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Voice atypicalities in Schizophrenia; replicability of machine learning approaches

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Abstract

Can machine learning (ML) applied to voice data be used as a tool to help diagnose people with schizophrenia? Numerous studies have shown high accuracies when classifying schizophrenia, but results are widely heterogenous, as concluded in the latest meta study within the field (Parola et al., 2019). Little work has investigated the validity and robustness of the previous findings, and few replications shed light on the generalizability of the studies. Currently there is no consensus on which machine learning pipeline should be applied for optimal classification of schizophrenic patients.

This study provides a proposal for a general machine learning pipeline suitable for future research into this topic, along with the information necessary for implementing both rigorous and conservative machine learning models. As the pipeline is meant to be broad and general, an example of its more specific implementation is also provided for clarifying purposes. It is exemplified through a replication of the promising study by Chakraborty et al (Chakraborty et al., 2018), and thus also has the benefit of contributing to science within this area that is largely deprived of replications. A macro average F1-score of 0.70 was found – notably lower than the original study’s 0.77. As the replication employed a dissimilar dataset and slightly diverging methods, these differences were discussed in relation to the results. Subsequently, the proposed overall pipeline was scrutinized and given its limitations, further development on the pipeline was suggested. Finally, this paper advocates for a more open and cumulative scientific community.Keywords: schizophrenia, speech signal, acoustic features, biomarker, machine learning

# 1. Introduction

## 1.1 Schizophrenia and voice as a biomarker

Schizophrenia has been associated with several language and voice differences (Andreasen et al., 1995; Cohen et al., 2012; Covington et al., 2005; Kuperberg, 2010; Parola et al., 2019). These language and speech disturbances are used in the clinical assessment process and proven helpful for identifying those individuals that are at a high risk for developing psychosis – even before onset (Bearden et al., 2011; DeVylder et al., 2014; Sichlinger et al., 2019). They have furthermore allowed for tracking psychotic symptoms and predicting progression in symptoms (Bearden et al., 2011; Corcoran et al., 2020; Morice & Ingram, 1983; Solomon et al., 2011). There is, however, a big drawback to the current use of speech in schizophrenia. Speech is being manually annotated or rated by expert raters, which is time extensive and requires training of the raters. This makes the procedure expensive and impractical on a large scale. Moreover, there is a chance that only the most extreme cases are picked up on, when using these manual assessments (Hitczenko et al., 2020). As the prospects of using speech clinically are ample but merely impractical on a larger scale, recent endeavors have been made to try and automate the assessment using supervised machine learning (ML) approaches.

## 1.2 Machine learning of acoustic patterns for detection of schizophrenia

### 1.2.1 Prospects of machine learning in classifying schizophrenia

Supervised ML classification works by learning patterns in some data set and can then subsequently be used to predict, using the learned patterns. The ‘learning’ part practically means building a model of the distribution of class labels (e.g. schizophrenic/non-schizophrenic) from predictor variables (e.g. acoustic features from speech). The ‘machine’ entails that the process is automated, which allows for finding complex, multivariate and sometimes non-linear relationships between multiple features in conjunction and class labels (Kotsiantis et al., 2007). After training a model, it can then be used to assign class labels to the testing instances where the class labels are unknown, but where the predictor values are known.

ML has the potential of supporting clinical evaluations. While the currently implemented manual assessment is impractical on a large scale, ML is not. It would allow for preemptively identifying those at risk for developing schizophrenia on a large scale and give clinicians an effortless way of tracking and predicting progressions in symptoms. Furthermore, judgements are objective given their automated nature (Hitczenko et al., 2020). Classification algorithms have been able to classify schizophrenia with accuracies between 70% and 95% (Martínez-Sánchez et al., 2015; Rapcan et al., 2010; Stassen et al., 1995; Tahir et al., 2019). If computational methods can achieve these rates of correct predictions, they may very well be applied clinically.

### 1.2.2 Limitations of machine learning methods in schizophrenia

Although the method of machine learning looks promising at first glance, some substantial hurdles in the way of instantiating these computational methods clinically.

One hurdle is the issue of overfitting that exists within the field (Vabalas et al., 2019; Voleti et al., 2019). Overfitting is the term for having models learn and rely on spurious correlations between features (acoustic features within this field) and a class (such as a diagnosis). Studies with overfit models might publish good performance, but the models have low generalizability and would predict poorly new data (Dietterich, 1995).

Another hurdle is the potential bias of the models. A large discrepancy in results across studies has been found within the field, which undermines belief in the generalizability of the models (Hitczenko et al., 2020). Much literature has not controlled for sociodemographic factors such as age, education, sex and race and as a result, have produced biased models that fail to generalize to new data (Vabalas et al., 2019).

