

**MESSAGE SENT ON BEHALF OF
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ASSOCIATE DEAN FOR RESEARCH**

Computational Biology Initiative and the UTSA Department Of Computer Science will host a workshop:

A Hands-on Introduction to MATLAB for Bioinformatics & Computational Biology

This workshop is free and open to the public. Experts from Mathworks will be presenting. Advanced registration is required. To register, please fill out this online registration form at http://www.cbi.utsa.edu/matlabws_registration.

For more information, please email Zhiwei Wang (zwang@cs.utsa.edu).

Date: May 20, 2008

Time: 9:00 am - 4:00 pm

Place: Science Building (SB) 3.02.02, UTSA 1604 campus.

Agenda

1. Introduction to Data Analysis with MATLAB

- Import data from common file formats (Excel, .csv) and databases
- Easy visualization and manipulation of data
- Automate manual tasks via auto-generated scripts
- Report generation with a single click
- Develop and deploy customized Graphical User Interfaces (GUI)

2. Introduction to Microarray Data Analysis (Bioinformatics toolbox)

- Import data from common file formats - Affymetrix, Illumina, GEO
- Pre-process raw data using various normalization and filtering techniques

- Overview of visualization and data mining features
- Hierarchical and K-means Clustering, Support Vector Machines

(SVM),

Principal Component Analysis (PCA)

3. Introduction to Sequence Analysis Techniques (Bioinformatics toolbox)

- Import data from web-based databases (EMBL, NCBI, GeneBank)
- Perform pair-wise and multiple sequence alignments
- Create and visualize phylogenetic trees

4. Processing and Analysis of Mass Spectroscopy Data (Bioinformatics toolbox)

- Overview of various spectra processing techniques
- Baseline removal
- Profile alignment
- Smoothing

- Peak detection

5. Modeling Biochemical Pathways with SimBiology

- Build and configure reaction pathways using SimBiology's graphical interface
- Simulate and analyze pathway models - sensitivity analysis, parameter scan, parameter estimation