Samantha Klasfeld, PhD

Computational Biologist, Bioinformatics

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Summary

- Bioinformatician committed to leveraging data and cutting-edge advancements to effectively build reproducible work and understand complex biological systems.
- Postdoctoral work: Improved analyses of genetic variants in cardiomyopathy, a rare heart condition, by means of state-of-the-art predictions to refine statical power and calculated the significant impact of common variants on cardiomyopathy outcomes in rare variant carriers through regression models.
- PhD work: Optimized, standardized, and published epigenetics data analysis and characterized regulatory pathways involved in cell fate reprogramming.

Technical Skills

- **Workflow development:** published ChIP-seq methods, experience with Github, Docker, conda, Nextflow, Snakemake
- **Programming languages**: Unix/Linux, Python, R programming, command line, git, SQL, Apache spark, Matlab, Perl, and Java
- **Genomics software**: BWA, Bowtie, Bowtie2, STAR, kallisto**,** MACS2, UMAP, Blacklist, DiffBind, DESeq2, EdgeR, sleuth**,** DANPOS2, DANPOS3**,** FASTQC, bedtools, samtools, deeptools, MEME, HOMER, AHA, PBJelly, miRDeep2, miRDeep*, miREAP, miRdentify, Centroidfold, CAP-miRSeq
- **Databases**: UK Biobank, gnomAD, GTex, ClinVar, dbNSFP, Clingen, Genebass, dbSNP
- **Genetics software**: PLINK, VCFtools, bcftools, VEP, LOFTEE, MutPred2, ESM1b, AlphaMissense

Professional Experience

Postdoctoral Fellow, Feb 2022 – Present (3 years)
Pfizer, Internal Medicine Research Unit and Rare Disease Research Unit, Cambridge, MA

- Organized genetic and medical data leveraged from self-reports, electronic health records, and ~500K exomes in the UK biobank and generated version-controlled code with git to ensure reproducibility
- Leveraged latest update of UK Biobank to identify a sufficiently sized cohort of known and novel cardiomyopathy variant carriers to improve upon previous studies without adequate statistical power
- Calculated PRS from relevant GWAS and evaluated logistic, cox, and linear regression to quantify the association of common variants on disease penetrance, onset, and severity among the rare pathogenic variant carriers and use the results to provide genetic insight for decreasing disease outcomes
- Articulated technical genetic study in internal symposiums to showcase my work to multidisciplinary audiences including nonsubject matter experts (eg. biologists, leadership)

Graduate Student Researcher, Aug 2015 – Feb 2022 (6 years)
University of Pennsylvania, Philadelphia, PA

- Developed Greenscreen method to accurately identify and mask false-positive ChIP-seq peaks with efficacy in *Arabidopsis, Drosophila,* and *Oryza sativa* resulting in 1st author publication
- Designed and orchestrated Next Generation Sequencing (NGS) data analysis (eg. ChIP-Seq, RNA-seq, MNase-seq) to measure the activity and outcomes of mobile and DNA binding proteins functional in cellular reprogramming*,* resulting in three 2nd author publications

Postbaccalaureate Fellow, Aug 2014 – June 2015 (1 year)
National Institutes of Health, National Human Genome Research Institute, Bethesda, MD

- Collaborated with computational biologists to analyze the genomes of *Hydractinia echinata* and *Hydractinia symbiolongicarpus* by designing and implementing analysis of novel small RNAs during head regeneration for publication
- Employed a domain architecture search strategy to identify TRAF immune genes in the genomes of multiple eukaryotes to explore cnidarian evolution

Summer Undergraduate Researcher, Jun 2013 – Aug 2013 (3 months)
J. Craig Venter Institute, Rockville, MD

- Investigated novel microRNAs in parasitic nematode *Rotylenchulus reniformis*
- Assessed AHA and PBJelly as gap closing and scaffold tools for *Medicago truncatula* PacBio sequencing data

Summer Undergraduate Researcher, Jun 2012 – Aug 2012 (3 months)
Boyce Thompson Institute, Ithaca, NY

- Improved methods to classify known and novel virus siRNA sequences from sweet potato samples more effectively

Undergraduate Researcher, Aug 2010 – May 2014 (4 years)
Cornell University, Plant Breeding Department, Ithaca, NY

- Compared Genotype by Sequencing data from different restriction enzymes to *Cucurbita pepo* transcript sequences using BLAST
- Developed and tested KASP markers for relevant genes in peppers to make available for breeding work
- Extracted DNA and utilized PCR and DNA sequencing to determine whether a mutation in a predicted gene was responsible for the observed phenotype in peppers.

