



Statistics and Actuarial Science Seminar

Title: Accounting for overlapping functional annotations as biological priors in Bayesian genomic prediction models of complex

Speaker: Andrea Rau (INRAE - GABI)

Date: Thu 7th March 2024 at 3:00PM

Location: E0.32 (beside Pi restaurant)

Abstract: It is now widespread to build whole-genome regression models using genomic data to predict complex traits in a wide range of fields, including farm animal and plant breeding and human genetics. Functional genomic annotations, such as the accessibility of chromatin or methylation status in relevant tissues, have the potential to provide valuable insight into the position and effect size of causal genetic variants underlying complex traits. In the H2020 GENE-SWitCH project, we aimed to develop and validate Bayesian models able to fully leverage such complex functional annotations for improved accuracy and interpretability of genomic predictions in the pig and poultry breeding sectors. To this end, we defined and implemented a flexible framework for genomic prediction called BayesRCO to simultaneously take advantage of the availability of multiple functional genomic annotations. In this talk, I'll describe the intuition behind our proposed model and discuss some of our key take-away messages from early use cases. <https://doi.org/10.1186/s12859-022-04914-5>
<https://github.com/FAANG/BayesRCO>

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