

Sébastien Roch

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Employment

Vilas Distinguished Achievement Professor, Department of Mathematics, UW–Madison (2024–)
Professor, Department of Mathematics, UW–Madison (2016–)

- Other affiliations: Affiliate Faculty, Department of Statistics, UW–Madison

Associate Professor (with tenure), Department of Mathematics, UW–Madison (2013–2016)

Tenure-track Assistant Professor, Department of Mathematics, UW–Madison (2012–2013)

Tenure-track Assistant Professor, Department of Mathematics, UCLA (2009–2012)

- Other affiliations: Core Member, UCLA Interdepartmental Program in Bioinformatics

Post-Doctoral Researcher, Microsoft Research (2007–2009)

Education

Ph.D., Statistics, UC Berkeley (2007)

M.Sc.A., Applied Mathematics, Polytechnique de Montréal, Canada (2003)

B.Eng., Engineering Physics, Polytechnique de Montréal, Canada (2002)

Diplôme d'Ingénieur, Ecole Polytechnique, France (2001)

Selected Honors

Plenary Speaker, SIAM Conference on Discrete Mathematics (DM24)

2024 IMS Medallion Lecture

Vilas Distinguished Achievement Professorship (2024–)

Van Vleck Research Professorship Award (2023–2027)

2022 Fellow of the Institute of Mathematical Statistics (IMS)

Vilas Associates Award, UW-Madison (2019–2021)

Best Paper Award, RECOMB 2018

2018 Simons Fellow in Mathematics

Honorable Mention – 2018 Marcus W. Feldman Prize in Theoretical Population Biology

NSF CAREER Award (2012-2017)

Kavli Fellow, National Academy of Sciences (2014, 2017)

Invited Address, AMS Central Fall Sectional Meeting (2015)

Alfred P. Sloan Research Fellowship (2012-2014)

Funding

Current

Vilas Distinguished Achievement Professorship Award (2024-2026)

Van Vleck Research Professorship Award (2023-2027)

NSF grant DMS-2308495 (2023-2026), “Principled phylogenomic analysis without gene tree estimation,” PI, \$295,263

NSF grant DMS-2023239 (2020-2025), “TRIPODS: Institute for Foundations of Data Science,” co-PI, \$4,583,262 (overall institute budget: \$12.5 million)

Past

NSF grant DMS-1916378 (2019-2023), “Scalable Statistical Inference in Small-World Networks,” PI, \$299,999

NSF grant DMS-1902892 (2019-2023), “Scalable Model-Based Reconstruction of Network Evolution,” co-PI, \$724,239

Vilas Associates Award (2019-2021)

NSF grant CCF-1740707 (2017-2021), “TRIPODS: Institute for Foundations of Data Science,” co-PI, \$1,499,523

NSF grant DMS-1614242 (2016-2020), “Probability Questions in Phylogenetics,” PI, \$194,000

Simons Fellowship (2018-2019)

SQuaRE on “Mathematical modeling of adaptive biological networks,” American Institute of Mathematics (AIM), jointly with Karen Alim, Eleni Katifori, Marcus Roper (2015-2016)

NSF grant DMS-1149312 (2012-2017), “CAREER: Phylogenomics - New Computational Methods through Stochastic Modeling and Analysis,” PI, \$444,405

Alfred P. Sloan Research Fellowship (2012-2014)

NSF grant DMS-1007144 (2010-2013), “Probabilistic Techniques in Mathematical Phylogenetics,” PI, \$171,000

Professional Activities

Boards

Governing Board and Site Committee, Institute for Foundations of Data Science (TRIPODS Phase II), University of Washington/UW–Madison/UCSC/UChicago (2020-)

Executive Committee, Institute for Foundations of Data Science (TRIPODS Phase I), UW–Madison (2017-2020)

Editorial Boards and Program Committees

Great Lakes Bioinformatics Conference (GLBIO), 2019, 2021, 2024

Workshop on Algorithms in Bioinformatics (WABI), 2019, 2021, 2022

Associate Editor, *Annals of Applied Probability* (2013-2018)

Annual International Conference on Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB), 2013-2016

ACM-SIAM Symposium on Discrete Algorithms (SODA), 2009

Organizational Work

Co-organizer, Workshop on “Contemporary challenges in large-scale sequence alignments and phylogenies: bridging theory and practice,” IMSI (to be held August 2025)

Organizing committee, Program on “Meeting the Genomics Data Challenge: Theory, Methods, and Applications of Quantitative Phylogenomics” at the Institute for Computational and Experimental Research in Mathematics (ICERM) (to be held Fall 2024; leads: Elizabeth Allman, Laura Kubatko).

Organizing committee, Program on “Mathematics of Evolution-Phylogenetic Trees and Networks” at the Institute for Mathematical Sciences (IMS) of the National University of Singapore (Sep 2023; leads: Louxin Zhang, Daniel Huson).

