

### Education

- 2015-2018 **PhD in Bioinformatics**, *INRA - INRIA team Genscale*, Rennes, France.  
Development and application of bioinformatics tools for insect metagenomics
- Analysis of multi-scale genomic diversity in metagenomic datasets
  - Software development for targetted assembly from metagenomic data
- 2012-2015 **Diplôme d'ingénieur agronome (MsC in life sciences)**, *Agrocampus Ouest*, a french *Grande École*, Rennes, France.  
Specializing in applied statistics for 2 years
- 2010-2012 **Classe préparatoire**, *Lycée Chateaubriand*, Rennes, France.
- 2010 **Baccalauréat**, *Lycée Saint Charles*, Saint Brieuc, France, with honours.

### Work and research experience

#### Placements and projects

- February 2015 **Statistics and Bioinformatics Internship**, *CNRS Lyon*, supervised by *Franck Picard*,  
– August 2015 Fonctionnal Poisson regression applied to peak detection in Chip-Seq NGS data.
- July 2014 **Collaborating with a freelance statistician**, R programming, statistical analysis.
- September 13 **Bioinformatics Internship**, *Rothamsted Research*, Harpenden, United Kingdom,  
– February 2014 Setting up a Galaxy pipeline to represent gene abundances in metagenomic datasets.

#### Teaching

- 2016 **Master 1**, Simulation for biostatistics.  
In charge of a 64h course of statistics and programming for medecine 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

- 2017 **Supervising**, *Wesley Delage (Master 1 Bioinformatique et Génomique, Université de Rennes 1)*.  
Development of an innovative method based on a reference guided assembly for the genome reconstruction of a bacteriophage APSE

#### Organization

- 2018 **Volunteer**, in RECOMB 2018 organization, Paris.
- 2016 **Scientific dissemination**, 2<sup>nd</sup> jury prize of Sciences en court(s).

### Foreign Languages

- French Native speaker
- English Fluent : TOEIC test in June 2014 : 970/990 , Several months in England and Ireland
- German Basic

## Skills

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

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

Statistics Statistical learning, modelling, factor analysis, bayesian methods, experimental design

Other Bash, Git, Latex, Docker

Proficient with Windows and GNU/Linux, including computing clusters

## Publications

### Peer reviewed publications

Cervin Guyomar, Fabrice Legeai, Emmanuelle Jouselin, Christophe Mougél, Lemaitre, and Jean-Christophe Simon. Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. . *In revision in Microbiome*, 2018.

Andrew L. Neal, Martin Blackwell, Elsy Akkari, Cervin Guyomar, 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, Cervin Guyomar, 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.

### Oral presentations

Cervin Guyomar, 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.

Cervin Guyomar and Jean-Christophe Simon. Aphid microbiota, from field ecology to metagenomics. In *Journée d'animation BioGenOuest*, Rennes, France, 2016.

### Posters

Cervin Guyomar, Wesley Delage, Fabrice Legeai, Christophe Mougél, Jean-Christophe Simon, and Claire Lemaitre. Reference guided genome assembly in metagenomic samples. RECOMB 2018, 2018. Poster.

Cervin Guyomar, Fabrice Legeai, Christophe Mougél, Claire Lemaitre, and Jean-Christophe Simon. Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. JOBIM 2017 - Journées Ouvertes en Biologie, Informatique et Mathématiques, July 2017. Poster.