Automatic pathology detection from PCG signals

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Overview

1. *Problem definition*
2. *Database collection*
3. *Processes involved in building an automatic system*
4. *Software tool developed*

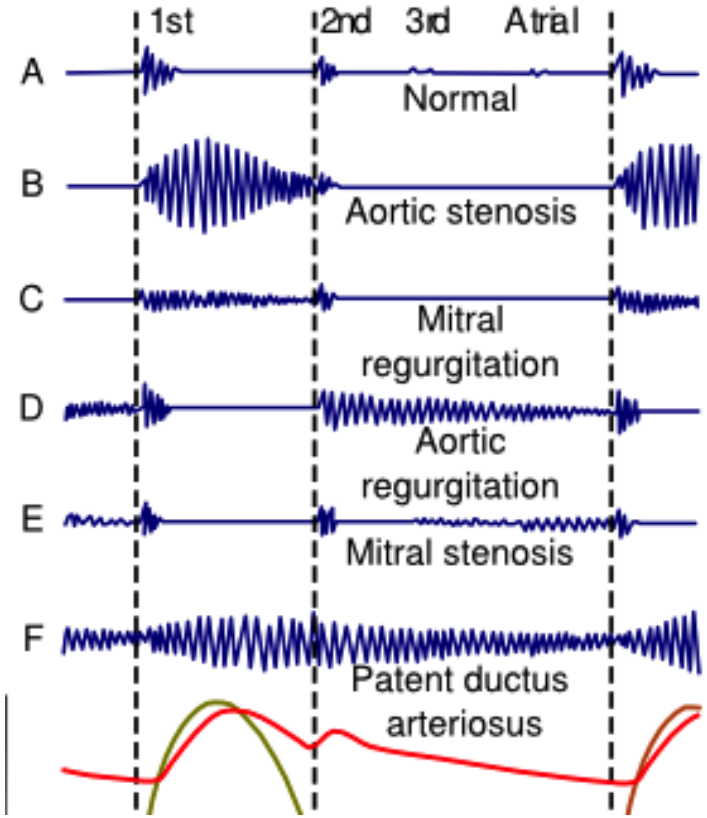
Problem definition

Detection of heart defect risk via processing heart sounds (Phonocardiogram (PCG))

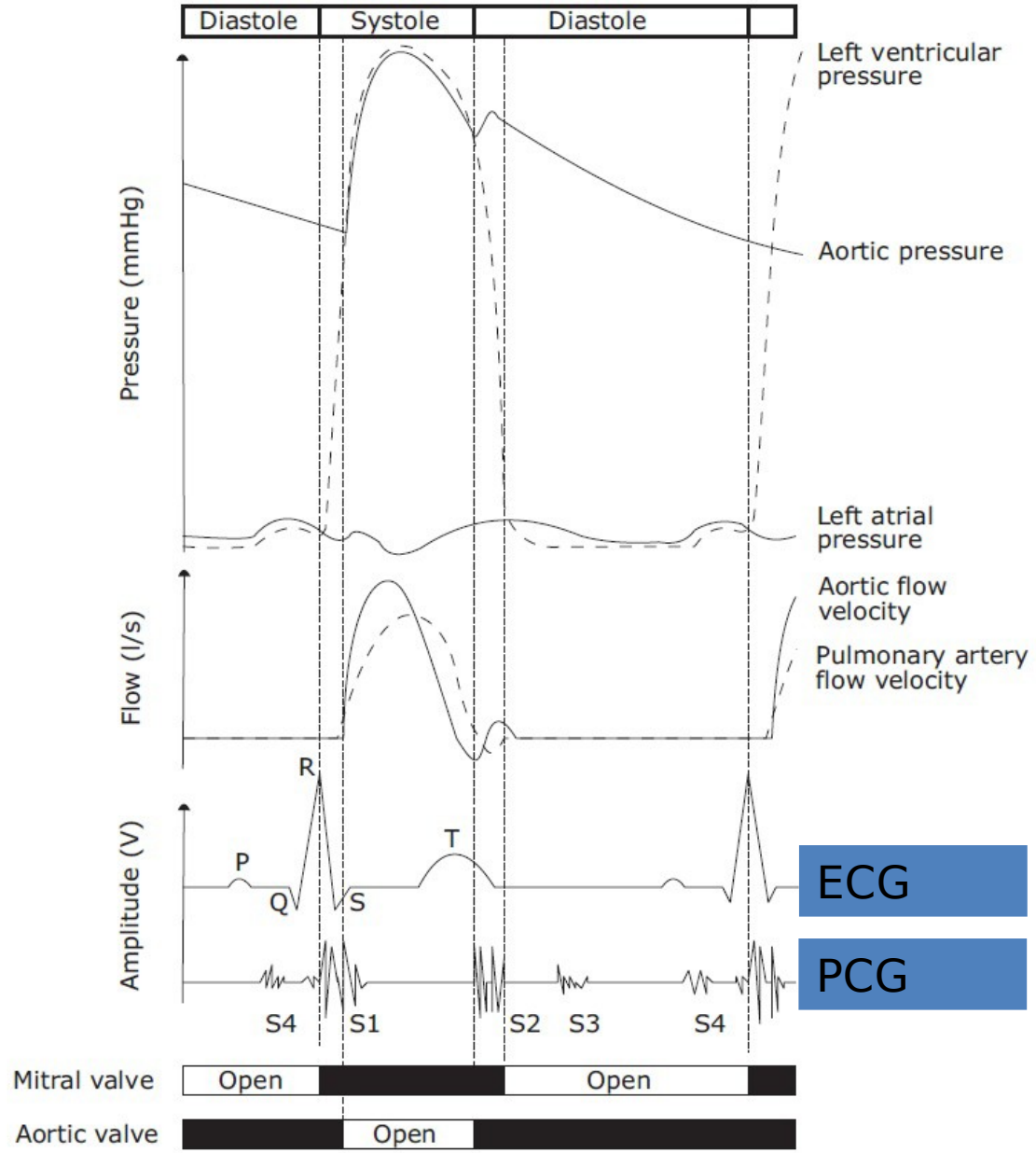
Classes:

- Normal and abnormal
- With murmur, without murmur
- Innocent murmur, pathological murmur

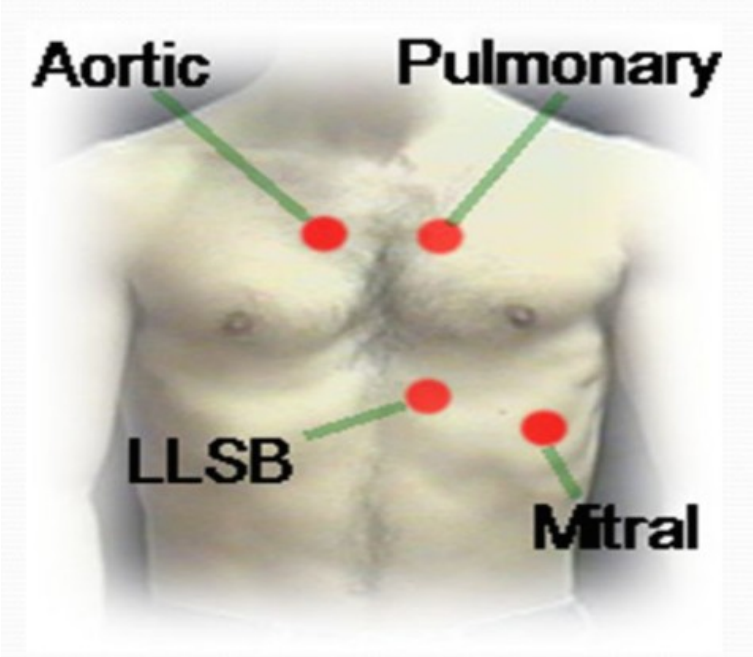
Heart sounds versus murmurs

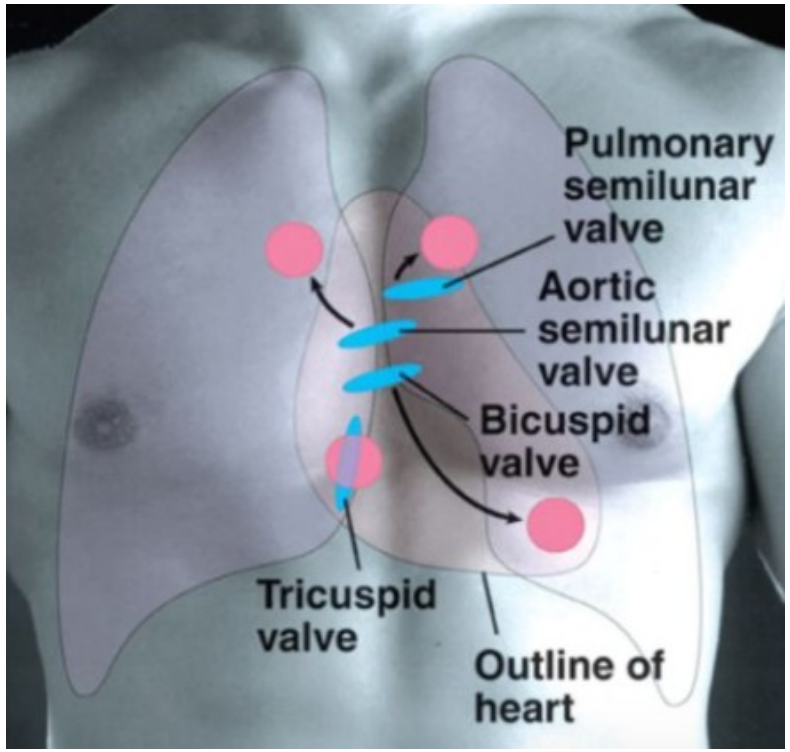


http://www.textbookofcardiology.org



Database collection





Murmurs are not audible in all recordings.
Expert labels 'single best'

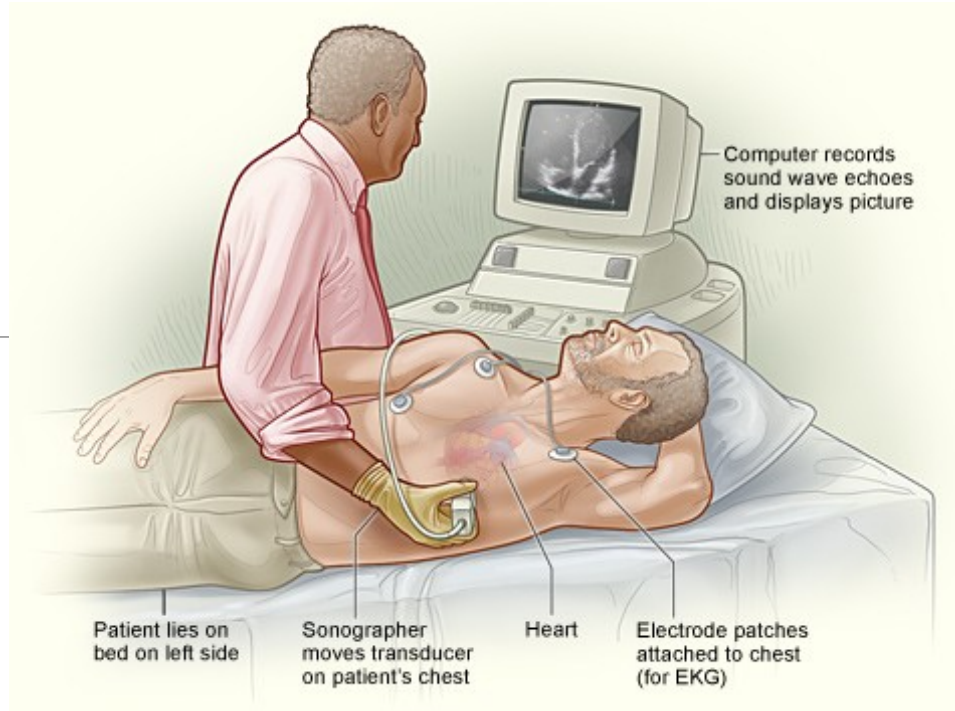
…our database includes one more recording location

