Schedule "to go"

Workshops, Tutorials and Satellite Meetings

Venue: see tables below to check event location

FORUM: Faculty of Medecine of Strasbourg: 4 Rue Kirschleger, Strasbourg.
PMC: Palais de la Musique et des Congrès, Place de Bordeaux - Avenue Schutzenberger, Strasbourg.

Registration

Unless otherwise indicated, one hour before the beginning of the event

Saturday, September 6

FORUM   **Faculty of Medecine of Strasbourg: 4 Rue Kirschleger, Strasbourg**.

W07	Workshop on Integrative Dynamic Analyses of Large Biomedical Network Data	**Room 3**	9:00	18:00
W09	Workshop on Machine Learning for Systems Biology (Day1)	**Amphi Forum**	9:00	18:00
W11	The 1st Unified Workshop on Proteome and Metabolome Informatics	**Room 2**	9:00	18:00
T01	Analysis of Cis-Regulatory Motifs from High-Throughput Sequence Sets	**Room 4**	9:00	18:00
T06	Reuse, Develop and Share Biological Visualisation with BioJS	**Room 1**	9:00	17:00
T07	Scientific Workflows for Analysing, Integrating and Scaling Bioinformatics Data: a Practical Introduction to Galaxy, Taverna and WS-PGRADE	**Room 5**	9:00	18:00
T09	TADbit: Automated Analysis and Three-Dimensional Modeling of Genomic Domains	**Room 6**	9:00	17:00

PMC   **Strasbourg Convention Centre, Place de Bordeaux - Avenue Schutzenberger, Strasbourg.**

W06	Workshop on Informatics based Approaches for Circular Dichroism Data	**Salon Rohan**	9:00	18:00
W08	Workshop on Logical Modelling and Analysis of Cellular Networks (Day1)	**Salon Boston**	9:00	18:00
W16	Workshop on Tools and Techniques for Analysis and Design of Macromolecular Structures	**Salon Stuttgart**	9:00	17:00
S01	European Student Council Symposium	**Salon Leicester**	9:00	18:00

Sunday, September 7

FORUM   **Faculty of Medecine of Strasbourg: 4 Rue Kirschleger, Strasbourg.**

W02	BioNetVisA Workshop: From biological network reconstruction to data visualization and analysis in molecular biology and medicine	**Room 3**	9:00	17:00
W04	Workshop on Computational and Systems Biology for Disease Comorbidities	**Room 2**	9:00	17:00

W09	Workshop on Machine Learning for Systems Biology (Day2)	**Amphi Forum**	9:00	17:00
T04	Multivariate projection methodologies for the exploration of large biological data sets. Application in R using the mixOmics package	**Room 5**	9:00	17:30
T05	Protein Evolution Analysis: on the Use of Phylogenetic Trees	**Room 4**	9:00	17:00

PMC	**Strasbourg Convention Centre, Place de Bordeaux - Avenue Schutzenberger, Strasbourg.**			
W01	RADIANT Workshop: Analysis of Differential Isoform Usage by RNA-seq: Statistical Methodologies and Open Software	**Salon Dresden**	9:00	18:00
W03	First Workshop on Computational Methods for Structural RNAs - CMRS'14	**Salon Bartholdi**	9:00	18:00
W05	Drug Development 2.0 - Computational integrative biology methods for drug repurposing, target discovery and translational research.	**Salon Boston**	9:00	18:00
W12	Workshop on Recent Computational Advances in Metagenomics	**Salon Orangerie**	9:00	17:30
W13	sbv IMPROVER Workshop	**Salon Leicester**	9:00	17:00
T02	Computational Tools to Define and Analyse Logical Models of Cellular Networks	**Salon Rohan**	13:30	18:00
T03	IMGT, the Global Reference in Immunogenetics and Immunoinformatics	**Salon Rohan**	9:00	13:00
T08	Statistics and Numerics for Dynamical Modeling	**Salon Stuttgart**	9:00	17:00

Main conference

Venue:

PMC: Palais de la Musique et des Congrès, Place de Bordeaux - Avenue Schutzenberger, Strasbourg.

Sunday, September 7 – Conference Opening

16:00	Conference registration opens	PMC – Main Floor
18:00	Conference opening and welcome	Auditorium ERASME
18:15	**Keynote 1: Jean-Marie LEHN**. *Perspectives in Chemistry: From Supramolecular Chemistry towards Adaptive Chemistry*.	
19:05	**Invited Talk:** Laurence LWOFF. *Biomedical Research and Human Rights: the case of biobanking.*	
19:30	Welcome Cocktail	Dining Room Contades
21:00	End of welcome cocktail	

Monday, September 8

7:45	Registration opens	
8:45	**Keynote 2: Patrick ALOY.** *A network biology approach to novel therapeutic strategies.*	Auditorium ERASME
9:35	Distribution in two parallel sessions	

