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**Monday, July 3**

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| <b>13:00</b> | Registration   |                          |
| 14:00-14:30  | Welcome  |                          |
| 14:30-15:30  | <b>Patrick Wincker</b><br><b>Holistic metagenomics in marine plankton communities</b>  | <b>Keynote – Pasteur</b> |
| 15:30-16:30  | Metagenomics   | Plenary – Pasteur        |
|              | Simka: Large Scale De Novo Comparative Metagenomics<br><i>Gaëtan Benoit, Pierre Peterlongo, Mahendra Mariadassou, Erwan Drezén, Sophie Schbath, Dominique Lavenier and Claire Lemaitre</i>   |                          |
|              | Food-Microbiomes Transfert, a Shotgun Metagenomic Tool and a Database to Analyze Cheese Ecosystems<br><i>Thibaut Guirimand, Anne-Laure Abraham, Sandra Derozier, Charlie Pauvert, Mahendra Mariadassou, Valentin Loux and Pierre Renault</i>   |                          |
|              | Reconstruction of Full-Length 16S rRNA Sequences for Taxonomic Assignment in Metagenomics<br><i>Pierre Pericard, Yoann Dufresne, Samuel Blanquart and Hélène Touzet</i>  |                          |
| 16:30-17:00  | Break  |                          |
| 17:00-18:00  | Integrative Biology  | Plenary – Pasteur        |
|              | FEELnc: an Alignment-Free Tool for Long Non-Coding RNAs Annotation<br><i>Valentin Wucher, Fabrice Legeai, Benoît Hédan, Guillaume Rizk, Laetitia Lagoutte, Edouard Cadieu, Audrey David, Nadine Botharel, Céline Le Béguéc, Catherine André, Christophe Hitte and Thomas Derrien</i> |                          |
|              | Analyse intégrative des ARN longs non-codant (lncRNAs) du génome canin<br><i>Céline Le Béguéc, Valentin Wucher, Laetitia Lagoutte, Edouard Cadieu, Benoît Hédan, Catherine André, Christophe Hitte and Thomas Derrien</i>  |                          |
|              | Analysis, Integration and Modeling of Cell Clustering Results in High-Dimensional Cytometry Data<br><i>Guillaume Gautreau, David Pejoski, Roger Le Grand, Antonio Cosma, Anne-Sophie Beignon and Nicolas Tchitchek</i>   |                          |
| 18:00-18:30  | JeBiF / bioinfo-fr.net / Bioinfuse   |                          |

