Genome Hunters:
A Quantitative Biology Course-Based Undergraduate Research Experience (CURE)

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Why a Q-Bio CURE?

Biology undergraduates vary in their attitudes towards and anxiety about math.1,2 However, modern biological problems require strong foundational skills in math and data literacy.3,4 An introductory Q-Bio CURE may improve student learning,5 build positive attitudes,6,7 and prepare and retain a diverse cohort of students8 for careers in quantitative biology.

Course Learning Goals

> Cultivate positive math-biology values
> Improve ability to collaborate in diverse teams
> Develop model thinking
> Build programming skills

Assessing Attitudes (Pre-Post)

> Math-biology values9, math anxiety10, and programming anxiety11
> Science attitudes (CURE survey)12

Student-designed Projects (weeks 4–10)

Peers use rubrics to review:
- initial idea pitches
- early results
- draft of full manuscript

Small-group workshops build skills:
- structuring an academic paper
- literature review13
- presentation best practices

What’s Next?

> Expand CURE to multiple sections
> Focus specifically on math-biology self-efficacy
> Bring in grad student and postdoc mentors7
> Flip more coding material using Swirl14

Acknowledgements

Sarah Andrews, Miranda Chen, and Nicole Chodkowski provided feedback on assessments. Marc Facciotti, John Albeck, Hyunsoo Kim, and Joel Rodriguez-Medina taught and provided input on assessment design and quantitative material. This project was funded by an HHMI grant to Mark Goldman.

Your Feedback

Thank you for any suggestions, questions, and ideas. Please swing by the July 27th community hour, 5–6pm ET, or email me (refurrow@ucdavis.edu) with any feedback.

Example Lessons

Genome assembly
1. Assemble physical “reads” of text
2. Formalize assembly algorithm
3. Use scaffolded R notebook to assemble example DNA reads and calculate coverage
4. Assess assembly quality of course genomes

Clustering
1. Visually cluster genomes by amino acid usage
2. Define a metric for distance between genomes
3. Use hierarchical clustering in R with their distance metric
4. Cluster the course genomes to infer halotolerance strategies

Salt ponds in the southern San Francisco Bay

Topic: Halophile Genomics

Students: 1st year undergraduates
Fall: culture microbes, quantitatively characterize halotolerance
Spring: bioinformatic analysis of the whole-genome sequences

Quantitative Labs (weeks 1–6)

1. Explore tangible example of concept
2. Design algorithm in small groups
3. Implement using code in R
4. Apply to novel microbial genomes

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