

# Md Abid Hasan

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## Overview

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I work to connect computer science to biological concepts. My job is to apply machine learning models on large biological dataset and interpret the results.

## Education

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<b>University of California Riverside</b> Ph.D. in Computer Science (Advisor: <b>Prof. Stefano Lonardi</b> )	09/2014–10/2019
<b>Islamic University of Technology</b> , Bangladesh M.Sc. in Computer Science (Advisor: <b>Prof. M. A. Mottalib</b> )	01/2011–12/2012
<b>Islamic University of Technology</b> , Bangladesh B.Sc. in Computer Science	01/2007–11/2010

## Work Experience

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<b>Roche Sequencing Solutions</b> – Bioinformatics Intern • BAM file generation from genetic variant information	06–09/2018
<b>University of California Riverside</b> – Graduate Student Researcher • Implementation of machine learning model on biomolecular data	09/2014–11/2019
<b>Islamic University of Technology</b> – Lecturer • Conducting undergraduate courses in Computer Science department	01/2011–08/2014

## Research Experience

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<b>Nucleosome stability prediction in <i>Plasmodium Falciparum</i></b> • Use sequence and chemical properties of nucleotides for prediction of nucleosome stability	Github repository
<b>Multiple cancer type classification with somatic point mutation data</b> • Classify 12 types of cancer using only somatic gene mutation frequency data	Github repository
<b>Deep learning model for gene essentiality prediction in microbes</b> • Using DNA and protein sequence feature to prediction essential genes with Deep neural network	Github repository
<b>Genome wide enhancer prediction with epigenetic markers</b> (on-going) • Use convolutional neural network to predict enhancers in multiple human cell-lines with epigenetics feature.	Github repository

## Selected Publications (full list in Google Scholar)

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- **Md Abid Hasan**, Stefano Lonardi, DeeplyEssential: A deep neural network for predicting essential genes in microbes. In *The 6th International Workshop on CNB: Modeling, Analysis, and Control, New York*, 2019, to appear in BMC Bioinformatics
- Stefano Lonardi, Mara MuozAmatrian, Qihua Liang, Shengqiang Shu, Steve I Wanamaker, Sassoum Lo, Jaakko Tanskanen, Alan H Schulman, Tingting Zhu, MingCheng Luo, Hind Alhakami, Rachid Ounit, **Abid Md Hasan**, Jerome Verdier, Philip A Roberts, Jansen RP Santos, Arsenio Ndeve, Jaroslav Doleel, Jan Vrna, Samuel A Hokin, Andrew D Farmer, Steven B Cannon, Timothy J Close “The genome of cowpea (*Vigna unguiculata* [L.] Walp.)”, *The Plant Journal*, 98 (5), 767-782, June 2019
- **Md Abid Hasan**, Stefano Lonardi, mClass: Cancer type classification with somatic point mutation data. In *16th International Conference RECOMB-CG, QC, Canada*, 2018
- Anton Polishko, **Md Hasan**, Weihua Pan, Evelien M Bunnik, Karine Le Roch, Stefano Lonardi ThIEF: Finding genome-wide trajectories of epigenetics marks. In *17th Workshop of Algorithm and Bioinformatics (WABI), Boston, USA*, 2017
- **Md Abid Hasan**, Md Kamrul Hasan, M Abdul Mottalib, Linear regression based feature selection for microarray data classification. In *Int. Journal of Data Mining and Bioinformatics*, 11(2), 167-179, 2015