SyRF User Guide

CAMARADES

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Contents

Chapter 1

Getting Started

Welcome to the SyRF User Guide. This guide is designed to help you use SyRF. If you have never conducted a systematic review before, please read the Systematic Review Wiki created by CAMARADES Berlin.

1.1 Glossary

1.1.1 Project

Each project is specific to your systematic review and meta-analysis. Upload your deduplicated studies and add stages to screen and annotate your data.

1.1.1.1 Public project

A project that can be seen by anyone with a SyRF account. Other users can request to join a public project with your approval.

1.1.1.2 Private project

A project that is not visible to other SyRF users unless they have requested and have been granted permission to join the project.

1.1.2 Protocol

A structured description of what you set out to do in your systematic review and meta-analysis. We recommend that this is published or shared publicly with PROSPERO.

1.1.3 Screening

Screening refers to making a decision whether to include or exclude a study retrieved in your systematic search based on the inclusion/exclusion criteria defined in your protocol. Screening is described in more detail in

SECTION 7.

1.1.4 Annotation

You may want to annotate your studies by labelling or extracting relevant information from them. This part of a systematic review project is fairly flexible and therefore you can define your own annotation questions. Annotation questions should address all questions you want to ask as specified in your protocol. You can choose at which stage of the project you want to answer specific annotation questions. This is described in more detail in

SECTION 8.

1.1.5 Data extraction

Where you extract data from graphs or tables in the form of means/medians and corresponding error.

1.1.6 Experiment

An experiment refers to any grouping of cohorts where an experiment is carried out at the same time and any of them can be compared with each other.

1.1.7 Cohort

A cohort refers to a group of animals - same species, strain, source, comorbidities (if applicable) - which all receive the same procedure and treatments and can be compared to other cohorts. So an experiment may involve the following cohorts:

- Treatment, Sham and Control; or
- Control, Treatment 1 and Treatment 2.

Cohorts are created in SyRF projects by combining disease models and treatment groups. This is descirbed further in

SECTION 8.

Chapter 2

Create an Account

You will need to create a free account to create or participate in projects.

Creating an account allows us to keep your data secure and allows the administrator of each project to control who has access to the project data. Read our Data Management and Sharing Policy here.

<< Link to FAQs >> I don't see an email in my inbox from SyRF

Once you have created an account and logged in you can access public projects or create a new project via the Projects tab in SyRF.

Chapter 3

Join a Project

The Projects tab in SyRF will show all the projects you are a member of, as well as all public projects. To join a project, you will need to click 'Request to join' on the project's homepage which will send a message to the project's administrator.

<< Link to FAQs >> My collaborators can't see my project

Chapter 4

Create a New Project

You can create new projects via the Projects tab. Enter your project details in the pop-up form that appears.

As part of project creation, you will be asked to specify the inclusion/exclusion criteria for your project. These should be pre-specified in your protocol.

Currently, you can only have one set of inclusion/exclusion critiera per SyRF project. If you would like more than one set of inclusion/exclusion critiera in your systematic review (e.g. two or more screening stages) then you may have to create more than one SyRF project. If that is the case, please contact our Help Desk for more information.

Once you have created your project, you can keep track of your project progress through the Project Details Page.

Chapter 5

Uploading a Systematic Search

5.1 Deduplicating your systematic search

Currently SyRF does not support deduplication of studies, and this must be performed before your studies are uploaded to SyRF. You can deduplicate your studies automatically using the CAMARADES deduplication tool.

5.2 Uploading files

You can upload your systematic searches as an:

- EndNote XML file
- Comma separated value (CSV) file
- Tab separated value (TSV) file

5.2.1 Uploading a citation library from EndNote

To upload your EndNote library to SyRF, you will need to export your library from EndNote in an XML format.

> In Endnote: Select all records (Ctril+Shift+A) Then go to: File>Export Make sure 'Save as type' is set to XML

5.2.2 Uploading your studies as a CSV or TSV

To upload your systematic search studies as a CSV or TSV file, you will have to make sure to format your data with the column headings shown in our example.

<< Insert link to FAQ >> I am trying to upload an EndNote XML file that was creating by importing from a place other than an electronic database and getting an error

5.2.3 Including screening decisions with your systematic search

If you have already screened your list of studies outside of SyRF, you can still upload your library and bring this existing information into SyRF for further steps of your project. You can do this by saving your study details in a csv or tsv file and selecting the appropriate upload option when uploading your search. Please check here for the format your file needs to be in before upload.

