Devang Thakkar

www.devangthakkar.com

EDUCATION

Duke University

Durham, NC

Aug 2018 - Present

Email: devang.thakkar@duke.edu GitHub: github.com/devangthakkar

PhD in Computational Biology and Bioinformatics

o Second year PhD student in the Dave Lab studying the cell of origin in cancers

CentraleSupélec

Paris, France

Échange Académique Ingénieur (Semester Exchange Program)

Aug 2016 - Jan 2017

Indian Institute of Technology Bombay

Mumbai, India

Bachelor and Master of Technology in Mechanical Engineering

Jul 2013 - Jul 2018

- $\circ~$ Minor in Biosciences and Bioengineering
- o Thesis: A Study on the Application of Multi-Agent Systems for Managing Reverse Supply Chain Networks

PUBLICATIONS

- 1. Shingleton JR, Wang J, Baloh C, Dave T, Davis N, Happ L, Jadi O, Kositsky R, Li X, Love CL, Panea RI, Qin Q, Reddy A, Singhi N, Smith E, **Thakkar D**, and Dave SS. (2020) *Non-Hodgkin Lymphomas: Malignancies Arising from Mature B Cells*. Leukemia and Lymphoma: Molecular & Therapeutic Insights, Cold Spring Harbor Perspectives in Medicine (In press)
- 2. Panea RI, Love CL, Shingleton JR, Reddy A, Bailey JA, Moormann AM, Otieno JA, Ong'echa JM, Oduor CI, Schroeder KMS, Masalu N, Chao NJ, Agajanian M, Major MB, Fedoriw Y, Richards KL, Rymkiewicz G, Miles RR, Alobeid B, Bhagat G, Flowers CR, Ondrejka SL, Hsi ED, Choi WWL, Au-Yeung RKH, Hartmann W, Lenz G, Meyerson H, Lin YY, Zhuang Y, Luftig MA, Waldrop A, Dave T, Thakkar D, Sahay H, Li G, Palus BC, Seshadri V, Kim SY, Gascoyne RD, Levy S, Mukhopadhyay M, Dunson DB, Dave SS. (2019) The whole genome landscape of Burkitt lymphoma subtypes. Blood DOI: 10.1182/blood.2019001880
- 3. **Thakkar D**, and Saini S. (2018) Estimating Optimal Lysogenic Propensity for Viruses in Stressed Environments. BiorXiv DOI: 10.1101/321372

RESEARCH

Ascertaining the Cell of Origin in Cancers

Advisor: Sandeep Dave

Sep 2019 - Present

- Identifying the putative cell of origin for different cancer types using scRNAseq and whole genome sequencing data
- o Compared tools for estimating copy number variation and validated against microarray sequencing results
- $\circ~$ Developing methods to understand the effect of tumor purity on copy number variation analysis

Clonal Analysis of Cardiomyocyte Growth and Regeneration

Advisors: Ed Iversen and Ravi Karra

May 2019 - Aug 2019

- o Created a statistical model to identify the distribution of proliferating cardiomyocyte cells in injured hearts
- Worked on understanding the relationship between cardiomyocyte proliferation and the vasculature of the heart

Computational Reconstruction of Immunoglobulin Sequences in Cancers

Advisor: Sandeep Dave

Jan 2019 - Apr 2019

- Reviewed and compared existing tools for clonotype detection from Whole Genome Sequencing (WGS) data
- o Developed pipelines for identification of tumor clonotype from WGS data of 101 Burkitt Lymphoma samples

Understanding Non-coding Transcripts in Yeast

Advisor: Alex Hartemink Sep 2019 - Dec 2019

- Worked on understanding how the expression of non coding transcripts depends on adjacent protein coding genes
- Used MNase-Seq data to understand the impact of heavy metal stress on non-coding transcripts in yeast

Modeling the Optimal Propensity of Lysogeny for Co-existing Populations

Advisor: Supreet Saini

Jun 2017 - May 2018

- o Developed a model for estimating the probability of viral lysogeny that maximizes coexistence as a function of Multiplicity of Infection under different environmental stresses for bacterial growth
- Performed Gillespie simulations to discretize the reactions and search a 2-D space for the optimal coexistence curve

Selecting Features from Sample Specific Coexpression Networks

Advisor: Chloé-Agathe Azencott

Dec 2016 - Mar 2017

- Studied existing weight transfer algorithms for the construction of sample-specific networks that incorporate gene expression data with a protein-protein interaction network
- Identified the relevant features using permutation importance in random forests from gene expression data

Posters

1. Thakkar D and Dave SS. (2019) Computational Reconstruction of Human Immunoglobulin Sequences. Duke Computational Biology and Bioinformatics Retreat, Wilmington, NC, Sep 2019

Fellowships

Kishore Vaignayik Protsahan Yojana (KVPY)

2012

Department of Science and Technology, Govt. of India

INPSIRE Scholarship for Higher Education

2012

Department of Science and Technology, Govt. of India

Industry Experience

Mumbai, India TransUnion

Data Architect Intern Aug 2018 - Present

- Developed pipelines for automated credit report creation on a 550M+ dataset with 50% reduction in execution time
- Led the team for the migration of the analysis pipelines from SAS to the open-source Hadoop ecosystem using Pig
- Performed regression analyses using Apache Spark to identify leading parameters affecting the rate of insolvency

TEACHING EXPERIENCE

Project Management, Graduate Teaching Assistant

2018

2017

Indian Institute of Technology Bombay

Mumbai, India

Industrial Engineering & Operations Research, Graduate Teaching Assistant

Indian Institute of Technology Bombay

Mumbai, India

Programming Skills

• Languages: Python, R, Java

• Technologies: Bash, Git, Hadoop