Introduction to Jalview

a guided tutorial

EMBL-EBI, Jan 21st, 2013.

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Plan for the Day

08:30-09:00	Arrival and Registration
09:00-09:10	**Welcome & Safety Notices**
09:10-10:30	***Introduction to Jalview*** – Manual Chapter 1
10:30-11:00	Coffee/Tea Break
11:00-12:30	***Introduction to Jalview*** – Manual Chapter 1
12:30-13:30	Lunch
13:30-14:30	**Geoff Barton** Multiple sequence alignment and analysis
14:30-15:00	***Alignment and analysis with Jalview***
15:00-15:30	Coffee/Tea Break
15:30-16:00	**Penny Coggil** Jalview and Pfam
16:00-16:50	Alignment and analysis with Jalview continued
16:50-17:00	Day 1 Wrap-up
17:00	Departure to accommodation
18:30-19:00	Meet for evening dinner @7 in Red Lion, Hinxton.

Day 2 - Tuesday

09:00-10:30 Advanced Jalview and Jalview Hackathon

10:30-11:00 Coffee/Tea Break

11:00-12:30 Advanced Jalview and Jalview Hackathon continued

12:30-13:30 Lunch

13:30-15:00 Jalview Clinic and Jalview Hackathon
15:00-15:30 Coffee/Tea Break
15:30-15:50 Jalview Clinic and Jalview Hackathon continued

15:50-16:15 Wrap-up

16:15 Departure

Course materials

Everything is (or will) be online at

http://www.jalview.org/tutorial/training-materials/2013/EBI/Jan/

- **These slides**
- **Jalview v2.8 Tutorial (v1.4.1)**

- **A copy of the tutorial is also on Penelope**

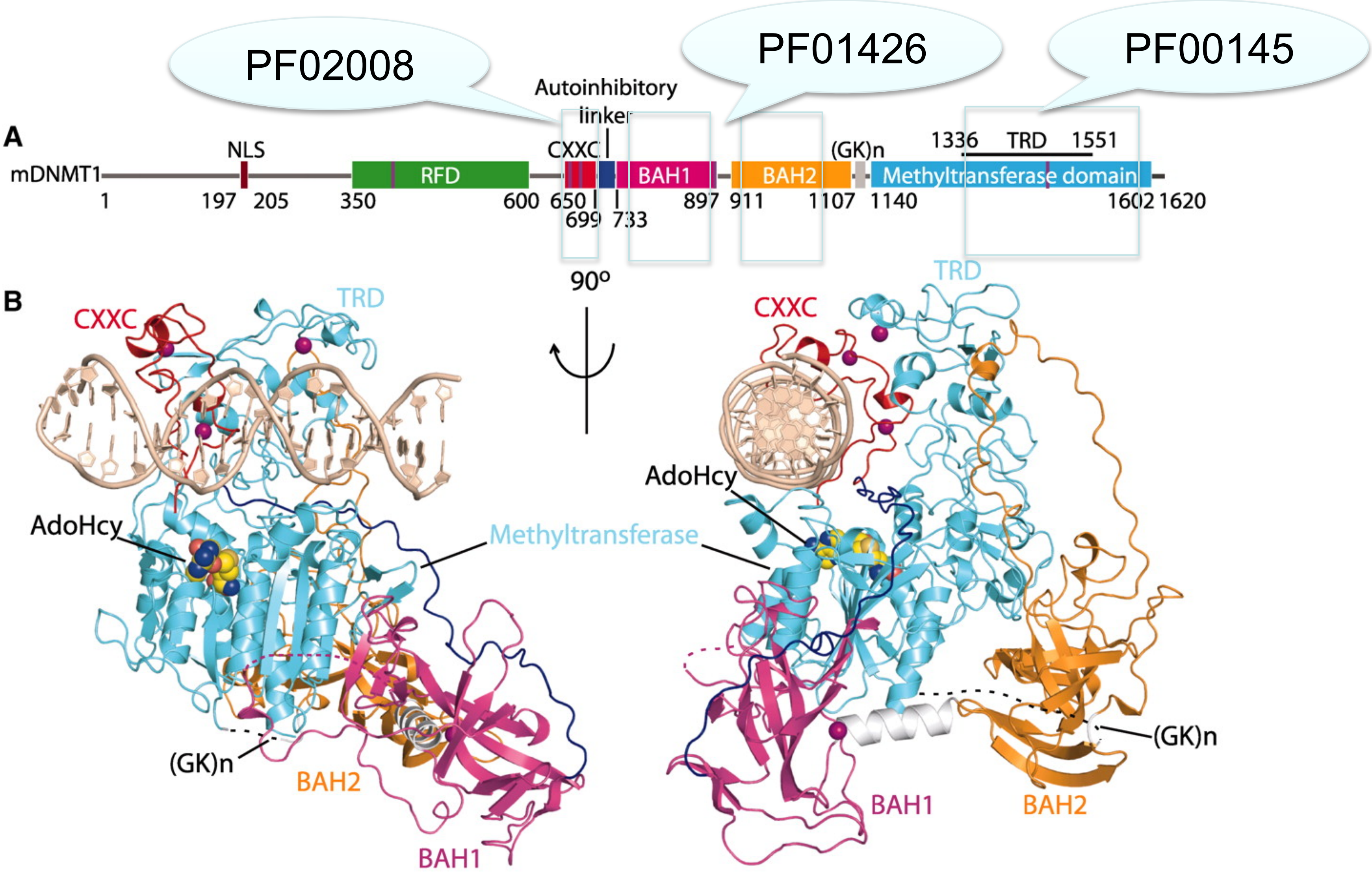
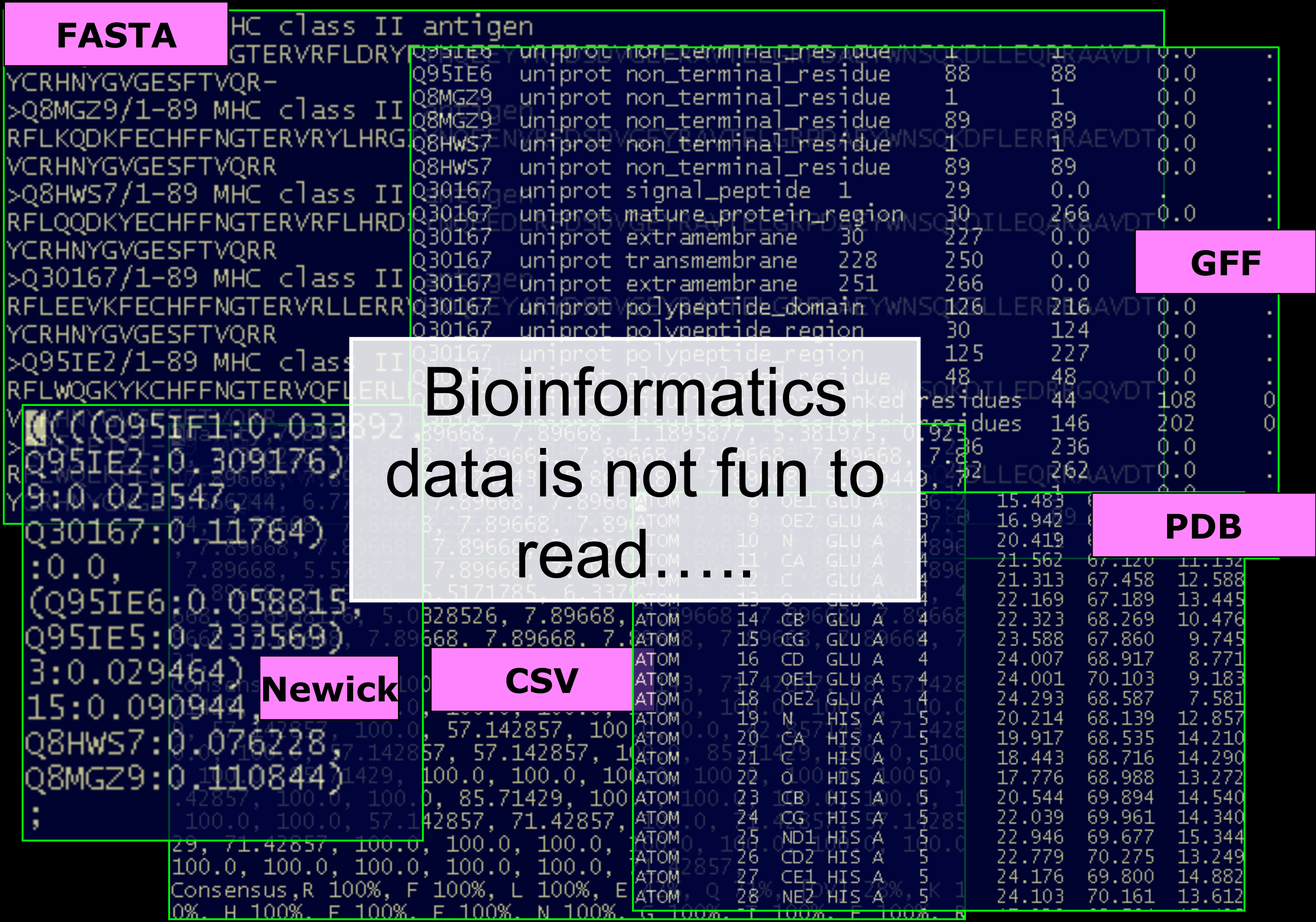


Fig. 1 Structural overview of mDNMT1(650–1602)–DNA 19-nucleotide oligomer complex with bound AdoHcy.

J Song et al. Science 2011;331:1036-1040

Published by AAAS

Bioinformatics data is not fun to read…..



