Learning bibliometrix

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Before the lesson:
Please make sure you got the latest RStudio and latest R version installed.

Lesson objectives:
* Learn to perform a search in academic literature database
* Download search results and import them into R
* Summarise bibliometric data
* Make a few types of simple bibliometric networks
* Plot bibliometric networks

Lesson outline:
* About this lesson
* Getting bibliometric data
* Summarising bibliometric data
* Creating bibliometric networks
* More resouces

About this lesson

This lesson is prepared for these who are already familiar with R coding language, R markdown and RStudio. By the end of this tutorial you should be able to create a simple html document containing markdown-formatted text, images and R code, all in RStudio.

Getting bibliometric data

You can do analyses of literature on any topic. In this lesson we will have a look at the academic literature related to the concept of Terminal Investment. Terminal Investment hypothesis predicts increased investment of resources into reproduction as the chances of survival decrease. This can be observed as increased reproductive effort in older animals or in animals challenged with factors signalling threat to their survival (e.g., predation, pathogenes, parasites).

Terminal investment in animals is usually studied in three main ways:
1. via observational studies of correlations of age and reproductive effort,
2. in experimantal studies where animals are subject to immune challenges and their subsequent reprodactive effort is compared to unchallenged aninmals of the same age,
3. in experimantal studies where reproductive response to immune challenge is compared between animals of older ages versus younger ages.

You can read more on this Wiki page: https://en.wikipedia.org/wiki/Terminal_investment_hypothesis

We hope the topic is quite appealing and quiet easy to understand.There are several published reviews on terminal investment hypothesis and we can expect many publications related to this topic, as well as many researchers working on it. Is this so?

Today, we will try to run bibliometric analyses on the relevant sample of literature. Note that ther are a few available R packages (and many other online/software tools, and new are being developed) that can perform some of the tasks which we will practice during this exercise, and often they can do much more. For your own project you may want to try to use some other tools, but there is no single “perfect” tool that fits all possible analyses and that is easy and usable for all disciplines and types of research questions. Also note that the main purpose of this exercise is to familiarize you with the basic principles/issues of bibliometric analyses. You can always learn more in your own time if you are interested.

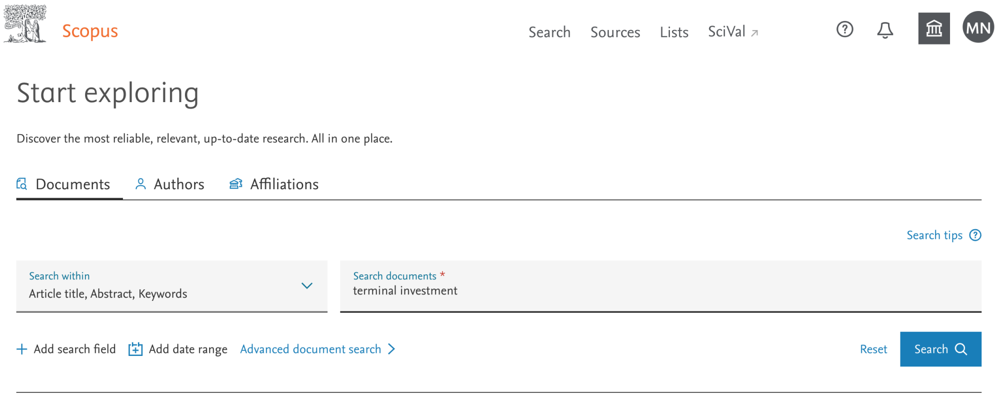
The search

First, we need to find a representative sample of academic publications on our topic of choice. For this, we will use cross-disciplianary database of academic literature, Scopus. This database has the largest coverage of the published literature and should give us the most complete picture. An alternative database, commonly used for broad academic literature searches and analyses, is Web of Science: https://www.webofknowledge.com/ (WoS; it has slightly different way of formatting serach strings).

You should have free access to Scopus and Wos database on campus, but you may not be able to access it from outside the campus unless you use UNSW VPN or other university proxy servers (try loging in via the Library). Free-access broad-coverage databases include BASe (Bielfield Academic Search Engine, https://www.base-search.net/) and Lens (lens.org). Google Scholar is not good, mainly because it is hard to export bibliometric records from the results list.

TASK 1

Go to Scopus search page: https://www.scopus.com/search/form.uri?display=basic and enter terminal investment in the basic search window, as follows:



Start exploring

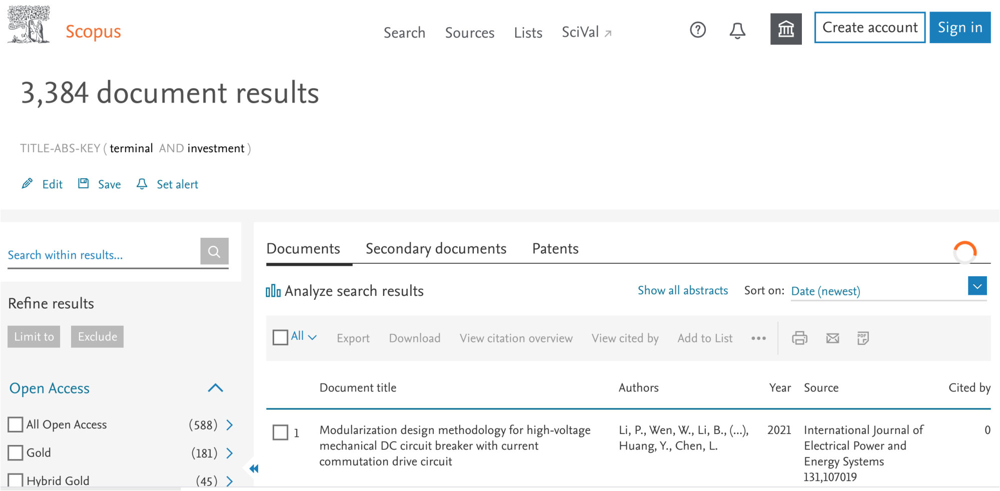
Discover the most reliable, relevant, up-to-date research. All in one place.

Search within: Article title, Abstract, Keywords

Search documents *: terminal investment

Figure 1:

Press “Search”" button.
You shoud see results like this:



3,384 document results

TITLE-ABS-KEY (terminal AND investment)

Refine results

Open Access

□ All Open Access (588)
□ Gold (181)
□ Hybrid Gold (45)

Sort on: Date (newest)

	Document title	Authors	Year	Source	Cited by
□ 1	Modularization design methodology for high-voltage mechanical DC circuit breaker with current commutation drive circuit	Li, P., Wen, W., Li, B., (...), Huang, Y., Chen, L.	2021	International Journal of Electrical Power and Energy Systems 131,107019	0

Figure 2:

Hey, this does not look good... - many documents were found, and mostof them are completely unrelated (e.g. on building shipping terminals).
Why is that?

This is because our search is too simple. It allows us only to find the papers that explicitly mention terminal AND investment words in their title, abstract or keywords. To find a more relevant set of bibliometric records for our analyses, we need a more sophisticated search string. Additionally, we will narrow down our topic a little bit more and aim to find papers that use immune challenge approach in wild or semi-wild animal species (so, we try to exclude established lab model species such as mice and rats, domesticated animals such as dogs and pigs, and humans). Finding the best search string is a bit of an art, so we just provide you with this one to save time:

```
TITLE-ABS-KEY ( ( "terminal investment"  OR  "reproductive effort"  OR  "fecundity compensation"  OR  "
```

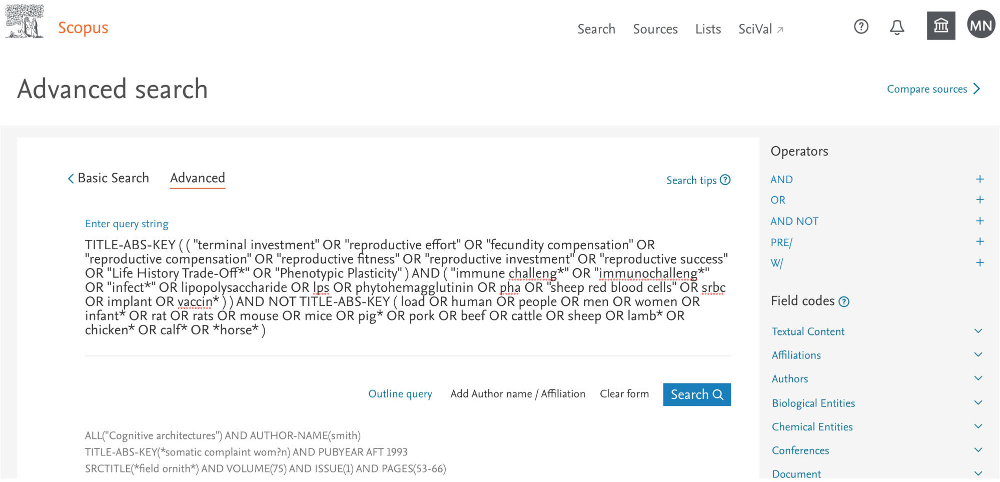
TASK 2

You need to copy and paste the above search string into the Avanced Search tab of the Scopus Search page:

Press “Search”" button. You shoud see results like this:

There are still over 1,300 records retrieved from the Scopus database. Ssome look relevant and many are not, but that is always the case, for a systematic review or a meta-analysis we would manually screen all an exclude all irrelevant papers).

On the left side of the results window you can see simple filters: year, most common author names, subject areas, etc. You can explore the whole set roughly by using “Analyze search results” link above the table of the hits:



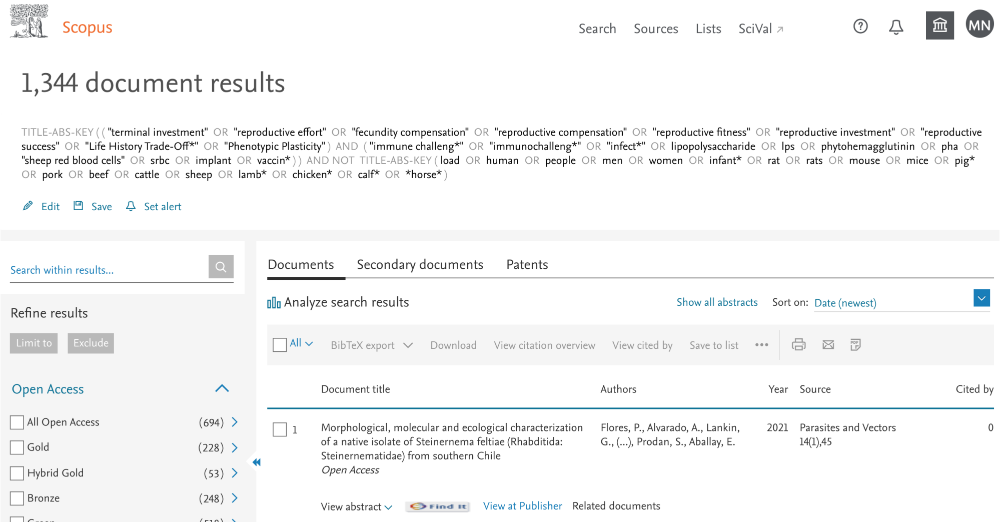
Advanced search

Enter query string

```
TITLE-ABS-KEY ( ( "terminal investment" OR "reproductive effort" OR "fecundity compensation" OR
"reproductive compensation" OR "reproductive fitness" OR "reproductive investment" OR "reproductive success"
OR "Life History Trade-Off*" OR "Phenotypic Plasticity" ) AND ( "immune challeng*" OR "immunochalleng*"
OR "infect*" OR lipopolysaccharide OR lps OR phytohemagglutinin OR pha OR "sheep red blood cells" OR srbc
OR implant OR vaccin* ) ) AND NOT TITLE-ABS-KEY ( load OR human OR people OR men OR women OR
infant* OR rat OR rats OR mouse OR mice OR pig* OR pork OR beef OR cattle OR sheep OR lamb* OR
chicken* OR calf* OR *horse* )
```

```
ALL("Cognitive architectures") AND AUTHOR-NAME(smith)
TITLE-ABS-KEY(*somatic complaint wom?n) AND PUBYEAR AFT 1993
SRCTITLE(*field ornith*) AND VOLUME(75) AND ISSUE(1) AND PAGES(53-66)
```

