

# Curriculum Vitae

## Ahsan Habib Polash

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(DOB: 1987-Nov-14, Age 32; Nationality: Bangladesh)



### Principal Research Areas:

- Cheminformatics/Chemoinformatics, Computational toxicology
- Computational Biology, Genomics, Transcriptomics
- Traceability and interpretability in machine learning

### Educational and Career History (most recent first):

- 2017 - present: **Doctoral Student**, Graduate School of Medicine, Kyoto University.  
Expected completion: March 2021
- 2016 - 2017: Research Student, Department of Radiation Genetics, Graduate School of Medicine, Kyoto University
- 2013 - 2016: **Lecturer**, School of Life Sciences, Independent University Bangladesh
- 2012 - 2013: Research Associate, Molecular Biology Lab, Department of Biochemistry and Molecular Biology, University of Dhaka (BMB-DU).
- 2010 - 2012: Masters of Science in Biochemistry and Molecular Biology, BMB-DU
- 2006 - 2010: Bachelor of Science in Biochemistry and Molecular Biology, BMB-DU

### Summary of Graduate Research Career:

- PhD Topics: Artificial intelligence for drug discovery and chemical toxicity
- Masters Thesis Topics: Analysis of salt stress responsive molecular pathways in Jute (*Corchorus olitorius* var. O-72)

### Selected Research Publications:

2020 : “Active learning efficiently converges on rational limits of toxicity prediction and identifies patterns for molecule design” *Computational Toxicology* 2020. (15), 100129

2019 : “Applicability Domain of Active Learning in Chemical Probe Identification: Convergence in Learning from Non-Specific Compounds and Decision Rule Clarification”, *Molecules* 2019, 24(15), 2716

2019 : Systematic approaches to build predictive models for rat oral toxicity. *CICSJ Bulletin* 2019, 37(1), 12

2018 : “Chemogenomic Active Learning's Domain of Applicability on Small, Sparse qHTS Matrices: A Study Using Cytochrome P450 and Nuclear Hormone Receptor Families”, *ChemMedChem* 2018, 13, 511.

\*Designated Very Important Paper based on peer review reports.

2018: Equal contribution of book chapter, “A Survey of Web-Based Chemogenomic Data Resources”. In: Brown J. (eds) *Computational Chemogenomics. Methods in Molecular Biology*, vol 1825. Humana Press, New York, NY

2015: A diverse community of jute (*Corchorus* spp.) endophytes reveals mutualistic host–microbe interactions. *Annals of Microbiology* (2015) 65: 1615

2013: “*In silico* prediction of structure and functions for some proteins of male-specific region of the human Y chromosome.”, *Interdisciplinary Sciences: Computational Life Sciences* (2013) 5: 258

**Technical Skills:**

- I. Data extraction/curation (RDKit and OpenEye Chemistry Toolkit), SAR analysis, 2D and 3D ligand similarity, Machine learning (Active learning, RF, SVM, DNN; scikit-learn, TensorFlow).
- II. NGS data analysis (CAGE, ChIP-Seq), Transcriptomics data curation and analysis from public databases (TCGA, ENCODE).
- III. DNA/RNA extraction, Molecular cloning, PCR, Immunostaining, Chromosome aberration assay, Clonogenic cell survival assay.

**Computer Skills:**

- I. Linux and Windows OS with common applications.
- II. Python (Fluent), R (Intermediate), Bash shell (Fluent)

**Language Skills:** Bengali (Native), English (Fluent), Japanese (elementary)

**Future Career Goals and Strategies in Research:**

- Contribution to academia through teaching and research
- Employ machine learning and structure based approaches for solving biology questions.
- Interested largely in advanced computational biology, i.e. next-generation sequencing, machine learning.
- Contribution to the fields of genetics and drug discovery through application of the above techniques on clinical or preclinical data.
- Development of practical tools for data visualization aimed at both students and researchers.

**Personality, Work Habits, and Leadership Experience:**

- Considered as a friendly and open minded person by faculty colleagues and students.
- Belief that a positive mindset can provide a significant boost to group performance.
- Capable of making tailored presentations on topics depending on the audience.
- Highly flexible in adapting to the personality of the person or colleague I am exchanging with.
- Able to maintain a dynamic yet well-organized working environment.
- Experience in leading and motivating groups of researchers or community members.
- As a biologist turned informatician, I recognize the critical importance of documentation in computer code, which leads to usability and improved work efficiency in a group. I stress high levels of self-evident documentation.