

# Book of Abstracts

of the 2<sup>nd</sup> Artificial Intelligence  
for Animal Science Conference



Book of Abstracts No. 43 (2026)  
Ghent, Belgium  
29-30 June, 2026



# Table of Contents

## Summary

<i>Welcome to the Artificial Intelligence 4 Animal Science Conference</i> .....	4
<i>The European Federation of Animal Science (EAAP)</i> .....	5
<i>Joint organizers</i> .....	6
<i>Organizers of the Artificial Intelligence 4 Animal Science Conference</i> .....	6
<i>Ghent university / KU LEUVEN / ILVO</i> .....	7
<i>Sponsors</i> .....	8
<i>Industry Members Club</i> .....	9
<i>Scientific Programme</i> .....	10
<i>Abstracts</i> .....	19
<i>Author index</i> .....	76

# Welcome to the Artificial Intelligence 4 Animal Science Conference

In recent years, artificial intelligence (AI) has demonstrated revolutionary potential in many sectors, and animal science is no exception. The organization of the second AI4animal science conference dedicated to this topic arises from the need to explore and leverage the opportunities offered by AI to improve efficiency, sustainability, and health and welfare in animal production. It is now well known that AI provides advanced tools to monitor and manage livestock farming activities more precisely and promptly. The analysis of data collected through sensors, IoT devices, and other technologies allows optimizing the nutrition, health, and welfare of animals, reducing waste and operational costs. One of the main challenges of modern agriculture is, to reduce environmental impact. AI can transform these challenges into opportunities through advanced data-analysis and decision support that minimize the use of natural resources and improve waste management, while simultaneously promoting more sustainable and environmentally friendly practices.

This 2-day conference, organized by EAAP, ILVO, KULeuven and Ghent university will offer a unique opportunity to showcase and discuss the newest developments in the field of AI for animal science. Through the scientific sessions, we aim to bring together researchers in AI for animal science, but also animal scientists, industry stakeholders and livestock sector partners with an interest in the future potential of AI in livestock farming. Focus will be on raising awareness of the importance and practical applications, but also challenges, of AI in animal husbandry. Through parallel scientific sessions and a plenary session, participants will be able to discuss and deepen their fundamental and applied knowledge and skills. It is well known that integrating AI into animal husbandry requires collaboration between different disciplines, including engineering, data science, computer science, biology, and, of course, animal husbandry. The Artificial-Intelligence-4-Animal-Science conference represents an ideal platform to facilitate the exchange of ideas and collaboration among experts from various fields, promoting an integrated and multidisciplinary approach.

In conclusion, the organization of the AI4animal science conference addresses the need to tackle current and future challenges in animal husbandry through the adoption of advanced technologies. AI has the potential to profoundly transform the sector, improving efficiency, sustainability, and animal welfare, and the workshop aims to be the starting point for this transformation.

# The European Federation of Animal Science (EAAP)

The main aims of the EAAP are to promote, by means of active co-operation between its members and other relevant international and national organisations, the advancement of scientific research, sustainable development and production systems; experimentation, application and extension; to improve the technical and economic conditions of the livestock sector; to promote the welfare of farm animals and the conservation of the rural environment; to control and optimise the use of natural resources in general and animal genetic resources in particular; to encourage the involvement of young scientists and technicians. More information on the organisation and its activities can be found at [www.eaap.org](http://www.eaap.org).

## Former Presidents

1949-1961	A.M. Leroy (France)
1961-1967	R. Trehane (United Kingdom)
1967-1972	J.M. Rijssenbeek (The Netherlands)
1972-1978	J.H. Weniger (Germany)
1978-1984	E.P. Cunningham (Ireland)
1984-1990	A. Roos (Sweden)
1990-1996	A. Nardone (Italy)
1996-2000	P. Solms-Lich (Germany)
2000-2004	A. Aumaitre (France)
2004-2008	J. Flanagan (Ireland)
2008-2012	K. Sejrsen (Denmark)
2012-2016	P. Chemineau (France)
2016-2020	M. Gauly (Germany)
2020-2024	I. Casasús (Spain)

## Council members

### President

- Jöel Berard (Switzerland)

### Vice-Presidents

- Sam de Campeneere (Belgium)
- Gunnfríður Elín Hreiðarsdóttir (Iceland)

### Council Members

- Peer Berg (Norway)
- Christian Lambertz (Germany)
- Nicolaj Ingemann Nielsen (Denmark)
- Moschos Korasidis (Greece)
- Nicolò Macciotta (Italy)
- Klemen Potocnik (Slovenia)
- Diana Ruska (Latvia)

### FAO Representative

- Badi Besbes

### Auditors

- Georgia Hadjipavlou (Cyprus)
- Zygmunt Maciej Kowalski (Poland)

### Alternate Auditor

- Jeanne Bormann (Luxembourg)

### Secretary General

- Andrea Rosati

The European Federation of Animal Science (EAAP) has close established links with its sister organizations of American Society of Animal Science (ASAS), American Dairy Science Association (ADSAS), Canadian Society of Animal Science (CSAS) and Asociación Latinoamericana de Producción Animal (ALPA) and is also member of the World Association for Animal Production (WAAP).



## Joint organizers



## Organizers of the Artificial Intelligence 4 Animal Science Conference

### Scientific Committee

- Matti Pastell - LUKE
- Jeroen Degroote - Ghent University
- Tomas Norton - KU Leuven
- Jarissa Maselyne - ILVO
- Mutian Niu - ETH Zurich
- Victor Cabrera - UW-Madison
- Mona Giersberg - Utrecht University
- Kai Liu - City University of Hong Kong
- Clément Allain - IDELE

### Organizing Committee

- Matti Pastell - LUKE
- Jeroen Degroote - Ghent University
- Tomas Norton - KU Leuven
- Jarissa Maselyne - ILVO
- Mutian Niu - ETH Zurich
- Riccardo Carelli - EAAP
- Andrea Rosati - EAAP

## **Ghent university**

Ghent University is a top 100 university, founded in 1817, and one of the major universities in Belgium with more than 50,000 students and 15,700 employees. Our 11 faculties offer more than 200 programs and conduct in-depth research within a wide range of scientific domains. Our credo is 'Dare to Think', challenging everyone to question conventional views and to dare to take a nuanced stand. We are a pluralistic university open to all, regardless of their ideological, political, cultural or social background. Ghent University Global Campus is also the first European university in Songdo, South Korea.

Ghent University's Faculty of Bioscience Engineering works in applied biological and life sciences, with education and research connected to a broad range of bioscience engineering domains. Its history goes back to 1920, when the first academic year at the State Agricultural University was opened, and in 1969 it officially became a faculty within Ghent University. The faculty departments focus on animal sciences and aquatic ecology, plants and crops, food technology, safety and health, green chemistry and technology, biotechnology, data analysis and mathematical modelling, environment, and agricultural economics. Within the Department of Animal Sciences and Aquatic Ecology, the LANUPRO research group focuses on feed evaluation and animal product quality, with significant efforts on modelling digestion processes in pigs, poultry and ruminants, and data-driven animal nutrition solutions.

## **KU LEUVEN**

KU Leuven is one of Europe's leading research-intensive universities. Founded in 1425, it is among the oldest universities in Europe and today combines academic excellence with strong international and industrial collaboration. Across its faculties, KU Leuven conducts fundamental and applied research in the life sciences, engineering and data science, with a long-standing focus on translating innovation into solutions for society. Animal science and the sustainable transformation of the agri-food sector are addressed in particular through the Faculty of Bioscience Engineering and its Department of Biosystems, where biological, technical and digital expertise are brought together.

Within the Department of Biosystems, the M3-BIORES (Measure, Model & Manage Bioresponses) research group of the Division of Animal and Human Health Engineering specializes in Precision Livestock Farming and the application of artificial intelligence to animal monitoring. The group develops sensor-, vision- and audio-based systems combined with machine learning to continuously assess animal health, behavior and welfare in real time. Through close collaboration with farmers, industry partners and international research consortia, M3-BIORES contributes to translating AI-driven technologies into practical, on-farm decision support tools that promote efficient, sustainable and welfare-oriented livestock production.

## **ILVO**

Flanders Research Institute for Agriculture, Fisheries and Food (ILVO) is a Belgian research organization dedicated to agriculture, fisheries, and food systems. It conducts applied and interdisciplinary research to support sustainable, innovative, and economically viable food production.

ILVO works closely with farmers, industry, policymakers, and researchers to develop practical solutions for real-world challenges such as climate change, animal welfare, food quality, and environmental impact. By combining scientific expertise with collaboration across the agri-food chain, ILVO aims to strengthen the transition toward resilient and sustainable food systems in Flanders and beyond.

## Sponsors



**AgrifoodTEF** at ILVO is accelerating the adoption of trustworthy AI and robotics in agriculture and food systems. It provides companies—especially SMEs and startups—access to advanced testing infrastructure, expertise, and real-world validation environments. AgrifoodTEF focuses on bridging innovation and practice, supporting the development of sustainable, efficient, and data-driven solutions. By combining technical expertise with real-world validation, AgrifoodTEF helps de-risk development and accelerate time-to-market. **AgrifoodTEF is funded under the European Union’s Digital Europe Programme, Grant Agreement No. 101100622**



**COST Action CA22112 - European Network on Livestock Phenomics (EU-LI-PHE)**

# Industry members

EAAP started in 2023 a new initiative to create closer connections between European livestock industries and the animal science network. Therefore, the “EAAP Industry Club” was shaped with the specific aim of bringing together the important industries of the livestock sector with our European Federation of Animal Sciences. All companies dealing with animal production (nutrition, genetic, applied technologies, etc.) are invited to join the “EAAP Industry Club” because industries will have opportunity to increase their visibility, to be actively involved in European animal science activities, and to receive news and services necessary to industries. In addition, through the Club, industries will enlarge their scientific network and will receive specific discounts on sponsoring activities.

The Industries that already joined the “EAAP Industry Club” are:



## The Club gives:

Visibility • Company name and logo at EAAP website and all relevant documents • Slides with name and logo at Official Events • Priority links with EAAP Socials • Invite, through EAAP dissemination tools and socials, people to events organized by your company • Information disseminated through a brand new Industry Newsletter • Networking • Joining the Study Commissions and Working Groups • Suggest topics to be considered for Annual Meetings Scientific Sessions • Organize Professional Panel through the EAAP platforms • One free registration to each Annual Meeting and at every meeting organized by EAAP • Five individual memberships at no cost • Many possible discounts (-30%) to sponsor and to increase company visibility through: EAAP Newsletter, EAAP website, EAAP Annual Meetings and workshops • Support young scientist by sponsoring scholarships named by the company • Co-Organize and sponsor webinars

Make yourself more visible within the livestock industry via the animal science network!

For more information, please contact [eaap@eaap.org](mailto:eaap@eaap.org).

# Scientific programme

## Session 1. Advancements in Data Collection, processing, standardization and integration

Date: Monday 29 June 2026; 8:30 - 12:00

Chair: Norton, Niu

### Theatre Session 1

<b>Case Study: Preparing Video Data for Behavioral Annotation, Visualization, and Machine Learning in Livestock Systems</b>	19
<i>D. Foy, T. Smith, J. Reynolds, J. Peralta</i>	
<b>Instance segmentation of pigs for automatic assessment of animal welfare related parameters during controlled atmosphere stunning</b>	19
<i>K. Zavyalova, J. Knöll, I. Wilk, H. Schomburg</i>	
<b>AI-Powered Voice Assistant for Routine Livestock Monitoring</b>	20
<i>M. Nourry, P. Marie, M. Querné, M. Marcon</i>	
<b>Role of environmental and signal parameters in stabilizing sniffer methane measurements in dairy cows.</b>	20
<i>R. Colleluori, G. Visentin, V. Indio, D. Cavallini, L. Zambianchi, F. Ghiaccio, M. Lamanna, L. Mammi, A. Formigoni</i>	
<b>DALM: an in-house developed mobile data acquisition and edge processing system</b>	21
<i>S. Coussement, M. Poelman, L. Ingelbrecht, J. Maselyne, P. J. De Temmerman</i>	
<b>Evaluation of ZELP Sense™ against Respiration Chambers for Methane Emissions Measurement in Cattle</b>	21
<i>S. Silvestri, R. Bica, M. Battelli, L. Rapetti</i>	
<b>Paired Computed Tomography and Standard X-ray Workflow for Artificial Intelligence-Assisted Post-Mortem Broiler Carcass Health Assessment</b>	22
<i>E. Kritsi, K. Libera, A. Bossers, L. A. M. Smit, L. Mughini-Gras, L. Heres</i>	
<b>Improved prediction of interaction with enrichment material in weaned fattening pigs using machine learning approaches</b>	22
<i>H. Taghvafard, B. Han, F. Veldkamp, R. De Mol, I. C. De Jong, D. Schokker, M. J. Counotte</i>	
<b>Validating an accelerometer-based smart collar for automated behavioural monitoring in grazing dairy cattle – a new gold standard for research?</b>	23
<i>C. Ducrue, C. Allain, T. Dechaux, U. Jean-Louis, C. Littlejohn, Z. Guy</i>	
<b>ViT-Cow: Self-Supervised Video Pretraining for Few-Shot Dairy Cow Behavior Recognition</b>	23
<i>J. Allyndrée, M. Charles, M. Frere, D. Glaizal, M. Meier, C. Tibi, A. Madouasse, A. Cornuéjols, C. Martin</i>	
<b>Reconstructing representative daily Fourier transform mid-infrared milk spectra from partial milking robot samples using machine learning</b>	24
<i>C. Sneessens, S. Franceschini, P. E. Jacoby, E. Reding, J. Leblois, H. Soyeurt</i>	
<b>Federated Learning for Bovine Respiratory Disease Prediction Across European Veterinary Laboratories</b>	24
<i>S. Noor, J. Degroote, B. Pardon, G. Van Schaik, M. Hostens</i>	

<b>Application of GreenDA for GreenFeed® data processing and analysis: a bovine case study</b>	<b>25</b>
<i>S. Jeon, F. Picard, N. Baleret, Y. Gaudron, S. Fresco, R. Boré, B. Deroche, C. Martin</i>	
<b>European Network on Livestock Phenomics (EU-LI-PHE): integrating Artificial Intelligence and phenotyping data for Precision Livestock Farming and animal breeding</b>	<b>25</b>
<i>G. Schiavo, S. Bovo, J. Maselyne, T. Norton, L. Fontanesi, &amp; Eu-Li-Phe Consortium</i>	

## Session 2. Emerging AI Applications in Precision Livestock Farming

Date: Monday 29 June 2026; 8:30 - 12:00

Chair: Allain, Eerdeken

### Theatre Session 2

<b>Application of Machine Learning to Predict Enteric Methane Emissions and Enhance Dairy Cattle Farm Management</b>	<b>26</b>
<i>A. Mansouri, D. Cavallini, R. Colletuori, G. Visentin, A. Formigoni, D. Remondini, A. De Cesare</i>	
<b>Tracking problematic behaviors of cage-free hens with machine vision technologies in the USA</b>	<b>26</b>
<i>L. Chai, R. Bist, X. Yang, S. Subedi, B. Paneru, A. Dhungana, S. Dahal</i>	
<b>Computer Vision-Based Multi-Feature Extraction and Regression for Precise Egg Weight Measurement in Laying Hen Farms</b>	<b>27</b>
<i>Y. Jiang</i>	
<b>Gait Analysis of Chickens: Predicting Expert Scores Using accelerometer Data</b>	<b>27</b>
<i>A. Eerdeken, C. Lopes Carvalho, G. Antonissen, F. Tuytens, E. De Poorter, D. Peralta, L. Martens, W. Joseph, M. Deruyck</i>	
<b>Towards quantitative behavioural indicators related to perinatal pig mortality</b>	<b>28</b>
<i>M. Perneel, P. J. De Temmerman, B. Garré, L. Ingelbrecht, D. Maes, M. Aluwé, J. Maselyne</i>	
<b>Automatic quantification of play behaviour in dairy calves from ultra-wideband location sensors and its associations with health</b>	<b>28</b>
<i>J. A. Vázquez-Diosdado, C. Doidge, E. Bushby, F. Occhiuto, J. Kaler</i>	
<b>Keypoint-Based Nest-Building Behaviour Detection in Sows Using Top-View Video Analysis</b>	<b>29</b>
<i>S. Malik, R. Sagevik, H. Quas, Ø. Nordbø</i>	
<b>Fiducial marker assisted animal tracking to quantify individual feeding time in group housed piglets</b>	<b>29</b>
<i>T. Van De Putte, R. Wang, S. Heirbaut, M. Hostens, J. Degroote</i>	
<b>Predictive Analytics in Dairy Farming: Machine Learning for Calving Outcome and Milk Yield Prediction</b>	<b>30</b>
<i>C. Bonenberger, L. Dale, E. Frenken, T. Kramer, R. Miller, C. Schmidt, M. Schneider</i>	
<b>Optimizing Dairy Cow Replacement Decisions Using Deep Reinforcement Learning in an Evolving Stochastic Environment</b>	<b>30</b>
<i>Y. Gong, L. Da Silva, V. Cabrera</i>	

<b>Prompting experience and image-transfer choices have limited impact on Gemini’s recognition of the Equine Pain Face</b>	<b>31</b>
<i>D. B. Jensen, S. H. Knudsen, C. Lindegaard, K. Gleerup, M. M. Gyldenkerne</i>	
<b>From Pasture to Prompt: Measuring LLM Effectiveness in Beef Cattle Outreach and Education</b>	<b>31</b>
<i>R. Strong, S. Talcott, S. Talcott, M. Hartel</i>	
<b>Dairylens: AI-enabled decision support for data driven decisions and time savings, life quality and reduced environmental footprint in dairy systems</b>	<b>32</b>
<i>M. Atzori, I. E. Cigagna, C. Mariani</i>	
<b>Holistic Animal Management with Agentic AI</b>	<b>32</b>
<i>A. Arsenos, O. Filippopoulos, N. Stavrou, A. Arsenou</i>	

### Session 3. Farm and Industry Adoption of AI in Animal Science

Date: Monday 29 June 2026; 13:30 - 17:00

Chair: Degroote, Chai

#### Theatre Session 3

<b>AI-assisted Animal Welfare: potential and applications</b>	<b>33</b>
<i>J. L. Rault, P. Taylor</i>	
<b>Sensor prototype development for automated monitoring of integument damage of laying hens using suitable artificial intelligence models</b>	<b>33</b>
<i>A. Gruen, P. Bhattacharya, S. Rose, G. Bieber, H. Oz</i>	
<b>A Lightweight Acoustic Model for Panic Stress Recognition of Caged Laying Hens</b>	<b>34</b>
<i>Z. Wang, B. Chen, M. Di, Y. Jiang, S. He, H. Lin, J. Pan</i>	
<b>Technological Innovations in Automated Monitoring of Pig and Broiler Welfare at the Slaughterhouse: progress of the aWISH project</b>	<b>34</b>
<i>N. Van Noten, F. Tuytens, Awish Consortium, J. Maselyne</i>	
<b>Automated image analytics to reveal changes in drinking and eating behavior after vaccination</b>	<b>35</b>
<i>S. Van Poucke, J. Ceia, J. Defoort, J. Maselyne, P. J. De Temmerman</i>	
<b>Automated welfare monitoring through tear staining assessment in pigs at slaughter</b>	<b>35</b>
<i>S. Verlinde, A. Ramon-Perez, J. Reixach, S. Gol, P. Llonch Obiols, J. Maselyne, J. Verwaeren</i>	
<b>Long-term Sound Monitoring and Classification for Detecting Suspicious Events in Pig Farming</b>	<b>36</b>
<i>M. Wutke, H. Geffert, I. Reker, I. Traulsen</i>	
<b>Beyond Accuracy in Precision Livestock Farming: Distribution-Aware Evaluation for Large-Scale Poultry Weight Monitoring</b>	<b>36</b>
<i>G. Toth, M. Alexy</i>	
<b>Cleanliness evaluation of poultry carcasses using deep learning analysis of images</b>	<b>37</b>
<i>V. Belik, L. Buhre, C. Ruhland, D. Meemken, N. Langkabel</i>	
<b>Unlocking digital twins in dairy herd through dynamic stochastic modelling</b>	<b>37</b>
<i>K. K. Johansen, J. Ettema, S. Østergaard</i>	

<b>Machine Learning for Lactation Curve Forecasting: Predicting 305-Day Dairy Production from Partial Observations</b>	<b>38</b>
<i>J. Ganitzer, C. Egger-Danner, P. Roth</i>	
<b>User-Centered Explainable AI for Decision Support Systems in Dairy Farming</b>	<b>38</b>
<i>M. B. Girmay</i>	
<b>Robustness of derivative-based AI pipelines for inferring herbage consumption from milk FT-MIR indicator</b>	<b>39</b>
<i>K. Dichou, D. Veselko, A. Marvuglia, H. Soyeurt</i>	
<b>AI ready individual animal data collection for fattening pigs using transponder ear tags: practitioner expectations and implications for cross stage digital integration</b>	<b>39</b>
<i>J. Exler, V. Beck</i>	

## Session 4. AI for Science

Date: Monday 29 June 2026; 13:30 - 17:00

Chair: Pastell, Bovo

### Theatre Session 4

<b>Found in translation: building explainable model for transparent decision making and interdisciplinary communication in precision livestock farming</b>	<b>40</b>
<i>Y. Xue, L. Foldager, K. Thodberg, G. Gebreyesus</i>	
<b>Explainable Machine Learning with SHAP for SNP-Based Prediction of Robustness-Related Longevity Indicators in Angler Dairy Cows.</b>	<b>40</b>
<i>A. Seidel, K. Schröder, G. Thaller, N. Krattenmacher</i>	
<b>Reduced Labelling Effort with Generalisable Computer Vision Models for Pigs, Cattle, and Poultry</b>	<b>41</b>
<i>P. J. De Temmerman, J. Maselyne</i>	
<b>Testing synthetic data integration for automated fish detection on beam trawl vessels</b>	<b>41</b>
<i>H. De Rijcke, L. Snoeck, S. Delacauw</i>	
<b>Thinking outside the black box: rethinking the use of machine learning for automated behaviour analysis</b>	<b>42</b>
<i>S. P. Brouwers, N. McLaughlin</i>	
<b>A Deep Learning system for automating head direction annotation in ungulates</b>	<b>42</b>
<i>A. Kaki, J. Deutsch, S. Lebing, S. Döpjan, C. Nawroth</i>	
<b>Quantification of Fading in Melanin-based Operculum Spots as Stress Response in Atlantic Salmon using Computer Vision</b>	<b>43</b>
<i>T. Laique, M. Gunnes, Ø. Øverli, H. Ullah</i>	
<b>AI-driven exploration of molecular data in animal science: applications in genomics and metabolomics to dissect the animal phenome</b>	<b>43</b>
<i>S. Bovo, G. Schiavo, M. Bolner, F. Bertolini, L. Fontanesi</i>	
<b>Prediction of milk coagulation properties using prior-fitted transformers</b>	<b>44</b>
<i>T. J. Curik, D. Domović, N. Mikulec, B. Lukic, M. Spehar, I. Curik</i>	

<b>DairySleepNet: a multichannel state space architecture for dairy sleep classification</b>	<b>44</b>
<i>C. Guo, E. Ternman, K. Liu, M. Niu</i>	
<b>Artificial neural networks outperform partial least squares models for fatty acids estimation using FT-MIR spectrometry on bovine milk: a first step towards transfer learning on small ruminants.</b>	<b>45</b>
<i>E. Cabaraux, I. Alexakis, S. Franceschini, O. Christophe, C. Grelet, M. Calmels, C. Lecomte, C. Bertozzi, D. Veselko, F. Dehareng, H. Soyeurt</i>	
<b>Development of robust neural network architectures for federated FT-MIR prediction of enteric methane emissions in dairy cows</b>	<b>45</b>
<i>H. Soyeurt, F. Dehareng, N. Gengler, S. Mcparland, M. Kreuzer, M. Bell, P. Lund, C. Martin, B. Kuhla, A. Vanlierde</i>	
<b>Fitting and Predicting Dairy Lactation Curves based on Test-Day Records</b>	<b>46</b>
<i>C. Frauzino, S. Canuto, V. Cabrera, E. Noronha</i>	
<b>LivestockMind: A Large Language Model for Livestock Health Caring</b>	<b>46</b>
<i>Z. Guo, L. Lyu, Z. He, K. Liu</i>	

## Poster Session A

Date: Monday 29 June 2026; 17:30 - 17:30:00

<b>Overcoming Data Silos in Bovine Reproduction: The Minimum Information Model for Bull Fertility Data (MI-BFD) for Data-Driven, Multi-Center AI Applications</b>	<b>60</b>
<i>A. Abu Dayeh, E. Kutafina, O. Beyan</i>	
<b>SENSTAR: Advancing Sensor-Based Indicators and Modeling of Animal Resilience, Health, and Welfare in Precision Livestock Farming</b>	<b>61</b>
<i>D. Foy, J. . Gautier, B. Foris, C. Morgan-Davis, L. Dale, P. P. Nielson, G. Franchi, X. Díaz De Otálora</i>	
<b>GLOBAL: a 10-year experiment to describe lifetime health in dairy cows</b>	<b>61</b>
<i>N. Gafsi</i>	
<b>Digital twin for fattening pig growth and behaviour</b>	<b>62</b>
<i>J. Sloomans, T. Norton, J. Maselyne</i>	
<b>AgriScienceFM: Foundation Models for Biological, Environmental and Management Data</b>	<b>62</b>
<i>P. J. De Temmerman, J. Maselyne, I. Athanasiadis</i>	
<b>Integrating AI-Driven Bioacoustics and Affective Neuroscience for Objective Sheep Welfare Assessment: A Methodological Framework</b>	<b>63</b>
<i>E. Emsen, B. Ödevci, M. Kutluca Korkmaz, N. Küçükay</i>	
<b>Smart herds: AI in feeding, monitoring, and welfare of dairy cattle</b>	<b>63</b>
<i>J. Fabjanowska, E. Kowalczyk-Vasilev, S. Milewski, G. Rogowska, R. Klebaniuk</i>	
<b>An LLM-Powered Intelligent Agent for Early Disease Diagnosis in Dairy Cattle using a Domain-Specific Knowledge Graphs</b>	<b>64</b>
<i>Z. Yang, Y. Yang, K. Sima, M. Li</i>	
<b>Machine learning-based genomic prediction of feed conversion ratio using SNP markers in Latvian sheep breeding.</b>	<b>64</b>
<i>M. Martins, N. Paramonova, S. Plavina, D. Malakovska, N. Krasnevska, J. Paramonovs, D. Kairisa, I. Trapina</i>	

<b>Artificial intelligence in precision poultry feeding: data integration, predictive models, and applications in production</b>	<b>65</b>
<i>S. Milewski, J. Fabjanowska, G. Rogowska, E. Kowalczyk-Vasilev, B. Kiczorowska</i>	
<b>Proof-of-Concept: AI-Based Classification of Cow Behavioral Responses using Neck-Mounted Accelerometers in Pasture</b>	<b>65</b>
<i>I. A. Saeed, K. Stetter, M. S. Teitscheid, A. M. Kurz, J. Langbein, S. Rose</i>	
<b>Automatic monitoring of piling behaviour in laying hens using convolutional neural networks</b>	<b>66</b>
<i>M. M. Gyldenkerne, D. B. Jensen</i>	
<b>Benchmarking Multiple Piglet Tracking and Detection in Crowded Farrowing Pens</b>	<b>66</b>
<i>J. Gao, I. Kyriazakis, S. P. Brouwers, X. Yang, D. Morris, M. Benjamin, N. McLaughlin</i>	
<b>Eco-Catch: AI-Driven Monitoring and Reduction of Protected Species Bycatch in European Waters</b>	<b>67</b>
<i>L. Ingelbrecht, P. J. De Temmerman, J. Maselyne, H. De Rijcke, S. Delacauw</i>	

## Session 5. Plenary Session

Date: Tuesday 30 June 2026; 9:00 - 11:00

Chair: Maselyne, Pastell

### Theatre Session 5

<b>AI Foundation models for agricultural sciences - Challenges and opportunities</b>	<b>47</b>
<i>I. Athanasiadis</i>	
<b>Bridging Fragmented Agricultural Data with AI-Driven Semantic Translation</b>	<b>47</b>
<i>P. Hekmati, K. Reed, J. Waddell, V. Cabrera</i>	
<b>Applications of AI in animal feeding and management</b>	<b>48</b>
<i>A. Bach</i>	
<b>From Pixels to Insight: Challenges and opportunities for computer vision in animal monitoring</b>	<b>48</b>
<i>S. Leroux</i>	

### Poster Session B

Date: Tuesday 30 June 2026; 13:30 - 13:30:00

<b>Future-Proofing Agricultural Research for the Era of Artificial Intelligence</b>	<b>67</b>
<i>Y. Gong, C. Qian, H. Hu, Y. Jung, A. N. Negreiro, M. Wiedmann, V. E. Cabrera</i>	
<b>Artificial Intelligence-driven modelling of microclimatic and climatic effects on production, metabolic status, udder health and ammonia emission in dairy cows</b>	<b>68</b>
<i>K. Kuterovac, V. Gantner</i>	
<b>Automated Deep Learning-Based Quantification of Goblet Cells as a Digital Biomarker of Poultry Gut Health</b>	<b>68</b>
<i>D. Mezghiche, F. Diaz Bahamonde, C. Vidal Moreno De Vega, G. Antonissen, P. Claes</i>	

<b>Mentor::i: AI-Powered, Secure Bioinformatics for Rapid Animal Health Discovery</b>	<b>69</b>
<i>D. Schokker, V. Bianchi</i>	
<b>Forecasting of Ammonia Concentrations in Commercial Growing Pig Houses Based on Deep Learning Models</b>	<b>69</b>
<i>D. A. Méndez Reyes, M. Jarque, S. Calvet Sanz</i>	
<b>From trait prediction to system-level inference: a machine learning framework for intrinsic product quality investigation</b>	<b>70</b>
<i>A. Mouhanna, L. Rey-Cadilhac, L. Darrigade, B. Martin, S. De Smet</i>	
<b>Data-Driven Genomic Analysis of Population Structure and Breed Differentiation of Latvian Dark-head Sheep.</b>	<b>70</b>
<i>I. Trapina, M. Martins, S. Plavina, D. Malakovska, N. Krasnevskaja, J. Paramonovs, D. Kairisa, N. Paramonova</i>	
<b>Whole-Chamber AI-Based Enumeration of Eimeria Oocysts for Objective OPG Quantification</b>	<b>71</b>
<i>D. Mezghiche, M. Verstraete, C. Vidal Moreno De Vega, G. Antonissen, P. Claes</i>	
<b>Prediction of Post-Freezing Semen Quality Using Pre-Freezing Semen Quality</b>	<b>71</b>
<i>A. Rehman, A. Tresch, K. Kupisiewicz</i>	
<b>Deep-learning inference models for canine diffuse large B cell lymphoma</b>	<b>72</b>
<i>K. Ancheta, A. Psifidi, S. Le Calvez, A. Yale, J. Williams</i>	
<b>Visual Re-Identification via Collar Patterns for Identity Recovery in Multi-Goat Tracking Systems</b>	<b>72</b>
<i>D. A. Méndez Reyes, D. Liu, T. Norton, S. Calvet Sanz, A. Costantino</i>	
<b>Multi-omics integration reveals coordinated rumen hydrogen turnover and energy metabolism underlying feed efficiency in Angus cattle</b>	<b>73</b>
<i>A. Nunes, C. Faleiros, M. Poleti, G. Marcelli, J. B. Ferraz, H. Fukumasu</i>	
<b>AI-Enabled Bioelectrical Impedance Digital Biomarkers for Non-Invasive Detection of Caseous Lymphadenitis in Goats</b>	<b>73</b>
<i>A. Klingler, A. Siddique, R. Kota, A. Rubio-Villa, D. Brown, P. Batchu, J. Van Wyk, T. Terrill</i>	
<b>AI-Enabled Radiofrequency Digital Biomarkers for Non-Invasive Anemia Phenotyping in Goats</b>	<b>74</b>
<i>S. R. Neelagiri, A. Siddique, D. Brown, Z. Carlton, J. Van Wyk, T. Terrill</i>	
<b>Validation of an automated AI image analysis system for in-line green ham quality assessment</b>	<b>74</b>
<i>V. Bonfatti, A. Rosolen, K. Ivanov, N. Guzzo, S. Faggion, P. Carnier</i>	
<b>Predictive modeling of bacteriophages endolysins structural features as a decision-support framework for targeting rumen microorganisms</b>	<b>75</b>
<i>C. Faleiros, A. Nunes, O. Gonçalves, M. Poleti, H. Fukumasu</i>	

## Session 6. Datasets and benchmarks

Date: Tuesday 30 June 2026; 14:30 - 16:00

Chair: Cabrera, Noronha

### Theatre Session 6

- Big Data and Machine Learning to Improve Culling Decision-Making in Dairy Herds** 49  
*L. Da Silva, Y. Gong, V. Cabrera*
- Multi-object tracking benchmark for livestock** 49  
*H. Fred, D. Liu, P. De La Vallée, L. Ruotsalainen, M. Pastell, T. Norton*
- Bridging Animal Science and Human Nutrition through INSIGHT: A Retrieved-Augmented Agentic Model** 50  
*R. Strong, L. Tedeschi, K. Kaniyamattam, J. Tao, D. Mudireddy, P. Surabhi, N. Greer, A. Wang*
- Using AI to find veterinary data sources in Europe** 50  
*R. Petie, V. Bianchi, E. Pacholewicz*
- FacEDiM++: A Probabilistic Evaluation Framework for Few-Shot Cross-Species Face Verification** 51  
*D. Lukamba Nsadisa, S. Mwasimuke Tsongo, B. Twite Ndeze, R. Vaishampayan, M. C. Oveneke, J. Ambukiyenyi Onya*
- Drone-Based AI System for Automated Sheep Counting Using Detection and Tracking Models** 51  
*L. Helary, A. Lebreton, A. Lauront, E. Nicolas, T. Dechaux*

## Session 7. Advancing Digital Biomarkers and Phenotypes with AI

Date: Tuesday 30 June 2026; 14:30 - 17:15

Chair: Liu, Heirbaut

### Theatre Session 7

- Image-derived digital similarity matrices as a scalable proxy for pedigree and genomic relationship matrices** 52  
*M. Billah, M. Bermann, C. Y. Chen, B. Valente, E. Psota, J. Holl, S. M. Bhandarkar, I. Misztal, D. Lourenco*
- Thermal Signatures as Biomarkers of Podal Inflammation in Cattle and Ovine** 52  
*L. Helary, Y. Do, J. Manceau, V. Gauthier, M. Doucet, A. Duvauchelle Waché*
- Automatic recognition of herbage prehensions in grazing ewes** 53  
*S. Bognanno, R. Avanzato, L. Beritelli, F. Beritelli, F. Gimmillaro, M. Avondo*
- Artificial intelligence-driven plasma metabolomics identifies metabolic signatures of feed efficiency in beef cattle** 53  
*A. Nunes, C. Faleiros, M. Poleti, Y. López-Hernández, D. Wishart, H. Fukumasu*
- Non-invasive eye temperature monitoring in dairy calves using computer vision and infrared technology** 54  
*J. A. Vazquez Diosdado, F. Occhiuto, M. Thomas, J. Kaler*

<b>Evaluating standing and lying behaviors measured with collar-mounted accelerometers for lameness detection in dairy cows</b>	<b>54</b>
<i>J. Allyndrée, C. Harrouet, A. Cornuéjols, C. Martin, A. Madouasse</i>	
<b>Zero-shot computer vision analysis of social behaviour in group-housed sows</b>	<b>55</b>
<i>N. Ipek, J. Verwaeren, B. De Baets, F. A. M. Tuytens</i>	
<b>AI-Driven Temporal Behavioral Pattern Mining for Digital Health Monitoring in Livestock</b>	<b>55</b>
<i>T. Terrill, A. Siddique, S. Panda, A. Mahapatra, E. Morgan, J. Van Wyk</i>	
<b>Validation of computer vision for automated detection of pig movement during Open Field and Novel Object tests</b>	<b>56</b>
<i>T. Ede, M. Parada Sarmiento, L. Sabei, T. Parsons</i>	
<b>2D to 3D Pose modeling: A scalable framework for individualized detection of tail-biting interactions in group-housed pigs</b>	<b>56</b>
<i>K. Ivanov, V. Bonfatti, C. Kasper, H. R. Nasser</i>	
<b>Vision-based detection of pain and nest-building behaviors in sows within commercial farrowing pens</b>	<b>57</b>
<i>P. Helf, M. Oczak</i>	

## **Session 8. Ethical, environmental and social implications of AI**

Date: Tuesday 30 June 2026; 16:30 - 18:00

Chair: Giersberg, Liu

### **Theatre Session 8**

<b>Support for whom? – Proposing an alternative approach to digital technologies in animal science</b>	<b>57</b>
<i>M. F. Giersberg, F. L. B. Meijboom</i>	
<b>Using AI to optimise animal welfare: opportunities and ethical challenges</b>	<b>58</b>
<i>M. Campbell</i>	
<b>Modelling Fish Welfare Law using Artificial Intelligence</b>	<b>58</b>
<i>L. Northwood</i>	
<b>Ethical and practical trade-offs in AI- and sensor-based disease detection in dairy cattle</b>	<b>59</b>
<i>J. Roelofs, A. Van Kneysel</i>	
<b>Virtual herding for real animals: healthy farming craftsmanship in a data-rich environment</b>	<b>59</b>
<i>F. L. B. Meijboom, M. Admiraal</i>	
<b>A proof-of-concept framework for machine learning to link coccidiosis-related performance losses to changes in the carbon footprint</b>	<b>60</b>
<i>J. Gickel, C. Visscher</i>	

**Case Study: Preparing Video Data for Behavioral Annotation, Visualization, and Machine Learning in Livestock Systems**

D. Foy<sup>1,2</sup>, T. Smith<sup>1</sup>, J. Reynolds<sup>3</sup>, J. Peralta<sup>3</sup>

<sup>1</sup> AgriGates, Philadelphia, 19146 Pennsylvania, United States, <sup>2</sup> DAT-AI-LAB, NBC, Kennett Square, 19348 Pennsylvania, United States, <sup>3</sup> Western University College of Veterinary Medicine, Pomona, 91766 California, United States

Cameras and video data are increasingly used in animal science to capture continuous or intermittent behavioral data at high temporal resolution. However, the preparation and management of video files, post-collection, and prior to annotation and analysis, remain a major time bottleneck in behavioral research and machine learning (ML) workflows. Inconsistent file naming, missing timestamps, and fragmented metadata can significantly limit the usability and reproducibility of video-derived datasets. This project presents a practical and scalable workflow for preparing video files for behavioral annotation and visualization that adds value to downstream ML modeling using dairy calf behavior and activities as a case study. A total of approximately 62 hours of video footage was analyzed, collected from individual and group-housed calves (12 single-housed and four pens of three calves group-housed). Video segments averaged ~1 hour in length and focused on key management periods of the day that included first feeding and health checks. All video files were standardized using a deterministic timestamp-based naming convention (YYYY-MM-DD\_HHMMSS). Behavioral annotation was conducted using multi-layer coding, including posture (lying/standing), location (in hutch/out of hutch), and human interaction (health checks and bottle placement/removal). Annotation outputs were exported as binary time-series CSV files and integrated into Power Query, given a relational data structure and calculations for visualization and exploratory analysis using Power BI. This enabled individual or group-level and day-of-life behavioral summaries for bout analysis and temporal pattern exploration. This work demonstrates that video annotation is not the primary limiting factor in behavioral AI pipelines; rather, data organization and temporal standardization account for the majority of project efforts. Establishing reproducible file naming, metadata alignment, and annotation structures is critical for scalable behavioral modeling, multi-sensor integration, and future federation of livestock video datasets.

