

JOBIM 2019

UNIVERSITÉ DE NANTES

Inserm La référence pour la santé. Pour répondre à la santé.

sfbi Société Française de Bioinformatique

INSRA SCIENCE & IMPACT

CHRS GDR BIM

ifb Institut Français de Bioinformatique

CENTRALE NANTES

MERIEUX NutriSciences

Ifremer

Nantes Métropole

sviesan alliance nationale pour les sciences de la vie et de la santé

lnria

FRANCE GÉNOMIQUE

Biogenouest

SFR - Santé

GDR GÉNOMIQUE ENVIRONNEMENTALE

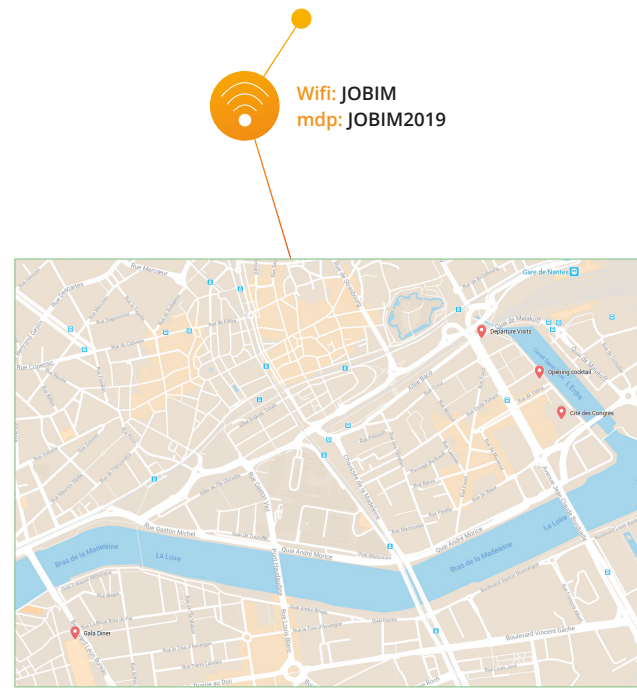
MethodOmics

FONDATION ARC POUR LA RECHERCHE SUR LE CANCER

lena by enano The fastest genomic compressor

Life & Soft Make IT easier

Création graphique: Jeremy Segard



#jobim2019

- July 2, 18:35
Opening cocktail: Brasserie Felix
1 rue Lefèvre-Utile
- July 3, 18:30
Social events: Pedestrian bus from Cité des congrès to departure points
- Visits:** Departure from Cité des congrès
- Boats:** Departure from Gare Fluviale
Place Waldeck Rousseau
- July 4, 19:30
Gala diner: Les Machines de l'île
Parc des Chantiers

JOBIM 2019

JOURNÉES OUVERTES DE BIOLOGIE INFORMATIQUE & MATHÉMATIQUES

> Nantes
2-5 juillet
Cité des Congrès

JOBIM 2019

UNIVERSITÉ DE NANTES

Inserm La référence pour la santé. Pour répondre à la santé.

