Wisdom of crowds – data explorer

Getting started

The data files are automatically loaded, and the viewer is ready for immediate use.

Tabs

Preloaded data

This page displays the list of the uploaded files.

Tables

Through a dropdown menu, users can select one of the uploaded files ("*Hazard*", "*Genes*", "*Properties*") and inspect its original content.

Expert

Users can select the anonymized experts and review their responses for each material.

Hazard Visualization, Gene Visualization, Properties Visualization

Each of these tab displays data related respectively to material concern scores, weighted gene expression, or weighted physico-chemical properties against different endpoints. The structure of the tabs are almost identical.

Hazard Visualization in detail

All possible interactions within this tab are based on the material concern score heatmap, which appears upon clicking "*Visualize*" button.

Users can interact with the heatmap in several ways:

- *Clicking on a heatmap cell*: displays an informative panel about the selected cell (value, coordinates, and labels of the original uploaded datatable) at the bottom of the page. It also enables the "*Material Categories*" button, showing aside the "*Material class*" of the selected cell.
- *Brushing an area on the heatmap*: displays a sub-heatmap and two scatterplots at the bottom of the window, representing the mean score vs endpoints for "*Specific Material*" and "*Material Category*".
- *"Sparse selection" checkbox:* if enabled, it allows users to select not-contiguous rows and/or columns of the heatmap by dedicated dropdown menus. Clicking "*Visualize Sparse Selection*" opens a new modal window with the heatmap representing selected data. If no entry is selected, the new heatmap will be identical to the original.

Fig. 1 – Structure of "Hazard Visualization" tab. Dropdown menus for rows and columns automatically appears when "sparse selection" is ticked.

Clicking "*Material Categories*" button opens a new modal window whose structure, characteristics and potentialities are similar to "*Hazard Visualization*" tab. The new heatmap shows the scores vs the endpoints for all materials in the same material class as the selected cell in the "*Hazard Visualization*" heatmap.

The sub-heatmap, created with the *InteractiveComplexHeatmap* R package, can be resized by dragging its bottom-right corner. Its menu bar on the left-bottom corner allows users to configure the sub-heatmap, export data to a downloadable table, save the image, and manually adjust the size.
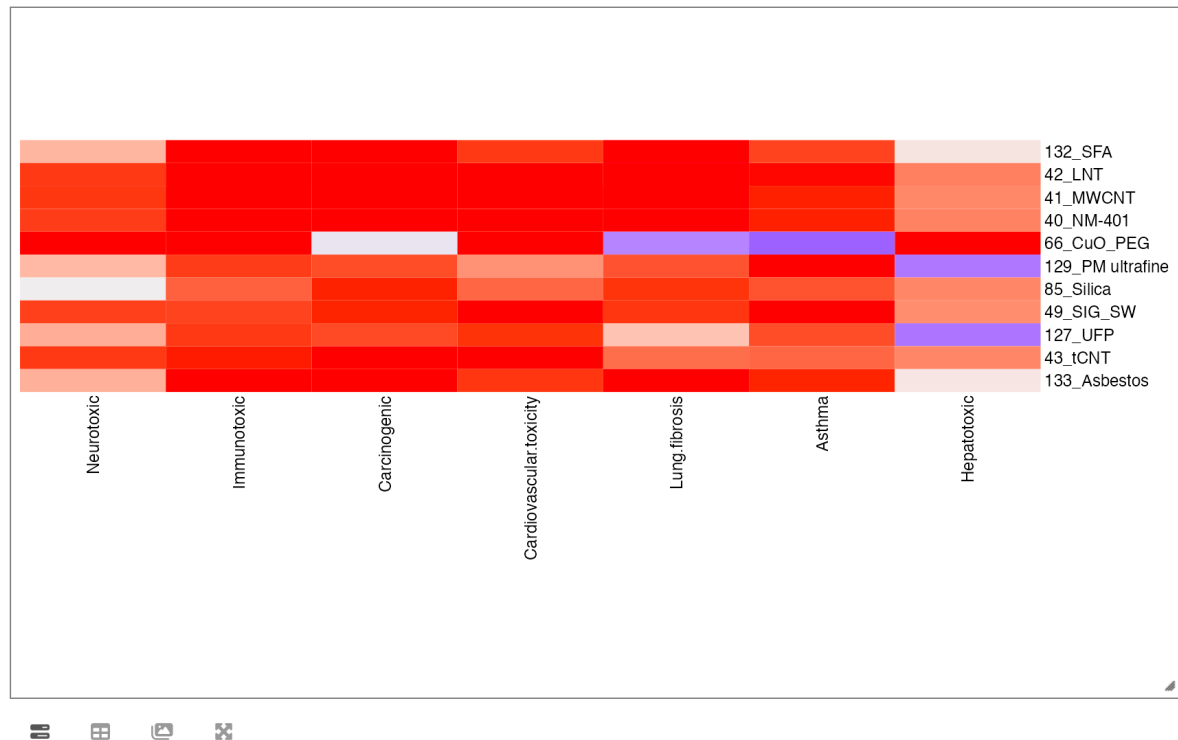
Selected sub-heatmap

