**EEOB563 final project outline**

Past studies on fossil and anatomy have suggested phylogenetic trees for the 18 extant orders of placental mammals. DNA sequences have suggested a few of the proposed superordinal groups, which are Paenungulata (elephants, sea cows and hyraxes) and Cetartiodactyla (artiodactyls and whales). Little is known about the relationships among placental mammals. This project aims to answer the questions of the relationships among placental mammals and whether parallel adaptive radiations were present among placental mammals.

Concatenations of individual genes can be employed to achieve high resolving power when trying to elucidate phylogenetic relationships. This dataset consists of concatenated DNA sequences for mitochondrial RNA genes and three nuclear genes (A2AB, IRBP, vWF) for 26 placental taxa. An independent data set from 3 kilobases (kb) of exon 11 of the single-copy breast and ovarian cancer susceptibility gene 1 (*BRCA1*) for 33 taxa is used for hypothesis testing with independent data sets. The BRCA1 data set contains all placental orders and one marsupial outgroup. These datasets are obtained from Madsen, O., Scally, M., Douady, C. *et al.* Parallel adaptive radiations in two major clades of placental mammals. *Nature* **409**, 610–614 (2001). <https://doi.org/10.1038/35054544>.

I plan to analyze both of these independent molecular data sets and compare the tree topologies. I will also run parsimony analysis, distance analysis, neighbor joining analysis, maximum likelihood analysis, bootstrap analysis and MCMC analysis.