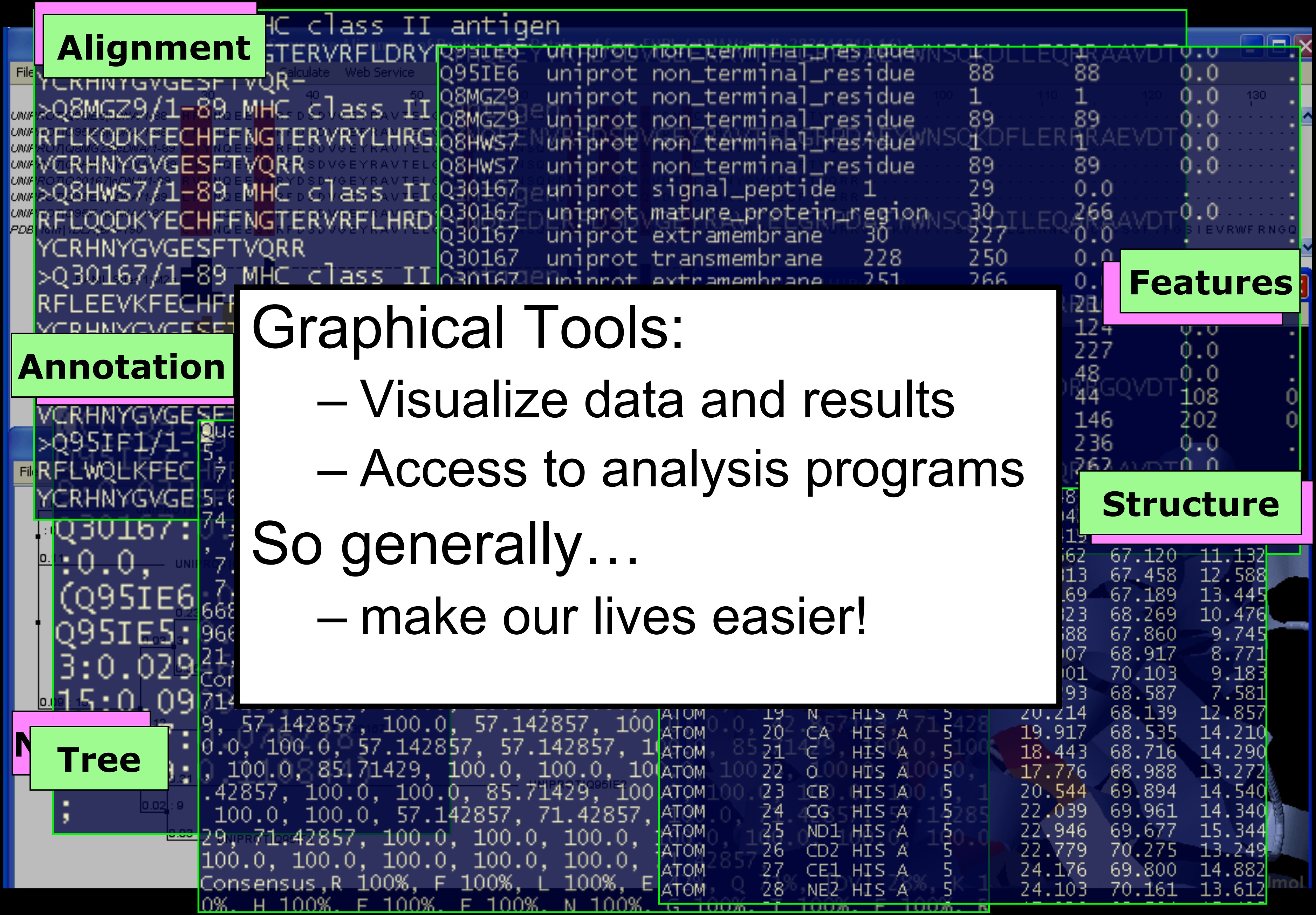
```
HC class II antigen
GTERVRFLDRY
YCRHNYGVGESFTVQR-
>Q8MGZ9/1-89 MHC class II
RFLKQDKFECHFFNGTERVRYLHRG
VCRHNYGVGESFTVQRR
>Q8HWS7/1-89 MHC class II
RFLQQDKYECHFFNGTERVRFLHRD
YCRHNYGVGESFTVQRR
>Q30167/1-89 MHC class II
RFLEEVKFECHFFNGTERVRLLERR
YCRHNYGVGESFTVQRR
>Q95IE2/1-89 MHC class II
RFLWQGKYKCHFFNGTERVQFLERL
```

```
Q95IE6  uniprot non_terminal_residue    88     88     0.0  .
Q8MGZ9  uniprot non_terminal_residue    1      1      0.0  .
Q8MGZ9  uniprot non_terminal_residue    89     89     0.0  .
Q8HWS7  uniprot non_terminal_residue    1      1      0.0  .
Q8HWS7  uniprot non_terminal_residue    89     89     0.0  .
Q30167  uniprot signal_peptide  1       29     0.0    .    .
Q30167  uniprot mature_protein_region   30     266    0.0  .
Q30167  uniprot extramembrane   30      227    0.0    .
Q30167  uniprot transmembrane   228     250    0.0    .
Q30167  uniprot extramembrane   251     266    0.0    .
Q30167  uniprot polypeptide_domain      126    216    0.0  .
Q30167  uniprot polypeptide_region      30     124    0.0  .
Q30167  uniprot polypeptide_region      125    227    0.0  .
```

```
((((Q95IF1:0.033892,
Q95IE2:0.309176),
9:0.023547,
Q30167:0.11764)
:0.0,
(Q95IE6:0.058815,
Q95IE5:0.233569)
3:0.029464)
15:0.090944,
Q8HWS7:0.076228,
Q8MGZ9:0.110844)
;
```

```
100.0, 100.0, 100.0, 100.0, 100.0,
Consensus,R 100%, F 100%, L 100%, E
```

```
ATOM     14  CB  GLU A   4      22.323  68.269  10.476
ATOM     15  CG  GLU A   4      23.588  67.860   9.745
ATOM     16  CD  GLU A   4      24.007  68.917   8.771
ATOM     17  OE1 GLU A   4      24.001  70.103   9.183
ATOM     18  OE2 GLU A   4      24.293  68.587   7.581
ATOM     19  N   HIS A   5      20.214  68.139  12.857
ATOM     20  CA  HIS A   5      19.917  68.535  14.210
ATOM     21  C   HIS A   5      18.443  68.716  14.290
ATOM     22  O   HIS A   5      17.776  68.988  13.272
ATOM     23  CB  HIS A   5      20.544  69.894  14.540
ATOM     24  CG  HIS A   5      22.039  69.961  14.340
ATOM     25  ND1 HIS A   5      22.946  69.677  15.344
ATOM     26  CD2 HIS A   5      22.779  70.275  13.249
ATOM     27  CE1 HIS A   5      24.176  69.800  14.882
ATOM     28  NE2 HIS A   5      24.103  70.161  13.612
```



Graphical Tools:

- Visualize data and results
- Access to analysis programs

So generally…

- make our lives easier!

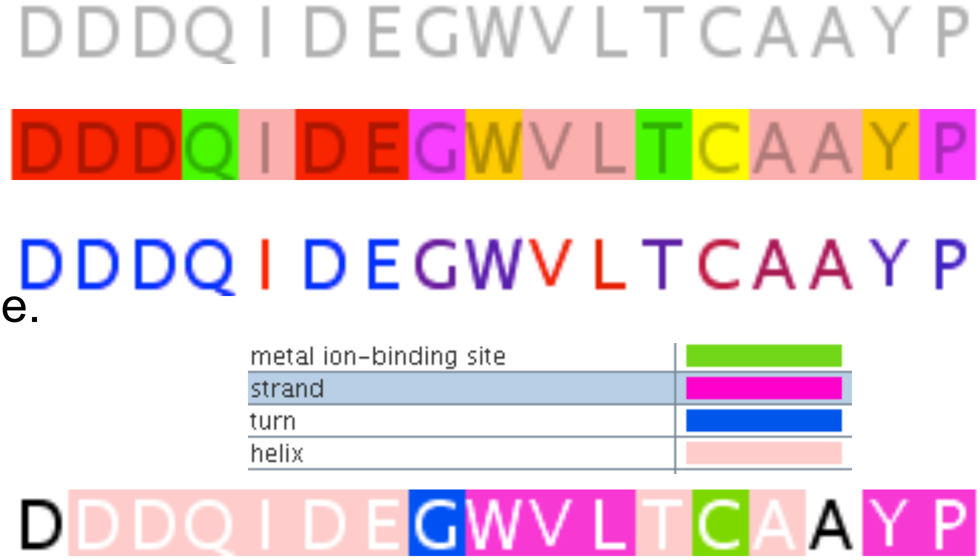
1D Protein Visualization

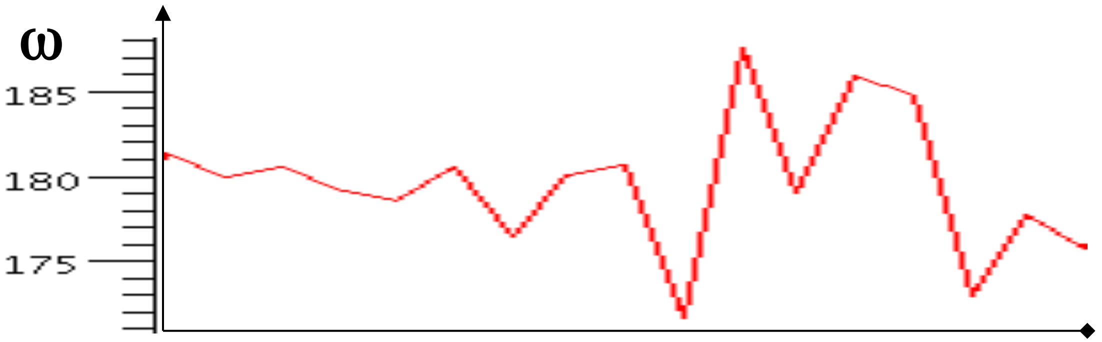
- Visualize information at each position in sequence
- Amino Acid Properties
  - Discrete colour schemes
  - Quantitative Scales
    - Hydrophobicity, polarity, size.
- Protein Features
  - Discrete annotations
  - Observations & Predictions
  - Measurements

    e.g. Omega torsion

    (reflects planarity

    of peptide bond)





Multiple Alignments

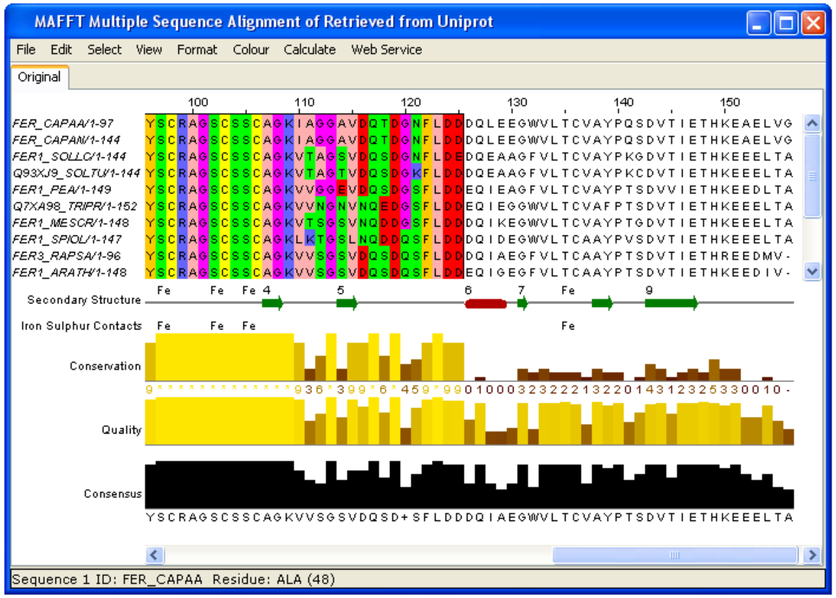
- Generated by heuristic optimization algorithm
  - Alignments sometimes need manual curation
- Correct alignments conserve common properties
- Shading can highlight differences

```
FER_CAPAA/28-82      AEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLEEGWVLTCVAYPQ
FER_CAPAN/75-129     AEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLEEGWVLTCVAYPQ
FER1_LYCES/75-129    AEEEGHDLPYSCRAGSCSSCAGKVTAGSVDQSDGNFLDEDQEAAGFVLTCVAYPK
Q93XJ9_SOLTU/75-129  AEEEGHDLPYSCRAGSCSSCAGKVTAGTVDQSDGKFLDDDQEAAGFVLTCVAYPK
FER1_PEA/80-134      AEEVGIDLPYSCRAGSCSSCAGKVVGGEVDQSDGSFLDDEQIEAGFVLTCVAYPT
Q7XA98_TRIPR/83-137  AEEVGIELPYSCRAGSCSSCAGKVVNGNVNQEDGSFLDDEQIEGGWVLTCVAFPT
FER1_MESCR/79-133    AEEAGIDLPYSCRAGSCSSCAGKVTSGSVNQDDGSFLDDDQIKEGWVLTCVAYPT
FER1_SPIOL/78-132    AEEEGIDLPYSCRAGSCSSCAGKLKTGSLNQDDQSFLDDDQIDEGWVLTCAAYPV
FER3_RAPSA/28-82     AEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDDQIAEGFVLTCAAYPT
FER_ARATH/80-134     AEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDEQIGEGFVLTCAAYPT
FER_BRANA/28-82      AEEAGIDLPYSCRAGSCSSCAGKVVSGFVDQSDESFLDDDQIAEGFVLTCAAYPT
FER2_ARATH/80-134    AEEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDEQMSEGYVLTCVAYPT
FER1_MAIZE/80-134    AEEDGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQIADGWVLTCHAYPT
O80429_MAIZE/72-126  AEEEGIDLPFSCRAGSCSSCAGKVVSGSVDQSDQSFLNDNQVADGWVLTCAAYPT
```

What is Jalview ?

