

# Group labels

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*Version 1.3.0, by Giorgio Bianchini*

**Description:** Highlights monophyletic groups with a label.

**Module type:** Plotting

**Module ID:** 7ef15916-4383-4ee7-b4bd-bd44a7be1849

This module is used to highlight monophyletic groups by adding "bars" with labels next to the tree. It can only be used with *Rectangular* or *Circular* coordinates (module Ids 68e25ec6-5911-4741-8547-317597e1b792 and 92aac276-3af7-4506-a263-7220e0df5797 ), respectively.

## Parameters

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### Attribute

**Control type:** Text box

This parameter specifies the attribute used to determine the text of the labels.

### 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 nodes, the label is only shown on nodes 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.

## Only on last ancestor

**Control type:** Check box

**Default value:** Unchecked

If this check box is checked, the label is only shown for nodes that have a value for the specified [attribute](#) that differs from their ancestor's value. For example, this makes it possible to use the Propagate attribute module to propagate an attribute (e.g. a gene name or a phylum) to the last common ancestor of all taxa that have that attribute (i.e. all orthologs of that gene or all members of that phylum), and then show a group label for that LCA.

## Distance

**Control type:** Number spin box

**Default value:** 100

**Range:**  $(-\infty, +\infty)$

If the tree is drawn using *Rectangular* coordinates, this determines the distance of the line containing labels from the root node. If the tree is drawn using *Circular* coordinates, this determines the radius of the circle containing the labels.

## Margin

**Control type:** Number spin box

**Default value:** 5

**Range:**  $(-\infty, +\infty)$

This parameter determines the margin to use when drawing the label. If this is greater than 0, the label is larger than the leaves that belong to it, while if it is lower than 0, the label is smaller than the leaves that belong to it.

## Height

**Control type:** Number spin box

**Default value:** 20

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

This parameter determines the height of the label.

## Prevent overlap

**Control type:** Check box

**Default value:** Checked

If this check box is checked, the module will make sure that no two labels overlap, by shifting some of the labels further away. This happens automatically; if you wish to have more control, disable this option and enable multiple instances of the module using different attributes.

## Row margin

**Control type:** Number spin box

**Default value:** 5

**Range:**  $( -\infty, +\infty )$

If [Prevent overlap](#) is enabled, this parameter determines the margin between consecutive rows of labels.

## Gravity

**Control type:** Drop-down list

**Default value:** Bottom

**Possible values:**

- Bottom
- Top

If [Prevent overlap](#) is enabled, this parameter determines whether the labels are clustered towards the top or the bottom.

## Invert arrangement


**Control type:** Check box

**Default value:** Unchecked

If [Prevent overlap](#) is enabled, this parameter determines whether larger labels are closest or farthest from the tree.

## Fill colour

**Control type:** Colour (by node)


**Default value:**  #000000 (opacity: 0%)

**Default attribute:** `LabelFillColor`

This parameter determines the colour of the background of the label.

## Stroke colour

**Control type:** Colour (by node)

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

**Default attribute:** `LabelStrokeColour`

This parameter determines the colour of the outline of the background of the label.

## Stroke thickness

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

**Default value:** 0

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

**Default attribute:** `LabelThickness`

This parameter determines the thickness of the outline of the background of the label.

## Font


**Control type:** Font

**Default value:** Helvetica-Bold 10pt

This parameter determines the font used to draw the labels.

## Text colour

**Control type:** Colour (by node)

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

**Default attribute:** `Color`

This parameter determines the colour of the text used to draw the labels.

## Text alignment

**Control type:** Drop-down list

**Default value:** Center

**Possible values:**

- Near
- Center
- Far

This parameter determines the alignment of the text within the label.

## Text margin

**Control type:** Number spin box

**Default value:** 0

**Range:** (  $-\infty$ ,  $+\infty$  )

This parameter determines the margin between the edge of the label and the start of the text.

## Further information

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This module cannot detect automatically the best value for the various layout parameters, therefore you will have to tweak these manually. In particular, on very large trees it may seem at first that the module is not doing anything; if this is the case, please try increasing the [Font](#) size or the other parameters.

Multiple instances of this module can be used to obtain various effects; e.g. one instance could be used to draw the labels, while another can be used to draw coloured bars.

Here are two examples of this module in action on a tree with *Rectangular* and *Circular* coordinates, respectively:

