

Date of birth: 10 July 1996

GitHub: <https://github.com/aLiehrmann>

2023 **PhD** in computational biology & statistics – SDSV, Uni. Paris-Saclay, France
 2020 **Master** in computational biology – GENIOMHE, Uni. Paris-Saclay, France
 2018 **Bachelor** in computational biology, Uni. Paris-Saclay, France

Since 2024 **Postdoctoral researcher** in computational biology & statistics, CQSB, Sorbonne Uni., France.

- “*Interspecies analysis of transcriptome: methodological developments*” supervised by Élodie Laine (bioinformatics, Sorbonne Uni.) and Hugues Richard (statistics, RKI)
- Collaboration I initiated: Paul Bastide (statistics, Uni. Paris Cité), Méлина Gallopin (statistics, Univ. Paris-Saclay) and Maëlle Daunesse (genomics, Institut Pasteur)

2020–2023 **PhD student** in computational biology & statistics, Uni. Paris-Saclay, France. [Link](#)

- “*Multiscale analysis of transcriptome: methodological and algorithmic developments*” supervised by Guillem Rigai (statistics) and Benoît Castandet (molecular biology)
- My work was conducted between:
 - (1) a Plant genomics lab (IPS2)
 - (2) an applied mathematics lab (LaMME)

2018–2020 **Research intern**

- I completed three research internships, including six months in the Machine Learning team at Northern Arizona Uni. in Flagstaff, **USA**, where I worked on supervised segmentation models applied to genomics data (ChIP-Seq). [Link](#)

Total: 12 articles + 3 *in preparation* (~ 77 citations)
 Started after my PhD defense: 5 articles + 3 *in preparation*

RESEARCH ACHIEVEMENTS

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

Computational Statistics

- Statistical inference: changepoint detection (segmentation), penalized likelihood
- Algorithms: dynamic programming, functional pruning

Biostatistics/Bioinformatics for Molecular Biology

- Models: segmentation, generalized linear models, phylogenetic comparative methods
- Data: RNA-Seq, Ribo-Seq, ChIP-Seq, RIP-Seq
- Package development: R/C++/python

1 - [A. Liehrmann](#), E. Delannoy, B. Castandet and G. Rigai. 2023. [Link](#)

DiffSegR: an RNA-Seq data driven method for differential expression analysis using changepoint detection. **NAR Genomics and Bioinformatics**

- DiffSegR is the segmentation method I developed during my PhD. From RNA-Seq data alone, it recovers the full set of annotated transcriptomic regulations in the Arabidopsis chloroplast, something no competing method achieves (best at 80%), while finding new ones. Its genericity is demonstrated through its application to sequencing data [4, 5], and its conclusions hold at nuclear genome scale [2].

Showcasing my expertise in applying segmentation methods to sequencing data (& others)

2 - V. Brunaud, G. Rigai, and [A. Liehrmann](#). *manuscript in prep.*

DiffSegR2: genome-scale data-driven differential expression analysis

- We show that the method DiffSegR remains robust at the scale of whole nuclear genomes.

3 - M. Abakarova, M. I. Freiburger, [A. Liehrmann](#), M. Rera and É. Laine. 2026. [Link](#)

Proteome-wide prediction of the functional impact of missense variants with ProteoCast.

Nature Communications

- I applied segmentation to predicted protein mutational landscapes to identify putative binding and regulatory sites in unstructured regions, outperforming competing methods.

4 - K. Baudry, S. Skiada, C. Burstein, V. Liveanu et al. (incl. [A. Liehrmann](#)). 2026. [Link](#)

The GT1 domain of RNase J ensures RNA quality control through dsRNA binding in Arabidopsis plastids. **Nucleic Acids Research**

- Using DiffSegR on RNA-Seq data from multiple RNase J mutants in *Arabidopsis*, I showed that mutants accumulate high levels of dsRNA in the chloroplast.

5 - H. C. Tran, V. Schmitt, S. Lama, C. Wang et al. (incl. [A. Liehrmann](#)). 2023. [Link](#)
An mTRAN-mRNA interaction mediates mitochondrial translation initiation in plants.
Science

- Using DiffSegR on RIP-Seq data, I showed that *Arabidopsis* mTRAN factors bind preferentially to 5' regions of mitochondrial mRNAs.

6 - [A. Liehrmann](#), G. Rigaiil and T. D. Hocking. 2021. [Link](#)
Increased peak detection accuracy in over-dispersed ChIP-seq data with supervised segmentation models. **BMC Bioinformatics**

- I showed that supervised segmentation of ChIP-Seq data yields higher-quality histone modification peak tracks than bioinformatics heuristics.

Showcasing my expertise in fine-grained modeling of transcriptomic and proteomic data

7 - [A. Liehrmann](#), L. Carrel Billiard, P. Bastide, M. Gallopin, H. Richard and É. Laine. *preprint*. [Link](#)
phyloDS: An RNA-Seq Driven Method for Differential Splicing Analysis Across Species.

- First method for inter-species differential splicing analysis from RNA-Seq data.