## Session 1

## Theatre 2

**Instance segmentation of pigs for automatic assessment of animal welfare related parameters during controlled atmosphere stunning**

K. Zavyalova<sup>1</sup>, J. Knöll<sup>1</sup>, I. Wilk<sup>1</sup>, H. Schomburg<sup>1</sup>

<sup>1</sup> Friedrich-Loeffler-Institut, Institute of Animal Welfare and Animal Husbandry, Dörnbergstr. 25/27, 29223 Celle, Germany

Effective pre-slaughter stunning is mandatory to prevent pain, fear and suffering [Council Regulation (EC) No 1099/2009]. CO<sub>2</sub> stunning in controlled atmosphere stunners (CAS) is currently the most common method for pigs. Pigs are stunned in groups within gondolas by lowering these into an atmosphere of high concentration CO<sub>2</sub> for a defined exposure duration. Direct observations of the behavior and stunning progress is hindered by stunner design and occupational safety limitations. Video surveillance would be data and labor intensive and require trained observers and behavior assessment guidelines. Automated detection of parameters related to animal behavior and stunning progress could be used to continuously monitor the animals and detect potential markers for animal welfare issues or risk factors for requiring backup stunning. This study provides the groundwork for automated computer-vision-based analysis of in-stunner video footage during CAS stunning. Video data, collected in a previous project from stunning 1300 pigs (groups of 2), was analyzed. As motion of components of the stunning system and subtle animal movements create a challenging visual environment, robust segmentation is key. By now, a total of 100 frames were manually annotated [Label Studio (HumanSignal) + Segment Anything Model, instance brush annotation]. These annotations (80 train, 20 test) were used to train a pig instance segmentation model using YOLOv8n-seg model by ultralytics (v. 8.4.14). The model achieved preliminary box mAP50-95 of 0.870 and mask mAP50-95 of 0.841, enabling reliable separation and identification of animals despite dynamic background conditions. Current development includes testing the model under varying illumination conditions and stages of stunning with different activity levels. The next steps would be extracting the specific animal welfare parameters from the segmented areas. The dataset includes manual annotations for categorized movement events and information on need of re-stunning for each animal, allowing comparison between manual and automated movement detection. This work was co-funded by the European Union's Horizon Europe project 101136346 EUPAHW.

**AI-Powered Voice Assistant for Routine Livestock Monitoring**

M. Nourry<sup>1</sup>, P. Marie<sup>1</sup>, M. Querné<sup>1</sup>, M. Marcon<sup>1</sup>

<sup>1</sup> IFIP institut du porc, R&D and IT, 9 Bd du Trieux, 35740 Pacé, France

Routine livestock monitoring requires frequent data recording, yet traditional manual input methods are time-consuming and impractical in farm environments. Dictapig is an AI-based solution designed to facilitate hands-free vocal note-taking during regular livestock checks. The application enables farmers and technicians to register key events such as births, deaths, piglet counts, and individual animal information using natural speech. Dictapig relies on speech-to-text (STT) processing combined with audio signal analysis to isolate relevant numerical and semantic information from spoken input. Extracted data are automatically converted into structured database queries and stored in the specialized livestock management database. The system also supports data retrieval, by providing a pig's identifier, users can access previously stored records through voice commands. The application provides multimodal feedback, displaying information on a smartphone screen while simultaneously delivering results via natural language text-to-speech (TTS) in French. Dictapig operates as a multi-platform solution, accessible through a web interface hosted on a dedicated server, ensuring flexibility, scalability, and ease of deployment in agricultural settings. This work demonstrates how AI-driven voice interfaces can significantly improve data collection efficiency, accuracy, and usability in precision livestock farming.

**Role of environmental and signal parameters in stabilizing sniffer methane measurements in dairy cows.**

R. Colleluori<sup>1</sup>, G. Visentin<sup>1</sup>, V. Indio<sup>1</sup>, D. Cavallini<sup>1</sup>, L. Zambianchi<sup>1</sup>, F. Ghiaccio<sup>1</sup>, M. Lamanna<sup>1</sup>, L. Mammi<sup>1</sup>, A. Formigoni<sup>1</sup>

<sup>1</sup> University of Bologna, Department of Veterinary Medical Sciences, Via Tolara di Sopra, 50, 40064 Ozzano Emilia, Italy

The sniffer technique is widely adopted for large-scale methane phenotyping in dairy cows; however, high intra-cow variability may compromise the robustness of measurements. This study aimed to assess the influence of environmental and signal parameters on the reliability of sniffer CH<sub>4</sub>/CO<sub>2</sub> ratio recordings, to explore their role in developing data-driven quality indicators. A total of 13,801 breath recordings were collected from 92 lactating dairy cows during robotic milkings. All raw data were processed through an automated pipeline based on custom Python scripts, to ensure standardized synchronization, aggregation and parameter extraction. Relative humidity and CH<sub>4</sub> peak amplitude ( $\Delta$ CH<sub>4</sub>) were categorized into quartiles to identify recordings potentially associated with stronger eructation events, reduced head movement and minimal dilution due to barn airflows. Linear mixed models were fitted on CH<sub>4</sub> concentration and CH<sub>4</sub>/CO<sub>2</sub> ratio, considering cows as a random effect. Mean CH<sub>4</sub> concentrations increased progressively across humidity quartiles (119.6, 190.4, 227.6 and 249.2 ppm;  $p < 0.01$ ) and  $\Delta$ CH<sub>4</sub> quartiles (73.4, 161.0, 234.2 and 339.7 ppm;  $p < 0.01$ ). In parallel, the coefficient of variation of CH<sub>4</sub>/CO<sub>2</sub> decreased from 58% to 34% and from 86% to 26% across humidity and  $\Delta$ CH<sub>4</sub> quartiles, respectively. Comparison of absolute residuals confirmed reduction in intra-cow dispersion between Q1-Q2 and Q2-Q3 ( $p < 0.01$ ). Inclusion of humidity reduced residual intra-cow variance by about 4%,  $\Delta$ CH<sub>4</sub> by about 5% and their combination by approximately 12%, while inter-cow variance remained stable. The findings demonstrate that environmental and signal parameters not only increase CH<sub>4</sub> signal strength but also reduce intra-cow measurement noise. Integrating humidity and  $\Delta$ CH<sub>4</sub> into a measurement quality index may facilitate the automatic identification of less disturbed recordings, improving the repeatability of sniffer methane measurements. This study was carried out within the Agritech National Research Center and received funding from the European Union – NextGenerationEU (Task 5.3.2., Project CN00000022).

**DALM: an in-house developed mobile data acquisition and edge processing system**

S. Coussement<sup>1</sup>, M. Poelman<sup>1</sup>, L. Ingelbrecht<sup>1</sup>, J. Maselyne<sup>1</sup>, P. J. De Temmerman<sup>1</sup>

<sup>1</sup> ILVO (Flanders Research Institute for Agriculture, Fisheries and Food), Burgemeester van Gansberghelaan 115, 9820 Merelbeke-Melle, Belgium

To enable on-farm operation of computer-vision models and process data of IoT sensors for automated animal behavior analysis, there is a need for a flexible data acquisition system capable of capturing and reliably storing data. Barn environments impose challenges: higher ammonia levels, dust particles, humidity and dirt. Next to environmental robustness, operational practicality is also a must. The system needs to be compact and mobile and needs to withstand thoroughly cleaning. Commercial solutions such as off-the-shelf video recording systems and cameras do not meet requirements for harsh environments and are not interoperable with other devices and sensors. Therefore, the DALM (Data Acquisition and Logging Machine) was developed, that allows storing data from different PoE sensors and devices. The core of the DALM is a NAS equipped with two 20 TB hard drives, in RAID 1, able to store video streams from up to 8 HD cameras, connected through an internal PoE switch, locally during approximately 35 weeks of recording. The platform can be extended with an extra module adding 8 more PoE connections, e.g. to extend the system with RFID readers, additional camera's and other IoT sensors. The components are housed in a rigid, IP66-rated enclosure. When the system needs to be cleaned, internal components can be easily removed to thoroughly clean the enclosure. The setup can be remotely accessed, through an integrated 4G router and Ethernet connection. For in barn interactions and privacy concerns a Human-Machine Interface screen allows operators to temporarily disable the cameras for 30 minutes with a each button press. A warning light and sound alerts the user when recording resumes. Overall, the DALM functions as a rugged, interoperable system of powering and storing data from PoE-enabled cameras, sensors, and edge devices while maintaining reliable, redundant storage under normal livestock farming conditions. As future development on-edge processing, such as deep learning processing algorithms, will be implemented. A solar-powered variation of this platform can also be build, allowing deployment in remote locations without access to the power grid.

## Session 1

## Theatre 6

**Evaluation of ZELP Sense™ against Respiration Chambers for Methane Emissions Measurement in Cattle**

S. Silvestri<sup>1</sup>, R. Bica<sup>1</sup>, M. Battelli<sup>2</sup>, L. Rapetti<sup>2</sup>

<sup>1</sup> Zelp, Animal Science Department, Unit B, 449 Holloway Rd, N7 6LJ London, United Kingdom, <sup>2</sup> University of Milan, Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy, University of Milan, 20133 Milan, Italy

Introduction Enteric methane (CH<sub>4</sub>) emissions by ruminants contribute consistently to ongoing climate change. Effective emissions monitoring is key to inform appropriate reduction strategies. Respiration chambers (RC) are the current gold standard methane measurement technique and, whilst precise, they are costly, labour-intensive and limited in their widespread usability. To address these drawbacks, ZELP is developing Sense, a wearable, field-deployable device that can be used for emissions monitoring in operative environments. In this study, we compare the methane measurements provided by ZELP Sense with those provided by RC. Materials and Methods: Four dry Holstein Friesian cows were used for this study. Each spent four separate test periods (of four days each) in a RC, whilst wearing the Sense device. There was a 10 day rest period between each test period. Sense uses sensors to track ventilation rate and methane concentrations in gas exhaled by the animal. ZELP's Machine Learning models then use this data to calculate daily emission totals. Results: Statistical analysis is still in progress, but preliminary results show methane measurements to be relatively comparable between methods. Using RC as a reference, the percentage error during the first test period ranged from -18.02% to 9.90%, with a mean percentage error of 9.33%. Conclusions: We conclude that this device can offer a promising alternative to RC for the monitoring of methane emissions in cattle. As it is field deployable it also addresses some of the usability limitations associated with RC. Further work will allow for improvements in performance and for its ability across a broad range of conditions to be demonstrated.

**Paired Computed Tomography and Standard X-ray Workflow for Artificial Intelligence-Assisted Post-Mortem Broiler Carcass Health Assessment**

E. Kritsi<sup>1</sup>, K. Libera<sup>1</sup>, A. Bossers<sup>1</sup>, L. A. M. Smit<sup>1</sup>, L. Mughini-Gras<sup>1</sup>, L. Heres<sup>1</sup>

<sup>1</sup> Institute for Risk Assessment Sciences (IRAS), Department of Population Health Sciences, Utrecht University, Yalelaan 2, 3584 CM Utrecht, Netherlands

Poultry slaughterhouses process thousands of carcasses per hour, with post-mortem inspection performed under time pressure. This makes organ health assessment challenging when relying solely on visual inspection. In prior work, we showed that computed tomography (CT) combined with artificial intelligence (AI) can support the detection of heart and liver abnormalities in broiler chickens (accuracy ~0.92 for heart classification with deep learning; ~0.79 for liver classification with logistic regression based on radiological features) [1]. Building on this work, we aimed to operationalize the approach by developing a repeatable imaging workflow and a paired CT/X-ray dataset. We linked (i) carcass-level scans, (ii) scans of isolated healthy and diseased hearts and livers, and (iii) scans using 3D positioning structures that mimic organ pose in a body-cavity context. For each specimen, we acquired a matched CT volume and dual-view X-ray images (anteroposterior and lateral), enabling within-specimen comparisons and faster screening evaluation. These data support three AI model components: two organ-specific healthy-versus-diseased classifiers (EfficientNetV2\_s for the heart and liver, trained on CT and dual-view X-ray), and a U-Net segmentation/localization model to identify heart and liver regions, as a step towards carcass-level imaging. We assembled balanced, inspection-relevant cohorts (approximately equal numbers of healthy and diseased organs per organ type) and a repeatable imaging protocol to allow within-specimen benchmarking of CT against dual-view plain X-ray. Our study addresses: CT versus dual-view X-ray classification performance, performance under faster X-ray screening, and transfer from isolated-organ imaging to body-cavity positioning. Overall, this work provides an AI-ready protocol and paired dataset to benchmark CT against a more practical X-ray alternative, supporting future decision support for fitness-for-consumption under high-throughput slaughterhouse conditions. [1] Libera et al., Food Control (2026), doi:10.1016/j.foodcont.2025.111581.

**Improved prediction of interaction with enrichment material in weaned fattening pigs using machine learning approaches**

H. Taghvafard<sup>1</sup>, B. Han<sup>1</sup>, F. Veldkamp<sup>2,3</sup>, R. De MoP<sup>2</sup>, I. C. De Jong<sup>2</sup>, D. Schokker<sup>1</sup>, M. J. Counotte<sup>1</sup>

<sup>1</sup> Wageningen University & Research, Wageningen Bioveterinary Research, Houtribweg 39, 8221 RA Lelystad, Netherlands, <sup>2</sup> Wageningen University & Research, Wageningen Livestock Research, De Elst 1, Building 122, 6708 WD Wageningen, Netherlands, <sup>3</sup> Wageningen University & Research, Adaptation Physiology Group, De Elst 1, Building 122, 6708 WD Wageningen, Netherlands

Continuous behavioral monitoring is increasingly used in precision livestock farming. Accelerometers mounted on enrichment materials enable non-invasive monitoring of pig-enrichment interactions, but the resulting data are temporal and require appropriate analytical approaches. In many studies, such data are analyzed as independent observations, limiting the use of behavioral dynamics. We reanalyzed accelerometer data from enrichment chains in pens of weaned pigs from one of our previous studies, using manual observations as ground truth. We tested whether behavior detection can be improved by applying signal-level feature extraction over fixed time windows (TWs) combined with time-series-appropriate machine-learning models. Signals were segmented into 1–15 s TWs and statistical movement-based features were extracted. Random Forest and CatBoost classifiers were evaluated under different data-splitting strategies. Model performance was improved with increased TW length, with optimal results for TWs  $\geq 6$  s. CatBoost outperformed Random Forest. Features describing acceleration magnitude and variability were most informative across all TWs and models. Models trained and tested within the same animal group performed better than cross-group models. These results show that explicitly accounting for temporal structure through signal-level feature extraction and time-series-aware machine learning improves detection of pig-enrichment interactions. The proposed workflow provides a generalizable strategy for behavioral monitoring using environmental sensors and contributes to robust digital behavioral phenotyping in animal science.

**Validating an accelerometer-based smart collar for automated behavioural monitoring in grazing dairy cattle – a new gold standard for research?**

C. Ducrue<sup>1</sup>, C. Allain<sup>1</sup>, T. Dechaux<sup>1</sup>, U. Jean-Louis<sup>1</sup>, C. Littlejohn<sup>1</sup>, Z. Guy<sup>1</sup>

<sup>1</sup> Institut de l'Élevage, 149 rue de Bercy, 75595 Paris, France

Behavioural monitoring is a key component of livestock research, yet traditional ethological observations remain labour-intensive and require specialised expertise, limiting their integration into large-scale experimental designs. Sensor-based technologies offer opportunities to automate behavioural recording. However, most commercial systems are designed for farm management rather than research, and often lack the data accessibility, configurability, and acquisition frequency required in experimental settings. This study evaluates Tauro Smart Collars (Embeint), a new research-oriented device designed to address these limitations. The collars combine local data storage, solar power supply, and high-frequency 3-axis accelerometer, gyroscope, and GPS measurements. Behavioural classification relies on the eGrazor algorithm (CSIRO), which predicts six behaviours: grazing, rumination, resting, walking, drinking, and other. Thirteen Normande cows were equipped with the devices and monitored at pasture. For ground-truth data, each cow underwent  $2 \times 2$  h focal behavioural observations following a protocol matching the six eGrazor categories. Overall, the system achieved a global accuracy of 81.77% and a Cohen's kappa of 0.744, indicating substantial agreement between predictions and observations. Major behaviours—grazing, rumination, and resting—were reliably detected, with Matthews Correlation Coefficients (MCC) exceeding 0.78. Performance was lower for minority behaviours: walking tended to be underestimated and often misclassified as grazing, while drinking was markedly overestimated and frequently confused with rumination. These results demonstrate promising performance for predominant behaviours but highlight the need to improve the detection of less frequent activities. Future work will focus on expanding the behavioural repertoire to include additional research-relevant behaviours and on extending validation to indoor housing conditions. To achieve this, we plan to initiate the development of new classification algorithms capable of integrating all sensor modalities, including gyroscope and GPS data, to enhance behavioural resolution and robustness across contexts.

## Session 1

## Theatre 10

**ViT-Cow: Self-Supervised Video Pretraining for Few-Shot Dairy Cow Behavior Recognition**

J. Allyndrée<sup>1,2</sup>, M. Charles<sup>2</sup>, M. Frere<sup>2</sup>, D. Glaiza<sup>2</sup>, M. Meier<sup>2</sup>, C. Tibi<sup>2</sup>, A. Madouasse<sup>1</sup>, A. Cornuéljols<sup>2</sup>, C. Martin<sup>2</sup>

<sup>1</sup> Oniris, INRAE, BIOEPAR, 101 Rte de Gachet, 44300 Nantes, France, <sup>2</sup> Université Paris-Saclay, INRAE, AgroParisTech, UMR MIA-PS, 22 place de l'Agronomie, 91120 Palaiseau, France

Behaviors such as eating and drinking are widely used as proxies for animal health and welfare, as changes in behavior often signal conditions such as lameness. However, annotating behaviors is a time-consuming and costly process, which limits the development of supervised machine learning models for behavior recognition. In dairy farming especially, datasets are scarce, rarely publicly available and typically cover a limited range of behaviors. Self-supervised learning offers a promising alternative by leveraging unlabeled data to learn meaningful visual representations without the need for extensive manual annotation. Combined with a small labeled dataset, these representations enable training accurate behavior recognition models with limited annotations, and support few-shot learning for rare or previously unseen behaviors. In this work, we introduce ViT-Cow, a Self-Supervised Vision Transformer model to learn meaningful representations directly from domain-specific dairy cow videos. This allows the model to capture behavioral dynamics and posture variations characteristic of dairy cows, resulting in more relevant and transferable representations. The learned embeddings serve as robust behavioral descriptors, enabling pseudo-labeling, dataset expansion, and transfer to related animal monitoring tasks. The transformer is trained using a video reconstruction pretext task on unlabeled video data recorded in 5 different commercial dairy farms, totalling more than 90,000 unannotated video clips (for a total of ~280 hours) and around 2500 annotated video clips of cows performing 11 different behaviors. We evaluate the learned representations on a downstream few-shot behavior classification task using limited labeled data, and compare performance against a YOLO-based supervised baseline trained from scratch on the same annotations. This setup directly measures the benefit of domain-specific self-supervised pretraining under limited-label conditions. Model weights, data, and final results will be publicly released upon publication.

### Reconstructing representative daily Fourier transform mid-infrared milk spectra from partial milking robot samples using machine learning

C. Sneessens<sup>1</sup>, S. Franceschini<sup>1</sup>, P. E. Jacoby<sup>2</sup>, E. Reding<sup>2</sup>, J. Leblois<sup>2</sup>, H. Soyeurt<sup>1</sup>

<sup>1</sup> Gembloux Agro-Bio Tech, TERRA Research and Teaching Centre, 2, Passage des déportés, 5030 Gembloux, Belgium, <sup>2</sup> AWé groupe, 32, chemin du Tersoit, 5590 Ciney, Belgium

Automated milking systems (AMS) are increasingly adopted on dairy farms to improve herd monitoring through automatically collected measurements. However, obtaining a representative daily milk sample for milk recording from those systems remains challenging because milk composition varies throughout the day and cows are milked voluntarily. In 2002, Peeters and Galesloot developed an ICAR-certified method to estimate daily fat content (%FAT24h), but not to reconstruct a representative Fourier-transform mid-infrared (FT-MIR) spectrum (SPECT24h) suitable for predicting multiple milk components. So, this study aimed to develop models allowing the estimation of %FAT24h and SPECT24h from partial milkings. 51,861 milk samples were collected from historical database and new milk recording events. Two sampling protocols were evaluated: RZ (one milking) and RM (two milkings), using three estimation methods: M1 (based on Peeters and Galesloot), M2 (weighted average), and M3 (linear regression). For the RZ protocol, M1 provided the most accurate %FAT24h estimates (RMSE = 0.275%). For RM, accuracy improved (RMSE = 0.193%). Optimal performance was observed when sampled milkings accounted for 40–60% of the daily milk volume. M2 became the most accurate when this proportion exceeded 60% (RMSE = 0.190%), while M3 did not outperform the other methods. The second step focuses on reconstructing an FT-MIR spectrum that should be representative of the day. From this spectrum, any prediction equation is applicable, but this study presents performance for predicting fat content. Daily spectra reconstructed from partial milking samples enabled %FAT24h prediction with accuracy equal to or greater than traditional methods. For M1, RMSE was 0.272% (RZ) and 0.193% (RM). For M2, reconstructed spectra slightly improved accuracy (RMSE = 0.182%). These results demonstrate the feasibility of reconstructing spectra from partial milkings and using them to predict milk fat content, potentially enabling the full usage of milk recording FT-MIR spectra for management and monitoring in farms using AMS.

## Session 1

## Theatre 12

### Federated Learning for Bovine Respiratory Disease Prediction Across European Veterinary Laboratories

S. Noor<sup>1,2</sup>, J. Degroote<sup>1</sup>, B. Pardon<sup>2</sup>, G. Van Schaik<sup>3</sup>, M. Hostens<sup>1,4</sup>

<sup>1</sup> Ghent University, Department of Animal Sciences and Aquatic Ecology, Faculty of Bioscience Engineering, Coupure Links 653, 9000 Ghent, Belgium, <sup>2</sup> Ghent University, Department of Internal Medicine, Reproduction and Population Medicine, Faculty of Veterinary Medicine, Salisburylaan 133, 9820 Merelbeke, Belgium, <sup>3</sup> Utrecht University, Department of Population Health Sciences, Unit Farm Animal Health, Yalelaan 7, 3584 CL Utrecht, Netherlands, <sup>4</sup> Cornell University, Department of Animal Science, 149 Morrison Hall, NY 14853 Ithaca, United States

Background: The European Cattle Barometer shows historical Bovine Respiratory Disease (BRD) trends but lacks predictive capability. Transforming it into a predictive tool requires multi-laboratory data, yet privacy regulations prevent direct data sharing. Federated Learning enables collaborative training without centralizing raw data, but heterogeneous feature spaces pose challenges for model aggregation. Methods: We developed an ontology-driven horizontal federated learning system combining a Graph Convolutional Network (GCN) with GRU and the Live-stock Health Ontology (LHO). The GCN captures spatial relationships (geographic neighbors, pathogen similarity) via SPARQL queries, while the GRU models temporal patterns. The LHO ensures consistent feature encoding across laboratories. Model aggregation follows FedAvg. Evaluation used Cattle Barometer data (2016-2025) from 6 laboratories across 4 European countries, comprising 164,814 records for 7 BRD pathogens: Bovine coronavirus, Bovine respiratory syncytial virus, Bovine parainfluenza virus type 3, Histophilus somni, Mycoplasma bovis, Mannheimia haemolytica, and Pasteurella multocida, to predict one-month-ahead BRD-positive sample rates. Results: The federated model achieved  $R^2=0.58$ , MAE=10.6%, RMSE=15% (aggregated across all countries and pathogens), comparable to centralized training ( $R^2=0.62$ , MAE=10.6%, RMSE=14%) while keeping all data local. The slight  $R^2$  reduction and marginal increase in RMSE indicate minor trade-offs, while the identical MAE confirms equivalent average prediction accuracy. Conclusion: Minimal performance loss demonstrates ontology-driven federated learning as a viable approach for privacy-preserving collaborative disease surveillance without centralizing sensitive data.

**Application of GreenDA for GreenFeed® data processing and analysis: a bovine case study**

S. Jeon<sup>1</sup>, F. Picard<sup>1</sup>, N. Baleret<sup>1</sup>, Y. Gaudron<sup>1</sup>, S. Fresco<sup>2,3</sup>, R. Boré<sup>4</sup>, B. Deroche<sup>4</sup>, C. Martin<sup>1</sup>

<sup>1</sup> INRAE, UMRH, Rte de Theix, 6122 Saint-Genès-Champagnelle, France, <sup>2</sup> INRAE, Université Paris-Saclay, Domaine de Vilvert, 78350 Jouy-en-Josas, France, <sup>3</sup> Eliance, 149 rue de Bercy, 75595 Paris, France, <sup>4</sup> Idele, 42 rue Georges Morel, 49000 Beaucouzé, France

The GreenFeed® system (GF) is globally used to measure enteric methane (CH<sub>4</sub>) emission in ruminants without restricting their behaviour. A single GF unit can be used by approximately 20-25 animals simultaneously, generating large and complex datasets through repeated visits by each animal. However, a common accessible tool for analysing such large dataset is currently lacking. To address this gap, we developed GreenDA, an R Shiny based application designed as a locally installed, user-friendly button driven tool. The application does not require users to have any programming experiences or advanced data analysis expertise. GreenDA integrates functions for data processing (i.e. outlier cleaning), descriptive statistical analyses (e.g. average, variation) and calculations (e.g. repeatability), visualization, and automated reporting at different analytical levels (herd, animal, treatment) and time scales (e.g. hourly, daily). The functionality of GreenDA was demonstrated using data from 53 cattle monitored over a 105-day indoor period and allocated to two treatments in a 2 x 2 factorial design. Using the default GreenDA setting (i.e. airflow < 26 L/s, stay duration < 2 min, and values outside ± 3 standard deviations from the mean), 124 out of 19,749 records (0.63%) were identified as outliers and removed. The results showed that CH<sub>4</sub> emission data followed a normal distribution, and the repeatability coefficient shows that averaging data over 5 days reliable CH<sub>4</sub> values. Daily kinetics of CH<sub>4</sub> emission closely reflected daily intake patterns, without observed differences between treatments. The peak hourly visitation was observed between 1 AM and 2 AM, whereas the minimum visitation rate occurred between 2 AM and 3 AM. By following the downloadable user manual provided with GreenDA, users can replicate these analyses with their own dataset. Through the development of GreenDA, we aimed to provide not only a practical tool but also structured guidance for GF data analysis.

**European Network on Livestock Phenomics (EU-LI-PHE): integrating Artificial Intelligence and phenotyping data for Precision Livestock Farming and animal breeding**

G. Schiavo<sup>1</sup>, S. Bovo<sup>1</sup>, J. Maselyne<sup>2</sup>, T. Norton<sup>3</sup>, L. Fontanesi<sup>1</sup>, & Eu-Li-Phe Consortium<sup>1</sup>

<sup>1</sup> University of Bologna, Animal and Food Genomics Group, Dept. of Agricultural and Food Sciences, Viale Fanin 46, 40127 Bologna, Italy, <sup>2</sup> ILVO (Flanders Research Institute for Agriculture, Fisheries and Food), Technology and Food Science Unit, Burg. Van Gansberghelaan 115 bus 1, 9820 Merelbeke, Belgium, <sup>3</sup> KU Leuven, Department of Biosystems, Kasteelpark Arenberg 30, 3000 Leuven, Belgium

Artificial Intelligence (AI) is redefining the future of livestock production systems, offering opportunities to enhance sustainability, resilience, and animal welfare. In this landscape, livestock phenomics, seen as systematic and high-resolution characterization of the animal phenotype, represents a strategic pillar to achieve innovation in animal science. However, the effective application in real world production systems requires adequate infrastructures, harmonized data, shared standards, and a strong governance framework. The European Network on Livestock Phenomics (EU-LI-PHE), funded by the European Cooperation in Science and Technology (COST), is a multidisciplinary network for advances in livestock phenomics. It takes actions by promoting interoperability, metadata harmonization and big datasets managing, and it aims to apply AI not just as a set of analytical tools, but as a strong infrastructure for integrating sensor data, “omics” information, environmental records, and farm management systems into knowledge. This approach supports the development of innovative phenotyping technologies and advanced genome to phenotype analytical methods. EU-LI-PHE consists of approximately 500 working group members from more than 50 countries. By promoting multi-disciplinary collaboration and innovation, EU-LI-PHE aims to become a reference platform for livestock phenomics in Europe and beyond, contributing to the development of sustainable and resilient livestock production systems, while promoting novel approaches in phenotyping and Precision Livestock Farming (PLF), always with continuous attention to regulatory frameworks for societal and ethical implication of livestock phenomics. Acknowledgment: EU-LI-PHE (CA22112) is funded by the European Union – COST European Cooperation in Science & Technology.

**Application of Machine Learning to Predict Enteric Methane Emissions and Enhance Dairy Cattle Farm Management**

A. Mansouri<sup>1</sup>, D. Cavallini<sup>1</sup>, R. Colleluori<sup>1</sup>, G. Visentin<sup>1</sup>, A. Formigoni<sup>1</sup>, D. Remondini<sup>2</sup>, A. De Cesare<sup>1</sup>

<sup>1</sup> University of Bologna, Department of Veterinary Medical Sciences, Via Tolara di Sopra 50, 40064 Ozzano dell'Emilia, Italy; <sup>2</sup> University of Bologna, Department of Physics and Astronomy, viale Berti Pichat 6/2, 40127 Bologna, Italy

Ruminant livestock are estimated to emit between 80 and 95 million tonnes of methane (CH<sub>4</sub>) annually, at global level. Approximately 80.7% of these emissions originate from enteric fermentation in dairy cattle. Effective monitoring and management of CH<sub>4</sub> emissions are therefore crucial to enhance the environmental sustainability of livestock production systems. In this study, we developed two machine learning models: 1) a model to predict the daily enteric CH<sub>4</sub> emissions at the dairy cattle farm level; 2) a probabilistic Bayesian model to support farmers in optimizing their daily farming practices, such as reducing CH<sub>4</sub> emissions, while maintaining milk production yield. Both models were developed using a set of 25 variables measured at the DIMEVET experimental dairy cattle farm, housing approximately 100 dairy cows. Data were recorded over a period of 252 days and included enteric CH<sub>4</sub> measurements, obtained from sniffers, environmental parameters, milk production yield and composition, animal variables, such as body weight and parity. In addition, detailed information on feed type and ingredients were also recorded. The first version of the two models showed good predictive performance (R-Squared = 0.79; Mean Absolute Error = 2397 L/Day with observed CH<sub>4</sub> = [30929, 61704] L/Day), with further improvements expected as data collection continues. Upon completion and validation, both models will be available as simple and user-friendly web applications to support farmers, policy makers and other stakeholders in enhancing environmental sustainability of livestock production systems. This study has been funded by the Italian Ministry of Agriculture, Food Sovereignty and Forests under the Contratto di Filiera, Stalla modello, DMI n. 0673777 del 22/12/2021, V Avviso n. 0182458 del 22/04/2022 e s.m.

## Session 2

## Theatre 2

**Tracking problematic behaviors of cage-free hens with machine vision technologies in the USA**

L. Chai<sup>1</sup>, R. Bist<sup>1</sup>, X. Yang<sup>1</sup>, S. Subedi<sup>1</sup>, B. Paneru<sup>1</sup>, A. Dhungana<sup>1</sup>, S. Dahal<sup>1</sup>

<sup>1</sup> University of Georgia, Poultry Science, 120 DW Brooks Dr, 30602 Athens, United States

The table egg production is shifting from conventional caged system to cage-free (CF) housing in the USA due to concerns of animal welfare. The market share of CF eggs has increased from 10% in 2015 to 40% in 2025. However, the current CF housing system is facing many challenges. For instance, CF hens tend to have higher injury rates or health issues such as severe pecking (cannibalism), footpad lesion or dermatitis, and keel bone damages than hens in conventional caged systems. Besides, mislaying behavior results in floor eggs, which could lead to increased labor cost and foot safety concerns. The objective of this study was to develop and optimize deep learning models to monitor welfare and behaviors of CF hens for improving egg production efficiency and animal wellbeing. The YOLO (You Only Look Once) family models have gained significant prominence due to their exceptional speed and accuracy in object detection tasks in recent years. In this study, two deep learning models, i.e., YOLOv5x-pecking and YOLOv5s-pecking, were developed and tested with up to 85% of precision in monitoring CF hens' pecking behaviors and damages. For bumblefoot detection (BFD), the performance of three newly developed deep learning models (i.e., YOLOv5s-BFD, YOLOv5m-BFD, & YOLOv5x-BFD) were compared. The results show that the YOLOv5m-BFD model had the highest precision (93.7%) and F1-score (89.0%) compared with other models. For footpad lesion detection (FLD), YOLOv8 models (YOLOv8n, YOLOv8s, YOLOv8m, YOLOv8l, and YOLOv8x) and YOLOv7 models (YOLOv7 and YOLOv7x) were comparatively evaluated for predicting footpad scores. According to the results, the YOLOv8l outperformed other models, with higher recall (96.6%) and F1-score (95%). Those new deep learning methods provide new solutions for improving animal welfare management in CF housing systems in the USA and beyond.

