

Ashok Rajaraman

Experience

March 2019– **Data Scientist Specialist**, ACCENTURE , Bengaluru, KA, India.

Member of the Data and Applied Intelligence team, involved in designing machine learning models and providing descriptive summaries for various client requirements.

- Designing and deploying machine learning models for inferring project types from text data associated with historical projects.

January 2016– **Postdoctoral Research Associate**, CARNEGIE MELLON UNIVERSITY.

December 2018 Worked with Jian Ma in the School of Computer Science on developing and implementing mathematical and statistical models for inferring and analyzing changes in cancer genome structure and associated functions.

- Designed statistical inference models and algorithms for inferring cancer genome structure.
- Developed a convex optimization scheme for improved graphical representations of cancer genomes.
- Analysed correlations between combinatorial structures in graphical representations of genomes and functional characteristics.

May 2015– **Postdoctoral Research Associate** , UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN.

December 2015 Worked with Jian Ma in the College of Engineering on developing and implementing models for inferring and analyzing changes in genome structure and associated function, in the context of ancestral genomics.

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

January 2010– **Research Assistant**, SIMON FRASER UNIVERSITY.

April 2015 Worked with Cedric Chauve in the Department of Mathematics on generalizing problems on interval graphs, developing and applying related algorithms in a real-world context.

- 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**, *developed in collaboration with Jian Ma.*

MultiRes is a heuristic convex optimization method for improved consensus ancestral reconstruction.

2015 **DeClone**, *developed in collaboration 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**, *developed in collaboration with Cédric Chauve and Eric Tannier.*

FPSAC is a pipeline for scaffolding ancestral genomes using extant genomic data.

2012 **ANGES**, *developed in collaboration with Cédric Chauve, Brad 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, XGBoost, Numba, Gurobi, Matplotlib, Git, Docker.

Education

- 2015 **Doctor of Philosophy in Mathematics**, SIMON FRASER UNIVERSITY.
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, .

Publications

Google Scholar profile.

- 2018 **Rajaraman, A.** and Ma, J. Toward recovering allele-specific cancer genome graphs. *Journal of Computational Biology, originally published in the proceedings of RECOMB 2017*, 25(7):624–636,
- 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., and others (including **Rajaraman, A.**). 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.