Co-organizer, IFDS-MADLab Summer School 2021, UW-Madison (July 2021; hybrid)

Scientific Committee, 41st Midwest Probability Colloquium, Northwestern University (October 2019)

Co-organizer, Special Session on “Recent Trends in the Mathematics of Data,” AMS Fall Central Sectional Meeting, UW–Madison (September 2019)

Organizer, Invited Session on “Biomedical Applications of Stochastic Processes,” 41st Conference on Stochastic Processes and their Applications (SPA) (July 2019)

Organizing committee, Summer School on “Fundamentals of Data Analysis,” Institute for Foundations of Data Science, UW–Madison (July 2018)

Co-organizer, Special session on “Probability Theory,” AMS Central Fall Sectional Meeting (October 2015)

Co-organizer, Workshop on “Multiple Sequence Alignment,” IPAM (January 2015)

Co-organizer, Second reunion workshop on “High-Throughput Genomics,” Lake Arrowhead, IPAM (June 2014)

Co-organizer, First reunion workshop on “High-Throughput Genomics,” Lake Arrowhead, IPAM (June 2013)

Organizing committee, Long program on “Mathematical Approaches in High-Throughput Genomics,” IPAM (Fall 2011)

Chair, Workshop on “Evolutionary Genomics,” IPAM (November 2011)

Co-organizer, Tutorials on “High-Throughput Genomics,” IPAM (September 2011)

Co-organizer, Special session on “Probability and Related Fields,” AMS Western Fall Sectional Meeting (October 2010)

Co-organizer, Computational Aspects of Biological Information Workshop, Microsoft Research (December 2007)

Organizer, Session on “Bioinformatics,” INFORMS Annual Meeting (October 2008)

Reviewer

Journals: Algorithms for Molecular Biology, American Mathematical Monthly, Annals of Applied Probability, Annals of Combinatorics, Annals of Probability, Annals of Statistics, Applied Mathematics Letters, Bioinformatics, Bioinformatics Advances, Biometrika, Computational Biology and Chemistry, Electronic Communications in Probability, Electronic Journal in Probability, Genome Biology and Evolution, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Transactions on Automatic Control, Information and Inference: A Journal of the IMA, Journal of Applied Probability, Journal of Classification, Journal of Computer and System Sciences, Journal of Mathematical Biology, Journal of the Royal Statistical Society: Series B, Journal of Theoretical Biology, Molecular Biology and Evolution, Nature Communications, Proceedings of the National Academy of Sciences (PNAS), PLOS ONE, PLOS Computational Biology, Random Structures and Algorithms, Science, SIAM Journal on Applied Algebra and Geometry, SIAM Journal on Computing, SIAM Journal on Discrete Mathematics, Soft Computing, Systematic Biology, Theoretical Population Biology.

Conferences: ACM Conference on Electronic Commerce (EC), ACM-SIAM Symposium on Discrete Algorithms (SODA), ACM Symposium on Theory of Computing (STOC), Algorithmic Learning Theory (ALT), Conference on Learning Theory (COLT), IEEE Symposium on Foundations of Computer Science (FOCS), Great Lakes Bioinformatics Conference (GLBIO), International Conference on Intelligent Systems for Molecular Biology (ISMB), Innovations in Theoretical Computer Science (ITCS), Pacific Symposium on Biocomputing (PSB), International Workshop on Randomized Techniques in Computation (RANDOM), Annual International Conference on Research in Computational Molecular Biology (RECOMB), Workshop on Algorithms in Bioinformatics (WABI).

University/Departmental Committees

UW–Madison: served on Ad hoc committee for Applied Math Masters (chair), Awards Committee, Budget Committee, Cluster Hire Search Committee (chair), Colloquium Committee, Computer Sciences and Statistics Liaison, Data Science Major Program Committee, Early Undergraduate Program Committee, Faculty Affairs Committee, Faculty Senate, Fundraising/Newsletter Committee, Graduate Admissions Committee, Graduate Program Committee, Hiring Committee, L&S Academic Planning Council, L&S Data Science Major Working Group, MA Advising Committee, Salary Committee (chair), Undergraduate Advising Committee

UCLA: served on Analysis Qualifying Exam Committee, Bioinformatics Interdepartmental Program, Graduate Studies Committee, Graduate Admissions Committee, Mathematics/Economics

Interdepartmental Program, Program in Computing Committee, Staff Search Committee, UCLA Systems and Integrative Biology (SIB) Training Program

Academic Visits

Fall 2018-Spring 2019: Wisconsin Institute for Discovery, Madison, WI

Spring 2017: Research member, MSRI, Berkeley

Spring 2014: Long-term visitor, Simons Institute for the Theory of Computing, UC Berkeley

Fall 2011: Program organizer, Institute for Pure and Applied Mathematics (IPAM), UCLA

Fall 2009: Visiting scholar, Institute for Pure and Applied Mathematics (IPAM), UCLA

September 2007: Visitor, Phylogenetics Programme, Isaac Newton Institute, Cambridge

Summer 2006: Intern, Microsoft Research, Redmond, WA

Summer 2005: Visitor, Program for Evolutionary Dynamics, Harvard

Summer 2004: Visitor, Computer Science and Artificial Intelligence Laboratory, MIT

Courses Taught

UW-Madison

Spring 2024: MATH 535 – Mathematical Methods in Data Science (Undergraduate)

Fall 2023: MATH 833 – Topics in the Theory of Probability (Graduate)

Spring 2023: MATH 632 – Introduction to Stochastic Processes (Undergraduate)

Fall 2022: MATH 535 – Mathematical Methods in Data Science (Undergraduate)

Spring 2022: 2×MATH 535 – Mathematical Methods in Data Science (Undergraduate)

Fall 2021: MATH 888 – Topics in Mathematical Data Science (Graduate)

Fall 2020: MATH 833 – Topics in the Theory of Probability (Graduate)

Fall 2020: MATH 535 – Mathematical Methods in Data Science (Undergraduate)

Spring 2020: MATH 535 – Mathematical Methods in Data Science (Undergraduate)

Fall 2019: MATH 431 – Introduction to the Theory of Probability (Undergraduate)

