

SCOPE: Analysis of the publicly available PTB ECG dataset.

CODE STRUCTURE: The analysis is done in 5 separate steps, each assigned to a different script. Two additional utility scripts are used (config.py & utils.py). To launch the analysis, simply call the Makefile on the terminal.

The code uses the sklearnex optimization module to speed up all Scikit-learn operations.

```
main:
$(PYTHON) 00_get_patient_info.py
$(PYTHON) 01_get_cohort_statistics.py
$(PYTHON) 02_eda.py
$(PYTHON) 03_data_preprocessing.py
$(PYTHON) 04_modelling.py
$(PYTHON) 05_plot_model_results.py
```

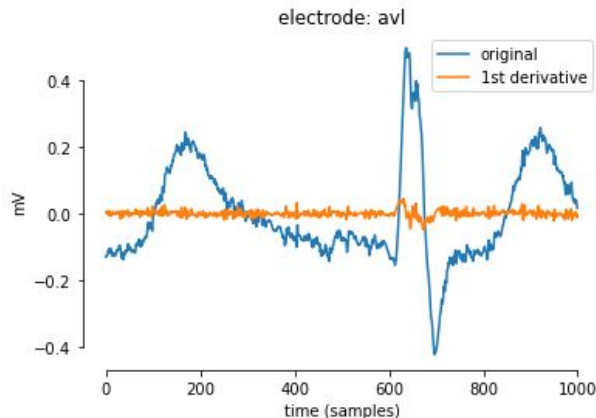
Fully parallelized at the patient level.

```
> code
> data
  > preprocessed
  > raw
> images
> info
> logs
  └─ results.log
> params
  └─ best_params.pkl
  └─ metadata_inference
  └─ README.md
> results
  > healthy_control_vs_bundle_branch_block
  > healthy_control_vs_cardiomyopathy
  > healthy_control_vs_dysrhythmia
  > healthy_control_vs_heart_failure_(nyha_2)
  > healthy_control_vs_heart_failure_(nyha_3)
  > healthy_control_vs_heart_failure_(nyha_4)
  > healthy_control_vs_hypertrophy
  > healthy_control_vs_myocardial_infarction
  > healthy_control_vs_myocarditis
  > healthy_control_vs_palpitation
  > healthy_control_vs_stable_angina
  > healthy_control_vs_unstable_angina
  > healthy_control_vs_valvular_heart_disease
  > metadata_inference
```

Logging is used for info and errors.

2 FEATURE EXTRACTION

For each patient, and each recording, a series of 6 features were extracted for every sensor.



The 1st derivative is calculated as a measurement of abrupt changes in the signal. Essentially, a way to identify the “R” peaks without presupposing any threshold.

	channel_variance	mean_amplitude	median_amplitude
i	0.024413	-0.000109	0.00700
ii	0.040936	-0.000213	0.00600
iii	0.046602	0.000089	0.02975
avr	0.021060	0.000060	-0.02600
avl	0.025254	0.000152	-0.02400
avf	0.037704	-0.000217	0.00450
v1	0.056249	-0.000162	-0.04550
v2	0.055694	0.000073	-0.03850
v3	0.096480	-0.000186	-0.00700
v4	0.042223	-0.000233	0.02000
v5	0.015040	-0.000087	0.02150
v6	0.009127	-0.000228	0.01500
vx	0.010746	-0.000169	0.00300
vy	0.016321	0.000093	0.02400
vz	0.011712	-0.000026	-0.01600

mean_derivative_value	median_derivative_value
9.895833e-06	0.00000
1.266927e-05	0.00050
2.805990e-06	0.00025
-1.129557e-05	-0.00025
3.554687e-06	-0.00025
7.740885e-06	0.00025
-1.263021e-06	0.00050
5.240885e-06	0.00025
2.988281e-06	0.00050
-4.941406e-06	0.00050
-8.287760e-06	0.00050
-9.401042e-06	0.00025
2.148438e-06	0.00000
-1.822917e-07	0.00000
9.635417e-07	0.00000

power_spectral_density_max
6.031482
10.737300
20.342330
3.256591
9.977706
14.301136
20.320052
20.124919
23.515985
8.118481
6.339899
4.516602
2.432285
10.376660
2.815476

