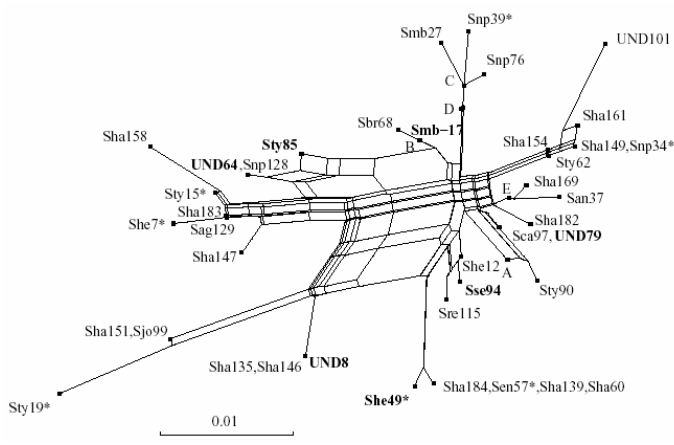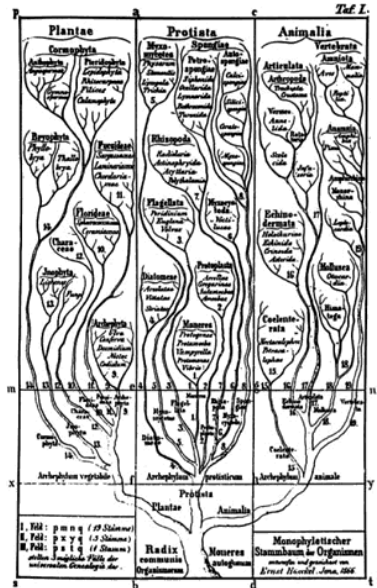# Phylogenetics

3 September to 21 December 2007

Organisers: *Professor D Huson (Tübingen), Professor V Moulton (East Anglia), Professor M Steel (Canterbury, NZ)*

This programme is concerned with a fundamental problem that has been of interest since Charles Darwin first proposed the theory of evolution. Namely, how can one use the present-day characteristics of a group of species to infer, in their evolution from a common ancestor, the historical relationships between these species? Typically these historical relationships are represented in the form of an evolutionary (phylogenetic) tree. Determining this tree for groups of species, or groups of populations, is fundamental to many questions in evolutionary biology as well as for related areas such as conservation genetics and epidemiology.

Phylogenetics - the field concerned with the reconstruction and analysis of phylogenetic trees and networks - is a flourishing area of interaction between the mathematical sciences and biology. It is widely used in molecular biology and in areas of classification such as linguistics, and has both led to and benefited from the development of new mathematical, statistical and computational techniques. Even though the foundations of phylogenetics were laid down in the last century, the field is growing at a dramatic rate due to the wealth and types of new biological data that are becoming increasingly more available.

This programme will bring together leading theoreticians and biologists to push forward the boundaries of phylogenetics and its associated theories. It will seek answers to questions such as how to represent and model reticulate evolution, how to incorporate new data types (such as whole genome and expression data) into evolutionary analyses, how to construct the Tree-of-Life, and how to store and manage large collections of phylogenetic trees. This will involve addressing contemporary mathematical, statistical and computational challenges in topics such as the combinatorics of phylogenetic trees, algorithms for phylogenetic analysis, and stochastic models of evolution.

Much of the work in the programme will be motivated by contemporary biological problems in areas of study such as molecular evolution, biodiversity, comparative genomics, phylogeography and epidemiology. As a result, we hope that the programme will not only help provide solutions to pressing problems arising in these fields, but also lead to fascinating new research directions in the mathematical sciences.