

# Whole Genome Analysis with wga1m

**Date:** Sunday, 1 December 2019

**Time:** 9am – 5pm

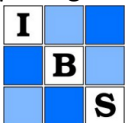
**Location:** University of Adelaide, North Terrace Campus, Barr Smith South 2052 Teaching Room

**Cost:** AU\$200 (IBS Member), AU\$250 (Non-member), AU\$100 (Concession)

**URL:** <https://ausbiometric2019.org/workshops/>

The advent of high-throughput genotyping methods has allowed the low-cost generation of high dimensional genetic marker sets for dissection and analysis. In plant and animal breeding research these analyses usually involve the incorporation of the complete set of genetic markers into a complex linear mixed model (LMM). In these models the goal is usually to determine the underlying genetic architecture of phenotypic traits through various whole genome analysis techniques such as quantitative trait loci (QTL) analysis, genome wide association studies (GWAS) or genomic selection (GS).

There are many LMM methods for QTL, GWAS and GS analysis. This course will provide a theoretical and computational introduction to the newly updated genetic analysis R package, WGA1M, that builds on the highly flexible LMM computational architecture of ASReml-R V4. The course will initially introduce LMM theory and the necessary extensions required for QTL, GWAS and GS analysis approaches. The functionality of the package will then be exemplified through a walk-through of the computational genetic analysis pipeline. Workshop participants will have a chance to gain hands on experience with the package features through practical sessions. A good working knowledge of R is assumed.



International Biometrics Society Australasian Region Conference, 3-6 December 2019

**Dr Julian Taylor** is a Senior Research Biometrician at the University of Adelaide. A substantial component of this research is whole genome analysis methods such as quantitative trait loci (QTL) analysis, genome wide association analyses (GWAS) and genomic selection (GS). Additionally, he is the co-author and maintainer of statistical software packages R/ASMap, R/wgaim and R/hett written in the open source R statistical computing environment.



**Dr Beata Sznajder** has expertise in linear mixed models, particularly for statistical genetics (associative mapping, linkage analysis, population structure, multiple testing). She has extensive experience with genetic marker analysis for cereal breeding. Application of Bayesian approaches to associative mapping. Expertise in statistical programming, parallelisation and management of data in R and SAS.

