

KEYNOTE SPEAKER

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Topic:

Novel biometric tools for managing and improving populations in the era of mega-scale genomics

Abstract:

The field of genetics has recently experienced tremendous growth and this pace will accelerate. When Gregor Mendel discovered the key principles of genetics, he had no knowledge of the inheritance mechanism. Similarly, Ronald Fisher almost singlehandedly defined the field of quantitative genetics without the knowledge of genome. These, and other, key genetics principles were recently unleashed with the affordable generation of genomic data. Animal and plant breeding are at the forefront of applying genomic data to accelerate genetic improvement. This improvement is much needed to address increasing demand for food in the face of climate change. In this contribution, I will highlight our work in using or developing novel biometric tools for improving agricultural populations.

First, I will summarise the concept of genomic prediction and selection, where we regress observed phenotype values on genome-wide markers to estimate allele substitution effects, which are then used to predict genetic value for any genotyped individual. I will show how such genomic predictions can significantly improve a hybrid plant breeding programme. Combined with environmental data, such genomic predictions are now starting to unravel the challenging genotype-

by-environment interactions. These methods hold promise for personalised medicine.

Second, I will summarise our animal breeding work in adopting genomic selection, optimising model fitting with millions of genotyped individuals, and analysing trends in genetic mean and variance in animal breeding programmes, particularly dairy cattle. Our results show that genomic selection increased the rate of genetic change, both in mean and variance. To better understand global genetic variation in cattle, we are studying whole-genome genealogies, efficiently encoded with tree sequences. I will show first results of inferring whole-genome genealogies from the 1000 bull genomes project.

Third, insects have been used for food and feed production for millennia, but have only recently been recognised as a major future source of feed and food. I will show our results on studying genetic variation in honey bees by inferring whole-genome genealogies across 30 sub-species. I will also summarise our collaboration with black soldier fly breeders to boost future insect protein production.

Much of our work involves simulating quantitative genetic data and breeding programmes, for research and education. To this end we have create a free on-line course on “Breeding programme modelling with AlphaSimR” – register at <https://edin.ac/3wfGSEj>.