- A java alignment viewer
  - ***j***ava ***al***ignment ***view***er

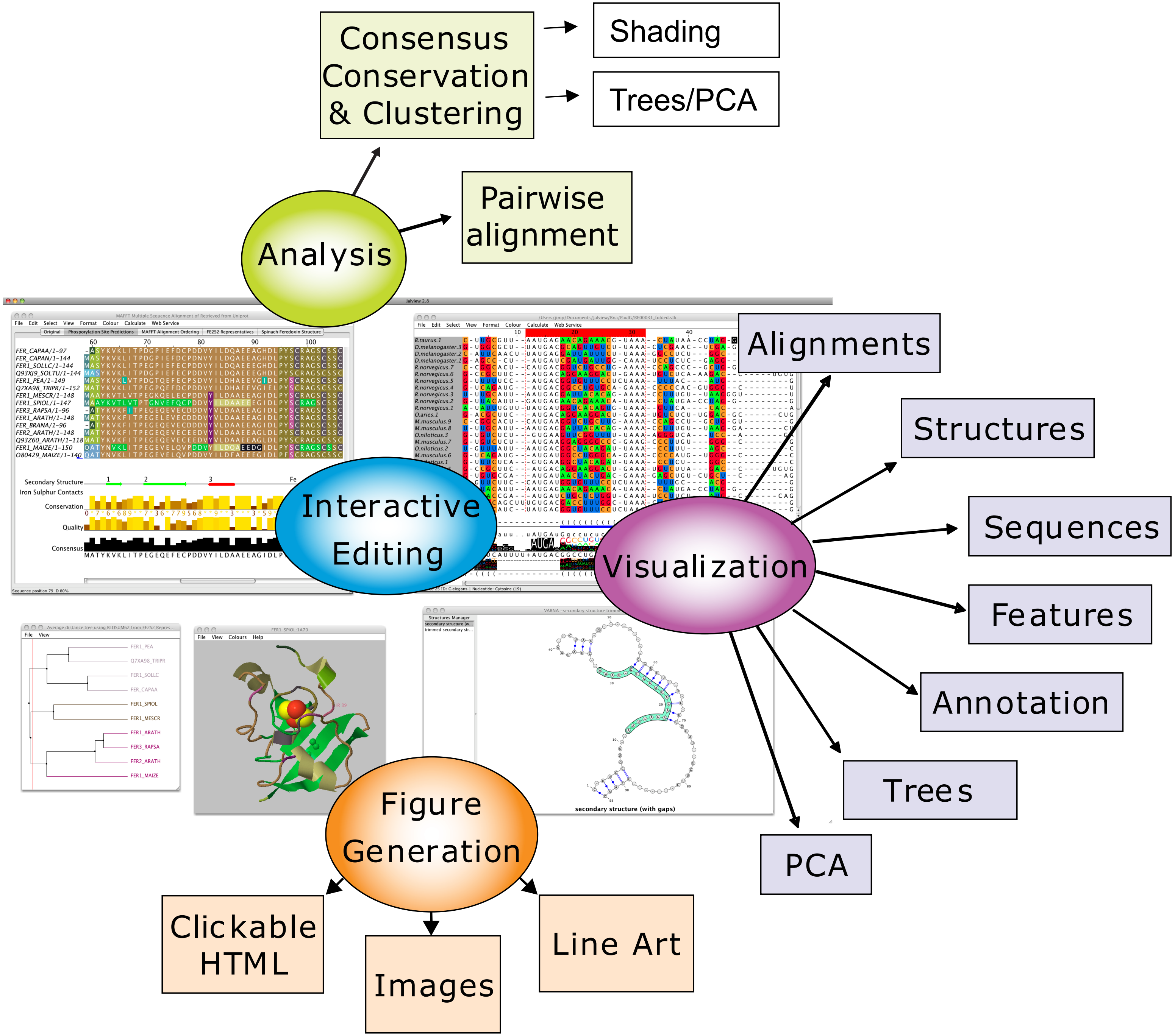
    .. but not just for viewing..
- Java ?
  - Programming language
    - Platform independence
    - Standalone or web based tool



```
FER_CAPAA/1-97      YSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLEEGWVLTCVAYPQSDVTIETHKEAELVG
FER_CAPAN/1-144     YSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLEEGWVLTCVAYPQSDVTIETHKEAELVG
FER1_SOLLC/1-144    YSCRAGSCSSCAGKVTAGSVDQSDGNFLDEDQEAAGFVLTCVAYPKGDVTIETHKEEELTA
Q93XJ9_SOLTU/1-144  YSCRAGSCSSCAGKVTAGTVDQSDGKFLDDDQEAAGFVLTCVAYPKCDVTIETHKEEELTA
FER1_PEA/1-149      YSCRAGSCSSCAGKVVGGEVDQSDGSFLDDEQIEAGFVLTCVAYPTSDVVIETHKEEDLTA
Q7XA98_TRIPR/1-152  YSCRAGSCSSCAGKVVNGNVNQEDGSFLDDEQIEGGWVLTCVAFPTSDVTIETHKEEELTA
FER1_MESCR/1-148    YSCRAGSCSSCAGKVTSGSVNQDDGSFLDDDQIKEGWVLTCVAYPTGDVTIETHKEEELTA
FER1_SPIOL/1-147    YSCRAGSCSSCAGKLKTGSLNQDDQSFLDDDQIDEGWVLTCAAYPVSDVTIETHKEEELTA
FER3_RAPSA/1-96     YSCRAGSCSSCAGKVVSGSVDQSDQSFLDDDQIAEGFVLTCAAYPTSDVTIETHREEDMV-
FER1_ARATH/1-148    YSCRAGSCSSCAGKVVSGSVDQSDQSFLDDEQIGEGFVLTCAAYPTSDVTIETHKEEDIV-

Conservation        9*************936*399*6*459*990100032322213220143123253300 10-
Consensus           YSCRAGSCSSCAGKVVSGSVDQSD+SFLDDDQIAEGWVLTCVAYPTSDVTIETHKEEELTA
```

Sequence 1 ID: FER_CAPAA Residue: ALA (48)



Analysis

Consensus Conservation & Clustering

Shading

Trees/PCA

Pairwise alignment

Interactive Editing

Visualization

Alignments

Structures

Sequences

Features

Annotation

Trees

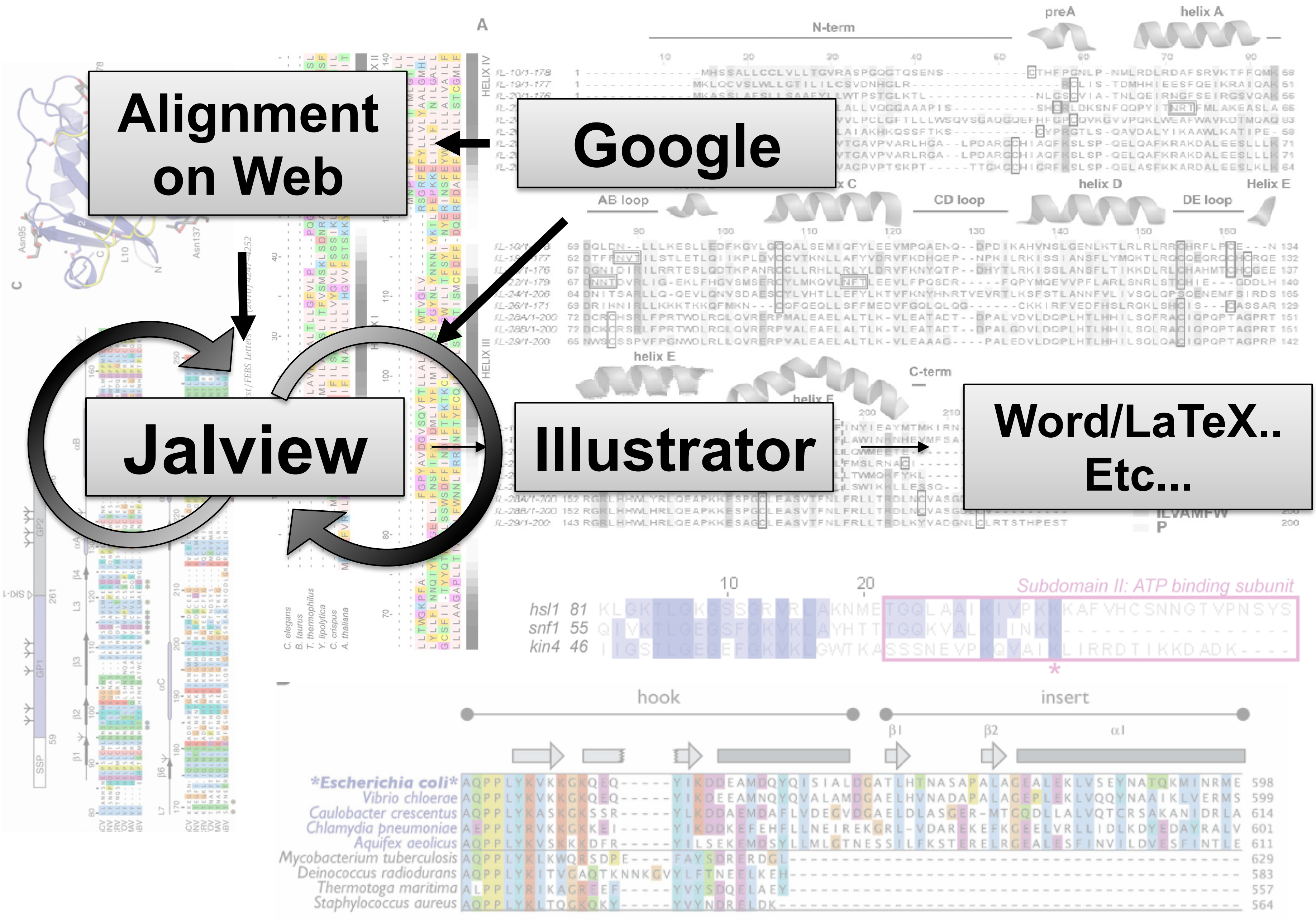
PCA

Figure Generation

Clickable HTML

Images

Line Art



Alignment on Web

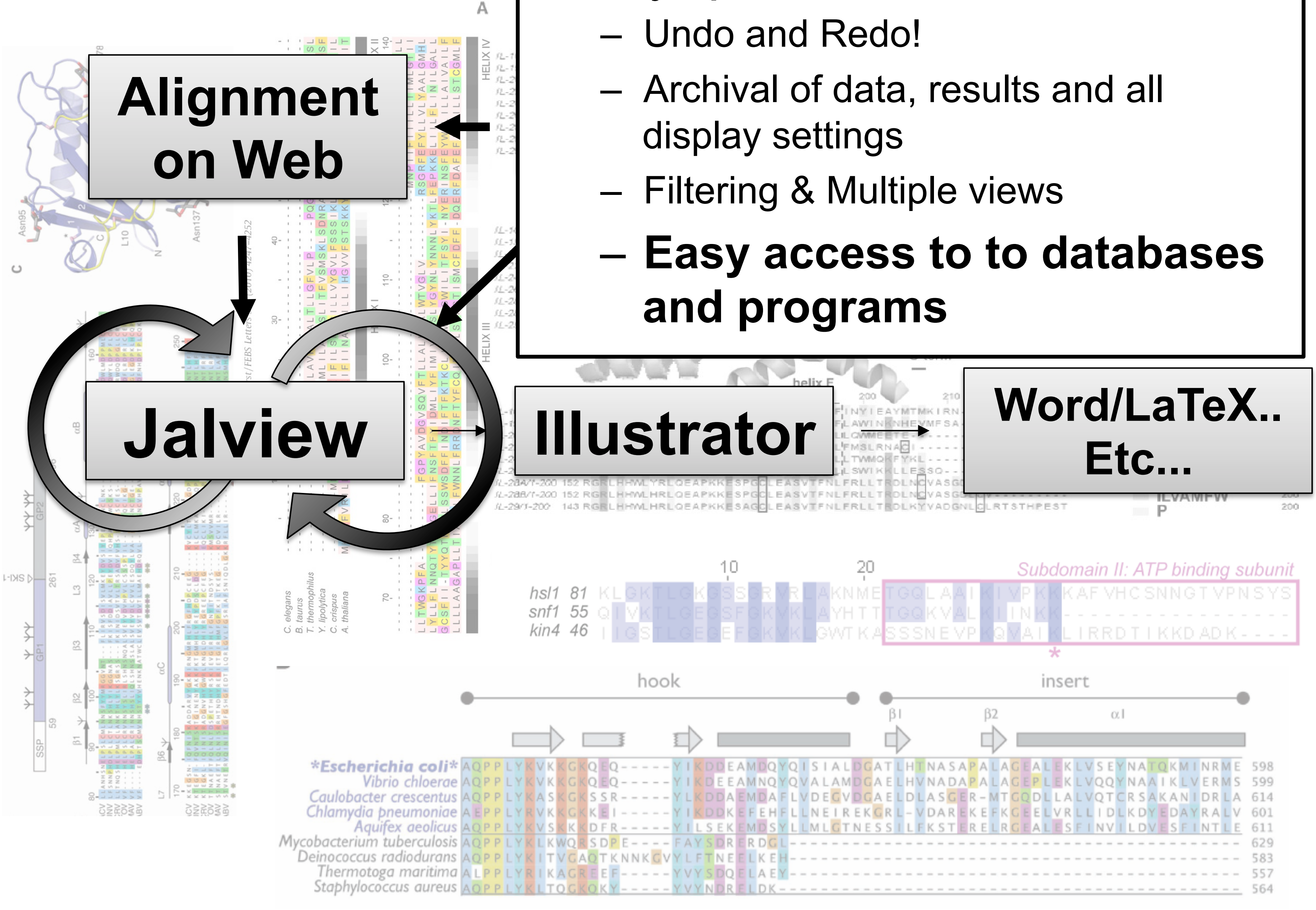
Google

Jalview

Illustrator

Word/LaTeX..
Etc...

