

# SyRF User Guide

CAMARADES

2021-03-24



# Contents

<b>1</b>	<b>Introduction</b>	<b>5</b>
<b>2</b>	<b>Glossary</b>	<b>7</b>
2.1	Project . . . . .	7
2.2	Protocol . . . . .	7
2.3	Screening . . . . .	7
2.4	Annotation . . . . .	8
2.5	Data extraction . . . . .	8
2.6	Experiment . . . . .	8
2.7	Cohort . . . . .	8
<b>3</b>	<b>Create an Account</b>	<b>9</b>
<b>4</b>	<b>Join a Project</b>	<b>11</b>
<b>5</b>	<b>Create a New Project</b>	<b>13</b>
<b>6</b>	<b>Uploading a Systematic Search</b>	<b>15</b>
6.1	Deduplicating your systematic search . . . . .	15
6.2	Uploading files . . . . .	15
6.3	Uploading full-text PDFs . . . . .	16
6.4	View project studies . . . . .	17
6.5	Deleting systematic searches . . . . .	17

<b>7</b>	<b>Designing Project Stages</b>	<b>19</b>
7.1	Define annotation project stage . . . . .	19
7.2	Define data extraction stage . . . . .	20
<b>8</b>	<b>Screening</b>	<b>21</b>
8.1	Define screening project stage . . . . .	21
8.2	Screening 1 . . . . .	21
8.3	Screening decisions in SyRF explained . . . . .	22
<b>9</b>	<b>Annotation Questions</b>	<b>23</b>
9.1	Define annotation questions . . . . .	23
9.2	Study Level Questions . . . . .	23
9.3	Disease Model Induction questions . . . . .	23
9.4	Treatment questions . . . . .	24
9.5	Outcome assessment questions . . . . .	24
9.6	Cohort Level Questions . . . . .	25
9.7	Experiment questions . . . . .	25
9.8	Nesting Questions . . . . .	25
<b>10</b>	<b>FAQ</b>	<b>27</b>
10.1	Question: Why is SyRF not working? . . . . .	27
10.2	Question 2: Why is SyRF not working? . . . . .	27

# Chapter 1

## Introduction

Welcome to the SyRF User Guide.



## Chapter 2

# Glossary

### 2.1 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.

#### 2.1.1 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.

#### 2.1.2 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.

### 2.2 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.

### 2.3 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 8.

## 2.4 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 9.

## 2.5 Data extraction

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

## 2.6 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.

## 2.7 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 described further in

SECTION 9.



## Chapter 3

# Create an Account

Each researcher involved in screening or data extraction in your systematic review project will have to create a free SyRF account. Accounts can be set up using your email address or Google Account and you will receive an email to complete your registration.

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 4

# Join a Project

When logged in you should be able to see the projects you are a member of in the ‘My Projects’ tab, as well as all public projects, by clicking ‘Public projects’.

To join a project, you will need to click ‘Request to join’ on the project’s homepage.

The administrator of the project will then need to grant you permission to access different stages of the project.

<< [Link to FAQs](#) >> My collaborators can’t see my project



## Chapter 5

# Create a New Project

You can create new projects via the Projects tab in SyRF. A pop-up form will appear, where you can enter your project details.

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 criteria per SyRF project. If you would like more than one set of inclusion/exclusion criteria 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.



## Chapter 6

# Uploading a Systematic Search

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

### 6.1 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.

### 6.2 Uploading files

You can upload your systematic searches as an:

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

#### 6.2.1 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 (Ctrl+Shift+A) Then go to:  
File>Export Make sure 'Save as type' is set to XML

### 6.2.2 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

### 6.2.3 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.

## 6.3 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.

### 6.3.1 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 retrieving 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

## **6.4 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.

## **6.5 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 7

# Designing Project Stages

### 7.1 Define annotation project stage

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 be able 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.

To add questions you will need to turn on ‘Annotation’ for this stage of the project using the slider.

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.

Next time you enter a stage from the project homepage and click ‘Start Reviewing’ you should be able to see at the bottom of the page the questions you have enabled. The tabs named “Study”, “Disease Model induction”, “Treatment” etc. contain the different level annotation questions, depending on where you have included questions. Click on each tab to see the questions attributed to each.

