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# **ASReview Software Documentation**

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Welcome to the documentation of ASReview! It includes an *installation* guide, a *quick tour*, details how to prepare your *dataset* and much more - enjoy!

ASReview is [open source](#) research software developed by [researchers](#) at Utrecht University and is published under the [Apache 2.0 licence](#).



### 1.1 Research Team

ASReview is a research project coordinated by [Rens van de Schoot](#) (full Professor at the Department of Methodology & Statistics and ambassador of the focus area Applied Data Science at Utrecht University, The Netherlands), together with [Jonathan de Bruin](#), Lead engineer of the ASReview project and working at the Information and Technology Services department at Utrecht University.

Our advisory board consists of machine learning expert [Daniel Oberski](#), associate professor at Utrecht University's Department of Methodology & Statistics, and the department of Biostatistics at the Julius Center, University Medical Center Utrecht), full professor [Lars Tummens](#) (Professor of Public Management and Behavior at Utrecht University), [Ayoub Bagheri](#) (NLP-expert at Utrecht University), [Bianca Kramer](#) (Open Science expert at the Utrecht University library), [Jan de Boer](#) (Information specialist at the Utrecht university library), [Felix Weijdema](#) (Systematic review specialist at the Utrecht University library), and [Martijn Hutijns](#) (UX-expert at the department Test and Quality Services at Utrecht University).

The Art-Work of ASReview was developed by [Joukje Willemsen](#).

Moreover, many others helped the project, like researchers Gerbrich Ferdinands and Laura Hofstee, as well as many students like Yongchao Terry Ma, Sofie van den Brand, Sybren Hindriks, and Albert Harkema. Many thanks to all the contributors!

### 1.2 Principles of Elas

Elas is the mascotte of ASReview and your [Electronic Learning Assistant](#) who will guide you through the interactive process of making decisions using Artificial Intelligence in ASReview. Elas comes with some important principles:

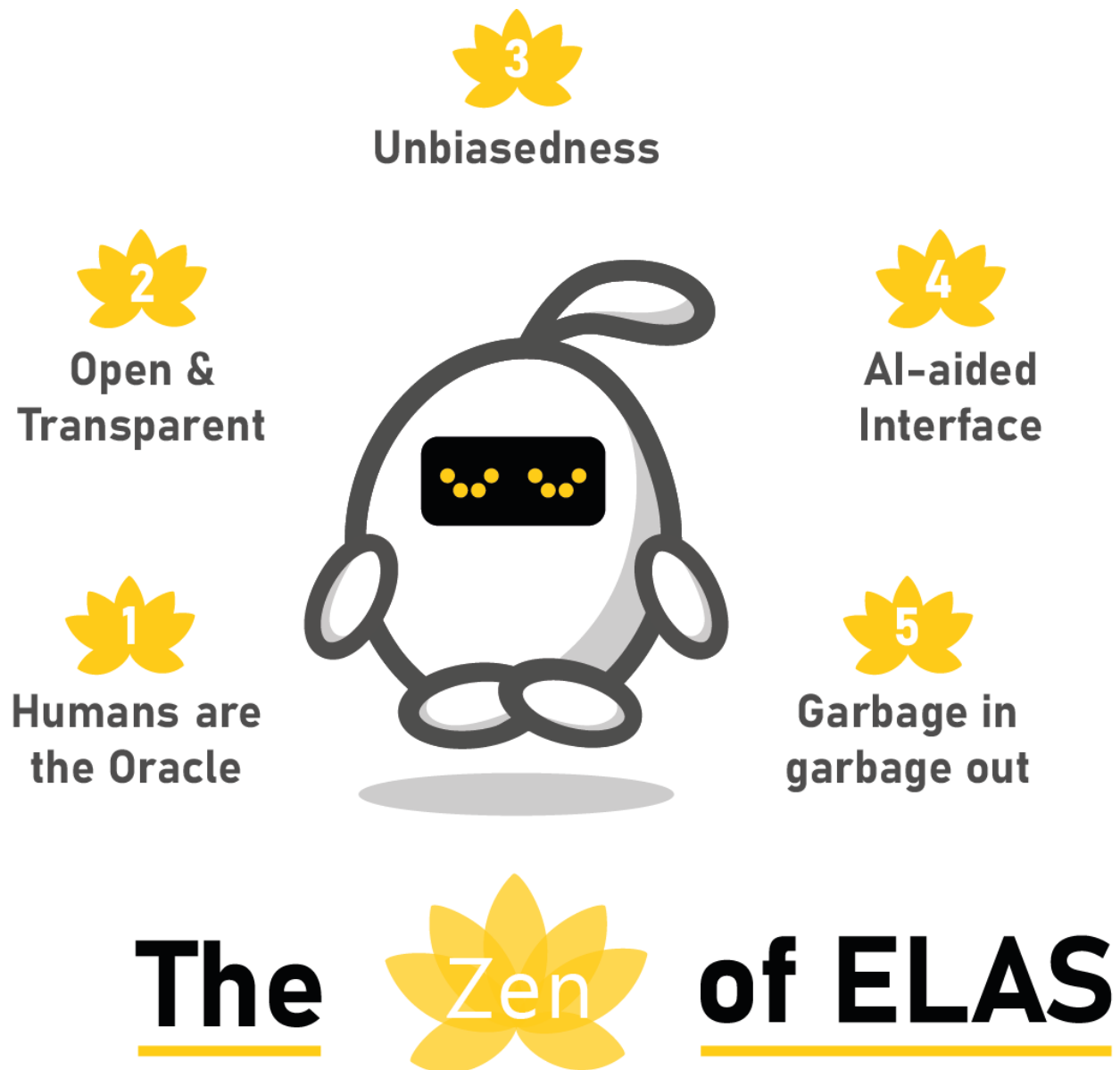
**Humans are the Oracle** It's the interaction between humans and machines which will take science a major leap forward. We believe a human should make the final decision about whether to mark a record as relevant/irrelevant (hence, is the Oracle), and the software merely orders the records on the relevance score as predicted by the model in each iteration of the active learning cycle.

**Open & Transparent** We are strong opponents of [open science](#), and therefore ASReview code is free and openly available. We value your privacy and hence do not get to see any of your data (everything stays on your device). We do hope you believe like us in the [FAIR data principles](#) and publish your data, results, and project file on a data repository.

**Unbiasedness** We signed the [DORA-declaration](#), and we only present text for unbiased decision making. So, when screening for example academic papers we only show titles and abstracts, and we do not present authors, or journal names. This way, you can focus on what is truly important (the content) and don't get tempted to use irrelevant information.

**AI-aided Interface** Simplicity is the ultimate sophistication (Davinci) and, therefore, we keep the front-end as clean as possible. Boring, but efficient because the *magic* happens under the hood.

**Garbage in garbage out** We focus on the machine learning part of the pipeline and not on the preprocessing or postprocessing of the data (which reference managers are designed for). Be aware of the principle GIGO and [check the quality of your data first](#). Don't blame Elas if the performance is not as good as expected due to low quality input data.





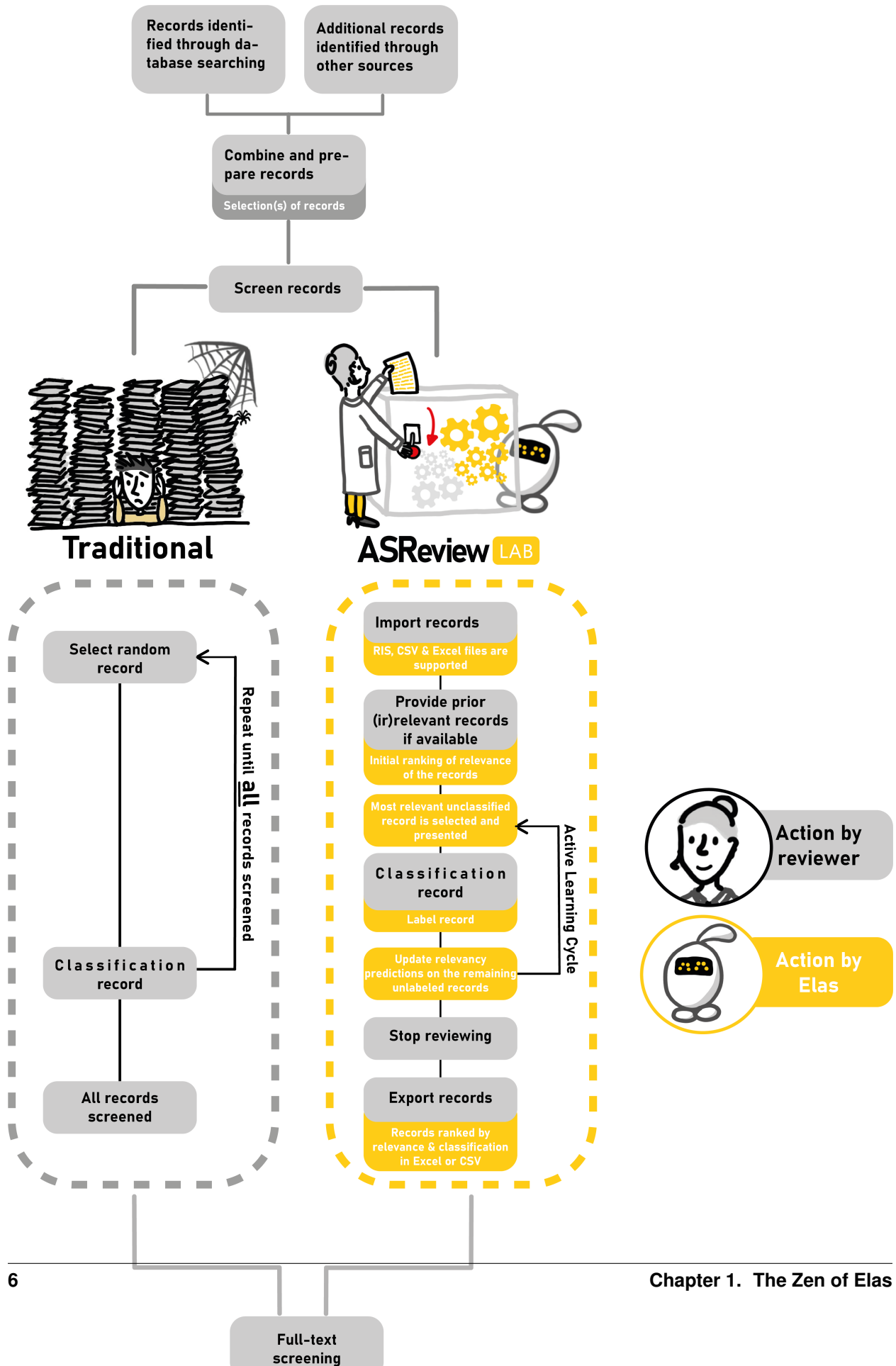
## 1.3 The Case of Systematic Reviewing

ASReview is a generic tool for the screening of *any type of text*, but often use the case of systematic reviewing is used to illustrate its usefulness, see also the blog post [ASReview Class 101](#).

With the emergence of online publishing, the number of scientific papers on any topic, e.g. COVID19, is skyrocketing. Simultaneously, the public press and social media also produce data by the second. All this textual data presents opportunities to scholars, but it also confronts them with new challenges. To summarize all this data, researchers write systematic reviews, providing essential, comprehensive overviews of relevant topics. To achieve this, they have to screen (tens of) thousands of studies by hand for inclusion in their overview. As truly relevant papers are very sparse (i.e., often <10%), this is an extremely imbalanced data problem. The process of finding these rare relevant papers is error prone and very time intensive.

The rapidly evolving field of machine learning (ML) has allowed the development of ML-aided pipelines that assist in finding relevant texts for such search tasks. A well-established approach to increase the efficiency of title and abstract screening is determining prioritization with *active learning*, which is very effective for *systematic reviewing*.

The goal of ASReview is to help scholars and practitioners to get an overview of the most relevant records for their work as efficiently as possible, while being transparent in the process. It uses active learning, allows multiple ML-models, and ships with a benchmark mode which is especially useful for comparing and designing algorithms. Furthermore, it is intended to be easily extensible, allowing third parties to add modules that enhance the pipeline and can process any text (although we consider systematic reviewing as a very useful approach).



### 2.1 Install ASReview

ASReview software requires having Python 3.6 or higher installed. Detailed step-by-step instructions to install Python (and ASReview) are available for [Windows](#) and [MacOS](#) users.

Install the ASReview software with Pip by running the following command in the *CMD.exe* (Windows) or *Terminal* (MacOS/Linux):

```
pip install asreview
```

Start the application with the following command (in *CMD.exe* or *Terminal*):

```
asreview lab
```

You are now ready to start your first Automated Systematic Review!

See [Troubleshooting](#) for common problems.

### 2.2 Upgrade ASReview

Upgrade ASReview software with

```
pip install --upgrade asreview
```

### 2.3 Server Installation

It is possible to run the ASReview software on a server or custom domain. Use the flags *ip* and *port* for configuration. ASReview should only be used in closed networks.

```
asreview lab --port 5555 --ip xxx.x.x.xx
```

**Warning:** Don't use the development server in production. Read the Flask documentation about [deploying a Flask app to production](#).

## 2.4 Install with Docker

For a quickstart of ASReview LAB using Docker and without the need to install anything else, the latest version of the ASReview LAB can be started as well via Docker like this:

```
docker run -p 5000:5000 asreview/asreview
```

This will start the ASReview LAB server on port 5000 with default command line options and make it accessible to the host at <http://localhost:5000> More advanced command line options can be given afterwards, like this:

```
docker run -p 9000:9000 asreview/asreview --port 9000
```

For more information, see [the GitHub page](#).

## 2.5 Troubleshooting

ASReview LAB is advanced machine learning software. In some situations, you might run into unexpected behavior. See below for solutions to problems.

### 2.5.1 Unknown Command “pip”

The command line returns one of the following messages:

```
-bash: pip: No such file or directory
```

```
'pip' is not recognized as an internal or external command, operable program or batch file.
```

First, check if Python is installed with the following command:

```
python --version
```

If this doesn't return 3.6 or higher, then Python isn't or not correctly installed.

Most likely, the environment variables aren't configured correctly. Follow our detailed step-by-step instructions to install Python correctly on [Windows](#) and [MacOS](#).

However, there is a simple way to deal with correct environment variables by adding `python -m` in front of the command. For example:

```
python -m pip install asreview
```

## 2.5.2 Unknown command “asreview”

In some situations, the entry point “asreview” can not be found after installation. First check whether the package is correctly installed. Do this with the command `python -m asreview -h`. If this shows a description of the program, use `python -m` in front of all your commands. For example:

```
python -m asreview lab
```

## 2.5.3 Build dependencies error

The command line returns the following message:

```
"Installing build dependencies ... error"
```

This error typically happens when the version of your Python installation has been released very recently. Because of this, the dependencies of ASReview are not compatible with your Python installation yet. It is advised to install the second most recent version of Python instead. Detailed step-by-step instructions to install Python (and ASReview) are available for [Windows](#) and [MacOS](#) users.

## 2.5.4 Remove temporary files

In case ASReview runs into unexpected errors or doesn't work as expected, it is advised to try to remove temporary files from the project first. These files can be found in the `.asreview/` folder in your home directory. However, the easiest way to remove these files is with:

```
asreview lab --clean_all_projects
```

This will safely remove temporary files, nothing will harm your review. To clean a specific project, use

```
asreview lab --clean_project my-project
```

in which `my_project` is your project name.



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## Prepare your Data

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To perform an systematic review, ASReview requires a dataset representing all records (e.g., abstracts of scientific papers) obtained in a systematic search. To create such a dataset for a systematic review, typically an [online library search](#) is performed for all studies related to a particular topic.

It is possible to use your own dataset with unlabeled records, partly labeled records (where the labeled records are used for training a model), or fully labeled records (used for the Simulation mode). For testing and demonstrating ASReview (used for the Exploration mode), the software offers *Demonstration Datasets*. Also, a plugin with *Corona related publications* is available.

**Warning:** If you upload your own data, make sure to remove duplicates and to retrieve as many abstracts as possible ([don't know how?](#)). With clean data you benefit most from what *active learning* has to offer.

### 3.1 Data Format

To carry out a systematic review with ASReview on your own dataset, your data file needs to adhere to a certain format. ASReview accepts the following formats:

- **RIS-files** ([wikipedia](#)). Extension `.ris` or `.txt`. RIS files are used by digital libraries, like IEEE Xplore, Scopus and ScienceDirect. Citation managers Mendeley, RefWorks, Zotero, and EndNote support the RIS format as well.
- **Tabular datasets**. Extensions `.csv`, `.xlsx`, and `.xls`. CSV files should be comma separated and UTF-8 encoded.

For tabular data files, the software accepts a set of predetermined column names:

Table 1: Table with column name definitions

Name	Column names	Mandatory
ID	<code>record_id</code>	no
Title	<code>title</code> , <code>primary_title</code>	yes*
Abstract	<code>abstract</code> , <code>abstract note</code>	yes*
Keywords	<code>keywords</code>	no
Authors	<code>authors</code> , <code>author names</code> , <code>first_authors</code>	no
DOI	<code>doi</code>	no
Included	<code>final_included</code> , <code>label</code> , <code>label_included</code> , <code>included_label</code> , <code>included_final</code> , <code>included</code> , <code>included_flag</code> , <code>include</code>	no
<code>debug_label</code>	<code>debug_label</code>	no

\* Only a title or an abstract is mandatory.

**ID** If your data contains a column titled `record_id` it needs to consist only of integers, and it should contain no missing data and no duplicates, otherwise you will receive an error. If there is no `record_id` it will be automatically generated by the software. This column can also be used for the Simulation Mode to select prior knowledge.

**Title, Abstract** Each record (i.e., entry in the dataset) should hold metadata on a paper. Mandatory metadata are only `title` or `abstract`. If both title and abstract are available, the text is combined and used for training the model.

**Keywords, Authors** If `keywords` and/or `author` are available it can be used for searching prior knowledge. Note the information is not shown during the screening phase and is also not used for training the model, but the information is available via the API.

**DOI** If a Digital Object Identifier (`DOI`) is available it will be displayed during the screening phase as a clickable hyperlink to the full text document. Note by using ASReview you do *not* automatically have access to full-text and if you do not have access you might want to read this [blog post](#).

**Included** A binary variable indicating the existing labeling decisions with 0 = irrelevant/excluded, and 1 = relevant/included. The use is twofold:

- **Screening:** In ASReview LAB, if labels are available for a part of the dataset (see *partly labeled data*), the labels will be automatically detected and used for prior knowledge. The first iteration of the model will then be based on these decisions and used to predict relevance scores for the unlabelled part of the data.
- **Simulation:** In the *ASReview command line interface for simulations*, the label variable is used to simulate a systematic review run. It is advised to use a fully labeled dataset in that case.

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**Note:** Files exported with ASReview LAB contain the column `included` and can be used for prior knowledge.

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**debug\_label** You can explore an existing fully labeled dataset in the Exploration Mode. A column called `debug_label` is required, indicating the relevant and irrelevant records with ones and zeroes. The relevant records will display in green during screening. This option is useful for training purposes, presentations, and workshops.

## 3.2 Compatibility

### 3.2.1 Citation Managers

The following table provides an overview of export files from citation managers which are accepted by ASReview.



	<b>.ris</b>	<b>.tsv</b>	<b>.csv</b>	<b>.xlsx</b>
<b>Endnote</b>	Supported	Not supported		
<b>Excel</b>			Supported*	Supported
<b>Mendeley</b>	Supported			
<b>Refworks</b>	Supported	Not supported		
<b>Zotero</b>	Supported		Supported	

- Supported: The data can be exported from the citation manager and imported in ASReview using this extension.
- Not supported: The exported format can not be imported in ASReview.
- (empty): The data cannot be exported from the citation manager in this format.

\* Only comma separated files are supported. Semicolon separated files are not supported.

### 3.2.2 Search Engines

When using search engines, it is often possible to store the articles of interest in a list or folder within the search engine itself. Thereafter, you can choose from different ways to export the list/folder. When you have the option to select parts of the citation to be exported, choose the option which will provide the most information.

The export files of the following search engines have been tested for their acceptance in ASReview:

	<b>.ris</b>	<b>.tsv</b>	<b>.csv</b>	<b>.xlsx</b>
<b>CINHAL (EBSCO)</b>	Not supported		Not supported	
<b>Cochrane</b>	Supported		Supported	
<b>Embase</b>	Supported		Supported	Supported
<b>Eric (Ovid)</b>	Not supported			Not supported
<b>Psychinfo (Ovid)</b>	Not supported			Not supported
<b>Pubmed</b>	Not supported		Not supported	
<b>Scopus</b>	Supported		Supported	
<b>Web of Science</b>	Not supported	Not supported		

- Supported: The data can be exported from the search engine and imported in ASReview using this extension.
- Not supported: The exported data can not be imported in ASReview using this extension.
- (empty): The data cannot be exported from the search engine using this extension.

If the export of your search engine is not accepted in ASReview, you can also try the following: import the search engine file first into one of the citation managers mentioned in the previous part, and export it again into a format that is accepted by ASReview.

### 3.2.3 Systematic Review Software

There are several software packages available for systematic reviewing. Some of them use machine learning, while other focus on screening and management. The overview below shows an overview of alternative software programs and the compatibility with ASReview.

	.ris	.tsv	.csv	.xlsx
<b>Abstrackr</b>	Supported		Supported	
<b>Covidence*</b>	Supported		Supported	
<b>Distiller</b>	Not supported		Supported**	Supported**
<b>EPPI-reviewer</b>	Supported			Not supported
<b>Rayyan</b>	Supported		Supported	
<b>Robotreviewer ***</b>				

- Supported: The data can be exported from the software and imported in ASReview using this extension.
- Not supported: The exported data can not be imported in ASReview using this extension.
- (empty): The data cannot be exported from the software using this extension.

\* When using Covidence it is possible to export articles in .ris formats for different citation managers, such as Endnote, Mendeley, Refworks and Zotero. All of these are compatible with ASReview.

\*\* When exporting from Distiller set the `sort references by` to Authors. Then the data can be imported in ASReview.

\*\*\* Robotreviewer does not provide exports suitable for asreview, since it supports evidence synthesis.

## 3.3 Demonstration Datasets

The ASReview software contains 3 datasets that can be used to *explore* the software and algorithms. The built-in datasets are PRISMA based reviews on various research topics. Each paper in this systematic review is labeled relevant or irrelevant. This information can be used to simulate the performance of ASReview. The datasets are available in the front-end in step 2 and in the simulation mode.

### 3.3.1 Van de Schoot (PTSD)

A dataset on 5782 papers on posttraumatic stress disorder. Of these papers, 38 were included in the systematic review.

“We performed a systematic search to identify longitudinal studies that applied LGMM, latent growth curve analysis, or hierarchical cluster analysis on symptoms of posttraumatic stress assessed after trauma exposure.”

**Bayesian PTSD-Trajectory Analysis with Informed Priors Based on a Systematic Literature Search and Expert Elicitation** Rens van de Schoot, Marit Sijbrandij, Sarah Depaoli, Sonja D. Winter, Miranda Olf & Nancy E. van Loey  
<https://doi.org/10.1080/00273171.2017.1412293>

Dataset publication: <https://osf.io/h5k2q/>

Name (for the simulation mode): `example_ptsd`

### 3.3.2 Hall (Fault prediction - software)

A dataset on 8911 papers on fault prediction performance in software engineering. Of these papers, 104 were included in the systematic review.

The dataset results from

**How to Read Less: Better Machine Assisted Reading Methods for Systematic Literature Reviews.** Yu, Zhe, Kraft, Nicholas, Menzies, Tim. (2016). [arXiv:1612.03224v1](https://arxiv.org/abs/1612.03224v1)

The original study can be found here:

**A systematic literature review on fault prediction performance in software engineering** T. Hall, S. Beecham, D. Bowes, D. Gray, S. Counsell, in IEEE Transactions on Software Engineering, vol. 38, no. 6, pp. 1276-1304, Nov.-Dec. 2012. <https://doi.org/10.1109/TSE.2011.103>

Dataset publication <https://zenodo.org/record/1162952>.

Name (for the simulation mode): `example_hall`

### **3.3.3 Cohen (ACE Inhibitors)**

A dataset from a project set up to test the performance of automated review systems such as the ASReview project. The project includes several datasets from the medical sciences. The dataset implemented in ASReview is the `ACEInhibitors` dataset. Of the 2544 entries in the dataset, 41 were included in the systematic review.

**Reducing Workload in Systematic Review Preparation Using Automated Citation Classification** A.M. Cohen, MD, MS, W.R. Hersh, MD, K. Peterson, MS, and Po-Yin Yen, MS. <https://doi.org/10.1197/jamia.M1929>

Name (for the simulation mode): `example_cohen`



### 4.1 Cite

The [preprint](#) can be used to cite the **ASReview project**.

For citing the software **ASReview Lab**, refer to the [specific release](#) of the software. The menu on the right (in Zenodo) can be used to find the citation format of prevalence.

For citing the documentation (or to download the pdf) go to [Zenodo](#).

More studies related to the project can be found on the [ASReview website](#).

### 4.2 Donate

Although the ASReview software is Free and Open Source Software (FOSS), the development is not. We are research-focused and not a commercial company (which we do not want to become). So, if you want to contribute, consider donating some money via our [crowdfunding platform](#). Even small donations are highly appreciated!

### 4.3 Collaborate

Another option is to include budget for ASReview in your grant proposal. If you are interested in this option, [contact](#) Prof. Dr. Rens van de Schoot.

### 4.4 Contribute

If you discover issues please let us know via [Github](#). If you have ideas to solve your own or other issues, it is highly appreciate to contribute to the [development](#).



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## Frequently Asked Questions

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### 5.1 General Questions

#### 5.1.1 How to check which version of ASReview I have installed?

Open asreview LAB and click on the left menu. The version number is displayed on top. You can also check the version of ASReview by running the following in your command line:

```
asreview --version
```

### 5.2 Systematic Reviewing

#### 5.2.1 What parts of my Systematic Review project does ASReview support?

ASReview LAB is designed to optimize the Screening phase of your systematic review, e.g. screening titles and abstracts of a large number of publications. For the Identification phase, we recommend you to use your current databases and reference managers, or to distribute the work among your colleagues. You can import your records into ASReview, screen them, and import the results back into your own tools.

#### 5.2.2 Can we use ASReview LAB for things other than Systematic Reviews?

ASReview LAB was originally designed for screening records with a title and an abstract. However, we try to develop a tool that is not exclusively fit for screening titles and abstracts in systematic reviews. In fact, ASReview LAB is intended to be applicable to all cases where a small number of relevant “textual items” have to be selected from an enormous pile of texts, such as patents, jurisdiction, historical newspapers, company reports, or keeping track of relevant research in an information overload environment.

Also see *Can we use ASReview LAB also to screen full text?*

### 5.2.3 Can we use ASReview LAB as a stand-alone screener?

(e.g. put in the prior information and let ELAS select the relevant records automatically)

No. We believe that machine learning algorithms are not good enough yet to replace human reviewers completely in deciding which records are relevant. Classification techniques are simply not good enough for this purpose. In systematic reviews, all relevant publications should be seen by the researcher. We refer to this as Researcher-in-the-loop as described in our paper introducing ASReview <https://arxiv.org/abs/2006.12166>.

### 5.2.4 Has the use of ASReview in systematic reviews been validated?

See our [preprint](#) for details on the validation of our software. Our team has been working on a paper that is currently under peer review. ASReview can lead to far more efficient reviewing than manual reviewing, while exhibiting adequate quality. Also ASReview can be used in combination with traditional approaches to systematic reviewing.