sfbi Société Française de Bioinformatique

INSRA SCIENCE & IMPACT

CHRS GDR BIM

ifb Institut Français de Bioinformatique

CENTRALE NANTES

MERIEUX NutriSciences

Ifremer

Nantes Métropole

sviesan alliance nationale pour les sciences de la vie et de la santé

lnria

FRANCE GÉNOMIQUE

Biogenouest

SFR - Santé

GDR GÉNOMIQUE ENVIRONNEMENTALE

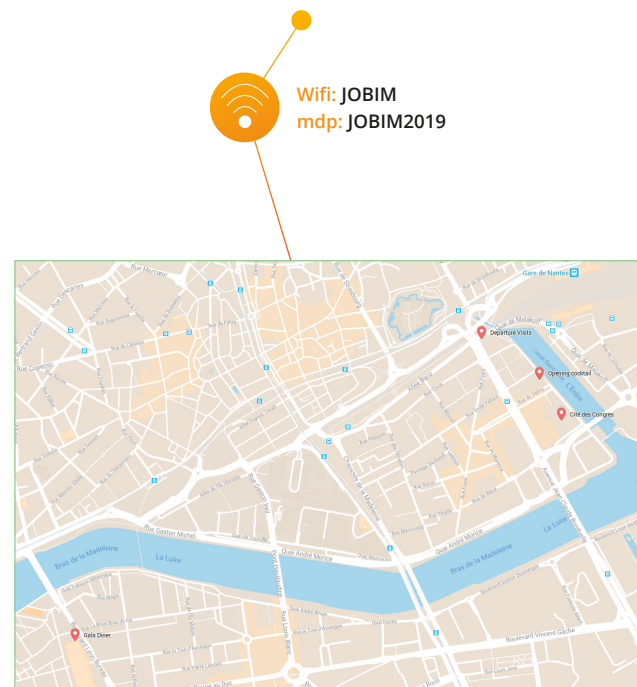
MethodOmics

FONDATION ARC POUR LA RECHERCHE SUR LE CANCER

lena by enano The fastest genomic compressor

Life & Soft Make IT easier

Création graphique: Jeremy Segard



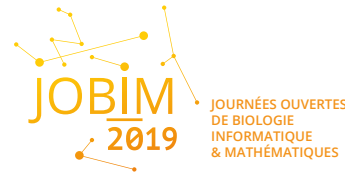
#jobim2019

- July 2, 18:35
Opening cocktail: Brasserie Felix
1 rue Lefèvre-Utile
- July 3, 18:30
Social events: Pedestrian bus from Cité des congrès to departure points
- Visits:** Departure from Cité des congrès
- Boats:** Departure from Gare Fluviale
Place Waldeck Rousseau
- July 4, 19:30
Gala diner: Les Machines de l'île
Parc des Chantiers

JOBIM 2019

JOURNÉES OUVERTES DE BIOLOGIE INFORMATIQUE & MATHÉMATIQUES

> Nantes
2-5 juillet
Cité des Congrès



DAY 1 - TUESDAY JULY 2ND

12:00 - 14:00	Registration
Auditorium 450	
14:00 - 14:30	Welcome speech and JOBIM opening
14:30 - 15:30	Keynote: Olivier Delaneau, <i>Chromatin three-dimensional interactions mediate genetic effects on gene expression</i>
15:30 - 15:50	Genotyping Structural Variations using Long Reads data, <i>Lolita Lecompte</i>
15:50 - 16:10	Sequana coverage: detection and characterization of genomic variations using running median and mixture models, <i>Thomas Cokelaer</i>
16:10 - 16:30	mCNA: a new methodology to improve high-resolution copy number variation analysis from next generation sequencing using unique molecular identifiers, <i>Pierre-Julien Vially</i>
16:30 - 17:00	Coffee Break
17:00 - 17:20	How to build up soil bacterial co-occurrence networks from wide spatial scale sampling?, <i>Battle Karimi</i>
17:20 - 17:40	Reference-guided genome assembly in metagenomic samples, <i>Cervin Guyomar</i>
17:40 - 18:00	Deciphering intra-species bacterial diversity of meat and seafood spoilage microbiota using gyrB amplicon sequencing: A comparative analysis with 16S rDNA V3-V4 amplicon sequencing, <i>Olivier Rué</i>
18:00 - 18:35	Bioinformatics associations overview
18:35 - 20:15	Opening cocktail