- Key qualities for a workbench
  - Undo and Redo!
  - Archival of data, results and all display settings
  - Filtering & Multiple views
  - **Easy access to to databases and programs**



Alignment on Web

Jalview

Illustrator

Word/LaTeX.. Etc...

Jalview Flavours

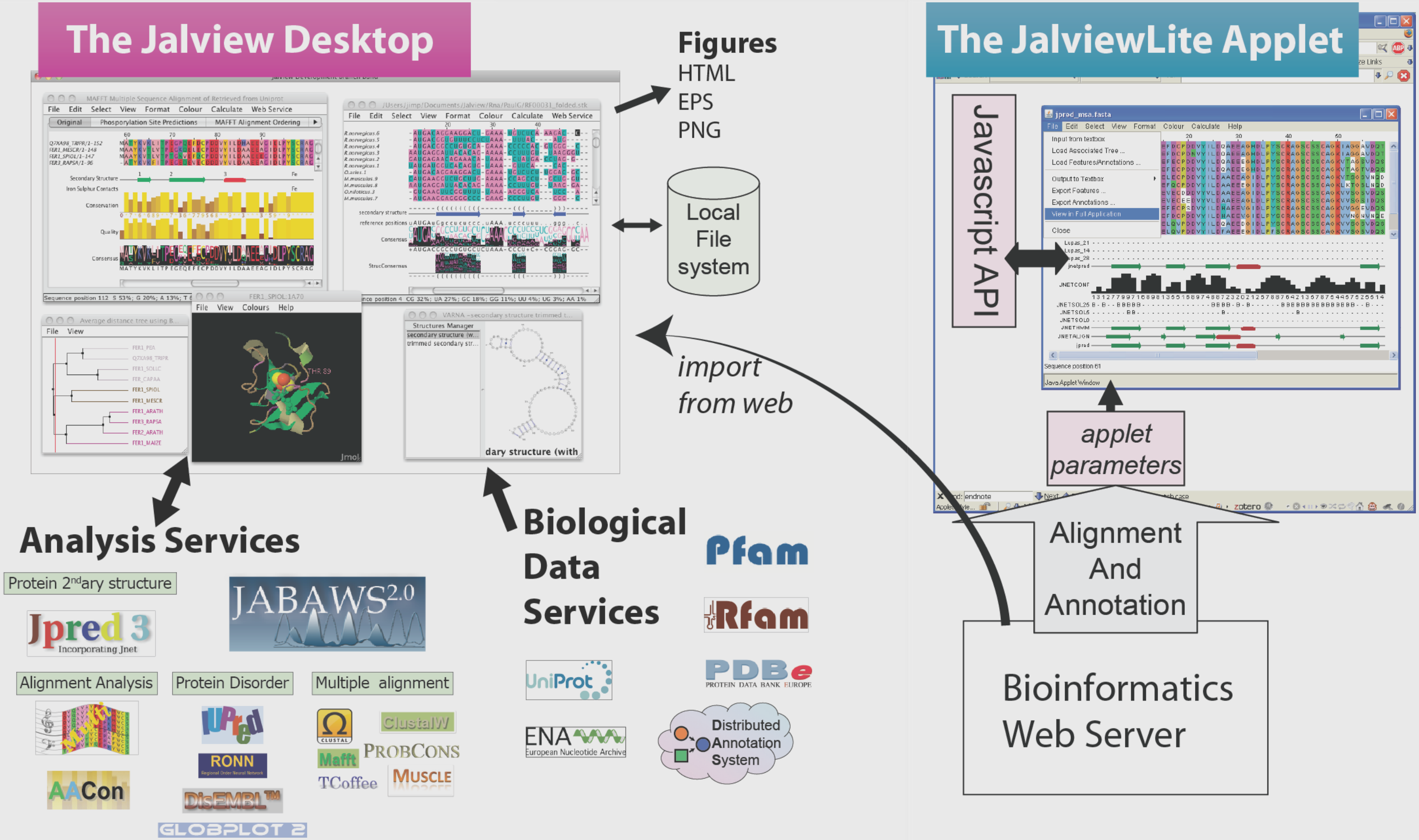
Multi-windowed UI

Visualization & Analysis

Common Data & Analysis
Editing, messaging and
File Input/Output

Lightweight UI

Integrate with web sites



The Jalview Desktop

Figures
HTML
EPS
PNG

Local
File
system

import from web

The JalviewLite Applet

Javascript API

applet parameters

Alignment
And
Annotation

Bioinformatics
Web Server

Analysis Services

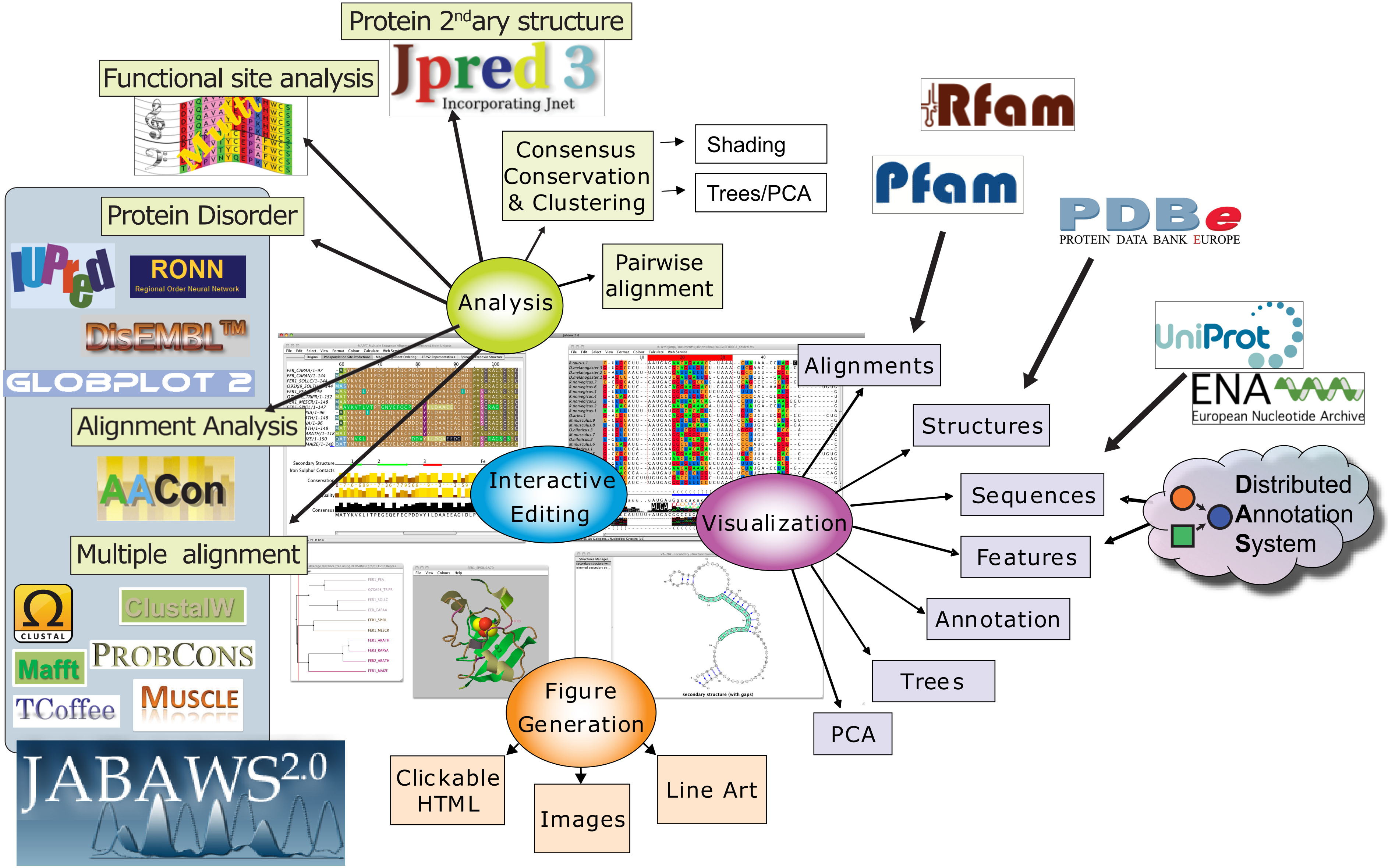
Protein 2ndary structure

Alignment Analysis

Protein Disorder

Multiple alignment

Biological Data Services



Protein 2ndary structure

Jpred 3 Incorporating Jnet

Functional site analysis

Protein Disorder

IUPred

RONN Regional Order Neural Network

DisEMBL™

GLOBPLOT 2

Alignment Analysis

AACon

Multiple alignment

CLUSTAL

ClustalW

Mafft

ProbCons

TCoffee

Muscle

JABAWS$^{2.0}$

Consensus Conservation & Clustering

Shading

Trees/PCA

Pairwise alignment

Analysis

Interactive Editing

Visualization

Figure Generation

Clickable HTML

Images

Line Art

Rfam

Pfam

PDBe PROTEIN DATA BANK EUROPE

UniProt

ENA European Nucleotide Archive

Alignments

Structures

Sequences

Features

Annotation

Trees

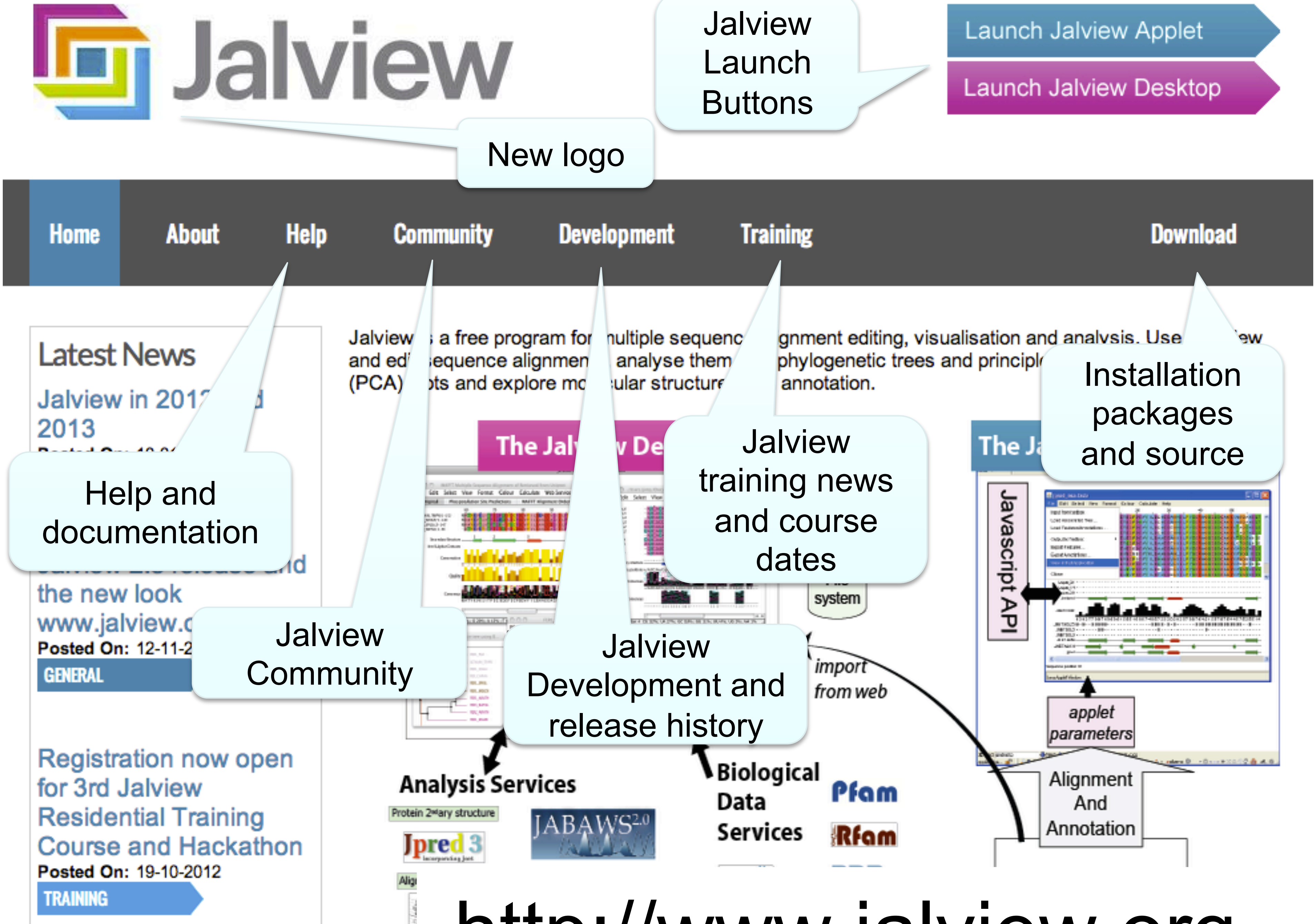
PCA

Distributed Annotation System

Ex 1 – starting Jalview

PAGE 7

Use the Development version via the development page



