• End of Session 1
  • Loading/saving
  • Navigation/Selecting
  • Colouring & Figures

• Session 2
  • Alignment & analysis
    • Trees
    • PCA
    • Subfamily analysis
Jalview alignment
Section 2.4 Exercise 25

• Tasks
  – Align sequences using different methods
    • Use the Webservices’ ‘alignment’ submenu
  – Explore how hidden regions affect alignment jobs.
Jalview alignment
Section 2.4 Exercise 25

• Tasks
  – Align sequences using different methods
    • Use the Webservices’ ‘alignment’ submenu
  – Explore how hidden regions affect alignment jobs.

• Questions
  – Why does jalview run several jobs if the input includes hidden regions ?
  – What does ‘re-alignment’ mean ?
Alignment Job Parameter Settings

- Browse or edit to change name of set
- Buttons appear to create, update, rename or delete user settings.
- Text box to add notes for the parameter set
- Parameters contain more complex settings
- Start job with current settings or cancel.
- Tooltips give brief description and link (right click) to further info
Why change alignment parameters?
Jaba Alignment Exercise

• Task
  – Run the alignment from step b of ex. 25 using the JABA clustalW service
    1. Run with default settings
    2. Use the ‘Edit parameters’ dialog to run an alignment with the following:
       • Gap opening (internal and end gaps) = 3
       • Gap Extension = 0.05
  – Compare the two alignments. You may want to save them for later, too.

• Questions
  – What effect has modifying the gap penalties had on the ferredoxin alignment?
• Session 2
  • Alignment & analysis
    • Trees
    • PCA
    • Subfamily analysis
Alignment analysis – Section 2.2

- Principal component analysis
- Phylogenetic trees
- Redundancy removal
- Tree based conservation analysis
- Subdividing alignment by mutation
Phylogenetic analysis and Jalview

• Built in tree methods
  – UPGMA
    • Fast, simple, but not reliable for phylogenetic inference
  – Neighbour joining
    • Slower than UPGMA
    • Useful for a first approximation
      – NJ does not work well for very divergent sequence sets
        » Need to add in close relatives to get an idea of topology

• Import trees from elsewhere
  – Load a Newick format tree file onto an alignment from another program
PCA and Phylogeny Section 2.2
Exercise 17 and 18

• Tasks
  – Calculate Principal component analyses (PCAs) and trees on the ferredoxin alignment
  – Explore the use of the interactive tree viewer
    • Use it to select subgroups on the alignment.
PCA and Phylogeny Section 2.2
Exercise 17 and 18

• Tasks
  – Calculate Principal component analyses (PCAs) and trees on the feredoxin alignment
  – Explore the use of the interactive tree viewer
    • Use it to select subgroups on the alignment.

• Questions
  – What is the role of BLOSUM62, PAM250 and ‘Percentage Identity’ in the tree building process?
Tree based conservation analysis
Sect. 2.2.3 Exercise 19

• “Poor man’s” character inference analysis
  – Compare conservation patterns within and between branches of a tree

• Task
  • Use interactive tree viewer to subdivide alignment and identify difference in conservation pattern
Tree based conservation analysis
Sect. 2.2.3 Exercise 19

• “Poor man’s” character inference analysis
  – Compare conservation patterns within and between branches of a tree

• Task
  • Use interactive tree viewer to subdivide alignment and identify difference in conservation pattern

• Question
  – How can you tell which differences are important?
Sub-groups and Sub-group Annotation

Exercise 21

• Task
  – Use the group consensus sequence logos to more easily compare tree subgroups
  – Use ‘Make groups for selection’ to subdivide groups by specific mutation
Sub-groups and Sub-group Annotation
Exercise 21

• Task
  – Use the group consensus sequence logos to more easily compare tree subgroups
  – Use ‘Make groups for selection’ to subdivide groups by specific mutation

• Question
  – How can you navigate the sub-groups of a large alignment?