**Tuesday, July 4**

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| 9:00-10:00  | <b>Tobias Marschall</b><br><b>A Guided Tour to Computational Haplotyping</b>   | <b>Keynote – Pasteur</b> |
| 10:00-10:40 | High Throughput Sequencing   | Plenary – Pasteur        |
|             | GenomeOnRails: Depicting Microbial Species Diversity Via a Pangenome Graph<br><i>Guillaume Gautreau, Rémi Planel, Amandine Perrin, Marie Touchon, Eduardo Rocha, Christophe Ambroise, Catherine Matias, Stéphane Cruveiller, Claudine Médigue and David Vallenet</i>   |                          |
|             | Assembly of Heterozygous Genomes Using High-Order de Bruijn Graphs<br><i>Antoine Limasset, Camille Marchet, Pierre Peterlongo and Jean-Francois Flot</i>   |                          |
| 10:40-11:05 | Break  |                          |
| 11:05-11:25 | Proteomics   | Plenary – Pasteur        |
|             | Rapid Spectra Comparison with Data-Mining Algorithms: Accessing Post-Translational Modification Profiles on a sample scale<br><i>Matthieu David, Guillaume Fertin, Hélène Rogniaux and Dominique Tessier</i>   |                          |
| 11:25-12:40 | Posters (odd numbers)  |                          |
| 12:40-13:40 | Lunch  |                          |
| 13:40-14:40 | <b>Julio Saez-Rodriguez</b><br><b>Network Models to Understand and Combat Cancer: from Clinical Genomics to Biochemical Modelling</b>  | <b>Keynote – Pasteur</b> |
| 14:40-15:40 | Systems biology  | Plenary – Pasteur        |
|             | Rare and Common Epilepsies Converge on a Shared Gene Regulatory Network Providing Opportunities for Novel Antiepileptic Drug Discovery<br><i>Andrée Delahaye-Duriez, Prashant Srivastava, Kirill Shkura, Sarah R. Langley, Liisi Laaniste, Aida Moreno-Moral, Bénédicte Danis, Manuela Mazzuferi, Patrik Foerch, Elena Gazina, Kay Richards, Steven Petrou, Rafal Kaminski, Enrico Petretto and Michael R. Johnson</i> |                          |
|             | Prediction of Disease-associated Genes by advanced Random Walk with Restart on Multiplex and Heterogeneous Biological Networks<br><i>Alberto Valdeolivas, Elisabeth Remy, Laurent Tichit, Gaëlle Odelin, Claire Navarro, Sophie Perrin, Pierre Cau, Nicolas Levy and Anaïs Baudot</i>  |                          |
|             |  CRCMapper: Models of Core Transcriptional Regulatory Circuitries<br><i>Violaine Saint-André, Alexander J. Federation, Charles Y. Lin, Brian J. Abraham, Jessica Reddy, Tong Ihn Lee, James E. Bradner and Richard A. Young</i>   |                          |
| 15:40-16:05 | Break  |                          |
| 16:05-17:45 | Systems biology  | Parallel 1/2 – Matisse   |
|             | Network Inference of Dynamic Models by the Combination of Spanning Arborescences<br><i>Anthony Coutant and Céline Rouveirol</i>  |                          |
|             |  Long-term Tracking of Budding Yeast Cells with CellStar<br><i>Cristian Versari, Szymon Stoma, Kirill Batmanov, Artémis Llamasi, Filip Mroz, Adam Kaczmarek, Matt Deyell, Cédric Lhoussaine, Pascal Hersen and Gregory Batt</i>   |                          |
|             |  Listeriomics: A Multi-Omics Interactive Web Platform for Systems Biology of the Model Pathogen Listeria<br><i>Christophe Becavin, Mikael Koutero, Nicolas Tchitchek, Franck Cerutti, Pierre Lechat, Nicolas Maillet, Claire Hoede, Hélène Chiappello, Christine Gaspin and Pascale Cossart</i>                                     |                          |
|             |  AskOmics, a Web Tool to Integrate and Query Biological Data Using Semantic Web Technologies<br><i>Xavier Garnier, Anthony Bretaudeau, Olivier Filangi, Fabrice Legeai, Anne Siegel and Olivier Dameron</i>   |                          |
|             |  Regulatory and Signaling Network Assembly through Linked Open Data<br><i>Marie Lefebvre, Jérémie Bourdon, Carito Guziolowski and Alban Gaignard</i>  |                          |
| 16:05-17:45 | Software Development and Workflows   | Parallel 2/2 – Pasteur   |
|             | Scientific Workflows for Computational Reproducibility in the Life Sciences: Status, Challenges and Opportunities<br><i>Sarah Cohen-Boulakia, Khalid Belhajame, Olivier Collin, Jérôme Chopard, Christine Froidevaux, Alban Gaignard, Konrad Hinsén, Pierre Larmande, Yvan Le Bras, Frédéric Lemoine, Fabien Mareuil, Hervé Ménager, Christophe Pradal and Christophe Blanchet</i>                                     |                          |
|             |  Sequanix: A Dynamic Graphical Interface for Snakemake Workflows<br><i>Dimitri Desvillechabrol, Rachel Legendre, Christiane Bouchier, Sean Kennedy and Thomas Cokelaer</i>  |                          |
|             |  Biosphere Web : un portail haut niveau pour une utilisation bioinformatique des clouds<br><i>Bryan Brancotte, Mohamed Bedri, Jonathan Lorenzo, Sandrine Perrin, Frédéric Séné, Awa Sepou Ngailo, Christophe Blanchet and Jean-François Gibrat</i>  |                          |
|             |  Biodjango, an Open Framework for Bioinformatics Publishing<br><i>Ennys Gheyouché and Stéphane Téletchéa</i>  |                          |
|             |  New Generation Phylogeny.fr: Refactoring Phylogeny.fr for Innovative Phylogenetic Services<br><i>Damien Correia, Vincent Lefort, Olivia Doppelt-Azeroual, Fabien Mareuil, Sarah Cohen-Boulakia and Olivier Gascuel</i>   |                          |
| 18:00       | Social events  |                          |

