Karel **BŘINDA**

Inria, Irisa, Univ. Rennes, France

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Research Interests

Bioinformatics / Computational Biology: Algorithms, Genomics, Pathogens, Rapid Diagnostics of Antibiotic Resistance

Academic Appointments

2022–present **Inria: French National Institute for Research in Digital Science and Technology**
Inria Starting Faculty (a permanent PI position), GenScale team, Inria Rennes, France

2022–present **Irisa: Research Institute for Computer Science and Random Systems** (UMR 6074)
Associate Member, Irisa Rennes, France

2017–2021 (5y) **Harvard Medical School & Harvard T.H. Chan School of Public Health**
2019–2021 *Research Associate*, Department of Biomedical Informatics
2018–2019 *Research Associate*, Department of Epidemiology, Center for Communicable Disease Dynamics
2017–2018 *Postdoctoral Research Fellow*, Department of Epidemiology, Center for Communicable Disease Dynamics
Advisors: Michael Baym & William P. Hanage

Education

2013–2016 **Ph.D.**, Computer Science, University of Paris-Est (Paris, France)
Advisors: Gregory Kucherov (CNRS) and Valentina Boeva (Curie Institute & Cochin Institute)
Dissertation: *Novel computational techniques for mapping and classification of Next-Generation Sequencing data*

2011–2013 **MSc (Ing)**, Mathematical Computer Science (with honors), Czech Technical University in Prague, Faculty of Nuclear Sciences and Physical Engineering (Prague, Czechia)

2008–2011 **BSc**, Mathematical Computer Science, Czech Technical University in Prague, Faculty of Nuclear Sciences and Physical Engineering (Prague, Czechia)

Selected Awards and Distinctions

2026 **RECOMB Best Poster Award**, Léo Ackermann, supervised Ph.D. student (senior-author role)
2024 **Stanislav Hanzl Prize**, Veronika Hendrychová, supervised student
2024 **Dean's Prize for Best Computer Science BSc Thesis**, Ondřej Sladký, co-supervised student
2024 **SVOČ winner, best TCS/ML undergraduate thesis in Czechia**, Ondřej Sladký, co-supervised student
2019 **Best Poster Award**, first author, Marvin Zelen Data Science Symposium, Dana-Farber Cancer Institute
2018 **Most Innovative Poster Award**, first author, Lake Arrowhead Microbial Genomics Conference

Funding (>€1M since 2022)

2025–2029 **French National Research Agency: *Young Researchers Program***, Sole PI, €493,385
ReAll: Real-Time Read Alignment to All Bacterial Genomes on Laptops (ANR-24-CE45-1226)

2024–2027 **Inria: *Moyens Incitatifs Ph.D. funding***, Sole PI, equiv. €120,000
Developing Efficient Algorithms for Sublinear Search in Large Genome Databases

2024–2027 **Irisa/University of Rennes: *CDO Ph.D. funding***, Sole PI, equiv. €120,000
Computational Methods for Phylogenetic Compression

2025–2026 **Campus France: *PHC Barrande***, PI, €8,000
EffiMas: Efficient Indexing of Large Genome Collections via Masked Superstrings of k-mers

2024–2026 **Rennes Métropole: *Allocation d'installation scientifique***, Sole PI, €10,000
Développement d'algorithmes efficaces pour la recherche sublinéaire dans de grandes bases de données génomiques

2023–2026 **Inria: *Exploratory Action***, Sole PI, equiv. €275,000
BARD(e): Bacterial Antibiotic Resistance Diagnostics (Enhanced)

2023–2024 **Campus France: *PHC Procope***, PI, €7,600
ReSLo: Novel Reference Structures for Long-Read Dataset Search

2023 **University of Rennes: *Scientific Challenges 2023*** (Interdisciplinary Research Section), PI, €15,000
Development of a Computational Method for Rapid Detection of Antibiotic Resistance in Enterococci

Publications

Complete list: https://scholar.google.com/citations?user=TTaAd_MAAAAJ **>3K citations, h-index 16**

*Shared first-author contribution. †Joint senior authorship.

