

Ashok Rajaraman

Experience

- January 2016– **Postdoctoral Research Associate**, *Carnegie Mellon University, School of Computer Science.*
- Designing statistical inference models and algorithms for problems in structural genomics.
 - Developed a convex optimization scheme for improved graphical representations of cancer genomes.
 - Analysing correlations between combinatorial structures in graphical representations of genomes and functional characteristics.
- May 2015– **Postdoctoral Research Associate**, *University of Illinois at Urbana-Champaign, College of Engineering*.
- December 2015
- Developed a convex optimization algorithm for multiresolution reconstruction of ancestral genomes.
- January 2010– **Research Assistant**, *Simon Fraser University, Department of Mathematics.*
- April 2015
- Devised a semidefinite approximation for vertex ordering in hypergraphs.
 - Developed polynomial time and fixed parameter tractable algorithms for generalizations of the consecutive ones property.
 - Implemented models and algorithms for ancestral genome reconstruction and phylogenetics.
 - Used combinatorial techniques to reconstruct the genome of the ancestral Black Death bacterium.

Published software

- 2016 **MultiRes**, *Inferring ancestral gene orders using extant gene and syntenic orders, with Jian Ma.*
MultiRes is a heuristic convex optimization method for improved consensus ancestral reconstruction.
- 2015 **DeClone**, *Predicting and sampling ancestral adjacency evolution in reconciled gene trees, with Cédric Chauve, Yann Ponty and João Zañetti.*
DeClone is an integrated method for sampling solutions to a phylogenetic problem, and for parameter inference.
- 2013 **FPSAC**, *Fast Phylogenetic Scaffolding of Ancient Contigs, with Cédric Chauve and Eric Tannier.*
FPSAC is a pipeline for scaffolding ancestral genomes using extant genomic data.
- 2012 **ANGES**, *Reconstructing ANcestral GENomeS maps, with Cédric Chauve, Bradley Jones and Eric Tannier.*
ANGES is a suite of combinatorial and spectral algorithms for ancestral genome reconstruction.

Skills

Research expertise, Convex and combinatorial optimization, statistical inference models, machine learning, graph algorithms, data representation.

Programming expertise.

Highly experienced

- Python
- C++
- L^AT_EX

Extensively used

- Shell script
- MATLAB

Familiar

- Perl
- R

Toolkit: Numpy/Scipy, Scikit-Learn, TensorFlow, Pandas, Matplotlib, Git, SVN, Docker.

Education

- 2015 **Doctor of Philosophy in Mathematics**, *Simon Fraser University, Burnaby, BC.*
Supervisor Cédric Chauve
Thesis title *Variants of the Consecutive Ones Property: Algorithms, Computational Complexity and Applications in Genomics.*
- 2009 **Bachelor of Technology in Metallurgical and Materials Engineering**, *Indian Institute of Technology Roorkee, Roorkee, Uttarakhand, India.*

Publications

Google Scholar profile.

- 2017 **Rajaraman, A.** and Ma, J. Towards recovering allele-specific cancer genome graphs. In S.C. Sahinalp, editor, *Research in Computational Molecular Biology: 21st Annual International Conference, RECOMB 2017, Hong Kong, China, May 3-7, 2017, Proceedings*, pages 224–240. Springer International Publishing, Cham, 2017. ISBN 978-3-319-56970-3.
- 2016 **Rajaraman, A.** and Ma, J. Reconstructing ancestral gene orders with duplications guided by synteny level genome reconstruction. *BMC Bioinformatics*, 17(14):201–212, 2016. ISSN 1471-2105.
- Rajaraman, A.**, Zanetti, J.P.P., Mañuch, J., and Chauve, C. Algorithms and complexity results for genome mapping problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, PP(99):1–1, 2016. ISSN 1545-5963.
- 2015 **Rajaraman, A.**, Chauve, C., and Ponty, Y. Assessing the robustness of parsimonious predictions for gene neighborhoods from reconciled phylogenies. In *Bioinformatics Research and Applications - 11th International Symposium, ISBRA 2015, Norfolk, VA, USA, June 7-10, 2015 Proceedings*, pages 260–271. 2015.
- Neafsey, D.E., Waterhouse, R.M. et al. Highly evolvable malaria vectors: The genomes of 16 anopheles mosquitoes. *Science*, 347(6217), 2015.
- 2013 **Rajaraman, A.**, Tannier, E., and Chauve, C. FPSAC: Fast Phylogenetic Scaffolding of Ancient Contigs. *Bioinformatics*, 29(23):2987–2994, 2013.
- Chauve, C., Patterson, M., and **Rajaraman, A.**. Hypergraph covering problems motivated by genome assembly questions. In *Combinatorial Algorithms - 24th International Workshop, IWOCA 2013, Rouen, France, July 10-12, 2013, Revised Selected Papers*, pages 428–432. 2013.
- 2012 Jones, B.R., **Rajaraman, A.**, Tannier, E., and Chauve, C. ANGES: Reconstructing ANcestral GEnomeS maps. *Bioinformatics*, 28(18):2388–2390, 2012.

Invited Talks

- 2015 **PIMS Discrete Mathematics Seminar, Simon Fraser University, Burnaby, British Columbia.**
Vertex ordering problems for hypergraphs: Connections to the consecutive ones property.
- 2014 **Centre for Systems Genomics, Pennsylvania State University, State College, Pennsylvania.**
A simple scaffolding pipeline, with application to ancient genomes.
- 2013 **PIMS IGTC in Mathematical Biology Summit, Banff, Alberta.**
Scaffolding the genome of the Black Death agent.

Academic Honours

- Michael Stevenson Graduate Scholarship (2014–2015)
- SFU President’s PhD Scholarship (Spring 2014)
- PIMS International Graduate Training Centre Fellowship in Mathematical Biology (2012–2014)
- Faculty of Science Graduate Fellowship (Summers 2010, 2012–2014)
- Travel and Minor Research Award (Fall 2011, 2012)

References

On request.