Figure 3:



1,344 document results

```
TITLE-ABS-KEY ( ( "terminal investment" OR "reproductive effort" OR "fecundity compensation" OR "reproductive compensation" OR "reproductive fitness" OR "reproductive investment" OR "reproductive
success" OR "Life History Trade-Off*" OR "Phenotypic Plasticity" ) AND ( "immune challeng*" OR "immunochalleng*" OR "infect*" OR lipopolysaccharide OR lps OR phytohemagglutinin OR pha OR
"sheep red blood cells" OR srbc OR implant OR vaccin* ) ) AND NOT TITLE-ABS-KEY ( load OR human OR people OR men OR women OR infant* OR rat OR rats OR mouse OR mice OR pig*
OR pork OR beef OR cattle OR sheep OR lamb* OR chicken* OR calf* OR *horse* )
```

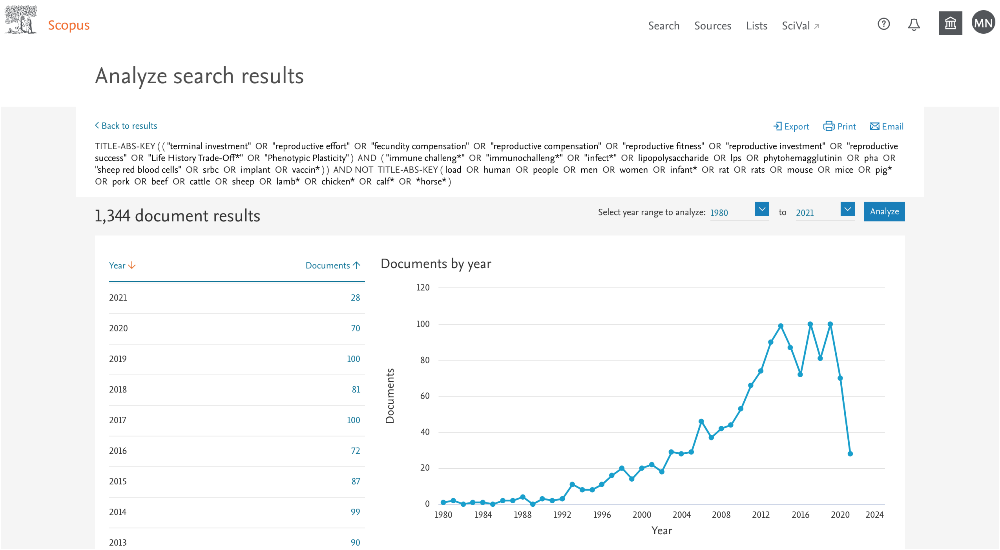
Sort on: Date (newest)

Open Access

□ All Open Access	(694)	>
□ Gold	(228)	>
□ Hybrid Gold	(53)	>
□ Bronze	(248)	>

		Document title	Authors	Year	Source	Cited by
□	1	Morphological, molecular and ecological characterization of a native isolate of Steinernema feltiae (Rhabditida: Steinernematidae) from southern Chile *Open Access*	Flores, P., Alvarado, A., Lankin, G., (...), Prodan, S., Aballay, E.	2021	Parasites and Vectors 14(1),45	0

Figure 4:



Analyze search results

< Back to results

TITLE-ABS-KEY (("terminal investment" OR "reproductive effort" OR "fecundity compensation" OR "reproductive compensation" OR "reproductive fitness" OR "reproductive investment" OR "reproductive success" OR "Life History Trade-Off*" OR "Phenotypic Plasticity") AND ("immune challeng*" OR "immunochalleng*" OR "infect*" OR lipopolysaccharide OR lps OR phytohemagglutinin OR pha OR "sheep red blood cells" OR srbc OR implant OR vaccin*)) AND NOT TITLE-ABS-KEY (load OR human OR people OR men OR women OR infant* OR rat OR rats OR mouse OR mice OR pig* OR pork OR beef OR cattle OR sheep OR lamb* OR chicken* OR calf* OR *horse*)

1,344 document results

Select year range to analyze: 1980 to 2021

Year ↓	Documents ↑
2021	28
2020	70
2019	100
2018	81
2017	100
2016	72
2015	87
2014	99
2013	90

Figure 5:

There are more graphs below, and you can expand and customise them a bit too - have a look!

TASK 3

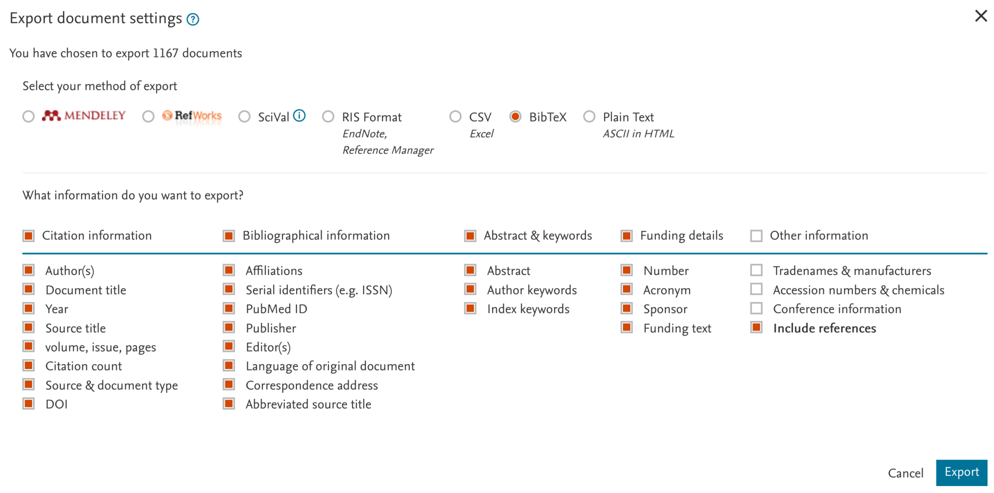
Next, we can export the bibliometric records for more detailed bibliometric analyses in R. To do so, close the Scopus analyses window and go back to the list of records found. First, select all records by clicking box "All" in the left top of the list of references. Then click the "Export" link to the right.

A pop-up window with the export options will appear.
First, select the format of the export: we will uses .bib file (BibTex format of references, one of the standard ones).
Second, select which fields have to be exported by clicking the boxes on top of each column (or as needed). For bibliometric analyses on the citations among papers, it is essential to tick the box next to "Include references" (i.e. data on the cited documents).

Note that, unfortunately, Scopus limits number of exported records to 2000. For longer listes of records, you will need to split them in smaller chunks for the export and then merge into a single larger dataset (not covered in this tutorial; WoS export limits are 500 records).

Click "Export" button. A file named "Scopus" (with extension matching your export type file, e.g., bib) will be saved to your downloads folder.
Note that when you export references with their reference lists included in the records, the resulting files are quite large (in our case around 16Mb).

In case you did not succeed exporting the files (or wish to work with exactly the same ones we used, or you cannot acces Scopus), the files downloaded on 27/05/2019 are provided (the standard way is to store them in a "/data" subdirectory).



Export document settings ⓘ

You have chosen to export 1167 documents

Select your method of export

○ MENDELEY ○ RefWorks ○ SciVal ⓘ ○ RIS Format *EndNote, Reference Manager* ○ CSV *Excel* ● BibTeX ○ Plain Text *ASCII in HTML*

What information do you want to export?

☑ Citation information
- ☑ Author(s)
- ☑ Document title
- ☑ Year
- ☑ Source title
- ☑ volume, issue, pages
- ☑ Citation count
- ☑ Source & document type
- ☑ DOI

☑ Bibliographical information
- ☑ Affiliations
- ☑ Serial identifiers (e.g. ISSN)
- ☑ PubMed ID
- ☑ Publisher
- ☑ Editor(s)
- ☑ Language of original document
- ☑ Correspondence address
- ☑ Abbreviated source title

☑ Abstract & keywords
- ☑ Abstract
- ☑ Author keywords
- ☑ Index keywords

☑ Funding details
- ☑ Number
- ☑ Acronym
- ☑ Sponsor
- ☑ Funding text

☐ Other information
- ☐ Tradenames & manufacturers
- ☐ Accession numbers & chemicals
- ☐ Conference information
- ☑ **Include references**

Figure 6:

TASK 4

Create a new Rmarkdown file to save your code (you can do this within new RStudio project). Install and upload *bibliometrix* R package:

```
install.packages("bibliometrix", dependencies=TRUE) ### installs bibliometrix package and dependencies
library(bibliometrix)   #uploads the package
# Note: output not displayed for this chunk
```

Upload the file exported from Scopus (you can use the one provided) into RStudio (note that the file path you may need to use on your computer may be different, e.g., “H:/Users/z1234567/Downloads/scopus.bib”). Then, convert the data from that file into internal *bibliometrix* format.

```
bib <- convert2df("data/scopus.bib", dbsource = "scopus", format = "bibtex") # Convert to a bibliometri
#>
#> Converting your scopus collection into a bibliographic dataframe
#>
#> Done!
#>
#>
#> Generating affiliation field tag AU_UN from C1:  Done!
names(bib)
#>  [1] "AU"         "DE"         "ID"         "C1"         "CR"
#>  [6] "JI"         "AB"         "AR"         "coden"      "RP"
#> [11] "DT"         "DI"         "BE"         "FU"         "BN"
#> [16] "SN"         "SO"         "LA"         "TC"         "PN"
#> [21] "page_count" "PP"         "PU"         "PM"         "DB"
#> [26] "TI"         "url"        "VL"         "PY"         "FX"
#> [31] "AU_UN"      "AU1_UN"     "AU_UN_NR"   "SR_FULL"    "SR"
#write.csv(bib, "data/bib_as_df.csv", row.names = FALSE) #if you want to save this data frame as a csv
```

After some processing, an object called “bib” is created. It contains a data frame with each row corresponsing to one exported publication from Scopus and with each column corresponding to a field exported from Scopus online database. If you tried to achieve this by exporting a csv file directly from Scopus, you would sonetimes get a meessy data frame, due to missing field values shifting the cells between columns.