Fall 2019: 2×MATH 431 – Introduction to the Theory of Probability (Undergraduate)

Spring 2018: MATH 734 – Theory of Probability II (Graduate)

Fall 2017: MATH 833 – Topics in the Theory of Probability (Graduate)

Fall 2017: MATH 431 – Introduction to the Theory of Probability (Undergraduate)

Fall 2016: 2×MATH 632 – Introduction to Stochastic Processes (Undergraduate)

Spring 2016: 2×MATH 632 – Introduction to Stochastic Processes (Undergraduate)

Fall 2015: MATH 632 – Introduction to Stochastic Processes (Undergraduate)

Spring 2015: MATH 632 – Introduction to Stochastic Processes (Undergraduate)
Fall 2014: MATH 833 – Topics in the Theory of Probability (Graduate)
Fall 2014: MATH 632 – Introduction to Stochastic Processes (Undergraduate)
Fall 2013: MATH 331 – Introduction to Probability and Markov Chains (Undergraduate)
Fall 2013: MATH 632 – Introduction to Stochastic Processes (Undergraduate)
Fall 2013: MATH 733 – Theory of Probability I (Graduate)
Fall 2012: MATH 213 – Calculus and Introduction to Differential Equations (Undergraduate)
Fall 2012: MATH 833 – Topics in the Theory of Probability (Graduate)

UCLA

Spring 2012: MATH 32B – Calculus of Several Variables (Undergraduate)
Spring 2012: MATH 285J – Applied Probability: An Introduction (Graduate)
Winter 2012: MATH 32B – Calculus of Several Variables (Undergraduate)
Winter 2012: MATH 275B – Probability Theory (Graduate)
Spring 2011: MATH 182 – Algorithms (Undergraduate)
Winter 2011: MATH 275B – Probability Theory (Graduate)
Fall 2010: MATH 275A – Probability Theory (Graduate)
Spring 2010: MATH 285K – Topics in Probability: Stochastic Processes in Evolution and Genetics (Graduate)
Winter 2010: MATH 275B – Probability Theory (Graduate)

Ecole Polytechnique–Montréal

Fall 2002: MTH 2305 – Probability for Engineers [in French] (Undergraduate)

Students and Postdocs

Postdocs Mentored

David Clancy, Van Vleck Assistant Professor/IFDS Postdoc, UW–Madison, Mathematics (2022-)
Wai-Tong (Louis) Fan, Van Vleck Assistant Professor, UW–Madison, Mathematics (2015-2018);
currently Tenure-track assistant professor at Indiana University Bloomington

Graduate Students Supervised

Hongyi Huang, Ph.D., Mathematics, UW–Madison (2022-)
Max Bacharach, Ph.D., Mathematics, UW–Madison (graduated 2023)
Yu Sun, Ph.D., Mathematics, UW–Madison (graduated 2023)

Shuqi Yu, Ph.D., Mathematics, UW–Madison (graduated 2023)
Changhun Jo, Ph.D., Mathematics, UW–Madison (graduated 2022)
Brandon Legried, Ph.D., Mathematics, UW–Madison (graduated 2020)
Harrison Rosenberg, Master of Science, ECE, UW–Madison (graduated 2019)
Kun-Chieh (Jason) Wang, Ph.D., Mathematics, UW–Madison (graduated 2017)

Ph.D. Prelim and/or Thesis Committee Member

Lloyd Kirk, UW–Madison, Integrative Biology
Sijia Fang, UW–Madison, Statistics
Jingcheng Xu, UW–Madison, Statistics
Lorenzo Najt, UW–Madison, Mathematics
Aidan Howells, UW–Madison, Mathematics
Jeffrey Covington, UW–Madison, Mathematics
Fan Chen, UW–Madison, Statistics
Changhun Jo, UW–Madison, Mathematics
Christopher McAllester, Genetics
Benjamin Mark, UW–Madison, Mathematics
Yilin Zhang, UW–Madison, Statistics
Heng Guo, UW–Madison, Computer Sciences
Lam Si Tung Ho, UW–Madison, Statistics
Gautam Dasarathy, UW–Madison, ECE
Hakan Seyalioglu, UCLA, Mathematics
Pejman Mahboubi, UCLA, Mathematics
Alexander Vandenberg-Rodes, UCLA, Mathematics

REU Students Supervised

Spring/Summer 2023: Carina Guo (through WISCERS)
Fall 2022: Achutha Balaji, Yuheng Cai, Laura Huang, Megan Lolling, Mengwei Sun (through Madison Experimental Mathematics (MXM) Lab)
Spring 2022: Achutha Balaji, Binhao Chen, Nitit Jongsawatsataporn, Jingde Wang (through Madison Experimental Mathematics (MXM) Lab)
Summer 2016: Periwinkle Doerfler, Zonglin Han, Calvin Kosmatka, Sonya Loberger (supported by NSF CAREER)
Summer 2010: Angela Dauer (supported by UC LEADS program)

Talks

Invited Lectures & Plenary Talks

Plenary Talk, SIAM Conference on Discrete Mathematics (DM24) (July 2024)

IMS Medallion Lecture, Seminar on Stochastic Processes, Rice University (March 2024)

Workshop on “Foundations of Phylogenetic Networks,” Program on “Mathematics of Evolution – Phylogenetic Trees and Networks,” Institute for Mathematical Sciences, NUS, Singapore (September 2023)

Southeastern Probability Conference, UNC-Chapel Hill (August 2022)

Session on “Probabilistic Models in Biology,” Bernoulli-IMS One World Symposium (August 2020; pre-recorded talk and live session)