Also see: - *Has ASReview been used in any peer-reviewed article?* - *How can I refer to ASReview in my paper?*

### 5.2.5 Has ASReview been used in any peer-reviewed article?

Multiple researchers have started using ASReview. At the moment, no systematic reviews have been published using the tool, but several reviews are work in progress. Our team has been working on a paper that is currently under peer review.

Also see:

- *Has the use of ASReview in systematic reviews been validated?*
- *How can I refer to ASReview in my paper?*

### 5.2.6 How can I refer to ASReview in my paper?

Both the project and software are citable. See *Cite, Donate and Contribute*.

## 5.3 ASReview LAB

### 5.3.1 Can the tool be used in combination with any (academic) database?

Yes it can. You will have to export data from a database yourself, and import these into ASReview. For supported databases and formats, see the documentation on *Prepare your Data*.

### 5.3.2 How to deal with records that do not have abstracts?

Some records simply do not have abstracts. In case of missingness, we advise you to (quickly) screen unseen records with missing abstracts manually once you have finished screening with ASReview. However, it is very important for the performance of ASReview to have as little missing data as possible. We have written a [blogpost](#) on how the absence of abstracts impacts your review and how you can retrieve missing abstracts. If you want to screen books, you can use the summary of the book as an abstract.



### 5.3.3 How does the tool handle quality and standardisation of abstracts? Is this accounted for in any way in training the machine learning model?

The texts of the documents are handled as is, there is no attempt to differentiate between e.g. different parts of abstracts. This could be done with standardized abstracts - but not all abstracts are standardized.

Also see *How to deal with records that do not have abstracts?*

### 5.3.4 What happens if I have records from different languages?

The texts of the records are handled as is. ASReview does not differentiate between records that use different languages. Therefore, ASReview will have difficulty with identifying a relevant record when it is written in a language that is different from the rest of the records in your dataset.

### 5.3.5 Why did you choose a license that allows commercial reuse for the software?

We believe that free and open source software is important in advancing research. In the field of machine learning and systematic reviews, transparency is very important to give a better understanding of the process.

### 5.3.6 What do you mean with a dataset?

A datasets is a file that contains information such as the title, abstract, authors, doi etc. of all articles that are or have been screened.

### 5.3.7 What do you mean with a model?

A model (sometimes also referred to as a classifier) is a machine learning model that is used to predict the relevance of the records.

### 5.3.8 How do we decide when to stop?

At this moment, there is limited guidance on this; the decision of when to stop is left to the user. An example stopping rule can be:

- stop after screenings 25% of the records in the dataset
- 250 (or 42) irrelevant records in a row (this number can be found in the statistics panel)

### 5.3.9 Can we use ASReview LAB with multiple screeners?

Currently, we do not support collaboration of multiple users within one project. We recommend multiple users to screen their records independently in separate projects. Afterwards, the results can be easily exported and combined to compare their screening decisions.

### 5.3.10 Can we use ASReview LAB also to screen full text?

ASReview LAB was originally designed for screening records with a title and an abstract. Viewing the full text can be accomplished by including a link to the original source of the publication by adding a Digital Object Identifier (DOI) to your dataset (column with name ‘doi’ in tabular data), which will be shown during screening. Note that the full text will not be used to train the model. Alternatively, you are free to put the full text into the abstract field of your dataset. When you put full-text in the abstract field, the full-text is used for display and training purposes.

Also see: *Can we use ASReview LAB for things other than Systematic Reviews?*

### 5.3.11 Which classifier should I choose in ASReview LAB?

In ASReview, you need to choose which classifier you want to use to predict relevancy of your documents. Currently, we always advise to use the Naive Bayes classifier since it performs very well and needs little computation time. We have performed several simulation studies to evaluate performance of different classifiers on several datasets. See *Simulation results*. We do not advise specific classifiers for specific jobs because we’ve not found enough evidence (yet) to make such recommendations.

### 5.3.12 I already started labeling before I came across ASReview. How can I keep my former screening decisions when starting a new project in ASReview?

You can keep your former labeling decisions by adding an extra column in your dataset called ‘included’ or ‘label\_included’. In this column, you can indicate previous screening decisions on records with 0s (irrelevant) and 1s (relevant). ASReview will use this information to train the model.

### 5.3.13 Related question: How can I add more publications while I are already started screening in ASReview?

You can export the results of ASReview you have so far and add your new publications to this file. Make sure that for your new publications the column *included* is empty and rename or delete the column of *record\_id*. This latter will save you from running into errors. Then simply import this updated file to ASReview and you can continue the screening process.

### 5.3.14 Is it possible to get the inclusion likelihood for unlabeled papers?

Unfortunately, no. Getting unbiased estimates for inclusion probabilities is a hard problem, especially in combination with active learning. Internally, we have scores that signify which papers are more likely included, but to avoid confusion, we do not put these in the export file. They are however available in the state files.

### 5.3.15 How can I make my previously labeled records green, like in the example datasets?

You can explore a previously labeled dataset in ASReview LAB by adding an extra column called ‘debug\_label’, indicating the relevant and irrelevant records with ones and zeroes.

### 5.3.16 How do I remove duplicate publications?

ASReview LAB works best with deduplicated datasets. One can use software like EndNote to remove duplicates. See the following article for examples:

Bramer, W. M., Giustini, D., de Jonge, G. B., Holland, L., & Bekhuis, T. (2016). De-duplication of database search results for systematic reviews in EndNote. *Journal of the Medical Library Association : JMLA*, 104(3), 240–243. <https://doi.org/10.3163/1536-5050.104.3.014>

Third-party manuals for removing duplicates in Zotero, Mendeley, and RefWorks, can found in the folder **4. Deduplication** by Staaks (2020).

Staaks, J. (2020, October 15). Systematic Review Search Support. <https://doi.org/10.17605/OSF.IO/49T8X>



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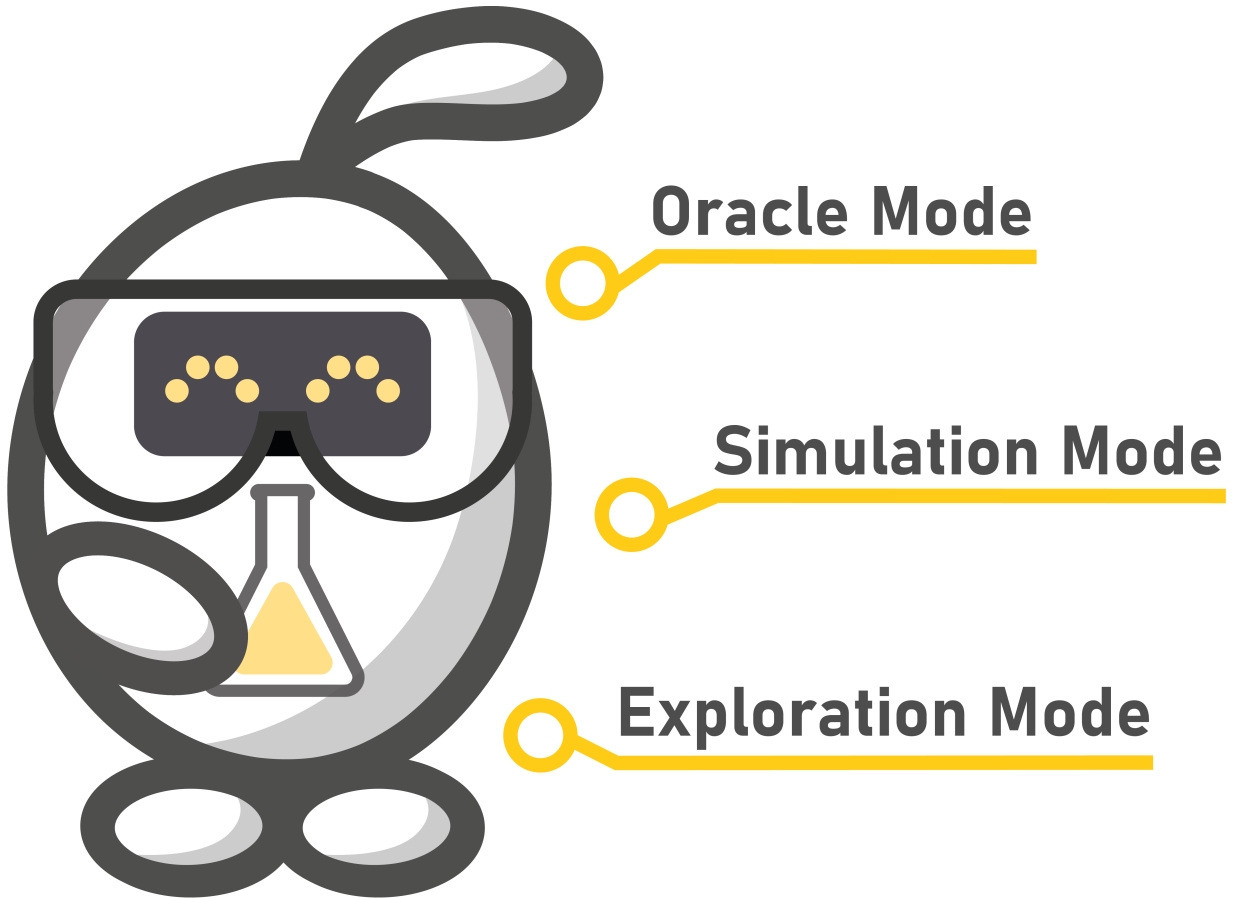
## Overview

---

ASReview LAB is user-friendly software for exploring the future of AI in systematic reviews. The software implements an *Oracle Mode*, an *Exploration Mode*, and a *Simulation Mode*. The oracle mode provides a screening interface that can be used to perform an AI-aided systematic review with the interaction of the reviewer (the oracle). The simulation mode can be used to simulate the performance of ASReview on existing systematic reviews. The exploration mode can be used for exploring a fully labeled dataset in combination with the user-friendly screening interface of the oracle mode. This mode is excellent for teaching purposes.

The source code of ASReview is available open source under an Apache-2.0 license on [GitHub](#). Compiled and packaged versions of the software are available on the [Python Package Index](#) or [Docker Hub](#).

If you encounter any issues during the process, first consult the [Frequently Asked Questions](#) or the Troubleshooting in the [installation manual](#). If you cannot find your problem, we ask you to file an issue via [Github](#).



# ASReview **LAB**

Research software to explore the future of AI in Systematic Reviews

---

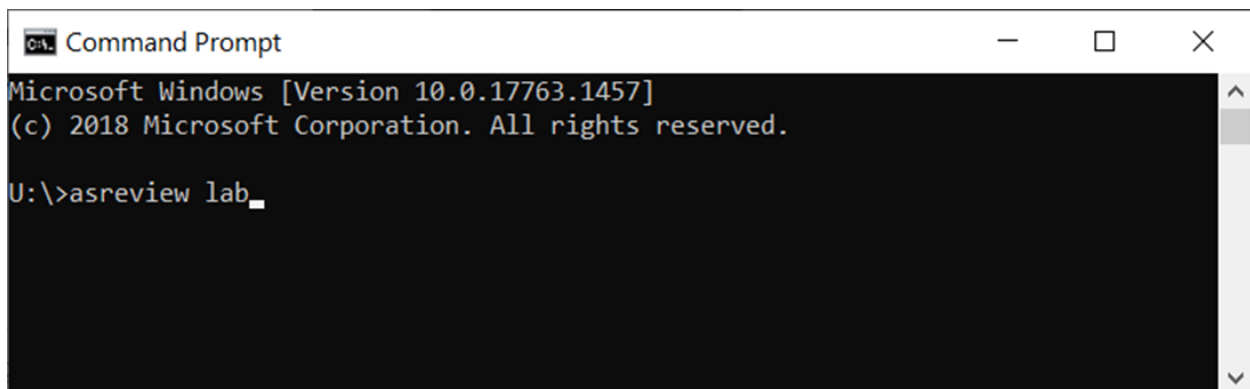
## Start, Open and Import a Project

---

This is a quick tour on launching ASReview and basic project routines like starting, opening and importing a project. It assumes you have ASReview installed. If this is not the case, see the [Installation](#) guide.

### 7.1 Launch ASReview Lab

Launch ASReview LAB by running the following command in the command line (*CMD.exe* for Windows or *Terminal* for MacOS/Linux):

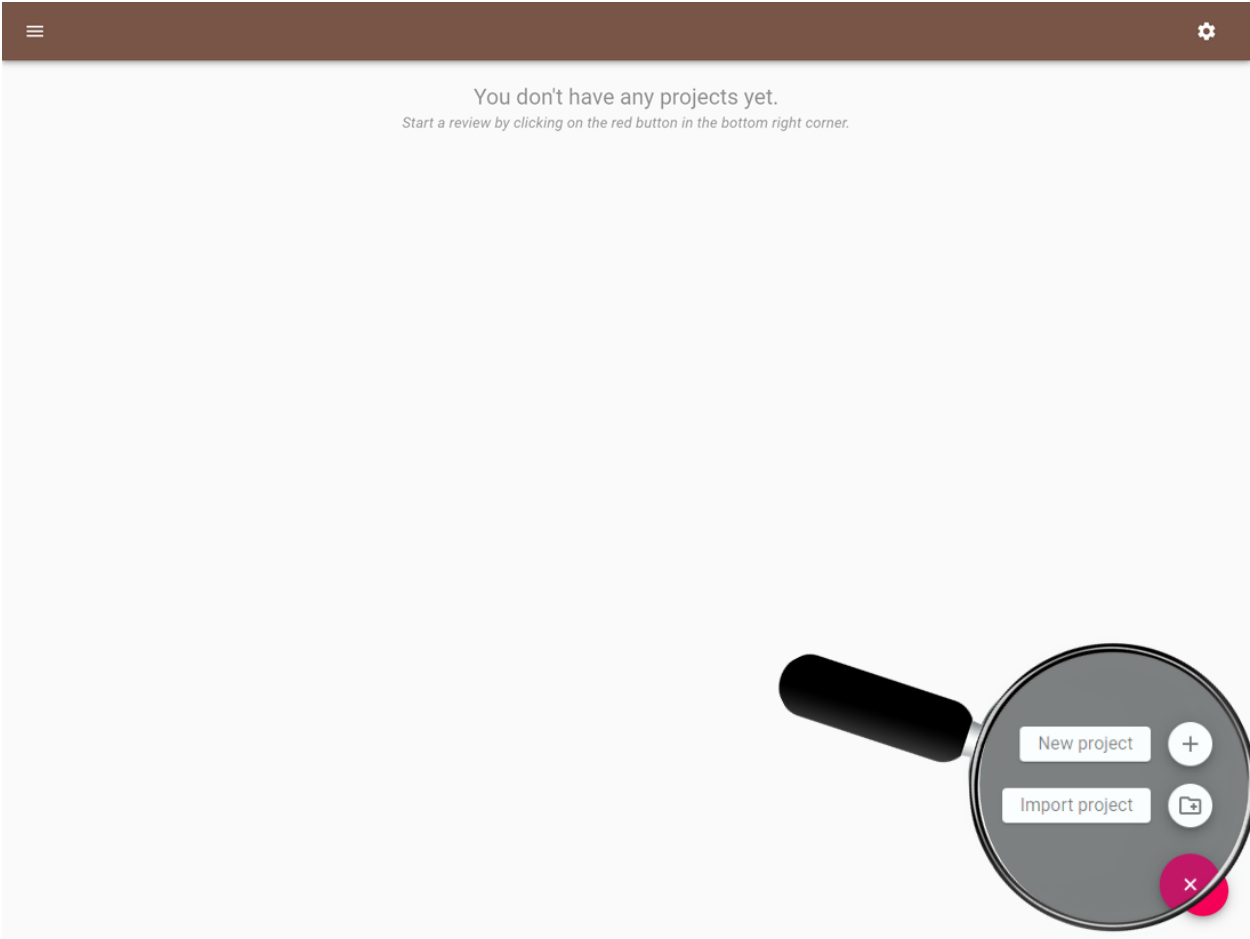


```
Command Prompt
Microsoft Windows [Version 10.0.17763.1457]
(c) 2018 Microsoft Corporation. All rights reserved.

U:\>asreview lab_
```

### 7.2 Create a New Project

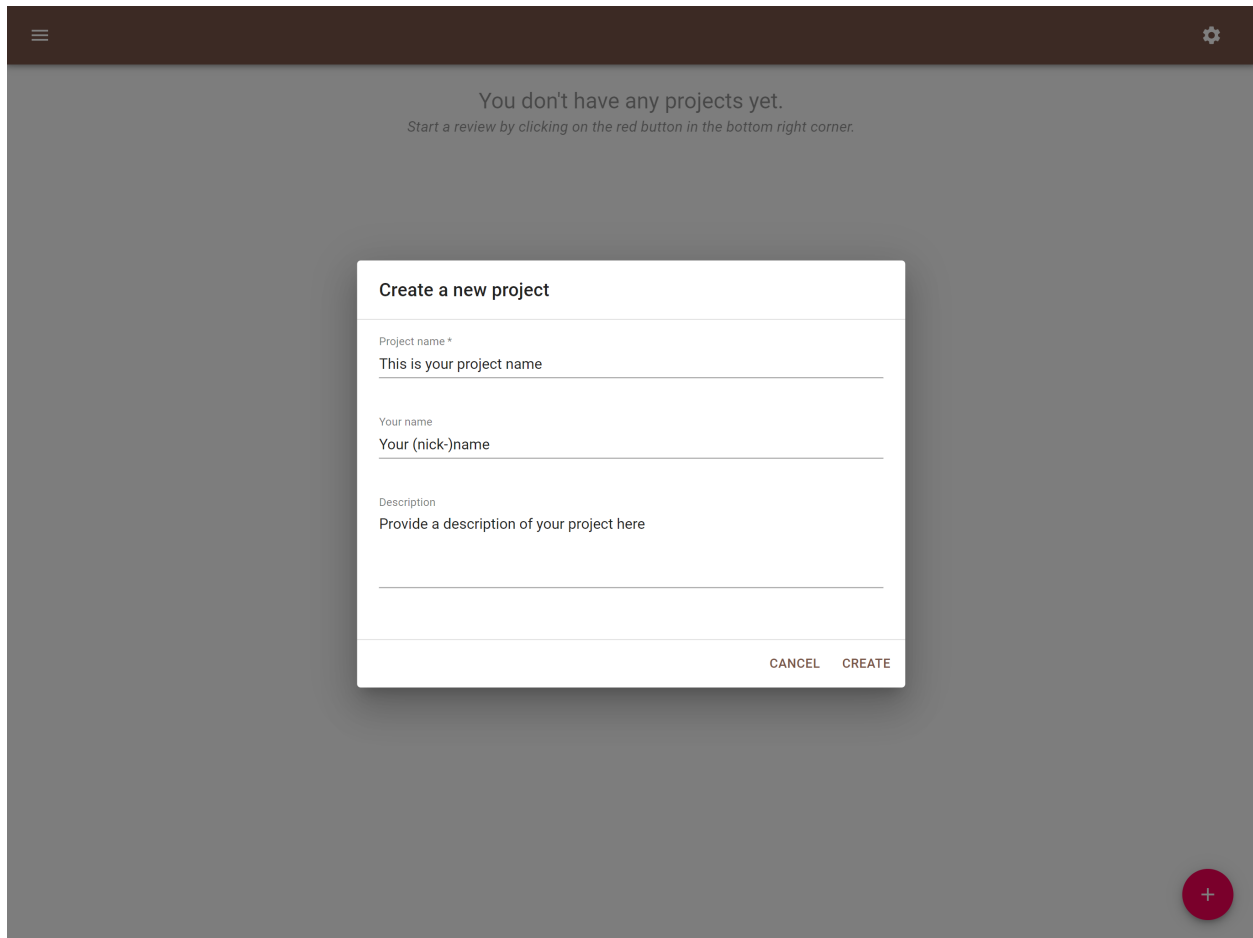
To start reviewing a dataset with ASReview LAB, you first need project to initialize a project. Click on the red button in the bottom right corner, select **new** and a pop-screen will appear.





## 7.3 Provide Project Info

Next, provide a project name (obligatory), your name and a short description on your systematic review project.



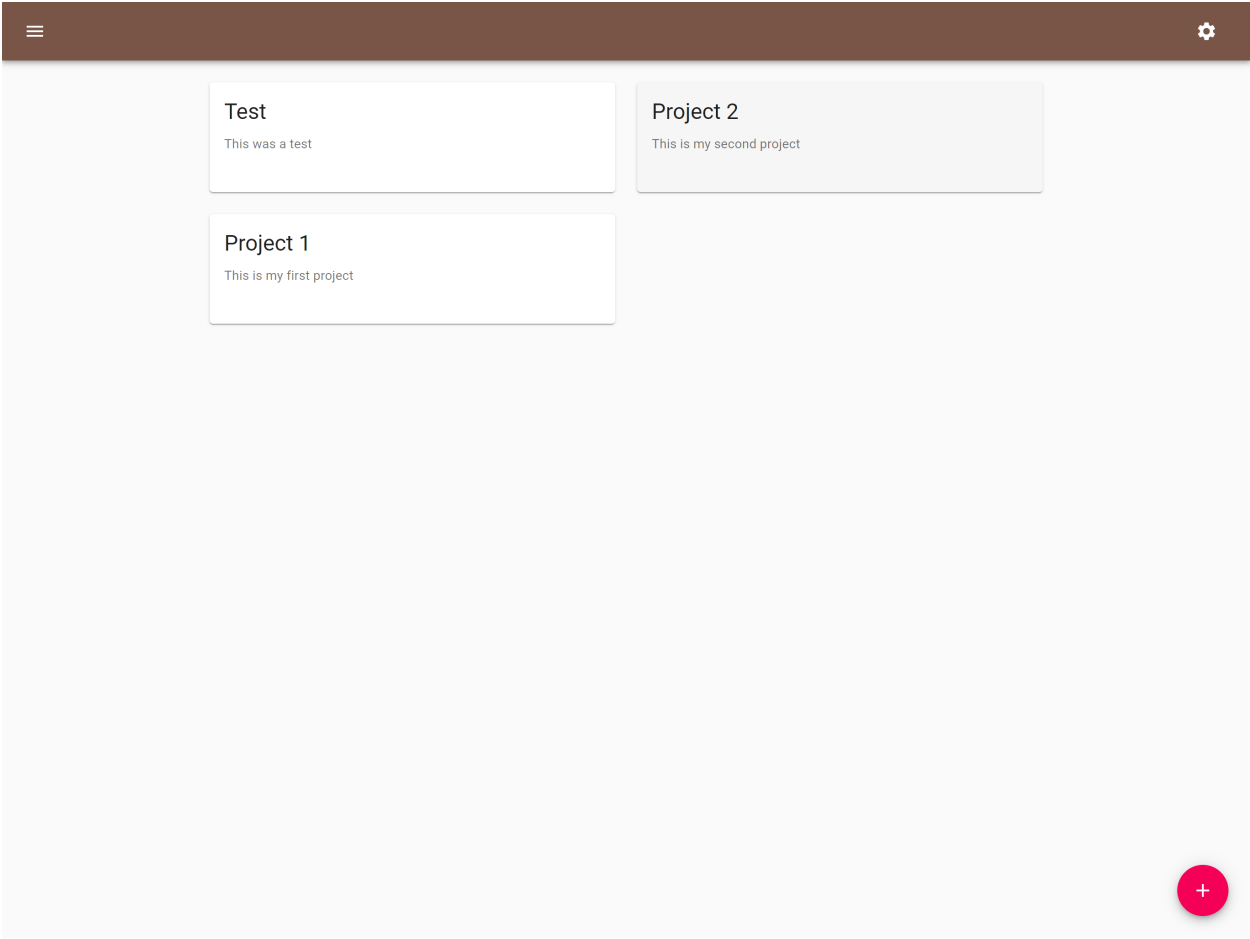
The screenshot displays the ASReview software interface. At the top, a dark header bar contains a menu icon on the left and a settings gear icon on the right. The main content area is a light gray background with a message: "You don't have any projects yet. Start a review by clicking on the red button in the bottom right corner." In the center, a white dialog box titled "Create a new project" is open. It contains three input fields: "Project name \*" with the placeholder "This is your project name", "Your name" with the placeholder "Your (nick-)name", and "Description" with the placeholder "Provide a description of your project here". At the bottom right of the dialog are "CANCEL" and "CREATE" buttons. In the bottom right corner of the main interface, there is a red circular button with a white plus sign.

## 7.4 Open a Project

If you want to continue with an existing project, simply click on the title.

## 7.5 Import a Project


Another option is to import an ASReview project file (.asreview extension). Usually, this is a project exported from ASReview LAB via the *Export Project* panel. Importing can be done by clicking the red button in the bottom right corner of the home page. In the pop-up screen choose the project file from your computer and click *Import*. After a successful project initialization, a project dashboard will be shown.



## 7.6 Project Dashboard

After a successful project initialization, a project dashboard will be shown and you are ready to continue with setting-up the project, like uploading data for the *Oracle Mode* or the *Exploration Mode*. The other options in the project dashboard are described in the *features section*.

☰ Project Dashboard ⚙️



# This is your project name

This is a description of your project

START SETUP

### Statistics

Statistics aren't available yet. Please finish the setup first.

### Publication and export

<b>Download results</b>
Download a file with all decisions. Various download formats are available.
<b>Export this project</b>
Download a complete copy of this project. Ideal to share or import later on.
<b>Mark screening as finished</b>
Stop reviewing and mark the screening process as finished.

### Danger Zone



This is a quick tour in using the ASReview LAB software in Oracle Mode, which is the user-friendly frontend for active learning in systematic reviews for unlabeled data with interaction by the user. A more elaborate instruction can be found in this [blogpost](#) on the ASReview website.

This tutorial assumes you have already installed Python and ASReview. If this is not the case, check out the [Installation](#) page. Also, you should have created a [project](#).

## 8.1 Select Dataset

Select the dataset you want to use, which should contain at least the titles and/or abstracts of all documents (records) you want to screen.

There are four ways to select a dataset:

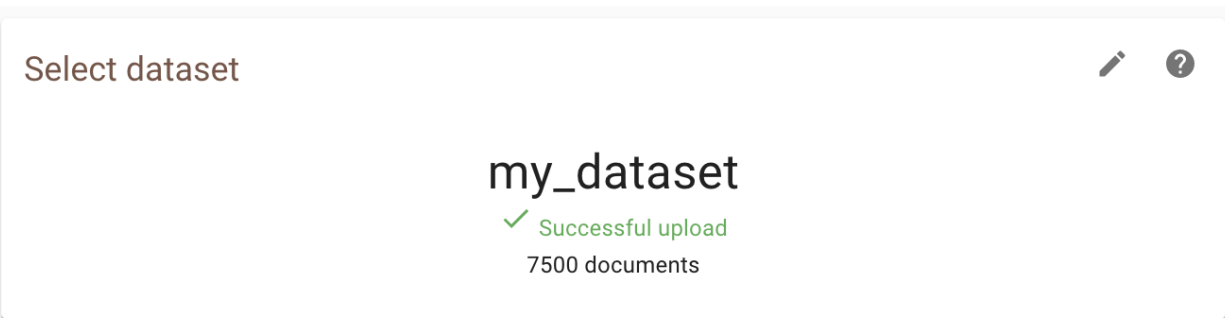
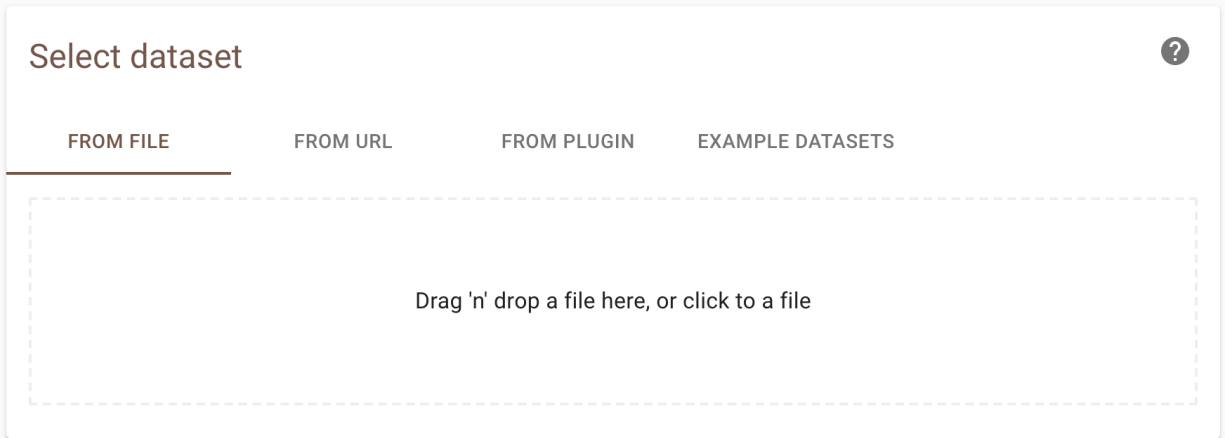
- Upload your own dataset. Read more about the format on [Prepare your Data](#).
- Import a dataset with an URL. Read more about the format on [Prepare your Data](#).
- Select a dataset from an [extension](#) (for example to use the [COVID-19 extension](#)).
- Choose one of the built-in [built-in data sets](#).