Jalview in 201 d 2013

Posted On: 19-0

the new look www.jalview.c

Posted On: 12-11-2

GENERAL

Registration now open for 3rd Jalview Residential Training Course and Hackathon

Posted On: 19-10-2012

TRAINING

Jalview a free program for nultiple sequenc gnment editing, visualisation and analysis. Use ew and edi sequence alignmen analyse them phylogenetic trees and principl (PCA) ots and explore mo ular structure annotation.

Jalview Launch Buttons

New logo

Help and documentation

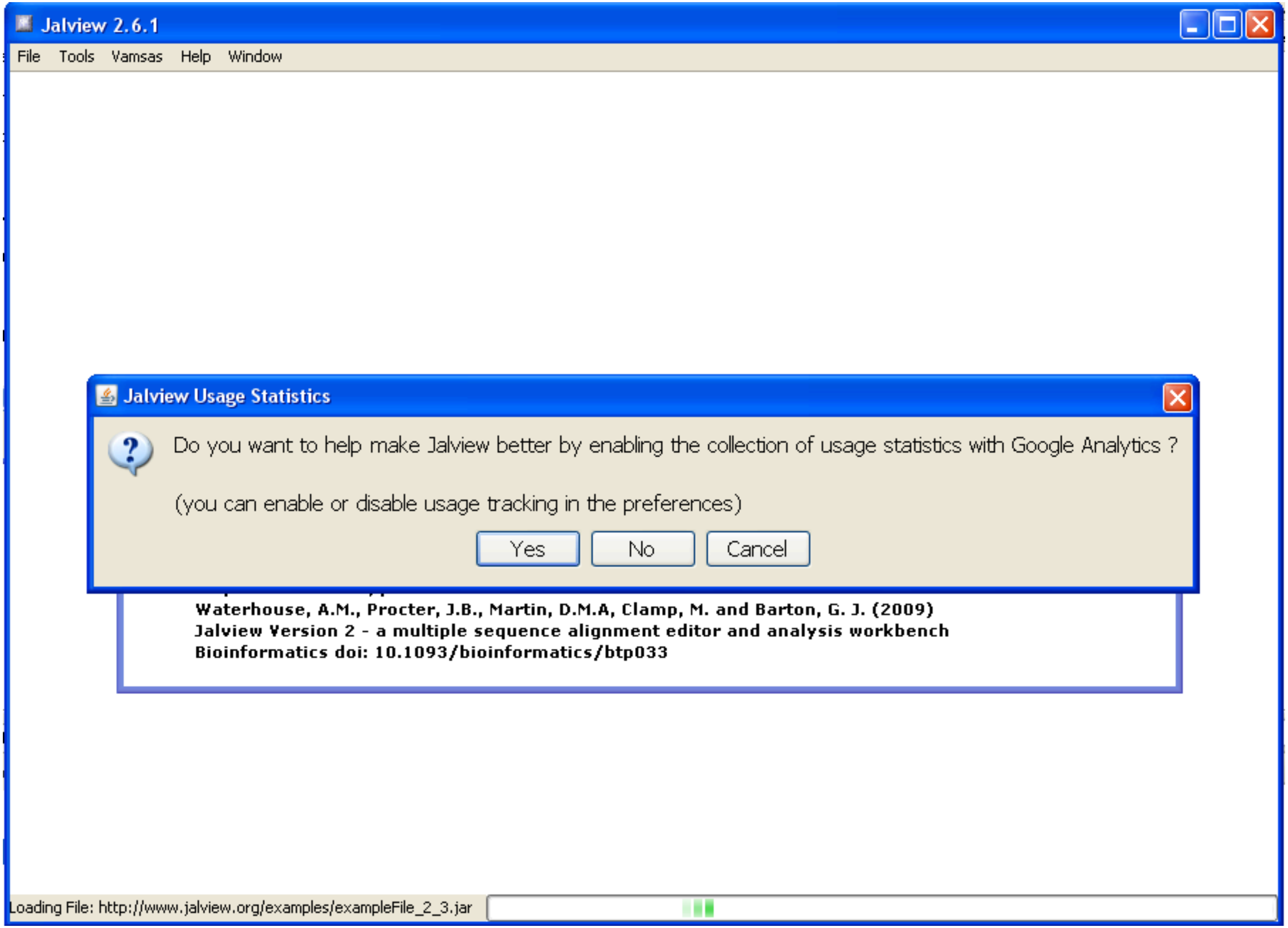
Jalview Community

Jalview Development and release history

Jalview training news and course dates

Installation packages and source

http://www.jalview.org



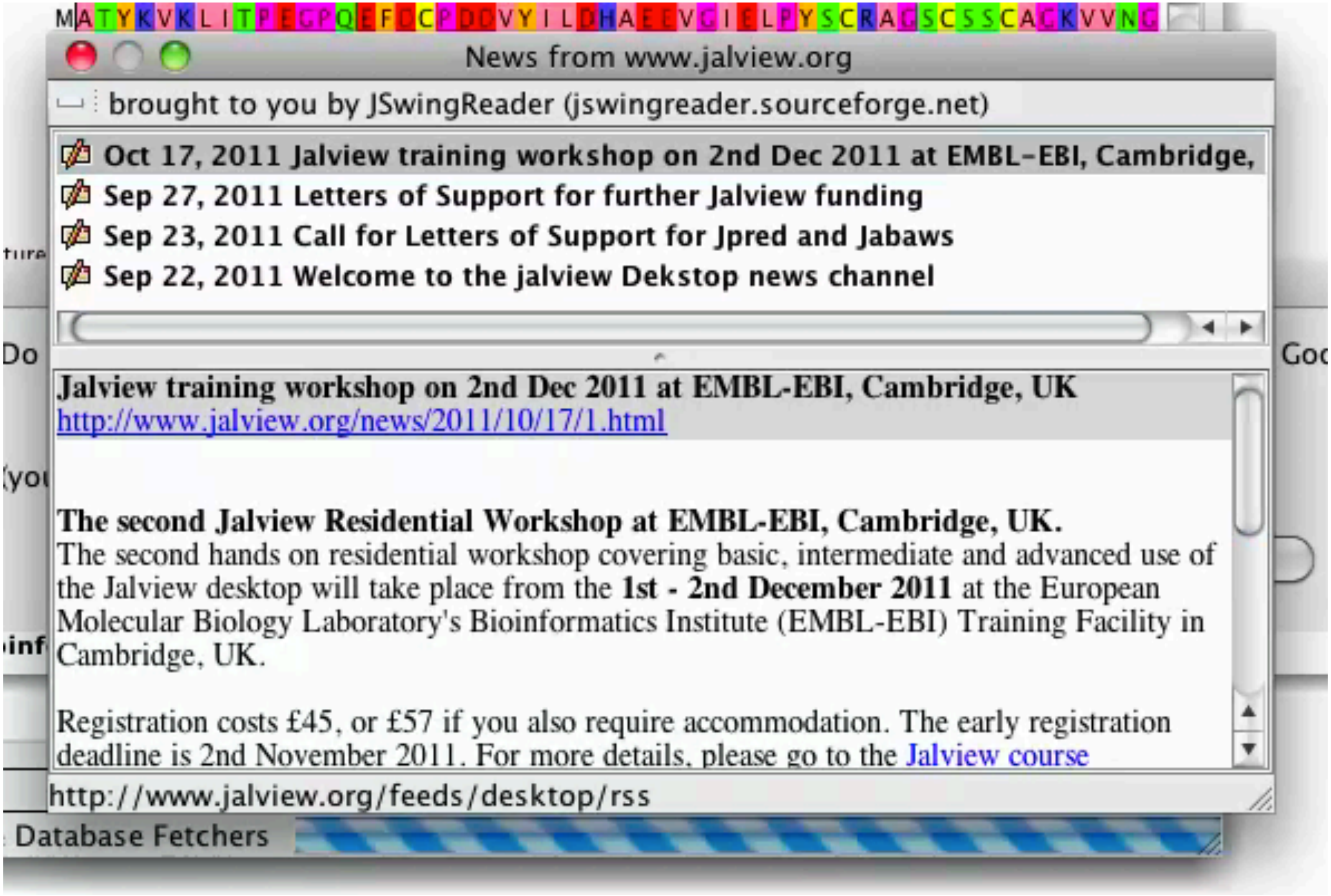
Do you want to help make Jalview better by enabling the collection of usage statistics with Google Analytics ?

(you can enable or disable usage tracking in the preferences)

Waterhouse, A.M., Procter, J.B., Martin, D.M.A, Clamp, M. and Barton, G. J. (2009)
Jalview Version 2 - a multiple sequence alignment editor and analysis workbench
Bioinformatics doi: 10.1093/bioinformatics/btp033

Loading File: http://www.jalview.org/examples/exampleFile_2_3.jar

Jalview News



News from www.jalview.org

brought to you by JSwingReader (jswingreader.sourceforge.net)

- Oct 17, 2011 Jalview training workshop on 2nd Dec 2011 at EMBL-EBI, Cambridge,
- Sep 27, 2011 Letters of Support for further Jalview funding
- Sep 23, 2011 Call for Letters of Support for Jpred and Jabaws
- Sep 22, 2011 Welcome to the jalview Dekstop news channel

