Case study

Discovering new family trees of biblical manuscripts .

Background

Until the arrival of the printing press, all documents had to be copied by hand – and every time a substantial document is copied by hand the copyist makes mistakes. For example the new manuscript might miss out lines, contain mis-spellings or even incorporate corrections to previous errors (or perceived errors) etc. These changes in the text are analogous to genetic mutations in species' DNA. Therefore the tools used in the field of phylogenetics to study the evolution of species can also be used to study the evolution of texts of a given work.

Method

The International Greek New Testament Project transcribed 1,659 manuscripts of chapter 18 of the Gospel of John into electronic form, which were then collated using specialist software. They divided the text into 401 logical units. I then encoded this data in the form of a matrix with over 650,000 pieces of information. Each individual manuscript is then represented by a string of 401 letters analogous to a DNA sequence.

The software used in this research is MrBayes (http://mrbayes.sourceforge.net/).

MrBayes is a powerful open source application that runs the Metropolis-Coupled Markov Chain Monte Carlo (MC^3) algorithm to perform Bayesian inference for phylogenetic and evolutionary models. It is MPI-capable, and therefore highly suitable for making use of BlueBEAR's parallel processing. I executed MrBayes incrementally ten times for this dataset, equating to approximately three weeks of continuous use of eight processors. This is the equivalent of running the analysis for several months on my laptop. After this time the MC^3 chains had converged and produced fascinating results.

Results

The resulting phylogenetic tree for John 18 contains many interesting features. For example, one sub-tree corresponds to the famous "Ferrar Group" of New Testament manuscripts. Here the group membership identified by MrBayes agrees with the conclusions of recent more traditional research – even though none of the traditional criteria for group membership are found in John 18:

Further work

I am in the process of applying this method to a number of other datasets. For example, I have applied this method to some Latin manuscript data of John's gospel with promising results.

This is only possible thanks to BlueBEAR's many processors. At times I have been running several different analyses at once. For example, one night in June 2015 I scheduled the use of 256 processors (16 different datasets each using 16 processors).

I am grateful to the College of Arts and Law for awarding me a doctoral scholarship for the rest of my research .

Client Profile
Andrew Edmondson
Institute for Textual Scholarship and Electronic   Editing
School of Philosophy, Theology and Religion
College of Arts and Law
University of Birmingham
B15 2TT

Contact Details
Email : ACE209@student.bham.ac.uk

Product Used
MrBayes

Contributors
Professor David Parker
Dr Hugh Houghton