DAY 2 - WEDNESDAY JULY 3RD

Auditorium 450	
09:00 - 10:00	Keynote: Alessandra Carbone, <i>Evolutionary conservation</i>
10:00 - 10:20	Flash poster presentation odd numbers (4x5')
10:20 - 10:40	Coffee Break
Auditorium 450	
Room 200	
10:40	A review of different ways to insert known RNA modules into RNA secondary structures, <i>Louis Becquey</i>
11:00	Allele-specific analysis of epigenetic and transcriptomic data to study Drosophila developmental cis-regulatory architecture, <i>Swann Flac'Hlay</i>
11:20	SPIP: Splicing Prediction Pipeline addressing the diversity of splice alterations, validated on a curated diagnostic set of 2,784 exonic and intronic variants, <i>Raphael Leman</i>
11:40 - 12:40	Signature analysis of Structural Variants reveals a new subclass of hepatocellular carcinoma characterized by Cyclin A2/E1 alterations, <i>Quentin Bayard</i>
12:40 - 14:00	Adaptation to animal sources of Salmonella enterica subsp. enterica deciphered by Genome Wide Association Study and Gene Ontology Enrichment Analysis at the pangenomic scale, <i>Vila Nova Meryl</i>
14:00 - 15:00	Merging of phenotypic information from cytometric profiles at the single-cell resolution, <i>Nicolas Tchitchek</i>
11:40 - 12:40	Poster and Demo session odd numbers
12:40 - 14:00	Lunch
Auditorium 450	
14:00 - 15:00	Keynote: Christophe Dessimoz, <i>Big Data: opportunities, pitfalls, and remedies</i>
15:00 - 16:30	Thematic workshops: 1 Bioimage informatique : la generation de phenomique en bioimagerie Room H 2 Methods for single-cell omics data analysis Room 200 3 Omics dark matter Auditorium 450 4 Predictive approaches for biological systems engineering Room G 5 Protein structure and design: from sequence to function Room I
16:30 - 17:00	Coffee Break

17:00 - 18:00 Thematic workshops (second part)
18:00 - 20:20 Social events

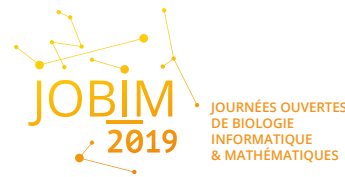
DAY 3 - THURSDAY JULY 4TH

Auditorium 450	
09:00 - 10:00	Keynote: Alexander Bockmayr, <i>Understanding cellular behaviours through mathematical optimization</i>
10:00 - 10:20	Flash poster presentation even numbers (4x5')
10:20 - 10:40	Coffee Break
Auditorium 450	
Room 200	
10:40	Architecture and evolution of blade assembly in β -propeller lectins, <i>François Bonnardel</i>
11:00	Novel insight on molecular dynamics trajectories: local equilibrium viewed by kappa-segmentation, <i>Sharad Goulam</i>
11:20 - 12:20	CISPER: Computational Identification of Switch Points (in a Metabolic Network) within an Environmental Range, <i>Francis Mairet</i>
12:20 - 13:30	A new method for evaluating the impacts of semantic similarity measures on the annotation of gene sets, <i>Aarón Ayllón-Benitez</i>
11:20 - 12:20	Poster and Demo session even numbers
12:20 - 13:30	Lunch
Auditorium 450	
13:30 - 14:30	Keynote: Chloe-Agathe Azencott, <i>Structured feature selection for biomarker discovery in precision medicine</i>
14:30 - 15:10	IFB invited speaker: Guy Cochrane, <i>European Nucleotide Archive: connectivity and community</i>
Parallel session Auditorium 450	
15:10 - 15:25	AskOmics: a user-friendly interface to Semantic Web technologies for integrating local datasets with reference resources, <i>Xavier Garnier</i>
15:25 - 15:40	WAVES: a Web Application for Versatile Enhanced bioinformatic Services, <i>Vincent Lefort</i>
15:40 - 15:55	DevOps bioinformatics services with Docker, GitLab CI, and Kubernetes, <i>Bryan Brancotte</i>

15:55 - 16:10	Shiny and Galaxy interactive software for multi-source data analysis, <i>Etienne Camenen</i>
16:10 - 16:30	NNCR IFB : Les ressources Core Cluster et Cloud de l'IFB, <i>Nicole Charrière, David Benaben</i>
Parallel session Room 200	
15:10 - 15:30	Exploring the uncharacterized human proteome using neXtProt, <i>Lydie Lane</i>
15:30 - 15:50	Redesign of IPPI-DB, a database for modulators of Protein-Protein Interactions, <i>Rachel Torchet</i>
15:50 - 16:10	ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research, <i>David Christiany</i>
16:10 - 16:30	UniFIRE: the UniProt Functional annotation Inference Rule Engine, <i>Rabie Saidi</i>
16:30 - 17:00	Coffee Break
Auditorium 450	
17:00 - 18:00	AG SFBI
18:00 - 18:30	Meeting GDR BIM
18:30 - 19:00	Meeting IFB
19:30 - 02:00	Gala dinner and more

