

# Critical Assessment of Genome Interpretation (CAGI) Developer (Programmer/Analyst)



**Research Group of Steven Brenner  
University of California, Berkeley**

*Establish the state-of-the-art in genome interpretation*

We are seeking a developer for the Critical Assessment of Genome Interpretation (CAGI, \k̄ājē), a community experiment to evaluate the prediction of phenotypes from genetic variation. CAGI objectively assesses computational methods for predicting the phenotypic impacts of genomic variation, particularly in the context of human disease and personalized medicine. In this experiment, modeled on the Critical Assessment of Structure Prediction (CASP), participants are provided genotypic data and make predictions of resulting molecular, cellular, or organismal phenotypes. Independent assessors evaluate these predictions against experimental and clinical characterizations. Community workshops are held to disseminate results, assess our collective ability to make accurate and meaningful phenotypic predictions, and better understand progress in the field. From this experiment, we identify bottlenecks in genome interpretation, inform critical areas of future research, and connect researchers from diverse disciplines whose expertise is essential to methods for genome interpretation. The third CAGI experiment assessed 188 predictions for ten diverse computational challenges. These predictions were made by 82 predictors hailing from labs located in 15 countries. The fourth CAGI experiment is being organized now.

The CAGI Developer will be responsible for development, maintenance, and operation of the CAGI data resources including the website, as well as providing user support. This involves having a robust information system that can securely store the prediction data and make challenges available, implementing automated assessment protocols developed in conjunction with the CAGI Lead Scientist and assessors, developing systematic ways of receiving predictions, providing appropriate access permission on prediction submissions for assessors, and providing access to meeting results (including videos of meetings and other resources) via the CAGI website.

For more information, see <http://compbio.berkeley.edu>  
<http://genomeinterpretation.org>

Other related positions may be available; inquire with [jobs@compbio.berkeley.edu](mailto:jobs@compbio.berkeley.edu).

## **The Berkeley academic environment**

The Brenner lab is an interdisciplinary research group at the University of California, Berkeley, one of the world's premiere research universities. We are associated with the Department of Plant and Microbial Biology, the Department of Molecular and Cell Biology, the Department of Bioengineering, the Center for Computational Biology, and the California Institute for Quantitative Biosciences, as well as the University of California, San Francisco, and Lawrence Berkeley National Lab.

The University of California, Berkeley ranks first nationally in the number of graduate programs in the top 10 in their fields, according to the most recent National Research Council study.

CAGI is jointly run with the John Moulton lab at the University of Maryland. Funding is provided by the National Human Genome Research Institute and the National Cancer Institute of the NIH.

Collaborators in this project include members of the Berkeley Center for Computational Biology, biologists and engineers at Tata Consulting Services, and clinicians at UCSF. The CAGI experiment engages a vibrant community. In addition to predictors, it includes dataset providers, advisory board and scientific council, and assessors: *Advisory Board*: Russ Altman, George Church, Tim Hubbard, Sean Mooney, Pauline Ng, Susanna Repo; *Scientific Council*: Patricia Babbitt, Atul Butte, Garry Cutting, Laura Elnitski, Reece Hart, Ryan Hernandez, Rachel Karchin, Robert Nussbaum, Michael Snyder, Shamil Sunyaev, Joris Veltman, Liping Wei; *Data providers for previous CAGIs include*: Adam Arkin, Madeleine Price Ball, Jason Bobe, George Church, Andre Franke, Nina Gonzaludo, Emma D'Andrea, Lisa Elefanti, Joe W. Gray, Linnea Jansson, John P. Kane, Pui-Yan Kwok, Rick Lathrop, Angel C. Y. Mak, Mary J. Malloy, Chiara Menin, John Moulton, Robert Nussbaum, Lipika R. Pal, Clive R. Pullinger, Jasper Rine, Maria Chiara Scaini, Jeremy Sanford, Nicole Schmitt, Jay Shendure, Michael Snyder, Tim Sterne-Weiler, Paul L. F. Tang, Sean Tavtigian, Silvio Tosatto; *Assessors*: Rui Chen, Roland Dunbrack, Iddo Friedberg, Gad Getz, Rachel Karchin, Alexander Morgan, Sean Mooney, John Moulton, Robert Nussbaum, Jeremy Sanford, David B. Searls, Artem Sokolov, Josh Stuart, Shamil Sunyaev, Sean Tavtigian, Silvio Tosatto.

### **Qualifications**

Bachelors degree or equivalent in computer science or related field. Candidates must have knowledge of web development platforms and languages (e.g. Drupal, CGI, etc.). Experience in web design and development in a professional environment is preferred. Candidates must have knowledge of database development, as well as the ability to read, write, and modify software in scripting languages (e.g. Python, Perl, etc.). Knowledge of statistical analysis is preferred. Candidates must also have skills necessary to communicate effectively both in writing and verbally.

### **To Apply**

Please apply by email to [jobs@compbio.berkeley.edu](mailto:jobs@compbio.berkeley.edu).

Interested individuals should include a 1 page statement of interest, transcripts, and a current resume. Applicants should also arrange for 3 letters of reference to be sent to Dr. Brenner's attention at [jobs@compbio.berkeley.edu](mailto:jobs@compbio.berkeley.edu).

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination affirmative action policy see: <http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct>.