Sarah G. Odell

Curriculum Vitae

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Education

2017 - Current	**PhD Candidate in Plant Biology**, *University of California, Davis*, Davis, CA.
2017 - 2022	**Master of Science, Plant Biology**, *University of California, Davis*, Davis, CA, GPA: 3.8.
2012 - 2016	**Bachelor of Science, Plant Science**, *Cornell University*, Ithaca, NY, GPA: 3.74.

Work Experience

2017 - Current   **PhD Candidate**, *University of California, Davis*.
- Dissection of agronomic quantitative traits in a maize multi-parent population
- Comparison of statistical power to detect quantitative trait loci using a variety of methods
- Differential expression analysis of a maize multi-parent population under drought and control conditions

2016 - 2017   **Database Curator**, *USDA Western Regional Research Center*.
- Develop scripts for incorporating large batches of published data into a genome database and creating links between different datasets
- Analyze published scientific literature and format peer-reviewed data into GrainGenes, a genome database for Triticeae and Avena species

2014 - 2015   **Student Research Assistant in Buckler Lab for Maize Genetics and Diversity**, *Cornell University*.
- Used variance partitioning variation to determine the amount of variation in resistance to a fungal pathogen that was explained by selected candidate gene families a diverse maize population
- Performed cross- and self-pollinations on maize plants, and maintained nursery populations of maize
- Collected phenotypic data for flowering time, plant height, and grain weight in maize
- Optimized PCR primers to function across multiple diverse maize lines

Publications

Odell, SG, Hudson, AI, Praud, S, Dubreuil, P,Tixier, MH, Ross-Ibarra, J, Runcie, DE. (2022) ***Modeling Allelic Diversity of Multi-parent Mapping Populations Affects Detection of Quantitative Trait Loci***. G3 Genes|Genomes|Genetics, jkac011; doi: https://doi.org/10.1093/g3journal/jkac011

Hudson, AI, **Odell, SG**, Dubreuil, P, Tixier, MH, Praud, S, Runcie, DE, Ross-Ibarra, J. (2022) ***Analysis of genotype by environment interactions in a maize mapping population***. G3 Genes|Genomes|Genetics, jkac013; doi: https://doi.org/10.1093/g3journal/jkac013

Blake, VC, Woodhouse, MR, Lazo, GR, **Odell, SG**, Wight. CP, Tinker, NA, Wang, Y, Gu, YQ, Birkett, CL, Jannink JL, Matthews DE, Hane, DL, Michel, SL, Yao, E, Sen, TZ. (2019) ***GrainGenes: centralized small grain resources and digital platform for geneticists and breeders***, Database, Volume 2019. https://doi.org/10.1093/database/baz065

Odell, SG, Lazo, GR, Woodhouse, MR, Hane, DL, and Sen, TZ. (2017) ***The art of curation at a biological database: Principles and application***. Current Plant Biology, 11-12, pp. 2-11. https://doi.org/10.1016/j.cpb.2017.11.001

Mabaya, E, Mandhania, A, Van der Elst, SC, Xue, K, Li, H, and **Odell, SG**. (2016) ***Challenges and opportunities in South Africa's indigenous plants industry: De Fynne Nursery***. International Journal on Food System Dynamics, 7(2), pp.131-142. https://doi.org/10.18461/ijfsd.v7i2.726

Teaching and Mentorship

2022	Teaching Assistant for BIS 2C: Introductory Biology (UC Davis)
2022	Teaching Assistant for PLS 205: Experimental Design and Analysis (UC Davis)
2021	Teaching Assistant for BIT 150: Applied Bioinformatics (UC Davis)
2018 - 2019	Teaching Assistant for BIS 101D: Genes and Gene Expression (UC Davis)
2019 - 2022	Undergraduate Mentor: Xiaofei Wei

Programs

magicsim (R package), *https://github.com/sarahodell/magicsim*.
- Simulates recombination events along chromosomes using a genetic map as input
- Object-oriented structure allows for the simulation of large populations
- Simulated individuals can be converted into Variant Call Format (VCF) files for downstream analysis
- Functions for visualization of simulated recombinant chromosomes

Skills

Programming:	Python, R, UNIX shell, SQL
High Performance Computing:	SLURM, Snakemake, conda, git
Software:	scikit-learn, R/qtl2, PLINK, bcftools, GATK
Wet Lab:	DNA/RNA Extraction, PCR, Gel Electrophoresis, Media Preparation, Sterile Technique
Other:	Research Proposals, Grant Writing, Public Speaking

Presentations & Posters

Talks:

2019	"Reproducible and Interpretable Data Management: Looking Out for Future You (And Other People Too)", Plant and Animal Genome Conference
2018	"Using Statistical Inference of Genotypes to Increase Power in Multi-parent QTL Mapping", UC Davis Plant Biology Colloqium

Posters:

2019	"Haplotype Analysis of a Maize Multi-parent Population to Increase Power in Finding QTL", Maize Genetics Conference
2017	"GrainGenes Update: Curating new resources for the small grains community", 10th International Biocuration Conference

Fellowships and Awards

2019	Henry A. Jastro Graduate Research Award, UC Davis ($1,400)
2019	University of Seattle Summer Short Course in Statistical Genetics Scholarship ($1,500)
2018 - 2022	Department of Plant Sciences Graduate Research Fellowship, UC Davis ($80,000)
2013 - 2016	Cornell University Dean's List
2014	Pi Alpha Xi National Horticultural Honors Society
2012	Marvin L. Lindner Scholarship ($3,000)

Service

2019 - 2020   WiLD (Women in Life Sciences Davis) Administrative Committee

2018 - 2019   Graduate Student Assocation Representative for Plant Biology Graduate Group

2018 - 2019   UC Davis Plant Science Symposium Organization Committee

References

Daniel Runcie
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University of California, Davis
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Jeffrey Ross-Ibarra
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Taner Sen
Supervisor, GrainGenes Team Leader
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Edward Buckler
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Cornell University (Ithaca, NY)
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