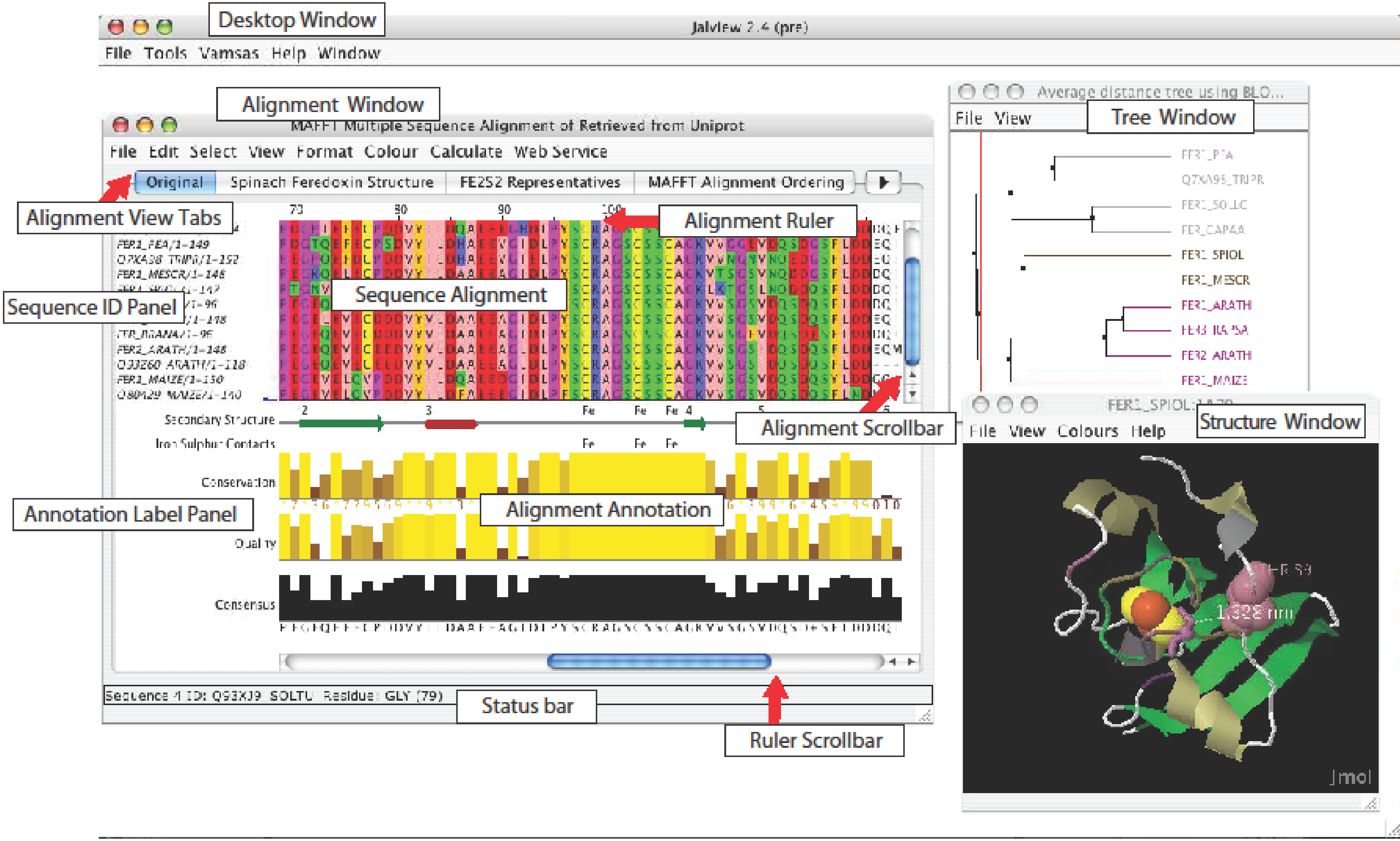
Jalview training workshop on 2nd Dec 2011 at EMBL-EBI, Cambridge, UK
http://www.jalview.org/news/2011/10/17/1.html

The second Jalview Residential Workshop at EMBL-EBI, Cambridge, UK.
The second hands on residential workshop covering basic, intermediate and advanced use of the Jalview desktop will take place from the **1st - 2nd December 2011** at the European Molecular Biology Laboratory's Bioinformatics Institute (EMBL-EBI) Training Facility in Cambridge, UK.

Registration costs £45, or £57 if you also require accommodation. The early registration deadline is 2nd November 2011. For more details, please go to the Jalview course

http://www.jalview.org/feeds/desktop/rss

Anatomy of Jalview: Figure 1.7



Sequence 1 ID: Q93XJ9_SOLTU Residue: GLY (79)

Ex 1 – starting Jalview

- Tasks
  - Modify user preferences
  - Test that you can load the example file manually
    - http://www.jalview.org/examples/exampleFile_2_7.jar

Ex 1 – starting Jalview

- Tasks
  - Modify user preferences
  - Test that you can load the example file manually
    - http://www.jalview.org/examples/exampleFile_2_7.jar
- Questions
  - Where to find help ?
  - How to report a bug ?

Jalview Community

- Mailing lists
  - – Discussion forum and developers forum
  - – Links from http://www.jalview.org/community
- Jalview bug database
  - – http://issues.jalview.org
    - Also indexed on google
- Jalview development info
  - – http://www.jalview.org/development

Ex 2 - Navigation

- Tasks
  - Open the overview window for a view
  - Jump to a specific row and column with keyboard mode

Ex 2 - Navigation

- Tasks
  - Open the overview window for a view
  - Jump to a specific row and column with keyboard mode
- Questions
  - How do you locate a sequence or sequence position if you don’t know its row/column ?
  - How do you find a sequence motif ?

Ex 3 Getting data into Jalview

- Tasks
  - Importing an alignment via a url, local file, or cut’n’paste
  - Getting an alignment from Pfam

Ex 3 Getting data into Jalview

- Tasks
  - Importing an alignment via a url, local file, or cut’n’paste
  - Getting an alignment from Pfam
- Questions
  - What happens when you drag a file onto an existing alignment ?
  - What is different about the alignment retrieved from Pfam ?
  - What if you want to load a *really* big alignment ?

Ex 4. Saving alignments

- Tasks
  - Save alignments in different formats

Ex 4. Saving alignments

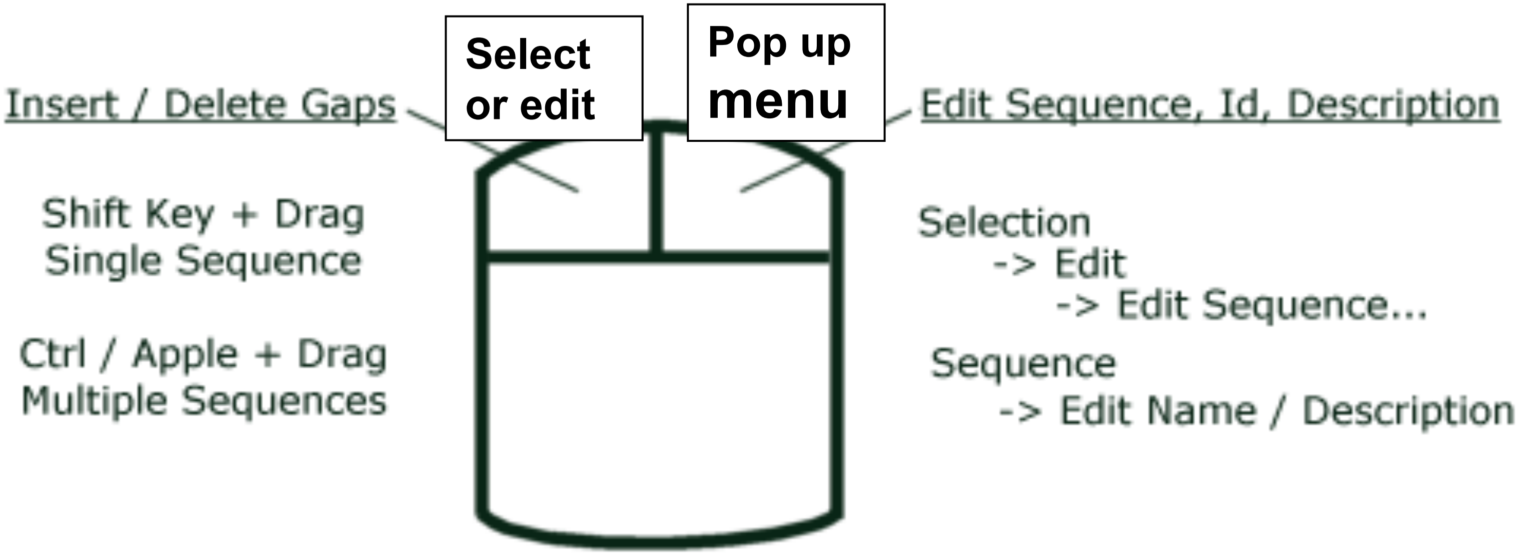
- Tasks
  - Save alignments in different formats
- Questions
  - What’s the biggest difference between a BLC file and a pileup file ?
  - Why are Jalview projects useful ?

Ex 5,6,7,8 and 9 selecting, editing, hiding and showing

- Tasks
  - Get used to the mouse and keyboard based selection and alignment editing controls
  - Learn how to work on specific parts of an alignment

- Exercise 8 and 9 let you practice mouse and keyboard based editing techniques ….
  - If you don’t finish them now, do them when you have a spare 15 mins.

