

# FastTree

The *Building Phylogenetic Tree* dialog for the *FastTree* method has the following view:

The screenshot shows a software dialog box titled "Build Phylogenetic Tree". At the top, there is a blue header bar with a small icon on the left and question mark and close buttons on the right. Below the header, the "Tree building method" is set to "FastTree" in a dropdown menu. There are two tabs: "FastTree options" (which is active) and "Display Options". Under the "FastTree options" tab, the text "Command line options for FastTree:" is followed by a large empty text box for input. To the right of this text box is a button labeled "View all options". Below the text box are two unchecked checkboxes: "Speed up the neighbor joining phase (>50,000 sequences)" and "Use pseudo-counts (recommended for highly gapped sequences)". At the bottom left, there is a "Save tree to" label followed by an empty text field and a small button with three dots. Below this are two buttons: "Save Settings" and "Restore Default". At the bottom right, there are three buttons: "Build", "Cancel", and "Help".

The full list of available parameters you can find [here](#).

Press the *Build* button to build a tree with the parameters selected.