# Manuscript drafts

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# Introduction

Systematic reviews are top of the bill in building evidence in research. A systematic review attempts to bring together all studies relevant to answer a specific research question [**PRISMA-PGroup2015**]. Systematic reviews inform practice and policy [**Gough2002**] and are key in developing clinical guidelines [**Chalmers2007**].

Systematic reviews are costly. Conducting a systematic review involves the manual screening of thousands of titles and abstracts, identifying publications relevant to answering the research question. An experienced reviewer takes on average 30 seconds to screen one title and abstract, whereas an inexperienced reviewer takes even longer [**Wallace2010**]. Conducting a systematic review typically requires over a year of work from a team of researchers [**Borah2017**].

Systematic reviewers face competing demands. The production of a systematic review is a time-consuming process, but is often bound to a limited budget and timeframe. Currently, the demand for systematic reviews exceeds the available time and resources by far [**Lau2019**]. Especially when the need for guidelines is urgent - such as in the context of the current COVID-19 crisis - it is almost impossible to provide a review that is both timely and comprehensive. To ensure a timely review, reducing workload in systematic reviews is imperative.

With advances in Artificial Intelligence (AI), there has been wide interest in tools to reduce workload in systematic reviews [**Harrison2020**]. More specifically, the field of AI-aided title and abstract screening is rapidly evolving. Various learning models have been proposed, aiming to detect whether a given publication is relevant or irrelevant to the systematic review. Findings suggest that such models potentially reduce workload with 30-70% at the cost of losing 5% of relevant publications (95% recall) [**OMara-Eves2015**].

Screening prioritization is a well-established approach in increasing efficiency in title and abstract screening [**Cohen2009**, **Shemilt2014**]. In screening prioritization, the learning model reorders publications to be screened by their likeliness to be relevant, aiming to present the reviewer with the most relevant publications first. Such an approach allows for substantial time-savings in the screening process: Reviewing relevant publications early facilitates a faster transition of those publications to the next steps in the review process [**Cohen2009**].
Moreover, when combined with a stopping criterion, screening prioritization can be used to reduce the number of publications needed to screen. Additionally, several studies report increasing efficiency beyond reducing workload [**OMara-Eves2015**].

Recent studies have demonstrated the effectiveness of screening prioritization by means of active learning models [**Yu2019**, **Yu2018**, **Miwa2014**]. Active learning is when the model can iteratively improve its predictions by allowing the model to choose the data from which it can learn [**Settles2012**]. Active learning has proven to be an efficient strategy in large datasets where labels are scarce, which makes identifying relevant publications an ideal candidate for such models.
When applied in the screening process, an active learning model can iteratively improve its relevancy predictions by interacting with the reviewer. The model decides which publication it wants the reviewer to screen next, who then provides the model with a label ('relevant', 'irrelevant'). In this active learning cycle, the model can incrementally improve its predictions on the relevancy of the remaining unlabeled publications. Based on previous labelling decisions by the reviewer, the model constantly reorders the remaining publications in the dataset.

Although the application of (active) learning models in reducing workload of systematic reviews has been extensively studied, the complex nature of the field is making it difficult to draw overarching conclusions about best practice. Moreover, the lack of replication on data outside the biomedical sciences makes it impossible to draw conclusions about the general effectiveness of such technologies [**OMara-Eves2015**]. The question remains how different active learning models for screening prioritization perform across different review contexts. Hence, additional evaluations of active learning models are required.

The purpose of this paper is to increase the evidence base of active learning models for reducing workload in title and abstract screening in systematic reviews. Combining latest insights from this area, we present a pipeline of active learning for prioritization screening, called `ASReview`. `ASReview` is an open source and generic tool such that users can adapt and add modules as they like, encouraging fellow researchers to replicate findings from previous studies. Working towards a general consensus in this emerging field, this study implements various active learning models (in `ASReview`). Models are evaluated by performing a simulation on data from six existing systematic reviews from various research areas. All data presented in this study are openly published, hoping to facilitate usability and acceptability of AI-assisted title and abstract screening in the field of systematic review.

The remaining part of this paper is organized as follows. The Technical Details section will cover the workings of active learning models for study selection in systematic reviews on a conceptual level. The method section describes ... The results section reports ... The discusssion section summarises the findings, comments on them and summarises the main findings, discusses discuss limitations, draw conclusion and

[**Marshall2020**]

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**summarise models used**

**propose pipeline**

**and specific components?**

**summarise datasets tested**

## Background

[**OMara-Eves2015**] literature review

[**Yu2018a**], [**Yu2019**] simulated 32 svm classifiers, on software engineering. A popular classifier is SVM. succes with HUTM (fastread), uncertainty, mix of weighting and agressive undersampling, In terms of Yu et al, we adopt .CT.

SVM - tf-idf on medical data, uncertainty sampling, agressive undersampling. [**Wallace2010**]

abstrackr

SVM + Weighting + uncertainty (bow) produced good methods [**Miwa2014**] Also include social sciences data besides medical data.

[**Cohen2006**] perceptron-based classifier (neural network)

SVM on legal documents (no balancing, certainty ) [**Cormack2014**] in limitations section mentions that LR yields about same results, nb inferior results.

