

# **General Introduction**

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# Filippo Biscarini



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### Oscar González-Recio



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### Christian - in a slide

- University of Gießen (BSc Agricultural Science)
- University of Gießen (MSc Crop Production)
- University of Gießen (PhD Plant Breeding)
- University of Edinburgh (*Post-doc*)
- Excellence in Breeding CIMMYT (QG Scientist)









### Oscar- in a slide

- Agricultural Engineer (Madrid)

- Animal Science (MSc degree, Madrid)

- Animal Genetics & Quantitative Genetics (UPM-Madrid & UW-Madison)

- University of Wisconsin-Madison (*Post-doc*)

- Dept. Environment and Primary
Industries-Melbourne, Australia (Senior Research
Scientist)

- INIA - Madrid (Senior Research Scientist)







### Filippo - in a slide

Physala Courses

- Roma (born)
- Perugia (MSc degree)
- Cork, ICBF (Web-design & Database)
- Cremona, ANAFI (Quantitative Genetics)
- Guelph, CGIL (Visiting Scientist)
- Wageningen, WUR (PhD)
- Göttingen University (post-doctoral researcher)
- Lodi, PTP ('omics in animals, plants, humans)
- Milan CNR (tenured researcher)
- Cardiff University (biostatistician)
- Milan CNR (senior researcher)
- Bruxelles ERC (seconded national expert)





### now you – round of introduction

- who
- where from
- type of research / work
- what's your interest on GWAS / motivation



### outline of this lecture

- 1. Laying out the topic
- 2. Overview and intuition on GWAS

#### course - in a slide



#### the course website:

- Introduction to GWAS
- Advanced R libraries
- Basic GWAS models
- Data exploration preprocessing
- Imputation of missing genotypes
- Experimental design
- Building a pipeline for GWAS
- Collaborative exercise
- GWAS model extensions
- post-GWAS analysis

Flexibility!



- GWAS: background and intuition
- Linkage disequilibrium
- Linear 'or' logistic regression
- Practicalities and set up
- Linux
- Advanced R libraries



- Exploratory Data Analysis
- Data Preprocessing
- **Imputation** theory
- Experimental design
- Statistical Power
- Population stratification
- Multiple testing



- Practical Imputation
  - Beagle
  - KNNI
- The full model
- Getting prepared for the pipeline
  - the stand-alone GWAS script(s)
  - revising the steps



- Bioinformatic pipelines
- Introduction
- Snakemake
- Continuous phenotype
- Binary phenotype
- Collaborative exercise



- GWAS model extensions
- post-GWAS analysis
- Kahoot quiz