

Phylogenetics project presentations

Project presentations will take place on December 12th from 5:30pm to 8:30pm.

For students in 03-727:

- Presentations should be 15 – 20 minutes long, allowing 10 minutes for questions between presentations.
- Project papers are due Sunday, December 17th at 8:00am. Final papers will typically be 3 – 5 pages, not including appendices. Examples of several papers from previous years are given on the web site.

For students in 03-327:

- Hand in an evaluation of each of the six presentations by 4pm on Friday, December 15th. A project evaluation will typically be 400 to 700 words.

In preparing and/or evaluating a presentation, the following are some points to consider. Not all of these points will be relevant to all projects.

Introduction

- Was the phylogenetic question clearly articulated? Context: what genes and species are under consideration in this study?
- Did the presentation provide the appropriate background and motivation for the study?

Methods

- General
 - Were the methods used well motivated and clearly explained?
 - Was the selection of the methods and parameter settings appropriate to the analysis?
 - What measures were taken to ensure the robustness of the results? Did different methods or software give different results?
 - Were the programs appropriately cited?
- Sequence retrieval
 - How were sequences selected for this analysis? Were the sequences used in the analysis appropriate for the phylogenetic question? Considerations include the type of sequence (DNA versus amino acid sequences), the taxonomic distribution of the sequences, and measures to avoid sample bias. Was the analysis restricted to orthologous sequences or were paralogous sequences included?

- Multiple sequence alignments
 - How were the sequences aligned? Did the alignment pose any particular challenges (e.g., high sequence divergence, different domain architectures, or different sequence lengths)? Was the alignment refined manually, and if so, why?
 - What approach was used to trim the sequences prior to alignment?
- Model selection
 - Which evolutionary model was used for this analysis? How was the model selected?
- Tree building
 - Are the methods that were used appropriate for the phylogenetic question and for the data set? How were parameter settings chosen? Did the results vary with when different programs and/or different parameter settings were used?
 - Are rooted trees required in this analysis? If so, how was the root of the tree inferred?
 - How was tree accuracy assessed?

Results/Discussion

- What are the results of the analysis? What conclusions can be drawn from these results?
- Do the results answer the original question? If not, did the presentation explain why not?
- Is gene family evolution considered in the context of species evolution?
- Were the results discussed in light of prior results in the literature? Do the results make “predictions” that can be compared with known biological relationships?
- Does the presentation address limitations of the methodology or the data and the potential impact of these limitations on the results? How robust are the conclusions?
- Future work: Does the presentation make recommendations for further study? If it was not possible to resolve the original question, what additional analyses could be carried out in a future study?