Ashok Rajaraman

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EDUCATION

SIMON FRASER UNIVERSITY

Doctorate in Mathematics
April 2015 | Burnaby, BC
Supervisor: Cedric Chauve
Thesis topic: *Algorithms and complexity results for variants of the consecutive ones property.*

IIT ROORKEE

B.Tech in Metallurgical and Materials Engineering
June 2009 | Roorkee, Uttarakhand, India

PROJECTS

DeClone: 2015
FPSAC: 2013
ANGES: 2012

WORKSHOPS

PIMS IGTC Mathematical Biology Summit
November 2013 | Banff, Alberta

ENUMEX
September 2012 | Bertinoro, Italy

IPAM Evolutionary Genomics
November 2011 | Los Angeles, CA

AWARDS

Michael Stevenson Scholarship: 2014
SFU President's PhD Scholarship: 2014
PIMS IGTC Fellowship: 2012-2014
SFU Travel Awards: 2011,2012
SFU Graduate Fellowship: 2010,2012

SKILLS

Programming:
(Most used first)
Python ▪ C++ ▪ shell ▪ perl
Mathematical software:
MATLAB ▪ R
Typesetting/markup:
LaTeX ▪ HTML

REFERENCES

On request

EXPERIENCE

CARNEGIE MELLON UNIVERSITY | Postdoctoral Research Associate, Computational Biology Department, School of Computer Science
January 2016 - | Pittsburgh, PA

UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN |
Postdoctoral Research Associate, Department of Bioengineering, College of Engineering
May 2015 – December 2015 | Urbana, IL
Host: Jian Ma. Research on mathematical models in computational genomics.

RESEARCH

COMPUTATIONAL MODELS IN COMPARATIVE GENOMICS

- Integrated ancestral genome reconstruction at multiple resolutions.
- Hypergraph models for genome mapping problems.
- Dynamic programming algorithms in phylogenetics.
- Approximations for generalized vertex ordering problems.

PUBLICATIONS

Accept Rajaraman, A. and Ma, J. Reconstructing ancestral gene orders with duplications guided by synteny level genome reconstruction. In *RECOMB-CG 2016*.

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. 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 neighbourhoods 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.

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. In *JOBIM 2013 (Extended abstract)*.

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