



CroP-BioDiv

ZNANSTVENI CENTAR IZVRSNOSTI ZA BIORAZNOLIKOST I MOLEKULARNO OPLEMENJIVANJE BILJA  
CENTRE OF EXCELLENCE FOR BIODIVERSITY AND MOLECULAR PLANT BREEDING

## Day 3 (26 September 2018)

Morning session (09:00 – 13:00):

- Breeding program design and GS  
(Ian Mackay, ~2.5 hours)
  - a. What we know about genomic selection
  - b. Small scale application of GS
    - i. Outbreeders
    - ii. Inbreeders
    - iii. Perceptions of GS
  - c. Things to come
    - i. Objectives and technologies
  - d. Conclusion
  - e. An example in R

### Coffee break

- Wrap up: Ian Mackay, Marcos Malosetti & Fred van Eeuwijk, ~1.5 hours



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## WORKSHOP

### High-throughput genotyping

Genomic selection/molecular breeding

25-27 September 2018, Krk, Island Krk, Croatia

Organized by  
**COE CroP-BioDiv – ‘Biodiversity and Molecular Plant Breeding’**  
KK.01.1.1.01.0005

### INVITED LECTURERS:

Fred van Eeuwijk and Marcos Malosetti  
Wageningen University & Research, Wageningen, the Netherlands

Ian Mackay  
IMplant Consultancy, Chelmsford, UK

### ORGANIZING COMMITTEE:

Jerko Gunjača  
Hrvoje Šarčević  
Mario Franić  
Igor Palčić  
Smiljana Goreta Ban  
Zlatko Šatović



Europska unija  
Zajedno do fondova EU



Projekt je sufinancirala Europska unija iz Europskog fonda za regionalni razvoj.  
Sadržaj emitiranog materijala isključiva je odgovornost  
Znanstvenog centra izvrnosti za bioraznolikost i molekularno oplemenjivanje bilja (ZCI CroP-BioDiv).



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## WORKSHOP PROGRAMME:

### Day 1 (24 September 2018)

Workshop foreword (18:30-19:30):

Zlatko Šatović - Presentation of Center of excellence for biodiversity and molecular plant breeding

Jerko Gunjača - Workshop programme and lecturer presentation

Welcome party (19:30)

### Day 2 (25 September 2018)

Morning session (09:00 – 13:00):

• Breeding theory revision, MAS and GS  
(Ian Mackay, ~2.5 hours)

- a. Introduction: the breeders' equation
- b. Marker assisted selection
  - i. Indirect selection and molecular score
  - ii. Estimating effects by regression
  - iii. Problems: the winners curse, over parametrisation
- c. Genomic selection
  - i. Overview
  - ii. Some simple examples
  - iii. Methods
  - iv. Digression: matrix algebra
  - v. Combining information
- d. An example in Excel

### Coffee break



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EUROPSKI STRUKTURNI  
I INVESTICIJSKI FONDOVI



Operativni program

KONKURENTNOST

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• Experimental design & spatial modelling  
(Marcos Malosetti / Fred van Eeuwijk, ~1.5 hours)

- a. Intro: basic principles
- b. Designs (and models) for large number of treatments (as in GS)
  - i. Alpha designs
  - ii. (Resolvable) row-column designs
- c. Spatial modelling
  - i. Models for the R matrix (AR1 x AR1)
  - ii. 2D P-splines approach (SpATS)

### Lunch

Afternoon session (15:00 – 19:00):

• Genotype to Phenotype models in multiple environments  
(Fred van Eeuwijk, ~2.5 hours)

- a. GxE concepts
- b. Linear and bilinear models for GxE
- c. Mixed models for GxE
- d. QTL and GWAS models for multiple environments

### Coffee break

• Genomic prediction in multiple environments  
(Marcos Malosetti, ~1.5 hours)

- a. Set the stage: a single environment prediction model
- b. The incomplete GxE table and the prediction problem
  - i. Untested genotypes in tested environments
  - ii. Tested genotypes in untested environments
  - iii. Untested genotypes in untested environments
- c. Illustration I with a barley data set
- d. Illustration II with a simulated wheat data set

### Dinner



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