

Division of Biostatistics

Seminar Talk: *A unified linear mixed model for familial relatedness and population structure in genetic association studies*

JOIN US! *Tuesday, November 16, 2021 3:30 – 4:30 PM*

Presented virtually by:



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In human population, both familial relatedness (FR) and population structure (PS) can further break down into additive and dominant components to account for potential additive and dominant genetic effects. In this study, besides the classical additive genomic relationship matrix, a dominant genomic relationship matrix is introduced. A link between the additive (or dominant) genomic relationship matrix and the (or double) coancestry coefficients is established. A unified linear mixed model is proposed to account for both the additive and dominance effects of FR and PS correlations as well as their possible random interactions. This unified linear mixed model is also applied to some real data from UK Biobank.