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

- Session 2
  - Alignment & analysis
    - Trees
    - PCA
    - Subfamily analysis

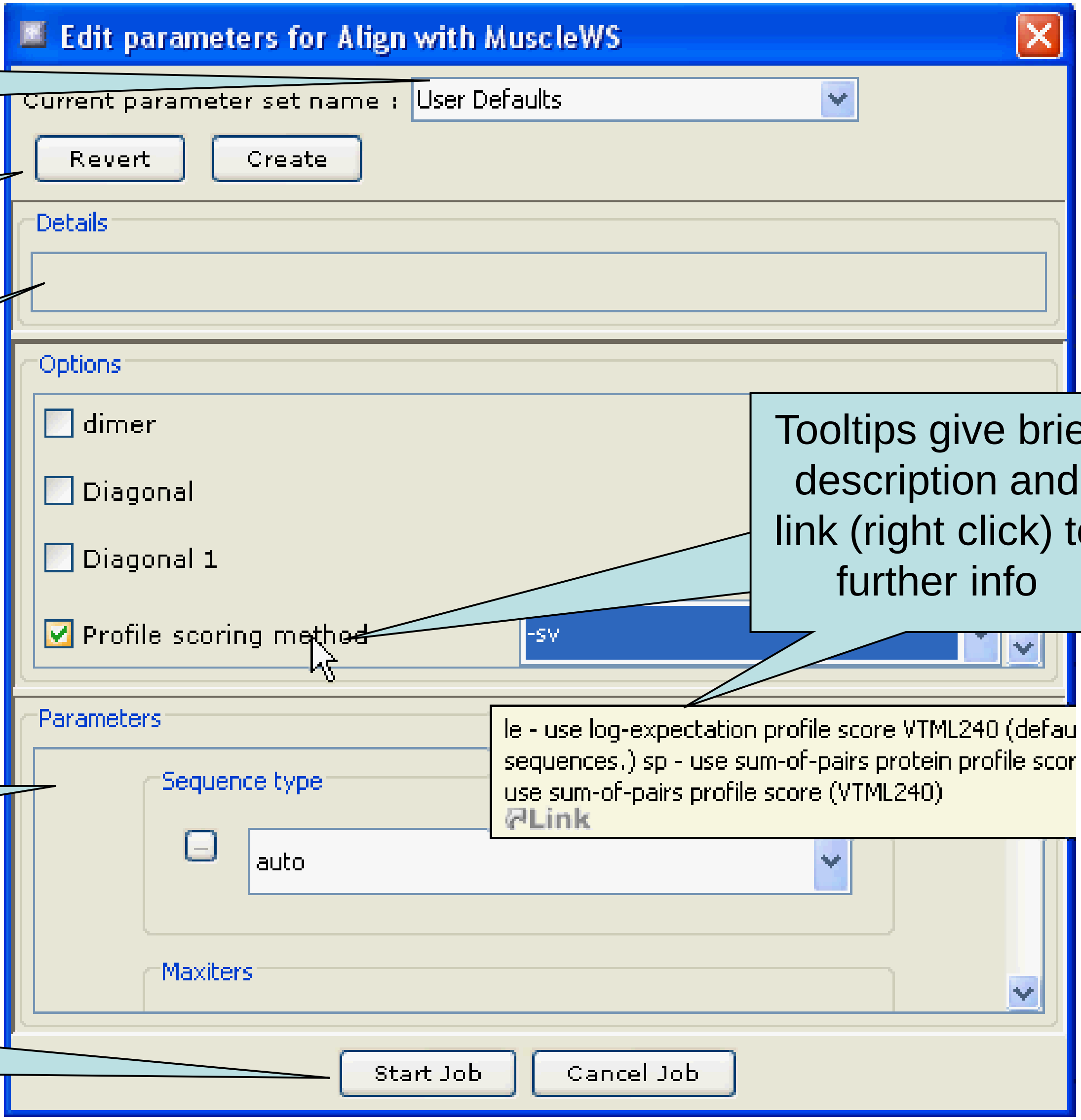
Jalview alignment
Section 2.4 Exercise 25

- 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



Current parameter set name : User Defaults

☐ dimer

☐ Diagonal

☐ Diagonal 1

☑ Profile scoring method -sv

Sequence type: auto

Maxiters

le - use log-expectation profile score VTML240 (defau
sequences.) sp - use sum-of-pairs protein profile scor
use sum-of-pairs profile score (VTML240)
Link

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

Tooltips give brief description and link (right click) to further info

Parameters contains more complex settings

Start job with current settings or cancel.

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 feredoxin 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 inferrence
  - 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 feredoxin 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 ?