

Vatsal Mehra

Bioinformatician, Software Developer

Personal Info

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vatsalmehra.com

github.com/rdbcasillas

Education

MS Bioinformatics, 2016

Marquette University - Milwaukee, USA

BS Computer Engineering, 2010

NMIMS - Mumbai, India

Skills

Expert

- Python
- Bash Shell Scripting
- Javascript
- HTML 5
- CSS3, Bootstrap & JQuery
- D3js

Proficient

- Vuejs/AngularJS
- Flask Web Framework
- R
- Make/SnakeMake
- Vim
- NodeJS / ExpressJS
- Git & Mercurial version control systems

Basic

- MySQL, MongoDB
- Docker
- AWK & SED
- Linux Administration
- Amazon Web Services

Projects Live Online

- mousebraindev.com - interactive visualizations to gain novel insights from time series NGS experiments on murine whole cortex
- 3dmousebrain.com - 2D and 3D interactive visualizations for quantifying spinal neurons

Podcast

[Cerebral](#) - a podcast exploring human biases to improve thinking and decisions

Experience

Bioinformatician, Biomedical Sciences, Marquette University

Milwaukee, USA | Dec 2019 - Jan 2021

- Created a web tool that allows scientists to visualize ATAC-Seq, RNA-seq and Histone Chip-Seq datasets across different time points in development of mice.
- Developed a website that visualizes and quantifies supra spinal neurons with projections to the cervical, thoracic and lumbar segments.

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 lists of genes.

Bioinformatics Support Analyst, Blood Center of Wisconsin

Milwaukee, USA | Oct 2016 - March 2018

- Developed web-based tools using the Flask framework, that automate and simplify the Bioinformatics workflow of Molecular Diagnostics Lab
- Human clinical genomics- Monitored NGS workflow, develop variant calling and variant annotation pipelines
- Designed and created an interactive web tool VIRAS, that provides a graphical view to analyze nucleotide mismatches between patients [10.1016/j.bbmt.2018.12.006](https://doi.org/10.1016/j.bbmt.2018.12.006)
- Designed and implemented data visualization tools using d3.js to help investigators analyze NGS workflow and patient report data

Consultant Bioinformatician, Biomedical sciences, Marquette University

Milwaukee, USA | May 2016 - Oct 2016

Developed custom shell scripts that automate RNA-Seq, and ChIP-Seq workflows

Research Assistant, Marquette University & Blood Center of Wisconsin

Milwaukee, USA | Aug 2015 - May 2016

Designed & developed *SNPpredict*, 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

- Co-occupancy analysis reveals novel transcriptional synergies for axon growth Venkatesh I, **Mehra V**, Wang Z, Blackmore M doi: <https://doi.org/10.1101/2020.06.12.146159> . *Nature Communications* (in press)
- 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. *Scientific Reports* <https://www.nature.com/articles/s41598-018-31101-5>
- Direct HLA Genetic Comparisons Identify Highly Matched Unrelated Donor/Recipient Pairs with Improved Transplant Outcome. Vazirabad I, **Mehra V**, Chhabra S, Nytes J, Hari P and Anderson M. *Transplantation and Cellular Therapy*