Session on “Stochastic Population Models,” 41st Conference on Stochastic Processes and their Applications (SPA 2019) (July 2019)

Special Session on “Combinatorial and Experimental Methods in Mathematical Phylogeny,” AMS Spring Central and Western Joint Sectional Meeting 2019 (March 2019)

Tutorial speaker, 40th Midwest Probability Colloquium (October 2018)

Tutorial on “Probability on Graphs: Techniques and Applications to Data Science,” Summer School on “Fundamentals of Data Analysis,” Institute for Foundations of Data Science, UW-Madison (July 2018)

Session “Stochastic models and phylogenetics,” 40th Conference on Stochastic Processes and Their Applications (SPA 2018) (July 2018)

LPSM (Laboratoire de Probabilités, Statistiques et Modélisation) Kickoff Conference (July 2018)

EURANDOM workshop on “Community detection and network reconstruction” (declined)

Minisymposium on “Discrete Mathematical Biology,” SIAM Annual Meeting, July 2017

Southeast Probability Conference, Duke, May 2017

Bernard Moret’s Festschrift, UC Berkeley, June 2017 (declined)

BIRS Workshop on “Mathematical Approaches to Evolutionary Trees and Networks,” 2017 (declined)

Evolution 2016 spotlight session on “Next-generation Phylogenetic Inference” (June 2016)

2016 Phylogenomics Symposium and Software School, Austin, TX (June 2016)

Plenary talk, Frontier Probability Days 2016, University of Utah, Salt Lake City, UT (May 2016)

Invited Address, 2015 AMS Central Fall Sectional Meeting (October 2015)

CIRM Conference on Probability and Biological Evolution (2015) (declined)

IPAM Workshop on “Multiple Sequence Alignment” (2015)

Session on “Origin and Evolution of Bacterial Genomes,” 2014 Canadian Mathematical Society Winter Meeting (declined)

Session on “Hidden Markov Models,” 2014 Latin American Congress on Probability and Mathematical Statistics (declined)

IPAM Second Reunion Workshop for “High-throughput Genomics” (2014)

Workshop on “New Directions in Probabilistic Models of Evolution,” Simons Institute for the Theory of Computing (2014)

Seminar on Stochastic Processes 2014, held at University of California, San Diego (March 2014)

2013 Meeting on Mathematical Statistics, Centre International de Rencontres Mathématiques (CIRM), Luminy, France (December 2013)

Workshop on “Branching Diffusions and Random Trees,” Thematic Semester on Biodiversity and Evolution, Centres de Recherches Mathématiques (CRM), Montréal (August 2013)

IPAM First Reunion Workshop for “High-throughput Genomics” (2013)

Guest lecture in a course on “Advanced Topics in Machine Learning and Decision Making” (STAT 241B), UC–Berkeley (April 2013)

Special Session on “Probabilistic and Multiscale Modeling Approaches in Cell and Systems Biology,” AMS Spring Central Sectional Meeting, Iowa State University, Ames, IA (April 2013)

Symposium and Workshop on “New Methods for Phylogenomics and Metagenomics,” UT–Austin (February 2013)

Fourth Annual University of Wisconsin–Madison Symposium on Integration of Mathematical and Biological Sciences (MathBio 4: Scale), Wisconsin Institute of Discovery (2012)

IPAM Workshop on “Mathematical Challenges in Graphical Models and Message-Passing Algorithms” (2012)

Theory of Computation as a Lens on the Sciences, UC Berkeley (2011)

Stochastic Networks Workshop (2010)

Southern California Probability Symposium (2009)

IPAM Workshop on “Probabilistic Techniques and Applications” (2009)

Computational Aspects of Biological Information Workshop, Microsoft Research (2008)

Session on “Applications of Algebraic Geometry,” AMS Fall Western Section Meeting (2008)

Complexity in Jerusalem (2008)

BIRS Workshop on “Phase Transitions, Hard Combinatorial Problems and Message Passing Algorithms” (2008)

Bay Area Biosystematists Meeting (2007)

IPAM Workshop on “Random and Dynamic Graphs and Networks” (2007)

DIMACS Workshop on “Phase Transitions in Random Structures and Algorithms” (2007)

Seminars & Colloquia

2023-2024: Statistics Seminar, Northwestern (January 2024); Mathematical Biology Seminar, UPenn (April 2024)

2021-2022: SILO Seminar, UW-Madison; IFDS Monthly Seminar, University of Washington, Seattle (virtual)

2020-2021: Graduate Colloquium, Northern Illinois University; Probability Seminar, UIUC; Probability Seminar, UC Davis

2019-2020: Statistics Seminar, University of Michigan; Statistics Seminar, Ohio State; Evolution Seminar, UW-Madison

2018-2019: Mathematics Colloquium, University of Delaware

2017-2018: IFDS Brown Bag, UW-Madison; Probability Seminar, UW-Madison

2016-2017: Computational Biology, Ecology, & Evolution (ComBEE) group meeting (declined), UW-Madison; Stochastics and Statistics Seminar, MIT

2015-2016: Probability Seminar, UW-Madison (October 2015); Applied Algebra Seminar, UW-Madison; Mathematical Biology Seminar, UPenn; QBio Seminar, UW-Madison; ORFE Colloquium, Princeton; Statistics Colloquium, UC Davis (declined); Probability Seminar, UW-Madison (March 2016); Probability Seminar, UIUC (cancelled)

2014-2015: Statistics Colloquium, Penn, Wharton School of Business; Probability Seminar, University of Chicago

