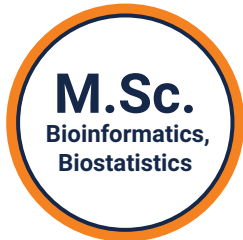


Simon BESSON-GIRARD

05/10/1990, French nationality
Munich, Germany
+49 152 265 739 14
simon.bessongirard@med.uni-muenchen.de



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

2018

Education

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

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.*

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

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 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 years – Sep.2009 - Jun.2011 Lyon-Est, UCBL - Lyon, France

Medicine University

First year studies then end of term competition

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

2009

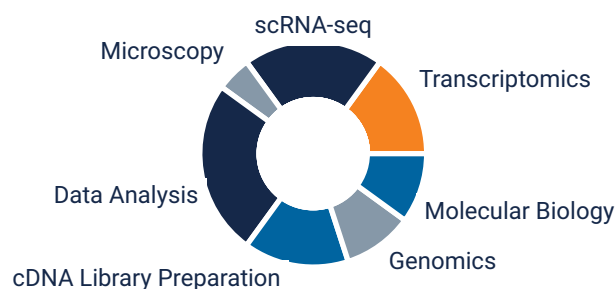
RESEARCH EXPERIENCE

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 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 31st, 2018** ISD, Munich
CSD Seminar - 30' talk
scRNA-seq: assessment of cellular development regulators and cell capture methods.