Fig. 2 – Structure of the sub-heatmap obtained by brushing the original heatmap. The bottom displays the interactive menu bar (left) and dragging corner (right).

The sub-heatmap can be set as interactive, opening a new modal window that displays on the left the now interactive sub-heatmap and the selections on the right. The process can be repeated recursively.

The mentioned charts are plotted with the *plotly* R package, offering several interactive options through a menu bar on the top-right corner of the plot (download, pan, zoom, and compare). Clicking on chart legend entries can add/remove data points, while hovering on chart dots reveals more information.
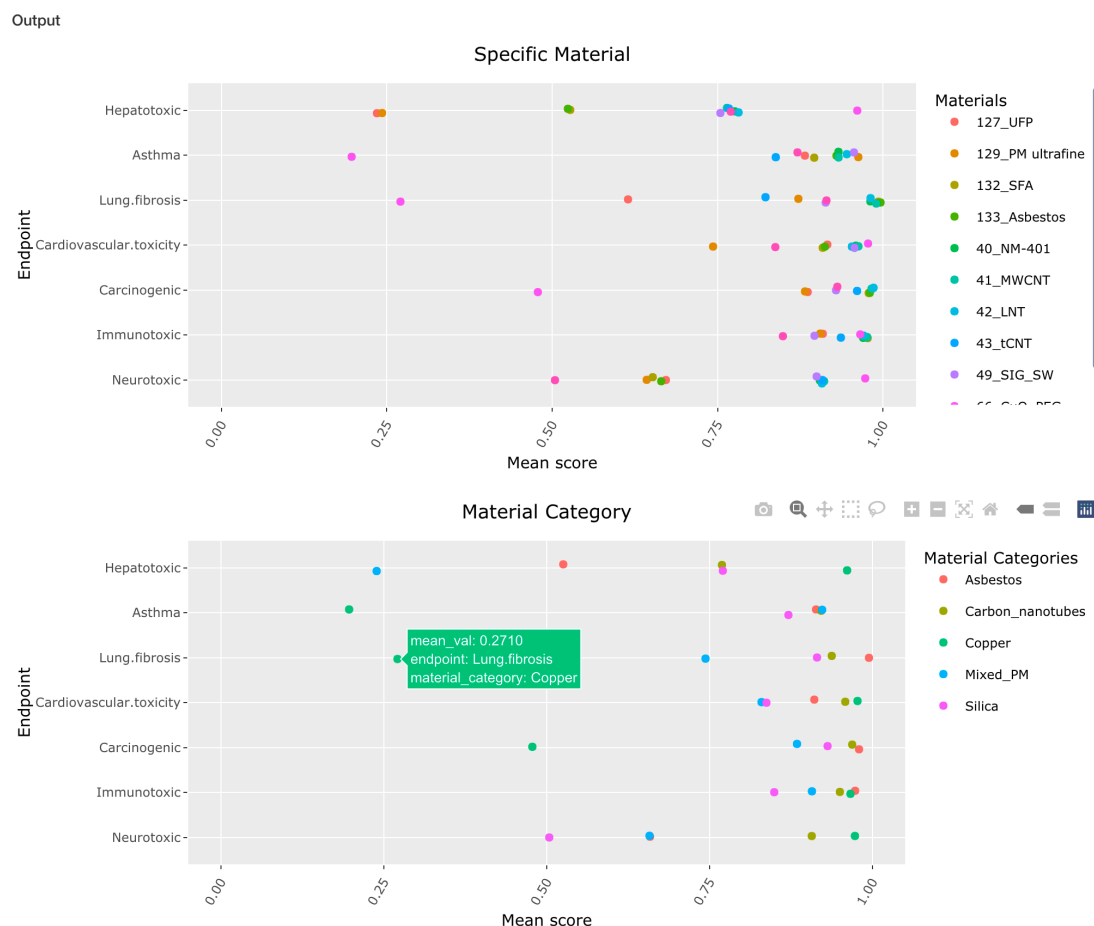
Fig. 3 – The scatterplots resulting from brushing the original heatmap. The bottom chart displays the interactive menu bar at the top right corner and the informative panel provided when users click on data dot.

