

Relevance Analysis

Relevance Analysis is to let user to run genes' relevance ranking for given grouping assignment and region boundary.

User may also run shuffle which is to shuffle the gene data into a randomly given category with a given number of shuffles.

The screenshot shows the 'Relevance Analysis' software window. It features a menu bar with 'File' and 'Help'. Below the menu is a 'Category List (1-N)' containing four items: '1 1_sham', '2 2_2h', '3 3_6h', and '4 4_24h'. Below the list are several input fields: 'Group Category, EX: 2 3, 1 6, 4 5' with a text box containing '1 3, 2 4'; 'Display top ranking:' with a text box containing '30'; and 'Region Boundary -- 1:' with three text boxes containing '-0.5', '0.5', and '3:'. At the bottom, there are four buttons: 'Shuffle', 'Reset', 'RUN', and 'Save'. Below these is a 'Shuffle Profile' section with a 'Number of Shuffle:' text box and a 'RUN Shuffle' button. Red arrows point from the text above to the 'Category List', the 'Group Category' text box, the 'Display top ranking' text box, the 'Region Boundary' text boxes, the 'RUN' button, and the 'RUN Shuffle' button.