

Self-presentations

1 slide, 1 minute per participant

GREEKC Training-hackathon
Marseille, Apr 23-26, 2019

Babic Tamara

- **Lab:** Laboratory for Molecular Biology
- **Institution:** Institute of Molecular Genetics and Genetic Engineering
- **Country:** Serbia
- **City:**
- **Skills relevant to this hackathon:**
 - concepts in molecular biology, e.g gene expression
- **Interests:**
 - interested in going through public databases regarding transcriptome, proteome and methylome



- **Lab:** TAGC
- **Institution:** INSERM (French NIH)
- **Country:** France
- **City:** Marseille
- **Skills relevant to this hackathon:**
 - Resource - ReMap
 - data provider
 - NGS data analysis
- **Interests:**
 - Gene regulations
 - Non coding regions (the famous junk dna)
 - TF Binding regions
 - Repeats
 - DNA replication sites



Basharat, Zarrin

- **Lab:** Laboratoire Génomique, Bionformatique, et Chimie Moléculaire (GBCM)
- **Institution:** Conservatoire National des Arts et Métiers
- **Country:** France
- **City:** Paris
- **Skills relevant to this hackathon:**
 - Knowledge of biological terms, user experience of various databases and concepts in biology
- **Interests:**
 - Genomic sequence interpretation, big data analysis, variant and expression analysis etc.

Ivan Berest

- **Lab:** Zaugg Lab SCB unit
- **Institution:** EMBL
- **Country:** Germany
- **City:** Heidelberg
- **Skills relevant to this hackathon:**
 - Experience in various NGS data analysis
 - Snakemake
 - R
- **Interests:**
 - Scientific - multiomics, personalised medicine, ML in biology, 3D structure of chromatin.
 - Computer games, football, travelling



Jaime Castro-Mondragon

- **Lab:** Computational Biology & Gene Regulation
- **Institution:** Centre for Molecular Medicine Norway, University of Oslo
- **Country:** Norway
- **City:** Oslo
- **Skills relevant to this hackathon:**
 - Analysis of NGS data
 - Developer of resources
 - JASPAR - jaspar.genereg.net
 - RSAT - <http://rsat.eu>
 - Programming with R and snakemake
- **Interests:**
 - Development of tools to analyze TF binding sites (with their respective negative controls :P)
 - Machine learning and bayesian inference
 - Reproducibility in science



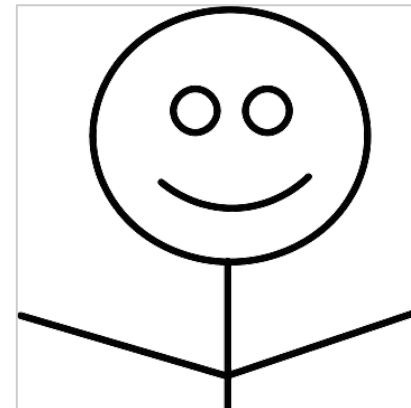
Noemi Del Toro Ayllon

- **Lab:** Molecular Interactions (IntAct + Complex Portal)
- **Institution:** EMBL-EBI
- **Country:** UK
- **City:** Hinxton (Cambridge)
- **Skills relevant to this hackathon:**
 - Expertise in molecular interaction data standards and data distribution
 - PSICQUIC
 - Java Software Engineer
- **Interests:**
 - Gene regulation in the context of molecular interactions
 - Data sharing and interoperability



Radoslav Davidović

- **Lab:** Laboratory for Bioinformatics and Computational Chemistry
- **Institution:** Institute of Nuclear Sciences Vinča
- **Country:** Serbia
- **City:** Belgrade
- **Skills relevant to this hackathon:**
 - concepts of molecular genetics, ontologies, protein function prediction, JAVA
- **Interests:**
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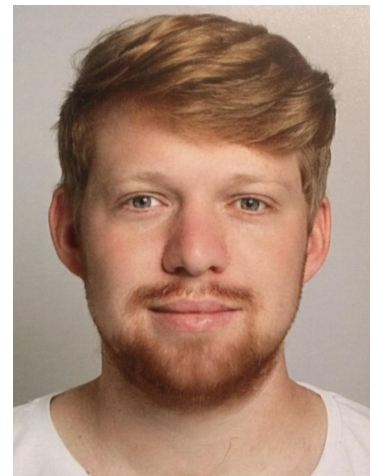
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Alban Gaignard