TASK 5

What are the contents of the columns of our "bib" data frame? Columns are labelled with a two-letter tags: AU, DE, ID, C1, CR, JI, AB, AR, coden, RP, DT, DI, BE, FU, BN, SN, SO, LA, TC, PN, page_count, PP, PU, PM, DB, TI, url, VL, PY, FX, AU_UN, AU1_UN, AU_UN_NR, SR_FULL, SR.
For a complete list and descriptions of field tags used in *bibliometrix* you can have a look at this file: http://www.bibliometrix.org/documents/Field_Tags_bibliometrix.pdf
Our data frame contains just a subset of these codes. Which ones?

Note that column **bib$AU** contains authors of each paper (as surenames and initials) separated by semicolon (;). We can easily split these strings and extract a list of all author names to a vector:

```r
# head(bib$AU) #have a look at the few few records on your sceen
authors <- bib$AU
authors <- unlist(strsplit(authors, ";")) #split the records into individual authors
authors <- authors[order(authors)] #order alphabetically
head(authors) #have a look again
#> [1] "ABBOTT J"        "ABE A"           "ABEDON ST"       "ABO-SHEHADA M"
#> [5] "ABOUL-SOUD MAM" "ABRANTES N"
# View(unique(authors)) #use to see all the values
# write.csv(authors, "data/author_list_uncleaned.csv", row.names = FALSE) #if you want to save this dat
```

TASK 6

Cited references for each included paper are in the CR column of the "bib" data frame. They are in a single string, also seperated by semicolon (;). We can have a look at them and check whether familiar names were cited, e.g.:

```r
dim(bib) #dimensions of the data frame
#> [1] 1167   35
names(bib) #names of the columns of the data frame
#>  [1] "AU"         "DE"         "ID"         "C1"         "CR"
#>  [6] "JI"         "AB"         "AR"         "coden"      "RP"
#> [11] "DT"         "DI"         "BE"         "FU"         "BN"
#> [16] "SN"         "SO"         "LA"         "TC"         "PN"
#> [21] "page_count" "PP"         "PU"         "PM"         "DB"
#> [26] "TI"         "url"        "VL"         "PY"         "FX"
#> [31] "AU_UN"      "AU1_UN"     "AU_UN_NR"   "SR_FULL"    "SR"
#bib$CR[1] #display a list of cited references for the first paper in the data frame
#(we are not displaying it in this doucment as it is a very long string! - examine it on your screen in
#look whether some of these names are cited:
grep("NAKAGAWA, S.", bib$CR)
#>  [1]   2   6   7  20  33  36  37  56  72  75 102 109 121 145 152 166 207 222 249
#> [20] 285 293 312 330 361 362 368 370 401 440 455 471 475 489 501 512 560 562 573
#> [39] 590 620 655 690 713 730 770
grep("CORNWELL, W.", bib$CR)
#> [1] 15
bib[grep("CORNWELL, W.", bib$CR), c(1:3)] #who is citing?
#>
#> MULETZ-WOLZ CR, 2019, J EVOL BIOL MULETZ-WOLZ CR;BARNETT SE;DIRENZO GV;ZAMUDIO KR;TOLEDO LF;JAMES TY
#>
#> MULETZ-WOLZ CR, 2019, J EVOL BIOL AMPHIBIANS;  BATRACHOCHYTRIUM DENDROBATIDIS;  CHYTRID;  CLIMATE;  
#>                                                                                  ID
#> MULETZ-WOLZ CR, 2019, J EVOL BIOL AMPHIBIA;  BATRACHOCHYTRIUM DENDROBATIDIS;  FUNGI
```

Summarising bibliometric data

TASK 7

Luckily, *bibliometrix* package has a handy function that summarises the information contained in the “bib” data frame, so we can get some quick facts about our set of papers.

Note: this and the following tasks require quite a bit of computational power, they may be slow or even halt on your computer.
In such case, for this exercise, make your data frame smaller by subsetting it, e.g.:
“bib <- bib[1:500,] #taking first 500 records”. However, the results and plots you will produce with a subsetted data frame will differ from the ones presented in this document.

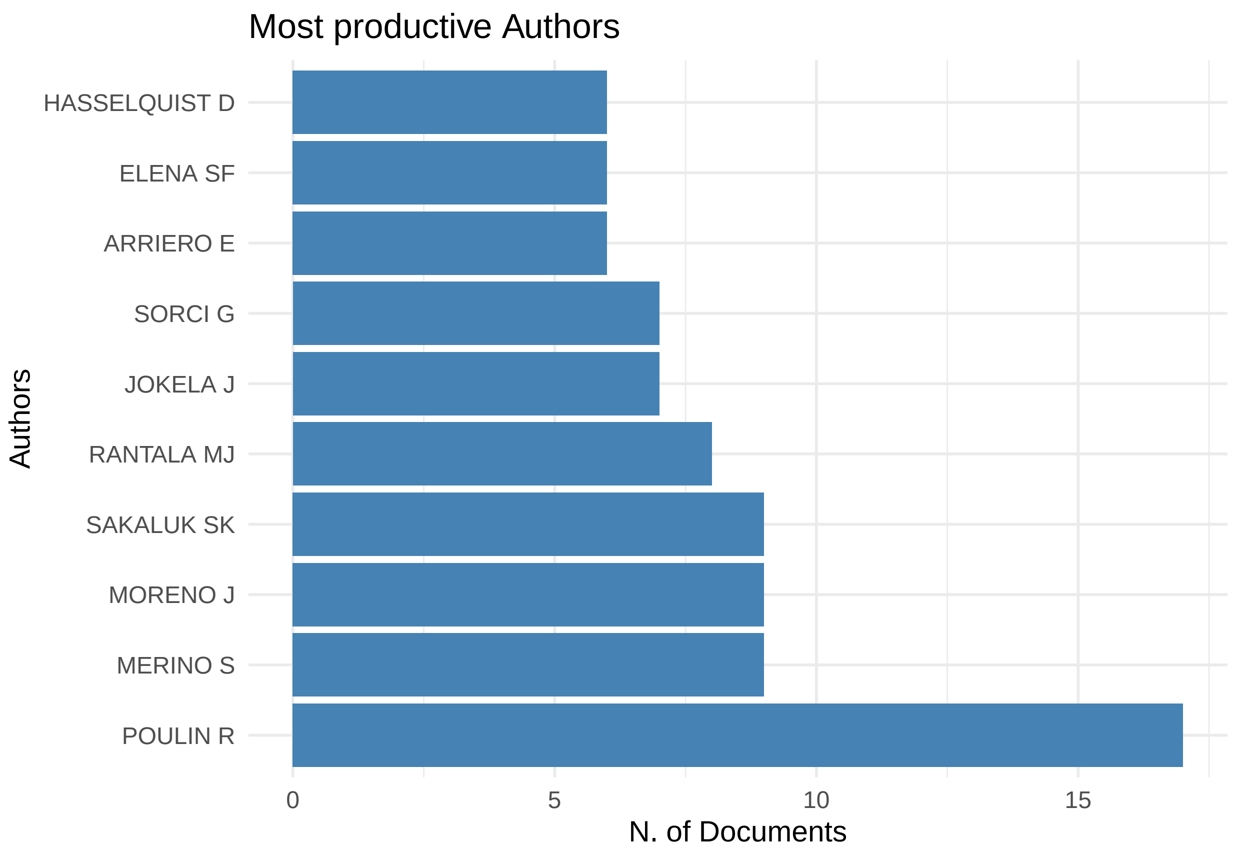
```
# Preliminary descriptive analyses
results <- biblioAnalysis(bib, sep = ";")
#summary(object = results, k = 10, pause = TRUE) #display a series of summary tables

# Reduce the dataset to the subset first 500 records
bib <- bib[1:500, ] #taking first 500 records
#summary(object = results, k = 10, pause = TRUE) #display a series of summary tables
```

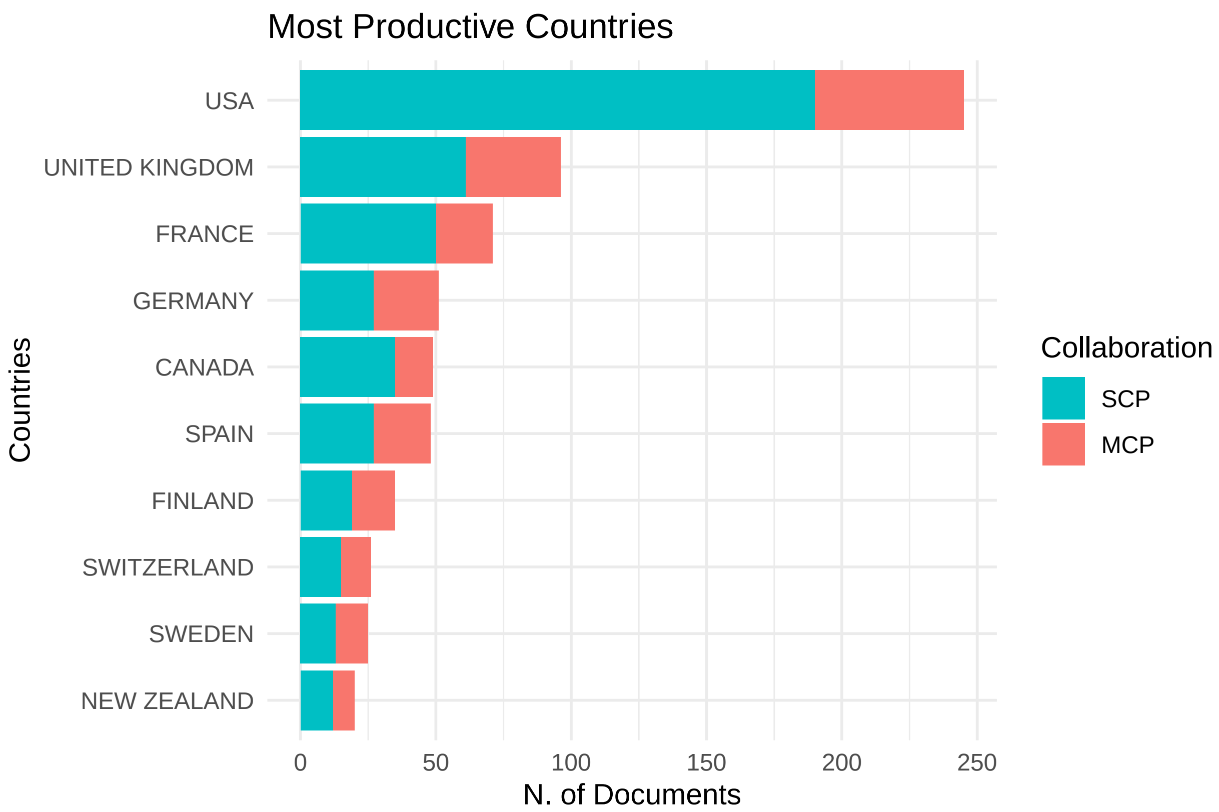
Using *summary* function on *bibliometrix* results, you get several screens with various tables summarising bibliometric data from our data frame - how many documents, journals, keywords, authors, publicatons timespan, collaboration index, annual publication growth rate, most prolific authors, publications per country, per journal, per keywords, etc.

