

# MEI<sup>BIO</sup> ENG16

# Modelling Physiological Time Series with Sequential Machine Learning

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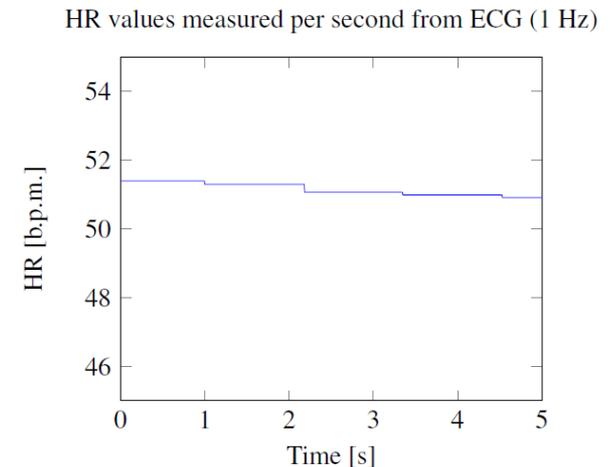
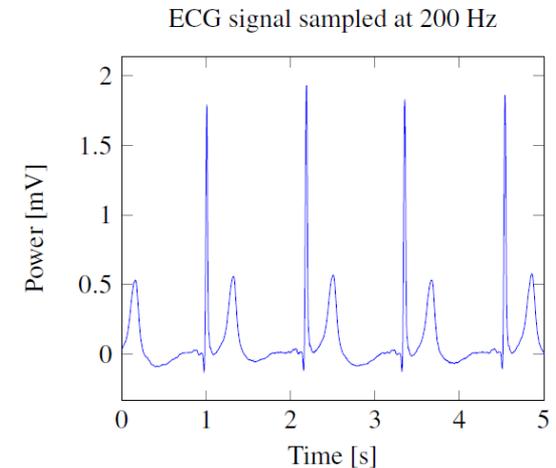
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# Outline

- Introduction
- Data Overview
- Hidden Markov Models
- Preprocessing with Gaussian Process
- Long Short-Term Memory Architecture
- Long Short-Term Memory Results
- Conclusion
- Future Work

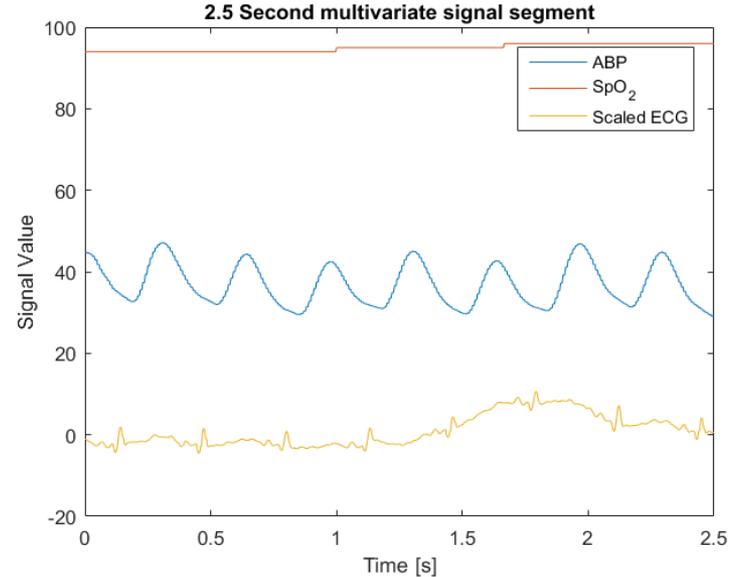
# Introduction

- Deep learning enables extraction of features from big data, that would otherwise go unnoticed
- Aims:
  - Provide probabilistic prediction of patient physiological status
  - Reverse engineer to learn
- Our study compared HMMs and LSTMs
- We argue that high-res data and LSTMs provide the best solution