2013-2014: Very Informal Seminar, Wisconsin Institute of Discovery; Probability Seminar, UC Davis; Ideas and Open Problems Session, Simons Institute for the Theory of Computing; Algebraic Statistics Seminar, UC-Berkeley (declined)

2012-2013: Probability Seminar, University of Wisconsin, Madison; Applied and Computational Mathematics Seminar, University of Wisconsin, Madison; SILO Seminar, University of Wisconsin, Madison; Statistics Seminar, University of Wisconsin, Madison; Probability Seminar, Cornell; Theory Colloquium, MIT

2011-2012: High-Throughput Genomics Seminar, IPAM; Biomathematics Seminar, Penn; Statistics Colloquium, University of Chicago; Probability Seminar, Ohio State University; Probability Seminar, UBC; Department Colloquium, UBC; Departmental Colloquium, University of Toronto; Statistics Seminar, University of Michigan, Ann Arbor; Mathematics Colloquium, University of Michigan, Ann Arbor; Mathematics Colloquium, University of Wisconsin, Madison;

2010-2011: Theory Colloquium, MIT; Probability Seminar, UC Berkeley; Algorithms and Randomness Center (ARC) Colloquium, GA Tech; Probability Seminar, UCLA

2009-2010: Applied Mathematics Colloquium, UCLA; Bioinformatics Seminar, UC Berkeley; Bioinformatics Retreat, UCLA; Statistics Seminar, UCLA; IPAM Retreat, Lake Arrowhead; Bioinformatics Seminar, UCLA; CIPRES Meeting, UC Berkeley

2008-2009: Probability Seminar, MIT; Center for Computational Molecular Biology Seminar, Brown University

2007-2008: Neyman Seminar, UC Berkeley; Mathematics Colloquium, UBC; Probability Seminar, UBC; Statistics Seminar, Columbia University; Probability Seminar, Duke University; Probability Seminar, UCSD; Applied Math Seminar, University of Minnesota, Twin Cities; Probability Colloquium, UCLA; Probability Seminar, Cornell University; Phylogroup Meeting, Isaac Newton Institute

2006-2007: Probability Seminar, UCSD; Mathematics Seminar, MIT; Theory Seminar, Microsoft Research; Probability Seminar, Cornell University; Probability Seminar, UC Berkeley;

Posters

Max Hill, Sebastien Roch, “Anomalous Inference Under the Multispecies Coalescent with Intralocus Recombination,” WABI 2021

Zonglin Han, Calvin Kosmatka, Sebastien Roch, Jason Wang, “A Multilocus Approach to Species Tree Reconstruction with Recombination,” 19th Annual Undergraduate Symposium, UW–Madison, April 2017

Sebastien Roch, Jason Wang, “Phylogenetic Network Reconstruction from Distorted Metrics,” Midwest Mathematical Biology Conference, UW–La Crosse, May 2016

Sebastien Roch, Jason Wang, “Phylogenetic Network Reconstruction from Distorted Metrics,” qbio2016 Symposium & Workshop, UW–Madison, April 2016

Outreach

Math Club, Madison Area Technical College, 2017

Mathematics of the Tree of Life, “Why Math Matters,” UW–Madison, 2016

Publications

(Papers available at <http://people.math.wisc.edu/~roch/>)

Books

1. Sebastien Roch. *Mathematical Methods in Data Science (with Python)*. To be published by Cambridge University Press. <https://people.math.wisc.edu/~roch/mmids/>.
2. Sebastien Roch. *Modern Discrete Probability: An Essential Toolkit*. Cambridge Series in Statistical and Probabilistic Mathematics. Cambridge University Press, 2024. <https://people.math.wisc.edu/~roch/mdp/>.

Lecture Notes, Surveys and Book Reviews

3. Sebastien Roch. Lecture notes for a graduate course on “Measure-Theoretic Probability.” <https://people.math.wisc.edu/~roch/grad-prob/>
4. Sebastien Roch. Lecture notes for a graduate course on “Stochastic Processes in Evolutionary Genetics.” <https://people.math.wisc.edu/~roch/evol-gen/>
5. Sébastien Roch. Hands-on introduction to sequence-length requirements in phylogenetics. In Tandy Warnow, editor, *Bioinformatics and Phylogenetics: Seminal Contributions of Bernard Moret*, pages 47–86. Springer International Publishing, Cham, 2019.

6. Sebastien Roch. *Phylogeny—discrete and random processes in evolution* [book review of MR3601108]. *Bull. Amer. Math. Soc. (N.S.)*, 56(3):572–533, 2019.

Preprints

7. Fan Chen, Sebastien Roch, Karl Rohe, and Shuqi Yu. Estimating graph dimension with cross-validated eigenvalues. *Preprint*; <https://arxiv.org/abs/2108.03336>, 2021.
8. Yilin Zhang, Karl Rohe, and Sebastien Roch. Reducing seed bias in respondent-driven sampling by estimating block transition probabilities. *Preprint*; <https://arxiv.org/abs/1812.01188>.

