Tag and Word Clouds

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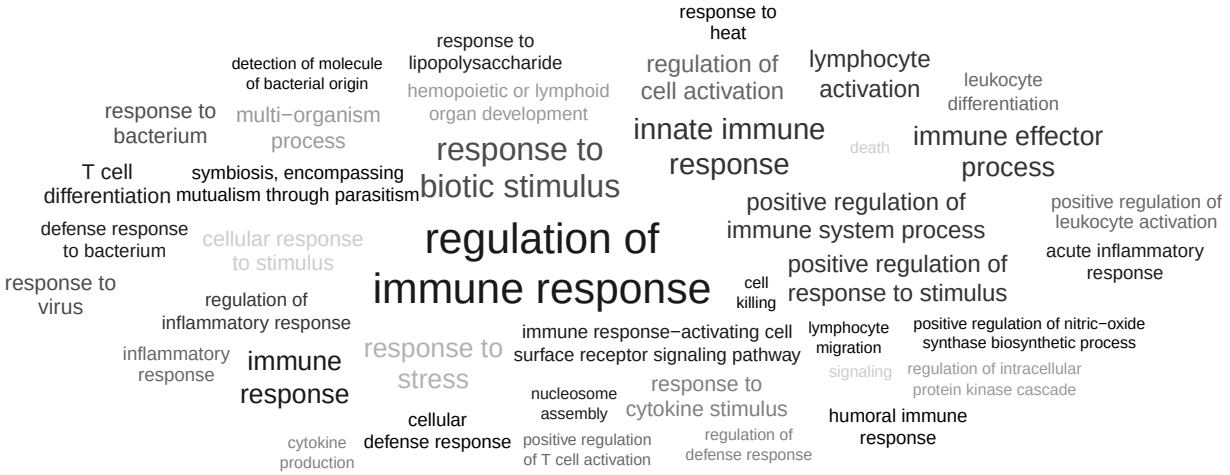
Introduction

`tagcloud` command creates various styles of tag and word clouds. In it simplest form, it takes a character vector (vector of tags) as an argument. Optionally, one can add different weights, colors and layouts. Here is an advanced example of a typical GO-Term cloud, where colors and weights (font size) which correspond to the effect size and P-value, respectively:

```
library(tagcloud)
```

```
## Loading required package: Rcpp
```

```
data(gambia)
tags <- strmultline(gambia$Term)[1:40]
weights <- -log(gambia$Pvalue)[1:40]
or <- gambia$OddsRatio[1:40]
colors <- smoothPalette(or, max=4)
tagcloud(tags, weights=weights, col=colors)
```

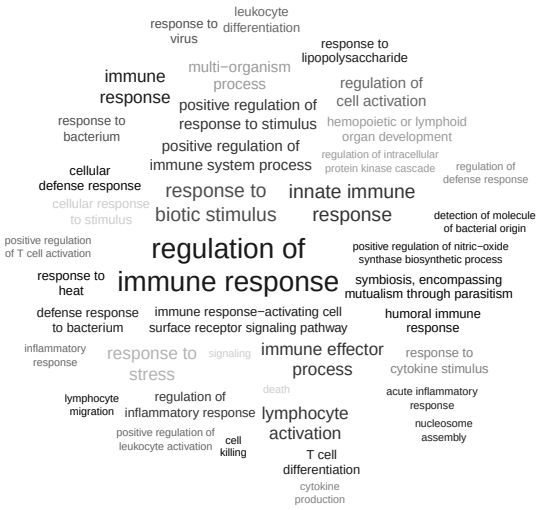


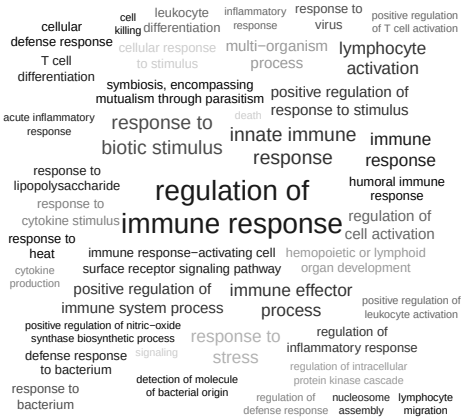
Notes. The geometry of the cloud will reflect the geometry of the plotting area: simply resize the plot and re-run `tagcloud` to get a different look. `smoothPalette` automagically converts a numeric vector into a vector of a color gradient of the same length. `strmultline` breaks long, multi-word lines, which otherwise mess up the figure.

