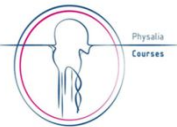


Towards the GWAS pipeline: revising the steps



Christian Werner

(Computational biologist and quantitative geneticist) **EiB**, **CIMMYT**, Texcoco (Mexico)

Filippo Biscarini

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



HerrFaloppio

Oscar González-Recio

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



OscarGenomics



the stand-alone **GWAS** scripts

- Run GWAS programmatically
 - gwas_rrblup.R
 - gwas_statgengwas.R
 - gwas_sommer.R



step 1 - getting the data

- **1.get_data.sh**
 - Download the data
 - Prepare the data



step 2 - filter the data

- **2.steps_filtering.sh**
 - Filter genotype data:
 - MAF
 - Missing rate



step 3 - **imputing** missing genotypes

- **3.step_imputation.sh**
 - Impute missing genotype data:
 - LHCI



step 4 - run the GWAS

- **4.gwas.sh**
 - Run GWAS through the stand-alone script
 - (try multiple scripts: gwas_rrblup.R, gwas_statgengwas.R, gwas_sommer.R)



NEXT LECTURE

Collaborative **exercise**

