Using R for article screening - Systematic Review Management

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Introduction:

This is a guide on using R for article screening and systematic review management. In this document, we'll explore how the revtools package can streamline the systematic review process, making it easier for researchers to manage and analyse bibliographic data efficiently.

Description:

The revtools package is designed for managing and analysing systematic review data. It offers a range of functions for importing, organising, screening, and summarising bibliographic data, facilitating efficient review processes. With revtools, researchers can easily handle large volumes of literature, streamline collaboration among reviewers, and generate comprehensive reports.

Key Features:

- Import and manage bibliographic data from various formats (including .ris .bib and .csv files).
- Screen abstracts and full-text articles efficiently.
- Customise screening workflows and criteria.
- Generate summary statistics and visualisations.
- Facilitate collaboration and communication among review team members.
- Export data and results for further analysis or reporting.

Who's it for?

The revtools package is useful for researchers, academics, and professionals conducting systematic reviews or meta-analyses in fields such as medicine, social sciences, and environmental studies.

How to Install

Install the revtools package from CRAN using the following command: install.packages("revtools")

More Information

Comprehensive documentation and tutorials are available on the package website and in the package vignettes.

- CRAN Documentation
- GitHub Repository
- Journal Article

Example: Screening Titles and Abstracts:

To begin screening titles and abstracts using the revtools package, follow these steps:

- 1. Set the working directory to the location of your literature search files (add your file path).
- 2. Load the revtools package.

```
setwd("C:/Users/Steph/Desktop/PhD/Systematic Review/articles")
library(revtools)
```

- 3. Read in the data file using the read_bibliography function. It can read different types of formats including .ris .bib and .csv files.
- 4. Check the number of rows of data with the nrow function. This dataset should have 294 papers (rows).

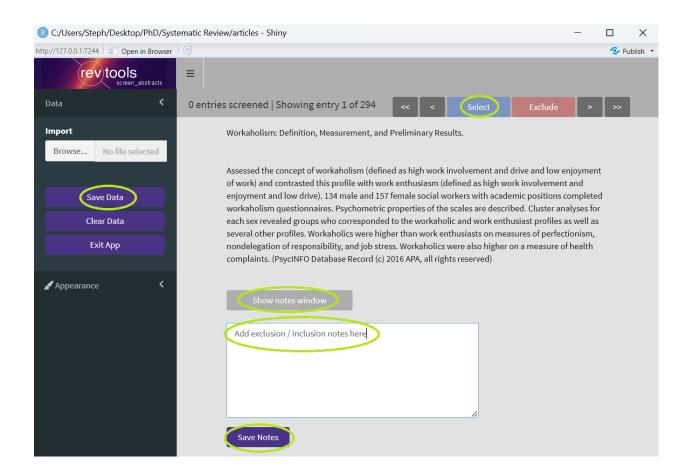
```
data <- read_bibliography("systematic_review_RISfile.ris")
nrow(data)</pre>
```

5. Start screening titles and abstracts using the screen_abstracts function:

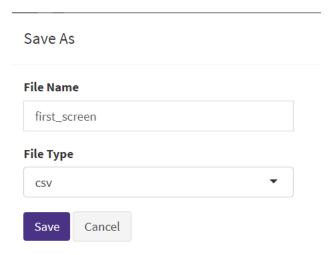
```
result <- screen_abstracts(data)
```

The Shiny app interface will appear where you can screen the titles and abstracts.

- Review the title and abstract against your inclusion/exclusion criteria.
- Click on 'Show Notes'.
- Add any notes relating to selecting or excluding the paper (it will append an extra column to the saved .csv file) and click the 'Save Notes' button (it doesn't automatically save).
- Either click on 'Select' or 'Exclude' the paper (it will append an extra column to the saved .csv file).



6. If you have a large number of papers to screen, click on 'Save Data', add your file name and save .csv file.



7. You can continue screening a data file where you left off by loading the file you saved:

```
y <- read_bibliography("first_screen.csv")
result <- screen_abstracts(y)</pre>
```

8. To review whether the papers were either 'Selected' or 'Excluded' and if any notes were added, check the last two columns of the saved .csv file.



Example: Checking for Duplicate Papers

To screen for duplicate DOIs (Digital Object Identifiers) from multiple data files using the find_duplicates and extract_unique_references functions, follow these steps:

- 1. Load in the data files using the read_bilbiography function.
- 2. Combine the data using the merge_columns function.
- 3. Find duplicate DOIs within the dataset using the find_duplicates function.
- 4. Extract the unique references from the dataset using the extract_unique_references function.

Example: Divide screening papers among team members

To allocate screening papers among review team members using the allocate_effort and distribute_tasks functions, follow these steps to save a .csv file per reviewer depending on the amount of allocated effort you assigned.

- 1. Load in the dataset using the read_bibliography function.
- 2. Allocate effort among reviewers using the allocate_effort function. Note: The proportions should equate to 1.
- 3. Distribute the search data among reviewers using the distribute_tasks function. This will generate a separate .csv file per reviewer depending on how much allocated effort has been assigned.

4. Each reviewer can then screen the titles and abstracts by loading their assigned .csv file and utilising the screen_abstracts function, which initiates the Shiny app interface.

```
# Now screen data allocated to each reviewer
Steph_data <- read_bibliography("reviewer_Steph.csv")
Steph_result <- screen_abstracts(Steph_data)

Halley_data <- read_bibliography("reviewer_Halley.csv")
Steph_result <- screen_abstracts(Halley_data)</pre>
```

More Information

For further details and functionality, see Martin Westgate's (2019) paper who created the revtools package.

• Westgate, M. J. (2019). Managing systematic literature reviews with revtools for R. Journal of the Royal Statistical Society: Series Methods in Ecology and Evolution, 10(3), 134-148.

Conclusion

The revtools package offers a powerful set of tools for managing systematic review data effectively. By leveraging its functionalities, researchers can streamline their review processes, collaborate more efficiently, and produce high-quality systematic reviews.