How do I edit sequences in Jalview
http://www.jalview.org/examples/editing.html



Select or edit

Pop up menu

Insert / Delete Gaps

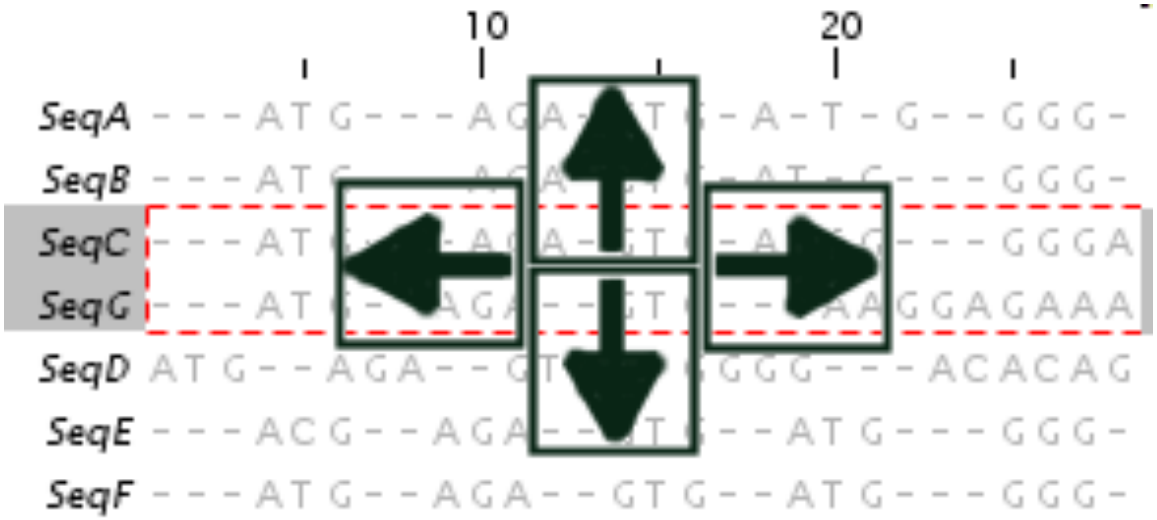
Shift Key + Drag
Single Sequence

Ctrl / Apple + Drag
Multiple Sequences

Edit Sequence, Id, Description

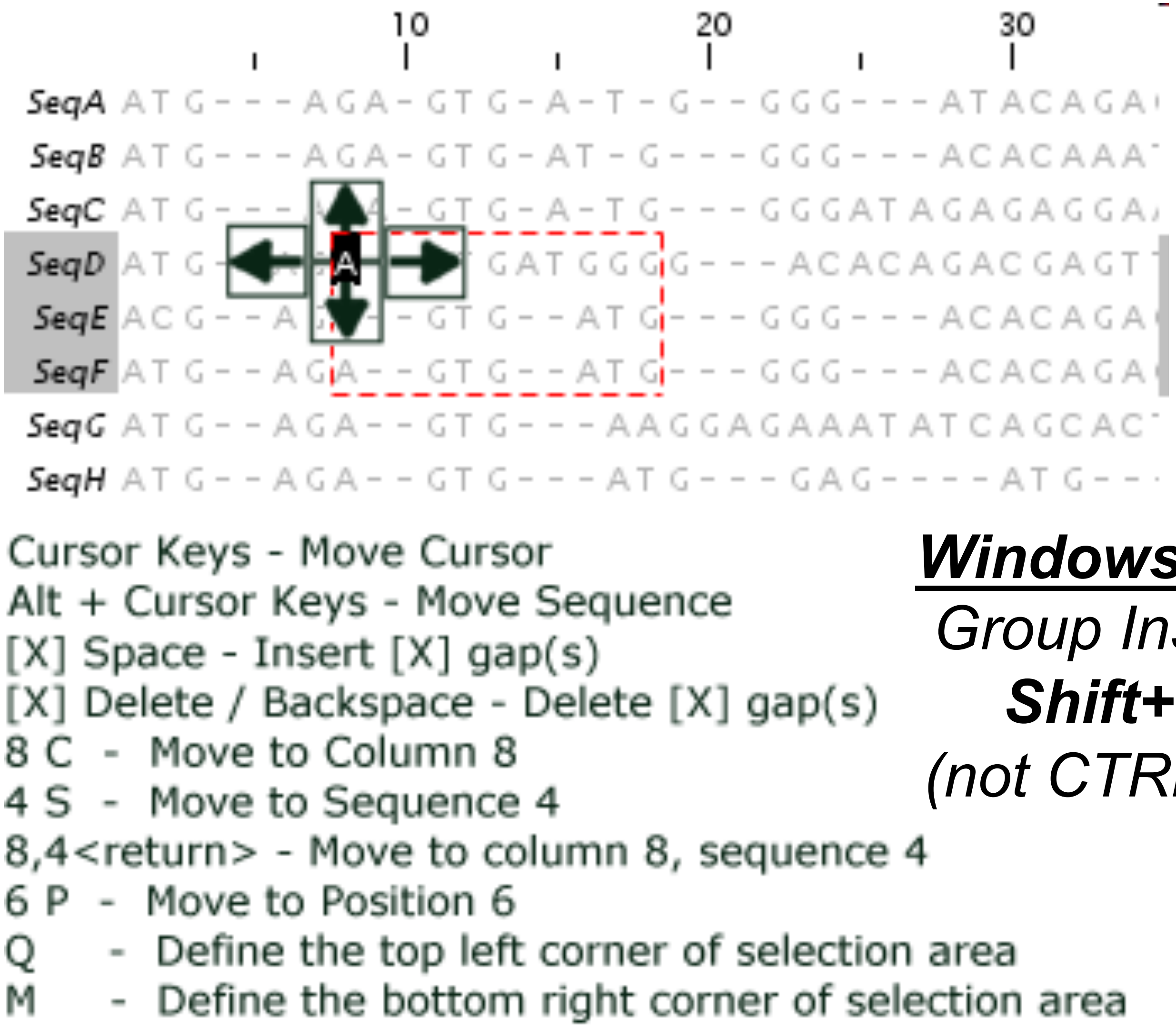
Selection
-> Edit
-> Edit Sequence...

Sequence
-> Edit Name / Description



Selected sequences can be moved up and down or slid from left to right http://www.jalview.org/examples/editing.html

F2 enables/disables keyboard mode



Cursor Keys - Move Cursor
Alt + Cursor Keys - Move Sequence
[X] Space - Insert [X] gap(s)
[X] Delete / Backspace - Delete [X] gap(s)
8 C - Move to Column 8
4 S - Move to Sequence 4
8,4<return> - Move to column 8, sequence 4
6 P - Move to Position 6
Q - Define the top left corner of selection area
M - Define the bottom right corner of selection area

Windows 7 Users:

Group Insert - use
Shift+Space
(not CTRL+Space)

Ex 5,6,7,8 and 9 selecting, editing, hiding and showing

- Tasks
  - Get used to the mouse and keyboard based selection and alignment editing controls
  - Learn how to work on specific parts of an alignment
- Questions
  - Why would you create representative sequences ?
  - How do you insert a gap in the middle of a sequence without affecting the rest of its alignment ?

Ex 10 & 11 : Colouring

- Tasks
  - Learn how to colour all, or part of the alignment by
    - Amino acid property
    - Annotation

Ex 10 & 11 : Colouring

- Tasks
  - Learn how to colour all, or part of the alignment by
    - Amino acid property
    - Annotation
- Questions
  - Why is colouring the alignment useful ?
  - How would you highlight acidic residues in your alignment ?

Ex 12,13 – alignment layout and export

- Tasks
  - Adjust the alignment formatting options
    - Wrap
    - Sequence id margin
  - Export the alignment as a figure
    - HTML, EPS and PNG

Lunch

Ex 12,13 – alignment layout and export

- Tasks
  - Adjust the alignment formatting options
    - Wrap
    - Sequence id margin
  - Export the alignment as a figure
    - HTML, EPS and PNG
- Questions
  - How do you control the number of columns shown in wrapped mode ?
  - How can you easily experiment with different alignment figure layouts ?
  - What programs can edit EPS files ?

- End of Session 1
  - Loading/saving
  - Navigation/Editing
  - Colouring/Annotation
  - Figure export

- Session 2
  - Alignment with JABAWS
- Section 2.4

PAGE 58 IN MANUAL

  - Alignment analysis

Next

- Section 2.4
  - Alignment with JABAWS.

PAGE 58 IN MANUAL

- End of Alignment analysis
  - PCA and Trees
  - Subfamily analysis

End of anli

- Section 2.4
  - Alignment with JABAWS.

PAGE 58 IN MANUAL

- End of Alignment analysis
  - PCA and Trees
  - Subfamily analysis

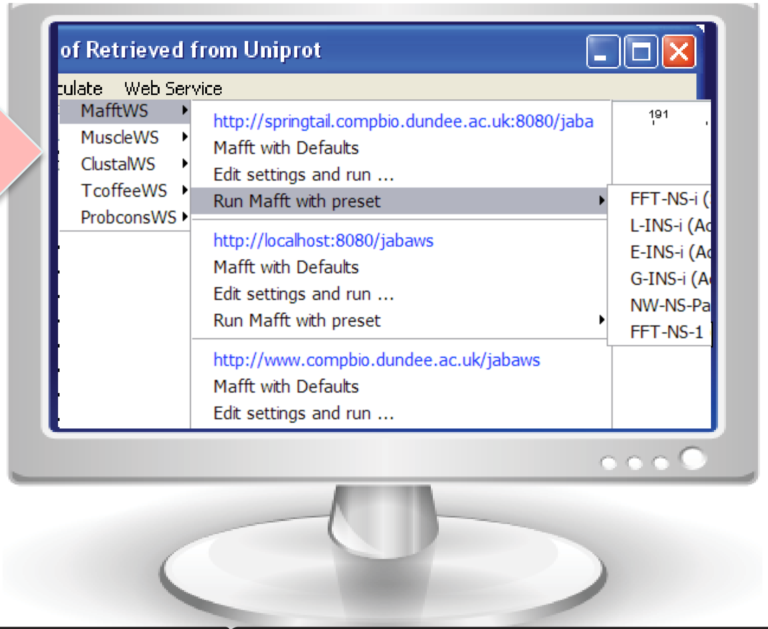
www.compbio.dundee.ac.uk/jabaws

JABAWS:MSA Troshin et al. 2011, *Bioinformatics.*

JABAWS 2 In Preparation.

Jalview Web Service GUI

JABAWS Java Client



JABAWS Virtual Appliance for your private use.

vmware™

Native JABAWS installs on a range of platforms

Apache Tomcat

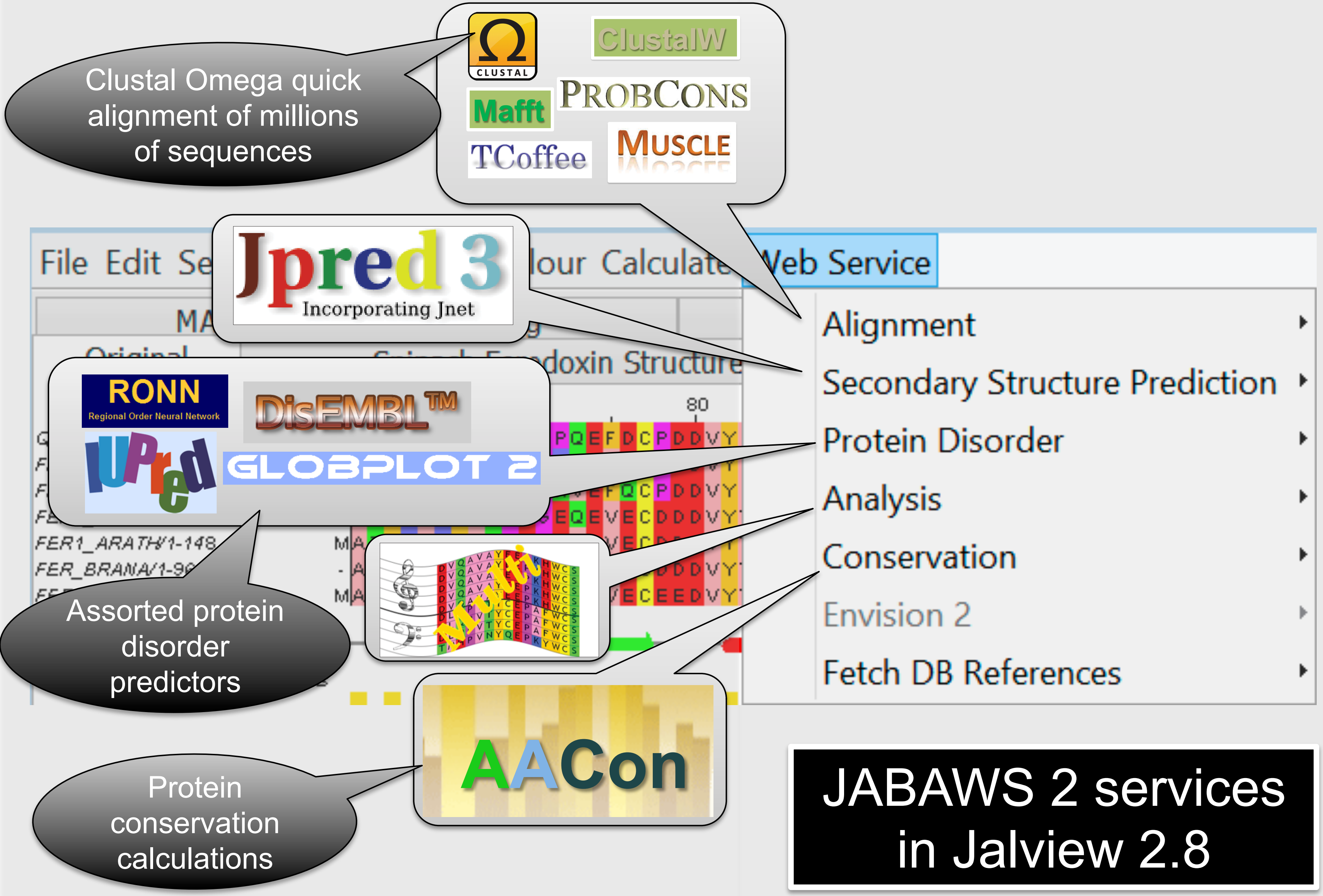
DRMAA
Distributed Resource Management Application API — www.drmaa.org