- **Lab:** l'institut du thorax, Nantes, France
- **Institution:**
 - CNRS (French National Center for Scientific Research)
 - IFB (French Institute for Bioinformatics) : interoperability working group co-lead + integrative bioinformatics project co-lead
- **Country:** France
- **City:** Nantes
- **Skills relevant to this hackathon:**
 - Semantic web, federated query processing, scientific workflows, provenance
 - Life Science ontologies (BioPax)
 - Pathway databases (PathwayCommons)
 - Python / Java / RDF / SPARQL / Rest APIs
- **Interests:**
 - Systems Biology (regulatory/signaling networks)
 - Machine- & Human- oriented data integration (imaging/omics)

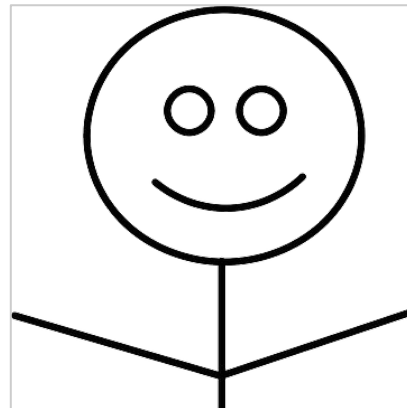


- **Lab:** AG Saez-Rodriguez (Saezlab)
- **Institution:** Institute for Computational Biomedicine
- **Country:** Germany
- **City:** Heidelberg
- **Skills relevant to this hackathon:**
 - TF-target inference from genomic and transcriptomic data
 - Maintainer and (future) developer of DoRothEA
(<https://saezlab.github.io/DoRothEA/>)
 - Estimation of TF-activity from gene expression using enriched regulon analysis
 - Programming in R following tidyverse' principles
- **Interests:**
 - Improving regulon quality by integrating more omics data (e.g. chromatin status, methylation)
 - Learning about new data analysis tools/platforms (e.g. snakemake)



Sandro Hurtado

- **Lab:** Department of Computer Sciences and Languages
- **Institution:** University of Málaga
- **Country:** Spain
- **City:** Málaga
- **Skills relevant to this hackathon:**
 - Health engineer
 - programming skills: Python and JAVA
 - Concepts of ontologies and GRN inference algorithm
- **Interests:**
 - Machine Learning in medical applications



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Lucie Khamvongsa-Charbonnier

- **Lab:** Theory and Approaches of Genome Complexity (TAGC), Aix-Marseille Université (AMU) / Marseille Cancer Research Centre (CRCM)
- **Institution:** Aix-Marseille Université (AMU)
- **Country:** France
- **City:** Marseille
- **Skills relevant to this hackathon:**
 - Analysis of NGS data
 - Programming with R and snakemake
 - Integrative omics data analysis and reproducibility
- **Interests:**
 - Omics data integration
 - Regulation of gene expression



- **Lab:** Computational Biology & Gene Regulation
- **Institution:** Centre for Molecular Medicine Norway, University of Oslo
- **Country:** Norway
- **City:** Oslo
- **Skills relevant to this hackathon:**
 - Resource and REST API development
 - Developer of resources
 - JASPAR - jaspar.genereg.net
 - UniBind - unibind.uio.no
 - dbSUPER - asntech.org/dbsuper
 - Integrative omics data analysis and reproducibility
- **Interests:**
 - Regulatory genomics and epigenomics
 - Development of tools and resource to understand transcriptional gene regulation
- More details - <https://asntech.github.io/>
- I often tweet about open science, reproducibility and preprints [@khanaziz84](https://twitter.com/khanaziz84)