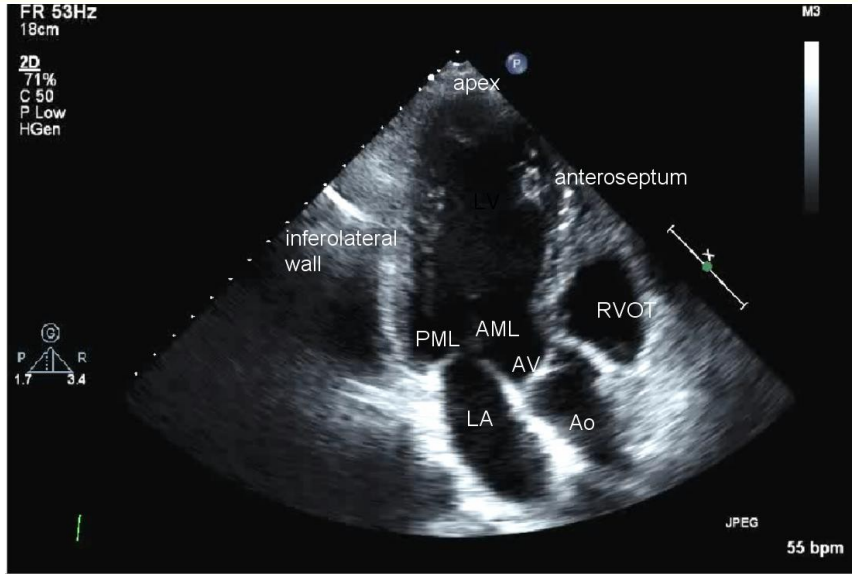
UoC Pcg database

Three categories:
No murmur, innocent/musical murmur, pathological murmur

Recordings from 5 locations, 1 selected

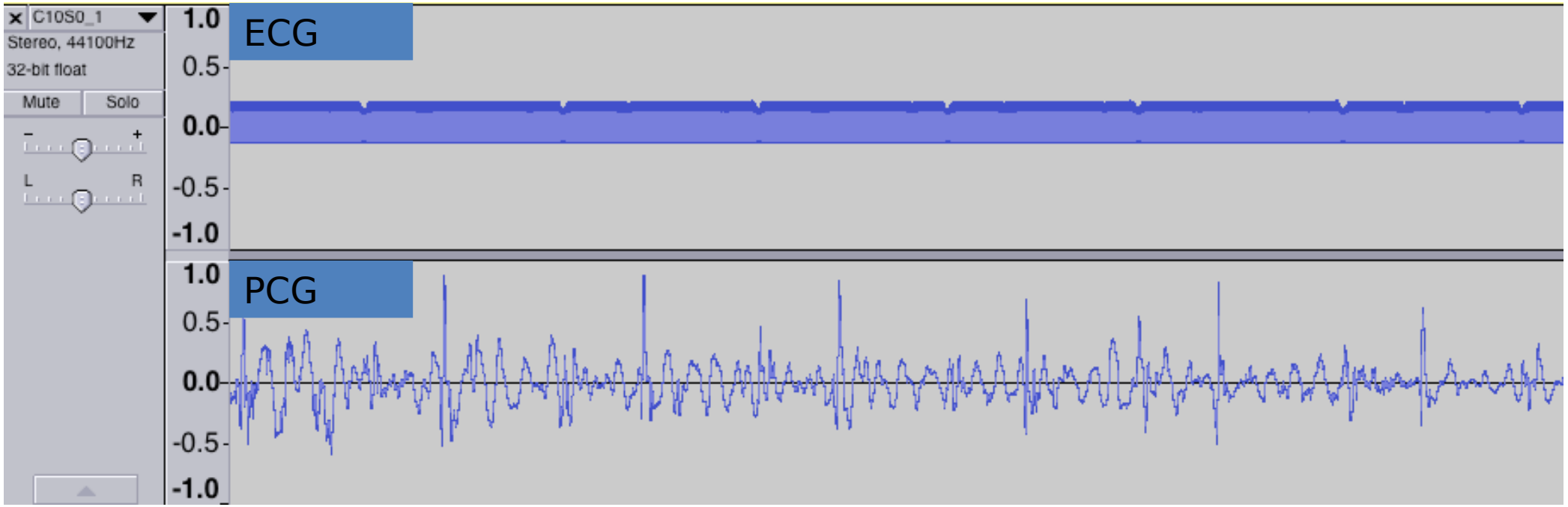
Validation:
- Echocardiogram
- Audio validation during consultation



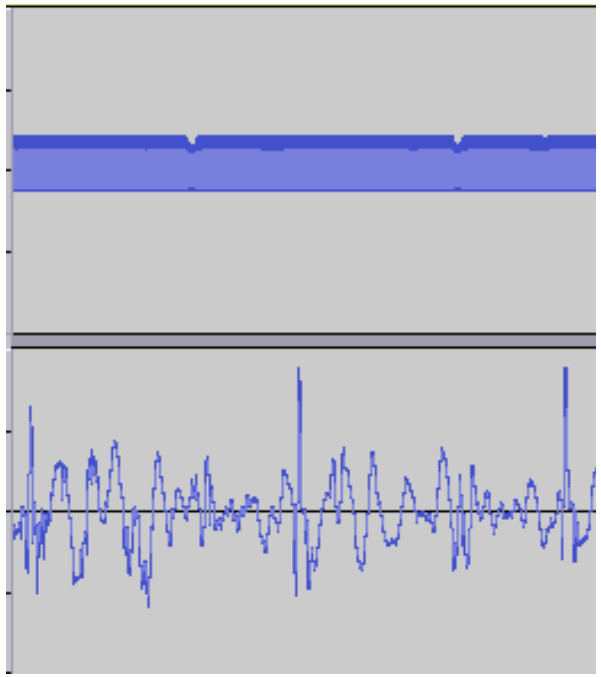


UoC Pcg database

Most devices would use proprietary coding schemes and bound users to a specific user interface and data analysis tool

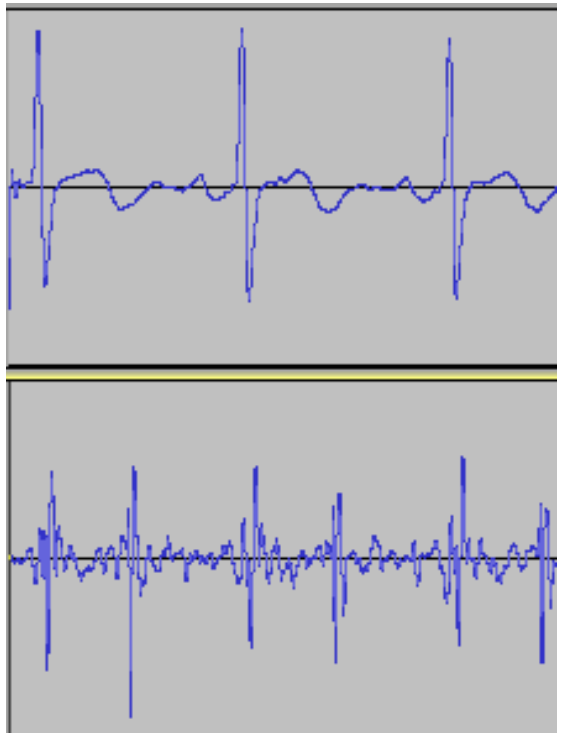


Processes involved in building an automatic system



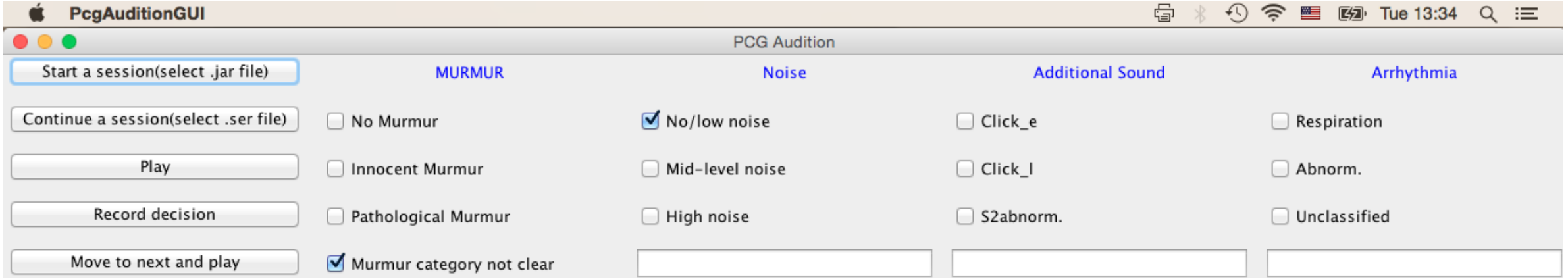
Pre-processing

- Separate channels
- Down-sample
- LP Filter
- Re-group for classification tests



!! All Phyton libraries are not reliable for signal processing. Scipy-resampling introduces artifacts

Blind validation



Tool implemented in Java

report_validation.txt

```
\WaveFiles\C13S7_mono.wav      Mur:1   Noise:0 AddSound:000    Arrhy:000
\WaveFiles\C11S54_mono.wav     Mur:0   Noise:1 AddSound:000    Arrhy:001
\WaveFiles\C15S7_mono.wav      Mur:0   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C12S16_mono.wav     Mur:0   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C11S18_mono.wav     Mur:0   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C15S23_mono.wav     Mur:1   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C12S37_mono.wav     Mur:0   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C13S28_mono.wav     Mur:1   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C13S33_mono.wav     Mur:0   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C16S12_mono.wav     Mur:0   Noise:1 AddSound:000    Arrhy:000
\WaveFiles\C13S21_mono.wav     Mur:0   Noise:2 AddSound:000    Arrhy:000
\WaveFiles\C15S12_mono.wav     Mur:1   Noise:0 AddSound:000    Arrhy:000
\WaveFiles\C11S43_mono.wav     Mur:1   Noise:0 AddSound:000    Arrhy:000
```

Experts feedback: sounds including high-noise and/or clicks should be excluded

Final database after duplicate removals

TRAIN

	NoMur	MurMus	MurPat	Total
NumWav	719	336	130	1185
NumPer	252	327	117	696

Files re-grouped and stored in folders automatically: trainNoMur, trainMurMus, trainMurPat … as two channels: ecg, pcg

TEST

(other position recordings of patients in TRAIN)

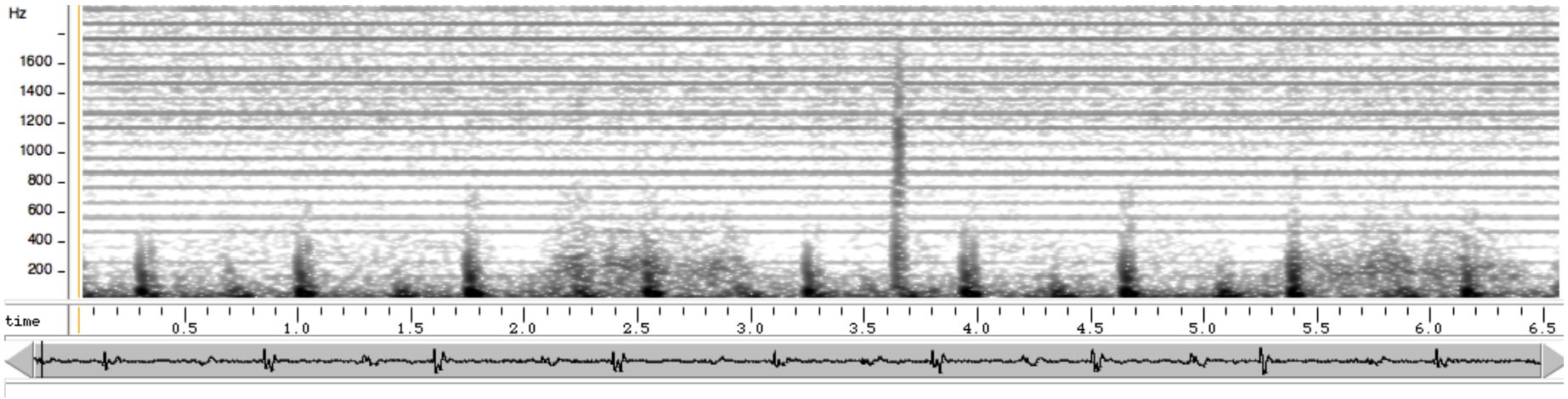
	NoMur	MurMus	MurPat	Total
NumWav	24	569	170	763
NumPer	8	183	58	249

Most reliable part of the database: 31.8Mbytes (after re-samp.)

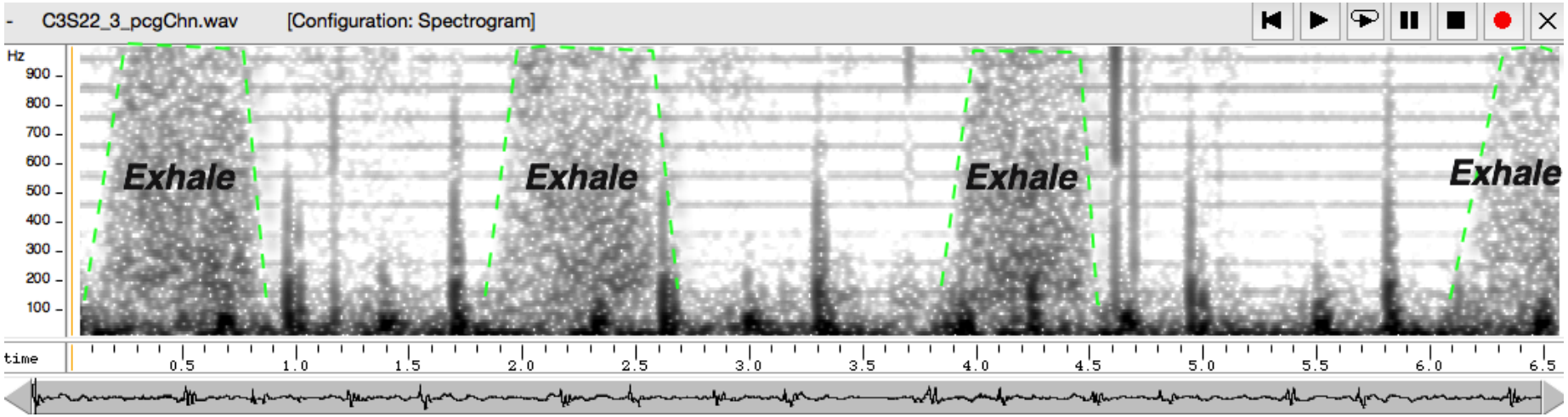
Not used due to lack of blind audio validation

Noise

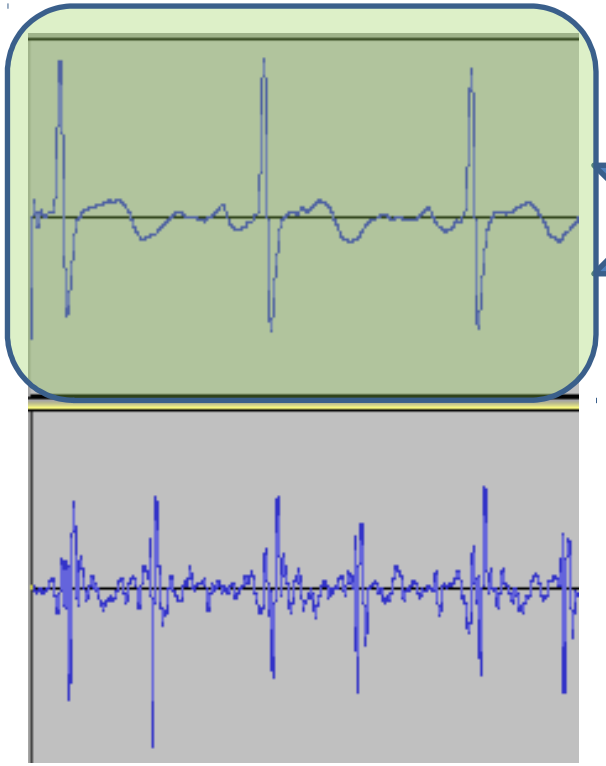
Various types of noise exist



In existence of breath, murmurs may be inaudible. Breath has similar signal characteristics as murmur