After a successful upload of the data, move to the next step.

**Warning:** If you upload your own data, make sure to remove duplicates and to retrieve as many abstracts as possible ([don't know how?](#)). With clean data you benefit most from what [active learning](#) has to offer.

## 8.2 Select Prior Knowledge

The first iteration of the [active learning cycle](#) requires some prior knowledge to work. This knowledge is used to train the first model. In this step you need to provide at least one relevant and one irrelevant document. To facilitate this,



it is possible to *search for specific records* within your dataset (for finding prior relevant papers), ask the software to present a couple of *random documents* (for prior irrelevant papers), or to upload *partly labeled data*.

### 8.3 Select Active Learning Model

In the next step of the setup, you can *select a model*. The default setup (Naïve Bayes, tf-idf, Max) overall has fast and *excellent performance*, but many more options are *davaialble*. After choosing your model, click on *Finish*. You will return to the project page and the model is trained for the first time.

### 8.4 Start Reviewing

As soon as the model is ready, a button appears with **Start Review**. Click the button to start screening. ASReview LAB presents you a document to screen and label. If you have selected certainty-based sampling it will be the document with the highest relevance score.

You are asked to make a decision: relevant or irrelevant?

While you review the documents, the software continuously improves its understanding of your decisions, constantly updating the underlying model.

As you keep reviewing documents and providing more labels, the number of unlabeled docuemtns left in the dataset will decline. When to stop is left to the user and we provide some tips in our [blogpost](#).

Select prior knowledge



3 relevant documents  
5 irrelevant documents

✓ Enough prior knowledge, feel free to go to the next step.

SEARCH

RANDOM

NEXT

Select Active learning model



Classifier: Naïve Bayes

Query strategy: Max

Feature extraction: tf-idf

☰ Review
↓ ⚙

---

## ASReview: Open Source Software for Efficient and Transparent Active Learning for Systematic Reviews

For many tasks - including but not limited to systematic reviews for research fields - the scientific literature needs to be checked systematically. Currently, scholars and practitioners might screen thousands of studies by hand to determine which studies to include in their review. This process is error prone and inefficient, because of the extremely imbalanced data: only a very small fraction of the studies screened will be relevant. The future of systematic reviewing will be an interaction with machine learning algorithms to deal with the enormous increase of available text. We therefore developed an open source machine learning-aided pipeline applying active learning: ASReview. We demonstrate by means of simulation studies that ASReview can yield far more efficient reviewing than manual reviewing, while exhibiting adequate quality. Furthermore, we describe the different options of the free and open source research software, we show how it can be used for screening the COVID19 literature, and we present the results from a series of user experience tests. We invite the community to contribute to open source projects such as our own, that provide measurable and reproducible improvement over current practice.

> Statistics

Project

Project name: AI-software

Authors: Van de Schoot et al.

Number of publications: 5782

---

Progress

Total reviewed: 303 (5.24%)

Since last relevant: 106

✕ Irrelevant
♥ Relevant

## 8.5 Download Results

During the screening or via the *dashboard* you can download the results with your decisions by clicking the download icon. A dialog will show the download options. Choose from the menu whether you would like to download your results as a CSV or an Excel file and click *Download*.

## 8.6 Return to Project Dashboard

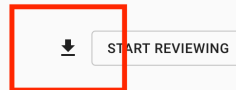
If you want to return to the project dashboard, click the hamburger menu (top left) and click **Project Dashboard**.



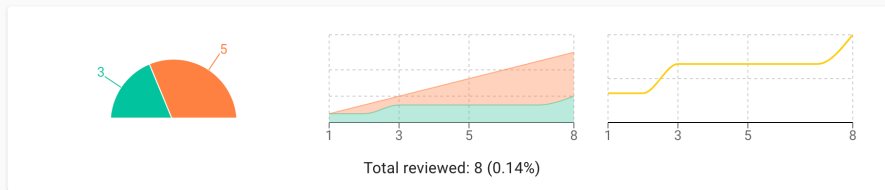


# PTSD-Trajectory Analysis

Bayesian PTSD-Trajectory Analysis with Informed Priors Based on a Systematic Literature Search and Expert Elicitation



## Statistics





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## Exploration Mode

---

This tutorial shows how the active learning software and the performance of *different algorithms* can be explored on already labeled data. In this mode relevant articles are displayed in green and a so-called recall curce can be obtained.

This tutorial assumes you have already installed Python and ASReview. If this is not the case, see *Installation*. Also, you should have created a *project* - the name is not relevant, but is adviced to have a test-prefix.

### 9.1 Upload Data for Exploration Mode

You can explore a previously labeled dataset in ASReview LAB by adding an extra column called ‘debug\_label’ to your dataset. This column should indicate the relevant (1) and irrelevant (0) records. The relevant records will show up green during screening.

1. Open ASReview LAB.
2. Start a new project.
3. Click the *Start Setup* button.
4. Select your labeled dataset containing the ‘debug\_label’.

### 9.2 Upload a Built-in dataset


Select one of the three *test-datasets* available. The datasets available are PTSD, Hall and AceInhibitors:

1. The PTSD data containing the results of a systematic search for longitudinal studies that applied unsupervised machine learning techniques on longitudinal data of self-reported symptoms of posttraumatic stress assessed after trauma exposure (<https://doi.org/10.1080/00273171.2017.1412293>). The total number of papers found was 5,782 of which only 38 were included (0.66%);
2. Results for a systematic review by Hall et al. of studies on fault prediction in software engineering (10.1109/TSE.2011.103 ) with 8,911 papers of which 104 inclusions (1.17%);

- Results for a systematic review on the efficacy of Angiotensin-converting enzyme (ACE) inhibitors, from a study collecting various systematic review datasets from the medical sciences (<https://doi.org/10.1197/jamia.M1929>) with 2,544 papers of which 41 inclusions (1.61%).


### Select dataset ?

FROM FILE
FROM URL
FROM PLUGIN
EXAMPLE DATASETS



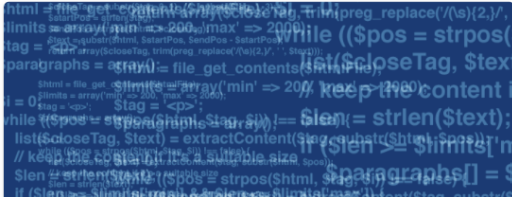
**PTSD - Schoot**

Bayesian PTSD-Trajectory Analysis with Informed ...



**ACEInhibitors - Cohen**

Systematic Drug Class Review Gold Standard Data



**Fault prediction - Hall**

A systematic literature review on fault prediction ...

### 9.3 Prior Inclusions

In the next step, you are asked to add prior inclusions. Select two (or more) papers of your choice and copy-paste the title in the search bar. For the test datasets you can use the following titles of papers:

PTSD:

- Latent trajectories of trauma symptoms and resilience: the 3-year longitudinal prospective USPER study of Danish veterans deployed in Afghanistan
- A Latent Growth Mixture Modeling Approach to PTSD Symptoms in Rape Victims
- Peace and War: Trajectories of Posttraumatic Stress Disorder Symptoms Before, During, and After Military Deployment in Afghanistan

- The relationship between course of PTSD symptoms in deployed U.S. Marines and degree of combat exposure
- Trajectories of trauma symptoms and resilience in deployed US military service members: Prospective cohort study

Hall:

- Predicting Defect-Prone Software Modules at Different Logical Levels
- Quantitative analysis of faults and failures in a complex software system
- A Comprehensive Empirical Study of Count Models for Software Fault Prediction
- Predicting fault prone modules by the Dempster-Shafer belief networks
- Robust prediction of fault-proneness by random forests

ACE:

- Quinapril in patients with congestive heart failure: controlled trial versus captopril.
- Clinical effects of early angiotensin-converting enzyme inhibitor treatment for acute myocardial infarction are similar in the presence and absence of aspirin: systematic overview of individual data from 96,712 randomized patients. Angiotensin-converting Enzyme Inhibitor Myocardial Infarction Collaborative Group.
- Efficacy of different drug classes used to initiate antihypertensive treatment in black subjects: results of a randomized trial in Johannesburg, South Africa.
- Long-term mortality in patients with myocardial infarction: impact of early treatment with captopril for 4 weeks.
- Comparison of perindopril versus captopril for treatment of acute myocardial infarction.

## 9.4 Prior Exclusions

Mark five papers as irrelevant.

## 9.5 START reviewing

Start reviewing the first 50, 100 or even 200 papers. Abstracts in green are relevant papers and abstracts in black are irrelevant. This is based on a fully labeled dataset.

For the **PTSD** dataset we expect you to find about 7 out of 38 relevant papers (in red) after screening 50 papers, 19 after screening 100 papers and 36 after 200 papers.

For the **Hall** dataset we expect you to find 25 out of 104 relevant papers (in red) after screening 50 papers, 48 after screening 100 papers and 88 after 200 papers.

For the **ACE** dataset we expect you to find 16 out of 41 relevant papers (in red) after screening 50 papers, 27 after screening 100 papers and 32 after 200 papers.

## 9.6 Results

For all three datasets, the animated plots below show how fast you can find the relevant papers by using ASReview LAB compared to random screening papers one by one. These animated plots are all based on a single trial per dataset in which only one paper was added as relevant and one as irrelevant.

PTSD:

38 inclusions out of 5,782 papers

Hall:

104 inclusions out of 8,911 papers)

ACE:

41 inclusions out of 2,544 papers

# CHAPTER 10

---

## Simulation Mode

---

At the moment, the ASReview simulation mode is only available in the command line interface. When using the *ASReview command line interface for simulation*, a fully labeled dataset is required (labeling decisions: 0 = irrelevant, 1 = relevant).

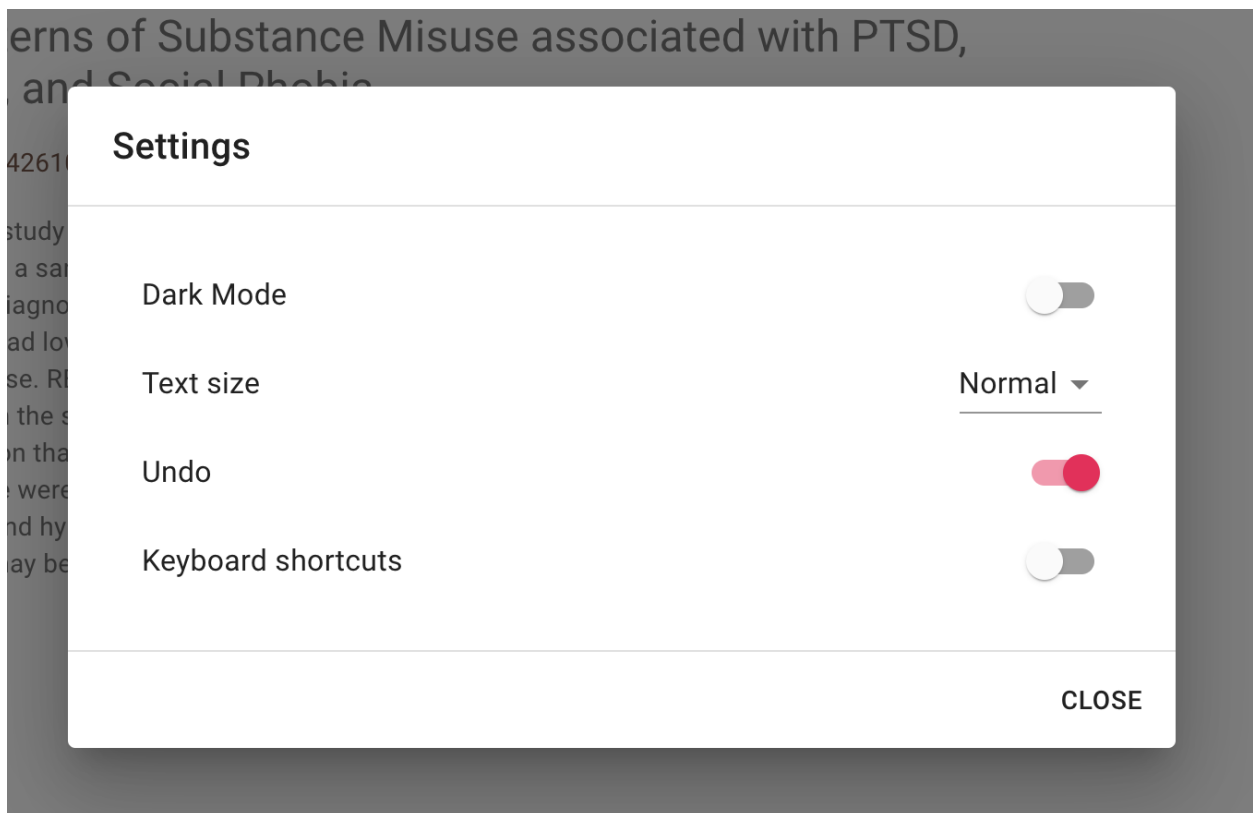
See the following resources for information on running a simulation:

- *ASReview command line interface for simulation*
- *Simulation results*
- *Simulation*

**Warning:** If you upload your own data, make sure to remove duplicates and to retrieve as many abstracts as possible (don't know how?). With clean data you benefit most from what *active learning* has to offer.



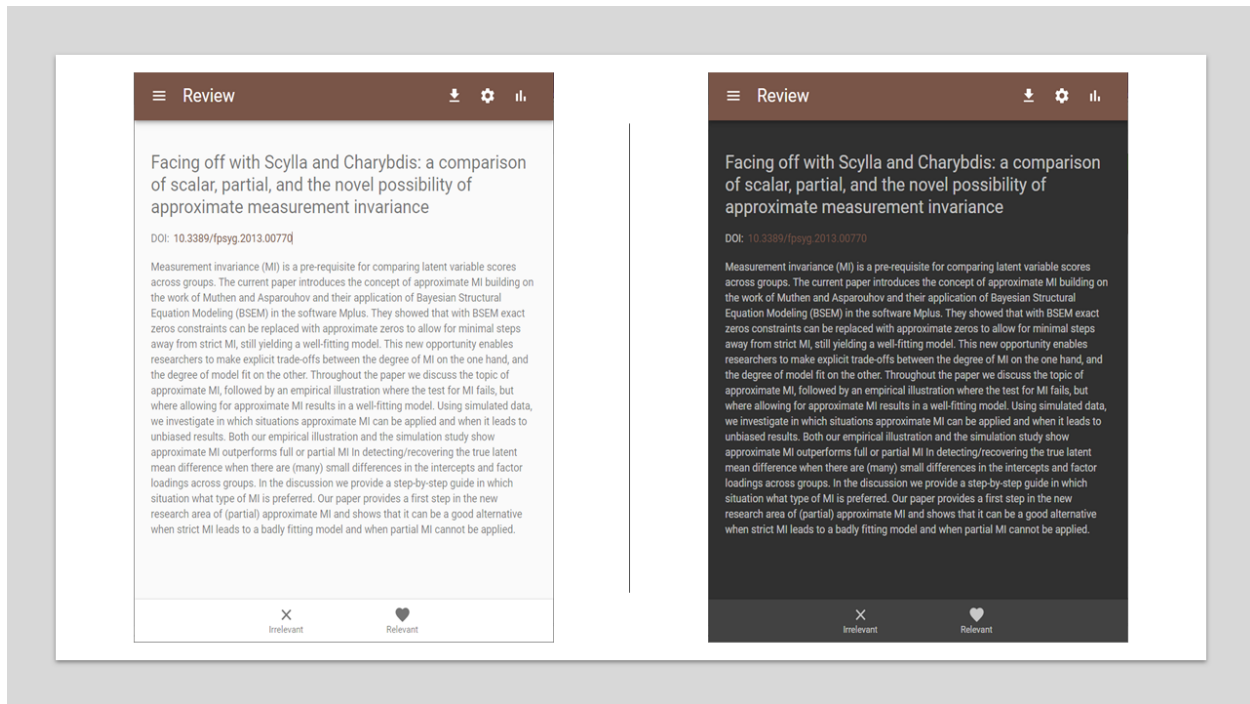




## 11.1 Dark Mode

ASReview LAB supports dark mode. By default, the dark mode is disabled. Enable the dark mode as follows:

1. Open ASReview LAB.
2. Click on the settings icon (top right).
3. Toggle the **Dark Mode** field.



---

**Note:** Your preference is saved in the browser.

---

## 11.2 Text Size

ASReview LAB supports different text sizes. By default, the text size is set to normal. Change the text size as follows:

1. Open ASReview LAB.
2. Click on the settings icon (top right).
3. Select the size in the **Text Size** field.

Resulting in:

---

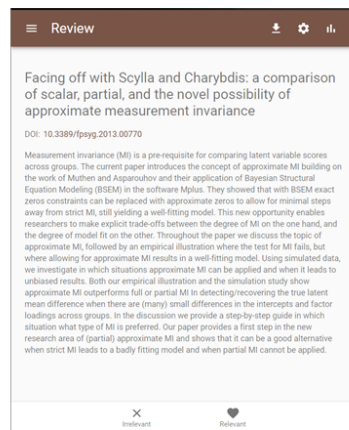
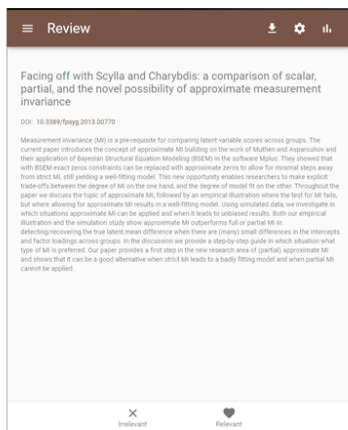
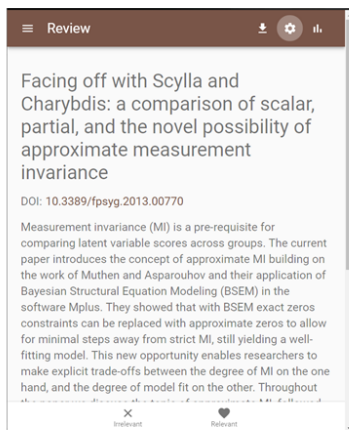
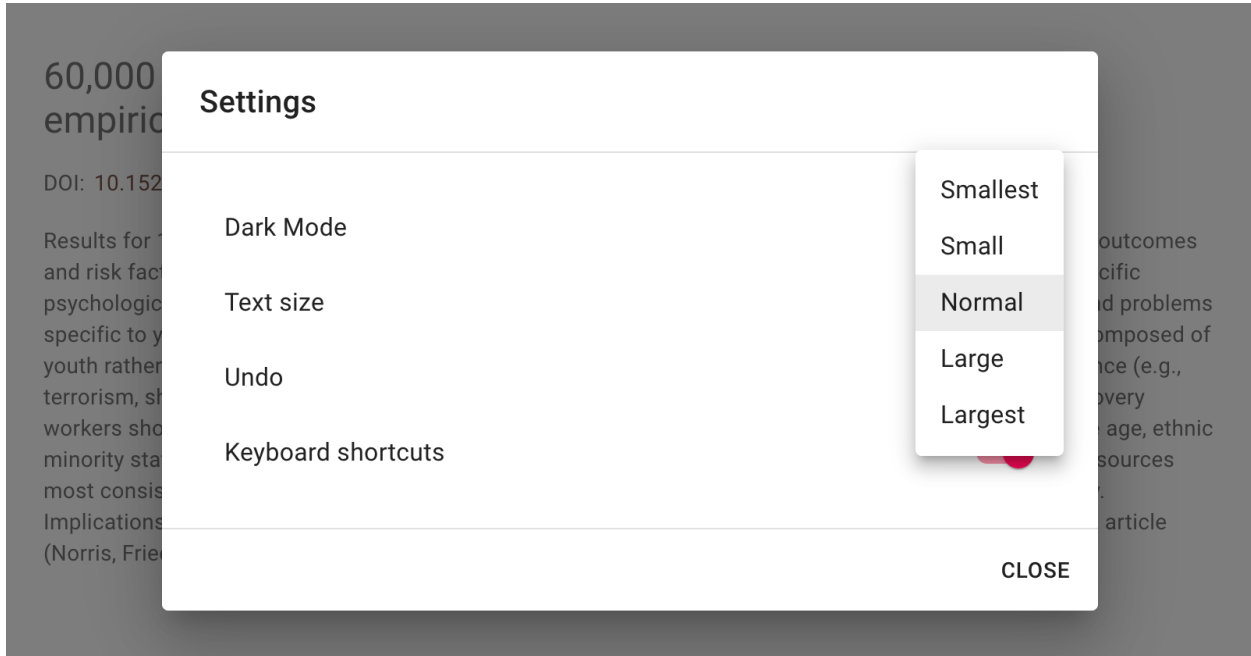
**Note:** Your preference is saved in the browser.

---

## 11.3 Toggle Undo option

It is possible to enable or disable the *undo option* in the settings menu:

1. Open ASReview LAB.



2. Click on the settings icon (top right).
3. Uncheck the **Undo** field.

### 11.4 Toggle Shortcuts

ASReview LAB supports the use of *keyboard shortcuts* during screening. By default, keyboard shortcuts are disabled. Enable the shortcuts as follows:

1. Open ASReview LAB.
2. Click on the settings icon (top right).
3. Check the **keyboard settings** field.

Before you can actually start screening you have to initialize a project, select a dataset, prior knowledge and a model.

### 12.1 Start Setup

After you have started a project, you are redirected to the project dashboard and you will first be asked to initialize the setup.

1. Open ASReview LAB.
2. Start a new project.
3. Click the *Start Setup* button.

Already in this project dashboard some of the features are available which are described in the *Post-Screening* section.

### 12.2 Select Dataset

To select a dataset:

1. Open ASReview LAB.
2. Start a new project.
3. Click the *Start Setup* button.
4. Choose one of the four options to select a dataset and click upload:

**Warning:** If you upload your own data, make sure to remove duplicates and to retrieve as many abstracts as possible (don't know how?). With clean data you benefit most from what *active learning* has to offer.



# PTSD-Trajectory Analysis

Bayesian PTSD-Trajectory Analysis with Informed Priors Based on a Systematic Literature Search and Expert Elicitation

START SETUP

## Statistics

Statistics aren't available yet. Please finish the setup first.

Publication and export

## Select dataset



FROM FILE

FROM URL

FROM PLUGIN

EXAMPLE DATASETS

Drag 'n' drop a file here, or click to a file

### 12.2.1 From File

Upload your file by *Drag 'n' Drop*, or select your file via the browser. The data needs to adhere to a *specific format*. If a file is uploaded and recognized as one of the available formats, it will display the message *Successful upload* and provides the number of records in the dataset.

### 12.2.2 From URL

Fill in a link to a file on the Internet. For example, a link from this [dataset repository](#).

### 12.2.3 From Plugin

Select a file available via a plug-in like the *COVID-19 plugin*.

### 12.2.4 Example Datasets

Select one of the *example datasets*.

## 12.3 Partly Labeled Data

If you want to include decisions you've already made prior to setting up your project, you can upload a partly labeled dataset containing labels for part of the data and unlabeled records you want to screen with ASReview. This might be very helpful if you switch from screening in another tool to screening with ASReview, or when updating an existing systematic review with more recent publications.

Currently, this can be done by merging your dataset with labeled and unlabeled records via Excel or another reference manager. Your dataset should contain a column, called *label\_included* (or: *final\_included*, *label*, *label\_included*, *included\_label*, *included\_final*, *included*, *included\_flag*, *include*) which is filled with 1's or 0's for the publications that you have already screened, and is empty for the records that you still need to screen using ASReview.

To use a partly labeled dataset:

1. Open ASReview LAB.
2. Start a new project.
3. Click the *Start Setup* button.
4. Select your partly labeled dataset.

ASReview will recognize the column with the labels and show you the number of prior relevant/irrelevant papers in the section *Prior Knowledge*.

## 12.4 Select Prior Knowledge

The first iteration of the *active learning cycle* requires prior knowledge to work. This knowledge is used to train the first model. In this step you need to provide at least one relevant and one irrelevant document. To facilitate this, it is possible to search within your dataset (for finding prior relevant papers) or ask the software to present a couple of random documents (for prior irrelevant papers).

1. Open ASReview LAB.

2. Start a new project.
3. Click the *Start Setup* button.
4. Select a dataset.
5. Click **Search** or **Random** to select your prior knowledge.

Select prior knowledge ?

0 relevant documents  
0 irrelevant documents

You don't have prior knowledge yet. Find yourself prior knowledge by searching relevant documents and label some random documents.

After selecting some prior information, you can click **Next**.

Select prior knowledge ✎ ?

3 relevant documents  
5 irrelevant documents

✓ Enough prior knowledge, feel free to go to the next step.

### 12.4.1 Search

Let's start with finding a prior relevant document. Probably the most efficient way to do this is by searching for a specific document you already know is relevant. Click the search button and search your dataset by authors, keywords or title, or a combination thereof. Enter your search terms (Use 'enter' to start searching).

Click the document you had in mind and click Relevant (Clicking Irrelevant results in an irrelevant document).

The Prior Knowledge step will now show 1 relevant document. This is already enough to proceed to the next step. Note that there are no restrictions on the number of publications you need to provide, but preferably provide 1-5 relevant documents.



## Select prior knowledge



1 relevant documents  
1 irrelevant documents

✓ Enough prior knowledge, however a bit more would help!

SEARCH

RANDOM

Search for a document of interest.

latent growth PTSD



Search result: latent growth PTSD

Latent Growth Mixture Models to estimate PTSD trajectories  
Van de Schoot, R.

Using Bayesian statistics for modeling PTSD through Latent Growth Mixture Modeling: implementation and discussion  
Depaoli, S., van de Schoot, R., van Loey, N., Sijbrandij, M.

A Latent Growth Mixture Modeling Approach to PTSD Symptoms in Rape Victims  
Armour, C., Shevlin, M., Elklit, A., Mroczek, D.

Heterogeneity in signaled active avoidance learning: Substantive and methodological relevance of diversity in instrumental defensive responses to threat cues  
Galatzer-Levy, I. R., Moscarello, J., Blessing, E. M., Klein, J., Cain, C. K., LeDoux, J. E.

636,120 Ways to Have Posttraumatic Stress Disorder  
Galatzer-Levy, I. R., Bryant, R. A.

