

Karthik R. Padmanabhan, Ph.D.

San Francisco, CA 94117
✉ karthikrp@gmail.com ☎ 812-325-0180 🌐 karthikrp.com in padmanak

PROFESSIONAL SUMMARY

- Bioinformatics Analyst with 9 years of hands-on experience in development of next-gen sequencing pipelines
- Expert in analysis of high-throughput sequencing data, highly collaborative with excellent communication skills

TECHNICAL SKILLS

Software/Tools

- Unix OS, R Bioconductor, RStudio, AWS, bioinformatics tools used in downstream analysis (QC, trimming, alignment, peak-calling, variant calling, sequence annotation, etc.), pathway/regulatory network analysis (iPathwayGuide), visualization (Cytoscape, R Shiny), Machine learning and feature selection (Random forests, Genetic Algorithms, Support Vector Machines), \LaTeX

Languages/Pipeline Development

- R, Python, Perl, JavaScript, Snakemake, Docker, Singularity, slurm, Torque, version control (CVS, git), Jupyter Notebook

Databases

- UCSC Genome Browser, NCBI, KEGG, Reactome, GEO, SRA, ENCODE, Gene Ontology, TCGA

BIOINFORMATICS EXPERIENCE

Staff Scientist, Bioinformatics

Jan 2021- present

Takara Bio USA

San Jose, CA

- Worked on algorithm and UI development for Embgenix PGT-A software for aneuploidy detection (low pass sequencing CNV detection) in embryos
- Collaborated with bench scientists to address bioinformatics needs in DNA-Seq, particularly in reproductive health
- Developed and maintained pipelines and software to aid design of new products in R&D using Python, Shiny and JavaScript

Bioinformatician/Computational Biologist

Sep 2016 - Jan 2021

University of Michigan

Ann Arbor, MI

- Developed, tested and maintained bioinformatics pipelines using Snakemake, R, Python, and open-source bioinformatics tools
- Worked with scientists to develop analysis plans and budgets for bioinformatics/epigenomics research groups
- Applied computational and statistical tools to interpret results from high dimensional genomics experiments derived from high-throughput sequencing (ChIP-Seq, ERRBS/WGBS, bulk/single-cell ATAC-Seq, RNA-Seq, Exome-Seq)
- Organized pre- and post-analysis consultations, generated detailed analysis reports and interpreted results effectively to non-expert audience

Research Assistant

Aug 2012 - Jul 2016

Purdue University

West Lafayette, IN

- Analyzed NGS data (*de novo* transcriptome analysis) from giant ragweed to identify genes responsible for disease resistance
- Performed domain co-occurrence analysis using statistical models for identifying the pairwise probability of protein domains

Data Science Intern

May 2015 - Aug 2015

Monsanto

Chesterfield, MO

- Investigated the effect of metabolites and genes on selected yield-related phenotypes in corn using machine learning algorithms and feature selection methods, generated a list of predictive features affecting the yield of corn
- Collaborated with multi-state teams to design and develop web applications in R Shiny, communicated results effectively with non-specialist scientists from other teams

EDUCATION

Ph.D. Biological Sciences (Computational Life Sciences Program)