### Computer Vision-Based Multi-Feature Extraction and Regression for Precise Egg Weight Measurement in Laying Hen Farms

Y. Jiang<sup>1</sup>

<sup>1</sup> Zhejiang University, 866 Yuhangtang Road, Xihu District, Hangzhou City, Zhejiang Province, China, 310058 Hangzhou, China

Egg weight monitoring provides critical data for calculating the feed-to-egg ratio, and improving poultry farming efficiency. Installing a computer vision monitoring system in egg collection systems enables efficient and low-cost automated egg weight measurement. However, its accuracy is compromised by egg clustering during transportation and low-contrast edges, which limits the widespread adoption of such methods. To address this, we propose an egg measurement method based on a computer vision and multi-feature extraction and regression approach. The proposed pipeline integrates two artificial neural networks: Central differential-EfficientViT YOLO (CEV-YOLO) and Egg Weight Measurement Network (EWM-Net). CEV-YOLO is an enhanced version of YOLOv11, incorporating central differential convolution (CDC) and efficient Vision Transformer (EfficientViT), enabling accurate pixel-level egg segmentation in the presence of occlusions and low-contrast edges. EWM-Net is a custom-designed neural network that utilizes the segmented egg masks to perform advanced feature extraction and precise weight estimation. Experimental results show that CEV-YOLO outperforms other YOLO-based models in egg segmentation, with a precision of 98.9%, a recall of 97.5%, and an Average Precision (AP) at an Intersection over Union (IoU) threshold of 0.9 (AP90) of 89.8%. EWM-Net achieves a mean absolute error (MAE) of 0.88 g and an R<sup>2</sup> of 0.926 in egg weight measurement, outperforming six mainstream regression models. This study provides a practical and automated solution for precise egg weight measurement in practical production scenarios, which is expected to improve the accuracy and efficiency of feed-to-egg ratio measurement in laying hen farms.

## Session 2

## Theatre 4

### Gait Analysis of Chickens: Predicting Expert Scores Using accelerometer Data

A. Eerdeken<sup>1</sup>, C. Lopes Carvalho<sup>2</sup>, G. Antonissen<sup>2</sup>, F. Tuytens<sup>3,4</sup>, E. De Poorter<sup>5</sup>, D. Peralta<sup>5</sup>, L. Martens<sup>1</sup>, W. Joseph<sup>1</sup>, M. Deruyck<sup>1</sup>

<sup>1</sup> WAVES-Imec, Department of Information Technology, Technologiepark 126, 9052 Ghent, Belgium, <sup>2</sup> Ghent University, Department of Pathobiology, Pharmacology and Zoological Medicine, Faculty of Veterinary Medicine, Salisburylaan 133, 9820 Merelbeke-Melle, Belgium, <sup>3</sup> Flanders Research Institute for Agriculture, Fisheries, and Food (ILVO), Burgemeester van Gansberghelaan 92 bus 1, 9820 Merelbeke-Melle, Belgium, <sup>4</sup> Ghent University, Department of Veterinary and Biosciences - Ethology and Animal Welfare, Salisburylaan 133, 9820 Merelbeke-Melle, Belgium, <sup>5</sup> IDLab, Department of Information Technology, Technologiepark 126, 9052 Ghent, Belgium

Broiler locomotion disorders pose significant welfare and economic challenges. Subjective visual scoring limits scalability, highlighting the need for automated monitoring systems. In this study, we investigated the feasibility of predicting expert-assigned gait scores using wearable accelerometer data and a Gradient Boosting Machine classifier. Sixteen broiler chickens were equipped with dorsally mounted tri-axial accelerometers sampling at 20 Hz, sufficient to capture stride-level locomotion dynamics. Birds were scored at day 23 and day 38 using a four-point locomotion scale. Peak-based segmentation of accelerometer data from -7 to +5 days around day 38 (50 samples per window) yielded 4,931 labeled windows across 16 birds (1,329 Good; 2,909 Fair; 693 Poor). Twenty time-domain features were extracted per window, including distributional, variability, and peak-based metrics. A Gradient Boosting Machine (100 trees, learning rate 0.1, depth 3) classified locomotion using a 70/30 train-test split. The model achieved 67% accuracy, demonstrating the feasibility of accelerometer-based gait phenotyping. While camera-based studies report strong flock-level gait prediction, this work addresses individual-level classification using wearable sensors. Peak width differed significantly between extreme gait score groups, with the largest peak widths observed in chickens with the poorest locomotion scores. Notably, absolute and relative gait metrics were significantly influenced by backpack attachment. These findings support the use of AI-driven wearable sensing for objective welfare monitoring in poultry production systems.

### **Towards quantitative behavioural indicators related to perinatal pig mortality**

M. Perneel<sup>1</sup>, P. J. De Temmerman<sup>1</sup>, B. Garré<sup>1,2</sup>, L. Ingelbrecht<sup>1</sup>, D. Maes<sup>2</sup>, M. Aluwé<sup>1</sup>, J. Maselyne<sup>1</sup>

<sup>1</sup> ILVO, Burgemeester van Gansberghelaan 92 bus 1, 9820 Merelbeke-Melle, Belgium, <sup>2</sup> Ghent University, Salisburylaan 133, 9820 Merelbeke-Melle, Belgium

One of the biggest issues in pig production with regard to animal health and welfare is perinatal pig mortality. Despite careful management by farmers, it is not uncommon to observe a loss of 20 to 25% of piglets due to stillbirth and neonatal pig mortality. Several risk factors for perinatal pig mortality were already identified in the past, e.g. farrowing duration, inter-piglet birth interval, birth weight and colostrum intake. However, studies examining the influence of sow and piglet behaviour onto perinatal pig mortality are relatively scarce. Additionally, quantifying these risk factors is often too labour intensive to be economically justified. Therefore, we build a mobile video monitoring setup and developed an integrated computer vision based pipeline which is not only able to monitor sow and piglet behaviour, but also can be used to monitor the onset and progress of farrowing in an automated way. Several behavioural indicators were developed to quantify sow restlessness, suckling frequency, total suckling time, piglet activity and piglet dispersal. Each of these quantitative indicators was determined for litters of over fifty sows and combined with records of piglet mortality and cause of death. Our mobile setup will be used to monitor the behaviour of sows and piglets temporarily on commercial farms, allowing to provide the farmer with tailored advice to reduce perinatal pig mortality. Moreover, our research demonstrates the potential of computer vision as a labour-efficient approach to determine quantitative behavioural indicators which can be used as selection criteria during breeding programmes. Additionally, our pipeline can be deployed to evaluate the influence of adaptations of feeding, housing and management practices onto animal behaviour and perinatal pig mortality in a reproduceable and efficient way, which will facilitate future research.

### **Automatic quantification of play behaviour in dairy calves from ultra-wideband location sensors and its associations with health**

J. A. Vázquez-Diosdado<sup>1</sup>, C. Doidge<sup>1</sup>, E. Bushby<sup>1</sup>, F. Occhiuto<sup>1</sup>, J. Kaler<sup>1</sup>

<sup>1</sup> University of Nottingham, School of Veterinary Medicine and Science, Sutton Bonington Campus, University of Nottingham, LE12 5RD Nottingham, United Kingdom

Although play behaviour is often considered an indicator of positive animal welfare, quantifying it can be challenging. Visual observations are time consuming, meaning that they can only be performed for limited periods, and automated measures can be subject to overestimation due to the classification methods. This study aims to improve upon the current methods by automatically classifying and quantifying locomotor play behaviour in dairy calves. Location data were collected from 46 calves for a period of 18 weeks using collar mounted ultra-wide band sensors. A total of 101.36 h of video footage were labelled and an AdaBoost ensemble learning algorithm was used to classify play behaviour. An adjusted count technique was implemented to the outputs of the classifier to account for the overestimation, which is often seen in low-prevalence behaviours such as play. Once the duration and instances of play behaviour were quantified, two generalized linear mixed models were fitted to measure the effect of age, health and weaning on play over the 18 weeks of monitoring. The algorithm identified play behaviour with high accuracy (>94%) and only 16% overestimation compared to the labelled video footage, which is an improvement compared to previous studies. Increasing age and sickness significantly decreased the instances and duration of play behaviour per day ( $p < 0.01$  and  $p = 0.03$  respectively), whilst play behaviour significantly increased during and after weaning ( $p < 0.01$ ). These results prove that location data can be used to successfully classify and quantify play behaviour and this is the first study to monitor play long-term, which provides unique insight into welfare status in calves. This method could also be used to detect and monitor other low prevalence behaviours from location data, and these could then be useful as non-invasive automated indicators of health and welfare in farm animals.

**Keypoint-Based Nest-Building Behaviour Detection in Sows Using Top-View Video Analysis**S. Malik<sup>1</sup>, R. Sagevik<sup>1</sup>, H. Quas<sup>2</sup>, Ø. Nordbø<sup>1</sup><sup>1</sup> Norsvin, Storhamargata 44, 2317 Hamar, Norway, <sup>2</sup> South Westphalia University of Applied Sciences, Lübecker Ring 2, 59494 Soest, Germany

Accurate detection of nest-building behaviour in sows is important for understanding pre-farrowing activity, assessing maternal readiness, and supporting automated phenotyping of maternal traits. Nest building in sows involves subtle ear and nose movements rather than large-scale body motion, causing the conventional bounding-box displacement measures to miss low-movement events. This highlights the need for fine-scale anatomical descriptors while remaining computationally efficient for large-scale monitoring. We developed a keypoint-based detection framework that models sow posture and localised movement using six top-view, frame-level anatomical landmarks: tail, back, shoulder, left ear, right ear, and nose. A YOLOv11 pose model was trained on a dataset of 1,000 images evenly distributed across varying sow postures. Model validation performance was high, with bounding-box precision of 0.9997, recall of 0.9951, mAP@0.5 of 0.995, and mAP@0.5–0.95 of 0.9449. Keypoint estimation achieved an mAP@0.5 of 0.995 and mAP@0.5–0.95 of 0.9835, supporting reliable extraction of six landmarks. Model throughput was ~5.5 ms/frame (~180 FPS), enabling real-time analysis. Nest-building behaviour detection is performed by analysing per-frame displacement of these keypoints using a set of movement thresholds. Frames are filtered to exclude implausible motion (>300 px), and stability of the back region is enforced by requiring  $|\text{back displacement}| \leq 50$  px. Nest-building activity is then identified when ear and nose displacement exceeds the back displacement by 12–200 px, capturing the characteristic pattern of pronounced anterior motion combined with a relatively stable torso. In ground-truth evaluation, 19 out of 20 video clips (~15 s each) showed nest-building behaviour that was correctly detected within the defined displacement thresholds. These results indicate that keypoint-level motion features provide an effective and computationally efficient method for scalable detection of nest-building behaviour.

## Session 2

## Theatre 8

**Fiducial marker assisted animal tracking to quantify individual feeding time in group housed piglets**T. Van De Putte<sup>1</sup>, R. Wang<sup>1</sup>, S. Heirbaut<sup>1</sup>, M. Hostens<sup>1,2</sup>, J. Degroote<sup>1</sup><sup>1</sup> Ghent University, Faculty of Bioscience Engineering, Department of Animal Sciences and Aquatic Ecology, Coupure Links 653, 9000 Ghent, Belgium, <sup>2</sup> Cornell University, Department of Animal Science, 616 Thurston Ave, NY 14853 Ithaca, United States

Adequate feed intake is a key determinant of piglet health in the immediate post-weaning phase. To explore feeding behaviour under practical conditions, a non-intrusive computer-vision pipeline was designed that combines object-detection-based tracking with fiducial-marker recognition on piglets' earmarks to enable persistent re-identification of individual animals in the proximity of the feeder. During the first week post-weaning, 36 piglets were housed in six pens (n = 6 per pen) and continuously video monitored with cameras focused on the feeder zone. Piglets were equipped with standard ear tags bearing printed ArUco markers. Video streams were processed into individual estimates of time spent eating by fusing intermittent fiducial-marker reads with near-continuous ear detections (YOLOv5) and a custom multi-target tracking algorithm. Feeding was defined when an ear detection overlapped a predefined mask covering the accessible, deeper feeder area. Algorithm output was benchmarked against manual annotations across pens (precision 92.8%, recall 83.8%, F1 score 88.1%). Approximately 16% of true feeding was missed and 7% of detected feeding reflected non-feeding or misattributed bouts, primarily due to identity swaps during tracking. Marker readability remained stable during the one-week validation period, although greater wear was observed afterwards, highlighting the need for fiducial tags that better tolerate oblique angles, motion blur, and dirt. The presented approach offers a scalable and cost efficient solution for persistent animal re-identification, while enabling individual level behavioural analysis within group housed systems. Beyond estimating feeding time, the resulting individual time series were analysed for their diurnal and ultradian organisation of feeding activity, resulting in the extraction of interpretable behavioural features and characterisation of social interactions (including potential dominance or hierarchy formation), creating insights for linking early feeding behaviour to short-term growth performance.

### Predictive Analytics in Dairy Farming: Machine Learning for Calving Outcome and Milk Yield Prediction

C. Bonenberger<sup>1</sup>, L. Dale<sup>4</sup>, E. Frenken<sup>2</sup>, T. Kramer<sup>5</sup>, R. Miller<sup>1</sup>, C. Schmidt<sup>3</sup>, M. Schneider<sup>1</sup>

<sup>1</sup> Hochschule Ravensburg-Weingarten, Institute for Artificial Intelligence, Leibnizstr. 15, 88250 Weingarten, Germany, <sup>2</sup> Förderverein Bioökonomieforschung e.V., Adenauerallee 174, 53113 Bonn, Germany, <sup>3</sup> Hochschule Weihenstephan-Triesdorf, Markgrafenstr. 16, 91746 Weidenbach, Germany, <sup>4</sup> LKV Baden-Württemberg, Heinrich-Baumann Str. 1, 70190 Stuttgart, Germany, <sup>5</sup> Rinderunion Baden-Württemberg e.V., Ölkofer Str. 41, 88518 Herbertingen, Germany

Modern dairy farming systems generate large amounts of structured data through herd management, milk recordings and genetic evaluation systems. These data provide a basis for improving animal welfare, resource efficiency, and economic sustainability via data-driven decision support. In this study, we present two applied machine learning (ML) use cases based on routine herd data from commercial farms in Baden-Württemberg, Germany, and discuss practical challenges in defining and implementing ML in the dairy farming context. The first use case focuses on the prediction of calving outcomes at the time of insemination using historical performance, health, fertility, and pedigree information. This facilitates the timely identification of animals at increased risk for calving difficulties or suboptimal reproductive performance. The prediction is based on decision tree bagging (LGBM), with a focus on different labeling strategies, including heuristic labels incorporating health data (ROC AUC  $\approx$  0.63) and purely data-driven labeling relying exclusively on evaluations of calving ease (ROC AUC  $\approx$  0.76). The second use case addresses individual-animal milk yield prediction based on production and health records using classical ML approaches. The underlying dataset comprises records from approximately 200 dairy farms over a five-year period and includes the predominant regional breeds Simmental, Holstein, and Brown Swiss. The focus of future evaluations will also include evaluating the added value of integrating genomic data and body weight data. Overall, the results indicate the practical feasibility of applying ML pipelines on routine herd data and underline their potential to support precision livestock farming, breeding strategies, and economically viable dairy production systems.

### Session 2

### Theatre 10

### Optimizing Dairy Cow Replacement Decisions Using Deep Reinforcement Learning in an Evolving Stochastic Environment

Y. Gong<sup>1</sup>, L. Da Silva<sup>1</sup>, V. Cabrera<sup>1</sup>

<sup>1</sup> University of Wisconsin–Madison, Animal and Dairy Sciences, 1675 Observatory Dr., 53706 Madison, United States

Replacement decisions are critical for dairy profitability but are inherently complex due to the stochastic nature of cow performance and volatile market conditions. This study introduces a deep reinforcement learning (DRL) framework for optimizing monthly keep-or-replace decisions in dairy cows. The problem was formulated as a finite-state Markov decision process, with cow states defined by parity (1–12), month after calving (1–20), month in pregnancy (0–9), and clinical mastitis status (0/1). A Deep Q-Network (DQN) learned the optimal policy through interaction with the simulated stochastic environment over 500,000 episodes. While transition probabilities governed the environment, they were not accessible to the agent, which learned exclusively from observed transitions and rewards. Policies were developed for a 2025 baseline scenario and four additional market scenarios, which combined varying heifer supply (oversupply vs. undersupply) with different milk market conditions (good vs. bad). Across all scenarios, the DRL framework demonstrated stable and plausible learning outcomes. Under the baseline scenario, the learned policy achieved an expected annual return of \$3,082 per cow stall, with a total annual culling rate of 23.5% (including 2.7% mortality) and a mean herd parity of 2.49. The policy also yielded interpretable replacement boundaries: parity-1, open, healthy cows were replaced at 11 months after calving, whereas those with mastitis were replaced earlier, at 7 months. These thresholds shifted earlier with increasing parity, reflecting declining future productive potential. Value-function contrasts further quantified key biological–economic tradeoffs: the marginal value of pregnancy averaged \$262 when conception occurred at 61 DIM and declined with increasing parity and delayed conception, whereas the economic cost of clinical mastitis averaged \$373 in early lactation and decreased over time. Overall, the DRL framework generated economically coherent and biologically plausible replacement policies in simulated environments, demonstrating its potential as a scalable, adaptive, data-driven decision support tool under evolving herd and market conditions.

**Prompting experience and image-transfer choices have limited impact on Gemini's recognition of the Equine Pain Face**

D. B. Jensen<sup>1</sup>, S. H. Knudsen<sup>1</sup>, C. Lindegaard<sup>1</sup>, K. Gleerup<sup>2</sup>, M. M. Gyldenkerne<sup>1</sup>

<sup>1</sup> University of Copenhagen, , Grønnegårdsvej 2, 1870 Frederiksberg, Denmark, <sup>2</sup> Dyr læge Karina Gleerup ApS, Elleorevej 9, 4000 Roskilde, Denmark

Pain in ridden horses is often misread as “conflict” behaviour and can remain unnoticed even when welfare is compromised. Facial expressions such as the Equine Pain Face (EPF) may support earlier recognition, but in practice they still depend on consistent human scoring. In this pilot, we asked: can freely available multimodal large language models (LLMs) provide a useful first-pass EPF decision from photographs? We used data from videos of 9 horses before and after surgery for a painful condition. All horses were judged by a blinded expert to display the EPF before surgery, but not after. From each video, a single frame was selected where the authors’ judged that the stereotypical indicators of EPF were visible (EPF positive videos) or not visible (EPF negative videos) in the frame. Three free Gemini models (gemini-3-flash-preview, gemini-2.5-flash, gemini-2.5-flash-lite) were prompted to act as an equine veterinarian and to return a binary EPF decision (Yes/No) based on EPF indicators. We varied (i) the stated clinical experience in the role prompt (0, 5, 10, 20, 50, 100 years) and (ii) how images were supplied to the API (inline vs upload). Performance was summarised using sensitivity, specificity and Major Mean Accuracy (MMA). Across models and settings, MMA mostly clustered around 0.50–0.60, i.e., near chance-level discrimination. The best observed condition was gemini-2.5-flash with inline images and a 5-year prompt (MMA = 0.72), driven by perfect specificity (1.00) but modest sensitivity (0.44). This pattern suggests the model tended to under-call pain rather than over-call it. In a linear model of MMA, neither stated experience nor image-transfer method showed a detectable effect (both  $p > 0.6$ ), and between-model differences were small and not statistically clear in this sample. Overall, these results suggest that zero-shot prompting of free multimodal LLMs is unlikely to be reliable for EPF-based welfare screening without further calibration.

## Session 2

## Theatre 12

**From Pasture to Prompt: Measuring LLM Effectiveness in Beef Cattle Outreach and Education**

R. Strong<sup>1</sup>, S. Talcott<sup>1</sup>, S. Talcott<sup>1</sup>, M. Hartel<sup>1</sup>

<sup>1</sup> Texas A&M University, 2116 TAMU, 77843-2116 College Station, United States

The Texas beef cattle industry remains a central economic and cultural engine, contributing tens of billions of dollars to the state economy while sustaining extensive rural employment across the supply chain. We evaluated ExtensionBot as a decision-support tool evidence-based, and context-specific extension standards. Our framework combined expert rating panels, gold-standard benchmarking, scenario vignettes, task-based evaluations, trust diagnostics, and mixed quantitative–qualitative analysis to judge accuracy, relevance, clarity, usefulness, and safety. Findings indicate ExtensionBot reliably synthesizes practical guidance on prickly pear cactus, identifying it as a moisture-rich but nutritionally limited emergency feed that can help sustain hydration and provide modest fermentable energy during forage shortfalls, while correctly emphasizing the need for supplemental protein and other nutrients and encouraging forage testing when use extends beyond short-term grazing. Integrating Precision Livestock Farming, we show that geo-referenced cactus mapping, repeatable photo points, and cattle behavior signals (from GPS collars, ear-tag accelerometers, water-point sensors, or systematic pasture-use records) can pinpoint avoidance patterns, quantify losses in grazing efficiency, and prioritize patches for control where animal flow, water access, or hay operations elevate reinfestation risk. Management implications include rotating grazing to maintain competitive plants, applying targeted mechanical removal to sever roots and prevent re-rooting, planning workflows to avoid fragmentation, and using selective herbicides only where density justifies them then closing the loop with scheduled re-scouting and patch-status updates. AI guidance must be paired with empirical forage analyses and local expertise for ration formulation and risk management. ExtensionBot shows promise as a complementary educational tool that accelerates synthesis, flags decision points, and routes producers to validated resources. Responsible deployment requires embedding the system within established extension protocols, curated and current datasets, and professional judgment to ensure safety, regulatory compliance, and durable value in beef systems.

### **DairyLens: AI-enabled decision support for data driven decisions and time savings, life quality and reduced environmental footprint in dairy systems**

M. Atzori<sup>1</sup>, I. E. Cigagna<sup>1</sup>, C. Mariani<sup>1</sup>

<sup>1</sup> Dairy Lens SrL, Via Santa Chiara, 17, 09092 Arborea, Italy

DairyLens: AI-enabled decision support for data driven decisions and time savings, life quality and reduced environmental footprint in dairy systems Atzori M., Cigagna I.E., Mariani C. Decision making in a dairy farm remains time-consuming, fragmented, and cognitively demanding. The challenge is transforming routine farm reports into actionable decisions that improve performance without increasing workload. DairyLens is an AI-driven decision-support platform that converts standard farm reports into structured cross-domain analysis. The system integrates heterogeneous datasets through rule-based validation layers and machine-learning pattern recognition, producing management priorities via a generative AI assistant. Farmers and advisors interact with DairyLens through a chatbot interface. After uploading routine reports, users receive: (1) a prioritized action list, (2) quantified impact estimates (economic and performance-related), and (3) contextual explanations linking indicators across health, nutrition, and reproduction. Users can ask follow-up questions, enabling iterative exploration without requiring advanced data-analysis skills. Commercial pilot applications across dairy farms show consistent operational gains. Early field data indicate strong reduction in report analysis time, improved interventions within the first 60 days, and measurable reductions in many inefficiency indicators. In several cases, corrective actions were implemented within weeks rather than months, reducing economic leakage and stabilizing performance trends. By accelerating decision cycles and highlighting “hidden losses” across interconnected domains, DairyLens enhances management precision while lowering cognitive load. Such improvements indirectly contribute to reduced GHG load per unit of milk produced. The platform also supports documentation needs aligned with EU sustainability frameworks. This demonstrates how AI in livestock systems can shift from passive data reporting to active strategic guidance—delivering measurable time value, economic resilience, environmental co-benefits, and improved farmer well-being. Keywords: artificial intelligence, dairy management, decision support, time efficiency, carbon footprint.

### **Holistic Animal Management with Agentic AI**

A. Arsenos<sup>1,2</sup>, O. Filippopoulos<sup>1,2</sup>, N. Stavrou<sup>1,2</sup>, A. Arsenou<sup>2,3</sup>

<sup>1</sup> National & Kapodistrian University of Athens, Digital Industry Technologies, Euripus Campus, 34400 Euboea, Greece, <sup>2</sup> ArtinisLabs S.A., Sotiriou Gkioka 8, 19200 Elefsina, Greece, <sup>3</sup> Newcastle University, Electrical and Electronic Engineering, Merz Court, NE1 7RU Newcastle upon Tyne, United Kingdom

Livestock production systems are evolving into complex, data-rich environments where biological, environmental, and operational variables continuously interact. Yet farm data remains fragmented across sensors, equipment vendors, and manual records, limiting holistic and real-time decision-making. This work presents an Agentic AI framework for integrated farm-level intelligence that unifies heterogeneous data into dynamic digital twins of animals, housing, and production processes. The system operates as a farm-centric data layer, ingesting environmental measurements like humidity, ammonia, feeding and watering data, production logs, veterinary inputs, and computer vision streams. These inputs are contextualised into multi-scale digital representations (animal, group, building, farm). On top of this model, specialised AI agents monitor welfare and performance indicators, producing interpretable insights and actionable recommendations. A key component is edge-based vision monitoring. AI models analyse continuous camera feeds to estimate weight, growth, mobility, activity, and early signs of health issues such as lameness or abnormal clustering. Detected anomalies are automatically correlated with environmental and production variables, enabling root-cause analysis rather than isolated alerts. The agentic architecture supports autonomous reasoning and task coordination, correlating feed efficiency, microclimate conditions, and behavioural deviations to prioritise interventions and support compliance documentation. Instead of static dashboards, the framework delivers adaptive decision support that learns farm-specific patterns while remaining interoperable with existing infrastructure. Preliminary deployments in intensive livestock systems show improved situational awareness, earlier detection of welfare deviations, and reduced manual workload. The results demonstrate how Agentic AI can shift livestock management from reactive monitoring to proactive, data-driven orchestration, positioning AI as an operational co-pilot for scalable and welfare-centered production.

### AI-assisted Animal Welfare: potential and applications

J. L. Rault<sup>1,2</sup>, P. Taylor<sup>3</sup>

<sup>1</sup> University of Veterinary Medicine Vienna, Animal Welfare Science Unit, Veterinärplatz 1, 1210 Vienna, Austria, <sup>2</sup> NexWelfare consulting, Kleingartenverein Hochau 4, 2103 Langenzersdorf, Austria, <sup>3</sup> University of Melbourne, VIC, 3010 Parkville, Australia

Animal welfare is a dynamic and multidimensional state emerging from interactions between animal characteristics, farm management and environment, with implications for productivity, sustainability and societal acceptance of animal production systems. Current welfare assessment approaches remain largely reactive and reductionist, limiting their ability to capture this complexity. Precision Livestock Farming enables continuous, non-invasive monitoring of animals through multimodal data streams such as video, audio, feeding and environmental sensors. AI can integrate these large volumes of heterogeneous data and model non-linear relationships. Combined PLF-AI systems could help detect emerging health and welfare related changes. To illustrate this potential, we analysed a longitudinal dataset of commercial free-range broilers with continuous sensor-based ranging and weekly welfare data. Ranging data could predict later welfare outcomes: birds that ranged more frequently had better gait scores later (week 6), even after accounting for pre-ranging (day 7) weight ( $P < 0.001$ ), and lower odds of lameness ( $P = 0.034$ ). Birds could be grouped into distinct ranging profiles, and lameness prevalence was 65.7% in birds with the lowest ranging frequency compared to 36.4% in those with the highest at week 6. These results show the potential for predictive AI-assisted welfare management to support early risk detection, interpretable welfare assessment and adaptive management decisions. This provides a practical pathway from reactive monitoring toward more preventive, responsive and evidence-based animal management. Beyond detecting data pattern changes, generative AI can now produce natural-language data interpretation for farmers, generate individual competence profiles, adaptively recommend adjustments (e.g. enrichment timing, climate control), and simulate alternative management scenarios to support timely, context-specific decisions under human oversight. The implementation of AI approaches could realistically help operationalise animal management on-farm through more evidence-based decision-support tools.

### Session 3

### Theatre 2

#### Sensor prototype development for automated monitoring of integument damage of laying hens using suitable artificial intelligence models

A. Gruen<sup>1</sup>, P. Bhattacharya<sup>2</sup>, S. Rose<sup>1</sup>, G. Bieber<sup>3</sup>, H. Oz<sup>4</sup>

<sup>1</sup> University of Rostock, Faculty of Agriculture, Civil and Environmental Engineering, Professorship for Agricultural Process Engineering, Justus-von-Liebig-Weg 6, 18059 Rostock, Germany, <sup>2</sup> University of Rostock, Faculty of Computer Science and Electrical Engineering, Fraunhofer Institute for Computer Graphics Research IGD, Joachim-Jungius-Str. 11, 18059 Rostock, Germany, <sup>3</sup> Fraunhofer Institute for Computer Graphics Research IGD, Joachim-Jungius-Str. 11, 18059 Rostock, Germany, <sup>4</sup> Ege University, Ege Vocational Training School, Kazimdirik Street, 35100 Izmir, Turkey

AI-application development for real-farm environments is crucial for the flexible, continuous assessment of a large number of individual laying hens. It contributes to evolve welfare assessments from solely herd level management towards a more holistic framework. Therefore, a camera sensor prototype that automatically monitors individual hens was installed on a farm located in Mecklenburg-Western Pomerania, Germany. The mobile unit was placed in the litter area and used by the hens mainly for grooming that allowed continuous, stress-free data collection. A Raspberry Pi gave remote access to the video data for subsequent transfer and annotation on a local server processing unit. Regular manual assessment of several dorsal and ventral body areas delivered suitable target markers and positions for the camera model. Integument damage was evaluated using a four-stage scale (0 = minor, 1 = moderate, 2 = significant, 3 = severe;  $n = 50$  hens). Since the detection of specific target markers was highly sensitive to lighting conditions and image resolution, further studies are being conducted for better image clarity. Foundation models (SAM3, Florence 2, Grounding DINO, Gemini) were integrated in a customized semi-automated AI-annotation tool delivering first promising results. High-quality training sets are used by combining deep learning and large language models (LLM) within a Python-based interface. Locally running inference models (Qwen, Llava, Gemma and own solution) are currently being selected and fine-tuned to achieve optimal detection accuracy and classification performance. Subsequently, the AI-system will be transformed into a smart livestock farming tool application.

**A Lightweight Acoustic Model for Panic Stress Recognition of Caged Laying Hens**Z. Wang<sup>1</sup>, B. Chen<sup>1</sup>, M. Di<sup>1</sup>, Y. Jiang<sup>1</sup>, S. He<sup>1</sup>, H. Lin<sup>1</sup>, J. Pan<sup>1</sup><sup>1</sup> Zhejiang University, College of Biosystems Engineering and Food Science, No. 866, Yuhangtang Road, 310058 Hangzhou, China

Panic stress represents a widespread environmental challenge in poultry facilities, significantly undermining bird immunity and egg yields. Conventional monitoring techniques, such as manual observation and physiological testing, are labor-intensive and inherently invasive. Notably, the invasive nature of blood sampling can inadvertently trigger secondary stress in the flock. Furthermore, vision-based monitoring encounters substantial obstacles in high-density tiered cages due to severe line-of-sight obstructions. Conversely, acoustic sensing demonstrates superior applicability in these complex environments, benefiting from its high information density and robust penetration. Leveraging these acoustic advantages, we developed the Lightweight Time Delay Neural Network (Light-TDNN) for acoustic-based stress recognition. The network's development relied on a dataset specifically constructed to capture a diverse range of stressor-induced sounds. To optimize performance, the Light-TDNN incorporates three distinctive modules: (i) a Dilated-Shuffle module that achieves substantial model compression while capturing temporal dependencies through a wider receptive field; (ii) a Time-Frequency Attention module designed to focus on discriminative features and enhance the recognition of easily confused sounds, such as panic-induced cage noise and feeding sounds; and (iii) a Relational Knowledge Distillation (RKD) strategy that elevates the student model's efficiency without increasing computational overhead. Validation in authentic farm scenarios yielded a precision of 96.44% and a recall of 93.75%. With an efficient footprint of only 0.34 million parameters and 39.86 million FLOPs, this model provides real-time processing capabilities that exceed traditional monitoring benchmarks. In conclusion, the Light-TDNN successfully optimizes the trade-off between accuracy and lightweight design for on-farm edge implementation. Furthermore, it provides a quantitative metric for assessing the animal-robot compatibility of automated equipment, such as inspection robots, thereby guiding the advancement of welfare-oriented smart farming.

## Session 3

## Theatre 4

**Technological Innovations in Automated Monitoring of Pig and Broiler Welfare at the Slaughterhouse: progress of the aWISH project**N. Van Noten<sup>1,2</sup>, F. Tuytens<sup>1</sup>, Awish Consortium<sup>2</sup>, J. Maselyne<sup>2</sup><sup>1</sup> Flanders Research Institute for Agriculture Fisheries and Food (ILVO), Animal Sciences, Burg. Van Gansberghelaan 119, 9090 Merelbeke-Melle, Belgium, <sup>2</sup> Flanders Research Institute for Agriculture Fisheries and Food (ILVO), Technology and Food Science, Burg. Van Gansberghelaan 115, 9090 Merelbeke-Melle, Belgium

aWISH is a four-year Horizon Europe project focusing on the automated monitoring of animal-based indicators at slaughterhouses to document and improve the welfare of broilers and pigs during the on-farm, transport, and slaughter phases. During the project, sixteen new sensor technologies were developed, tested, and validated in six pilots across Europe. Each pilot consists of a slaughterhouse with a local research partner, associated farms, and various technology providers. Pig pilots are located in the Netherlands, Spain, Austria, and Serbia, while the broiler pilots are located in France and Poland. Each of these pilots accommodates several technologies. Most technologies rely on camera systems integrated with computer vision methods to automatically assess animal welfare indicators, such as ear, skin, and tail lesions, tail length, tear staining, stunning effectiveness, body weight, lung lesions, footpad lesions, hock burns, catching lesions, and activity. Additionally, three AI-driven sound analysis systems were developed that selectively detect stress vocalisations of pigs and broilers or coughs from pigs. These technologies are mainly installed in the slaughterhouse, but some are also installed on-farm. While certain technologies were designed and implemented from scratch, others were advanced through the incorporation of supplementary modules and algorithms into pre-existing frameworks, resulting in TRL levels currently ranging from 2 to 7, with an average of 6. All these sensor data are complemented by metadata from focal farms and are stored and processed on the aWISH data platform. Stakeholders across the production chain receive feedback through interactive dashboards presenting individual and aggregated welfare indicators, enabling time-series analysis and benchmarking. Further development and implementation of the aWISH approach allow cost-effective monitoring of the welfare of meat-producing livestock.

**Automated image analytics to reveal changes in drinking and eating behavior after vaccination**S. Van Poucke<sup>1</sup>, J. Ceia<sup>1</sup>, J. Defoort<sup>2</sup>, J. Maselyne<sup>3</sup>, P. J. De Temmerman<sup>3</sup><sup>1</sup> SYN+ BV, Boswegel 37, 9870 Olsene, Belgium, <sup>2</sup> PROVET DAP, Talpestraat 2, 8610 Kortemark, Belgium, <sup>3</sup> ILVO, Burg. Van Gansberghelaan 115/119, 9820 Merelbeke, Belgium

**Background & objectives** Vaccination of piglets to control porcine circovirus type 2 (PCV2) and *Mesomycoplasma hyopneumoniae* (Mh) is a common strategy in pig farming. Some vaccines, however, may trigger side effects. This study aimed to compare the effects of 2 bivalent PCV2/Mh vaccines on the lying down behavior and the feeding and drinking behavior by means of computer vision analysis. **Materials & methods** At the age of 32 days, 511 animals in the T1 group and 510 animals in the T2 group were subjected to a vaccination with 2ml of a commercial bivalent vaccine. Visual data collection relied on 2 Copeeks platforms. Three AI models were trained: a YOLOv11 animal segmentation model, a pig behavior segmentation model and a ViTPose 24-keypoint model. In addition, the average daily water consumption was registered. **Results** Before vaccination, lying behavior averaged 73% in T1 and 68% in T2, increasing to 88% and 91% on D0 and returning to baseline by D+1. Feeding among standing pigs decreased from 25–27% to 14–16% on D0 and recovered by D+1, while drinking showed a similar transient reduction (11–16% to 6–8%), with normalization the following day. Water counter data indicated a mean water intake per pig of 0.56 L/day at D–1, decreasing to 0.34 L/day on D0, and increasing to 0.78 L/day at D+1 in the T1 group. For the T2 group this was 0.63 L/day at D–1, decreasing to 0.38 L/day on D0, and increasing to 0.81 L/day at D+1. **Discussion & conclusion** Computer vision analytics successfully captured transient behavioral changes associated with vaccination, including increased inactivity and reduced feeding and drinking behavior on the day of vaccination, followed by rapid recovery within 24 hours. These findings were corroborated by independent water intake measurements, supporting the biological relevance and accuracy of the automated behavioral classifications. The changed behavior was temporary and similar for both vaccines. The vicinity of drinking and feeding spaces on the Roxell feeder was a challenge for training the models.

