## Make a table of the articles

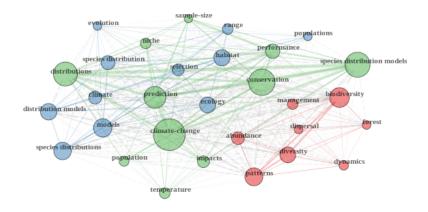
```
review, year, author, title, keywords
```

```
Much of the following code is adapted from https://cran.r-project.org/web/
packages/bibliometrix/vignettes/bibliometrix-vignette.html.
if (!(any(installed.packages()[, 1] == "bibliometrix"))){
    install.packages("bibliometrix")
library(bibliometrix)
## To cite bibliometrix in publications, please use:
##
## Aria, M. & Cuccurullo, C. (2017) bibliometrix: An R-tool for comprehensive science mapping
##
##
## http://www.bibliometrix.org
##
##
## To start with the shiny web-interface, please digit:
## biblioshiny()
bib.df <- convert2df("../docs/bib/combined.bib", dbsource = "wos", format = "bibtex")
##
## Converting your wos collection into a bibliographic dataframe
##
## Done!
##
##
## Generating affiliation field tag AU_UN from C1: Done!
                                          # restrict to articles
bib.df <- bib.df[bib.df[, "DT"] == "ARTICLE", ]</pre>
year <- bib.df[, "PY"]</pre>
ead <- do.call(rbind, strsplit(bib.df[, "early.access.date"], " "))[, 2]</pre>
year[is.na(year)] <- ead[is.na(year)]</pre>
if (!(any(dir("../data/") == "genm_biblio.csv"))){
    author <- sapply(bib.df[, "AU"], function(x) strsplit(x, ";")[[1]][1], USE.NAMES = FALS</pre>
    review <- grepl("REVIEW", bib.df[, "TI"], ignore.case = TRUE) |</pre>
        grepl("REVIEW", bib.df[, "DE"], ignore.case = TRUE) |
        grepl("REVIEW", bib.df[, "ID"], ignore.case = TRUE) |
        grepl("REVIEW", bib.df[, "web.of.science.categories."], ignore.case = TRUE)
    review <- as.numeric(review)</pre>
```

```
kw <- apply(bib.df[, c("DE", "ID")], 1, paste, collapse = "; ")
kw <- gsub(";;", ";", kw)
kw <- gsub(";;;", ";", kw)
kw <- lapply(kw, function(x) unique(strsplit(x, split = "; ")[[1]]))
kw <- unlist(lapply(kw, paste, collapse = "; "))
kw <- as.character(kw)
gene <- grepl("gene", bib.df[, "TI"], ignore.case = TRUE) |
    grepl("gene", kw, ignore.case = TRUE) |
    grepl("gene", bib.df[, "web.of.science.categories."], ignore.case = TRUE)
gene <- as.numeric(gene)
out <- data.frame(year, author, title = bib.df[, "TI"], review, gene, kw)
out <- out[order(as.numeric(out[, "year"]), decreasing = TRUE),]
    write.csv(file = "../data/genm_biblio.csv", out, row.names = FALSE)
}</pre>
```

## **Figures**

## **Keyword Co-occurrences**



CS <- conceptualStructure(bib.df, field="ID", method="CA", minDegree=4, clust=5,

## stemming=FALSE, labelsize=10, documents=20)