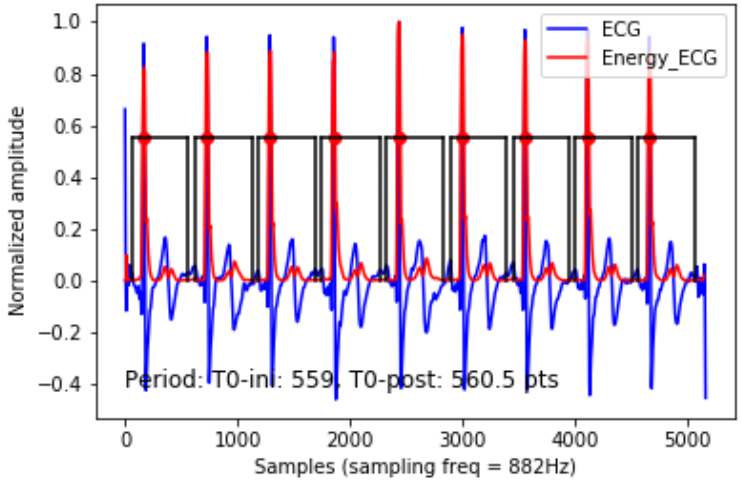


Segmentation using ECG signals



Segmentation

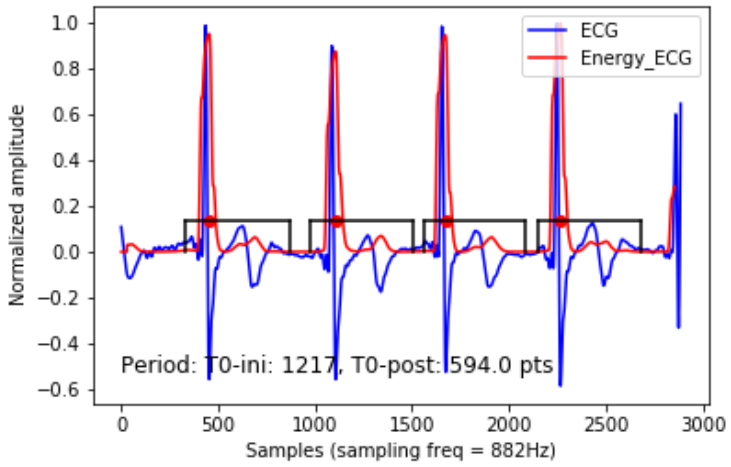
- Compute energy
- Re-shape to enhance peaks
- Detect period (auto-corr.)
- Estimate # of periods
- Detect 3*# peaks via thresh.
- Filter out spurious peaks

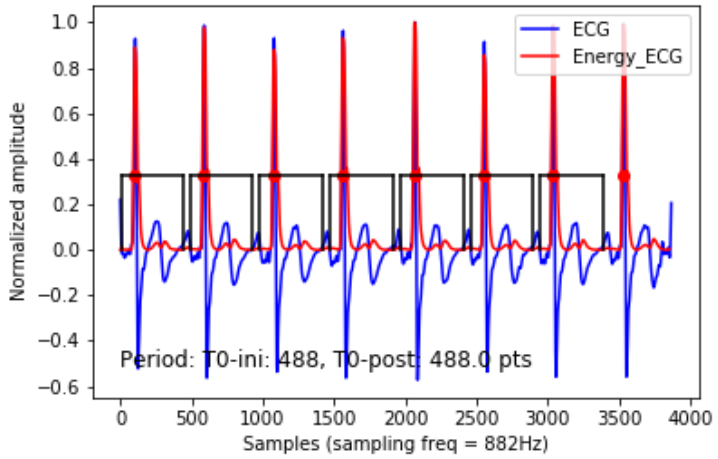


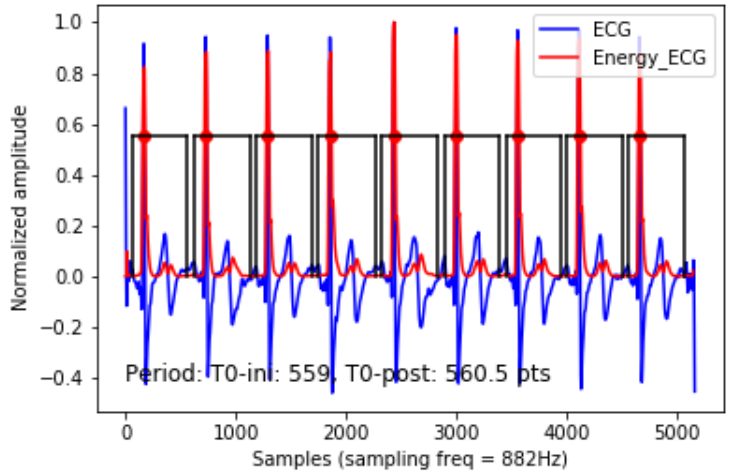
Different strategies may be applied for framing:

- **Syncr. Frames (1/2/3 period len)**
- **Syncr. Frames (0.5/1/2 sec. len)**
- **ASyncr. Frames (0.5/1/2 sec. len)**

Processes involved in building an automatic system: Period marking from ECG signals [examples]

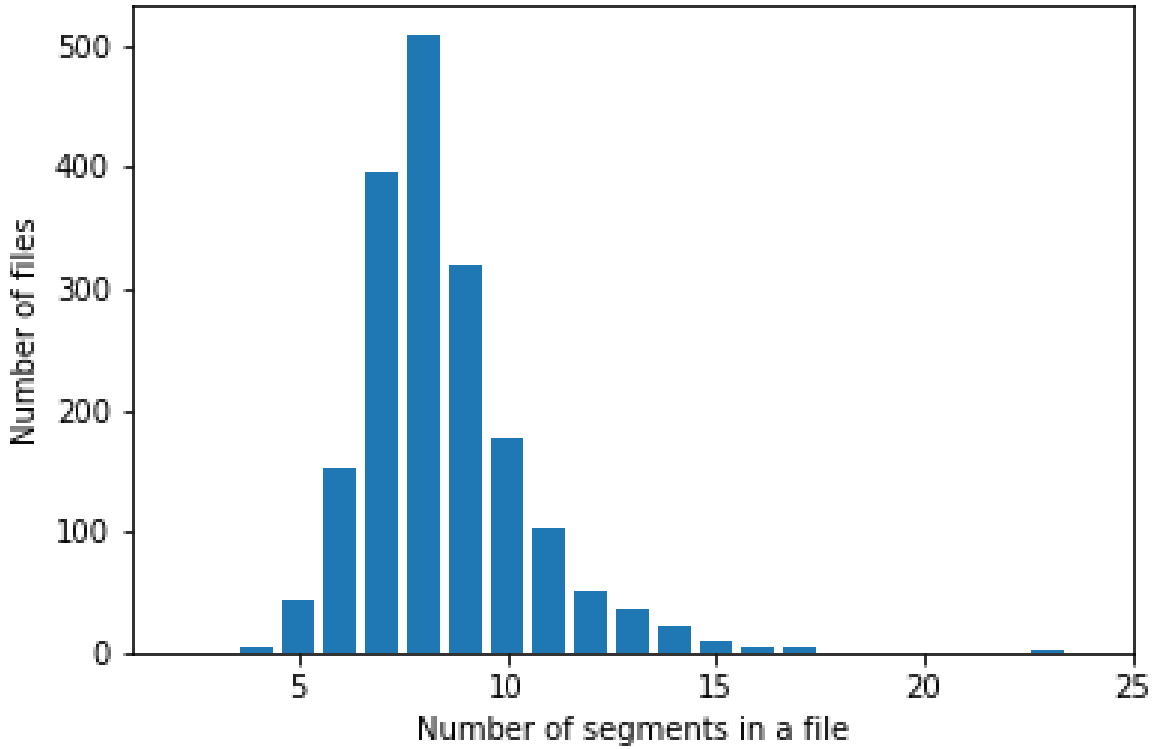






- Window-based amplitude normalization applied to get rid-off sudden energy jumps
- Reliable in most of the cases

Processes involved in building an automatic system: Period marking from ECG signals [examples]

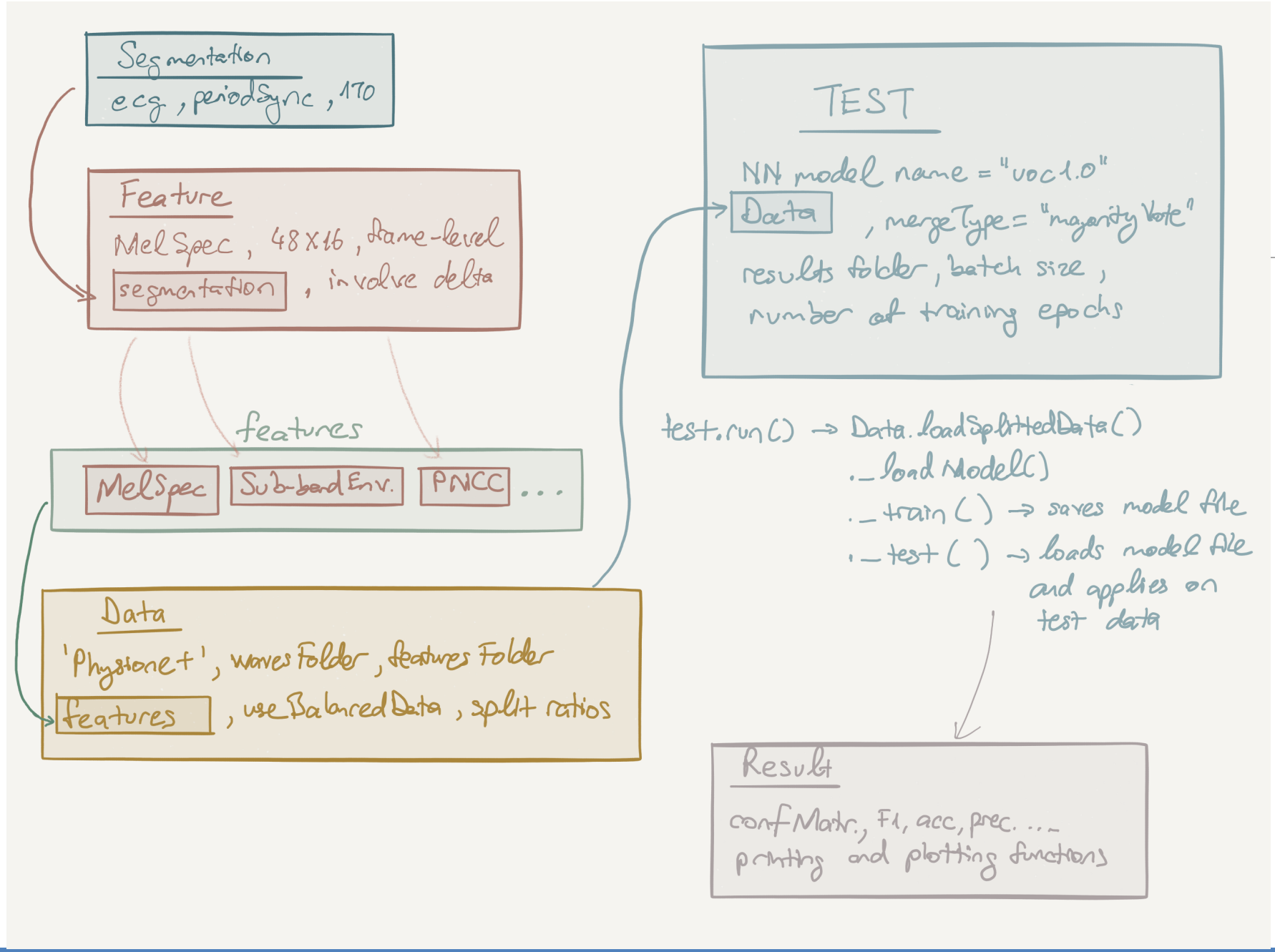


On average there are 8 periods per file

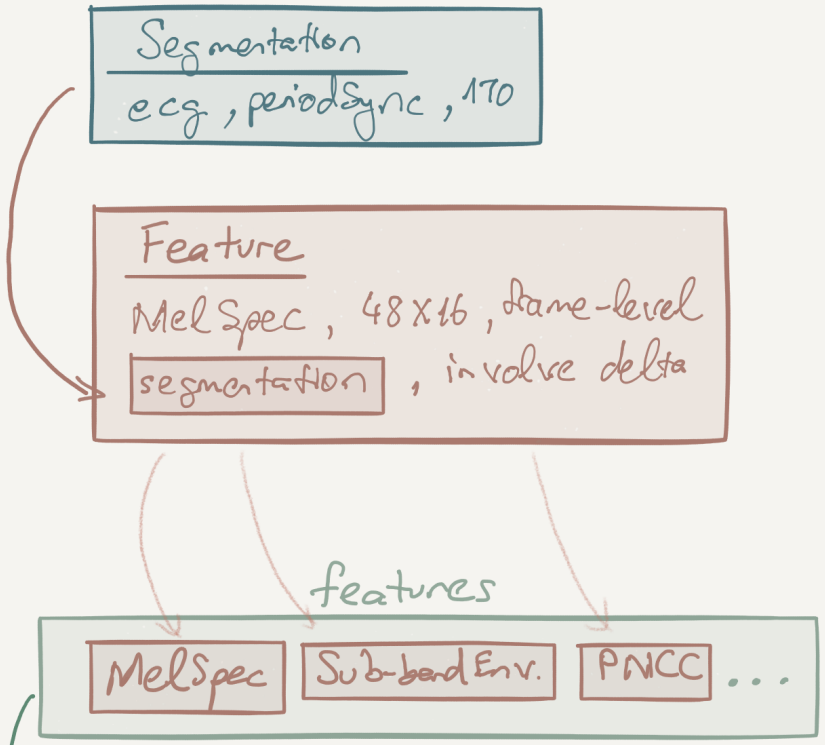
Feature extraction

Frame-level feature computation:

- MFCC (with/without delta coefficients) [librosa]
- Mel-Spectrum (with/without delta coefficients) [librosa]
- Sub-band envelopes:
  - Use auditory filter banks to create sub-band filters
  - Filter the signal to get sub-band signals
  - Compute (Hilbert)envelopes of sub-band signals and re-sample
- Sub-band signals
  - The first two steps above



Designed tool to carry combinational testing in a simple way




```
#%% Define segmentation strategies
ecg1perSegments=Segmentation("ecg",periodSync=True,sizeType="1period")
ecg2perSegments=Segmentation("ecg",periodSync=True,sizeType="2periods")
ecg3perSegments=Segmentation("ecg",periodSync=True,sizeType="3periods")
pcg1perSegments=Segmentation("pcg",periodSync=True,sizeType="1period")
```

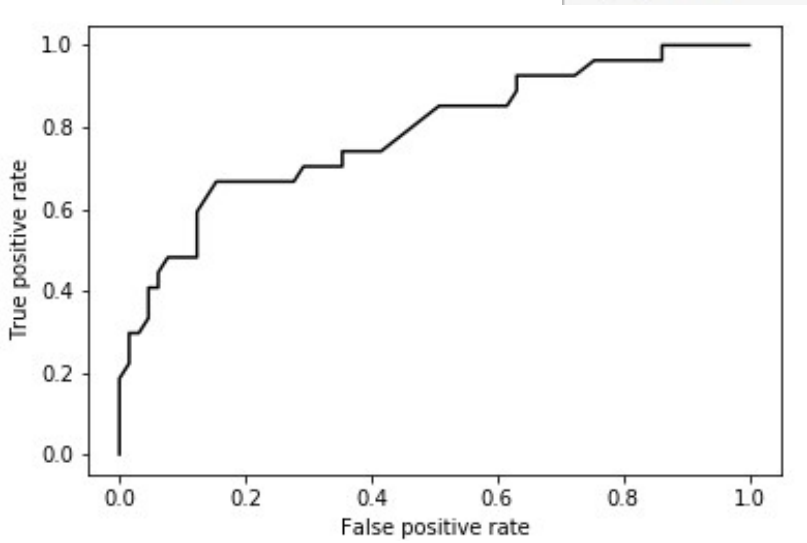
```
#Segmentation strategies to be tested for the SubEnv feature:
segStrategies=[ecg1perSegments,ecg2perSegments,ecg3perSegments]
```

```
#Define features to be used
features=[]
for featName in ['SubEnv','SubSig','MelSpec','MFCC']:
    for segType in segStrategies:
        for timeDim in [32,64,128,256]:
            for freqDim in [8,16,24,32]:
                features.append(Feature(featName,[timeDim,freqDim],"frame",segType,involveDelta=False))
                if featName=='MelSpec' or featName=='MelSpec':#for MFFC and MelSpec, also add involve data coeffs.
                    features.append(Feature(featName,[timeDim,freqDim],"frame",segType,involveDelta=True))
```

288 different feature settings defined here

Comparing outputs

We prefer high sensitivity, so better to apply different threshold(than 0.5) to probability outputs



results

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JAVA
Bass

Name | Date Modified

M_uocSeq0MelSpec32by32_eSyn11_10h_maj_results.txt

```
53.0     |12.0    |
9.0      |18.0    |

Sensitivity =    0.6666666666666666
Specificity =    0.8153846153846154
Accuracy    =    0.7717391304347826
F1          =    0.631578947368421
Matthews CC =    0.46824735250351485
```

M_uocSeq1MFCC48by16_eSyn11_10t_maj_results.txt

```
50.0     |15.0    |
10.0     |17.0    |

Sensitivity =    0.6296296296296297
Specificity =    0.7692307692307693
Accuracy    =    0.7282608695652174
F1          =    0.576271186440678
Matthews CC =    0.38133692943535785
```

M_uocSeq1MFCC64by16_eSyn21_10t_maj_results_ROC.png	3 Jun 2017 03:54
M_uocSeq1MFCC64by16_eSyn21_10t_maj_results.txt	3 Jun 2017 03:54
M_uocSeq1MFCC64by16_eSyn21_10t.h5maj.pkl	3 Jun 2017 03:54
M_uocSeq1MFCC64by16_eSynf2_10t_maj_acc.png	3 Jun 2017 04:00
M_uocSeq1MFCC64by16_eSynf2_10t_maj_loss.png	3 Jun 2017 04:00
M_uocSeq1MFCC64by16_eSynf2_10t_maj_results_ROC.png	3 Jun 2017 04:00
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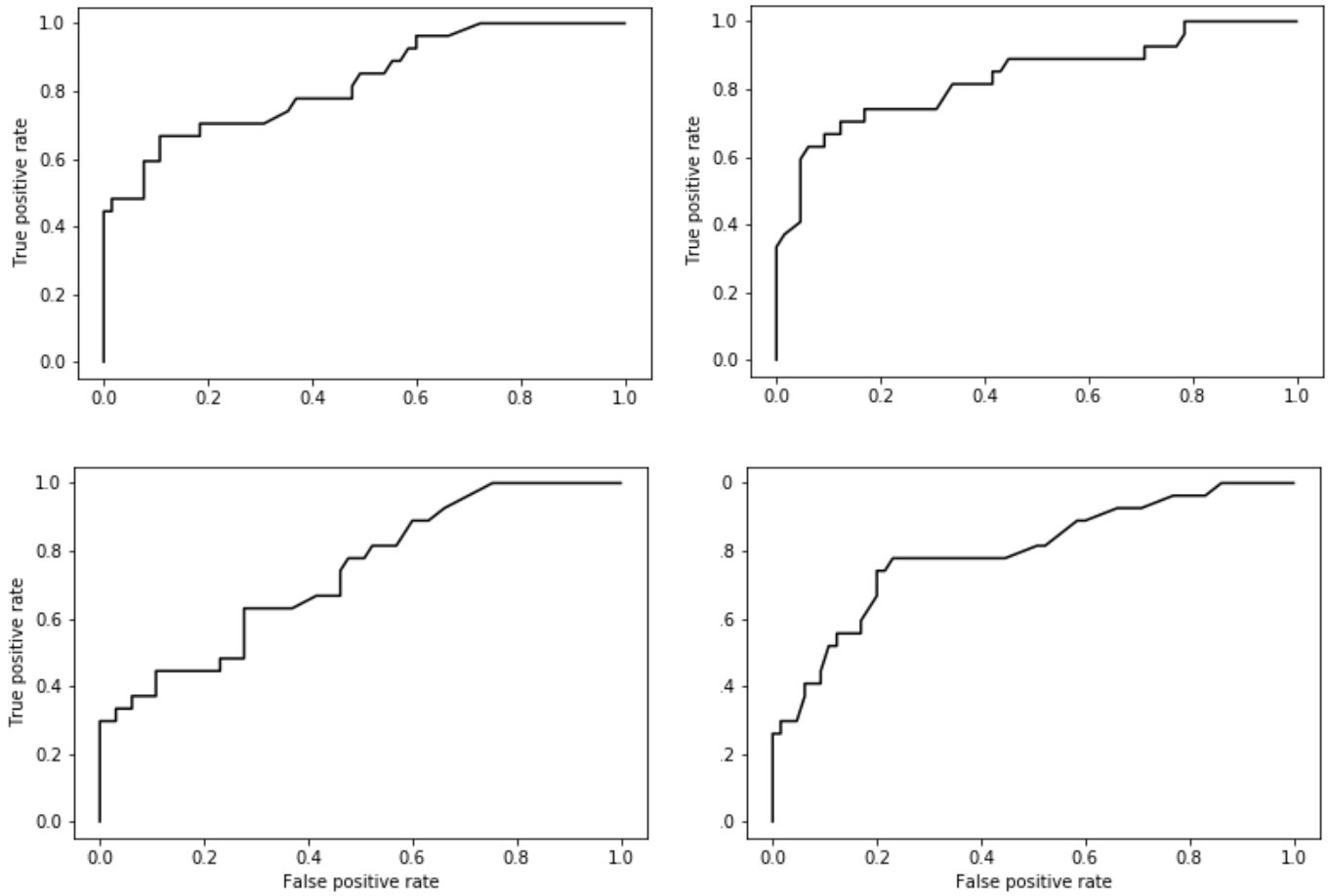
M_uocSeq1SubEnv32by32_eSyn11_10h_maj_loss.png	3 Jun 2017 01:30

Selecting a system among many using the ROC curve

Main Criteria:

High sensitivity:
We don’t want to miss any pathological cases, it is ok to misclassify some normal cases as pathological.

We target selecting several systems that can be further fused to obtain improved classification



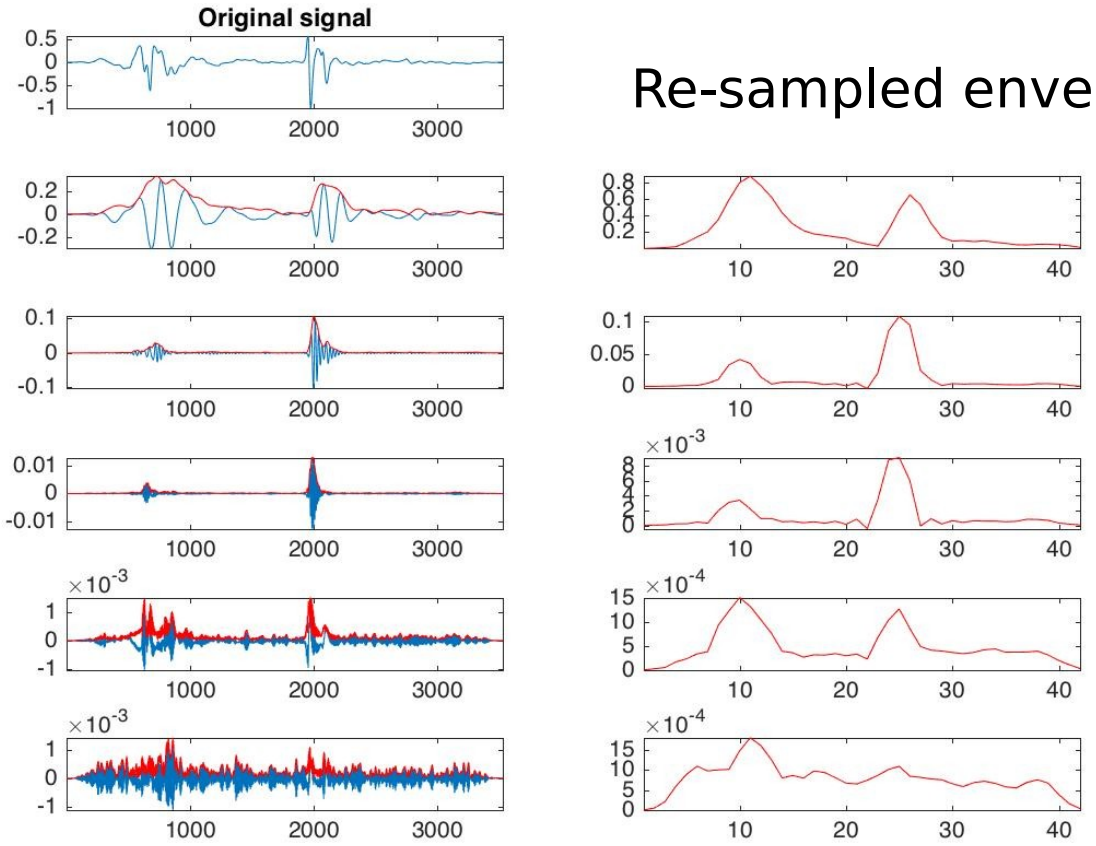
Processes involved in building an automatic system

Feature computation: Sub-band signal envelopes

Sub-band 1

Sub-band 2

Sub-band 3



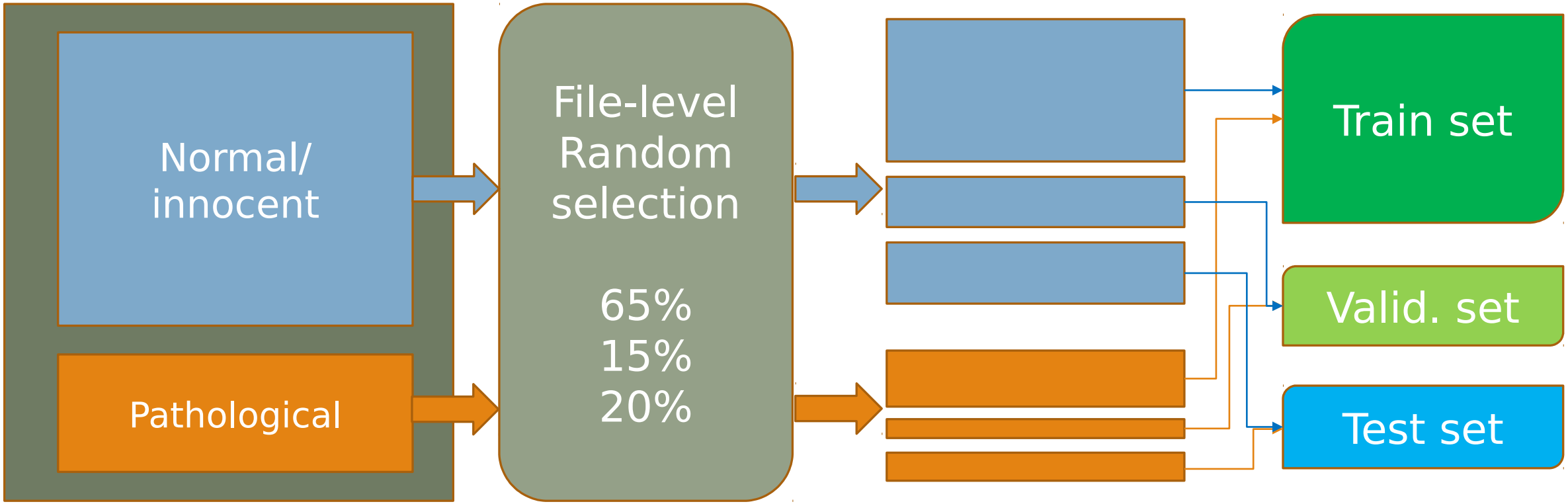
In a later step, logarithmic compression is applied since energy is generally too low in higher bands

