Plot alignment

Version 1.0.0, by Giorgio Bianchini

Description: Adds the plot of an alignment to the tree.

Module type: Plotting

Module ID: `ea7e246b-e93f-4d0d-a67a-88af05479b48`

This module reads an alignment file in FASTA format from an attachment and adds the alignment to the tree plot. Clicking on a sequence in the alignment selects the corresponding tip in the tree and vice versa.

Parameters

FASTA alignment

Control type: Attachment

This parameter is used to select the attachment containing the alignment file. The alignment must be in FASTA format (see e.g. FASTA format on Wikipedia).

Start

Control type: Number spin box

Default value: 1

Range: [1, +∞)

This parameter determines the first nucleotide of the alignment that is shown.

End

Control type: Number spin box

Default value: 1

Range: [1, +∞)

This parameter determines the last nucleotide of the alignment that is shown.

Anchor

Control type: Drop-down list

Default value: Bottom-center

Possible values:

- Node
- Top-left
- Top-center
- Top-right
- Middle-left
- Middle-center
- Middle-right
- Bottom-left
- Bottom-center
- Bottom-right

This parameter is used to select the anchor used to determine the position of the alignment plot. If the selected value is `Node`, the specified node is used as an anchor. Otherwise, the selected point on the tree plot is used. Note that these positions refer to the *tree* plot and do not take into account the presence of labels and other elements.

Node

Control type: Node

If the [Anchor](#) was set to `Node`, this control is used to select the node that acts as an anchor.

Alignment

Control type: Drop-down list

Default value: Top-center

Possible values:

- Top-left
- Top-center
- Top-right
- Middle-left
- Middle-center
- Middle-right
- Bottom-left
- Bottom-center
- Bottom-right

This parameter controls to which point on the alignment plot the selected [Anchor](#) corresponds.

Position

Control type: Point

Default value: (0, 0)

This parameter determines how much the alignment plot is shifted with respect to the position determined by the Anchor and the Alignment.

Label position

Control type: Drop-down list

Default value: Left

Possible values:

- Neither
- Left
- Right
- Both

This parameter determines the position of the labels for the sequences in the alignment (if any).

Label font

Control type: Font

Default value: Helvetica-Oblique 6pt

This parameter determines the font used to draw the labels for the sequences in the alignment.

Label attribute

Control type: Attribute selector

Default value: Name

This parameter specifies the attribute used to determine the text of the labels. By default the `Name` of each node is drawn.

Attribute type

Control type: Attribute type

Default value: String

Possible values:

- String
- Number

This parameter specifies the type of the attribute used to determine the text of the labels. By default this is `String`. If the type chosen here does not correspond to the actual type of the attribute (e.g. `Number` is chosen for the `Name` attribute, or `String` is chosen for the `Length` attribute), no label is drawn. If the attribute has values with different types for different leaves, the label is only shown for leaves whose attribute type corresponds to the one chosen here.

Attribute format

Control type: Attribute formatter

This parameter determines how the value of the selected attribute is used to determine the text of the label. By default, if the [Attribute type](#) is `String` the text of the label corresponds to the value of the attribute, while if the [Attribute type](#) is `Number` the text of the label corresponds to the number rounded to 2 significant digits.

Identity label

Control type: Text box

Default value: Identity

This parameter determines the label used for the line showing the % identity at each residue in the alignment.

Gaps label

Control type: Text box

Default value: Gaps

This parameter determines the label used for the line showing the % of gaps at each residue in the alignment.

Residue width

Control type: Number spin box

Default value: 0.25

Range: [0, +∞)

This parameter determines the width of each residue in the alignment.

Sequence height

Control type: Number spin box (by node)

Default value: 5

Range: [0, +∞)

Default attribute: `SequenceHeight`

This parameter determines the height of each sequence in the alignment. The value can be changed on a per-node basis, but the lines showing the % identity and % gaps will always use the default value defined here.

Margin

Control type: Number spin box (by node)

Default value: 2

Range: [0, +∞)

Default attribute: `SequenceMargin`

This parameter determines the space between a sequence and the next in the alignment. The value can be changed on a per-node basis, but the lines showing the % identity and % gaps will always use the default value defined here.

Colour mode

Control type: Drop-down list

Default value: By sequence

Possible values:

- By sequence
- By residue

This parameter determines how each sequence in the alignment is coloured. If the selected value is `By sequence`, each sequence is coloured using a single colour. If the selected value is `By residue`, each residue in the sequence is coloured with a different colour. Note that colouring each residue with a different colour will likely cause reduced performance and is not recommended for alignment files containing many sequences or long sequences.

Auto colour by node

Control type: Check box

Default value: Unchecked

If this check box is checked, the colour of each sequence is determined algorithmically in a pseudo-random way designed to achieve an aestethically pleasing distribution of colours, while being reproducible if the same tree is rendered multiple times.

Opacity

Control type: Slider

Default value: 100 %

Range: [0 %, 100 %]

This parameter determines the opacity of the colour used if the Auto colour by node option is enabled.

Colour

Control type: Colour (by node)

Default value: ▮ #0072B2 (opacity: 100%)

Default attribute: `SequenceColour`

If the selected Colour mode is `By sequence`, this parameter determines the colour of each sequence; otherwise, it only controls the colour of the label for each sequence.

Residue colours

Control type: Colour (by node)

Default value: ▢ #FFFFFF (opacity: 0%)

Default attribute: `(N/A)`

If the selected Colour mode is `By residue`, this parameter determines the colour used for each residue. While this uses a "Colour by node" control, the colours are actually determined based on the residues, rather than on attributes of the tree. The colours associated with each residue can be changed (or additional residues can be added) by modifying the formatter code for this parameter.

Residue style buttons

Control type: Buttons

Buttons:

- DNA/RNA
- Protein

These buttons can be used to reset the default [Residue colours](#) for nucleotide sequences or protein sequences.

Identity colour

Control type: Colour

Default value: ■ #009E9E (opacity: 100%)

This parameter is used to determine the colour to use when drawing the line with the % identity.

Gaps colour

Control type: Colour

Default value: ■ #CC7979 (opacity: 100%)

This parameter is used to determine the colour to use when drawing the line with the % of gaps.

Draw residue letters

Control type: Check box

Default value: Unchecked

If this check box is checked, the letters corresponding to the sequences are also drawn with the alignment. Note that this will likely cause reduced performance and is not recommended for alignment files containing many sequences or long sequences. If necessary, the letters will be compressed so that they do not overflow the alignment.

Residue font

Control type: Font

Default value: Courier-Bold 6pt

The font used to draw the letters in the alignment.

Letter colour

Control type: Colour

Default value: ■ #000000 (opacity: 100%)

The colour used to draw the letters in the alignment.