Martin Kuiper

- **Lab:** Systems Biology group, Dept. of Biology
- **Institution:** Norwegian University of Science and Technology
- **Country:** Norway
- **City:** Trondheim
- **Skills relevant to this hackathon:**
 - organisational skills :-)
 - BioGateway
 - TFcheckpoint
- **Interests:**
 - develop the knowledge commons (KC) for computational biology
 - test parts of the KC for network biology
 - improve ontologies for KC queries
 - develop Use Cases for next hackathon
 - Raise interests from hackers in STSMs

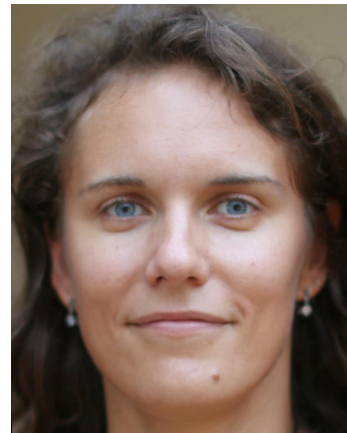


- **Lab:** Systems Oncology, Faculty of Medicine
- **Institution:** Norwegian University of Science and Technology
- **Country:** Norway
- **City:** Trondheim
- **Skills relevant to this hackathon:**
 - Molecular cellular biology
 - Cancer systems biology
 - Gene regulation, signal transduction
 - Gene regulation knowledge management
- **Interests:**
 - wide multidisciplinary in systems biology
 - the knowledge commons
 - responsible research and innovation



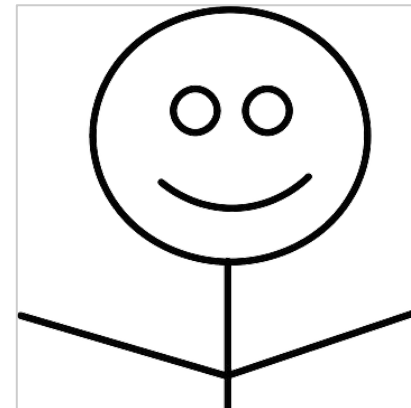
Yulia Medvedeva

- **Research Group:** Regulatory transcriptomics and epigenomics
- **Institution:**
 - Research Center of Biotechnology, Russian Academy of Science
 - Moscow Institute of Physics and Technology (MIPT)
- **Country:** Russia
- **City:** Moscow
- **Skills relevant to this hackathon:**
 - R, bash
 - EpiFactors, HOCOMOCO db
- **Interests:**
 - lncRNA in regulatory genomics, in particular in epigenetic regulation
 - Epigenetic regulation of gene expression
 - Epigenetics and lncRNA in diseases
 - Reprogramming and transdifferentiation



Ferran Moratalla

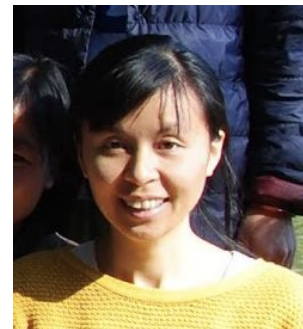
- **Lab:** Oncology Analytics Data Program
- **Institution:** Catalan Institute of Oncology
- **Country:** Spain
- **City:** Barcelona
- **Skills relevant to this hackathon:**
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- **Interests:**
 - Omics data integration
 - Development of new gene regulatory analysis methods



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Thi Thuy Nga NGUYEN

- **Lab:** IBENS
- **Institution:** Institut de Biologie de l'Ecole Normale Supérieure
- **Country:** France
- **City:** Paris
- **Skills relevant to this hackathon:**
 - RESTful API using Flask
- **Interests:**
 - Swagger - tool for automatically generating documentation for Restful API



Novkovic Mirjana

- **Lab:** Laboratory for Molecular Biology
- **Institution:** Institute of Molecular Genetics and Genetic Engineering (IMGGE)
- **Country:** Serbia
- **City:**
- **Skills relevant to this hackathon:**
 - molecular biology, bioinformatics (basic)
- **Interests:**
 - better utilization of public and specific databases regarding gene variants,
 - TFBS prediction,
 - prediction of effect of genetic variants on protein structure and function