# Data Overview

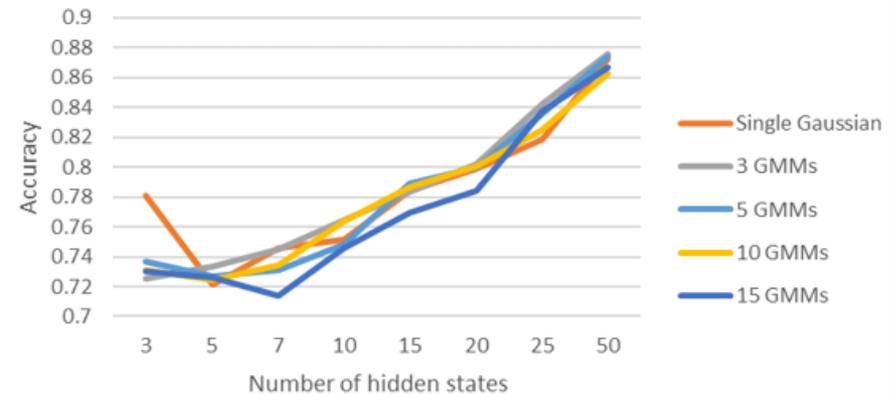
- NICU (60 Hz | 3 patients)
  - Outcomes: Death, IVH, or Good
  - Input channels: ABP, ECG, SpO<sub>2</sub>
- ICU (40 Hz | 4 patients)
  - Outcomes: Death or Good
  - Input channels: ICP, ABP
- TBI (0.2 Hz | 101 patients)
  - Outcomes: GOS 1 or 5 (Death or Good)
  - Input channels: ICP, CPP, ABP, ECG, SpO<sub>2</sub>, RR, temp, PRx, age
- MIT-BIH Arrhythmia (360 Hz | 48 patients)
  - ECG beat classification: normal, RBBB, LBBB, paced, premature ventricular



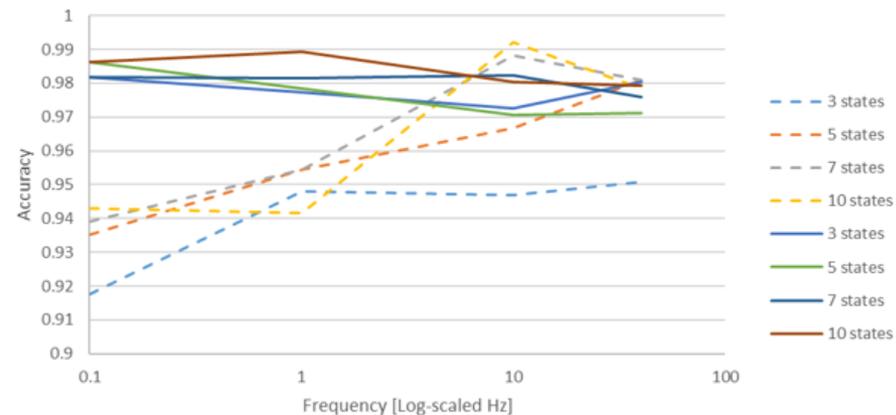
# Hidden Markov Models

- Classification based on highest log-likelihood
- 50:50 split
- Short dropouts (<20 time steps) replaced with interpolated values

