Master project: **Understanding transcriptional and epigenetic heterogeneity in human cancers**

Starting date: January 2019 or later

This project seeks to understand the causes of transcriptional and epigenetic heterogeneity in cancer potentially leading to a poor patient survival and escape from treatment. You will aim to discover novel genomic, epigenetic or transcriptional biomarkers related to changes in cellular identity of cancer cells and increase in intratumor heterogeneity. You will analyze genetic events with a potential to change expression status of transcription factors in cancer, and correlate these changes with changes in transcriptional programs. Changes of transcriptional programs will be characterized on the level of activation of signaling pathways, gain of metastatic potential, increase in proliferation and escape from the immune surveillance.

This project will leverage ChIP-seq, RNA-seq and genomic data available for hundreds of cancer samples. Integration of these data will allow understanding the shaping of transcriptional and epigenetic landscapes that provides evolutional advantages to cancer cells.

You will work on this project in the laboratory of Computational Epigenetics of Cancer (**Institut Cochin, Paris**) and in a collaboration with the laboratory of Genetics, epigenetics and cellular stress in bone pathology (PI: Benjamin Ory, **Nantes University**). Our teams are the national leaders in the analysis of cancer epigenetic data. We also work in close collaboration with clinicians and biologists from the Curie Institute, the Cochin Hospital, and Gustave Roussy Institute. In Cochin, we have a dynamic international environment (French, Russian, Algerian and Polish researchers in our lab), a big work-space with a view on the top of the Eiffel tower and excellent expertise in the bioinformatics analysis of high-throughput sequencing data from cancer samples, motif discovery methods, epigenetics and cancer biology.

Selected publications by the team:

- Heterogeneity of neuroblastoma cell identity defined by transcriptional circuitries. V. Boeva, et al. *Nature Genetics*, 2017. 49(9):1408-1413. **Key paper.**
- QuantumClone: Clonal assessment of functional mutations in cancer based on a genotype-aware method for clonal reconstruction. P. Deveau, et al. *Bioinformatics.* 2018. 34(11):1808-1816.
- HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics. H. Ashoor, et al. *Nucleic Acids Research*. 2017. 45(8):e58.
- Comparative analyses of super-enhancers reveal conserved elements in vertebrate genomes. Y.A. Pérez-Rico, V. Boeva, et al. *Genome Research*, 2017. 27(2):259-268.
- Analysis of genomic sequence motifs for deciphering transcription factor binding and transcriptional regulation in eukaryotic cells. V. Boeva. *Frontiers in Genetics*. 2016. 7:24.

Candidate requirements:

- Experience in data analysis with R
- Good knowledge of Linux environment (bash, awk, grep,…)
- General understanding of the biological processes involved in gene transcription and transcriptional regulation
- Good level of spoken English

Team webpage: www.boevalab.com

Team location: 5th floor of the Faculty building, Institut Cochin, 24 rue du Faubourg Saint-Jacques, 75014 Paris

Contact: valentina.boeva@inserm.fr – please send a short motivation letter, your CV and names of two references.