Exploring the association between posttraumatic growth and PTSD: National Study of Jews and Arabs following the 2006 Israeli-Hezbollah War  
Hall, Brian J., Hobfoll, Stevan E., Canetti, Daphna, Johnson, Robert J., Palmieri, Patrick A., Galea, Sandro

Prior trauma and PTSD among homeless mothers: Effects on subsequent stress appraisals, coping, posttraumatic growth, and health outcomes  
Schuster, Jennifer Lynn

The course of PTSD symptoms among Gulf War veterans: A growth mixture modeling approach  
Orcutt, H. K., Erickson, D. J., Wolfe, J.

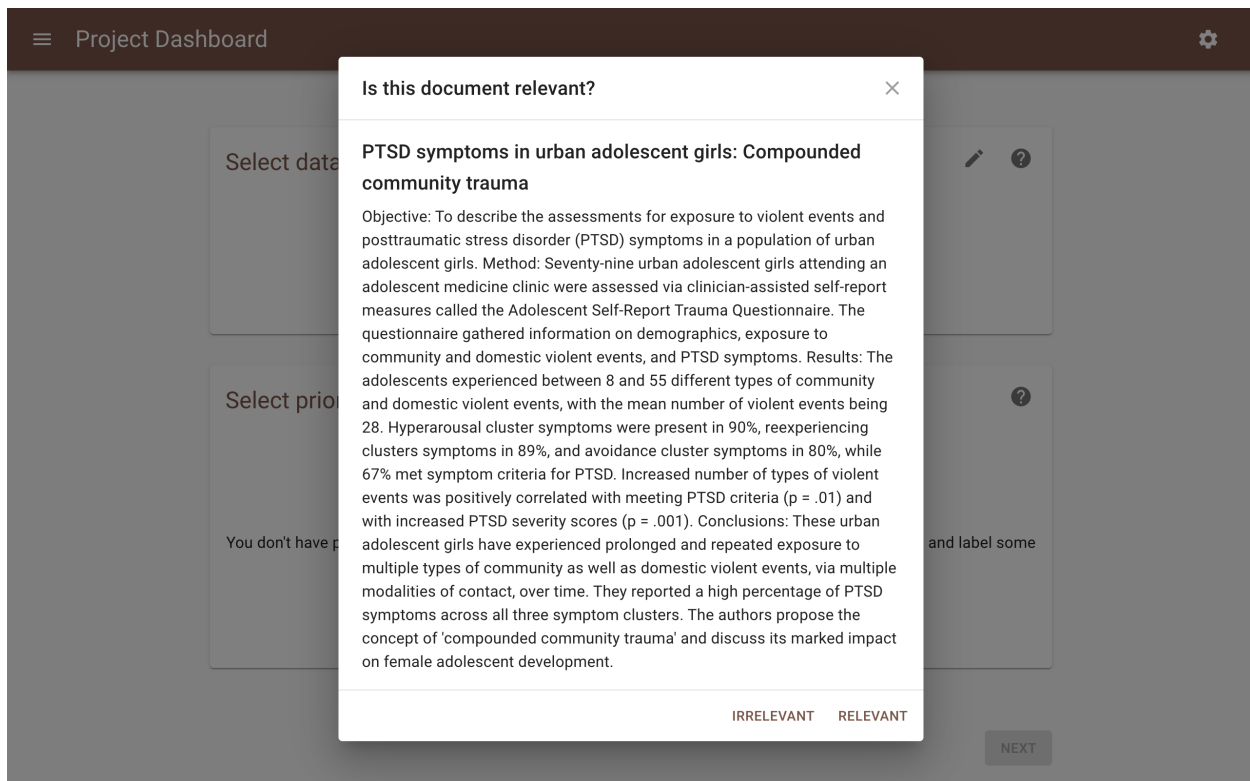
Posttraumatic stress after a motor vehicle accident: a six-month follow-up study utilizing latent growth modeling  
Wu, K. K., Cheung, M. W.

Heterogeneity in threat extinction learning: substantive and methodological considerations for identifying individual difference in response to stress  
Galatzer-Levy, I. R., Bonanno, G. A., Bush, D. E., Ledoux, J. E.

If you are done click **Next**.

### 12.4.2 Random

You also need to provide at least one prior irrelevant document and we will use the random option. Given that the majority of documents in the dataset is probably irrelevant (extreme imbalanced data problem), the documents presented here will most probable be irrelevant for your study. Click on random to and a couple of random documents will be shown. Indicate for each document whether it is relevant or irrelevant.



After labeling a couple of randomly selected documents, ASReview LAB will ask you whether you want to stop. Click on **STOP** and click **Next**.

## 12.5 Select Model

It is possible to change the settings of the Active learning model. There are three ingredients that can be changed in the software: the type of classifier, the query strategy and the feature extraction technique.

To change the default setting:

1. Open ASReview LAB.
2. Start a new project, upload a dataset and select prior knowledge.
3. Click on the **edit** icon (top right).
4. Using the drop-down menu select a different classifier, query strategy or feature extraction technique.
5. Click Finish.

## Select Active learning model



Classifier: Naïve Bayes  
Query strategy: Max  
Feature extraction: tf-idf

The classifier is the machine learning model used to compute the relevance scores. The available classifiers are Naive Bayes, Support Vector Machine, Logistic Regression, and Random Forest. More classifiers can be selected via the [API](#). The default is Naive Bayes, though relatively simplistic, it seems to work quite well on a wide range of datasets.

The query strategy determines which document is shown after the model has computed the relevance scores. With certainty-based is selected the document with the highest relevance score is showed followed by the 2nd in line, etcetera, untill a new model is trained with new relevance scores. When uncertainty-based is selected, the most uncertain docuemtn is sampled according to the model (i.e. closest to 0.5 probability). When random is selected, as it says, randomly select samples with no regard to model assigned probabilities. **Warning:** selecting this option means your review is not going to be accelerated by ASReview.

The feature extraction technique determines the method how text is translated into a vector that can be used by the classifier. The default is TF-IDF (Term Frequency-Inverse Document Frequency) from [SKLearn](#). It works well in combination with Naive Bayes and other fast training models. Another option is Doc2Vec provided by the [gensim](#) package which needs to be installed manually. To use it, install the gensim package manually:

```
pip install gensim
```

It takes relatively long to create a feature matrix with this method. However, this only has to be done once per simulation/review. The upside of this method is the dimension-reduction that generally takes place, which makes the modelling quicker.



The screen in which you provide labels for records shown to you by the software is kept as simple as possible. This is because we want you to focus on the content of the text so that you can make your decision as a true Oracle. There are few features you can access during screening which we present below.

### 13.1 Autosave

Your work is saved automatically. There is no need to press any buttons to save your work anywhere in ASReview LAB.

### 13.2 Label options

Below the text, ASReview provides two labeling options: *Relevant* or *Irrelevant*.

To make a decision:

1. Open ASReview LAB.
2. Open a project.
3. Click on either the button Relevant or Irrelevant.
4. The next record is presented. Repeat the process of labeling.

**Warning:** If you are in doubt, think harder and take your time to make a decision, you are the oracle. Based on your input, a new model will be trained in the background. If you make decisions faster than the model needs for computing new relevance scores, you will simply be presented with the record next in line (etcetera) until the model is done training.



☰ Review
↓ ⚙

## ASReview: Open Source Software for Efficient and Transparent Active Learning for Systematic Reviews

For many tasks - including but not limited to systematic reviews for research fields - the scientific literature needs to be checked systematically. Currently, scholars and practitioners might screen thousands of studies by hand to determine which studies to include in their review. This process is error prone and inefficient, because of the extremely imbalanced data: only a very small fraction of the studies screened will be relevant. The future of systematic reviewing will be an interaction with machine learning algorithms to deal with the enormous increase of available text. We therefore developed an open source machine learning-aided pipeline applying active learning: ASReview. We demonstrate by means of simulation studies that ASReview can yield far more efficient reviewing than manual reviewing, while exhibiting adequate quality. Furthermore, we describe the different options of the free and open source research software, we show how it can be used for screening the COVID19 literature, and we present the results from a series of user experience tests. We invite the community to contribute to open source projects such as our own, that provide measurable and reproducible improvement over current practice.

> Statistics

Project

Project name: AI-software

Authors: Van de Schoot et al.

Number of publications: 5782

Progress

Total reviewed: 303 (5.24%)

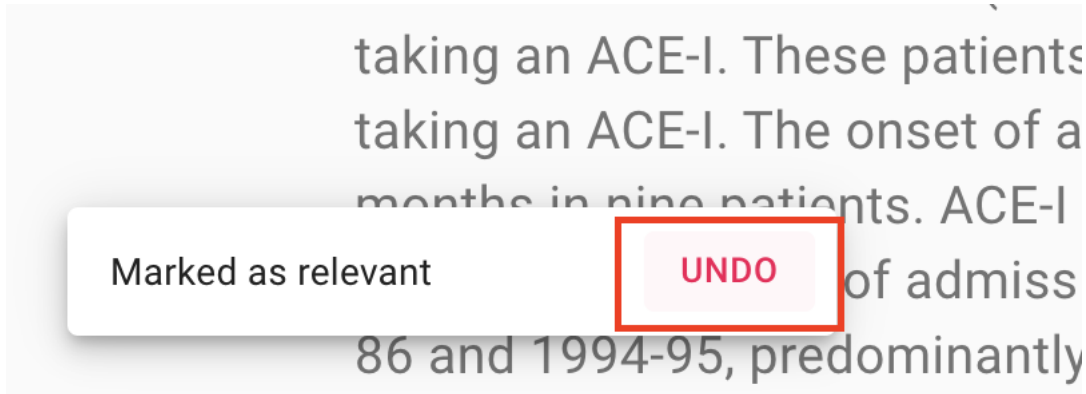
Since last relevant: 106

✕ Irrelevant
♥ Relevant

## 13.3 Undo Last Decision

In some cases, you might want to change your previous decision. The screening interface of ASReview LAB can be used to return to the previous decision.

1. Open ASReview LAB.
2. Open or create a project.
3. Label the record displayed in the screen as relevant or irrelevant.
4. Click on **Undo** (See picture below).



5. Click on **Keep (ir)relevant** or **Convert to (ir)relevant**
6. Continue labeling.

## 13.4 Statistics Panel

For unlabeled data, ASReview LAB offers some insightful graphs to keep track of your screening process so far. To open the statistics panel:

1. Open ASReview LAB.
2. Open a project.
3. Start screening.
4. Click the **statistics** icon in the upper-right corner.
5. To close the panel click on the '>' icon.

In the top of the statistics panel the project name, authors and total number of records in the dataset are displayed.

The pie chart on the presents an overview of how many relevant (green) and irrelevant (orange) records have been screened so far. Also, the total number of records screened is displayed, as well as the percentage screened relative to the total number of records in the dataset.

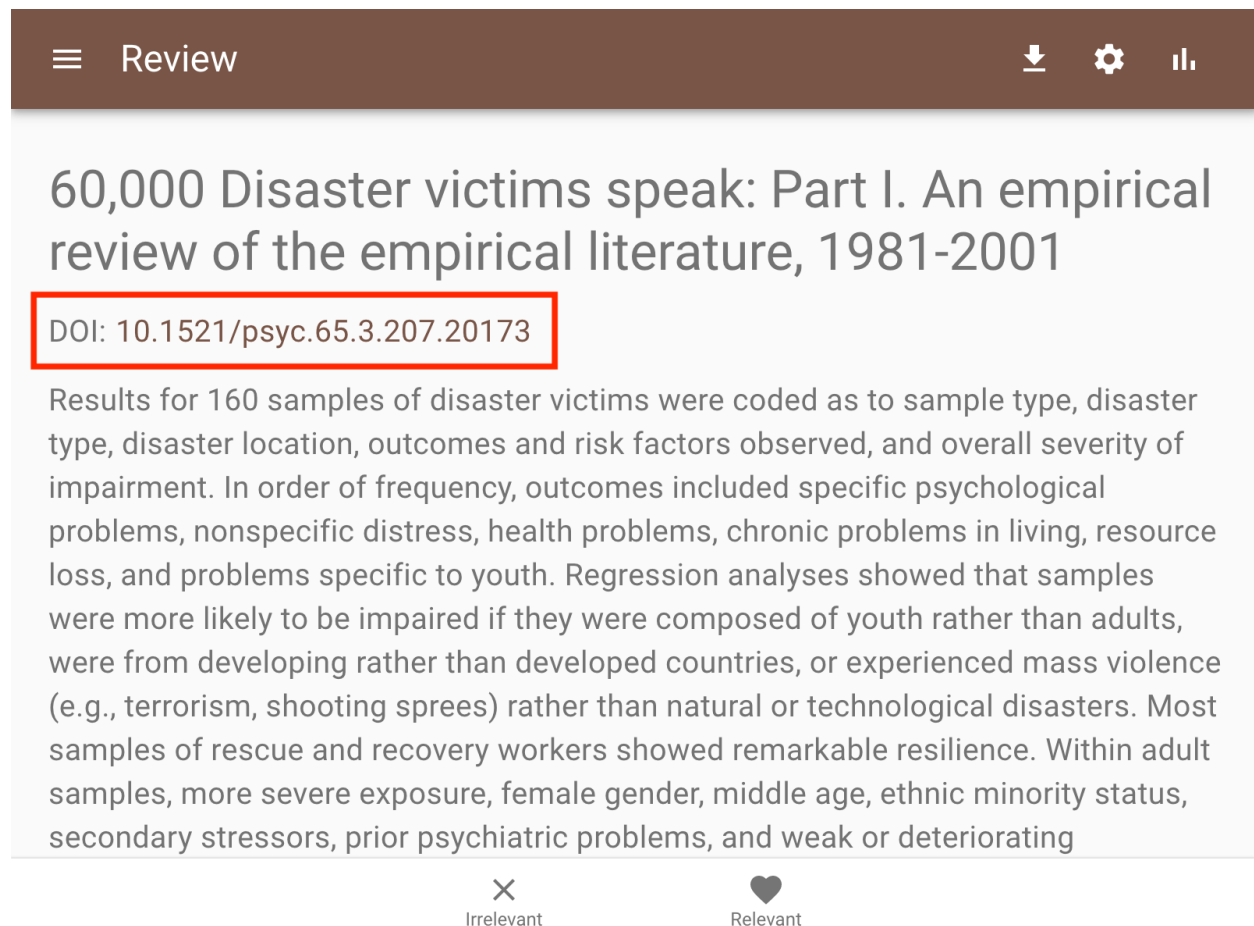
The second plot is a progress plot. On the x-axis the number of records screened is tracked. The y-axis shows a moving average. It displays the ratio between relevant and irrelevant records for a batch of 10 labeled records. If you hover over the plot you can see the moving average for any batch of 10 labeled records.

Underneath the progress plot, the number of irrelevant records after the last relevant is shown. This statistic might help in deciding when to stop reviewing.

## 13.5 DOI

If a column with Digital Object Identifiers (DOI) is available in the metadata of your dataset, ASReview Lab will display the DOI with hyperlink during screening. Most of the time, DOIs point to the full-text of a publication. See *datasets* for more information on including DOI values to your datasets. To access the full text:

1. Open ASReview LAB.
2. Open a project
3. Start screening.
4. As soon as a record contains a DOI number, it will be presented below the title.



The screenshot shows the ASReview Lab interface. At the top, there is a dark brown header bar with a hamburger menu icon on the left, the word "Review" in the center, and three icons (download, settings, and list) on the right. Below the header, the main content area displays the title "60,000 Disaster victims speak: Part I. An empirical review of the empirical literature, 1981-2001". Below the title, the DOI "10.1521/psyc.65.3.207.20173" is highlighted with a red rectangular box. Below the DOI, there is a paragraph of text describing the results of 160 samples of disaster victims. At the bottom of the interface, there are two buttons: "Irrelevant" with a red 'X' icon and "Relevant" with a red heart icon.

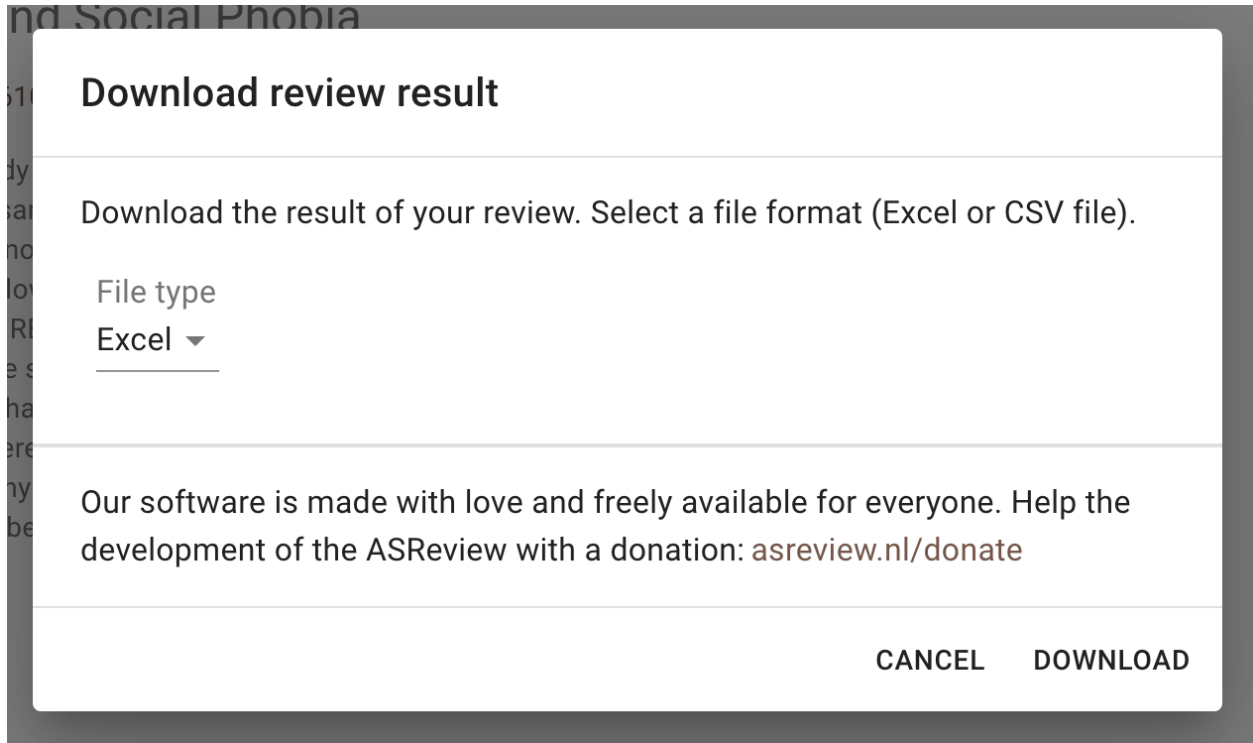
## 13.6 Download Results

A file containing all metadata including your decisions can be downloaded any time during the screening process. To download your results:

1. Open ASReview LAB.
2. Open a project.
3. Start screening.



4. Click the **download** icon in the upper-right corner.
5. You will be asked whether you want to save an Excel or a CSV file.
6. You will be asked where to save the file.



## 13.7 Hamburger menu

Via the hamburger menu in the left-upper corner you can:

1. Navigate back to the [overview](#) page containing all your projects (or to start a new project).
2. You can access the [Project Dashboard](#).
3. Navigate to the documentation via the [HELP](#) button.
4. Provide feedback or [contribute](#) to the code.
5. Donate some money via our [crowdfunding platform](#)
6. Quit the software (your progress was saved automatically)

## 13.8 Keyboard shortcuts

ASReview LAB supports the use of keyboard shortcuts during screening. The table below lists the available keyboard shortcuts.

Action	Shortcut
Label record as relevant	<b>r</b> or <b>Shift + r</b>
Label record as irrelevant	<b>i</b> or <b>Shift + i</b>
Return to previous decision	<b>u</b> or <b>Shift + u</b>

After you stop screening, or anytime you want to take a break, you can return to the project dashboard by clicking the hamburger menu on the top-left. Below we will explain the options in the project dashboard.

### 14.1 Download Results

A file containing all meta-data including your decisions can be downloaded any time during the screening process. To download your results:

1. Open ASReview LAB.
2. Start a new project, upload a dataset and select prior knowledge.
3. Navigate to the Project Dashboard.
4. Click the *download* icon (see screenshot below), or click on *Download Results*.
5. You will be asked whether you want to save an excel or a csv file.
6. You will be asked where to save the file.


Three columns will be added to your dataset:

The column titled **included** contains the labels as provided by the user: 0 = not relevant, 1 = relevant and if missing it means the record is not seen during the screening process. First, all relevant records are presented in the order these shown during the screening process. Then, all records not seen during the screening proces are presented ordered from most to least relevant according to the last iteration of the model. At end of the file all non-relevant records are presented in the order these are shown during the screening proces.

The column titled **asreview\_ranking** contains an identifier to preserve the rank ordering as described above.

If present, the column **record\_id** contains the values of the original **record\_id** as included by the user. If not available, ASReview generates a new **record\_id**, based on the row number and starting at 0.

☰ Project Dashboard⚙️




# PTSD-Trajectory Analysis

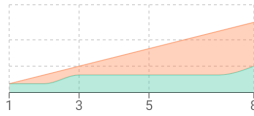
Bayesian PTSD-Trajectory Analysis with Informed Priors Based  
on a Systematic Literature Search and Expert Elicitation

↓START REVIEWING

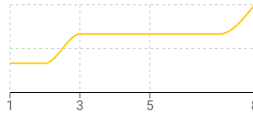
Statistics



3 5



1 3 5 8



1 3 5 8

Total reviewed: 8 (0.14%)

## 14.2 Export Project

An ASReview project file can be downloaded containing all information needed to replicate the project or to import the project on a different device. To export your project:

1. Open ASReview LAB.
2. Start a new project, upload a dataset and select prior knowledge.
3. Navigate to the Project Dashboard.
4. Click on *Export this project*.
5. You will be asked where to save the ASReview file (extension *.asreview*).

## 14.3 Finished

When you are done with the review, you can mark the project as finished. To mark your project as finished:

1. Open ASReview LAB.
2. Open a project.
3. Click on *Mark Screening as finished*.

The button to continue screening is now disabled. This can be undone by clicking again on *Mark Screening as finished (undo)*.

## 14.4 Delete a Project

To permanently delete a project, including ALL files:

1. Open ASReview LAB.
2. Start a new project, upload a dataset and select prior knowledge.
3. Navigate to the Project Dashboard.
4. Click on *Delete this project*.
5. This action cannot be made undone, ASReview LAB will ask you to confirm by typing in the project title.



ASReview has support for extensions. Extensions are a nice way to extend the functionality of the *ASReview LAB* software or the *command line interface*. See the following officially supported extensions of ASReview:

- *ASReview against COVID-19*: Make literature on COVID-19 available in ASReview.
- *ASReview-visualization*: Plotting functionality for state files produced by ASReview.
- `asreview-statistics`: Tool to give some basic properties of a dataset, such as number of papers, number of inclusions. [GitHub](#)
- `asreview-hyperopt`: Optimize the hyperparameters of the models in ASReview. [GitHub](#)

If an extension is not on this list, or you make one and want it added to this list, make an issue on [github](#).







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## ASReview against COVID-19

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For many questions from medical doctors, journalists, policy makers the scientific literature on COVID-19 needs to be checked in a systematic way to avoid biased decision-making. For example, to develop evidence-based medical guidelines to transparently support medical doctors. Medical guidelines rely on comprehensive systematic reviews. Such reviews entail several explicit and reproducible steps, including identifying all likely relevant papers in a standardized way, extracting data from eligible studies, and synthesizing the results into medical guidelines. They need to scan hundreds, or even thousands of COVID-19 related studies, by hand to find relevant papers to include in their overview. This is error prone and extremely time intensive; time we do not have right now!

The software relies on *Active learning* which denotes the scenario in which the reviewer is labeling data that are presented by a machine learning model. The machine learns from the reviewers' decisions and uses this knowledge in selecting the reference that will be presented to the reviewer next. In this way, the COVID-19 related papers are presented ordered from most to least relevant based on the input from the user. The goal of the software is to help scholars and practitioners to get an overview of the most relevant papers for their work as efficiently as possible, while being transparent in the process.

### 16.1 ASReview plugin

To help combat the COVID-19 crisis, the ASReview team has decided to [release](#) a plugin that provides three datasets on COVID-19. These are integrated automatically into ASReview once we install the correct packages, so reviewers can start reviewing the latest scientific literature on COVID-19 as soon as possible!

### 16.2 CORD-19 dataset

Two versions of the CORD-19 dataset (publications relating to COVID-19) are made available in ASReview:

- Full [CORD-19 dataset](#) .
- Custom made subset of the CORD-19 dataset with publications from December 2019 onwards.

The Cord19 database, developed by the [Allen Institute for AI](#), with all publications on COVID-19 and other coronavirus research (e.g. SARS, MERS, etc.) from PubMed Central, the WHO COVID-19 database of publications, the preprint servers bioRxiv and medRxiv and papers contributed by specific publishers.

In addition to the full dataset, we construct automatically a daily subset of the database with studies published after December 1st, 2019 to search for relevant papers published during the COVID-19 crisis.

The datasets are updated in ASReview plugin shortly after the release by the Allen Institute for AI.

### 16.3 Pre-print dataset

A separate dataset of COVID-19 related [preprints](#), containing metadata of preprints from over 15 preprints servers across disciplines, published since January 1, 2020. The preprint dataset is updated weekly by the maintainers (Nicholas Fraser and Bianca Kramer) and then automatically updated in ASReview as well. As this dataset is not readily available to researchers through regular search engines (e.g. PubMed), its inclusion in ASReview provided added value to researchers interested in COVID-19 research, especially if they want a quick way to screen preprints specifically.

### 16.4 Installation and usage

The COVID-19 plug-in requires ASReview 0.8 or higher. Install ASReview by following the instructions in [Installation](#).

Install the extension with pip:

```
pip install asreview-covid19
```

The datasets are immediately available after starting ASReview.

```
asreview lab
```

The datasets are selectable in Step 2 of the project initialization. For more information on the usage of ASReview, have a look at the [Oracle Mode](#).



## 16.5 License

The ASReview software and the plugin have an Apache 2.0 LICENSE. For the datasets, see the license of the CORD-19 dataset <https://www.semanticscholar.org/cord19>.



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## ASReview-visualization

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ASReview-visualization is a plotting and visualization supplemental package for the [ASReview](#) software. It is a fast way to create a visual impression of the ASReview with different datasets, models and model parameters.

### 17.1 Installation

The easiest way to install the visualization package is to install from PyPI:

```
pip install asreview-visualization
```

After installation of the visualization package, `asreview` should automatically detect it. Test this by:

```
asreview --help
```

It should list the ‘plot’ modus.

### 17.2 Basic usage

State files that were created with the same ASReview settings can be put together/averaged by putting them in the same directory. State files with different settings/datasets should be put in different directories to compare them.

As an example consider the following directory structure, where we have two datasets, called `ace` and `ptsd`, each of which have 8 runs:

```
├── ace
│   ├── results_0.h5
│   ├── results_1.h5
│   ├── results_2.h5
│   ├── results_3.h5
│   ├── results_4.h5
│   └── results_5.h5
```

(continues on next page)

(continued from previous page)

```
├── results_6.h5
├── results_7.h5
└── ptsd
    ├── results_0.h5
    ├── results_1.h5
    ├── results_2.h5
    ├── results_3.h5
    ├── results_4.h5
    ├── results_5.h5
    ├── results_6.h5
    └── results_7.h5
```

Then we can plot the results by:

```
asreview plot ace ptsd
```

By default, the values shown are expressed as percentages of the total number of papers. Use the `-a` or `--absolute-values` flags to have them expressed in absolute numbers:

```
asreview plot ace ptsd --absolute-values
```

## 17.3 Plot types

There are currently four plot types implemented: *inclusion*, *discovery*, *limit*, *progression*. They can be individually selected with the `-t` or `--type` switch. Multiple plots can be made by using `,` as a separator:

```
asreview plot ace ptsd --type 'inclusion,discovery'
```

### 17.3.1 Inclusion

This figure shows the number/percentage of included papers found as a function of the number/percentage of papers reviewed. Initial included/excluded papers are subtracted so that the line always starts at (0,0).