[**Kilicoglu2009**] - SVM, naive bayes, boosting and combinations. future work should optimize parameters. “Regarding the base classifiers used in identifying method- ologically rigorous studies, boosting consistently strikes the best balance between precision and recall, whereas naive Bayes in general performs well on recall (demonstrating a tradeoff between recall and precision), as does polynomial SVM on precision. The AUC results are mixed, although boosting has a slight edge overall. These results demonstrate that different classifiers can be used to satisfy different information needs (SVM for specificity, naive Bayes for sensitivity, and boosting for balance between the two, for example).”

Our extensions is that we try different classifiers, on more datasets.

Goal: evaluate performance of different models of the ASReview tool. The screening process is simulated using ASReview, seeing if the original inclusions replicate. What would happen if the citation screening would have been performed using asreview? All datasets accompanying the systematic reviews are openly published. We built several machine learning models to perform automated systematic reviews, who are then applied on existing systematic reviews.

When no balancing is applied, the training data set = labeled data set $\mathcal{L}$ The model can query the labels, who serve as the reviewer, active learning then perform active learning to detect inclusions.

a machine learning-based citation classification tool to reduce workload in systematic reviews of drug class efficacy. Using a perceptron classifier, WSS@95% = 56.61 in [**Cohen2006**]. (5x2 crossvalidation). Can we beat this? The data

Openness, reproducible,

Benefits:

Adopting some sort of stopping criterion (outside scope of the current thesis) the reviewer can quit reviewing after having read only a fraction of candidate studies. meaning the screening process can be finished after reading a fraction of all candidate studies. Saving hours of time and resources.

paper organization:

The goal is to gain insight in classifiers other than the widely applied SVM, overall various research areas. So not only medical sciences.

Although considerable research has been devoted to . . . , less attention has been paid to the comparison of different classifiers. Few studies have evaluated different classifiers in any systematic way different models to use haven't been investigated in a systematic way (only in software engineering)

1) the lack of replication of methods is making it impossible to draw any overall conclusions about best practice/ best approaches of the problem of reducing workload in screening.
2) screening prioritization is appealing to systematic reviewers because . . .
3)
4) implemantation: usabliity and acceptability of such tools amongst researchers conducting a systematic review.

lack of studies investigating the effect of different methods over different research areas. (yu but only software engineering, miwa perhaps?) There is also a significant lack of examples outside of healthcare with the exception of one example in software engingeering

However, there is a need for consensus () and transparancy?

So far, however, there has been little discussion about the different classifiers to be used. Support Vector Machine has been the default in almost all studies.

Several algorithms to assist the reviewer in the abstract screening process have been proposed. (they are available in many shapes/sorts).

**indicating the structure of the writing)** principle findings:

For truly evaluate the effectiveness of such methods,

automatically (by machine learning techniques) In the current study we focus on the effectiveness of different machine learning models in reducing workload in the citation screening process. Assisting the reviewer. Combining various machine learning techniques. Combining recent insights on, we propose ASReview. Approaching the citation screening phase as a classfication task, The benefit is that ASReview is dynamic, user can decide open source, multiple classifiers and other settings,

The current study focus is on reducing workload by prioritizing the most relevant abstracts. Presenting the abstracts orders the abstracts by likelihood of relevance, e.g. th The reviewer sees the most relevant abstracts first, If the model performs well all relevent abstracts will be seen much earlier than when abstracts are read at a random order.

Such a solution can save time and resources. Time saving is not the only benefit: and help to minimize bias..

**Proposed solution** This study is about how machine learning models can increase efficiency in systematic reviews. Their main objective is to identify ..

The strategy to reduce workload proposed in the current study is by prioritizing publications that are deemed most relevant to the systematic review. As the relevant publications are screened first, the reviewing process can be quit earlier.

The stage of abstract screening where abstracts are systematically screened is where a lot is to be gained. This stage is the target of possible learning algorithms that can assist the reviewer in selecting the relevant papers. Together with the reviewer /human machine interaction. The algorithm aims to compute which papers in the pool need to be excluded and which need to be included, based on the reviewers decisions. It learns from the reviewers decisions and asks the reviewer to provide more labels, incrementally improving its class predictions.

The goal of the algorithm defined in the current study is to reduce to number of abstracts needed to screen (maybe not right term, bit biomedical). To be more specific, the algorithm aims to present the reader with the primary studies as soon as possible. This means that at some point you probably have seen all relevant abstracts and are only viewing excluded papers, which means you can stop reviewing much earlier (theoretically spoken). Also reviewing is now much more fun. As compared to when you have to review all abstracts and you perhaps see only one relevant abstract every other week/day.

### Background

. . . starts with a search for potentially relevant publications. This initial set of candidate studies need to be manually screened to identify the publications relevant for answering the research question. Because the initial set often consists of thousands of papers and the

To gather the findings relevant to answering the research question, a systematic search is performed. A systematic search starts with collecting all publications that meet pre-specified eligibility criteria. From this collection of candidate studies the researcher has to identify the publications relevant for answering the research question. Of all candidate studies only a fraction is relevant [. . . ].

As more and more papers are published and reproducibility crisis has emerged, A systematic search often results in thousands of candidate studies. Relevant publications are then identified by screening title and abstract of all candidate studies. This screening process is a manual task often executed by multiple reviewers to ensure reliability. This is a time consuming process that weighs heavily on resources.

Most often the SVM classifier is used, popular and very good results. Also lots of other configurations. However, other classifiers have not been tested a lot (polygon thing by cohe, naïve bayes and random forest by . . . ), but mostly SVM still. Also, most research in the medical sciences (well there are some exceptions of course [conversation between cohen and matwill]

A solution is . . .