DAY 4 - FRIDAY JULY 5TH

Auditorium 450	
09:30 - 10:30	Keynote: Juliette Martin, <i>Protein-protein interactions: the tip of the iceberg</i>
10:30 - 11:00	Coffee Break
11:00 - 11:20	eIPrep 4: A high-performance tool for sequence analysis, <i>Roel Wuyts</i>
11:20 - 11:40	CONSENT: Scalable self-correction of long reads with multiple sequence alignment, <i>Pierre Morisse</i>
11:40 - 12:00	A De Novo Robust Clustering Approach for Amplicon-Based Sequence Data, <i>Alexandre Bazin</i>
12:00 - 12:30	Closing and farewell JOBIM 2019 Presentation of JOBIM 2020



DAY 1 - TUESDAY JULY 2ND

12:00 - 14:00	Registration
Auditorium 450	
14:00 - 14:30	Welcome speech and JOBIM opening
14:30 - 15:30	Keynote: Olivier Delaneau, <i>Chromatin three-dimensional interactions mediate genetic effects on gene expression</i>
15:30 - 15:50	Genotyping Structural Variations using Long Reads data, <i>Lolita Lecompte</i>
15:50 - 16:10	Sequana coverage: detection and characterization of genomic variations using running median and mixture models, <i>Thomas Cokelaer</i>
16:10 - 16:30	mCNA: a new methodology to improve high-resolution copy number variation analysis from next generation sequencing using unique molecular identifiers, <i>Pierre-Julien Vially</i>
16:30 - 17:00	Coffee Break
17:00 - 17:20	How to build up soil bacterial co-occurrence networks from wide spatial scale sampling?, <i>Battle Karimi</i>
17:20 - 17:40	Reference-guided genome assembly in metagenomic samples, <i>Cervin Guyomar</i>
17:40 - 18:00	Deciphering intra-species bacterial diversity of meat and seafood spoilage microbiota using gyrB amplicon sequencing: A comparative analysis with 16S rDNA V3-V4 amplicon sequencing, <i>Olivier Rué</i>
18:00 - 18:35	Bioinformatics associations overview
18:35 - 20:15	Opening cocktail

DAY 2 - WEDNESDAY JULY 3RD

Auditorium 450	
09:00 - 10:00	Keynote: Alessandra Carbone, <i>Evolutionary conservation</i>
10:00 - 10:20	Flash poster presentation odd numbers (4x5')
10:20 - 10:40	Coffee Break
Auditorium 450	
Room 200	
10:40	A review of different ways to insert known RNA modules into RNA secondary structures, <i>Louis Becquey</i>
11:00	Allele-specific analysis of epigenetic and transcriptomic data to study Drosophila developmental cis-regulatory architecture, <i>Swann Flac'Hlay</i>
11:20	SPIP: Splicing Prediction Pipeline addressing the diversity of splice alterations, validated on a curated diagnostic set of 2,784 exonic and intronic variants, <i>Raphael Leman</i>
11:40 - 12:40	Signature analysis of Structural Variants reveals a new subclass of hepatocellular carcinoma characterized by Cyclin A2/E1 alterations, <i>Quentin Bayard</i>
12:40 - 14:00	Adaptation to animal sources of Salmonella enterica subsp. enterica deciphered by Genome Wide Association Study and Gene Ontology Enrichment Analysis at the pangenomic scale, <i>Vila Nova Meryl</i>
14:00 - 15:00	Merging of phenotypic information from cytometric profiles at the single-cell resolution, <i>Nicolas Tchitchek</i>
11:40 - 12:40	Poster and Demo session odd numbers
12:40 - 14:00	Lunch
Auditorium 450	
14:00 - 15:00	Keynote: Christophe Dessimoz, <i>Big Data: opportunities, pitfalls, and remedies</i>
15:00 - 16:30	Thematic workshops: 1 Bioimage informatique : la generation de phenomique en bioimagerie Room H 2 Methods for single-cell omics data analysis Room 200 3 Omics dark matter Auditorium 450 4 Predictive approaches for biological systems engineering Room G 5 Protein structure and design: from sequence to function Room I
16:30 - 17:00	Coffee Break

