# Syed Hussain Ather

hussainather.com • https://www.linkedin.com/in/syed-hussain-ather-049919137/ • github.com/hussainather
shussainather@gmail.com • +317 701 1491 • 6270 Canterbury Dr • Zionsville, IN 46077

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## Research Experience

- **University of Toronto**                                                                                  **Toronto, ON**
  *Ph.D. student, Medical Science*                                                               *Adviser: John Griffiths*
  *02/2020 – Present*

  – Performing dynamic causal modeling of neuroimaging data.

- **Google Summer of Code, International Neuroinformatics Coordinating Facility (INCF)**     **Stockholm, Sweden**
  *Summer intern (remote)*                                                          *Advisers: John Griffiths, Rick Gerkin*
  *05/2020 – 09/2020*

  – Performed a Boolean stability test for the equilibria of FitzHugh-Nagumo models.

- **National Institutes of Health**                                                                        **Bethesda, MD**
  *Post-baccalaureate Researcher*                                               *Advisers: Sinisa Pajevic, Harold Burgess*
  *06/2018 – 05/2019*

  – Created an RNA-Seq protocol for analyzing single-cell sequencing data of the zebrafish brain.
  – Simulated the neuronal dynamics of various models.
  – Analyzed potential of machine learning methods in creating more accurate predictions of genetic expression.
  – Performed large-scale simulations of neural circuitry and synapse models for parameter optimization and linear regression through modeling.
  – Examined the statistics of spike trains for determining correlation strength.
  – Engaged in workshops for statistical design and data exploration and analysis of imaging data.
  – Modeled membrane channel dynamics to assess stochastic, deterministic, and statistical features using NEURON and the Blue Brain Project.
  – Compared processes in statistical physics using stochastic differential equations.
  – Compared statistical techniques in R for challenges in genetics and neuroscience.
  – Solved programming puzzles for the heuristics and methods behind them.
  – Surveyed techniques across neuroscience, mathematics, physics, computer science, biology, and philosophy.

- **National Institutes of Health**                                                                        **Bethesda, MD**
  *Bioinformatics Trainee*                                                             *Advisers: Ryan Dale, Elissa Lei*
  *06/2017 – 05/2018*

  – Created a Snakemake workflow for performing ChIP-Seq, RNA-Seq differential splicing, and colocalization analysis from FASTQ files through called peaks which is run in parallel on NIH's Biowulf cluster.
  – Performed Fisher's exact test and Jaccard index in detecting colocalization events.
  – Used deeptools and bedtools in determining the differences between peak-callers.
  – Detected and fixed errors in PeakSeg supervised peak-calling algorithm.
  – Visualized output from ChIP-Seq peak-calling algorithms to understand their differences in terms of biases, underlying assumptions, and applicability to particular datasets.
  – Manually created labels of peak-calling output for learning a model to optimize ChIP-Seq peak-callers.
  – Lead a group of researchers to create `SeqAcademy.org`, a self-guided educational tutorial for RNA-Seq and ChIP-Seq analysis.
  – Used machine learning methods, including exploratory data analysis and feature engineering, with the goal of creating a publishable tool to decide which parameters should be used on a particular dataset.

- **Indiana University-Bloomington**                                                                       **Bloomington, IN**
  *Bioinformatics Undergraduate Research Assistant*                                           *Adviser: Matthew Hahn*
  *09/2013 – 05/2017*

  – Engineered software for constructed gene trees reconciled with MUL-trees to identify and resolve polyploidy events in simulated organisms; parallelized pipeline to increase effectiveness of heavy-input reconciliations.
  – Compared the effectiveness of whole-genome alignment methods in detecting indel mutations.
  – Created algorithms for bioinformatics solutions including sorting, searching, and performing operations on biological data such as splice junctions, de Brujin graphs, and RNA strings.
  – Summarized and discussed implications and methods of research papers during meetings.
  – Created Pac-Man game that eats DNA bases and produces strings of amino acids.

- **Conte Center for Computational Neuropsychiatric Genomics**                                            **Chicago, IL**
  *Undergraduate Research Intern*                                                               *Adviser: Chunyu Liu*
  *06/2015 – 07/2015*

- – Performed RNA-Seq analysis using STAR aligner to analyze genetic expression for significantly expressed genes in the human brain.
- – Updated human brain transcriptome from long reads of PacBio Iso-Seq data; used differential equations and graphs to visualize new isoforms uncovered.

- **Indiana University-Bloomington** **Bloomington, IN**
  *Physics Undergraduate Research Assistant* *Advisers: Adam Szczepaniak, Geoffrey Fox*
  *09/2014 – 05/2015*

  - – Converted scripts between programming languages Python and Fortran for Monte Carlo particle physics simulations; performed statistical analyses of energy and momenta collisions between particles.

- **Boyce Thompson Institute** **Ithaca, NY**
  *Undergraduate Research Intern* *Adviser: Zhangjun Fei*
  *06/2014 – 07/2014*

  - – Performed RNA-Seq analysis using Tuxedo suite on tomatoes to extract genetic information; explored mechanisms behind transcription and protein synthesis.
  - – Implemented novel algorithms to optimize run-times of virus detection software.

