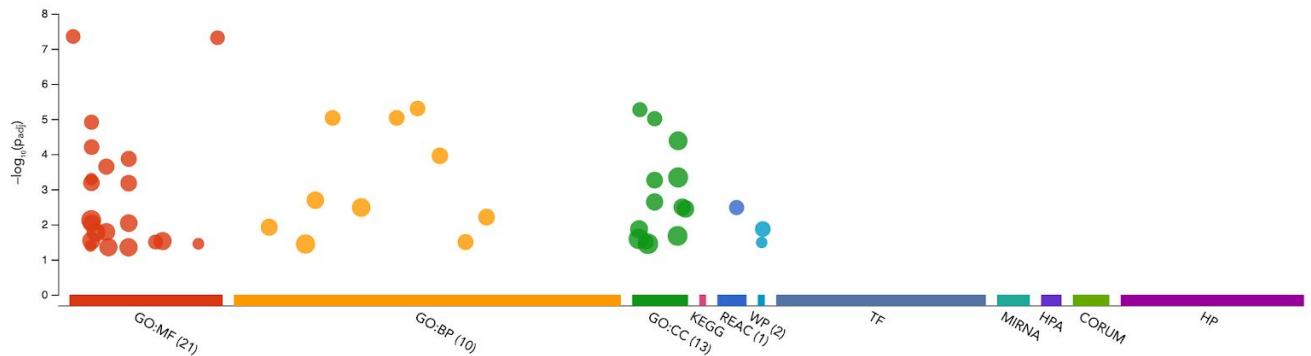


## [g:Profiler](#)

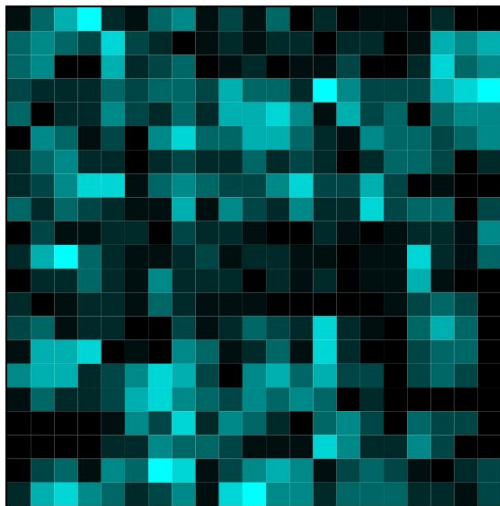
### Example:



**Description:** This is a manhattan plot. It appears to have x-axis labelled with gene sets, y-axis is labelled with p-values (on a negative log scale). When you hover over the circles, they display the gene name, it's description, and the p-value. I'm not exactly sure what the size of the circles represents (probably count?). I found the paper describing this update and it says that they are the first to use a Manhattan plot to visualize enrichment analysis results. I think that this plot is useful in the beginning stages of enrichment analysis but in general when presenting findings and writing a paper I would imagine that most people would want to look at a smaller subset of gene sets.

## [Network2Canvas](#)

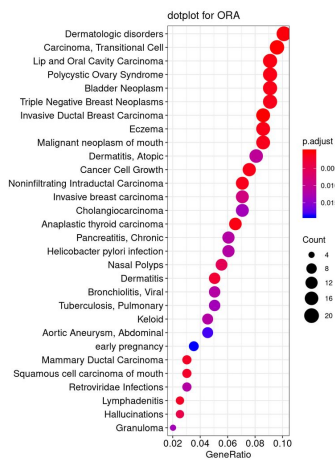
### Example:



**Description:** I believe the example above is just random, but I was not able to find any gene sets that showed any meaningful results from the sample genes! It seems like this offers similar features to what Enrichr currently offers - networks and some type of cluster gram.

## [cluserProfiler Chapter 12: Visualization of Functional Enrichment Result](#)

### Example:



**Description:** The dotplot shown is similar to a bar graph, but allows for additional information to be shared in the sizes of the circles (count). There are also more interesting examples in the chapter linked.

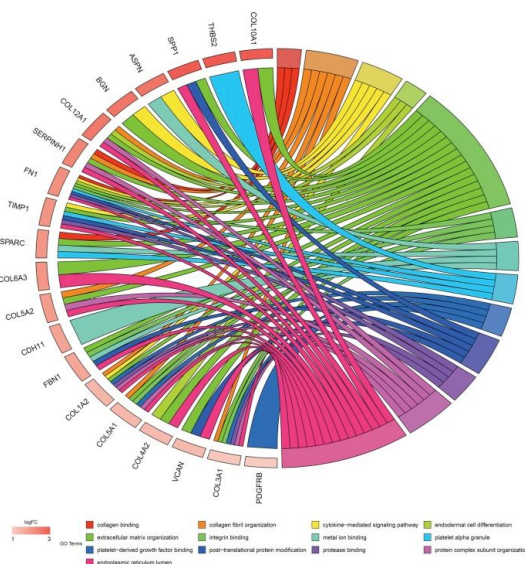
### [Paper on Osteoporosis](#)

**Example:** dot plots that look just like the one above

**Description:** Used enrichment analysis data specifically from Enrichr to create this dot plot.

### [Paper on Gastric Cancer in Asia that cites Enrichr](#)

### Example:



**Description:** I'm not totally sure that this visualization does not require analysis methods other than what Enrichr provides, but I think this one is particularly eye-catching. It's not the most clear in terms of information but when combined with other plots it can be useful.