

### Research experience

- January 2020- **Research engineer**, *INRAE, Unités LPGP et IGEPP*, Rennes, France.
- Microtranscriptome annotation and biomarker identification for the rainbow trout
  - Detection of large structural variants for the downy mildew genome
- January 2019 - **Post-doctoral researcher**, *iDiv, Bioinformatics Unit*, Leipzig, Germany.
- December 2019
- Member of the bioinformatics support group (BIU)
  - Assembly of highly heterozygous genomes using third generation data (Pacbio - 10X)
  - Transcriptomics
  - Population genomics (RAD-seq)
- 2015-2018 **PhD student**, *INRA - INRIA team Genscale*, Rennes, France.
- Development and application of bioinformatics tools for insect metagenomics
- Analysis of multi-scale genomic diversity in large metagenomic datasets
  - Development of MinYS, a tool for targetted genome assembly from metagenomic data
- February 2015 – **Statistics and Bioinformatics intern**, *CNRS Lyon, supervised by Franck Picard*,
- August 2015 Functionnal Poisson regression applied to peak detection in Chip-Seq NGS data.
- September 2013 - **Bioinformatics intern**, *Rothamsted Research*, Harpenden, United Kingdom,
- February 2014 Setting up a Galaxy pipeline to represent gene abundances in metagenomic datasets.

### Education

- 2018 **PhD in Bioinformatics**, *University of Rennes*, Rennes, France.
- Development and application of bioinformatics tools for insect metagenomics. Supervisors :
- Jean-Christophe Simon (INRA, IGEPP)
  - Claire Lemaitre (Inria, IRISA)
  - Christophe Mougel (INRA, IGEPP)
- 2012–2015 **Diplôme d'ingénieur agronome (MsC in life sciences)**, *Agrocampus Ouest*, Rennes, France.
- Specializing in applied statistics for 2 years
- 2010–2012 **Classe préparatoire**, *Lycée Chateaubriand*, Rennes, France.
- 2010 **Baccalauréat**, *Lycée Saint Charles*, Saint Briec, France, with honours.

### Teaching and supervising

#### Teaching

- 2019 **Master 2**, Molecular evolution course.
- 8h of practical work : assembly, alignment, phylogeny
- 2016 **Master 1**, Simulation for biostatistics.
- In charge of a 64h course of statistics and programming for medicine students.
- R programming, random variable generation, stochastic modelling
- 2017 **Master 1**, Statistical learnings.
- Supervising 32h of statistics practical work.
- Statistics and introduction to machine learning

#### Supervising

- 2020 **Tutoring**, *Manon Paineau (PhD student INRAE UMR SAVE)*.
- Variant calling and population genomics for the downy mildew genome

- 2020 **Tutoring**, Eugene Bayahmetov (PhD student university of Cracow).  
Introduction to bioinformatics and assembly of a plant genome using PacBio reads
- 2017 **Supervising**, Wesley Delage (Master BIG, Université de Rennes 1).  
Development of an innovative method based on a reference guided assembly for the genome reconstruction of a bacteriophage
- [Other](#)
- 2018 **Volunteer**, in RECOMB 2018 organization, Paris.
- 2016 **Scientific dissemination**, 2<sup>nd</sup> jury prize of Sciences en court(s).

## Languages

French Native speaker  
German Basic

English : Fluent ; TOEIC in 2014 : 970/990

## Skills

Bioinformatics and NGS : Assembly, variant calling, high volume datasets, metagenomics...

Programming R : ★★★★★ Python : ★★★★★ Julia : ★★★★★ C++ : ★★★★★

Software Developer of MineYourSymbiont (<https://github.com/cguyomar/MinYS>)  
Codeveloper of MindTheGap (<https://github.com/GATB/MindTheGap>)

Statistics Statistical learning, GLM, factor analysis, data exploration and visualization

Other Bash, Git, Latex, software distribution (Conda, Docker, NextFlow)  
Proficient with Windows and GNU/Linux, including computing clusters

## Publications

### Peer reviewed publications

**Guyomar, Cervin**, Wesley Delage, Fabrice Legeai, Christophe Mougél, Jean-Christophe Simon, and Claire Lemaitre. Minys: Mine your symbiont by targeted genome assembly in symbiotic communities. *Accepted in NAR Genomics and Bioinformatics* (link to preprint), 2020.

**Guyomar, Cervin**, Fabrice Legeai, Emmanuelle Jouselin, Christophe Mougél, Claire Lemaitre, and Jean-Christophe Simon. Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. *Microbiome*, 6(1):181, 2018.

Andrew L. Neal, Martin Blackwell, Elsy Akkari, **Guyomar, Cervin**, Ian Clark, and Penny R. Hirsch. Phylogenetic distribution, biogeography and the effects of land management upon bacterial non-specific Acid phosphatase Gene diversity and abundance. *Plant and Soil*, pages 1–15, jun 2017.

Andrew L. Neal, Maïke Rossmann, Charles Brearley, Elsy Akkari, **Guyomar, Cervin**, Ian M. Clark, Elisa Allen, and Penny R. Hirsch. Land-use influences phosphatase gene microdiversity in soils. *Environmental Microbiology*, 19(7):2740–2753, jul 2017.

### Book chapter (in press)

**Cervin Guyomar** and Claire Lemaitre. Métagénomique et métatranscriptomique. In *Du texte aux graphes : méthodes discrètes pour la bioinformatique*. Éditions ISTE, 2020.

### Conferences (selection)

**Guyomar, Cervin**, Wesley Delage, Fabrice Legeai, Christophe Mougél, Jean-Christophe Simon, and Claire Lemaitre. Reference-guided genome assembly in metagenomic samples. In *JOBIM*, Nantes, France, 2019.

**Guyomar, Cervin**, Fabrice Legeai, Christophe Mougél, Claire Lemaitre, and Jean-Christophe Simon. Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. In *International Conference on Holobionts*, Paris, France, April 2017.