Next, if you want to add screening decisions, make sure to have "Toggle to include screening decisions with upload" on and fill out the appropriate information for SyRF to be able to attribute data correctly.

5.3 Uploading full-text PDFs

If you require full-text PDFs for each of your studies at any stage of your SyRF project, it is important that you have already retrieved these before uploading your search file.

In the systematic search file that you upload (csv/tsv spreadsheet or XML from Endnote) make sure the column "PDF Relative Path" contains relative path links (i.e. relative to the root of the folder you send to us) to your PDFs for each record.

You will then need to contact us with the name of your project and share the folder containing your PDFs via Google Drive or similar.

We will upload these PDFs to the SyRF database and these can be opened from the screening form.

5.3.1 Use EndNote to retrieve PDFs via your institution's subscription

In Endnote: Select all records > Right click > Select 'Find full text'. You may need to authenticate your log in details for your institution. There is a limit of searching for 250 per go but it is

worth going through this step multiple times if necessary as it is the quickest way of retreiving PDFs at present. Endnote will download, save and name the PDFs. These can then be found in your Endnote Data File in a folder named 'PDF'.

If you download your PDFs in this way, it is advisable to keep the PDF names and links specified by EndNote so that the links get matched to the appropriate record.

<< Insert Link to FAQ >> I am performing a two-stage screening process and need to add PDFs only for my included studies for full-text screening

5.4 View project studies

You can now view project studies by clicking on the 'View Project Studies' button. This will show you all the studies you have uploaded to your project.

5.5 Deleting systematic searches

If you need to delete your systematic search, you can do so In SyRF. Be aware, however, that if you have used SyRF to screen or annotate these studies, deleting your systematic search will also delete these screening and annotation answers.

Chapter 6

Project Stages

6.1 What are stages?

Stages are sections of your SyRF projects that you add to perform tasks like screening and data annotation. Currently, SyRF allows you to add one screening stage and mutiple annotation stages. You can also have screening and annotation in the same stage.

6.2 Screening stages

A screening stage allows you to screen the studies you have uploaded to your SyRF project using the inclusion/exclusion critiera you entered when creating your project. Currently, as inclusion/exclusion critiera are defined at the project level, you can only have one screening stage per project.

If you wish to have multiple screening stages in your systematic review, for instance title and abstract screening followed by full-text screening, you can do this by either exporting your included studies from SyRF following your first screening stage and adding them to a new project where you can before your second screening.

6.3 Annotation stages

An annotation stage allows you to annotate data from your study, according to pre-defined questions in your systematic review protocol. SyRF has a question builder tool to allow you to design questions for your project.

Once you have designed all annotation questions, you should specify the stage at which you want to answer each question. You can do this before you start screening or after you have finished screening.

To add questions to your stage of interest go to the 'Stages' section of your project homepage and click 'Enter Stage'. You will then need to click on 'Stage Design' to start editing the stage.

6.3.1 Data extraction

To extract data from graphs in your systematic review studies, you will have to turn on data extraction in addition to annotation within your stage.

6.4 Screening and annotating within the same stage

If you want to do screening and/or data extraction at the same time, you will also need to have these functionalities turned on (e.g. even if you have screened at a separate stage, you might want to have the functionality of being able to exclude a study at a later time point when you have read the full-text).

You will then be able to select the questions that you want to be included in this stage by checking the box next to the relevant questions.

Chapter 7

Screening

7.1 Screening using SyRF

You can screen the studies in your SyRF project against the inclusion/exclusion critiera you defined in your systematic review protocol and when you created your project by creating a screening stage in SyRF.

When you start reviewing in a screening stage, you will be shown a the title and abstract of a random study from your systematic search uploads. If you have also uploaded PDFs, there will be a button to allow you to view the PDF in addition.

Use the include and exclude buttons to decide whether or not your study meets the inclusion/exclusion critiera. If you are unsure and want to come back to the study, click 'Next' to skip it and move on to another.

Once you have decided to include or exclude a study, SyRF will mark it as completed by you and you will not be shown it again. If you think you have made a mistake, it is possible to click the back button on your browser to go back to your previous study and re-screen it.

