

# Ashok Rajaraman

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## Experience

- January 2016– **Postdoctoral Research Associate**, *Computational Biology Department, Carnegie Mellon University*.  
Postdoctoral researcher working with Jian Ma.
- May 2015– **Postdoctoral Research Associate**, *College of Engineering, University of Illinois at Urbana-Champaign*.  
January 2015 Postdoctoral researcher working with Jian Ma.
- January 2011– **Research Assistant**, *Department of Mathematics, Simon Fraser University*.  
August 2012 Research on combinatorial models in genomics and phylogenetics with Cédric Chauve.

## Education

- 2015 **Doctor of Philosophy**, *Department of Mathematics, Simon Fraser University, Burnaby, British Columbia*.  
Supervisor Cédric Chauve  
Thesis title *Variants of the Consecutive Ones Property: Algorithms, Computational Complexity and Applications in Genomics*.
- 2011 **Master of Science**, *Department of Mathematics, Simon Fraser University, Burnaby, British Columbia*.
- 2009 **Bachelor of Technology**, *Department of Metallurgical and Materials Engineering, Indian Institute of Technology, Roorkee, Uttarakhand, India*.

## Publications

- Accept Rajaraman, A. and Ma, J. Towards recovering allele-specific cancer genome graphs. *Accepted for RECOMB 2017*,
- 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 Neafsey, D.E., Waterhouse, R.M. et al. Highly evolvable malaria vectors: The genomes of 16 anopheles mosquitoes. *Science*, 347(6217), 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.

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1/3

- 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.
- 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.
- 2012 Jones, B.R., Rajaraman, A., Tannier, E., and Chauve, C. ANGES: Reconstructing ANcestral GENomeS maps. *Bioinformatics*, 28(18):2388–2390, 2012.

## Talks

- 2015 **International Symposium on Bioinformatics Research and Applications**, *Norfolk, Virginia*.  
Assessing the robustness of parsimonious predictions for gene neighbourhoods from reconciled phylogenies.  
**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.

## Workshops

- 2012 **ENUMEX**, *Bertinoro, Italy*.  
School on enumeration algorithms and exact methods for exponential problems in computational biology.
- 2011 **IPAM Genomics Workshop**, *Los Angeles, California*.  
Workshop on mathematical and computational approaches in evolutionary genomics.

## Software Collaborations

- MultiRes: Software for inferring ancestral gene orders using extant gene and syntenic orders.
- DeClone: Software for the prediction of ancestral adjacencies in reconciled gene trees, with Cédric Chauve, Yann Ponty and João Zannetti.
- FPSAC: Fast Phylogenetic Scaffolding of Ancient Contigs, with Cédric Chauve and Eric Tannier.
- ANGES: Reconstructing ANcestral GENomeS maps, with Cédric Chauve, Bradley Jones and Eric Tannier.

## Academic Honours

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2/3

- Michael Stevenson Graduate Scholarship, awarded for 2014–2015.
- SFU President's PhD Scholarship, awarded for Spring 2014.
- PIMS International Graduate Training Centre Fellowship in Mathematical Biology, awarded for 2012–2014.
- Faculty of Science Graduate Fellowship, awarded for Summer 2010, 2012–2014.
- Travel and Minor Research Award, awarded for Fall 2011 and 2012.

## Relevant skills

### Experienced

- Python
- C++
- L<sup>A</sup>T<sub>E</sub>X

### Used occasionally

- shell script
- MATLAB

### Used sporadically

- perl
- R

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3/3