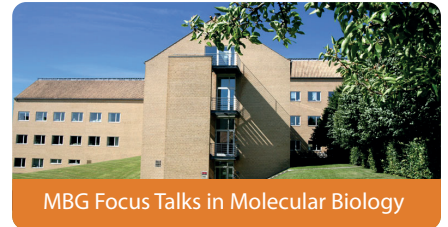


MBG FOCUS TALK

hosted by Erik Østergaard Jensen



Wednesday October 30 at 9:15 - 10:00

iNano Auditorium, 1593-012

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Gene mapping and genomic prediction with GxG and GxE interactions

Approaches for gene mapping and genomic prediction are often limited to additive effects, such as in the standard GWAS and GBLUP methods. It is interesting, both scientifically and for practical breeding, to expand these approaches to non-linear and interaction effects. However, simply expanding standard mapping approaches to scan every locus-by-locus or locus-by-environment effect will suffer from (extreme) low power. Various kernel approaches can be more efficient to tackle GxG and GxE problems, but these approaches suffer from over-simplification by assuming all interactions to contribute equally. I will describe several new approaches to model GxG and GxE interactions that are intermediate between either extreme, such as modelling of locus by genetic-background interactions, globally weighted GxG interactions, heterogeneous contributions of environments to GxE interactions, and approaches to break-up kernels in multiple components with different levels of interactions. Power to retrieve interactions may be further improved by use of smarter experimental designs, use of multi-omics data and use of detailed 'environome' information. When interest is in mapping, efficient procedures have been described, for the additive GWAS approach, to back-solve GWAS from a kernel-method like GBLUP, and similar approaches can be developed for GxG and GxE models. Some examples described include the study of GxG interactions between species, and use of environome data for GxE predictions.