## Session 3

## Theatre 6

**Automated welfare monitoring through tear staining assessment in pigs at slaughter**S. Verlinde<sup>1,2</sup>, A. Ramon-Perez<sup>3</sup>, J. Reixach<sup>4</sup>, S. Gol<sup>4</sup>, P. Llonch Obiols<sup>3</sup>, J. Maselyne<sup>2</sup>, J. Verwaeren<sup>1</sup><sup>1</sup> Ghent University, Department of Data Analysis and Mathematical Modelling, Coupure Links 653, 9000 Gent, Belgium, <sup>2</sup> ILVO (Flanders Research Institute for Agriculture, Fisheries and Food), Burg. Van Gansberghelaan 115 bus 1, 9820 Merelbeke-Melle, Belgium, <sup>3</sup> Universitat Autònoma de Barcelona, Department of Animal and Food Science, Travessera dels Turons, 08193 Barcelona, Spain, <sup>4</sup> Selecció Batallé S.A., Dels Segadors, s/n, 17421 Riudarenes, Spain

In recent years, tear staining has been proposed as a novel indicator of pig welfare, with links to physiological stress, suboptimal environmental conditions and social stress. Despite variation in shape and colour, current assessment schemes primarily focus on the visibly stained area relative to the corresponding eye area, allowing for non-invasive visual evaluation. As these protocols rely solely on human-based scoring, scalability remains therefore a key bottleneck. Driven by advances in computer vision, this study presents the development of an automated tear staining assessment system deployed in a commercial slaughterhouse as a step towards centralised pig welfare monitoring. In March 2025, two synchronised RGB cameras were installed at a bleeding line behind a protective glass panel, providing separate views of the left and right sides of pigs. Data was collected over four days, recording more than 2000 pigs. A computer vision pipeline was developed to extract per-animal tear staining measurements from video data. The pipeline combines three deep learning models: (i) a detection model (YOLOv11) tracking individual pigs, (ii) a segmentation model (DynUNet) identifying relevant tear staining regions, and (iii) a classification model (DenseNet) predicting the staining severity scores. Cross-camera correspondence between left- and right-side recordings was established using a simple timestamp-based matching strategy. The pipeline demonstrates stable pig-level tracking (mAP = 0.95), while segmentation and classification performance is lower (Dice = 0.71, F1 = 0.67), mainly due to image degradation caused by glass fogging and contamination. This study presents key challenges, feasibility and initial performance of automated tear staining assessment under commercial slaughterhouse conditions.

### Long-term Sound Monitoring and Classification for Detecting Suspicious Events in Pig Farming

M. Wutke<sup>1</sup>, H. Geffert<sup>1</sup>, I. Reker<sup>2</sup>, I. Traulsen<sup>1</sup>

<sup>1</sup> Christian-Albrechts-University Kiel, Institute of Animal Breeding and Husbandry, Hermann-Rodewald-Straße 6, 24118 Kiel, Germany, <sup>2</sup> Chamber of Agriculture Lower Saxony, Division Agriculture, Mars-la-Tour-Str. 6, 26121 Oldenburg, Germany

PLF methods show substantial potential to improve pig husbandry systems by offering continuous, data driven monitoring of welfare parameters and environmental conditions. In contrast to computer vision approaches, which are usually computationally more intensive and can be negatively affected by factors like suboptimal lighting conditions or object occlusions, methods from the fields of bioacoustics and AI can be an efficient alternative, enabling long-term monitoring and early detection of critical situations in terms of animal welfare and management. Recent studies have shown that convolutional neural networks (CNNs) can reach state-of-the-art results for audio-based classification of pig vocalizations, such as screams. However, most of this work remains centered on model development and evaluation within the bounds of the collected datasets, emphasizing classification performance rather than investigating how these models behave when deployed over a longer period within a practical setting. To address this gap, we applied a CNN-based scream detection approach not as an isolated task, but as an operational element within a real-time animal monitoring system, where scream activity is continuously quantified, and threshold exceedances are used to support the detection of suspicious events. For training and validation, we curated a binary dataset comprising 3,500 scream and 5,400 non-scream samples and trained a YOLOv12 classification model using Mel-spectrogram representations, achieving an accuracy of 0.972. In addition, using a novel pig scream benchmark dataset, the proposed model achieved a precision of 0.944, a recall of 0.810 and a F1-score of 0.872. Subsequently, the model was deployed for real-time monitoring over five weeks within a sliding-window approach to process whole video instances. The proposed method enabled the detection of events associated with atypical feed intake, external disturbances, behaviorally relevant post-mixing situations, and pain-related incidents, allowing earlier, more targeted welfare and management interventions on commercial farms.

### Beyond Accuracy in Precision Livestock Farming: Distribution-Aware Evaluation for Large-Scale Poultry Weight Monitoring

G. Toth<sup>1</sup>, M. Alexy<sup>2</sup>

<sup>1</sup> Eötvös Loránd University, Faculty of Informatics, Egyetem tér 1-3, 1053 Budapest, Hungary, <sup>2</sup> Óbuda University, John von Neumann Faculty of Informatics, Bécsi út 96b., 1034 Budapest, Hungary

Traditional evaluation of AI-based weight estimation in poultry production still relies heavily on mean-based metrics such as Mean Absolute Error or Mean Absolute Percentage Error. In practice, these averages can mask systematic biases across time, flocks, or production conditions, and they offer little insight into how well a model captures the full variability in animal weights. In this contribution, we highlight these limitations on real broiler and duck datasets and propose a shift toward distribution-aware evaluation. Instead of judging models only by a single error number, we recommend using metrics that directly compare the predicted and true weight distributions, such as kernel-based distances and Wasserstein-type measures. We show how these metrics reveal effects of seasonality, camera setup, and sampling bias that remain invisible under MAE/MAPE-only reporting, and how they can change conclusions about which model is “better” for on-farm decision-making. This perspective aims to support more robust, interpretable analysis in Precision Livestock Farming and to guide the design of monitoring and feedback loops that remain reliable under real farm variability.

**Cleanliness evaluation of poultry carcasses using deep learning analysis of images**

V. Belik<sup>1</sup>, L. Buhre<sup>2</sup>, C. Ruhland<sup>2</sup>, D. Meemken<sup>2</sup>, N. Langkabel<sup>2</sup>

<sup>1</sup> System Modeling Group, Institute of Veterinary Epidemiology and Biostatistics, School of Veterinary Medicine, Freie Universität Berlin, Königsweg 67, 14163 Berlin, Germany, <sup>2</sup> Working Group Meat Hygiene, Institute of Food Safety and Food Hygiene, School of Veterinary Medicine, Freie Universität Berlin, Königsweg 67, 14163 Berlin, Germany

According to European Union regulations, only clean animals are accepted for slaughter avoiding microbial contaminations. European guidelines are lacking, but in Germany the German General Administrative Regulation on Food Hygiene (AVV LmH) enforces visual assessment of cleanliness of poultry batches to distinguish between clean or not clean delivery batches. For humans, determination of the cleanliness level is a laborious task in industrial broiler abattoirs with a slaughter line speed of more than three carcasses per second which involves visual examination of selected data samples. Its automation would help to reduce costs and improve the hygienic management and food safety. We developed a computational pipeline for the assessment of the level of cleanliness of poultry carcasses using video analysis by deep learning. We implemented our computational pipeline as a two-step procedure. First, we detect video frames with centered carcasses in a video sequences. Then we classify the carcasses into clean and dirty classes using three grades for dirty carcasses (slightly, moderate and highly contaminated). Here we combined moderate and high grade contaminated carcasses into a single category (dirty). Both steps were utilizing ResNet architecture implemented in pytorch and pretrained on ImageNet dataset. Our preliminary results were based on the evaluation of ca. 500 images of each class. For cleanliness prediction we achieved accuracy of over 0.91, F1 score of 0.90, sensitivity (recall) of 0.922, specificity of 0.900 and AUC of 0.96. Our study demonstrates that a relatively simple setup allows efficient and continuous assessment of the cleanliness of poultry carcasses in slaughter houses thus improving hygiene management, food safety and animal welfare.

## Session 3

## Theatre 10

**Unlocking digital twins in dairy herd through dynamic stochastic modelling**

K. K. Johansen<sup>1</sup>, J. Ettema<sup>1</sup>, S. Østergaard<sup>1,2</sup>

<sup>1</sup> Simherd A/S, Niels Pedersens Alle 2, DK-8830 Tjele, Denmark, <sup>2</sup> Aarhus University, Department of Animal and Veterinary Sciences - ANIVET Management and Modelling, Blichers Alle 20, DK-8830 Tjele, Denmark

Digital twins are emerging as a powerful tool for scenario testing and decision support in dairy herd management. Advances in real-time sensors and automated data recording enable continuously updated virtual representations of herds. When combined with biological and economical simulation models, such digital twins enable structured “what-if” analyses of management strategies. SimHerd, a stochastic, dynamic herd model, has effectively served this function since 1992. The model simulates animal- and herd-level state transitions to evaluate the biological and economic consequences of management decisions. State changes are driven by probabilistic events such as disease, heat detection, conception, mortality, and culling. SimHerd is a consequence-simulation model rather than an optimization tool. It quantifies expected biological and economic outcomes under herd-specific assumptions. Model parameters are calibrated using routinely recorded data, including milk yield, reproduction, and health records. The model is currently linked to the Danish National Cattle Database, allowing direct import of approximately 100 parameters. A full digital twin implementation would extend this setup with continuous synchronization of incoming data streams, making it implementable in other countries. We demonstrate how such digital twins support strategic and tactical decision-making through scenario analyses and economic evaluation of interventions. Applications include breeding and reproduction strategies, such as combinations of beef and sexed semen; health and welfare management, including the economic potential of reducing disease prevalence; replacement and youngstock strategies, such as extending productive life and lactations; and carbon footprint mitigation through improved yields and herd structure planning. All applications are based on real scenarios used by farmers, breeding advisors or researchers. Extending herd simulation models into fully synchronized digital twins moves their role beyond monitoring toward systematic evaluation of economic potential, risk, and uncertainty associated with alternative management strategies.

### Machine Learning for Lactation Curve Forecasting: Predicting 305-Day Dairy Production from Partial Observations

J. Ganitzer<sup>1,3</sup>, C. Egger-Danner<sup>1</sup>, P. Roth<sup>2,3</sup>

<sup>1</sup> ZuchtData EDV-Dienstleistungen GmbH, Dresdner Straße 89/B1/18, 1200 Vienna, Austria, <sup>2</sup> Webster Vienna Private University, Palais Wenkheim, Praterstraße 23, 1020 Vienna, Austria, <sup>3</sup> Graz University of Technology, Institute of Visual Computing, Inffeldgasse 16/II, 8010 Graz, Austria

Standard lactation curves describe the temporal dynamics of milk production across a dairy cow's 305-day lactation. Predicting these curves from early partial observations enables proactive herd management decisions, and early disease detection. This work presents a comprehensive investigation of machine learning approaches for dairy lactation curve forecasting. We leverage records from automatic milking systems combined with monthly control measurements, and static covariates (breeding values, breed, parity). The dataset comprises lactation records from commercial dairy operations with chronologically split sets (train/validation/test). We enforce strict boundaries to avoid leakage across individual cow timelines: training uses historical lactations, and validation/test sets contain latest lactations. Our data pipeline implements missing data handling through fill mechanisms and observation masks. Multi-cutoff evaluation at different days in milk (DIM 10, 50, 100, 150, 200, 250) reflects predictions at different stages of a lactation. We benchmark three conceptual neural architectures: Parametric (Curve-as-Parameters): Models that predict Wood curve parameters which fully specify a smooth production trajectory. Multi-Output Prediction: Models output one predicted yield per day across 305 days. Autoregressive: Models iteratively predict from the cutoff point forward, either via teacher forcing (training) or autoregressive rollout (inference). Overall, our best models achieve a mean absolute error (MAE) of 3.43 kg and a R2 score of 0.71 across multiple cutoff points. Early predictions (DIM 10–50) show higher error rates (MAE approx. 4 kg) due to a limited observation window. The error decreases with later cutoff points and longer observations windows (MAE = 2.70 kg at 200 DIM). This work demonstrates that modern machine learning methods outperform classical curve-fitting and simple baselines in early dairy production prediction, enabling farmers to identify projected yield curves and intervene early.

### Session 3

### Theatre 12

### User-Centered Explainable AI for Decision Support Systems in Dairy Farming

M. B. Girmay<sup>1</sup>

<sup>1</sup> University of Kaiserslautern-Landau, Gottlieb-Daimler-Straße, 67663 Kaiserslautern, Germany

Artificial Intelligence (AI) promises transformative opportunities in many application domains. A compelling example is the dairy farming sector, where large amounts of data could be used to optimize farm management. Decision support systems (DSSs) bridge raw data and practice by transforming it into actionable insights, enabling applications such as automated health monitoring or support in reproductive management. However, despite their potential, most DSSs face limited adoption. Key barriers include their complexity and black-box nature, making it difficult for farmers to understand how data is interpreted and on what basis recommendations are generated. This opacity can undermine trust, particularly when recommendations contradict farmers' intuition and experience. Explainable AI (XAI) directly addresses this by providing insight into how recommendations are generated, enabling users to better evaluate their validity. However, XAI research has predominantly focused on supporting AI developers rather than end users, and the dairy farming sector remains relatively unexplored compared to domains such as healthcare, autonomous driving, and finance. This presentation addresses both gaps. Through direct farmer engagement, we surveyed current DSS usage and aggregated feedback to derive general insights into DSS quality and explainability needs. We investigated which explanation output formats farmers find most useful, including rule-based formats and natural language, and explored preferences regarding explanation detail and data privacy. We clustered farmers by demographic characteristics into user personas capturing distinct explainability requirements. Our findings highlight the importance of involving end users in XAI-enabled system design and point toward concrete directions for future evaluation studies.

**Robustness of derivative-based AI pipelines for inferring herbage consumption from milk FT-MIR indicator**

K. Dichou<sup>1</sup>, D. Veselko<sup>2</sup>, A. Marvuglia<sup>3</sup>, H. Soyeurt<sup>1</sup>

<sup>1</sup> University of Liège, Gembloux Agro-Bio Tech, TERRA Research and Teaching Centre - Avenue de la Faculté d'Agronomie 41/13, 5030 Gembloux, Belgium, <sup>2</sup> Comité du Lait, Route de Herve, 104, 4651 Battice, Belgium, <sup>3</sup> Luxembourg Institute of Science and Technology (LIST), Avenue des Hauts-Fourneaux, 5, 4362 Esch-sur-Alzette, Luxembourg

At present, the dairy sector relies on grazing calendars and farm inspections to assess grazing practices for milk production. These methods are labour-intensive, costly, and hard to standardise at scale. Indicators derived from Fourier-transform mid-infrared (FT-MIR) milk spectra provide a promising alternative for automated, reproducible monitoring of feeding practices. This approach could enable to count grazing days, supporting verification of pasture-related labels. In a previous work, we developed a continuous indicator derived from milk constituents' estimates, including fatty acid profiles, protein fractions, and acidity-related traits obtained from FT-MIR analysis of bulk tank milk. This indicator reflects the proportion of herbage in the cows' diet on a scale from 0 to 1. In this study, we assess the robustness of a rule-based, derivative-driven AI pipeline designed to infer herbage consumption dynamics from FT-MIR-derived indicators. Derivative-based rules are used to extract discrete grazing periods from continuous time series. Using data from 2181 dairy farms in Wallonia for 2023 and 2024, we evaluate the influence of key algorithmic parameters, including smoothing intensity (4, 7 and 10 days) and derivative order (4, 7 and 10 days), on inferred metrics. Results show that inferred grazing duration was moderately sensitive to parameter choices, with mean annual grazing duration across farms ranging from 193.5 to 222.3 days depending on algorithmic settings, while between-farm variability remained stable (SD  $\approx$  40–46 days). This work highlights both the potential and the limitations of low-complexity, explainable algorithms such as this rule-based, derivative-driven AI pipeline. Although this study lacks precise validation based on in-farm data, it demonstrates clear potential as a screening tool that could be applied to large database to determine the associated number of grazing days, which may prove particularly useful for pasture-related labels.

## Session 3

## Theatre 14

**AI ready individual animal data collection for fattening pigs using transponder ear tags: practitioner expectations and implications for cross stage digital integration**

J. Exler<sup>1</sup>, V. Beck<sup>2</sup>

<sup>1</sup> Brand Qualitätsfleisch GmbH & Co. KG, Procurement of live pigs, Brandstr. 21, 49393 Lohne, Germany, <sup>2</sup> Brand Qualitätsfleisch GmbH & Co. KG, Sustainability Management, Brandstr. 21, 49393 Lohne, Germany

The increasing use of AI, sensor systems and IoT technologies in livestock production enhances possibilities for real time monitoring, optimisation of animal health and welfare, and improved sustainability across production stages. In the pork sector, demand for full chain traceability is rising, together with expectations regarding transparency on husbandry practices, veterinary treatments and carcass quality. Individual animal data infrastructures offer a basis for AI supported analytics that extend beyond traceability and may contribute to more consistent information flow. This study examines how farmers perceive the introduction of an individual animal identification system using transponder ear tags, focusing on practical benefits, barriers and the potential integration of AI based decision support. Eleven farm managers from the Agropole Innovates project were interviewed using a literature informed, semi structured guideline. Interviews were recorded, transcribed and analysed through qualitative content analysis (MaxQDA) with quantitative coding counts. Across interviews, nine farmers already use digital documentation, but all rely mainly on group level evaluation. Most expect increased workload, while several associate benefits with earlier detection of health or behavioural deviations. Usability and workflow compatibility were key requirements. To complement the qualitative results, descriptive analyses of initial transponder-based datasets from pilot farms were conducted, including read event frequencies, transponder retention observations and matching rates between transponder IDs and slaughter numbers. These metrics indicate technical feasibility and provide baselines for future AI modelling, although the current dataset size does not yet allow conclusions regarding predictive performance or economic impact. Overall, farmers recognise possible advantages of individual animal data collection, but adoption will depend on practical workflows, manageable workload and transparent cross stage value creation rather than expectations of AI driven optimisation alone.

**Found in translation: building explainable model for transparent decision making and interdisciplinary communication in precision livestock farming**Y. Xue<sup>1</sup>, L. Foldager<sup>2,3</sup>, K. Thodberg<sup>2</sup>, G. Gebreyesus<sup>1</sup><sup>1</sup> Aarhus University, Center for Quantitative Genetics and Genomics, C. F. Møllers Allé 3, bld. 1130, 8000Aarhus, Denmark, <sup>2</sup> Aarhus University, Department of Animal and Veterinary Sciences, Blichers Alle 20, 8830Tjele, Denmark, <sup>3</sup> Aarhus University, Section for Bioinformatics and Computational Biology, Universitetsbyen 81, building 1872, 3rd floor, 8000 Aarhus, Denmark

Artificial intelligence (AI) is increasingly applied in precision livestock farming for decision support. While AI-based models often achieve high predictive accuracy, their limited interpretability constrains adoption and trust among users outside computer science. Moreover, expert-confirmed annotations required for supervised learning are expensive and time-consuming to obtain, particularly regarding veterinary and management. These challenges are amplified in interdisciplinary settings, where differences in terminology, evaluation metrics, and conceptual frameworks hinder effective communication, validation, and deployment. Consequently, there is a growing need for explainable models that improve both predictive performance and interpretability while facilitating cross-disciplinary understanding. In this study, we illustrate two complementary approaches to classify slaughter-age images according to early-life docking severity in pigs under European welfare legislation. We conducted controlled experiments where pigs were assigned shortly after birth to three categories: intact, half-docked, or quarter-docked, and followed until slaughter for detailed tail measurements and image collection. The first approach relies on 13 predefined biologically meaningful image features and 6 derived features as inputs to a random forest regression model. Preliminary results show strong performance with 97% accuracy for intact and half-docked tails, while misclassifications mainly occur between quarter- and half-docked categories. To address this finer-scale challenge, we further explore a concept-based explainable AI (C-XAI) approach that integrates semantic concepts describing tail morphology directly into model training. Together, these strategies demonstrate how explainable models can enhance interpretability and practical usability of AI-based systems across disciplines in precision livestock farming.

## Session 4

## Theatre 2

**Explainable Machine Learning with SHAP for SNP-Based Prediction of Robustness-Related Longevity Indicators in Angler Dairy Cows.**A. Seidel<sup>1</sup>, K. Schröder<sup>1</sup>, G. Thaller<sup>1</sup>, N. Krattenmacher<sup>1</sup><sup>1</sup> Institute of Animal Breeding and Husbandry, Kiel University, Olshausenstr. 40, 24118 Kiel, Germany

Robustness and functional longevity are key breeding goals in dairy cattle, particularly in locally adapted breeds such as Angler cattle. Genomic prediction of health- and management-related traits remains challenging, as genetic effects may be heterogeneous and partly non-linear. While machine-learning approaches can capture such complexity, their limited interpretability has often restricted practical use in breeding. We compared classical linear genomic prediction (rrBLUP) with gradient boosting (XGBoost) and interpreted marker contributions using SHAP (Shapley additive explanations) in 972 genotyped Angler cows. Genotypes were derived from commercial 50k bovine SNP arrays and harmonized across chip versions. After quality control and LD-based clumping, approximately 24,680 autosomal SNPs were retained for analysis. Two robustness-related traits were analysed: lactation number at culling as a longevity indicator and stayability beyond the second lactation. Models were evaluated using five-fold cross-validation with identical SNP sets. For the longevity indicator, XGBoost achieved higher accuracy than rrBLUP (RMSE 0.93 vs 0.98; Spearman 0.51 vs 0.47). For stayability, discrimination was also slightly improved (AUC 0.79 vs 0.77). Out-of-sample marker contributions enabled model interpretation and comparison of marker importance between models. Within each trait, marker importance estimates showed moderate agreement between models, with Spearman  $\rho$  values of 0.33 and 0.30 for the longevity indicator and stayability, respectively. Several top-ranked SNPs were consistently identified across models, indicating shared additive signals. In contrast, XGBoost concentrated importance on a smaller subset of loci, suggesting non-additive effects that may not be captured by the additive model. These results indicate that explainable machine learning can complement classical genomic prediction by modestly improving accuracy while retaining biological interpretability, supporting transparent marker prioritization and practical decision-making for robustness and longevity breeding.

**Reduced Labelling Effort with Generalisable Computer Vision Models for Pigs, Cattle, and Poultry***P. J. De Temmerman<sup>1</sup>, J. Maselyne<sup>1</sup>**<sup>1</sup> ILVO (Flanders Research Institute for Agriculture, Fisheries and Food), Technology and Food, Burg. van Gansberghelaan 115, 9820 Merelbeke-Melle, Belgium*

The development of computer vision models for livestock behaviour monitoring is currently constrained by the need for large amounts of labelled data for each species, camera setup, and housing layout, making model creation time-consuming. Published models are often developed and tested under optimised conditions, reducing reproducibility on other farms. While open or historic datasets offer potential, integrating them into generalisable models remains challenging. For reproducibility and commercial farm applications, workflows must support fast and iterative development. To address this, an end-to-end workflow for generalisable computer vision models for pigs, poultry, and cattle was developed, covering labelling, segmentation, pose estimation, and behaviour inference. To form the basis for segmentation and pose estimation models, diverse datasets were collected across multiple species, farms, housing types, and camera setups. This resulted in labeling 1,662 training, 472 validation, and 250 testing images containing 34,902 animals (40% pigs, 30% cattle, 30% poultry) for segmentation, and 1,136 animals from 262 images labeled with 24 keypoints representing head, body, and distal landmarks for pose estimation. Body keypoints were visible in over 80% of images, head keypoints in ~60%, and distal extremities in ~20%. The model performance on these heterogeneous datasets demonstrates the workflow's ability to generalise across species and farm conditions. The YOLOv11-based segmentation model achieved an animal detection precision of 0.88, while a ViT-based pose estimation model reached a COCO AP of 0.65. By combining these models with infrastructure information, behaviour can be inferred without additional labelling for new farms or conditions. The presented workflow provides reusable models leveraging existing datasets, reducing labelling effort for new species, farms, and camera setups. Its modular design allows components to be replaced or extended, enabling adaptation to additional species, housing layouts, or behaviours. This approach demonstrates a scalable framework for generalisable computer vision models that facilitate reduced labelling effort in animal monitoring.

## Session 4

## Theatre 4

**Testing synthetic data integration for automated fish detection on beam trawl vessels***H. De Rijcke<sup>1</sup>, L. Snoeck<sup>1</sup>, S. Delacauw<sup>1</sup>**<sup>1</sup> ILVO, Marine, Jacobsenstraat 1, 8400 Oostende, Belgium*

Reliable on-board species identification is essential for modern fisheries monitoring, yet current practices still rely heavily on manual reporting. Automated camera-based systems offer a scalable alternative, but their performance is limited by the availability, diversity, and quality of training data. In demersal trawl fisheries, controlled imagery collection is especially challenging due to mixed catches, overlapping individuals, and variable lighting, while rare or protected species exacerbate data scarcity. Within the SynFish project, we systematically assess how synthetic imagery affects model performance and robustness across varying synthetic-real training ratios. High-resolution photogrammetry is used to generate detailed 3D models, which form the basis for rendered synthetic images. Body pose, lighting, colour, and background are systematically varied to approximate on-board conditions. In parallel, real-world datasets were collected under controlled laboratory conditions using brill and plaice, a small-scale conveyor belt, adjustable lighting, and non-target objects, as well as on beam trawl vessels and at the fish auction. The contribution of synthetic data is studied by varying the synthetic-real ratio from fully synthetic to fully real in 10% increments. Three training strategies are compared: simple mixed, fine-tuned real (pretrained on synthetic, then fine-tuned on real), and fine-tuned synthetic (pretrained on real, then refined on synthetic). Experiments progressively increase visual complexity, including fish overlap, background clutter, lighting conditions, orientation, and number of species. This study builds on prior research in similar experimental designs, notably outside the fisheries domain. Previous work shows that models fine-tuned on real data outperform baseline approaches. Initial experiments on controlled laboratory datasets indicate an overall preference for fine-tuned real, evidenced by higher accuracy and mAP50 values. However, near-optimal real imagery likely introduces bias by limiting visual variability and reducing the synthetic-real domain gap. Further evaluation will be extended to assess robustness under operational on-board variability, and to identify conditions where synthetic data benefits automated fisheries monitoring.

### Thinking outside the black box: rethinking the use of machine learning for automated behaviour analysis

S. P. Brouwers<sup>1</sup>, N. McLaughlin<sup>2</sup>

<sup>1</sup> Teagasc, Pig and Poultry Research and Knowledge Transfer Department, Moorepark, P61 C996 Fermoy, Ireland, <sup>2</sup> Queen's University Belfast, School of Electronics, Electrical Engineering and Computer Science, 16A Malone Road, BT9 5BN Belfast, United Kingdom

Automated behaviour analysis (ABA) promises to transform applied ethology by enabling scalable behavioural measurement with minimal human labour. However, despite recent advances in machine learning (ML) and computer vision, the real-world impact of ABA remains limited. This is largely due to several key challenges. First, traditional ethograms impose discrete behavioural categories onto inherently continuous phenomena, creating label ambiguity and limiting model performance. Second, traditional ML models rely on large volumes of annotated data, which is scarce in ethology. As a result, ML models are often trained on small, homogeneous datasets, making them susceptible to shortcut learning and limiting their ability to generalise across environments. To address these limitations, we explore several alternative approaches to the development of ABA that make more efficient use of scarce manual effort while improving its robustness and biological relevance. Firstly, annotation and model outputs may be shifted away from interpretive behavioural labels towards phenomenological descriptors, such as postural configurations, movement trajectories, relative distances, and velocities. This approach better reflects the continuous nature of behaviour and allows biological interpretation to occur downstream of model output. Secondly, there is a need for open data sharing to create diverse large-scale datasets. This would allow robust supervised models to be trained and permit out-of-distribution generalisation testing. Thirdly, we discuss using foundation models and unsupervised learning for zero-shot identification of behavioural motifs, which would significantly reduce the need for low-level manual annotations. Finally, model evaluation should be complemented by biological validation to support meaningful biological inference, and a closer integration between animal science, data science, and engineering is needed to ensure that ABA development remains aligned with its core objective of generating biologically meaningful, scalable insights into animal behaviour in real-world settings.

### Session 4

### Theatre 6

#### A Deep Learning system for automating head direction annotation in ungulates

A. Kaki<sup>1</sup>, J. Deutsch<sup>1</sup>, S. Lebing<sup>1</sup>, S. Döpjan<sup>1</sup>, C. Nawroth<sup>1</sup>

<sup>1</sup> Research Institute for Farm Animal Biology (FBN), Working Group Animal Behaviour & Welfare, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany

Behavioural paradigms that assess looking time hold significant potential for investigating cognitive processes and welfare states in farm animals, particularly through attention bias tasks. However, the subsequent data analysis typically relies on laborious manual annotation, creating a significant bottleneck for scalability. In this study, we present a Deep Learning-based system to fully automate the annotation of head direction in dwarf goats (*Capra aegagrus hircus*) within a looking-time experimental paradigm. Our system utilises computer vision to detect key facial features (eyes, nose, and horns), and algorithmically calculates a looking direction vector based on the geometric relationship between these points. To address the challenge of lateral eye placement and occlusion in freely moving animals, we integrated a fallback mechanism that utilises horn position to estimate the gaze vector when eyes are not visible. We systematically evaluated three distinct object detection architectures: a one-stage detector (YOLOv8-Medium), a two-stage Faster R-CNN with a ResNet-101 backbone, and a two-stage Faster R-CNN with a Vision Transformer (ViT) backbone. The models were evaluated on a manually annotated test set of 2,566 frames. The ViT-based model achieved a final classification accuracy of 90.2%, substantially outperforming both the ResNet-101 (80.8%) and YOLOv8-Medium (81.7%) models. These results indicate that the Vision Transformer's attention mechanisms, which capture global context rather than local features alone, are significantly more effective for pose estimation in ungulates than traditional CNN baselines. We demonstrate that automated computer vision systems can achieve high reliability in unconstrained animal settings. By replacing manual coding with this automated pipeline, researchers can drastically reduce analysis time, enabling the efficient processing of large datasets necessary for robust animal welfare and cognition research.

**Quantification of Fading in Melanin-based Operculum Spots as Stress Response in Atlantic Salmon using Computer Vision**

T. Laique<sup>1</sup>, M. Gunnes<sup>1</sup>, Ø. Øverli<sup>1</sup>, H. Ullah<sup>1</sup>

<sup>1</sup> Norwegian University of Life Sciences, Faculty of Life Sciences (Biovit), Oluf Thesens vei 6, 1433 Ås, 1433 Ås, Norway

Intensive Atlantic salmon farming is challenged by high mortality rates, and the aquaculture industry urgently requires innovative, non-invasive indicators of stress and welfare. Currently, the indicators used in the industry are invasive and often provide signals only after a problem has already developed (e.g., scale loss, wounds). We hypothesized that melanin-based operculum spots fade in response to stress and tested this hypothesis by photographing 130 salmon before and after 18 hours of confinement stress. In this study, we present a methodology that leverages computer vision to quantify fading in operculum spots. The approach involves detecting the operculum region in out-of-water salmon images, followed by the detection and segmentation of spots within the operculum. Grayscale pixel intensity based and geometry based features were computed for each spot, and fading was quantified by comparing pre- and post-stress measurements. We also developed a tool that integrates our trained models with state-of-the-art computer vision models to segment operculum spots and quantify spot fading. Furthermore, correlations were observed between pigmentation fading and different physiological parameters, supporting the validity of our findings. Overall, the results suggest that fading of melanin-based operculum spots may serve as a promising non-invasive indicator of stress and welfare in Atlantic salmon and could provide valuable insights for improving welfare monitoring in aquaculture.

**AI-driven exploration of molecular data in animal science: applications in genomics and metabolomics to dissect the animal phenome**

S. Bovo<sup>1</sup>, G. Schiavo<sup>1</sup>, M. Bolner<sup>1</sup>, F. Bertolini<sup>1</sup>, L. Fontanesi<sup>1</sup>

<sup>1</sup> University of Bologna, Animal and Food Genomics Group, Dept. of Agricultural and Food Sciences, Viale Fanin 46, 40127 Bologna, Italy

Artificial Intelligence (AI) provides powerful tools to extract biologically meaningful information from high-dimensional omics datasets. Here, we present the application of Boruta, a Random Forest-based feature selection algorithm, to genomic and metabolomic data in pigs, highlighting its value for dissecting complex phenotypes. Using high-density Single Nucleotide Polymorphism arrays from over than 1,000 pigs across local and commercial breeds. Boruta identified reduced subsets of informative markers capable of allocating pigs to their corresponding breeds with high accuracy. Additionally, Boruta was applied to metabolomics datasets derived from plasma, serum and urine samples across multiple pig and cattle cohorts to explore the molecular phenome in relation to complex traits, including breed differences, sexual dimorphism, heat stress, and variation in production traits. Machine learning enabled the identification of stable metabolomic signatures capturing metabolic shifts at different biological levels. Overall, AI-driven analysis of genomic and molecular phenomics data represents a practical strategy to identify robust biomarkers, supporting innovative breeding and precision feeding programs in the era of big data. Research funded by the European Union – NextGenerationEU under the National Recovery and Resilience Plan (PNRR) – FEEDTHEPIG, proposal code P2022FZMJ9 – CUP J53D23018310001 and the European Union’s Horizon Europe research and innovation programme under the grant agreement No. 101059609 (Re-Livestock).

**Prediction of milk coagulation properties using prior-fitted transformers**

T. J. Curik<sup>1</sup>, D. Domović<sup>2</sup>, N. Mikulec<sup>2</sup>, B. Lukic<sup>3</sup>, M. Spehar<sup>4</sup>, I. Curik<sup>5,6</sup>

<sup>1</sup> Maastricht University, Paul-Henri Spaaklaan 1, 6229GS Maastricht, Netherlands, <sup>2</sup> University of Zagreb, Svetošimunska 25, 10000 Zagreb, Croatia, <sup>3</sup> J.J. Strossmayer University of Osijek, Vladimira Preloga 1, 31000 Osijek, Croatia, <sup>4</sup> Croatian Agency for Agriculture and Food, Gorice 68 B, 10000 Zagreb, Croatia, <sup>5</sup> Hungarian University of Agriculture and Life Sciences, Guba Sándor 40, 7400 Kaposvár, Hungary, <sup>6</sup> University of Zagreb, Svetošimunska 25, 10000 Zagreb, Croatia

While cheese production is a key value-added component of the global dairy sector, selection for cheese-making traits remains insufficiently incorporated into genetic improvement programs. Mid-infrared (MIR) spectroscopy provides a rapid, low-cost approach for predicting milk coagulation properties (MCP) and improving its predictive accuracy could enable their use as selection criteria for cheese-focused breeding. We evaluated TabPFN, a prior-data-fitted transformer recently shown to outperform conventional methods on small tabular datasets, for predicting six MCP traits (RCT, k20, a30, a60, a2r, and amax) from MIR spectra of 1,134 Holstein cow milk samples. All models evaluated (TabPFN, penalized regression, ensemble tree methods, kernel methods, and neural networks), except partial least squares (PLS), were trained on PLS-derived latent variables, which reduced spectral dimensionality and ensured a common input representation for fair comparison. Evidence of temporal confounding motivated a leave-one-batch-out cross-validation design. Sampling batch explained 6.1% of total spectral variance (PERMANOVA), and batch membership could be predicted from spectra with 89–99% accuracy. Under random cross-validation,  $R^2$  declined by 0.02–0.14 across traits with temporal blocking, demonstrating that shared temporal structure inflates performance estimates. Under this stricter validation, TabPFN achieved the highest  $R^2$  across all six traits, exceeding the PLS baseline by 0.02–0.06 depending on trait. For RCT, this corresponds to 68% of the empirical performance ceiling derived from duplicate Formagraph measurements. Our results show that TabPFN applied to MIR spectra enhances the prediction of MCP, marking an important step toward their implementation in dairy breeding programs, milk payment systems, and industrial milk separation.