A final obstacle within the literature is the diversity in ways of conducting research. As this field of research is relatively new, no universally accepted way of conducting ML exists. As a result, studies vary considerably in methods, method quality, transparency and documentation. Not only does this make it hard to compare studies, but it also makes it difficult to pinpoint which methods, feature sets, or datatypes produces the best results. When a study finds a classification rate of 87.5% (Martínez-Sánchez et al., 2015), while another finds a rate of 79.5% (Chakraborty et al., 2018), it can be hard to investigate why. The difference in performance might be due to one study using LDA classification as a method, while the other uses SVM. It could also be due to one study using features related to emotion as predictors, while the other does not. Furthermore, studies also vary in their way of documenting both methods and results. If the methods or the results are inadequate for comparing across studies, then it is hard to pinpoint which factors cause what (Hitczenko et al., 2020).

## 1.3 Alleviating current limitations

### 1.3.1 Through replications and conservative ML implementation

Replications and conservative ML implementation might prove to diminish the limitations. Replications and studies differing slightly from past work (such as on nationality of participants) give clear insights into the impact of specific factors (e.g. showing that cross-cultural differences impact results). Proper ML implementation ensures that these inferences can be made, as this ensures that studies are:

a) replicable – the studies must be transparent and properly document the entire process of conducting the study,

b) using proper and conservative methods – results are only insightful if the models producing them do not suffer from problems of overfitting or bias.

To alleviate limitations within this research area, we must ensure that the two previously mentioned criteria are met. But what constitutes a proper conservative ML implementation? This paper will attempt to provide a general pipeline that guides proper conservative ML implementation. The workflow that the pipeline suggests will allow for better ML practice as well as an improvement of the conditions for comparisons of results between studies.

### 1.3.2 A general pipeline for ML using voice

A pipeline consists of several steps to train a model and operate workflow guidelines, from which predictive algorithms can be created. It can be used to support and streamline research, as well as easing comparison to other work (Guzzetta et al., 2010; Olson & Moore, 2016; Samad & Witherow, 2018). In turn, this will enable insights of the impact of specific methods, features or data on machine learning within this research field.

The pipeline that this paper is presenting is general and broad, with aspirations of being widely inclusive. Its intended use is within ML research using voice as a predictor and may be directly applicable to research within the fields of autism or depression. The pipeline will narrow in the range of options to ensure that the necessary requirements for good ML conduct are being met. The pipeline will be divided up into 9 steps, visualized in figure 1. The pipeline will not specify exactly how they ought to be carried out. Proper and transparent documentation is therefore critical – just as in all research, but perhaps especially within a field that suffers from little replicability and poor documentation.

*Data acquisition.* Knowledge of the data that is going to be processes is important for avoiding pitfalls. A number of factors from data can confound a study if neglected – however, these factors pose no threats if dealt with appropriately. First, it is important to be wary of any bias that might arise in the model as a result of sociodemographic factors. Educational level, age, race, sex have been known to cause a wide array of harmful bias across research fields, but additional factors such as medication and severity of symptoms might also contribute to biases (Blodgett et al., 2020; Cohen et al., 2016; Hitczenko et al., 2020). Secondly, data quantity is important. Internal and external validity of a study have been found to undermined by small sample sizes (Faber & Fonseca, 2014), and there has been found an association between small sample sizes and biased performance in ML studies classifying diagnosis from voice (Vabalas et al., 2019). Thirdly, the task from which the recordings are derived has to be taken into account, as cognitive and social load has been found to increase the effects of schizophrenia in the acoustic signal (Parola et al., 2019). Finally, irrelevant recording identifiers must be controlled for. Background noise, room ambience or recording settings should ideally be uniform across diagnosis. Having all schizophrenics all be recorded within one room and the healthy controls in another could cause potential problems as acoustic features of participants might be altered by room acoustics (Olsen, 2018).

*Preprocessing.* Preprocessing includes noise removal and data augmentation. This step may alleviate the data of confounds such as room acoustics or differences in microphone settings (Olsen, 2018).Since raw recordings cannot be used to predict, features also must be extracted from the speech within this step. The choice of features set can be driven by theory, by choices of past studies or can be entirely explorative.

*Data partitioning.* Train/test splits have found to be more robust and provide less balanced results in comparison to K-fold cross-validation (Vabalas et al., 2019). Train/test splits are therefore recommended. Further dividing the training set up, into a training and a validation set can further allow better hyperparameter tuning (Schratz et al., 2019). The ratio of train/test has an impact. Larger training sets allow for the model to better learn the patterns in the data, while a larger test set allows for a more accurate measure of performance. Having for example only three voice recordings to in the test set could only result in an accuracy of either 0, 33.33, 66.67 or 100 percent accuracy even given a true accuracy 70 percent. Although there is some basis for choosing the split, there is no scientific consensus on what is optimal. 70/30 or 80/20 is often used. \* cite \*.  
Given an unbalanced dataset, some precautionary measures ought to be taken for partitioning. An unbalanced training set of for example 4 male patients and 2 female controls, might simply lead to the model predicting ‘schizophrenic’ to all cases where the acoustic features are specific to males. A model might end up biased, if it learns the acoustic patterns of males instead of those for schizophrenia. However, if the testing set and not the training set is unbalanced another problem may occur. A test set with for example very few females does not allow for accurately seeing whether the model is, in fact biased.

