Simon BESSON-GIRARD

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M.Sc.
Bioinformatics, Biostatistics
as latest degree from
University Claude Bernard

After starting medicine school, I discovered bioinformatics and changed for a **B.Sc. in Biology** with a specialization in **Biostatistics, Modelling and Bioinformatics**. I continued in the same direction with the **M.Sc.** and performed my Masters' internship at the **RIKEN in Japan** where I developped analyses for **Single-Cell RNA-Seq** data. I further came to Munich as a PhD Student in the **Systems Neuroscience Group** of the Institute for Stroke and Dementia Research (**ISD**) where I extend my knowledge of the data analysis *in silico* to the biological experimental design and the sample preparation *in vitro* and *in vivo* in the context of neurological disorders.

EDUCATION AND EXPERIENCE

2018

Experience

Ongoing since Jan.2017
with Ozgun Gokce, PhD, group leader at the Institute for Stroke and Dementia Research - Systems Neuroscience Group - Munich, Germany – Graduate School of Systemic Neurosciences GSN-LMU
PhD Student: Single-cell RNA-Seq to Study Neurological Disorders
- Set-up and personalization of single-cell cDNA library preparation
- Development of the full analysis pipeline after sequencing

6 months – Feb.2016 - Aug.2016
with Charles Plessy, PhD, unit leader at RIKEN - CLST - DGT - Genomics Miniaturization Technology Unit - Yokohama, Japan
Master thesis: Single-cell RNA-Seq Data Analysis
Title: "Vizection: an interactive application for the analysis of big datasets from single-cell transcriptomics studies"
- Familiarisation with single-cell related technologies
- Design of a statistical analysis pipeline (classification, dimension reduction analyses, etc.)
- Implementation of an R/Shiny application and encapsulation in a package

2 months – Apr.2015 - May.2015
with Sam Meyer, PhD, docent at INSA - Laboratory MAP - UMR5240 - Villeurbanne, France
Internship: DNA Supercoiling as a Transcriptional Regulator
Title: "Analysis of thermodynamic properties of bacterial promoter sequences and modelling of DNA topology role in transcriptional regulation genome-wide"
- Implementation of Python/R scripts to extract the transcription start sites of genes sensitive to DNA supercoiling

2 months – May.2013 - Jun.2013
Novadiscovery - Lyon, France
Internship: "Research for Proof of Concept of *in silico* in the Last 20 Years Scientific Publications"
- Design of a research protocol
- Manipulation of bibliographic tools

Education

2 years – Sep.2014 - Aug.2016 University Claude Bernard - Villeurbanne, France
M.Sc. Mathematics and Computer Sciences for Biology – *honours: "Bien"*
keywords: *bioinformatics, biostatistics, data analysis, evolution, genomics, transcriptomics, etc.*

3 years – Sep.2011 - Jul.2014 University Claude Bernard - Villeurbanne, France
B.Sc. Biology – *honours: "Assez Bien"*
Specialization in Modelling and Computer Sciences for Life Sciences

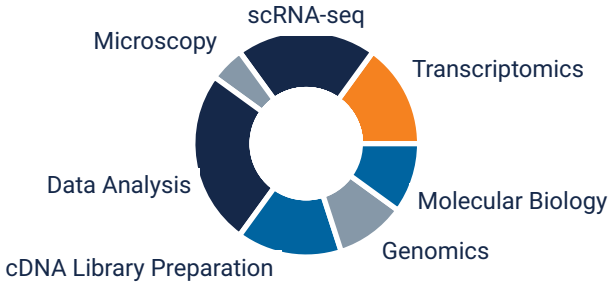
2 years – Sep.2009 - Jun.2011 Lyon-Est, UCBL - Lyon, France
Medicine University
First year studies then end of term competition

2009

RESEARCH EXPERIENCE

During my B.Sc. of Biology, I already specialized myself in bioinformatics and biostatistics. During my M.Sc. I continued to emphasize in genomics and data analysis.

For my Masters' first year internship I studied the impact of DNA supercoiling on the gene expression and thus acting as a regulation factor. We investigated the statistical link between DNA supercoiling and the AT-content of bacterial promoters. We found that supercoiling sensitive genes that are induced by DNA relaxation had a higher AT-content than those repressed by relaxation. We also defined an interval of 6nt on which no contact with a regulation or transcription protein is known. The AT-content on this interval may act as a discriminant factor into the differential reponse in front of supercoiling regulation.



For my Masters' thesis I built an interactive tool to qualitatively and quantitatively analyse single-cell transcriptomic datasets. Each step is expected to answer a specific point as for example identify the outliers, define sub-populations or identify the genes contributing the most to these sub-populations. I developped this tool in close collaboration with the molecular biologists preparing the samples before sequencing, thus responding to the needs and taking account for the technical specificities.

In the Systems Neuroscience Group at the ISD, I make usage of the single-cell knowledge I obtained until now and use it in one of the most relevant field for single-cell analyses due to its strong heterogeneity: neurobiology. I am currently reponsible for the development of the cDNA library preparation from single-cell and the full analysis pipeline after sequencing. We integrate cutting-edge technology to optimize the preparation of this library such as liquid handling machines, flow cytometry and laser capture microdissection.

INSTRUMENTS AND SOFTWARES

Instruments

- Brightfield Microscopy
- Confocal Microscopy
- Laser Capture Microdissection
- Flow cytometry cell sorting
- Liquid Handling Machine
- HPC Linux Cluster

Softwares and Programming

- Demultiplexing softwares
- FASTQ/BAM Quality Control
- Mapping/Alignment
- R/Shiny, Python, Bash
- LaTeX, Markdown, Sweave
- Cluster job submission

LANGUAGES

- French – native
- English – TOEIC 910/990, English workplace since February 2016
- Spanish – B1/B2
- German – notions - ongoing tuition
- Japanese – 2 years of studies & 9 months in Japan
- Taiwanese Mandarin – notions & 2 months of private tuition

POSTERS

1. August 8^{th}, 2017 ISD, Munich
   ISD Advisory Board
   "scRNA-Seq to Study Neurological Disorders"
2. December 20^{th}-21^{st}, 2017 MPI Martinsried
   ToPAG Symposium
   "scRNA-Seq to Study Neurological Disorders"

TALKS

1. July 4^{th}, 2017 Ammersee
   ISD Retreat - 20' talk
   Description of the scRNA-seq technology and how we plan to use it in the context of neurological disorders.
2. July 4^{th}, 2018 Ammersee
   ISD Retreat - 20' talk
   scRNA-seq transcriptomics to study somatic instability.
3. July 31^{th}, 2018 ISD, Munich
   CSD Seminar - 30' talk
   scRNA-seq: assessment of cellular development regulators and cell capture methods.