Journals

9. Brandon Legried and Sebastien Roch. Pairwise sequence alignment at arbitrarily large evolutionary distance. *The Annals of Applied Probability*, 34(3):2714 – 2732, 2024.
10. Max Hill, Sebastien Roch, and Jose Israel Rodriguez. Maximum Likelihood Estimation for Unrooted 3-Leaf Trees: An Analytic Solution for the CFN Model. *Bulletin of Mathematical Biology*, 86(9):106, July 2024.
11. Yasamin Tabatabaee, Sebastien Roch, and Tandy Warnow. QR-STAR: A polynomial-time statistically consistent method for rooting species trees under the coalescent. *Journal of Computational Biology*, 30(11):1146–1181, 2023. PMID: 37902986.
12. Sebastien Roch. Expanding the Class of Global Objective Functions for Dissimilarity-Based Hierarchical Clustering. *Journal of Classification*, 40(3):513–526, November 2023.
13. Max Hill and Sebastien Roch. Inconsistency of triplet-based and quartet-based species tree estimation under intralocus recombination. *Journal of Computational Biology*, 29(11):1173–1197, 2022. PMID: 36048557.
14. Wai-Tong Louis Fan, Brandon Legried, and Sebastien Roch. An impossibility result for phylogeny reconstruction from k-mer counts. *The Annals of Applied Probability*, 32(6):4893–4913, 2022.
15. Max Hill, Brandon Legried, and Sebastien Roch. Species tree estimation under joint modeling of coalescence and duplication: Sample complexity of quartet methods. *The Annals of Applied Probability*, 32(6):4681–4705, 2022.
16. Gautam Dasarathy, Elchanan Mossel, Robert Nowak, and Sebastien Roch. A stochastic Farris transform for genetic data under the multispecies coalescent with applications to data requirements. *Journal of Mathematical Biology*, 84(5):36, April 2022.
17. Brandon Legried, Erin K. Molloy, Tandy Warnow, and Sébastien Roch. Polynomial-time statistical estimation of species trees under gene duplication and loss. *Journal of Computational Biology*, 28(5):452–468, 2021. PMID: 33325781.

18. Sébastien Roch and Kun-Chieh Wang. Sufficient condition for root reconstruction by parsimony on binary trees with general weights. *Electronic Communications in Probability*, 26:1–13, 2021.
19. Wai-Tong Louis Fan, Brandon Legried, and Sébastien Roch. Impossibility of Consistent Distance Estimation from Sequence Lengths Under the TKF91 Model. *Bulletin of Mathematical Biology*, 82(9):123, September 2020.
20. Yuling Yan, Bret Hanlon, Sébastien Roch, and Karl Rohe. Asymptotic seed bias in respondent-driven sampling. *Electronic Journal of Statistics*, 14(1):1577–1610, 2020.
21. Wai-Tong Fan and Sébastien Roch. Statistically consistent and computationally efficient inference of ancestral DNA sequences in the TKF91 model under dense taxon sampling. *Bulletin of Mathematical Biology*, 82(2):21, January 2020.
22. Sébastien Roch, Michael Nute, and Tandy Warnow. Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. *Systematic Biology*, 68(2):281–297, 03 2019.
23. Sébastien Roch and Karl Rohe. Generalized least squares can overcome the critical threshold in respondent-driven sampling. *Proceedings of the National Academy of Sciences*, 115(41):10299–10304, 2018.
24. Zvi Rosen, Anand Bhaskar, Sébastien Roch, and Yun S. Song. Geometry of the sample frequency spectrum and the perils of demographic inference. *Genetics*, 210(2):665–682, 2018.
25. S. Shekhar, S. Roch, and S. Mirarab. Species tree estimation using ASTRAL: How many genes are enough? *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1738–1747, Sept 2018.
26. Wai-Tong (Louis) Fan and Sébastien Roch. Necessary and sufficient conditions for consistent root reconstruction in Markov models on trees. *Electron. J. Probab.*, 23:24 pp., 2018.
27. Elchanan Mossel and Sébastien Roch. Distance-based species tree estimation under the coalescent: Information-theoretic trade-off between number of loci and sequence length. *Ann. Appl. Probab.*, 27(5):2926–2955, 10 2017.
28. Sébastien Roch and Allan Sly. Phase transition in the sample complexity of likelihood-based phylogeny inference. *Probability Theory and Related Fields*, 169(1):3–62, Oct 2017.
29. Cécile Ané, Lam Si Tung Ho, and Sébastien Roch. Phase transition on the convergence rate of parameter estimation under an Ornstein–Uhlenbeck diffusion on a tree. *Journal of Mathematical Biology*, 74(1):355–385, 2017.
30. Sébastien Roch and Tandy Warnow. On the robustness to gene tree estimation error (or lack thereof) of coalescent-based species tree methods. *Systematic Biology*, 64(4):663–676, 2015.
31. Gautam Dasarathy, Robert D. Nowak, and Sébastien Roch. Data requirement for phylogenetic inference from multiple loci: A new distance method. *IEEE/ACM Trans. Comput. Biology Bioinform.*, 12(2):422–432, 2015.

