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P1

Responsible sense-making of the digital transformation of agri-food systems

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Digital technologies are often seen as an opportunity to enable sustainable futures in agriculture and rural areas. They, however, often have impacts that go beyond use of the digital technology, but also includes social, economic, institutional, etc., aspects, which can be difficult to foresee and understand. Digital transformation is thus a process that comes with uncertainties, expectations and the need for sense-making by different stakeholders.

This sense-making involves understanding how different stakeholders perceive and deal with the digital transformation at an organisational, value chain or at agri-food system level. It often starts with generating awareness at an organisational level and understanding what and how they need to adapt in order to benefit from a digital transformation process (1). The next step in digital transformation often focusses on data sharing along a value chain. A key element for data sharing is trust, both in the technology, as well as in other stakeholders in the value chain (2). I.e. how they are organised in terms of data management and governance, and more importantly how used are they to collaborating in a competitive environment?

Moving from individual organisations and various value chains towards a sustainable agri-food system generates a new set of ethical and social questions, since digital technologies and the related transformation are not inherently good and can have negative impacts. For example people or organisations are excluded (3) through 1) limited access to digital technologies; 2) the design of these technologies; or 3) the complexity of the digital innovation system that encompasses all the social, cyber and physical elements and the relations between them (4). On the other hand people and organisations may (unknowingly) be included, which may also have negative consequences for them (3). This shows a reinforcement of technological lock-ins, competitive behaviour and existing power structures and raises questions such as: who is responsible and/or accountable for these (potential) impacts (4)?

To deal with such ethical and social aspects caused by the uncertainties of digital transformation it is crucial to consider ambidexterity (e.g. a balance between explorations and exploitation), collaboration, trust, reciprocity, and between relevant stakeholders, to allow for a joint process of assessing the appropriate level of digital, allowing space for alternative pathways in both content and process (5). In other words: because it is technologically possible it doesn't mean that must be done from a societal perspective.

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P2

Integration of (Big) Data for Optimizing Animal Health, Welfare, and Productivity in Norwegian Aquaculture: Producing knowledge for decision-making processes

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In the modern world, (big) data is no longer just a tool, but the driving force behind decision-making processes at all levels, including animal health and welfare. Norwegian aquaculture, with its complex and dynamic nature, is uniquely positioned when it comes to the need for data analysis and understanding. With access to extensive datasets spanning multiple aspects of aquaculture, we are able to delve deeper into the challenges and opportunities that lie within.

This presentation will focus on integrating these rich data sources to promote knowledge relevant for the management of Norwegian aquaculture. We will explore how these diverse datasets can be used to improve animal health, welfare, and productivity in aquaculture, and how to make the results accessible for the public through online tools such as R-Shiny applications.

Further, I will touch some of the deeper scientific questions related to the use of data, to shed light on the hidden pitfalls that can distort our understanding and influence decision-making.

I will demonstrate how the careful interpretation of extensive data can be used to promote a more sustainable and productive aquaculture system, with focus on disease and parasite propagation. The goal is to continue our development of robust methods for data analysis and interpretation, contributing to better management and policy within Norwegian aquaculture.

P3

From reporting to impact: leveraging aquaculture data for insights as a government agency

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The amount of data produced worldwide is increasing exponentially – a fact no less true within the aquaculture industry. As a government agency this represents an enormous opportunity be even more precise in our risk-based approach, simplify compliance processes, and digitize supervision activities. Simultaneously, this increase in data challenges traditional approaches, particularly regarding how reporting is collected, used and stored – challenges which must be solved in partnership. The talk will showcase how data can be seen as a core asset in a future data-driven ecosystem, and how this will support a sustainable growth in the aquaculture industry

P4

An early warning system for disease outbreaks in aquaculture using unspecific health-related data

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Mortality is a major problem in salmon aquaculture. In 2022, there were more than 56 million registered salmon deaths in Norway. This represented a yearly probability of death of 16.1% for marine reared salmon [1]. There are many possible causes for the salmon deaths, and infectious diseases are one of the main ones [2]. Pancreas disease (PD) is an example of a viral disease caused by salmonid alphavirus associated with increased mortality and indirect economic losses due to reduced growth of salmon. This disease can be considered endemic in some salmon production areas of Norway and is nationally notifiable. Commercial salmon farming gathers a large amount of data, primarily collected for production management purposes. Such data can potentially be useful for disease surveillance, in particular for syndromic surveillance (SyS). This type of surveillance relies on the detection of aberrations in unspecific health-related data tracked historically and with regular updates. With applications in early warning tools, SyS is a desirable component in animal health surveillance systems with potential to detect disease outbreaks before traditional methods, e.g. clinical investigations and laboratory diagnosis [3]. We conducted a study with the objective to investigate how salmon mortality data reported to competent authorities could be useful for detecting PD outbreaks. Our study population consisted of all aquaculture sites in one of the 13 salmon production areas (PA) of Norway where PD is endemic, i.e. PA 3. Using monthly data reported by farmers, we developed a generalized linear model with individual fish death as the dependent variable. The model contained other production and environmental variables as independent variables as well as an offset to account for the number of fish at risk of dying in a month. We established a training period for the model using data from 2014 to 2017. Data from 2018 to 2021 served for parametrization and evaluation of the performance of an algorithm to trigger alarms if monthly mortality was above a pre-defined cutoff or higher than expected by the model. We adjusted the settings of the algorithm to optimize sensitivity, but with a good balance between sensitivity and specificity that is a typical approach in SyS. The performance tests compared PD outbreaks detected by the proposed SyS and the current surveillance programme for PD in Norway. We found that the SyS method had high sensitivity (87%) for detecting PD outbreaks and that PD was not diagnosed in 94% of the production months without alerts; the SyS method had a high percentage of false alarms (48%). Detection of PD outbreaks by SyS occurred overall 1 month after the current surveillance program (range: 3 months earlier to 4 months later). Our results indicate usefulness of the method for monitoring mortality and disease outbreaks in salmon aquaculture, but it was unspecific in our evaluation that considered only a single disease.

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P5

Machine learning for milk prognosis of individual lactations and aggregated herd milk production

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The main source of income from a dairy herd is the milk produced. At the same time, feed represents the highest cost in production [1]. Being able to predict the milk production and feed requirement are key factors to optimize the production on a dairy farm, both to increase revenue and limit the cost. Traditional modeling of lactation curves for single lactations has been based on the ideas of [1] and curve fitting and has since been generalized to consider curves of a more general shapes [2]. Lately, machine learning techniques have become more popular to model milk production [4,5].

We have developed a machine learning model for predicting single lactations. The overall model is based upon the gradient boosted decision tree method. One model is trained on running lactations and predicts accumulated milk yield in 15-day periods for a total of 345 days. This is combined with another model with the same output that predicts milk yield for lactations that has not yet started.

The data used for training are collected from milking robots which record the yield of each milking. These data are used in combination with the less frequent farmer milk weighing's to ensure a versatile model applicable for all Norwegian dairy farmers.

When putting the machine learning model in context with a stochastic herd modeling approach utilizing information about e.g., animal age, parturitions, insemination, mating, historical milk production and historical culling we predict the aggregated herd production.

The machine learning model accuracy is measured by the absolute relative error and the test data collected from about 200 000 individual lactations with at least 120 days prediction length. The median error is 11.9% with an interquartile range of 5.6 – 20.9 %.

When aggregating to a herd level we obtain a median of 12.3 %, and IQR 5.8% - 21.1 %.

We will demonstrate both the machine learning model and the stochastic herd model and show the results and accuracy.

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P6

Integrating weather data to improve grass production

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Weather data, e.g., temperature and precipitation, is key for several aspects related to plant growth. An early review on the effect of temperature was presented by [1]. A more recent discussion of extreme temperatures in the context of climate change can be found in [2]. Plants require water to grow [2], and in [4] the authors studied the relationship between plant growth and precipitation patterns using satellite data and vegetation maps. They found that changes in precipitation patterns cause non-linear changes in plant growth.

A key factor for agricultural plant cultivation is fertilization, which ensures that the plants have access to appropriate amounts of nutrients, mainly nitrogen, potassium, and phosphorus [3]. This can be achieved by fertilizing with a combination of manure and mineral fertilizers. The correct amount of fertilizer to add depends on temperature and precipitation [4].

We will present three use cases integrating publicly available Norwegian weather data and field specific information to optimize grass production: 1) Fertilization planning using historical rainfall data to estimate run off, 2) modeling mineralization [5] of manure to optimize fertilizer distribution throughout the growing season and 3) field specific temperature sums [6] for decision support to determine harvest timing.

We will demonstrate how integrating weather data actively into these processes gives decision support and improves grass production.

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P7

Combining milk, herd recording and dairy sensor data to improve the life and sustainability of dairy cows

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The Food and Agricultural Organization (FAO) estimates that 14.5% of greenhouse gas emissions are caused by livestock, and the most effective way to reduce the carbon footprint from this sector is to improve fertility and improve the cow’s health. Both will increase the number of productive days during the lactation (1). Improving the health situation for dairy cows, will also contribute to sustainability by reducing the use of antibiotics (2) in the food chain.