- **Lab:** Ensembl
- **Institution:** EMBL-EBI
- **Country:** United Kingdom
- **City:**
- **Skills relevant to this hackathon:**
 - Resources - Ensembl
- **Interests:**
- **Email:** aparton@ebi.ac.uk
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Rafel Riudavets Puig

- **Lab:** Department of Biology
- **Institution:** NTNU
- **Country:** Norway
- **City:**
- **Skills relevant to this hackathon:**
 - NGS data analysis
 - Molecular Biology
 - R
- **Interests:**
 - Omics data integration
 - Machine Learning
 - Music, photography, outdoor sports



Thomas Rosnet

- **Lab:** TAGC
- **Institution:** French Institute of Bioinformatics (IFB)
- **Country:** France
- **City:** Marseille
- **Skills relevant to this hackathon:**
 - Bioinformatics
 - Web development
- **Interests:**
 - Ontology
 - Interoperability



David Salgado

- **Lab:** Marseille Medical Genetics
- **Institution:** INSERM
- **Country:** France
- **City:** Marseille
- **Skills relevant to this hackathon:**
 - NGS data analysis, mutations identification
 - Web Services and web technologies
- **Interests:**
 - Sciences : Various fields of bioinformatics, Machine Learning, Textmining, 3D reconstruction, ...
 - Others : Sports, music, travelling



Jacques van Helden



Campus de Luminy
(view from the Aiguille
Guillemain in the Calanques)

- **Lab:** Theory and Approaches of Genome Complexity (TAGC)
- **Institution:**
 - Institut Français de Bioinformatique (IFB)
 - Aix-Marseille Université (AMU)
- **Country:** France
- **City:** Marseille
- **Skills relevant to this hackathon:**
 - Analysis of regulatory sequences
 - RSAT project (<http://rsat.eu/>)
 - Statistical analysis + R coding
- **Interests:**
 - Integration of bioinformatics resources for gene regulation
 - Representation of knowledge about gene regulation
 - Reproducible science
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- **Lab:** Theory and Approaches of Genome Complexity (TAGC)
- **Institution:** Aix-Marseille Université (AMU)
- **Country:** France
- **City:** Marseille
- **Skills relevant to this hackathon:**
 - Replace the downloads and manual analyses by R programmatic accesses.
- **Interests:**
 - Integration of bioinformatics resources to detect disease-associated regulatory SNPs.
 - Interoperability



Vasundra Touré

- **Lab:** Department of Biology
- **Institution:** NTNU
- **Country:** Norway
- **City:** Trondheim
- **Skills relevant to this hackathon:**
 - standards, programming (Java, R)
- **Interests:**
 - Causal relationships
 - knowledge management - standardisation
 - data extraction



- **Lab:** Molecular Embryology
- **Institution:** CABD-CSIC
- **Country:** Spain
- **City:** Seville
- **Skills relevant to this hackathon:**
 - Basic-Intermediate programming skills in R and Perl
 - Analysis of ATAC-seq and RNA-seq data
 - Strong background in Molecular Biology (e.g. gene expression regulation, three-dimensional organization of chromatin)
- **Interests:**
 - Integration of data from several bioinformatic resources
 - Regulation of gene expression
 - Travelling



John Zobolas

- **Research Group:** DrugLogics
- **Institution:** Norwegian University of Science and Technology (NTNU)
- **Country:** Norway
- **City:** Trondheim
- **Skills relevant to this hackathon:**
 - Java (maven), R (Rstudio), Javascript (npm)
- **Interests:**
 - Reproducible Research and Software Engineering
 - Clean code
 - Testing code (JUnit, Roxygen, Chai.js)
 - Nice documentation (e.g. gitbook)
 - Mathematical Modeling of cancer cell systems
 - DrugLogics pipeline for predicting beneficial drug combinations