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## Education

- **University of Toronto, Ph.D., Medical Science**
  *01/2021 – Present*

- **Foundation for Advanced Education in the Sciences Graduate School at the National Institutes of Health**
  *09/2017 – 05/2019*

- **Indiana University-Bloomington, B.A., Physics**
  *08/2013 – 05/2017*

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## Online Coursework

- **Complexity Explorer**

  - **The Santa Fe Institute**
    - * *Nonlinear Dynamics: Mathematical and Computational Approaches*

- **Coursera**

  - **Duke University**
    - * *Medical Neuroscience*

  - **Stanford University**
    - * *Probabilistic Graphical Models 1: Representation*
    - * *Probabilistic Graphical Models 2: Inference*
    - * *Probabilistic Graphical Models 3: Learning*

  - **University of California, San Diego, and National Research University Higher School of Economics**
    - * *Advanced Algorithms and Complexity*
    - * *Genome Assembly Programming Challenge*

  - **University of California, Santa Cruz**
    - * *Bayesian Statistics: From Concept to Data Analysis, with Honors*

  - **University of Michigan**
    - * *Introduction to Data Science in Python*

  - **University of Washington**
    - * *Computational Neuroscience*
    - * *Machine Learning: Clustering & Retrieval*
    - * *Machine Learning: Classification*
    - * *Machine Learning: Regression*
    - * *Machine Learning Foundations: A Case Study Approach*

- **edX**

  - **Harvard University**
    - * *Fundamentals of Neuroscience, Part 1: The Electrical Properties of the Neuron*
    - * *Fundamentals of Neuroscience, Part 2: Neurons and Networks*
    - * *Fundamentals of Neuroscience, Part 3: The Brain*
    - * *High-Dimensional Data Analysis*

– **Swiss Federal Institute of Technology, Lausanne**
  - ✳ *Computational Neuroscience: Neuronal Dynamics of Cognition*
  - ✳ *Neuronal Dynamics*
  - ✳ *The Multi-Scale Brain*

## Publications

- Ather, S. H. (2021) Catastrophe theory in work from heartbeats to eye movements. In *Biological Cybernetics*.

- Ather, S. H. (2020) Computational approaches to precise toxicology research. In Waste Management: A Reference Handbook, ABC-CLIO.

- Ather, S. H., Awe, O., Butler, T. J., Denka, T., Semick, S., Tang, W. (2018) SeqAcademy: an educational pipeline for RNA-Seq and ChIP-Seq analysis. In *F1000Research.*

- Thomas, G., Ather, S. H., Hahn, M. (2017) Gene-tree reconciliation with MUL-trees to resolve polyploidy events. In *Systematic Biology.*

- Ather, S. H., Zheng, Y., Fei, Z. (2015). RNA-Seq Analysis of lncRNAs and cisNATs in tomato ripening. In *Indiana University Journal of Undergraduate Research*, 1, 34.

## Awards

Rosalind Bioinformatics Contest Finalist, 2019.
Rosalind Bioinformatics Contest Finalist, 2018.
National Association of Science Writers Undergraduate Travel Fellow, 2017.
Second place in Biological Sciences at Emerging Researchers National Conference in STEM, 2016.
Honorable Mention, Academic Excellence, Indiana University-Bloomington Department of Philosophy, 2016.

## Workshops

NEURONUS, Jagiellonian University, 2020
NeuroHackademy, University of Washington, 2020
Krembil Centre for Neuroinformatics, Centre for Addiction and Mental Health, Toronto, Summer School 2020
Columbia Workshop on Brain Circuits, Memory and Computation 2020
Lattices: Algorithms, Complexity, and Cryptography Boot Camp, Simons Institute for the Theory of Computing, 2020
Data Science Hackathon, National Institutes of Health, 2018-2019
Brainhack, 2018-2020
Mathematics of Vision, University of Toronto, 2019
Large Scale Simulations and Data Processing, Society for Neuroscience, 2019
Diving DEAP into Adolescent Brain Cognitive Development (ABCD) Study Data workshop, Society for Neuroscience, 2019
Modeller's Workshop for the Brain Dynamics Toolbox, 2019

## Technical Experience

**Programming Languages:** Julia, Python, R, Perl, MATLAB, Haskell, Unix, HTML, CSS, C, LaTeX, SQL, XML.
**Natural Languages:** Fluent in English, advanced in Arabic, German, Spanish, and Urdu.
**Research Software:** bedtools, BioPython, BluePyOpt, Brain Dynamics Toolbox, Bokeh, CAFFE, Conda, cutadapt, DESeq, deeptools, Django, dupRadar, eFEL, Elephant, Flask, GEKKO, ggplot2, HISAT, intervalstats, kallisto, Keras, Matplotlib, Neo, Neurodynex, NeuroM, NEURON, NiBabel, Nitime, NLTK, pandas, PsychoPy, pygame, PySqlite, PyTorch, qutip, RStan, salmon, scikit-learn, scipy, seaborn, SimPy, Slurm, Snakemake, STAR-aligner, statsmodels, Subread, SymPy, TensorFlow, Tuxedo Suite, XGBoost.