



1st session of International Theoretical & Practical School on Quantitative Genetics

“Using whole-genome data in plant breeding: GWAS and Genomic Selection to genetically characterize key traits in large germplasm collections”

July 2018, VIR, St Petersburg

Program

Registration : Sunday, July 22nd, 09h00-9h30					
Time/Day	9h30-11h	11h-11h30	11h30-13h	13h-14h	14h-17h30
Sunday, July 22nd	Lecture of Prof. Dmitry Afonnikov (Institute of Cytology and Genetics, Novosibirsk, to be announced)	<i>Coffee break</i>	Lecture of Prof. Vladimir Brukhin, (Dobzhansky Center for Genome Bioinformatics, St. Petersburg (to be announced))	<i>Lunch</i>	The School Sponsor’s presentation Welcome Party
	8:30-11:00	11:00-11:30	11:30-13:00	13:00-14:00	14:00-17:30
Monday July 23rd	General introduction: « Genetics of quantitative resistance to <i>Verticillium</i> wilt in <i>M. truncatula</i> » as a redline of the course. -Theory: RCBD and Linear Mixed Models, LMM analysis with R.	<i>Coffee break</i>	How to make the best of large-scale phenotyping raw datasets: Focus on some useful experimental designs for GWAS and biostatistics with R -Theory: Augmented Block Designs;	<i>Lunch</i>	-‘How to?’ <i>guided practice</i> : R for semi-beginners: How to organize your data in a spreadsheet? How to analyse data quality? How to draw nice & informative graphs with R? - ‘By yourself’ <i>practice to code an</i>

	<ul style="list-style-type: none"> - <i>'How to?'</i> guided practice: Getting started with R: Generalities about the R environment: interface, data import, basic syntax, graphics. - <i>Guided practice on case study #1:</i> RCBD applied to genetic analysis of quantitative traits (heterosis, ploidy). 		<ul style="list-style-type: none"> Power of tests and independence concepts. - <i>Guided practice on case study #2:</i> Augmented-block designs for large-scale genotype collection evaluation. - <i>ePosters presentation</i> 		<ul style="list-style-type: none"> <i>analysis:</i> * <i>Case study #3:</i> RCBD applied to plant quantitative genetics studies. * <i>Case study #4:</i> Augmented-block designs for GWAS. - <i>ePosters presentation</i>
	8h30-11h	11h-11h30	11h30-13h	13h-14h	14h-17h30
Tuesday July 24th	How to deal with large-scale SNP raw datasets : Focus on some useful bioinformatics pipelines (no computational practice)	<i>Coffee break</i>	Analysis of genetic structure of populations - <i>Theory and case study</i> : Presentation of basic concepts of popular methods for pop. structure, using SNPs or SSRs. - <i>ePosters presentation</i>	Lunch	Analysis of genetic structure of populations, relationships with covariates and geography - <i>Guided practice on case study:</i> Analysis of genetic structure of populations in the model legume <i>Medicago truncatula</i> . - <i>ePosters presentation</i>
	8h30-10h30	10h30-11h	11h-12h30	12h30-13h30	13h30-17h
Wednesday July 25th	Genome Wide Association Study (GWAS) - <i>Theory:</i> Linkage disequilibrium (LD), General Linear Models (GLM)	<i>Coffee break</i>	- <i>Guided practice on case study:</i> GWAS on agronomical traits in legumes with GLM and LD analysis. - <i>ePosters presentation</i>	Lunch	Excursion – Social event
	8h30-11h	11h-11h30	11h30-13h	13h-14h	14h-17h30

Thursday July 26th	Genome Wide Association Study (GWAS)	Coffee break	Genome Wide Association Study (GWAS)	Lunch	Genomic Selection (GS)
	- <i>Theory</i> : Mixed Linear Models (MLM) including population structure and kinship.		- <i>Guided practice on case study</i> : GWAS on agronomical traits in legumes with MLM and kinship computation. - <i>ePosters presentation</i>		- <i>Theory</i> : Principle of GS, Breeding Values, Heritability - <i>Guided practice on case study</i> : Computation of Best Linear Unbiased Estimator (BLUEs), Best Linear Unbiased Predictor (BLUPs), Pedigree vs. Kinship matrix, Imputation. - <i>ePosters presentation</i>
	8h30-10h30	10h30-11h	11h-12h30	12h30-14h	14h-17h30
Friday July 27th	Genomic Selection (GS)	Coffee break	Genomic Selection (GS)	Lunch	Plant GWAS and GS Challenge.
- <i>Theory</i> : One-step models using G-BLUP and RR-BLUP models. - <i>Guided practice on case study</i> : genomic prediction of agronomical traits of interest in crop species	- <i>Theory and case study</i> : One-step and two-step models. Cross Validation, Accuracy. Factors affecting GS, optimization of training populations. - <i>Guided practice on case study</i> : Accuracy computation for genomic prediction of agronomical traits of interest in crop species, using different GS models. - <i>ePosters presentation</i>		<i>'By yourself' practice on complex case studies: GWAS and GS on agronomical traits in crops.</i>		
					Using whole-genome data in plant breeding: promises, challenges and limits. GWAS <i>and/or</i> GS, MAS, functional validation of candidate genes. Questions and Open Discussion. Delivery of certificates