Peter Acuña Combs

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Summary of Qualifications

- Computational biologist with strong bioinformatics skills, quantitative training, and significant bench experience.
- Experienced creating visualizations for complex, multidimensional datasets to highlight interesting and statistically validated biological results.
- Focus on efficient, scalable, and reproducible computational analyses.
- Strong record presenting results at local and national conferences, and in preparing peer-reviewed journal articles.

Relevant Experience

Bioinformatics Data Scientist **May 2019-Present**

Dry Lab Operations Data Science Group, Invitae, San Francisco, CA.

- Worked with cross-functional teams to diagnose issues in the production lab, analyze performance of new assays, and identify and implement process improvements to reduce costs and improve turnaround time.
- Developed and deployed dashboards and tools to empower teammates to monitor production process.
- Mentored colleagues working to gain data science skills.

Postdoctoral Researcher and Staff Research Scientist **2015-2019**

Fraser Lab, Department of Biology, Stanford University.

- Designed experiments and built statistical analysis pipelines to use RNA-seq and other data for probing evolutionary and molecular consequences of diverged cis-regulatory sequences.
- Validated hits using CRISPR/Cas9 Genome Editing
- Pioneered ongoing projects on genetic selection in human and Dictyostelium.
- Managed SLURM server cluster and trained grad students on high throughput reproducible analyses.

Graduate Researcher **2010-2015**

Eisen Lab, Department of Molecular and Cell Biology, University of California, Berkeley.

- Rotation project and PhD research developing methods for spatially resolved RNA-seq expression profiles in order to study regulation of gene expression.
- Validated and improved low-volume RNA-seq methods.
- Explored and managed large scale data sets.

Course Organizer and Instructor **2010-2013**

QB3 Institute, Berkeley, CA.

- Organized and taught wildly popular introductory Python Programming course for biologists.
- Redesigned curriculum and gathered experimental next-gen sequencing data for sample analysis.
- Collaborated with other instructors to assign lectures to maximize learning opportunities for lecturers.

Teaching Assistant and Head Teaching Assistant **2007-2009**

The Summer Science Program, Socorro, NM.

- Prepared and gave lectures on programming with goal of completing data analysis.
- Organized astronomical observing schedules, adjusting for weather and data necessity.
- Led and collaborated with team of TAs to assign duties and grading.

Skills

- Programming Languages: Python (pandas/matplotlib/scipy/scikit-learn), Snakemake, R, SQL, Datalog, Matlab, d3.js, Unix/Linux/awk/bash, C
- Bioinformatics: samtools, bedtools, tophat/cufflinks, STAR, DESeq, BLAST, GATK, git, SLURM, SRA/GEO, etc.
- Bench techniques: Next-gen sequencing, CRISPR/Cas9 editing, molecular cloning, hybrid capture, *in situ* hybridization, other standard molecular biology techniques

For code samples, see https://github.com/petercombs/

Education

2015. PhD in Biophysics. University of California, Berkeley, CA.
Dissertation: Genome-wide Spatial Patterning Data Reveal Mechanisms of Gene Regulation; Advisor: Michael Eisen

2008. AB in Physics, Certificate in Quantitative and Computational Biology. Princeton University, Princeton, NJ.
Senior Thesis: Probing Cell Structural Forces in Escherichia coli; Advisor: Joshua Shaevitz

Selected Publications and Presentations

1. **Article** Spatially varying cis-regulatory divergence in *Drosophila* embryos elucidates cis-regulatory logic. Combs PA, Fraser HB. PLOS Genetics. 2018 14(11): e1007631. https://doi.org/10.1371/journal.pgen.1007631
2. **Article** Tissue-specific cis-regulatory divergence implicates a fatty acid elongase necessary for inhibiting interspecies mating in *Drosophila*. Current Biology. 2018; 28(24):3969-3975. https://doi.org/10.1016/j.cub.2018.10.036
3. **Presentation** March 2017: Cold Spring Harbor Systems Biology Conference, Cold Spring Harbor, NY; Platform presentation, “Spatially varying allele specific expression in Drosophila Hybrids”
4. **Article** Sequencing mRNA from cryo-sliced Drosophila embryos to determine genome-wide spatial patterns of gene expression. Combs PA, Eisen MB. PLoS One. 2013;8(8):e71820. doi: 10.1371/journal.pone.0071820. eCollection 2013.
5. **Article** Cytoplasmic dynein moves through uncoordinated stepping of the AAA+ ring domains. DeWitt MA, Chang AY, Combs PA, Yildiz A. Science. 2012 Jan 13;335(6065):221-5. doi: 10.1126/science.1215804. Epub 2011 Dec 8.
6. **Article** Fine-mapping cis-regulatory variants in diverse human populations. A Tehranchi, B Hie, M Dacre, I Kaplow, K Pettie, P Combs, HB Fraser. eLife 8, e39595
7. **Article** Genome-wide measurement of spatial expression in patterning mutants of Drosophila melanogaster. PA Combs, MB Eisen. F1000Research 6
8. **Article** Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. PA Combs, MB Eisen. PeerJ 3, e869 18 2015
9. **Article** A new system for comparative functional genomics of Saccharomyces yeasts. AA Caudy, *et al.* Genetics 195 (1), 275-287
10. **Article** Actin-like cytoskeleton filaments contribute to cell mechanics in bacteria. S Wang, H Arellano-Santoyo, PA Combs, JW Shaevitz. Proceedings of the National Academy of Sciences 107 (20), 9182-9185

For complete list of publications see http://scholar.google.com/citations?user=kykfLtQAAAAJ