

Dates: 13-17 January, 2020
 Venue: AGROSAVIA station, Bogotá, Colombia

Teachers:

Institut National de Recherche Agricole (INRA), France

- Michel Naves

Universidad Complutense of Madrid (UCM), Spain

- Oscar Cortés (OC)

University of Lisbon (ULisboa)

- Andreia J. Amaral (AJA)
- Luís Telo da Gama (LTG)

Day 1: Monday 13th January 2020		
8:00-9:00	Welcome	Director of the AGROSAVIA Research station in Tibaitata u Carlos Lucero
9:00-10:00	Introduction	LTG & OC
10:00-10:15	Coffee break	
10:15-12:00	Review of concepts related with the measure of genetic diversity; AnGRs of Argentina	LTG, OC and Maria Antonia Revidatti
12:00-13:00	Lunch	
13:00-14:00	Genomic tools and their use in conservation genetics and management of populations	OC
14:00-15:00	SNP chip panels: conception and usage. Conventional data formats for genotype data. Public databases for genomic data	AJA
15:00-15:15	Coffee break	
15:15-16:15	Analysis software: introduction on basic functions	OC & AJA
Day 2: Tuesday 14th January 2020		
08:00-09:00	Analysis software: conclusion	OC & AJA
09:00-10:00	Principles of genetic characterization and estimation parameters	LTG
10:00-10:15	Coffee break	
10:15-12:00	Using runs of homozygosity (ROH) and estimation of linkage disequilibrium (LD) decay. Estimating ancestral effective population size (Ne).	OC
12:00-13:00	Lunch	
13:00-15:00	Practical: estimating ROH and LD using PLINK. Estimating ancestral Ne using SNeP	OC & AJA
15:00-15:15	Coffee break	
15:15-16:15	Organization of working groups. Kick-off of group projects	AJA, LTG & OC

Day 3: Wednesday 15th January 2020		
8:00-9:00	Detecting selection signatures across genomes	AJA
9:00-10:00	Practicals: Introduction to linux; How to access to a remote server and perform basic operations using BASH	AJA
10:00-10:15	Coffee break	
10:15-12:00	Practical: Introduction to R and data manipulation in R environment	AJA
12:00-13:00	Lunch	
13:00-14:00	Practical: Introduction to principal component analysis (PCA). Using it to identify signatures of selection and genetic markers associated with adaptation (pcadapt R package)	AJA
14:00-15:00	Practical: Detection of signatures of selection by identifying FST outliers with an inferred neutral distribution (The OutFLANK R package)	AJA
15:00-15:15	Coffee break	
15:15-16:15	Relationships between breeds and Principal component analysis	OC
Day 4: Thursday 16th January 2020		
08:00-09:00	Practical: admixture analysis	LTG
09:00-10:00	Linking phenotype and genotype: principals of genome-wide association analysis	LTG
10:00-10:15	Coffee break	
10:15-12:00	Practical: performing GWAS using PLINK Functional impact of selection: biological processes and pathways	AJA
12:00-13:00	Lunch	
13:00-14:00	Principals of genomic selection	LTG
14:00-16:15	Working in groups	AJA & OC & LTG
Day 5: Friday 17th January 2020		
08:00-12:00	Working in groups	AJA & OC & LTG
12:00-13:00	Lunch	
13:00-15:45	Presentation of groups' projects	AJA & OC & LTG
15:45-16:30	Plenary discussion: The way forward for the preservation of AnGR in latin America	AJA & OC & LTG & Maria António Ravidatti