Despite large amounts of data being captured on dairy farms most of the decisions made on a dairy farm are not databased (3). We hypothesise that by merging data streams we will be able to provide farmers, and breeders novel and increasingly accurate biomarkers and phenotypes to drive data-based decisions. Loss in body weight (BW) and body condition are important markers for energy deficits, and loss in body condition score (BCS) of more than 0.5 on a five-point scale is associated with increased risk of ketosis and impaired reproductive function in Norwegian dairy cows (4). However, visible changes in body condition first appear at a time when corrective measures may be less effective in preventing unwanted health, reproduction, and welfare effects (5), such that reliable estimates of BW changes is better obtained by sensor information.

We have used Transform Infrared (FTIR) spectroscopy of dried milk to build milk fatty acid profiles. These profiles have been used as early bio-indicators of energy deficits (subclinical ketosis) and impaired reproduction in Norwegian dairy cows (6, 7). Currently, we are merging data from different sources, including traditional milk and cow level data, sensor information on BCS and FTIR-derived fatty acid profiles to identify cows with subclinical ketosis within the three first weeks of lactation. Preliminary analyses show an ability to detect “at risk” cows with a specificity of 95% and a sensitivity of 70% with traditional multivariate regression techniques. This way, we can identify cows with major energy deficits before changes in BCS becomes visible to the human eye. A high specificity is the most important characteristic of decision support systems, as false negative alarms will discourage its use by farmers. The sensitivity of our diagnostic tests might be increased by adding more information to the current model, or by serial (repeat) testing. It is our hope to improve the models by including more data on a cows previous disease and breeding history in our assessments.

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P8

PigAtlas – Metamorphosis of geek statistics to an industrial asset during the decade of artificial intelligence

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Pig carcasses are fabricated into wholesale cuts, using knives, saws, and other mechanical equipment. The wholesale cuts include the shoulder, loin, belly, and ham. These primal cuts are standardized trade goods with different uses and monetary value, consequently their relative proportions are of crucial importance for the overall value. The size and specifications of these cuts varies between countries.
Topigs Norsvin (TN) is the worlds second largest pig breeding company Worldwide, with markets in 52 different countries in Europa, North and South America, Asia and Africa. More than 100 million slaughter pigs with TN genetical origin are slaughtered annually. In 2021 TN included “Selection for primal yields” in their breeding program [1], a result of extensive research during the previous decade. TN included computed tomography (CT) as part of their breeding program in 2008. Approximately 3000 boars of purebred Landrace and Duroc were tested each year for *in vivo* carcass traits. These numbers expanded till around 3000 in Norway and 5000 in Canada by 2022, including 2 new breeds, in total 4 breeds, 2 terminal and 2 maternal. Prior to 2021, phenotypes obtained from CT scanning was restricted to overall body composition, and surveillance of potential illnesses like osteochondrosis.
“Selection for primal yields” was initiated by Lars Erik Gangsei’s PhD work (2013-16), where the construction of an anatomical three-dimensional pig template, “PigAtlas”, for primal yields, was essential [2]. The template was an ensemble of triangular meshes, defining the primal cuts. Based on this result, Norsvin initiated a new project named “PigAtlas” (2016-20). The time period for the project coincided with a rapid development in artificial intelligence, consequently the original mesh-based Atlas was utilized to annotate 2D images, which in turn were utilized for training AI models for semantic segmentation. The distribution of primal cuts obtained by the AI models were shown to be heritable [3], a prerequisite for their inclusion as useful phenotypes in a breeding program. Finally, the PigAtlas project came to fruition by the “Selection for primal yields” in TN breeding program.

The newest AI-model for carcass cuts was implemented autumn 2022. This resnet-based [4] model was trained on predictions of 85 animals stratified sampled across from a previous AI-model, but now using human corrections of predictions, prior to training. High heritability’s of primal cuts (h^2:45-58%) demonstrates the accuracy of the AI generated phenotypes. The methods and models are still subject to improvement and development, with high emphasis on visceral organs and bone health, in order to further improve swine health and robustness through selective breeding.

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P9

Improving udder health in Norwegian dairy herds through machine learning and transmission modelling

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Mastitis is one of the main health issues in dairy herds and one of the most economically important diseases in dairy farming, so detection and management of the disease at an early stage would be beneficial. Today, many dairy farms use automatic milking systems (AMS) which have enabled access to data on several traits from each milking, such as online cell count (OCC), electrical conductivity and milk yield. TraWel is a project at NMBU Faculty of Veterinary Medicine that aims to develop methods for early detection of mastitis in cattle using the large amount of data collected through the AMS. For the Green Data Lab Conference, we will present plans for the interdisciplinary project, selected results from this first study and some challenges.

The methods used in the project include data analysis and pre-processing of large amount of data. A better understanding of the differences between physiological and pathological changes in the milking traits can be achieved by comparing changes in the milking traits against bacteriological culture results and through the use of machine learning. Machine learning methods will also be used for feature selection and mathematical modelling will be used to develop the transmission model.

One of the projects objectives is to develop a transmission model for subclinical mastitis within a herd. Such a model would provide useful predictions of potential transmission of infection and the effect of control measures. In order to develop such a model, it is necessary to distinguish between susceptible and infectious cows. Milking trait values varies a lot between cows, and between repeated measurements from the same cow. Udder infections are known to affect several milking traits, and the first part of the PhD project is to assess pathogen-specific patterns in relevant milking traits. The results from this study include which of the pathogens appear to have the largest effect on the traits and that the patterns from these pathogens should be in focus when trying to detect contagious infections. All the studied pathogens increased both level and variability in the measurements of OCC and regression analysis found the pathogens to have a significant effect on this trait.

Challenges related to this project include common issues when working with medical data, like missing data and an uneven distribution between healthy and sick cows. Because of the large variation in the measurements, we are looking for methods for transformation of the data that preserve the variation that is relevant for detecting infection. Currently, we are working with data from one herd and a challenge related to this is making models that are general enough to be used in different herds. For subclinical mastitis there exists no perfect reference test to determine infection, and this will cause some uncertainty when using bacteriology as target in supervised machine learning models.

The plan forward is to continue the search for features that are relevant for detecting infection at an early stage and start working on the transmission model for subclinical mastitis. Prediction of subclinical mastitis will constitute a useful decision-support tool for the farmers and contribute to better udder-health in dairy herds

P10

Causal Modelling (for Improving Animal Health)

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The development of causal graphs has made causal inference more tractable and available for any researcher with basic statistical training. Overall, the presentation emphasizes the importance of developing a robust causal inference workflow to accurately estimate causal effects and improve the reliability of scientific findings (1). My presentation will present a workflow for causal inference intended for engineers, food scientists, and data scientists working within the food research industry. The case example analyzes the relationship between risk factors and prevalence ascites in chickens.

Ascites is a condition in which fluid accumulates in the abdominal cavity, caused by progressive heart failure. Ascites is a common and significant health issue in broilers. Therefore, knowing more about the risk factors for ascites and thereby finding ways to reduce disease prevalence under field conditions is important.

While experimental study designs are traditionally used to ensure that statistical association is causation, the vast amount of observed data in modern science makes it necessary to develop additional steps for causal inference. A causal inference workflow involves at least seven stages, including (1) stating the causal question, (2) drawing a causal Directed Acyclic Graph (DAG) to determine identification, (3) testing the statistical assumptions in the DAG, (4) find an estimator, (5) estimating the model, (6) report results and (7) validate/verify the results through prediction.

In addition to its significance for animal health, ascites is an important economic issue for the broiler chicken industry. Ascites is a complex condition with multiple potential risk factors, and understanding the causal relationships between these factors can help identify effective interventions to reduce its prevalence. As presented in this work, a robust causal inference workflow can provide a systematic and transparent approach to estimating causal effects from observational data and ultimately lead to more reliable and accurate findings in the food research industry.

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P11

DHP – Norwegian electronic solution for Food Chain Information

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Digital technologies will not only exchange analogue technologies, but alter the way we work, stakeholders' natural roles, and division of labour [1].

It is mandatory for food animal producers to provide the Meat Inspection services with Food Chain Information (FCI) before animals are sent to slaughter. The abattoirs receives the information and forwards the FCI and their assessment to the Meat Inspection services 24 hours before the animals arrive the abattoirs. FCI is information about the health condition and medical treatments that can have an adverse effect on meat safety. FCI is intended to support a risk-based meat inspection [2].

In the innovation project EyeAM – digital transformation of meat inspection, a system thinking approach was applied to illustrate how data and information flows among interconnected stakeholders with the application Dyrehelseportalen (DHP) [3,4]. The ambition is to apply automatic epidemiological analyses to extract more useful information than the minimum legislative demands.

An animation has been developed assisted by NMBU Læringsenteret to ease understanding of the complex system. Mattilsynet, the Norwegian Food Safety Authority, has made a complimentary system, MAKKS, to receive the electronic information. DHP + MAKKS is unique in Europe and a very successful example of Norwegian public-private collaboration for digital transformation.

The animation will be shown for the first time at the conference.

