

Michael S. Chimenti, PhD

R, Linux, Git, Excel, NextFlow, Python, AWS

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Director of Bioinformatics - Iowa Institute of Human Genetics, Univ of Iowa. Iowa City, IA. 7/19 - Present

- Lead and manage team of four computational professionals serving University of Iowa researchers
- Improved team revenue ~80% over several years by adopting "agile" project management
- Co-authored >14 publications in high impact journals
- Informatics Testing Director for CAP/CLIA-certified *KidneySeq*[™] targeted NGS panel
- Cofounder of UIHC "10X Visium Spatial Transcriptomics Consortium"

Senior Scientific Advisor and Bioinformatics Consultant - FBB Biomed Remote. 11/22-Present

- Advising development of an RNA-based liquid biopsy diagnostic for neurological disease and cancer
- Leveraging AWS cloud to build back-end infrastructure with S3, AWS Healthomics, SageMaker
- Predictive modeling of RNAseq data using ML tools (PCA, sPLS-DA and XG-boost) resulting in a major provisional patent filing (<https://fbbbio.com/>)

Assistant Research Scientist - Iowa Institute of Human Genetics, U of Iowa. Iowa City, IA. 7/15 - 7/19

- Created IIHG YouTube Channel (18+ technical videos, ~1500 subscribers)
- Co-authored several publications in high impact journals
- Collaborated on a wide array of human and mouse genomics projects (RNA-seq, ChIP-seq, 10X SC-RNAseq, WGS/WES, Illumina PsychArray GWAS, etc.)
- Won \$20,000 research grant for machine-learning on targeted NGS data

Postdoctoral Researcher - University of California at San Francisco, San Francisco, CA. 08/11 - 06/15

- Worked as a lead computational biologist on a discovery team for novel small molecule inhibitors
- Performed computational predictions of ligand binding, providing critical guidance for organic chemists
- I validated binding predictions by performing advanced structural NMR with selective labeling

Postdoctoral Scholar - University of California at San Francisco, San Francisco, CA. 08/09 - 07/11

- Devised and performed computational simulations of a large protein-protein binding complex to study electrostatic interactions. I validated my computational predictions in the laboratory resulting in a highly cited paper.

EDUCATION

The Johns Hopkins University, 2009.

Ph.D., Program in Molecular and Computational Biophysics

The University of Iowa, 2003.

B.Sc. in Biochemistry (with Honors)

AWARDS

1st place in UCSF "Idea to IPO" biotechnology business plan competition (2012), Chapman Charitable Trust *Young Investigator* Fellowship (2003-2009), Student Travel Award PANIC NMR industry conference (2014)

ACTIVITIES

Creator of michaelchimenti.com, a bioinformatics blog awarded 'Top 75 on the Web For Bioinformatics' by FeedSpot.com. **Volunteer Analyst** (Patient Response Team) at the Rare Genomics Institute (2017-2019).

Member, International Society for Computational Biology (2017-present).

CONTINUING EDUCATION AND CERTIFICATIONS

AWS Cloud Practitioner Essentials (AWS); Project Management Foundations (LinkedIn Learning); Strategic Thinking (LinkedIn Learning); Leadership: Practical Skills (LinkedIn Learning); Data Science and Machine Learning Bootcamp with R (Udemy); Machine Learning A-to-Z (Udemy); Algorithms for DNA sequencing (Coursera); Statistics for Genomic Data Science (Coursera); Bioconductor for Genomic Data Science (Coursera); Python for Genomic Data Science (Coursera)

SELECTED PUBLICATIONS

Thurman, Andrew L; Ratcliff, Jason A; Chimenti, Michael S; Pezzulo, Alejandro A. "Differential gene expression analysis for multi-subject single cell RNA sequencing studies with aggregateBioVar" **BMC Bioinformatics**. 2021.

Wang, Zhaoming; Chimenti, Michael S; Strouse, Christopher; Weiner, George J. "T cells, particularly activated CD4+ cells, maintain anti-CD20-mediated NK cell viability and antibody dependent cellular cytotoxicity." **Cancer Immunology, Immunotherapy**. 1-13, 2021.

Merritt, Nicole; Garcia, Keith; Rajendran, Dushyandi; Lin, Zhen-Yuan; Zhang, Xiaomeng; Mitchell, Katrina A; Borcharding, Nicholas; Fullenkamp, Colleen; Chimenti, Michael S; Gingras, Anne-Claude. "TAZ-CAMTA1 and YAP-TFE3 alter the TAZ/YAP transcriptome by recruiting the ATAC histone acetyltransferase complex" **Elife**, 10:e62857. 2021.