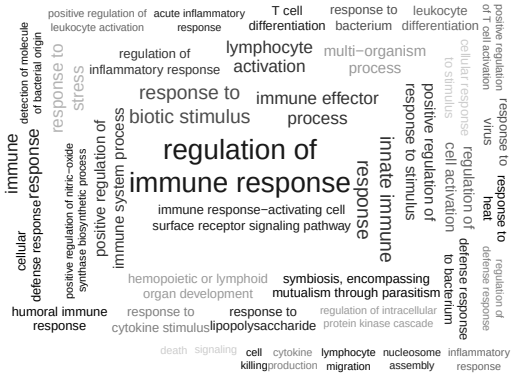
Layouts

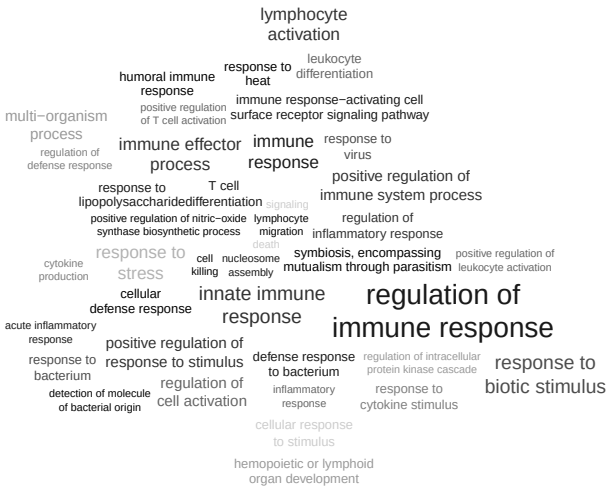
There is a number of algorithms that allow you to create different layouts.

```
par( mfrow=c( 3, 2 ) )
tagcloud(tags, weights=weights, col=colors, algorithm="oval")
tagcloud(tags, weights=weights, col=colors, algorithm="fill")
tagcloud(tags, weights=weights, col=colors, algorithm="snake")
tagcloud(tags, weights=weights, col=colors, algorithm="random")
tags2 <- gambia$Term[1:20]
cols2 <- colors[1:20]
wei2 <- weights[1:20]
tagcloud(tags2, weights=wei2, col=cols2, algorithm="list")
tagcloud(tags2, weights=wei2, col=cols2, algorithm="clist")
```









regulation of immune response
response to biotic stimulus
positive regulation of immune system process
immune response−activating cell surface receptor signaling pathway
positive regulation of response to stimulus
innate immune response
immune effector process
lymphocyte activation
immune response
regulation of inflammatory response
hemopoietic or lymphoid organ development
response to stress
regulation of cell activation
multi−organism process
response to cytokine stimulus
cellular response to stimulus
leukocyte differentiation
response to bacterium
T cell differentiation
response to virus

Another parameter to tune is `fvert`, the proportion of tags that are displayed vertically (which is 0 by default).

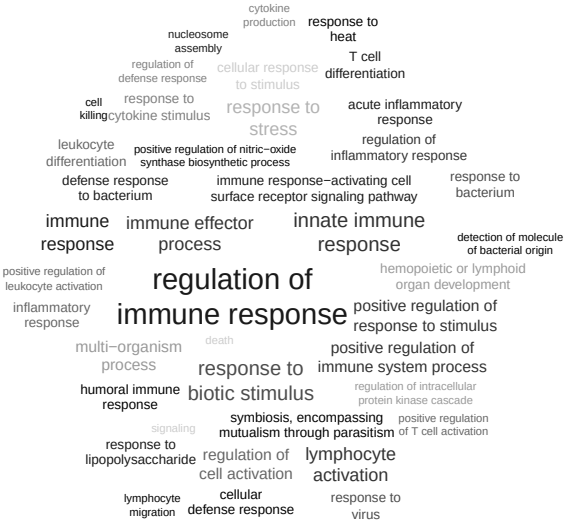
```
par(mfrow=c(1, 2))
tagcloud(tags, weights=weights, col=colors, fvert=0.3)
tagcloud(tags, weights=weights, col=colors, fvert=0.7)
```