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P12

Implementing whole genome sequencing for surveillance, outbreak detection and investigation

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The use of whole genome sequencing (WGS) data for monitoring microbial pathogens is increasing. WGS data can be used to compare and characterize microbes, and has proven to be very useful for surveillance and for outbreak detection and investigation. However, such activities are made significantly easier if there are systems available to support them. In our experience, there are two main requirements that such systems need to satisfy: 1) the methods need to be well implemented and integrated into the OH process, and 2) the methods need to be available to the people who will make decisions based on the results, and the people in question need to be able to interpret the results in appropriate ways. We have at the NVI implemented an analysis system that in our experience satisfies both requirements.

The system we have selected to implement and adapt is the web based IRIDA system (irida.ca), which has been developed by The Public Health Agency of Canada and other actors. IRIDA uses Galaxy as an analyses engine and comes with pipelines, visualization tools and a project-based data management system that allows for fine grained data access control. In addition to the pre-existing pipelines we have extended the system with our own pipelines to cover the needs of the NVI. In this system several different analyses are available, such as virulence characterization, antimicrobial detection, MLST and serotyping, and clustering via cgMLST and phylogeny.

Within the NVI, this new system is currently being integrated into our work processes, and we are establishing guidelines regarding what analyses will be used for which purposes. The information needed to solve outbreaks is not necessarily the same as is needed for surveillance purposes, and the characteristics of the pathogen may also influence the choice of analysis. These factors need to be integrated into the analysis guidelines to ensure that the results that are being produced are fit for purpose.

The system itself as well as the guidelines are being developed in collaboration between bioinformaticians, microbiologists, computer scientists, veterinarians and other domain specialists to ensure that there are no misunderstandings in the analysis pathway. This process has not been without its challenges. In this presentation we will describe how the NVI has worked with the implementation of this system, describe the solutions we have come up with so far, and discuss how we will proceed further with integration and implementation of WGS analysis.

P13

Using machine learning for cattle growth prognoses

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The cattle live and slaughter weight is important for several players in agriculture. For the farmer the liveweight is key for correct feeding strategy [1], and thus also herd management. The live weight and growth rate is related to the animal energy and protein requirement and feed intake. Thus, also a climate impact. The slaughter weight determines the slaughter value of the carcass for the farmer and can be used also for optimizing the logistics of slaughterhouses. Being able to prognose cattle growth is therefore key for production optimization and to monitor climate footprint.

Traditional methods for growth estimation mainly consists of different variants of curve fitting logistic-like functions through an appropriate selection of data [2]. The weakness of such approaches is that it is difficult and cumbersome to consider the variability from animal to animal, and herd-to-herd, in a general way. Lately, machine learning techniques have emerged as a viable alternative to address this challenge [3].

We have developed a machine learning method based on a gradient boosted decision tree approach that estimates live weight and slaughter weight ahead in time simultaneously for individual animals. The data source is Mimiro's database containing data on most animals in Norwegian dairy herds and some beef herds. We utilize available live weight measurements and slaughter weights as data for training. Each animal is described by a set of features such as historical live weight measurements, body condition score, chest girth, age, breed, and owner. We train separate models for each gender, and separate models for animals with/without previous live weight measurements. We use a standard randomized train/validate/test split of data in combination with cross validation to avoid overfitting, and hyperparameter search was performed to optimize the model. The training data was limited to 150 000 animals due to computational limitations.

When considering prognoses one year ahead in time the median error for liveweight and slaughter weight on the test dataset was 0.5% and 0.28%, respectively, for animals with historical live weights. The corresponding inter quartile ranges (IQR) were -14% - 14% and -16% - 16%. For animals without historical live weight measurements the corresponding medians were 1.6% and 5%, respectively, and the IQRs -17% - 17% and -19% - 19%.

We will explain the construction of the models, show the accuracy and output, and discuss some applications of the model.

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P14

The role of spectrometer design in optimising data quality and enabling digitalisation

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The digital representation of physical systems and objects is the foundation of sustainable digital solutions. By feeding robust data into a digital twin or advanced algorithms, you can reach the full potential of the solution and build trust with the operators who use it on a daily basis. Spectrometers are valuable sensors that are suited to digitising food and agricultural quality parameters, as they enable the measurement of many complex biological and chemical components. However, they are instruments that are susceptible to matrix effects and, on top of this, natural biological variations add to the complexity of the measurement challenge, beyond the spectrometer design itself. The trend towards black-box AI analytics and the miniaturisation of spectrometers pushes us in the direction of systems that are built on less solid foundations, whereas prioritising data quality, explainable data analytics and understanding deviations in data make it possible to build more trustworthy systems. This talk will discuss the role of spectrometer design in digitalisation, and how understanding and knowing your data can make a difference.

P15

Using shared spectroscopy data with calibration transfer

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There is an increasing number of datasets available for download on the internet. Combined with calibration transfer, this opens a new possibility in spectroscopy: to calibrate a spectrometer without creating a calibration set. This removes one of the largest disadvantages of spectroscopy, the costly and time-consuming calibration. A few samples are still required for tuning and validation, but that number is much smaller than what is usually required for a full calibration. Most traditional calibration transfer methods require samples that have been measured on both spectrometers, and that the spectrometers are similar. To make full use of the advantage of shared dataset, our calibration transfer methods will need to work without using samples with spectra acquired on both spectrometers and be able to handle very different spectrometers. Here we present a calibration transfer method able to do this, as well as a few examples where it has been applied.

The calibration transfer method works in three steps: first, the wavelength correspondence is matched between the spectrometers. In the examples used here, the wavelengths supplied by the spectrometer manufacturer have been used. Other methods are available if those are not sufficiently accurate. Second, a PLS model is trained using data from the source spectrometer using a few spectra from the target spectrometer to select the number of components. Third, the predictions in the target spectrometer are slope-and-bias corrected. A few samples and references are required for selecting the number of PLS components and doing the slope and offset correction, but much fewer samples than required for a full calibration.

This kind of calibration transfer is an important step in sharing data: it enables user to benefit from shared data. Ideally, any field with the potential to share data should have methods for using that shared data. Those methods should also be simple and robust so to make the data sharing easy on both sides, both the sender and receiver should be able to participate in the sharing easily, regardless of instrumentation and scenario. Any data available should be sharable because some user may benefit from it, even if it is incomplete.

P16

From laboratory to process: Understanding industrial process variations with FTIR Spectroscopy

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The Norwegian food and feed industry is committed to significantly reducing food loss, and a major challenge is to effectively handle and utilize all available bioresources of different origins and quality in the best possible way. Smart sensors for controlling and optimizing industrial processing are one key step in solving this challenge, and Fourier Transform Infrared (FTIR) spectroscopy is a highly relevant sensor in this respect. FTIR is a well-established laboratory method for qualitative and quantitative analysis of chemical compounds, and the technique is adopted in several industry segments (e.g., pharmaceutical, and dairy industries). However, industrial implementations of FTIR to characterize and analyze complex bioprocesses are still scarce. Today, FTIR approaches for industrial analysis are becoming available. Thus, understanding the FTIR behaviour towards industrial samples is very important. FTIR spectroscopy is a sensitive probe for protein analysis, and in our previous studies, we have shown that FTIR is a potential tool to predict the composition of complex protein products obtained from enzymatic protein hydrolysis [1]. Also, previous work has shown that raw material composition and process parameters affect protein composition in small-scale and highly controlled laboratory settings [2, 3]. In a recent large-scale industry experiment, we have been able to do frequent product sampling and FTIR analysis from an industrial hydrolysis process with designed variations in raw material composition and processing conditions. In the presentation we will show that FTIR is sensitive enough to capture subtle product differences induced by variations in raw material and processing conditions, suggesting that FTIR is a promising tool for process monitoring and quality control in the industry.

Keywords: Fourier Transform Infrared Spectroscopy, Protein Hydrolysates, Process Parameters, Quality Control

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P17

In-line Raman Spectroscopy for Characterization of an Industrial Poultry Raw Material Stream

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The inherent raw material variation of foods reduces process efficiency and increases waste and variation in food products. Thus, developing sensors to monitor and control this variation is an important aid in developing sustainable food processes. One example is found in the poultry processing industry, where enzymatic protein hydrolysis (EPH) has been adapted as a strategy to recover and valorize constituents from by-products (e.g. carcasses and mechanical deboning residues). In this process, proteins from the by-products are digested and solubilized by proteases. The raw materials entering the hydrolysis process are typically very heterogeneous, consisting of different mixes of e.g. water, meat, skin, tendons and bone from chicken and turkey. This variation is a challenge when specific and stable product quality is important. It has been found that poultry raw material variation impacts quality parameters such as peptide size distribution and amino acid composition. Furthermore, the product quality is a function of raw material composition in combination with different process parameters. This motivates in-line measurements of the raw materials input to the hydrolysis, which could provide the means for real time process control, potentially leading to better raw material utilization and help prevent batches of hydrolysates being discarded from the human market. Raman spectroscopy is a promising spectroscopic technique for in-line food analysis, with the advantage that both gross components, including fat, proteins and bone, can be targeted at the same time as more detailed information on protein composition, e.g. the concentration of collagen. The main aim of the present study was therefore to use in-line Raman spectroscopy for characterisation of an industrial poultry raw material stream. In the work, calibrations based on Raman measurements of fat, protein, ash (proxy for bone) and hydroxyproline (HYP, proxy for collagen) in ground poultry rest raw material were established. Subsequently, the obtained calibrations were tested for continuous monitoring of a ground poultry by-product stream at a commercial hydrolysis facility over the course of two days. To the best of our knowledge, this is the first time a Raman probe has been tested in-line under relevant measurement conditions in the food industry.

