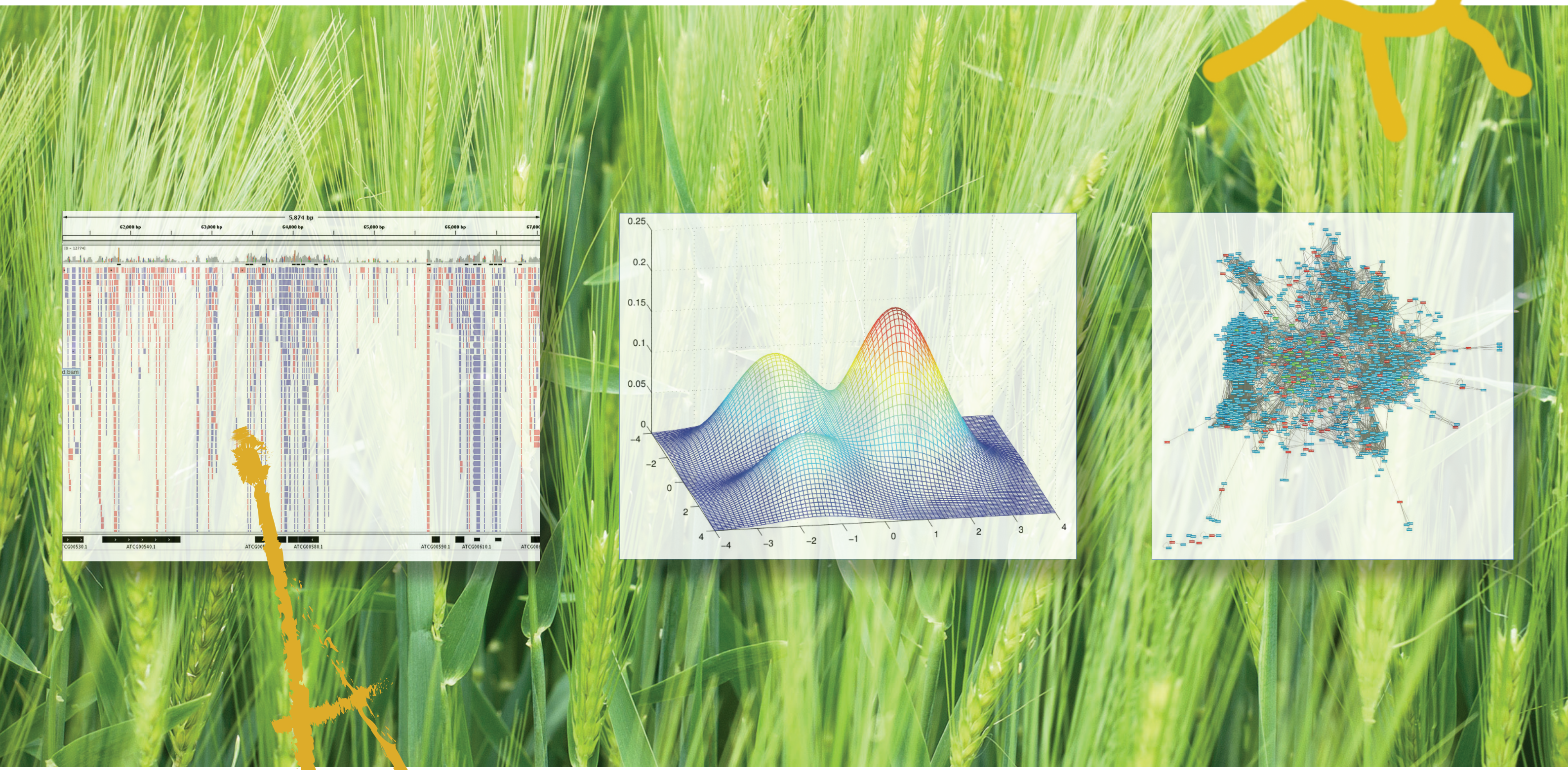
SPS Summer School 2016

From gene expression to genomic network

July 17th to 22nd 2016

Programme



SACLAY PLANT SCIENCES

Contents

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INRA
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Venue

Centre Port-Royal
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Planning at a glance

