Ali Razzak

Structural Bioinformatician ∘ Data scientist

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I am a Structural Bioinformatician and data scientist who has spent 5 years mastering and implementing big data analysis tools within a Biomedical Context. I developed and integrated computational methods that systematically modelled terabytes of data sets composed of 20+ million data points using machine learning. This was used to identify key elements within intricate molecular systems that contributed towards pharmaceutical and biomedical science and contended with experimental research. Academia has honed my computational prowess and expertise which I am eager to develop.

Employment

06/2018 - 06/2020 | Universitat Basel - Scientific researcher

- Constructed analytical pipelines using **CHARMM**, **GROMACS**, and **CGENFF** and **statistically quantified terabytes of data** using **Python, R, and C++** to investigate **molecular phenomena**.
- Implemented thorough **machine learning algorithms** in **Python and R** using **big data** of **20+ million data points** to identify **critical elements** which govern protein molecular movement.
- Exhaustively **prototyped and bug fixed analytical software** used to handle **big science data** using **C++**.
- Routinely compiled **reports demonstrating project progress** to the science community using 3D histograms, PCA, scatter plots, and correlation matrices in **Python, R, and SQL**.

06/2018 - 06/2020 | Universitat Basel - Practical instructor and Teaching assistant

- Endowed **25+ second year chemistry students** with advanced computational techniques and theory in **quantum mechanics, thermodynamics, and biochemistry** in a comprehensive, and digestible manner.
- Ensured robust **production**, **analysis**, and **visualisation** methods of biomolecular scientific data.
- Mastered guiding students through understanding **quintessential scientific methods and report writing** outlining their scientific learning and understanding using **LaTex, xmgrace and Microsoft Office**.

03/2016 - 06/2018 | University of Auckland - Lab demonstrator (BIOSCI 201, 107, and 95F)

- Taught classrooms of **40+ students** the essentials of effectively **working in a lab environment**.
- Communicated complex **biochemical knowledge** while retaining the **core theory** and ensuring learning.
- Supervised students through correctly using **Excel, MATLAB** and scientific apparatus while conducting scientific experiments.

Education

10/2016 - 03/2018 | University of Auckland - MSc in Bioinformatics Science, First Honours (GPA: 3.5)

- Discovered **novel molecular dynamics** produced through **HPC** in **GROMACS** and **CGENFF**.
- Computationally **modelled interactive networks** between using **Perl, Python, C++, and R**.
- Oversaw **collaborative projects** between the University of Auckland and Massey University.
- Implemented advanced **Computational** Biology applications and findings alongside **experimentalists**.

02/2015 - 10/2016 | University of Auckland - PgDipSci in Biomedical Science, First Honours (GPA: 3.75)
Structural Bioinformatics, immunology, Mathematics, programming, data analysis, statistical modelling.

02/2012 – 10/2014 | University of Auckland - BSc in Biomedical Science (GPA: 3.0)
Microbiology, structural biology, and cancer physiology, immunology.

Key Skills

Data analysis ∘ Statistical analysis ∘ Machine learning ∘ Prototyping and debugging ∘ Handling big data ∘ Biochemical comprehension ∘ Team and objective orientated ∘ Innovative, critical and dialectical problem solver ∘ Dexterous with computational tools ∘ Adaptable to new languages and tools ∘ Focused and conscientious work ethic ∘ Meticulous project planner ∘ Thrive in collaborative projects ∘ Decisive and informed decision maker ∘ English fluency interdisciplinary approach ∘ Bioinformatician ∘ Mastery in code development and execution ∘ Independently driven

Technical Skills

Programming
Proficient: Python (Beautiful Soup, matplotlib, numpy, pandas, plot.ly, sklearn, scipy, selenium, scrappy), R (bio3d), SQL, MongoDB, MATLAB, JavaScript (React, P5, Mongoose, Expression), shell, HTML, CSS, PHP.
Familiar: Perl, C++, shell

Operating Systems
Used: Windows, Linux, Mac OS.

Software
General: Jupyter, Adobe Creative suite, Tensor Flow, Git, Google suite, Excel, Powerpoint, MySQL, R-Studio.
Science: GROMACS, CHARMM, NAMD, VMD, Pymol, gaussian, Chimera, SURFNET.

Core competencies
Used: machine learning (linear regression, k-nearest neighbour, neural networks), statistical modeling (hypothesis testing, ANOVA, multivariate regression, principal component analysis), High performance computing (NeSi, NCCR, SNSF), full stack web development (LAMP, MERN, Django), Cloud Computing (Slurm, SGE).

Relevant conferences

- **Virus Versus Hackathon 2020**
  - Guided implementation of machine learning process to enhance insight of an education app.
- **MUST2018 conference**
  - International conference on Molecular Ultrafast Science and Technology
- **1st CHARMM-GUI CECAM School**
  - Participated to improve CHARMM and Computational ability
- **28th Annual Queenstown Molecular Biology Meeting**
  - Presented Master's work at poster session
- **5th Annual INMS Post-graduate Student's Conference**
  - Presented seminar on Master's work

Additional

- **Selfharm:** organise an international reading group of 40+ participants on contemporary fashion.
- **Cutthwice:** website created using HTML5 frontend with a Jquery, PHP and MySQL backend.
- **Design**: design, print and paste posters, web design, digital animation and leatherwork.
- **Film**: shoot and edit experimental footage, and adamantly believe in the profound language of film.
- **Gigs**: obsessively attend loud and *gnarly* gigs/shows against my better judgement.
- **Writing**: Involved in critical writing of niche Cinema and Fashion literature.