P18

Combining LC-MS/MS analysis with chemometrics: getting the most out of mycotoxin surveys.

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Mycotoxins are toxic fungal metabolites. Screening for them is crucial to ensure the safety of our food system. Occurrence data forms the basis for risk mitigation strategies, the reduction of exposure, as well as for the estimation of the economic impact of these toxins [1]. Liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) is considered the gold standard for mycotoxin analysis, as it allows for selective and sensitive multi-toxin screening. Quantification of several hundred fungal secondary metabolites is doable with LC-MS/MS [2]. However, the method is usually only used to screen for a few regulated mycotoxins.

In this study, we paired chemometrics with targeted LC-MS/MS analysis of Austrian maize and wheat samples from two years and of different geographical origin. We screened for 1000 secondary metabolites, as such an extension of analytes hardly increases the measurement time and is in good accordance with green analytical chemistry, where ideally as many analytes as possible are measured with every analysis [3]. We found a total of 88 secondary metabolites produced by different microbes, of which 12 are regulated mycotoxins. By using principal component analysis, differences in metabolite occurrence between the crops, years, and regions could be visualized. Partial least squares discriminant analysis was used to identify metabolites responsible for these differences. Out of the 88 found metabolites, 19 are discriminative between the crops, years, and regions.

In the end, this demonstrates that by increasing the number of analytes towards non-regulated metabolites yearly, regional and crop-associated effects can be studied in parallel to mycotoxin surveys. The additional information obtained with every analysis could thereby help to understand the effect of climate change on fungal pathogen occurrence, as well as the influence of non-mycotoxigenic fungi on the agronomical performance of crops.

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P19

Spectroscopic sensor data for sustainable food production

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The agrifood sector is challenged to produce sufficient, high quality food for a rapidly growing population, while reducing its impact on the environment. To reach this goal, the productivity should be increased with minimal use of energy, water, fertilizers and pesticides. While automation technologies have strongly increased the labor efficiency in this sector, they do not necessarily make the production processes more sustainable. For example, the possibility to farm larger areas and herds has reduced the time available to the farmer for monitoring his plant and animal production systems, while these are typically more variable than technical systems.

The aim of Smart Farming is to increase agricultural resource efficiency by applying the right treatment at the right time to every individual plant and animal. In an analogous way the food industry aims to maximize their resource efficiency by taking the right decisions. Thanks to their large information content, non-destructive character and high measurement speed, spectroscopic sensors have high potential in this context. In this talk, recent developments in the use of spectroscopic sensor data for increasing the resource efficiency of the agrifood sector will be discussed with examples from plant and animal production.

P20

Fatty Acid Measurements in Salmon Fillets using an AI-powered Robotic Raman Spectroscopy Framework

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Assessing food quality parameters using non-destructive methods is a frontier in research and development projects; these parameters benefit consumer health and thus profits for the food industry. Current methodologies include Raman spectroscopy and NIR Hyperspectral Imaging to estimate bone concentration in ground chicken [1], omega-3 fatty acids [1, 2] and Astaxanthin content in salmon fillets [3]. These measurements are conducted manually in the laboratory, which are tiresome, erroneous and impractical for a large sample space. An automatic system to qualify every salmon for in-line measurements process prior to sale is beneficial to the producer and consumer; thus, demanding a robotic solution. We present a proof-of-concept (PoC) robotic solution to measure the omega-3 fatty acids in salmon fillets using Raman spectroscopy in a simulated industrial environment [4]. The PoC system successfully uses image-based detection, accurately tracks a salmon on a conveyor module and measures Raman spectra in real-time using a 6-axis robot arm equipped with a Raman probe. The measured signals from salmon fillet movement at low (10 mms^{-1}) and high (100 mms^{-1}) conveyor speeds have an average SNR of 30, whereas manual measurements presented in the literature [1, 2] have an average SNR of 60. Thus, there is a need for improvement and robustness for the PoC system. We enhance the robotic system to account for varying breeds, trims, sizes of salmon using state-of-the-art Artificial Intelligence (AI) models and Computer Vision (CV) methods [5] to achieve a better SNR. The current progress is a robotic system that is significantly immune to parameter variations such as lighting and prior sample training/preprocessing. Processing salmon includes, but is not limited to, sorting post a Raman scan, database creation, and removal of damaged/undesired melanin sections. The fully integrated system is envisioned to be flexible to measure and manipulate food samples at a pilot scale production in real scenarios along the food value chain in the near future.

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P21

Multidimensional Characterization of Natural Organic Matter in Water: Harnessing EEM-PARAFAC with Aggregate and Fractional Analysis

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Climate change and growing population pose risks to drinking water quality by increasing long-term exposure to disinfection by-products. Variability in dissolved organic matter (DOM) composition, driven by rising temperatures and shifting precipitation patterns, affects water treatment processes. It is vital that treatment processes adapt dynamically to the real-time composition of DOM to minimize harmful by-products in treated water.

Natural organic matter (NOM) significantly impacts water treatment processes and is associated with adverse health effects. Optimizing NOM removal is crucial for managing fluctuations in NOM concentration and composition driven by climate change. Real-time quantification and characterization of NOM are essential to predicting its reactivity and removal during water treatment, but this remains challenging due to the diversity of molecules and their low concentrations.

We employed EEM-PARAFAC analysis combined with aggregate and fractional properties of NOM from Norwegian surface water samples. Our hypothesis posits that utilizing NOM characteristics from EEM and UV-VIS spectra alongside aggregate parameters will reveal further associations between NOM fluorescence and functional properties.

Our results identified six informative variables from three measurement clusters, obtained from principal component analysis of EEM and UV-VIS spectra, as well as aggregate and fractional characteristics of NOM.

This study demonstrates that combining fluorescence EEMs and PARAFAC offers an alternative method for characterizing and evaluating NOM removal in drinking water treatment processes. The approach can be used to optimize treatment facility design and operational effectiveness. However, limited selectivity in fluorescence measurements and environmental factors restrict EEM-PARAFAC's broader application. Coupling fluorescence measurements with UV-VIS and aggregate NOM assessments can enhance EEM-PARAFAC's selectivity, paving the way for more robust and versatile applications in the future.

P22

Sparse spectroscopic sensor data for food quality testing: data analysis modelling approaches

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To be able to assess food quality and safety is important to avoid food losses along the value chain. An assessment of the food shelf live can be crucial to make the right decisions in the distribution of food to customers. Infrared spectroscopy has been used since several decades for assessing food quality and safety in a lab environment. To bring the possibility for assessing food quality closer to the food chain, there is a need for cheaper, faster, and portable infrared devices to perform in-situ quick analysis of food quality. Therefore, instruments with smaller, and cost-effective components (such as bandpass filters, single channel detectors, and laser-based light sources e.g., inter-band and quantum cascade lasers) are being implemented. Such instruments often provide measurements in form of sparse data, which include a collection of single-frequency channels or a collection of channels covering very narrow spectral ranges depending on the component comprising the instrument. The number, quality, and in general specifications of these components, will affect the final price, but also the performance of the instruments. Therefore, the number of measurement points (i.e. channels) needs often be kept at minimum. Modelling and preprocessing of the data however need a sufficient number of channels to perform the task. Calibration methods for sparse data analysis, such as multiple linear regression (MLR), cannot handle highly collinear variables such as narrow band spectral data. Methods commonly used in multivariate analysis, such as partial least squares regression (PLSR) and random forest (RF), are not particularly suited for sparse data with very few single-frequency channels.

In this study we suggest an approach to sampling wavelength channels to perform calibration modelling to predict fatty acid composition of milk and fungi of existing FTIR datasets, by simulating the sparse data. The aim was to understand how different sampling approaches affect modelling results, and which method should be used for different sparse data. Compared to prediction models based on broadband data, PLSR obtained good prediction models with only few multi-frequency channels, i.e., channels covering narrow spectral region. In contrast, RF regression and MLR models did not gain in performance compared to the models built using single-frequency channels. However, more single-frequency channels are required for successful modelling using MLR and RF algorithms.

The sampling strategy of wavelength channels suggested in this study, namely extending few single-frequency channels to multi-frequency channels comprising of narrow regions, has a direct application for laser industry. The lasers can be built such that they can be tuned to measure in a narrow region instead of single frequency. The results therefore can provide an important insight and suggest optimal approach for selecting wavelength channels. [1-4]

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P23

Application of UAV imagery for phenotyping of agronomically important traits in faba bean

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Faba bean (*Vicia faba* L.) is a globally cultivated cool-season grain pulse crop that possesses high seed protein content, making it an excellent source of food and animal feed [1]. Faba bean has the potential to meet the increasing global demand for plant-based protein and it is suitable for sustainable agricultural systems due to its capacity to improve soil nitrogen fertility [1]. Faba bean breeding program aims to develop adapted, disease-resistant, high-yielding, and stable germplasm. High throughput phenotyping as a useful method in breeding can be achieved using UAV remote sensing platforms equipped with various sensors including RGB and multispectral cameras, to quickly asses traits such as yield, plant height, and disease outbreak in the field [2]. In this study, a spring faba bean trial of 38 cultivars with 4 replicates was conducted at Vollebekk Research Farm, at the Norwegian University of Life Sciences (NMBU), in South-Eastern Norway in 2022. The study aimed to evaluate the relationship between the faba bean manual plant height and UAV plant height estimation by RGB camera and assess changes in multispectral-based vegetation indices over the growing season in order to investigate their effectiveness in identifying faba bean phenology. Additionally, the study aimed to identify the optimal development stage of faba bean yield prediction using two machine learning algorithms, Support Vector Regression (SVR) and Random Forest (RF) with two feature selection methods, Pearson correlation coefficient (PCC) and Sequential feature selection (SFS).

