Janani Ravi

Pathobiology and Diagnostic Investigation,
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Work Experience

Senior Research Associate   **2018–Present**
Pathobiology and Diagnostic Investigation, Michigan State University, East Lansing, MI

Postdoctoral Research Associate   **2013–2017**
Public Health Research Institute, Rutgers University, Newark, NJ

Visiting Scientist   **Feb–Mar '17**
National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD

Visiting Scientist   **Jan–Feb '15**
Broad Institute, Boston, MA

Postdoctoral Research Associate   **2012–2013**
Dept. of Mathematics, Rutgers University, Piscataway, NJ

Graduate Research Assistant   **2006–2011**
Virginia Tech, Blacksburg, VA

Student Researcher   **2004–2006**
Supercomputing Education Research Centre, Indian Institute of Science, India   2005–2006
Molecular Reproduction, Development and Genetics, Indian Institute of Science, India Summer '05
Center for DNA Fingerprinting and Diagnostics, India   Summer '04

Education

Ph.D. Genetics, Bioinformatics and Computational Biology   **2006–2011**
Virginia Tech, Blacksburg, VA
Dissertation: *Mathematical modeling of pathways involved in cell cycle regulation and cell differentiation*

B.Tech. Industrial Biotechnology   **2002–2006**
Anna University, Chennai, India

Research Interests

- Unraveling molecular mechanisms common between genetic and infectious diseases, to guide targeted drug repurposing
- Identifying genomic signatures, functions, and mechanisms relevant to host-pathogen interactions, to enable understanding and guide diagnosis
- Developing tools and resources for seamlessly relating sequence, structure, and function of genes/proteins in poorly characterized pathogens to enable and guide better prevention, diagnostic and treatment regimen

- Mathematical/statistical modeling of signaling and regulatory networks: host-pathogen interactions, metabolic pathways, and cellular processes.

Publications

- **Ravi J**, Anantharaman V, Aravind L, Gennaro ML. Evolution of the phage shock protein response system across the tree of life. *In preparation.*
- **Ravi J**, Anantharaman V, Aravind L, Gennaro ML. Variations on a theme: Evolution of the phage-shock-protein system in Actinobacteria. Antonie Van Leeuwenhoek. 2018 May;111(5):753-760. PMID: 29488183. [GitHub](#)
- **Ravi J***, Kaufman G*, Rey-Jurado E, Mehra S, Nikolaev EZ, Kaushal D, Sontag ED, Pine R, Tyagi S, Gennaro ML. Single-cell analysis of genes involved in lipid droplet accumulation in *Mycobacterium tuberculosis* infected macrophages. *In preparation.*
- Thorne C, **Ravi J**, Tyson JJ, Lee E. Modeling bistability in the canonical Wnt ⬚signaling pathway. *Submitted.*
- **Ravi J**, Tyson JJ. Modeling the START transition in the budding yeast cell cycle. *Submitted.*
- Chauhan R, **Ravi J**, Datta P, Chen T, Schnappinger D, Bassler K, Balázsi G, Gennaro ML. (2016) Reconstruction and topological characterization of the sigma factor regulatory network of Mycobacterium tuberculosis. *Nature communications.* 7:11062. PMID: 27029515. [GitHub](#)
- Datta P, **Ravi J**, Guerrini V, Chauhan R, Hancioglu B, Igoshin O, Neiditch M, Gennaro ML. (2015) The Psp system of *Mycobacterium tuberculosis* integrates envelope stress sensing and envelope preserving functions. *Molecular Microbiology*. 97: 408-422. PMID: 25899163. [GitHub](#)
- Salamon H, Bruiners N, Lakehal K, Shi L, **Ravi J**, Yamaguchi KD, Pine R, Gennaro ML. (2014) Cutting Edge: Vitamin D regulates lipid metabolism in *Mycobacterium tuberculosis* infection. *Journal of Immunology* 193: 30-34. PMID: 24899504.