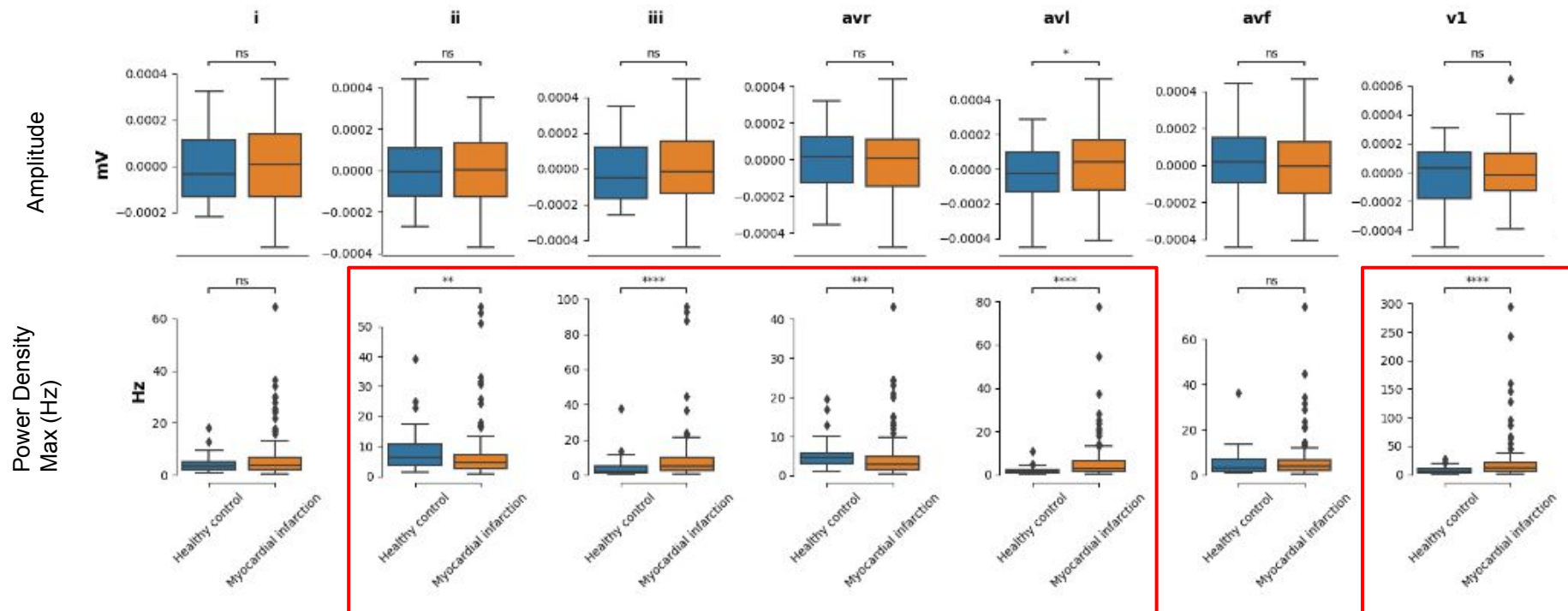
* These operations took place for all recordings of a given patient. The corresponding script (“03_data_preprocessing.py”) is parallelized at the patient level.

Maximum of power spectral density estimated using Welch's method (in Hz).

3 EXPLORATORY DATA ANALYSIS

* A full list of comparisons is available at the "images" directory.

