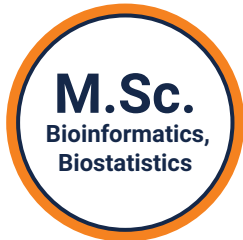


Simon BESSON-GIRARD

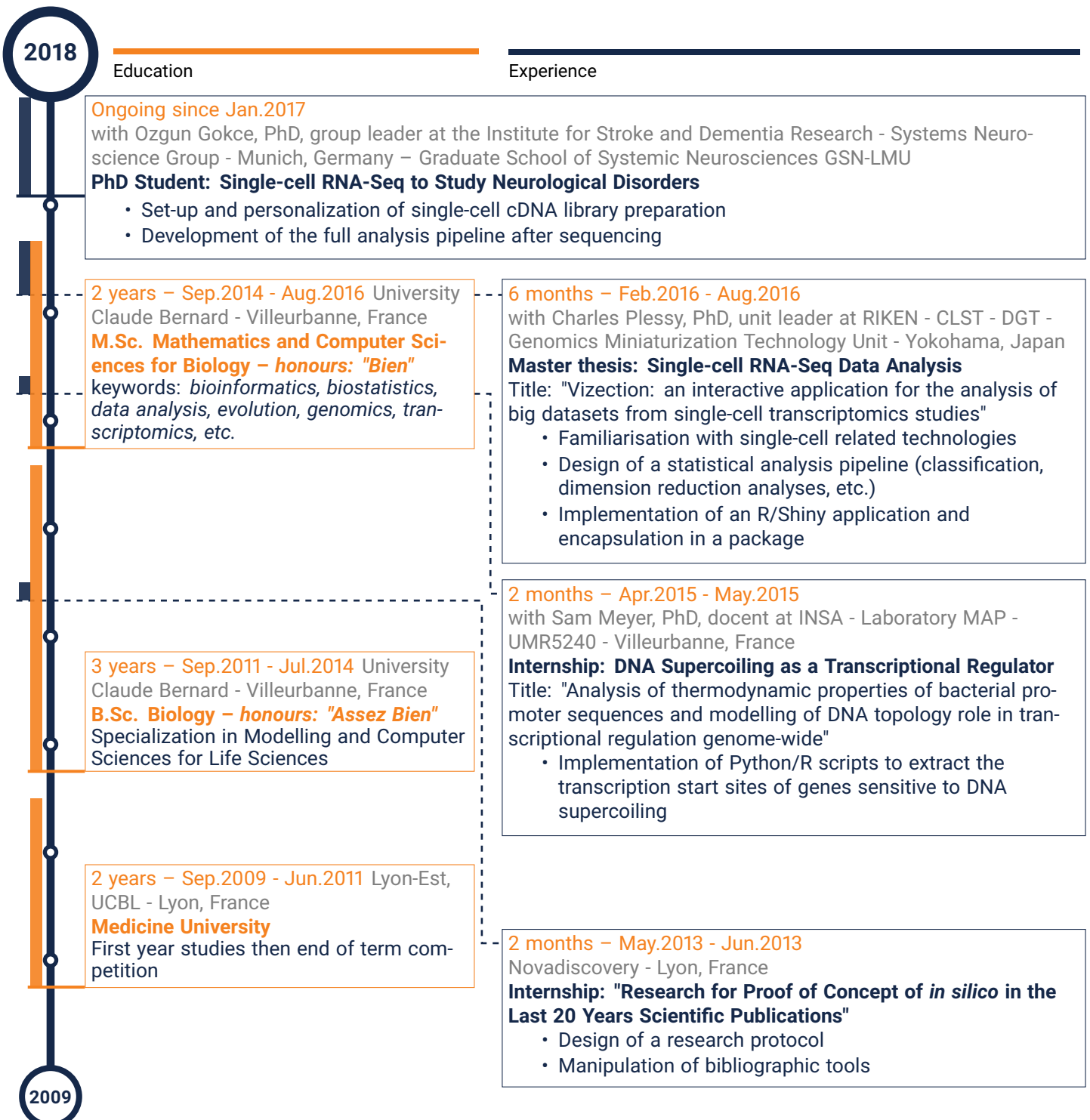
05/10/1990, French nationality
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as latest degree from
University Claude Bernard

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 developed 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



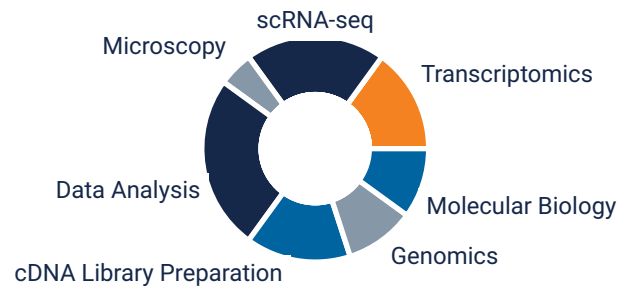
RESEARCH EXPERIENCE

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 response 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 developed 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 responsible 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 8th, 2017** ISD, Munich
ISD Advisory Board
"scRNA-Seq to Study Neurological Disorders"
2. **December 20th-21st, 2017** MPI Martinsried
ToPAG Symposium
"scRNA-Seq to Study Neurological Disorders"

TALKS

1. **July 4th, 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 4th, 2018** Ammersee
ISD Retreat - 20' talk
scRNA-seq transcriptomics to study somatic instability.
3. **July 31th, 2018** ISD, Munich
CSD Seminar - 30' talk
scRNA-seq: assessment of cellular development regulators and cell capture methods.