Vivek Rai

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Education

Indian Institute of Technology Kharagpur, India
B.Tech & M.Tech, *Biotechnology*
GPA: **8.65** (out of 10), **first** in class. 2012-2017

Skills

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

Areas Bioinformatics, Computational modeling, Open source, Data visualization

Tools GNU/Linux (*nix), Vim, Git, LaTeX

Publications

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

Conferences and Seminars

Winter School Dec 2015 — Selected for **Winter School on Quantitative Systems Biology 2015** organized at International Centre for Theoretical Science, Bangalore in association with ICTP, Italy.

Short Term Course Mar 2014 — Attended a set of seminars as a part of **Short Term Course on Computational Biology** organized at Indian Institute of Technology Kharagpur.

Research Experience

B.Tech thesis
IIT Kharagpur
August 2015–present

Bioinformatic analysis of protein knots and their knotting mechanism.

- Delivered an in-house talk with comprehensive review of the topic and formulated my research problem statement.
- Investigating sequence properties and pattern (amino acid nature and distribution, for example) in the protein knot core.

Research Intern
MRDG, IISc
May 2015–July 2015

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

- Extracted, purified and labeled (fluorescence) the 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 Experience[1]

WIGI, Wikimedia
May 2015–present

A Wikimedia project to quantify gender biases in Wikipedia and create quantitative indicators. The project is supported by an *inspire* 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.js** improving overall application architecture, usability, and modularity.

Afra
Dec 2014–Jan 2014

Improved frontend of the gene annotation platform for intuitive visual feedback and better user experience, while backend work constituted of handling annotation data, managing user sessions and editing features etc.,

Coursework

Term Paper
Feb 2014–Feb 2014

Comparison of Fuzzy Guided Gene Prediction Methods

- Reviewed the future prospects and application strategies of support vector machines, neural network and heuristic techniques (genetic algorithm, fuzzy logic) based learning combined as hybrid methods for improved annotation of raw genomic data.

Subjects taken
Sem I–Sem VII

(+L) includes laboratory

- Cell and Molecular Biology
- Microbiology
- Genetics
- Biochemistry (+L)
- Gene Expression
- Bioinformatics (+L)
- Protein Engineering
- Probability and Statistics
- Statistical Modelling
- Mathematics I & II
- Discrete Structures
- Bioanalytical Labs (L)
- Data Analytics
- Computational Neuroscience

Other

iGEM Wet lab team member and content writer for the iGEM IIT Kharagpur team. 2015

Hackerrank Author of tutorial problems for Ruby, Python & Linux section. 2015

en Wikipedia Experienced editor with over **30** english articles and more than 1600 edits. 2012–Now

metaKGP Contributor and administrator of the first Comprehensive campus Wiki. 2015

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