Arjun Arkal Rao

220 Auburn Ave, Santa Cruz CA 95060. Ph. No.: +1 (847) 943–7524
aarjunrao@soe.ucsc.edu

Personal Statement

I am an experienced, determined individual who is interested in the immune response to cancer. My research under the guidance of Dr. David Haussler includes the prediction of MHCI and MHCII displayed epitopes in tumors that can be used to elicit a T-cell response in the patient.

Academic Qualification

- Doctoral student - Department of Biomolecular Engineering, University of California Santa Cruz (September 2013 – Current)
- Bachelor of Engineering (Biotechnology) from Peoples Educational Society Institute of Technology (PESIT) Bangalore Affiliated to Visvesvaraya Technological University, Belgaum, Karnataka, India (2008-2012) CGPA: 8.71/10.0

Internships/research experience

- Doctoral research – Haussler Lab. UC Santa Cruz (Sept 2013 – Current)
  - Prediction of MHCI and MHCII displayed epitopes for precision cancer Immunotherapy
- Junior Research Fellow – Somasundaram Lab. Indian Institute of Science, Bangalore, INDIA (June 2012-July 2013)
  - Identification of recurrent fusion genes and alternative splice variant patterns in sequencing data of Glioblastoma obtained from TCGA
- Intern – GANIT Labs, Bangalore, INDIA (August 2011 – December 2011)
  - Developed an algorithm to simulate NGS data that could incorporate SNVs, INDELs and CNVs into the files such that they could be used to test variant callers..
  - Tool published in BMC Bioinformatics. CNV simulation model used to test a tool published in PLoS One.
- Summer Intern – GANIT Labs, Bangalore, INDIA (Summer 2010)
  - Developed an algorithm to identify CNVs in shotgun sequencing data using the read counts seen in dynamically sized sliding windows.

Programming proficiency

- Proficient in Python and C
- Proficient in R for statistics and data visualization
- Proficient in shell scripting
- Comfortable using the Linux/Unix Interface, and working with clusters.

Publications

- Pattnaik, S., Gupta, S., **Rao, A. A**. & Panda, B. SInC: An accurate and fast error-model based simulator for SNPs, Indels and CNVs coupled with a read generator for short-read sequence data. BMC Bioinformatics. 2014; 15: 40.
- Krishnan, N. M., Gaur, P., Chaudhary, R., **Rao, A. A**. & Panda, B. COPS: A Sensitive and Accurate Tool for Detecting Somatic Copy Number Alterations Using Short-Read Sequence Data from Paired Samples. PLoS ONE 7, e47812 (2012)