*Feature scaling.*Feature scaling is a necessary step for most algorithms to function properly. It has been known to improve performance, as well as decrease the computational load and avoid convergence issues \*cite\*. Regardless of scaling method, it is important to avoid scaling the pooled features from the training and holdout set – instead the scaling of both the training and holdout set should only use information (e.g. min-max values if using min-max normalization) from the training set. This ensures that no information can flow from the training to the test set, which otherwise would result in overfitting (Myrianthous, 2020).

*Feature selection:*It can be necessary to select a subset of features, given many extracted features. Feature selection is carried out in order to improve predictive power and interpretability as well as to reduce complexity and need for computational power.  
Features must only be selected on basis of information in the training set, and not on the pooled training and testing data. Selecting relevant features based on what is relevant in the test set is going to produce problems with overfitting and low generalizability (Vabalas et al., 2019).   
Numerous feature selection techniques exist, and although choosing a technique might seem an arbitrary choice, it is not. They do in theory perform the same task, but in practice they do not perform equally well (Oreski et al., 2017). There simply is no silver bullet method, however, as the best individually performing feature selection technique depends on both dataset and classifier algorithm (Jović et al., 2015).

*Model training, tuning and testing.*Supervised machine learning covers a wide range of algorithms that all produce models based on some set of data. Common to most of them is the embedded use of hyperparameters - parameters with values that control the learning process of a given algorithm. Performance is dependent on hyperparameter settings and they must be specified before training a model (Hutter et al., 2014). However, determining the appropriate values can be complex (Claesen & De Moor, 2015). Some software implements automated ways of doing so, but at the present time, they do not necessarily determine the optimal values (Feurer & Hutter, 2019; Mantovani et al., 2016; Olson et al., 2017; Sanders & Giraud-Carrier, 2017; Thornton et al., 2013). Optimal values can, however, be discovered semi-manually. One of the benefits of partitioning the data up into a training, a validation and a test set is the possibility of validating the model on the validation set. After having the model trained on the training set with a given set of hyperparameters, its performance can be explored via the validation set. The hyperparameters can then again be tuned and repeatedly be validated until the optimal hyperparameter settings have been found. Since the model has been validated without the use of the test set, we can be assured that the model has not been overfit to the test set, thus making the test set suitable for as an evaluation of true performance.

*Validation.* When evaluating performance on the test set, confusion matrices are critical. They provide the complete picture of performance and all relevant metrics of performance can be calculated solely using the information from the matrix. They ought to be supplemented by additional evaluation metrics, however. Accuracy – the percentage of correct classifications – is regarded common practice but can often misleading, which is why other measures such as precision, recall and F1-scores ought to be provided (Hossin & Sulaiman, 2015).

### 1.3.3 Purpose of paper

To summarize; voice proves to be an important biomarker for schizophrenia with prospects of widespread application if automated. Machine learning proves promising and appear to be able to distinguish and schizophrenia. However, the field of machine learning within this topic have issues with overfitting, bias, and problems with comparability of results between studies as a result of large differences in methods between studies.

To alleviate these problems, this study provides a pipeline which assist in diminishing issues of overfitting and bias as well as improving conditions for comparison of results between studies. As a way of facilitating replications and providing an exemplification of the pipeline, this study will furthermore perform a replication of the study by Chakraborty and colleagues from 2018 (Chakraborty et al., 2018). Finally, the implementation of the pipeline in the replication will be evaluated - and the potential limits and prospects of the pipeline will be discussed.

# 2. Methods

## 2.1 Pipeline implementation – an overview of the methods

The replication of this paper follows and provides an exemplification of general pipeline. The methods section will provide a detailed description of the choices for each step in the pipeline.  
To provide an overview of the process and showcase how it followed the general pipeline, a short summary will be provided below. Additionally, two figures will be provided. One figure attempts to visualize the pipeline (figure 1) and one attempts to visualize the complex multi-leveled process of partitioning (figure 2).

Diagram

Description automatically generated

Figure 1.

*An overview of the proposed pipeline. Purple boxes refer to the general pipeline whereas the green refer to the specific choices of this replication.*

The pipeline for this replication is divided up into 8 steps which are as follows:  
**1) Data acquisition.** Recorded voice data from 4 studies was acquired. **2)** **Data preprocessing.** Prior to this study, all data had gone through a cleaning process and all 988 features extracted in the original experiment were extracted from the data in this replication. **3) Partitioning.** The data was partitioned into a training and a holdout set of 80% and 20%, respectively. **4) Feature scaling.** Features were min-max normalized. **5) Feature selection.** The training data was split up into 5 folds. These folds were used in 5 different splits – with each split having a training set consisting of 4 out of the 5 folds and a validation set consisting of the remaining fold. All training sets had their features L2 regularized; meaning that the less important features were removed. In short, this process thus resulted in 5 validation sets and 5 training sets, each with an appertaining feature set. For an overview, see figure 2.

