

VIVEK RAI

🌐 <http://vivekiitkgp.github.io>
🌐 <http://github.com/vivekiitkgp>

✉ vivekrai@iitkgp.ac.in
☎ + (91) 8013291569

EDUCATION

Indian Institute of Technology Kharagpur, 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 stack), Ruby, JavaScript, C, BASH
Bioinformatics BLAST+, BioPython, Primer design, Sequence analysis
Tech Linux, Vim, Git, L^AT_EX, Scientific computing

PUBLICATIONS

in prep Priyam A, **Rai V**, Woodcroft BJ, & Wurm Y, "SequenceServer: BLAST searching made
2015 easy." <http://sequenceserver.com>

PROFESSIONAL EXPERIENCE¹

**Indian Institute of
Science, Bangalore**
May 2015–July 2015

Fluorescent Labeling and lipid phase dependence study of ClyA pore forming toxin.
– Extracted, identified and purified wild type and mutant proteins (for fluorescent tagging) from expression vectors.
– Assessed toxin activity using hemolytic assay and calcein leakage assay; required liposome preparation and dynamic light scattering experiment.
– Qualitatively demonstrated a lipid phase dependent kinetic behavior of Cytolysin A; one of the foremost such study for the toxin.

SequenceServer
Jun 2014–Current

A project to provide biologists with an intuitive and easy to setup custom BLAST server to effectively query and handle large sequence data.
Total contribution translates to over **110** commits and eight months of activity.
– Implemented BLAST+ output parser module and back-end data-layer in **Ruby**, thereby improving application architecture, usability, and modularity.
– Designed graphical overview scheme for BLAST hits information using **D3** (<http://www.d3js.org>), a javascript visualization library.

Afra
Dec 2014–Jan 2014

A gene annotation platform inspired by crowdsourcing approaches including Foldit, Galaxy Zoo and Crowdfunder, but with easier learning curve.
– 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.,

¹ An exhaustive list of projects can be found on my website.

Jigsaw Solver	Program to solve large piece jigsaw puzzle (randomly shuffled pieces of an image)
Feb 2014–Mar 2014	<ul style="list-style-type: none"> – Evaluated different techniques based on genetic algorithm; implemented mutation strategie; could solve up to 1000 pieces. – Programmed the algorithm entirely from scratch in C++ using OpenCV image processing library.

LAB EXPERIENCE

- | | | |
|----------------------|-----------------------|----------------------------|
| – Microscopy | – Assay techniques | – DNA cloning |
| – Basic microbiology | – HPLC, FPLC | – Dynamic Light Scattering |
| – Cell culture | – Spectrophotometry | |
| – Cell Fractionation | – Gel electrophoresis | |

COURSEWORK

Short Term Course	<i>Computational Systems Biology</i>
Mar 2014–Apr 2014	<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	<i>Comparison of Fuzzy Guided Gene Prediction Methods</i>
Feb 2014–Feb 2014	<ul style="list-style-type: none"> – Reviewed existing computational techniques to analyze and annotate whole organism’s genome in an automated way to predict genes and other regions of interest; – Critiqued the future prospects and application strategies of SVM, NN learning and heuristic techniques (GA, Fuzzy Logic) combined as hybrid methods for better annotation of raw genomic data.

Subjects taken	<i>Core courses</i>	<i>(T)heory and (L)aboratory</i>
Sem I–Sem VI	<ul style="list-style-type: none"> – Cell and Molecular Biology (T/L) – Microbiology (T/L) – Genetics – Biochemistry (T/L) – Biochemical, and Bio-analytical Labs. – Bioinformatics (T/L) – Protein Engineering 	<ul style="list-style-type: none"> – Probability and Statistics – Statistical Decision Modelling – Mathematics I & II – Computational Neuroscience – Gene Expression – Data Analytics – Bioprocess Technology
	<i>Additional courses</i>	
	<ul style="list-style-type: none"> – Discrete Structures 	<ul style="list-style-type: none"> – Soft Computing Tools in Engineering

OTHER

iGEM	Core team member of the iGEM 2015 team.	2015
WIGI	Developer in a \$25k Wikimedia sponsored inspire project called WIGI.	2015–Now
en Wikipedia	Contributed over thirty english articles and more than 1600 edits.	2012–Now
Hackerrank	Authored of tutorial problems for Ruby, Python & Linux sections.	2015–Now