Classroom crowdscience: UC students challenged to detect schizophrenia genes

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Teaching big data to future scientists means having them think creatively about ways to harness the terabytes of information available to them. To that end, systems biologist Trey Ideker used his UC San Diego School of

Medicine's Biological Networks and Biomedicine graduate course to host a classroom competition tasking students with detecting genes associated with schizophrenia. The winning technique was quick, flexible, and outperformed previously published methods. The details appear April 24 in the journal *Cell Systems*.

"The challenge was interesting because you typically try to directly answer a problem with the most obvious, least risky solution," says Yue Qin, a second year Ph.D. student in the Bioinformatics and Systems Biology program at UC San Diego, and whose group won the challenge. "But because we had several groups all working on the same problem, we could take creative risks and explore the current techniques available to us in ways you wouldn't under normal research conditions."

The competition involved ten groups of two to three students utilizing open-source codebases to identify gene networks associated with schizophrenia. Nearly half of the class followed a pipeline that outlined the steps necessary to complete the analysis, making small adjustments along the way, while the other half, although still following the same pipeline, diverged more drastically from the provided format.

"It may just be that any time you have people in groups, you're going to find a dominant mode and then the real diversity is going to be on the tail of that distribution," says Ideker, the Director of the National Resource for Network Biology.

He notes that although Qin's group's method performed best, other approaches may have seen similar success had the students been provided more time with which to perfect their techniques. "You can't get out of the time limitation, and you feel that acutely through the course," he says.

Overall, Ideker recommends this course style to his colleagues, and his

students view it as an effective learning opportunity. "As a graduate student, all you want is to work on a novel research project and apply the information you've been learning," says Isaac Shamie, a third year Ph.D. student in Bioinformatics and Systems Biology who is the teaching assistant for the class's second semester. "And this class was an opportunity to do just that."

A second article describing the winning team's findings was published in the journal *iScience*. The method, known as Network Assisted Genomic Association (NAGA), recovered 33 known schizophrenia genes in the top-ranked 100, ran the analysis in under five minutes, and outperformed previously published approaches, the authors write. Further, by utilizing an open-source codebase of protein networks, the technique is not only accessible, but also able to incorporate up-to-date gene associations.

"This outcome was exactly what I was hoping for; students are getting a higher degree to do science and to start their career as a researcher, and this class allows them to do that," Ideker says. "I'm excited to teach the class again this year."

  More information: *Cell Systems*, Fong et al.: "Strategies for Network GWAS Evaluated using Classroom Crowd Science" www.cell.com/cell-systems/full … 2405-4712(19)30116-4 , DOI: 10.1016/j.cels.2019.03.013

iScience, Carlin and Fong et al: "A fast and flexible framework for network assisted genomic association" - Publication forthcoming.

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