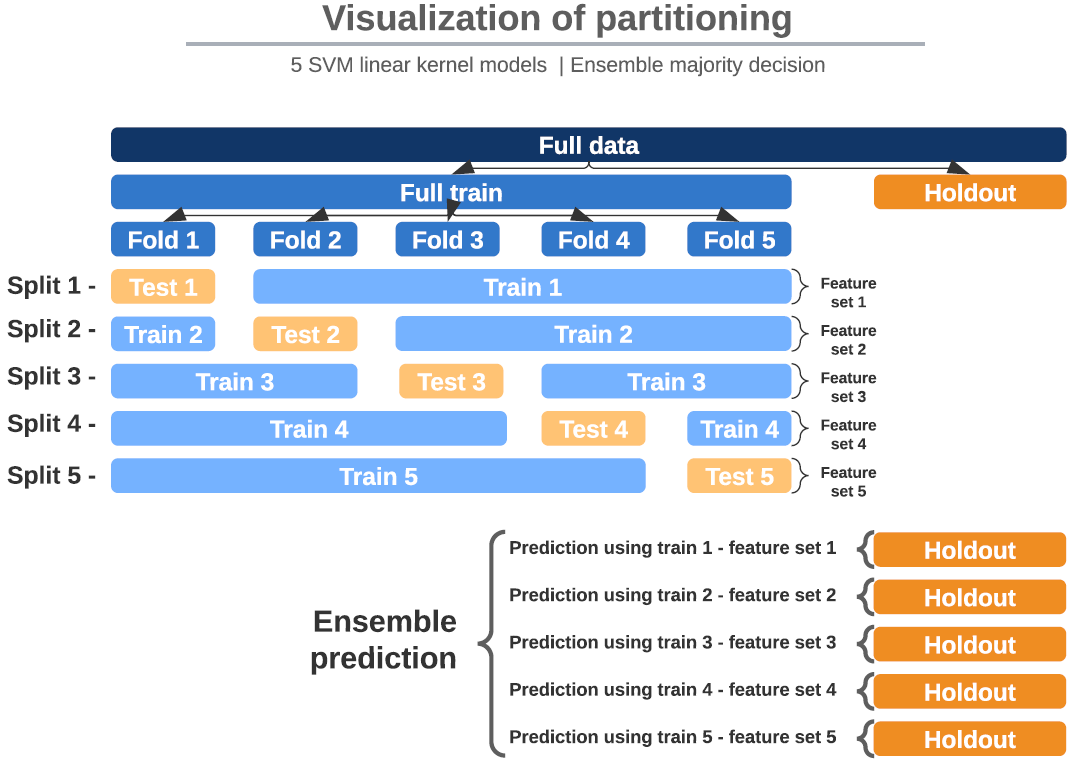


Figure 2.  
*A visualization of the data structures used for this ML replication. Shows the process of partitioning and dividing the data up into multiple folds and outlines which sets were used for what.*

**6), 7), 8) Model training, parameter tuning, model testing.** 5 SVM linear kernel models were then constructed to classify patients from controls. Each of these models were fit on the 5 training sets using the respective feature sets. The fit models were then validated on the matching validation set. Hyperparameters (C and gamma) where then tuned and the models were validated again. The process was repeated until the performance was found to be optimal.

**9) Validation.** Finally, the 5 models were tested on the test set. An ensemble model was also constructed. This model predicted the holdout data by the use of the majority vote of the other 5 models. Performance on the holdout set was then evaluated for the 6 models using relevant metrics.

## 2.2 Literature search for choice of replication

A literature search for papers, dissertations and unpublished manuscripts was conducted for finding a paper to replicate. The complete list of papers listed in the meta-analysis by Parola et al. in 2019 (Parola et al., 2019) was manually screened – first by title and since by content. As their search was last updated as of April 12, 2018, the search was continued from that date forward to Sep 15, 2020 when the continued search took place. The continuation of the search used the same search terms (schizo\* AND machine learning AND prosody OR inflection OR intensity OR pitch OR fundamental frequency OR speech rate OR voice quality OR acoustic OR intonation OR vocal). This search yielded an additional 709 papers that were manually screened for relevance by title. Relevant papers, were then explored by content looking for papers that 1) implemented ML to classify schizophrenia patients from healthy controls using acoustic features, 2) were transparent and well-documented, 3) were thorough in applying proper ML methods, 4) had large amounts of data. This narrowed the number of papers down to 8 papers (see appendix, 7.1). The study by Chakraborty and colleagues from 2018 was chosen for replication after carefully assessment. (Chakraborty et al., 2018).

## 2.3 Data

### 2.3.1 Data sources

The data used in this paper consists of speech recordings gathered from 3 published studies (Beck et al., 2020; Bliksted et al., 2014, 2019) and an unpublished study by Vibeke Bliksted.

Participants from all studies went through the same tasks; namely the Frith Happé animations task (Abell et al., 2000). All participants went through 8 such trials that were recorded, except for in the study from 2014 by Bliksted et al., where the they also recorded 2 practice trials – meaning this dataset included voice recordings from 10 trials (Bliksted et al., 2014). This totaled in 1900 recordings (mean duration = 18.18 sec. SD duration = 14.84). Recording settings and equipment was constant within study, but unique across studies.

