

## CAGI5 Post-conference survey feedback (60% of attendees responded)

### 1. Did you enjoy the conference?

I had a great time! 61%      Yes 39%      No 0%

### 2. Did the conference impact your research direction in any way?

Yes, significantly 46%      Yes, slightly 33%      No 21%

### 3. How useful was the conference to you?

Extremely useful 39%  
Moderately useful 49%  
Slightly useful 12%  
Neither useful nor useless 0%  
Useless 0%

### 4. How was the food?

Delicious 70%      Edible 30%      Ugh 0%

### 5. Did you make use of the lactation and family room accommodations?

Yes 0%      No 100%

### 6. Did you receive a CAGI Fellowship?

Yes 27%      No 73%

### 7. What have you found valuable about CAGI? (if any collaborative activity arose from CAGI and during the conference please let us know)

It was our lab's first CAGI experience and it was wonderful. Scientifically, we are working on predicting various levels of mutational effects, a topic CAGI fosters; and I was strongly impressed by the width and the depth of the related scientific problems present in CAGI challenges. Importantly, these carefully-made challenges brought us closer to real-world healthcare challenges which are now made computationally tangible and rationally accessible with proper problem/scope definition and data availability. The experiences help me better define, formulate, and approach certain scientific problems to advance on the overarching challenges about genotype-phenotype relationships. I would like to take the opportunity to thank the CAGI organizers again for the great efforts to foster the scientific community to work on the big challenges.

Its great to come together with the variant interpretation community on these shared challenges to see what is working and what is not.

It's good to observe that sometimes CAGI academic predictors are doing a better job than standard companies in handling these challenges.

Small meeting facilitates discussions with other participants.

understanding the complexity of data sharing

A collaborative plan with all the people trying to annotate variants in proteins

I have found contact with other CAGI participants extremely useful, and have indeed, co-authored papers based on CAGI. I can't point to specific collaborative activities that arose from this conference, but my participation re-invigorated research that is, by its nature, highly likely to result in collaboration.

Got an awareness of the methods and approaches others are taking to solve missense impact predictions methods. It also helped me to expand my scientific network with amazing PIs, grad students and PostDocs.

Making connections within the industry

I liked to see the different approaches used to address each challenge. Also, some discussions/comments were very insightful, e.g. how splice effects can complement pathogenicity predictors.

Meeting data providers and predictors

Insightful discussion sessions of each topic

I've found valuable perspective on the state of the art on variant interpretation, including excellent perspective on how the state of the art might further improve.

Networking

***8. Comments or suggestions for the organizers, including about meeting structure, location, the mix of talks***

It's good so far.

Very well organized!

create incentives for people to not be on devices.

I like the formula. Only remark: it would be extremely useful to know the evaluations a little bit in advance and not during the meeting

Too late announcement! Otherwise location was good. Sunlight for jetlag people :-). Also food/coffee/tee provided (extreme improvement compared to the ISMB)

No comments.

Some assessments were very poor, using only limited (e.g one) criteria for success. Perhaps the organizers can help the assessors by providing guidelines with multiple suggested criteria for success. Also, it will be nice to understand which method performed best overall, and whether different methods performed best for different criteria of success (these were not clear in several of the assessments). Perhaps, the assessor should present a slide with an overview of the worth to mention (if not all) predictor approaches (prepared by each predictor), as it is understood that there was no time for multiple predictors to present. I appreciated the assessors gave emphasis to predictors that worked well and not to methods that did not work well, as inappropriate use/adjustments to a method can make it look bad. However, it would be nice if someone (the assessor or any CAGI personel) could try to apply as many of the currently available state-of-the-art methods (not just SIFT and PolyPhen).

Need better organization and design of the assessment.

The last meeting included an emphasis on how variant prediction needs to evolve to address clinical needs. It would be great to have the perspective of a clinician, such as a genetic counselor. I especially recommend Barry Tong at UCSF.

The evaluators should be given ample time to analyze, interpret and provide a thorough presentation of their work. The presentations were often preliminary and difficult to contextualize for discussions.

Schedule should have been decided weeks in advance

CAGI rocks.