It is important reflect on research by giving an overview of research areas which is typically done by a systematic review [. . . ].

To review a specific research area, one starts out with an initial search of thousands of academic papers. All these papers abstracts need to be screened to find an initial batch of possibly relevant papers. With now hopefully only a couple of hundred papers left, the researcher needs to read these papers full-text to arrive at a final selection of papers that are relevant for the final systematic review [this is prisma process?]. This whole processes costs this and this much time [shelmilt].

**Technical details** So you might wonder, how does such an algorithm actually work? Active learning strategy, starting with a pool of unlabeled abstracts (U). The reviewer starts labeling some instances in U, creating L. The algorithm utilizes L to predict labels for all abstracts (classifier), by using a set of features from the papers called X, for example the text in the abstract (feature extraction method). Now, it made an initial classification. The algorithm now aims to improve its classification by which paper from U will be presented to the reviewer next. By labeling the next paper, the reviewer provides the algorithm with new information which the algorithm uses to update its prediction.

We approach asr as a classification problem: All papers obtained in the systematic search form a pool of instances x. All instances x need to be classified, e.g. we want to give them a label y. all x are now part of U,. Binary classification, either inclusion or exclusion. We want to classify based on some features from the instances $x$, feature vector $\mathbf{X}$.

By starting of with L, the algorithm utilizes characteristics of X to predict labels in U.

We want to classify the papers in Where the whole collection of papers in the systematic search form a pool of instances x, with unknown label y. <x,y>.

```
input:
    a pool of unlabeled abstracts $\mathcal{U}$
    oracle labels a few initial papers, from $\mathcal{U}$, $\mathcal{L}$,

  M = train($\mathcal{L}$)
  Query x isin mathcal{U} (<x, y=?)
  oracle <x, y>
```

- pool unlabeled abstracts $\mathcal{U}$
- labeled data set $\mathcal{L}$,
- instance $x$, label $y$
- utility measure $\phi_A(\cdot)$
- $x^*_A$ best query instance according to $\phi_A(\cdot)$

Now there are a few technical details. Many different versions of such algorithms exist. Many of such algorithms have been described in the active learning literature and have been applied in the systematic reviewing process. Not exhaustive, but the algorithm can apply many different strategies to arrive at its predictions, which can be divided in following parameters: classifier, feature extraction strategy, balancing, query strateg y.

To perform all these computations the research was carried out using the ASReview software by Utrecht University, which has a simulation mode that you can just input your labelled review file into and perform a simulation study with it. To be found on GitHub. It has many adjustable components/is very versatile.

Then if we still have time left we explore the effect of another feature extraction method, namely doc2vec. This might possibly increase performance as it performs better at grasping structure/hidden relations/hierarchy between words in the texts. So, it could be interesting in more 'fuzzy' research areas. A downside is that it takes more computing time.

Then if there's even more time we might want to compare a different balance strategy.

A SR can be divided into phases. Everything starts with a **systematic search**, leading to then citation screening is performed, then full-text screening [**PRISMA-PGroup2015**]

What must be the objective of our tool?: It is the tedious task citation screening part where loads of time can be saved.

models are designed in a 'realistic' way (you have some inclusions)

Selecting papers is a two-step process: abstract & fulltext screening

Binary classification problem. predict whether a paper in the pool is an inclusion or exclusion, based on labeled instances from $\mathcal{L}$ and use training data to understand how input variables are related to class.

We're building active learning model who takes X as an input an predicts class using labels from training set. Model improves by deciding asking more information from the reviewer (oracle), accounting for imbalance.

The researcher has some prior knowledge about the pool, some papers ought to be included in the SR.

#### Assumptions

1) decisions of the original SR are **ground truth** (benchmark) (oracle)

The inclusion rate is ... data is imbalanced. what is the philosophy False negatives must be avoided ... The cost of a false negative outweighs the cost of a false positive. Note that we assume the oracle/original user to hold the truth. This is of course not always the case.

There are two classes in the data: exlusions and inclusions. The inclusions are clearly the minority class.

Datasets from the medical and social sciences, software engineering and public administration. Medical sciences SRs are viewed as more 'strict'/'structured' and social sciences more messy.

## active learning for systematic reviews

corpus = all the text:

Active learning = increasing classification performance with every query. The query strategy determines the way unlabeled papers are queried to the researcher.

[**modAL2018**]

RQ1 - what are good classifiers RQ2 - what are good optimization strategies

# Methods

This study was approved by the Ethics Committee of the Faculty of Social and Behavioural Sciences of Utrecht University, filed as an amendement under study 20-104.

All simulations were run using through cartesius EINF-156

Performance of several machine learning models was demonstrated on six systematic review datasets.
study design: retrospective

## Models

$x$ machine learning models ($M$) were built. The models consist of multiple components, of which the classifier and the feature extraction strategy varied over the models.

**Classifiers** Every model applies a classifier $c$ to predict the relevance of publications in the data. The classfiier predicts the class of a publication in the dataset expediting a training dataset $\mathcal{L}$, predicts the class of an instance given input features $\mathbf{X}$

Logistic Regression (LR) - L2-regularized logistic regression. Logistic models the posterior directly, naive bayes has higher bias but lower variance, logistic might perform better when trainign set increases. [**Ng2002**] Naive Bayes (NB) - Naive Bayes assumes all features are independent given the class value. This is obviously not the case but still the algorithm performs impressively [**Zhang2004**]. Especially at ... tasks.