Sunday 17th	Monday 18th	Tuesday 19th	Wednesday 20th	Thursday 21st	Friday 22nd
	8:30 AM Session I	8:30 AM Session II	8:30 AM Session VI	8:30 AM Session IV	8:30 AM Session V
	10 AM Coffee break	10 AM Coffee break	10 AM Coffee break	10 AM Coffee break	10 AM Coffee break
	10:30 AM Session VI	10:30 AM Session II	10:30 AM Session VI	10:30 AM Session IV	10:30 AM Session V
	12:30 PM Lunch	12:30 PM Lunch	12:30 PM Lunch	12:30 PM Lunch	12:30 PM Lunch
		1:30 PM Session III			
2 PM Introduction	2 PM Session II			Free time	2PM Session V
		3 PM Coffee break		3 PM Session IV	
3:30 PM Coffee break	3:30 PM Coffee break	3:30 PM Session III			3:30 PM Conclusions
4 PM Introduction	4 PM Session II		Free time		
				4:30 PM Coffee break	
5 PM Session I		5 PM Coffee break		5 PM Session VI	
	5:30 PM Coffee break	5:30 PM Session VI			
	6 PM Session VI				
6:30 PM Poster session					
	8 PM Dinner	8 PM Dinner		8 PM Dinner	
8:30 PM Dinner			8:30 PM Dinner		

Bioinformatics analysis of raw RNA-seq data (assembly, mapping, counting)

Statistical analysis of RNA-seq from normalisation to differential analysis

Coexpression analysis by mixture models

Network inference by Graphical Models

Omics integration using mixOmics

Biological interpretation of the previous statistical outputs

Sunday 17th of July

2 PM - 3 PM: Introduction with presentation of SPS and Hadamard LabeX

3 PM - 3:30 PM: Presentation of the training

3:30 PM - 4 PM: Coffee break

4 PM - 5 PM: Introduction of the participants

5 PM - 6:30 PM: Bioinformatics for RNAseq data (part 1)

6:30 PM - 8 PM: Poster session

8:30 PM: Diner

Monday 18th of July

8:30 AM - 10 AM: Bioinformatics for RNAseq data (part 2)

10 AM - 10:30 AM: Coffee break

10:30 AM - 12 PM: Biological interpretation of the bioinformatics analysis

12:30 PM: Lunch

2 PM - 3:30 PM: Normalization of RNA-seq data

3:30 PM - 4 PM: Coffee break

4 PM - 5:30 PM: Differential analysis (part1)

5:30 PM - 6 PM: Coffee break

6 PM - 7:30 PM: Biological interpretation of the differential analysis

8 PM: Diner

Tuesday 19th of July

8:30 AM - 10 AM: Differential analysis (part 2)

10 AM - 10:30 AM: Coffee break

10:30 AM - 12 PM: Differential analysis (part 3)

12:30 PM: Lunch

1:30 PM - 3 PM: Co-expression analysis (part1)

3 PM - 3:30 PM: Coffee break

3:30 PM - 5 PM: Co-expression analysis (part 2)

5 PM - 5:30 PM: Coffee break

5:30 PM - 7 PM: Biological interpretation of the coexpression

8 PM: Diner

Wednesday 20th of July

8:30 AM - 10 AM: Integrative Model of Sepal Primordium Polarity (part 1)

10 AM - 10:30 AM: Coffee break

10:30 AM - 12 PM: Integrative Model of Sepal Primordium Polarity (part 2)

12:30 PM: Lunch

Free afternoon

8 PM: Diner

Thursday 21st of July

8:30 AM - 10 AM: Network inference (part 1)

10 AM - 10:30 AM: Coffee break

10:30 AM - 12 PM: Network inference (part 2)

12:30 PM: Lunch

3 PM - 4:30 PM: Network inference (part 3)

4:30 PM - 5 PM: Coffee break

5 PM - 6:30 PM: Cytonuclear interactions of *Arabidopsis thaliana*

8 PM: Diner

Friday 22nd of July

8:30 AM - 10 AM: MixOmics (part 1)

10 AM - 10:30 AM: Coffee break

10:30 AM - 12 PM: MixOmics (part 2)

12:30 PM - 2 PM: Lunch

2 PM - 3:30 PM: MixOmics to investigate cytonuclear interactions

3:30 PM - 4 PM: Conclusions of the Summer School

SPEAKERS

Richard Berthomé
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Richard Berthomé is a research scientist at the French National Institute for Agronomical Research (INRA) in the Plants Microorganisms Interaction laboratory (LIPM) (team ”Plant resistance pathways dynamics and adaptation to global warming”).