	Auditorium ERASME	Room SCHUMANN
	Session Mon1: Pathways and Molecular Networks (1)	**Session Mon5: Evolution and Population Genetics (1)**
9:40	*PP01 - HubAlign: An accurate and efficient method for global alignment of protein-protein interaction networks.* Daniela Boernigen	*PP11 - Polytomy Refinement for the Correction of Dubious Duplications in Gene Trees.* Manuel Lafond
10:05	*PP02 - Alignment-free protein interaction network comparison.* Waqar Ali	*PP12 - RidgeRace: Ridge regression for continuous ancestral character estimation on phylogenetic trees.* Christina Kratsch
10:30	*PP03 - Fast randomisation of large genomic datasets while preserving alteration counts.* Francesco Iorio	*PP13 - Point estimates in phylogenetic reconstructions.* Philipp Benner
10:55	Coffee Break	Main Floor & 1st Floor
	Session Mon3: Sequencing and Sequence Analysis for Genomics (1)	**Session Mon6: Evolution and Population Genetics (2)**
11:15	*PP06 - Lambda: The local aligner for massive biological data.* Hannes Hauswedell	*PP14 - ASTRAL: Genome-scale coalescent-based species tree estimation.* Siavash Mirarab
11:40	*PP07 - Fiona: a parallel and automatic strategy for read error correction.* Marcel Schulz	**Highlight Talk:** *HP03 - Patterns of positive selection in seven ant genomes.* Julien Roux
12:05	**Highlight Talk**: *HP02 - Comparison of mapping algorithms used in high-throughput sequencing: application to Ion Torrent data.* Ségolène Caboche	
12:30	LUNCH	Dining Room Contades
13:30	**Industrial and Demo Track**	See corresponding pages
14:35	**Keynote 3: Alice McHardy.** *Gaining Insight into the Uncultured Microbial World by Computational Metagenome Analysis.*	Auditorium ERASME
15:25	Distribution in two parallel sessions	
	Auditorium ERASME	Room SCHUMANN
	Session Mon4: Sequencing and Sequence Analysis for Genomics (2)	**Session Mon7: Structural Bioinformatics (1)**
15:30	*PP08 - FastHap: fast and accurate single individual haplotype reconstruction using fuzzy conflict graphs.* Sepideh Mazrouee	*PP15 - Assessing the local structural quality of transmembrane protein models using statistical potentials (QMEANBrane).* Gabriel Studer
15:55	*PP09 - Probabilistic single-individual haplotyping.* Volodymyr Kuleshov	*PP16 - A new statistical framework to assess structural alignment quality using information compression.* James Collier
16:20	*PP10 - cnvOffSeq: detecting intergenic copy number variation using off-target exome sequencing data.* Evangelos Bellos	*PP17 - Entropy driven partitioning of the hierarchical protein space.* Nadav Rappoport
16:45	Coffee Break	Main Floor & 1st Floor
	Session Mon2: Pathways and Molecular Networks (2)	**Session Mon8: Structural Bioinformatics (2)**
17:05	*PP04 - Identifying transcription factor complexes and their roles.* Thorsten Will	*PP18 - PconsFold: Improved contact predictions improve protein models.* Mirco Michel
17:30	*PP05 - Personalized identification of altered pathways in cancer.* Taejin Ahn	*PP19 - Microarray R-based analysis of complex lysate experiments with MIRACLE.* Markus List
17:55	**Highlight Talk:** *HP01 - Wiring miRNAs to pathways: a topological approach to integrate miRNA and mRNA expression profiles.* Enrica Calura	**Highlight Talk:** *HP04 - Comprehensive analysis of DNA polymerase III alpha subunits and their homologs in bacterial genomes.* Ceslovas Venclovas
18:20	Break – Moving to Poster Session	

18:30	**Poster Session (Odd numbers)**	1st Floor
19:30	**Poster Session (Even numbers)**	1st Floor
20:30	Launching Ice-Breaking Event	Main Floor
20:45	Ice-breaking Event	