CNN architectures tested

```
if modelName=="uocSeq0":#Model with single convolutional layer
    model = Sequential()
    model.add(Conv2D(32, kernel_size=(3, 3), strides=(1, 1), padding='valid', activation='relu', input_shape=input_shape))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.5))
    model.add(Flatten())
    model.add(Dense(32,kernel_regularizer=regularizers.l1(0.0005), activation='relu'))
    model.add(Dropout(0.5))
    model.add(Dense(num_classes, activation='softmax'))
    model.compile(loss=keras.losses.categorical_crossentropy,
                  optimizer=keras.optimizers.Adam(lr=0.0003, beta_1=0.9, beta_2=0.999, epsilon=1e-08, decay=0.0),
                  metrics=['accuracy'])#learning rate default: 0.001
```

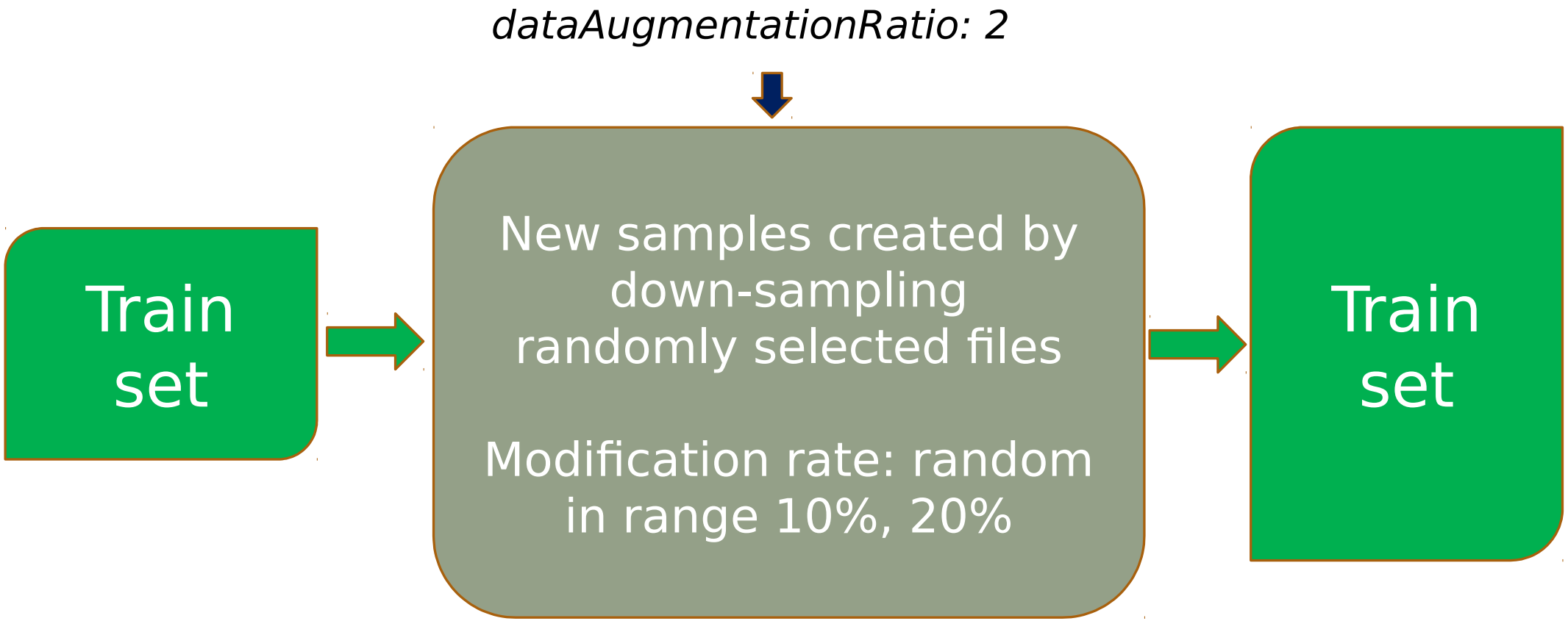
```
elif modelName=="uocSeq1":#Model with two convolutional layers
    model = Sequential()
    model.add(Conv2D(32, kernel_size=(3, 3), strides=(1, 1), padding='valid',activation='relu', input_shape=input_shape))
    model.add(Conv2D(32, (3, 3), strides=(1, 1), padding='valid', activation='relu'))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.5))
    model.add(Flatten())
    model.add(Dense(64, activation='relu'))
    model.add(Dropout(0.5))
    model.add(Dense(16,kernel_regularizer=regularizers.l1(0.0002)))
    model.add(Dense(num_classes, activation='softmax'))
    model.compile(loss=keras.losses.categorical_crossentropy,
                  optimizer=keras.optimizers.Adam(lr=0.001, beta_1=0.9, beta_2=0.999, epsilon=1e-08, decay=0.0),
                  metrics=['accuracy'])#learning rate default: 0.001

elif modelName=="uocSeq2":
    model = Sequential()#Model with 4 convolutional layers
    model.add(Conv2D(32, kernel_size=(3, 3), strides=(1, 1), padding='valid', activation='relu', input_shape=input_shape))
    model.add(Conv2D(32, kernel_size=(3, 3), strides=(1, 1), padding='valid', activation='relu', input_shape=input_shape))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.5))
    model.add(Conv2D(32, kernel_size=(3, 3), strides=(1, 1), padding='valid', activation='relu', input_shape=input_shape))
    model.add(Conv2D(32, kernel_size=(3, 3), strides=(1, 1), padding='valid', activation='relu', input_shape=input_shape))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.5))
    model.add(Flatten())
    model.add(Dense(32,kernel_regularizer=regularizers.l1(0.0001), activation='relu'))
    model.add(Dropout(0.5))
    model.add(Dense(16,kernel_regularizer=regularizers.l1(0.0001), activation='relu'))
    model.add(Dropout(0.5))
    model.add(Dense(num_classes, activation='softmax'))

    sgd = SGD(lr=0.01, decay=1e-6, momentum=0.9, nesterov=True, clipnorm=5)
    model.compile(loss='categorical_crossentropy', metrics=['accuracy'], optimizer=sgd)
```

Test design:
Splitting data into train/validation/test



Selection results in ~25 pathological samples in test set. Each random selection results in varying numbers of ‘difficult to classify cases’. So, tests should be repeated and results averaged.

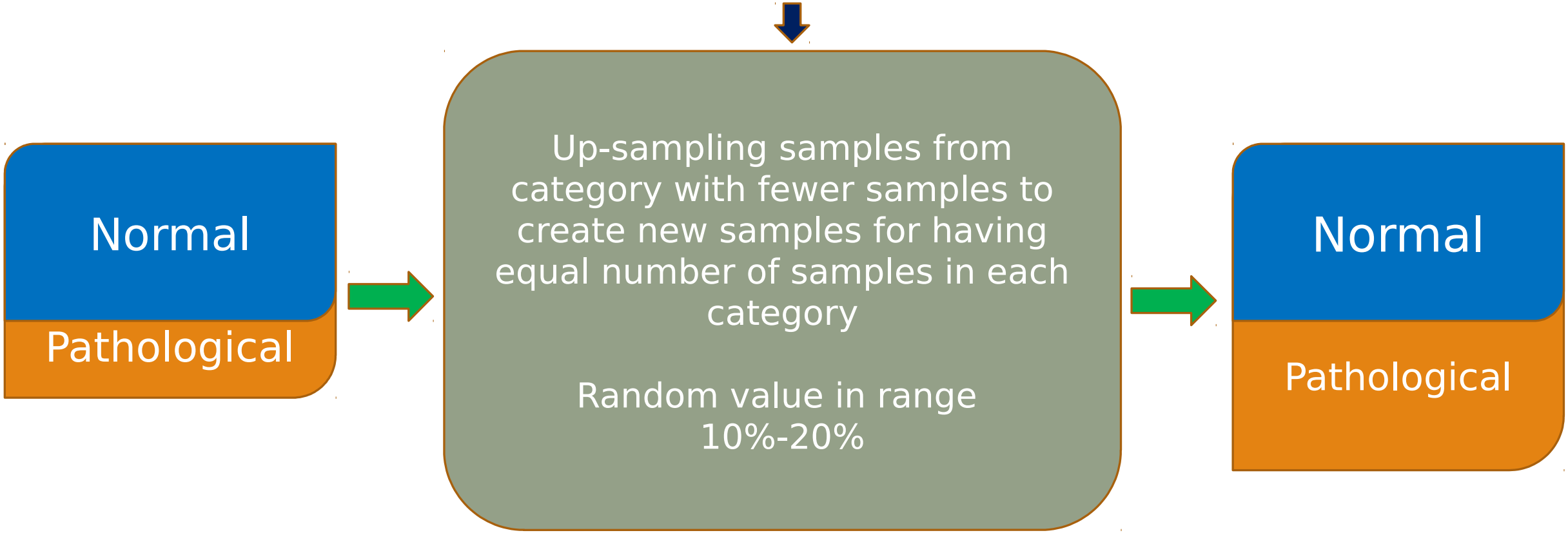
Test design:
Data augmentation [**Applied on train set**]



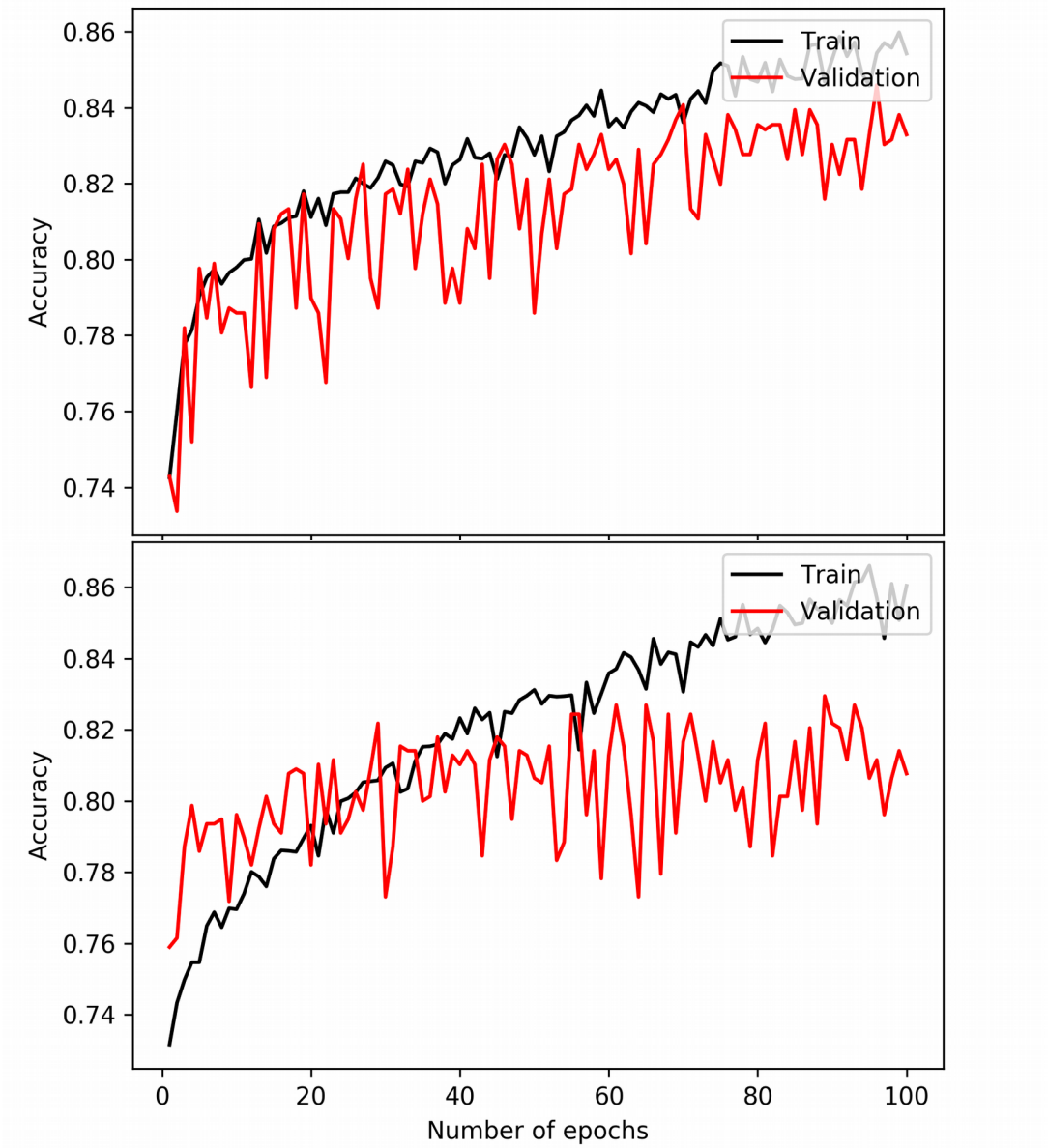
Test design:

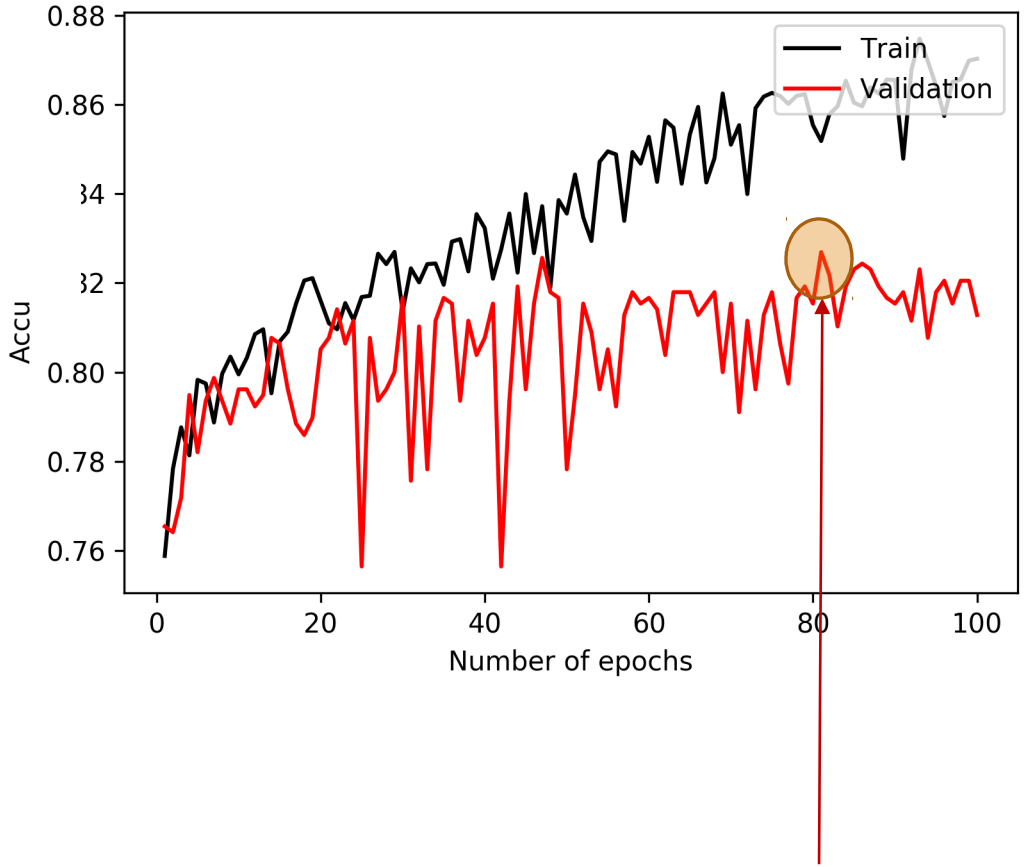
Balancing the data via creating new samples for the small sized category [**Applied on train and validation sets**]

useBalancedData: True



Sample learning curves



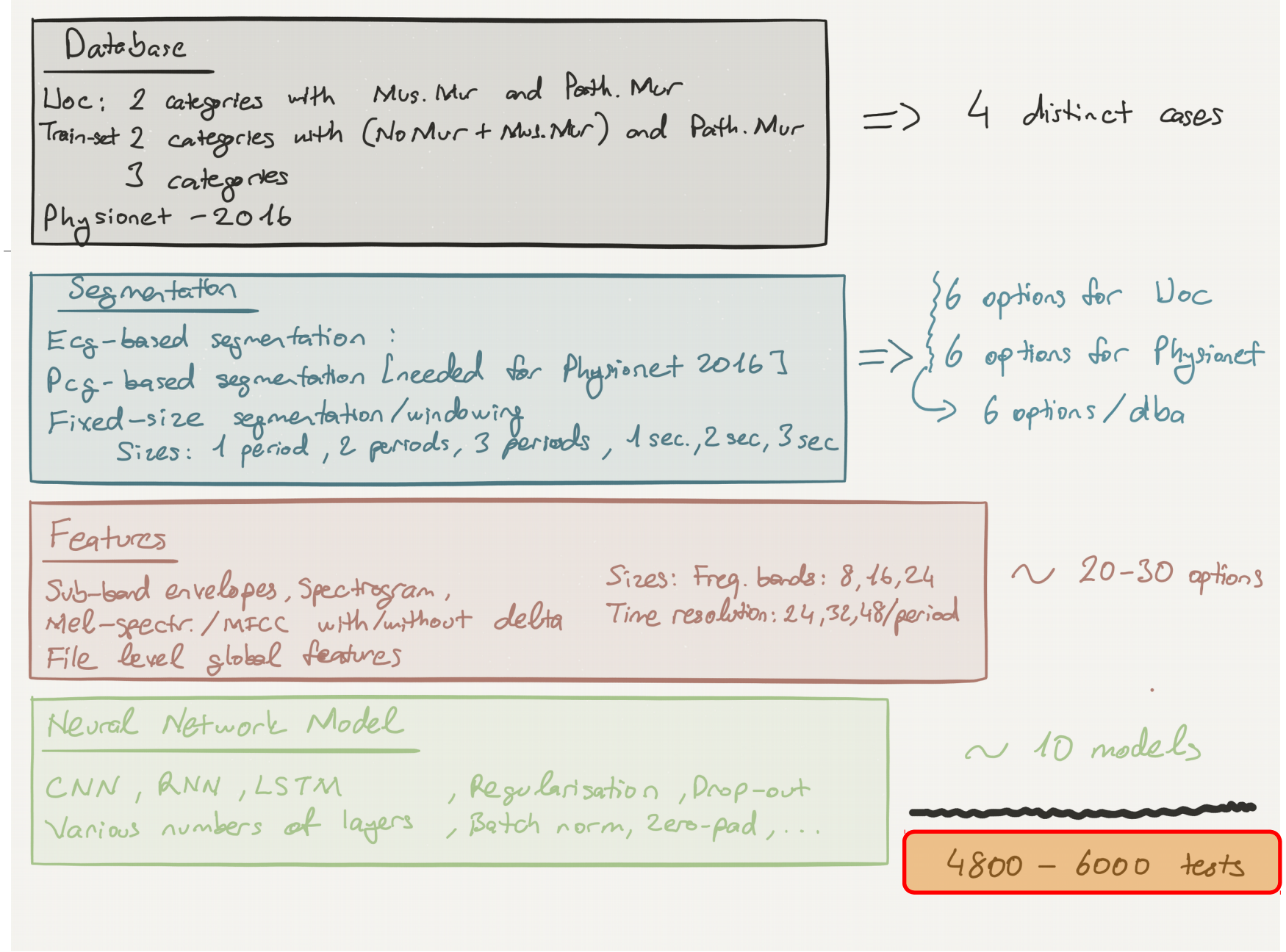


We store the system with highest validation accuracy as the final model

User defined number of epochs=100 for these tests

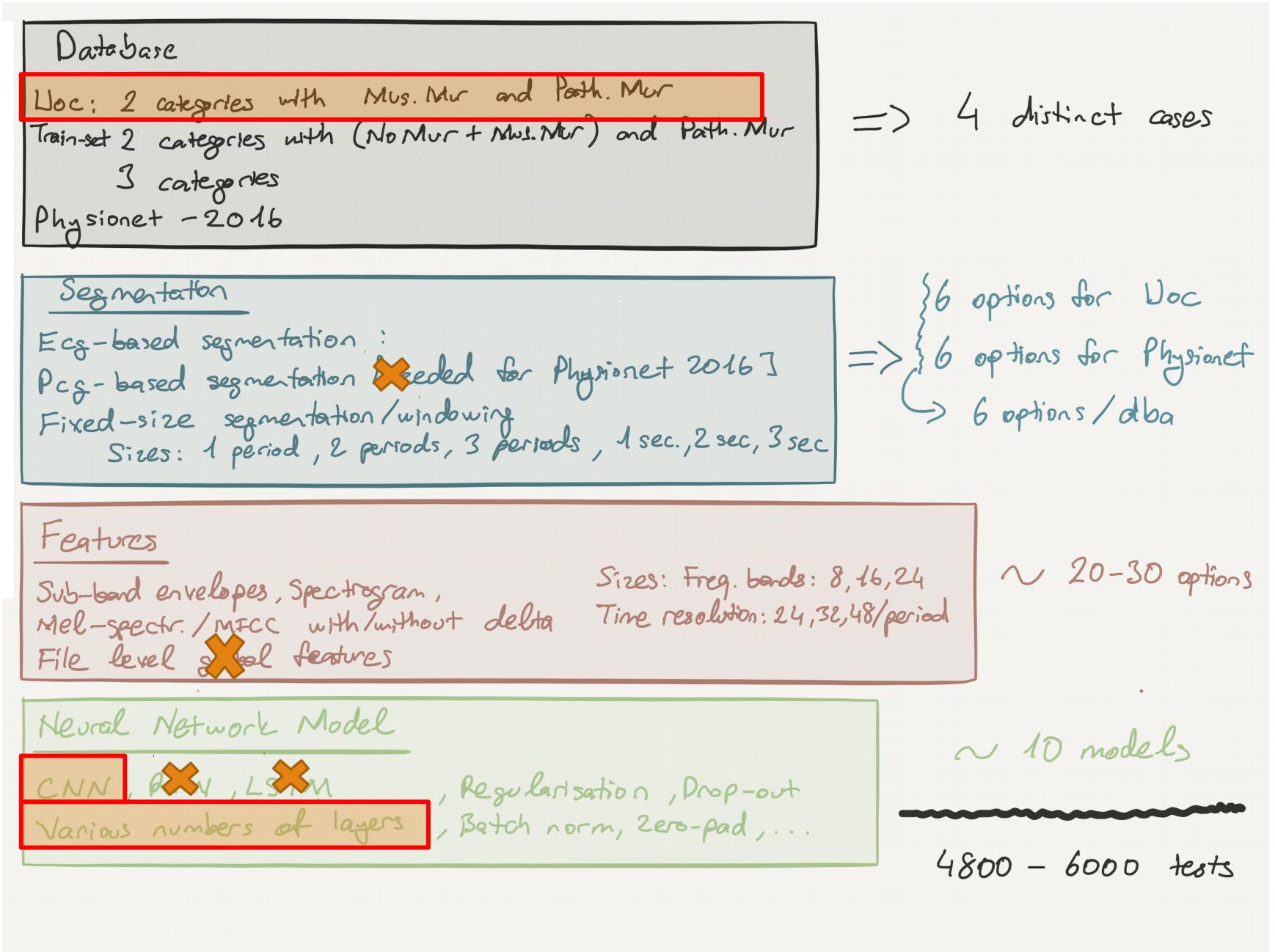
Extensive testing with various settings is unavoidable for arriving at a good design.

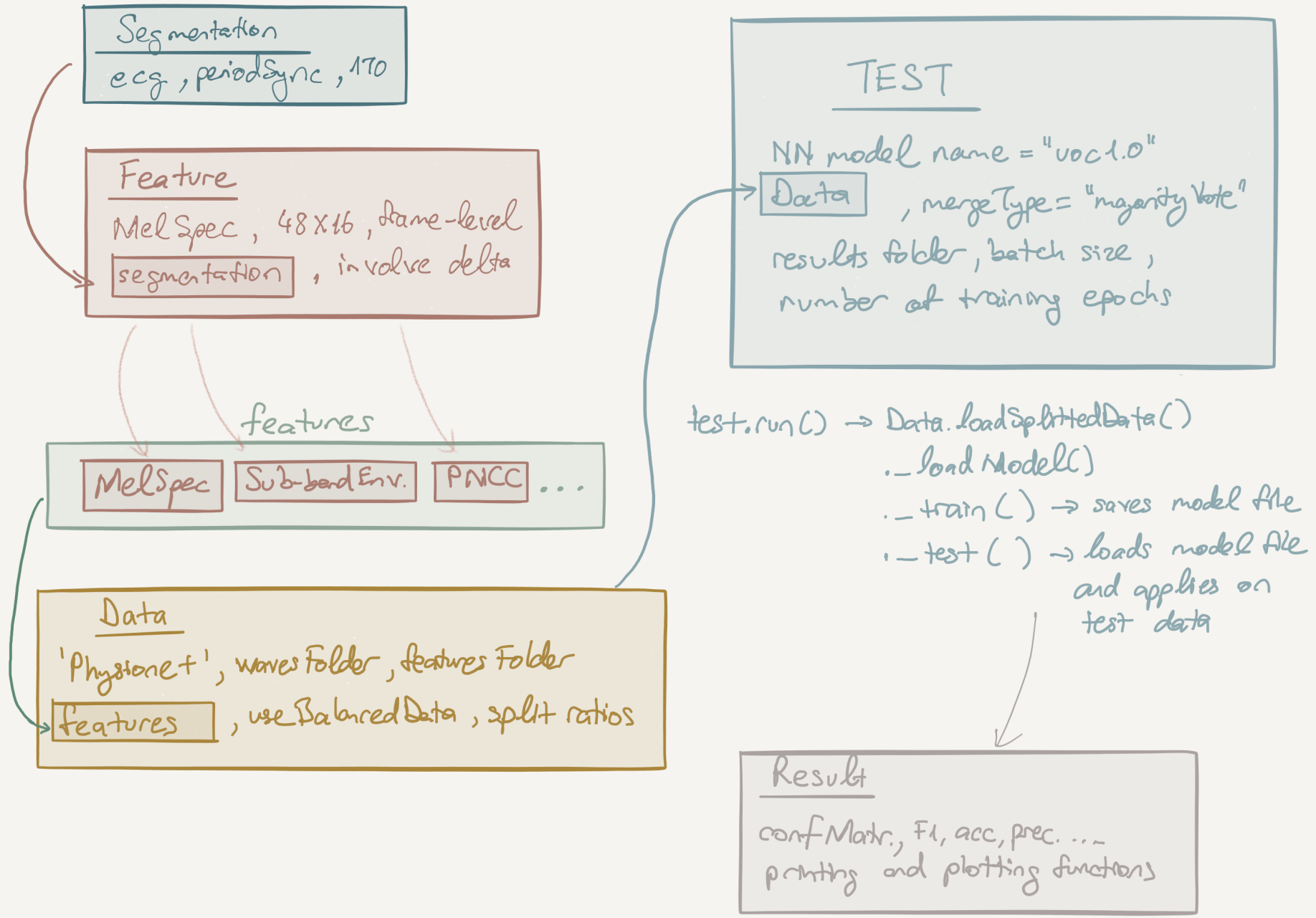
Designing systematic tests and reporting the results may be our contribution to the community.



