



Incorporating known functional annotations into Bayesian genomic prediction models

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Keywords:

Genomic prediction, integrative analysis, functional annotation, Bayesian models, multi-omics

Summary:

Genomic selection has been successfully implemented in many livestock breeding programs in the last decade, and one recently proposed means for improvement is the use of underlying biology as an additional source of information to guide predictions for complex traits. The aim of this thesis project is to develop and validate genomic prediction models able to weight SNPs to incorporate information extracted from functional annotation maps obtained at different molecular levels on top of the commonly used phenotypic and genotypic data. Subsequently, the extent to which this may increase prediction accuracy will be investigated. The candidate will develop novel cutting-edge statistical models to integrate new functional information into existing genomic predictions methods and validated in commercial populations. In particular, the thesis will focus on the development of a computationally tractable empirical Bayesian genomic prediction model that incorporates functional annotation into prior distributions to weight the likelihood that a given genetic variant is functional or has predicted functional impact on a phenotype. This thesis project thus represents the development of an innovative and impactful approach, making use of statistically robust approaches, to potentially have a major influence on breeding practices.

The thesis project is anchored in data that will be collected in the multi-actor GENE-SWitCH (The regulatory GENome of SWine and CHicken: functional annotation during development) EU Horizon 2020 Research and Innovation project. GENE-SWitCH supports the efforts of the ongoing [Functional Annotation of ANimal Genomes](#) (FAANG) consortium, a worldwide consortium of 350+ contributors with the global goal of establishing reference functional maps of domesticated animal genomes. GENE-SWitCH will produce new genomic information to enable the characterization of genetic and epigenetic determinants of complex traits in the two monogastric species (chicken and pigs) that are the primary sources of meat worldwide. In particular, by producing comprehensive reference functional annotation maps at several

molecular levels (RNA-seq, ATAC-seq, ChIP-seq, Hi-C) in tissues of relevance to sustainable production at different time points (from embryo/fetus to adult life), the GENE-SWitCH project aims to integrate functional information into genomic selection schemes to improve their effectiveness in the pig and poultry sectors. The large amount of biological information that will be generated in the GENE-SWitCH project will thus provide an excellent opportunity to empirically investigate the potential benefit of using functional annotation in genomic prediction.

Candidates:

All candidates should hold a Master's degree (or equivalent) in a relevant biological (genomics, epigenomics, bioinformatics, animal science, agrobiolgy) or quantitative field (statistics, biostatistics). In addition, successful candidates will have:

- Strong interest in quantitative work, including coding and statistical analyses (e.g., in R) and wrangling large complex datasets;
- Experience with or willingness to learn Linux and an additional programming language, as needed (e.g. C++). Experience with high performance computing is a plus;
- Good organizational and proficient (written/spoken) communication skills in English;
- Willingness to travel nationally and internationally to attend project meetings and conferences;
- Collaborative and creative spirit, with enthusiasm for innovative scientific research and the ability to work both independently and in a large and diverse group of researchers;
- Knowledge of Bayesian / empirical Bayesian models is a plus, and experience with genomic data and/or genomic prediction models would be an advantage but is not necessarily required.

Funding and location:

The gross monthly salary for this thesis project 1770€.

This Ph.D. project is half-funded by the GENE-SWitCH grant, and half-funded by the INRA Animal Genetics department. The GENE-SWitCH grant will provide funding for travel to major scientific conferences as well as for participation in relevant training courses and workshops. In addition, the candidate will communicate results and present the methods developed in this thesis in peer-reviewed journal articles and national and international conferences. An international dimension to this project will naturally arise from interactions with other GENE-SWitCH partners, including one or several short stays at Wageningen University during model development and application to pig data.

The thesis will take place in the [Genomics, Biodiversity, Bioinformatics, and Statistics](#) (GiBBS) and [Bovine Genetics and Genomics](#) (G2B) teams of the [Animal Genetics and Integrative Biology](#) (GABI) research unit at [INRA](#) in Jouy en Josas, France. The thesis work will be supervised at GABI by Dr. Andrea Rau and Dr. Pascal Croiseau and will feature close collaborations with Dr. Elisabetta Giuffra, Dr. Herve Acloque (INRA GABI), Dr. Helene Gilbert, and Dr. Andres Legarra (INRA GenPhySE). Throughout the thesis, the candidate will have

access to the necessary computational resources (e.g., a laptop, access to a computational cluster) as well as a supportive scientific environment, including strong interactions with biologists, bioinformaticians and statisticians (both permanent staff and other trainees) in the GABI research unit.

Start date: September or October 2019 (negotiable)

Duration: 3 years

How to apply: Interested candidates should send a brief statement of motivation/research interests, a CV, and the names of two references in a single PDF document to andrea.rau@inra.fr and pascal.croiseau@inra.fr. For further information and informal inquiries, please contact Dr. Andrea Rau and Dr. Pascal Croiseau directly at the same addresses.