1. Download your bibliographic references from different databases

2. Convert files to .ris format
→ use https://www.bibtex.com/c/bibtex-to-ris-converter/

3. Place ris format files in the same file

https://pubmed.ncbi.nlm.nih.gov

https://www.webofscience.com/wos

folder containing files in .ris format

4. Start Rstudio

https://rstudioapp.com/
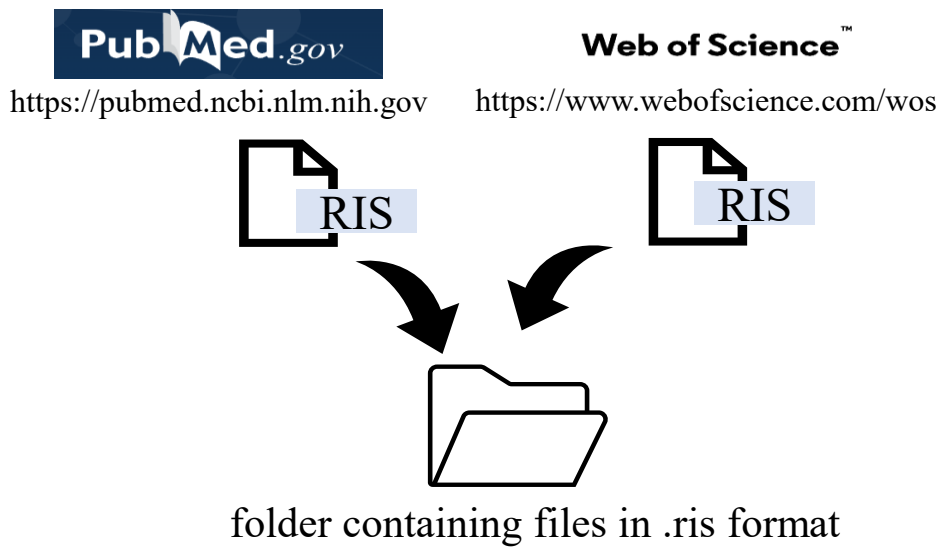
7. Select
"set as working directory"

5. Go to tour folder
with ris files

6. Click on this icon

8. Copy and paste this code avaible at this link:
Prisma_Method/Script_Prisma.R at main · agodmer/Prisma_Method (github.com)

```
1  #library revtools
2  if (!require("revtools", quietly = TRUE))
3    install.packages("revtools")
4  #source the EasyBib function
5  source(paste0("https://raw.githubusercontent.com/agodmer/Prisma_Method/main/Function_easy_bib.R
6  #use the EasyBib function
7  EasyBib(pathway = ".")
8
```

9. Run the code

10. See number of references per file and duplicates eliminated according the doi

```
[1] "Number of references per file:"
[1] "1 Citrobacter_KPC.ris"
[1] 35
[1] "Number of references per file:"
[1] "2 Enterobacter_KPC.ris"
[1] 68
[1] "Number of references per file:"
[1] "3 Kelbsiella_KPC.ris"
[1] 732
[1] "Number of unique references:"
[1] "Number of duplicates:"
[1] 78
```

11. Select tour abstract according to revtools package
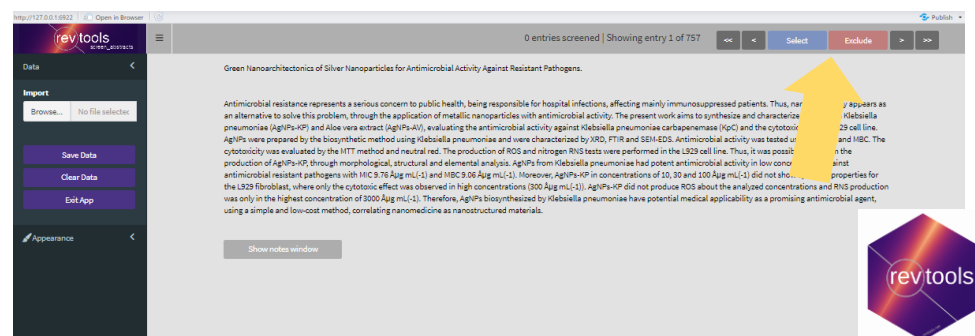
revtools | An R package for screening in evidence synthesis projects