**Wednesday, July 5**

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| 9:00-10:00  | <b>Franca Fraternali</b><br><b>Unraveling the Good and the Bad in Protein Networks: Functional versus Dysfunctional Interactions</b>   | <b>Keynote – Pasteur</b> |
| 10:00-10:40 | High Throughput Sequencing   | Parallel 1/2 – Matisse   |
|             | HG-CoLoR: Hybrid Graph for the error Correction of Long Reads<br><i>Pierre Morisse, Thierry Lecroq and Arnaud Lefebvre</i>   |                          |
|             |  PhylOligo: a Package to Identify Contaminant or Untargeted Organism Sequences in Genome Assemblies<br><i>Ludovic Mallet, Tristan Bitard-Feildel, Franck Cerutti and H  l  ne Chiapello</i> |                          |
| 10:00-10:40 | Proteins   | Parallel 2/2 – Pasteur   |
|             | Use of Cross-Docking Simulations for Identification of Protein-Protein Interactions Sites: The Case of Proteins with Multiple Binding Sites<br><i>Nathalie Lagarde, Lydie Vamparys, Benoist Laurent, Alessandra Carbone and Sophie Sacquin-Mora</i>                          |                          |
|             | In silico developments for the study of glycosylation applied to extracellular matrix proteins<br><i>Camille Besan  on, Alexandre Guillot, S  bastien Blaise, Manuel Dauchez, Jessica Jonquet, Nicolas Belloy and St  phanie Baud</i>  |                          |
| 10:40-11:05 | Break  |                          |
| 11:05-11:45 | Genome visualization   | Parallel 1/2 – Matisse   |
|             |  Dynamix: Dynamic Visualization by Automatic Selection of Informative Tracks from Hundreds of Genomic Data Sets<br><i>Matthias Monfort, Eileen Furlong and Charles Girardot</i>             |                          |
|             |  GeneSpy, a Simple Tool to Explore Genomic Context<br><i>Pierre Simon Garcia, Fr  d  ric Jauffrit, Christophe Grangeasse and C  line Brochier-Armanet</i>                                   |                          |
| 11:05-11:45 | High Throughput Sequencing   | Parallel 2/2 – Pasteur   |
|             |  MCXpress: An R Package for Functional Interpretation of Single Cell RNA-Seq Data Using Multivariate Analysis<br><i>Akira Cortal and Antonio Rausell</i>                                    |                          |
|             |  Deciphering the Functional Effects of Genetic Variation with UniProt Annotations<br><i>Benoit Bely, Andrew Nightingale and Maria Martin</i>  |                          |
| 11:45-12:50 | Posters (even numbers)   |                          |
| 12:50-13:50 | Lunch  |                          |
| 13:50-14:50 | <b>John Huelsenbeck</b><br><b>Bayesian inference in phylogeny for genome-scale data</b>  | <b>Keynote – Pasteur</b> |
| 14:50-15:50 | Phylogeny  | Plenary – Pasteur        |
|             | Extreme Halophilic Archaea Derive from Two Distinct Methanogen Class II Ancestors<br><i>Monique Aouad, Najwa Taib, Anne Oudart, Michel Lecocq, Manolo Gouy and C  line Brochier-Armanet</i>  |                          |
|             | Origin and Evolution of Multiple Haem Copper Oxidases in Archaea<br><i>Anne Oudart, Simonetta Gribaldo and C  line Brochier-Armanet</i>  |                          |
|             |  Genomicus – New tools for Comparative Genomics and Evolution in Eukaryotes<br><i>Alexandra Louis, Nga Thi Thuy Nguyen and Hugues Roest Crolius</i>                                       |                          |
| 15:50-16:15 | Break  |                          |
| 16:15-17:15 | SFBI – assembl  e g  n  rale   | Pasteur                  |
| 17:15-17:45 | GdR BIM (BioInformatique Mol  culaire) – assembl  e g  n  rale   |                          |
| 17:45-18:15 | IFB (Institut Fran  ais de Bioinformatique)  |                          |
| 18:30       | Bus departure for the Gala Dinner  |                          |
| 19:00-23:55 | Gala Dinner  |                          |

Thursday, July 6

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|-------------|---|--------------------------|
| 9:00-10:00  | <b>Céline Brochier</b><br><b>The growing tree of Archaea: changing perspectives on the diversity and evolution of the third domain of life</b>  | <b>Keynote – Pasteur</b> |
| 10:00-10:40 | <b>Integrative Biology</b><br>Probing Factor-Dependent Long-Range Contacts Using Regression with Higher-Order Interaction Terms<br><i>Raphaël Mourad, Lang Li and Olivier Cuvier</i><br>An Integrative Approach for Predicting the RNA Secondary Structure for the HIV-1 Gag UTR Using Probing Data<br><i>Afaf Saaidi, Yann Ponty and Bruno Sargueil.</i> | Plenary – Pasteur        |
| 10:40-11:10 | Break   |                          |
| 11:10-11:50 | <b>Integrative Biology</b><br>NCBoost: a machine-learning method to detect disease-causing non-coding variants<br><i>Barthelemy Caron and Antonio Rausell</i><br>Context-Specific Prioritization of Non-Coding Variants Implicated in Human Diseases<br><i>Lambert Moyon, Yves Clément, Camille Berthelot and Hugues Roest Crolius</i>                    | Plenary – Pasteur        |
| 11:50-12:30 | Announce RECOMB 2018 (Paris)<br>Prix SFBI<br>Announce JOBIM 2018<br>Clôture   | Plenary – Pasteur        |