

Téo Lemane

16 avenue Darblay

91540 Mennecy

France

📞 0623314420

✉ teo.lemane@genoscope.cns.fr

📁 [tlemane.github.io](https://github.com/tlemanegithub)

🌐 [tlemane](https://tlemane.github.io)



Education

- 2022 **Ph.D in computer science**, *University of Rennes 1, France.*
- 2019 **Master's Degree in bioinformatics, with high honours**, *University of Rennes 1, France.*
Subjects: Algorithmic, sequence analysis, programming, semantic web, combinatorial optimization, machine learning, biological networks, structural biology
- 2017 **Bachelor's Degree: biology of organisms**, *University of Rennes 1, France.*
- 2013 **High School Diploma, scientific option**, *Lycée André Malraux, Allonnes, France.*

Research experiences

- Postdoc** **Metagenomic read classification using pangenome graphs.**
Since January 2025 **Supervisor:** *David Vallenet*
CNRS/Genoscope
LABGeM team
Development of bioinformatic methods to classify and quantify metagenomic reads using pangenome graphs.
- Postdoc** **Large-scale sequence indexing.**
05/2023 - 12/2024 **Supervisor:** *Eric Pelletier*
CEA/Genoscope
LAGE team
Development of bioinformatic methods and tools for large-scale indexing of biological sequences with abundances, including powerful interfaces for end-users.
- Ph.D thesis** **Indexing and analyses of large sequencing collections using k -mer matrices.**
2019 - 2022 **Supervisors:** *Pierre Peterlongo, Rayan Chikhi*
Inria Rennes
GenScale team
Development of bioinformatic methods for constructing k -mer matrices from large sequencing collections. This project focused on making the computational tools necessary to scale up and enable indexing and downstream analyses of these collections.
- MSc2 Internship** **Search engine for genomic sequencing data.**
January - July 2019 **Supervisor:** *Pierre Peterlongo*
Inria Rennes
GenScale team
Study and development of algorithms and methods for indexing sequencing data.
Key words: Algorithmic, probabilistic data structures, indexing, C++ implementation, metagenomic
- MSc1 Internship** **Curation of the metabolic network of *Tisochrysis lutea* using heterogeneous methods.**
April - July 2018 **Supervisor:** *Jeanne Got*
Inria Rennes
Dyliss team
Improvement of the metabolic network quality of *Tisochrysis lutea*, especially the metabolic pathways related to vitamin B12.
Key words: GEMs (Genome-scale metabolic models), flux balance analysis, topological analysis

Publications





- 2024 [preprint] Lucas Elliott, Frédéric Boyer, **Téo Lemane**, Inger Alsos, and Eric Coissac. wholeskim: Utilizing genome skims for taxonomically annotating ancient DNA metagenomes. September 2024 [preprint].
- 2024 Beatriz Willink, Kalle Tunström, Sofie Nilén, Rayan Chikhi, **Téo Lemane**, Michihiko Takahashi, Yuma Takahashi, Erik I. Svensson, and Christopher West Wheat. The genomics and evolution of inter-sexual mimicry and female-limited polymorphisms in damselflies. *Nature Ecology & Evolution*, volume 8, pages 83–97, January 2024. Publisher: Nature Publishing Group.
- 2024 **Téo Lemane**, Nolan Lezsoche, Julien Lecubin, Eric Pelletier, Magali Lescot, Rayan Chikhi, and Pierre Peterlongo. Indexing and real-time user-friendly queries in terabyte-sized complex genomic datasets with kmindex and ORA. *Nature Computational Science*, volume 4, pages 104–109, February 2024. Publisher: Nature Publishing Group.

- 2023 Camila Duitama González, Riccardo Vicedomini, **Téo Lemane**, Nicolas Rascovan, Hugues Richard, and Rayan Chikhi. decOM: similarity-based microbial source tracking of ancient oral samples using k-mer-based methods. *Microbiome*, volume 11, page 243, November 2023.
- 2022 **Téo Lemane**, Paul Medvedev, Rayan Chikhi, and Pierre Peterlongo. kmtricks: efficient and flexible construction of Bloom filters for large sequencing data collections. *Bioinformatics Advances*, volume 2, page vbac029, January 2022.
- 2022 **Téo Lemane**, Rayan Chikhi, and Pierre Peterlongo. kmdiff, large-scale and user-friendly differential k-mer analyses. *Bioinformatics*, volume 38, pages 5443–5445, December 2022.
- 2022 Yoann Dufresne, **Téo Lemane**, Pierre Marijon, Pierre Peterlongo, Amatur Rahman, Marek Kokot, Paul Medvedev, Sebastian Deorowicz, and Rayan Chikhi. The K-mer File Format: a standardized and compact disk representation of sets of k-mers. *Bioinformatics*, volume 38, pages 4423–4425, September 2022.
- 2021 Grégoire Siekaniec, Emeline Roux, **Téo Lemane**, Eric Guédon, and Jacques Nicolas. Identification of isolated or mixed strains from long reads: a challenge met on *Streptococcus thermophilus* using a MinION sequencer. *Microbial Genomics*, volume 7, page 000654, 2021. Publisher: Microbiology Society,.