### 2.3.2 Participants

222 Danish participants were included in this study. Out of the 222 participants 106 were clinically diagnosed with schizophrenia by the standards of ICD-10 DCR (Zivetz, 1992). Patients were recruited through OPUS, Aarhus University Hospital Risskov.  
The patient group was originally matched one-to-one with healthy control subjects (N = 116), using the following criteria: age, sex, handedness, ethnicity, community of residence and parental social economic status and educational level. Healthy control subjects were recruited via advertisements in four local newspapers. The control group (and their first-degree relatives) had no history of psychological disorders. 14 patients and 4 controls were excluded due to poor recording quality or other similar factors. This explains the uneven number of participants within each group. For further information on participants, see table 1.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Study | N() | Diagnosis | N(Females) | N(Males) | Mean(Age) | SD(Age) | Range(Age) |
| Beck et al., 2020 | 70 | SZ | 16 | 18 | 22.8 | 3.13 | 18-31 |
| HC | 17 | 19 | 22.7 | 3.19 | 18-30 |
| Bliksted et al., 2014 | 46 | SZ | 6 | 17 | 23.3 | 3.94 | 18-33 |
| HC | 7 | 16 | 23.7 | 3.61 | 18-34 |
| Bliksted et al., 2019 | 48 | SZ | 11 | 8 | 40.8 | 12.4 | 20-61 |
| HC | 13 | 16 | 37.5 | 13.1 | 21-62 |
| Bliksted et al., n.d. | 58 | SZ | 12 | 18 | 24.8 | 3.66 | 18-31 |
| HC | 13 | 15 | 24.4 | 4.65 | 18-34 |
| Total | 106 | SZ | 45 | 61 | 26.7 | 9.02 | 18-61 |
| 116 | HC | 50 | 66 | 26.7 | 9.22 | 18-62 |

Table 1:  
*Demographic data within each of the original studies. N, SD, HC, SZ refers to number, standard deviation, healthy controls and the schizophrenia group respectively.*

### 2.3.2 Task

The participants from all studies went through the Frith Happé animations task (Abell et al., 2000). This task consisted of watching 2D top-view videos of animated triangles moving around on the screen. After watching an animation, the participants were interviewed and asked to describe what happened in the animation. Each description of a trial thus ended up as a single .wav file.

## 2.4 Preprocessing

### 2.4.1 Cleaning of audio files

The cleaning of the audio files was carried out by Ludvig Olsen in 2018 (Olsen, 2018)  
The audio files were converted to 16-bit .wav files, with a sample rate of 16k. They were subsequently denoised by stacking multiple instances of the Voice De-noise and De-hum tools in the iZotope RX 6 audio editor (iZotope Inc., 2018). A small equalizer tilt was applied at 1085Hz with the Fabfilter Pro-Q2 equalizer to bring more brightness to the signal (FabFilter Software Instruments, 2018). The signal was normalized to peak at -1dB both before and after the cleaning steps.

### 2.4.2 Feature extraction

The toolkit openSMILE 2.3.0 was used for extracting the features needed for the classification algorithm. The ‘emobase’ base-set configuration file of 988 emotion recognition features was used to extract features from the recordings. The ‘emobase’ feature set contained 26 LLDs, a delta regression coefficient for each LLD and 19 functionals for each of the LLDs and for each of the delta regression coefficients (for full list of features, see appendix). The process of feature extraction was executed on each of the speech recordings, yielding a single feature vector for each trial of each participant. These feature vectors functioned as data points for the model.

## 2.5 Partitioning

To be able to evaluate the performance of the model the dataset was partitioned into a training set and a test set consisting of 80% and 20% of the data, respectively. The partitioning was done using the package groupdata2 and was carried out semi-randomly (Olsen, 2020). The partitioning kept each participant ID only within either the resulting training set or the resulting test set. Moreover, the test set was forced balanced – both on the account of sex and diagnosis. The test set contained feature vectors for each trial from 23 controls (11 female) and 21 patients (10 female)

## 2.6 Normalization

All feature parameters were normalized using the min-max feature scaling formula in order to achieve a dataset with a common scale without losing information or distorting differences in the range of values. Normalization was carried out separately for the training and the test set – both using the min-max values from the training set



## 2.7 Feature selection

Feature selection was carried out using the Least Absolute Shrinkage and Selection Operator (LASSO) analysis regression. The R package ‘glmnet’ was utilized for the purpose of this paper. (Friedman et al., 2010). LASSO optimizes beta estimates for all features through a loss function based on misclassification error and an added regularization term. The latter term utilized lambda.1se - the lambda value resulting in the fewest number of features within 1 SE of the lambda value that minimized the loss function. As the full training data had been divided up into 5 splits (see fig. 2), LASSO was performed on the 5 training sets separately which resulted in a feature set for each (see appendix x\*). An illustration of the feature selection for one of these splits can be seen below in figure 4.

Graphical user interface, diagram

Description automatically generated

Figure 4:  
*Figure showing the process of feature selection on train 1:  
The training data is divided up into 5 folds. One fold is then excluded (yellow). Using cross-validation, the LASSO regression fit a range of lambda values, to find the optimal value. This entire procedure is then repeated for each of the remaining 4 training splits.*

## 2.8 Model training, testing and parameter tuning

Using the 5 training sets and the appertaining feature sets for each split, 5 SVM linear kernel classifier models were constructed using the Scikit-learn module in Python (Pedregosa et al., 2011; Van Rossum & Drake, 2009). SVM classifiers were then validated on the appropriate validation sets, repeatedly using a range of C-parameters, and performance was tracked using the metrics specified in section 2.7. The default C-parameter of 1 was found optimal for classification.

