Lucile Vigué

Computational biologist specialized in genomic data analysis and modeling

Professional experience

Sept. 2020 – now **PhD candidate: population genetics of 81,000 E. coli strains**
Université de Paris Cité, Institut Cochin, Paris, France. *Use of Python, R, SQL.*

Feb. – June 2020 **Inference of the effect of mutations using statistical physics: application to E. coli**
Research intern, IAME research center, Paris, France. *Use of Python.*

June – Sept. 2019 **Performance of alternative bayesian estimation algorithms in pharmacokinetic/pharmacodynamic**
Industry intern, Merck Serono S. A., Aubonne, Switzerland. *Non-linear mixed effect models and optimal design of clinical trials. Use of R, Stan, PopED, NONMEM.*

Apr. – Aug. 2018 **Comparative population genetics of Neisseria meningitidis and Neisseria gonorrhoeae**
Research intern, University of Sussex, Falmer, United Kingdom. *Use of Python, R.*

June – Aug. 2017 **Data visualisation**
Industry intern, Thales Alenia Space, Cannes, France. *Project of digitalisation of Thales Group. Use of Angular, TypeScript, D3.js.*

Oct. 2015 – Apr. 2016 **Teacher**
Detention Center, Villefranche-sur-Saône, France. *Provided courses to the prison population.*

Education

2018 – 2020 **EPFL**, Lausanne
Life Sciences and Technology Master, specialization in Computational Biology

2015 – 2018 **École polytechnique**, Paris
Key subjects studied: Physics, Biology & Computer Science.

2013 – 2015 **Classe Préparatoire aux Grandes Écoles (PCSI-PC*)**, *Lycée Fermat*, Toulouse
Key subjects studied: Maths, Physics & Chemistry.

Projects

E. coli database SQL database of 81,000 genomes of *E. coli*: sequence clustering, gene annotation, phylogenies, ancestral sequence reconstruction and mutation effect inference. 1 publication, others in progress.

DNA barcodes analysis Evolution experiment: clustering of DNA barcodes to correct sequencing errors, bayesian approach to infer establishment times and fitness of mutations. Publication in progress.

Microbiota analysis Developed a pipeline to analyse and visualize 16S sequence data from gut microbiota. This pipeline led to 2 publications (others in progress) and is used in 2 labs for day-to-day activities.

Publications

2022 Vigué, Croce, *et al.* Deciphering polymorphism in 61,157 *Escherichia coli* genomes via epistatic sequence landscapes. *Nat Com*

2022 Hobson, Vigué *et al.* A microbiota-dependent response to anticancer treatment in an *in vitro* human microbiota model *Front. cell. infect*

2022 Hobson, Vigué *et al.* MiniBioReactor Array (MBRA) *in vitro* gut model: a reliable system to study microbiota-dependent response to antibiotic treatment. *JAC-AMR*

2019 Vigué and Eyre-Walker The comparative population genetics of *Neisseria meningitidis* and *Neisseria gonorrhoeae*. *PeerJ*

Prizes & Distinctions

2022 **Young Talent France** awarded by Fondation L'Oréal, UNESCO, and the French Academy of Science. 35 awardees among 660 candidates. Grant of 15,000 €.

2020 **Best average grade award** of the *Life Sciences and Technology* Master at EPFL.

2019 **EPFL Excellence fellowship** of CHF 16,000 per academic year.

2018 **Outstanding Investment** for my participation in the associative life of École polytechnique.

Languages

French Native speaker

English Fluent (TOEIC L&R: 960/990)

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