17:00 - 18:00 Thematic workshops (second part)
18:00 - 20:20 Social events

DAY 3 - THURSDAY JULY 4TH

Auditorium 450	
09:00 - 10:00	Keynote: Alexander Bockmayr, <i>Understanding cellular behaviours through mathematical optimization</i>
10:00 - 10:20	Flash poster presentation even numbers (4x5')
10:20 - 10:40	Coffee Break
Auditorium 450	
Room 200	
10:40	Architecture and evolution of blade assembly in β -propeller lectins, <i>François Bonnardel</i>
11:00	Novel insight on molecular dynamics trajectories: local equilibrium viewed by kappa-segmentation, <i>Sharad Goulam</i>
11:20 - 12:20	CISPER: Computational Identification of Switch Points (in a Metabolic Network) within an Environmental Range, <i>Francis Mairet</i>
12:20 - 13:30	A new method for evaluating the impacts of semantic similarity measures on the annotation of gene sets, <i>Aarón Ayllón-Benitez</i>
11:20 - 12:20	Poster and Demo session even numbers
12:20 - 13:30	Lunch
Auditorium 450	
13:30 - 14:30	Keynote: Chloe-Agathe Azencott, <i>Structured feature selection for biomarker discovery in precision medicine</i>
14:30 - 15:10	IFB invited speaker: Guy Cochrane, <i>European Nucleotide Archive: connectivity and community</i>
Parallel session Auditorium 450	
15:10 - 15:25	AskOmics: a user-friendly interface to Semantic Web technologies for integrating local datasets with reference resources, <i>Xavier Garnier</i>
15:25 - 15:40	WAVES: a Web Application for Versatile Enhanced bioinformatic Services, <i>Vincent Lefort</i>
15:40 - 15:55	DevOps bioinformatics services with Docker, GitLab CI, and Kubernetes, <i>Bryan Brancotte</i>

15:55 - 16:10	Shiny and Galaxy interactive software for multi-source data analysis, <i>Etienne Camenen</i>
16:10 - 16:30	NNCR IFB : Les ressources Core Cluster et Cloud de l'IFB, <i>Nicole Charrière, David Benaben</i>
Parallel session Room 200	
15:10 - 15:30	Exploring the uncharacterized human proteome using neXtProt, <i>Lydie Lane</i>
15:30 - 15:50	Redesign of IPPI-DB, a database for modulators of Protein-Protein Interactions, <i>Rachel Torchet</i>
15:50 - 16:10	ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research, <i>David Christiany</i>
16:10 - 16:30	UniFIRE: the UniProt Functional annotation Inference Rule Engine, <i>Rabie Saidi</i>
16:30 - 17:00	Coffee Break
Auditorium 450	
17:00 - 18:00	AG SFBI
18:00 - 18:30	Meeting GDR BIM
18:30 - 19:00	Meeting IFB
19:30 - 02:00	Gala dinner and more

DAY 4 - FRIDAY JULY 5TH

Auditorium 450	
09:30 - 10:30	Keynote: Juliette Martin, <i>Protein-protein interactions: the tip of the iceberg</i>
10:30 - 11:00	Coffee Break
11:00 - 11:20	eIPrep 4: A high-performance tool for sequence analysis, <i>Roel Wuyts</i>
11:20 - 11:40	CONSENT: Scalable self-correction of long reads with multiple sequence alignment, <i>Pierre Morisse</i>
11:40 - 12:00	A De Novo Robust Clustering Approach for Amplicon-Based Sequence Data, <i>Alexandre Bazin</i>
12:00 - 12:30	Closing and farewell JOBIM 2019 Presentation of JOBIM 2020