## PhD positions in Systems biology and Biocomputing

The Popescu group at the Institute for Genomics, Biocomputing and Biotechnology (IGBB) seeks applicants for PhD positions that offers interdisciplinary training in systems biology and bioinformatics. The PhD students will lead and participate in NSF-funded research exploring the systems biology of peptidase activity, redox signaling and plant stress responses, focusing on understanding the role of controlled proteolysis in signaling circuits that enable plants to withstand oxidative stress. The project employs a model to elucidate the contributions of the proteolytic pathways mediated by TOP1 and TOP2 thimet oligopeptidases (doi: 10.1111/tpj.12320) through integrated biochemical, proteomics, and systems biology approaches (doi: 10.3389/fpls.2015.00327).

**Qualifications**: Bachelor's or Master's degree in bioinformatics, computational sciences, systems biology or a related field.

**Requirements:** Experience in computational biology and bioinformatics; good computer programming skills; a strong interest in developing quantitative biology methods applied to cell signaling and molecular plant biology; good communication skills and an ability to work as part of a multi-disciplinary team. How to Apply: Applicants are encouraged to email a one-page cover letter and CV (including skills, previous research/education, GPA, GRE/TOEFL, and the contacts of three references)

to <u>gvp18@msstate.edu</u>. Please set the email subject line as "[PhD\_application] Full name". The Mississippi State University is an EEO employer (http://www.policies.msstate.edu/policypdfs/0302.pdf). **IGBB** 

Popescu's group at IGBB focuses on computational and high-throughput quantitative approaches to study biological networks and processes in order to understand evolution and dynamics at the molecular and cellular levels. We seek to infer plant protein interactions, analyze the properties of biochemical networks, and study the dynamics of signaling pathways. We are pursuing a multidisciplinary approach that includes high-throughput genomics and proteomics (doi: 10.1101/gad.1740009), mathematical and computational modeling and bioinformatics tool development.