Cervin Guyomar

Research engineer in bioinformatics

Professional experience

Novembre 2020 - current
Research engineer, *INRAE GenPhySE*, Toulouse, France.
Member of the Dynagen group and Sigenae platform
- Functional annotation of animal genomes (associated with the FAANG consortium)
- MenicroRNA annotation and characterization
- Genotyping by sequencing for animal populations
- Bioinformatic and biostatistic support for -omics data analysis

January 2020 - July 2020
Research engineer, *INRAE, Unités LPGP et IGEPP*, Rennes, France.
- Microtranscriptome annotation and biomarker identification for the raindow trout
- Detection of large structural variants for the downy mildew genome

January 2019 - December 2019
Research engineer, *iDiv, Bioinformatics Unit*, Leipzig, Germany.
- 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 – August 2015
Statistics and Bioinformatics intern, *CNRS Lyon, supervised by Franck Picard*,
Functionnal Poisson regression applied to peak detection in Chip-Seq NGS data.

September 2013 - February 2014
Bioinformatics intern, *Rothamsted Research*, Harpenden, United Kingdom,
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 Brieuc, 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 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

2024 **Supervising**, *Océane Carpentier (Master BIG, Université de Rennes 1).*
Multi omics intergration to discover expression regulation paterns

2022 **Supervising**, *Martin Racoupeau (Master bioinformatique, Université de Toulouse).*
Comparing miRNA annotation tools

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**, 2nd jury prize of Sciences en court(s).

Languages

French Native speaker   English Proficient
German Intermediate

Skills

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

Programming R: ★★★★ Python: ★★★☆ Nextflow: ★★★☆ Julia: ★★☆☆ C++: ★☆☆☆
Software Developer of software (MinYS) and bioinformatic pipelines (TAGADA, PARSEC, pegASE)
Statistics Inferential and descriptive statistics, data visualization
Other Bash, Git, Latex, software distribution (Conda, Singularity, NextFlow)
Proficient with Windows and GNU/Linux, including computing clusters

Publications

Peer reviewed publications

Laura Frohn, Diogo Peixoto, **Guyomar, Cervin**, Carla Teixeira, Frédéric Terrier, Pierre Aguirre, Sarah Mama n Haddad, Julien Bobe, Benjamin Costas, Nadège Richard, Karine Pinel, and Sandrine Skiba-Cassy. Yeast extract improves growth in rainbow trout (Oncorhynchus mykiss) fed a fishmeal-free diet and modulates the hepatic a nd distal intestine transcriptomic profile. *Aquaculture*, 579, January 2024. Publisher: Elsevier.

Sarah Janati-Idrissi, Mariana Roza de Abreu, **Guyomar, Cervin**, Fernanda de Mello, Thaovi Nguyen, Nazim Mechkou ri, Stéphanie Gay, Jérôme Montfort, Anne Alicia Gonzalez, Marzieh Abbasi, Jérôme Bugeon, Viole tte Thermes, Hervé Seitz, and Julien Bobe. Looking for a needle in a haystack: de novo phenotypic target identification reveals Hippo pathway-mediated miR-202 reg ulation of egg production. *Nucleic Acids Research*, 52(2):738–754, January 2024.

Cyril Kurylo, **Guyomar, Cervin**, Sylvain Foissac, and Sarah Djebali. TAGADA: a scalable pipeline to improve genome annotations with RNA-seq data. *NAR Genomics and Bioinformatics*, 5(4):lqad089, October 2023.

Thomas Desvignes, Philippe Bardou, Jérôme Montfort, Jason Sydes, **Guyomar, Cervin**, Simon George, John H Pos tlethwait, and Julien Bobe. FishmiRNA: An evolutionarily supported microRNA annotation and expression database for ray-finned fishes. *Molecular Biology and Evolution*, 39(2):msac004, January 2022. Publisher: Oxford University Press (OUP).

Rebekka Sontowski, Yvonne Poeschl, Yu Okamura, Heiko Vogel, **Guyomar, Cervin**, Anne-Marie Cortesero, and Nicole M. van Dam. A high-quality functional genome assembly of Delia radicum L. (Diptera: Anthomyiidae) annotated from egg to adult. *Molecular Ecology Resources*, 22(5):1954–1971, July 2022. Publisher: Wiley/Blackwell.

Rebekka Sontowski, **Guyomar, Cervin**, Yvonne Poeschl, Alexander Weinhold, Nicole M van Dam, and Danie l G Vassão. Mechanisms of Isothiocyanate Detoxification in Larvae of Two Belowground Herbivores, Delia radicum and D. f loralis (Diptera: Anthomyiidae). *Frontiers in Physiology*, 13:17 p., April 2022. Publisher: Frontiers.

Evgenii Baiakhmetov, **Guyomar, Cervin**, Ekaterina Shelest, Marcin Nobis, and Polina D Gudkova. The first draft genome of feather grasses using SMRT sequencing and its implications in molecular studies of Stipa. *Scientific Reports*, 11(1):15345, July 2021. Publisher: Nature Publishing Group.

Emilie Cardona, **Guyomar, Cervin**, Thomas Desvignes, Jérôme Montfort, Samia Guendouz, John H Postlethwait, Sandrine Skiba-Cassy, and Julien Bobe. Circulating miRNA repertoire as a biomarker of metabolic and reproductive states in rainbow trout. *BMC Biology*, 19(1), December 2021.

Guyomar, Cervin, Wesley Delage, Fabrice Legeai, Christophe Mougel, Jean-Christophe Simon, and Cla ire Lemaitre. MinYS: mine your symbiont by targeted genome assembly in symbiotic communities. *NAR Genomics and Bioinformatics*, 2(3):1–11, September 2020.

Guyomar, Cervin, Fabrice Legeai, Emmanuelle Jousselin, Christophe Mougel, Claire Lemaitre, and Jean-Christophe Simon. Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. *Microbiome*, 6(1):181, December 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*, 427(1-2):175–189, June 2018.

Andrew L. Neal, Maike 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, July 2017.

Book chapters

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

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