He realized his Ph.D. (1995-1999) and his first post-doc (1999-2000) at the Cellular biology laboratory (INRA, Versailles center) under the supervision of Dr. M. Tepfer and Dr. H. Vaucheret, respectively. During this period, he developed strategies devoted to confer resistance to viruses on an ornamental crop (Pelargonium) and studied PTGS (post-transcritpional gene suppression of transgenes) mechanism involved in natural resistance to viruses. Following this, he did a one-year post-doctoral fellowship in the Dr J.Traas's group (Cellular Biology laboratory at INRA, Versailles) and in the Dr D. Inzé's laboratory (VIB, Gend, Belgium) aimed at studying the role of the cell cycle in the shoot apical meristem organization control.

He was recruited as researcher in 2001 at the Genetic and Plant Breeding unit (IJPB-INRA, Versailles) in the « Organites and Reproduction" team. The project developed was dedicated to study the involvement of mitochondria in plant development and more particularly in sexual reproduction. In 2007, he joined the functional Genomic of Arabidopsis group of the Plant Genomics Research Unit (INRA-EVRY) to engineer a new system allowing tissue specific RNA labeling/transcriptome analysis and to study to the plant genome expression regulation in fluctuating environments, more particularly in response to abiotic stresses (cell differentiation process, nitrogen starvation, salt stress, organic pollutant). He integrated the LIPM in 2012. His main focus of interest is now on biotic-abiotic stress response interplay using the Arabidopsis thaliana/ Ralstonia solanacearum (Rs) pathosystem, well characterized in the team. His priorities are the analysis of (i) molecular mechanisms involved in the RPS4/RRS1-R immunity inhibition following a faint and permanent increase of temperature and (ii) to identify the genetic basis involved in resistance mechanisms remaining efficient at 30°C.

From 2005 to 2012, he has contribute as a biologist to several modules in Master level teaching on plant sexual reproduction, animal and plant genomics, genomics and plant productivity, functional genomics and biotechnology. Currently, he participates in two master level modules (signaling and gene regulation in microorganisms and plants; Symbiotic and pathogenic interactions) as lecturer and in workshops.

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Véronique Brunaud is an engineer of research in Bioinformatic at the French National Institute for Agronomical Research (INRA) in the Institute of Plant Sciences Paris-Saclay (IPS2).

In 1997 she has got a PhD in Bioinformatic from University Pierre et Marie Curie. During her PhD she worked on the characterization of DNA box allowing DNA reparation in the genome of Bacillus subtilis and the conception and management of a genomic database for bacteria.

She has been recruited in 1999 in a plant genomic research unit (URGV) to develop the databases of different platforms of this laboratory. She was in charge of the conception and management of CATdb (Trancriptomic platform), UTILLdb (platform of mutant TILLiNG), a collection of mutants (FLAGdb/FST). During these 16 years passed to URGV, her research activity has focus on the characterization of the gene function on Arabidopsis genome. For instance, she has been co-supervisor of a PhD in characterization of regulatory motifs fixed by the transcriptional factors.

In 2015, she has moved to the new Institute of Plant Science of Paris-Saclay (IPS2) in the team 'Genomic Networks' leaded by Marie-Laure Martin Magniette. The main projects of this team turns around the functional prediction of gene function with transversal tools (bioinformatics, statictics) and integration of various types of omic data. V. Brunaud is in charge of some projects dealing with the expresion of the genes, their regulations and the characterization of particular group of genes like "housekeeping genes". She manages the bioinformatic developments on the transcriptomic platform POPS and follows the evolution of research technologies in this domain.

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Françoise Budar is a senior scientist at the French Institute for Agronomical Research, in the Jean-Pierre Bourgin Institute in Versailles, where she leads the group "Organelles and Reproduction".

She realized her PhD under the Direction of Pr M. Van Montagu, on the genes of the T-DNA (for transferred DNA) of Agrobacterium tumefaciens. She was recruited at INRA as a plant molecular geneticist, in 1986.

She has been working on the interactions between nuclear and organelle genes since 1987. With her colleagues, she identified the genes responsible for male sterility and for restoration of fertility of the Ogu-INRA cytoplasmic male sterility (CMS) system, which has become the most used for seed production of Brassica crops hybrids in Europe. She acquired an internationally recognized expertise in CMS systems. Her work on this CMS system contributed to the understanding of some features of plant mitochondrial gene expression.