The quicker the line goes to a 100%, the better the performance.

### 17.3.2 Discovery

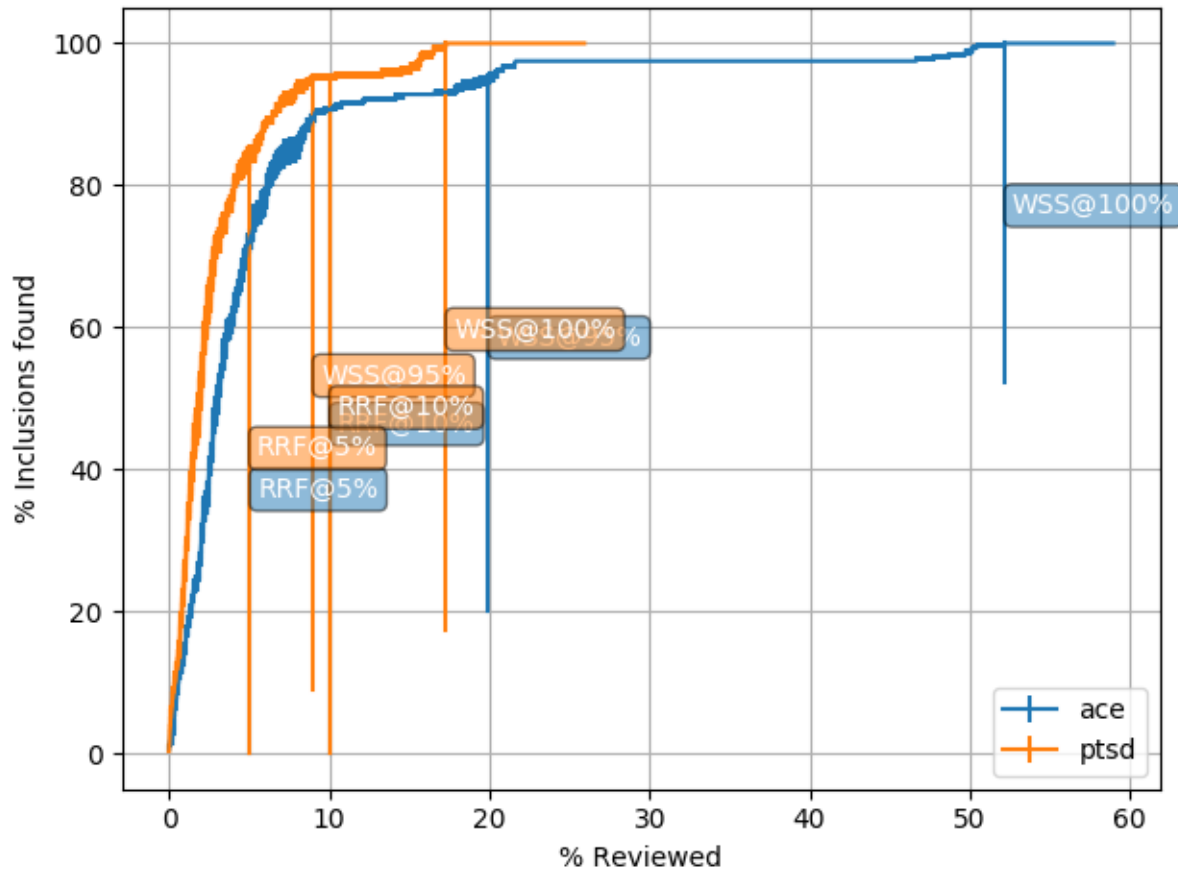
This figure shows the distribution of the number of papers that have to be read before discovering each inclusion. Not every paper is equally hard to find.

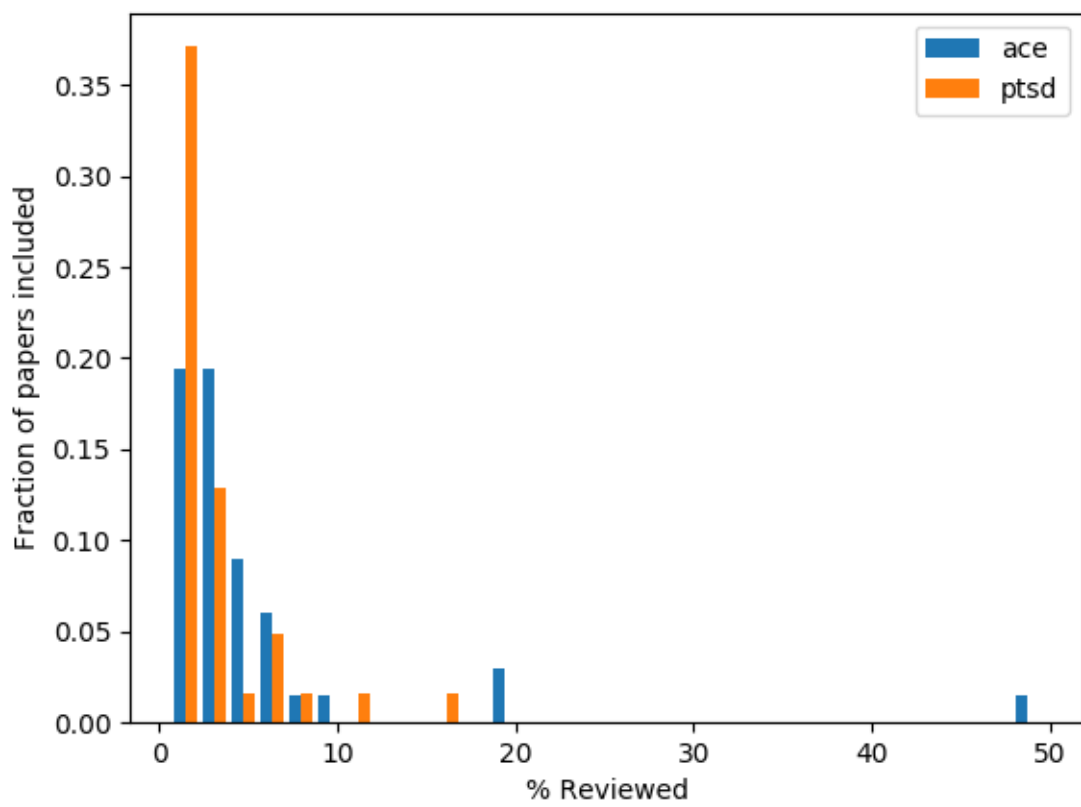
The closer to the left, the better.

### 17.3.3 Limit

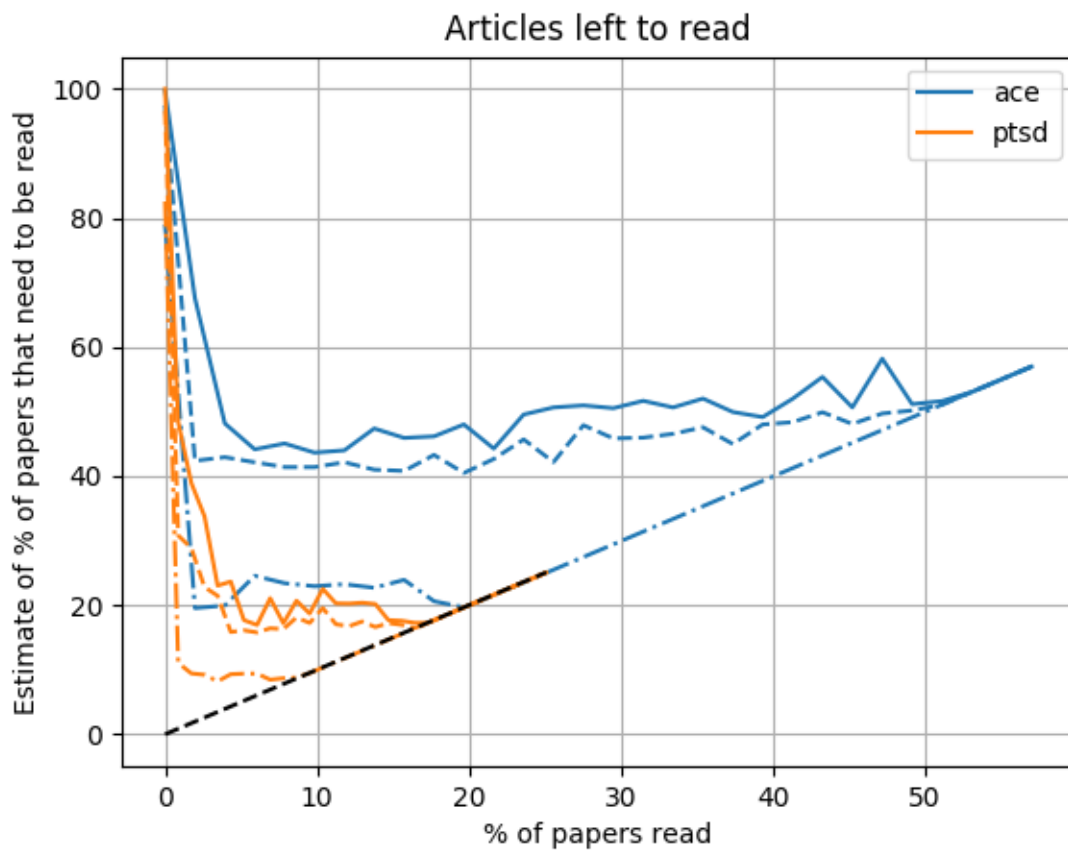
This figure shows how many papers need to be read with a given criterion. A criterion is expressed as “after reading  $y$  % of the papers, at most an average of  $z$  included papers have been not been seen by the reviewer, if he is using max sampling”. Here,  $y$  is shown on the y-axis, while three values of  $z$  are plotted as three different lines with the same color. The three values for  $z$  are 0.1, 0.5 and 2.0.

The quicker the lines touch the black ( $y=x$ ) line, the better.



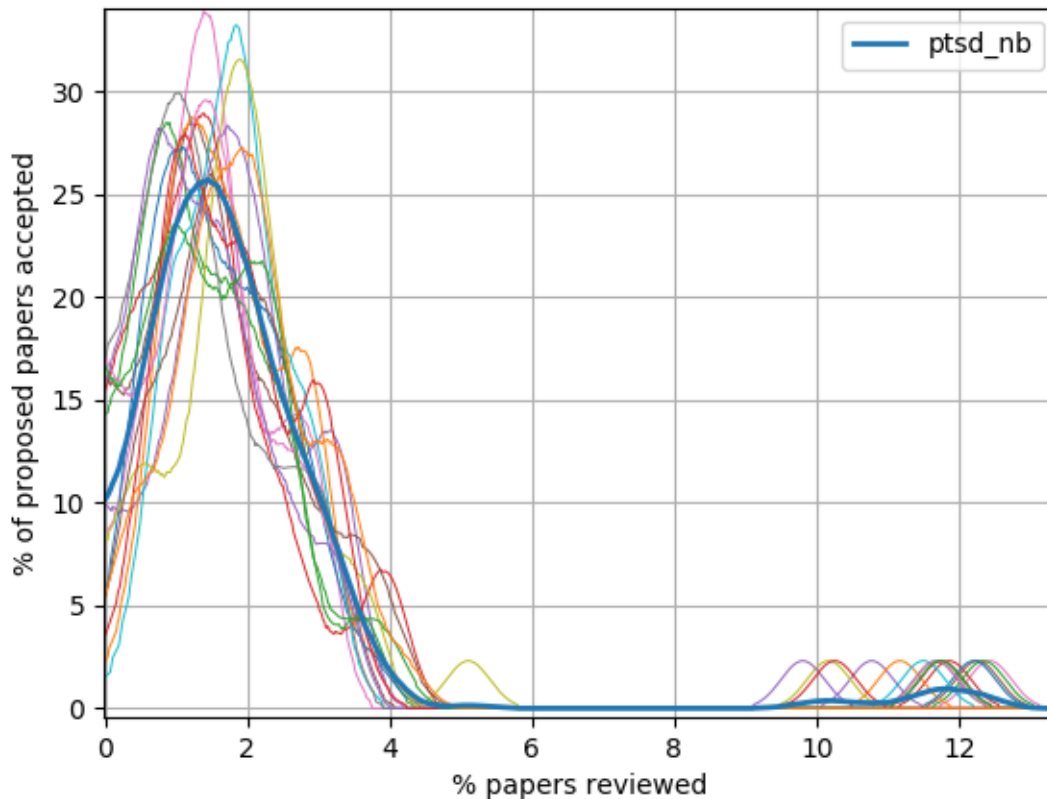






### 17.3.4 Progression

This figure shows the average inclusion rate as a function of time, number of papers read. The more concentrated on the left, the better. The thick line is the average of individual runs (thin lines). The visualization package will automatically detect which are directories and which are files. The curve is smoothed out by using a Gaussian smoothing algorithm.



## 17.4 API

To make use of the more advanced features, you can also use the visualization package as a library. The advantage is that you can make more reproducible plots where text, etc. is in the place *you* want it. Examples can be found in module `asreviewcontrib.visualization.quick`. Those are the scripts that are used for the command line interface.

```
from asreviewcontrib.visualization.plot import Plot

with Plot.from_paths(["PATH_1", "PATH_2"]) as plot:
    inc_plot = plot.new("inclusion")
    inc_plot.set_grid()
    inc_plot.set_xlim(0, 30)
    inc_plot.set_ylim(0, 101)
    inc_plot.set_legend()
    inc_plot.show()
    inc_plot.save("SOME_FILE.png")
```

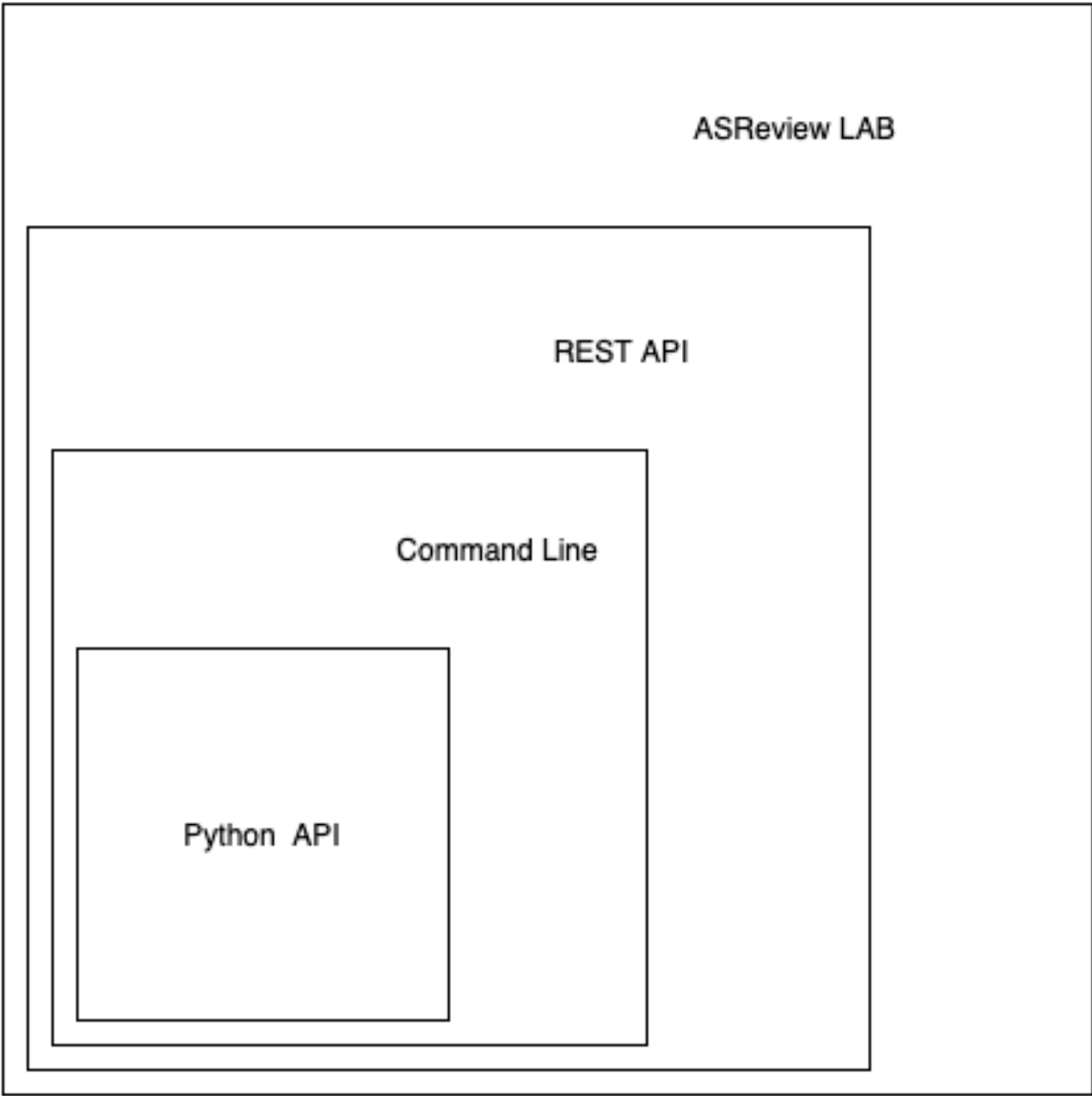
Of course fill in `PATH_1` and `PATH_2` as the files you would like to plot.

If the customization is not sufficient, you can also directly manipulate the `self.ax` and `self.fig` attributes of the plotting class.



ASReview provides users an API to interact directly with the underlying ASReview machinery. This provides researchers an interface to study the behavior of algorithms and develop custom workflows. The following figure shows the available interfaces for interacting with the ASReview software:

- The REST API uses a Flask REST API to provide a method to let the React front-end communicate with the backend and algorithms. The REST API is not documented at the moment and should be considered ‘internal use only’.
- The *Command Line* is an interface to open ASReview LAB, to run simulations, and more. See *Simulation* for example usage.
- The *API Reference* is a low level Python interface for ASReview. This interface requires detailed knowledge about the workings of the software. There is extensive documentation available on the functions, classes, modules. An outline for usage can be found in *Programming Interface (API)*.



ASReview provides a powerful command line interface for running tasks like simulations. For a list of available commands, type `asreview --help`.

### 19.1 Lab

**asreview lab** launches the ASReview LAB software (the frontend).

```
asreview lab [options]
```

- ip** IP  
The IP address the server will listen on.
- port** PORT  
The port the server will listen on.
- clean\_project** CLEAN\_PROJECT  
Safe cleanup of temporary files in project.
- clean\_all\_projects** CLEAN\_ALL\_PROJECTS  
Safe cleanup of temporary files in all projects.
- embedding** EMBEDDING\_FP  
File path of embedding matrix. Required for LSTM models.
- seed** SEED  
Seed for the model (classifiers, balance strategies, feature extraction techniques, and query strategies). Use an integer between 0 and  $2^{32} - 1$ .
- h, --help**  
Show help message and exit.

## 19.2 Simulate

**asreview simulate** measures the performance of the software on existing systematic reviews. The software shows how many papers you could have potentially skipped during the systematic review.

```
asreview simulate [options] [dataset [dataset ...]]
```

Example:

```
asreview simulate YOUR_DATA.csv --state_file myreview.h5
```

### **dataset**

A dataset to simulate

**-m, --model** MODEL

The prediction model for Active Learning. Default: nb. (See available options below: *Classifiers*)

**-q, --query\_strategy** QUERY\_STRATEGY

The query strategy for Active Learning. Default: max. (See available options below: *Query strategies*)

**-b, --balance\_strategy** BALANCE\_STRATEGY

Data rebalancing strategy. Helps against imbalanced datasets with few inclusions and many exclusions. Default: double. (See available options below: *Balance strategies*)

**-e, --feature\_extraction** FEATURE\_EXTRACTION

Feature extraction method. Some combinations of feature extraction method and prediction model are not available. Default: tfidf. (See available options below: *Feature extraction*)

**--embedding** EMBEDDING\_FP

File path of embedding matrix. Required for LSTM models.

**--config\_file** CONFIG\_FILE

Configuration file with model settings and parameter values.

**--seed** SEED

Seed for the model (classifiers, balance strategies, feature extraction techniques, and query strategies). Use an integer between 0 and  $2^{32} - 1$ .

**--n\_prior\_included** N\_PRIOR\_INCLUDED

The number of prior included papers. Only used when `prior_idx` is not given. Default 1.

**--n\_prior\_excluded** N\_PRIOR\_EXCLUDED

The number of prior excluded papers. Only used when `prior_idx` is not given. Default 1.

**--prior\_idx** [PRIOR\_IDX [PRIOR\_IDX ...]]

Prior indices by rownumber (0 is first rownumber).

**--prior\_record\_id** [PRIOR\_RECORD\_ID [PRIOR\_RECORD\_ID ...]]

Prior indices by record\_id.

New in version 0.15.

**--included\_dataset** [INCLUDED\_DATASET [INCLUDED\_DATASET ...]]

A dataset with papers that should be included. Can be used multiple times.

**--excluded\_dataset** [EXCLUDED\_DATASET [EXCLUDED\_DATASET ...]]

A dataset with papers that should be excluded. Can be used multiple times.

**--prior\_dataset** [PRIOR\_DATASET [PRIOR\_DATASET ...]]

A dataset with papers from prior studies.



- 
- state\_file** STATE\_FILE, **-s** STATE\_FILE  
Location to store the (active learning) state of the simulation. It is possible to output the state to a JSON file (extension `.json`) or [HDF5 file](#) (extension `.h5`).
- init\_seed** INIT\_SEED  
Seed for setting the prior indices if the `prior_idx` option is not used. If the option `prior_idx` is used with one or more index, this option is ignored.
- n\_instances** N\_INSTANCES  
Number of papers queried each query. Default 1.
- n\_queries** N\_QUERIES  
The number of queries. By default, the program stops after all documents are reviewed or is interrupted by the user.
- n** N\_PAPERS, **--n\_papers** N\_PAPERS  
The number of papers to be reviewed. By default, the program stops after all documents are reviewed or is interrupted by the user.
- verbose** VERBOSE, **-v** VERBOSE  
Verbosity
- h, --help**  
Show help message and exit.
- 

**Note:** Some classifiers (models) and feature extraction algorithms require additional dependencies. Use `pip install asreview[all]` to install all additional dependencies at once.

---

### 19.2.1 Feature Extraction

Name	Reference	Requires
<code>tfidf</code>	<code>asreview.models.feature_extraction.Tfidf</code>	
<code>doc2vec</code>	<code>asreview.models.feature_extraction.Doc2Vec</code>	<code>gensim</code>
<code>embedding-idf</code>	<code>asreview.models.feature_extraction.EmbeddingIdf</code>	
<code>embedding-lstm</code>	<code>asreview.models.feature_extraction.EmbeddingLSTM</code>	
<code>sbert</code>	<code>asreview.models.feature_extraction.SBERT</code>	<code>sentence_transformers</code>

### 19.2.2 Classifiers

Name	Reference	Requires
<code>nb</code>	<code>asreview.models.classifiers.NaiveBayesClassifier</code>	
<code>svm</code>	<code>asreview.models.classifiers.SVMClassifier</code>	
<code>logistic</code>	<code>asreview.models.classifiers.LogisticClassifier</code>	
<code>rf</code>	<code>asreview.models.classifiers.RandomForestClassifier</code>	
<code>nn-2-layer</code>	<code>asreview.models.classifiers.NN2LayerClassifier</code>	<code>tensorflow</code>
<code>lstm-base</code>	<code>asreview.models.classifiers.LSTMBaseClassifier</code>	<code>tensorflow</code>
<code>lstm-pool</code>	<code>asreview.models.classifiers.LSTMPoolClassifier</code>	<code>tensorflow</code>

### 19.2.3 Query Strategies

Name	Reference	Requires
max	<code>asreview.models.query.MaxQuery</code>	
random	<code>asreview.models.query.RandomQuery</code>	
uncertainty	<code>asreview.models.query.UncertaintyQuery</code>	
cluster	<code>asreview.models.query.ClusterQuery</code>	

### 19.2.4 Balance Strategies

Name	Reference	Requires
simple	<code>asreview.models.balance.SimpleBalance</code>	
double	<code>asreview.models.balance.DoubleBalance</code>	
triple	<code>asreview.models.balance.TripleBalance</code>	
undersample	<code>asreview.models.balance.UndersampleBalance</code>	

## 19.3 Simulate-batch

**asreview simulate-batch** provides the same interface as the **asreview simulate**, but adds an extra option (`--n_runs`) to run a batch of simulation runs with the same configuration.

```
asreview simulate-batch [options] [dataset [dataset ...]]
```

**Warning:** The behaviour of some arguments of **asreview simulate-batch** will differ slightly from **asreview simulate**.

**dataset**

A dataset to simulate

**--n\_runs**

Number of simulation runs.

## 19.4 Algorithms

New in version 0.14.

**asreview algorithms** provides an overview of all available active learning model elements (classifiers, query strategies, balance strategies, and feature extraction algorithms) in ASReview.

```
asreview algorithms
```

---

**Note:** **asreview algorithms** lists models added via extensions as well. See [Extensions](#) for more information on creating an model extension.

---

ASReview has support for extensions, which enable you to integrate your programs with the ASReview framework seamlessly. These extensions can extend the software with new classifiers, query strategies, balance strategies, and feature extraction techniques. It is also possible to extend ASReview with a completely new subcommand (like `lab` or `simulate`).

The extensibility of the framework is provided by the entrypoints of `setuptools`. You will need to create a package and install it (for example with `pip`). If you have no experience with creating packages, look at the [visualization extension](#) and modify it to suit your needs.

## 20.1 Usage

This section shows how to use an extension. In this example, the `asreview-visualization` extension is used. The extension extends ASReview to create basic plots from ASReview state files.

Install the extension with

```
pip install asreview-visualization
```

After installation, the subcommand `plot` is available in the command line. See `asreview -h` for this option.

```
$ asreview -h
usage: asreview [-h] [-V] [subcommand]

Automated Systematic Review (ASReview).

positional arguments:
  subcommand          The subcommand to launch. Available commands:

                        lab [asreview-0.13]
                        Graphical user interface for ASReview.

                        simulate [asreview-0.13]
```

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```

        Simulate the performance of ASReview.

simulate-batch [asreview-0.13]
    Parallel simulation for ASReview.

plot [asreview-visualization-0.2.2]
    Plotting functionality for logging files produced by ASReview.

optional arguments:
  -h, --help      show this help message and exit
  -V, --version   print the ASR version number and exit

```

With this extension installed, a plot can be made with an ASReview state file. The following example shows how a plot is made of the file `example_run_1.h5`.

```
asreview plot example_run_1.h5
```

## 20.2 Create subcommand

Extensions in ASReview are Python packages. Extension packages can extend the subcommands of `asreview` (see `asreview -h`) or add new algorithms.

The easiest way to create an extension is by defining a class that can be used as a new entry point for ASReview. This class should inherit from `asreview.entry_points.BaseEntryPoint`. Add the functionality to the class method `execute`.

