



**Department of Computer Science**  
Texas Southern University



## **MONTHLY RESEARCH SEMINAR**

### **Bioinformatics, Phylogenetics and Parallel Computing**

by

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**September 17, 2013**

**3:00-4:00 PM, Nabrit Science Center Room 106**

#### **Abstract**

The future of medicine is in genomics. Biology is fast becoming more computational as advances in molecular biology accelerate in concert with advances in computational technology. Here, I discuss the theoretical underpinnings of the most widely used methods for phylogenetic reconstructions; the distance approach, cladistic, maximum likelihood, and most popularly, Bayes. I also present the role of molecular evolution models, common statistical tests such as bootstrapping, the applications for handling and assembling large DNA datasets, and some practical examples of the use of these applications running in Unix. As science moves from sequencing single genes to whole genomes, phylogenomic inference becomes more daunting, and many applications will be rewritten to run in parallel to meet those challenges.



**Hector C. Miranda, Jr Ph D**