The 5 models were then implemented into an ensemble model that was tested on the test set. This model merely predicted using the majority vote of the 5 previously mentioned constituent models. If for example 3 out of 5 models predicted ‘schizophrenia’ for a recording, then this was also the vote of the ensemble model.

## 2.9 Evaluation metrics

For evaluating the performance of the models, several metrics conveying information about the classification was provided. Information on precision, recall and F1-scores for each class (controls and patients) was provided, along with a macro average F1-score, accuracy and baseline accuracy. Moreover, confusion matrices are provided as they convey the whole picture of performance and provide all the information needed for calculations of all evaluation metrics.



*Where,   
tp, fp, tn, fn, refers to true positives, false positives, true negatives, false negatives - while i and N refers to class and number of classes respectively.*

## 2.10 Differences between replication and original study

This replication employed principles from the proposed general pipeline, which meant that it diverged from the original study on several aspects. These discrepancies can all be seen in table x \* below.

|  |  |  |
| --- | --- | --- |
|  | **Original** | **Replication** |
| **N (participants)** | 78 | 222 |
| **Female rate** | 52.6% | 42.8% |
| **SZ rate** | 66.67% | 48.2% |
| **Origin** | Malay, Indian, Chinese | Danish |
| **Task  language** | English | Danish |
| **N (recordings)** | 78 (1 per  participant) | 1900 (8-10 per participant) |
| **Mean (recording length)** | 26 min | 18.8 sec |
| **Feature  selection** | PCA | LASSO regularization |
| **Feature scaling** | Min-max  normalization | No information |
| **ML  algorithm** | Single SVM | Majority vote ensemble – SVM |
| **Final  testing set** | Cross- validation (full dataset) | Holdout (separate set for final test) |

Table x \* :  
*An overview of the differences between the original paper by Chakraborty et al. and this replication.*

# 3. Results

This section presents the performance of the ML models when predicting various parts of the full data. A crude overview of the performance of the 5 models on the various test sets is given in table 2. An in-depth look at the ensemble models performance; both for controls and for the patient group is provided in table 3. The latter also provides insight into performance differences between the sexes. Finally, a confusion matrix (table 4) provide the necessary details that would underlie calculations for any and all additional performance metrics. The latter uses the abbreviations HC and SZ which mean ‘healthy controls’ and ‘schizophrenia”, respectively.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Testing set** | **Training and feature set** | **Macro avg. F1-score** | **Accuracy** | **Baseline accuracy** |
| Train 1 | Train 1 | 0.896 | 89.64% | 53.05 |
| Train 2 | Train 2 | 0.930 | 93.03% | 51.52 |
| Train 3 | Train 3 | 0.897 | 89.73% | 52.21 |
| Train 4 | Train 4 | 0.899 | 89.91% | 51.89 |
| Train 5 | Train 5 | 0.898 | 89.85% | 51.80 |
|  | | | | |
| Test 1 | Train 1 | 0.687 | 68.68% | 51.85 |
| Test 2 | Train 2 | 0.630 | 63.05% | 54.34 |
| Test 3 | Train 3 | 0.678 | 67.84% | 51.62 |
| Test 4 | Train 4 | 0.613 | 61.31% | 52.94 |
| Test 5 | Train 5 | 0.658 | 65.80% | 53.29 |
|  | | | | |
| Holdout | Train 1 | 0.644 | 64.44% | 51.87% |
| Train 2 | 0.652 | 65.19% | 51.87% |
| Train 3 | 0.735 | 73.51% | 51.87% |
| Train 4 | 0.740 | 74.05% | 51.87% |
| Train 5 | 0.716 | 71.64% | 51.87% |
| **Ensemble (majority vote of set 1:5)** | **0.703** | **70.32%** | **51.87%** |

Table 2:  
*Prediction performance for all 5 SVM linear kernel models, on various testing data.  
Within-sample prediction performance can be seen in row 1-5, while row 5-10 depicts performance tested on the 5 validation sets. Finally, the performance for the models’ predictions on the test set along with the majority decision vote can be seen in the bottommost 6 rows.*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Test set | Model | Sex | Acc. | Baseline acc. | Class | Precision | Recall | F1-score |
| Holdout | Ensemble | Male | 70.62% | 52.58% | SZ | 0.664 | 0.772 | 0.714 |
| HC | 0.759 | 0.647 | 0.698 |
| Female | 70.00% | 51.11% | SZ | 0.689 | 0.705 | 0.697 |
| HC | 0.711 | 0.696 | 0.703 |
| Both | 70.32% | 51.87% | SZ | 0.675 | 0.739 | 0.706 |
| HC | 0.734 | 0.670 | 0.700 |

Table 3:  
*Performance of the ensemble model - within both each sex and within HC/SZ.*

|  |  |  |  |
| --- | --- | --- | --- |
| N = 374  *(m = 194,*  *f = 180)* | Predicted group | | |
| True group |  | HC | SZ |
| HC | 130  *(m = 66*  *f = 64)* | 64  *(m = 36*  *f = 28)* |
| SZ | 47  *(m = 21*  *f = 26)* | 133  *(m = 71*  *f = 62)* |

Table 4:  
*Confusion matrix for the ensemble model predictions. Information on the proportion of males (m) and females (f) is also provided.*

# 4. Discussion

This discussion section will first compare the results of this replication with the results of the original paper. A potential model bias coming from the physiological difference between the sexes, will furthermore be investigated in relation to the results.

