





VIVEK RAI

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EDUCATION

Indian Institute of Technology Kharagpur, India
Dual Degree (B.Tech & M.Tech), *Biotechnology and Biochemical Engineering*
GPA: 8.65 (out of 10), first in class.

2012-2017

SKILLS

LANGUAGES Python (+scipy), SQL, Ruby, JavaScript, C, R, MATLAB, BASH

AREAS Scientific computing, Bioinformatics, Computational modeling, Data visualization

TOOLS *nix, Vim, Git, L^AT_EX

PUBLICATIONS

in prepration 2015 Priyam *et al*, "Sequenceserver: rapid creation of assistive graphical BLAST frontends for custom sequence databases" <http://sequenceserver.com>

RESEARCH EXPERIENCE

B.TECH THESIS
IIT KHARAGPUR
August 2015–present

Bioinformatic analysis of protein knots and the knotting mechanism.

- Delivered an in-house talk assessing latest developments in concerned field.
- Reviewing existing literature to formulate the research problem statement.

RESEARCH INTERN
MRDG, IISc
May 2015–July 2015

Fluorescent labeling and lipid phase dependence study of *E.coli* ClyA toxin.(Report)

- Extracted, purified and fluorescently labeled wild type and mutant proteins obtained from expression vectors.
- Assessed toxin activity and qualitatively demonstrated a lipid phase dependent kinetic behavior of Cytolysin A; one of the foremost such study of the toxin.

DEVELOPMENT EXPERIENCE¹

WIGI, WIKIMEDIA
May 2015–present

A Wikimedia project to quantify gender biases in Wikipedia and create quantitative indicators. The project is supported by a grant of \$ 22,500.

- Analyzed raw Wikidata information to visualize gender information across categories and perform statistical analyses; also developed the corresponding portal for hosting results.
- Assisted in research and community efforts by writing writing blog posts, reports and reviewing paper.

SEQUENCESERVER
Jun 2014–Current

Contributed more than 110 commits over an year log period and co-authored the paper.

- Implemented BLAST+ output parser module, back-end data-layer in Ruby and designed graphical overview scheme for BLAST hits information using D3 improving overall application architecture, usability, and modularity.

¹Please find an exhaustive list of projects on my website.

AFRA Dec 2014–Jan 2014	<p>A gene annotation platform inspired by crowdsourcing approaches including Foldit, Galaxy Zoo and Crowdfunder, but with easier learning curve.</p> <ul style="list-style-type: none"> – Frontend work with JavaScript, JQuery to design and improve the overall user experience and provide intuitive visual feedback to the user. – Backend work constituted of handling annotation data, providing tab synchronization between multiple user sessions, extending edit track features etc.,
JIGSAW SOLVER Feb 2014–Mar 2014	<p>Program to solve large piece jigsaw puzzle (randomly shuffled pieces of an image) based on genetic algorithm; implemented entirely from scratch in C++ using OpenCV image processing library.</p>
READ SIGN LANGUAGE Apr 2014–May 2014	<p>Developed an application to recognize basic American Sign Language alphabets through gestures with a kNN classifier trained on contour based features.</p>

LAB EXPERIENCE

- Microscopy
- Basic microbiology
- Cell culture
- Cell fractionation
- Assay techniques
- HPLC, FPLC
- Spectrophotometry
- Gel electrophoresis
- DNA cloning
- Dynamic Light Scattering
- Western blotting
- Fermenter operation

COURSEWORK

SHORT TERM COURSE IIT KHARAGPUR Mar 2014–Apr 2014	<p>COMPUTATIONAL SYSTEMS BIOLOGY</p> <ul style="list-style-type: none"> – Learned about latest techniques and ongoing research in the field of sequencing, systems biology, protein interactions, modeling, and metabolic engineering.
TERM PAPER Feb 2014–Feb 2014	<p>COMPARISON OF FUZZY GUIDED GENE PREDICTION METHODS</p> <ul style="list-style-type: none"> – Reviewed the future prospects and application strategies of support vector machines, neural network based learning and heuristic techniques (genetic algorithm, fuzzy logic) combined as hybrid methods for better annotation of raw genomic data.

SUBJECTS TAKEN Sem I–Sem VII	(L) includes laboratory		
	– Cell & Molecular Biology	– Bioinformatics (L)	– Bioprocess Technology
	– Microbiology	– Protein Engineering	– Bioanalytical Labs (L)
	– Genetics	– Probability and Statistics	– Data Analytics
	– Biochemistry (L)	– Statistical Modelling	– Computational
	– Gene Expression	– Mathematics I & II	Neuroscience

Additional courses

- Discrete Structures
- Soft Computing Tools in Engineering

OTHER

METAKGP	Contributor and administrator of our first Comprehensive campus Wiki.	2015
iGEM	Core team member of the iGEM 2015 team.	2015
HACKERRANK	Author of tutorial problems for Ruby, Python & Linux sections.	2015
EN WIKIPEDIA	Experienced editor with over 30 english articles and more than 1600 edits.	2012–Now