Random Forests (RF) is where a large number of decision trees are fit on bootstrapped samples of the original data. All trees cast a vote on the class, which are aggregated into a class prediction for each input $\mathbf{X}$ [**Breiman2001**].

Support Vecor Machine (SVM) - finds a multidimensional hyperplane to separate classes. [**Tong2001**]

**Word representation** To predict the class of a publication class (e.g. whether a publication should be included or excluded), the classifier uses information from the publications in the dataset. Examples of such information are titles and abstracts. However, the classifier cannot predict the publication class from titles and abstracts as they are. Their textual content to needs to be mapped to feature vectors. This process of numerically representing textual content is called 'word embeddings'.

A classical example of word embeddings a 'bag of words' representation. For each text in the data set, the number of occurrences of each word is stored. This leads to n features, where n is the number of distinct words in the texts [**scikit-learn**]. The bag-of-words method is simplistic and will highly value often occuring but otherwise meaningless words such as "and". Term-frequency Inverse Document Frequency (TF-IDF) [**Ramos2003**] circumvents this problem by adjusting a term frequency in a text with the inverse docuement frequency, the frequency of a given word in the entire data set.

The model expedits features of previously labeled publications and Based on features of the previously labeled inclusions and exclusions, the model

The features used are title and abstract from every publication. - this is what is prescribed by prisma, (check!)

(TF-IDF) (Doc2Vec)

**Fixed components** All models $M$ apply the same query strategy of certainty sampling, in which the presented publication is always the one of which the model is most certain for it to be relevant.

To decrease the class imbalance in the training data, the model rebalances the training set by Dynamic Supersampling (DS). DS decreases the number of irrelevant papers in the training data, whereas the number of relevant papers are increased (by copy) such that the total number of samples remains the same. The ratio between relevant and irrelevant papers is not fixed, but dynamically updated and depends on the number of training samples, the total number of publications and the ratio between relevant and irrelevant publications.

## Datasets

Six Systematic Reviews from various research areas were used to simulate the automated systematic review process. Data were preprocessed from the original source into a test dataset, containing all publications obtained in the systematic search. The test datasets are labelled indicating the relevant and irrelevant publications. Using these labels, a computer simulation of an automated systematic review can be performed on the systematic review data.

The test datasets contain title information on all publications obtained in the search strategy. The instances in the data consist of a title and an abstract and were labeled to indicate which publications were included in the systematic review. Instances with missing abstracts and duplicate instances were removed from the data. The data preprocessing scripts can be found on the GitHub[1]

Cohen et al. collected systematic review datasets from the medical sciences [**Cohen2006**]. All systematic reviews in this database are on drug efficacy. The *ace* dataset used in the current study comes from a systematic review on the efficacy of Angiotensin-converting enzyme (ACE) inhibitors.

The *software* dataset is retrieved from [**Yu2018a**], who collected datasets on literature reviews from the software engineering field. This dataset is on fault prediction in software engineering by [**Hall2012**].

The *nudging* dataset comes from a review from the behavioural public administration area. The SR includes studies on nudging healthcare professionals [**Nagtegaal2019**]. The data was stored on the Harvard Dataverse [**Nagtegaal2019a**].

A literature review from field of psychology, *ptsd*. The SR is on studies applying latent trajectory analyses on posttraumatic stress after exposure to trauma [**vandeSchoot2017**]. The corresponding data can be found on the Open Science Framework [. . . ].

*wilson*, a dataset from the medical sciences [**Appenzeller-Herzog2020**]. TA review on effectiveness treatments of Wilson disease [**Appenzeller-Herzog2019**].

All datasets started with an initial pool of thousands of papers. A fraction of these papers where deemed relevant for the SR, with inclusion rates around 1-2 percent with one outlier of about 5 percent (Table 1).

Table 1: Statistics on datasets from original systematic reviews.

| | Original study | | | Test collection | | |
|---|---:|---:|---:|---:|---:|---:|
| Dataset | Candidate studies | Final inclusions | Inclusion rate (%) | Candidate studies | Final inclusions | Inclusion rate (%) |
| ace | 2544 | 41 | 1.61 | 2235 | 41 | 1.83 |
| nudging | 2006 | 100 | 4.99 | 1847 | 100 | 5.41 |
| ptsd | 6185 | 38 | 0.61 | 5031 | 38 | 0.76 |
| software | 8911 | 104 | 1.17 | 8896 | 104 | 1.17 |
| wilson | 3453 | 26 | 0.75 | 2333 | 23 | 0.99 |

### Optimizing hyperparameters

Every model component contains hyperparameters, leading to a unique set of hyperparameters for each model. To maximize model performance, we need to find optimal values for the hyperparameters. For every model the optimal hyperparameter values are determined by optimizing on the data $d$. The hyperparameters

[1] https://github.com/GerbrichFerdinands/asreview-thesis

are optimized by running several hundreds of optimization trials, in which hyperparameter values are sampled from their possible parameter space. A description of all hyperparameters and their sample space can be found in the appendix.

Maximum model performance is defined as the average time it takes to find an inclusion in the data, or more specific: the loss function minimizes the average number of papers needed to screen to find an inclusion (e.g. the area above the curve in the inclusion plot).

