

8/19/09

Postdoctoral Research Fellow in Statistical inference tools for computationally intensive genome wide association mapping

Available: October 2009 till...

Location: Plant Sciences: University of California, Davis

As part of the iPlant Grand Challenge Initiative, a cross-disciplinary research team is developing computational tools to exploit genome wide association mapping using statistical inference tools. The successful candidate will work as part of a team to develop tools to facilitate a better and broader use of quantitative genomics by the general research community. This project will largely focus on computational analysis of existing genome wide association data potentially utilizing computational integration into supercomputing or distributed grid systems to allow for more complex algorithms to better identify causal genotype variation. Additionally, the project will work to develop packages that allow for the inclusion of network models within the statistical analysis to better incorporate multiple data sources and phenotypic information for genome wide association mapping and QTL mapping. The positions are sponsored by the iPlant Collaborative (<http://iplantcollaborative.org>), which implements cyberinfrastructure support for Grand Challenge research across the plant sciences.

Individuals will work in a team setting with other postdoctoral researchers and computational programmers to have a key role in issues related to genotype-to-phenotype cyberinfrastructure development. There are five working groups are broadly defined as NextGen Sequence Analysis, Statistical Inference Tool Development (this project), Modeling Tool Development, Data Visualization and Analytic Tools and Data Integration. Indeed, travel between participating labs and Institutions of the G2P consortium is strongly encouraged and will be supported through iPlant funding. This project's working group will involve interactions with groups that allow for phenotypic datasets coming from Arabidopsis, maize, rice and other species. This will allow for the generation of novel and publishable insights into network analysis of pre-existing datasets as well as essential input into the development and analysis of new datasets from external funding sources as a part of the working group. We anticipate that the PDF's will help connect working groups providing exciting challenges and opportunities to help shape the future of plant science.

Qualifications include familiarity with quantitative genetics (preferably, but not necessarily, plant-centered) and bioinformatic tools; programming experience (at the level of a scripting language such as PERL or Python). Top applicants will have experience in computational analysis, quantitative genetics and plant biology. The position is available immediately but the start date is flexible. Salary will be commensurate with experience; the position also includes health insurance and other benefits.

The iPlant group and Kliebenstein laboratory are interactive groups at the forefront of applying genomics techniques to understanding the molecular basis of phenotypic generation in both an ecological and applied context. We have numerous international collaborations and opportunities with an excellent track record of placing individuals in advanced positions.

For more information contact Dr. Kliebenstein via phone at (530) 754-7775 or via e-mail. The position will become available October 1. A full description of the iPlant G2P project can be found online at <http://ipg2p.iplantcollaborative.org>.