You can automatically plot some of these tables (hit “return”" to display next graph, and later you can use arrows in the top left of the plots pane to move back and forth between consecutive plots saved in the RStudio memory):

```
plot(results, k = 10, pause=TRUE) #this takes top 10 values from each plottable table
#> Hit <Return> to see next plot:
```

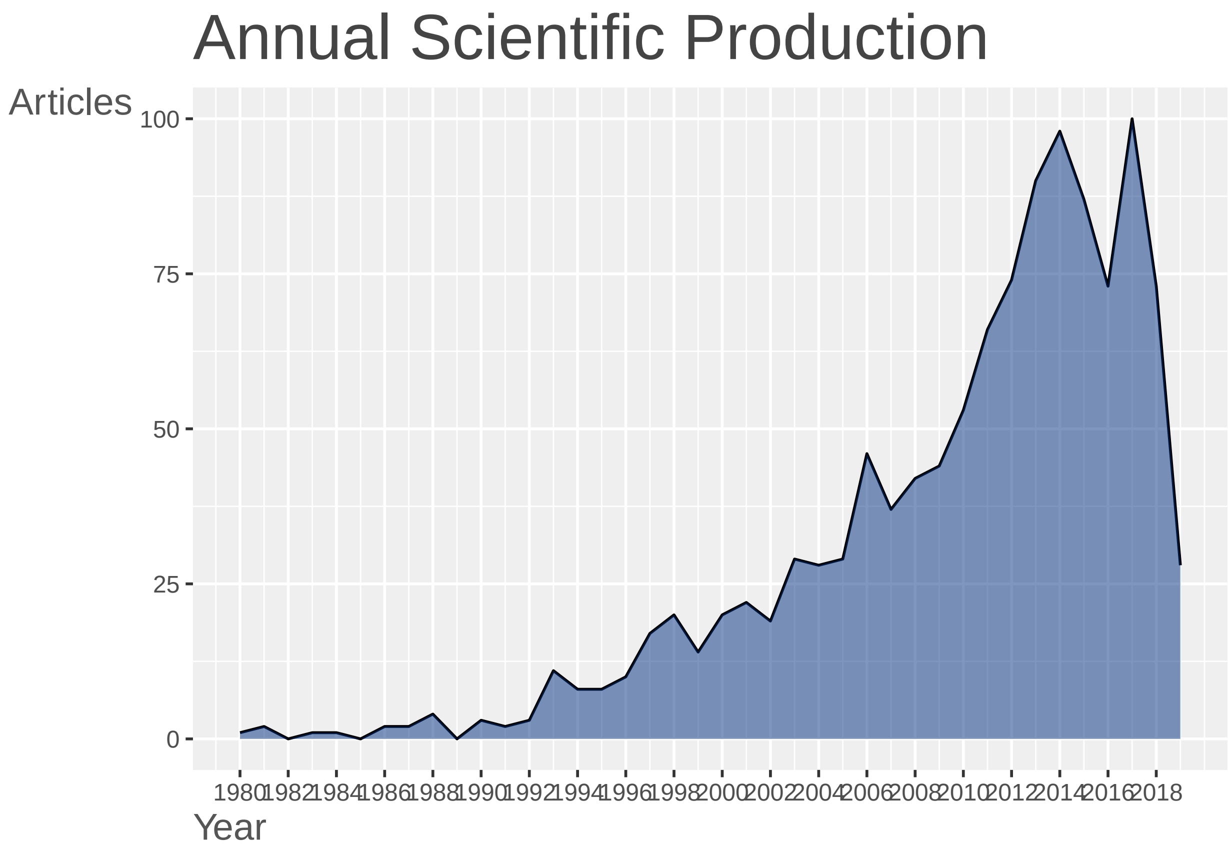


```
#> Hit <Return> to see next plot:
```

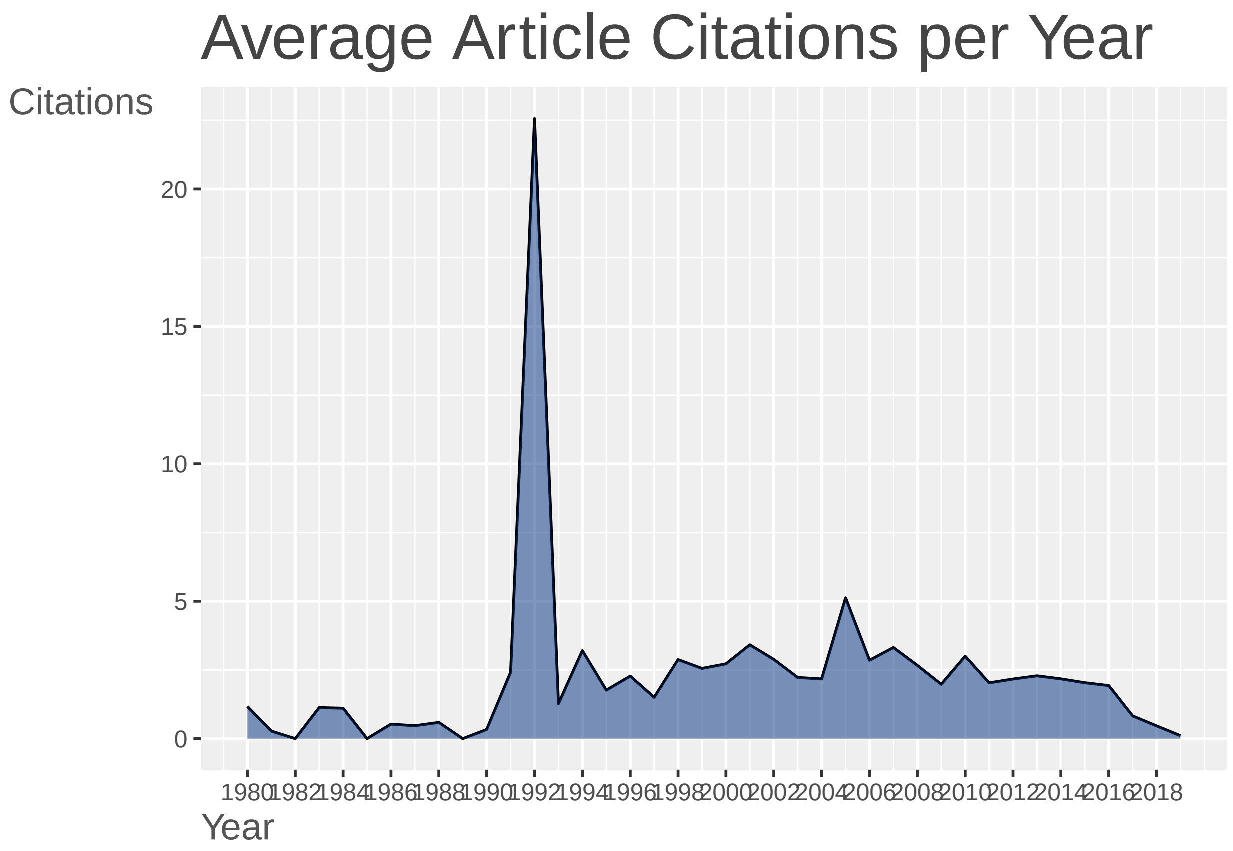


SCP: Single Country Publications, MCP: Multiple Country Publications

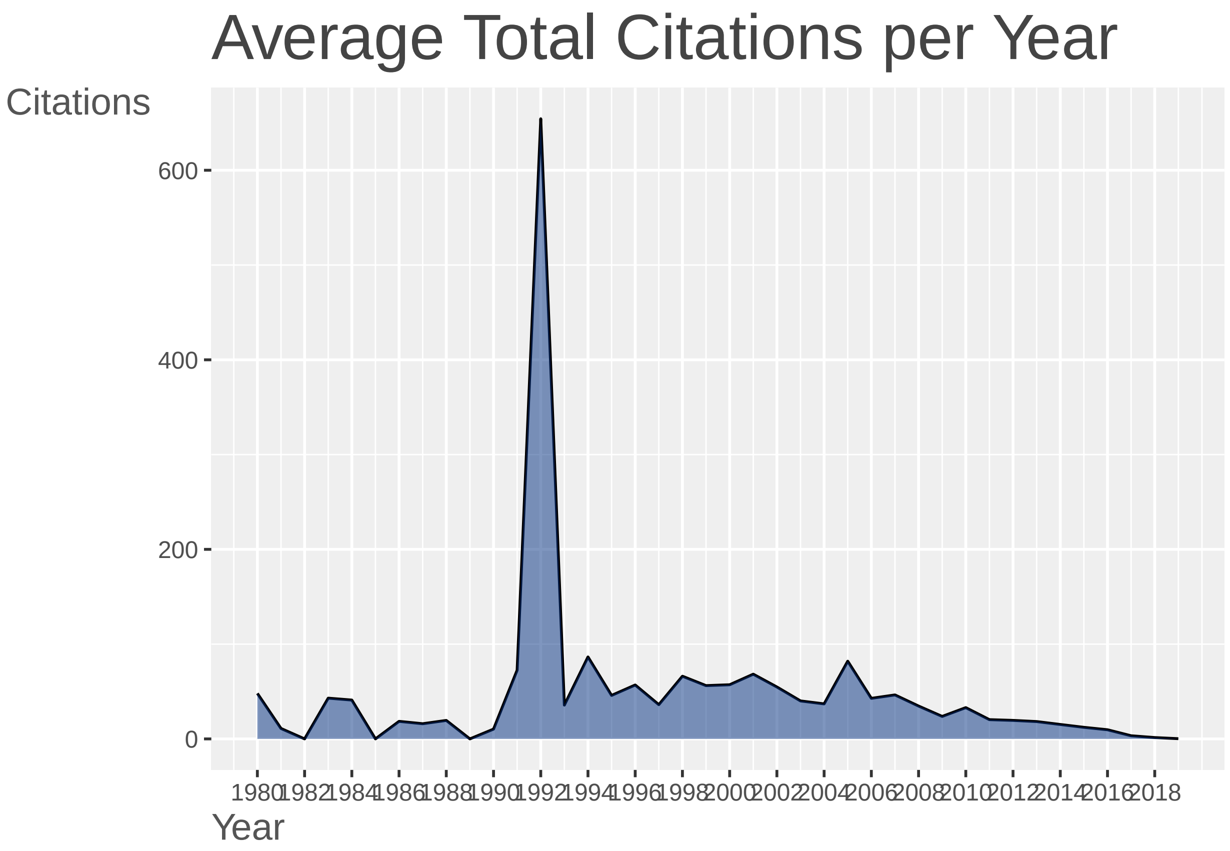
```
#> Hit <Return> to see next plot:
```



```
#> Hit <Return> to see next plot:
```



```
#> Hit <Return> to see next plot:
```



```
#the code below is for saving these plots into a pdf:
# pdf(file = "plots/bib_descriptive_plots.pdf", height = 8, width = 8, pointsize=10) #
# plot(results, k = 20, pause=FALSE) #this takes top 20 values from each plottable table
# dev.off()
```

TASK 8

The cited papers from the CR field of the data frame can be analysed using function *citations*. Function *citations* makes it easy to generate the frequency tables of the most cited papers or the most cited first authors.