The result showed a high correlation (0.97) between manual and UAV plant height measurements during the season. The height profiles of cultivars provided by RGB camera identified the occurrence of lodging which is a common physiological disorder during faba bean growth and development [3]. The trend of 8 spectral indices during the growing season showed that the Normalized Difference Vegetation Index (NDVI), Enhanced Vegetation Index (EVI), and Normalized Green Red Difference Index (NGRDI) could trace the different development stages of faba bean as flowering, pod development, and maturation. These indices increased after germination til flowering and decreased at maturation. Furthermore, EVI effectively demonstrated the outbreak of chocolate spot (*Botrytis fabae* L.) in the field at two development stages. This fungal disease resulted in a significant reduction in EVI which was highly correlated with disease severity in different cultivars. Spectral indices could predict faba bean yield at four different development stages, flower bud present, first flower open, first pod reached final length, and beginning of pod ripening. However, the best yield prediction was at stage 2 (first flower open) by SVR and using PCC as feature selection (R^2 0.83, RMSE 0.53). Our findings will facilitate the development of a non-destructive and high-throughput method to estimate plant height, lodging, disease occurrence, and yield of faba bean. This will accelerate the screening of germplasm and breeding materials in breeding programs, facilitating the development of resistance and high-yielding cultivars.

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P24

Sharing data for creating value and transparency – Reflections by NCE Seafood Innovation

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With the goal to tackle the sea lice challenge collaboratively, the data sharing platform AquaCloud was started as a project by NCE Seafood Innovation in 2017. Since then, a lot of work has been put into establishing the platform, a common language and standards that are necessary for succeeding with data sharing.

More and more data are collected, and the time is ripe for harvesting actual results as well as scale data sharing and extend it to further fields of application.

Data sharing can be a significant driver for value creation if done properly. It is a must if the aquaculture industry wants to 1) improve operational performance and 2) secure its 'license to operate' and deliver on demand for more transparency in the value chain. Solutions to challenges in areas such as fish health or environmental footprint rely on data sharing and cannot be found or established by single companies.

NCE Seafood Innovation plays an important role in facilitating industry collaboration and is a strong advocate and convinced of the necessity of data sharing. Against this backdrop, the cluster has put together an easy-to-understand report on data sharing based on close to 40 in-depth interviews with key persons from stakeholders throughout the value chain. The report provides a clear value proposition of data sharing, outlines the breeding ground for it and defines seven enabling factors that the success of data sharing depends on.

Dominik Flatten, who has been leading this project, will share reflections and learnings from making the report that is meant to push the development of a strong 'data sharing culture' and provide an overview over what it entails, requires and – most important – what possibilities it gives.

P25

The Digital Salmon: Why collaborate on data analysis in production biology?

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Sustainable aquaculture is poised to be a vanguard and early adopter of data science and integrative systems biology. Private companies are accruing operational data and searching for the most relevant sensor and monitoring technologies, applying cutting-edge big data analysis for purposes of operations monitoring, feeding, welfare monitoring and sea louse forecasting. However, it remains challenging to generate value from data through mathematical models. The reasons are partly technical and organizational, in connecting and integrating expertise on biology, operations, business and analytics. This can to a large extent be addressed with common standards for data acquisition and interchange, and proper labeling of data and models, making them easier to overview and navigate. However, another barrier is fear of sharing -- of giving away the value inherent in one's data, or exposing business secrets. There is a need for new role models for business concepts and data sharing agreements that address the interests of the necessary participants. I will comment on these issues, drawing upon examples from the Green Data Lab workshop.

P26

In silico feed trials suggest candidate feed recipes

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Aquaculture has become a large part of global food production. Salmon is the most important aquaculture species in cold water, and among the reared animals with lowest co2 footprint.

However, the growing industry has a shrinking pool of available resources. Novel feed ingredients are needed for the industry to prosper and develop further in a sustainable manner.

The metabolic model SALARECON [1] represents the network of chemical reactions catalyzed by the enzymes encoded by the Atlantic salmon genome. This model is a step towards a predictive evaluation of feed ingredients.

Feed trials were simulated using the molecular compositions of feed ingredients to constrain a version of SALARECON with expanded lipid metabolism. The results suggest optimal feed recipes, combined with predictions of fatty acid composition of the resulting salmon filet.

Data on price, co2-footprint and digestibility were used to constrain the simulations further if available, showing potential for adaptable feed formulations evaluated by multiple metrics.

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P27

DIGIHEART - prediction at the heart of fish mortality

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Fish mortality is a significant challenge for the Nordic aquaculture industry, impacting sustainability, ethics, and the economy. In Norway in 2022, mortality rates for farmed Atlantic salmon during the grow-out stage at sea exceeded 20%, with evidence indicating that cardiac failure related to heart morphology or disease is a leading cause [1]. Addressing the issue of cardiac morphology in farmed Atlantic salmon is essential for sustainable production and growth in the industry. As cardiac morphology is a promising predictor of mortality risk [2], there is a pressing need to develop tools for on-site evaluation that are both efficient and standardized.

The DigiHeart project aims to enhance fish welfare and biological performance in salmon farming by developing insights, diagnostic tools, and predictive models. To standardize data on cardiac morphology, the project has developed deep learning models for automating cardiac morphology measurements in farmed salmonids. To understand the causes of morphological deviations, the project collects data sets and hearts from fish groups in Norway and at the Faroe Islands, linking production practices and events to the development of cardiac deformities. Furthermore, the project aims to connect cardiac morphology to cardiac function and mortality to understand how deformities contribute to poor health and death.

By combining this knowledge and these tools, the DigiHeart project seeks to improve forecasting of disease progression and mortality events, empowering informed decisions and preventive measures. Ultimately, the project's efforts will help mitigate production losses, reduce the industry's environmental footprint, and enhance fish welfare in aquaculture.

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Digital phenotyping for larger scale individual morphological welfare traits in Atlantic salmon (*Salmo salar*)

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Ensuring individual animal welfare is a moral and legal imperative, which is increasingly in focus in Norwegian society and research. The sheer scale of aquaculture operations, and the operational and biological limitations of recording fish out of water, have further spurred new research into rapid and non-invasive digital phenotyping methods. FISHWELL is a standardised set of ‘operational welfare indicators’ (OWIs) widely used in Norway (Noble et al., 2018), including number of ectoparasites, presence and severity of skin wounds, and fin condition. Trained observers score these OWIs, which entails a rapid assessment of as many as 20 different traits. A conundrum while recording is that individual welfare should not be compromised by the act of measuring OWIs themselves. However high precision is required for the most statistically powerful analysis with the least fish. The longer a fish remains out of water while being handled, the higher the chance of harming its welfare. We present potential rapid, non-invasive, digital phenotypes in development to address these challenges. We developed an imaging system with rapid delivery of fish via conveyor belts to a hyperspectral camera which can image both sides of an anesthetised fish in under 30 seconds. By handling the fish with care and monitoring their recovery post-anaesthesia, none of the measured fish showed impaired welfare. The images undergo image analysis and deep learning methods to determine numerous traits including fin morphology, presence of wounds, as well as salmon lice numbers. We present standardised *in vivo* lice challenge models, where large numbers of fish (2000 – 3000) must be counted for lice within a 2-3 day period with between 0 -180 lice per fish, before the chalimus lice (<1 mm in length) become motile. To this end, we have digitally recorded more than 1200 genotyped smolt infected with over 18000 salmon lice. We have successfully recorded more than 2500 Atlantic salmon parr and post-smolts for presence and severity of damage to dorsal fins after smoltification and have concurrent scores on a subset of 234 post-smolt for the presence or absence of damaged dorsal fins and the severity (0 – 3) using two human observers.

All new methods must be compared to the appropriate gold standard methods to benchmark the level of their agreement. In the case of lice counting this was done with genetic correlations to the manual human count which was very high and positive at >= 0.90. In the case of operational welfare traits, the agreement between human observers and hyperspectral analysis was done using Cohen’s Kappa which was 0.81 and 0.90 respectively. Accuracy between the fin haemorrhaging index and the human observers for wound severity was moderate (0.61 and 0.57) and on par with the agreement between the two human observers (0.68) (Lindberg et al., 2023). Importantly, this work shows that digital methods can be adapted to meet the needs of fish biology and large-scale experimental numbers. A paradigm shift from relying on minute human-scored operational welfare traits to large-scale rapid, image-based methods is feasible with more extensive testing. Benefits include reducing the burden on the fish being measured but also the financial burden of requiring human resources.