Secondly, the implementation of the general pipeline in this replication will be discussed – going into depth with the choices for each step. The question; “*How did an implementation of the pipeline work out in this replication?* “, will be addressed. This will be done on two levels:  
1) with regards to this specific replication (evaluating the choices for the 9 steps) and  
2) with regards to the original paper (what differed in the replication, and what impact did it have?)

Finally, the use of the proposed general pipeline will be assessed using the insights gained from this replication. Future research using the pipeline will also be discussed, looking into both benefits, limitations and development.

## 4.1 Performance results and comparison of performance to original study

This section will compare performance of the original paper with the performance of the ensemble model. Performance on the test set will be investigated as this is what gives information about the out-of-sample capabilities of the model - as opposed to looking at the predictions on the training or validation set which would not give an idea of the generalizability of the model.

The original paper had a macro average F1-score of 0.77 – higher than that of this replication (0.703). When looking at the isolated F1-scores for classifying patients and controls, both models classified controls equally well. The model from the original study did, however, achieve a higher F1-score when classifying patients (0.84) compared to this study (0.706). Moreover, both models also had an evenly balanced rate between recall and precision – the metrics that constitute the basis for the F1-score calculation.

As voice is modulated by the physiological differences between the sexes, the models may have elicited biases. The ensemble model classified equally well between males and females with macro average F1-scores of 0.706 for males and 0.7 for females. No information was provided by Chakraborty et al. on this issue.

All performance measures considered, a moderate difference in performance was found with this replication seemingly having slightly worse classification capabilities. This can be interpreted in various ways. Was it due to the differences in data? Or was it due to not applying the optimal methods in this replication? To shed light on the difference in performance the specifics of the pipeline implementation and their divergence from the original study will be evaluated.

## 4.2 Evaluating specific pipeline implementation (and discussing differences from original study)

The proposed general pipeline did not provide a rigid guide to the specific execution; therefore, the specific choices must be evaluated. Furthermore, the impact of the deviation between the studies will also be discussed (for an overview of deviations, see table x \* ).

**1) Data acquisition.** This study used data corpora of diverse speech recordings from multiple studies. This meant that the data was more diverse data since the recording setting differed across study. The ML model is therefore likely to be slightly more robust, in that it is less bound to only learning patterns within a certain setting.  
All participants in this study were Danish while the original study employed Malay, Indian and Chinese participants. This means that the data differs from the original study. Culture has been known to modulate symptoms of schizophrenia – with for example westerners eliciting stronger depressive behavior (*Lundbeck Institute Campus*, 2016; Sartorius et al., 1986). Moreover, sociodemographic factors have been known to play a role in the acoustic differences as well (Hitczenko et al., 2020). The original study furthermore instructed their participants to speaking English during their recordings– a non-native language. As cognitive load has been found to show larger symptomatologic effects for voice in patients (Parola et al., 2019), this might have elicited stronger patterns for the model to pick up and correspondingly better predictions.

The number of recordings for this study (N = 1900) was significantly greater than the original study (N = 78), as a result of having 8-10 recordings for each participant in the replication. Since each recording only produced a single datapoint, the algorithm had more data to learn from in this replication. The recordings in the study by Chakraborty et al., did however have much longer recordings, which meant that for each data point, the true features values were more accurately captured. \* Mangler info om impact??? \* \* Se om nogen har svaret på stackexhange \*.

**2) Preprocessing.** For feature extraction, the ‘emobase’ feature set was utilized to capture the acoustics of the emotional impairment of schizophrenia (Eyben et al., 2010). However, many other feature sets could have been used. It would have been interesting to use multiple feature sets – such as the features from DigiVoice, either in conjunction or for comparison (Zhang et al., 2019).

**3) Partitioning.** This study was roughly balanced on sex and diagnosis. The holdout set included enough male (N = 194) and female recordings (N = 180) to allow for insights into whether the slightly fewer numbers of females in the training data confounded the results. As discussed in 4.1.1 the model was unbiased in terms of sex. The original study was balanced but offered no information on potential bias.

**4) Feature scaling.** Feature were scaled using a min-max normalization. Alternatively, they could have been standardized as this method has the benefit of not being as affected by outliers as normalization is \* cite \*. The scaling of both the training and holdout set solely used information from the training set to avoid overfitting (Géron, 2019; Myrianthous, 2020; Vabalas et al., 2019) (Myrianthous, 2020). As no information was provided in the original paper, it is unclear whether they scaled similarly. They might have scaled prior to the cross-validation that they used – allowing for overfitting - or instead within each step of the cross-validation. Given the former option performance would appear better, but it would more poorly reflect out-of-sample performance.