Ten most cited papers:

```
mostcitedP <- citations(bib, field = "article", sep = ";")
cbind(mostcitedP$Cited[1:10]) #first 10
#>
#> LOCHMILLER, R.L., DEERENBERG, C., TRADE-OFFS IN EVOLUTIONARY IMMUNOLOGY: JUST WHAT IS THE COST OF IM
#> MORET, Y., SCHMID-HEMPEL, P., SURVIVAL FOR IMMUNITY: THE PRICE OF IMMUNE SYSTEM ACTIVATION FOR BUMBL
#> ANDERSON, R.M., MAY, R.M., COEVOLUTION OF HOSTS AND PARASITES (1982) PARASITOLOGY, 85, PP. 411-426
#> ROLFF, J., SIVA-JOTHY, M.T., INVERTEBRATE ECOLOGICAL IMMUNOLOGY (2003) SCIENCE, 301, PP. 472-475
#> CLUTTON-BROCK, T.H., REPRODUCTIVE EFFORT AND TERMINAL INVESTMENT IN ITEROPAROUS ANIMALS (1984) AM. N
#> MINCHELLA, D.J., LOVERDE, P.T., A COST OF INCREASED EARLY REPRODUCTIVE EFFORT IN THE SNAIL BIOMPHALA
#> SHELDON, B.C., VERHULST, S., ECOLOGICAL IMMUNOLOGY: COSTLY PARASITE DEFENCES AND TRADE-OFFS IN EVOLU
#> AHMED, A.M., BAGGOTT, S.L., MAINGON, R., HURD, H., THE COSTS OF MOUNTING AN IMMUNE RESPONSE ARE REFL
#> FORBES, M.R.L., PARASITISM AND HOST REPRODUCTIVE EFFORT (1993) OIKOS, 67, PP. 444-450
#> HAMILTON, W.D., ZUK, M., HERITABLE TRUE FITNESS AND BRIGHT BIRDS: A ROLE FOR PARASITES? (1982) SCIEN
```

Ten most cited authors:

```
mostcitedA <- citations(bib, field = "author", sep = ";")
cbind(mostcitedA$Cited[1:10]) #first 10
#>                 [,1]
#> POULIN R         181
#> SCHMID HEMPEL P  179
#> HASSELQUIST D    160
#> WINGFIELD J C    147
#> MLLER A P        121
#> SHELDON B C      117
#> HOFFMANN A A     116
#> READ A F         113
#> RANTALA M J      106
#> BENSCH S         104
```

Function *localCitations* generates the frequency table of the **locally** most cited authors. Locally means that citations are counted only within the given data set - i.e. how many times an author/paper that is in this data set has been cited by other authors/papers also in the data set.

Ten most frequent local cited authors and papers:

```
mostcitedLA <- localCitations(bib, sep = ";")
mostcitedLA$Authors[1:10,]
#>               Author LocalCitations
#> 1179     LPEZ-GMEZ M              9
#> 1927 VERDEJO-LUCAS S              9
#> 164       BILLINGS G              8
#> 433         DAVIS BM              8
#> 879       HUBBARD TP              8
#> 1125        LEUNG KY              8
#> 1159           LIU Q              8
#> 1439         PARK JS              8
#> 1960       WALDOR MK              8
#> 1972          WANG Q              8
mostcitedLA$Papers[1:10,]
#>                                    Paper                                DOI Year
#> 323             ASGHAR M, 2015, SCIENCE            10.1126/science.1261121 2015
#> 448          LEVENTHAL GE, 2014, AM NAT                     10.1086/675242 2014
#> 312             BOWERS EK, 2015, AM NAT                     10.1086/681017 2015
#> 254  SCHWENKE RA, 2016, ANN REV ENTOMOL 10.1146/annurev-ento-010715-023924 2016
#> 440       PODMOKA E, 2014, J AVIAN BIOL   10.1111/j.1600-048X.2013.00284.x 2014
#> 500 GONZLEZ-TOKMAN DM, 2013, FUNCT ECOL            10.1111/1365-2435.12072 2013
#> 320          VZILIER J, 2015, BIOL LETT             10.1098/rsbl.2014.0840 2015
#> 192       GIEHR J, 2017, R SOC OPEN SCI                10.1098/rsos.170547 2017
#> 236       BRANNELLY LA, 2016, OPEN BIOL                10.1098/rsob.150251 2016
#> 273        CROSSIN GT, 2016, FUNCT ECOL            10.1111/1365-2435.12482 2016
#>     LCS GCS
#> 323   9 166
#> 448   8  15
#> 312   6  30
#> 254   5  67
#> 440   5  20
#> 500   5  17
#> 320   4  14
#> 192   3   9
#> 236   3  18
#> 273   3  44
```

Creating bibliometric networks

So far, we looked only at the numbers - who or what gets cited most, either from the main papers list or from the lists of the references within these papers. Now it is time to look at the actual networks of citations and also other types of networks that can be created using our data set.

To do so, we will be creating various rectangular matrices which reflect connections of different attributes of Papers/Authors. These matrices than can be plotted as bipartite networks and analysed.

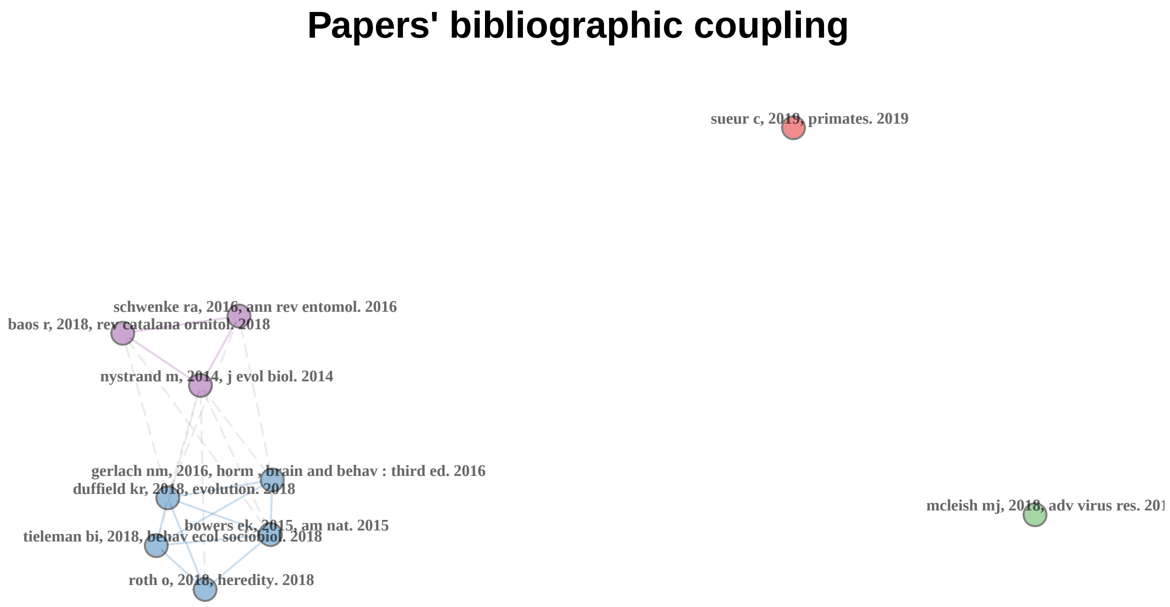
Co-citation or coupling networks are a special type of networks build from the information on scientific papers containing references to other scientific papers.

Package *bibliometrix* contains function *biblioNetwork* which makes creating bibliographic networks easy. This function can create the most frequently used coupling networks: Authors, Sources, and Countries.

TASK 9

Bibliographic coupling - two articles are bibliographically coupled if they share at least one reference from their reference lists, i.e. at least one cited source appears in the reference lists/bibliographies of both papers (Kessler, 1963).

```
NetMatrix <- biblioNetwork(bib, analysis = "coupling", network = "references", sep = ";")
net = networkPlot(NetMatrix, weighted = NULL, n = 10, Title = "Papers' bibliographic coupling", type =
```



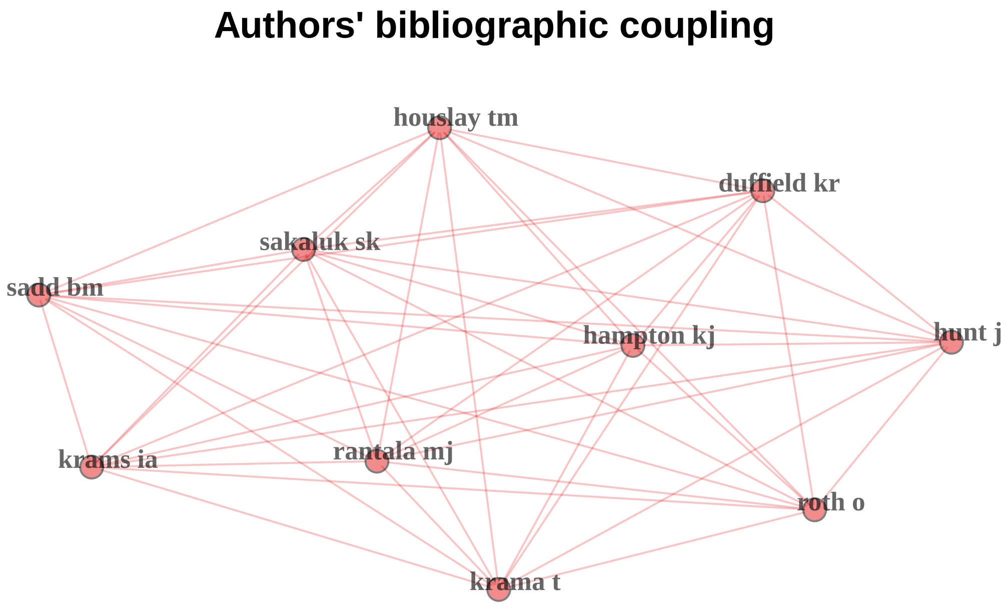
Above, we plotted only the top 10 most coupled papers (n=10). Try increasing this number to 100 (would not recommend further increasing the number of displayed nodes - it gets slow and messy).
What happens and why?

