

Kevin L. Keys

SENIOR BIOINFORMATICS SCIENTIST

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Summary

Bioinformatics and Computational Biology for human disease. 15+ years of interdisciplinary research experience in human genomics and computational science. Interested in making genomic medicine equitable and available for all.

Skills

Analysis

statistical genetics, RNA-Seq, scRNA-Seq, differential expression analysis, single cell expression analysis, multiomic analysis, genetic admixture, ancestry estimation, genetic risk scores, human genetic diversity, linear modeling, predictive modeling, machine learning, penalized regression, parallel computing, scientific computing, scientific software engineering

Bioinformatics

PLINK, ADMIXTURE, vcftools, bcftools, samtools, RFMix, EAGLE, GCTA, BOLT-LMM, PrediXcan, limma, GATK, RSEM, STAR, bbtools, FastQC, MultiQC, Cromwell, Nextflow, CellRanger, SPAdes, Seurat, GSEA

Computing

R, Bioconductor, Julia, MATLAB, Python, BASH, LaTeX, Git, SGE, AWS (EC2,S3,ECR,Batch), Docker, PostgreSQL, Terraform, Jupyter, RMarkdown, RShiny

Languages

English, Spanish, Catalan, Portuguese

Experience

AmplifyBio

South San Francisco, CA

SENIOR BIOINFORMATICS SCIENTIST

Feb 2023 - current

- Design and implement cloud-enabled bioinformatics pipelines
- Maintain scalable cloud research computing infrastructure
- Execute statistical analyses of high-dimensional genomic data for cancer immunotherapy

Ambys Medicines

South San Francisco, CA

SENIOR SCIENTIST I, COMPUTATIONAL BIOLOGY

July 2022 - Nov 2022

- Wrote and deployed pipelines for analysis of multi-omic data
- Cleaned and analyzed genomic data in the cloud
- Provided analytic and statistical support for assays into liver function and regeneration
- Structured and organized heterogeneous data sources into a centralized view for rapid therapeutic development

Ambys Medicines

South San Francisco, CA

SCIENTIST II, COMPUTATIONAL BIOLOGY

June 2020 - July 2022

University of California, San Francisco

San Francisco, CA

POSTDOCTORAL SCHOLAR

September 2016 - June 2020

- Studied the ability of transcriptome prediction models to predict across populations for integrative genomic analyses
- Supervised 8 students in projects covering genetic epidemiology and statistical genetics
- Provided data management and interpretation for large-scale whole genome and transcriptome analysis of complex disease

University of California, Los Angeles

GRADUATE STUDENT

Los Angeles, CA

September 2012 - August 2016

- Worked on parallel computing frameworks for high dimensional statistical analysis with ADMM
- Developed proximal algorithms for high-dimensional mathematical (non)convex optimization
- Produced open-source software for hard thresholding algorithms for penalized regression in GWAS
- Summer intern at Freie Universität Berlin implementing support vector machine in SAP HANA Predictive Analytics library for cancer classification

Stanford University

VISITING GRADUATE RESEARCHER

Stanford, CA

September 2014 - June 2015

- Developed mathematical optimization code in Julia
- Translated signals processing algorithms into software suitable for penalized regression in GWAS

Universitat Pompeu Fabra

FULBRIGHT STUDENT RESEARCHER

Barcelona, Spain

September 2010 - June 2011

- Studied fine-grained signals of molecular evolution in human metabolome
- Used BioPerl to query Ensembl gene ontologies and KEGG networks
- Analyzed molecular evolution in aligned primate and rodent orthologous genes with PAML software
- Provided computational and data management support in BASH, R, and Perl
- Summer intern at University of Oxford modeling metabolic network evolution with hidden Markov random fields

The University of Arizona

STUDENT RESEARCH ASSISTANT

Tucson, AZ

June 2007 - May 2010

- Modeled population dynamics and coevolution of languages and genes in eastern Indonesia with genetic, linguistic, and cultural data
- Performed PCR, restriction enzyme assays, and linguistic phylogenetic construction with Swadesh word lists
- Studied hidden Markov models for haplotype imputation

Education

University of California, Los Angeles

PH.D BIOMATHEMATICS

Los Angeles, CA

September 2011 - September 2016

- Dissertation title: Projection algorithms for large scale optimization and genomic data analysis
- Advisor: Kenneth Lange

University of California, Los Angeles

M.S. BIOMATHEMATICS

Los Angeles, CA

September 2011 - December 2012

The University of Arizona

B.S. MATHEMATICS AND B.A. LINGUISTICS

Tucson, AZ

August 2006 - May 2010

Honors & Awards

2020-2025 **Career Development Award (K01 HL153100)**, NIH

San Francisco, CA

2018-2020 **Data Science Fellow**, BIDS-UCSF BCHSI

Berkeley, CA

2015-2016 **Dissertation Year Fellowship**, UCLA (declined)

Los Angeles, CA

2012-2016 **Graduate Research Fellowship**, National Science Foundation

Los Angeles, CA

2011-2012 **Graduate Opportunity Fellowship**, UCLA

Los Angeles, CA

2010-2011 **Student Research Fellow**, Fulbright

Barcelona, Spain

2006-2010 **National Hispanic Scholar Award**, UA

Tucson, AZ