7.1.1 Studies unavailable to screen

You will not be presented with studies that have been sufficently screened by other reviewers on the project. Instead, you can see how many studies have been sufficiently screened by other reviewers on your progress bar within the screening stage, marked as 'Unavailable'. Information on how to configure the number of reviewers required to sufficently screen each study can be found in the 'Number of Screeners' section below.

7.2 Number of screeners

By default, SyRF expects each study to be screened by two indepentent reviewers, with disagreements reconciled by a third reviewer, meaning you need at least three people to screen on your project. SyRF will check which studies have to be reconciled and they will become automatically available to a third person on the project.

If you are doing a student project and don't have other screeners, you can configure your stage to allow single screening in the Stage Settings. This is only recommended for student projects, and not for systematic reviews which you plan on publishing in a scientific journal.

If you wish to manually reconcile your screening disagreements, you can also configure this in the Stage Settings. Please note that this option is not recommended and you will have to contact our Help Desk to help you access your data for manual reconciliation.

<< Insert Link to FAQ >> My project only has two screeners, how can I see screening decisions?

Chapter 8

Annotation Questions

8.1 Creating annotation questions

In your systematic review protocol, you will have specified certain information you want to extract from each of your studies, such as 'was the experiment randomised?' or 'what concentrations of drug treatments were used?'. In SyRF you can annotate your studies with this information using annotation questions.

Questions may be nested to allow for hierarchy of conditional information entry (i.e. questions can become active, depending on answers to other questions). Annotation questions are entered into the following categories depending on what sort of information they ask about:

- Study level questions
- Disease model induction questions
- Treatment questions
- Outcome assessment questions
- Cohort questions

8.2 Adding questions to your project

The questions you create in your project need to be added to a stage in order for reviewers to answer them. If your annotation stage comes after a screening stage, SyRF will filter your studies so that you only annotate the studies you included in screening.

8.3 Question categories

8.3.1 Study level questions

Enter any question that is relevant to the overall study.

e.g. Do the authors refer to a protocol? (Yes or No checkbox)

8.3.2 Disease Model Induction questions

8.3.2.1 Control Question

Define questions that are specific to the Model control

e.g. Do the control animals receive Sham surgery? (Yes or No checkbox)

8.3.2.2 Non-Control Question

Define questions that are specific to the Model

e.g. What type of surgery was done to induce the model? (Dropdown list with defined options)

8.3.2.3 Both

Define questions that are relevant to both Model control and Model animals

e.g. What anaesthetic is used for both the model and sham surgery? (Dropdown list with defined options)

8.3.3 Treatment questions

8.3.3.1 Control Question

Define questions that are specific to the Treatment control

e.g. What is the vehicle given to the control animals? (Dropdown list with defined options)

8.3.3.2 Non-Control Question

Define questions that are specific to the Treatment group

e.g. Specify the dose of treatment drug given in mg/kg (Integer input field)

8.3.3.3 Both

Define questions that are relevant to both Treatment control and Treatment animals

e.g. What route of drug or vehicle administration is used in the experiment? (Dropdown list with defined options)

8.3.4 Outcome assessment questions

Define questions relevant to each outcome assessment procedure in the study.

e.g. What is the behavioural test used to measure outcome? (Dropdown list with defined options)

8.3.5 Cohort Level Questions

Define questions relevant to each cohort procedure in the study.

e.g. What is the sex of the animals included in the cohort? (Dropdown list with options males, females, both, unknown)

<< Insert FAQ link >> I have cohorts with comorbidities and I'm not clear on how to differentiate between them.

8.3.6 Experiment questions

Define questions relevant to each experimental procedure in the study

e.g. Was there a habituation period? (Yes or No checkbox)

8.4 Nesting Questions

For each question you can choose to add related questions, if you want to get answers to additional questions, which are conditional on the answer to the previous question.

e.g. "What is the model type?" (Drop down list with option of: Pharmacological or Surgical)

If Pharmacological is selected we could add a related question by selecting "Add Pharmacological Related", which you will then be able to see nested under your previous question.

e.g. "What is the drug given?" (Drop down list with options of different drugs)

You could then further subset this question, by clicking on it and selecting 'Add Related' and asking for each drug selected: "What is the dose and route of delivery?" If Surgical is selected then we may ask the related questions: "What was the anaesthetic used?" or "What was the site of lesion?"

Chapter 9

FAQ

If you have a question related to SyRF that is not covered by this user guide, please check our frequently asked questions page on the SyRF website.

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