GILLES THOMAS **BIOINFORMATICS FACILITY**

Expertise

- Whole Genome Analysis
- Whole Exome Analysis
- Targeted Sequencing
- RNAseq
- Microarrays (CGH/SNP/Cytoscan/ Oncoscan/RNA expression)
- Methylation arrays

Bioinformatics Pipelines

- Quality control
- Genome Mapping
- Transcriptome Mapping
- Somatic SNV/CNV/SV detection
- Alternative transcripts
- Clonal analysis
- Annotation
- A la carte

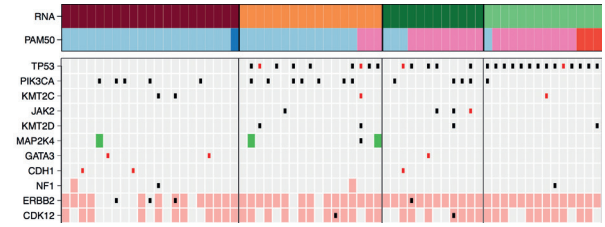
Biostatistics

- Experimental design
- Differential Expression analysis
- Univariate and multivariate analysis, Classification
- Survival analysis
- Molecular subtypes assignment and predictors
- Microenvironment cell population characterization
- Signatures of mutational processes
- GWAS
- A la carte

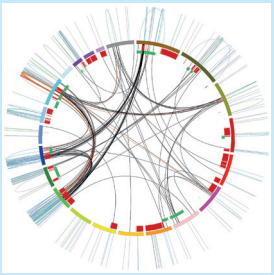
Computation and data storage resources

- Data storage
- HPC environment

Since its establishment in 2007, the **Gilles Thomas Bioinformatics Facility**, operated by Foundation Synergie-Lyon Cancer, is working in close collaboration with biologists and clinicians to the **analysis of large integrative cancer research projects** including the International Cancer Genome Consortium (ICGC) on Breast, Prostate and Gynecological Carcinosarcoma.
The facility provides high-quality computational, bioinformatical and biostatistical solutions with a special emphasis on large-scale genomics, transcriptomics, proteomics and personalized medicine.



Bioinformatics
Specialized in the analysis of high-throughput NGS data, we provide expertise in analyzing whole genome/whole exome/targeted sequencing as well as RNAseq and microarray data.
The analysis pipelines include publicly available tools as well as in-house software developments and databases to get the best out of the data.



Biostatistics
The facility has a strong experience in the area of biostatistics and data mining and offers assistance and consulting services to accompany researchers and clinicians in their projects.
We proposes various solutions for any need that may arise during a project: from advice on the experimental design to complete statistical data analysis and interpretation.

Computational Infrastructure/Databases and Training
The facility operates two dedicated computational and storage clusters (total of 750 cores and 0.6 Pb) and provides access to computational and storage resources on a per-user or per-project basis. It also creates and maintains biological databases to support fundamental research projects and clinical studies, such as the Profiler study. Finally, it also organizes training sessions in bioinformatics (programming basis, omics-data analysis) dedicated to biologists and clinicians.

Need help?

- You feel lost with your NGS data ?
- You need to access publicly available data ?
- You do not understand some software?
- You want to build new analysis tools?

Mention us in your publications!

To allow our platform to pursue its objectives, we need you to mention our work in your publications as follows:
Plateforme de Bioinformatics Gilles Thomas, Synergie Lyon Cancer, Lyon France
Département de Recherche Translationnelle et d'Innovations, Centre Léon Bérard, Lyon, France

Project workflow

Initial contact (contact-pgt@lyon.unicancer.fr)

Short project request

Need some advice ?	*Need assistance ?*	*Need more help?*
Consulting service	**Assistance service & custom analysis**	**Research collaboration**
Advice on bioinformatic/biostatistic methods, tools, analyses and resources Help with grant applications	Basic bioinformatics and biostatistics analysis Access to computational resources Training	For research or clinical projects that need a specific design or new methodological developments we work on a collaborative basis

Alain Viari PhD

– Scientific director

Alain Viari, PhD in molecular biophysics, has a senior researcher position at the Institut National de Recherche en Informatique et en Automatique (INRIA). Since 2012, he is the deputy scientific director at INRIA in charge of Biology, Medicine and Environment. He is the head of the Gilles Thomas bioinformatics facility since 2014.

Anthony Ferrari

– Bioinformatics operations manager

Anthony Ferrari is a bioinformatician with a solid background in mathematics and computer science.
He is working in cancer research since 2006 and has been mainly involved in cancer genomics projects involving array and sequencing data analysis. Lately, he has been focusing on building automated pipelines dedicated to the analysis of complex datasets combining whole genome, exome and RNAseq data.

Janice Kielbassa PhD

– Biostatistics operations manager

Janice Kielbassa has been a research engineer in statistical modeling for more than 10 years. She is currently responsible for the statistical data analysis of high-dimensional omics data, such as RNAseq, microarrary and methylation.She provides statistical expertise and can accompany you in your projects from proposal to completion.

Contacts

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Submission form and more infos:
www.cancer-research-lyon.com