8 - M. Gallopin, M. Daunesse, O. Lespinet, [A. Liehrmann](#), P. Bastide. *preprint*. [Link](#)
Interspecies Differential Gene Expression Analysis with Regularized Phylogenetic Linear Model.

- First method to correctly control the false discovery rate for inter-species differential expression analysis from RNA-Seq data.

9 - L. Carrel Billiard, [A. Liehrmann](#), H. Richard and É. Laine. *manuscript in prep*.
Charting the Evolution of Protein Splice Variations Across More Than One Billion Years.

- First framework integrating evolutionary splicing graphs with protein-scale datasets to reconstruct the evolutionary history of alternative splicing across species.

10 - M. Guilcher, [A. Liehrmann](#), C. Seyman, T. Blein et al. 2021. [Link](#)
Full length transcriptome highlights the coordination of plastid transcript processing.
International Journal of Molecular Sciences

- First method to detect transcriptome-wide co-maturations between pairs of RNA processing events from long-read RNA-Seq data.

Showcasing my expertise in developing statistically grounded and fast segmentation methods

11 - [A. Liehrmann](#), G. Romano, P. Fearnhead, G. Rigaiil. *Poster GDR IASIS & manuscript in prep*.
Papillon: pruning dynamic programming for changepoint detection by comparing means

- A pruning rule for exact changepoint detection, as simple to implement as PELT and almost as efficient as functional pruning, that only compares segment means; C with R and Python ports.

12 - [A. Liehrmann](#) and G. Rigaiil. 2024. [Link](#)
Ms.FPOP: a fast exact segmentation algorithm with a multiscale penalty.
Journal of Computational and Graphical Statistics

- A global optimization algorithm for multi-scale penalties implemented in R/C++.

Showcasing my commitment to making protocols and results accessible to the community

- 13 - M. Abakarova, M. I. Freiburger, [A. Liehrmann](#), M. Rera and É. Laine. 2026. [Link](#)
ProteoCast: a web server to predict, validate, and interpret missense variant effects.
Journal of Molecular Biology
- 14 - E. Delannoy, [A. Liehrmann](#) and B. Castandet. 2024. [Link](#)
The Use of Nanopore Sequencing to Analyze the Chloroplast Transcriptome Part II:
Bioinformatic Analyzes and Virtual RNA Blots. **Plastids: Methods and Protocols, Springer US**
- 15 - S. Skiada, A. Launay-Avon, [A. Liehrmann](#), E. Delannoy et al. 2024. [Link](#)
The Use of Nanopore Sequencing to Analyze the Chloroplast Transcriptome Part I: Library
Preparation. **Plastids: Methods and Protocols, Springer US**

Showcasing my commitment to disseminating my research

I have 10 abstracts accepted as talks or posters in national and international conferences and workshops (JOBIM, SMPGD, Gordon Research Conference, SFBBM, JdS-SFdS, Paris-Saclay change-point workshop, German Conference on Bioinformatics).

PEER RECOGNITION

Invited short-term researcher in international laboratories

Since 2025	Robert Koch Institute, Berlin, Germany	(1 month)
2024	Department of Mathematics and Statistics, Lancaster Uni., United Kingdom	(1 week)

Invited presentations at lab-seminars

2025	Young Researchers' Seminar, Robert Koch Institute, Germany	(for bioinformaticians)
2024	LBCPLM Seminar, IBPC, France	(for biologists)
2024	MAV Seminar, LPSM, France	(for statisticians)

Invited presentations at conferences and workshops

2026	JOBIM, Strasbourg, France	(for bioinformaticians)
2024	K-mers mini symposium, Dijon, France	(for bioinformaticians)
2022	StatScale ECR meeting, Brighton, United Kingdom	(for statisticians)
2022	GRC post-transcriptional gene regulation, Maine, USA	(for biologists)

Invited PhD lecture

Since 2024	Introduction to changepoint detection, application to genomics	(for bioinformaticians)
	• GDR BIMMM Early-Career Researchers' School, France	
2025	Introduction to changepoint detection from first principles	(for statisticians)
	• PhD Program Data Science, Uni. La Sapienza, Roma, Italy	

2021	Introduction to differential expression analysis	(for biologists)
	• Genopole Summer School, France	

Reviewer for journals and conferences

Since 2021	Reviewer for ISMB, ECCB, and NAR Genomics and Bioinformatics.	(>10)
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OTHER CONTRIBUTION TO RESEARCH

Supervision of Master students

2 co-supervised Master's students are now PhD students

- Benjamin Vacus (6 months, 2022)
- Chloé Seyman (3 months, 2021)

[Link](#)

[Link](#)

1 co-supervised Master's student will start her PhD in early 2027

- Milica Urosevic (6 months, 2025)

Teaching

Since 2022	Detection of transcriptional variants	(Total: 12 h)
	• First-year Master's students in Biology, Uni. Paris-Saclay	

2020	Introduction to statistics	(Total: 27 h)
	• Second-year Bachelor's students in Biology, Uni. Évreux Val d'Essonne	