



# VIVEK RAI

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

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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<sup>A</sup>T<sub>E</sub>X

## 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 EXPERIENCE<sup>1</sup>

**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.

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<sup>1</sup>Please find an exhaustive list of projects on my website.

<b>SEQUENCESERVER</b> Jun 2014–Current	Contributed more than <b>110 commits</b> over an year log period and co-authored the paper. – Implemented BLAST+ output parser module, back-end data-layer in <b>Ruby</b> and designed graphical overview scheme for BLAST hits information using <b>D3</b> improving overall application architecture, usability, and modularity.
<b>AFRA</b> 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 edit features etc.,
<b>JIGSAW SOLVER</b> Feb 2014–Mar 2014	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.
<b>READ SIGN LANGUAGE</b> Apr 2014–May 2014	Developed an application to recognize basic American Sign Language alphabets through gestures with a kNN classifier trained on contour based features.

## LAB EXPERIENCE

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

## COURSEWORK

<b>SHORT TERM COURSE</b> <b>IIT KHARAGPUR</b> Mar 2014–Apr 2014	<b>COMPUTATIONAL SYSTEMS BIOLOGY</b> – Learned about latest techniques and ongoing research in the field of sequencing, systems biology, protein interactions, modeling, and metabolic engineering.
<b>TERM PAPER</b> Feb 2014–Feb 2014	<b>COMPARISON OF FUZZY GUIDED GENE PREDICTION METHODS</b> – 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

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

## OTHER

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