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P29

Optimized data analysis for predicting Omega-3 fatty acids in Atlantic salmon for sustainable breeding

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Atlantic salmon is a rich source of Omega-3 fatty acids and accounts for the largest portion of aquaculture production in Norway. However, the industry faces a complex challenge to maintain the high contents of Omega-3, while at the same time receiving less dietary Omega-3 fatty acids due to a shift toward greener and more sustainable feed resources [1] . Atlantic salmon has the ability to generate Omega 3 fatty acids like EPA and DHA *de novo* and this has been found to be heritable [2] . However, in order to breed for increased Omega-3 contents we need to be able to measure Omega-3 fatty acid content in a sufficiently large population (typically 10^3-10^4 related fish) [3] . The gold standard method for measurement is extremely costly, time-consuming, and destructive and is therefore a significant bottleneck. Rapid non-destructive methods which employ vibrational spectroscopy, such as NIR and Raman, are therefore widely used to detect or measure the chemical compounds in the research area [4] . Spectroscopic data are inherently high-dimensional, and partial least square regression (PLSR) is regularly used to overcome challenges in multicollinearity to predict variables like Omega-3 fatty acids.

Typically, models are built with the aim of maximizing the R^2 and minimizing the root mean square error (RMSE) on a subset of samples that are sent for the costly reference analysis. Subsequently, this calibration (training data) is used for predicting the remaining samples in the population. When the final purpose is for breeding programs, it is not possible to conduct a genetic validation as concurrent reference measurements and vibration spectra are needed on 10^3-10^4 related fish. We had unique access to 613 adult Atlantic salmon with both Raman and NIR spectral measurements concurrently with Omega-3 fatty acid measures[5]. With this data, we have unprecedented possibilities to optimize the data analysis for the genetic prediction of Omega-3 fatty acids.

One question which arises is which subset of the measured samples should be selected for the costly reference analysis? If *a priori* models are not available, model selection methods are needed, and we investigated Random Sampling (RS) and Kennard-Stone (KS). Recently, variable selection methods like Markov blanket (MB) based on the Bayesian networks have also further boosted milk spectra prediction in dairy cows, will a similar benefit be obtained in Atlantic salmon? Lastly, which combinations are optimal for improving breeding programs?

The results show that 1) NIR spectroscopy benefited the most from using KS, whilst RAMAN did equally well with KS and RS approaches, 2) MB variable selection further improved predictions for both NIR and Raman spectra, 3) Overall Raman spectroscopy outperformed NIR. Remarkably, the predicted EPA and DHA from the optimal Raman model was significantly heritable (h^2= 0.38 – 0.43 and very highly genetically correlated (Rg = 0.83 – 0.99) to the reference values. Demonstrating, the high potential for inclusion in breeding programs of Atlantic salmon in Norway.

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P30

Digitalizing large scale genetic trials of whole-body fat measurements in *Atlantic salmon* through non-invasive NIR and Distell spectroscopy

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Maintaining an optimal level of body fat is essential for the survival in Atlantic salmon, but higher levels can result in costly harvest waste and economic losses. Breeding programs could in principle, incorporate whole body fat as a trait and thus contribute to more sustainable and cost-efficient fish farming. However, high throughput and cost-effective methods for phenotyping whole-body fat in thousands of fish are currently lacking. The reference Folch lipid extraction method is destructive, highly laborious, and expensive. Two rapid non-invasive methods, namely the Distell fat meter which is a highly portable dielectric spectrometer and a new semi-automated Near-infrared (NIR) system offer the possibility to change this, but require further validation.

To address this issue, we conducted a large-scale genetic validation study on ~3000 Atlantic salmon with the goal of 1) comparing the accuracy and reliability of digital NIR and Distell spectroscopy methods for estimating total body fat; and 2) examining the pattern of total body fat across three different life phases. The studied non-invasive methods showed strong agreement with the reference method (r_p= 0.80 -0.88). Moderate to high genetic estimates were obtained for Distell ($h^2 = 0.48_{\pm 0.08}$ - $0.56_{\pm 0.10}$) and NIR ($h^2 = 0.57_{\pm 0.04}$ - $0.63_{\pm 0.06}$), indicating the potential use in selective breeding.

For the first time, the flexibility offered by these methods made it possible to investigate genetic links between fat at different life phases. We found substantial variation in total body fat across the different life phases, with an average of $11.32_{\pm 1.23}$ % in parr, $33.80_{\pm 2.6}$ % in pre-smolt, and $14.98_{\pm 1.27}$ % in post-smolt fish. A significant decrease in phenotypic and genetic correlation was observed between fresh water and sea water stages, suggesting that selection at the parr and/or pre-smolt stage has little impact on total body fat content in adult fish. In all, genetic validation proves the potential of Distell and NIR methods for measuring whole body fat at different life stages without killing or damaging it, and their usefulness depends on the users' specific needs and preferences.

P31

Early warning through video monitoring: dissolved hydrogen sulphide (H_2S) affects Atlantic salmon swimming behavior in recirculating aquaculture systems.

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Hydrogen sulphide (H_2S) poses a major threat in marine land-based recirculating aquaculture systems (RAS) leading to acute mortality in sensitive fish species such as Atlantic salmon [1]. To date, little is known about the effects of sub-lethal H_2S on the physiology and behaviour of the species.

The present study analysed swimming behaviour in Atlantic salmon in response to H_2S in a controlled trial. The setup consisted of two RAS in parallel. The control RAS comprised of one fish tank (800L, 10 Kg fish/m3 (≈ 70 fish)) and one biofilter, while the exposure RAS included two fish tanks (800L; 10 and 30 Kg fish/m3 (≈ 70 and 200 fish)) connected to one biofilter. Swimming behaviour was monitored via both a submerged custom-built stereo camera system and an overhead surveillance camera system filming from above. Fish (smolt, ≈ 114g) were exposed once a day for 10 consecutive days to increasing H2S concentrations, from ≈ 1- up to ≈ 68-µg/L (2 µM). Dissolved H_2S, O_2 and CO_2 were measured continuously using Aquasense real-time monitoring system (SeaRAS Bergen, Norway). Three parameters were extrapolated from video recordings using artificial intelligence: i) average swimming speed, ii) swimming pattern (representing whether the fish swim in a straight or zigzagging direction) and iii) asynchronization (indicating to what degree the fish maintain a schooling behaviour). The results demonstrated that fish quickly react to H_2S, showing a panic response characterised by faster swimming speed, erratic pattern, and loss of schooling behaviour. The response was concentration-dependent, increasing linearly up to 30-40 µg/L, above which a clear threshold was present. At concentrations around 40-50 µg/L, the change in behavior was significantly higher compared to lower concentrations, and additionally raising H_2S did not result in further changes in behavior. Swimming parameters quickly returned to basal levels once H_2S was no longer present in the water.

This study provides new insights on the sensitivity of Atlantic salmon to acute H_2S exposure and highlights the potential behind the use of artificial intelligence and video-monitoring as early warning tools for poor water quality in RAS.

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P32

Creating a Data Space in the Norwegian Agriculture Sector with Open Standards and Open Source

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GAIA-X Data Spaces[1] is a concept that describes how a common data sharing eco-system for a constellation of actors can bring benefits through effective and secure sharing of data.

One of the challenges for projects and industries looking to build data spaces is that there is a lack of, or at least a lack of visibility of, how to engineer these data spaces. Data spaces need to include many actors in the eco-system, from small research teams publishing data, to large enterprise data aggregators and then onwards to those building Digital Twin applications.

MIMIRO have long been involved as a central data sharing organisation in the Norwegian Dairy industry. Additional experience in the DEMETER and Iliad EU projects, as well as membership of the ICAR[2] technical working group has led us to develop open source and open standards that directly address the issue of how to build the technical infrastructure needed to support an industrial data space.

The main enabler for creating the data space is the creation and adoption of a Universal Data API (UDA) [3] designed specifically for the synchronisation of data between willing participants. While the world has become more API centric this does not resolve the issue of reliable semantic exchange, at scale and amongst many parties.

In this paper we present the history of data sharing protocols of the last 20 years, and how the properties inherent in these works have influenced the design of the UDA protocol. We present the UDA protocol itself and describe the way in which adoption in the Norwegian agrilcultural sector has led to improved data sharing and value to the entire industry.

We also reflect on how the provision of open source software that implements standard protocols accelerates the adoption and creation of an industrial data space.

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P33

A Norwegian experience of a fully automatic scoring system of pleurisy in slaughtered pigs

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This study investigates the application of artificial intelligence (AI) in assessing porcine respiratory disease complex (PRDC) at slaughterhouses, focusing on *Actinobacillus pleuropneumoniae* (App) as a causative agent of porcine pleuropneumonia (Gottschalk 2019). PRDC is a multifactorial health issue causing significant economic losses in the pig industry worldwide. The Slaughtered Pleurisy Evaluation System (SPES) grid is widely used to estimate the impact of App in pig herds (Merialdi *et al.* 2012), while the alternative Pleurisy Evaluation on Parietal Pleura (PEPP) method allows scoring pleurisy using digital images (Di Provvido *et al.* 2019).