**5) Feature selection.** Feature selection was in both the original and in this replication carried out using only information from the training set which avoided overfitting – a measure often neglected within this field (Vabalas et al., 2019). LASSO regularization and Principal Component Analysis (PCA) which was utilized in this replication and the original study respectively have been found to be similar in performance, with great improvements of classification algorithms (Abdi & Williams, 2010; Sun et al., 2019). Given that they perform similarly, it is unlikely that all variation in performance between the studies can be attributed to feature selection technique. If the method for using the acoustic features from ‘emobase’ for classification truly is robust and reliable, then either should – at least in theory - work. For this paper, it could have been informative to explore PCA and the many other techniques and compare their performance to shed light on this topic.

**6, 7, 8) Model training, model testing and parameter tuning.** SVM linear kernel models were utilized in both the replication and the original study. However, the use of an ensemble model was different. Combining or utilizing multiple models within a single model has been seen to have benefits for performance and generalizability (Buracas & Albright, 1994; Hong & Page, 2004; Sechidis, 2020; Tang et al., 2006). The ensemble model can be hypothesized to give more robust results, but given it was only tested on a single holdout set this speculation would require further testing across datasets.

**9) Validation.** Validation of the models was similarly carried out in this replication and the original. Discussion of result has been provided in section 4.1. Supplementary metrics could have been provided. ROC-curves show the tradeoff between false positives and false negatives at different classification thresholds – knowledge that is important to know before applying such models clinically. Given that research has not yet established the generalizability and ecological validity of these ML algorithms, they were deemed unnecessary and thus omitted.

In summary; this replication is unlikely to have been confounded by problems related to data, bias on the basis of sex or overfitting. The differences in performance between the original and this replication is likely to be due to a) a difference in data, b) a difference in methods, or c) the very conservative nature of this replication. Since the data differs widely between studies, it is reasonable to assume that data has had an impact – it is however unfeasible to deciphering exactly how and to which magnitude since other factors were not controlled for.

## 4.3 Limitations and prospects of the proposed overall pipeline

By providing a general pipeline for classification of schizophrenia patients, it is the hopes that the conditions for both replicability and comparisons of results can be improved. It is also the aim to alleviate future problems of overfitting and bias within the literature. However, the proposed pipeline is not an exhaustive solution. The pipeline does hold some limitations, some of which have become apparent through its use in this replication.

One of the limitations has to do with the broadness of the proposed pipeline. The pipeline was meant to inclusive and broadly applicable. However, the generalist nature of the pipeline has a downside. Many of the choices for good ML conduct are still up in the air, which hosts room for error. Choices for algorithms and feature selection technique are still left up to the practical experience of the individual researcher. The problem of knowing which algorithm to use for instance is not aided by the proposed pipeline. Choosing ensemble modeling and LASSO feature selection in this replication, for instance, was mostly based upon individual experience and knowledge of the existing methods. It is important to note, that although the proposed pipeline still does narrow down the number of potential choices to the most feasible choices.

Another limitation that has become apparent has to do with how difficult it can be to compare own results to other studies – even when applying thorough ML implementation. Using this replication as a case example, it is apparent that it proves difficult to pinpoint what drove the performance differences. It could be attributed to the difference in data – participants came from different backgrounds; they spoke different languages and were also presented to task of dissimilar nature. However, overfitting could have played a minor role, since the original did not document whether feature scaling was performed on the combined training and testing set or not.

The future use of testing across datasets combined with the use of a rigorous pipelines could potentially help solve the problem (Hitczenko et al., 2020; Vijayakumar & Cheung, 2018). Testing across datasets would shed light on true out-of-sample performance, while a pipeline would contribute by streamlining research in order to make comparisons of models easier. Open-science conduct such as sharing of data, scripts and models would further allow for transparency of methods and cumulative science.

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# 6. Appendix

## 6.1 Relevant studies

(Chakraborty et al., 2018; Gosztolya et al., 2018; Kliper et al., 2016; Martínez-Sánchez et al., 2015; Püschel et al., 1998; Rapcan et al., 2010; Stassen et al., 1995; Tahir et al., 2019)

## 6.2 Feature lists after L2 Regularization

\*

## 6.3 ‘Emobase’ feature set

Intensity, Loudness, 12 MFCC’s, F0 Pitch, Probability of voicing, F0 envelope, 8 LSFs (Line Spectral Frequencies), Zero-Crossing Rate. Delta regression coefficients are then computed from all these previously mentioned low-level descriptors (LLD). Both the LLDs and their delta coefficients are smoothed by a moving average window that filters with a window size of 3 seconds. Furthermore, the following functionals are applied to the LLDs and the delta coefficients: Max./Min. values and their respective relative position within input, range, arithmetic mean, 2 linear regression coefficients and linear and quadratic error, standard deviation, skewness, kurtosis, quartile 1-3, and 3 inter-quartile ranges.