Preprints

[1] V. Hendrychová and **K. Břinda**, "Why phylogenies compress so well: combinatorial guarantees under the Infinite Sites Model," ***bioRxiv*** 2026.03.18.712055, presented at RECOMB-Seq 2026, 2026. doi:10.64898/2026.03.18.712055.

[2] A. Kaul, F. W. Rossine, **K. Břinda**, and M. Baym, "Novel genes arise from genomic deletions across the bacterial tree of life," ***bioRxiv*** 2026.01.05.697752, 2026. doi:10.64898/2026.01.05.697752.

[3] F. Brunetti and **K. Břinda**, "Optimized k-mer search across millions of bacterial genomes on laptops," ***bioRxiv*** 2025.11.23.690050, 2025. doi:10.1101/2025.11.23.690050.

[4] M. Budia-Silva, A. C. Carroll, H. Ghosh, A. McGeer, T. Giani, G. M. Rossolini, **K. Břinda**, W. P. Hanage, H. Grundmann, D. R. MacFadden, and S. Reuter, "Neighbour typing using long read sequencing provides rapid prediction of sequence type and antimicrobial susceptibility of ***Klebsiella pneumoniae***," ***bioRxiv*** 2025.09.03.673989, 2025. doi:10.1101/2025.09.03.673989.

Journal Articles

[5] J. Plachý, O. Sladký, **K. Břinda**†, and P. Veselý†, "Pareto optimization of masked superstrings improves compression of pan-genome k-mer sets," to appear in ***Journal of Computational Biology***, 2026. doi:10.1177/15578666261491601.

[6] O. Sladký, P. Veselý, and **K. Břinda**, "From superstring to indexing: a space-efficient index for unconstrained k-mer sets using the Masked Burrows-Wheeler Transform (MBWT)," ***Bioinformatics Advances*** **6**(1), p. vbaf290, 2026. doi:10.1093/bioadv/vbaf290.

[7] A. C. Carroll, L. Mortimer, H. Ghosh, S. Reuter, H. Grundmann, **K. Břinda**, W. P. Hanage, A. Li, A. Paterson, A. Purssell, A. M. Rooney, N. R. Yee, B. Coburn, S. Able-Thomas, M. Antonio, A. McGeer, and D. R. MacFadden, "Prediction of genetic relatedness of ***Escherichia coli*** using neighbor typing: a tool for rapid outbreak detection," ***Antimicrobial Agents and Chemotherapy*** **70**(3), p. e01071-25, 2026. doi:10.1128/aac.01071-25.

[8] **K. Břinda**, L. Lima, S. Pignotti, N. Quinones-Olvera, K. Salikhov, R. Chikhi, G. Kucherov, Z. Iqbal, and M. Baym, "Efficient and robust search of microbial genomes via phylogenetic compression," ***Nature Methods*** **22**(4), pp. 692–697, 2025. doi:10.1038/s41592-025-02625-2.

[9] A. C. Carroll, L. Mortimer, H. Ghosh, S. Reuter, H. Grundmann, **K. Břinda**, W. P. Hanage, A. Li, A. Paterson, A. Purssell, A. Rooney, N. R. Yee, B. Coburn, S. Able-Thomas, M. Antonio, A. McGeer, and D. R. MacFadden, "Rapid inference of antibiotic susceptibility phenotype of uropathogens using metagenomic sequencing with neighbor typing," ***Microbiology Spectrum*** **13**(1), p. e01366-24, 2025. doi:10.1128/spectrum.01366-24.

[10] N. B. Wikle*, T. N.-A. Tran*, B. Gentilesco, S. M. Leighow, E. Albert, E. R. Strong, **K. Břinda**, H. Inam, F. Yang, S. Hossain, P. Chan, W. P. Hanage, M. Messick, J. R. Pritchard, E. M. Hanks, and M. F. Boni, "SARS-CoV-2 epidemic after social and economic reopening in three U.S. states reveals shifts in age structure and clinical characteristics," ***Science Advances*** **8**(4), p. eabf9868, 2022. doi:10.1126/sciadv.abf9868.