32. Sébastien Roch and Mike Steel. Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent. *Theoretical Population Biology*, 100:56 – 62, 2015.
33. Sébastien Roch and Sagi Snir. Recovering the treelike trend of evolution despite extensive lateral genetic transfer: a probabilistic analysis. *J. Comput. Biol.*, 20(2):93–112, 2013.
34. E. Mossel, S. Roch, and A. Sly. Robust estimation of latent tree graphical models: Inferring hidden states with inexact parameters. *Information Theory, IEEE Transactions on*, 59(7):4357–4373, 2013.
35. Elchanan Mossel and Sébastien Roch. Identifiability and inference of non-parametric rates-across-sites models on large-scale phylogenies. *Journal of Mathematical Biology*, 67(4):767–797, 2013.
36. Constantinos Daskalakis and Sébastien Roch. Alignment-free phylogenetic reconstruction: sample complexity via a branching process analysis. *Ann. Appl. Probab.*, 23(2):693–721, 2013.
37. Elchanan Mossel and Sébastien Roch. Phylogenetic mixtures: concentration of measure in the large-tree limit. *Ann. Appl. Probab.*, 22(6):2429–2459, 2012.
38. Alexandr Andoni, Constantinos Daskalakis, Avinatan Hassidim, and Sébastien Roch. Global alignment of molecular sequences via ancestral state reconstruction. *Stochastic Processes and their Applications*, 122(12):3852 – 3874, 2012.
39. Elchanan Mossel, Sébastien Roch, and Allan Sly. On the inference of large phylogenies with long branches: How long is too long? *Bulletin of Mathematical Biology*, 73:1627–1644, 2011. 10.1007/s11538-010-9584-6.
40. Yuval Peres and Sébastien Roch. Reconstruction on trees: Exponential moment bounds for linear estimators. *Electron. Comm. Probab.*, 16:251–261 (electronic), 2011.
41. Constantinos Daskalakis, Elchanan Mossel, and Sébastien Roch. Phylogenies without branch bounds: Contracting the short, pruning the deep. *SIAM J. Discrete Math.*, 25(2):872–893, 2011.
42. Constantinos Daskalakis, Elchanan Mossel, and Sébastien Roch. Evolutionary trees and the ising model on the Bethe lattice: a proof of Steel’s conjecture. *Probability Theory and Related Fields*, 149:149–189, 2011. 10.1007/s00440-009-0246-2.
43. Shankar Bhamidi, Ram Rajagopal, and Sébastien Roch. Network delay inference from additive metrics. *Random Structures Algorithms*, 37(2):176–203, 2010.
44. Sébastien Roch. Toward Extracting All Phylogenetic Information from Matrices of Evolutionary Distances. *Science*, 327(5971):1376–1379, 2010.
45. Elchanan Mossel and Sébastien Roch. Submodularity of influence in social networks: From local to global. *SIAM J. Comput.*, 39(6):2176–2188, 2010.

46. Elchanan Mossel and Sébastien Roch. Incomplete lineage sorting: Consistent phylogeny estimation from multiple loci. *IEEE/ACM Trans. Comput. Biology Bioinform.*, 7(1):166–171, 2010.
47. Elchanan Mossel, Sebastien Roch, and Mike Steel. Shrinkage effect in ancestral maximum likelihood. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):126–133, 2009.
48. Martin Nowak and Sebastien Roch. Upstream reciprocity and the evolution of gratitude. *P. Roy. Soc. B Bio.*, 274(1610):605–609, 2007.
49. Sébastien Roch. On learning thresholds of parities and unions of rectangles in random walk models. *Random Struct. Algorithms*, 31(4):406–417, 2007.
50. Elchanan Mossel and Sébastien Roch. Slow emergence of cooperation for win-stay lose-shift on trees. *Machine Learning*, 67(1-2):7–22, 2007.
51. Sébastien Roch. A short proof that phylogenetic tree reconstruction by maximum likelihood is hard. *IEEE/ACM Trans. Comput. Biology Bioinform.*, 3(1):92–94, 2006.
52. Elchanan Mossel and Sébastien Roch. Learning nonsingular phylogenies and hidden Markov models. *Ann. Appl. Probab.*, 16(2):583–614, 2006.
53. Jean-Pierre Dussault, Patrice Marcotte, Sébastien Roch, and Gilles Savard. A smoothing heuristic for a bilevel pricing problem. *European Journal of Operational Research*, 174(3):1396–1413, 2006.
54. Sébastien Roch. Bounding fastest mixing. *Electron. Comm. Probab.*, 10:282–296 (electronic), 2005.
55. Sébastien Roch, Patrice Marcotte, and Gilles Savard. An approximation algorithm for stackelberg network pricing. *Networks*, 46(1):57–67, 2005.
56. Wolfgang König, Neil O’Connell, and Sébastien Roch. Non-colliding random walks, tandem queues, and discrete orthogonal polynomial ensembles. *Electron. J. Probab.*, 7:no. 5, 24 pp. (electronic), 2002.
57. Hristina Hristova, Sébastien Roch, Peter J. Schmid, and Laurette S. Tuckerman. Transient growth in Taylor–Couette flow. *Physics of Fluids*, 14(10):3475–3484, 2002.
58. Hristina Hristova, Sebastien Roch, Peter J. Schmid, and Laurette S. Tuckerman. Transient growth in exactly counter-rotating Couette–Taylor flow. *Theoretical and Computational Fluid Dynamics*, 16(1):43–48, 2002.

Refereed Proceedings

59. Yasamin Tabatabaee, Sébastien Roch, and Tandy Warnow. Statistically consistent rooting of species trees under the multispecies coalescent model. In Haixu Tang, editor, *Research in Computational Molecular Biology*, pages 41–57, Cham, 2023. Springer Nature Switzerland.

