

VIVEK RAI

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EDUCATION

Indian Institute of Technology Kharagpur, Kharagpur, India
Dual Degree, *Biotechnology and Biochemical Engineering*
CGPA: **8.53** (out of 10), **first** in class.

2012-2017

SKILLS

Languages Python (+scipy stack), Ruby, JavaScript, C, BASH, Haskell
Bioinformatics BLAST+, BioPython, Primer design, Sequence analysis
Topics Data visualization, Data analysis, Computational modeling, Algorithms
Tech Linux, Vim, Git, L^AT_EX, Scientific computing

PUBLICATIONS

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

PROFESSIONAL EXPERIENCE

SequenceServer A project to provide biologists with an intuitive and easy to setup custom BLAST server
Jun 2014–Current 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 obtained hit information using **D3** (<http://www.d3js.org>), a javascript visualization library.

Afra A gene annotation platform inspired by crowdsourcing approaches including Foldit,
Dec 2014–Current 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.,

Jigsaw Solver Program to solve large piece jigsaw puzzle (randomly shuffled pieces of an image)
Feb 2014–Mar 2014
– 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.

Torn Paper Mosaicing Mar 2014–Mar 2014	<p>Program to digitally stitch manually torn paper pieces to reconstruct original document with minimal loss and manual effort.</p> <ul style="list-style-type: none"> – Familiarized myself with Object Oriented Design pattern, OpenCV image processing algorithms (Canny, Douglas-Peucker etc.), feature extraction and analysis techniques.
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LAB EXPERIENCE

– Microscopy	– Cell Fractionation	– Chromatography
– Aseptic Techniques	– Assay techniques	– Gel Electrophoresis
– Centrifugation	– HPLC, FPLC	– DNA Amplification (PCR)
– Staining, Culture, and Isolation	– Photometry & fluorometry	– Nucleic acid & Protein Isolation and Purification

COURSEWORK

Short Term Course Mar 2014–Apr 2014	<p><i>Computational Systems Biology</i></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.
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Term Paper Feb 2014–Feb 2014	<p><i>Comparison of Fuzzy Guided Gene Prediction Methods</i></p> <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) as hybrid methods for better annotation of raw genomic data.
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Subjects taken Sem I–Sem VI	<p><i>Core courses</i> <i>(T)heory and (L)aboratory</i></p> <table> <tr> <td>– Cell and Molecular Biology (T/L)</td><td>– Bioinformatics (T/L)</td></tr> <tr> <td>– Microbiology (T/L)</td><td>– Protein Engineering</td></tr> <tr> <td>– Genetics</td><td>– Probability and Statistics</td></tr> <tr> <td>– Biochemistry (T/L)</td><td>– Statistical Decision Modelling</td></tr> <tr> <td>– Biochemical, and Bio analytical Labs.</td><td>– Mathematics I & II</td></tr> </table> <p><i>Additional courses</i></p> <table> <tr> <td>– Discrete Structures</td><td>– Soft Computing Tools in Engineering</td></tr> </table>	– Cell and Molecular Biology (T/L)	– Bioinformatics (T/L)	– Microbiology (T/L)	– Protein Engineering	– Genetics	– Probability and Statistics	– Biochemistry (T/L)	– Statistical Decision Modelling	– Biochemical, and Bio analytical Labs.	– Mathematics I & II	– Discrete Structures	– Soft Computing Tools in Engineering
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OTHER

iGEM	Core team member of the iGEM 2015 team.	2015
en Wikipedia	Authored over thirty articles and cotributed more than 1600 edits.	2012–Now
Hacker Rank	Contributing tutorial problems to the Ruby, Python & Linux sections.	2015–Now