The study was carried out in a medium-sized Norwegian slaughterhouse between September and December 2022. A camera robot prototype was used to take images of half-carcasses as they moved along the slaughter chain. An ad hoc algorithm screened multiple images of each half-carcass and selected one for analysis by a convolutional neural network (CNN) trained on the PEPP method (Trachtman *et al.* 2020). The CNN's performance was optimized using a small set of approximately 300 images collected under the same slaughterhouse conditions.

Out of 37,798 pictures taken, 19,029 were considered suitable for analysis. Pleurisy was detected in 1,948 half-carcasses (10.24%), with 323 pigs scoring 1 (1.7%), 894 pigs scoring 2 (4.7%), and 731 pigs scoring 3 (3.84%) according to Trachtman et al. (2020). These findings indicate the potential of AI-based technologies for large-scale data collection in livestock production, with the goal of improving pig health status and overall profitability.

The prevalence of pleurisy in this study is lower than that reported in other countries, such as Italy, but is consistent with data on pleurisy prevalence detected in Norway as part of meat inspection and stored in the Extended Disease Registration (USR) system, which recorded a prevalence of 6-7% between 2016 and 2020. The USR data will be preliminarily validated against the results provided by the Automatic Detection of Abattoir Lesions (ADAL) system used in this study.

It is important to note that Norway is free from *Mycoplasma hyopneumoniae* (M.hyo) and PRRS virus (PRRSv) infections, which play a key role in PRDC's etiology. Although M.hyo and PRRSv cannot cause pleurisy independently, they can trigger the pathogenic activity of other bacteria, including App. This study serves as a preliminary field trial, further confirming the potential of AI-based technologies in livestock production for the efficient and effective collection of health data at slaughterhouses, ultimately contributing to the improvement of pig health status and farm profitability.

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P34

Mathematical optimization for fruit and vegetable logistics

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At Bama, the potential of mathematical optimization is being explored to manage the distribution of over 500,000 tonnes of fresh produce each year efficiently. This presentation will demonstrate how these techniques are employed to reduce costs while ensuring freshness and sustainability. The focus will be on ongoing projects related to operational and tactical transportation planning, as well as an exploration of potential supply chain designs for Norwegian fruits and vegetables.

P35

Digital technology and agriculture

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About the "Digital technology and agriculture" presentation

Real example of how digital technology and data are enabling innovation and development of new business models and their evolvements to eventually solve some of the most precious issues in the world related to agriculture.

P36

Quality control of fruits & vegetables powered by machine learning

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Using state-of-the-art of machine learning models, BAMA has transformed the quality control process of fresh fruits and vegetables. Their model is trained on extensive historical data to predict real-time product quality and identify products that need a closer look. This approach ensures fewer substandard products slip through the net, optimizing customer satisfaction and operational efficiency.

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Models and data for industry 4.0 implementation in biomanufacturing

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Industry 4.0 can potentially transform biomanufacturing, yielding better control of processes and opening up towards increased automation. Digital twins, virtual copies of a physical process interacting with that process, are assumed to play an important role in this transformation. This presentation has focus on two important aspects of such a digital twin: models, and data.

A digital twin of a process (or part of a process) can be considered a virtual copy of the process that exchanges data/information with the process in real-time: data are sent from the physical process to the virtual copy, and are processed to yield predictions about the ongoing biomanufacturing process. Subsequently, model predictions are sent from the digital twin to the real process, with the purpose of achieving improved operation. As such, there is a clear similarity with model predictive control. In this presentation, the focus will be on different modelling approaches that can be used to obtain a Digital Twin of a process. Issues related to model validation are highlighted.

Furthermore, the need for improved data collection is presented, and application examples of the use of several more advanced measurement techniques on a fermentation process are presented, including spectroscopy and electrochemical sensors.

Finally, interactions between model and data are discussed. Biomanufacturing operations at industrial scale are traditionally known to be relatively poor in on-line data, compared to the lab environment that is used to develop such processes. In that respect, it is interesting to reflect on the data aspect, where availability of more and better on-line data can have a strong impact on the application of digital twins in biomanufacturing.

Digital Twins of Ecosystems

***Einar Broch Johnsen**, Eduard Kamburjan, Rudolf Schlatte, [Text Wrapping Break]Laura Ann Slaughter, Silvia Lizeth Tapia Tarifa*

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Digital twins of natural environments have an enormous and largely unexplored potential [1, 2], due to their ability to explore alternatives in predictive ("what-may-happen") and prescriptive ("what-if") analyses. Bringing a natural system into a "virtual laboratory" enables us to perform experiments on the twin that would be impossible to perform on the real system: Digital twins could be used to explore the impact of temperature increase on fragile ecosystems. More generally, digital twins may be used to study the effects of climate-associated changes on fragile ecosystems or of interventions on pandemics [8], but also for digitalization and advanced automation in farming [10].

A digital twin turns a model of a natural system into a live replica by directly connecting the model to observations of the natural system in near real-time. Whereas digital twins play a major role in the on-going digital transformation in industry (e.g., [9]), they are criticized for being brittle, inflexible, monolithic, and difficult to both maintain and scale [6]. Our research targets flexible, modular and open-source digital twin solutions that couple heterogeneous models with streams of real-world observations, together with advanced analysis support: We develop digital twin architectures (e.g., [5]) that leverage domain knowledge, formalized using semantic technologies [4], with simulators and sensor data to explore hypothetical what-if scenarios. Currently, we also work on digital twins for resource management in, e.g., logistics [7] and cloud computing [3].

Currently, we develop digital twin technology in the context of ecosystems. For example, we conduct lab experiments on plants in an in-door greenhouse, where our digital twins connect data streams from sensors monitoring the environment, e.g., humidity, temperature. These streams, together with explicitly formulated domain knowledge, control actuators, such as water pumps, lamps, in order to study automated optimization and decision making. We also develop a digital twin of the Oslo Fjord, where we connect sensor data to a fjord circulation model and study the effects of climate change (e.g., extreme weather events) on the physical processes in the fjord and on its ecosystems. In this talk, we discuss our work on digital twin technologies that integrate models, domain knowledge and sensor data for decision making and what-if analyses. We will discuss the capture and use of knowledge about processes, interactions, and dynamics in the ecosystem, such as how plants interact with their environments. We further discuss the potential of this technology for monitoring and model-based analysis of ecosystems, illustrated by our current case studies.

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Performances and uses of Digital Twin technology in spatial planning – a critical literature review

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The main applications of Digital Twin technology (DT) are complex calculation, simulation, visualisation, monitoring, testing, and prediction, in particular within the fields of engineering, medicine, operation training, and infrastructure management. DTs thus belong to a natural science framework where a common method is experimental testing in a controlled environment. Lately we can observe how the uses of DTs are expanding, without taking fully into consideration the consequences of transiting into other fields of application. A question, then, is whether the transition to new environments can be made without reconsidering some of the basic tenets that DT research is based on. *Prediction*, for instance, may be a quite different matter in a closed system compared to open ones, or when related to spatial vs mechanical issues. The ongoing Twin Fjord project uses DT to develop a support system for sustainable land-use management in the Norwegian region of Geiranger. The present paper has a double aim within that project: to specify the need for knowledge about uses of DT in spatial planning, and, through a literature review, to outline how planning support systems (PSS) are currently understood and appreciated, identifying the state-of-the-art with respect to the specific research agenda of Twin Fjord project.

The paper first presents the specific problem structure of the Twin Fjord research project. Sustainable land-use management involves challenges of information flow and decision-making inconsistencies. To cope with these challenges, within a framework of sustainable community values, co-creation is selected as a preferred approach. It implies a focus on initiatives and interactive dynamics of place-making. Properties and functionalities of DT technology are then identified and appreciated based on their relevance to the specific field of application. After this framework is outlined, the core of the paper is presented as a critical literature review to identify the state-of-the-art of PSS. The review proceeds by extracting the most common definitions of PSS, which in the planning literature is far from unison. To explain the reasons for this variegated landscape of concepts and definitions, the paper provides an overview of historical relationships between spatial planning rationales, knowledge needs and data modelling. An alignment with the evolution of automation and digital technology allows a historical overview of the main paradigms of computer-aided planning. The review ends with an account of a wide array of roles attributed to current PSS concepts.

The specified and focused quest for a state-of-the-art in this paper, with its tailored literature review, leads to fundamental interrogations on the phenomenon of DT when transitioning into land-use management: spatial planning issues may be highly contextual, posing important interrogations to the purposefulness of exhaustive and exact data models; and when technology is employed as an interactive tool, it may assume a social role beyond current expectations to DTs. Potentially it also enables searches for new paths of application and innovation where DT is reconceptualised within a sociotechnical framework of interaction, co-creation, and decision-making.

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Conceptualising a DT-based support system for sustainable land-use management – a diary from real life testing experiences

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The NFR funded research project Twin Fjord explores the potentials of Digital Twin technology (DT) conceptualised as a support system for sustainable land-use management. The project draws its title from its testing ground, defined by the West Norwegian fjord landscape areas of Geiranger and Tafjord, figuring on the UNESCO world heritage list. The point of departure is a set of challenges related to sustainable land-use management: information and processes are often fragmented, and it is hard to secure conherent and consistent decisions over a wider geographical area and over time.

