

MTCS COLLOQUIUM

Olga Nikolova

will present

GENEVA Gene Expression and Visualization Application

3:30 pm

Tuesday, September 27th

Violette Hall 1236

DNA microarrays allow for the investigation of the expression levels of tens of thousands of genes in a single experiment. Microarray analysis generates large sets of raw data to which automated and manual processing is applied to extract usable biologically relevant information. The Gene Expression and Visualization Application (GENEVA) was designed to store, maintain, and facilitate the annotation process of the thousands of expressed sequence tags (ESTs). The application automates techniques previously used by researchers to manually retrieve important information. GENEVA has significantly improved the speed and quality of the EST annotation process. This work is part of a project to analyze the genes involved in shoot apical meristem organization and leaf initiation in maize and is mentored by Dr. Jon Beck (MTCS) and Dr. Brent Buckner and Dr. Diane Janick-Buckner (Science).

Cookies and Refreshments!!!