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– December 2015   **Postdoctoral Research Associate**, *University of Illinois at Urbana-Champaign, College of Engineering* .

- Developed a convex optimization algorithm for multiresolution reconstruction of ancestral genomes.

January 2011– August 2012   **Research Assistant**, *Simon Fraser University, Department of Mathematics*.

- 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 synteny 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 Zanetti*.
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	Extensively used	Familiar
Python	Shell script	Perl
C++	MATLAB	R
LATEX		

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.

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Publications

Google Scholar profile.

2017   **Rajaraman, Ashok** 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, Ashok** 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, Ashok, Zanetti, J.P.P., Maňuch, 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, Ashok**, 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, Ashok**, Tannier, E., and Chauve, C. FPSAC: Fast Phylogenetic Scaffolding of Ancient Contigs. *Bioinformatics*, 29(23):2987–2994, 2013.

     Chauve, C., Patterson, M., and **Rajaraman, Ashok**. 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, Ashok**, 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

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