JABAWS Amazon Machine Image on EC2

powered by amazon web services™

the cloud market

JABAWS 2 services in Jalview 2.8

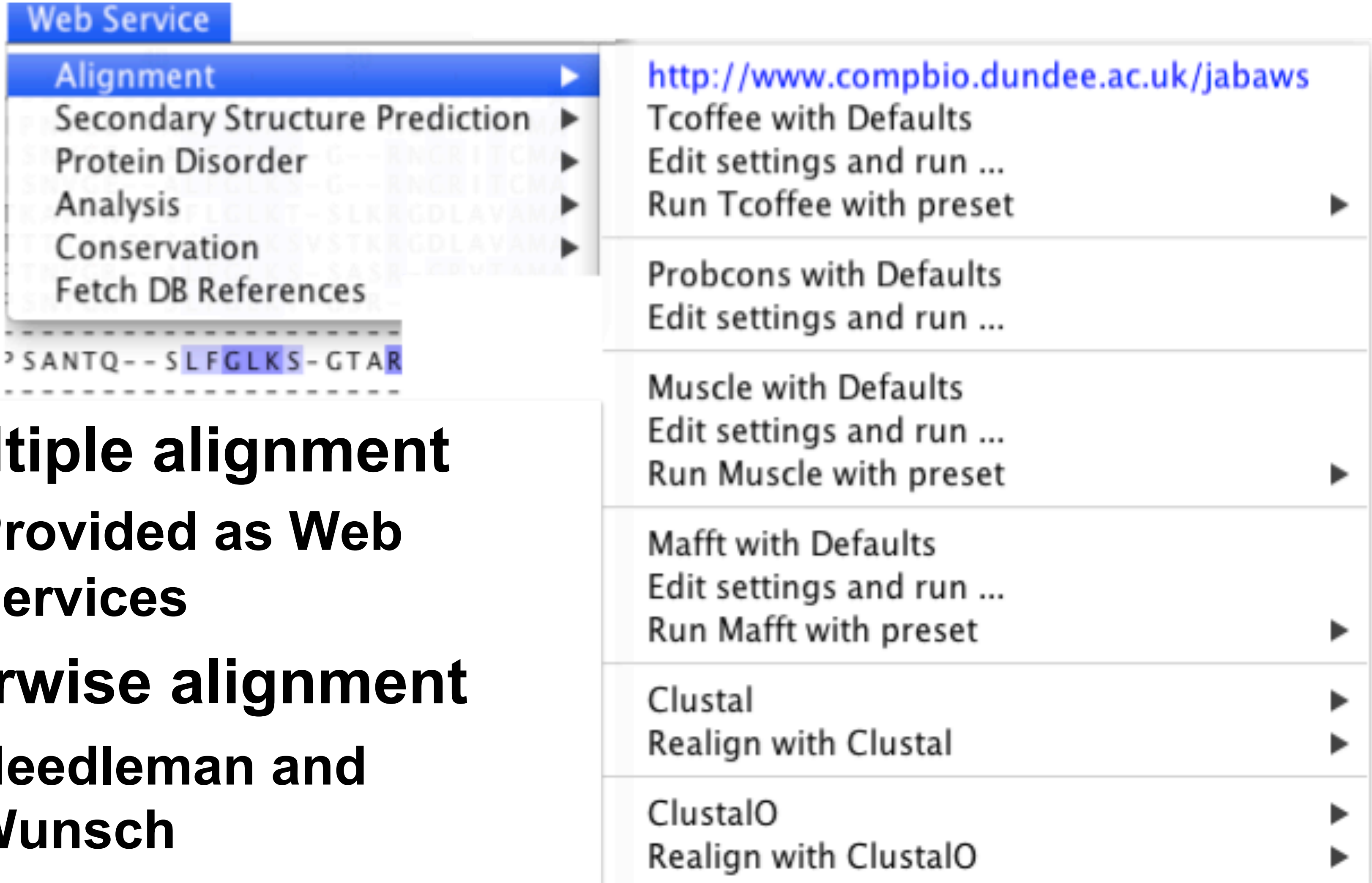


Clustal Omega quick alignment of millions of sequences

Assorted protein disorder predictors

Protein conservation calculations

Jalview's Alignment Methods



- **Multiple alignment**
  - **Provided as Web Services**
- **Pairwise alignment**
  - **Needleman and Wunsch**
    - Mostly used internally (described in section 2.2.7)

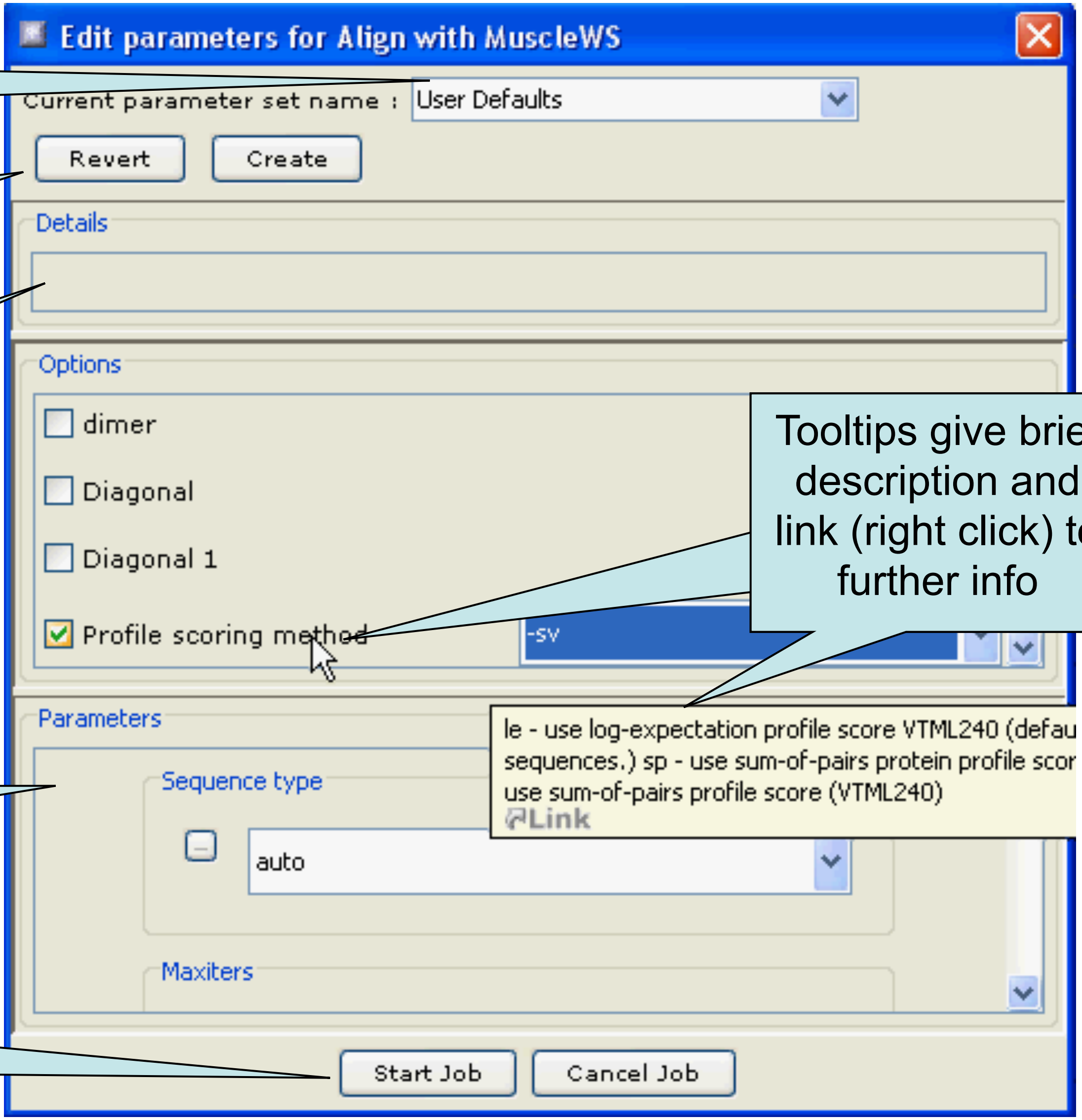
Jalview alignment exercise 25 (sect. 2.4)

- Tasks
  - Align sequences using different methods
    - Use the Webservices' 'alignment' submenu
  - Explore how hidden regions affect alignment jobs.

Jalview alignment exercise 25 (sect. 2.4)

- 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



Edit parameters for Align with MuscleWS

Current parameter set name : User Defaults

☐ dimer

☐ Diagonal

☐ Diagonal 1

☑ Profile scoring method: -sv

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

Sequence type: auto

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 contains more complex settings

Start job with current settings or cancel.

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

Modifying 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 ?

Alignment Analysis

Using jalview to analyse the relationships between aligned sequences.

Alignment analysis – Section 2.2

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

=> If there’s time, carry on to session 3

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 Exercises
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 Exercises 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 or 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
- Questions
  - How can you tell which differences are important ?
  - How can you navigate the sub-groups of a large alignment ?

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

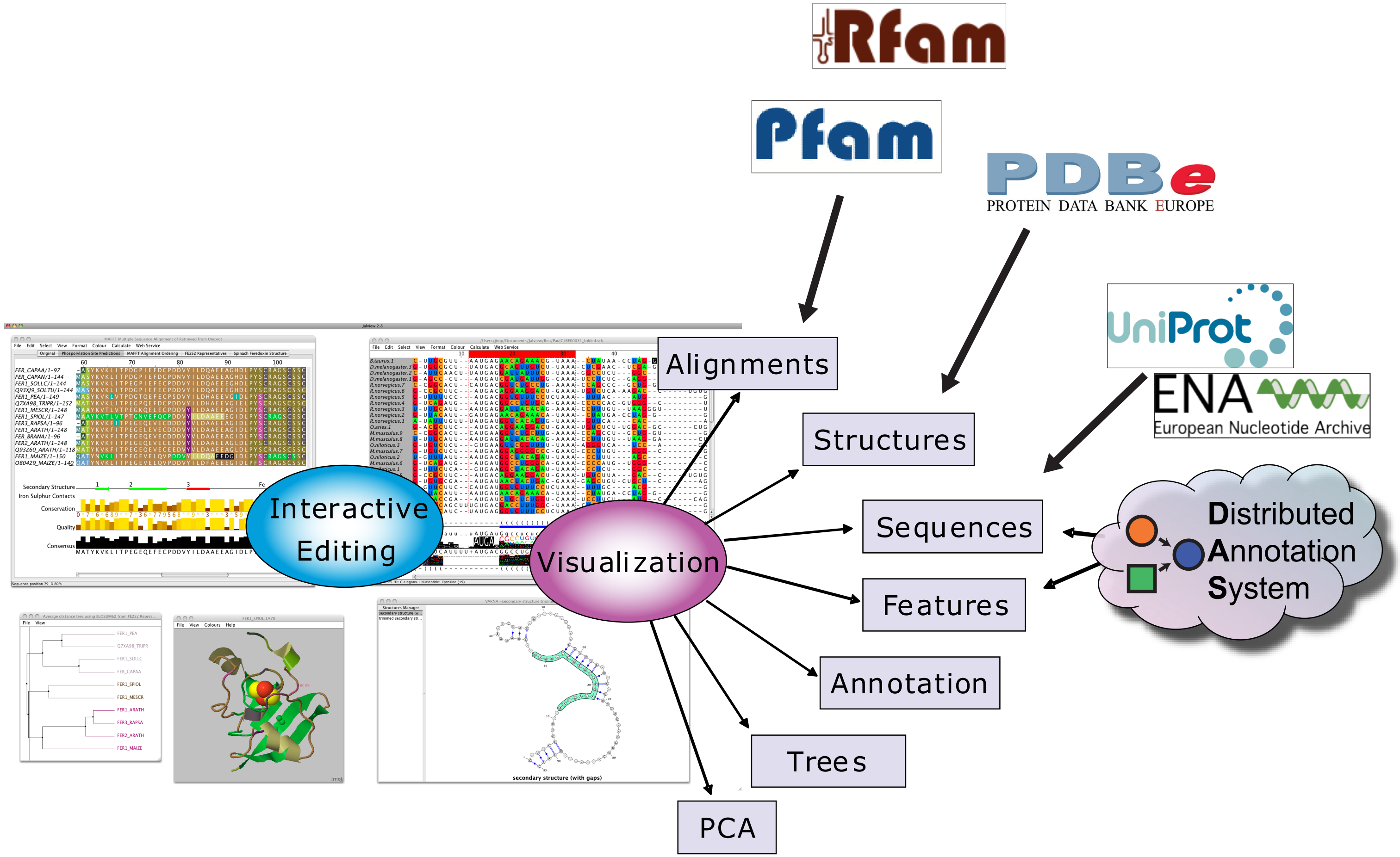
- Task
  - Use the group consensus sequence logos to more easily compare tree subgroups
  - Use ‘Make groups for selection’ to subdivide groups by specific mutation
- Questions
  - How can you work out which group is associated with which annotation row ?

- End of Session 2
  - Alignment
  - Alignment analysis

- Session 3
  - Sequence DB refs and Sequence Features
  - Protein secondary structure prediction
  - Alignment annotation

Getting and working with sequence features and annotation

- Sequence Databases
- Sequence feature sources
  - DAS Sequence feature retrieval
  - GFF and Jalview feature files
- Visualizing features
  - Highlighting annotated regions
  - Shading and reordering based on scores and labels



Rfam

Pfam

PDBe
PROTEIN DATA BANK EUROPE

UniProt

ENA
European Nucleotide Archive

Interactive Editing

Visualization

Alignments

Structures

Sequences

Features

Annotation

Trees

PCA

Distributed **A**nnotation **S**ystem

Jalview and Sequence Databases
Sec 2.9.1 Ex. 29

- Can retrieve new sequences or match against existing records using IDs
- Task
  - Recover the Uniprot annotation for the ferredoxin sequences using their IDs
    - **make sure you are using the latest 2.8 Build**

  - Verify retrieval by examining sequence annotation