For a detailed description of the features, please refer to the respective R package documentation (*InteractiveComplexHeatmap*, *plotly*).

Gene and Properties Visualization tabs in detail

Since these tabs differ only slightly from the "*Hazard Visualization*" tab, a dedicated explanation is not provided.

The only major difference refers to Gene tab, where clicking or brushing the main heatmap results in a table displaying Ensembl ID, gene description and the corresponding Ensembl url of non-null selected genes.

Selected sub-heatmap

Intestinal.toxicity

Environmental.hazard

MT1G
SLC30A1
SYNGR2
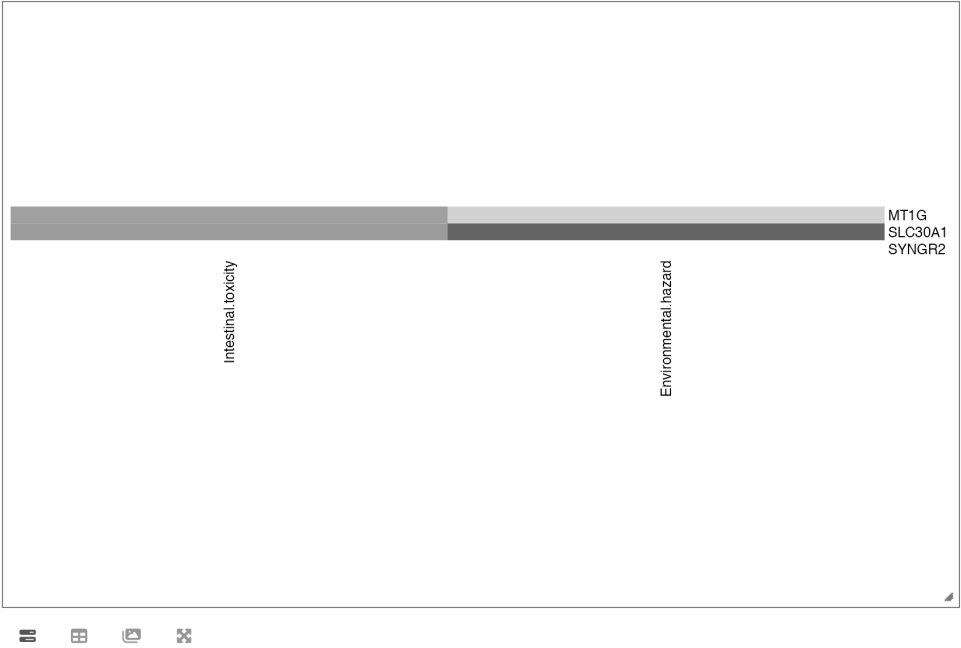
Output

Non-null selected genes

Ensembl url	Ensembl ID	Gene description
MT1G	ENSG00000125144	metallothionein 1G [Source:HGNC Symbol;Acc:HGNC:7399]
SLC30A1	ENSG00000170385	solute carrier family 30 member 1 [Source:HGNC Symbol;Acc:HGNC:11012]

Showing 1 to 2 of 2 entries

Fig. 4 — Sub-heatmap and non-null gene information resulting from the area brushed on the original gene heatmap.