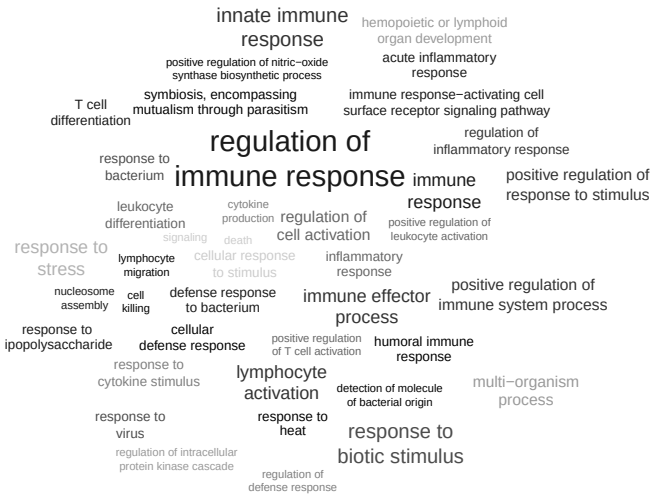
Finally, using the parameter `order` you can also influence the layout of the word cloud:

- `size`: tags are ordered by size, that is, their effective width multiplied by their effective height. Default.
- `keep`: keep the order from the list of words provided
- `random`: randomize the tag list
- `width`: order by effective screen width
- `height`: order by effective screen height

Starting with the tag with the largest weight typically makes this tag at the center of the cloud. Sometimes, however, a randomized order results in a more interesting output.

```
par(mfrow=c(1, 2))
tagcloud(tags, weights=weights, col=colors, order="size")
tagcloud(tags, weights=weights, col=colors, order="random")
```



