



## Bioinformatics in Jouy

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### ► To cite this version:

Jean-François Gibrat. Bioinformatics in Jouy. Bioinformatics in Jouy, Institut National de Recherche Agronomique (INRA). UR Mathématique, Informatique et Génome (1077)., Oct 2009, Jouy-en-Josas, France. 18 p. hal-02812808

**HAL Id: hal-02812808**

**<https://hal.inrae.fr/hal-02812808>**

Submitted on 6 Jun 2020

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# Bioinformatics in Jouy

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Jouy, October 5 2009

- Bioinformaticians scattered in “wet” biology laboratories
- Bioinformatics laboratories
  - Mathématique et Informatique Appliquées (MIA-Jouy)
  - Mathématique, Informatique et Génome (MIG)
- INRA matrix organization :  
research divisions x local research centers
- Each laboratory is located at the interface of two networks :
  - a methodological network
  - a thematic network

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# Mathématique et Informatique Appliquées (MIA-Jouy) laboratory

- Groups mostly mathematicians and computer scientists.
- Belongs to the research division : Applied Mathematics and Informatics
- MIA-Jouy has 24 permanent staff members
  - 13 scientists
  - 7 engineers
  - 4 technicians and administrative staff members
- MIA-Jouy has 10 non-permanent staff members
  - 8 PhD students
  - 1 post-doc
  - 1 engineer

## Two research groups

- **MathRisq** : risk evaluation (13 permanent + 7 non-permanent staff members)
  - animal and plant epidemiology
  - food safety
- **MathCell** : analysis and modelling of biological systems at different scales (6 permanent + 3 non-permanent staff members)
  - molecules
  - cells
  - physiological functions
  - populations

- Ab initio prediction of the 3D structure of proteins
- **Statistical inference of biological interaction networks**
- Proteomics management and analysis software (PARIS)
- Analysis and modelling of the nuclear spatial organization
- Analysis and modelling of membrane traffic
- Heterosis and selection of wine yeasts
- Modelling of bovine trophoblast growth
- **Modelling of anaerobic digestion in the human colon**
- Computational biology for metagenomics Experiments
- Comparative analysis of metagenomic data of the intestinal flora of healthy and obese people



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# Mathématique et Informatique Appliquées (MIA-Jouy) laboratory

- **Methological network**

- INRA-Jouy : MIG, AMIB, MIMA2 platform (microscopy)
- INRIA Rocquencourt
- Paris 11 university
- Ecole Polytechnique
- AgroParisTech

- **Thematic network**

- INRA-Jouy : BioBAC, UEPSD, BDR, NOPA, GPL, etc.
- INRA-Versailles : Biologie Cellulaire, Génétique Végétale
- Curie Institute
- CEA Fontenay

- **Skills**

- statistics : experimental design, inference, stochastic process
- modelling of dynamic systems
- image processing
- computational geometry

# Mathématique, Informatique et Génome (MIG) laboratory

- Groups together mathematicians, computer scientists, physical-chemists and biologists for the analysis of genomic data.
- Belongs to 3 INRA research divisions :
  - **Applied Mathematics and Informatics**
  - Microbiology and the Food Chain
  - Animal Physiology and Livestock Systems
- MIG has a permanent staff of 26 people
  - 12 scientists
  - 9 engineers
  - 5 technicians and administrative staff
- MIG hires 24 people on temporary contracts (grants)
  - 6 post-docs
  - 10 engineers
  - 8 PhD students

MIG has 2 main tasks :

① to develop methods and tools for analyzing genomic data :

- Genomes and evolution ►
- Bibliome : automatic text analysis, data mining ►
- System biology ►

② to lend support to INRA biologists involved in genomic researches :

- ▷ by collaborating with biologists about bioinformatics aspects of genomics projects
  - 25 European or ANR (French research funding agency) projects
- ▷ by making available a bioinformatics platform ►

# MIG interaction network

## ● Methological network

- INRA-Jouy : MIA-J, INRA-Montpellier (MIA Res. Div.)
- INRIA Rennes (IRISA, TEWMEX)
- CNRS
- Paris 11 , Paris 6, Paris 13, Paris-Dauphine universities
- Ecole Polytechnique, Ecole Normale Supérieure
- Pasteur Institute
- NIH, NICTA (Australia)
- ▷ “Statistics for Systems Biology”, SSB network
- ▷ “Inference and Networks” (MIA methodological network)
- ▷ ReNaBi (national network of bioinformatics platforms)

## ● Thematic network

- INRA-Jouy : BioBAC, UEPSD, NOPA, FLEC, VIM, UBLO, GENMIC, etc.
- INRA-Versailles, INRA-Rennes, INRA-Theix, INRA-Montpellier
- Paris 11 university
- Several European projects
- companies (HOSPITEX, JOUVE)

# Genome and evolution

- Integration of genomic data
- Annotation of prokaryotic genomes
- Analysis of metagenomic data
- Comparative genomics
- Models of evolution
- Statistical analysis of sequences
- Relationship : sequence – 3D structure – function of proteins





- Textual documents are a major source of information in biology
- Bibliome, a bioinformatics field :
  - extracts, analyzes, manages and proposes interpretative models from data, for the understanding of biological processes.
- Semantic analysis, knowledge acquisition
  - Relevant for many document-based applications
  - Several intermediate computational linguistic analysis steps are needed
  - Each step requires specific domain knowledge (e.g., terminology, ontology)
- Bibliome research group develops methods for automatizing knowledge acquisition from textual document and integrate them in on-line services.



- Goal : to understand the basic rules that control a biological system through the quantitative description of its components and their interactions
  - ① Inference of cell interaction network models (genetic, metabolic, signaling)
  - ② Analysis of interaction network properties to understand mechanisms underlying miscellaneous cell functions.



Two main objectives :

- Development of a scientific computation infrastructure devoted to genomic data analysis
  - ▷ provides access to computing resources : CPU, storage, memory
  - ▷ makes available genomic data
  - ▷ allows usage of bioinformatics tools to process the data
- Dissemination of bioinformatics “know-how”
  - ▷ training for researchers
  - ▷ scientific and technical assistance, expertise
  - ▷ conception and development of applications for processing and analyzing user's data.

