

General Introduction

Christian Werner

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

Filippo Biscarini



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

Oscar González-Recio



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

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

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)
- 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).