

General Introduction

Christian Werner

(Quantitative geneticist and biostatistician) **EiB, CIMMYT**, Texcoco (Mexico)

Filippo Biscarini

(Biostatistician, bioinformatician and quantitative geneticist) **CNR-IBBA**, Milan (Italy)



HerrFalloppio

Oscar González-Recio

(Computational biologist and quantitative geneticist) **INIA-UPM**, Madrid (Spain)

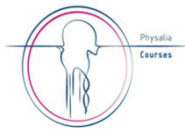


OscarGenomics



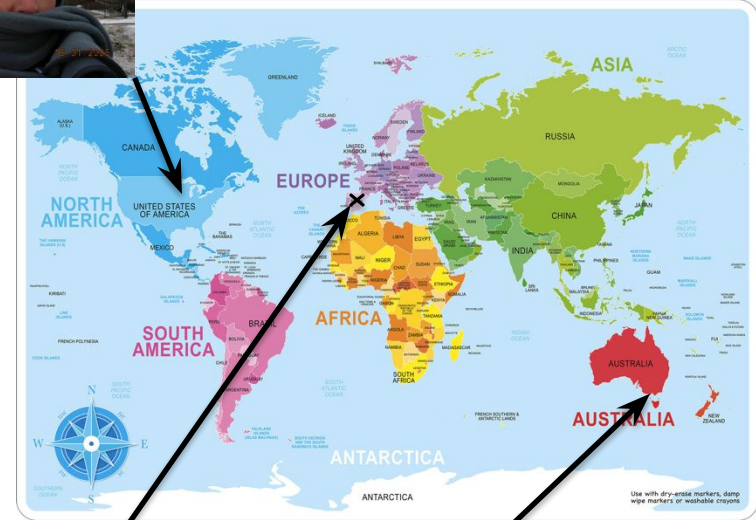
Christian - in a slide

- University of Gießen (*BSc Agricultural Science*)
- University of Gießen (*MSc Crop Production*)
- University of Gießen (*PhD Plant Breeding*)
- Roslin Institute, University of Edinburgh (*Post-doc in QG*)
- Excellence in Breeding, CGIAR / 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

- 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*)
- Milan - CNR (*senior scientist*)



now you – round of introduction

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



course - in a slide

the course [website](#):

- Introduction to GWAS
- Linear regression, linkage disequilibrium, population structure, ...
- Experimental design, sample size and statistical power
- Data exploration and preprocessing
- Imputation of missing genotypes
- Basic GWAS models (in R)
- Linux and the Shell
- Scaling up: building a pipeline for GWAS
- Collaborative exercise
- post-GWAS analysis
- GWAS model extensions

Flexibility!



laying out the **topic**

- https://filippob.github.io/introduction_to_gwas/
-

introduction_to_gwas

https://filippob.github.io/introduction_to_gwas/

[View the Project on GitHub](#)
filippob/introduction_to_gwas

introduction_to_gwas

Material for the course “Introduction to genome-wide association studies (GWAS)”

Instructors: *Filippo Biscarini, Oscar Gonzalez-Recio, Christian Werner*

This course will introduce students, researchers and professionals to the steps needed to build an analysis pipeline for Genome-Wide Association Studies (GWAS). The course will describe all the necessary steps involved in a typical GWAS study, which will then be used to build a reusable and reproducible bioinformatics pipeline.

Each day the course will start at **14:00** and end at **20:00** (CET). As a general rule, we'll have a longer break (30 minutes) at 16:00 and two shorter breaks (10-15 minutes) later on during the day (to be decided flexibly depending on the sessions).