Research Experience

Postdoctoral Research, PHRI, Rutgers University   **2013–2017**
PI: Maria Laura Gennaro

- *Delineating the phylogeny and evolution of the phage-shock-protein response system across the tree of life.*
  Collaborators: Vivek Anantharaman and L Aravind (NIH), Matthew Neiditch (Rutgers University), Oleg Igoshin (Rice University), Sarah Fortune (Harvard University).
- *Understanding transcriptional response in Mycobacterium tuberculosis-infected macrophages*:
  - Lipid metabolism genes and pathways that are ⬚induced by *M. tuberculosis* infection of human macrophages under various small molecule perturbations using transcriptomics and single-cell analyses.
  Collaborators: Sanjay Tyagi, Eduardo Sontag and Richard Pine (Rutgers University), Deepak Kaushal (Tulane University), Hugh Salamon (Knowledge Synthesis).
- *Reconstruction and analysis of the sigma factor network in Mycobacterium tuberculosis.*
  Collaborator: Gabor Balázsi (SUNY, Stony Brook).
- *Understanding the commonalities and differences in the deregulation of lipid metabolism between tuberculosis and other disorders, infectious diseases*.
  Collaborator: Arjun Krishnan (Michigan State University).

Postdoctoral Research, Dept. of Mathematics, Rutgers University   **2012–2013**

PI: Eduardo Sontag

- *Modeling bacterial chemotaxis/aerotaxis*:
  - Building a mathematical framework for chemotaxis and aerotaxis in bacteria.
  - Understanding bacterial response in the presence of counter-gradients of nutrients/oxygen.
  Collaborator: Roman Stocker (MIT).

Graduate Research, Virginia Tech   **2006–2011**

PI: John Tyson

- *Modeling the START transition in the budding yeast cell cycle:*
  - Built a detailed mathematical model (~100 ODEs, ~150 parameters) for the START transition in yeast and integrated it with our published model of the whole cell cycle.
  - Model addresses outstanding issues related to the precise mechanism and timing of transcriptional, post-translational and localization events, as well as size control under varying growth conditions.
  - Model consistent with ~200 experimental mutant phenotypes pertaining to the START transition and rest of the cell cycle.
  - Built a basic model for the nutritional effect of size control in budding yeast cells.
  - This mechanism has been incorporated into the existing model of the yeast cell cycle to explain an initial set of START mutants.
- *Modeling bistability in the canonical Wnt pathway:*
  - Built a simplified model based upon the core module of the Wnt canonical pathway, and incorporated additional key regulatory interactions.
  - Model shows that the Wnt signaling pathway can display bistability, in agreement with preliminary experimental results.
  Collaborators: Ethan Lee (Vanderbilt University), Curtis A. Thorne (University of Arizona).

Undergraduate Research, Anna University   **2002–2006**

- **Bachelor's thesis at Indian Institute of Science**   **2005–2006**
  PI: Debnath Pal
  - Reconstruction of the cMyc signaling network for modeling cMyc deregulation in cancer.
  - Construction of a generic mathematical model for cell competition and compensatory proliferation between epithelial cell populations in the wings of *Drosophila melanogaster*.
- **Summer research at Indian Institute of Science**   **May–Jun'05**
  PI: Annapoorni Rangarajan
  - Making stable siRNA constructs for ß-actin to be used in Notch experiments.
- **Summer research at Center for DNA Fingerprinting and Diagnosis**   **May–Jun'04**
  PI: Radha Ramadevi
  - Study of the impact of MTHFR gene polymorphisms on fetal viability in the context of gender bias.

Technical Skills

- *Programming:* R, Matlab, Python, C, C++, Unix/Linux.
- *Data science — analysis & visualization:* Wrangling, exploratory analysis, statistical and machine learning, and visualization of complex data using R programming.