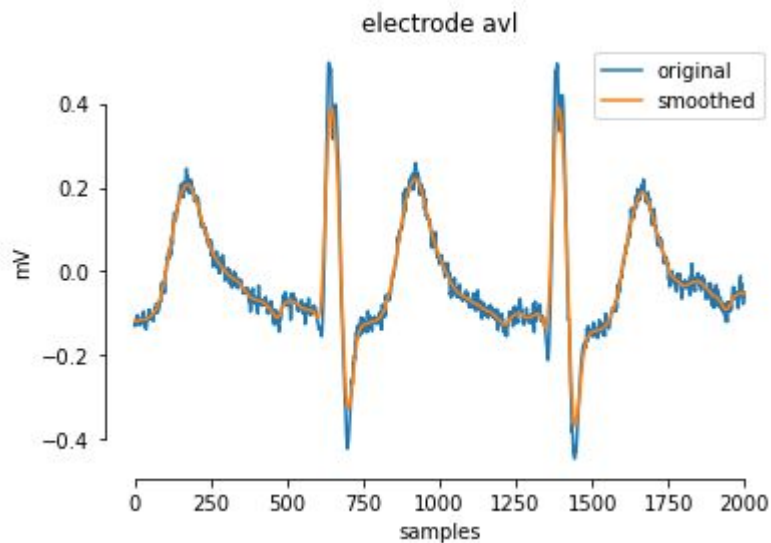
Healthy control VS Myocardial Infarction



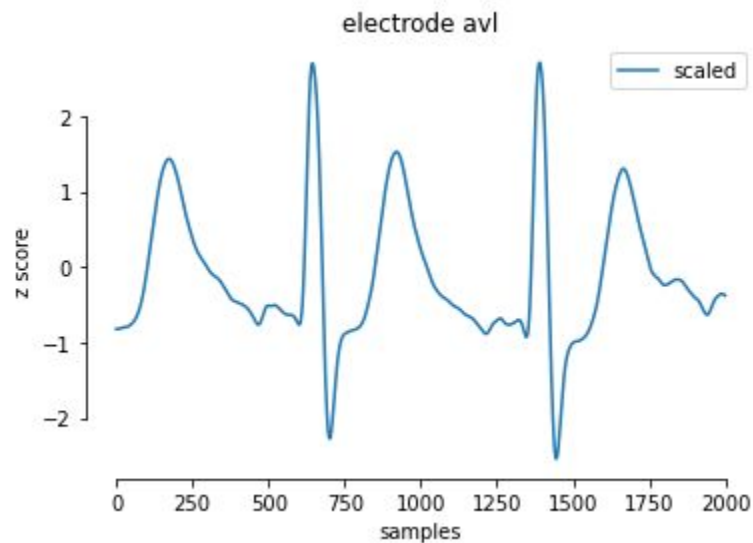
We observe a statistically significant difference in multiple electrodes ($p < 0.05$; Mann-Whitney test, corrected with Bonferroni corrections for multiple comparisons) for the power density feature, but not this amplitude. This type of analysis can help us build more interpretable models or identify limitations of existing ones.

3 PREPROCESSING

- (i) The time series were smoothed with a 10ms Gaussian Kernel.

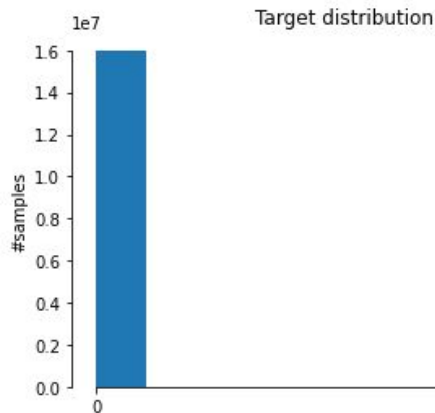


- (ii) The smoothed signal was scaled to zero mean and unit variance.

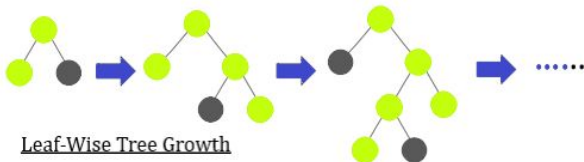


* These operations took place for all recordings of a given patient. The corresponding script ("03_data_preprocessing.py") is parallelized at the patient level. The data are stored in the "preprocessed" directory,

4 MODELLING



The target distribution is skewed. This indicates that I cannot use metrics such as F1 or accuracy to evaluate our model, AND that I must use a STRATIFIED k-Fold approach to avoid overfitting.