[11] Y. Che, X. Xu, Y. Yang, **K. Břinda**, W. P. Hanage, C. Yang, and T. Zhang, "High-resolution genomic surveillance elucidates a multilayered hierarchical transfer of resistance between WWTP- and human/animal-associated bacteria," ***Microbiome*** **10**(1), p. 16, 2022. doi:10.1186/s40168-021-01192-w.

[12] **K. Břinda**, M. Baym†, and G. Kucherov†, "Simplitigs as an efficient and scalable representation of de Bruijn graphs," ***Genome Biology*** **22**(1), p. 96, 2021. doi:10.1186/s13059-021-02297-z.

[13] Y. Che, Y. Yang, X. Xu, **K. Břinda**, M. F. Polz, W. P. Hanage, and T. Zhang, "Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes," ***Proceedings of the National Academy of Sciences*** **118**(6), p. e2008731118, 2021. doi:10.1073/pnas.2008731118.

[14] T. N.-A. Tran, N. B. Wikle, E. Albert, H. Inam, E. R. Strong, **K. Břinda**, S. M. Leighow, F. Yang, S. Hossain, J. R. Pritchard, P. Chan, W. P. Hanage, E. M. Hanks, and M. F. Boni, "Optimal SARS-CoV-2 vaccine allocation using real-time attack-rate estimates in Rhode Island and Massachusetts," ***BMC Medicine*** **19**(1), p. 162, 2021. doi:10.1186/s12916-021-02038-w.

[15] **K. Břinda**, A. Callendrello, K. C. Ma, D. R. MacFadden, T. Charalampous, R. S. Lee, L. Cowley, C. B. Wadsworth, Y. H. Grad, G. Kucherov, J. O'Grady, M. Baym, and W. P. Hanage, "Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbour Typing," ***Nature Microbiology*** **5**(3), pp. 455–464, 2020. doi:10.1038/s41564-019-0656-6.

[16] D. R. MacFadden, B. Coburn, **K. Břinda**, A. Corbeil, N. Daneman, D. Fisman, R. S. Lee, M. Lipsitch, A. McGeer, R. G. Melano, S. Mubareka, and W. P. Hanage, "Using genetic distance from archived samples for the prediction of antibiotic resistance in *Escherichia coli*," ***Antimicrobial Agents and Chemotherapy*** **64**(5), p. e02417-19, 2020. doi:10.1128/AAC.02417-19.

[17] B. Grüning*, R. Dale*, A. Sjödin, B. A. Chapman, J. Rowe, C. H. Tomkins-Tinch, R. Valieris, J. Köster, and The Bioconda Team (incl. **K. Břinda**), "Bioconda: sustainable and comprehensive software distribution for the life sciences," ***Nature Methods*** **15**(7), pp. 475–476, 2018. doi:10.1038/s41592-018-0046-7.

[18] **K. Břinda**, V. Boeva, and G. Kucherov, "RNF: a general framework to evaluate NGS read mappers," ***Bioinformatics*** **32**(1), pp. 136–139, 2016. doi:10.1093/bioinformatics/btv524.

[19] **K. Břinda***, M. Sykulski*, and G. Kucherov, "Spaced seeds improve k-mer-based metagenomic classification," ***Bioinformatics*** **31**(22), pp. 3584–3592, 2015. doi:10.1093/bioinformatics/btv419.

[20] **K. Břinda**, E. Pelantová, and O. Turek, "Balances of m-bonacci words," ***Fundamenta Informaticae*** **132**(1), pp. 33–61, 2014. doi:10.3233/FI-2014-1031.

[21] L. Balková, **K. Břinda**, and O. Turek, "Abelian complexity of infinite words associated with quadratic Parry numbers," ***Theoretical Computer Science*** **412**(45), pp. 6252–6260, 2011. doi:10.1016/j.tcs.2011.08.016.

Peer-Reviewed Conference Articles

[22] O. Sladký, P. Veselý, and **K. Břinda**, "Towards efficient k-mer set operations via function-assigned masked superstrings," in *Proceedings of the Prague Stringology Conference 2025 (PSC 2025)*, J. Holub and J. Žďárek, eds., pp. 26–40, 2025. Available from bioRxiv 2024.03.06.583483.

