

# Plot alignment

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*Version 1.1.2, 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.

The module can be used in two ways, depending on the value of the [Mode](#) parameter: if this is `Alignment block`, the alignment is drawn as a single block that can be positioned on the tree plot; if this is `Sequences at nodes`, each sequence is drawn individually at a position corresponding to the node it refers to. In this case, the sequences may not appear "aligned" in the plot, unless the [Anchor type](#) is set to `Origin`.

## Parameters

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### 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,  $+\infty$  )

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

### End

**Control type:** Number spin box

**Default value:** 1

**Range:** [ 1,  $+\infty$  )

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

## Mode

**Control type:** Drop-down list

**Default value:** Alignment block

**Possible values:**

- Alignment block
- Sequences at nodes

This parameter determines whether the alignment is drawn as a single "block" positioned somewhere on the tree plot, or as individual sequences positioned at the tips they refer to. In the second case, the lines showing the % identity and the % of gaps are not 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

If the [Mode](#) is `Alignment block`, 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.

## Anchor type

**Control type:** Drop-down list

**Default value:** Node

**Possible values:**

- Node
- Origin

If the [Mode](#) is `Sequences at nodes` , this parameter is used to determine how the position of each sequence is computed. If the selected value is `Node` , each sequence is positioned at the node it corresponds to; if the selected value is `Origin` , the position of each sequence depends on the current Coordinates module:

Coordinates module	Origin
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<i>Rectangular</i>	A point corresponding to the projection of the node on a line perpendicular to the direction in which the tree expands and passing through the root node. Usually (i.e. if the tree is horizontal), this means a point with the same horizontal coordinate as the root node and the same vertical coordinate as the current node.
<i>Radial</i>	The root node.
<i>Circular</i>	The root node.

## Position

**Control type:** Point

**Default value:** ( 0, 0 )

If the [Mode](#) is `Alignment block`, this parameter determines how much the alignment plot is shifted with respect to the position determined by the [Anchor](#) and the [Alignment](#). If the [Mode](#) is `Sequences at nodes`, instead, each sequence is shifted by the specified amount with respect to the [Reference](#).

## Orientation

**Control type:** Slider

**Default value:** 0°

**Range:** [ 0°, 360° ]

This parameter determines the orientation of the sequence with respect to the [Reference](#), in degrees. If this is 0°, the sequence is parallel to the reference (e.g. the branch), if it is 90° it is perpendicular to the branch and so on.

## Reference

**Control type:** Drop-down list

**Default value:** Branch

**Possible values:**

- Horizontal
- Branch

This parameter (along with the [Orientation](#)) determines the reference for the direction along

which the sequence flows. If this is `Horizontal`, the sequences are all drawn in the same direction, regardless of the orientation of the branch to which they refer. If it is `Branch`, each sequence is drawn along the direction of the branch connecting the node to its parent.

## 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:**  $[0, +\infty)$

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

## Sequence height

**Control type:** Number spin box (by node)

**Default value:** 5

**Range:**  $[0, +\infty)$

**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:**  $[0, +\infty)$

**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 aesthetically 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.