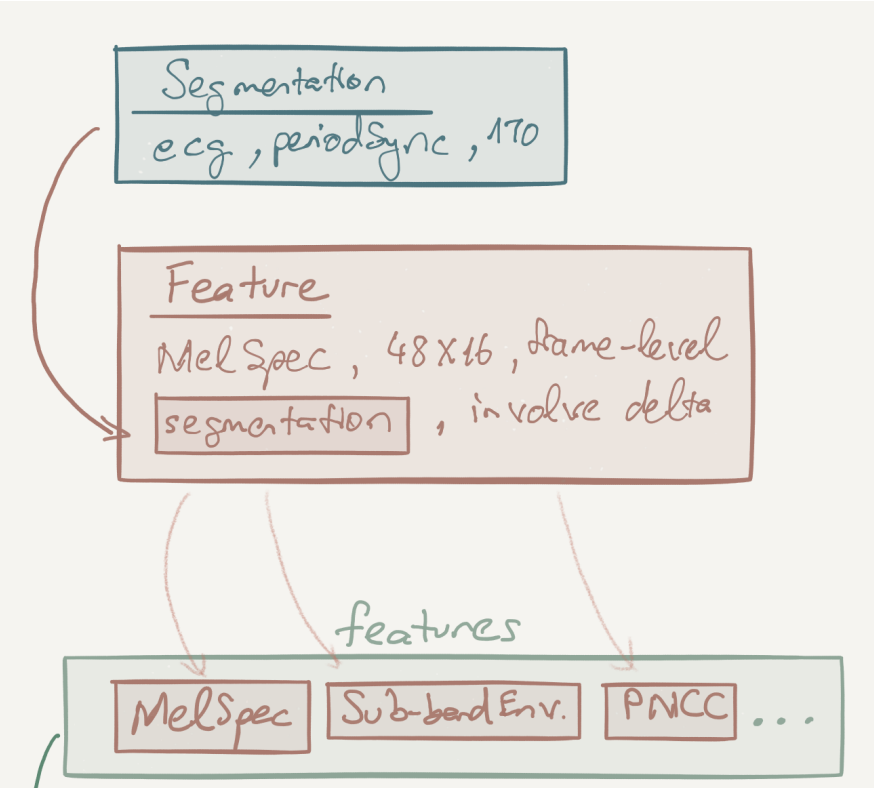
After several attempts, I figured out this is impractical and decided to:

- Reduce number of tests
- Apply on a single dataset
- Pick limited number of best(?) systems
- Re-run experiments several times (%20->5)
- Test these few systems on several databases





Designed an Object-oriented tool to carry combinational testing in a simple way



Sample code lines

```
#%% Define segmentation strategies
ecg1perSegments=Segmentation("ecg",periodSync=True,sizeType="1period")
ecg2perSegments=Segmentation("ecg",periodSync=True,sizeType="2periods")
ecg3perSegments=Segmentation("ecg",periodSync=True,sizeType="3periods")
pcg1perSegments=Segmentation("pcg",periodSync=True,sizeType="1period")
```

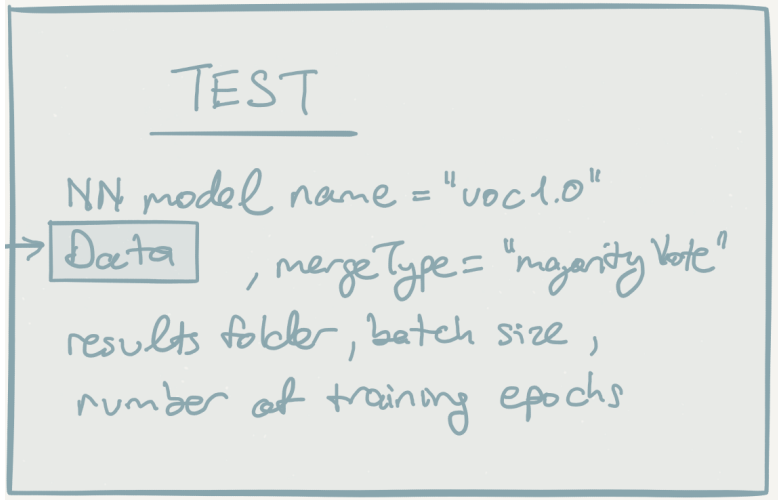
```
#Segmentation strategies to be tested for the SubEnv feature:
segStrategies=[ecg1perSegments,ecg2perSegments,ecg3perSegments]
```

```
#Define features to be used
features=[]
for featName in ['SubEnv','SubSig','MelSpec','MFCC']:
    for segType in segStrategies:
        for timeDim in [32,64,128,256]:
            for freqDim in [8,16,24,32]:
                features.append(Feature(featName,[timeDim,freqDim],"frame",segType,involveDelta=False))
                if featName=='MelSpec' or featName=='MelSpec':#for MFFC and MelSpec, also add involve data coeffs.
                    features.append(Feature(featName,[timeDim,freqDim],"frame",segType,involveDelta=True))
```

288 different feature settings defined here

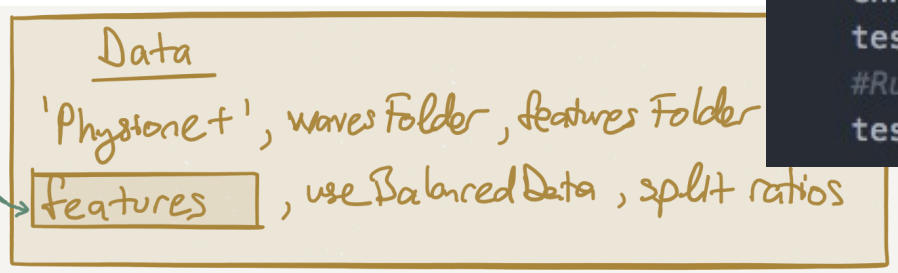
For a single experiment:
~10 lines of code

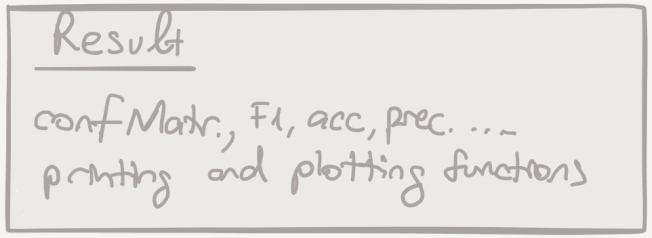
For hundreds of experiments:
~20-30 lines of code



- Does not re-compute features if feature-files are available.
- The user can specify train/valid./test sets or use random splits

```
#Define data specifications
data=Data(dbaName,wavFolder,featureFolder,features,useBalancedData,splitRatios,info)

for i in range(3):#this loop for setting models by name
    #Define test specifications
    CnnModelName="uocSeq"+str(i)
    test4SubEnv=Test(CnnModelName,data,mergeType,resultsFolder,batch_size=128,num_epochs=200)
    #Run the tests
    test4SubEnv.run()
```

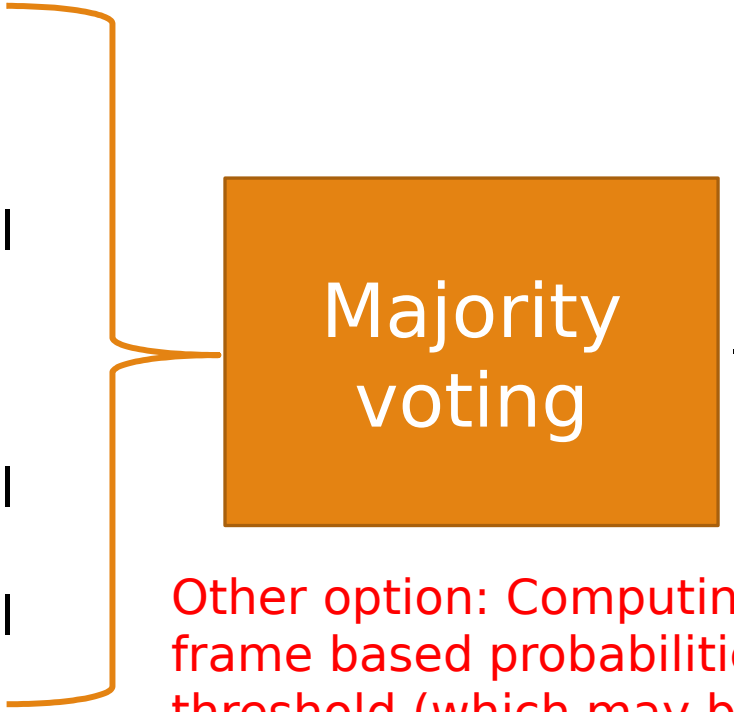




Frame-based decision to file-level decision

Probabilities for normal and pathological for frames of a file:

[0.21741118, 0.78258884] -> pathological
[0.17369123, 0.82630873] -> pathological
[0.59241056, 0.4075895] -> normal
[0.23323412, 0.76676589] -> pathological
[0.57892609, 0.42107388] -> normal
[0.52060699, 0.47939304] -> normal
[0.33756566, 0.6624344] -> pathological
[0.18149786, 0.81850213] -> pathological
[0.208248 , 0.79175204] -> pathological
[0.22317596, 0.77682412] -> pathological

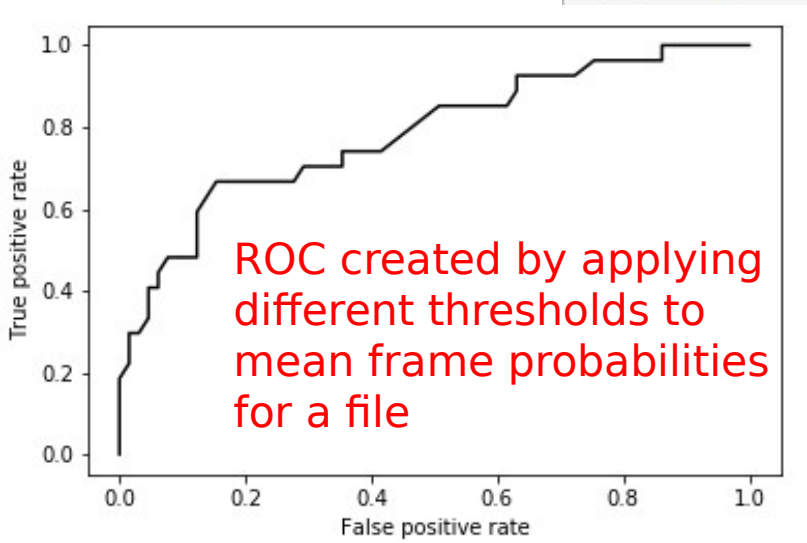


-> pathological

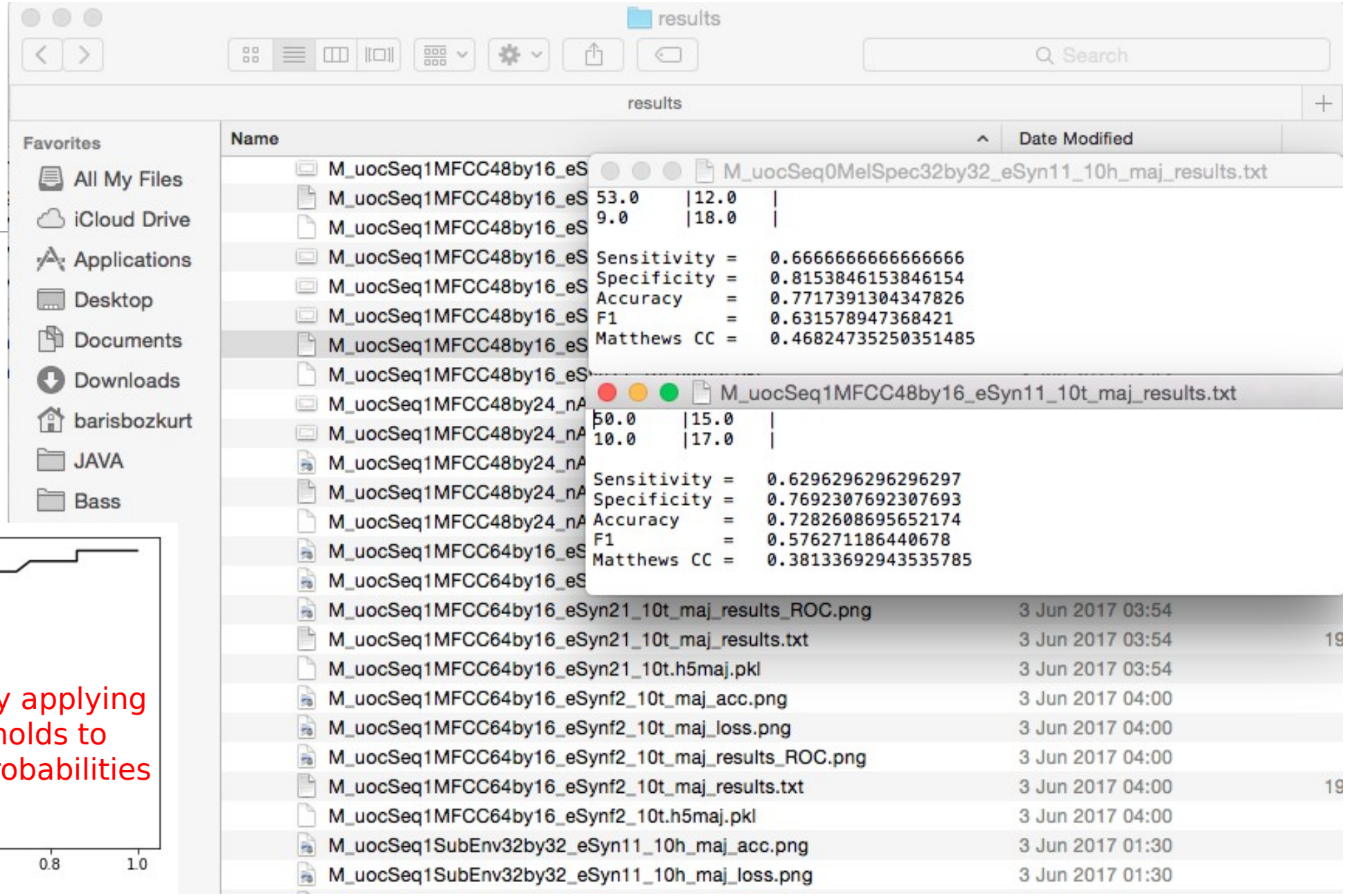
Other option: Computing mean of all frame based probabilities and applying a threshold (which may be lower than 0.5 for increasing sensitivity)

Comparing systems

How to compare hundreds of systems in a reliable way?



