3rd BeNeLuxFra Student Symposium



Thursday 6 and Friday 7 July 2017

INRIA Lille



Welcome to Lille | 3rd BeNeLuxFra Student Symposium

The story of BeNeLuxFra Student symposium started in September 2014 during ECCB in Strasbourg. Bart Cuypers from RSG Belgium was giving a "course" to me on the differences between trapist and abbey beers. After a few beers, we talked of organizing joint event between RSG Belgium and RSG France. We invited also RSG Luxembourg and RSG Netherlands who were immediately enthusiastic and joined the project.

In 2015, RSG Belgium launched the very first BeNeLuxFra Student Symposium as a satellite meeting of the BBC 2015 in Antwerp. This edition was also the time to celebrate the creation of RSG Luxembourg.

The second edition was organized by RSG Luxembourg in 2016 in the middle of Belval's former blast furnace that have been rehabilitated for the university of Luxembourg.

This year, it was RSG France's turn to organize this event. We hope you will enjoy it as much as we enjoyed organizing it for you and that networking and beers will let you have new crazy ideas.

Julien Fumey Chair, RSG France President

Funding |

We would like to thanks funders of 3rd BeNeLuxFra Student Symposium :





Twitter |

Official hashtag is #BNLF17. You can tweet all presentation except "no tweet" is explicitly request by the speaker.

The venue |

INRIA Lille Bât B 40 Avenue du Halley Villeneuve d'Ascq How to come ? By Public transportation : Take Metro Line 1 Station 4 Cantons Grand Stade

By Car : From Lille, Take A1, E42, A27 and D952



Schedule |

Thursday 6 July		
13h00 - 14h00	Registration	
14h00 - 14h30	Opening remarks Julien Fumey - Chair, RSG France President Presentation RSG Luxembourg - Eugen Bauer, President RSG Belgium - Daniele Parisi, President RSG Netherlands - Joske Ubels, President	
14h30 - 15h30	Keynote Long term information integration : evolutio Paulien Hogeweg - Utrecht University, The Netherlands	Chairman : Bart Cuypers n of evolution
15h30 - 16h00	Coffee break	
16h00 - 17h00	Keynote Natural and synthetic control of resource al Hidde de Jong - <i>Inria Grenoble, France</i>	Chairman : Daniele Parisi location in bacteria
17h00 - 17h45	RSG France General Assembly	
19h	Social Event Au Boudin Bar o place Schuman Lille	How to go there ? You can follow organizers! Take metro line 1 Station Rihour The bar is at a 6-7 minutes walk (Follow green or red dashed line on the maps)

Friday 7 July	
08h30 - 09h30	Registration
09h30 - 09h45	Epilepsy Subgroup Identification Based On Shared Comorbidity Risk Factors And Pleiotropic Findings, Using Data-Mining And Disease-Modeling Approaches Nora Filep - Fraunhofer SCAI, Germany
09h45 - 10h00	Ligand-protein interaction analysis for drug-target interaction prediction in drug repositioning Daniele Parisi - <i>KU Leuven, Belgium</i>
10h00 - 10h15	Analysis of the molecular network underlying left ventricular remodeling after myo- cardial infarction Marie Cuvelliez - Institut Pasteur de Lille, France
10h15 - 10h30	Black box revelation of linkage between two disparate levels of pathophysiology "Genetics/Imaging" using integrated multi-scale modelling Sepehr Golrizkhatami - Fraunhofer Institute, Germany
10h30 - 11h00	Coffee Break
	Chairman : Léopold Carron
11h00 - 11h15	Genome-wide SNP analysis reveals distinct origins of Trypanosoma evansi and Trypanosoma equiperdum Bart Cuypers - University of Antwerp, Belgium
11h15 - 11h30	Design and modeling of a database dedicated to Medicinal Plants - Herbal Medic Ouissam El Andaloussi - Centre des Études en Sciences et Technique, Morocco
11h30 - 11h45	Study of recent coalescence events in contemporaneous landscapes : C++ tem- plate library for Approximate Bayesian Computation Arnaud Becheler - EGCE, France
11h45 - 12h00	Evaluation of methodologies for the characterization of plant mosaic genomes Aurélien Cottin - CIRAD - UMR AGAP, France
12h00 - 12h15	Bi-Objective Integer Programming For RNA Secondary Structure Prediction With Pseudoknots Audrey Legendre - <i>IBISC, France</i>
12h15 - 12h30	Bioinfo-fr.net Gwenaëlle Lemoine - <i>Centre de recherche du CHU de Québec, Université Laval, Canada</i>
12h30 - 14h00	Lunch

14h00 - 14h15	Labsquare Aurélien Béliard - <i>Université Lille 1, France</i>
14h15 - 15h15	Chairwoman : Gwenaëlle Lemoine Keynote Challenges of high-dimensional data for machine learning in precision medicine Chloé-Agathe Azencott - CBIO MinesParisTech, France
15h15 - 15h45	Coffee Break
	Chairman : Hugo Pereira
15h45 - 17h30	Round Table How to popularize science? Mathias Kasiulis - <i>Le Projet Lutétium</i> Martin Clavey - <i>Sound of Science</i> Pierre Kerner - <i>Université Paris Diderot; Café des Sciences</i> Julie Rode - <i>Objectif Sciences International</i>
17h30 - 17h45	Concluding remarks Julien Fumey - <i>Chair, RSG France President</i>

