BiographI at CSU: Improving Students Graph Interpretation and Broadening Science Identities

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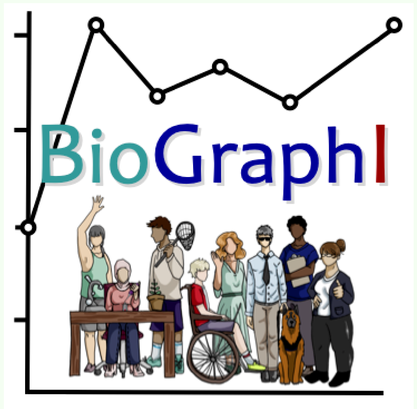
What is BiographI?

- Biologists and Graph Interpretation (BioGraphI) is a Research Coordination Network of faculty who work collaboratively to increase student persistence in biology through improving representation of diverse scientists in the curriculum and incorporating data interpretation skills



BioGraphI modules

- address data literacy while fostering diversity in undergraduate biology classrooms.
- lessons about graph and data interpretation,
- featuring the research of biologists who are members of historically excluded groups (HEGs).
- include video interviews with these biologists, allowing students to hear directly from HEGs about their discoveries.

BioGraphI Faculty Mentoring Network

- Meet every other week Fall 2023
- Discussed Inclusive Teaching
- Developed a BiographI module
- Worked to align with Universal Design for Learning principles

Our Module: *Mysteries of the Heart: Discovering genes that may be associated with atrial fibrillation*

Content learning objective(s) :

- Define Atrial Fibrillation and its associated risks
- Describe what noncoding RNA is and its characteristics
- Explain the possible role of PANCR in heart development

Quantitative learning objective(s)

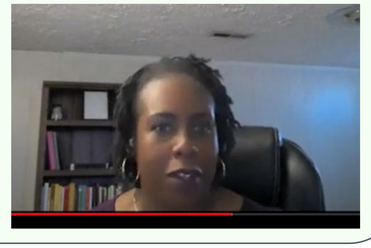
- Interpret graphs and/or data figures related to the concepts from this lesson
- Reflect on your perceptions about using graphs or figures in biology.

Diversity/equity/inclusion learning objective(s)

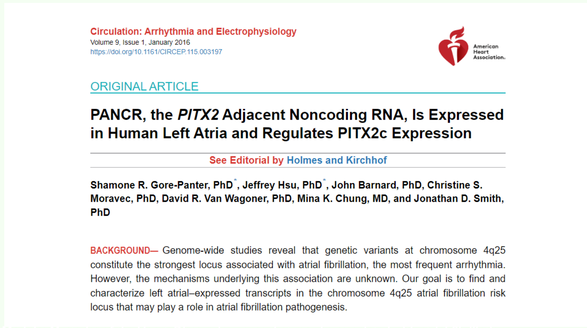
- Reflect on your perceptions of people who do biology.
- Compare your own interests and/or identities to those of people who do biology.

Interview with Dr. Shamone Gore Panter

Researcher, Educator and Medical Student



Module Focus: Dr. Gore Panter's cardiovascular research



Circulation: Arrhythmia and Electrophysiology
Volume 9, Issue 1, January 2016
https://doi.org/10.1161/CIRCEP.115.003197

American Heart Association.

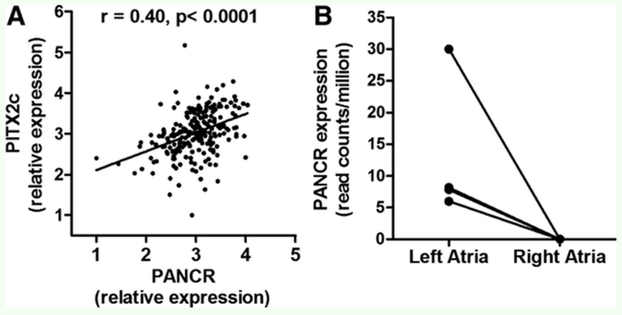
ORIGINAL ARTICLE

PANCR, the *PITX2* Adjacent Noncoding RNA, Is Expressed in Human Left Atria and Regulates PITX2c Expression

See Editorial by Holmes and Kirchhof

Shamone R. Gore-Panter, PhD, Jeffrey Hsu, PhD, John Barnard, PhD, Christine S. Moravec, PhD, David R. Van Wagoner, PhD, Mina K. Chung, MD, and Jonathan D. Smith, PhD

BACKGROUND— Genome-wide studies reveal that genetic variants at chromosome 4q25 constitute the strongest locus associated with atrial fibrillation, the most frequent arrhythmia. However, the mechanisms underlying this association are unknown. Our goal is to find and characterize left atrial–expressed transcripts in the chromosome 4q25 atrial fibrillation risk locus that may play a role in atrial fibrillation pathogenesis.



Next steps:

- Finish module development
- Publish module on QUBES
- Co-lead the Summer 2024 Cohort

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