The optimization data $d$ consists of (a subset from) the six systematic review datasets $D$ mentioned above. Three different approaches in composing $d$ are explored:

- **one**, where hyperparameters are optimized on only one of the six datasets, $d \in D$. Such hyperparameters are expected to lead to maximum performance in the same dataset $d$.
- **n**, where hyperparameters are optimized on all six data sets, $d = D$. This optimization approach intends to serve in producing the most optimal hyperparameters overall.
- **n-1**, where hyperparameters are optimized on all six datasets but one, $d \subset D$. Serving as a sensitivity analysis for the former condition, e.g. how sensitive are the hyperparamters. also as a cross-validation later on: hyperparameters obtained by training data, test data is never seen before. where d are all datasets but the one where we want to simulate later on. This results in $6 + 6 + 1 = 13$ sets of hyperparameters for every model.

Results were visually inspected to check if an optimum (minimal loss) has been reached. More trials were run if the loss still seemed to go down at a quick pace.

The hyperparameter values that were found to lead to a minimum loss value were visually inspected.

### Optimization results

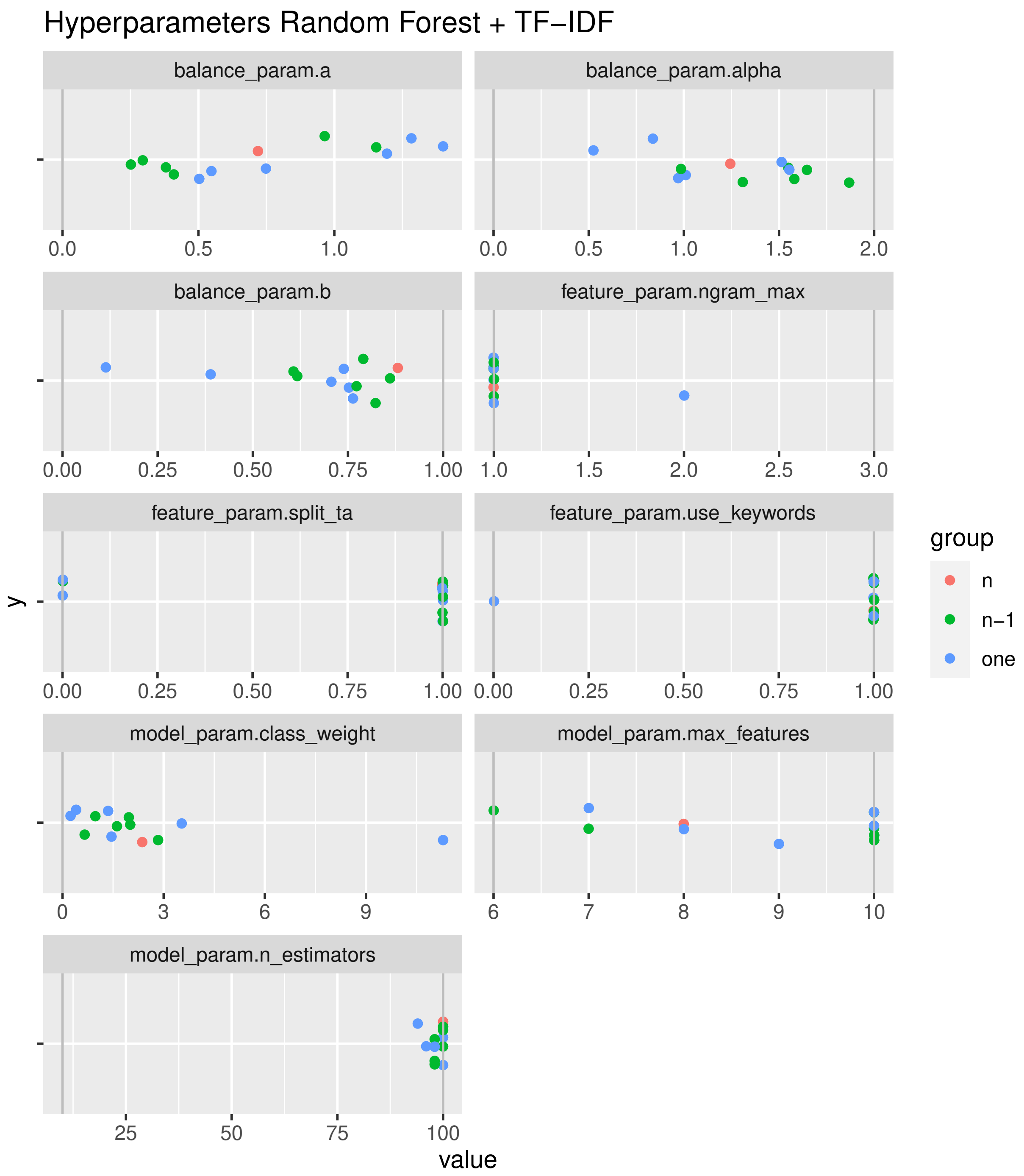
For every model, 13 sets of hyperparameters were optimized.

*to include: plotting the loss reduction over trials*

Optimal values of the hyperparameters were visually inspected.

As an example, the hyperparameters of the RF_TF-IDF model are presented in Figure 1. A panel displays the optimal values for a certain hyperparameter, where the blue colored dots represent the **one** condition, the green dots the **n-1** condition and the orange dot represents the optimal hyperparameter value when optmizing over all datasets (**n**). The x-axis represents the possible parameter space where the vertical grey lines mark the boundaries of the hyperparameter space (if possible). Note that the feature parameters ngram_max, split_ta, use_keywords and model parameters max_features and n_estimators are categorical.