- *Genomic analyses:* Analysis of NGS gene-expression data; Transcriptional regulatory network inference, analysis and visualization; Phylogenetic patterns and functional conservation of regulatory proteins. Software tools: GenomeSpace, IGVtools, SAMtools, Tuxedo Suite, R pipelines for RNA-Seq analysis, Roary for pangenomes, MEME Suite, Cytoscape.
- *Phylogenetic and evolutionary analyses:* Bioinformatics tools including R and shell scripts, and command line execution of BLAST+ package, NR databases, JACKHMMER, BLASTCLUST, HHPRED, Kalign, DaliLite, TMHMM, SignalP, Phobius, Interpro.
- *Dynamical systems and mathematical modeling:* Dynamic Bayesian networks; Construction and simulation of large quantitative models of cellular processes; Deterministic and stochastic modeling (including conversion to differential equations, simulation, parameter estimation, bifurcation analysis). Software tools: XPPaut, Oscill8, JigCell (ModelBuilder, RunManager), PET (Parameter Estimation Toolkit), CRNT (Chemical Reaction Network Toolbox), Copasi, Cell Designer.

Poster, Oral Presentations & Workshops

Workshop & presentation material: jananiravi.github.io/talk
- Introduction to Tidy Data with R workshop. *R-Ladies East Lansing, East Lansing, MI* (Nov 2018)
- Introduction to Data Visualization with R workshop. *R-Ladies East Lansing, East Lansing, MI* (Oct 2018)
- ISMB 2018, *Chicago, IL* (July 2018)
- ASM Tuberculosis 2017, *New York, NY* (April 2017)
- ASM Microbe 2016, *Boston, MA* (June 2016)
- Lipid Research Symposium at the Rutgers Center for Lipid Research, *Rutgers University, New Brunswick, NJ* (November 2015)
- *Institute for Mathematical Sciences, Chennai, India* (October 2014)
- Computational Cell Biology Meeting. *Cold Spring Harbor Laboratories, Long Island, NY* (March 2011)
- Signal Transduction and Gene Regulatory Networks Workshop. *Mathematical Biosciences Institute, OSU, Columbus, OH* (November 2010)
- Gordon Research Conference on Cell Growth and Proliferation. *Colby College, Waterville, ME* (July 2009)
- Computational Cell Biology Meeting. *Cold Spring Harbor Laboratories, Long Island, NY* (March 2009)
- Biological Sciences Research Symposium. *Virginia Tech, Blacksburg, VA* (February 2009)

Meetings

- Computational Genomics workshop. *Center for Cell Circuits, Broad Institute, Boston, MA* (Sep 2014)
- Biomarkers for Tuberculosis: New Questions, New Tools. *Chantilly, VA* (Sep 2013)
- The Cell Cycle Meeting. *Cold Spring Harbor Laboratories, Long Island, NY* (May 2010)
- Joint meeting of the National Centers of Integrative and Systems Biology 2007. *Boston, MA* (Jun 2007)
- Summer Symposium on Systems Biology of Cancer. *Koch Institute for Integrative Cancer Research. MIT, Boston, MA* (Jun 2007)
- ASBMB Meeting. *Washington DC* (Apr–May 2007)

Grants, Awards, Achievements

- 2019 Harvey J Fiege Endowed Research Fund: $25000 for 1 yr, College of Veterinary Medicine, Michigan State University.
- 2018 ISMB: Conference registration grant award.
- 2017 ASM Tuberculosis: Travel grant award.
- 2017 ORAU/ORISE fellowship: Visiting scientist program at NCBI, NIH.
- 2007 P.E.O. International Peace Scholarship: Graduate Research.
- 2006: Graduated with distinction in B. Tech. Industrial Biotechnology at Anna University.

Professional Memberships, Education and Outreach

2006 — 2011	Member and Co-organizer, Asha for Education, Virginia Tech
2014—2015	Member, Postdoc Association, New York Academy of Sciences
2015 —	Member, American Society of Microbiology
2018 —	Member, International Society for Computational Biology Member, American Thoracic Society
2018 —	Founder and Organizer, RLadies East Lansing (https://rladieseastlansing.github.io)