Education

University of Pennsylvania | Perelman School of Medicine | Philadelphia, PA
Doctor of Philosophy in Genomics and Computational Biology, 2015-2021
Cornell University | College of Agriculture and Life Sciences | Ithaca, NY
Bachelor of Science in Biology, Concentration in Computational Biology, 2010-2014

Publications and Presentations

- **Klasfeld, S.**, Fauman, E.B., Miller, M.R., Moccia, R., & Kim, H.I. (2024, November 5). Coding cis pQTLs from proteogenomic data allow evaluation of the performance of missense variant effect predictions and the utility of their application to rare variant association analyses. [Poster]. American Society of Human Genetics, Denver, CO.
- **Klasfeld, S.**, Moccia, R., Knutson, A., Berghout, J., & Kim, H.I. (2023, November 1). Common genetic modifiers influence disease risk in carriers of rare pathogenic cardiomyopathy variants [Poster]. Pfizer Worldwide Research, Development and Medical Postdoc Symposium, Cambridge, MA.
- Schnitzler, C. E., …, **Klasfeld, S.**, ..., & Baxevanis, A. D. (2023). The genome of the colonial hydroid *Hydractinia* reveals their stem cells utilize a toolkit of evolutionarily shared genes with all animals. bioRxiv.
- **Klasfeld, S.**, Moccia, R., Knutson, A., Berghout, J., & Kim, H.I. (2023, November 2). Genetic modifiers illuminate clinical phenotype penetrance in carriers of rare cardiomyopathy-causal variants [PowerPoint slides]. Pfizer Worldwide Research, Development and Medical Postdoc Symposium, Cambridge, MA.
- **Klasfeld, S.**, Moccia, R., & Berghout, J. (2022, November 2). Genetic modifiers illuminate frequency and penetrance of clinical and subclinical phenotypes in carriers of rare cardiomyopathy-causal variants [Poster]. Pfizer Worldwide Research, Development and Medical Postdoc Symposium, Cambridge, MA.
- **Klasfeld, S.**, & Wagner, D. (2022). Greenscreen decreases Type I Errors and increases true peak detection in genomic datasets including ChIP-seq. bioRxiv.
- Zhu, Y., **Klasfeld, S.**, & Wagner, D. (2021). Molecular regulation of plant developmental transitions and plant architecture via PEPB family proteins–an update on mechanism of action. Journal of Experimental Botany.
- Jin, R., **Klasfeld, S.**, ... & Wagner, D., (2021). LEAFY is a pioneer transcription factor and licenses cell reprogramming to floral fate. Nature communications, 12(1), 1-14.
- Zhu, Y., **Klasfeld, S.**, …, & Wagner, D. (2020). TERMINAL FLOWER 1-FD complex target genes and competition with FLOWERING LOCUS T. Nature communications, 11(1), 1-12. • **Klasfeld, S.**, & Wagner, D. (2019, June 12). Improving resolution of protein binding sites by filtering conserved ultra-high signal in Arabidopsis [Poster]. University of Pennsylvania Genomics and
- Computational Biology Graduate Group Retreat, The College of Physicians of Philadelphia, Philadelphia, PA.
- **Klasfeld, S.**, & Wagner, D. (2018, November 15). Resolving the mechanism of PRC2 during plant stress [Poster]. University of Pennsylvania Epigenetics Retreat, Independence Seaport Museum, Philadelphia, PA.
- **Klasfeld, S.**, & Wagner, D. (2017, October 13). The characterization and discovery of novel Polycomb and Trithorax Recruitment Elements in plants [Poster]. University of Pennsylvania Epigenetics Retreat, Citizens Bank Park, Philadelphia, PA.
- Xiao, J., …, **Klasfeld, S.**, ..., & Wagner, D., (2017). Cis and trans determinants of epigenetic silencing by Polycomb repressive complex 2 in Arabidopsis. Nature genetics, 49(10), p.1546.
- **Klasfeld, S.,** Baxevanis, A., & Schnitzler, C. (2015, October 22). Small RNA discovery and expression during regeneration in the colonial hydroid, Hydractinia [PowerPoint slides]. Bioinformatics Scientific Interest Group (BSIG), NIH.

Selected Awards

- Outstanding Poster Award at NIH Post Baccalaureate Poster Day 2015
- Bioinformatics-Scientific Interest Group 3rd Annual Poster Day Winner (First Place)
- Honorable Mention of the 2016 National Science Foundation (NSF) Graduate Research Fellowship

Leadership Experience

2024	Volunteer for Cambridge Tutoring Plus to aid 8th grade students in their academic, personal, and social growth through free and individualized mentoring (weekly during the school year)
2024	Women in Bioinformatics in Boston Meetup Organizer
2019 – 2021	University of Pennsylvania Data Science Group kaggle team VP (online **machine learning** competitions with a focus on text data). For more information: https://www.kaggle.com/sklasfeld
2020 – 2021	Weekly lessons to teach lab mates ChIP-seq and RNA-seq analysis (22+ lectures)
2020 – 2021	University of Pennsylvania Data Science Group Journal Club VP
2016 – 2020	Choreographed python programming course for graduate students (6-8 lectures/year)
2018	Genomics and Computational Biology Graduate Program Representative
2016	Content developer: discoveringthegenome.org (2 modules)
2015	Philadelphia Science Education Academy teacher to support 1st grade science education (4 classes)