

# Curriculum vitae

## Romain Groux

Bioinformatics software developer /  
bioinformatician

32 years old, Swiss

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### Strenghts

PhD in bioinformatics

Bioinformatics software developer

NGS data specialist

Naturally curious and always eager to learn

### Professional experience:

**04.2015 - 09.2019 EPFL, scientific assistant** in the laboratory of "Computational Cancer Genomics".

- Development of a software predicting transcription factor binding sites (C). This software predicts which regions of a genome are bound given a specificity model. This software is currently the most efficient available for this type of problem.
- Development of unsupervised classification methods (C++) for genomic region of interest, based on i) the sequence of the regions and ii) diverse NGS sequencing profiles (ChIP-seq, DNase-seq, ATAC-seq, MNase-seq). These methods allow to identify i) functionally different families of regions and ii) their signatures.
- Development, maintenance and optimization of diverse software components and analysis pipelines hosted on the laboratory web server backend.
- Curator for a public database containing NGS data (ChIP-seq, DNase-seq, ATAC-seq, MNase-seq, etc).

### Technical skills:

**Developing and maintaining of software and analysis pipelines** in C++11 (STL, Boost, SFML, SeqAn) Python 2.7/3.6 (STL), R 2.X/3.X (diverse libraries) and bash.

**Testing code** using dedicated libraries in C++ (Unittest++) and Python (unittest)

**Measuring and optimizing the performances** of code and analysis pipelines.

**Handling and processing of NGS data** using dedicated softwares/libraries (samtools, bedtools, pysam), mapping (bowtie, bowtie2) and data quality control, etc.

**Genomic data analysis using machine learning methods** (unsupervised classification algorithm) and function prediction (transcription factor binding prediction).

**Algorithm understanding** and ability to implement and optimize them.

### Academic projects:

**PhD project** : setting up and pursuing a research project studying i) transcription factor binding specificity in the human genome (development of methods allowing to model their sequence preferences, training of sequence preference models and performance assessments of the models) and ii) the chromatin structure in the vicinity of transcription factor binding sites in the human genome by the developing dedicated analysis methods. These methods were then applied on NGS datasets (ChIP-seq, DNase-seq, ATAC-seq, etc) in order to characterize some regions of the human genome.

**Master project** : studying the regulation of gene expression as part of a swiss consortium (CycliX). I worked on i) the development of a pipeline that performs data processing/formatting and quality control (bash, Python et R), ii) the development of different software modules required for the data analysis and iii) the application of the above for the data analysis (Python et R).

### Education:

2016 - 2020

2013 - 2014

2010 - 2013

2006 - 2009

**PhD** in bioinformatics, EPFL

**Master** in bioinformatics, UNIL

**Bachelor** in biology, UNIL

**CFC** of biology laboratory technician, EPFL

## Languages:

French  
English  
German

mother tongue  
fluent written and spoken (equivalent to C1)  
basic scholar knowledge

## References:

### **Dr. Philipp Bucher**

Head of the “Computational Cancer Genomics” laboratory of EPFL  
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### **Dr. René Dreos**

Senior biostatistician at the Integrative Center for Genomics of UNIL  
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### **Dr. Giovanna Ambrosini**

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### **Dr. Vincent Gardeux**

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