HMM accuracy for different emission distributions



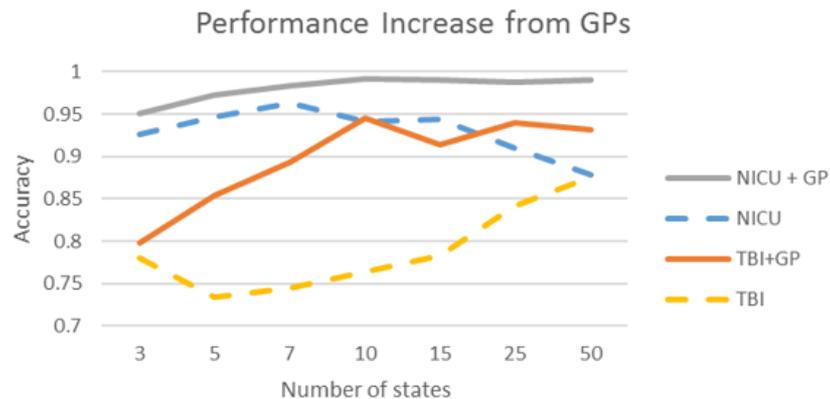
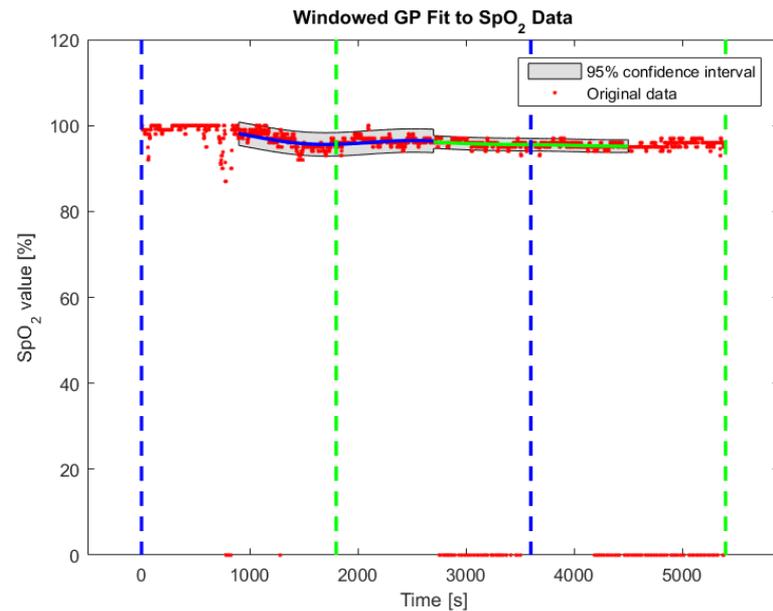
HMM performance on ICU data



# Preprocessing with Gaussian

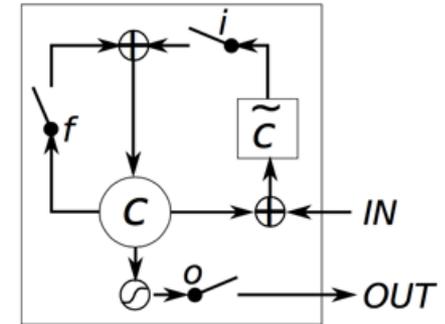
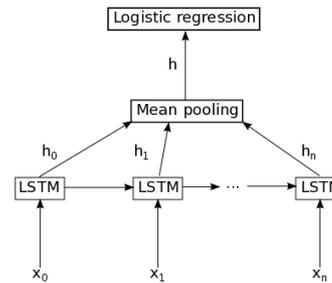
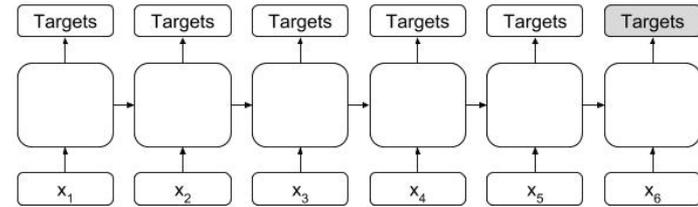
## Processes

- Windowed approach (30 minute)
- Regressed mean replaces noise and dropouts
- Standard deviation serves as confidence measure
- Outputs fed to HMMs



# Long Short-Term Memory Architecture

- Target replication and average pooling
- Dropout
- RMSprop and SGD-NAG
- Drop\_mask

