

# Billie A. Gould

San Mateo, CA      [billie.a.gould@gmail.com](mailto:billie.a.gould@gmail.com)      607-220-6005  
<https://www.linkedin.com/in/billiegould>      <https://bitbucket.org/billiegould/>

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## Professional Experience

### Senior Computational Biologist Freenome Inc.

Nov. 2019 - present  
South San Francisco, CA

- Multi-omic data analysis for development of early cancer detection focusing on genomic methylation data.
- Technical lead for multi-cancer modeling and biomarker discovery efforts. Organizes and assigns objectives and key results to team members. Communicates important findings to stakeholders.
- Interviews and returns extensive feedback on incoming Computational Biology job candidates in order to grow out team functionality.

### Bioinformatics Scientist II Guardant Health

April - Sept 2019  
Redwood City, CA

- Genomic data analysis in support of CLIA and FDA certification of CDx ctDNA assays and software validation.

### Computational Biologist Myriad Women's Health (formerly Counsyl Inc.)

Oct. 2017 - April 2019  
South San Francisco, CA

- Modeling and bioinformatic analysis for improvement of NGS disease risk assays and cfDNA prenatal screening.
- Polygenic risk assessment, novel variant detection, application of machine learning methodology to NGS analysis.
- Drafts and carries out early development research proposals in close collaboration with wet lab scientists.

### Data Science Fellow Insight Health Data Science Fellowship

May - July 2017  
San Francisco, CA

- Designed and optimized an RF machine learning model that predicts disease spread in lung cancer patients using transcriptome-wide expression profiles from the Cancer Genome Atlas.

### Postdoctoral Research Associate Dept. of Plant Biology, Michigan State University

Feb 2015-May 2017  
East Lansing, MI

- RNAseq expression analysis and statistical modeling to detect genotype by environment interactions and allele-specific expression patterns (*Mimulus guttatus*).
- Conducted and published statistical analyses of genome-wide association data incorporating diverse environmental and phenotypic data (*Panicum hallii*). Joint Genome Institute collaboration.
- Identified adaptive genes through analyses of genome-wide differentiation, diversity, and selective signatures in a 100-population genomic pool (*Mimulus guttatus*).

### Postdoctoral Research Associate Dept. of Ecology and Evolutionary Biology, University of Toronto

Jan 2013-Feb 2015  
Toronto, ON

- Identified genomic variants controlling climate adaptation in the model plant (*Arabidopsis*) through population genomic analysis of re-sequence data.

## Education

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### Cornell University, Ithaca, NY, February 2013

Doctor of Philosophy, Ecology and Evolutionary Biology (Evolutionary Genetics)

Dissertation: The genetic basis of adaptation to soil aluminum toxicity in wild sweet vernal grass.

### Brandeis University, Waltham, MA, May 2002

Bachelor of Science, Biology, minor in Environmental Studies, *Cum laude*

## **Skills**

- **Python** (i.e. numpy, scikitLearn, pandas, pysam), SQL, cluster computing, Linux environment, BASH, git, Google Cloud Services, Jupyter Notebooks.
- **Statistical computing in R and Python**
  - Supervised and unsupervised machine learning, generalized linear modeling, multivariate statistics, differential expression analysis (RNAseq), clustering, GWAS, outlier analyses, population genetics, Bayesian models/inference, data viz.
  - Bioconductor (e.g. limma, caret, lme, DESeq2, SNPRelate, APE, edgeR, randomForest, WGCNA)
- **Bioinformatics pipeline construction:** (i.e. Snakemake, WDL) read processing, alignment, quality control, and SNP calling, structural variation, in-house and open source tools (i.e. FastQC, BWA/Bowtie, Samtools, GATK/VarScan/SNAPE, VCFtools).
- **Laboratory:** experimental design, NGS library construction, standard nucleic acid isolation, molecular cloning, PCR and other standard molecular biology techniques, microbial culture, flow cytometry.

## **Relevant Publications**

16. **Gould, B**, Palacio-Mejia, JD, Mamidi, S, Barry, K, Jenkins, J, Shmutz, J, Juenger, T, Lowry, D. Population genomics and climate adaptation of a C4 perennial grass, *Panicum hallii* (Poaceae) *BMC Genomics* 19:792
15. **Gould BA**, Chen Y, Lowry DB. Gene regulatory divergence between locally adapted ecotypes in their native habitats. *Molecular Ecology*. 2018. 27:4174-4188
13. **Gould, B**, Chen, Y, Lowry, DL. Pooled Ecotype Sequencing Reveals Candidate Genetic Mechanisms for Adaptive Differentiation and Reproductive Isolation. (2016) *Molecular Ecology*. DOI: 10.1111/mec.13881
11. **Gould, B** and Stinchcombe, J (2016). Population genomic scans suggest novel genes underlie convergent flowering time evolution in the introduced range of *Arabidopsis thaliana*. *Molecular Ecology*. DOI: 10.1111/mec.13643
7. **Gould, B**, McCouch, S, and Geber, M. (2015) *De novo* transcriptome assembly and identification of gene candidates for rapid evolution in response to soil aluminum toxicity in *Anthoxanthum odoratum* at the Park Grass Experiment. *PLOS One* 10:7:e0124424
6. **Gould, B**, McCouch, S, and Geber, M. (2014). Variation in soil aluminum tolerance genes is associated with local adaptation to soils at the Park Grass Experiment. *Molecular Ecology*. 24:6058-72
  - Perspective article: von Wettberg, E, Vance, W, and Rowland, DL. (2014) The Park Grass Experiment and next generation approaches: local adaptation of sweet vernal grass revisited. *Mol. Ecology* 24:5931-5933
4. **Gould, B**, Moeller, DA, Eckhart, VM, Tiffin, P, Fabio, E, and Geber, M. (2013) Local adaptation and range boundary formation in response to complex environmental gradients across the geographical range of *Clarkia xantiana* ssp. *xantiana*. *Journal of Ecology*. 1:95-107
3. **Gould, B**, Leon, B, Buffen, A, and Thompson, L. (2010) Evidence of a high-Andean, mid-Holocene plant community: An ancient DNA analysis of glacially preserved remains. *American Journal of Botany*, 9:1579-84
1. Kramer, EM, Holappa, L, **Gould, B**, Jamarillo, MA, Setnikov, D, and Santiago, PM. (2007) Elaboration of B gene function to include the identity of novel floral organs in the lower eudicot *Aquilegia*. *Plant Cell*, 19:750-766