



THE UNIVERSITY OF  
MELBOURNE

# Mechanical Engineering 2010 Tewksbury Seminar

## Data Analysis on Phylogenetic Trees.

*Trees come up in many contexts, not only in phylogenetics but also in the analysis of a variety of physical, organizational, and data-type structures. Because of their topological nature, trees are difficult to represent in a way that can be analyzed along classical statistical lines.*

*We introduce the concept of tree space, a representational format for labeled trees first introduced by Billera, Holmes and Vogtmann. Tree space allows statistical tools such as means, variances, and principal component analysis to be applied to trees in realistic ways. As well, the structure of tree space enables powerful search techniques to be applied to solve the associated computational problems.*

*We present a description of tree space, give some of its properties, and outline some basic algorithmic tools for working on this space.*

*We give two applications, one involving consensus trees in phylogenetics, and one involving the analysis of arterial systems in the human brain.*

### Prof J Scott Provan

Department of Statistics and Operations  
Research  
University of North Carolina

Wednesday 9th June, 11am

Lecture Theatre

Level 3

Mechanical Engineering

Building 170

#### MORE INFORMATION

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