

POSITIONS IN COMPUTATIONAL GENETICS – THE MARTH LABORATORY/UNIVERSITY OF UTAH



MAY 7, 2016

Gabor Marth's laboratory (http://marthlab.org) develops novel computational algorithms for analyzing genomic variants and mutations, and for elucidating cancer evolution. We participate in large genomic consortium projects (e.g. the Human Genome Structural Variation Consortium and the Simon's Foundation Autism Research Initiative), and in translational research together with clinical researchers and diagnostic clinicians. Our main projects are:

- Graph approaches for genome representation, mapping, genetic variant discovery, and variant interpretation
- Reference-free methods for detecting germline or somatically acquired de novo mutations
- Algorithms for reconstructing tumor subclone evolution to dissect cellular heterogeneity in cancer patients
- Web-based analysis tools for interactive analysis of genomic big data (http://iobio.io).

We have several position openings for postdoctoral researchers, graduate students, as well as scientific and web programmers, to drive genomic analysis algorithm and software development. We are looking for scientists with a strong interest and background in computational algorithm design, and experience with software development. Familiarity with genomics and computational biology is a plus. Successful candidates will join a vibrant community of computational and experimental scientists, as part of the USTAR Center for Genetic Discovery (http://ucgd.genetics.utah.edu). We are located within the Eccles Institute of Human Genetics on the University of Utah Medical School campus in Salt Lake City, UT, lying at the interface between basic and clinical sciences, with ample opportunities for interdisciplinary studies. The institution is set in a unique recreational and geographical landscape that attracts a very diverse and productive scientific community.

For more information or to apply please contact Dr. Mary Anne Karren at makarren@genetics.utah.edu.

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