Overall, the optimal values are distributed over the parameter space. Outlying values all belong to the **one** condition where optimization was dependent on one dataset only. Fore example, the class_weight parameter has an outlying value of 11.3 that belongs to the nudging dataset. (Why this is the case I can only speculate, but it is worth mentioning that this dataset has a relatively high inclusion rate of 5.41%, compared to the other datasets).



## Appendix x - Hyperparameters and their sample space

Classifier hyperparameters

```
class_weight: normal(0,1) constrained to be > 0
class weight of the inclusions.
```

Logistic Regression

```
c: float. normal(0,1), constrained to be > 0
```

Support Vector Machine

```
gamma: ["auto", "scale"],
Gamma parameter of the SVM model.

C:
C parameter of the SVM model.

kernel:
SVM kernel type.["linear", "rbf", "poly", "sigmoid"]
```

Naive Bayes

```
"model_param.alpha", # exp(normal(0,1))
```

Random Forest

```
max_features: int (between 6 and 10)
    Number of features in the model.

n_estimators: int between 10 and 100
    Number of estimators.

model_param.n_estimators" #quniform(10,100,1)
```

Balance strategy hyperparameters: Dynamic supersampling:

```
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.
```

Feature extraction strategy hyperparameters

```
split_ta: 0 or 1
   whether titles and abstracts are split

use_keywords: 0 or 1
    whether keywords should be used
```

TF-IDF

```
ngram_max: 1, 2 or 3
    Can use up to ngrams up to ngram_max. For example in the case of
    ngram_max=2, monograms and bigrams could be used.
```

Doc2Vec

```
vector_size: int (between 32 and 127)
    Output size of the vector.

epochs: int (between 20 and 50)
    Number of epochs to train the doc2vec model.


min_count: int (between 1 and 3)
    Minimum number of occurences for a word in the corpus for it to be
    included in the model.

window: int (between 5 and 9)
    Maximum distance over which word vectors influence each other.

dm_concat: int 0 or 1
    Whether to concatenate word vectors or not.

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 0 or 1
    Whether to train the word vectors using the skipgram method.
```

## Simulations

To demonstrate the models, simulations are performed of the models on six original systematic reviews. With the labeled datasets, the systematic review can be reproduced but with now using a machine learning model to optimize the reviewing process.

The initial training set of the active learning model in the simulation is one prior included publication and one prior excluded publication, randomly sampled from the data. This demonstrates a ‘worst case scenario’ where the reviewer has minimal prior knowledge on publications in the data. For this simulations there is no need for a human reviewer since the labels in the data can be queried. The oracle is not the reviewer but the labels in the data. The model retrains every time after a label is provided by the oracle. The simulation ends when all publications in the dataset have been queried.

To account for variance, every simulation is repeated for 15 trials $t$.

### Statistical analysis

Results are aggregated over 15 runs of every simulation.

#### measures

#### comparison over conditions

## The software

ASReview takes the following parameters/arguments: We now have 75 combinations. for every for every model (5), for every dataset (5) and for every set of optimized hyperparameters (3), a simulation study consisting trials is performed. From these $5 * 5 * 3 = 75$ simulation studies, performance of the different models is evaluated.

| | Configurations |
|---|---|
| Models | 2-Layer Neural Network, Naive Bayes, Random Forest, Support Vector Machine, Logistic Regression |
| Query Strategies | Cluster Sampling, Maximum Sampling, Cluster * Maximum Sampling, Maximum * Uncertainty Sampling, Maximum * Random Sampling, Cluster * Uncertainty Sampling, Cluster * Random Sampling |
| Feature extraction strategies | Doc2Vec, TF-IDF, sbert, embeddingIdf |

Use these inputs to predict relevance of papers.

#### Stage 1: hyperparameter optimization

Or, more specific:

| Models | Feature extraction strategies |
|---|---|
| dense_nn | doc2vec |
| nb | tfidf |
| rf | tfidf |
| svm | doc2vec |
| lr | tfidf |

**Performance metrics** For each model, Several metrics are used to compare performance of different models over datasets,

| Dataset | Naive Bayes | Random Forests | Support Vector Machine | Logistic Regression | Dense Neural Network |
|---|---|---|---|---|---|
| ptsd | ? | | | | |
| ace | ? | | | | |
| hall | ? | | | | |
| nagtegaal | ? | | | | |
| .... | ? | | | | |

The goal is twofold: we want to identify all relevant papers, as fast as we can. Tradeoff: identifying all relevant papers and reducing workload. A good metric to evaluate this is..

What is more important: recall or precision?

Recall more highly valued than precision.

What about class imbalance?

**RRF** Amount of relevant references found after having screened a certain percentage of the total number of abstracts.

**Work saved over sampling (WSS)** Indicates how much time can be saved, at a given level of recall. WSS is in terms of the percentage of abstracts that don't have to be screened by the researcher. Typically, WSS is measured at a recall of 0.95. Reasonable because..

$$\texttt{WSS} = \frac{TN + FN}{N} - (1 - recall)$$

**Raoul**

**Utility?**

**F-measure**

**ROC/AUC** Is performance related to some characteristic (n, inclusion rate, ...)

? How to compare outcomes of 3 different optimization strategies?