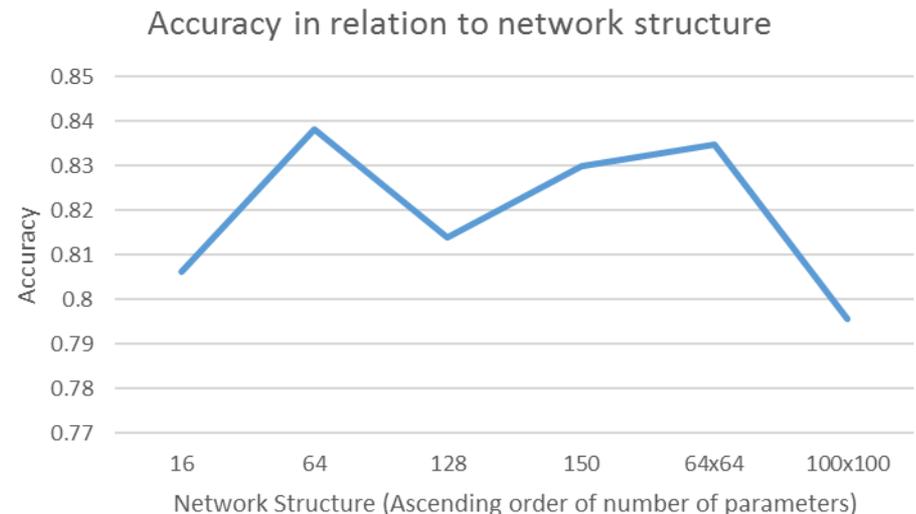
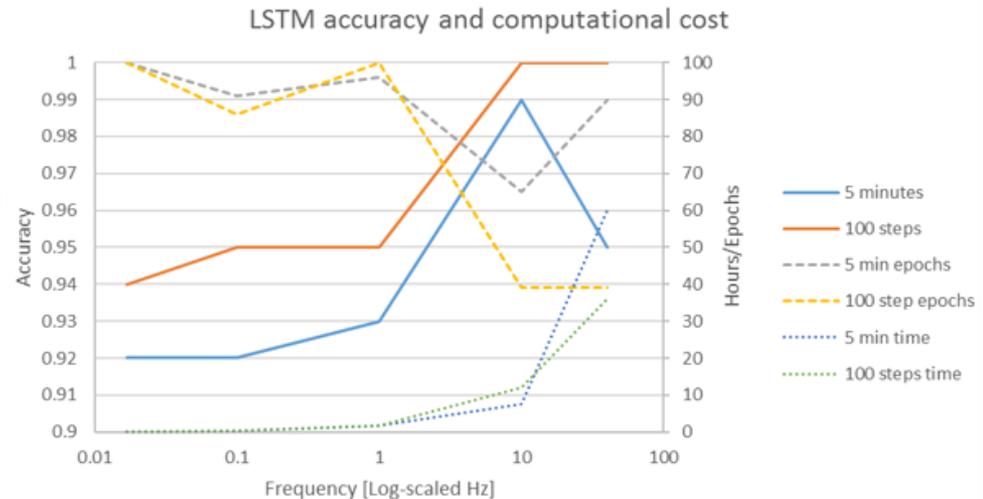


Graves [2013]

$$\mathbf{P} = (\mathbf{W}\mathbf{X}) \left( \sum_{k=1}^K \frac{\mathbf{W}_k}{\mathbf{D}_k \mathbf{W}_k} \right)$$

# LSTM Results

- Accuracy increases with resolution
- No correlation with network structure
- Cannot deal with long sequences (>300 time steps)



# Conclusion

- Overall LSTMs outperform HMMs
- GPs significantly improve HMM performance, but are not practical
- Need for semi-supervised approach in medicine

Dataset	HMM	LSTM
NICU	0.96	0.985
ICU	0.99	1
TBI	0.875	0.86
MIT-BIH	N/A	0.96

# Future Work

- Apply LSTMs to more data
- Implement LSTM autoencoders combined with t-SNE for semi-supervised clustering
- Implement Neural Turing Machines and stacked LSTMs to allow longer sequence analysis.



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Thank You

**wellcome**trust

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