Since 2005, she studies cytonuclear interactions in the model plant Arabidopsis thaliana. She explored the natural genetic diversity of cytoplasmic genomes and discovered a cryptic CMS in this species. With the Versailles Arabidopsis Resource Centre, she developed new genetic resources for the study of cytonuclear interactions, by cytoplasmic exchange among natural accessions.

She has been involved in Master level teaching since 2005, when she created a teaching module on plant sexual reproduction. She has contributed as a biologist to a teaching module for young scientists in biology on statistical modeling since 2007.

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Julien Chiquet is a researcher at the French National Institute for Agronomic Research (INRA) in the department of Applied Mathematics and Computer Science. After a MSc. In Computer Science, he received in 2007 his PhD in applied mathematics at the University of Technologies of Compiègne (UTC), which was supported by the French Nuclear Agency (CEA). His PhD dealt with the development of stochastic approaches for application to reliability problems. In 2008 he got a position as an assistant professor in Statistics at the Université d'Évry-Val-d'Essonne. There, he turned to statistical learning, motivated by the need for renewed statistical methods and algorithms for analyzing genomics data. He has been working ever since on the problem of biological network reconstruction and modeling among other challenging problems in genomics. His favorite tools entails Gaussian graphical model and sparse regularizing methods. He received his "habilitation" in mathmatics at the Université of Évry in 2015. In 2016, he joined the INRA as a researcher at AgroParisTech, where he diversifies his fields of application to genetics and agronomy by elaborating more involved regularized methods to a broader class of problems.

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My research focuses on the regulation of organelle gene expression during stress responses with a particular emphasis on the role of the members of the pentatricopeptide repeat protein (PPR) family. Through genetics, interactomics and transcriptomics approaches and their integration using bioinformatics and biostatistics, my aim is to infer the plastid and mitochondrial gene networks and to understand how they cope with biotic and abiotic stresses. I'm also interested in how some pathogens can use PPR proteins to manipulate organelle gene expression during infection.

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Dr Kim-Anh Lê Cao (University of Queensland Diamantina Institute) was awarded her PhD in 2008 at Université de Toulouse, France. She then moved to Australia as a postdoctoral fellow at the University of Queensland.

She is now working at the University of Queensland Diamantina Institute as a National Health and Medical Research Council (NHMRC) Career Development Fellow. Her team focuses on the development of statistical approaches for the analysis and the integration of large biological data sets for studies in several types of cancer, and diseases involving the immune system, including arthritis, chronic infections, and diabetes. Since 2009, her team has been working on developing a statistical software dedicated to the integrative analysis of `omics' data, to help researchers make sense of biological big data (http://www.mixOmics.org). The mixOmics team currently includes 3 core members and 3 developers. Together they continue developing methodologies for the R package, to analyse and integrate 'omics and microbiome studies.

Since working at the University of Queensland, Kim-Anh has been teaching Statistics as a 'UQ ResTeach' recipient to undergraduate students, and since 2011 for the UQ Bioinformatics Masters program. She also teaches a yearly seminar series entitled `Statistics for frightened bio-researchers' to UQ institutes (http://www.imb.uq.edu.au/statistics) and 2-day mixOmics workshops .

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Marie-Laure Martin-Magniette is strongly involved in the analyses of genomic data and is at the interface between statistics and molecular biology. She has been for 11 years in charge of the statistical analyses of the data produced by the transcriptomic platform of the Plant Genomics Research Unit. Since 2003, she has acquired a strong expertise on the data normalization and the differential analysis for microarray and High- Throughput Sequencing technologies. She has also investigated the analysis of chIP-chip data to detect enriched regions and differentially methylated regions.

Since 2005 she has been focused on the discovery and characteristics of underlying structures in genomic data with mixture models and Hidden Markov Models. She conceived these models in close collaboration with fellow biologists and statisticians. Since September 2013, she has led the team Bioinformatics for predictive genomics of the Plant Genomics Research Unit. Her team project is highly interdisciplinary and deals with the construction of genomic networks of the plant model Arabidopsis thaliana for the discovery of functional modules and the prediction of functions of orphean genes involved in stress responses.

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Françoise Monéger is a senior scientist at the Centre National de la Recherche Scientifique, in the laboratory Reproduction et Développement des Plantes, located at the Ecole Normale Supérieure of Lyon. She is part of the Floral Meristem team.

She realized her PhD in 1990 under the supervision of Régis Mache on the analysis of chloroplastic and mitochondrial genome during microsporogenesis in maize. She then worked for 5 years in Chris Leaver's laboratory (Oxford, UK) on the molecular basis of cytoplasmic male sterility in sunflower. She was recruited at the CNRS in 1994. With her colleagues, she identified the first genes located on plant sex chromosomes in Silene latifolia. This discovery allowed to trace the evolutionary history of sex chromosomes.

