Ashok Rajaraman

Experience

March 2019– **Data Scientist Specialist**, ACCENTURE OPERATIONS .
Member of the Data and Applied Intelligence team, involved in designing machine learning models and providing descriptive summaries for various client requirements.
- Developing unsupervised and supervised machine learning models for invoice flagging and tagging for multiple clients.
- Developing methods for summarizing data and optimizing the number of chargeback cases faced by client based on historical data.
- 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.

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.

Skills

Research expertise, Machine learning, statistical inference models, convex and combinatorial optimization, graph algorithms, data representation.

Programming expertise.

Highly experienced	Extensively used	Familiar
- Python	- Shell script	- Perl
- C++	- MATLAB	- R
- LaTeX		

Toolkit: Numpy/Scipy, Scikit-Learn, Keras, TensorFlow, XGBoost, Elasticsearch, Numba, Gurobi, Matplotlib, Git, Docker.

Education

2015 **Simon Fraser University**, *Burnaby, BC, Canada* , DOCTOR OF PHILOSOPHY IN MATHEMATICS.
   Supervisor   Cédric Chauve
   Thesis title   *Variants of the Consecutive Ones Property: Algorithms, Computational Complexity and Applications in Genomics.*

2009 **Indian Institute of Technology Roorkee**, *Roorkee, Uttarakhand, India* , BACHELOR OF TECHNOLOGY IN METALLURGICAL AND MATERIALS ENGINEERING.

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.

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Selected 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.**, 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   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.

      Rajaraman, **A.**, Tannier, E., and Chauve, C. The genome of the medieval Black Death agent, 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.

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