## Results

| | ace | nudging | ptsd | software | virus | wilson |
|---|---|---|---|---|---|---|
| BCTD | 0 | 0 | 0 | 0 | 0 | 0 |
| RCTD | 0 | 0 | 0 | 0 | 0 | 0 |
| SCTD | 0 | 0 | 0 | 0 | 0 | 0 |
| LCTD | 0 | 0 | 0 | 0 | 0 | 0 |
| NCTD | 0 | 0 | 0 | 0 | 0 | 0 |
| BCDD | 0 | 0 | 0 | 0 | 0 | 0 |
| RCDD | 0 | 0 | 0 | 0 | 0 | 0 |
| SCDD | 0 | 0 | 0 | 0 | 0 | 0 |
| LCDD | 0 | 0 | 0 | 0 | 0 | 0 |
| NCDD | 0 | 0 | 0 | 0 | 0 | 0 |

# Discussion

- we look for final inclusions but we screen only the abstracts (do they satisfy the imformation need (blake (page 19 omara et evs)))

future research: - stopping rule is not discussed - computation/retraining time

strengths:

- open data
- different research areas
- different models on same dataset
- different datasets on same model

limitations

future research - all models save time, difficult to distinguish performance over datasets, especially when applied on a dataset of which no prior information is known (e.g. inclusions isn't known in practice). Perhaps go for other criteria like the fastest model, replicate study with computation time?

Simulating the title and abstract screening process, models are evaluted on their capability/speed of detecting the final inclusions. However, in a manual SR these final inclusions are selected after reading the fulltext. Information the text mining tool does not have. To truly assess the added value of such a tool, models should be evaluated on their capability of detecting the abstract inclusions. Call for systematic reviewers to openly publish need for open data containing abstract inclusions, not only final inclusions!

# Appendix A - list of definitions

### Feature Extraction Strategies

split_ta = overall hyperparameter

### TF-IDF

### hyperparameters

```
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.
```

**Doc2Vec** Predicts words from context. Aims at capturing the relations between word (man-woman, king-queen). [**Le2014**]. Using a neural network.

using Continuous Bag-of-Words (CBOW), Skip-Gram model, .... Word vector $W$ and extra: document vector $D$, trained to predict words in the text.

From gensim [**Rehurek2010**].

```
    Arguments
    ---------
    vector_size: int
        Output size of the vector.
    epochs: int
        Number of epochs to train the doc2vec model.
    min_count: int
        Minimum number of occurences for a word in the corpus for it to
        be included in the model.
    workers: 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 metho
```

**SBERT** BERT-base model with mean-tokens pooling [**Reimers2019**]

**embeddingIdf** 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

### Models

**Naive Bayes** Naive Bayes assumes all features are independent given the class value. [**Zhang2004**]

ASReview uses the `MultinomialNB` from the scikit-learn package [**scikit-learn**], that implements the naive Bayes algorithm for multinomially distributed data. `nb`

Hyperparameters

- alpha - accounts for features not present in learning samples and prevents zero probabilities in further computations.

**Random Forests** A number of decision trees are fit on bootstrapped samples of the original data, [**Breiman2001**] RandomForestClassifier from sklearn

Arguments ——— n_estimators: int Number of estimators. max_features: int Number of features in the model. class_weight: float Class weight of the inclusions. random_state: int, RandomState Set the random state of the RNG. `"""`

**Support Vector Machine** Arguments ——— gamma: str Gamma parameter of the SVM model. class_weight: class_weight of the inclusions. C: C parameter of the SVM model. kernel: SVM kernel type. random_state: State of the RNG.

**Logistic Regression**

**Dense Neural Network**

### Query Strategies

- Max - Choose the most likely samples to be included according to the model
- Uncertainty - choose the most uncertain samples according to the model (i.e. closest to 0.5 probability) [**Lewis1994**]
- Random - randomly selects abstracts with no regard to model assigned probabilities.
- Cluster - Use clustering after feature extraction on the dataset. Then the highest probabilities within random clusters are sampled

The following combinations are simulated:

- cluster
- max
- cluster * random
- cluster * uncertainty
- max * cluster
- max * random
- max * uncertainty

**Balance Strategies**

**amount of training data**

- n_instances = number of papers queried each query
- n_queries = number of queries
- n_prior_included: 5
- n_prior_excluded:

# Combinations

This leads to 119 combinations of configurations.

- Naive bayes only goes with tfidf feature extraction.
- For the feature extraction strategies we will focus on doc2vec and tfidf. (but will compute all 4)
- This leads to 3 * 7 * 4 * 3 + 1 * 7 * 1 * 3 = 273 combinations.

See appendix A for a table containing all 273 combinations.

## Cross-validation

Should give an accurate estimate of maximum performance / future systematic reviews to be performed.