____

TASK 10

Author's bibliographic coupling - two authors are bibliographically coupled if they share at least one reference form their reference lists.

```
NetMatrix <- biblioNetwork(bib, analysis = "coupling", network = "authors", sep = ";")
net = networkPlot(NetMatrix, weighted = NULL, n = 10, Title = "Authors' bibliographic coupling", type =
```

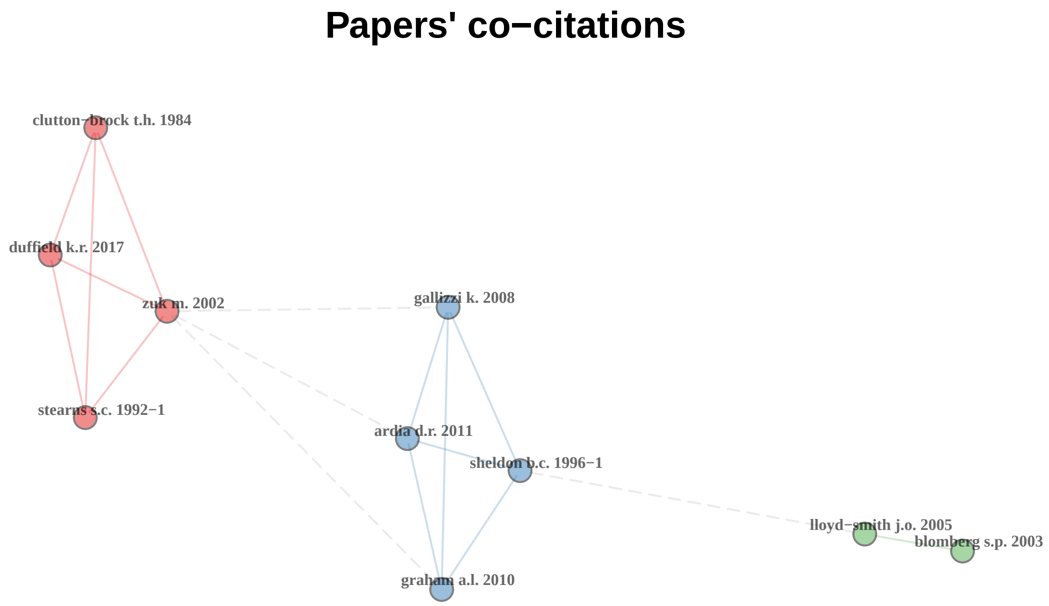


Above, we plotted only the top 10 most coupled authors (n=10). Try increasing this number to 100 (would not recommend further increasing the number of displayed nodes to >50 - it gets slow and messy). What happens and why?

TASK 11

Bibliographic co-citation is kind of opposite to bibliographic coupling, in so that two papers are linked by co-citation when both are cited in a third paper.

```
NetMatrix <- biblioNetwork(bib[1:50,], analysis = "co-citation", network = "references", sep = ";")
net = networkPlot(NetMatrix, weighted=NULL, n = 10, Title = "Papers' co-citations", type = "fruchterman
```

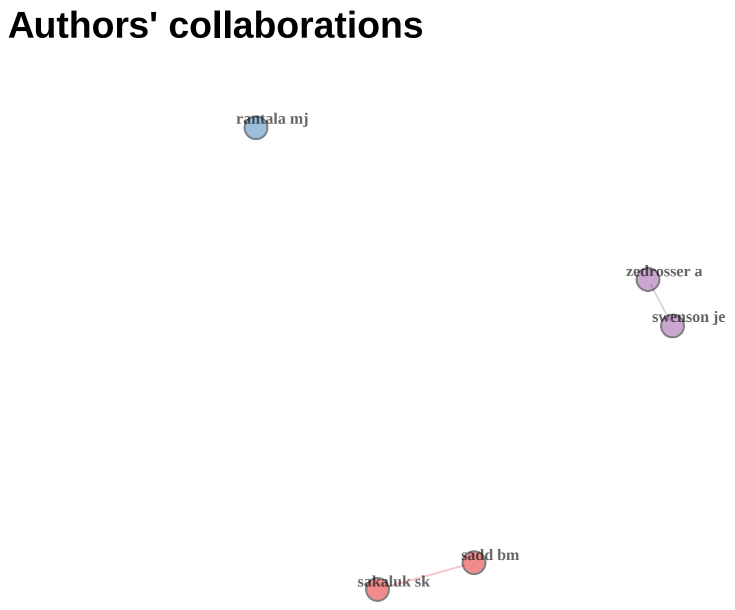


Note that for creating this matrix we only used first 50 papers from our data set - this is because the resulting matrix is a matrix of ALL cited papers and it gets HUGE). Also, we plotted only the top 10 most coupled papers (n=10). Try increasing this number to 20 (would not recommend further increasing the number of displayed nodes to >50 - it gets slow and messy).
What happens and why?

TASK 12

Bibliographic collaboration is a network where nodes are authors and links are co-authorships of the papers.

```
NetMatrix <- biblioNetwork(bib, analysis = "collaboration", network = "authors", sep = ";")
net = networkPlot(NetMatrix, weighted = NULL, n = 10, Title = "Authors' collaborations", type = "fruchte
```

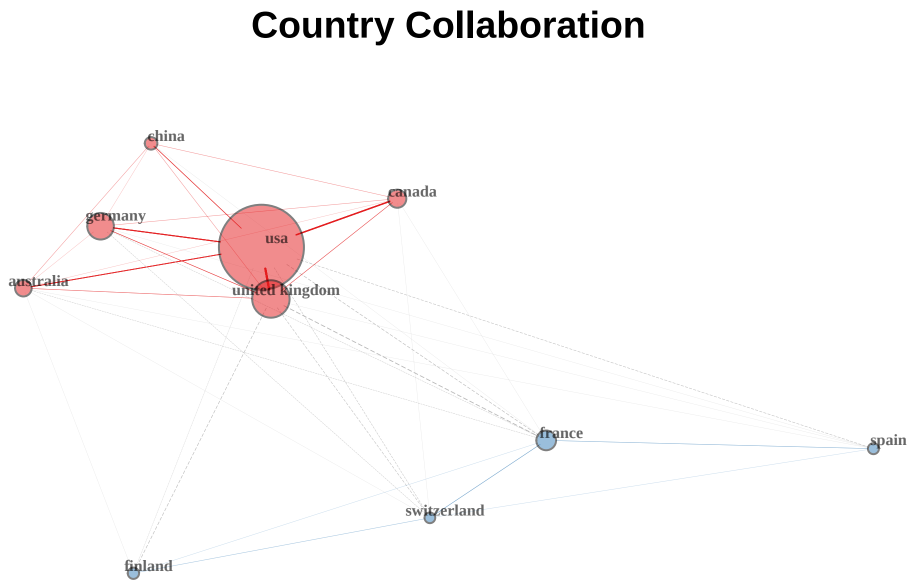


Above, we plotted only the top 10 most collaborating authors (n=10). Try increasing this number to 100 (would not recommend further increasing the number of displayed nodes - it gets slow and messy). What happens and why?

TASK 13

Country Scientific Collaboration - we can visualise authors from which countries publish papers together most frequently.

```
bib <- metaTagExtraction(bib, Field = "AU_CO", sep = ";") #we need to extract countries from the affili
NetMatrix <- biblioNetwork(bib, analysis = "collaboration", network = "countries", sep = ";")
net = networkPlot(NetMatrix, n = 10, Title = "Country Collaboration", type = "auto", size = TRUE, remove
```

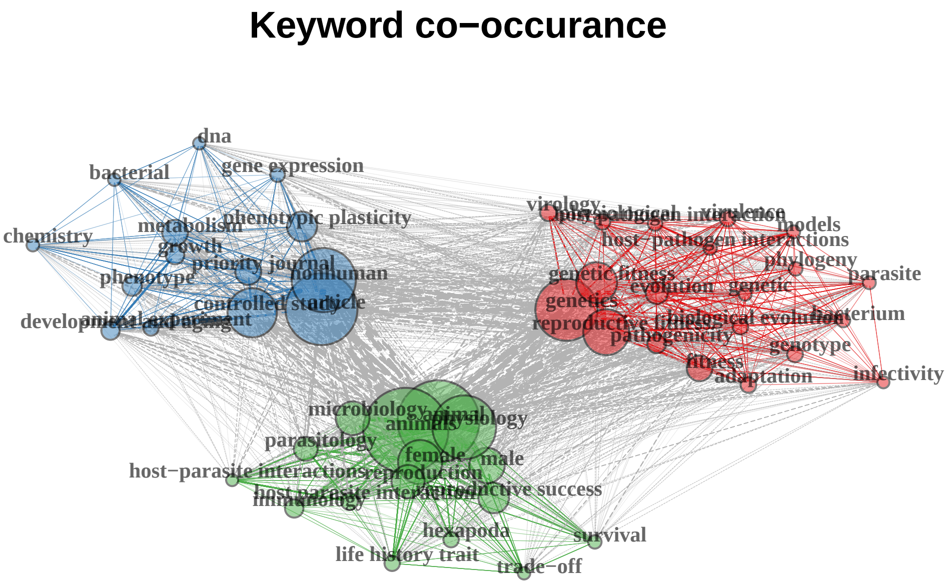


Above, we plotted only the top 10 most collaborating countrie (n=10). Try increasing this number to 50 (would not recommend further increasing the number of displayed nodes to >100 - it gets slow and messy). What happens and why?

TASK 14

Keyword co-occurrences - we can also visualise which papers share most keywords (from Scopus database).

```
NetMatrix <- biblioNetwork(bib, analysis = "co-occurrences", network = "keywords", sep = ";")
net = networkPlot(NetMatrix, n = 50, Title = "Keyword co-occurance", type = "fruchterman", size = T, rem
```



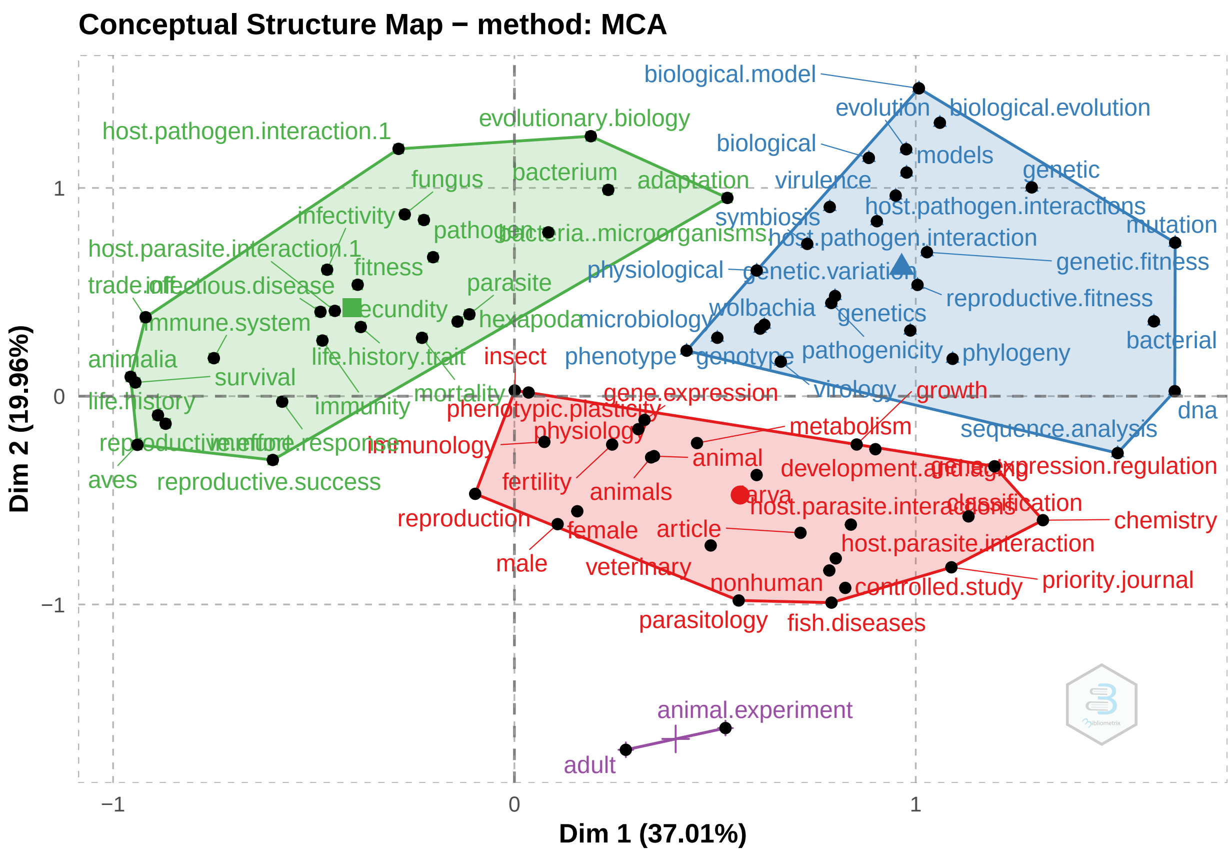
Try replacing network = “keywords” with network = “author_keywords” and see what happens. You can also try to display fewer/more keywords in the plot.