## Session 4

## Theatre 10

**DairySleepNet: a multichannel state space architecture for dairy sleep classification**

C. Guo<sup>1,2</sup>, E. Ternman<sup>3</sup>, K. Liu<sup>2</sup>, M. Niu<sup>1</sup>

<sup>1</sup> Institute of Agricultural Sciences, Department of Environmental Systems Science, ETH Zürich, 8092 Zürich, Switzerland, <sup>2</sup> Department of Infectious Diseases and Public Health, Jockey Club College of Veterinary Medicine and Life Sciences, City University of Hong Kong, 0000 Hong Kong SAR, China, <sup>3</sup> Faculty of Biosciences and Aquaculture, Nord University, 8049 Steinkjer, Norway

Accurate sleep classification is essential for assessing animal welfare and health in precision livestock farming. However, automated sleep monitoring in cattle remains challenging due to the complexity of physiological signals and the scarcity of labelled data. This study presents a deep learning framework based on the selective state space model (Mamba) for automated sleep classification in dairy cows using multimodal physiological signals. A dataset comprising 77 hours of synchronized recordings was collected from 7 Holstein cows housed in a tie-stall barn, including 9-channel polysomnography (PSG) signals and 4-channel accelerometer and pressure data from a halter sensor. Sleep stages were manually annotated in 30-second epochs following a standardized protocol, yielding three classes: Awake, Rumination, and Sleep. In our method, raw signals were transformed into time-frequency spectrograms via short-time Fourier Transform and fed into channel-wise Mamba encoders. A cross-channel fusion module with residual connections aggregates multimodal representations, followed by fully connected layers for prediction. Subject-level cross-validation was performed with weighted sampling to address class imbalance. The proposed method achieved macro F1-scores of 0.86, 0.69, and 0.85 for PSG-only, accelerometer-only, and combined modalities, outperforming random forest baselines (0.78, 0.73, 0.81). For the minority Sleep class, the model attained F1-score of 0.74 with PSG compared to 0.69 for baseline, while accelerometer-based models achieved only 0.55, highlighting the advantage of time-frequency representations in capturing sleep-related patterns, while accurate sleep prediction using halter data alone remains challenging. These results demonstrate the potential of state space models for automated sleep scoring in livestock, though further on-farm validation is warranted.

### Artificial neural networks outperform partial least squares models for fatty acids estimation using FT-MIR spectrometry on bovine milk: a first step towards transfer learning on small ruminants.

E. Cabaraux<sup>1,2</sup>, I. Alexakis<sup>1</sup>, S. Franceschini<sup>1</sup>, O. Christophe<sup>3</sup>, C. Grelet<sup>3</sup>, M. Calmels<sup>4</sup>, C. Lecomte<sup>5</sup>, C. Bertozzi<sup>6</sup>, D. Veselko<sup>7</sup>, F. Dehareng<sup>3</sup>, H. Soyeurt<sup>1</sup>

<sup>1</sup> TERRA Teaching and Research Centre, Gembloux Agro-Bio Tech, Passage des déportés 2, 5030 Gembloux, Belgium, <sup>2</sup> Scientific Research Fund, FRS - FNRS, Rue d'Egmont 5, 5000 Bruxelles, Belgium, <sup>3</sup> Wallon Agricultural Research Centre, Chaussée de Namur 24, 5030 Gembloux, Belgium, <sup>4</sup> Seenovia, Boulevard des Loges 141, 53940 Saint Berthevin, France, <sup>5</sup> Eliance, Rue de Bercy 149, 75595 Paris, France, <sup>6</sup> Walloon Breeding Association, Rue des Champs Elysées 4, 5590 Ciney, Belgium, <sup>7</sup> Comité Du Lait, Route de Herve 104, 4651 Battice, Belgium

Fourier transform mid-infrared (FT-MIR) spectrometry in milk can improve production, milk quality and animal welfare. However, its application in dairy ewes and goats remains limited, despite widespread use in dairy cattle. To reduce equation development costs, transfer learning could be used to adapt FT-MIR models from dairy cattle to dairy sheep and goats. However, this transfer requires artificial neural networks (ANN) but these bovine ANN models do not yet exist. This study aims to develop multi-layers perceptron ANN for fatty acids. The ANN models were then directly applied to goat milk to evaluate the potential of transductive learning. The database (n=1942) contained 42 individual and groups of fatty acids measured by gas chromatography and their associated standardized bovine milk spectra. Validation R<sup>2</sup> values ranged from 0.1223 to 0.9890 for PLS models and from 0.2050 to 0.9886 for ANN models. Compared with PLS models, ANN reduced prediction errors (RMSE) by 0.08 to 47.27% for 39 fatty acids, while the remaining fatty acids models are outperformed by the traditional PLS. After applying the built ANN models on the goat dataset (n=345), only 10 fatty acids have a positive R<sup>2</sup> from 0.1228 to 0.9410, one showed an R<sup>2</sup> equal to zero, and 28 exhibited aberrant R<sup>2</sup> values, indicating poor cross-species generalization. In conclusion, ANN models improved predictive performance compared with PLS models. Transductive transfer learning confirms that cattle-specific models cannot be directly applied to small ruminants and opens the door to testing other transfer learning methods.

### Development of robust neural network architectures for federated FT-MIR prediction of enteric methane emissions in dairy cows

H. Soyeurt<sup>1</sup>, F. Dehareng<sup>2</sup>, N. Gengler<sup>1</sup>, S. Mcparland<sup>3</sup>, M. Kreuzer<sup>5</sup>, M. Bell<sup>6</sup>, P. Lund<sup>7</sup>, C. Martin<sup>4</sup>, B. Kuhla<sup>8</sup>, A. Vanlierde<sup>2</sup>

<sup>1</sup> University of Liège, Gembloux Agro-Bio Tech, Passage des Déportés 2, 5030 Gembloux, Belgium, <sup>2</sup> CRA-W, Chaussée de Namur 24<sup>ème</sup> de Namur, 5030 Gembloux, Belgium, <sup>3</sup> Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, P61C996 Cork, Ireland, <sup>4</sup> Université Clermont Auvergne - INRAE, UMR Herbivores, Route de Theix, 63122 Saint-Genès-Champanelle, France, <sup>5</sup> ETH Zurich, Environmental Systems Science, Eschikon 27, 8315 Lindau, Switzerland, <sup>6</sup> AFBI, Large Park, BT26 6DR Hillsborough, United Kingdom, <sup>7</sup> Aarhus University, Animal Science, Blichers Allé 20, 8830 Tjele, Denmark, <sup>8</sup> FBN, Nutrition Biochemistry, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany

Previous studies have demonstrated the potential of milk FT-MIR spectroscopy to predict enteric CH<sub>4</sub> emissions in dairy cows. Sufficient accuracy of CH<sub>4</sub> reference measurements to reliably capture the underlying population trend requires many observations. But, the sharing of such data can be limited due to confidentiality constraints. Federated learning (FL) offers a promising solution as it enables a neural network trained by one research group to be transferred to another without sharing raw data. The second group can further train the model on its own data and share the updated network, preserving data privacy while improving predictive performance. So, the development of a robust neural architecture is essential. This study aims to compare PLS regression with multilayer perceptrons (MLP) and convolutional neural networks (cANN). A dataset of 1,879 records was used. A total of 289 spectral variables were selected and preprocessed using a first derivative, followed by regression on second-order Legendre polynomials according to days in milk. Three MLP architectures (one to three hidden layers) and three cANN models were evaluated, the latter using spectral data reshaped into 3 × 289 images. Cross-validation performances were consistent with expectations : R<sup>2</sup> from 0.60 to 0.80; mean error around 51 g CH<sub>4</sub>/day. The MLP with two hidden layers achieved the best results. ANN slightly outperformed PLS and, more importantly, open new perspectives for implementing FL frameworks to improve CH<sub>4</sub> prediction models.

### Fitting and Predicting Dairy Lactation Curves based on Test-Day Records

C. Frauzino<sup>1</sup>, S. Canuto<sup>1</sup>, V. Cabrera<sup>2</sup>, E. Noronha<sup>1</sup>

<sup>1</sup> Federal Institute of Goiás, Informatic, Rua 75, 46, Centro, 74055110 Goiânia, GO, Brazil, <sup>2</sup> University of Wisconsin-Madison, Animal & Dairy Science, 1675 Observatory Drive 266 Animal Sciences Building, 53706-1205 Madison, WI, United States

Predicting and reconstructing lactation curves from test-day milk yield records plays a central role in modern dairy herd management. Despite the growing use of automated milking systems, periodic test-day data remain the primary and most accessible data source for monitoring production performance across diverse herds and environments. Accurate reconstruction of these curves enables better estimation of total milk yield, early detection of production disturbances, and informed decisions regarding herd management, genetic selection, and reproductive planning, which directly influence farm efficiency and profitability. However, traditional lactation models, typically constrained by fixed functional forms, often introduce bias and exhibit limited predictive capacity, particularly when applied to incomplete or ongoing lactations. Recent advancements in artificial intelligence have introduced data-driven lactation models, but these often rely on extensive input features beyond standard milk records and parity. We introduce a new data-driven autoencoder model that learns patterns from historical test-day records to reconstruct complete lactation curves. The proposed method is compared against five lactation benchmarks and remains robust with limited data, outperforming traditional models by achieving a 12.5% lower RMSE than the next-best model (Wood) under a 30-day sampling interval. A key advantage is the model's ability to provide an unbiased prediction, eliminating the systematic over- and under-prediction characteristic of the benchmark models in different lactation stages. The autoencoder also shows notable robustness and data efficiency, delivering competitive performance when trained on as little as 5% of the original training dataset. This data-driven approach, validated for its accuracy, lack of bias, and robustness to sparse data, offers a promising avenue for developing advanced decision support systems that empower dairy farmers with more reliable predictive tools for herd management.

### Session 4

### Theatre 14

### LivestockMind: A Large Language Model for Livestock Health Caring

Z. Guo<sup>1</sup>, L. Lyu<sup>1</sup>, Z. He<sup>1</sup>, K. Liu<sup>1,2</sup>

<sup>1</sup> City University of Hong Kong, Infectious Disease and Public Health, CityU, 999077 Hong Kong, China, <sup>2</sup> City University of Hong Kong Qingdao Research Institute, CityU, 266000 Qingdao, China

Ensuring livestock health and welfare is a cornerstone of sustainable agricultural productivity. Despite its importance, accessing actionable veterinary expertise remains a significant bottleneck. Traditional information retrieval relies on time-intensive manual reviews, which often fail to provide the rapid insights needed for complex pathologies, leading to missed therapeutic windows and significant economic losses. While general Large Language Models offer a potential solution, their clinical deployment is hindered by domain-specific hallucinations and an inability to reason through intricate veterinary cases. To bridge this gap, we present LivestockMind, a specialized LLM based on the Qwen2.5-7B-Instruct architecture engineered for high-precision veterinary care. Our methodology adopts a multi-stage optimization strategy to enhance clinical reasoning. First, we integrate a custom Retrieval-Augmented Generation (RAG) architecture leveraging 60 authoritative Elsevier livestock textbooks to ground outputs in verified clinical evidence. Second, we utilize Low-Rank Adaptation (LoRA) to fine-tune the model on a high-quality corpus of 30,000 veterinary Q&A pairs, enabling the internalization of complex domain expertise. To ensure cognitive rigor, we incorporate a Chain-of-Thought (CoT) mechanism trained on 30,000 reasoning samples, forcing the model to articulate logical, step-by-step thinking. Finally, Direct Preference Optimization (DPO) is employed using 2,000 curated entries to align model behavior with professional ethical standards and suppress erroneous advice. Experimental evaluations demonstrate that LivestockMind significantly outperforms state-of-the-art models including Llama 3, DeepSeek 3.2, and Qwen Max. Specifically, it achieved a peak BERTScore F1 of 0.8979, demonstrating superior semantic alignment with authoritative literature. In double-blinded machine evaluations, LivestockMind earned the highest mean expert-alignment score of 91/100. These results suggest that LivestockMind establishes a offline, reliable, and scalable decision-support infrastructure, offering transformative value for veterinary practitioners, farm management, and clinical education.

**AI Foundation models for agricultural sciences - Challenges and opportunities***I. Athanasiadis<sup>1</sup>**<sup>1</sup> Wageningen University and Research, Artificial Intelligence (AIN) group, Droevendaalsesteeg 1, 6708 PB Wageningen, Netherlands*

Foundation models, developed with self-supervised methods using unlabeled and multimodal multidisciplinary corpora, offer a new pathway for AI-driven discoveries in agricultural sciences. In this paper, we identify key challenges inherent to AI research in agricultural sciences, and advocate that an emerging new generation of agricultural AI, in the form of foundation models is necessary to kickstart data-driven discoveries in agricultural sciences. We argue that foundation models have the potential to act as jumpboards and enable a new generation of AI models for agricultural sciences, offering power and adaptability to accelerate innovation. By reflecting on agricultural science challenges, data, and theory, we identify pathways for model development and evaluation that will enable agricultural researchers to build on shared foundations instead of training new models from scratch for each application and location.

**Bridging Fragmented Agricultural Data with AI-Driven Semantic Translation***P. Hekmati<sup>1,2</sup>, K. Reed<sup>3</sup>, J. Waddell<sup>4</sup>, V. Cabrera<sup>1</sup>**<sup>1</sup> University of Wisconsin–Madison, Department of Animal and Dairy Sciences, 1675 Observatory Drive, WI 53706-1205 Madison, United States, <sup>2</sup> Pasalica, 971 US Highway 202N STE N, NJ 08876 Branchburg, United States, <sup>3</sup> KFR Consulting LLC, Sault Sainte Marie, 49783 Michigan, United States, <sup>4</sup> Dairy Management Inc., 10255 W. Higgins Rd., Illinois 60018-5616 Rosemont, United States*

Agricultural systems are fragmented across incompatible schemas, units, and metadata, requiring manual integration through schema mapping, and static converters that scale poorly. This talk presents an AI-based approach to semantic translation across heterogeneous systems using LLM-assisted schema alignment, ontology-aware discovery, and semantic search. The result enables dynamic integration, reduces engineering effort, and improves accessibility and analytics for complex modeling platforms.

**Applications of AI in animal feeding and management**A. Bach<sup>1,2</sup><sup>1</sup> University of Lleida, Dep. Animal Science, Av. Roure 191, 25198 Lleida, Spain, <sup>2</sup> Agrotecnio, Av. Roure 191, 25198 Lleida, Spain

The continuous progress in milk production is challenging the ability of cows to consume sufficient nutrients to sustain all their physiological functions. This demands for accurate models to predict nutrient requirements of cows as well as their response to different diets. Nutritionists have estimated requirements and responses defining a reference cow, initially using factorial models and more recently a mixture of mechanistic and factorial approaches. These models assume that all cows would respond, on average, in the same manner as the reference cow to a given nutrient supply. But cows from different herds respond differently in terms of milk yield when fed an exact same diet. These models disregard economic parameters as it is assumed that more milk implies greater profits. But, within any given group of cows, when additional nutrients are supplied, a subset of cows may fail to respond with increased milk yield. Feeding more nutrients to non-responding cows leads to economic losses as they consume a more expensive feed without improving output. Models should predict group responses rather than those of a single reference cow. Algorithms based on artificial intelligence (AI) use large sets of data to recognize patterns and learn or predict an outcome. Animal scientists have been progressively using AI to improve different aspects of dairy production such as heat detection, health assessment, etc... But, the most important contribution of AI is perhaps its application to predict economic responses upon dietary modifications, pen movements, or oscillations in environmental conditions. An effective integration and exchange among different platforms that collect data from different aspects of the dairy farm (i.e., nutrition, prices, milk production, reproduction, health) hinders the opportunity of using AI to facilitate management and nutritional decisions. Examples of these opportunities include deciding the optimum level of nutrients to maximize profit, when to change a ration, when to move cows from different production groups, whether to breed or not a cow, or how much feed should each cow receive while visiting a milking robot. These opportunities are already available, and as they become further developed and advanced they are likely to re-define dairy production.

## Session 5

## Theatre 4

**From Pixels to Insight: Challenges and opportunities for computer vision in animal monitoring**S. Leroux<sup>1</sup><sup>1</sup> Ghent University - imec, Technologiepark-Zwijnaarde 126, 9052 Ghent, Belgium

The fields of computer vision and machine learning are moving at an unprecedented pace. New approaches and models are being proposed daily, and it is often hard to keep up to date with the latest and greatest developments. Especially for an application area such as animal monitoring, it is not always clear how these new techniques transfer from the traditional computer vision datasets to real world environments. In this talk, we will go over a few recent developments and discuss how they might improve the capabilities of animal monitoring systems. More specifically, we will address the rise of self-supervised methods that can reduce the need for manually annotated dataset, the move from single modality to multi-modal data and finally, a trend towards more efficient models that can be deployed on edge devices, close to the data source instead of relying on cloud computing.

**Big Data and Machine Learning to Improve Culling Decision-Making in Dairy Herds***L. Da Silva<sup>1</sup>, Y. Gong<sup>1</sup>, V. Cabrera<sup>1</sup>**<sup>1</sup> University of Wisconsin–Madison, Animal and Dairy Sciences, 1675 Observatory Dr., 53706 Madison, United States*

The culling of animals in dairy herds generally results from the interaction between managerial decisions and biological processes inherent to animal physiology and health, being influenced by multiple productive, reproductive, and environmental variables. Consequently, estimating the probability of survival in future scenarios becomes a strategic tool for decision-making, in addition to enabling the early identification of critical points that influence culling risks. Hence, we studied survival curves incorporating a broad set of productive and reproductive variables using routine records from farms located in the United States. We built two machine learning predictive models to estimate survival probability of a cow over the years. Both models were trained using data from the Council on Dairy Cattle Breeding (CDCB) collected between 2006 and 2017, totaling 6,729,954 individual records. We implemented the XGBoost AFT regression algorithm (GB) and the nonparametric Kaplan–Meier estimator (KM), both in Python in the Google Colab environment. Performance evaluation was based on MAE, RMSE, and  $R^2$  metrics. The results showed that the GB model is technically feasible for survival predictions, achieving an  $R^2$  of 0.74, MAE of 0.14 years, and RMSE of 0.18 years. The KM model, in turn, showed superior performance ( $R^2 = 0.99$ ; MAE = 0.01 years; RMSE = 0.01 years). Although GB presented lower metrics than KM, its performance was satisfactory and, in some circumstances, desired since this model allows the integration of a larger number of productive, reproductive, and managerial variables. Thus, the tested machine learning–based models offered a promising path for more realistic and individualized survival estimates, incorporating heterogeneity among cows and management practices. In summary, both models demonstrated strong predictive capacity; however, machine learning approaches such as GB may allow more accurate predictions tailored to the unique reality of each producer.

## Session 6

## Theatre 2

**Multi-object tracking benchmark for livestock***H. Fred<sup>1,3</sup>, D. Liu<sup>2</sup>, P. De La Vallée<sup>2</sup>, L. Ruotsalainen<sup>3</sup>, M. Pastell<sup>1</sup>, T. Norton<sup>2</sup>**<sup>1</sup> Natural Resources Institute Finland, Latokartanonkaari 9, 00790 Helsinki, Finland, <sup>2</sup> KU Leuven, Biosystems 1, Kasteelpark Arenberg 30, B-3001 Leuven, Belgium, <sup>3</sup> University of Helsinki, PL 68, Pietari Kalmin katu 5, 00014 Helsinki, Finland*

Visual tracking of individual animals is a key problem in precision livestock farming, supporting the measurement of behaviour, activity and welfare at scale. Despite rapid progress in multi-object tracking (MOT) methods, progress in livestock applications is limited by the lack of standardized, domain-specific benchmark datasets that allow fair and reproducible comparison of algorithms. This work presents an ongoing effort to develop a benchmark for livestock visual tracking. The benchmark is constructed by curating and harmonizing existing livestock video datasets into an openly available resource for MOT. A central contribution is the use of oriented bounding boxes (OBB), which more accurately represent animal pose than conventional axis-aligned boxes, particularly in dense housing conditions and under frequent rotations. In addition, the benchmark jointly covers two major livestock species, dairy cattle and pigs, enabling cross-species evaluation of tracking performance within a single framework. We describe the data acquisition conditions and a harmonized annotation protocol across both species. Statistical summaries characterize scene types, animal densities, sequence lengths, and annotation properties. To establish reference performance, well-known baseline tracking models, including Simple Online and Real-time Tracking (SORT), as well as OBB-specific tracking approaches, are evaluated using standard MOT metrics, highlighting current strengths and limitations when applied to livestock data with oriented annotations. The main outcomes of this work are (1) an open benchmark dataset for visual tracking of dairy cows and pigs, (2) a harmonized OBB annotation protocol across species, and (3) baseline tracking results on oriented bounding boxes. The dataset and associated resources will be released openly via Zenodo. By lowering the barrier for computer vision researchers to work on livestock tracking problems, this benchmark aims to stimulate methodological advances beyond individual projects and accelerate the development of robust computer vision tools for precision farming applications.

**Bridging Animal Science and Human Nutrition through INSIGHT: A Retrieved-Augmented Agentic Model**

R. Strong<sup>1</sup>, L. Tedeschi<sup>1</sup>, K. Kaniyamattam<sup>1</sup>, J. Tao<sup>1</sup>, D. Mudireddy<sup>1</sup>, P. Surabhi<sup>1</sup>, N. Greer<sup>1</sup>, A. Wang<sup>1</sup>

<sup>1</sup> Texas A&M University, 2116 TAMU, 77843-2116 College Station, United States

Animal production research has generated vast knowledge about how feed, environment, genetics, and management influence animal-source food quality. Yet translating these findings into human-nutrition guidance remains slow and fragmented, costing billions annually. We present INSIGHT (Intelligent System for Integrating Global Human & Animal Health Technology), a multi-stage Retrieval Augmented Generation (RAG) system that synthesizes animal science and human nutrition literature to deliver evidence-grounded recommendations. INSIGHT integrates domain-specific corpora, controlled vocabularies (e.g., AGROVOC) for entity normalization, and human-in-the-loop gates to maintain provenance and reduce hallucinations. The system employs a multi-stage pipeline: query expansion, hybrid retrieval (dense embeddings + BM25), Reciprocal Rank Fusion, cross-encoder reranking, and LLM-as-a-Judge verification. Experimental deployment demonstrates that INSIGHT shortens literature-to-practice cycles, facilitates cross-disciplinary grant development, and reveals actionable links between production practices and nutrient outcomes. This represents the first AI-powered knowledge integration system bridging animal science and human nutrition research domains. INSIGHT provides real-time, contextually relevant insights that bridge disciplinary silos between animal science and human nutrition research. The system's implementation aims to accelerate the translation of literature to practice, strengthen cross-disciplinary proposal competitiveness, and support evidence-based recommendations where production methods directly impact human nutritional outcomes. Through this integrated approach, INSIGHT enables enhanced cross-disciplinary collaboration, accelerated innovation cycles, and improved nutritional and economic outcomes of animal production systems as agricultural research continues to generate vast quantities of specialized knowledge. Tools like INSIGHT become essential for ensuring that this scientific investment translates into meaningful improvements in food system sustainability and human health outcomes.

## Session 6

## Theatre 4

**Using AI to find veterinary data sources in Europe**

R. Petie<sup>1</sup>, V. Bianchi<sup>1</sup>, E. Pacholewicz<sup>1</sup>

<sup>1</sup> Wageningen Bioveterinary Research, Houtribweg 39, 8221 RA Lelystad, Netherlands

Distributed over countries and institutes in Europe there are many veterinary relevant data sources, hosted by national governments, universities, research institutes, environmental agencies, veterinarians, insurance companies and more. Our goal was to systematically locate at least ten such data sources per country across all European Economic Area (EEA) member states (all EU countries plus Norway, Iceland and Liechtenstein), using AI-assisted methods. Here we present the methods we used to locate these data sources with the help of AI and, maybe more importantly, the limitations and pitfalls of using AI in this context. We will share the steps in our workflow including the structure of the prompts used. We used Google's Gemini AI and developed a three-step prompting pipeline in R, taking advantage of the gemini.R package: 1) identifying potential holders of veterinary data per EEA country, 2) searching for specific data sources held by those data holders, and 3) conducting a broad search not limited by institute, to capture sources not identified in step two. In addition to this fully automated pipeline, we developed a dedicated prompt for use in Gemini's web interface to verify and enrich results with reliable URLs. The automated R pipeline was able to quickly locate the names and countries of potential data holders. However, adding reliable URLs for the data sources required an additional web-interface step, making a human-in-the-loop approach essential for accuracy. Despite this, the overall process was considerably faster than manual searching using traditional search engines operations. This led us to the identification of a total 388 new sources, reaching our goal of ten sources per country for all EEA countries.

**FacEDiM++: A Probabilistic Evaluation Framework for Few-Shot Cross-Species Face Verification**

*D. Lukamba Nsadasa<sup>1</sup>, S. Mwasimuke Tsongo<sup>2</sup>, B. Twite Ndeze<sup>2</sup>, R. Vaishampayan<sup>1</sup>, M. C. Oveneke<sup>1,2</sup>, J. Ambuki-yenyi Onya<sup>1,2</sup>*

*<sup>1</sup> NEOTEX BELGIUM, Artificial Intelligence Research Lab, Boulevard Lambert 129, B-1030 Brussels, Belgium, <sup>2</sup> NEOTEX RDC, Artificial Intelligence Research Lab, 5573, avenue Kauka, Q. Batetela, C. Gombe, CO-01204 Kinshasa, Congo, Democratic Republic of the*

Reliable biometric face verification is increasingly important in precision livestock farming, supporting automated identification for health monitoring, traceability, and individualized management. A major challenge is data scarcity for both training and evaluation, as only limited images are typically available per animal. Under such few-shot conditions, conventional deterministic similarity thresholds provide unstable performance estimates and limited insight into verification reliability. We propose FacEDiM++, a probabilistic evaluation framework for few-shot animal face verification. A fixed deep backbone network is used to extract embeddings, and each identity is modeled as a probability distribution in embedding space using sampling-by-augmentation. Verification is formulated through information-geometric distance measures between identity distributions, enabling principled estimation of false rejection and false acceptance rates under limited data. We evaluate the framework on approximately 3,000 cattle and 1,500 goats, with 5 to 10 real images collected per identity, gathered from online sources and field acquisitions in Kenya, the Democratic Republic of the Congo, and India. Sampling-by-augmentation is applied up to 20-fold per image to estimate embedding distributions. For cattle, FacEDiM++ attains a false rejection rate of 4.8% at a false acceptance rate of 1%, while for goats it reaches a false rejection rate of 3% at a false acceptance rate of 1%, demonstrating reliable verification despite severe data constraints and heterogeneous acquisition conditions. FacEDiM++ provides a generic, distribution-aware quality assurance layer for animal biometric systems in data-constrained scenarios, with future work extending to additional species.

**Drone-Based AI System for Automated Sheep Counting Using Detection and Tracking Models**

*L. Helary<sup>1</sup>, A. Lebreton<sup>1</sup>, A. Lauront<sup>1</sup>, E. Nicolas<sup>1</sup>, T. Dechaux<sup>1</sup>*

*<sup>1</sup> Institut de l'Élevage, 149 rue de Bercy, 75012 Paris, France*

Accurate sheep counting remains a challenging and labor-intensive task in livestock management, often relying on manual techniques that are time-consuming and error-prone. Artificial intelligence (AI), particularly deep learning-based object detection, offers a promising solution by enabling automated detection and counting of animals. However, in the agronomical domain, the development of robust detection models is frequently hindered by the scarcity of diverse, high-quality, and publicly available annotated datasets. In the context of precision livestock farming (PLF), standardized benchmarks are essential to evaluate detection and tracking models under real-world field conditions. Within the ICAERUS project, we developed and released a series of open datasets dedicated to aerial livestock monitoring using drone imagery. These datasets include 5696 images and 50 videos of sheep, goats, and bovines acquired in real farm environments under diverse conditions (variations in breed, background, lighting, weather, and animal density). Among them, 1903 images were annotated for object detection and 8 videos were annotated for multi-object tracking evaluation. Using these datasets, we established benchmarking experiments for sheep detection and counting from drone footage. A YOLOv8n model was first trained on a generic dataset and then fine-tuned on our annotated data to assess the impact of domain-specific diversity. The fine-tuned model achieved a precision of 0.97, recall of 0.97, and mAP<sub>50-95</sub> of 0.97. Tracking-based counting experiments on unseen videos further enabled evaluation of full-pipeline robustness under practical field conditions. All datasets (annotated and raw), trained models, and evaluation pipelines are publicly available on Zenodo and GitHub. By providing standardized data and baseline performance metrics, this work contributes to new open benchmarks for AI-based livestock monitoring and supports reproducible research in animal science. It also permits to provide a validated proof of concept for drone-based automated livestock counting and lays the foundation for scalable decision-support tools for farmers.

### Image-derived digital similarity matrices as a scalable proxy for pedigree and genomic relationship matrices

M. Billah<sup>1</sup>, M. Bermann<sup>1</sup>, C. Y. Chen<sup>2</sup>, B. Valente<sup>2</sup>, E. Psota<sup>2</sup>, J. Holl<sup>2</sup>, S. M. Bhandarkar<sup>3</sup>, I. Misztal<sup>1</sup>, D. Lourenco<sup>1</sup>

<sup>1</sup> University of Georgia, Department of Animal and Dairy Science, 425 River Rd, 30602 Athens, United States,

<sup>2</sup> Genus PIC, 100 Bluegrass Commons Blvd, 37075 Hendersonville, United States, <sup>3</sup> University of Georgia, School of Computing, Boyd Graduate Studies Research Center, 30602 Athens, United States

Digital images capture a vast array of phenotypic information capable of explaining variation in economically important traits within genomic evaluation frameworks. In this study, we present a deep learning framework to extract latent features from images of pigs for downstream analyses, including attribute-specific characterization, trait disentanglement, and the construction of digital similarity matrices. Our methodology begins by segmenting images to isolate the body, followed by the extraction of high-dimensional latent features using a custom  $\beta$ -Variational Autoencoder ( $\beta$ -VAE) alongside four Vision Transformer (ViT) variants, ViT-B and ViT-L with 16 and 32 patch sizes, pretrained on ImageNet. We calculated attribute-specific vectors for contemporary groups, birth year-month, farm, sex, and litter to assess systematic variation within the latent space. Feature disentanglement was evaluated by comparing latent representations against body weight, loin depth, and backfat thickness, followed by the development of three methods for constructing digital similarity matrices. Our results demonstrate that latent embeddings reveal structured covariance across adjacent temporal windows and demographic groups. Moderate to high correlations between latent variables and ground-truth measurements, reaching 0.43 for body weight, 0.42 for loin depth, and 0.32 for backfat thickness, suggest that latent representations capture biologically relevant variation in growth and body composition. Finally, the similarity matrix constructed from ViT embeddings exhibited higher correlations with both genomic ( $r = 0.27$ ) and pedigree-based ( $r = 0.31$ ) relationship matrices compared with  $\beta$ -VAE embeddings. These findings establish a robust foundation for integrating deep learning-derived latent representations into mixed-model frameworks, offering a scalable approach to refine the partitioning of genetic and environmental variances through high-dimensional phenomics.

### Session 7

### Theatre 2

#### Thermal Signatures as Biomarkers of Podal Inflammation in Cattle and Ovine

L. Helary<sup>1</sup>, Y. Do<sup>1</sup>, J. Manceau<sup>2</sup>, V. Gauthier<sup>2</sup>, M. Doucet<sup>1</sup>, A. Duvauchelle Waché<sup>1</sup>

<sup>1</sup> Institut de l'Élevage, 149 rue de Bercy, 75012 Paris, France, <sup>2</sup> NeoTec Vision,, 9 allée de la Planche Fagline, 35740 Pacé, France

Foot lesions represent major welfare and economic challenges in bovine and ovine production systems as they can lead to productivity losses, chronic pain, and premature culling. Foot lesions can be detected through observation of lameness; however, this clinical sign appears late, and not all lesions result in visible mobility issues. Early identification of foot lesions is therefore essential for effectively preventing and controlling lameness. The Thermopod project aims to investigate the feasibility of developing a non-invasive, AI-driven phenotyping system for early detection of inflammatory foot lesions, if possible before the onset of lameness, using thermal imaging. The proposed approach leverages thermal signatures as digital biomarkers of inflammation to automatically classify foot health status. In the experimental protocol, bovine and ovine animals passed through a restraining chute equipped with eight thermal cameras that captured images of their feet from multiple angles. The sanitary status of the feet was established by a veterinarian in order to generate ground-truth labels. Once all data were collected, the feet were annotated in the images obtained from each camera using Roboflow software. Preliminary results obtained in cattle demonstrate promising deep learning performance, with an accuracy of 84% in distinguishing healthy from inflamed feet using a YOLO11n classification model trained on images from a single camera. This approach contributes to the development of digital biomarkers for precision livestock farming, enabling early detection and management of health issues while reducing handling stress and optimizing labor efficiency. Ongoing work focuses on improving model robustness and training additional classification models.

**Automatic recognition of herbage prehensions in grazing ewes**

S. Bognanno<sup>1</sup>, R. Avanzato<sup>2</sup>, L. Beritelli<sup>3</sup>, F. Beritelli<sup>2</sup>, F. Gimmillaro<sup>1</sup>, M. Avondo<sup>1</sup>

<sup>1</sup> University of Catania, Agriculture, Food and Environment, Via S.Sofia 100, 95123 Catania, Italy, <sup>2</sup> University of Catania, Electrical, Electronic and Computer Engineering, Via S.Sofia 64, 95123 Catania, Italy, <sup>3</sup> University of Catania, Mathematics and Computer Science, Viale Andrea Doria 6, 95125 Catania, Italy

Detection of the number of herbage prehensions represents the key element for calculating total herbage intake in grazing ruminants. The reference is to the well-known definition of intake which arises from the product eating time x bite rate x bite mass. The study presents a deep learning-based approach for the automatic recognition of prehension in ewes using audio signals. Mono audio files, sampled at 16 kHz, were transformed into spectrograms and segmented into 500 ms time windows, which were subsequently labeled into two classes: prehension and non-prehension. A YOLOv11n model in classification configuration was trained on these time-frequency representations. The dataset shows a slightly unbalanced distribution between classes, which is reflected in the metrics obtained on the test set: the overall accuracy reached approximately 0.83 with a macro F1-score of ~0.69. Performance highlights a strong discriminative ability for the non-prehension class (precision ≈ 0.97, recall ≈ 0.84), while the prehension class shows a high recall (≈ 0.75) but a lower precision (≈ 0.36), suggesting the presence of false positives. The same study on cattle (data not published) yielded better results. This is because the ingestion behavior of sheep, which is very different from that of cattle, is difficult to recognize due to their tendency to penetrating vegetation in search of their favorite species, thus producing very loud noises that can interfere with the recognition of prehension sounds. Nonetheless, global metrics showed higher micro and weighted accuracy values (≈ 0.83 and ≈ 0.90), indicating that the model maintains good overall performance despite the difficulty in recognizing the minority class. The results demonstrate the potential of spectrogram-based audio analysis and lightweight architectures for automatic behavioral monitoring in precision livestock farming, while also highlighting potential directions for improvement in the trade-off between sensitivity and accuracy of grasping events.

## Session 7

## Theatre 4

**Artificial intelligence-driven plasma metabolomics identifies metabolic signatures of feed efficiency in beef cattle**

A. Nunes<sup>1</sup>, C. Faleiros<sup>1</sup>, M. Poleti<sup>1</sup>, Y. López-Hernández<sup>2</sup>, D. Wishart<sup>2</sup>, H. Fukumasu<sup>1</sup>

<sup>1</sup> University of São Paulo, Department of Veterinary Medicine, Duque de Caxias St, 225, 13635-900 Pirassununga, Brazil, <sup>2</sup> University of Alberta, Departments of Biological Sciences and Computing Science, 11011 - 88 Avenue, T6G 2P5 Edmonton, Canada

Feed efficiency is a complex and economically important trait in beef cattle that is commonly evaluated using residual feed intake (RFI). As RFI is polygenic and strongly influenced by the environment, identifying reproducible metabolic biomarkers remains difficult. We applied artificial intelligence (AI) methods to targeted plasma metabolomics to characterize the metabolic signatures associated with feed efficiency. Phenotypic data and plasma samples were available for 360 animals. RFI was estimated within contemporary groups using linear models with dry matter intake as the response and metabolic body weight and average daily gain as predictors. The animals were ranked according to RFI, and individuals from the upper and lower quartiles were selected for metabolomic profiling. Metabolomic analyses were performed using liquid chromatography–tandem mass spectrometry and flow-injection analysis–tandem mass spectrometry. Supervised models (Random Forest, elastic net logistic regression, PCA–SVM, and XGBoost) were trained using repeated cross-validation on a balanced dataset (n = 164), and their performance was evaluated on an independent stratified hold-out test set. XGBoost yielded the best classification performance, and a cross-model consensus analysis identified recurrent predictors separating the groups: TG (16:1/32:0) and citric acid were higher in low-RFI group, and valine and phosphatidylcholines (PC aa C42:0/C42:6) were higher in high-RFI group. This pattern supports divergent nutrient partitioning, with low-RFI profiles reflecting a tighter coupling of central carbon metabolism to energy supply and lipid handling, whereas high-RFI animals display signatures of increased amino acid turnover and altered lipid remodeling, aligning with reduced feed efficiency. Overall, AI-guided targeted metabolomics revealed a coherent metabolic signature of feed efficiency in beef cattle, although the separation between groups was modest and warrants external validation.

