

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 has a menu bar with 'File' and 'Help'. Below the menu is a 'Category List (1-N)' box containing four items: '1 1_sham', '2 2_2h', '3 3_6h', and '4 4_24h'. Below this is a 'Group Category, EX: 2 3, 1 6, 4 5' label followed by a text input field containing '1 3, 2 4'. Below that is a 'Display top ranking:' label followed by a text input field containing '30'. Below that is a 'Region Boundary --' label followed by three text input fields: '1: -0.5', '2: 0.5', and '3:'. Below these are four buttons: 'Shuffle', 'Reset', 'RUN', and 'Save'. At the bottom is a 'Shuffle Profile' section with a 'Number of Shuffle:' label followed by a text input field and a 'RUN Shuffle' button. Red arrows point from the text above to the following UI elements: '1 1_sham', '2 2_2h', '3 3_6h', '4 4_24h', the 'Group Category' input field, the 'Display top ranking' input field, the 'Region Boundary' input fields, the 'RUN' button, and the 'RUN Shuffle' button.

Relevance Analysis

File Help

Category List (1-N)

1 1_sham
2 2_2h
3 3_6h
4 4_24h

Group Category, EX: 2 3, 1 6, 4 5: 1 3, 2 4

Display top ranking: 30

Region Boundary -- 1: -0.5 2: 0.5 3:

Shuffle Reset RUN Save

Shuffle Profile

Number of Shuffle: RUN Shuffle