```

from asreview.entry_points import BaseEntryPoint

class ExampleEntryPoint(BaseEntryPoint):

    description = "Description of example extension"
    extension_name = "asreview-example" # Name of the extension
    version = "1.0" # Version of the extension in x.y(.z) format.

    def execute(self, argv):
        pass # Implement your functionality here.

```

It is strongly recommended to define the attributes `description`, `extension_name`, and `version`.

The class method `execute` accepts a positional argument (`argv` in this example). First create the functionality you would like to be able to use in any directory. The argument `argv` are the command line arguments left after removing `asreview` and the entry point.

It is advised to place the newly defined class `ExampleEntryPoints` in the following package structure: `asreviewcontrib.{extension_name}.{your_modules}`. For example:

```

├── README.md
├── asreviewcontrib
│   └── example
│       ├── __init__.py
│       ├── entrypoint.py
│       └── example_utils.py
├── setup.py
└── tests

```

Create a `setup.py` in the root of the package, and set the keyword argument `entry_points` of `setup()` under `asreview.entry_points`, for example:

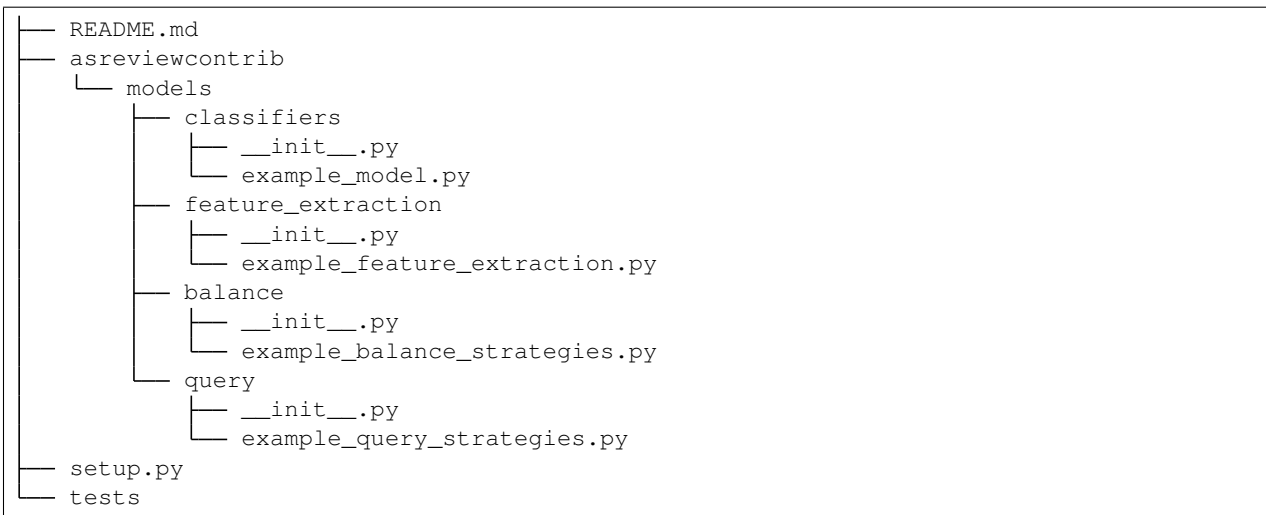
```
entry_points={
    "asreview.entry_points": [
        "example = asreviewcontrib.example.entrypoint:ExampleEntryPoint",
    ]
}
```

After installing this package. ASReview is extended with the `asreview example` subcommand.

If you are willing to share your work, the easiest way is to upload your package to GitHub and/or PyPi. Users can directly install the extension from these sources.

## 20.3 Add model

In the ASReview project, an active learning model consists of classifier, query strategy, balance strategy, or feature extraction technique. The easiest way to extend ASReview with a new classifier, query strategy, balance strategy, or feature extraction technique is by using the template [Template for extending ASReview](#). Create a copy of the template and add the new algorithms. It is advised to use the following structure of the package:



The next step is to add metadata to the `setup.py` file. Edit the name of the package and point the `entry_points` to the models.

```
entry_points={
    'asreview.models.classifiers': [
        'example = asreviewcontrib.models.classifiers.example_model:ExampleClassifier
→',
    ],
    'asreview.models.feature_extraction': [
        # define feature_extraction algorithms
    ],
    'asreview.models.balance': [
        # define balance_strategy algorithms
    ],
    'asreview.models.query': [
        # define query_strategy algorithms

```

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```
}  
},
```

This code registers the model with name `example`.

Install the package with pip:

```
pip install .
```

The new classifier is now available and can be used, for example, in the `simulate` command line.

```
asreview simulate example_data_file.csv -m example
```

## 21.1 Low level API

```
class asreview.review.BaseReview(as_data, model=None, query_model=None, balance_model=None, feature_model=None, n_papers=None, n_instances=1, n_queries=None, start_idx=[], state_file=None, log_file=None)
```

Base class for Systematic Review.

### Parameters

- **as\_data** (*asreview.ASReviewData*) – The data object which contains the text, labels, etc.
- **model** (*BaseModel*) – Initialized model to fit the data during active learning. See `asreview.models.utils.py` for possible models.
- **query\_model** (*BaseQueryModel*) – Initialized model to query new instances for review, such as random sampling or max sampling. See `asreview.query_strategies.utils.py` for query models.
- **balance\_model** (*BaseBalanceModel*) – Initialized model to redistribute the training data during the active learning process. They might either resample or undersample specific papers.
- **feature\_model** (*BaseFeatureModel*) – Feature extraction model that converts texts and keywords to feature matrices.
- **n\_papers** (*int*) – Number of papers to review during the active learning process, excluding the number of initial priors. To review all papers, set `n_papers` to `None`.
- **n\_instances** (*int*) – Number of papers to query at each step in the active learning process.
- **n\_queries** (*int*) – Number of steps/queries to perform. Set to `None` for no limit.

- **start\_idx** (*numpy.ndarray*) – Start the simulation/review with these indices. They are assumed to be already labeled. Failing to do so might result bad behaviour.
- **state\_file** (*str*) – Path to state file. Replaces log\_file argument.

**classify** (*query\_idx, inclusions, state, method=None*)  
Classify new papers and update the training indices.

It automatically updates the state.

#### Parameters

- **query\_idx** (*list, numpy.ndarray*) – Indices to classify.
- **inclusions** (*list, numpy.ndarray*) – Labels of the query\_idx.
- **state** (*BaseLogger*) – Logger to store the classification in.
- **method** (*str*) – If not set to None, all inclusions have this query method.

**log\_probabilities** (*state*)  
Store the modeling probabilities of the training indices and pool indices.

**n\_pool** ()  
Number of indices left in the pool.

**Returns** *int* – Number of indices left in the pool.

**query** (*n\_instances, query\_model=None*)  
Query records from pool.

#### Parameters

- **n\_instances** (*int*) – Batch size of the queries, i.e. number of records to be queried.
- **query\_model** (*BaseQueryModel*) – Query strategy model to use. If None, the query model of the reviewer is used.

**Returns** *numpy.ndarray* – Indices of records queried.

**review** (*\*args, \*\*kwargs*)  
Do the systematic review, writing the results to the state file.

#### Parameters

- **stop\_after\_class** (*bool*) – When to stop; if True stop after classification step, otherwise stop after training step.
- **instant\_save** (*bool*) – If True, save results after each single classification.

**settings**  
Get an ASReview settings object

**statistics** ()  
Get statistics on the current state of the review.

**Returns** *dict* – A dictionary with statistics like n\_included and last\_inclusion.

**train** ()  
Train the model.

**class** asreview.**ReviewSimulate** (*as\_data, \*args, n\_prior\_included=0, n\_prior\_excluded=0, prior\_idx=None, init\_seed=None, \*\*kwargs*)  
ASReview Simulation mode class.

#### Parameters



- **as\_data** (`asreview.ASReviewData`) – The data object which contains the text, labels, etc.
- **model** (`BaseModel`) – Initialized model to fit the data during active learning. See `asreview.models.utils.py` for possible models.
- **query\_model** (`BaseQueryModel`) – Initialized model to query new instances for review, such as random sampling or max sampling. See `asreview.query_strategies.utils.py` for query models.
- **balance\_model** (`BaseBalanceModel`) – Initialized model to redistribute the training data during the active learning process. They might either resample or undersample specific papers.
- **feature\_model** (`BaseFeatureModel`) – Feature extraction model that converts texts and keywords to feature matrices.
- **n\_prior\_included** (`int`) – Sample n prior included papers.
- **n\_prior\_excluded** (`int`) – Sample n prior excluded papers.
- **prior\_idx** (`int`) – Prior indices by row number.
- **n\_papers** (`int`) – Number of papers to review during the active learning process, excluding the number of initial priors. To review all papers, set `n_papers` to `None`.
- **n\_instances** (`int`) – Number of papers to query at each step in the active learning process.
- **n\_queries** (`int`) – Number of steps/queries to perform. Set to `None` for no limit.
- **start\_idx** (`numpy.ndarray`) – Start the simulation/review with these indices. They are assumed to be already labeled. Failing to do so might result bad behaviour.
- **init\_seed** (`int`) – Seed for setting the prior indices if the `-prior_idx` option is not used. If the option `prior_idx` is used with one or more index, this option is ignored.
- **state\_file** (`str`) – Path to state file. Replaces `log_file` argument.

**classify** (`query_idx`, `inclusions`, `state`, `method=None`)

Classify new papers and update the training indices.

It automatically updates the state.

#### Parameters

- **query\_idx** (`list`, `numpy.ndarray`) – Indices to classify.
- **inclusions** (`list`, `numpy.ndarray`) – Labels of the `query_idx`.
- **state** (`BaseLogger`) – Logger to store the classification in.
- **method** (`str`) – If not set to `None`, all inclusions have this query method.

**log\_probabilities** (`state`)

Store the modeling probabilities of the training indices and pool indices.

**n\_pool** ()

Number of indices left in the pool.

**Returns** `int` – Number of indices left in the pool.

**query** (`n_instances`, `query_model=None`)

Query records from pool.

#### Parameters

- **n\_instances** (*int*) – Batch size of the queries, i.e. number of records to be queried.
- **query\_model** (*BaseQueryModel*) – Query strategy model to use. If None, the query model of the reviewer is used.

**Returns** *numpy.ndarray* – Indices of records queried.

**review** (*\*args, \*\*kwargs*)

Do the systematic review, writing the results to the state file.

#### Parameters

- **stop\_after\_class** (*bool*) – When to stop; if True stop after classification step, otherwise stop after training step.
- **instant\_save** (*bool*) – If True, save results after each single classification.

#### settings

Get an ASReview settings object

#### statistics ()

Get statistics on the current state of the review.

**Returns** *dict* – A dictionary with statistics like `n_included` and `last_inclusion`.

#### train ()

Train the model.

## 21.2 Classifiers

**class** `asreview.models.classifiers.NaiveBayesClassifier` (*alpha=3.822*)

Naive Bayes classifier

Naive Bayes classifier. Only works in combination with the `asreview.models.feature_extraction.Tfidf` feature extraction model. Though relatively simplistic, seems to work quite well on a wide range of datasets.

The naive Bayes classifier is an implementation based on the sklearn multinomial naive Bayes classifier.

**Parameters** **alpha** (*float, default=3.822*) – Additive (Laplace/Lidstone) smoothing parameter (0 for no smoothing).

#### default\_param

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

#### fit (X, y)

Fit the model to the data.

#### Parameters

- **X** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

#### full\_hyper\_space ()

Get a hyperparameter space to use with hyperopt.

**Returns** *dict, dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**predict\_proba** (*X*)

Get the inclusion probability for each sample.

**Parameters** **X** (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

```
class asreview.models.classifiers.RandomForestClassifier (n_estimators=100,  
max_features=10,  
class_weight=1.0, ran-  
dom_state=None)
```

Random Forest classifier

The Random Forest classifier is an implementation based on the sklearn Random Forest classifier.

**Parameters**

- **n\_estimators** (*int, default=100*) – The number of trees in the forest.
- **max\_features** (*int, default=10*) – Number of features in the model.
- **class\_weight** (*float, default=1.0*) – Class weight of the inclusions.
- **random\_state** (*int or RandomState, default=None*) – Controls both the randomness of the bootstrapping of the samples used when building trees and the sampling of the features to consider when looking for the best split at each node.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**fit** (*X, y*)

Fit the model to the data.

**Parameters**

- **X** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

**full\_hyper\_space** ()

Get a hyperparameter space to use with hyperopt.

**Returns** *dict, dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**predict\_proba** (*X*)

Get the inclusion probability for each sample.

**Parameters** **X** (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

```
class asreview.models.classifiers.SVMClassifier (gamma='auto', class_weight=0.249,  
C=15.4, kernel='linear', ran-  
dom_state=None)
```

Support Vector Machine classifier

The Support Vector Machine classifier is an implementation based on the sklearn Support Vector Machine classifier.

#### Parameters

- **gamma** (*str*) – Gamma parameter of the SVM model.
- **class\_weight** (*float*) – class\_weight of the inclusions.
- **C** (*float*) – C parameter of the SVM model.
- **kernel** (*str*) – SVM kernel type.
- **random\_state** (*int, RandomState*) – State of the RNG.

#### default\_param

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

#### fit (*X, y*)

Fit the model to the data.

#### Parameters

- **x** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

#### full\_hyper\_space ()

Get a hyperparameter space to use with hyperopt.

**Returns** *dict, dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

#### param

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

#### predict\_proba (*X*)

Get the inclusion probability for each sample.

**Parameters** **x** (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

```
class asreview.models.classifiers.LogisticClassifier (C=1.0, class_weight=1.0, ran-  
dom_state=None, n_jobs=1)
```

Logistic regressions classifier

The Logistic regressions classifier is an implementation based on the sklearn Logistic regressions classifier.

#### Parameters

- **C** (*float*) – Parameter inverse to the regularization strength of the model.
- **class\_weight** (*float*) – Class weight of the inclusions.
- **random\_state** (*int, RandomState*) – Random state for the model.
- **n\_jobs** (*int*) – Number of CPU cores used.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**fit** (*X*, *y*)

Fit the model to the data.

**Parameters**

- **x** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

**full\_hyper\_space** ()

Get a hyperparameter space to use with hyperopt.

**Returns** *dict*, *dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**predict\_proba** (*X*)

Get the inclusion probability for each sample.

**Parameters** **x** (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

```
class asreview.models.classifiers.LSTMBaseClassifier (embedding_matrix=None,
                                                    backwards=True, dropout=0.4,
                                                    optimizer='rmsprop',
                                                    lstm_out_width=20,
                                                    learn_rate=1.0,
                                                    dense_width=128, ver-
                                                    bose=0, batch_size=32,
                                                    epochs=35, shuffle=False,
                                                    class_weight=30.0)
```

LSTM base classifier.

LSTM model that consists of an embedding layer, LSTM layer with one output, dense layer, and a single sigmoid output node. Use the `asreview.models.feature_extraction.EmbeddingLSTM` feature extraction method. Currently not so well optimized and slow.

---

**Note:** This model requires `tensorflow` to be installed. Use `pip install tensorflow` or install all optional ASReview dependencies with `pip install asreview[all]`

---

**Parameters**

- **embedding\_matrix** (*numpy.ndarray*) – Embedding matrix to use with LSTM model.
- **backwards** (*bool*) – Whether to have a forward or backward LSTM.
- **dropout** (*float*) – Value in [0, 1.0) that gives the dropout and recurrent dropout rate for the LSTM model.
- **optimizer** (*str*) – Optimizer to use.

- `lstm_out_width` (*int*) – Output width of the LSTM.
- `learn_rate` (*float*) – Learn rate multiplier of default learning rate.
- `dense_width` (*int*) – Size of the dense layer of the model.
- `verbose` (*int*) – Verbosity.
- `batch_size` (*int*) – Size of the batch size for the LSTM model.
- `epochs` (*int*) – Number of epochs to train the LSTM model.
- `shuffle` (*bool*) – Whether to shuffle the data before starting to train.
- `class_weight` (*float*) – Class weight for the included papers.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**fit** (*X*, *y*)

Fit the model to the data.

**Parameters**

- **X** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

**full\_hyper\_space** ()

Get a hyperparameter space to use with hyperopt.

**Returns** *dict*, *dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**predict\_proba** (*X*)

Get the inclusion probability for each sample.

**Parameters** **X** (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

```
class asreview.models.classifiers.LSTMPoolClassifier (embedding_matrix=None,  
                                                    backwards=True, dropout=0.4,  
                                                    optimizer='rmsprop',  
                                                    lstm_out_width=20,  
                                                    lstm_pool_size=128,  
                                                    learn_rate=1.0,           ver-  
                                                    bose=0,           batch_size=32,  
                                                    epochs=35,       shuffle=False,  
                                                    class_weight=30.0)
```

LSTM pool classifier.

LSTM model that consists of an embedding layer, LSTM layer with many outputs, max pooling layer, and a single sigmoid output node. Use the `asreview.models.feature_extraction.EmbeddingLSTM` feature extraction method. Currently not so well optimized and slow.

---

**Note:** This model requires `tensorflow` to be installed. Use `pip install tensorflow` or install all optional ASReview dependencies with `pip install asreview[all]`

---

### Parameters

- **embedding\_matrix** (*numpy.ndarray*) – Embedding matrix to use with LSTM model.
- **backwards** (*bool*) – Whether to have a forward or backward LSTM.
- **dropout** (*float*) – Value in [0, 1.0) that gives the dropout and recurrent dropout rate for the LSTM model.
- **optimizer** (*str*) – Optimizer to use.
- **lstm\_out\_width** (*int*) – Output width of the LSTM.
- **lstm\_pool\_size** (*int*) – Size of the pool, must be a divisor of `max_sequence_length`.
- **learn\_rate** (*float*) – Learn rate multiplier of default learning rate.
- **verbose** (*int*) – Verbosity.
- **batch\_size** (*int*) – Size of the batch size for the LSTM model.
- **epochs** (*int*) – Number of epochs to train the LSTM model.
- **shuffle** (*bool*) – Whether to shuffle the data before starting to train.
- **class\_weight** (*float*) – Class weight for the included papers.

### `default_param`

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

### `fit(X, y)`

Fit the model to the data.

#### Parameters

- **X** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

### `full_hyper_space()`

Get a hyperparameter space to use with hyperopt.

**Returns** *dict, dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

### `param`

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

### `predict_proba(X)`

Get the inclusion probability for each sample.

**Parameters** **X** (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

```
class asreview.models.classifiers.NN2LayerClassifier (dense_width=128,          op-  
                                                    timizer='rmsprop',  
                                                    learn_rate=1.0,          regu-  
                                                    larization=0.01,       ver-  
                                                    bose=0,                epochs=35,  
                                                    batch_size=32, shuffle=False,  
                                                    class_weight=30.0)
```

Dense neural network classifier.

Neural network with two hidden, dense layers of the same size.

Recommended feature extraction model is `asreview.models.feature_extraction.Doc2Vec`.

---

**Note:** This model requires `tensorflow` to be installed. Use `pip install tensorflow` or install all optional ASReview dependencies with `pip install asreview[all]`

---

**Warning:** Might crash on some systems with limited memory in combination with `asreview.models.feature_extraction.Tfidf`.

### Parameters

- **dense\_width** (*int*) – Size of the dense layers.
- **optimizer** (*str*) – Name of the Keras optimizer.
- **learn\_rate** (*float*) – Learning rate multiplier of the default learning rate.
- **regularization** (*float*) – Strength of the regularization on the weights and biases.
- **verbose** (*int*) – Verbosity of the model mirroring the values for Keras.
- **epochs** (*int*) – Number of epochs to train the neural network.
- **batch\_size** (*int*) – Batch size used for the neural network.
- **shuffle** (*bool*) – Whether to shuffle the training data prior to training.
- **class\_weight** (*float*) – Class weights for inclusions (1's).

### default\_param

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

### fit (X, y)

Fit the model to the data.

#### Parameters

- **X** (*numpy.ndarray*) – Feature matrix to fit.
- **y** (*numpy.ndarray*) – Labels for supervised learning.

### full\_hyper\_space ()

Get a hyperparameter space to use with hyperopt.

**Returns** *dict, dict* – Parameter space. Parameter choices; in case of hyperparameters with a list of choices, store the choices there.

### param

Get the (assigned) parameters of the model.



**Returns** *dict* – Dictionary with parameter: current value.

**predict\_proba** (*X*)

Get the inclusion probability for each sample.

**Parameters** *X* (*numpy.ndarray*) – Feature matrix to predict.

**Returns** *numpy.ndarray* – Array with the probabilities for each class, with two columns (class 0, and class 1) and the number of samples rows.

`asreview.models.classifiers.list_classifiers()`

List available classifiers.

**Returns** *list* – Names of available classifiers in alphabetical order.

`asreview.models.classifiers.get_classifier(name, *args, random_state=None, **kwargs)`

Get an instance of a model from a string.

**Parameters**

- **name** (*str*) – Name of the model.
- **\*args** – Arguments for the model.
- **\*\*kwargs** – Keyword arguments for the model.

**Returns** *BaseFeatureExtraction* – Initialized instance of classifier.

`asreview.models.classifiers.get_classifier_class(name)`

Get class of model from string.

**Parameters** **name** (*str*) – Name of the model, e.g. ‘svm’, ‘nb’ or ‘lstm-pool’.

**Returns** *BaseModel* – Class corresponding to the name.

## 21.3 Query

**class** `asreview.models.query.MaxQuery`

Maximum sampling query strategy.

Choose the most likely samples to be included according to the model.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**query** (*X, classifier, pool\_idx=None, n\_instances=1, shared={}*)

Query method for strategies which use class probabilities.

**class** `asreview.models.query.MixedQuery` (*strategy\_1='max', strategy\_2='random', mix\_ratio=0.95, random\_state=None, \*\*kwargs*)

Class for mixed query strategy.

The idea is to use two different query strategies at the same time with a ratio of one to the other. A mix of two query strategies is used. For example mixing max and random sampling with a mix ratio of 0.95 would mean that at each query 95% of the instances would be sampled with the max query strategy after which the remaining 5% would be sampled with the random query strategy. It would be called the *max\_random* query strategy. Every combination of primitive query strategy is possible.

**Parameters**

- **strategy\_1** (*str*) – Name of the first query strategy.
- **strategy\_2** (*str*) – Name of the second query strategy.
- **mix\_ratio** (*float*) – Portion of queries done by the first strategy. So a mix\_ratio of 0.95 means that 95% of the time query strategy 1 is used and 5% of the time query strategy 2.
- **\*\*kwargs** (*dict*) – Keyword arguments for the two strategy. To specify which of the strategies the argument is for, prepend with the name of the query strategy and an under-score, e.g. ‘max’ for maximal sampling.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**name**

`str(object=”) -> str str(bytes_or_buffer[, encoding[, errors]]) -> str`

Create a new string object from the given object. If encoding or errors is specified, then the object must expose a data buffer that will be decoded using the given encoding and error handler. Otherwise, returns the result of `object.__str__()` (if defined) or `repr(object)`. encoding defaults to `sys.getdefaultencoding()`. errors defaults to ‘strict’.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**query** (*X, classifier, pool\_idx=None, n\_instances=1, shared={}*)

Query new instances.

**Parameters**

- **X** (*numpy.ndarray*) – Feature matrix to choose samples from.
- **classifier** (*SKLearnModel*) – Trained classifier to compute probabilities if they are necessary.
- **pool\_idx** (*numpy.ndarray*) – Indices of samples that are still in the pool.
- **n\_instances** (*int*) – Number of instances to query.
- **shared** (*dict*) – Dictionary for exchange between query strategies and others. It is mainly used to store the current class probabilities, and the source of the queries; which query strategy has produced which index.

**class** `asreview.models.query.UncertaintyQuery`

Maximum uncertainty query strategy.

Choose the most uncertain samples according to the model (i.e. closest to 0.5 probability). Doesn’t work very well in the case of LSTM’s, since the probabilities are rather arbitrary.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**query** (*X*, *classifier*, *pool\_idx=None*, *n\_instances=1*, *shared={}*)  
 Query method for strategies which use class probabilities.

**class** `asreview.models.query.RandomQuery` (*random\_state=None*)  
 Random sampling query strategy.

Randomly select samples with no regard to model assigned probabilities.

**Warning:** Selecting this option means your review is not going to be accelerated by ASReview.

**default\_param**  
 Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**  
 Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**query** (*X*, *classifier*, *pool\_idx=None*, *n\_instances=1*, *shared={}*)  
 Query method for strategies which do not use class probabilities

**class** `asreview.models.query.ClusterQuery` (*cluster\_size=350*, *update\_interval=200*, *random\_state=None*)

Query strategy using clustering algorithms.

Use clustering after feature extraction on the dataset. Then the highest probabilities within random clusters are sampled.

#### Parameters

- **cluster\_size** (*int*) – Size of the clusters to be made. If the size of the clusters is smaller than the size of the pool, fall back to max sampling.
- **update\_interval** (*int*) – Update the clustering every x instances.
- **random\_state** (*int*, *RandomState*) – State/seed of the RNG.

**default\_param**  
 Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**  
 Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**query** (*X*, *classifier*, *pool\_idx=None*, *n\_instances=1*, *shared={}*)  
 Query method for strategies which use class probabilities.

`asreview.models.query.list_query_strategies` ()  
 List available query strategies.

This excludes all possible mixed query strategies.

**Returns** *list* – Names of available query strategies in alphabetical order.

`asreview.models.query.get_query_model` (*name*, *\*args*, *random\_state=None*, *\*\*kwargs*)  
 Get an instance of the query strategy.

#### Parameters

- **name** (*str*) – Name of the query strategy.
- **\*args** – Arguments for the model.
- **\*\*kwargs** – Keyword arguments for the model.

**Returns** *asreview.query.base.BaseQueryModel* – Initialized instance of query strategy.

`asreview.models.query.get_query_class(name)`

Get class of query strategy from its name.

**Parameters** **name** (*str*) – Name of the query strategy, e.g. ‘max’, ‘uncertainty’, ‘random’. A special mixed query strategy is also possible. The mix is denoted by an underscore: ‘max\_random’ or ‘max\_uncertainty’.

**Returns** *class* – Class corresponding to the name *name*.

## 21.4 Balance

**class** `asreview.models.balance.SimpleBalance`

No balancing.

Use all training data.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**sample** (*X*, *y*, *train\_idx*, *shared*)

Function that does not resample the training set.

**Parameters**

- **X** (*numpy.ndarray*) – Complete matrix of all samples.
- **y** (*numpy.ndarray*) – Classified results of all samples.
- **extra\_vars** (*dict*) – Extra variables that can be passed around between functions.

**Returns**

- *numpy.ndarray* – Training samples.
- *numpy.ndarray* – Classification of training samples.

**class** `asreview.models.balance.DoubleBalance` (*a=2.155*, *alpha=0.94*, *b=0.789*, *beta=1.0*,  
*random\_state=None*)

Dynamic Resampling balance strategy.

Class to get the two way rebalancing function and arguments. It super samples ones depending on the number of 0's and total number of samples in the training data.

**Parameters**

- **a** (*float*) – Governs the weight of the 1's. Higher values mean linearly more 1's in your training sample.

- **alpha** (*float*) – Governs the scaling the weight of the 1's, as a function of the ratio of ones to zeros. A positive value means that the lower the ratio of zeros to ones, the higher the weight of the ones.
- **b** (*float*) – Governs how strongly we want to sample depending on the total number of samples. A value of 1 means no dependence on the total number of samples, while lower values mean increasingly stronger dependence on the number of samples.
- **beta** (*float*) – Governs the scaling of the weight of the zeros depending on the number of samples. Higher values means that larger samples are more strongly penalizing zeros.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**sample** (*X, y, train\_idx, shared*)

Resample the training data.

**Parameters**

- **X** (*numpy.ndarray*) – Complete feature matrix.
- **y** (*numpy.ndarray*) – Labels for all papers.
- **train\_idx** (*numpy.ndarray*) – Training indices, that is all papers that have been reviewed.
- **shared** (*dict*) – Dictionary to share data between balancing models and other models.

**Returns** *numpy.ndarray, numpy.ndarray* – X\_train, y\_train: the resampled matrix, labels.

**class** asreview.models.balance.**TripleBalance** (*a=2.155, alpha=0.94, b=0.789, beta=1.0, c=0.835, gamma=2.0, shuffle=True, random\_state=None*)

Triple balance strategy.