Talks

- 2022 **Téo Lemane**, Paul Medvedev, Rayan Chikhi, and Pierre Peterlongo. kmtricks: creating bloom filters for indexing large sequencing data collections. JOBIM, 2022.
- 2021 **Téo Lemane**, Rayan Chikhi, and Pierre Peterlongo. Advances in k-mer matrix construction for analysis of large sequencing collections. SeqBIM, 2021.
- 2020 **Téo Lemane**, Paul Medvedev, Rayan Chikhi, and Pierre Peterlongo. kmtricks: Modular k-mer count matrix and Bloom filter construction for large read collections. SeqBIM, 2020.
- 2020 **Téo Lemane**, Rayan Chikhi, and Pierre Peterlongo. HowDeSBT and Simka wedding: what has been done and what we plan to do? DSB, 2020.

Softwares

- kmtricks **Modular k -mer count matrix and Bloom filter construction for large read collections.**
kmtricks is a generic tool suite along with a library for the construction of k -mer matrices and Bloom filters from large sequencing collections. It provides also a C++ plugin system to extend its features.
Availability:  tlemanek/kmtricks
- kmdiff **Large-scale and user-friendly differential k -mer analyses.**
kmdiff is a tool allowing differential k -mer analysis on large cohorts (hundreds of individuals). It uses the concept of k -mer matrix to find differentially represented k -mers between two cohorts, opening the door to large-scale downstream analysis like structural variant detection.
Availability:  tlemanek/kmdiff
- kmindex **Real-time k -mers query in TB-sized banks.**
kmindex is a tool for real-time querying of sequencing samples indexed using kmtricks. It allows to compute the percentage of shared k -mers between a query and each indexed sample. It is the indexing backend of the ORA (<https://ocean-read-atlas.mio.osupytheas.fr>) web service.
Availability:  tlemanek/kmindex
- kmviz **A generic web interface for exploring biological sequence indexes.**
kmviz is a generic web interface and a REST API for interacting with sequence indexes. It connects to multiple, local or distant, sequence indexes to performs sequence queries. Results and metadata can then be explored through interactive tables, plots, sequence views, or maps.
Availability:  tlemanek/kmviz

Teaching

- 2019 - 2022 **String algorithms and bioinformatics**, MSc1 Software Engineering, Istic Univ. Rennes 1, France.

Computer skills

- Systems GNU/Linux (CentOS, Arch, Debian, NixOS), basic knowledge of macOS
- Programming Advanced: C, C++ and Python, Intermediate: JavaScript, Nix and Java
- Perf Engineering Microbenchmarking (gbench, nanobench, hyperfine), Profiling (perf, gprofng, flamegraph), SIMD
- CI/CD Git, Github Actions, GitLab CI, Jenkins
- Packaging RPM, Nix, Conda, Poetry
- Containerization Docker, Singularity, Apptainer, Apptainer, Apptainer

Orchestration	Docker Swarm, basic knowledge of Kubernetes
Workflow	Nextflow, Snakemake
HPC	Slurm, SGE
Cloud	Microsoft Azure (Blob, Batch), basic knowledge of AWS

Languages

French Native
English Advanced

Popular science

- 2021 **Organization of "Sciences en cour[t]s".**
<http://sciences-en-courts.fr>
- 2020 **Production of an animated short film for "Sciences en cour[t]s".**
<http://sciences-en-courts.fr>

Referees

Dr. Pierre Peterlongo

Research Associate, Head of GenScale team

Inria, Rennes, France

✉ pierre.peterlongo@inria.fr

🌐 <http://people.rennes.inria.fr/Pierre.Peterlongo/>

Dr. Rayan Chikhi

Research Associate, Head of Sequence Bioinformatics team

Institut Pasteur, Paris, France

✉ rayan.chikhi@pasteur.fr

🌐 <http://rayan.chikhi.name>

Dr. Eric Pelletier

Research Associate

Genoscope, Évry-Courcouronnes, France

✉ eric.pelletier@genoscope.cns.fr