ROC created by applying different thresholds to mean frame probabilities for a file

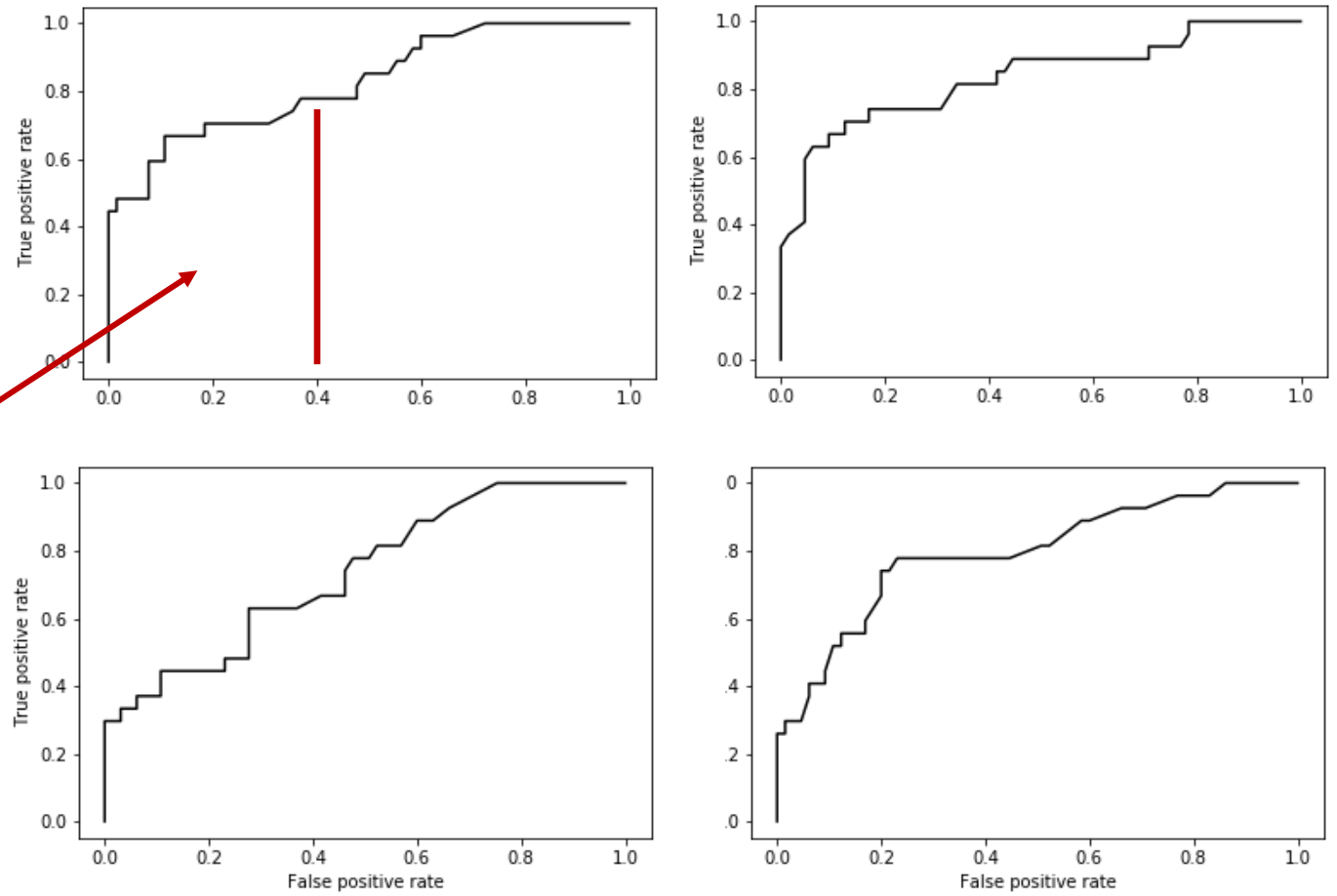


Selecting a system among many using the ROC curves

Main Criteria:

High sensitivity:
We don’t want to miss any pathological cases, it is ok to mis classify some normal cases as pathological.

Area under the left part of ROC curve (obtained by thresholding mean probabilities) may be a good measure together with sensitivity and specificity of the majority voting based decision



Selected systems sorted with respect to area under the curve

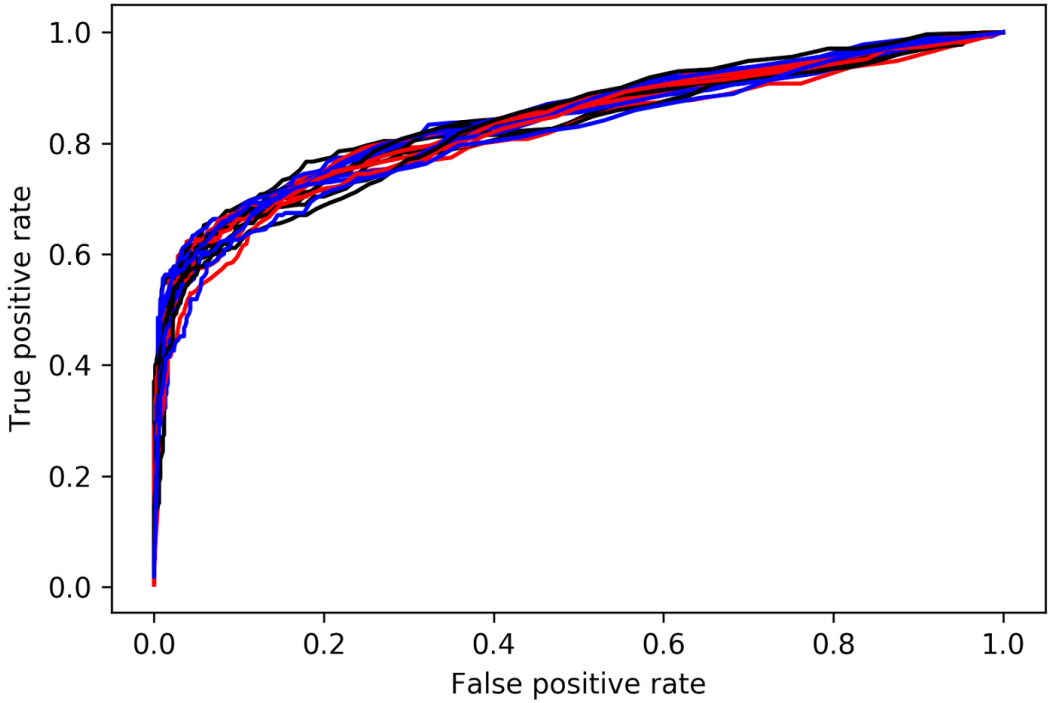
uocSeq2SubEnv32by16_eSyn500len: Sequential model 2, Sub-band envelopes size 32*16 computed on Ecg-synchronous 500 msec length frames.
uocSeq2SubEnv128by16_eSyn2000len
uocSeq2SubEnv64by16_eSyn1000len
uocSeq2SubEnv32by16_eSyn1000len
uocSeq2SubEnv128by16_nASyn2000len
uocSeq0SubEnv128by8_eSyn2000len
uocSeq2MelSpec128by16_nASyn2000len
uocSeq1SubEnv32by8_eSyn1per
uocSeq1SubEnv64by8_eSyn1per
uocSeq2SubEnv32by16_eSyn1per
uocSeq0SubEnv64by8_eSyn1000len
....

Observations:

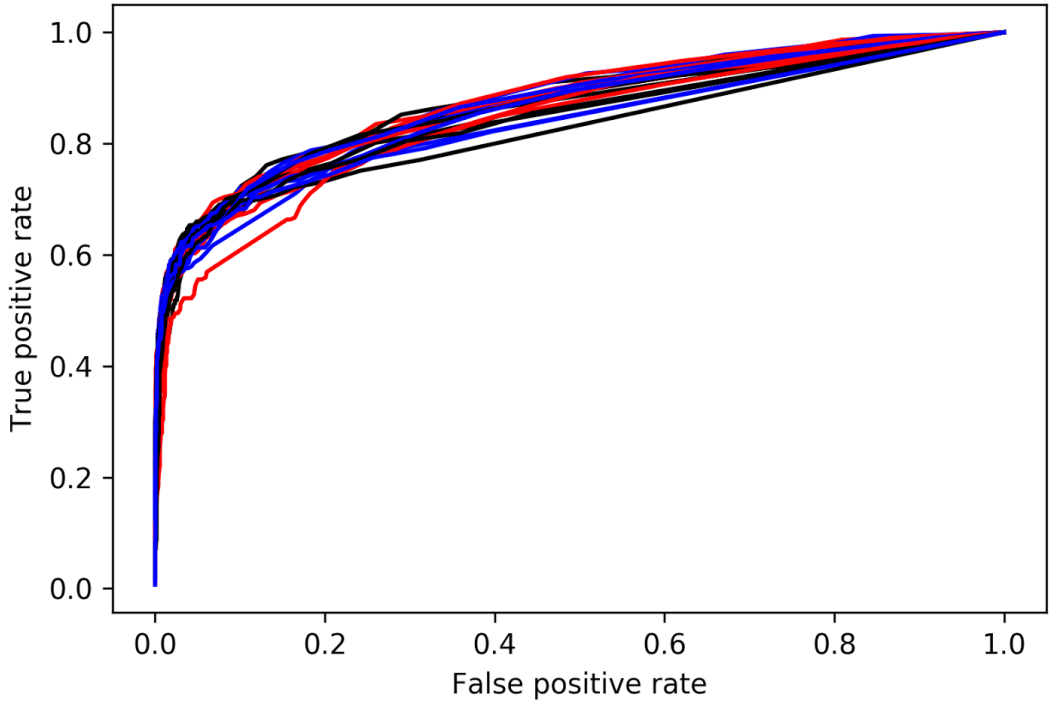
- Most of the selected systems use Sub-band envelopes
- More complex sequential models have higher performance
- While most of the selected systems use Ecg-synchronous frames, there are a few good systems selected to use a-synchronous frames. This is worth dedicating time.

ROC curves of best 20 systems (selected with respect to area under ROC)

Grp1: innocent vs pathological murmur



Grp2: normal vs pathological



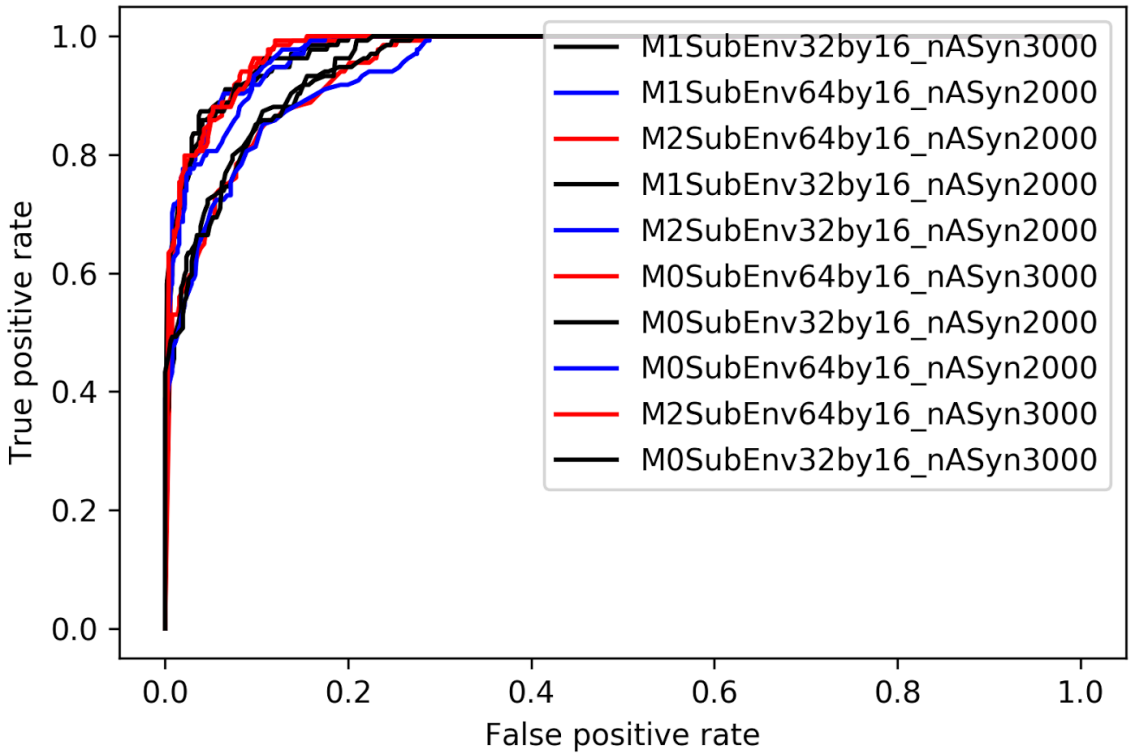
Preliminary test results for Physionet 2016

M_uocSeq1SubEnv64by16_nASyn2000len_1000hopt

File-level measures:
Confusion matrix:
Normal: 485 | 31
Pathological: 17 | 117
Sensitivity = 0.873, Specificity = 0.940,
Accuracy = 0.926, F1 = 0.830

Frame-level measures:
Confusion matrix:
Normal: 10045 | 663
Pathological: 424 | 2665
Sensitivity = 0.863, Specificity = 0.938

Best 10 systems ROCs for Physionet 2016



Result from literature [Potes et al, 2016]

Classifier	Sensitivity	Specificity	Overall Score
AdaBoost-abstain	0.70 (0.88)	0.88 (0.82)	0.79 (0.85)
CNN	0.79 (0.88)	0.86 (0.80)	0.82 (0.84)
Classifier ensemble	0.88 (0.96)	0.82 (0.80)	0.85 (0.89)