[23] O. Sladký, P. Veselý, and **K. Břinda**, "Masked superstrings as a unified framework for textual k-mer set representations," *RECOMB-Seq 2023*, 2023. Available from bioRxiv 2023.02.01.526717.

[24] P. Červenka, **K. Břinda**, M. Hanousková, P. Hofman, and R. Seifert, "Blind friendly maps: tactile maps for the blind as a part of the public map portal (Mapy.cz)," in *Proceedings of the 15th International Conference on Computers Helping People with Special Needs (ICCHP 2016)*, K. Miesenberger, C. Bühler, and P. Penaz, eds., *Lecture Notes in Computer Science* **9759**, pp. 131–138, 2016. doi:10.1007/978-3-319-41267-2_18.

[25] **K. Břinda**, "Languages of lossless seeds," in *Proceedings of the 14th International Conference on Automata and Formal Languages (AFL 2014)*, Z. Ésik and Z. Fülöp, eds., *Electronic Proceedings in Theoretical Computer Science* **151**, pp. 139–150, 2014. doi:10.4204/EPTCS.151.9.

Technical Reports

[26] **K. Břinda**, V. Boeva, and G. Kucherov, "Ococo: an online variant and consensus caller," *arXiv* 1712.01146 [q-bio.GN], 2018. doi:10.48550/arXiv.1712.01146.

[27] **K. Břinda**, V. Boeva, and G. Kucherov, "Dynamic read mapping and online consensus calling for better variant detection," *arXiv* 1605.09070 [q-bio.GN], 2016. doi:10.48550/arXiv.1605.09070.

Patents

[28] W. P. Hanage, **K. Břinda**, and M. Baym, "Rapid identification of strains from sequence data," ***United States Patent Application*** 17/251,343, US 2021/0246502 A1, 2021.

Theses

[29] **K. Břinda**, "Novel computational techniques for mapping and classification of Next-Generation Sequencing data." Ph.D. thesis, *University of Paris-Est*, 2016.

[30] **K. Břinda**, "Lossless seeds for approximate string matching." MSc thesis, *Czech Technical University*, 2013.

[31] **K. Břinda**, "Abelian complexity of infinite words." BSc thesis, *Czech Technical University*, 2011.

Selected Software

Complete list: `https://github.com/karel-brinda` **>4M downloads***

[SW1] **MiniPhy** – `https://github.com/karel-brinda/miniphy` — Python and Snakemake
Phylogenetic compression of extremely large genome collections.

[SW2] **Phylign** – `https://github.com/karel-brinda/phylign` — Python and Snakemake
BLAST-like alignment across all pre-2019 bacterial genomes on personal computers.

[SW3] **RASE** – `https://github.com/c2-d2/rase-pipeline` — Python, Snakemake, Make, R, and Bash
A proof-of-concept framework for Genomic Neighbor Typing for real-time predictions of antibiotic resistance using nanopore sequencing. Pipeline, tool, library, two species databases (***S. pneumoniae*** and ***N. gonorrhoeae***), skeleton for novel databases, and demonstrations of within-minutes diagnostics from isolates and metagenomes.

[SW4] **ProPhyle** – `https://prophyle.github.io` — Python, C, and C++
An accurate, resource-frugal, and deterministic metagenomic classifier, based on k-mer propagation, simplitigs, and k-mer indexing using the Burrows-Wheeler Transform. [2.4M downloads]

[SW5] **SAMsift** – `https://github.com/karel-brinda/samsift` — Python
Advanced filtering and tagging of SAM/BAM alignments using Python expressions. [606k downloads]

[SW6] **RNFtools** – `https://rnftools.github.io` — Python
A generic format for naming simulated sequencing reads using arbitrary tools and the associated toolkit and pipeline for read simulation and read mapper evaluation. [518k downloads]

[SW7] **Ococo** – `https://github.com/karel-brinda/ococo` — C++
Online variant and consensus caller, based on streaming and maintaining variant statistics in small counters per individual genomic position, which enables real-time analysis of unsorted SAM/BAM data. [128k downloads]

[SW8] **ProphAsm** – `https://github.com/prophyle/prophasm` — C++
A tool for rapid and memory-efficient computation of simplitigs and set operations with k-mer sets. [41k downloads]

* Cumulative sum of the statistics from Bioconda and Biocontainers

Teaching

2023–present **École normale supérieure de Rennes** (ENS Rennes)

BOX: Experimental Bioinformatics (MSc level, lecturer) [4 semesters]

- An introductory Bioinformatics course for ENS master's students in theoretical computer science.