In 2004, she decided to switch to the model plant Arabidopsis to adress fundamental question in developmental biology. With her colleagues, she identified target genes of several transcription factors involved in flower morphogenesis. She is now establishing links between transcription factors and cell wall remodelling components in order to understand how growth rates and directions are controlled and lead to proper morphogenesis. In parallel, she initiated a collaboration with computer scientists to reconstruct integrative genetic regulatory network, using the flower of Arabidopsis as a model. She is now participating to the Netbio working group to investigate the inference of genetic interaction network from transcriptomic data.

Every year, she is teaching at the ENS a course on polarity establishment in Arabidopsis flower.

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Andrea Rau is a research scientist at the French National Institute for Agronomical Research (INRA) in the Animal Genetics and Integrative Biology research unit (Populations, Statistics, and Genome team). She received her Ph.D. in 2010 from Purdue University (West Lafayette, Indiana, USA) for the development of statistical methods to infer gene regulatory networks from time-course microarray data. Following this, she did a one-year post-doctoral fellowship in the Model Selection and Statistical Learning (Select) team at Inria Saclay -- Île-de-France, with a focus on clustering RNA-seq data to identify groups of co-expressed genes. She was recruited as a researcher at INRA in the Animal Genetics department in 2011.

Dr. Rau's research interests focus on the development of appropriate statistical methodology for the analysis of high-dimensional genomic and transcriptomic data, and the implementation of these methods in open-source software packages. She is an active user and developer of the R programming language, and has developed or co-developed six R packages. Today, her work centers on the inference of causal regulatory networks from gene knock-out and knock-down experiments, as well as differential and co-expression analyses of RNA-seq data. Since 2014, she has been a work-package leader in the French National Research Agency (ANR) grant MixStatSeq, which seeks to develop mixture-based procedures for the statistical analysis of RNA-seq data.

Since 2011, Dr. Rau has worked in close collaboration with biologists on interdisciplinary problems at the interface of statistics and biology. She enjoys training students, and has taught courses on the statistical analysis of 'omics data at a variety of levels, from Master's level students to fellow researchers. She is also an active participant in the Statomique consortium, which gathers together more than 40 statisticians and bioinformaticians involved in high-throughput 'omics data analysis in France.

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Guillem Rigaill is Lecturer at Evry University. He is a member of Genomic Networks Team at the Institute of Plant Sciences Paris-Saclay. He received his PhD from AgroParisTech in 2010 for the development of algorithms and statistical methods for the analysis of breast cancer data.

His research interests focus on the development of efficient algorithms and appropriate statistical methodologies for the analysis of high-dimensional genomic and transcriptomic data. He has been developing new models for change-point detection and differential analysis and proposed inference procedures for these models that are both statistically and algorithmically efficient.Since 2007 he has applied those new tools in a number interdisciplinary projects involving cancer and plant biologists, bioinformaticians and statisticians.

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Nathalie Villa-Vialaneix is chargée de recherche at the French National Institute for Agronomical Research (INRA) in the Unit of Applied Mathematics and Computer Sciences in Toulouse. She is a member of the team "Statistics and Algorithm for Biology". She received her PhD of the University Toulouse 2 (Le Mirail) in Mathematics in 2005 for her work on functional data analysis and machine learning. She was involved in interdisciplinary research projects, especially with geographers and historians.

In 2006, she was recruited as an associate professor (maîtresse de conférences) at the University de Perpignan (IUT Carcassonne) and became a member of the SAMM team in the University Paris 1. She also started collaborations with researchers from the INRA of Toulouse and became a member of the working group "Biopuces" interested in microarray analyses and other types of 'omics data. Her research focused on developping methods for application in graph mining and inference for social sciences and biology.

Since 2014, she has been recruited at the INRA of Toulouse and is involved in several research projects for 'omics data integration, transcriptomic (microarray and RNAseq) data analysis and network inference and analysis. She has several collaborations with researchers of INRA and INSERM. She is also co-organizer of two working groups in biostatistics ("Biopuces" which is a monthly workshop about 'omics data analysis, "NETBIO" a network with a yearly two-day conference on Biological Network), a board member of the biostatistics platform in Toulouse and a board member of the French Statistical Association (SFdS).

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