### **Non-invasive eye temperature monitoring in dairy calves using computer vision and infrared technology**

*J. A. Vazquez Diosdado<sup>1</sup>, F. Occhiuto<sup>1</sup>, M. Thomas<sup>1</sup>, J. Kaler<sup>1</sup>*

*<sup>1</sup> University of Nottingham, School of Veterinary Medicine and Science, School of Veterinary Medicine and Science, Sutton Bonington Campus, LE125RD Sutton Bonington, United Kingdom*

Animal health and welfare are crucial elements of livestock production and sustainability. Infrared technology represents a unique non-invasive monitoring tool capable of retrieving eye temperature, which is considered to be an accurate representation of core body temperature, and therefore could be used for temperature monitoring in dairy calves. The development of a fully integrated architecture solution (hardware/software) with pretrained algorithms would provide the opportunity to continuously monitor the eye temperature of dairy calves in real time and assessing temperature changes in response to disease or stress. Such monitoring tool could easily be adapted for other species (farm and zoo animals) and provide automated non-invasive monitoring of their health and welfare. However, real long-term monitoring requires automated image processing over regions of interest (e.g. eyes) to generate reliable measure core temperatures. This observational study used IR images from 2 fixed thermal cameras (FLIR A65) located behind the automatic milk feeder, with a total of 3000 labelled IR images, from 32 heifer pre-weaned heifer calves. To identify the temperature of the eye of each calf in the images, two algorithms were used: the first to classify whether the image contained one or both of the eyes, and the second to locate the eye within the image. The algorithms were trained using deep learning techniques. The performance of the image classification algorithm to determine if there were no eyes, right eye, left eye or both eyes present in the image resulted in average sensitivity of 95.73%, precision of 97.2%, and F-score of 95.75%. Similarly, the eye location algorithm resulted in a high performance with an average sensitivity of 83.74%, precision of 100% and F-score of 84.71%. These results demonstrate the potential to automatically monitor eye temperature in calves with a high level of sensitivity and precision using fixed and handheld thermal cameras.

### **Evaluating standing and lying behaviors measured with collar-mounted accelerometers for lameness detection in dairy cows**

*J. Allyndrée<sup>1,2</sup>, C. Harrouet<sup>1</sup>, A. Cornuéjols<sup>2</sup>, C. Martin<sup>2</sup>, A. Madouasse<sup>1</sup>*

*<sup>1</sup> Oniris, INRAE, BIOEPAR, 101 Rte de Gachet, 44300 Nantes, France, <sup>2</sup> Université Paris-Saclay, INRAE, AgroParisTech, UMR MIA-PS, 22 place de l'Agronomie, 91120 Palaiseau, France*

Lameness affects 20% to 30% of dairy cows worldwide and is a major welfare and economic concern. Most commonly caused by foot lesions, it is painful from its early stages and can worsen over time, leading to chronic pain, reduced milk production, increased veterinary costs, and eventual culling. Early detection is therefore essential to limit its impact and improve animal welfare. However traditional detection methods such as visual locomotion scoring, require extensive training, are time-consuming, and difficult to implement in large herds. As a result, many cases remain undetected until the condition becomes severe. Therefore, there is a growing interest in developing automated and objective methods for lameness detection. While many studies have focused on identifying changes in behavior between healthy and lame cows, few have investigated the potential of using specific behaviors to predict lameness status. Various methods are being explored and using wearable sensors and Artificial Intelligence (AI) seems promising and scalable. In this work, we investigate a method to detect lameness based on the analysis of standing-up (SU) and lying-down (LD) behaviors using collar-mounted 3D-accelerometers. We collected data from 3 different commercial farms, equipping 126 cows with collars and manually recording their SU and LD behaviors over a two months period. Lameness scores were also recorded weekly by trained observers, leading to three scores for each cow. We then trained a Bi-LSTM model and a MiniRocket with XGBoost model to predict lameness scores based on the accelerometer data of the annotated behaviors. Using cow-level stratified evaluation to ensure strict separation between training and test animals, our best model (XGBoost) predicted lameness with an accuracy of 65% and an F1-score of 61%. While SU and LD behaviors showed clear visual differences in their expressions, they were not sufficiently predictive when measured using neck-mounted accelerometers, likely due to their limited ability to capture detailed leg movements.

**Zero-shot computer vision analysis of social behaviour in group-housed sows**N. Ipek<sup>1</sup>, J. Verwaeren<sup>1</sup>, B. De Baets<sup>1</sup>, F. A. M. Tuytens<sup>2,3</sup><sup>1</sup> Ghent University, Department of Data Analysis and Mathematical Modelling, Coupure links 653, 9000Ghent, Belgium, <sup>2</sup> ILVO, Animal Sciences Unit, Burgemeester Van Gansberghelaan 119, 9090 Ghent, Belgium,<sup>3</sup> Ghent University, Department of Veterinary and Biosciences, Salisburylaan 133, 9820 Ghent, Belgium

In most European production systems, sows are individually housed during farrowing and insemination before being regrouped into pens at the start of gestation. This regrouping of partly unfamiliar animals often provokes social instability, heightened aggression, and stress, posing welfare and productivity challenges. Among potential mitigation strategies, Pig Appeasing Pheromone (PAP) provides an ethologically grounded approach to reducing conflict during hierarchy formation. Evaluating such mitigation strategies relies on behavioural observations, yet traditional manual observation is often criticized as labour-intensive and subjective. While video-based observation is increasingly adopted to improve scalability and consistency, large-scale and longitudinal welfare assessment remains limited by the need for extensive annotation and by unreliable tracking in complex, multi-camera pen environments. In this study, we present a zero-shot self-supervised learning pipeline that can detect and segment animals without any annotations. The approach is species- and system-agnostic, enabling large-scale behavioural monitoring. When integrated with a multi-camera tracking algorithm, it supports automatic modelling of both individual-level and pairwise behaviours at fine temporal and spatial resolution. We evaluate the pipeline on over 800 hours of continuous video from moderately large groups (16–20) of gestating sows, assigned to pheromone or placebo treatment in a double-blind experiment. The proposed approach achieves robust multi-camera individual tracking, reaching 96.63% tracking accuracy. We further introduce a model-agnostic processing optimization that reduces computational requirements by 90.7% while preserving fine-scale behavioural information. Finally, a rule-based pairwise agonistic interaction detector, based on individual tracks, is used to automatically annotate fighting, fleeing, and displacement, achieving precisions of 0.82, 0.73, and 0.77, respectively.

## Session 7

## Theatre 8

**AI-Driven Temporal Behavioral Pattern Mining for Digital Health Monitoring in Livestock**T. Terrill<sup>1</sup>, A. Siddique<sup>1</sup>, S. Panda<sup>2</sup>, A. Mahapatra<sup>1</sup>, E. Morgan<sup>3</sup>, J. Van Wyk<sup>4</sup><sup>1</sup> Fort Valley State University, Department of Agricultural Sciences, 1005 State University Drive, 31030 FortValley, United States, <sup>2</sup> University of North Georgia, Institute for Environmental Spatial Analysis, 3820 MundyMill Road, 30566 Oakwood, United States, <sup>3</sup> Queen's University Belfast, Institute for Global Food Security,University Road, BT7 1NN Belfast, United Kingdom, <sup>4</sup> University of Pretoria, Faculty of Veterinary Science,

Private Bag x04, 0110 Onderstepoort, South Africa

Early detection of illness in small ruminants remains a major challenge in resource-limited production systems. This study advances a digital phenotyping framework using RFID-derived motion signals integrated with machine learning to classify health status based on behavior-derived digital biomarkers. Continuous RFID transponder data were collected from goats over two years, generating  $\sim 800 \times 7$  activity matrices per day, with signal intensities ranging from 0–255. After preprocessing, temporal and frequency-based behavioral features were extracted to characterize activity rhythms and circadian structure. Healthy animals exhibited stable digital behavior defined by 2–4 daytime activity peaks and consolidated nocturnal rest. In contrast, abnormal profiles demonstrated elevated nocturnal motion, fragmented rest cycles, and reduced grazing-associated daytime peaks, indicating disruption of circadian locomotor organization. These activity-derived features serve as candidate behavioral digital biomarkers of compromised health. Supervised learning models were developed to classify normal versus abnormal patterns. Random Forest achieved 76% accuracy, while K-Nearest Neighbors achieved 82%, demonstrating strong discriminative capability for identifying health-related motion anomalies. These findings establish RFID motion signal mining as a scalable digital phenotyping approach for livestock health surveillance. The integration of explainable machine learning with continuous behavioral monitoring provides an objective, low-cost diagnostic layer for precision herd management. This AI-enabled behavioral biomarker framework supports early disease detection, reduces productivity losses, and enhances resilience in climate-sensitive, resource-constrained livestock systems.

### Validation of computer vision for automated detection of pig movement during Open Field and Novel Object tests

T. Ede<sup>1</sup>, M. Parada Sarmiento<sup>1</sup>, L. Sabei<sup>1</sup>, T. Parsons<sup>1</sup>

<sup>1</sup> University of Pennsylvania, Swine Teaching and Research Center, 505 Byrd Road, 19348 Kennett Square, United States

Behavioral differences among individual animals are recognized as a significant contributor to research outcomes and as a driver of the study of behavioral phenotypes, often called temperament or personality. Behavioral tests such as the Open Field (OF) and Novel Object (NO) are common but require time-consuming manual coding of video recordings. Recent advances in computer vision have enabled automated animal tracking by detecting specific body parts. However, this approach has not been applied to OF/NO tests in pigs. Our objective was to investigate the use of computer vision to automate the extraction of pig movement data during OF/NO tests and compare it with manually coded data using common approaches for the study of behavioral phenotypes. Twenty-six commercial gilts underwent an OF for 5 min and following the introduction of a NO (yellow traffic cone) test for 5 min. Pig movement was recorded from a ceiling-mounted Sony HDR-AS30V. Moving, staying still, latency to touch NO, and contact with NO were manually coded from the recordings. A computer vision model was trained from the same recordings using SLEAP to detect gilts' head, shoulder, midsection, and hind. A total of 362 frames were labelled to achieve a model with 98.7% visibility precision, 100% visibility recall, and an average distance of ~6 cm between the ground truth and the prediction. Correlations between automated and manually identified behavioral measures were strong (0.66 to 0.93). PCAs based on either manually or automatically extracted behaviors yielded similar results. Two strong principal components (PC), reflecting Activity and NO Interest, accounted for 82-84% of the data's variation. Gilts' z-scores for either PC were highly correlated between both data sets (Activity:  $r = 0.92$ , NO Interest:  $r = 0.79$ ). These findings support the use of computer vision to reliably quantify pig movement during an OF/NO test and enable the automation of detailed behavioral analysis. This work promises to accelerate the study of behavioral phenotypes and is likely applicable to other species.

### 2D to 3D Pose modeling: A scalable framework for individualized detection of tail-biting interactions in group-housed pigs

K. Ivanov<sup>1</sup>, V. Bonfatti<sup>1</sup>, C. Kasper<sup>2</sup>, H. R. Nasser<sup>3</sup>

<sup>1</sup> University of Padova, Department of Comparative Biomedicine and Food Science, Viale dell'Università 16, 35020 Legnaro, Italy, <sup>2</sup> Agroscope, Animal GenoPhenomics, Rte de la Tiolleyre 4 Rte de la Tiolleyre 4, 1725 Posieux, Switzerland, <sup>3</sup> Agroscope, Digital Production, Rte de la Tiolleyre 4, 1725 Posieux, Switzerland

Accurate identification of harmful social interactions in group-housed pigs remains a major technical challenge due to occlusions, body overlap, and dynamic group behavior. In our research we propose a computational framework that extends conventional 2D multi-animal pose estimation toward structured flat-3D modeling to improve spatial interpretability and interaction analysis in dense pen environments. The pipeline consists of multi-animal detection and ID-aware tracking to maintain consistent pose-to-individual association across frames, even under occlusions and crossing events. 2D keypoint estimation extracts anatomically relevant landmarks, including snout and tail base positions, enabling detailed spatial relationship modeling. Instead of relying only on planar Euclidean distances, we introduce a flat-3D projection layer that embeds normalized 2D joint configurations into a pseudo-3D coordinate space. This reduces ambiguity caused by perspective compression and depth overlap in top-view recordings. Interaction logic is defined through spatial and temporal constraints applied in the reconstructed space. Snout-tail proximity, directional alignment, and persistence across consecutive frames are jointly modeled to detect behavioral anomalies and distinguish directed contacts from incidental proximity under high animal density. Pose outputs are stored as structured frame-wise keypoint tensors in .npz format, preserving coordinates, confidence scores, and track identifiers. Detections are reorganized into continuous individual trajectories with confidence-based filtering and interpolation of missing joints. Interaction analysis is then performed directly on reconstructed joint trajectories using vector-based computation of orientation and relative positioning. The proposed framework demonstrates how structured flat-3D modeling enhances robustness, interpretability, and interaction specificity in group-housed pigs.

### **Vision-based detection of pain and nest-building behaviors in sows within commercial farrowing pens**

P. Helf<sup>1</sup>, M. Oczak<sup>1</sup>

<sup>1</sup> *University of Veterinary Medicine Vienna, Precision Livestock Farming Hub, Clinical Department for Farm Animals and Food System Transformation, Veterinärplatz 1, 1210 Vienna, Austria*

Pain indicators and pre-parturient nest-building are precursors to the onset of farrowing, yet continuous quantification in commercial farrowing pens remains challenging. We developed a non-invasive computer vision approach to automatically detect pain-associated behaviors i.e. back-arching, tail-flicking, pulling the back leg forward, trembling and nest-building behaviors i.e. manipulation of pen fixtures/walls, pawing, exploration from top-view pen videos. RGB footage totaling 748 hours from 11 sows at 25 fps on a single farm was used. Recordings spanned 64 hours before farrowing until 4 hours after the first piglet was born. A total of 46,010 behavior events were annotated using a defined ethogram with inter-annotator agreement Cohen's  $\kappa=0.724$ . To assess generalization, data was split at the sow level i.e. 8 in the training set and 3 in validation. Behaviors were detected using a modified DeepEthogram pipeline. This approach combines RGB with optical flow. Both streams were processed by separate ResNet3D-34 encoders. Optical flow was estimated using a state-of-the-art DPFlow model. Training employed focal loss to address class imbalance, alongside geometric and photometric augmentations for robustness to camera placement and lighting. Videos were downsampled to 8 fps and video clips of 11 frames ( $\approx 1.375$  s) were used for the detection of behaviors. Preliminary results on the validation sows showed reliable detection of nest-building behaviors with F1=0.872 for manipulation, 0.722 for pawing and 0.777 for exploration. Pain behaviors achieved F1=0.624 for back-arching, 0.733 for tail-flicking, 0.791 for back leg forward, and 0.584 for trembling. These results indicate that pen-installed vision systems can identify key behaviors in a non-invasive way, supporting scalable monitoring by stockpersons and researchers. Limitations include modest dataset size and limited diversity i.e. single farm and single breed, which may constrain generalizability. Ongoing work will expand the dataset and explore how behavior dynamics can support time-to-farrowing estimation.

### Session 8

### Theatre 1

#### **Support for whom? – Proposing an alternative approach to digital technologies in animal science**

M. F. Giersberg<sup>1</sup>, F. L. B. Meijboom<sup>1</sup>

<sup>1</sup> *Utrecht University, Faculty of Veterinary Medicine, Yalelaan 2, 3584 CM Utrecht, Netherlands*

Artificial Intelligence (AI)-based and other digital technologies in animal science are often framed as 'supporting tools'. Previous research shows that this view seems to be consistent across groups of professionals and individuals, such as farmers, animal caretakers, advisors, veterinarians, and scientists. In this context, 'supportive' means that the technologies are seen as something 'additional' to the regular work of professionals. They either provide information that would otherwise be inaccessible to human observations or take over routine tasks, which gives professionals more time for animal care. This framing emphasizes the positive aspects of digital technologies for humans and animals, and probably addresses an underlying concern of professionals being replaced by technology. However, the development of advanced technologies, that for instance detect animal behavior more accurately and reliably than human observers, raises the question of how far framing as a 'supporting tool' is still a) empirically correct and b) beneficial for professionals working with these technologies. Framing a tool as 'supportive' when in fact one has become dependent on it can turn into a vulnerability that may lead to professional identity confusion, which has been associated with decreased job satisfaction and low professional wellbeing. In our presentation we will address this issue by proposing an alternative approach to digital technologies in animal science. First, we will argue how a different framing of digital technologies as non-human team members with whom one can and has to negotiate expertise boundaries and responsibilities may decrease the risks of dependency and vulnerability. Second, we will show how certain kinds of digital technologies, such as explainable and interactional AI, can enable this alternative approach. A realistic perspective on technologies is needed in order to use them responsibly for humans and animals.

**Using AI to optimise animal welfare:opportunities and ethical challenges**M. Campbell<sup>1</sup><sup>1</sup> *Animal Welfare Committee, Seacole Building, 2 Marsham Street, SW10 4DF London, United Kingdom*

Whilst the use of AI in veterinary medicine has been an actively-developing field, use of AI to optimise animal welfare (as distinct from health) is relatively nascent. Human ability to improve animal welfare is limited by our understanding of animals' physical and psychological welfare needs, our ability to meet them, and our recognition of behavioural indicators of animal emotions. The use of Artificial intelligence (AI) to analyse animal-derived data offers real opportunities to rapidly increase our understanding of animals' lived welfare experiences, and stimulate targeted human interventions. AI might also be used as a tool to reconcile the potential and complex conflicts between animal welfare and environmental/ sustainability objectives. Such opportunities are an apparent part of the current and upcoming work of the UK's Animal Welfare Committee (AWC). However, there are ethical challenges associated with the use of AI in animal welfare. This abstract outlines current uses, considers beneficial future applications, and describes associated ethical issues. Suggestions are made for future developments to support the effective and responsible use of AI in animal welfare, drawing on the Animal Welfare Committee's longstanding work on concepts such as enabling animals to have "lives worth living" and, ideally, "good lives". There is a particular need to focus on indicators of affective welfare states over and above health states. AI should be trained to recognise behavioural indicators of positive as well as negative states. Such training is currently limited by relatively underdeveloped human understanding of such positive indicators, particularly in aquatic, avian and invertebrate species. The potential of AI to improve animal welfare in such species, however, is huge.

**Modelling Fish Welfare Law using Artificial Intelligence**L. Northwood<sup>1</sup><sup>1</sup> *University of Edinburgh, Royal (Dick) Veterinary School, Easter Bush Campus,, EH25 9RG Midlothian, United Kingdom*

Modelling Fish Welfare Law using Artificial Intelligence There is a vast application for fish welfare legislation. Fish are subjected to human use at levels exceeding those of any other vertebrate group. In these fields, they are often not measured as individuals, but as biomass. They are also significant in the greater plan for humanity. The United Nations Sustainable Development Goals (SDGs) include Life Below Water (SDG14), Food Security (SDG2), Sustainable Consumption and Production (SDG12), and Global Partnership for Sustainable Development (SDG17). These plans have been severely affected by rising temperatures, associated increases in sea lice and disease, reduced oxygen levels in water, and decreased immunity. Human activity is heavily regulated, yet little attention is paid to animal welfare and, in particular, to the welfare of fish. However, a growing scientific understanding of fish's sentience raises our ethical obligations to minimise their suffering. These obligations have arisen amid a steep increase in the global importance of fish as a food source, an alarming rise in climate-related mass-mortality events (MMEs), an associated explosion in antibiotic use, and corresponding concerns about antimicrobial resistance (AMR). There is a clear imperative to pursue holistic, evidence-based fish welfare regulation. However, having humans do this work would be enormously complicated and time-consuming. In contrast, the nature of this task is an ideal match for the strengths of AI-supported legislative drafting, which emphasises its capacity to process data, benchmark, identify gaps, and simplify complex information within a consistent feedback loop. This presentation will consider the benefits and concerns associated with AI use in regulatory settings, i.e., data security, bias, transparency, and explainability. It would also consider what contributes to effective regulation, including clear frameworks, opportunities for comparison, and the ability to measure outcomes, as well as the challenges posed by regulations created by jurisdictions, socioeconomic conditions, and enforcement capacity.

### **Ethical and practical trade-offs in AI- and sensor-based disease detection in dairy cattle**

*J. Roelofs<sup>1</sup>, A. Van Knegsel<sup>1</sup>*

*<sup>1</sup> Wageningen University & Research, Adaptation Physiology Group, De Elst 1, 6708 WD Wageningen, Netherlands*

Since the development of precision livestock farming in the 1990s, sensor technologies and artificial intelligence have advanced rapidly. Nowadays, AI- and sensor-based systems can continuously monitor behaviour and detect deviations from normal patterns, generating early warnings for individual cows. While these systems have the potential to improve health through earlier interventions, their performance characteristics also bring practical and ethical trade-offs. This study reviews literature on system performance in disease detection and develops a conceptual framework linking performance to animal welfare and farmer decision-making. System performance can be evaluated using metrics such as sensitivity, specificity, precision, and the occurrence of false alerts and missed cases. The values of these metrics are not fixed but depend on how alert thresholds are defined. Different thresholds yield different outcomes. For example, increasing sensitivity often results in more false alerts and lower specificity. Animal welfare can be influenced by system performance. False alerts can lead to unnecessary handling or treatment. Missed cases may delay timely intervention and prolong or worsen health problems. Correct alerts might trigger too early intervention: not all early warnings for disease require immediate treatment but may resolve without intervention. Moreover, biological and behavioural variation between animals can complicate the interpretation of alerts. Performance characteristics also influence on-farm use and farmer decision-making. Alert frequency, perceived reliability, and interpretability affect trust in alerts and influence management responses. Excessive or inconsistent alerts can lead to a reluctance to respond. Furthermore, automated decision support may change observation routines and human-animal interactions. Evaluating these systems for practical use requires examining human–technology interaction. Taken together, these considerations indicate that AI- and sensor-based systems for disease detection cannot be assessed solely on technical accuracy. We propose a conceptual framework that integrates system performance, welfare implications, and farmer decision-making to evaluate such systems in a more holistic manner.

### Session 8

### Theatre 5

### **Virtual herding for real animals: healthy farming craftsmanship in a data-rich environment**

*F. L. B. Meijboom<sup>1</sup>, M. Admiraal<sup>2</sup>*

*<sup>1</sup> Utrecht University, Yalelaan 2, DT Utrecht, Netherlands, <sup>2</sup> Collie, DT, DT Amsterdam, Netherlands*

Behaviour, movement and physiology are increasingly translated into quantitative indicators of welfare. While this promises greater precision, it raises a key question: which aspects of animal welfare can be captured in data, and which forms of knowledge require direct experiential engagement with animals? Insights from animal and environmental science are not easily translated into livestock farming practice. In conventional systems animals cannot always express normal behaviour, for instance due to space restrictions or limited environmental complexity. Virtual fencing and herding technologies can accelerate implementation of such insights by enabling flexible outdoor grazing, protecting habitats, reducing emissions and supporting nature-inclusive farming. Through data technology farmers can manage grazing patterns with more flexibility. The case of Collie illustrates how these developments raise ethical and epistemological questions about the role of data in livestock farming. Collie has developed smart collars that use sound and vibration cues to guide cows, combined with an application that allows farmers to monitor and manage the herd. These systems generate datasets on animal behavior and location, providing insight into herd dynamics. However, the growing availability of behavioral data also raises questions about how such data shape farmers' perception of animals and animal welfare. Data can support decision-making and earlier detection of problems, but quantitative indicators may influence how farmers interpret what they see in their herd, narrowing attention to what can be measured. This raises questions about healthy farming craftsmanship in a data-rich environment. Good animal care relies not only on measurement but also on experience, observation and presence among animals. Some aspects of welfare such as herd social dynamics or subtle behavioural cues—remain difficult to translate into indicators. We analyse ethical dimensions at three levels: (1) animal-related questions about autonomy and welfare impacts of cues; (2) the role of digital monitoring in shaping the human–animal relationship and farming practice; and (3) interpretation and limits of welfare indicators in data-driven livestock systems.

### **A proof-of-concept framework for machine learning to link coccidiosis-related performance losses to changes in the carbon footprint**

J. Gickel<sup>1</sup>, C. Visscher<sup>1,2</sup>

<sup>1</sup> University of Veterinary Medicine Hannover, Science for innovative and sustainable poultry farming, Bünteweg 13, 30559 Hannover, Germany; <sup>2</sup> University of Veterinary Medicine Hannover, Institute for Animal Nutrition, Bischofsholer Damm 15, 30173 Hannover, Germany

Coccidiosis caused by *Eimeria* spp. impairs growth performance and feed efficiency in broiler production and may thereby increase the carbon footprint (CF). However, quantitative links between performance losses and environmental impact remain insufficiently explored. We developed a proof-of-concept machine learning framework to link coccidiosis-related performance changes to relative changes in CF. A structured literature search identified broiler challenge studies comparing experimentally infected and non-infected groups and reporting performance parameters, including average daily gain (ADG) and feed conversion ratio (FCR). Based on these published performance data, CF (kg CO<sub>2</sub>-equivalents per kg body weight gain) was calculated using a life cycle assessment (LCA) approach. For modelling, the extracted data were reorganised so that each analytical unit represented a direct within-study comparison between infected and non-infected groups under identical experimental conditions. Incomplete records were excluded, resulting in 41 independent comparisons from 33 challenge trials. A baseline linear regression and a random forest regression were implemented using an 80:20 training–test split. On independent test data, the linear model achieved moderate predictive performance ( $R^2 \approx 0.57$ ; RMSE  $\approx 13.3$ ), whereas the random forest improved explanatory power ( $R^2 \approx 0.70$ ; RMSE  $\approx 11.7$ ), indicating non-linear relationships between performance losses and CF changes. Variable importance analysis identified percentage changes in FCR and ADG as the dominant predictors of CF variation, whereas oocyst dose, trial duration and broiler genetics had minor influence. As a proof of concept, this study demonstrates the feasibility of applying machine learning to integrate animal health and sustainability metrics. However, the small sample size and heterogeneity of literature-derived data limit generalisability. Broader application requires larger, standardised datasets with harmonised reporting to enable robust validation.

### Session 9

### Poster 1

### **Overcoming Data Silos in Bovine Reproduction: The Minimum Information Model for Bull Fertility Data (MI-BFD) for Data-Driven, Multi-Center AI Applications**

A. Abu Dayeh<sup>1</sup>, E. Kutafina<sup>1</sup>, O. Beyan<sup>1</sup>

<sup>1</sup> University of Cologne, Institute for Biomedical Informatics, Kerpenerstraße 64, 50937 Cologne, Germany

Accurate prediction of bull fertility with machine learning depends on access to large, high-quality, multi-center datasets. Data produced by artificial insemination breeding centres — covering semen assessments, genomic profiles, and field fertility outcomes — are inherently multimodal and frequently trapped in institutional silos. Although broad agricultural ontologies exist, there is no domain-specific standard that captures the fine-grained workflows used in bovine AI (for example, CASA parameter settings, extender formulations, and specific processing protocols). This semantic fragmentation prevents automated integration of records from different centres and limits the utility of advanced computational models. To address this gap, we developed the Minimum Information Model for Bull Fertility Data (MI-BFD). Created through iterative expert consensus across the MSCA BullNet consortium, the MI-BFD defines a seven-stage workflow that links baseline bull phenotypes and laboratory processing metadata to field-level pregnancy outcomes. The model specifies essential variables and provenance metadata to support consistent quality control and cross-centre interoperability. We validated MI-BFD by assessing the compliance of independent datasets contributed by participating AI centres. Mapping legacy variables to the MI-BFD semantic framework revealed common deficiencies and opportunities for unit standardization and contextual metadata enrichment. Preliminary results show that harmonization using MI-BFD reduces semantic conflicts and enables direct comparison of previously incompatible measures, effectively assembling a denser, harmonized dataset from isolated sources. By providing a clear standard for data curation, MI-BFD establishes the input requirements for reproducible machine- and deep-learning studies aimed at improving the accuracy of fertility prediction.

### **SENSTARA: Advancing Sensor-Based Indicators and Modeling of Animal Resilience, Health, and Welfare in Precision Livestock Farming**

D. Foy<sup>1</sup>, J. Gautier<sup>2</sup>, B. Foris<sup>3</sup>, C. Morgan-Davis<sup>4</sup>, L. Dale<sup>5</sup>, P. P. Nielson<sup>6</sup>, G. Franchi<sup>7</sup>, X. Díaz De Otálora<sup>8</sup>

<sup>1</sup> AgriGates, Philadelphia, 19146 Philadelphia, United States, <sup>2</sup> Institut de l'Élevage, Castanet-Tolosan, 31320 Toulouse, France, <sup>3</sup> VetMedUni, Vienna, 1210 Vienna, Austria, <sup>4</sup> SRUC, Edinburgh, EH9 3JG Edinburgh, United Kingdom, <sup>5</sup> LKV Baden-Württemberg, Stuttgart, 70190 Stuttgart, Germany, <sup>6</sup> RISE Research Institutes of Sweden, Göteborg, 412 58 Göteborg, Sweden, <sup>7</sup> Aarhus University, Tjele, 8830 Tjele, Denmark, <sup>8</sup> Universitat Politècnica de València, València, 46022 València, Spain

Livestock production systems are increasingly challenged by on and off-farm factors. In this context, sensor-based technologies and associated metrics, data management, and analytical tools within Precision Livestock Farming (PLF) offer powerful tools to continuously monitor animals at both individual and group levels. However, a major limitation remains the translation of large, heterogeneous sensor datasets into robust, biologically meaningful, and actionable indicators that can be applied consistently across species, production systems, and environmental conditions. SENSTARA (Sensor and Standards Development for Research Activities in Animal Behavior and Biometrics) is an international Working Group within the European Federation of Animal Science (EAAP) PLF Commission that aims to advance sensor-based assessment and analytical tools. The primary objectives of the SENSTARA Working Group are to promote, coordinate, and communicate the development, validation, and harmonization of sensor-derived indicators, metrics, and models to improve methodological standardization across studies, species, and production systems. The scientific and technological scope of SENSTARA encompasses wearable, environmental, and physiological sensors; imaging technologies such as infrared thermography and video-based monitoring; acoustic and environmental sensing systems; and advanced data analytics methods and artificial intelligence approaches. By fostering collaboration among researchers, technology developers, industry stakeholders, and policy actors, SENSTARA provides an open, interdisciplinary platform to accelerate the translation of PLF innovations into practical, transparent, Standardized, and scalable decision-support tools in research.

### Session 9

### Poster 3

### **GLOBAL: a 10-year experiment to describe lifetime health in dairy cows**

N. Gafsi<sup>1</sup>

<sup>1</sup> Université Paris-Saclay, INRAE, ENVA UMR BREED, F-78350 Jouy-en-Josas, France, France

GLOBAL is a 10-year experiment at INRAE Le Pin designed to capture 'global health' throughout the productive lives of dairy cows. Females are followed from birth through successive lactations (up to five, if possible) under two contrasting management systems, enabling lifetime trajectories rather than isolated events to be studied. The herd is composed of 240 lactating cows (65% Holstein and 35% Normande breeds). Following a shared rearing period, the heifers are assigned to either a pasture-based system involving seasonal block calving and grouped dry-off, or an indoor, higher-input system operating year-round with ad libitum feeding and individual intake monitoring. Within the indoor system, a subset is milked using an Automated Milking System. Reproduction relies exclusively on artificial insemination, with the first calving targeted for around 24 months of age, with no hormonal treatments used. Data collection combines continuous sensors (activity collars, accelerometers and thermoboluses) with routine zootechnical performance recording (milk production, body weight and body condition score) and repeated milk sampling. Mid-infrared spectra (MIR) support phenotyping. To preserve long-term interpretability, we maintain backups, validate zootechnical and health records prior to analysis and document changes in equipment or protocols. Health-event records (initially from a phenotyping system of INRAE (CATI SICPA)) have been recoded to differentiate between group and individual treatments, and to maintain consistent disease categories across years. Tables share a minimal common key (table ID, animal ID and date) to balance interoperability and flexibility. Data access is managed via INRAE Nextcloud under a usage charter, with high-throughput data deposited through CATI SICPA and the INRAE data pathways. GLOBAL aims to provide a reference resource for developing health prediction, clustering and lifetime trajectory analysis methods.

**Digital twin for fattening pig growth and behaviour**

*J. Sloomans<sup>1,2</sup>, T. Norton<sup>1</sup>, J. Maselyne<sup>2</sup>*

<sup>1</sup> M3-BIORES, Department of Biosystems, Kasteelpark Arenberg 30, 3001 Heverlee, Belgium, <sup>2</sup> ILVO (Flanders Research Institute for Agriculture, Fisheries and Food), Technology and Food Science Unit, Burg. Van Gansberghelaan 115 bus 1, 9820 Merelbeke-Melle, Belgium

Monitoring fattening pigs has traditionally focused on group-level performance metrics such as body weight, feed intake and feed conversion ratio. Although software and hardware developments allow a shift towards individual pig monitoring, collected data is often scattered across different sensors, dashboards, machines, and storage devices, making it challenging to locate, integrate and interpret the data, thereby hindering the extraction of meaningful insights. A digital twin pig offers a potential solution as an integrated virtual representation of individual fattening pigs in the barn. This project aims to develop an expandable digital twin pig with a focus on individual pig growth and behaviour. Building on data from 2,786 pigs monitored over the past 14 years, the monitoring digital twin is capable of capturing the real-time state of each individual pig by monitoring all connected sensors. Precision livestock farming sensors stream data from RFID antennas, feeder stations, water flow meters, weight scales, cameras and climate sensors directly into the digital twin. Additionally, the aim for the digital twin is to predict future states and to simulate the impact of different strategies. The predictive digital twin combines established mechanistic models, such as InraPorc model for pig growth adapted to the individual pig, with state-of-the-art deep learning models for growth prediction and computer vision analysis. These models enable pig detection, tracking, keypoint detection, posture estimation, and the classification of social interactions. The models will also facilitate the estimation of hidden state variables and early warnings when newly measured data deviates from predictions. As such, the digital twin transcends traditional databases or models, functioning as an interconnected digital system built upon these components. The digital twin pig forms a promising next step in smart farming, building on decades of research to create an integrated digital system for monitoring, modelling and managing fattening pigs.

## Session 9

## Poster 5

**AgriScienceFM: Foundation Models for Biological, Environmental and Management Data**

*P. J. De Temmerman<sup>1</sup>, J. Maselyne<sup>1</sup>, I. Athanasiadis<sup>2</sup>*

<sup>1</sup> ILVO (Flanders Research Institute for Agriculture, Fisheries and Food), Burg. van Gansberghelaan 115, 9820 Merelbeke-Melle, Belgium, <sup>2</sup> Wageningen University and Research, Droevendaalsesteeg 3, Bode 536, 6708 PB Wageningen, Netherlands

Foundation Models (FMs) offer new opportunities to accelerate innovation in agricultural and livestock sciences by integrating biological, environmental, and management data. To exploit these opportunities, two major challenges must be addressed: the inherent complexity and multidisciplinary nature of agricultural systems, and the fragmented, diverse, and highly localized structure of the datasets on which these models are trained. In AgriScienceFM (Horizon Europe, GA 101293777), three interoperable foundation models are being developed to capture the core drivers of agricultural systems: Genetics (G), Environment (E), and Management (M). The G model represents the biological dimension, including phenotypes, genetic diversity, and organism-level processes. The E model incorporates the environmental layer, integrating earth observation imagery, climate and weather time series, soil information, and broader environmental context. The M model reflects the management dimension, encompassing farm-level operational decisions, management documentation, and practice-based data. By combining these biological, environmental, and management dimensions, the project presents cross-scale AI pipelines tailored to agriculture and livestock production systems. A key livestock use case focuses on the M model and integrates three data sources: farmer decision-making captured through management documents such as stable cards and veterinary records; sensor and camera streams that detect behavioral anomalies, stress indicators, and early warning signals of disease; and biophysical conditions derived from weather, soil, and climate data, including temperature, humidity, NH<sub>3</sub>, and CO<sub>2</sub>. By aligning knowledge across genetics, environment, and management, FMs enable earlier recognition of subtle health or welfare deviations, provide robust benchmarking across farms, and reduce manual annotation needs. For farmers and scientists, this translates into faster issue detection, improved decision support, and models that generalize across breeds, housing systems, and environmental conditions.