2019–2020 **Harvard Medical School – Department of Biomedical Informatics**

BMIF 201: Concepts in Genome Analysis (Ph.D. level, TA) [1 semester]

- An introductory Computational Biology course for Harvard Ph.D. students.
- Recitations, grading, mentoring the students, supervision of the final projects.
- Close collaboration with the four faculty members responsible for the course: Michael Baym, Heng Li, Cheng-Zhong Zhang, and Shamil Sunyaev.

2009–2013 **Czech Technical University in Prague – Faculty of Nuclear Sciences and Physical Engineering**

01ASTE Assistive Technology (MSc level, instructor) [3 semesters]

01SWP Software Project 1, 2 (MSc level, supervisor) [4 semesters]

Supervision

Awards are marked by ⋆

Postdoctoral Fellows

2023–2025 **Loren Dejoies**, *Inria*, Postdoctoral Researcher
– Currently: *Permanent Clinical Microbiologist @Limoges University Hospital*

Ph.D. Students

2024–present **Léo Ackermann**, *Inria*, Ph.D. student, co-supervised with P. Peterlongo
⋆ *RECOMB Best Poster Award 2026*

2024–present **Tam Truong**, *Irisa*, Ph.D. student, co-supervised with P. Peterlongo and D. Lavenier

2022–2026 **Francesca Brunetti**, *Sapienza University of Rome*, Ph.D. student, co-supervised with M. Conte

2023–2024 **Arya Kaul**, *Harvard Medical School*, visiting Ph.D. student
⋆ ***Chateaubriand fellow*** (program for outstanding American Ph.D. students to research in France)

Master's Students

2026–present **Ján Plachý**, *Charles University in Prague*, MSc project and thesis, co-supervised with P. Veselý

2025–2026 **Marie Picard**, *ENS Rennes*, MSc project, co-supervised with L. Ackermann

2023–2026 **Veronika Hendrychová**, *Czech Technical University in Prague*, MSc student
⋆ ***Stanislav Hanzl Prize 2024*** for the 9 best students at Czech Technical University

2024–2025 **Amory Antao**, *ENS Rennes*, MSc research project, co-supervised with R. Vicedomini

2022–2023 **Léo Laffeach**, *ENS Rennes*, MSc research project, co-supervised with P. Peterlongo and G. Gourdel

2017–2018 **Simone Pignotti**, MSc research project at *Harvard Medical School*, co-supervised with M. Baym
– Currently: *Bioinformatics Team Leader @Eligo Bioscience*

2015–2016 **Mikhail Dubov**, *University of Paris-Est*, MSc research project, co-supervised with G. Kucherov
– Currently: *Senior Machine Learning Engineer @Meta*

Bachelor Students

2026 **Mohamed Anas Malki**, *ENS Rennes*, summer internship

2022–2024 **Ondřej Sladký**, *Charles University in Prague*, BSc project and thesis, co-supervised with P. Veselý
⋆ ***Dean's Prize for the best CS BSc thesis*** (Faculty of Mathematics and Physics, Charles University)
⋆ ***Best 2024 TCS/ML undergrad thesis in Czechia*** (Winner of SVOČ 2024)
– Currently: *MSc student at ETH Zurich*

2024 **Ulysse McConnell**, *ETH Zurich*, summer internship project, co-supervised with D. Lavenier

2022–2023 **Veronika Hendrychová**, *Czech Technical University in Prague*, BSc thesis, co-supervised with Ľ. Dvořáková
⋆ ***2nd Place Award for Best Math undergrad thesis at Czech Tech. University*** (Rektorys Competition 2024)

2022–2023 **Ekaterina Milyutina**, *Charles University in Prague*, BSc thesis, co-supervised with P. Veselý

Related Work Experience

2005–2012 **Software Engineer / Assistive Technology Specialist**, Czech Technical University in Prague
Major achievement: Co-developed Hapticke.Mapy.com, automatically generated tactile maps for blind users. Time to create a tactile map for any part of the world *reduced from several weeks to under five minutes*. **Industrial collaboration with Seznam.cz, the biggest Czech Internet company.**

Selected Media Coverage

2026 **Radio Prague International – *Science without Borders*** — Link
An interview about my academic career and research.

