AI4Health Practical session:
omics data analysis for precision medicine

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Overview of the training

- Introduction to **molecular biology data** (sequencing data, bulk RNA-sequencing, single cell transcriptomics)
- **Bioinformatics** methods and tools for high-throughput data analysis
- Morning session: **bulk RNA-seq data** analysis for cancer patient stratification
- Afternoon session: **single cell data** analysis to study cell types

Aims of the training

→ Introduce concepts and methods to manipulate large-scale omics datasets

→ Get familiar with open source tools used by data scientists to analyse and visualize transcriptomic data

→ Develop strategies to extract relevant information and interpret results

→ 2 sessions, 6h

→ Morning session: 9h – 12h30 (coffee break at 10h30)

→ Afternoon session: 14h30 – 18h (coffee break at 16h)

Speakers

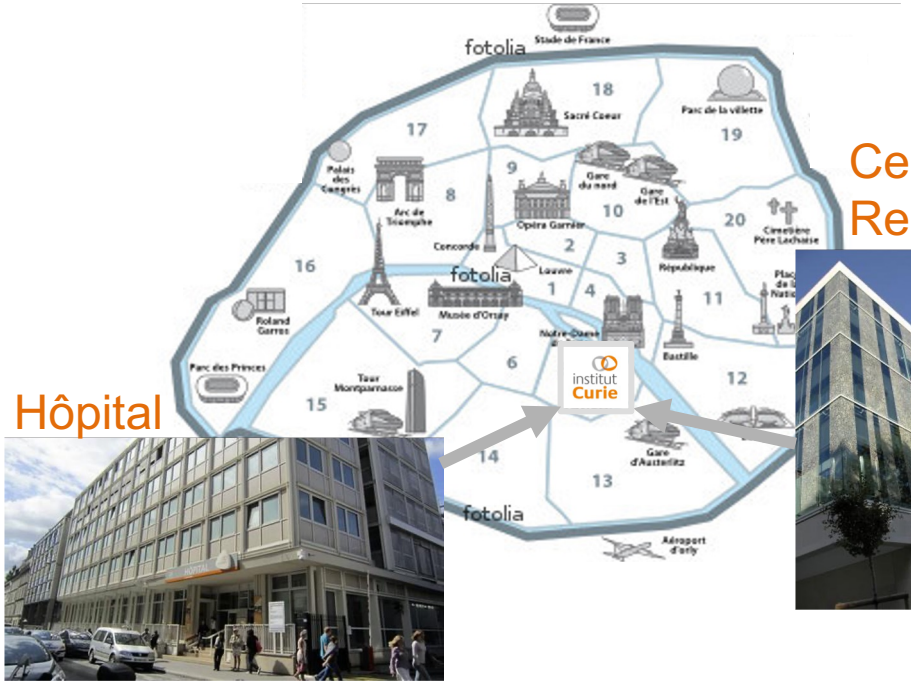
Lucie GASPARD-BOULINC
PhD student, Computational biology and Integrative genomics of cancer Team
(Institut Curie - Inserm U900)

Pierre GESTRAUD
Biostatistician, bioinformatics core facility CUBIC
(Institut Curie - Inserm U900)

Loredana MARTIGNETTI
PhD, Computational Systems Biology of Cancer Team
(Institut Curie - Inserm U900)

Institut Curie

- Cancer research and treatment center
- Interdisciplinary research in life sciences, physics, chemistry
- Founded in 1909
- 1200 people
- 90 research teams
- 74 nationalities



U900 research department at Institut Curie

6 research teams

- Genetic epidemiology of cancer
- Computational systems biology of cancer
- Statistical machine learning
- Statistical methods for precision medicine
- Computational biology and Integrative genomics of cancer
- Multiscale systems pharmacology

1 Core bioinformatics platform

- Data analysis
- Data integration
- Informatics support
- Training

Disclaimer

→ Examples and applications are mostly oriented to transcriptomics, but easily generalized to other omics

→ We would like an interactive classroom, do not hesitate to intervene / ask questions throughout the course