

# Vatsal Mehra

**Bioinformatician, Software Developer**

## Personal Info

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## Education

MS Bioinformatics, 2016  
Marquette University - Milwaukee, USA

BS Computer Engineering, 2010  
NMIMS - Mumbai, India

## Skills

Expert

- Python
- Flask Web Framework
- Bash Shell Scripting
- Javascript
- HTML
- CSS, Bootstrap & JQuery
- D3js
- R
- AngularJS / Angular2
- Vim

Proficient

- NodeJS / ExpressJS
- Git & Mercurial version control systems
- MySQL, MongoDB
- Docker
- AWK & SED

Basic

- Linux System Administration
- Amazon Web Services
- Common Workflow Language

## Bioinformatics Skills

### Data munging & Visualization

- SciPy, Pandas, Scikit-learn
- D3js, Plotly, circosJS, ggplot2, Matplotlib

### Next-Gen sequencing analysis

- DNA-Seq, RNA-seq, ATAC-Seq, ChIP-Seq & MEDIP-Seq

- Bioconductor packages & BioPython library

Highly driven Bioinformatician/Software Developer with over 5 years of experience creating and maintaining robust software for various disciplines ranging from corporate data servers to human genomics and molecular neuroscience.

## Experience

### Programmer Analyst, Medical College of Wisconsin

*Milwaukee, USA | Apr 2018 - July 2018*

- Developed a tool for the Rat Genome database that provides a unique way to seamlessly visualize and perform set operations on large gene lists.

### Bioinformatics Support Analyst, Blood Center of Wisconsin

*Milwaukee, USA | Oct 2016 - March 2018*

- Developed web-based tools using Python (with Flask), that automate and simplify the Bioinformatics workflow of Molecular Diagnostics Lab
- Human clinical genomics- Monitored NGS workflow, develop variant calling and variant annotation pipelines
- Routinely developed Python and Unix shell scripts to automate data manipulation and filtering of metadata associated with patient samples
- Created an interactive web tool that provides a graphical view to analyze nucleotide mismatches between patients

### Consultant Bioinformatician, Biomedical sciences, Marquette University

*Milwaukee, USA | May 2016 - Oct 2016*

- Developed custom shell scripts that automate RNA-Seq, ChIP-Seq & ATAC-Seq workflows
- Performed transcription factor regulatory network analysis using a suite of tools - WGCNA, TF footprinting (PIQ, CENTIPEDE)

### Research Assistant, Marquette University & Blood Center of Wisconsin

*Milwaukee, USA | Aug 2015 - May 2016*

Designed & developed *SNPredict*, a tool that predicts rare somatic variants using multiple machine learning training algorithms like kNN & LinearSVC

### Software Engineer, Tech Mahindra

*Pune, India | Aug 2010 - Nov 2013*

Lead production support duties. Designed, coded and maintained Bash shell scripts to automate tasks for checking and updating status of AT&T servers.

## Publications

- Developmental chromatin restriction of pro-growth gene networks acts as an epigenetic barrier to axon regeneration in cortical neurons. *Venkatesh I, Mehra V, Wang Z, Calliff B.* doi: <https://doi.org/10.1101/259408>. Dev Neurobiology.
- KLF6 and STAT3 co-occupy regulatory DNA and functionally synergize to promote axon growth in CNS neurons. *Wang Z, Mehra V, Simpson M, Maunze B, Eastwood E, Holan L, Blackmore M and Venkatesh I.* Nature Scientific Reports <https://www.nature.com/articles/s41598-018-31101-5>
- The Recipient is the Reference: Sequence level comparison of HLA loci in unrelated hematopoietic cell transplant (HCT) pairs. *Ibrahim Vazirabad, Vatsal Mehra, James Nytes, and Matthew W. Anderson.* Blood (Under Review)
- SNPredict: A Machine Learning Approach for Detecting Low Frequency Variants in Cancer. *Mehra V, Bozdog S* (in prep)