**Integrating AI-Driven Bioacoustics and Affective Neuroscience for Objective Sheep Welfare Assessment: A Methodological Framework**

E. Emsen<sup>1</sup>, B. Ödevci<sup>2</sup>, M. Kutluca Korkmaz<sup>3</sup>, N. Küçükay<sup>4</sup>

<sup>1</sup> United Arab Emirates University, Integrative Agriculture, Al Ain, 15551 Al Ain, United Arab Emirates, <sup>2</sup> Imona Technologies, Arı Teknonent, İstanbul Technical University, 34485 İstanbul, Turkey, <sup>3</sup> Malatya Turgut Ozal University, Animal Science, Malatya, 44210 Malatya, Turkey, <sup>4</sup> Dubai British School, Emirates Hills, Dubai, 37828 Dubai, United Arab Emirates

The growing demand for animal-derived products highlights the need for objective, scalable, and biologically grounded approaches to livestock welfare assessment. Precision livestock farming (PLF) increasingly relies on artificial intelligence (AI) to move welfare monitoring beyond subjective visual observations toward continuous, data-driven evaluation. In sheep production systems, conventional welfare assessment remains limited in detecting early alterations in affective and physiological states mediated by neural and sensory processing. Bioacoustics provides a non-invasive window into the neurophysiological and affective mechanisms underlying animal behaviour, as vocalizations are closely linked to central nervous system activity, emotional valence, and arousal. Variations in acoustic structure and temporal features of sheep vocalizations may reflect stress-related neural responses or altered affective states before overt behavioural or clinical signs emerge. We reviewed the progression of vocal signal analysis from traditional acoustic feature extraction to contemporary machine learning and deep learning models capable of capturing non-linear patterns associated with affective state modulation. While AI-based vocal analysis is well established in cattle and pigs, its application in sheep remains limited. We propose an integrative methodological framework combining bioacoustic, behavioural, and physiological indicators to support multimodal AI models of sheep welfare. Aligning bioacoustic signatures with affective neuroscience concepts enables earlier detection of welfare compromise and supports proactive, evidence-based management decisions, contributing to a more objective and biologically meaningful assessment of sheep welfare.

## Session 9

## Poster 7

**Smart herds: AI in feeding, monitoring, and welfare of dairy cattle**

J. Fabjanowska<sup>1</sup>, E. Kowalczyk-Vasilev<sup>1</sup>, S. Milewski<sup>1</sup>, G. Rogowska<sup>1</sup>, R. Klebaniuk<sup>1</sup>

<sup>1</sup> University of Life Sciences in Lublin, Institute of Animal Nutrition and Bromatology, Faculty of Animal Sciences and Bioeconomy, Akademicka 13, 20-950 Lublin, Poland

Artificial intelligence (AI) in dairy farming is a modern herd management strategy combining digital technologies in feeding, behaviour monitoring, and animal welfare support. The systems integrate data from environmental sensors, video cameras, automatic milking systems, and telemetric devices worn by cows (wearables, smart collars, stomach micro-sensors), enabling holistic herd management and considering individual animal needs. This analysis evaluates AI tools in feeding, behaviour monitoring, and cattle welfare, with a focus on machine learning, deep learning, heterogeneous data integration, and practical farm implementation. In feeding, decision support systems analyse milk yield, body condition, metabolic parameters, and feed composition. They generate individualised feed rations, optimising protein and energy balance, reducing feed waste and methane emissions, and improving feed conversion into milk. They account for individual herd variability, lactation stage, production level, and health status, outperforming traditional group nutrition methods. Behaviour monitoring relies on motion sensors, cameras, and computer vision algorithms. Convolutional networks and hybrid CNN-LSTM models detect early behavioural biomarkers, such as changes in locomotion, chewing rhythm, or social interactions, enabling early detection of mastitis, lameness, and ketosis. Individual cow recognition supports personalised health and performance cards, enabling individual care in large herds. Animal welfare is monitored through accelerometric, bioacoustic, and environmental data. Vocalisation analysis allows stress, pain, or disease to be detected before clinical symptoms appear. Intelligent AI systems, such as automatic cooling sprinklers, adjust operation to animal presence and environmental conditions, ensuring thermal comfort. AI in feeding, behaviour monitoring, and welfare improves productivity, herd health, reduces environmental impact, and increases farm economic efficiency. The development of 'smart herds' allows independent optimisation of feeding, health, and welfare, minimising losses and supporting sustainable farming.

**An LLM-Powered Intelligent Agent for Early Disease Diagnosis in Dairy Cattle using a Domain-Specific Knowledge Graphs**Z. Yang<sup>1</sup>, Y. Yang<sup>1</sup>, K. Sima<sup>1</sup>, M. Li<sup>1</sup><sup>1</sup> Northwest A&F University, Animal Science and Technology, No.3 Taicheng Road, 71210 Yangling, China

Early detection of diseases in dairy cattle is essential to minimize economic losses in large-scale farming and improve animal welfare. However, shortages of professional veterinarians and challenges in individual animal monitoring in intensive production systems continue to hinder timely diagnosis. This study introduces an automated early warning framework integrates a Dairy Disease Knowledge Graph (DDKG) with an LLM-powered Intelligent Agent. The DDKG was constructed by systematically extracting and structuring hierarchical, tree-like relationships from veterinary literature into a formal ontology, with clearly defined node types and relationships centered on diseases. To address variability in symptom description, an LLM-based synonym library normalizes non-standard user inputs to align with standard graph entities (derived from symptom nodes). The resulting graph was implemented in a Neo4j for efficient querying. The intelligent agent comprises three specialized modules: 1) Input Discrimination and Information Extraction, which employs LLMs to determine whether a query concerns dairy cattle disease symptoms and to extract relevant symptom entities and relations; 2) Knowledge Graph Reasoning and Disease Recall, which matches extracted terms against the synonym library, converts them into Cypher queries, and retrieves candidate diseases from the DDKG; and 3) Diagnosis and Consultation Generation, which integrates candidate disease sets from Knowledge graph reasoning retrieval and vector similarity recall via a rule-based fusion mechanism, narrowing down differentials for accurate localization while generating interpretable explanations and customized management recommendations (e.g., treatment protocols and preventive measures). On a dedicated test dataset, the input discrimination and information extraction modules achieved 98% accuracy. Graph retrieval and final disease localization reached 77% and 82% accuracy, respectively. These results indicate the framework's potential as a reliable, scalable tool for automated health monitoring in precision dairy farming, leveraging large language models and knowledge graphs to support decision-making and advance sustainable livestock management.

**Machine learning-based genomic prediction of feed conversion ratio using SNP markers in Latvian sheep breeding.**M. Martins<sup>1</sup>, N. Paramonova<sup>1</sup>, S. Plavina<sup>1</sup>, D. Malakovska<sup>1</sup>, N. Krasnevska<sup>1</sup>, J. Paramonovs<sup>1</sup>, D. Kairisa<sup>2</sup>, I. Trapina<sup>1</sup><sup>1</sup> The University of Latvia, Genomics and Bioinformatics Centre, Department of Pharmaceutical Sciences, Faculty of Medicine and Life Sciences, Jelgavas iela 1, LV-1004 Riga, Latvia, <sup>2</sup> Latvian University of Life Sciences and Technologies, Department of Animal Sciences, Faculty of Agriculture and Food Technology, Liela iela 2, LV-3001 Jelgava, Latvia

The economic benefit of sheep farmers depends on the level of feed conversion ratio (FCR) of lambs. The selection by FCR would produce higher quality, economically profitable lambs. FCR is complex, quantitative trait influenced by multiple genetic factors, making it suitable for data-driven modelling for marker-assisted selection. The study aims to use genetic markers from GeneSeek® Genomic Profiler™ Ovine 50K (Lansing, MI, USA) related to FCR in sheep breeds in Latvia to build machine-learning (ML) model that can predict. Genotyping results from 261 controlled fattening lambs of eight commonly grown breeds, with 51.72% belonging to the national breed Latvian Dark-head (LT). Genome-wide association analysis (GWAS) was used to find SNPs that are strongly linked to FCR of 60-day (90th-150th) fattening interval. One SNP, rs413876950, achieved genome-wide significance ( $p = 3.46 \times 10^{-8}$ ), while 1665 and 3549 markers met relaxed thresholds of  $p < 0.01$  and  $p < 0.05$ , respectively. The LT analysis produced 478 and 1994 markers at the same thresholds. Significant loci (5215 from different breeds; 2472 from LT) were combined with early-life variables to build supervised ML models for predicting pre-fattening FCR. The results showed that machine learning models using carefully chosen genetic features can make accurate predictions, even with a smaller number of samples and many variables. The results demonstrated the predictive capabilities of machine learning algorithms. Overall, the study found that using ML algorithms along with genotyping results could help improve breeding efforts in Latvia, particularly for the LT variety, which would boost breed improvement and competitiveness. Funded by UL Faculty of Medicine and Life Sciences internal student grant MG-2026/XXX, grant No. XXX and by the Latvian Council of Science, Latvia, projects LZP-2021/1-0489 and LZP-2024/1-0092.

**Artificial intelligence in precision poultry feeding: data integration, predictive models, and applications in production**

S. Milewski<sup>1</sup>, J. Fabjanowska<sup>1</sup>, G. Rogowska<sup>1</sup>, E. Kowalczyk-Vasilev<sup>1</sup>, B. Kiczorowska<sup>1</sup>

<sup>1</sup> University of Life Sciences in Lublin, Institute of Animal Nutrition and Bromatology, Faculty of Animal Sciences and Bioeconomy, Akademicka 13, 20-950 Lublin, Poland

Artificial intelligence (AI) is playing an increasingly important role in precision poultry nutrition by enabling the integration of data from RFID sensors, cameras, automated weighing systems, and platforms monitoring bird behaviour. The aim of this study was to review the available evidence on AI applications in poultry nutrition and to assess the implementation potential of these solutions in practice. Behavioural data analysis (locomotor activity and use of feeders and drinkers) supports individualized adjustment of feed allowances to body weight, age, and health status, and enables early detection of stress and health problems that may impair production performance. AI-based predictive models can forecast body weight gain, growth rate, and key efficiency indicators related to egg and meat production, while optimization algorithms support dynamic feed formulation by accounting for nutrient value, ingredient availability, and costs. Computer vision systems and deep learning methods (including convolutional neural networks and object detection) enable automated monitoring of body condition and posture, body weight, and activity at the individual level. Integrating multi-source data and analysing it in real time allows rapid responses to declines in feed intake and abnormal behavioural patterns. Linking AI with IoT networks additionally enables simultaneous monitoring of microclimatic conditions (temperature, humidity, ventilation, and lighting) that influence appetite and digestive efficiency, while automation of feeding and watering reduces human intervention and flock stress. The literature indicates that AI implementation may lower FCR, reduce raw material losses, and improve production efficiency, while supporting welfare and reducing the environmental footprint through more precise resource management.

**Proof-of-Concept: AI-Based Classification of Cow Behavioral Responses using Neck-Mounted Accelerometers in Pasture**

I. A. Saeed<sup>1</sup>, K. Stetter<sup>1</sup>, M. S. Teitscheid<sup>2</sup>, A. M. Kurz<sup>2</sup>, J. Langbein<sup>2</sup>, S. Rose<sup>1</sup>

<sup>1</sup> University of Rostock, Faculty of Agriculture, Civil and Environmental Engineering, Justus-von-Liebig-Weg 6, 18059 Rostock, Germany, <sup>2</sup> Research Institute for Farm Animal Biology (FBN), Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany

Accurate monitoring of cow behavior is crucial in Precision Livestock Farming, especially in pasture settings where monitoring is challenging. This study presents a proof-of-concept (PoC) structure for automatic cow behavior identification using neck-tags, carried out within the AutoPasture project. The experiment was conducted on nine cows, each equipped with an accelerometer during pasture access. Accelerometer signals were segmented into 10-second windows, and time-domain features, such as mean and standard deviation of each axis were computed. A comprehensive window-labeling strategy was adopted. Recorded videos were labeled using a predefined coding scheme and retained only clearly defined behaviors, providing ground-truth labels for foraging, standing, and walking activities. A Random Forest classifier was trained using window-level features and examined against labeled videos using weighted F1-score and confusion matrix analysis. A non-stratified train-test split was conducted due to the limited number of samples per behavior class, initially fit for the PoC appraisal. The model performed well, attaining a weighted F1-score of 0.74, showing the likelihood of identifying grazing-related behaviors using accelerometer data validated against video ground truth. Performance was further evaluated using five repeated random splits, producing a mean weighted F1-score of  $0.81 \pm 0.16$ , showing a stable performance. Confusion matrix analysis revealed high recognition accuracy for grazing behavior, whilst walking was more difficult to quantify because of its short bout, resulting in overlapping of neck-movement patterns within fixed time windows. Overall, the findings promise the deployment of accelerometers combined with machine learning for PoC behavior detection in pasture settings. Within the AutoPasture project, the study presents a validated behavioral monitoring baseline to assist data-driven, welfare-oriented pasture management, while emphasizing the use of additional sensing controls for precise movement recognition.

**Automatic monitoring of piling behaviour in laying hens using convolutional neural networks**M. M. Gyldenkerne<sup>1</sup>, D. B. Jensen<sup>1</sup><sup>1</sup> University of Copenhagen, Faculty of Health and Medical Sciences, Grønnegårdsvej 2, 1870 Frederiksbers, Denmark

Piling is an abnormal behaviour in poultry that raises significant welfare and production concerns. It is characterized by individual hens clustering closely together, escalating to suffocation in severe cases. Automated monitoring for both recorded and real-time videos can be crucial to facilitate the study of this behaviour and enable early alarm systems. Convolutional neural networks (CNNs) are artificial intelligence models for image processing that have shown potential for automated behaviour detection in livestock production systems. This study aimed to compare and evaluate six CNN architectures (VGG16, ResNet50V2, InceptionV3, Xception, MobileNetV2, EfficientNetB0) for automated piling detection in commercial laying hens under real production conditions. To train and build the CNN models, a dataset of 882,847 RGB images from 12 commercial flocks was used, varying in lighting conditions, housing systems, and camera perspectives. To compare the architectures, we first applied a systematic grid search using 2% of the dataset to analyse the effect of four structural aspects of CNN and determine the best performing configuration for each architecture. Then, we compared three different data management strategies and a fine-tuning strategy using the full dataset. All models achieved moderate performance (AUC: 0.62–0.74) and exhibited overfitting, suggesting that architectural complexity is not the primary limiting factor. Given the gradual nature of piling, the absence of temporal information in this CNN-based approach may partly explain these limitations. Future studies will aim at incorporating temporal feature extraction or large multimodal models (LMMs), which may yield more useful information for this case.

**Benchmarking Multiple Piglet Tracking and Detection in Crowded Farrowing Pens**J. Gao<sup>1</sup>, I. Kyriazakis<sup>1</sup>, S. P. Brouwers<sup>2</sup>, X. Yang<sup>3</sup>, D. Morris<sup>3</sup>, M. Benjamin<sup>3</sup>, N. McLaughlin<sup>1</sup><sup>1</sup> Queen's University Belfast, University Road, BT7 1NN Belfast, United Kingdom, <sup>2</sup> Teagasc, Pig and Poultry Research and Knowledge Transfer Department, Moorepark, P61 C996 Fermoy, Ireland, <sup>3</sup> Michigan State University, 524 S Shaw Ln, MI 48824 East Lansing, United States

We propose a new benchmark dataset for multiple piglet tracking and detection in highly crowded scenarios with visually similar piglets, which is particularly challenging for current object detection and multi-object tracking methods. Our dataset focuses on three piglet behaviours which are key indicators of piglet vitality: sucking, moving and resting. To ensure high biological variance and enable evaluation of generalisation capabilities of various computer vision models, videos and images were collected from two distinct facilities in the USA and Ireland. The tracking dataset comprises 20 high-resolution top-view videos containing 266 unique piglet tracks, captured in conventional farrowing pens with permanently crated sows covering the period from farrowing to weaning. Piglet tracks were manually labelled in Oriented Bounding Boxes (OBB) to enable precise localisation even under heavy occlusion, crowding, and non-rigid deformation. The detection dataset consists of 784 images with 14,614 piglets individually annotated with OBBs. Importantly, the detection images do not temporally overlap with the tracking videos, allowing independent training and evaluation of detection and tracking models. All annotations were produced by a team with expertise in both animal behaviour and computer vision. We established a comprehensive baseline by evaluating a range of state-of-the-art object detectors, including YOLO and DETR, and multi-object trackers, including ByteTrack and SAM3. Our piglet detector evaluation shows that learning from data in similar domains improves generalisation on the target domain. Our piglet tracking experiments demonstrate superior performance of segmentation-based tracking, compared to traditional tracking-by-detection approaches, with SAM3 achieving a HOTA score of 83.4 in our piglet tracking test set. Our experiments also highlight the difficulty of monitoring piglets in densely crowded sucking scenarios, where performance degrades even for the best models.

**Eco-Catch: AI-Driven Monitoring and Reduction of Protected Species Bycatch in European Waters**L. Ingelbrecht<sup>1</sup>, P. J. De Temmerman<sup>1</sup>, J. Maselyne<sup>1</sup>, H. De Rijcke<sup>1</sup>, S. Delacauw<sup>1</sup><sup>1</sup> ILVO, T&V115, Burg. Van Gansberghelaan 115, 9820 Merelbeke, Belgium

Eco-Catch outlines bycatch challenges in the Baltic Sea and North Sea, identifying vulnerable species and the fishing gears associated with high-risk interactions. Rather than focusing solely on large-scale automated monitoring, it aims to reduce manual review effort while safeguarding the detection of protected species. Key activities include the development of smart bycatch information systems for gillnet fisheries, the design and testing of BRD technologies (Bycatch Reduction Devices), and alternative fishing gears. Eco-Catch aims to monitor bycatch via AI-driven species recognition using onboard camera systems. These images are often of bad quality, due to challenging environmental conditions such as low light, turbidity, motion blur, and occlusions, which introduces an additional layer of complexity for automated species recognition. These data support both a detection model and a bycatch identification model, trained on a large-scale onboard imagery dataset comprising 9,759 annotated images (6,825 training, 1,948 validation, and 986 test images) across 14 target classes, with a strongly imbalanced class distribution reflecting real-world bycatch occurrence. The detection model achieves a precision of 96.7%, recall of 95.7%, mAP@50 of 98.0%, and mAP@50–95 of 86.7% on the independent test set. At an instance level (n = 732 test annotations), this corresponds to approximately 31 false negatives (≈4.3% missed detections) and 24 false positives, indicating a high overall accuracy while highlighting the remaining challenge of missed detections. Reducing false negatives remains a key priority, particularly for protected and endangered species. Initial efforts to address this issue included adapting the validation strategy to optimize recall rather than loss, though this resulted in only limited improvements. Current work therefore focuses on modifying the YOLO loss function itself to further penalize false negatives and shift the model's behaviour toward higher sensitivity.

## Session 10

## Poster 1

**Future-Proofing Agricultural Research for the Era of Artificial Intelligence**Y. Gong<sup>1</sup>, C. Qian<sup>2</sup>, H. Hu<sup>3</sup>, Y. Jung<sup>2</sup>, A. N. Negreiro<sup>1</sup>, M. Wiedmann<sup>2</sup>, V. E. Cabrera<sup>1</sup><sup>1</sup> University of Wisconsin-Madison, Department of Animal & Dairy Sciences, 1675 Observatory Dr., 53706Madison, United States, <sup>2</sup> Cornell University, Department of Food Science, 411 Tower Rd., 14853 Ithaca, UnitedStates, <sup>3</sup> Cornell University, Department of Animal Science, 507 Tower Rd., 14853 Ithaca, United States

The evolution of large language models (LLMs) is shifting Artificial Intelligence (AI) from specialized predictive models toward generalized reasoning capable of solving complex tasks, known as “agentic ability”. While this offers transformative potential for agricultural science, a data-rich, multidisciplinary field that integrates biology, environment, economics, and engineering, its realization is constrained by limited accessibility, standardization, and machine-readability of research outputs. We argue that agricultural research must proactively evolve to be “agent-actionable” by ensuring that underlying research outputs (including code, data, and models) are machine-readable, accessible, and accompanied by clear provenance. Building upon the established FAIR (Findable, Accessible, Interoperable, and Reusable) principles, we propose an enhanced framework of “Agent-actionability.” This framework redefines FAIR for the era of agentic AI: Findability evolves to enable agents to discover specific skills and tools; Accessibility moves beyond downloadable files to standardized interfaces for autonomous data retrieval; Interoperability prioritizes clear version control and metadata for explicit agent chain-of-thought; and Reusability ensures research software is modular, executable blocks for new applications. We outline implementation-ready practices across various modalities: structured text formats (LaTeX) with semantic tags (e.g., AGROVOC); multimedia signal isolation and slide synchronization; and packaging models into containerized services or agent skills. We also advocate for funding agencies to recognize data stewardship as a recommended budget item in grant proposals. These practices are crucial for converting static publications into computable assets, thereby enabling LLM-based systems to autonomously query and synthesize published research. Such a paradigm shift is essential for agricultural science to remain at the forefront of the AI-driven research ecosystem.

### Artificial Intelligence–driven modelling of microclimatic and climatic effects on production, metabolic status, udder health and ammonia emission in dairy cows

K. Kuterovac<sup>1</sup>, V. Gantner<sup>2</sup>

<sup>1</sup> Croatian Agency for Agriculture and Food, Ulica kardinala Alojzija Stepinca 17, 31000 Osijek, Croatia, <sup>2</sup> University of Josip Juraj Strossmayer Osijek, Faculty of Agrobiotechnical Sciences Osijek, Vladimira Preloga 1, 31000 Osijek, Croatia

Climate change and increasing thermal load represent major challenges for sustainable dairy production. The aim of this study was to quantify the effects of microclimatic and long-term climatic factors on milk production, metabolic status, udder health and indicators of ammonia emission in dairy cows in Croatia, and to develop Artificial Intelligence (AI)–based predictive models for risk assessment under future climate scenarios. Production data originated from the national milk recording database (Croatian Agency for Agriculture and Food, including daily milk yield, fat, protein, lactose, milk urea and somatic cell count). Microclimatic parameters (ambient temperature and relative humidity) were recorded on test day, and the temperature–humidity index (THI) was calculated. Ammonia emission was estimated from milk urea. Long-term climatic data (1990–2025) were obtained from the national meteorological database (Croatian Meteorological and Hydrological). Derived variables (THI classes, degree days and interaction terms) were generated following detailed logical and statistical data validation. Classical statistical approaches in SAS were combined with AI techniques (machine learning regression, classification algorithms and time-series modelling) to: predict milk yield and composition under varying THI conditions; classify the risk of metabolic disorders based on the fat-to-protein ratio (F/P), including subclinical ketosis and subacute ruminal acidosis; estimate the probability of elevated SCC and mastitis occurrence; and model ammonia emission risk associated with nutritional imbalance and climatic load. Regression-based climate trend analyses quantified long-term changes in temperature, humidity and THI, while AI-driven scenario modelling assessed potential future risks for productivity and sustainability of dairy farming in Croatia. The integration of national longitudinal datasets with advanced analytical approaches provided a framework for precision risk prediction and climate-resilient dairy management strategies.

### Automated Deep Learning–Based Quantification of Goblet Cells as a Digital Biomarker of Poultry Gut Health

D. Mezghiche<sup>1,2,3</sup>, F. Diaz Bahamonde<sup>1</sup>, C. Vidal Moreno De Vega<sup>1</sup>, G. Antonissen<sup>4</sup>, P. Claes<sup>2,3,5</sup>

<sup>1</sup> Poulpharm bvba, Prins Albertlaan 112, 8870 Izegem, Belgium, <sup>2</sup> KU Leuven, Department of Electrical Engineering, ESAT/PSI, Kasteelpark Arenberg 10 box 2441, 3001 Leuven, Belgium, <sup>3</sup> University Hospital Leuven, Medical Imaging Research Center, Herestraat 49, 3000 Leuven, Belgium, <sup>4</sup> Ghent university, Department of Pathobiology, Pharmacology and Zoological Medicine, Salisburylaan 133, 9820 Merelbeke, Belgium, <sup>5</sup> KU Leuven, Department of Human Genetics, Herestraat 49, 3000 Leuven, Belgium

Goblet cell density is a primary biomarker for intestinal mucosal integrity and host immune response in poultry. During enteric challenges such as coccidiosis (*Eimeria* spp.) and necrotic enteritis, mucus production is a vital defense mechanism. However, traditional quantification on PAS-stained sections is labor-intensive and subjective, restricting its use in high-throughput poultry research and large-scale field diagnostics. We developed an automated pipeline using the YOLOv8n (Nano) framework. The model was optimized via transfer learning and partial layer freezing to handle histological variability, then tested on an independent validation set of 84 images. The model achieved high performance with a mAP@0.5 of 0.883, an F1-score of 0.83, and a Recall of 0.88. It remained robust against staining artifacts and mucus depletion. The user-oriented workflow allows veterinarians to select a region of interest and receive objective density metrics in seconds, eliminating inter-observer variability. This AI-driven approach transforms a manual, error-prone task into a standardized, rapid, and objective digital biomarker. By maintaining high sensitivity and consistent performance across diverse slide morphologies, this tool bridges the gap between digital pathology and precision livestock management, supporting the development of targeted nutritional and therapeutic interventions in the poultry industry.

**Mentor::i: AI-Powered, Secure Bioinformatics for Rapid Animal Health Discovery**D. Schokker<sup>1</sup>, V. Bianchi<sup>1</sup><sup>1</sup> Wageningen Bioveterinary Research, Houtribweg 35, 8200AB Lelystad, Netherlands

In animal health research, the bottleneck is not the abundance of sequencing data but the speed with which that data can be transformed into actionable insights that protect livestock, companion animals, and wildlife. Rapid identification of genomic biomarkers, design of targeted vaccines, and profiling of immune responses are essential for early disease detection and One Health initiatives. Yet the journey from raw reads to publishable findings remains hampered by cumbersome, error prone bioinformatics pipelines that lock domain expertise into brittle scripts and dependency chains. To break this cycle, we developed Mentor::i, an open source, multi agent research platform that brings the full power of locally hosted and cloud based large language models (LLMs) to animal health scientists. Its modular architecture, Lead Researcher, Coder, Handyman, Editor, Synthesizer, automates code generation, file and web search management, and structured reporting, all within a secure sandbox. A Supervisor Agent continuously evaluates each execution step, triggering automatic retries when quality scores dip below thresholds, while a Librarian Agent preserves session memory for seamless multi query research. Mentor::i goes beyond code automation by integrating Retrieval Augmented Generation (RAG) with a Recursive Language Model (RLM) to explore scientific literature and generate claims that are fully traceable to primary sources. The Model Context Protocol (MCP) server exposes specialized tools, vision based figure analysis, web search with truth preservation, and domain specific annotation services, ensuring reproducibility, data privacy, and auditability. By enabling rapid, reproducible, and secure genomic and immunologic analyses, Mentor::i accelerates discovery in animal health, from aiding complex data analysis to identifying disease resistant genes in livestock. The platform democratizes advanced bioinformatics, shortens turnaround times, and safeguards sensitive data, thereby propelling the field of animal sciences forward.

**Forecasting of Ammonia Concentrations in Commercial Growing Pig Houses Based on Deep Learning Models**D. A. Méndez Reyes<sup>1</sup>, M. Jarque<sup>1</sup>, S. Calvet Sanz<sup>1</sup><sup>1</sup> Universitat Politècnica de València, Instituto de Ciencia y Tecnología Animal, Camí de Vera S/N, 46022 Valencia, Spain

Ammonia (NH<sub>3</sub>) concentrations in intensive swine production present significant environmental and health challenges, as elevated levels adversely affect animal welfare and worker health while contributing to soil acidification and water eutrophication. In naturally ventilated systems, indoor air quality is particularly difficult to predict due to high stochasticity influenced by animal performance, farm management, and fluctuating outdoor meteorological conditions. Accurate, real-time forecasting is essential for transition toward Precision Livestock Farming (PLF), enabling proactive interventions such as dynamic ventilation adjustments to reduce NH<sub>3</sub> accumulation. This study evaluated eight state-of-the-art forecasting architectures, TiDE, D-Linear, TSMixer, Temporal Fusion Transformers (TFT), N-HiTS, TCN, Transformer, and XGBoost, to predict NH<sub>3</sub> fluctuations in a commercial pig house. The methodology used a full-factorial experimental design conducted in Teruel, Spain, monitoring 864 pigs over a three-month period. Environmental parameters, including gas concentrations (NH<sub>3</sub>, CO<sub>2</sub>, H<sub>2</sub>S), microclimate data, and wind metrics, were recorded at one-minute resolution. Results identified data pre-processing as the dominant factor for accuracy, accounting for 68% of performance variability. Smoothing significantly outperformed aggressive outlier removal, which often eliminated essential high-frequency signals. Factorial analysis determined a 15-minute resampling frequency as the optimal "sweet spot" for capturing environmental dynamics while minimizing sensor noise. Among the models, TiDE and D-Linear demonstrated superior short-term forecasting capabilities. An optimized TiDE model achieved a peak R<sub>2</sub> of 0.913 for a 30-minute horizon. For extended 60-minute horizons, integrating future weather covariates (temperature and humidity) could improve forecast performance under high-stochastic conditions.

### From trait prediction to system-level inference: a machine learning framework for intrinsic product quality investigation

A. Mouhanna<sup>1</sup>, L. Rey-Cadilhac<sup>2</sup>, L. Darrigade<sup>3</sup>, B. Martin<sup>4</sup>, S. De Smet<sup>1</sup>

<sup>1</sup> Ghent University, Coupure Links, 9000 Ghent, Belgium, <sup>2</sup> Institut Agro, INRAE, La Prise, 35590 Saint-Gilles, France, <sup>3</sup> Université de Tours, INRAE, Nouzilly, 37380 Nouzilly, France, <sup>4</sup> Université Clermont Auvergne, INRAE, Route de Theix, 63122 Saint-Genès Champanelle, France

Farm-level outcomes such as the intrinsic quality of milk and meat are shaped by multiple interrelated farming practices. In high-dimensional observational data, signal and noise co-occur through (non)linear interactions, making it difficult to identify generalizable system-level patterns. Moreover, field data collection introduces constraints beyond measurement error (e.g., tied values, structural zeros reflecting system definitions), complicating conventional modeling approaches. Hence, linking farming practices to intrinsic quality in commercial settings is challenging. Machine learning (ML) offers a suitable framework to address this. We present a transferable ML framework to extract and validate system-level signals from high-dimensional observational farm data, demonstrated using fatty acids (FA) traits in milk and beef. Optimized Random Forest models first detect potential system-level signals under cross-validation. When performance meets predefined criteria (validation  $R^2 \geq 0.50$ ), selected farming practices are forwarded to an optimized Conditional Inference Tree model to test whether associations can be expressed as statistically supported management contrasts. The resulting partitions quantify differences in trait concentration between contrasting production configurations. Applied to multi-country livestock datasets from the INTAQT H2020 project, the approach shows heterogeneity in trait responsiveness, indicating that not all traits are equally influenced by farming practices. In both milk and beef, polyunsaturated FA models showed strong and stable performance, reflecting production-intensity gradients. In contrast, saturated and monounsaturated FA had weaker signals, suggesting limited responsiveness to the recorded practices. This framework limits over-interpretation by distinguishing traits with coherent system-level signal from those with insufficient evidence for system-level inference. This distinction is critical for claims about system-driven differences in product quality.

### Data-Driven Genomic Analysis of Population Structure and Breed Differentiation of Latvian Dark-head Sheep.

I. Trapina<sup>1</sup>, M. Martins<sup>1</sup>, S. Plavina<sup>1</sup>, D. Malakovska<sup>1</sup>, N. Krasnevska<sup>1</sup>, J. Paramonovs<sup>1</sup>, D. Kairisa<sup>2</sup>, N. Paramonova<sup>1</sup>

<sup>1</sup> Faculty of Medicine and Life Sciences, the University of Latvia, Genomics and Bioinformatics Centre, The Department of Pharmaceutical Sciences, Jelgava str 3, LV-1040 Riga, Latvia, <sup>2</sup> Faculty of Agriculture and Food Technology, Latvian University of Life Sciences and Technologies, Department of Animal Sciences, Liela str 2, LV-3001 Jelgava, Latvia

The Latvian Dark-head (LT) is the only sheep breed developed in Latvia, is fully adapted to local climatic conditions, and carries significant cultural, ecological, and socio-economic value. The growing dominance of commercially optimised breeds threatens indigenous genetic resources, underscoring the need for advanced genomic monitoring and data-driven conservation strategies. This study applies high-density genomic analysis to evaluate the genetic diversity of the LT breed and compare it with that of other widely used sheep breeds in Latvia. Lambs from leading sire lines were genotyped using the GeneSeek® Genomic Profiler™ Ovine 50K array, generating large-scale SNP datasets suitable for Principal Component Analysis and structure analysis. Bioinformatic and statistical pipelines were used to quantify minor allele frequency (MAF) distributions and to detect breed-specific genomic signatures by identifying fixed SNPs (MAF=0). The LT breed demonstrated high genomic variability, with 27,561 highly polymorphic SNPs (MAF 0.3–0.5), indicating substantial genetic differentiation from other breeds. A total of 2668 SNPs (5.45%) were fixed within the LT population, with 55–131 markers identified as breed-unique across comparisons. It enables detection of distinct genetic traits and interbreed differences, AI-assisted ancestry inference, and precision breeding applications. The Ovine50K platform, along with computational genomic analysis, makes it possible to find breed-specific markers on a large scale. It also helps create tools for selection and genetic monitoring for the Latvian national sheep breed. The results provide a base of information for future machine learning methods in evaluating sheep genetics and helping with decisions in sustainable animal breeding. This study was supported by the Latvian Council of Science, Latvia, projects LZP-2021/1-0489 and LZP-2024/1-0092.

### Whole-Chamber AI-Based Enumeration of Eimeria Oocysts for Objective OPG Quantification

D. Mezghiche<sup>1,2,3</sup>, M. Verstraete<sup>1</sup>, C. Vidal Moreno De Vega<sup>1</sup>, G. Antonissen<sup>4</sup>, P. Claes<sup>2,3,5</sup>

<sup>1</sup> Poulpharm bvba, Prins Albertlaan 112, 8870 Izegem, Belgium, <sup>2</sup> KU Leuven, Electrical Engineering, ESAT/PSI, Kasteelpark Arenberg 10 box 2441, 3001 Leuven, Belgium, <sup>3</sup> University Hospital Leuven, Medical Imaging Research Center, Herestraat 49, 3000 Leuven, Belgium, <sup>4</sup> Ghent university, Pathobiology, Pharmacology and Zoological Medicine, Salisburylaan 133, 9820 Merelbeke, Belgium, <sup>5</sup> Ku Leuven, Human Genetics, Herestraat 49, 3000 Leuven, Belgium

Accurate quantification of Eimeria oocysts per gram (OPG) is essential for monitoring coccidiosis dynamics, evaluating vaccine efficacy, and assessing trial outcomes in poultry production. The conventional McMaster method relies on manual counting of the chamber area under light microscopy, introducing sampling bias, human error, and inter-operator variability. In addition, the process is time-consuming. In this study, we developed a deep learning-based computer vision pipeline to automate oocyst detection and differentiation between the seven major Eimeria species affecting chickens. Randomly acquired images from different regions of the McMaster chamber were first used to train object detection models. Multiple architectures were evaluated, including YOLOv8 object detection framework, specifically comparing the Nano (YOLOv8n) and Small (YOLOv8s) variants, RetinaNet, and Faster R-CNN. Among them, YOLOv8n achieved the best overall performance, providing the optimal balance between detection accuracy, species differentiation capability. In the second phase, a slide scanner was used to digitize the entire McMaster chamber, enabling full-field analysis and eliminating partial sampling bias. Automated whole-chamber inference allowed complete enumeration across the entire counting area. Comparison with expert manual counting showed highly comparable results, with an average error rate of approximately 1.10%. These findings demonstrate the feasibility of replacing partial manual counting with ongoing refinement for reliable species classification and sporulation assessment, and fully automated whole-chamber OPG analysis.

