

Collaborative **exercise**

Christian Werner

(Quantitative geneticist and biostatistician) **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



GWAS workflow/pipeline - collaborative exercise


- Build your own workflow!
 - a. Download the data
 - b. Prepare the data (look at the phenotypes and genotypes!)
 - c. Filter the data
 - d. Impute missing genotypes
 - e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large White boars

(<https://zenodo.org/record/4081475#.YKPfmnUzZhE>)




from: <https://petpigworld.com/large-white-pigs-the-essential-guide/>

GWAS workflow/pipeline - collaborative exercise

- Build your own workflow!
 - a. Download the data
 -  **b. Prepare the data (look at the phenotypes and genotypes!)**
 - c. Filter the data
 - d. Impute missing genotypes
 - e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large White boars


 (<https://zenodo.org/record/4081475#.YKPfmnUzZhE>)




!! beware !! no missing SNP
genotypes (data already filtered
and imputed)

get data with missing SNP
genotypes from here:
http://www.jackdellequerce.com/data/GWAS_cohort.tar.gz

GWAS workflow/pipeline - collaborative exercise

- Build your own workflow!
 - a. Download the data
 -  **b. Prepare the data (look at the phenotypes and genotypes!)**
 - c. Filter the data
 - d. Impute missing genotypes
 - e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large White boars

 (<https://zenodo.org/record/4081475#.YKPfmnUzZhE>)



take a **subset of the SNPs** (to make calculations -and trial/errors- quicker), **e.g. chromosomes 10-14** (the mutation is on chromosome 12)



GWAS workflow/pipeline - collaborative exercise

- Build your own workflow!
 - a. Download the data
 - b. Prepare the data (look at the phenotypes and genotypes!)
 - c. Filter the data
 - d. Impute missing genotypes
 - e. Run the GWAS

- 1. Try on your own (individually, groups)
- 2. Let's do it all together!