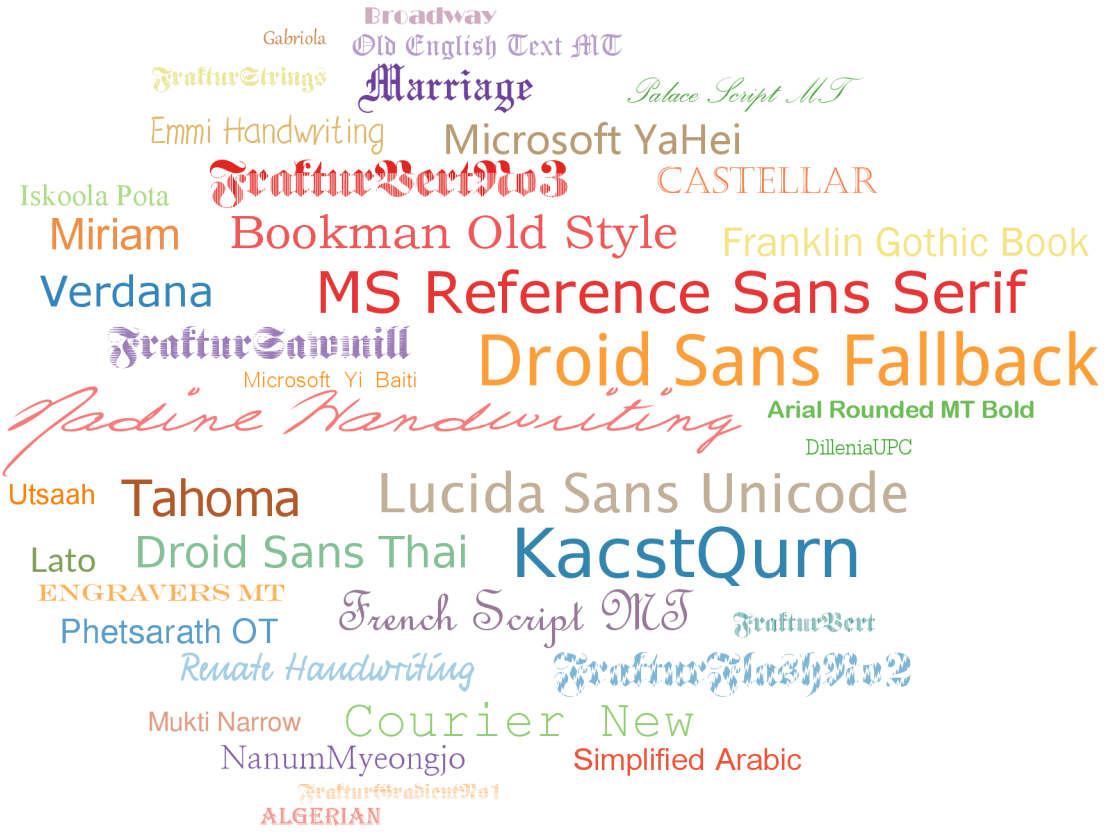


Fonts

Using the parameter `family`, you can specify the font family to be used. In the following, we use the excellent `extrafont` package[1]. However note that to produce correct PDFs, you should use the cairo engine, for example with `dev.copy2pdf( out.type="cairo", ... )`. Alternatively, use the `png()` device.

```
library(extrafont)
library(RColorBrewer)
fnames <- sample(fonts(), 40)
fweights <- rgamma(40, 1)
fcolors <- colorRampPalette( brewer.pal( 12, "Paired" ) )( 40 )
tagcloud( fnames, weights=fweights, col=fcolors, family=fnames )
```

[1] After installing the package, run `font_import` to import the fonts installed on the system

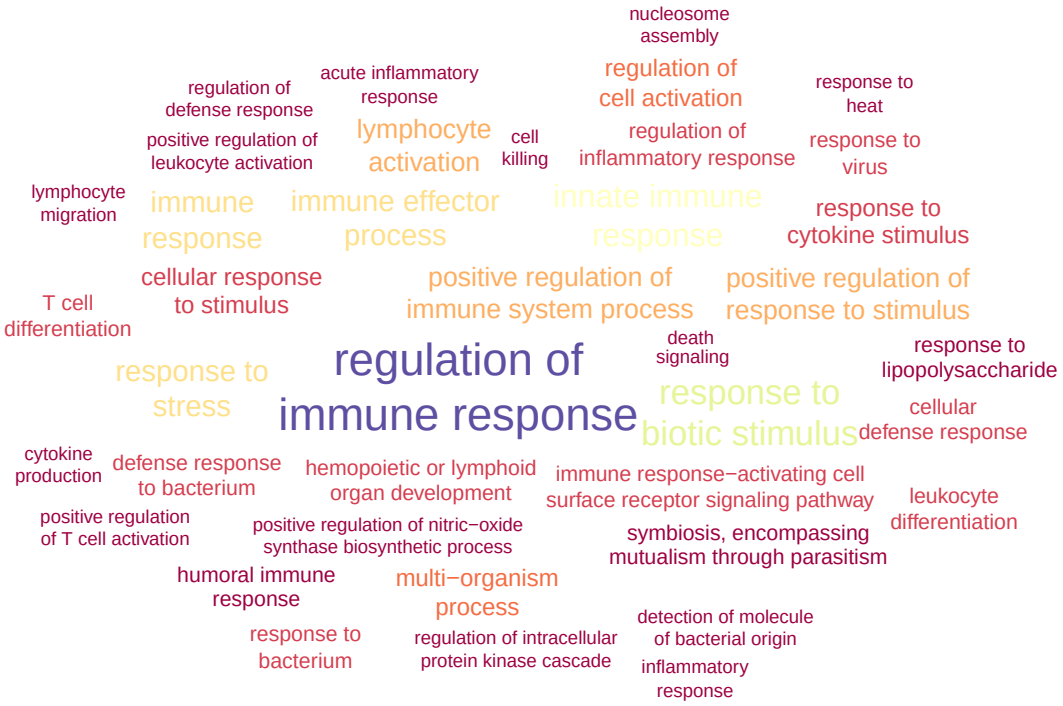


Colors

Using the tools `smoothPalette`, you can easily map a numeric vector onto colors. `smoothPalette` by default produces a grey-black gradient, but anything goes with the help of `RColorBrewer`. `smoothPalette` either takes a predefined palette (it will not expand it, however, so if you define three colors, three colors will be on the figure, no extrapolated colors in between), or an RColorBrewer palette.

In the example below, the weights are on purpose correlated to the color.

```
library(RColorBrewer)
colors <- smoothPalette(weights, pal= brewer.pal( 11, "Spectral" ) )
tagcloud(tags, weights=weights, col=colors, order="size")
```



Alternative way to specify the colors is to provide a function that can generate a palette – for example, the return value of `colorRampPalette`. This has the advantage that `smoothPalette` will generate, with the palette function, as many color steps as necessary.

```
palf <- colorRampPalette( c( "blue", "grey", "red" ) )
colors <- smoothPalette(weights, palfunc= palf )
tagcloud(tags, weights=weights, col=colors, order="size")
```