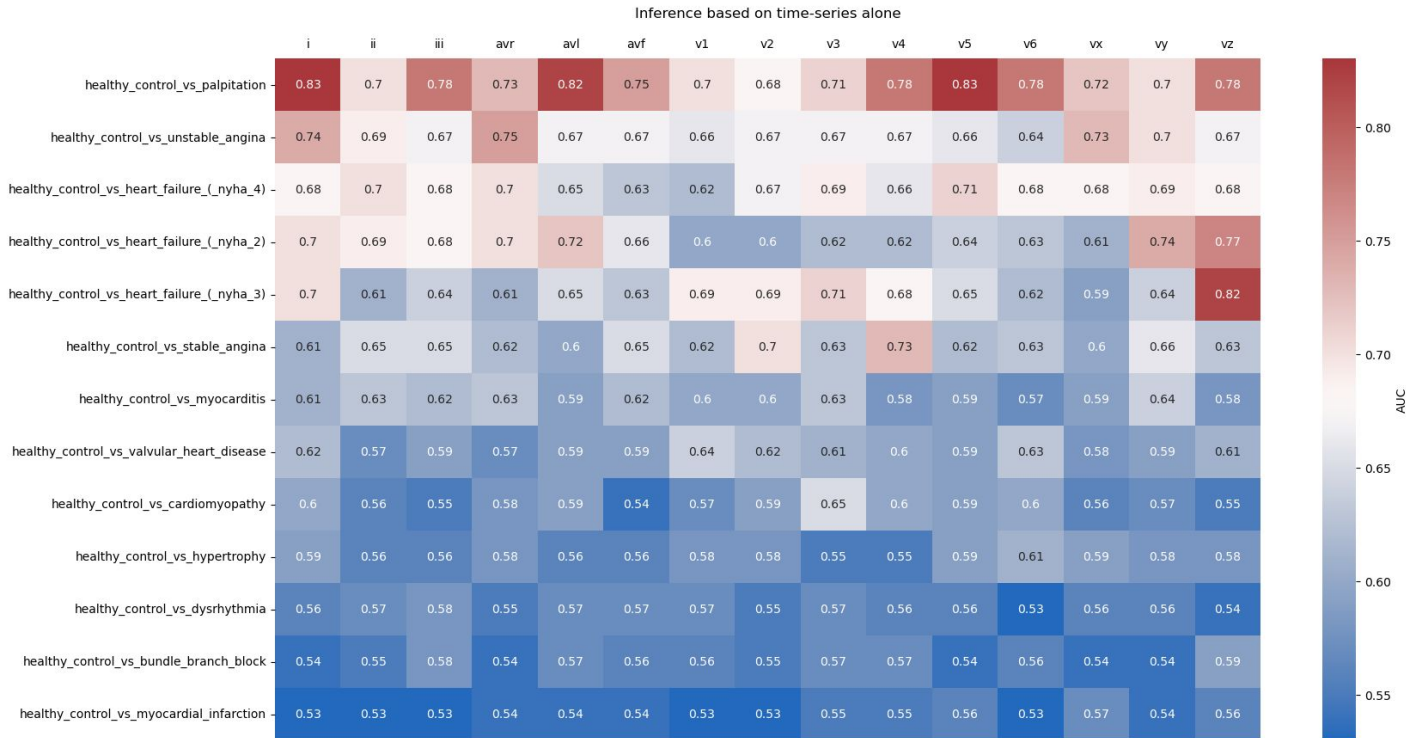


To computationally constrain the task, I transformed the classification to a univariate binary classification problem, essentially contrasting each population (e.g: “myocarditis”) against data from the healthy control group.

