Position: Assistant Project Scientist (Bioinformatics)
Field of Research: Plant Biology, Genomics, Bioinformatics, Computer Science or highly-related field

The Department of Botany & Plant Sciences, Institute for Integrative Genome Biology at the University of California, Riverside (UCR) is inviting applications for an Assistant Project Scientist under a recently awarded USDA grant to investigate the mechanisms of Plant-Microbe interactions on a genome scale. The project, entitled "***Design and Delivery of Therapeutic Proteins for HLB Protection***" will address the mechanisms of pathogenesis on a genome-scale (e.g. comparative analysis of multiple host-pathogen Protein Interaction Networks (PINs) that may allow us to identify conserved mechanisms of pathogen cellular invasion), and (ii) provide bioinformatics solutions / tools to visualize such PINs in a user-friendly way. The long-term goal of this project is to develop novel protein therapy to protect against HLB based upon enhancing innate immune defense in citrus.

Duration of Appointment and Salary: Initial appointment is for one year, reappointment for second year is possible and funding is in place. Salary is competitive and commensurate with experience. Renewal of the appointment will be contingent upon the availability of adequate funding and individual performance.

Principal Responsibilities:
The successful candidate will join the laboratories of Drs. Mikeal L. Roose and Rakesh Kaundal to develop systems bioinformatics approaches to decipher plant host-pathogen interaction networks. The appointee will focus on system and data integration, algorithm development and computational modeling of the interactions among *Candidatus* Liberibacter asiaticus (CLas) proteins and Citrus proteins using diverse data types or properties; specific responsibilities include: (i) Generate a series of data types / protein features from intra- and inter-species Protein-Protein Interactions (PPIs) for *Citrus-CLas* interaction system, (ii) Develop a Bayesian network from these properties and generate a decision layer, (iii) Validate the performances on experimentally-proven independent datasets and/or develop alternative approaches such as those based on machine learning, dual RNA-seq data, (iv) Implement a publicly available web server for predicting and visualizing the *Citrus-CLas* PINs. In addition, the candidate is also expected to work closely with other postdocs and students involved in this project, assist in the analysis of RNA-seq data for differential gene expression, etc.

Qualifications:
1. Ph.D. degree in Biology, Computer Science, Engineering, or related life sciences field.
2. Programming skills with Java, C/C++, or Perl and efficiency in Linux/Unix operating systems.
3. Independent problem solving skills.
4. Have good communication skills, strong team-work spirit, and self-learning abilities.

Preferred Qualifications:
1. Ph.D. degree in Plant Biology, Genomics, Bioinformatics, Computer Science or highly-related field.
2. Post-doctoral experience in Bioinformatics.
3. Experience in developing Bayesian-based models and large-scale data analysis systems.
4. Knowledge about PINs, graphical models such as the dynamic Bayesian networks.

Please submit a current CV, a brief statement of your research interests, and contact information for at least three references who can address your skills and abilities in science by e-mail to the Principal Investigator, Dr. Mikeal L. Roose at mikeal.roose@ucr.edu.

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