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Computational Biology Seminar Series for Undergraduates

Putting Together Genomic Jigsaw Puzzles and Decoding the Messages in a Genome**Maheshi Dassanayake, LSU**

Assistant Professor, Department of Biological Sciences

Life Sciences Building Annex A101
November 04, 2013 - 05:30 pm**Abstract:**

Today's Next Generation Sequencing (NGS) technologies have revolutionized the field of genetics by providing ways to explore the genetic code of any organism. Novel genomes allow novel ways of discovering and interpreting the genetic mechanisms underlying physiological and evolutionary processes. Insight gained from such processes will be needed in the development of crops in sustainable agriculture, biotechnology applications, drug discovery, and effective conservation strategies, especially in the face of climate change, overpopulation, and increasing demand for food and bioenergy crops. However, understanding the messages embedded in genomes continue to be a complex challenge. The challenge begins with first putting together a massive number of DNA sequences into a complex genomic jigsaw puzzle and then trying to decode the common and unique messages written in each genome. Assembling genomes, interpreting functional units, and comparing to other known genomes require massive computational power and new computational tools that are rapidly evolving in the field of genomics. In this talk I will use a plant genome of a wild relative of several crop species and discuss how we have assembled its genome and now trying to understand the unique message it carries about its past and present.

Speaker's Bio:

Maheshi Dassanayake is an assistant professor in the Department of Biological Sciences at LSU. She received her B.Sc. degree in Biology from the University of Colombo, Sri Lanka and her Ph.D. in Biology from the University of Illinois at Urbana-Champaign in 2009. She completed two years of postdoctoral research at the University of Illinois before joining as LSU faculty in January 2013. As a graduate student she studied stress adaptation mechanisms of mangrove plants and was taking the approach of studying one target gene at a time. This was the time (2008-2009) when next generation sequencing techniques were being introduced as a practical tool to study any type of organism. She embraced the opportunity to sequence the entire transcriptomes of mangrove species and was successful in publishing the first non-model plant transcriptomes assembled de novo exclusively with short sequence reads. As a postdoctoral researcher at the University of Illinois, she followed her passion for understanding genomes and adaptations to environmental stress in plant species that had virtually no genetic resources available prior to sequencing. This required her to learn, write, and use new and existing programs run on servers with large computational power. Her application of computational tools in studying plant genomics led her to be a recipient of the Discovery Early Career Researcher Award given by the Australian Research Council in 2012. Her research interests continue to revolve around understanding genomic signatures that govern phenotypic adaptations. In her lab they use a dual approach of developing computational pipelines to make in silico predictions that are complemented by wet lab experimental designs. Please visit www.lsu-genomics.org for more details.

This lecture has refreshments @ 05:00 pm