60. Max Hill and Sébastien Roch. On the effect of intralocus recombination on triplet-based species tree estimation. In Itsik Pe'er, editor, *Research in Computational Molecular Biology*, pages 143–158, Cham, 2022. Springer International Publishing.
61. Brandon Legried, Erin K. Molloy, Tandy Warnow, and Sébastien Roch. Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. In Russell Schwartz, editor, *Research in Computational Molecular Biology*, Lecture Notes in Computer Science, pages 120–135, Cham, 2020. Springer International Publishing.
62. Sébastien Roch. On the variance of internode distance under the multispecies coalescent. In *Comparative Genomics - 16th International Conference, RECOMB-CG 2018, Magog-Orford, QC, Canada, October 9-12, 2018, Proceedings*, pages 196–206, 2018.
63. Sébastien Roch and Kun-Chieh Wang. Circular networks from distorted metrics. In *Research in Computational Molecular Biology - 22nd Annual International Conference, RECOMB 2018, Paris, France, April 21-24, 2018, Proceedings*, pages 167–176, 2018.
64. Shubhanshu Shekhar, Sébastien Roch, and Siavash Mirarab. Species tree estimation using ASTRAL: how many genes are enough? In *RECOMB'17—Proceedings of the 21st Annual International Conference on Research in Computational Molecular Biology*, pages 393–395, 2017.
65. Constantinos Daskalakis and Sébastien Roch. Species trees from gene trees despite a high rate of lateral genetic transfer: A tight bound (extended abstract). In *Proceedings of the Twenty-Seventh Annual ACM-SIAM Symposium on Discrete Algorithms, SODA 2016, Arlington, VA, USA, January 10-12, 2016*, pages 1621–1630, 2016.
66. Elchanan Mossel and Sébastien Roch. Distance-based species tree estimation: Information-theoretic trade-off between number of loci and sequence length under the coalescent. In *Approximation, Randomization, and Combinatorial Optimization. Algorithms and Techniques, APPROX/RANDOM 2015, August 24-26, 2015, Princeton, NJ, USA*, pages 931–942, 2015.
67. Gautam Dasarathy, Robert D. Nowak, and Sébastien Roch. New sample complexity bounds for phylogenetic inference from multiple loci. In *2014 IEEE International Symposium on Information Theory, Honolulu, HI, USA, June 29 - July 4, 2014*, pages 2037–2041, 2014.
68. Sébastien Roch. An analytical comparison of multilocus methods under the multispecies coalescent: The three-taxon case. In *PSB'13—Proceedings of the Pacific Symposium on Biocomputing 2013*, pages 297–306.
69. Vahab S. Mirrokni, Sébastien Roch, and Mukund Sundararajan. On fixed-price marketing for goods with positive network externalities. In *WINE'12—Proceedings of the 8th International Workshop on Internet and Network Economics*, pages 532–538, 2012.
70. Sébastien Roch and Sagi Snir. Recovering the tree-like trend of evolution despite extensive lateral genetic transfer: A probabilistic analysis. In Benny Chor, editor, *Research in Computational Molecular Biology*, volume 7262 of *Lecture Notes in Computer Science*, pages 224–238. Springer Berlin / Heidelberg, 2012.

71. Constantinos Daskalakis and Sebastien Roch. Alignment-free phylogenetic reconstruction. In Bonnie Berger, editor, *Research in Computational Molecular Biology*, volume 6044 of *Lecture Notes in Computer Science*, pages 123–137. Springer Berlin / Heidelberg, 2010.
72. Alexandr Andoni, Constantinos Daskalakis, Avinatan Hassidim, and Sébastien Roch. Global alignment of molecular sequences via ancestral state reconstruction. In *ICS'10—Proceedings of the First Symposium on Innovations in Computer Science*, pages 358–369, 2010.
73. Constantinos Daskalakis, Elchanan Mossel, and Sebastien Roch. Phylogenies without branch bounds: Contracting the short, pruning the deep. In Serafim Batzoglou, editor, *Research in Computational Molecular Biology*, volume 5541 of *Lecture Notes in Computer Science*, pages 451–465. Springer Berlin / Heidelberg, 2009.
74. Sébastien Roch. Sequence length requirement of distance-based phylogeny reconstruction: Breaking the polynomial barrier. In *FOCS'08—Proceedings of the 2008 49th Annual IEEE Symposium on Foundations of Computer Science*, pages 729–738, 2008.
75. Elchanan Mossel and Sebastien Roch. On the submodularity of influence in social networks. In *STOC'07—Proceedings of the 39th Annual ACM Symposium on Theory of Computing*, pages 128–134. ACM, New York, 2007.
76. Christian Borgs, Jennifer Chayes, Constantinos Daskalakis, and Sebastien Roch. First to market is not everything: an analysis of preferential attachment with fitness. In *STOC'07—Proceedings of the 39th Annual ACM Symposium on Theory of Computing*, pages 135–144. ACM, New York, 2007.
77. Christian Borgs, Jennifer Chayes, Elchanan Mossel, and Sébastien Roch. The Kesten-Stigum reconstruction bound is tight for roughly symmetric binary channels. In *FOCS'06—Proceedings of the 47th Annual IEEE Symposium on Foundations of Computer Science*, pages 518–530, 2006.
78. Constantinos Daskalakis, Elchanan Mossel, and Sébastien Roch. Optimal phylogenetic reconstruction. In *STOC'06—Proceedings of the 38th Annual ACM Symposium on Theory of Computing*, pages 159–168, New York, 2006. ACM.
79. Elchanan Mossel and Sébastien Roch. Learning nonsingular phylogenies and hidden Markov models. In *STOC'05—Proceedings of the 37th Annual ACM Symposium on Theory of Computing*, pages 366–375, New York, 2005. ACM.

Theses

80. Sébastien Roch. *Markov Models on Trees: Reconstruction and Applications*. PhD thesis, University of California, Berkeley, 2007.
81. Sébastien Roch. Tarification optimale: Complexité et approximation [Optimal pricing: Complexity and approximation]. Master's thesis, Ecole Polytechnique, Montreal, 2003.