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Activity

The Institut Curie Bioinformatics platform is composed of thirty bioinformaticians, biostatisticians and software engineers who offer a multidisciplinary expertise to support the biotechnological platforms, the research units and the hospital in their daily activities. Our skills range from statistical data analysis, data management, software development and high performance computing. We have five main missions: (1) knowledge and data integration, (2) collaborative support to biologists or clinicians for bioinformatics and biostatistics data analysis, (3) delivering advices and training in biostatistics and bioinformatics, (4) support to high performance computing and (5) coordination of bioinformatics activities within Institut Curie.

Aims

- Statistical analysis of omics and clinical data obtained from high-throughput technologies such as next-generation sequencing, mass spectrometry, reverse-phase protein array, cellular phenotyping or microarray
- Development, maintenance and running of automatic bioinformatics pipelines, in particular for biotechnological platform data processing, including quality control and first level analysis
- Setting up of a seamless information system for knowledge and data sharing, data query, visualization and analysis
- Support to the precision medicine program and delivery of decision-making reports in real-time for physicians
- Research and development for new biostatistical methods and bioinformatics tools
- Support to high performance computing,
- Leveraging the high performance computing infrastructure with the use of big data technologies.



Networking

The Bioinformatics platform has conducted collaborations with virtually all units of the research center and many departments from the hospital within Institute Curie. For years, the Bioinformatics platform has also developed many partnerships in France and abroad (institut Pasteur, Mines ParisTech, INSERM, CNRS, APHP, Cancéropole...) and is involved in several key national or international initiatives. To name a few, let's mention our implication in France Génomique, the Institut Français de Bioinformatique, Institut National du Cancer, RENABI, the SIRIC network. We have been involved in several European projects such as ABS4NGS, FP7 MAARS, FP7 RAIDS.

Services

- Bioinformatics and biostatistics data analysis, including but not limited to NGS, mass spectrometry, RPPA, cellular phenotyping
- Data management
- Training in bioinformatics and biostatistics
- Advices in bioinformatics and biostatistics
- Access to high-performance computing
- Access to bioinformatics workstation
- Access to in-house and commercial analysis softwares

Equipment

The platform disposes of a substantial IT infrastructure, managed by the Institut Curie's Computer team: a 2 Petabyte storage system, a computational cluster with 1400 cores, along with individual customized bioinformatics workstations for each person in the group. An informatician in the Bioinformatics platform is dedicated to pipeline optimization leveraging this high-performance computing infrastructure with big data technologies. The management of the infrastructure is ensured in the Direction of Informatics by Jean-Gabriel Dick group.

Training

It is the platform policy to promote autonomous data analysis by biologists and clinicians as often as possible:

- All tools that are within biologist/clinician reach are offered on our platform through web interfaces to enable direct use by non-specialists (Ingenuity, Partek and the many interfaces)

that we developed);

- Training sessions are organized in collaborations with other bioinformaticians both within Institut Curie or for a wider audience, and both for the in house tools (microarray, NGS, network analysis), statistics or commercial software (Ingenuity, Partek) ;
- A consulting activity is offered for people seeking advice for the bioinformatics and biostatistics analysis they carry out themselves.

Key publications

Year of publication 2018

Forget Antoine, Martignetti Loredana, Puget Stéphanie, Calzone Laurence, Brabetz Sebastian, Picard Daniel, Montagud Arnau, Liva Stéphane, Sta Alexandre, Dingli Florent, Arras Guillaume, Rivera Jaime, Loew Damarys, Besnard Aurore, Lacombe Joëlle, Pagès Mélanie, Varlet Pascale, Dufour Christelle, Yu Hua, L. Mercier Audrey, Indersie Emilie, Chivet Anaïs, Leboucher Sophie, Sieber Laura, Beccaria Kevin, Gombert Michael, D. Meyer Frauke, Qin Nan, Bartl Jasmin, Chavez Lukas, Okonechnikov Konstantin, Sharma Tanvi, Thatikonda Venu, Bourdeaut Franck, Pouponnot Celio, Ramaswamy Vijay, Korshunov Andrey, Borkhardt Arndt, Reifenger Guido, Pouillet Patrick, D. Taylor Michael, Kool Marcel, M. Pfister Stefan, Kawauchi Daisuke, Barillot Emmanuel, Remke Marc, Ayrault Olivier (2018 Sep 10)

Aberrant ERBB4-SRC Signaling as a Hallmark of Group 4 Medulloblastoma Revealed by Integrative Phosphoproteomic Profiling

Cancer Cell : 34 : 379-395 : [DOI : 10.1016/j.ccell.2018.08.002](https://doi.org/10.1016/j.ccell.2018.08.002)

Year of publication 2015

Natasha Zamudio, Joan Barau, Aurélie Teissandier, Marius Walter, Maté Borsos, Nicolas Servant, Déborah Bourc'his (2015 Jun 26)

DNA methylation restrains transposons from adopting a chromatin signature permissive for meiotic recombination.

Genes & development : 1256-70 : [DOI : 10.1101/gad.257840.114](https://doi.org/10.1101/gad.257840.114)

Antonio Cappuccio, Raphaël Zollinger, Mirjam Schenk, Aleksandra Walczak, Nicolas Servant, Emmanuel Barillot, Philippe Hupé, Robert L Modlin, Vassili Soumelis (2015 Apr 21)

Combinatorial code governing cellular responses to complex stimuli.

Nature communications : 6847 : [DOI : 10.1038/ncomms7847](https://doi.org/10.1038/ncomms7847)

Servant N., Varoquaux N., Lajoie B.R., Viara E., Chen C.J., Vert J.P., Heard E., Dekker J., Barillot E.
(2015 Jan 1)

HiC-Pro: an optimized and flexible pipeline for Hi-C data processing

Genome biology : 16 : 1

Year of publication 2013

Dillies M.A., Rau A., Aubert J., Hennequet-Antier C., Jeanmougin M., Servant N., Keime C., Marot G., Castel D., Estelle J., Guernec G., Jagla B., Jouneau L., Laloë D., Le Gall C., Schaëffer B., Le Crom S., Guedj M., Jaffrézic F., Consortium F.S. (2013 Jan 1)

A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis.

Briefings in bioinformatics : 14 : 671-683 : [DOI : 10.1093/bib/bbs046](https://doi.org/10.1093/bib/bbs046)