

Chromista is a major eukaryotic kingdom comprising algae and former protozoa that is evolutionarily entirely distinct from the kingdoms Plantae and Protozoa (Cavalier-Smith 2007). Chromist chloroplasts were acquired secondarily by enslavement of a red alga, itself a member of kingdom Plantae, and have a unique membrane topology. The methodologies needed for this project is phylogeny inference (Felsenstein, 2003), sequence/genome alignment, database search and detection of horizontal transfers. Much of this can be done with available packages, but there is also scope for new models and implementations. There are several open questions relating to algal evolution that can only be settled by a variety methods testing dates, detecting horizontal transfer and aligning genomes.

The project should appeal to a student with general bioinformatics interests as it would give an all round experience in applying sequence analysis techniques. The project is motivated in a biological question, so there is also scope exploring interests in organismal biology. The project scales well into a DPhil at many levels as the increased availability of genomes will allow many classic questions to be investigated and the many genomes will pose many and interesting methodological challenges.