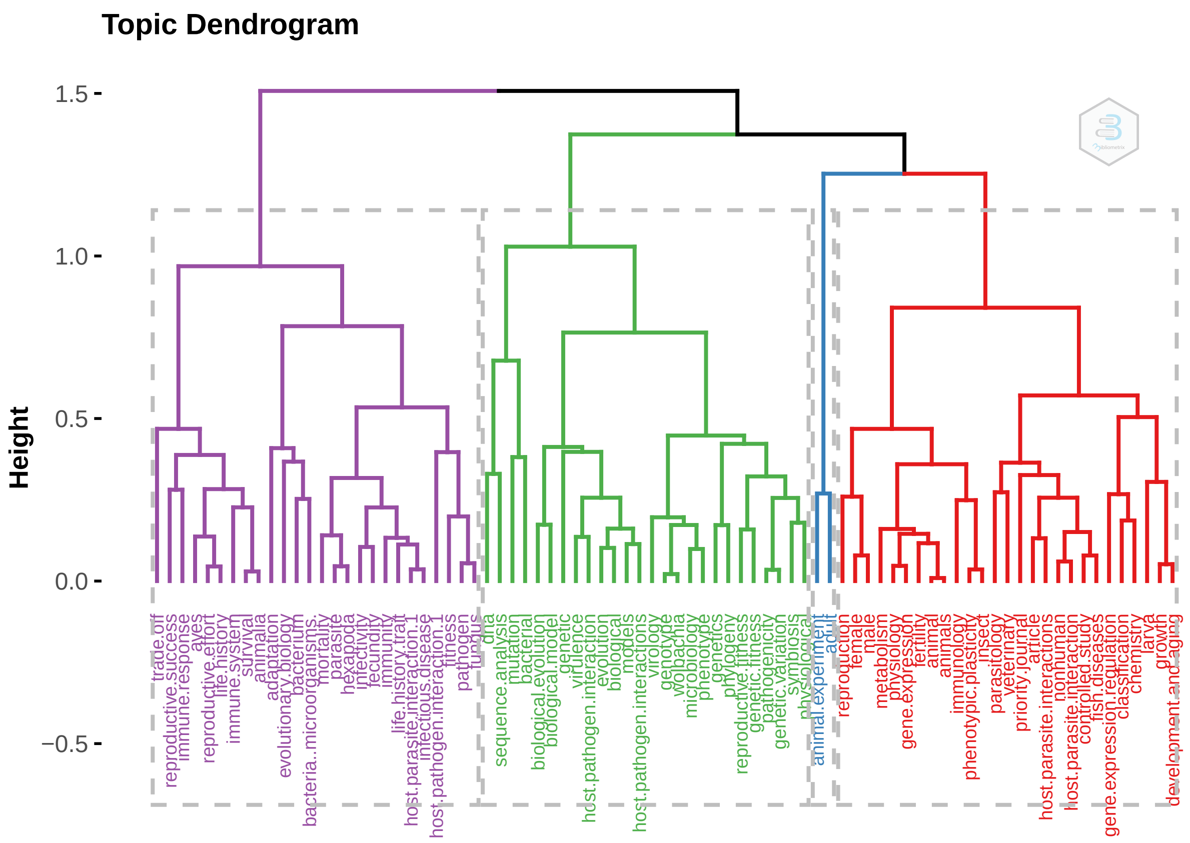
TASK 15

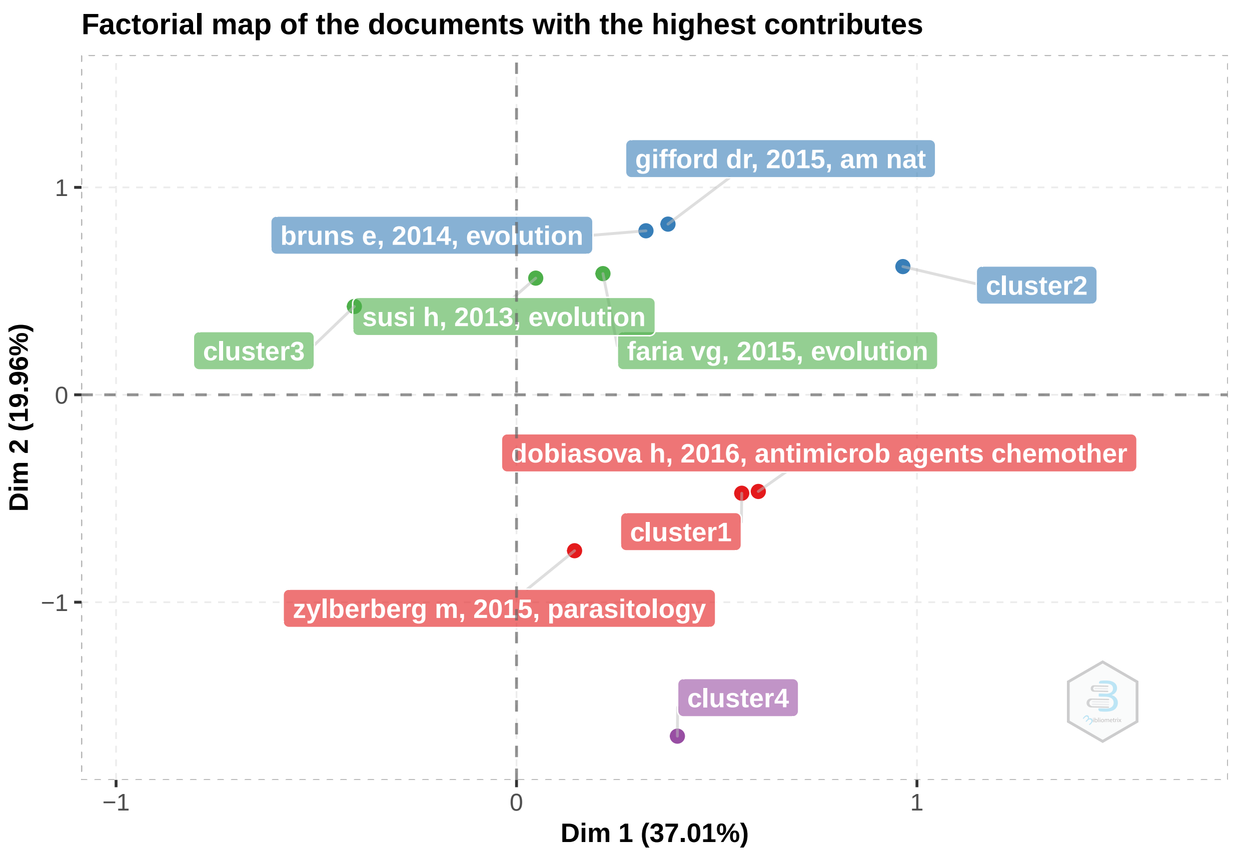
Note: you may want to skip this step on a big data set or a slow computer.

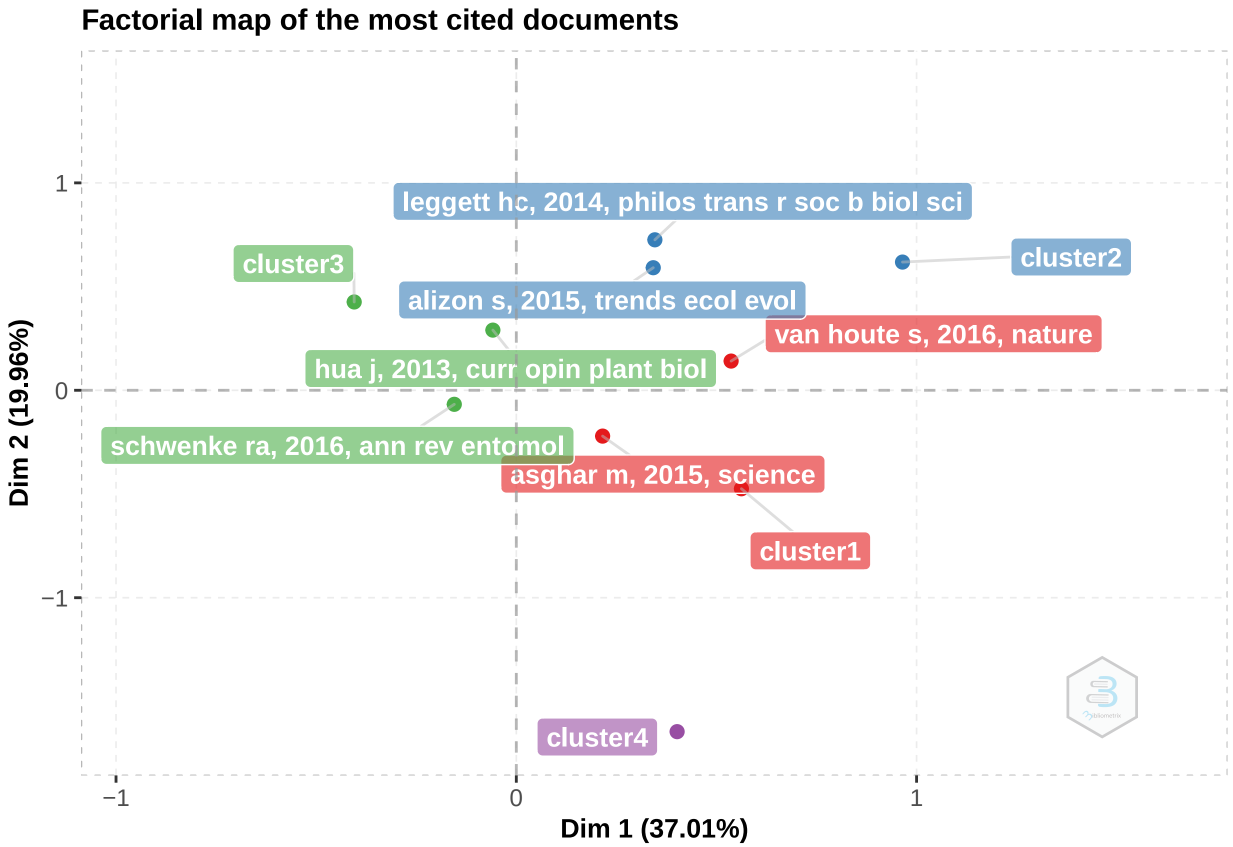
Co-Word Analysis - uses the word co-occurrences in a bibliographic collection to map the conceptual structure of research. It works via a separate function *conceptualStructure* that creates a conceptual structure map of a scientific field performing Correspondence Analysis (CA), Multiple Correspondence Analysis (MCA) or Metric Multidimensional Scaling (MDS) and Clustering of a bipartite network of terms extracted from keyword, title or abstract fields of the data frame. Note that three different graphs are created as an output.

```
CS <- conceptualStructure(bib, field = "ID", minDegree = 20, k.max = 5, stemming = FALSE, labelsize = 1
```