Committee |

Chair Julien Fumey, I2BC, Université Paris Saclay, Gif-sur-Yvette, France

Aurélien Béliard - Université Lille 1, France Marouen Ben Guebila - Luxembourg University, Belval, Luxembourg June Benvegnu-Sallou - Université Bordeaux II, France Léopold Carron - Université Pierre et Marie Curie, Paris, France Elsa Cirillo - Maastricht University, The Netherlands Gwenaëlle Lemoine - Centre de Recherche du CHU de Québec - Université Laval, Canada Florence Jornod - Muséum d'Histoire Naturelle, Paris, France Susanne Kirchen - Luxembourg University, Belval, Luxembourg Pierre Marijon - Université Lille 1, France Daniele Parisi - University of Leuven, Belgium Hugo Pereira - CEA - Genoscope - LABGeM, Evry, France Aubin Thomas - IGH, Montpellier, France Joske Ubels - UMC Utrecht, The Netherlands Athénaïs Vaginay - Institut Jacques Monod, Paris, France

Long term information integration: evolution of evolution

Keynote |

Paulien Hogeweg University of Utrecht

Thursday 6 July | 14h30

Phylogenetic analysis has uncovered many interesting and surprising patterns in both long term and short term evolution. I will use a non-supervised evolutionary modelling approach to asses how surprising these feature, in fact, are from Darwinian evolutionary viewpoint when we allow the genotype-phenotype to evolve and allow not only point mutations, but also INDELS of various sizes.



Giving enough degrees of freedom we recover a number

of the observed features, and conclude that these are generic properties of mutation/ selection processes.

Natural and synthetic control of resource allocation in bacteria

Keynote |

Hidde de Jong INRIA Grenoble - Rhône-Alpes, France

Thursday 6 July | 16h00

In the environment. This involves changes in the expression of a large number of genes, encoding proteins with a variety of cellular functions. Fundamentally, the reorganization of gene expression in response to changes in environmental conditions is a resource allocation problem. It poses the question how microorganisms redistribute their protein synthesis capacity



over different cellular functions when constrained by the changing environment. I will give an overview of recent work on resource allocation in bacteria, including novel insights gained by the application of optimal control theory. I will also present an approach to modify natural resource allocation schemes by putting the transcription of a key component of the gene expression machinery, RNA polymerase, under the control of an inducible promoter. By changing the inducer concentration in the medium, the RNA polymerase concentration can be adjusted and thereby bacterial growth switched between zero and the maximal growth rate supported by the medium. I will show that the proposed synthetic growth switch is a promising tool for gaining a better understanding of bacterial physiology and for applications in synthetic biology and biotechnology.

J. Izard, C. Gomez Balderas, D. Ropers, S. Lacour, X. Song, Y. Yang, A.B. Lindner, J. Geiselmann, H. de Jong. A synthetic growth switch based on controlled expression of RNA polymerase. Molecular Systems Biology, 11(11):840, 2015

N. Giordano, F. Mairet, J.-L. Gouzé, J. Geiselmann, H. de Jong. Dynamical allocation of cellular resources as an optimal control problem: Novel insights into microbial growth strategies. PLoS Computational Biology, 12(3): e1004802, 2016

H. de Jong, J. Geiselmann, D. Ropers . Resource reallocation in bacteria by reengineering the gene expression machinery. Trends in Microbiology, 25(6):480-93

Challenges of high-dimensional data for machine learning in precision medicine

Keynote |

Chloé-Agathe Azencott

CBIO MinesParisTech, Institut Curie, Inserm, France

Friday 7 July | 14h15

Differences in how patients experience disease can be explained in great part by their genomic differences. Enabling precision medicine, which tailors treatments to specificities of the patients rather than of the disease, hence requires identifying genomic features associated with disease risk, prognosis or response to treatment. This field depends on collecting considerable amounts of molecular data for large numbers of individuals, which is being enabled by thriving developments in genome sequencing and other high-throughput experimental technologies.



Unfortunately, we still lack effective methods to reliably detect, from

such data, which of the genomic features determine a phenotype such as disease predisposition or response to treatment. One of the major issues is that the number of features that can be measured is large (easily reaching tens of millions) with respect to the number of samples for which they can be collected (more usually of the order of hundreds or thousands), posing both computational and statistical difficulties.

In my talk I will discuss several ways to address this problem via the integration of additional data, and give a brief overview of the challenges and opportunities for machine learning in this field.

Contributed talks |

Friday 7 July | 09h30

Abstracts for Friday morning presentations are available on RSG France website : http://bit.ly/2rUpCBl You can also use the QR code on the right.



How to popularize science?

 Mathias Kasiulis

 Le Projet Lutétium

 Martin Clavey

 Round Table |
 Sound of Science

 Pierre Kerner

 Université Paris Diderot ; Café des Sciences

 Julie Rode

 Objectif Sciences International

Friday 7 July | 15h45

Science is everywhere in our life, it remains important to understand that all of this is not magic. However, scientific publication that could erase this illusion can be boring or dissuading for people not used to it. To renew the interest of people, it takes a new approach that get more and more effect those last years: the popularization of science! Nowadays science is being more and more popularized, but how to popularize science correctly?



RSG France - JeBiF

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