This divides the training data into three sets: included papers, excluded papers found with random sampling and papers found with max sampling. They are balanced according to formulas depending on the percentage of papers read in the dataset, the number of papers with random/max sampling etc. Works best for stochastic training algorithms. Reduces to both full sampling and undersampling with corresponding parameters.

**Parameters**

- **a** (*float*) – Governs the weight of the 1's. Higher values mean linearly more 1's in your training sample.
- **alpha** (*float*) – Governs the scaling the weight of the 1's, as a function of the ratio of ones to zeros. A positive value means that the lower the ratio of zeros to ones, the higher the weight of the ones.
- **b** (*float*) – Governs how strongly we want to sample depending on the total number of samples. A value of 1 means no dependence on the total number of samples, while lower values mean increasingly stronger dependence on the number of samples.
- **beta** (*float*) – Governs the scaling of the weight of the zeros depending on the number of samples. Higher values means that larger samples are more strongly penalizing zeros.
- **c** (*float*) – Value between one and zero that governs the weight of samples done with maximal sampling. Higher values mean higher weight.

- **gamma** (*float*) – Governs the scaling of the weight of the max samples as a function of the % of papers read. Higher values mean stronger scaling.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**sample** (*X*, *y*, *train\_idx*, *shared*)

Resample the training data.

**Parameters**

- **X** (*numpy.ndarray*) – Complete feature matrix.
- **y** (*numpy.ndarray*) – Labels for all papers.
- **train\_idx** (*numpy.ndarray*) – Training indices, that is all papers that have been reviewed.
- **shared** (*dict*) – Dictionary to share data between balancing models and other models.

**Returns** *numpy.ndarray, numpy.ndarray* – *X\_train*, *y\_train*: the resampled matrix, labels.

**class** `asreview.models.balance.UndersampleBalance` (*ratio=1.0*, *random\_state=None*)

Balancing class that undersamples the data with a given ratio.

This undersamples the data, leaving out excluded papers so that the included and excluded papers are in some particular ratio (closer to one).

**Parameters** **ratio** (*double*) – Undersampling ratio of the zero's. If for example we set a ratio of 0.25, we would sample only a quarter of the zeros and all the ones.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**sample** (*X*, *y*, *train\_idx*, *shared*)

Resample the training data.

**Parameters**

- **X** (*numpy.ndarray*) – Complete feature matrix.
- **y** (*numpy.ndarray*) – Labels for all papers.
- **train\_idx** (*numpy.ndarray*) – Training indices, that is all papers that have been reviewed.
- **shared** (*dict*) – Dictionary to share data between balancing models and other models.

**Returns** *numpy.ndarray, numpy.ndarray* – *X\_train*, *y\_train*: the resampled matrix, labels.

`asreview.models.balance.list_balance_strategies` ()

List available balancing strategies.

**Returns** *list* – Names of available balance strategies in alphabetical order.

`asreview.models.balance.get_balance_model(name, *args, random_state=None, **kwargs)`  
Get an instance of a balance model from a string.

**Parameters**

- **name** (*str*) – Name of the balance model.
- **\*args** – Arguments for the balance model.
- **\*\*kwargs** – Keyword arguments for the balance model.

**Returns** *BaseFeatureExtraction* – Initialized instance of features extraction algorithm.

`asreview.models.balance.get_balance_class(name)`  
Get class of balance model from string.

**Parameters** **name** (*str*) – Name of the model, e.g. ‘simple’, ‘double’ or ‘undersample’.

**Returns** *BaseBalanceModel* – Class corresponding to the name.

## 21.5 Feature extraction

**class** `asreview.models.feature_extraction.Tfidf` (*\*args*, *ngram\_max=1*,  
*stop\_words='english'*, *\*\*kwargs*)

Class to apply TF-IDF to texts.

Use the standard TF-IDF (Term Frequency-Inverse Document Frequency) feature extraction from [SKLearn](#). Gives a sparse matrix as output. Works well in combination with `asreview.models.NBModel` and other fast training models (given that the features vectors are relatively wide).

**Parameters**

- **ngram\_max** (*int*) – Can use up to ngrams up to `ngram_max`. For example in the case of `ngram_max=2`, monograms and bigrams could be used.
- **stop\_words** (*str*) – When set to ‘english’, use stopwords. If set to `None` or ‘none’, do not use stop words.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**fit** (*texts*)

Fit the model to the texts.

It is not always necessary to implement this if there’s not real fitting being done.

**Parameters** **texts** (*numpy.ndarray*) – Texts to be fitted.

**fit\_transform** (*texts*, *titles=None*, *abstracts=None*, *keywords=None*)

Fit and transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**transform** (*texts*)

Transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

**class** `asreview.models.feature_extraction.Doc2Vec` (*\*args*, *vector\_size=40*, *epochs=33*, *min\_count=1*, *n\_jobs=1*, *window=7*, *dm\_concat=0*, *dm=2*, *dbow\_words=0*, *\*\*kwargs*)

Base class for doc2vec feature extraction.

Feature extraction method provided by the [gensim](#) package. It takes relatively long to create a feature matrix with this method. However, this only has to be done once per simulation/review. The upside of this method is the dimension- reduction that generally takes place, which makes the modelling quicker.

---

**Note:** This feature extraction algorithm requires `gensim` to be installed. Use `pip install gensim` or install all optional ASReview dependencies with `pip install asreview[all]`

---

### Parameters

- **vector\_size** (*int*) – Output size of the vector.
- **epochs** (*int*) – Number of epochs to train the doc2vec model.
- **min\_count** (*int*) – Minimum number of occurrences for a word in the corpus for it to be included in the model.
- **n\_jobs** (*int*) – Number of threads to train the model with.
- **window** (*int*) – Maximum distance over which word vectors influence each other.
- **dm\_concat** (*int*) – Whether to concatenate word vectors or not. See paper for more detail.
- **dm** (*int*) – Model to use. 0: Use distribute bag of words (DBOW). 1: Use distributed memory (DM). 2: Use both of the above with half the vector size and concatenate them.
- **dbow\_words** (*int*) – Whether to train the word vectors using the skipgram method.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**fit** (*texts*)

Fit the model to the texts.

It is not always necessary to implement this if there's not real fitting being done.

**Parameters** **texts** (*numpy.ndarray*) – Texts to be fitted.

**fit\_transform** (*texts*, *titles=None*, *abstracts=None*, *keywords=None*)

Fit and transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.



**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**transform** (*texts*)

Transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

```
class asreview.models.feature_extraction.EmbeddingIdf (*args, embedding_fp=None,
                                                    random_state=None,
                                                    **kwargs)
```

Class for Embedding-Idf model.

This model averages the weighted word vectors of all the words in the text, in order to get a single feature vector for each text. The weights are provided by the inverse document frequencies.

---

**Note:** This feature extraction algorithm requires `tensorflow` to be installed. Use `pip install tensorflow` or install all optional ASReview dependencies with `pip install asreview[all]`

---

**Parameters** **embedding\_fp** (*str*) – Path to embedding.

**default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

**fit** (*texts*)

Fit the model to the texts.

It is not always necessary to implement this if there's not real fitting being done.

**Parameters** **texts** (*numpy.ndarray*) – Texts to be fitted.

**fit\_transform** (*texts, titles=None, abstracts=None, keywords=None*)

Fit and transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

**param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

**transform** (*texts*)

Transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

```
class asreview.models.feature_extraction.EmbeddingLSTM(*args, loop_sequence=1,
                                                    num_words=20000,
                                                    max_sequence_length=1000,
                                                    padding='post', truncating='post',
                                                    n_jobs=1,
                                                    **kwargs)
```

Class to create embedding matrices for LSTM models.

Feature extraction method for `asreview.models.classifiers.LSTMBaseClassifier` and `asreview.models.classifiers.LSTMPoolClassifier` models.

---

**Note:** This feature extraction algorithm requires `tensorflow` to be installed. Use `pip install tensorflow` or install all optional ASReview dependencies with `pip install asreview[all]`

---

### Parameters

- **loop\_sequence** (*bool*) – Instead of zeros at the start/end of sequence loop it.
- **num\_words** (*int*) – Maximum number of unique words to be processed.
- **max\_sequence\_length** (*int*) – Maximum length of the sequence. Shorter get truncated. Longer sequences get either padded with zeros or looped.
- **padding** (*str*) – Which side should be padded [pre/post].
- **truncating** – Which side should be truncated [pre/post].
- **n\_jobs** – Number of processors used in reading the embedding matrix.

### default\_param

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

### fit (texts)

Fit the model to the texts.

It is not always necessary to implement this if there's not real fitting being done.

**Parameters** **texts** (*numpy.ndarray*) – Texts to be fitted.

### fit\_transform (texts, titles=None, abstracts=None, keywords=None)

Fit and transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

### param

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

### transform (texts)

Transform a list of texts.

**Parameters** **texts** (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

**class** `asreview.models.feature_extraction.SBERT` (*split\_ta=0, use\_keywords=0*)  
Sentence BERT class for feature extraction.

Feature extraction method based on Sentence BERT. Implementation based on the `sentence_transformers` package. It is relatively slow.

---

**Note:** This feature extraction algorithm requires `sentence_transformers` to be installed. Use `pip install sentence_transformers` or install all optional ASReview dependencies with `pip install asreview[all]`

---

#### **default\_param**

Get the default parameters of the model.

**Returns** *dict* – Dictionary with parameter: default value

#### **fit** (*texts*)

Fit the model to the texts.

It is not always necessary to implement this if there's not real fitting being done.

**Parameters** *texts* (*numpy.ndarray*) – Texts to be fitted.

#### **fit\_transform** (*texts, titles=None, abstracts=None, keywords=None*)

Fit and transform a list of texts.

**Parameters** *texts* (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

#### **param**

Get the (assigned) parameters of the model.

**Returns** *dict* – Dictionary with parameter: current value.

#### **transform** (*texts*)

Transform a list of texts.

**Parameters** *texts* (*numpy.ndarray*) – A sequence of texts to be transformed. They are not yet tokenized.

**Returns** *numpy.ndarray* – Feature matrix representing the texts.

`asreview.models.feature_extraction.list_feature_extraction()`

List available feature extraction methods.

**Returns** *list* – Names of available feature extraction methods in alphabetical order.

`asreview.models.feature_extraction.get_feature_model` (*name, \*args, random\_state=None, \*\*kwargs*)

Get an instance of a feature extraction model from a string.

#### **Parameters**

- **name** (*str*) – Name of the feature extraction model.
- **\*args** – Arguments for the feature extraction model.
- **\*\*kwargs** – Keyword arguments for the feature extraction model.

**Returns** *BaseFeatureExtraction* – Initialized instance of feature extraction algorithm.

`asreview.models.feature_extraction.get_feature_class` (*name*)

Get class of feature extraction from string.

**Parameters** `name` (*str*) – Name of the feature model, e.g. ‘doc2vec’, ‘tfidf’ or ‘embedding-lstm’.

**Returns** *BaseFeatureExtraction* – Class corresponding to the name.

## 21.6 Data

**class** `asreview.ASReviewData` (*df=None*, *data\_name='empty'*, *data\_type='standard'*, *column\_spec=None*)

Data object to the dataset with texts, labels, DOIs etc.

### Parameters

- **df** (*pandas.DataFrame*) – Dataframe containing the data for the ASReview data object.
- **data\_name** (*str*) – Give a name to the data object.
- **data\_type** (*str*) – What kind of data the dataframe contains.
- **column\_spec** (*dict*) – Specification for which column corresponds to which standard specification. Key is the standard specification, key is which column it is actually in.

**append** (*as\_data*)

Append another ASReviewData object.

It puts the training data at the end.

**Parameters** `as_data` (*ASReviewData*) – Dataset to append.

**classmethod** `from_file` (*fp*, *read\_fn=None*, *data\_name=None*, *data\_type=None*)

Create instance from csv/ris/excel file.

It works in two ways; either manual control where the conversion functions are supplied or automatic, where it searches in the entry points for the right conversion functions.

### Parameters

- **fp** (*str*, *pathlib.Path*) – Read the data from this file.
- **read\_fn** (*callable*) – Function to read the file. It should return a standardized dataframe.
- **data\_name** (*str*) – Name of the data.
- **data\_type** (*str*) – What kind of data it is. Special names: ‘included’, ‘excluded’, ‘prior’.

**get** (*name*)

Get column with name.

**hash** ()

Compute a hash from the dataset.

**Returns** *str* – SHA1 hash, computed from the titles/abstracts of the dataframe.

**prior\_data\_idx**

Get prior\_included, prior\_excluded from dataset.

**prior\_labels** (*state*, *by\_index=True*)

Get the labels that are marked as ‘initial’.

**state:** *BaseState* Open state that contains the label information.

**by\_index:** *bool* If True, return internal indexing. If False, return record\_ids for indexing.

**Returns** *numpy.ndarray* – Array of indices that have the ‘initial’ property.

**record** (*i*, *by\_index=True*)

Create a record from an index.

**Parameters**

- **i** (*int*, *iterable*) – Index of the record, or list of indices.
- **by\_index** (*bool*) – If True, take the i-th value as used internally by the review. If False, take the record with `record_id==i`.

**Returns** *PaperRecord* – The corresponding record if *i* was an integer, or a list of records if *i* was an iterable.

**slice** (*idx*, *by\_index=True*)

Create a slice from itself.

Useful if some parts should be kept/thrown away.

**Parameters** **idx** (*list*, *numpy.ndarray*) – Record ids that should be kept.

**Returns** *ASReviewData* – Slice of itself.

**to\_csv** (*fp*, *labels=None*, *ranking=None*)

Export to csv.

**Parameters**

- **fp** (*str*, *NoneType*) – Filepath or None for buffer.
- **labels** (*list*, *numpy.ndarray*) – Current labels will be overwritten by these labels (including unlabelled). No effect if labels is None.
- **ranking** (*list*) – Reorder the dataframe according to these (internal) indices. Default ordering if ranking is None.

**Returns** *pandas.DataFrame* – Dataframe of all available record data.

**to\_dataframe** (*labels=None*, *ranking=None*)

Create new dataframe with updated label (order).

**Parameters**

- **labels** (*list*, *numpy.ndarray*) – Current labels will be overwritten by these labels (including unlabelled). No effect if labels is None.
- **ranking** (*list*) – Reorder the dataframe according to these `record_ids`. Default ordering if ranking is None.

**Returns** *pandas.DataFrame* – Dataframe of all available record data.

**to\_excel** (*fp*, *labels=None*, *ranking=None*)

Export to Excel xlsx file.

**Parameters**

- **fp** (*str*, *NoneType*) – Filepath or None for buffer.
- **labels** (*list*, *numpy.ndarray*) – Current labels will be overwritten by these labels (including unlabelled). No effect if labels is None.
- **ranking** (*list*) – Reorder the dataframe according to these (internal) indices. Default ordering if ranking is None.

**Returns** *pandas.DataFrame* – Dataframe of all available record data.

`to_file` (*fp*, *labels=None*, *ranking=None*)

Export data object to file.

RIS, CSV and Excel are supported file formats at the moment.

#### Parameters

- **fp** (*str*) – Filepath to export to.
- **labels** (*list*, *numpy.ndarray*) – Labels to be inserted into the dataframe before export.
- **ranking** (*list*, *numpy.ndarray*) – Optionally, dataframe rows can be reordered.

## 21.7 Utils

`asreview.load_embedding` (*fp*, *word\_index=None*, *n\_jobs=None*)

Load embedding matrix from file.

The embedding matrix needs to be stored in the FastText format.

#### Parameters

- **fp** (*str*) – File path of the trained embedding vectors.
- **word\_index** (*dict*) – Sample word embeddings.
- **n\_jobs** (*int*) – Number of processes to parse the embedding (+1 process for reading).
- **verbose** (*int*) – The verbosity. Default 1.

**Returns** *dict* – The embedding weights stored in a dict with the word as key and the weights as values.

`asreview.sample_embedding` (*embedding*, *word\_index*)

Sample embedding matrix

#### Parameters

- **embedding** (*dict*) – A dictionary with the words and embedding vectors.
- **word\_index** (*dict*) – A `word_index` like the output of Keras Tokenizer.`word_index`.
- **verbose** (*int*) – The verbosity. Default 1.

**Returns** (*np.ndarray*, *list*) – The embedding weights stored in a two dimensional numpy array and a list with the corresponding words.

## 21.8 State

`asreview.state.open_state` (*fp*, *\*args*, *read\_only=False*, *\*\*kwargs*)

Open a state from a file.

#### Parameters

- **fp** (*str*) – File to open.
- **read\_only** (*bool*) – Whether to open the file in `read_only` mode.

**Returns** *Basestate* – Depending on the extension the appropriate state is chosen: - `[".h5", ".hdf5", ".he5"]` -> HDF5state. - None -> Dictstate (doesn't store anything permanently). - Anything else -> JSONstate.

**class** `asreview.state.BaseState` (*state\_fp*, *read\_only=False*)

**add\_classification** (*idx*, *labels*, *methods*, *query\_i*)

Add training indices and their labels.

**Parameters**

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for training.
- **labels** (*list*) – A list of labels corresponding with the training indices.
- **i** (*int*) – The query number.

**add\_proba** (*pool\_idx*, *train\_idx*, *proba*, *query\_i*)

Add inverse pool indices and their labels.

**Parameters**

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for unlabeled pool.
- **pred** (*numpy.ndarray*) – Array of prediction probabilities for unlabeled pool.
- **i** (*int*) – The query number.

**close** ()

Close the files opened by the state.

Also sets the end time if not in read-only mode.

**delete\_last\_query** ()

Delete the last query from the state object.

**get** (*variable*, *query\_i=None*, *default=None*, *idx=None*)

Get data from the state object.

This is universal accessor method of the State classes. It can be used to get a variable from one specific query. In theory, it should get the whole data set if *query\_i=None*, but this is not currently implemented in any of the States.

**Parameters**

- **variable** (*str*) – Name of the variable/data to get. Options are: *label\_idx*, *inclusions*, *label\_methods*, *labels*, *final\_labels*, *proba*, *train\_idx*, *pool\_idx*.
- **query\_i** (*int*) – Query number, should be between 0 and *self.n\_queries()*.
- **idx** (*int*, *numpy.ndarray*, *list*) – Indices to get in the returned array.

**get\_current\_queries** ()

Get the current queries made by the model.

This is useful to get back exactly to the state it was in before shutting down a review.

**Returns** *dict* – The last known queries according to the state file.

**get\_feature\_matrix** (*data\_hash*)

Get feature matrix out of the state.

**Parameters** **data\_hash** (*str*) – Hash of *as\_data* object from which the matrix is derived.

**Returns** *np.ndarray*, *sklearn.sparse.csr\_matrix* – Feature matrix as computed by the feature extraction model.

**initialize\_structure** ()

Create empty internal structure for state

**is\_empty()**

Check if state has no results.

**Returns** *bool* – True if empty.

**n\_queries()**

Number of queries saved in the state.

**Returns** *int* – Number of queries.

**pred\_proba**

Get last predicted probabilities.

**restore(fp)**

Restore or create state from a state file.

If the state file doesn't exist, creates an empty state that is ready for storage.

**Parameters** *fp* (*str*) – Path to file to restore/create.

**save()**

Save state to file.

**Parameters** *fp* (*str*) – The file path to export the results to.

**set\_current\_queries(current\_queries)**

Set the current queries made by the model.

**Parameters** *current\_queries* (*dict*) – The last known queries, with {*query\_idx*: *query\_method*}.

**set\_final\_labels(y)**

Add/set final labels to state.

If *final\_labels* does not exist yet, add it.

**Parameters** *y* (*numpy.ndarray*) – One dimensional integer numpy array with final inclusion labels.

**set\_labels(y)**

Add/set labels to state

If the labels do not exist, add it to the state.

**Parameters** *y* (*numpy.ndarray*) – One dimensional integer numpy array with inclusion labels.

**settings**

Get settings from state

**startup\_vals()**

Get variables for reviewer to continue review.

**Returns**

- *numpy.ndarray* – Current labels of dataset.
- *numpy.ndarray* – Current training indices.
- *dict* – Dictionary containing the sources of the labels.
- *query\_i* – Current query number (starting from 0).

**to\_dict()**

Convert state to dictionary.

**Returns** *dict* – Dictionary with all relevant variables.



**class** `asreview.state.HDF5State` (*state\_fp*, *read\_only=False*)

Class for storing the review state with HDF5 storage.

**add\_classification** (*idx*, *labels*, *methods*, *query\_i*)

Add training indices and their labels.

#### Parameters

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for training.
- **labels** (*list*) – A list of labels corresponding with the training indices.
- **i** (*int*) – The query number.

**add\_proba** (*pool\_idx*, *train\_idx*, *proba*, *query\_i*)

Add inverse pool indices and their labels.

#### Parameters

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for unlabeled pool.
- **pred** (*numpy.ndarray*) – Array of prediction probabilities for unlabeled pool.
- **i** (*int*) – The query number.

**close** ()

Close the files opened by the state.

Also sets the end time if not in read-only mode.

**delete\_last\_query** ()

Delete the last query from the state object.

**get** (*variable*, *query\_i=None*, *idx=None*)

Get data from the state object.

This is universal accessor method of the State classes. It can be used to get a variable from one specific query. In theory, it should get the whole data set if *query\_i=None*, but this is not currently implemented in any of the States.

#### Parameters

- **variable** (*str*) – Name of the variable/data to get. Options are: *label\_idx*, *inclusions*, *label\_methods*, *labels*, *final\_labels*, *proba*, *train\_idx*, *pool\_idx*.
- **query\_i** (*int*) – Query number, should be between 0 and *self.n\_queries*() .
- **idx** (*int*, *numpy.ndarray*, *list*) – Indices to get in the returned array.

**get\_current\_queries** ()

Get the current queries made by the model.

This is useful to get back exactly to the state it was in before shutting down a review.

**Returns** *dict* – The last known queries according to the state file.

**get\_feature\_matrix** (*data\_hash*)

Get feature matrix out of the state.

**Parameters** *data\_hash* (*str*) – Hash of *as\_data* object from which the matrix is derived.

**Returns** *np.ndarray*, *sklearn.sparse.csr\_matrix* – Feature matrix as computed by the feature extraction model.

**initialize\_structure** ()

Create empty internal structure for state

**is\_empty()**

Check if state has no results.

**Returns** *bool* – True if empty.

**n\_queries()**

Number of queries saved in the state.

**Returns** *int* – Number of queries.

**pred\_proba**

Get last predicted probabilities.

**restore(fp)**

Restore or create state from a state file.

If the state file doesn't exist, creates an empty state that is ready for storage.

**Parameters** **fp** (*str*) – Path to file to restore/create.

**save()**

Save state to file.

**Parameters** **fp** (*str*) – The file path to export the results to.

**set\_current\_queries(current\_queries)**

Set the current queries made by the model.

**Parameters** **current\_queries** (*dict*) – The last known queries, with {*query\_idx*: *query\_method*}.

**set\_final\_labels(y)**

Add/set final labels to state.

If *final\_labels* does not exist yet, add it.

**Parameters** **y** (*numpy.ndarray*) – One dimensional integer numpy array with final inclusion labels.

**set\_labels(y)**

Add/set labels to state

If the labels do not exist, add it to the state.

**Parameters** **y** (*numpy.ndarray*) – One dimensional integer numpy array with inclusion labels.

**settings**

Get settings from state

**startup\_vals()**

Get variables for reviewer to continue review.

**Returns**

- *numpy.ndarray* – Current labels of dataset.
- *numpy.ndarray* – Current training indices.
- *dict* – Dictionary containing the sources of the labels.
- *query\_i* – Current query number (starting from 0).

**to\_dict()**

Convert state to dictionary.

**Returns** *dict* – Dictionary with all relevant variables.

**class** `asreview.state.JSONState` (*state\_fp*, *read\_only=False*)

Class for storing the state of a Systematic Review using JSON files.

**add\_classification** (*idx*, *labels*, *methods*, *query\_i*)

Add training indices and their labels.

#### Parameters

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for training.
- **labels** (*list*) – A list of labels corresponding with the training indices.
- **i** (*int*) – The query number.

**add\_proba** (*pool\_idx*, *train\_idx*, *proba*, *query\_i*)

Add inverse pool indices and their labels.

#### Parameters

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for unlabeled pool.
- **pred** (*numpy.ndarray*) – Array of prediction probabilities for unlabeled pool.
- **i** (*int*) – The query number.

**close** ()

Close the files opened by the state.

Also sets the end time if not in read-only mode.

**delete\_last\_query** ()

Delete the last query from the state object.

**get** (*variable*, *query\_i=None*, *idx=None*)

Get data from the state object.

This is universal accessor method of the State classes. It can be used to get a variable from one specific query. In theory, it should get the whole data set if *query\_i=None*, but this is not currently implemented in any of the States.

#### Parameters

- **variable** (*str*) – Name of the variable/data to get. Options are: *label\_idx*, *inclusions*, *label\_methods*, *labels*, *final\_labels*, *proba*, *train\_idx*, *pool\_idx*.
- **query\_i** (*int*) – Query number, should be between 0 and *self.n\_queries()*.
- **idx** (*int*, *numpy.ndarray*, *list*) – Indices to get in the returned array.

**get\_current\_queries** ()

Get the current queries made by the model.

This is useful to get back exactly to the state it was in before shutting down a review.

**Returns** *dict* – The last known queries according to the state file.

**get\_feature\_matrix** (*data\_hash*)

Get feature matrix out of the state.

**Parameters** *data\_hash* (*str*) – Hash of *as\_data* object from which the matrix is derived.

**Returns** *np.ndarray*, *sklearn.sparse.csr\_matrix* – Feature matrix as computed by the feature extraction model.

**initialize\_structure** ()

Create empty internal structure for state

**is\_empty()**

Check if state has no results.

**Returns** *bool* – True if empty.

**n\_queries()**

Number of queries saved in the state.

**Returns** *int* – Number of queries.

**pred\_proba**

Get last predicted probabilities.

**restore(fp)**

Restore or create state from a state file.

If the state file doesn't exist, creates an empty state that is ready for storage.

**Parameters** **fp** (*str*) – Path to file to restore/create.

**save()**

Save state to file.

**Parameters** **fp** (*str*) – The file path to export the results to.

**set\_current\_queries(current\_queries)**

Set the current queries made by the model.

**Parameters** **current\_queries** (*dict*) – The last known queries, with {*query\_idx*: *query\_method*}.

**set\_final\_labels(y)**

Add/set final labels to state.

If *final\_labels* does not exist yet, add it.

**Parameters** **y** (*numpy.ndarray*) – One dimensional integer numpy array with final inclusion labels.

**set\_labels(y)**

Add/set labels to state

If the labels do not exist, add it to the state.

**Parameters** **y** (*numpy.ndarray*) – One dimensional integer numpy array with inclusion labels.

**settings**

Get settings from state

**startup\_vals()**

Get variables for reviewer to continue review.

**Returns**

- *numpy.ndarray* – Current labels of dataset.
- *numpy.ndarray* – Current training indices.
- *dict* – Dictionary containing the sources of the labels.
- *query\_i* – Current query number (starting from 0).

**to\_dict()**

Convert state to dictionary.

**Returns** *dict* – Dictionary with all relevant variables.

**class** `asreview.state.DictState` (*state\_fp*, \*, \*\*\_)

Class for storing the state of a review with no permanent storage.

**add\_classification** (*idx*, *labels*, *methods*, *query\_i*)

Add training indices and their labels.

#### Parameters

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for training.
- **labels** (*list*) – A list of labels corresponding with the training indices.
- **i** (*int*) – The query number.

**add\_proba** (*pool\_idx*, *train\_idx*, *proba*, *query\_i*)

Add inverse pool indices and their labels.

