

Short Course in Statistical and Quantitative Genetics

March 13-16, 2023

SCHEDULE

Day	Time	Topic/Activity
Monday	8:30am-10:00am	Genetic and statistical sampling, Allele and genotype Frequencies.
	10:30am-12:00pm	Allele frequency variances, within- and between-populations.
	1:00pm-3:00pm	Computer exercises. 1000 Genomes data. Use of hierfstat, msprime, SNRelate.
	3:30pm-4:40pm	Phil Wilcox, Otago University: The Rakeiora project.
Tuesday	8:30am-10:00am	Allelic association testing.
	10:30am-12:00pm	Inbreeding and relatedness.
	1:0pm-3:00pm	Computer exercises. HardyWeinberg and hierfstat packages.
	3:30pm-4:30pm	Gertje Petersen, AbacusBio: Honeybee genetic studies.
Wednesday	8:30am-10:00am	Principal Components Analysis.
	10:30am-12:00pm	Genetic population structure.
	1:00pm-3:00pm	Computer exercises. SNPRelate, hierfstat and Gaston packages.
	3:30pm-5:00pm	Ken Dodd and Tim Bilton, AgResearch: Polyploid analyses.
Thursday	8:30am-10:00am	Quantitative trait models, GWAS.
	10:30am-12:00pm	Inbreeding depression, heritability.
	1:00pm-3:00pm	Wrap-up Session.

References

- Goudet J, Kay T, Weir BS. 2018. How to estimate kinship. *Mol. Ecol.* 27,4121-413.
- Graffelman J, Weir BS. 2022. The transitivity of the Hardy-Weinberg law. *Foren. Sci. Int. Genetics* 58, Article Number 102680.
- Ochoa A, Storey JD. 2021. Estimating F_{ST} and kinship for arbitrary population structures. *PLoS Genet.* 17,e1009241.
- Wainschtein P, Jain D, Zheng Z, et al. 2022. Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. *Nature Genetics* 54: 263273.
- Weir BS, Cockerham CC. 1984. Estimating F -statistics for the analysis of population structure. *Evolution* 38,1358-1374.
- Weir BS, Goudet J. 2017. A unified characterization for population structure and relatedness. *Genetics* 206,2085-2103.
- Yang J, Manolio TA, Pasquale LR, Boerwinkle E, et al. 2011. Genome partitioning of genetic variation for complex traits using common SNPs. *Nat. Genet.* 43:519-525.
- Yengo L, Zhu Z, Wray NR, Weir BS, et. al. 2017. Detection and quantification of inbreeding depression for complex traits from SNP data. *Proc. Natl. Acad. Sci. USA* 114,8602-8607.
- Zhang Q, Goudet, J. & Weir, B.S. Rank-invariant estimation of inbreeding coefficients. *Heredity* 128,1-10 (2022).