### Prediction of Post-Freezing Semen Quality Using Pre-Freezing Semen Quality

A. Rehman<sup>1</sup>, A. Tresch<sup>1</sup>, K. Kupisiewicz<sup>2</sup>

<sup>1</sup> University of Cologne, IMSB, Robert-Koch-Str. 10, Building 51 ("Zfs"), 50931 Cologne, Germany, <sup>2</sup> Viking Genetics, R&D, Agro Food Park 12, 8200 Aarhus, Denmark

The cryopreservation of bovine semen is a critical step in artificial insemination and semen quality is evaluated at ejaculate collection and after cryopreservation. Semen quality varies considerably between breeding bulls and between ejaculates from the same bull making it difficult to predict which ejaculate will pass post-thaw quality control. This uncertainty may lead to production inefficiencies and increase the cost. This study investigated whether pre-freezing semen quality parameters can reliably predict post-thaw status (approved / rejected) of the ejaculate using machine learning algorithms. Four machine learning models were evaluated – Logistic Regression (LR), Random Forest, Extreme Gradient Boosting (XGBoost), and Gradient Boosting Machine (GBM) – for their ability to predict post-thaw status of the ejaculate. Model performance was evaluated using accuracy, precision, sensitivity, specificity, F1 score, AUC and log-loss. Models were developed separately for conventional and sex-sorted semen using production data from commercial AI station. Training and testing datasets for conventional semen were generated using 80:20 split ratio and contained about 27K and 7K ejaculates respectively. Similarly, for sex-sorted semen about 11.5K and 3K ejaculates were in training and test datasets, respectively. To address class imbalance, inverse frequency class weights were applied to both classes of the target variable during model training. Results showed that for conventional semen the GBM was the best model (AUC = 0.86, log-loss = 0.41) followed by LR (AUC = 0.83, log-loss = 0.49). GBM was also the best model for sex-sorted semen (AUC = 0.71 and log-loss = 0.58), although overall performance metrics were lower compared to conventional semen. Variable importance analysis revealed initial motility of collected ejaculate as the best predictor for GBM, while in LR collection year was the top predictor. This study shows that machine learning tools like GBM and LR can successfully predict post-freezing semen quality based on pre-freezing parameters. Such models may serve as valuable decision-support tools to improve efficiency and optimize semen production in commercial AI programs.

**Deep-learning inference models for canine diffuse large B cell lymphoma**K. Ancheta<sup>1</sup>, A. Psifidi<sup>2</sup>, S. Le Calvez<sup>3</sup>, A. Yale<sup>2</sup>, J. Williams<sup>1</sup>

<sup>1</sup> Royal Veterinary College, Pathobiology & Population Sciences, Hawkshead Lane, North Mymms, AL9 7TA Hatfield, United Kingdom, <sup>2</sup> Royal Veterinary College, Clinical Science & Services, Hawkshead Lane, North Mymms., AL9 7TA Hatfield, United Kingdom, <sup>3</sup> IDEXX Laboratories Limited, Grange House, Sandbeck Way, LS22 7DN Wetherby, United Kingdom

Canine diffuse large B cell lymphoma (cDLBCL) is the most common lymphoma in dogs, with aggressive behaviour and ~20% one-year survival despite treatment. It is a heterogeneous lymphoid malignancy with distinct genomic and transcriptomic profiles, driving its pathogenesis, clinical behaviour, and response to therapy. However, key knowledge gaps remain compared to its human homolog, due to limited relevant cDLBCL “omics” studies. This study aims to fill this gap by exploring tissue analysis in histopathological slides using deep learning and infers clinically relevant information from digitised histopathology images. DNA derived from FFPE lymph nodes from cDLBCL (n=15; CD3-/CD20+) and reactive lymphoid hyperplasia (RLH; control; n=15) were whole genome sequenced (40×). The Genome Analysis Toolkit (v4.4) MuTect2 tumour-only workflow was adapted for somatic variant calling. Corresponding H&E-stained lymph node slides were scanned at 20× magnification using Zeiss Axio Scan.Z1. Whole slide images (WSIs) were tiled into 512×512-pixel images and stain-normalised. Cases were split into tumour mutational burden (TMB)-high and TMB-low groups based on the median TMB. TensorFlow (v2.10) was used to train convolutional neural network (CNN) models to distinguish these groups and performance was evaluated on held-out test sets. We identified 155,560 variants post-filter, with 12,721 significantly mutated genes (q<0.05). The TMB-inference model for cDLBCL achieved an area under the receiver operating characteristic curve of 0.64. Tile-level predictions overlaid on WSIs revealed subtle spatial patterns consistent with TMB status. CNNs can be trained to infer TMB status in cDLBCL with modest predictive value. Once refined, such models could support treatment selection and prognostication as in humans. Future work aims to improve performance and extend predictions to additional genomic and transcriptomic features directly from digitised histological images.

## Session 10

## Poster 11

**Visual Re-Identification via Collar Patterns for Identity Recovery in Multi-Goat Tracking Systems**D. A. Méndez Reyes<sup>1</sup>, D. Liu<sup>2</sup>, T. Norton<sup>2</sup>, S. Calvet Sanz<sup>1</sup>, A. Costantino<sup>1</sup>

<sup>1</sup> Universitat Politècnica de València, Ciencia y tecnología animal, Cami de Vera S/N, 46022 Valencia, Spain, <sup>2</sup> KU LUEVEN, Animal and Human Health Engineering (A2H), Kasteelpark Arenberg 30, 2472 Leuven, Belgium

Individual animal tracking is a cornerstone of precision livestock farming, providing real-time monitoring and lifelong traceability essential for welfare assessment and production management. Goat farming has gained prominence as a resilient and economically viable option, valued for its adaptability and dual-purpose production of meat and dairy. Currently, maintaining consistent identity assignment over goats’ entire production cycle remains challenging, since frequent occlusions, overlapping, and dynamic postures disrupt visual continuity. Conventional appearance-based re-identification strategies often fail under overhead view. To overcome this limitation, we implemented a collar displaying a unique color-pattern combination, designed for robust visual discrimination, using an architecture that balances accuracy and computational efficiency. The tracking pipeline begins with YOLO26 and RF-DERT, to localize goats within each video frame. To maintain consistent identities, we evaluated various tracking algorithms, both with and without specialized Re-Identification (Re-ID) components (SORT, ByteTrack, DeepSORT, BoT-SORT, StrongSORT). In these tracking-by-detection frameworks, embeddings are typically extracted from the detected bounding boxes (or cropped Regions of Interest) to facilitate data association when motion-based cues are ambiguous or fail. Our implementation enhances this process by replacing the generic appearance extractor with a collar-focused Re-ID model. By constraining embedding generation to the highly discriminative collar region rather than the entire animal body, we could reduce intra-class variance. Preliminary analyses of the metrics show that this targeted approach improves re-identification robustness, particularly in scenarios involving partial occlusions or complex postural changes. This approach is considered a practical pathway toward reliable, long-term individual tracking in group-housed small ruminants, with implications for behavior monitoring, health surveillance, and precision management in commercial goat production systems.

### Multi-omics integration reveals coordinated rumen hydrogen turnover and energy metabolism underlying feed efficiency in Angus cattle

A. Nunes<sup>1</sup>, C. Faleiros<sup>1</sup>, M. Poleti<sup>1</sup>, G. Marcellini<sup>1</sup>, J. B. Ferraz<sup>1</sup>, H. Fukumasu<sup>1</sup>

<sup>1</sup> University of São Paulo, Department of Veterinary Medicine, Duque de Caxias St, 225, 13635-900 Pirassununga, Brazil

Residual feed intake (RFI) is widely used to measure feed efficiency (FE) in cattle and captures coordinated variation in rumen fermentation and host metabolism. We integrated fecal 16S rRNA profiles and serum metabolomics from Angus cattle divergent for FE using DIABLO (mixOmics), a supervised multiblock sparse model that maximizes cross-omic covariance while selecting compact and interpretable biomarker panels. Phenotypic records and paired serum and fecal samples were available for 64 Black Angus bulls. RFI was estimated within contemporary groups using linear models with dry matter intake as the response and metabolic body weight and average daily gain as predictors. Individuals from the upper and lower RFI quartiles were selected for omics profiling. The integrated latent space separated high vs low RFI animals across microbiome and metabolome blocks, with strong cross-omic agreement ( $r = 0.82$ ), supporting a coordinated microbial–metabolic FE signature. Fecal communities from L-RFI (high-FE) animals were enriched for genera linked to enhanced fermentation efficiency and hydrogen turnover (e.g., Rikenellaceae RC9 gut group and Lachnospiraceae NK3A20). In contrast, the fecal microbiome of H-RFI (low-FE) animals showed higher contributions from *Anaerovibrio* and *Roseburia*, consistent with a rumen ecosystem more strongly shaped by biohydrogenation and a more acidogenic fermentation profile. These microbial patterns aligned with discriminant serum metabolites dominated by lipid transport and mitochondrial fuel handling, including phosphatidylcholines (PC ae C42:2; PC ae C24:0), sphingomyelin (SM C26:1), acylcarnitines (C10:2; C14:1-OH), and amino acids (e.g., taurine and lysine). Together, these results connect microbial hydrogen handling with systemic energy metabolism and highlight biomarker candidates to support FE classification in Angus cattle.

### AI-Enabled Bioelectrical Impedance Digital Biomarkers for Non-Invasive Detection of Caseous Lymphadenitis in Goats

A. Klingler<sup>1</sup>, A. Siddique<sup>1</sup>, R. Kota<sup>1</sup>, A. Rubio-Villa<sup>1</sup>, D. Brown<sup>1</sup>, P. Batchu<sup>1</sup>, J. Van Wyk<sup>2</sup>, T. Terrill<sup>1</sup>

<sup>1</sup> Fort Valley State University, Department of Agricultural Sciences, 1005 State University Drive, 31030 Fort Valley, United States, <sup>2</sup> University of Pretoria, Department of Veterinary Tropical Diseases, Private Bag x04, 0110 Onderstepoort, South Africa

Caseous lymphadenitis (CL) is a chronic infectious disease that compromises productivity and herd health in small ruminants. Early detection remains challenging due to reliance on clinical palpation and laboratory diagnostics. This study advances a digital biomarker framework using bioelectrical impedance analysis (BIA) integrated with machine learning to enable non-invasive phenotyping of CL status in goats. Multi-frequency impedance measurements were collected to capture resistance ( $R_s$ ), reactance ( $X_c$ ), phase angle, hematocrit (PCV), and frequency-dependent electrical signatures. Spectral responses were modeled using the Cole–Cole equation to derive dielectric parameters ( $R_0$ ,  $R_\infty$ ,  $\tau$ ,  $\alpha$ ), enabling extraction of digital biomarkers reflecting cellular membrane integrity and extracellular ionic conduction. CL-affected animals exhibited significantly elevated  $R_s$  and reduced  $X_c$  and phase angle, consistent with infection-associated shifts in membrane capacitance and tissue conductivity. These dielectric alterations indicate structural and inflammatory changes that can be quantified as objective digital phenotypes. Supervised machine learning models demonstrated robust diagnostic discrimination. Support Vector Machine achieved the highest ROC-AUC ( $\sim 0.92$ ), outperforming K-Nearest Neighbors and back-propagation neural networks. SHAP-based explainability confirmed phase angle and  $R_s$  as dominant predictors, mechanistically linked to infection-driven cellular and extracellular resistance shifts. A composite Diagnostic Index integrating  $R_s$ ,  $X_c$ , PCV, and phase angle improved separation between groups (AUC = 0.94). Decision curve analysis showed consistent net clinical benefit across threshold probabilities of 0.3–0.7, supporting translational viability. Collectively, these findings establish impedance spectroscopy features as AI-extracted digital biomarkers for CL detection to provide a scalable diagnostic framework suitable for real-time herd-health monitoring and field deployment.

**AI-Enabled Radiofrequency Digital Biomarkers for Non-Invasive Anemia Phenotyping in Goats**S. R. Neelagiri<sup>1</sup>, A. Siddique<sup>1</sup>, D. Brown<sup>1</sup>, Z. Carlton<sup>1</sup>, J. Van Wyk<sup>2</sup>, T. Terrill<sup>1</sup><sup>1</sup> Fort Valley State University, Agriculture Science, 1005 State University Drive, 31030 Fort Valley, United States,<sup>2</sup> University of Pretoria, Veterinary Tropical Diseases, Private Bag x04, 0110 Onderstepoort, South Africa

Anemia caused by gastrointestinal parasitism remains a major constraint to small ruminant productivity. This study advances a digital biomarker framework using radiofrequency-based non-destructive testing (RF-NDT) integrated with artificial intelligence to enable objective, non-invasive anemia phenotyping in goats. We hypothesized that anemia alters tissue dielectric properties due to changes in hemoglobin concentration, hydration status, and microcirculatory dynamics. RF spectral responses were extracted as candidate digital biomarkers and benchmarked against FAMACHA<sup>®</sup> categories as the biological reference phenotype. Unsupervised spectral clustering of the ten most discriminatory frequencies revealed structured dielectric signatures across anemia states. Healthy animals (FAMACHA 1) exhibited a dominant spectral cluster at 8.43 GHz explaining 93.7% of variance. Moderately affected animals (FAMACHA 2) shifted toward 9.33 GHz with reduced uniformity (88.7%). Borderline animals (FAMACHA 3) displayed bifurcated clusters at 9.89 and 8.23 GHz explaining 91.0% of variance, indicating progressive tissue heterogeneity. These frequency-domain signatures represent RF-derived digital biomarkers of anemia severity. Supervised learning confirmed predictive feasibility. Linear Regression achieved  $R^2 = 1.00$  (RMSE = 0.07), Random Forest achieved  $R^2 = 0.79$ , and classification models demonstrated strong categorical discrimination. A Multilayer Perceptron yielded the highest performance (Accuracy = 0.84; F1 = 0.83; ROC-AUC = 0.94), outperforming Support Vector Machine and K-Nearest Neighbors. These findings demonstrate that RF spectral features capture physiologically meaningful dielectric shifts and can serve as AI-extracted digital biomarkers for real-time anemia detection. The framework enables rapid phenotyping without blood sampling and supports precision deworming, reducing anthelmintic overuse. Future work includes longitudinal biomarker stability assessment, sensor miniaturization, and embedded neural classifiers for scalable on-farm deployment in climate-smart livestock systems.

## Session 10

## Poster 15

**Validation of an automated AI image analysis system for in-line green ham quality assessment**V. Bonfatti<sup>1</sup>, A. Rosolen<sup>1</sup>, K. Ivanov<sup>1</sup>, N. Guzzo<sup>1</sup>, S. Faggion<sup>1</sup>, P. Carnier<sup>1</sup><sup>1</sup> University of Padova, Comparative Biomedicine and Food Science, Viale dell'Università 16, 35020 Legnaro, Italy

Assessment of green ham quality for PDO dry-cured production relies on expert visual scoring, which is subjective and difficult to standardize. This study validates a 2D image analysis system installed in a commercial slaughterhouse, capable of capturing images of all hams in-line during processing. A dataset of 60,000 images was collected during routine production. For validation, a subset of 40 images per feature (skin area, visible veins, hematomas, overall fat area, subcutaneous fat area) was selected to ensure representative coverage of the full variability. Images were manually segmented by three independent experts. Automatic segmentations were compared to expert annotations using area-based Pearson correlations, Dice Similarity Coefficient (DSC), Intersection over Union (IoU), and 95th percentile Hausdorff Distance (HD95). Automatic vs human comparisons showed very high agreement: Pearson correlations exceeded 0.96 for overall fat, 0.98 for subcutaneous fat, and skin, and 0.91 for veins. DSC values ranged 0.84–0.88 for fat and 0.97 for skin, while HD95 confirmed close boundary correspondence (3.9–68.9 pixels depending on feature). Hematomas were more variable, with DSC values ranging from 0.64 to 0.68. Veins were skeletonized, and centerline-based metrics were used, showing centerline recall 0.43–0.56 reflecting partial but meaningful detection of elongated structures. Inter-annotator agreement was high for all features (Fleiss' Kappa 0.77–0.99). These results indicate that the system reliably reproduces expert segmentations, including elongated venous structures, while enabling high-throughput, objective, and in-line phenotyping. This approach supports scalable and reproducible assessment of green hams in commercial production, enabling industrial quality control and the generation of large-scale phenotypic datasets for breeding and research applications.

**Predictive modeling of bacteriophages endolysins structural features as a decision-support framework for targeting rumen microorganisms**

C. Faleiros<sup>1</sup>, A. Nunes<sup>1</sup>, O. Gonçalves<sup>2</sup>, M. Poleti<sup>1</sup>, H. Fukumasu<sup>1</sup>

<sup>1</sup> University of São Paulo, Av. Duque de Caxias Norte, 225 - Jardim Elite, 13635-90 Pirassununga, Brazil, <sup>2</sup> State University of the Midwest (Unicentro), Rua Salvatore Renna, 875, 85015-430 Guarapuava, Brazil

The bovine rumen microbiome is essential for digestion and productivity but remains poorly characterized, particularly regarding phage–bacteria interactions and microbial modulation. Bacteriophages produce modular endolysins that lyse the host cell wall, comprising catalytic domains adapted to cell wall composition and cell wall binding domains (CWBDs) that confer specificity. This study aimed to apply a predictive modeling approach based on structural and functional features of endolysins to predict associated rumen microbial genera. A dataset of 1,975 endolysins from abundant rumen genera was analyzed, including Gram-positive and Gram-negative bacteria and methanogenic archaea. Bacteriophage genomes with known hosts were retrieved from the Rumen Virome Database, annotated with Pharokka, aligned against the PhaLP database using BLAST, and characterized with InterProScan. A Random Forest model was trained using enzyme description, host Gram type, sequence length, and the size and type of catalytic and binding domains. The model achieved 76.7% accuracy and a kappa of 0.56, indicating moderate agreement. The most important variables identified by the model included sequence length, catalytic domain size, GH25 (muramidase activity;  $\beta$ -1,4 cleavage between NAM and NAG), MurNAc-L-Ala amidase (amide bond cleavage between N-acetylmuramic acid and L-alanine), and the peptide bond–cleaving domains Peptidase M15, NlpC/P60, and CHAP. Additionally, CWBD size and the presence of CW-7 repeats and putative PG-binding domains contributed to classification performance. CW-7 repeats were more common in Gram-positive bacteria, whereas putative PG-binding domains predominated in Gram-negative bacteria. Together, these findings support the use of structural characteristics and modular architecture of endolysins within a data-informed framework for the targeted selection of enzymes against rumen microorganisms. The Random Forest classifier shows promise as a decision-support tool, although further optimization is necessary to improve predictive reliability.

# Author index

## A

<i>Abu Dayeh, A.</i>	60
<i>Admiraal, M.</i>	59
<i>Alexakis, I.</i>	45
<i>Alexy, M.</i>	36
<i>Allain, C.</i>	23
<i>Allyndrée, J.</i>	23, 54
<i>Aluwé, M.</i>	28
<i>Ambukiyenyi Onya, J.</i>	51
<i>Ancheta, K.</i>	72
<i>Antonissen, G.</i>	27, 68, 71
<i>Arenos, A.</i>	32
<i>Arenou, A.</i>	32
<i>Athanasiadis, I.</i>	47, 62
<i>Atzori, M.</i>	32
<i>Avanzato, R.</i>	53
<i>Avondo, M.</i>	53
<i>Awish Consortium,</i>	34

## B

<i>Bach, A.</i>	48
<i>Baleret, N.</i>	25
<i>Batchu, P.</i>	73
<i>Battelli, M.</i>	21
<i>Beck, V.</i>	39
<i>Belik, V.</i>	37
<i>Bell, M.</i>	45
<i>Benjamin, M.</i>	66
<i>Beritelli, F.</i>	53
<i>Beritelli, L.</i>	53
<i>Bermann, M.</i>	52
<i>Bertolini, F.</i>	43
<i>Bertozzi, C.</i>	45
<i>Beyan, O.</i>	60
<i>Bhandarkar, S.M.</i>	52
<i>Bhattacharya, P.</i>	33
<i>Bianchi, V.</i>	50, 69
<i>Bica, R.</i>	21
<i>Bieber, G.</i>	33
<i>Billah, M.</i>	52
<i>Bist, R.</i>	26
<i>Bognanno, S.</i>	53
<i>Bolner, M.</i>	43
<i>Bonenberger, C.</i>	30
<i>Bonfatti, V.</i>	56, 74
<i>Boré, R.</i>	25

<i>Bossers, A.</i>	22
<i>Bovo, S.</i>	25, 43
<i>Brouwers, S.P.</i>	42, 66
<i>Brown, D.</i>	73, 74
<i>Buhre, L.</i>	37
<i>Bushby, E.</i>	28

## C

<i>C. De Jong, I.</i>	22
<i>Cabaraux, E.</i>	45
<i>Cabrera, V.</i>	30, 46, 47, 49
<i>Cabrera, V.E.</i>	67
<i>Calmels, M.</i>	45
<i>Calvet Sanz, S.</i>	69, 72
<i>Campbell, M.</i>	58
<i>Canuto, S.</i>	46
<i>Carlton, Z.</i>	74
<i>Carnier, P.</i>	74
<i>Cavallini, D.</i>	20, 26
<i>Ceia, J.</i>	35
<i>Chai, L.</i>	26
<i>Charles, M.</i>	23
<i>Chen, B.</i>	34
<i>Chen, C.Y.</i>	52
<i>Christophe, O.</i>	45
<i>Cigagna, I.E.</i>	32
<i>Claes, P.</i>	68, 71
<i>Colleluori, R.</i>	20, 26
<i>Cornuéjols, A.</i>	23, 54
<i>Costantino, A.</i>	72
<i>Coussement, S.</i>	21
<i>Curik, I.</i>	44
<i>Curik, T.J.</i>	44

## D

<i>Da Silva, L.</i>	30, 49
<i>Dahal, S.</i>	26
<i>Dale, L.</i>	30, 61
<i>Darrigade, L.</i>	70
<i>De Baets, B.</i>	55
<i>De Cesare, A.</i>	26
<i>De La Vallée, P.</i>	49
<i>De Mol, R.</i>	22
<i>De Poorter, E.</i>	27
<i>De Rijcke, H.</i>	41, 67
<i>De Smet, S.</i>	70
<i>De Temmerman, P.J.</i>	21, 28, 35, 41, 62, 67
<i>Dechaux, T.</i>	23, 51
<i>Defoort, J.</i>	35

<i>Degroote, J.</i>	24, 29		
<i>Dehareng, F.</i>	45		
<i>Delacauw, S.</i>	41, 67		
<i>Deroche, B.</i>	25		
<i>Deruyck, M.</i>	27		
<i>Deutsch, J.</i>	42		
<i>Dhungana, A.</i>	26		
<i>Di, M.</i>	34		
<i>Diaz Bahamonde, F.</i>	68		
<i>Díaz De Otdólor, X.</i>	61		
<i>Dichou, K.</i>	39		
<i>Do, Y.</i>	52		
<i>Doidge, C.</i>	28		
<i>Domović, D.</i>	44		
<i>Doucet, M.</i>	52		
<i>Ducrue, C.</i>	23		
<i>Düpjan, S.</i>	42		
<i>Duvauchelle Waché, A.</i>	52		
<b>E</b>			
<i>Ede, T.</i>	56		
<i>Eerdekens, A.</i>	27		
<i>Egger-Danner, C.</i>	38		
<i>Emsen, E.</i>	63		
<i>Ettema, J.</i>	37		
	25		
<i>Exler, J.</i>	39		
<b>F</b>			
<i>Fabjanowska, J.</i>	63, 65		
<i>Faggion, S.</i>	74		
<i>Faleiros, C.</i>	53, 73, 75		
<i>Ferraz, J.B.</i>	73		
<i>Filippopoulos, O.</i>	32		
<i>Foldager, L.</i>	40		
<i>Fontanesi, L.</i>	25, 43		
<i>Foris, B.</i>	61		
<i>Formigoni, A.</i>	20, 26		
<i>Foy, D.</i>	19, 61		
<i>Franceschini, S.</i>	24, 45		
<i>Franchi, G.</i>	61		
<i>Frauzino, C.</i>	46		
<i>Fred, H.</i>	49		
<i>Frenken, E.</i>	30		
<i>Frere, M.</i>	23		
<i>Fresco, S.</i>	25		
<i>Fukumasu, H.</i>	53, 73, 75		
<b>G</b>			
<i>Gafsi, N.</i>	61		
<i>Ganitzer, J.</i>	38		
<i>Gantner, V.</i>	68		
<i>Gao, J.</i>	66		
<i>Garré, B.</i>	28		
<i>Gaudron, Y.</i>	25		
<i>Gauthier, V.</i>	52		
<i>Gautier, J..</i>	61		
<i>Gebreyesus, G.</i>	40		
<i>Geffert, H.</i>	36		
<i>Gengler, N.</i>	45		
<i>Ghiaccio, F.</i>	20		
<i>Gickel, J.</i>	60		
<i>Giersberg, M.F.</i>	57		
<i>Gimmillaro, F.</i>	53		
<i>Girmay, M.B.</i>	38		
<i>Glaizal, D.</i>	23		
<i>Gleerup, K.</i>	31		
<i>Gol, S.</i>	35		
<i>Gonçalves, O.</i>	75		
<i>Gong, Y.</i>	30, 49, 67		
<i>Greer, N.</i>	50		
<i>Grelet, C.</i>	45		
<i>Gruen, A.</i>	33		
<i>Gunnes, M.</i>	43		
<i>Guo, C.</i>	44		
<i>Guo, Z.</i>	46		
<i>Guy, Z.</i>	23		
<i>Guzzo, N.</i>	74		
<i>Gyldenkerne, M.M.</i>	31, 66		
<b>H</b>			
<i>Han, B.</i>	22		
<i>Harrouet, C.</i>	54		
<i>Hartel, M.</i>	31		
<i>He, S.</i>	34		
<i>He, Z.</i>	46		
<i>Heirbaut, S.</i>	29		
<i>Hekmati, P.</i>	47		
<i>Helary, L.</i>	51, 52		
<i>Helf, P.</i>	57		
<i>Heres, L.</i>	22		
<i>Holl, J.</i>	52		
<i>Hostens, M.</i>	24, 29		
<i>Hu, H.</i>	67		

<b>I</b>	
<i>Indio, V.</i>	20
<i>Ingelbrecht, L.</i>	21, 28, 67
<i>Ipek, N.</i>	55
<i>Ivanov, K.</i>	56, 74
<b>J</b>	
<i>J. Counotte, M.</i>	22
<i>Jacoby, P.E.</i>	24
<i>Jarque, M.</i>	69
<i>Jean-Louis, U.</i>	23
<i>Jensen, D.B.</i>	31, 66
<i>Jeon, S.</i>	25
<i>Jiang, Y.</i>	27, 34
<i>Johansen, K.K.</i>	37
<i>Joseph, W.</i>	27
<i>Jung, Y.</i>	67
<b>K</b>	
<i>Kairisa, D.</i>	64, 70
<i>Kaki, A.</i>	42
<i>Kaler, J.</i>	28, 54
<i>Kaniyamattam, K.</i>	50
<i>Kasper, C.</i>	56
<i>Kiczorowska, B.</i>	65
<i>Klebaniuk, R.</i>	63
<i>Klingler, A.</i>	73
<i>Knöll, J.</i>	19
<i>Knudsen, S.H.</i>	31
<i>Kota, R.</i>	73
<i>Kowalczyk-Vasilev, E.</i>	63, 65
<i>Kramer, T.</i>	30
<i>Krasnevska, N.</i>	64, 70
<i>Krattenmacher, N.</i>	40
<i>Kreuzer, M.</i>	45
<i>Kritsi, E.</i>	22
<i>Küçükay, N.</i>	63
<i>Kuhla, B.</i>	45
<i>Kupisiewicz, K.</i>	71
<i>Kurz, A.M.</i>	65
<i>Kutafina, E.</i>	60
<i>Kuterovac, K.</i>	68
<i>Kutluca Korkmaz, M.</i>	63
<i>Kyriazakis, I.</i>	66
<b>L</b>	
<i>Laique, T.</i>	43
<i>Lamanna, M.</i>	20
<i>Langbein, J.</i>	65
<i>Langkabel, N.</i>	37
<i>Lauront, A.</i>	51
<i>Le Calvez, S.</i>	72
<i>Lebing, S.</i>	42
<i>Leblois, J.</i>	24
<i>Lebreton, A.</i>	51
<i>Lecomte, C.</i>	45
<i>Leroux, S.</i>	48
<i>Li, M.</i>	64
<i>Libera, K.</i>	22
<i>Lin, H.</i>	34
<i>Lindegaard, C.</i>	31
<i>Littlejohn, C.</i>	23
<i>Liu, D.</i>	49, 72
<i>Liu, K.</i>	44, 46
<i>Llonch Obiols, P.</i>	35
<i>Lopes Carvalho, C.</i>	27
<i>López-Hernández, Y.</i>	53
<i>Lourenco, D.</i>	52
<i>Lukamba Nsadsa, D.</i>	51
<i>Lukic, B.</i>	44
<i>Lund, P.</i>	45
<i>Lyu, L.</i>	46
<b>M</b>	
<i>Madouasse, A.</i>	23, 54
<i>Maes, D.</i>	28
<i>Mahapatra, A.</i>	55
<i>Malakovska, D.</i>	64, 70
<i>Malik, S.</i>	29
<i>Mammi, L.</i>	20
<i>Manceau, J.</i>	52
<i>Mansouri, A.</i>	26
<i>Marcilli, G.</i>	73
<i>Marcon, M.</i>	20
<i>Mariani, C.</i>	32
<i>Marie, P.</i>	20
<i>Martens, L.</i>	27
<i>Martin, B.</i>	70
<i>Martin, C.</i>	23, 25, 45, 54
<i>Martins, M.</i>	64, 70
<i>Marvuglia, A.</i>	39
<i>Maselyne, J.</i>	21, 25, 28, 34, 35, 41, 62, 67
<i>Mclaughlin, N.</i>	42, 66
<i>Mcparland, S.</i>	45
<i>Meemken, D.</i>	37
<i>Meier, M.</i>	23

<i>Meijboom, F.L.B.</i>	57, 59	<i>Parsons, T.</i>	56
<i>Méndez Reyes, D.A.</i>	69, 72	<i>Pastell, M.</i>	49
<i>Mezghiche, D.</i>	68, 71	<i>Peralta, D.</i>	27
<i>Mikulec, N.</i>	44	<i>Peralta, J.</i>	19
<i>Milewski, S.</i>	63, 65	<i>Perneel, M.</i>	28
<i>Miller, R.</i>	30	<i>Petie, R.</i>	50
<i>Misztal, I.</i>	52	<i>Picard, F.</i>	25
<i>Morgan, E.</i>	55	<i>Plavina, S.</i>	64, 70
<i>Morgan-Davis, C.</i>	61	<i>Poelman, M.</i>	21
<i>Morris, D.</i>	66	<i>Poleti, M.</i>	53, 73, 75
<i>Mouhanna, A.</i>	70	<i>Psifidi, A.</i>	72
<i>Mudiredy, D.</i>	50	<i>Psota, E.</i>	52
<i>Mughini-Gras, L.</i>	22	<b>Q</b>	
<i>Mwasimuke Tsongo, S.</i>	51	<i>Qian, C.</i>	67
<b>N</b>		<i>Quas, H.</i>	29
<i>Nasser, H.R.</i>	56	<i>Querné, M.</i>	20
<i>Nawroth, C.</i>	42	<b>R</b>	
<i>Neelagiri, S.R.</i>	74	<i>Ramon-Perez, A.</i>	35
<i>Negreiro, A.N.</i>	67	<i>Rapetti, L.</i>	21
<i>Nicolas, E.</i>	51	<i>Rault, J.L.</i>	33
<i>Nielson, P.P.</i>	61	<i>Reding, E.</i>	24
<i>Niu, M.</i>	44	<i>Reed, K.</i>	47
<i>Noor, S.</i>	24	<i>Rehman, A.</i>	71
<i>Nordbø, Ø.</i>	29	<i>Reixach, J.</i>	35
<i>Noronha, E.</i>	46	<i>Reker, I.</i>	36
<i>Northwood, L.</i>	58	<i>Remondini, D.</i>	26
<i>Norton, T.</i>	25, 49, 62, 72	<i>Rey-Cadilhac, L.</i>	70
<i>Nourry, M.</i>	20	<i>Reynolds, J.</i>	19
<i>Nunes, A.</i>	53, 73, 75	<i>Roelofs, J.</i>	59
<b>O</b>		<i>Rogowska, G.</i>	63, 65
<i>Occhiuto, F.</i>	28, 54	<i>Rose, S.</i>	33, 65
<i>Oczak, M.</i>	57	<i>Rosolen, A.</i>	74
<i>Ödevci, B.</i>	63	<i>Roth, P.</i>	38
<i>Østergaard, S.</i>	37	<i>Rubio-Villa, A.</i>	73
<i>Oveneke, M.C.</i>	51	<i>Ruhland, C.</i>	37
<i>Øverli, Ø.</i>	43	<i>Ruotsalainen, L.</i>	49
<i>Oz, H.</i>	33	<b>S</b>	
<b>P</b>		<i>Sabei, L.</i>	56
<i>Pacholewicz, E.</i>	50	<i>Saeed, I.A.</i>	65
<i>Pan, J.</i>	34	<i>Sagevik, R.</i>	29
<i>Panda, S.</i>	55	<i>Schiavo, G.</i>	25, 43
<i>Paneru, B.</i>	26	<i>Schmidt, C.</i>	30
<i>Parada Sarmiento, M.</i>	56	<i>Schneider, M.</i>	30
<i>Paramonova, N.</i>	64, 70	<i>Schokker, D.</i>	22, 69
<i>Paramonovs, J.</i>	64, 70	<i>Schomburg, H.</i>	19
<i>Pardon, B.</i>	24	<i>Schröder, K.</i>	40

<i>Seidel, A.</i>	40	<i>Van Wyk, J.</i>	55, 73, 74
<i>Siddique, A.</i>	55, 73, 74	<i>Vanlierde, A.</i>	45
<i>Silvestri, S.</i>	21	<i>Vazquez Diosdado, J.A.</i>	54
<i>Sima, K.</i>	64	<i>Vázquez-Diosdado, J.A.</i>	28
<i>Slootmans, J.</i>	62	<i>Veldkamp, F.</i>	22
<i>Smit, L.A.M.</i>	22	<i>Verlinde, S.</i>	35
<i>Smith, T.</i>	19	<i>Verstraete, M.</i>	71
<i>Sneessens, C.</i>	24	<i>Verwaeren, J.</i>	35, 55
<i>Snoeck, L.</i>	41	<i>Veselko, D.</i>	39, 45
<i>Soyeurt, H.</i>	24, 39, 45	<i>Vidal Moreno De Vega, C.</i>	68, 71
<i>Spehar, M.</i>	44	<i>Visentin, G.</i>	20, 26
<i>Stavrou, N.</i>	32	<i>Visscher, C.</i>	60
<i>Stetter, K.</i>	65	<b>W</b>	
<i>Strong, R.</i>	31, 50	<i>Waddell, J.</i>	47
<i>Subedi, S.</i>	26	<i>Wang, A.</i>	50
<i>Surabhi, P.</i>	50	<i>Wang, R.</i>	29
<b>T</b>		<i>Wang, Z.</i>	34
<i>Taghvafard, H.</i>	22	<i>Wiedmann, M.</i>	67
<i>Talcott, S.</i>	31	<i>Wilk, I.</i>	19
<i>Tao, J.</i>	50	<i>Williams, J.</i>	72
<i>Taylor, P.</i>	33	<i>Wishart, D.</i>	53
<i>Tedeschi, L.</i>	50	<i>Wutke, M.</i>	36
<i>Teitscheid, M.S.</i>	65	<b>X</b>	
<i>Ternman, E.</i>	44	<i>Xue, Y.</i>	40
<i>Terrill, T.</i>	55, 73, 74	<b>Y</b>	
<i>Thaller, G.</i>	40	<i>Yale, A.</i>	72
<i>Thodberg, K.</i>	40	<i>Yang, X.</i>	26, 66
<i>Thomas, M.</i>	54	<i>Yang, Y.</i>	64
<i>Tibi, C.</i>	23	<i>Yang, Z.</i>	64
<i>Toth, G.</i>	36	<b>Z</b>	
<i>Trapina, I.</i>	64, 70	<i>Zambianchi, L.</i>	20
<i>Traulsen, I.</i>	36	<i>Zavyalova, K.</i>	19
<i>Tresch, A.</i>	71		
<i>Tuyttens, F.</i>	27, 34		
<i>Tuyttens, F.A.M.</i>	55		
<i>Twite Ndeze, B.</i>	51		
<b>U</b>			
<i>Ullah, H.</i>	43		
<b>V</b>			
<i>Vaishampayan, R.</i>	51		
<i>Valente, B.</i>	52		
<i>Van De Putte, T.</i>	29		
<i>Van Knegsel, A.</i>	59		
<i>Van Noten, N.</i>	34		
<i>Van Poucke, S.</i>	35		
<i>Van Schaik, G.</i>	24		

