

SIDDHARTH S. TOMAR

PERSONAL INFORMATION

Born in India, 08 May 1994

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EDUCATION

Master of Science

2016-2018 KTH Royal Institute of Technology

Master's programme in Molecular Techniques in Life Science, a joint program with Karolinska Institutet and Stockholm University

Duration: 2 years (full time)

Date of graduation: 31-May-2018

Country: *Sweden*

Bachelor of Technology

2012-2016 Jaypee University of Information Technology

GPA: 8.6 out of 10 · *Specialization in Bioinformatics*

Duration: 4 years (full time)

Date of graduation: 09-July-2016

Country: *India*

BIOINFORMATICS SKILLS

<i>Workflows</i>	Genome/Transcriptome assembly, Quantification, Differential expression, Novel gene discovery, Time series analysis, Weighted correlation network analysis
<i>Programming</i>	C++/C (INCLUDING CUDA AND MPI), JAVA, PYTHON, PERL, R
<i>Databases</i>	MySQL
<i>Machine learning</i>	SCIKIT-LEARN, TENSORFLOW
<i>Documentation</i>	L ^A T _E X, MARKDOWN
<i>Version control</i>	GIT
<i>Model organisms</i>	HUMAN, MICE, <i>P. ABIES</i>

LAB SKILLS

<i>Genetic Engineering</i>	Gene cloning using bacteria, Gene disruption and gene replacement in bacteria
<i>General</i>	DNA isolation, RNA isolation, Plasmid and genomic DNA isolation, PCR, Sanger and Illumina sequencing

COURSEWORK - KEYWORDS

<i>Molecular biology</i>	Systems biology, Genetics, translational research in cardiology, neurodegenerative disorders, homology search, multiple sequence alignment, phylogeny reconstruction, protein topology prediction, biophysical chemistry, molecular dynamics, comparative genomics, proteomics, mass spectrometry, antibody assays, short and long read sequencing, microarrays, bead based assays, droplet barcoding, single cell sequencing, ChIP sequencing
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RESEARCH EXPERIENCE

- Jun'18–present* KAROLINSKA INSTITUTET - Sweden
- SciLifeLab - Stockholm* I am currently working as a research assistant in Dr Claudia Kutter's group in Science For Life laboratory, Stockholm. My current work builds upon my experience in my master's thesis and is more focused on the developmental dynamics of PIWI-interacting RNA (piRNA) in mice and their interplay with transposons. This project also involves an in-depth characterisation of piRNA genes concerning their function in regulating genomic integrity and as an individual class of genes.
Reference: Claudia KUTTER · +46-704933896 · claudia.kutter@ki.se
- Jun–Aug '17* KAROLINSKA INSTITUTET - Sweden
- SciLifeLab - Stockholm* After being awarded the SciLifeLab Summer Fellowship, I joined Dr Claudia Kutters group at the Karolinska Institute/SciLifeLab. My work focused on annotating various RNA classes from mice liver at different developmental stages by using total RNA sequencing data. This project involved methods for discovering novel developmental stage-specific noncoding RNAs and correlation with other meta-resources to mark functionality.
Reference: Claudia KUTTER
- Jun–Aug '15* INSTITUTE OF ONCOLOGY RESEARCH - Switzerland
- IOSI-IOR* I worked under Dr Francesco Bertoni's group at Institute of Oncology Research, Bellinzona, Switzerland on performance profiling of short read aligners (using Nvidia CUDA framework) for testing scalability in GPGPU environment. I studied the impact of GPU based tools on the next generation sequencing analysis pipeline and included cost versus performance analysis based on scaling.
Reference: Ivo KWEE +41-794283375 · ivo.kwee@ior.iosl.ch
- Master's thesis* *Micro-evolution of regulatory RNAs*
In this master thesis project, I investigated the functional contribution of regulatory RNA in speciation in closely related mice species. This involved studying the dynamics of their species-specific gene expression by utilising ChIP sequencing to define active promoters along with short and total RNA sequencing.
Supervisor: Claudia KUTTER
- Bachelor's thesis* *Improving the computation of positive selection using codon models*
In my bachelor's project, I was working on improving the computation of positive selection using codon models. In this project, I implemented the Branch-Site Model on GPU architecture, and test the efficiency gains which are potentially possible. I changed the underlying algorithm to reduce the redundancy and increase the sensitivity by optimising the subtree pruning. I mainly used (CUDA)C++ for this project. The primary challenge of this project was to implement the current model as it is, without any heuristics involved, and still archive exceptionally low runtimes.

PROJECTS

- 2017* KTH ROYAL INSTITUTE OF TECHNOLOGY
- Course Project* Assembling reference transcriptome for *P. abies* using massively parallel and PacBio real time sequencing data. This project involved utilization of large amount of data (>700 million reads) and optimization techniques for transcriptome assembly.
Reference: Lars ARVESTAD · +4687906436 · lars.arvestad@scilifelab.se
- 2017* STOCKHOLM UNIVERSITY
- Course Project* Constructing a SVM based predictor for classifying topological features of β barrels based on their sequence.
- 2014* Jaypee University of Information Technology
- Course Project* Identification of novel leads against dimeric interface(DBP) in *P. vivax* using computer-aided drug design. For this project, I investigated the structural dynamics of Duffy binding proteins with respect to the phylum Apicomplexa.

Course Project 2013 Jaypee University of Information Technology

Created an application written in Java for searching repeat content in a given genome. Simple machine learning technique was used, applying the Hidden Markov Model. Lempel–Ziv–Welch algorithm was also used and modified according to requirements. Perl was used as a wrapper and as text acquisition/annotation search engine.

POSTER PRESENTATION AND CONFERENCES

Poster 2018 2nd Uppsala Transposon Symposium

Micro-evolution of regulatory RNA in *M. domesticus* and *M. castaneus*

GRANTS

Nvidia 2015 - Nvidia GPU Grant Program

OTHER INFORMATION

Scholarships 2017 · Science for Life Laboratory summer fellowship
2017 · Karolinska Institutet Foundation scholarship

Languages ENGLISH · Fluent
HINDI · Native

Last updated on February 23, 2019