# Appendix B - combinations

| Model | Query Strategy | Feature extraction strategy |
|---|---|---|
| dense_nn | cluster | doc2vec |
| dense_nn | max | doc2vec |
| dense_nn | max * cluster | doc2vec |
| dense_nn | max * uncertainty | doc2vec |
| dense_nn | max * random | doc2vec |
| dense_nn | cluster * uncertainty | doc2vec |
| dense_nn | cluster * random | doc2vec |
| dense_nn | cluster | tfidf |
| dense_nn | max | tfidf |
| dense_nn | max * cluster | tfidf |
| dense_nn | max * uncertainty | tfidf |
| dense_nn | max * random | tfidf |
| dense_nn | cluster * uncertainty | tfidf |
| dense_nn | cluster * random | tfidf |
| dense_nn | cluster | sbert |
| dense_nn | max | sbert |
| dense_nn | max * cluster | sbert |
| dense_nn | max * uncertainty | sbert |
| dense_nn | max * random | sbert |
| dense_nn | cluster * uncertainty | sbert |

*(continued)*

| Model | Query Strategy | Feature extraction strategy |
|---|---|---|
| dense_nn | cluster * random | sbert |
| dense_nn | cluster | embeddingIdf |
| dense_nn | max | embeddingIdf |
| dense_nn | max * cluster | embeddingIdf |
| dense_nn | max * uncertainty | embeddingIdf |
| dense_nn | max * random | embeddingIdf |
| dense_nn | cluster * uncertainty | embeddingIdf |
| dense_nn | cluster * random | embeddingIdf |
| nb | cluster | tfidf |
| nb | max | tfidf |
| nb | max * cluster | tfidf |
| nb | max * uncertainty | tfidf |
| nb | max * random | tfidf |
| nb | cluster * uncertainty | tfidf |
| nb | cluster * random | tfidf |
| rf | cluster | doc2vec |
| rf | max | doc2vec |
| rf | max * cluster | doc2vec |
| rf | max * uncertainty | doc2vec |
| rf | max * random | doc2vec |
| rf | cluster * uncertainty | doc2vec |
| rf | cluster * random | doc2vec |
| rf | cluster | tfidf |
| rf | max | tfidf |
| rf | max * cluster | tfidf |
| rf | max * uncertainty | tfidf |
| rf | max * random | tfidf |
| rf | cluster * uncertainty | tfidf |
| rf | cluster * random | tfidf |
| rf | cluster | sbert |
| rf | max | sbert |
| rf | max * cluster | sbert |
| rf | max * uncertainty | sbert |
| rf | max * random | sbert |
| rf | cluster * uncertainty | sbert |
| rf | cluster * random | sbert |
| rf | cluster | embeddingIdf |
| rf | max | embeddingIdf |
| rf | max * cluster | embeddingIdf |
| rf | max * uncertainty | embeddingIdf |
| rf | max * random | embeddingIdf |
| rf | cluster * uncertainty | embeddingIdf |
| rf | cluster * random | embeddingIdf |
| svm | cluster | doc2vec |
| svm | max | doc2vec |
| svm | max * cluster | doc2vec |

*(continued)*

| Model | Query Strategy | Feature extraction strategy |
|---|---|---|
| svm | max * uncertainty | doc2vec |
| svm | max * random | doc2vec |
| svm | cluster * uncertainty | doc2vec |
| svm | cluster * random | doc2vec |
| svm | cluster | tfidf |
| svm | max | tfidf |
| svm | max * cluster | tfidf |
| svm | max * uncertainty | tfidf |
| svm | max * random | tfidf |
| svm | cluster * uncertainty | tfidf |
| svm | cluster * random | tfidf |
| svm | cluster | sbert |
| svm | max | sbert |
| svm | max * cluster | sbert |
| svm | max * uncertainty | sbert |
| svm | max * random | sbert |
| svm | cluster * uncertainty | sbert |
| svm | cluster * random | sbert |
| svm | cluster | embeddingIdf |
| svm | max | embeddingIdf |
| svm | max * cluster | embeddingIdf |
| svm | max * uncertainty | embeddingIdf |
| svm | max * random | embeddingIdf |
| svm | cluster * uncertainty | embeddingIdf |
| svm | cluster * random | embeddingIdf |
| lr | cluster | doc2vec |
| lr | max | doc2vec |
| lr | max * cluster | doc2vec |
| lr | max * uncertainty | doc2vec |
| lr | max * random | doc2vec |
| lr | cluster * uncertainty | doc2vec |
| lr | cluster * random | doc2vec |
| lr | cluster | tfidf |
| lr | max | tfidf |
| lr | max * cluster | tfidf |
| lr | max * uncertainty | tfidf |
| lr | max * random | tfidf |
| lr | cluster * uncertainty | tfidf |
| lr | cluster * random | tfidf |
| lr | cluster | sbert |
| lr | max | sbert |
| lr | max * cluster | sbert |
| lr | max * uncertainty | sbert |
| lr | max * random | sbert |
| lr | cluster * uncertainty | sbert |
| lr | cluster * random | sbert |
| lr | cluster | embeddingIdf |

*(continued)*

| Model | Query Strategy | Feature extraction strategy |
|---|---|---|
| lr | max | embeddingIdf |
| lr | max * cluster | embeddingIdf |
| lr | max * uncertainty | embeddingIdf |
| lr | max * random | embeddingIdf |
| lr | cluster * uncertainty | embeddingIdf |
| lr | cluster * random | embeddingIdf |

# Appendix C - supercomputer Cartesius

500,000 SBU

Running on Cartesius is charged in System Billing Units (SBUs), and charging is based on the wall clock time of a job. On fat and thin nodes, an SBU is equal to using 1 core for 1 hour (a core hour), or 1 core for 20 minutes on a GPU node. Since compute nodes are allocated exclusively to a single job at a time, you will be charged for all cores on that node - even if you are using less.

In the current study, the classifier and the feature extraction strategy are varied, whereas the query and balance strategy remain fixed. In the current study only a fraction of all possible configurations are tested for the sake of brevity. There are many more options available and open to exploration.