The MUSC Bioinformatics Core invites all faculty and staff to join Drs. Gary Hardiman and Sean Courtney as they discuss and demonstrate how to analyze DNA Microarray and High Throughput RNA Sequencing Data.

The confluence of robotics, biotechnology, computer sciences and the completion of genome sequencing efforts for several organisms have resulted in revolutionary changes in how biomedical research is carried out. In recent years high-density arrays of specified DNA sequences and high-throughput RNA sequencing approaches have gained in popularity. Genomics and informatics are playing increasingly important roles as discovery tools in the basic biological sciences, and as diagnostic and rational therapeutic aids in the clinical arena. This introductory bioinformatics 101 format class will provide both an introduction and detailed overview of good data analysis practices when exploiting microarray technology and high throughput RNA sequencing analysis.

There will be two presentations

**1-2 PM** Bioinformatics 101 - How to Analyze DNA Microarray and High Throughput Sequencing Data ? (Dr. Gary Hardiman)

**2-3 PM** Gene Ontology (GO) and Pathway Analysis using Advaita iPathway Guide (Dr. Sean Courtney)

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