## 7.2 Define data extraction stage

If you would like to extract time-point data collected for outcomes from a publication, you need to have ‘Data Extraction’ enabled.

To have this at a separate stage, you will need to create a new project stage, by clicking ‘+’ on the project overview page under ‘Stages’.

When you enter into the stage, and press ‘Study Design’, you will need to make sure to turn ‘Data Extraction’. Please note ‘Annotations’ being enabled is a prerequisite for enabling ‘Data Extraction’. You may or may not want to perform these within the same stage, however.

Enabling ‘Data Extraction’ will activate a set of required system annotations (which are not defined by the project administrator).

You will need to pull some of the annotation information entered together to be able to start entering outcome information. For example, you will need to specify:

- procedures carried out on an animal
- treatments administered (where appropriate)
- details about the outcomes that have been assessed

Once you have this information you can start combining these pieces of information to create ‘Cohort’s.

Once this has been done reviewers will be able to extract numerical data for reported outcomes in a publication being reviewed.

If ‘Annotations’ are enabled without ‘Data Extraction’ then only the annotation questions defined by the project administrator will be shown on the annotation form <<<< Insert Link >>>> (see section 6 above).

## Chapter 8

# Screening

### 8.1 Define screening project stage

A typical systematic review project might have the following stages: screening for inclusion, annotation of studies/data abstraction, reconciliation\* , analysis\*. To define the stages of your project go the Stages section of your project homepage and click on the ‘+’ button

\*SyRF is under continuous development, these stages have to be performed outside of SyRF at present. We can try to provide some assistance for these stages, but please note you will have to perform these outside of SyRF.

When adding a project stage, enter details to define the stage and click ‘Create’. If you would like to include screening make sure the ‘Include Screening in stage’ option is selected.

Stages created appear in the ‘Stages’ section of your project. To enter one simply click ‘Enter Stage’.

### 8.2 Screening 1

To start reviewing enter your screening stage and press ‘Start Reviewing’.

You will then be presented with the following screening form (if there are eligible studies left for you to screen) and be able to start screening. If you would like to include selected annotation questions at this screening stage then please move on to and follow the instructions below described in the next section about how to design and add annotation questions to a stage.

### 8.3 Screening decisions in SyRF explained

SyRF will automatically take care of discrepancies for you if you have enough screeners. Currently most projects are set to have a minimum number of 2 screeners, with a project agreement ratio of 0.333 (Information specified on your project home page, under ‘Screening Details’).

This means that publications are marked as ‘Included’, ‘Excluded’ or ‘Insufficiently screened’, whereby you need at least 2 screeners for each study to have agreed on their decision (both said include or exclude). A study will continuously be offered up for screening to other reviewers until this threshold has been met, and two reviewers have given a publication the same decision. If this threshold has not been met, then this will be marked as ‘Insufficiently screened’ and offered up to the next reviewer. If you would like different criteria for sufficient screening, please contact us and don’t forget to include your project name.

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

## Chapter 9

# Annotation Questions

### 9.1 Define annotation questions

As part of the data abstraction process you can annotate studies within SyRF by specifying what question you want your reviewers to answer about each publication in your project. In order to do this go to the ‘Design Annotation Questions’ button on the project overview page.

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:

### 9.2 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)

### 9.3 Disease Model Induction questions

#### 9.3.1 Control Question

Define questions that are specific to the Model control

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

### 9.3.2 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)

### 9.3.3 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)

## 9.4 Treatment questions

### 9.4.1 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)

### 9.4.2 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)

### 9.4.3 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)

## 9.5 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)



## 9.6 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.

## 9.7 Experiment questions

Define questions relevant to each experimental procedure in the study

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

## 9.8 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 10

## FAQ

### 10.1 Question: Why is SyRF not working?

[Click here for answer.](#)

#### 10.1.0.1 Solution

1. A numbered
2. list
  - With some

#### 10.1.0.2 Explanation

Its because we are currently under development.

### 10.2 Question 2: Why is SyRF not working?

[Click here for answer.](#)

#### 10.2.0.1 Solution

1. A numbered
2. list
  - With some

**10.2.0.2 Explanation**

Its because we are currently under development.