



**The Roslin Institute, University of Edinburgh and
MendTheGap project**

Organise workshop/course on:

**Modern plant and animal applied genomics driven by
genotype and sequence data**

17th-19th July 2018

University of Zagreb, Faculty of Agriculture, Department of Animal Science

The objective of this short workshop/course is to equip the participants with new techniques (e.g., simulation, sequence, genotype, phasing, imputation, phenomics, gene editing) and tools that are used in modern applied animal and plant genomics. The course targets graduate students and researchers interested in applied genomics and will consist of lectures interspersed with computer practicals.

For a maximum of 40 students/researchers the workshop/course is free of charge.

Please, send your intent of interest to dnovosel@agr.hr.

Each participant is expected to bring a laptop with R installed.

Instructors

John Hickey



Gregor Gorjanc



Martin Johnsson



<http://alphagenes.roslin.ed.ac.uk>



THE UNIVERSITY of EDINBURGH
The Royal (Dick) School
of Veterinary Studies



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Program

Tuesday 17th

- 09:00 Hickey: Why do we do artificial selection and breeding?
- 09:30 Gorjanc: Inheritance, genetics, genomes, and phenotypes
- 10:00 Gorjanc: Simulating selection and breeding programs
- 11:00 Gorjanc: Breeders' equation and manipulating its parameters
- 12:00 Lunch break
- 13:30 Gorjanc: Optimal contribution selection
- 14:15 Hickey: Genomic data
- 14:45 Hickey: Phasing genotype data using heuristic methods
- 15:30 Hickey: Imputing genotype data using heuristic methods
- 16:15 Hickey: Introduction to hidden Markov models for breeders

Wednesday 18th

- 09:00 Hickey: Generating and exploiting sequence data
- 10:15 Johnsson: Genome and variant annotation
- 11:15 Johnsson: The theory of deleterious load
- 12:00 Lunch break
- 13:30 Johnsson: Deleterious variant prediction methods
- 14:45 Johnsson: Deleterious variants 1: VEP and SIFT
- 15:30 Johnsson: Deleterious variants 2: Genome alignment and GERP

Thursday 19th

- 9:00 Wrap up discussions with question, own datasets, more examples.