The paper meanders through an abductive process, where a theoretical perspective and a search for experimental methodology are built by means of a back-and-forth movement between cogitation and testing experiences. Experimental navigation is based on the following premices: Firstly, two partner municipalities, Fjord and Stranda, have brought quite different cases into the project. The Valldal case (Fjord) starts from a single place-making initiative, allowing the local community to defragment information through a progressively collective process of local co-initiative, oriented towards an open time horizon. The Geiranger case (Stranda) on the other hand has a deadline, based on the Norwegian Parliament's decision to make the cruice traffic climate neutral by 2026; the case is characterised by urgency, and at the same time a kind of apathy in front of a purely restrictive approach, where no actor takes initiative. Secondly, in these situations DT is tested through a series of stake-holder workshops, broken down to the basic steps of co-creation: co-initiative, co-conceptualisation, and co-implementation. Thirdly, within this frame, the point of departure has been to conceptualise a support system based on DT's virtues as a visualisation tool, constructing optical relations between actors and reality. We experience, however, that in a co-creation process we cannot isolate the optical from haptic relations to reality, or from the social relations actors connect with eachother.

Through the testing our attention has been drawn towards a number of surprising impacts. The DT instantiates social and technical elements that engage communities in goal directed behaviour, shifting our perspective from the purely technological to a socio-technical effects. Further, we see that the presence of a tool may influence the actors' techniques and methods, potentially sharpening the understanding of their own roles, building mutual confidence, and improving the community's spatial planning methodology. The main purpose of the DT thus, conceptualised as a planning support system, is not its usual performance of calculation and predictability; it is to enable communities to think about space-time, and to consider initiatives collectively against a backdrop of sustainable development goals.

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Digital twin technology for bioreactor bioprocesses: applications in fungal fermentation and in-vitro cartilage growth

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The application of digital twin technology has shown great potential for optimizing and improving processes in manufacturing. Replacing part of the experimental development by a digital version of the process may reduce development costs considerably. Our study aims to investigate the potential of digital twin models for bioreactor bioprocesses. We consider two specific bioprocesses (1) microbial fermentation processes and (2) in-vitro bioreactor growth of cartilage growth.

As opposed to manufacturing processes, digital twins in bioprocesses need to deal with strong variability due to the nature of biological processes. To assess the stability of digital twin models is essential for understanding their effectiveness in predicting and optimizing bioreactor performance. For understanding the variability in bioprocesses, it is important to use efficient tools for measuring critical parameters of bioprocesses. E.g., for the development of a digital twin for microbial bioprocesses it is essential to estimate the consumption of media and the production of extra- and intracellular products.

To identify critical parameters for bioreactor processes, this study analyzes and compares various data sources, such as spectroscopic techniques, sensors, and other data sources, to determine which parameters are most indicative of bioreactor performance. Such data allows a more comprehensive understanding of the bioprocess and improve the accuracy of the digital twin model.

We explore various methods to estimate the stability of a digital twin model, such as model calibration and validation. Additionally, the study investigates techniques to improve the robustness of digital twins, such as incorporating process variability and uncertainty.

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From research to production by using artificial intelligence and remote sensing: new mapping activities at NIBIO

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The Norwegian Institute of Bioeconomy Research (NIBIO) is in charge of several mapping activities at the national scale. Recent advances in artificial intelligence, and particularly in machine and deep learning models, coupled with the availability of remote sensing data from multiple platforms with increasingly higher spatial and temporal resolutions, opened for new opportunities. The Geomatics department at the Maps and Survey division of NIBIO is in charge with the development and maintenance of several maps and geospatial services, taking into a production environment the results of research activities. This presentation will focus on three recent projects that combined research and development activities to produce maps by combining artificial intelligence and remote sensing. In particular will be presented and discussed:

- Map of land cover/land use changes supporting AR5 updating process;
- Map of green areas in built-up areas;
- Map of agricultural types.

The areal resource map of Norway (AR5) is the highest resolution map for Norway. It is based on images from airplane, and it is frequently updated. In order to facilitate the work of people working with the update, it has been implemented a deep learning model that identify areas with changes. By using the produced map, the update process is expected to be faster since operators focus on identified areas, rather than visually/manually identify those area by inspecting all images.

The Map of green areas in built-up areas is produced in order to identify areas with vegetation that currently are not mapped by any other map in Norway. In fact, courtyards, recreational areas, and other spaces cover by vegetation are usually considered as urban areas, but their correct identification is getting an increasing interest in relation to climate change and potential climate-related risks in urban areas. The main reason is that these areas contribute in a different way to greenhouse gasses emission and can play an important role in relation e.g., to urban floods in a context of climate change. It has been therefore developed a method that uses deep learning to identify those areas based on Very High-Resolution images from the Copernicus Contributing Missions. Further, the integration with laser scanning data, allows for the identification of different vegetation classes: grass, bushes, and trees.

The map of agricultural types is the first attempt to spatially identify crops in Norway during the growing season. The proposed approach identifies grain (without distinguishing yet different types of grain) and grass for entire Norway by using time series of Sentinel-2 images. The model is a temporal Convolution Neural Network and consider the changes of different bands/indicator through the growing season, from April to October, in order to identify the main crop type. The proposed approach does not currently go to a higher level of detail due to the lack of ground truth data, but it is expected that the availability of better ground truth data could allow to map different type of grains.

A more detailed presentation of the methods and an overview of the obtained results will be given in order to show the benefits of use artificial intelligence and remote sensing to support mapping activities also in a production environment.

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Hyperspectral Imaging for Mushy Halibut Syndrome Identification

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Mushy Halibut Syndrome (MHS) is a condition that appears in Greenland halibut and manifests itself as abnormally opaque, flaccid, and jelly-like flesh [1]. Fish affected by this syndrome show poor meat quality, which results in negative consequences for fishermen and food industry producers. The condition is often not discovered until the fish has been filleted, and its presence leads to complaints and the downgrading of the products on the market [2]. As far as we know, no technology exists for the early screening of MHS. However, the early identification of MHS could lead to an improved and more sustainable processing chain. Thus we evaluated if hyperspectral imaging, as a potential non-invasive technology, could be used to characterize and identify MHS [3], [4].

This work analyzed 62 individual Greenland halibut (2-3 kg), 56% of them were affected by the MHS, and 44% were not affected by the MHS. The presence of MHS was evaluated by visual inspection after filleting. Since the presence of MHS can be related to its chemical composition, loin sections (about 200 g) from 23 fish (11 with no MHS and 12 affected by MHS) were sent for biochemical analysis. Four hyperspectral images were acquired for each halibut: one image from each side of the fish and one for each fillet (two fillets per sample).

The hyperspectral data were recorded using the Maritech Eye, an industrial hyperspectral imaging system. The Maritech Eye comprises an interactance illumination system and a hyperspectral camera (HySpex Baldur V-1024N) covering the spectral range from 485-960 nm. When using interactance illumination, the light is measured after different internal scatterings have occurred inside the sample [5], allowing retrieval of information about the chemical composition beyond the surface.

We proposed two alternatives to exploit spectral information to identify MHS. First, to estimate the biochemical composition of the fish by using constrained spectral unmixing, and secondly to automatic identification of MHS from the spectral information using Partial Least-Squares Discriminant Analysis (PLS-DA). Regarding the estimation of the chemical composition, the proposed constrained spectral unmixing method showed some limitations and only produced reasonable estimations under specific circumstances. However, the detection of MHS using PLS-DA was precise for hyperspectral images from both fillets and whole fish, with lower bounds of 75% and 83% for precision and recall, respectively.

We concluded that the precise classification results obtained with PLS-DA suggest hyperspectral imaging could be used in industrial environments to screen MHS, allowing an automatic fish grading. Thus, improving the product sorting according to their quality, optimizing the processing chain, and preventing economic losses due to variable quality and complaints from the customers.

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Comparison of model- and data- based correction methods for infrared hyperspectral images

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Hyperspectral infrared (IR) imaging offers a wealth of information beyond conventional three-color channel cameras (red, green, blue) by capturing data across hundreds of spectral channels. Infrared irradiation interacts with the molecular structure of a sample, providing comprehensive information on the sample's chemical and morphological properties. This makes it invaluable for sustainability research in areas such as pollution monitoring, disease recognition, and the development of innovative green bioprocesses.

However, the complexity of hyperspectral IR data poses analytical challenges, as it contains intertwined chemical and morphological information. The analysis of microscopic samples, such as microorganisms and tissues of plants and animals, is further complicated by phenomena like Mie scattering, which nonlinearly alters the chemical profile of measured absorbance. To overcome these challenges and harness the full potential of hyperspectral imaging, we explore model- and data-driven approaches for restoring the pure chemical profiles of measured spectra.

Our research focuses on employing the model-based techniques (1–3) and data-based deep neural networks (DNNs) (4) to remove morphological information from spectra, leaving only chemical data. Choosing and setting up a suitable correction method can be complex, requiring a tradeoff between factors such as scattering type and complexity, data volume, computational and time resources, and the purpose of the correction.

During the presentation, we will discuss and compare these preprocessing methods, highlighting their strengths, weaknesses, and potential applications in research that addresses sustainability problems such as biorefinery.

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