

Alexandre Gouy | Data scientist, Bioinformatician

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Born in 1991

French citizen

Swiss work permit B

Professional profile

- Main areas of expertise: data analysis, data visualization, genomics, mentoring and training.
- 7 years of experience integrating, visualizing and analysing complex datasets using R and Python.
- Life sciences background and extensive knowledge of a broad range of biological data (genomes, brain imagery, networks, geospatial data, time series).

Professional experience

Since Jun. 2019 **Freelance data scientist | Gouy Data Consulting, Echandens, Switzerland**

- I developed machine learning solutions for disease risk prediction
- I realised dashboards for the interactive visualisation of data of interest for clients in the healthcare and agronomy sectors

Jul. 2015 - Dec. 2019 **PhD Candidate | University of Bern, Switzerland**

- I implemented and deployed statistical methods for the analysis of large-scale genomic datasets: DNA and RNA sequencing data analysis (bioinformatics, genomics, transcriptomics), and functional enrichment / differential expression analysis.
- I developed various statistical and machine learning algorithms (using Python, R and C++).
- I taught 180 hours of Genomics, Statistics and R classes (Bachelor to Master level).

Jun. 2013 - Jun. 2015 **Research internships | University of Montpellier and CNRS, Moulis, France**

- Three research internships (14 months total) dedicated to biological data analysis: genomics, R programming, C++ scientific software development, molecular biology (wet lab), field work.

Sep. 2012 - Jun. 2013 **Computer Science Tutor | University of Limoges, France**

- I trained people for an IT certificate (350 hours of teaching) and monitored databases (SQL).

Education

2019 **PhD *summa cum laude* | University of Bern, Switzerland**

- With training in Genomics, Theoretical and Applied Machine Learning, NGS data analysis, Markov models.

2015 **Master's degree *with highest honors* in Biology | University of Montpellier and Montpellier SupAgro, France**

- Focus on population genomics, advanced statistics, and mathematical modeling.

2013 **Bachelor's degree *with high honors* in Population Biology | University of Limoges, France**

Skills

Computer Science

Languages

- High proficiency in **R**, **Javascript/HTML/CSS**, **D3.js**
- Intermediate level in **Python**, **C#** and **C++**

Other

- Version control using git
- R package development
- Web applications
- High Performance Computing on clusters

Data Science

Statistical analysis

- **Machine learning** (Tensorflow, Keras, Pytorch): deep neural networks, random forests, support vector machines.
- **Exploratory analysis**: data mining, multivariate statistics.
- **Geospatial** statistics.
- **Simulation**-based inference, **maximum-likelihood** and **Bayesian** methods.

Data visualisation

- R and Python **plotting libraries**, **d3.js**, **dashboard** creation frameworks.
- **Shiny** and **Django** web application frameworks

Genomics and Bioinformatics

- **Next Generation Sequencing** data handling and analysis: variant calling, pipeline use and development in humans and non-model species
- Population **genomics**: genome-wide variant analysis
- Experience in **genome assembly and annotation**
- **Functional annotation** of variants of interest

Languages

- **French** (native speaker)
- **English** (fluent)
- **Spanish** (intermediate level)

Communication

- Scientific writing (including 8 publications in peer-reviewed journals)
- Oral presentation to both technical and non-technical audiences
- Knowledge of elements of typography and document design

Creativity

- Photography knowledge (+ Adobe Photoshop and Lightroom)
- Data-based artistic visualization and musical pieces
- 15 years of guitar playing

Publications

Non peer-reviewed

- **Gouy A.**, Hickner P., Severson D., Rousset F., Labbé P. (**in prep.**) Impacts of insecticide resistance on neutral genetic diversity in the mosquito *Culex pipiens*.
- **Gouy A.**, Excoffier L. (**submitted**) Polygenic selection and co-introgression of archaic variants contributed to modern humans' adaptation to pathogens.
- Armstrong E., Khan A., Taylor R., **Gouy A.**, Greenbaum G., Thiéry A., et al. (**submitted**) Recent evolutionary history of tigers highlights contrasting roles of genetic drift and selection.

Peer-reviewed

- Armstrong E., Khan A., Taylor R., **Gouy A.**, Greenbaum G., Thiéry A., et al. (**submitted**) Recent evolutionary history of tigers highlights contrasting roles of genetic drift and selection.
- **Gouy A.**, Excoffier L. (2020) Polygenic selection and co-introgression of archaic variants contributed to modern humans' adaptation to pathogens. **Molecular Biology and Evolution**, msz306.
- **Gouy A.** & Cruz-Dávalos D.I. (2020), Nothing stands still in the streams of life. In *The Beauty of Theoretical Biology*, Springer.
- Peischl S., Dupanloup I., Foucal A., Jomphe M., Bruat V., Grenier J.-C., **Gouy A.**, Gilbert K.J., Gbeha E., Bosshard L., Hip-Ki E., Agbessi M., Hodgkinson A., Vézina H., Awadalla P., Excoffier L. (2018). Relaxed selection during a recent human expansion. **Genetics** 208(2): 763-777
- **Gouy A.**, Daub J.T. & Excoffier L. (2017). Detecting gene subnetworks under selection in biological pathways. **Nucleic Acids Research** 45(16): e149
- **Gouy A.** & Zieger M. (2017). STRAF—A convenient online tool for STR data evaluation in forensic genetics. **Forensic Science International: Genetics** 30: 148-151
- Rousset F., **Gouy A.**, Martinez-Almoyna C., & Courtiol A. (2017). The summary likelihood method and its implementation in the Infusion package. **Molecular Ecology Resources** 17: 110-119