Arnaud Liehrmann

PhD. Student
Bioinformatics, Biostatistics

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Current Position

Nov 2020– Nov 2023 **PhD. Student in Bioinformatics / Biostatistics**,
Doctoral School of Structure and Dynamics of Living Systems,
Laboratory of Mathematics and Modeling of Evry, Stat. and Genome Team, Evry, France,
Institute of Plant Sciences of Paris-Saclay, Organellar Gene Expression Team & Genomic Networks Team, Gif-sur-Yvette, France,
Supervised by Rigaill Guillem and Castandet Benoît,
Development and application of changepoint detection methods for the automatic analysis of transcription variants in the chloroplast.

Research Themes

Description **My research focuses on the development and the application of statistical models, algorithms and methods for the analysis and interpretation of high throughput biological data**.

Computational Statistics :
> Models: multiple changepoint detection
> Statistical Inference : penalized likelihood
> Algorithms : dynamic programming, functional pruning

Biostatistics/Bioinformatics for molecular biology:
> Models: multiple changepoint and generalized linear models
> Data : RNA-Seq (small and long reads), ChIP-Seq
> Package developpement : R/C++

Scientific Experiences

Feb 2020– Aug 2020 **Master Research Internship**,
School of informatics, Computing, and Cyber Systems of Northern Arizona University, Machine Learning Team, Flagstaff, Arizona, United States,
Supervised by Hocking Toby Dylan and Rigaill Guillem,
Study of constrained multiple changepoint detection models applied to Chip-Seq data.

Apr 2019–Jul 2019 **Master Research Internship**,
Laboratory of Mathematics and Modeling of Evry, Stat. and Genome Team, Evry, France,
Supervised by Rigaill Guillem and Runge Vincent,
Design and implementation in R/Cpp of an algorithm for multiple changepoint detection with multi-scale penalty and application to DNA copy number variation profiles.

May 2018–July 2018	**Bachelor Research Internship**, *Institute of Plant Sciences of Paris-Saclay, Genomic Networks Team, Gif-sur-Yvette, France*, *Supervised by Boudet Nathalie and Tamby Jean Philippe*, **Comparison of orthology detection methods for plant genomes**.

Education

2018–2020	**Master of Bioinformatics: Genomics Informatics and Mathematics for Health and Environment**, *University of Paris-Saclay - University of Evry Val d'Essonne, Evry, France*.
2015–2018	**Bachelor of Bioinformatics**, *University of Paris-Saclay - University of Evry Val d'Essonne, Evry, France*.
2014–2015	**Bachelor of Computer Science (First year)**, *University of Paris-Saclay - University of Evry Val d'Essonne, Evry, France*.
2014	**French Baccalaureate, scientific section (French equivalent to A levels)**, *Parc des Loges High School, Evry, France*.

Publications

(soon)	**DiffSegR : an RNA-Seq data driven method for differential expression analysis using changepoint detection**, <u>Liehrmann Arnaud</u>, Etienne Delannoy, Benoît Castandet, Guillem Rigaill .
(soon)	**Ms.FPOP : an exact and fast segmentation algorithm with a multiscale penalty**, <u>Liehrmann Arnaud</u>, Guillem Rigaill.
2022	**Exponential integral solutions for fixation time in Wright-Fisher model with selection**, *Vincent Runge, <u>Liehrmann Arnaud</u>, Pauline Spinga*, arXiv.
2021	**Full length transcriptome highlights the coordination of plastid transcript processing**, *Guilcher Marine, <u>Liehrmann Arnaud</u>, Seyman Chloé, Blein Thomas, Rigaill Guillem, Castandet Benoît, Delannoy Etienne*, International Journal of Molecular Sciences.
2021	**Increased peak detection accuracy in over-dispersed ChIP-seq data with supervised segmentation models**, <u>Liehrmann Arnaud</u>, Rigaill Guillem, Hocking Toby Dylan, BMC Bioinformatics.

Talks

2023	**Ms.FPOP: an exact and fast segmentation algorithm with a multi-scale penalty**, *Paris-Saclay Change-Point Workshop, France*.
2022	**Ms.FPOP: an exact and fast segmentation algorithm with a multi-scale penalty**, *StatScale ECR Meeting, UK*.
2022	**DiffSegR : systematic identification of differential regulation events in RNA-Seq data using changepoint detection**, *Post-Trasncriptional Gene Regulation, Gordon Research Conference, US*.

2021 **DiffSegR : systematic identification of differential regulation events in RNA-Seq data using changepoint detection (poster)**,
Open Days in Biology, Computer Science and Mathematics (JOBIM), France.

2021 **DiffSegR : systematic identification of differential regulation events in RNA-Seq data using changepoint detection**,
Congress of French Society of Biochemistry and Molecular Biology, France.

2021 **Ms.FPOP: an exact and fast segmentation algorithm with a multi-scale penalty**,
52nd days of statistics of the French Statistical Society (SFDS), France.

Teachings

Fall 2022 **System Biology**, *Master 2 students in Biology, University of Paris-Saclay (3h).*

Fall 2021 **Differential Expression Analysis**, *PhD students, Genopole summer school, with Guillem Rigaill (3h).*

Fall 2021 **Statistics**, *2nd year Bachelor students in Biology, University of Evry Val d'Essonne (27h).*

Supervisions

2023 **Jeremy Ferraro, Master 2 Reasearch Internship**,
Integration of transcriptomic and metabolomic data for the study of the response to multiple stresses,
with Marie-Laure Martin-Magniette and Rigaill Guillem.

2022 **Benjamin Vaccus, Master 2 Reasearch Internship**,
Analysis of nanopore data to study co-maturations of the chloroplast transcriptome,
with Benoît Castandet and Rigaill Guillem.

2021 **Chloé Seyman, Bachelor Reasearch Internship**,
Coordination of plastid transcript processing analysis using nanopore sequencing data,
with Rigaill Guillem.

Others

2021 **Thematic School (JC)2BIM organized by GDR Molecular Bioinformatics**, *6-10 Dec, Rennes (training).*

Languages

French Native
English Advanced (B2)
German Beginner (A2)