As a first approach, I labelled each sample of the time-series based on the population where the patient belonged (e.g: all samples from healthy patients were labelled as 0 and all others as 1). Thus, this a time-resolved classification approach.

I chose the Light Gradient Boosting Machine classifier, which a lighter version of XGBoost, currently the state-of-the-art in ML classification.

5 RESULTS



The model performs very well on distinguishing patients suffering from palpitation against healthy controls. The lowest performance is achieved for the myocardial infarction patients. Interestingly, not all electrodes provide the same predictive power. Additionally, even though we observed differences in the frequency domain for the “myocardial infarction” patients, the time-resolved model remains at chance level across all electrodes. This indicates that this simple approach is not sufficient and the model more likely underfits due to the high temporal bias. More elaborated models are required to achieve high classification performance.

6 NEXT STEPS

(i)

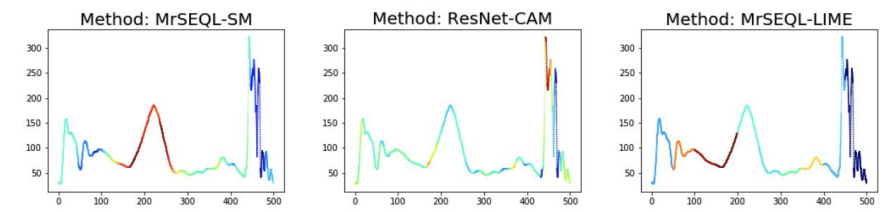
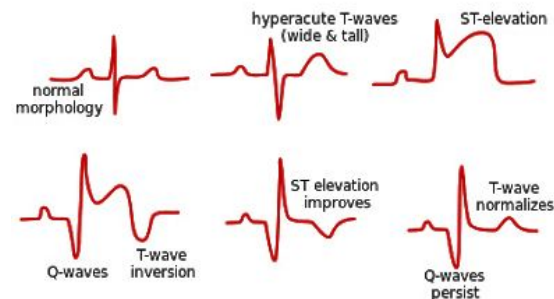


Fig. 1: Saliency map explanations for a motion time series obtained using different explanation methods. In this figure, the most discriminative parts are colored in deep red and the most non-discriminative parts are colored in deep blue.

(ii) Models more suited to handle temporal data (LSTMS)

(iii) “Epoching”. The data should be cropped around the “R” peak. Each segment is called an epoch. Then, different epochs will be averaged for each class. A time-resolved classifier can then be run on these average epochs. This will increase the statistical power of the analysis, and, importantly, will provide a time resolved picture on the segments that contribute the most to the difference (essentially building a saliency map but in a far less complicated way).

Explainable ECG classification with saliency maps (e.g: Le Nguyen, Thach, and Georgiana Ifrim. "A short tutorial for time series classification and explanation with MrSQM." *Software Impacts* 11 (2022): 100197.). In principle, the saliency maps should agree with the clinical practice.



7 What I would study next to enhance my skills.

(i) @COURSERA

Browse > Data Science > Machine Learning

Informed Clinical Decision Making using Deep Learning Specialization

Apply Deep Learning in Electronic Health Records. Understand the road path from data mining of clinical databases to clinical decision support systems

 [Fani Deligianni](#)

Offered By  University of Glasgow

(ii) PAPERS:

1. Faouzi, Johann. "Time Series Classification: A review of Algorithms and Implementations." *Machine Learning (Emerging Trends and Applications)* (2022).
2. Ismail Fawaz, H., Forestier, G., Weber, J., Idoumghar, L., & Muller, P. A. (2019). Deep learning for time series classification: a review. *Data mining and knowledge discovery*, 33(4), 917-963.
3. Gupta, Varun, et al. "A review of different ECG classification/detection techniques for improved medical applications." *International Journal of System Assurance Engineering and Management* (2022): 1-15.
4. Weimann, Kuba, and Tim OF Conrad. "Transfer learning for ECG classification." *Scientific reports* 11.1 (2021): 1-12.