Jul 2016

Purdue University

West Lafayette, IN

M.S. Bioinformatics

Jun 2011

Indiana University

Bloomington, IN

B.Tech. Industrial Biotechnology

May 2009

SASTRA University

Tamil Nadu, India

PUBLICATIONS AND PATENTS

- J. Foox, J. Nordlund, C. Lalancette, T. Gong, M. Lacey, S. Lent, B.W. Langhorst, V.K.C. Ponnaluri, L. Williams, **K. Padmanabhan**, et al. "The SEQC2 Epigenomics Quality Control (EpiQC) Study: Comprehensive Characterization of Epigenetic Methods, Reproducibility, and Quantification". *Genome Biology*. 2021 Dec. <https://doi.org/10.1186/s13059-021-02573-y>.
- Z.M. Laubach, J.R. Greenberg, J.W. Turner, T. Montgomery, M.O. Pioon, L. Smale, R. Cavalcante, **K. Padmanabhan**, et al. "Early-life social experience affects offspring DNA methylation and later life stress phenotype". *Nature Communications*. 2021 Jul. doi:10.1038/s41467-021-24583-x.
- N.J. Edwards, E. Hobson, D. Dey, A. Rhodes, C. Pagani, A.L. Strong MD, G.E. Hespe, A. Huber, **K. Padmanabhan**, et al. "High Frequency Spectral Ultrasound Imaging Detects Early Stage Post Traumatic Heterotopic Ossification in Rodent Models". *Stem Cells Dev*. 2021 May. doi: 10.1089/scd.2021.0011.
- C.A. Pagani, A.K. Huber, C. Hwang, S. Marini, **K. Padmanabhan**, et al. "Novel Lineage Tracing System to Identify Site-specific Ectopic Bone Progenitor Cells". *Stem Cell Reports*. 2021 Feb. doi: 10.1016/j.stemcr.2021.01.011.
- P. Venkatraman, I. Mills-Henry, **K. Padmanabhan**, et al. "Rods Contribute to Visual Behavior in Larval Zebrafish". *Investigative Ophthalmology and Visual Science*. 2020 Oct. doi:<https://doi.org/10.1167/iovs.61.12.11>
- A.K. Huber, N. Patel, C.A. Pagani, S. Marini, **K. Padmanabhan**, et al. "Immobilization after injury alters extracellular matrix and stem cell fate". *The Journal of Clinical Investigation*. 2020 Jul. doi: 10.1172/jci136142. - A.K Saha, R. Contreras-Galindo, Y.S. Niknafs, M. Iyer, T. Qin, **K. Padmanabhan**, et al. "The role of the histone H3 variant CENPA in prostate cancer". *Journal of Biological Chemistry*. 2020 May. doi: 10.1074/jbc.RA119.010080
- **K. Padmanabhan**, K. Segobye, S.C. Weller, B. Schulz, M. Gribskov. "Preliminary investigation of glyphosate resistance mechanism in giant ragweed using transcriptome analysis". *F1000 Research*. 2016 Jun. doi: 10.12688/f1000research.8932.1
- B. Schulz, S.C. Weller, M. Gribskov, **K. Padmanabhan**, K. Segobye, "Diagnostic Tools for Herbicide Resistance in Weeds", Application No. 61/910,770 ("Technology"), 2013

PRESENTATIONS

- **K. Padmanabhan**, K. Segobye, S.C. Weller, B. Schulz, M. Gribskov, "Transcriptome Analysis of giant ragweed", Office of Interdisciplinary Graduate Programs Spring Reception, Purdue University, 2015 (Poster Presentation)
- **K. Padmanabhan**, K. Segobye, M. Gribskov, B. Schulz, S.C. Weller, "Molecular Analysis of Glyphosate Resistance in Giant Ragweed", NCWSS Annual Meeting, Minneapolis, MN, December 3, 2014 (Oral Presentation)
- **K. Padmanabhan**, K. Segobye, M. Gribskov, B. Schulz, S.C. Weller, "Molecular Analysis of Glyphosate Resistance in Giant Ragweed", Graduate Student Retreat, Purdue University, 2014 (Oral Presentation)
- **K. Padmanabhan**, N.B. Best, M. Gribskov, S.C. Weller, B. Schulz, "Transcriptome Analysis of Glyphosate Resistance in Giant Ragweed", Joint Annual Meeting of WSSA and CWSS, Vancouver, BC, February 4, 2014 (Oral Presentation).

SELECTED AWARDS

- Purdue Graduate Student Government Travel Award, Purdue University, 2015
- Purdue Graduate Student Government Professional Award, Purdue University, 2014
- Student Innovator Award, Purdue University, 2014
- Summer Institutes in Statistical Genetics Travel Award, University of Washington, 2014
- Best Oral Presentation, Department of Biological Sciences, Purdue University, 2014
- Dr. P.T. Gilham Graduate Award. Purdue University, 2011

TEACHING AND LEADERSHIP

- Assistant Program Coordinator, LSAMP Summer Undergraduate Research Program, 2016
- President/Treasurer/Webmaster, Biological Graduate Student Council, Purdue University, 2012-15
- Organizer/Lead Instructor, Computational Interdisciplinary Graduate Programs RNA-Seq Workshop, 2015
- Webmaster, Society of Industrial and Applied Mathematics, Purdue University, 2012-13
- Teaching Assistant, Purdue University
 - Introduction to R and Bioconductor, Summer 2014
 - Human Anatomy and Physiology Fall 2011 – Spring 2013