#### Parameters

- **indices** (*list*, *numpy.ndarray*) – A list of indices used for unlabeled pool.
- **pred** (*numpy.ndarray*) – Array of prediction probabilities for unlabeled pool.
- **i** (*int*) – The query number.

**close** ()

Close the files opened by the state.

Also sets the end time if not in read-only mode.

**delete\_last\_query** ()

Delete the last query from the state object.

**get** (*variable*, *query\_i=None*, *idx=None*)

Get data from the state object.

This is universal accessor method of the State classes. It can be used to get a variable from one specific query. In theory, it should get the whole data set if *query\_i=None*, but this is not currently implemented in any of the States.

#### Parameters

- **variable** (*str*) – Name of the variable/data to get. Options are: *label\_idx*, *inclusions*, *label\_methods*, *labels*, *final\_labels*, *proba*, *train\_idx*, *pool\_idx*.
- **query\_i** (*int*) – Query number, should be between 0 and *self.n\_queries*() .
- **idx** (*int*, *numpy.ndarray*, *list*) – Indices to get in the returned array.

**get\_current\_queries** ()

Get the current queries made by the model.

This is useful to get back exactly to the state it was in before shutting down a review.

**Returns** *dict* – The last known queries according to the state file.

**get\_feature\_matrix** (*data\_hash*)

Get feature matrix out of the state.

**Parameters** *data\_hash* (*str*) – Hash of *as\_data* object from which the matrix is derived.

**Returns** *np.ndarray*, *sklearn.sparse.csr\_matrix* – Feature matrix as computed by the feature extraction model.

**initialize\_structure** ()

Create empty internal structure for state

**is\_empty()**

Check if state has no results.

**Returns** *bool* – True if empty.

**n\_queries()**

Number of queries saved in the state.

**Returns** *int* – Number of queries.

**pred\_proba**

Get last predicted probabilities.

**restore(\*, \*\*\_)**

Restore or create state from a state file.

If the state file doesn't exist, creates an empty state that is ready for storage.

**Parameters** **fp** (*str*) – Path to file to restore/create.

**save()**

Save state to file.

**Parameters** **fp** (*str*) – The file path to export the results to.

**set\_current\_queries(current\_queries)**

Set the current queries made by the model.

**Parameters** **current\_queries** (*dict*) – The last known queries, with {*query\_idx*: *query\_method*}.

**set\_final\_labels(y)**

Add/set final labels to state.

If *final\_labels* does not exist yet, add it.

**Parameters** **y** (*numpy.ndarray*) – One dimensional integer numpy array with final inclusion labels.

**set\_labels(y)**

Add/set labels to state

If the labels do not exist, add it to the state.

**Parameters** **y** (*numpy.ndarray*) – One dimensional integer numpy array with inclusion labels.

**settings**

Get settings from state

**startup\_vals()**

Get variables for reviewer to continue review.

**Returns**

- *numpy.ndarray* – Current labels of dataset.
- *numpy.ndarray* – Current training indices.
- *dict* – Dictionary containing the sources of the labels.
- *query\_i* – Current query number (starting from 0).

**to\_dict()**

Convert state to dictionary.

**Returns** *dict* – Dictionary with all relevant variables.

## 21.9 Analysis

**class** `asreview.analysis.Analysis` (*states*, *key=None*)

Analysis object to do statistical analysis on state files.

**avg\_time\_to\_discovery** (*result\_format='number'*)

Estimate the Time to Discovery (TD) for each paper.

Get the best/last estimate on how long it takes to find a paper.

**Parameters** `result_format` (*str*) – Desired output format: “number”, “fraction” or “percentage”.

**Returns** *dict* – For each inclusion, `key=paper_id`, `value=avg time`.

**close** ()

Close states.

**classmethod** `from_dir` (*data\_dir*, *prefix=""*, *key=None*)

Create an Analysis object from a directory.

**Parameters**

- `data_dir` (*str*) – Directory to read the state files from.
- `prefix` (*str*) – Only assume files starting with this prefix are state files. Ignore all other files.
- `key` (*str*) – Name for the analysis object.

**classmethod** `from_file` (*data\_fp*, *key=None*)

Create an Analysis object from a file.

**Parameters**

- `data_fp` (*str*) – Path to state file to analyse.
- `key` (*str*) – Name for analysis object.

**classmethod** `from_path` (*data\_path*, *prefix=""*, *key=None*)

Create an Analysis object from either a file or a directory.

**inclusions\_found** (*result\_format='fraction'*, *final\_labels=False*, *\*\*kwargs*)

Get the number of inclusions at each point in time.

Caching is used to prevent multiple calls being expensive.

**Parameters**

- `result_format` (*str*) – The format % or # of the returned values.
- `final_labels` (*bool*) – If true, use the `final_labels` instead of labels for analysis.

**Returns** *tuple* – Three numpy arrays with `x`, `y`, `error_bar`.

**limits** (*prob\_allow\_miss=[0.1]*, *result\_format='percentage'*)

For each query, compute the number of papers for a criterium.

A criterium is the average number of papers missed. For example, with 0.1, the criterium is that after reading `x` papers, there is (about) a 10% chance that one paper is not included. Another example, with 2.0, there are on average 2 papers missed after reading `x` papers. The value for `x` is returned for each query and probability by the function.

**Parameters** `prob_allow_miss` (*list*, *float*) – Sets the criterium for how many papers can be missed.

**Returns** *dict* – One entry, “x\_range” with the number of papers read. List, “limits” of results for each probability and at # papers read.

**rrf** (*val=10, x\_format='percentage', \*\*kwargs*)

Get the RRF (Relevant References Found).

**Parameters**

- **val** – At which recall, between 0 and 100.
- **x\_format** – Format for position of RRF value in graph.

**Returns** *tuple* – Tuple consisting of RRF value, x\_positions, y\_positions of RRF bar.

**wss** (*val=100, x\_format='percentage', \*\*kwargs*)

Get the WSS (Work Saved Sampled) value.

**Parameters**

- **val** – At which recall, between 0 and 100.
- **x\_format** – Format for position of WSS value in graph.

**Returns** *tuple* – Tuple consisting of WSS value, x\_positions, y\_positions of WSS bar.

## 21.10 Extensions

**class** `asreview.entry_points.BaseEntryPoint`

Base class for defining entry points.

**classmethod** `execute` (*argv*)

Perform the functionality of the entry point.

**Parameters** **argv** (*list*) – Argument list, with the entry point and program removed. For example, if `asreview plot X` is executed, then `argv == ['X']`.

**format** (*entry\_name='?'*)

Create a short formatted description of the entry point.

**Parameters** **entry\_name** (*str*) – Name of the entry point. For example ‘plot’ in `asreview plot X`



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## Active learning for Systematic Reviews

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The rapidly evolving field of artificial intelligence (AI) has allowed the development of AI-aided pipelines that assist in finding relevant texts for such search tasks[1]. A well-established approach to increase the efficiency of title and abstract screening is determining prioritization[2, 3] with active learning[4], which is very effective for systematic reviewing[5-15]. It works as follows: Just like with a classical pipeline, you start with the set of all unlabeled records (e.g., meta-data containing titles and abstracts of scientific papers) retrieved from a search (pool). This is followed by constructing a training set, which, in the example of systematic reviewing, consists of labeled data provided by the annotator (researcher) (e.g., some relevant and irrelevant abstracts). Then, the active learning cycle starts. Active learning denotes the scenario in which the reviewer is labeling references that are presented by a machine learning model. The machine learning model learns from the reviewers' decision and uses this knowledge in selecting the next reference that will be presented to the reviewer. The annotated dataset starts out small and iteratively grows in size:

1. The first step is feature extraction. That is, an algorithm cannot make predictions from the records as they are; their textual content needs to be represented more abstractly. The algorithm can then determine the important features that are necessary to classify a record, thereby drastically decreasing the search space;
2. A specific classification algorithm (i.e, machine learning model) is then chosen;
3. The chosen classifier is trained on the labeled records and estimates relevance scores for all unlabeled records. The model chooses a record to show to the user for the next iteration of the cycle;
4. The annotator screens this record and provides a label, relevant or irrelevant. The newly labeled record is moved to the training data set and it's back to step 1.

The interaction with the human can be used to train a model with a minimum number of labeling tasks and the trained model is the output which is then used to classify new data, also called Human-in-the-Loop machine learning[16]. In the general sense the key idea behind active learning is that, if we allow the model to decide for itself which data it wants to learn from, its performance and accuracy may improve and it requires fewer training instances to do so. Moreover, the dataset's informativeness is increased by having the reviewer annotate those references that are more informative to the model (**uncertainty-based sampling**).

The application of active learning to systematic reviewing is called Researcher-In-The-Loop (RITL)[17] with three unique components:

- (I) The primary output of the process is a selection of the pool with only relevant papers;

(II) All data points in the relevant selection should have been seen by a human at the end of the process (**certainty-based sampling**);

(III) The process requires a strong, systematic way of working. As such, it entails several explicit and reproducible steps, as outlined in the [PRISMA guidelines](#) for systematic reviewing. This procedure ensures (more or less) that all likely relevant publications are found in a standardized way based on pre-defined eligibility criteria, extracting data from eligible studies, and synthesizing the results.

In the active learning cycle, the model incrementally improves its predictions on the remaining unlabeled records, but hopefully all relevant records are identified as early in the process as possible. The reviewer decides to stop at some point during the process to conserve resources or when all records have been labeled. In the latter case, no time was saved and therefore the main question is to decide when to stop: i.e. to determine the point at which the cost of labeling more papers by the reviewer is greater than the cost of the errors made by the current model[18]. Finding 100% of the relevant papers appears to be almost impossible, even for human annotators[19]. Therefore, we typically aim to find 95% of the inclusions. However, in the situation of an unlabeled dataset, you don't know how many relevant papers there are left to be found. So researchers might either stop too early and potentially miss many relevant papers, or stop too late, causing unnecessary further reading[20]. That is, one can decide to stop reviewing after a certain amount of non-relevant papers have been found in succession[21], but this is up to the user to decide. We are currently implementing potential stopping rules based on estimating the number of potential relevant papers or finding an inflection point where [5, 8, 9, 11, 12, 22-24]. This is work in progress.

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Simulation results

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To provide insight into how much screening effort ASReview could potentially save, seven ASReview models were simulated on six existing systematic review datasets (Ferdinands, 2020). In short, for all six datasets ASReview could have saved at least 60% of screening effort (e.g. WSS@95% was > 40%). For some datasets, ASReview was even able to detect 95% of relevant publications after screening only 5% of relevant publications.

## 23.1 Datasets

To assess the generalizability of the models across research contexts, the models were simulated on data from varying research contexts. Data were collected from the fields of medicine (Cohen et al. 2006; Appenzeller-Herzog et al. 2019), virology (Kwok et al. 2020), software engineering (Yu, Kraft, and Menzies 2018), behavioural public administration (Nagtegaal et al. 2019) and psychology (van de Schoot et al. 2017). Datasets are available in the [ASReview systematic review datasets repository](#).

The data were preprocessed from their source into a dataset containing title and abstract of the publications obtained in the initial search. Candidate studies with missing abstracts and duplicate instances were removed from the data. All datasets consisted of thousands of candidate studies, of which only a fraction was deemed relevant to the systematic review. For the Virus and the Nudging dataset, the inclusion rate was about 5 per cent. For the remaining six datasets, inclusion rates were centred around 1-2 per cent.

**Table 1 - Statistics on the systematic review datasets**

Dataset	Candidate publications	Relevant publications	Inclusion rate (%)
Nudging	1847	100	5.41
PTSD	5031	38	0.76
Software	8896	104	1.17
Ace	2235	41	1.83
Virus	2304	114	4.95
Wilson	2333	23	0.99

## 23.2 Models

To assess the effect of different ASReview models, seven models were evaluated differing in terms of the classification technique (Naive Bayes, Linear Regression, Support Vector Machine, and Random Forest) and the feature extraction strategy they adopt (TF-IDF and Doc2vec). The Naive Bayes + TF-IDF model is the current default in ASReview. Note that the ASReview GUI currently only offers freedom of choice for a classification technique. However, the models presented here are not exhaustive as the ASReview backend implements various other configurations.

## 23.3 Evaluation

Model performance was assessed by two different measures, Work Saved over Sampling (WSS), and Relevant References Found (RRF). WSS indicates the reduction in publications needed to be screened, at a given level of recall (Cohen et al. 2006). Typically measured at a recall level of 0.95, WSS@95 yields an estimate of the amount of work that can be saved at the cost of failing to identify 5% of relevant publications. In the current study, WSS is computed at 0.95 recall. RRF statistics are computed at 10%, representing the proportion of relevant publications that are found after screening 10% of all publications.

Furthermore, model performance was visualized by plotting recall curves. Plotting recall as a function of the proportion of screened publications offers insight in model performance throughout the entire screening process (Cormack and Grossman 2014; Yu, Kraft, and Menzies 2018). The x-axis represents the proportion of screened publications, the y-axis represents the proportion of relevant publications found. The curves give information in two directions. On the one hand, they display the proportion of relevant publications found for any point during the screening process (on the x-axis), RRF. On the other hand, they present the proportion of publications that need to be screened to achieve a certain level of recall (on the y-axis), 1-WSS. The quicker the curve reaches towards the top of the y-axis, the better the performance.

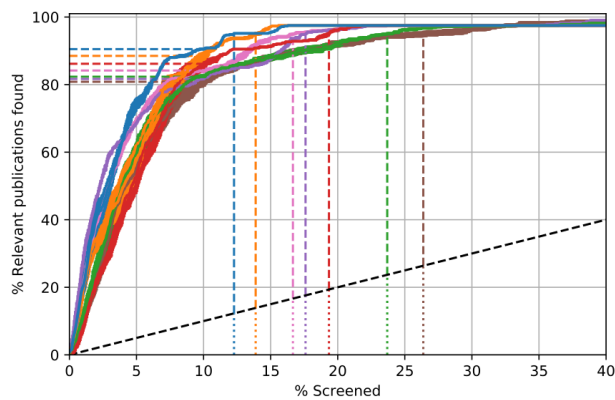
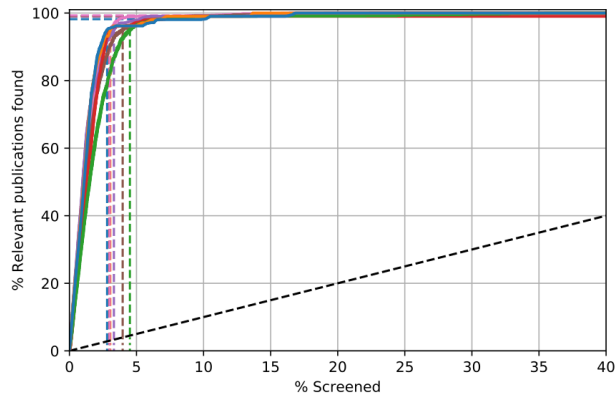
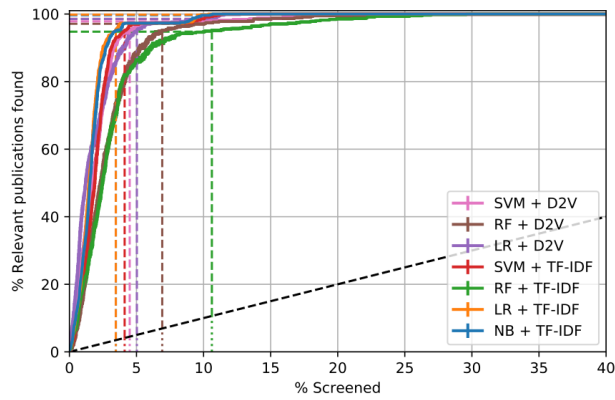
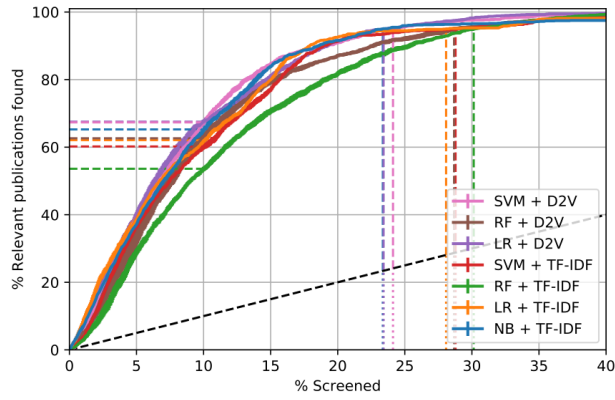
For every simulation, the RRF@10 and WSS@95, are reported as means over 15 trials. To indicate the spread of performance within simulations, the means are accompanied by an estimated standard error of the mean (hat s). To compare overall performance across datasets, median performance is reported for every dataset, accompanied by the Median Absolute Deviation (MAD), indicating variability between models within a certain dataset. Recall curves are plot for every simulation, representing the average recall over 15 trials (pm) the standard error of the mean.

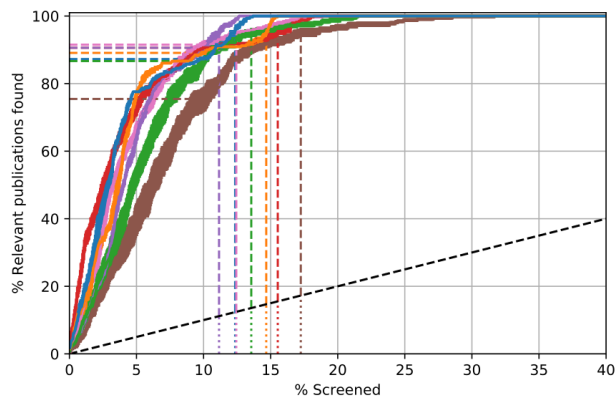
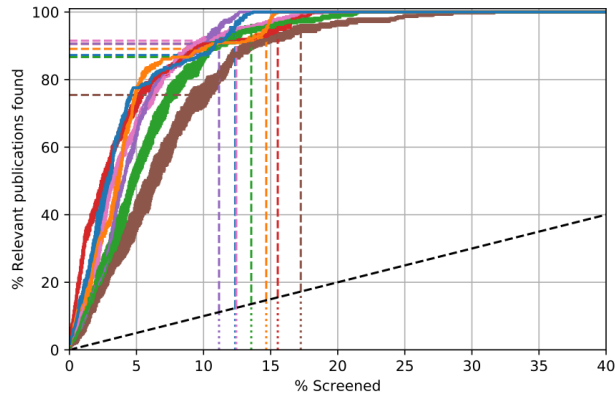
## 23.4 Results

The figures below show the recall curves of simulations for all model-dataset combinations. These curves plot recall as a function of the proportion of publications screened. The curves represent the average recall over 15 trials where the error margin represents the standard error of the mean in the direction of the y-axis. The x-axis is cut off at 40% since all for simulations, the models reached 95% recall after screening 40% of the publications. The dashed horizontal lines indicate the RRF@10 values, the dashed vertical lines the WSS@95 values. The dashed grey diagonal line corresponds to the expected recall curve when publications are screened in random order.

### 23.4.1 Recall curves

LRTB: Nudging dataset, PTSD dataset, Software dataset, Ace dataset, Virus dataset, Wilson dataset.





### 23.4.2 Between models comparison

For all datasets, the models were able to detect the relevant publications much faster compared to when screening publications at random order as the recall curves exceed the expected recall when screening at random order by far. While all models perform quite well, the NB + TF-IDF shows high performance on all measures across all datasets, whereas the RF + TF-IDF model never performed best on any of the measures across all datasets. Neither TF-IDF nor D2V feature extraction showed superior performance when simulated on certain datasets nor when combined with certain classification techniques.

### 23.4.3 Between datasets comparison

Firstly, models showed much higher performance for some datasets than for others. While performance on the PTSD and the Software dataset was quite high, the performance was much lower across models for the Nudging and Virus datasets. Secondly, the performance variability between models differed across datasets. Within the PTSD, Software and Virus datasets, model performance is less spread out than within the Nudging, Ace and Wilson dataset. Thirdly, the curves for the Ace (Figure 2c) and Wilson (Figure 2e) datasets show a larger standard error of the mean compared to other the other datasets. For these datasets, model performance seemed to be more dependent on the initial training dataset compared to others.

### 23.4.4 WSS and RRF tables

**Table 2 - WSS@95 values (mean, standard error) for all model-dataset combinations, and median (MAD) for all datasets**



	Nudging	PTSD	Software	Ace	Virus	Wilson
SVM + TF-IDF	66.2 (2.90)	91.0 (0.41)	92.0 (0.10)	75.8 (1.95)	69.7 (0.81)	79.9 (2.09)
NB + TF-IDF	71.7 (1.37)	91.7 (0.27)	92.3 (0.08)	82.9 (0.99)	71.2 (0.62)	83.4 (0.89)
RF + TF-IDF	64.9 (2.50)	84.5 (3.38)	90.5 (0.34)	71.3 (4.03)	63.9 (3.54)	81.6 (3.35)
LR + TF-IDF	66.9 (4.01)	91.7 (0.18)	92.0 (0.10)	81.1 (1.31)	70.3 (0.65)	80.5 (0.65)
SVM + D2V	70.9 (1.68)	90.6 (0.73)	92.0 (0.21)	78.3 (1.92)	70.7 (1.76)	82.7 (1.44)
RF + D2V	66.3 (3.25)	88.2 (3.23)	91.0 (0.55)	68.6 (7.11)	67.2 (3.44)	77.9 (3.43)
LR + D2V	71.6 (1.66)	90.1 (0.63)	91.7 (0.13)	77.4 (1.03)	70.4 (1.34)	84.0 (0.77)
median (MAD)	66.9 (3.05)	90.6 (1.53)	92.0 (0.47)	77.4 (5.51)	70.3 (0.90)	81.6 (2.48)

**Table 3 - RRF@10 values (mean, standard error) for all model-dataset combinations, and median (MAD) for all datasets**

	Nudging	PTSD	Software	Ace	Virus	Wilson
SVM + TF-IDF	60.2 (3.12)	98.6 (1.40)	99.0 (0.00)	86.2 (5.25)	73.4 (1.62)	90.6 (1.17)
NB + TF-IDF	65.3 (2.61)	99.6 (0.95)	98.2 (0.34)	90.5 (1.40)	73.9 (1.70)	87.3 (2.55)
RF + TF-IDF	53.6 (2.71)	94.8 (1.60)	99.0 (0.00)	82.3 (2.75)	62.1 (3.19)	86.7 (5.82)
LR + TF-IDF	62.1 (2.59)	99.8 (0.70)	99.0 (0.00)	88.5 (5.16)	73.7 (1.48)	89.1 (2.30)
SVM + D2V	67.3 (3.00)	97.8 (1.12)	99.3 (0.44)	84.2 (2.78)	73.6 (2.54)	91.5 (4.16)
RF + D2V	62.6 (5.47)	97.1 (1.90)	99.2 (0.34)	80.8 (5.72)	67.3 (3.19)	75.5 (14.35)
LR + D2V	67.5 (2.59)	98.6 (1.40)	99.0 (0.00)	81.7 (1.81)	70.6 (2.21)	90.6 (5.00)
median (MAD)	62.6 (3.89)	98.6 (1.60)	99.0 (0.00)	84.2 (3.71)	73.4 (0.70)	89.1 (2.70)

## 23.5 Conclusion

Overall, the findings confirm the great potential of active learning models in reducing workload for systematic reviewers. All models were able to detect 95% of the relevant publications after screening less than 40% of the total number of publications, indicating that active learning models can save more than half of the workload in the screening process. The results shed new light on the performance of different classification techniques, indicating that the Naive Bayes classification technique is superior to the widely used Support Vector Machine. As model performance differs vastly across datasets, this study raises the question of what causes models to yield more workload savings for some systematic review datasets than for others. To facilitate the applicability of active learning models in systematic review practice, it is essential to identify how dataset characteristics relate to model performance.

## 23.6 References

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## 24.1 Why run a simulation?

Doing simulations can be a great way to assess how well ASReview performs for your particular purposes. The user can run simulations on previously labeled datasets to see how much time the user could have saved using ASReview.

## 24.2 Doing the simulation

The ASReview simulation mode works through the dataset exactly like an ASReview user would, using the inclusions and exclusions in the dataset to learn in the active learning cycle. In this way, the entire screening process is replicated.

You can use the simulation mode that is provided with the ASReview package. It can be accessed directly from the command line, for example:

```
asreview simulate MY_DATASET.csv --state_file myreview.h5
```

This performs a simulation of a default active learning model, where `MY_DATASET.csv` is the path to the dataset you wish to simulate on and where `myreview.h5` is the file where the results will be stored.

More detail on specific model and simulation settings can be found in the Simulation options section. For how to prepare your data, see *Prepare your Data*.

## 24.3 Analyzing your results

The extensions `asreview-statistics` and `asreview-visualization` are useful tools to analyze results. Install them directly from PyPi:

```
pip install asreview-statistics asreview-visualization
```

Detailed information can be found on their respective GitHub pages. The following commands should give you at least a basic exploratory idea of the performance of your review:

```
asreview stat YOUR_DATASET.csv
asreview stat myreview.h5
asreview stat DIR_WITH_MULTIPLE_SIMULATIONS

asreview plot myreview.h5
asreview plot DIR_WITH_MULTIPLE_SIMULATIONS
```

For an example of results of a simulation study, see *Simulation results*.

## 24.4 Simulation options

ASReview provides an extensive simulation interface via the command line. An overview of the options are found on the *ASReview command line interface for simulation* page. This section highlights some of the more often used options here. When no additional arguments are specified in the `asreview simulate` command, default settings are used.

To make your simulations reproducible you can use the `--seed` and `--init_seed` options. ‘init\_seed’ controls the starting set of papers to train the model on, while the ‘seed’ controls the seed of the random number generation that is used after initialization.

By default, the model initializes with one relevant and one irrelevant record. You can set the number of priors by `-n_prior_included` and `-n_prior_excluded`. However, if you want to initialize your model with a specific set of starting papers, you can use `--prior_idx` to select the indices of the papers you want to start the simulation with.

The `--n_instances` argument controls the number of records that have to be labeled before the model is retrained again and is set at 1 by default. If you want to reduce the number of training iterations, for example to limit the size of your state file and the time to simulate, you can increase `--n_instances`.

You can select a classifier with the `-m` flag, which is set to be Naive Bayes by default. Names for implemented classifiers are listed on the `:ref: :classifiers-table` table.

Implemented query strategies are listed on the *Query Strategies* table and can be set with the `-q` option.

For feature extraction, supply the `-e` flag. Default is TF-IDF, more details on the table for *Feature Extraction*.

The last element that can be changed is the *Balance Strategies*, and is changed with the `-b` flag. Default is double balance.

---

## Programming Interface (API)

---

For more control over the workings of the ASReview software, an API is provided. For example, it is possible to define a new model or sampling strategy and use it with ASReview.

### 25.1 Simulation Mode

An example of use the API for the simulation mode:

```
import asreview
from asreview.models import LSTMBaseModel
from asreview.query_strategies import MaxQueryModel
from asreview.balance_strategies import SimpleBalanceModel
from asreview.feature_extraction import EmbeddingLSTM

# load data
as_data = asreview.ASReviewData.from_file(DATA_FILE)

train_model = LSTMBaseModel()
query_model = MaxQueryModel()
balance_model = SimpleBalanceModel()
feature_model = EmbeddingLSTM()

# Load the embedding matrix, only necessary for lstm models.
train_model.embedding_matrix = feature_model.get_embedding_matrix(
    as_data.texts, EMBEDDING_FILE)

# start the review process.
reviewer = asreview.ReviewSimulate(
    as_data,
    model=train_model,
    query_model=query_model,
    balance_model=balance_model,
```

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```
    feature_model=feature_model,  
    n_instances=10,  
)  
reviewer.review()
```

## CHAPTER 26

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### Indices and tables

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