

ALI MOHAMMED PIRANI

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SUMMARY

- Bioinformatics Specialist, carrying interdisciplinary experience and expertise in Software Engineering and bioinformatics driven microbial genomics research
- More than 5 years of experience working on various research projects that leverages genomics data to understand the epidemiology of healthcare and community associated infections.
- Expertise in the development and application of computational tools and pipelines for the analysis of Next Generation Sequencing (NGS) data with proficiency in different programming languages and data visualization techniques.
- Past IT industry experience in Web application and database development.

PROFESSIONAL EXPERIENCE

Title: Bioinfo-Comput Biologist Assoc, April 2020 - Present

Place: **The Snitkin Lab, University of Michigan**

Responsibilities:

- Develop novel and scalable Next Generation Sequencing (NGS) data analysis pipeline with on-premise High performance computing resources.
- Perform Quality control analysis to investigate data quality issues and work with wet-lab technicians to optimize processes for data generation.
- Architect and engineer processes that relate to bioinformatics data processing, laboratory information management, and large-scale dataset curation and analysis.
- Perform literature research and acquire new skills that could help adapt to latest technologies/algorithms for genomic analyses.
- Assist in designing and conducting Bioinformatic projects for research grants, in-house projects and formulate customized analysis solutions for collaborators.
- Work collaboratively with the team to analyze problems and continuously improve existing methods, discover new ways to analyze genomic dataset that help answer specific biological questions.
- Interpret and communicate analysis results to internal/external collaborators for efficient decision making.
- Improve the quality, speed and efficacy of current projects through evaluating and benchmarking new software tools and pipeline development.
- Document code and standard operating procedure for in-house pipelines, maintain code infrastructure using GitHub Version Control.
- Assist with manuscript preparation for publications.
- Prepare and teach a three day Microbial Genomics workshop every year to UMICH faculty and students.

Title: **Research Computer Specialist** Mar 2015 – Mar 2020

Place: **The Snitkin Lab, University of Michigan**

- Develop, customize and implement computational tools and programs to analyze sequencing data.
- Develop and maintain automated bioinformatics pipelines for analyzing lab-generated sequencing data and publicly available genetic data;
- Perform quality assessment, genome assembly, mapping, annotation, SNP/Indel analysis, RNA-seq data analysis and data visualization; develop bioinformatics strategies to mine and visualize data;
- Interpret and communicate analysis results to internal/external collaborators for efficient decision making.
- Adapt new skills and learn about latest technologies that could be incorporated in on-going projects and can enhance the pipelines in development.
- Maintain the computational infrastructure required for lab research.

Title: **Graduate Research Assistant** Dec 2013 – Jan 2014

Place: **Jordan lab, Georgia Institute of Technology**

- My research focused on developing an application framework specifically for typing bacterial strains employing k-mer based approach on next generation sequencing data.
- I was also involved in developing a novel genome-based Multi-locus sequence typing (MLST) scheme for *Bordetella pertussis*. I also collaborated with Pertussis lab(CDC) in analyzing the genome arrangements observed in 2014 Vermont and California B. Pertussis outbreak strains.
- I was also involved in the enhancement of Meningococcus Genome Informatics Platform (MGIP) by constantly upgrading, deploying and documenting its features using PHP and MYSQL for optimum outbreak data analysis.

Title: **Software Engineer** Mar 2012 – Jul 2013

Place: **CapGemini India PVT India**

- My responsibility involved development of products through the software lifecycle, from requirements definition through successful deployment of web application while maintaining documentation of activities. It involved design, use and implementation of client database, development of stored procedures to populate, parse, create and display data on web and interaction with clients and fellow software engineer for defining and analyzing the use cases.

ACADEMIC QUALIFICATION

Georgia Institute of Technology, Atlanta, GA
Master of Sciences in Bioinformatics

Aug 2013 - Dec 2014

The Oxford College of Engineering, Bangalore, India.
Bachelor of Engineering in Biotechnology

Aug 2007 - June 2011

TECHNICAL SKILLS

Areas	Technical Skills
Bioinformatics	Microbial NGS and Metagenomics Data Analysis: Quality Control; Comparative Genomics, Gene Expression and Variant Analysis, Bioinformatics pipeline development and visualization, 3- tier web application development, Docker containerization
Programming Languages	Scripting: PERL, BioPerl, AWK, Bash, Python, conda and R(Intermediate) OOP languages: C#, PHP, Linux and SQL Command line, MySQL, HTML/CSS, C(beginner), GitHub version control
Operating Systems	Windows and UNIX environment. Experience in LAMP and WAMP stack (Linux, Apache, MySql, PHP), HPC clusters, Microsoft Visual Studio, Netbeans, MS SQL SERVER, AWS

Publications

Wang, Joyce; Foxman, Betsy; **Pirani, Ali**; Lapp, Zena; Mody, Lona; Snitkin, Evan S; (2020) Application of Combined Genomic and Transfer Analyses to Identify Factors Mediating Regional Spread of Antibiotic-resistant Bacterial Lineages. *Clinical Infectious Diseases* 71 (10), e642-e649

Saund, Katie; Lapp, Zena; Thiede, Stephanie N; **Pirani, Ali**; Snitkin, Evan S; (2020) prewas: data pre-processing for more informative bacterial GWAS. *Microbial genomics* 6 (5)

Sintsova, Anna; Frick-Cheng, Arwen E; Smith, Sara; **Pirani, Ali**; Subashchandrabose, Sargurunathan; Snitkin, Evan S; Mobley, Harry; (2019) Genetically diverse uropathogenic Escherichia coli adopt a common transcriptional program in patients with UTIs. *Elife* 8, e49748

Forsyth, Valerie S; Armbruster, Chelsie E; Smith, Sara N; **Pirani, Ali**; Springman, A Cody; Walters, Matthew S; Nielubowicz, Greta R; Himpel, Stephanie D; Snitkin, Evan S; Mobley, Harry LT; (2018) Rapid growth of uropathogenic Escherichia coli during human urinary tract infection. *MBio* 9 (2)

Martin, Rebekah M; Cao, Jie; Wu, Weisheng; Zhao, Lili; Manthei, David M; **Pirani, Ali**; Snitkin, Evan; Malani, Preeti N; Rao, Krishna; Bachman, Michael A; (2018) Identification of pathogenicity-associated loci in Klebsiella pneumoniae from hospitalized patients. *Msystems* 3 (3)

Eaton, Kathryn; **Pirani, Ali**; Snitkin, Evan S; (2018) Replication Study: Intestinal inflammation targets cancer-inducing activity of the microbiota. *Elife* 7, e34364

Popovich, Kyle J; Snitkin, Evan S; Hota, Bala; Green, Stefan J; **Pirani, Ali**; Aroutcheva, Alla; Weinstein, Robert A; (2017) Genomic and epidemiological evidence for community origins of hospital-onset methicillin-resistant Staphylococcus aureus bloodstream infections. *The Journal of infectious diseases* 215 (11), 1640-1647

Snitkin, Evan S; Won, Sarah; **Pirani, Ali**; Lapp, Zena; Weinstein, Robert A; Lolans, Karen; Hayden, Mary K; (2017) Integrated genomic and interfacility patient-transfer data reveal the transmission pathways of multidrug-resistant Klebsiella pneumoniae in a regional outbreak. *Science translational medicine* 9 (417)

References

References available on request