2025 **Sciences Ouest (2025/9, N°431) – *Mieux caractériser l'antibiorésistance***
A popularization article about our research on antibiotic resistance.

2025 **Inria Émergences – *Diagnostiquer plus vite la résistance aux antibiotiques*** — Link
A popularization article about our research on faster resistance diagnostics.

2020 **BBC World Service – *Science in Action*** — Link
An interview about our paper on rapid diagnostics of antibiotic resistance by Genomic Neighbor Typing.

2020 **The Bioinformatics Chat – *Spectrum-preserving string sets and simplitigs*** — Link
An interview about our paper on simplitigs.

2020 **Massive Science – *Rapid DNA sequencing of unknown bacteria helps doctors choose which antibiotics to treat it with*** — Link
A popularization article on how our method of rapid diagnostics could help doctors prescribe antibiotics better.

Talks (last 10 years)

Invited Talks

2026 **Faculty of Medicine, Masaryk University**, Research Day 2026 – **Keynote**: *Across continents, languages, and disciplines: from combinatorics to rapid diagnostics of antibiotic resistance.* Brno, Czechia.

2026 **Sapienza University of Rome**, Department of Public Health and Infectious Diseases: ***From bacteria to bits and back again: towards faster, more accurate, and smarter diagnostics of antibiotic resistance.*** Rome, Italy.

2025 **Embassy of the Czech Republic in Paris**, Annual Czech-French Science Meetup – **Keynote**: ***From bacteria to bits and back again: faster, more accurate, and smarter diagnostics of antibiotic resistance.*** Paris, France.

2024 **EMBL-EBI**, K-mer/Sequence Indexing Workshop: ***Efficient search of microbial genomes via phylogenetic compression.*** Hinxton, UK.

2023 **Charles University in Prague**, Bioinformatics seminar: ***Efficient search of microbial genomes via phylogenetic compression.*** Prague, Czechia.

2023 **Sorbonne University**, Graphs and Bioinformatics 2023: ***K-mers and their graphs in computational biology.*** Paris, France.

2023 **Alpaca/Pangaia**, joint seminar of the two international pan-genomic consortia: ***Efficient and robust search of microbial genomes via phylogenetic compression.*** Online.

2023 **Institute of Medical Microbiology, University Hospital of Düsseldorf**, Dilthey group seminar: ***Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbor Typing.*** Düsseldorf, Germany.

2023 **École normale supérieure**, CPM 2023 Summer School: ***Under the hood: the role of string algorithms in contemporary biological research.*** Paris, France.

2022 **Irset University of Rennes / EHESP French School of Public Health**, The Irset Seminar: ***Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbor Typing.*** Rennes, France.

2022 **CRIStAL Lille**, Bioinformatics seminar: ***Efficient and robust search of microbial genomes via phylogenetic compression.*** Lille, France.

2022 **JOBIM 2022**, The Indexing Minisymposium: ***The tree of life enables efficient and robust compression and search of microbes.*** Rennes, France.

2021 **ICCMG 5**, Fifth International Conference on Clinical Metagenomics: ***Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbor Typing.*** Geneva, Switzerland (remote).

2021 **LIRMM Montpellier**, Methods and Algorithms for Bioinformatics Seminar: ***Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbor Typing.*** Montpellier, France (remote).

2020 **BAARN 2020**, Boston Area Antimicrobial Research Network Symposium: ***Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbor Typing.*** Boston, USA (remote).

2019 **Harvard MSI**, Microbiology Chalk Talk Seminar: ***Rapid inference of antibiotic resistance and susceptibility by Genomic Neighbor Typing.*** Cambridge, USA.

2019 **MIT CSAIL/MIT Department of Mathematics**, Bioinformatics Seminar: ***Lineage calling can identify antibiotic resistant clones within minutes.*** Cambridge, USA.