Tuesday, September 9

7:45	Registration opens	
8:45	**Keynote 4: Nada LAVRAC. *Advances in data mining for biomedical research.***	Auditorium ERASME
9:35	Distribution in the two parallel sessions	
	Auditorium ERASME	Room SCHUMANN
	Session Tue1: Computational Systems Biology (1)	**Session Tue4: Biological Knowledge Discovery from Data**
9:40	*PP20 - Stronger findings for metabolomics through Bayesian modeling of multiple peaks and compound correlations.* Tommi Suvitaival	*PP28 - Unveiling new biological relationships using shared hits of chemical screening assay pairs.* Monica Campillos
10:05	*PP21 - Causal network inference using biochemical kinetics.* Chris Oates	*PP29 - Identification of structural features in chemicals associated with cancer drug response: A systematic data-driven analysis.* Suleiman Ali Khan
10:30	**Highlight Talk:** *HP05 - High-dimensional Bayesian parameter estimation: Case study for a model of JAK2/STAT5 signaling.* Sabine Hug	**Highlight Talk:** *HP06 - Shaping the interaction landscape of bioactive molecules.* David Gfeller
10:55	Coffee Break	Main Floor & 1st Floor
	Session Tue2: Computational Systems Biology (2)	**Session Tue5: Gene Expression (1)**
11:15	*PP22 - Effects of small particle numbers on long-term behaviour in discrete biochemical systems.* Peter Dittrich	*PP30 - Estimating the activity of transcription factors by the effect on their target genes.* Rainer Koenig
11:40	*PP23 - TEMPI: Probabilistic modeling time-evolving differential PPI networks with multiple information.* Yongsoo Kim	*PP31 - Modeling DNA methylation dynamics with approaches from phylogenetics.* Dennis Kostka
12:05	*PP24 - Experimental design schemes for learning Boolean network models.* Nir Atias	**Highlight Talk:** *HP07 - Key regulators control distinct transcriptional programmes in blood and progenitor and mast cells.* Felicia Ng
12:30	LUNCH	Dining Room Contades
13:30	**Industrial and Demo Track**	See corresponding pages
14:35	**Keynote 5: Ewan Birney. *Big Data in Biology.***	Auditorium ERASME
15:25	Distribution in two parallel sessions	
	Auditorium ERASMUS	Room SCHUMANN
	Session Tue3: Bioinformatics of Health and Disease (1)	**Session Tue6: Gene Expression (2)**
15:30	*PP25 - OncodriveROLE classifies cancer driver genes in Loss of Function and Activating mode of action.* Michael Philipp Schroeder	*PP32 - Two-dimensional segmentation for analyzing HiC data.* Celine Levy-Leduc
15:55	*PP26 - ContrastRank: a new method for ranking putative cancer driver genes and classification of tumor samples.* Emidio Capriotti	*PP33 - Broad-Enrich: Functional interpretation of large sets of broad genomic regions.* Raymond Cavalcante

16:20	*PP27 - Drug susceptibility prediction against a panel of drugs using kernelized Bayesian multitask learning.* Mehmet Gönen	**Highlight Talk:** *HP08 - Chromatin position effects quantified from thousands of reporters integrated in parallel.* Lodewyk Wessels
16:45	Coffee Break - Poster Session begins	Main Foor & 1st Floor
17:30	1st departure to river boat trip (then every 15 min)	Main Floor
18:45	End of Poster Session	1st Floor
19:15	Last departure to river boat trip	Main Floor
From 19:00	Gala Evening at the Council of Europe or Ancienne Douane	

Wednesday, September 10

8:00	Conference registration opens	Main Floor
9:00	**Keynote 6: Doron LANCET**. ***Rational confederation of genes and diseases***.	Auditorium ERASME
	Session Wed1: Databases and Ontologies	
9 :50	*PP34 - The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective.* Yuxiang Jiang	
10:15	*PPE35 - Integration of molecular network data reconstructs Gene Ontology.* Vladimir Gligorijevic	
10 :40	Coffee Break	Main Floor
	Session Wed2: Bioinformatics of Health and Disease (2) and Bio-Imaging	Auditorium ERASME
11:00	*PP36 - Transcriptome-guided amyloid imaging genetic analysis via a novel structured sparse learning algorithm.* Jingwen Yan	
11:25	*PP37 - Large-scale automated identification of mouse brain cells in confocal light sheet microscopy images.* Paolo Frasconi	
11:50	**Highlight Talk:** *HP09 - Novel Developments in computational clinical breath analysis and biomarker detection.* Anne Christine Hauschild	
12:15	Moving to Dining Room	
12:30	LUNCH	Dining Room Contades
13:30	**Industrial and Demo Track**	See corresponding pages
	Session Wed3: Text Mining for Computational Biology	Auditorium Erasme
14:35	*PP38 - Extracting patterns of database and software usage from the bioinformatics literature.* Geraint Duck	
15:00	**Highlight Talk:** *HP10 - Text mining technologies for database curation.* Fabio Rinaldi	
	Session Wed4: RNA prediction	Auditorium Erasme
15:25	*PP39 - CRISPRstrand: Predicting repeat orientations to determine the crRNA-encoding strand at CRISPR loci.* Omer S. Alkhnbashi	
15:50	*PP40 - Towards a piRNA prediction using multiple kernel fusion and support vector machine.* Fariza Tahi.	
16:15	**Keynote 7: Eric WESTHOF**. ***The Detection of Architectural Modules in RNA sequences and the RNA-Puzzles Modeling Contest.***	
17:05	Prize Ceremony and Concluding remarks	
17:15	End of Conference – Farewell Coffee	Main Floor