Conceptual Structure Map − method: MCA
host.pathogen.interaction.1
evolutionary.biology
fungus
bacterium
adaptation
infectivity
pathogen
host.parasite.interaction.1
fitness
parasite
trade.off
infectious.disease
fecundity
hexapoda
immune.system
animalia
survival
life.history.trait
life.history
immunity
mortality
reproductive.effort
immune.response
aves
reproductive.success
biological.model
evolution
biological.evolution
biological
models
genetic
virulence
symbiosis
host.pathogen.interactions
mutation
bacteria..microorganisms
host.pathogen.interaction
physiological
genetic.variation
genetic.fitness
reproductive.fitness
wolbachia
microbiology
genetics
bacterial
phenotype
genotype
pathogenicity
phylogeny
virology
sequence.analysis
dna
insect
gene.expression
growth
phenotypic.plasticity
physiology
metabolism
immunology
animal
development.and.aging
gene.expression.regulation
fertility
animals
larva
host.parasite.interactions
classification
chemistry
reproduction
female
article
host.parasite.interaction
male
veterinary
nonhuman
controlled.study
priority.journal
parasitology
fish.diseases
animal.experiment
adult
1
0
−1
Dim 2 (19.96%)
−1
0
1
Dim 1 (37.01%)


Topic Dendrogram
Height
1.5
1.0
0.5
0.0
−0.5
trade.off
reproductive.success
immune.response
aves
reproductive.effort
life.history
immune.system
survival
animalia
adaptation
evolutionary.biology
bacterium
bacteria..microorganisms.
mortality
parasite
hexapoda
infectivity
fecundity
immunity
life.history.trait
host.parasite.interaction.1
infectious.disease
host.pathogen.interaction.1
fitness
pathogen
fungus
dna
sequence.analysis
mutation
bacterial
biological.evolution
biological.model
genetic
virulence
host.pathogen.interaction
evolution
biological
models
host.pathogen.interactions
virology
genotype
wolbachia
microbiology
phenotype
genetics
phylogeny
reproductive.fitness
genetic.fitness
pathogenicity
genetic.variation
symbiosis
physiological
animal.experiment
adult
reproduction
female
male
metabolism
physiology
gene.expression
fertility
animal
animals
immunology
phenotypic.plasticity
insect
parasitology
veterinary
priority.journal
article
host.parasite.interactions
nonhuman
host.parasite.interaction
controlled.study
fish.diseases
gene.expression.regulation
classification
chemistry
larva
growth
development.and.aging


Factorial map of the documents with the highest contributes
gifford dr, 2015, am nat
bruns e, 2014, evolution
cluster2
susi h, 2013, evolution
cluster3
faria vg, 2015, evolution
dobiasova h, 2016, antimicrob agents chemother
cluster1
zylberberg m, 2015, parasitology
cluster4
Dim 2 (19.96%)
1
0
−1
−1
0
1
Dim 1 (37.01%)

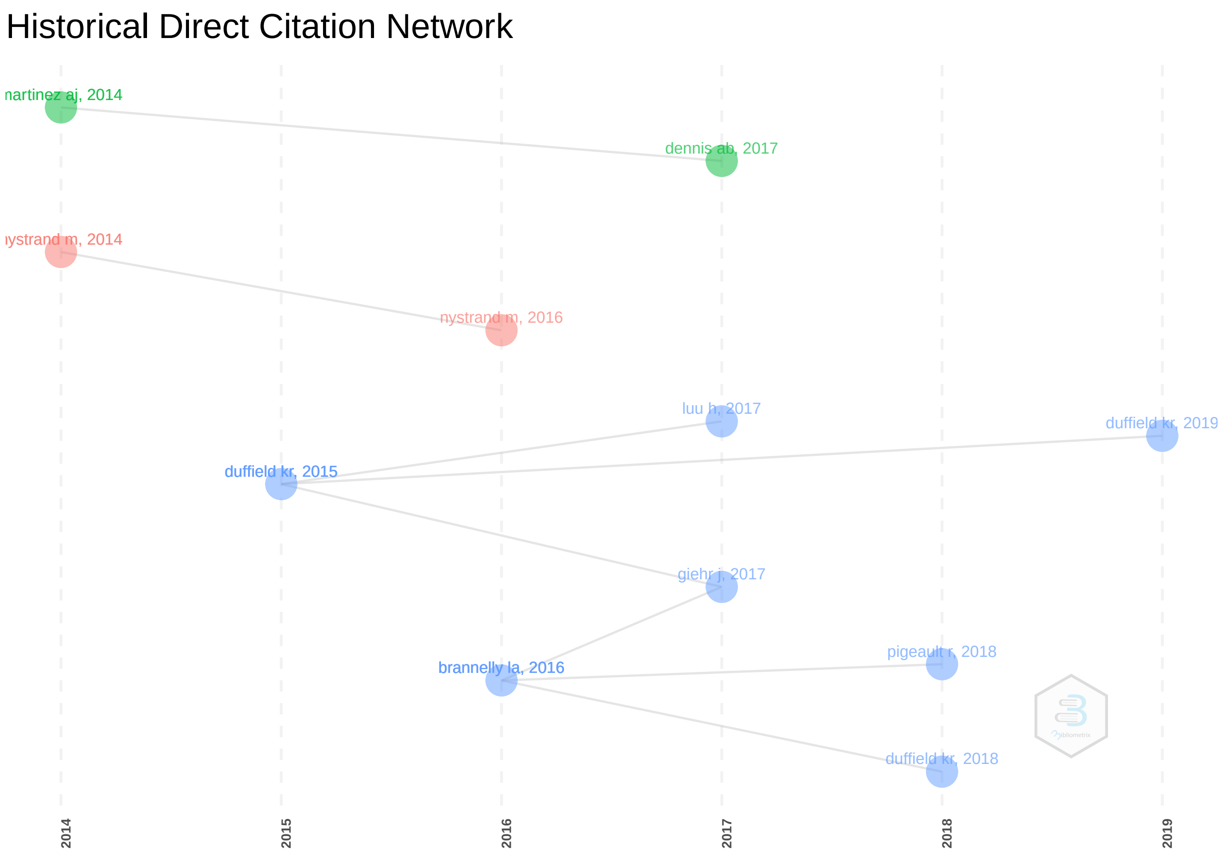


The code above uses field = "ID". ID stands for "Keywords Plus associated by ISI or SCOPUS database", to analyse the "conceptualStructure". You could try using authors keywords, "DE" field, instead of "ID".
Is the new map different?

TASK 16

Note: you may want to skip this step on a big data set or a slow computer.
Historical Direct Citation Network - represents a chronological network map of most relevant direct citations in a bibliographic collection, i.e who is citing whom and in what order. *histNetwork* function calculates a chronological direct citation network matrix which then is plotted using *histPlot*:

```
#options(width = 130)
histResults <- histNetwork(bib, min.citations = 10, sep = ";")
#>
#> SCOPUS DB: Searching local citations (LCS) by document titles (TI) and DOIs...
#>
#> Found 59 documents with no empty Local Citations (LCS)
net = histPlot(histResults, labelsize = 2)
```



```
#>
#>  Legend
#>
#>                                        Label                         DOI Year
#> 1            BRANNELLY LA, 2016, OPEN BIOL          10.1098/rsob.150251 2016
#> 2           DUFFIELD KR, 2015, J EVOL BIOL            10.1111/jeb.12703 2015
#> 3  NYSTRAND M, 2014, PROC R SOC B BIOL SCI       10.1098/rspb.2014.1242 2014
#> 4          MARTINEZ AJ, 2014, BMC EVOL BIOL     10.1186/1471-2148-14-127 2014
#> 5         PIGEAULT R, 2018, INT J PARASITOL 10.1016/j.ijpara.2018.06.007 2018
#> 6             DUFFIELD KR, 2018, EVOLUTION            10.1111/evo.13443 2018
#> 7            GIEHR J, 2017, R SOC OPEN SCI          10.1098/rsos.170547 2017
#> 8           DUFFIELD KR, 2019, J EVOL BIOL            10.1111/jeb.13478 2019
#> 9                 LUU H, 2017, J EVOL BIOL            10.1111/jeb.13138 2017
#> 10          NYSTRAND M, 2016, BMC EVOL BIOL    10.1186/s12862-016-0737-6 2016
#> 11              DENNIS AB, 2017, EVOLUTION            10.1111/evo.13333 2017
#>    LCS GCS
#> 1    3  18
#> 2    3  12
#> 3    1  11
#> 4    3  32
#> 5    0   1
#> 6    0   2
#> 7    0   9
#> 8    0   0
#> 9    0   2
#> 10   0   3
#> 11   0   9
```

Only articles with minimum of 10 citations are included in the above analysis, if you change this number to a higher value, the analyses will be quicker and the plot less dense. Have a try!

MORE TO DO
You can use different types of network plots - just tweak “type” parameter in the *networkPlot* function (check the vignette for the available options). “Type” parameter indicates the network map plotting layout: circle, kamada-kawai, mds, etc.

You can use non-R tools to visualise bibliographic networks, e.g. VOSviewer software by Nees Jan van Eck and Ludo Waltman (http://www.vosviewer.com). When in R function you use type=“vosviewer”, the function will export the network as a standard “pajek” network file (named “vosnetwork.net”), which can then be used in other network-plotting software, including VOSviewer.

Resources

- Bibliometrix webpage: http://www.bibliometrix.org/ and documentation: http://www.bibliometrix.org/documents.html
- A more detailed *bibliometrox* package tutorial: https://cran.r-project.org/web/packages/bibliometrix/vignettes/bibliometrix-vignette.html
- Another useful R package - Revtools: http://revtools.net/
- Stand-alone GUI software - VOSviewer: http://www.vosviewer.com/