Other Talks

2026 **RECOMB-Seq 2026**: *Why phylogenies compress so well: combinatorial guarantees under the Infinite Sites Model*. Thessaloniki, Greece.

2025 **Data Structures in Bioinformatics 2025**: *Masked superstrings as a compact, indexable, and dynamic representation of k-mer sets*. Pisa, Italy.

2024 **SeqBIM 2024**: *Masked superstrings as a compact, indexable, and dynamic representation of k-mer sets*. Rennes, France.

2024 **Stringmasters 2024**: *Developing the phylogenetic transform*. Czech Technical University in Prague, Czechia.

2023 **Pan-genomics – metagenomics workshop (PHC Procope)**: *Towards comprehensive sequence data search engines*. Heinrich Heine University Düsseldorf, Germany.

2022 **Data Structures in Bioinformatics 2022**: *Efficient and robust search of microbial genomes via phylogenetic compression*. Düsseldorf, Germany.

2021 **Data Structures in Bioinformatics 2021**: *All microbes on a flash drive*. Milan, Italy (remote).

2021 **Human Technopole**: *Genome search to combat antibiotic resistance*. Milan, Italy (remote).

2021 **Helmholtz Centre for Infection Research**: *Algorithms to combat antibiotic resistance*. Braunschweig, Germany (remote).

2020 **Human and Biotechnology at TU Graz**: *Algorithms to combat antibiotic resistance*. Graz, Austria (remote).

2018 **Jonathan Freeman Symposium on the Epidemiology of Infectious Disease 2018**: *Lineage calling can identify antibiotic resistant clones within minutes*. Boston, USA.

2017 **Permafrost workshop on bacterial evolution 2017**: *Efficient phylogeny-based metagenomic classification*. Bormio, Italy.

Service and Organization

Program Committees

2026 **SeqBIM 2026** Workshop Program Committee

2026 **ECCB 2026** Conference Program Committee

2025 **SeqBIM 2025** Workshop Program Committee

2025 **ISMB/ECCB 2025** Conference Program Committee

2024 **SeqBIM 2024** Workshop Program Committee

2023 **SeqBIM 2023** Workshop Program Committee

2023 **ISMB/ECCB 2023** Conference Program Committee

2022 **SeqBIM 2022** Workshop Program Committee

2021 **ISMB/ECCB 2021** Conference Program Committee

Organizing Committees

2026 **CiE 2026 (Computability in Europe)** Session on Natural Computing and Bioinformatics, co-organizer

2024 **SeqBIM 2024** Workshop Organizing Committee

2023 **Inria Rennes Intercultural Workshop** Organizing Committee

2022 **JOBIM 2022** Session on Indexing, co-organizer

Ph.D. Committees

2021–present **Doctoral Advisory Committees**
Emile Breton (Mathematics Institute of Rennes, Univ. Rennes, France)
Khodor Hannoush (Irisa, Univ. Rennes, France)

2022 **Dissertation Committee**
Yoshihiro Shibuya (LIGM, Gustave Eiffel University, France)

Reviewing Activities

2014–present **Reviewer for Journals**
Nature Biotechnology, Nature Communications, Genome Research, Genome Biology, Bioinformatics, ASM mSystems, PCI Math & Comp Biol, Microbial Genomics, NAR Genomics and Bioinformatics, PeerJ, Journal of Bioinformatics and Computational Biology

2014–present **Reviewer for Conferences**
RECOMB, ISMB, ECCB, HitSeq, WABI, SPIRE, WALCOM, ICCHP

Others

2014–2016 **Czech Students and Young Professionals Organization in France**
Organized events for incoming scholars, in collaboration with the *Embassy of the Czech Republic in Paris*.

2010–2013 **Academic Senate of the FNSPE Czech Technical University in Prague**
Served as an elected student representative and **vice-chair of the senate**.

2008–2013 **FNSPE Student Association, CTU International Student Club, Technical Break, AEGEE Prague**
Member and event organizer across Prague student associations (incl. summer/winter camps and scavenger hunts).

2010 **Ministry of the Interior** of the Czech Republic
Served as a member of the Working Group for Accessible Documents.