



WROCŁAW UNIVERSITY
OF ENVIRONMENTAL
AND LIFE SCIENCES

Deep Learning Architectures for Exploring High-Dimensional, Small- Sample Data in Microbiome

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Goals

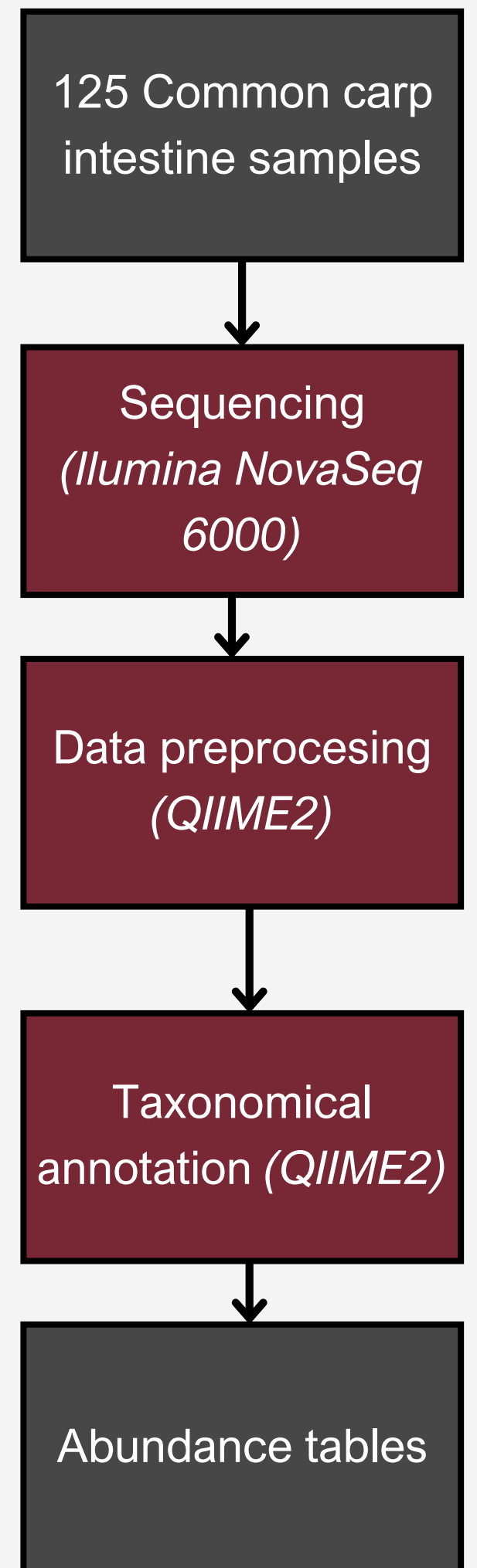
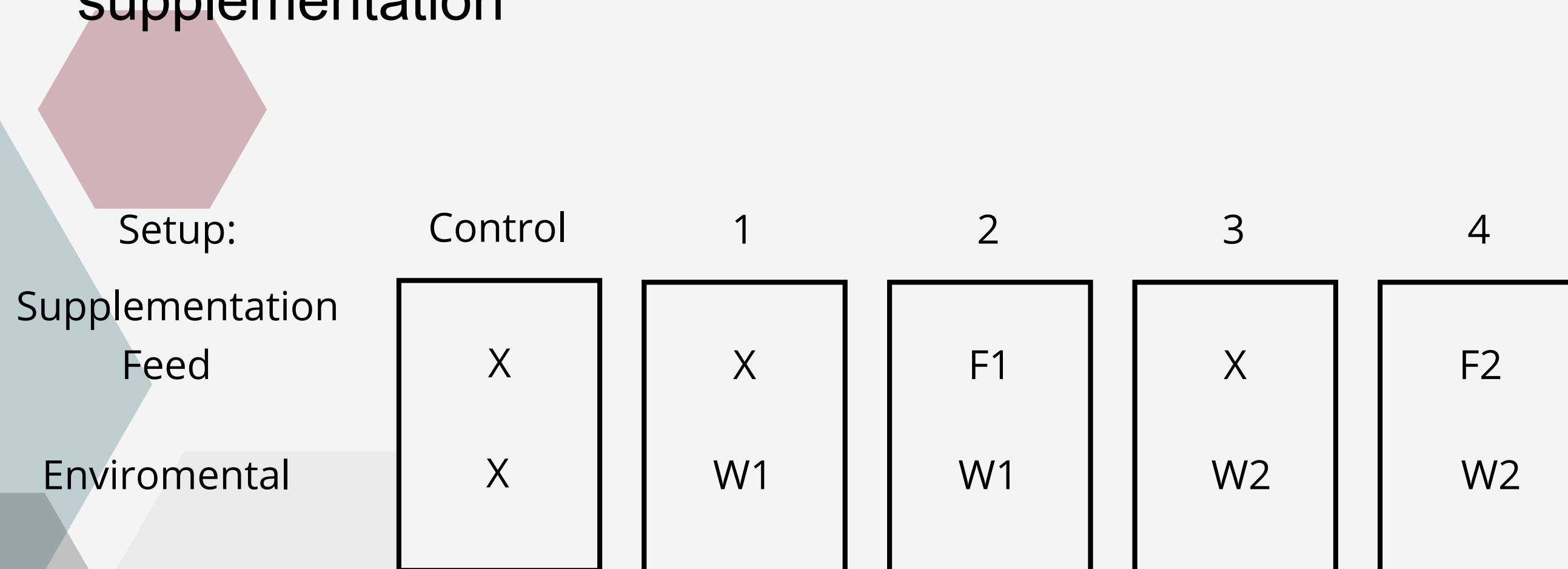
Deep Learning (DL) approaches in classification of high dimensional - small sample, sparse, biological data



Development of a DL model capable of classification based on differences in effective microorganism supplementation

Materials

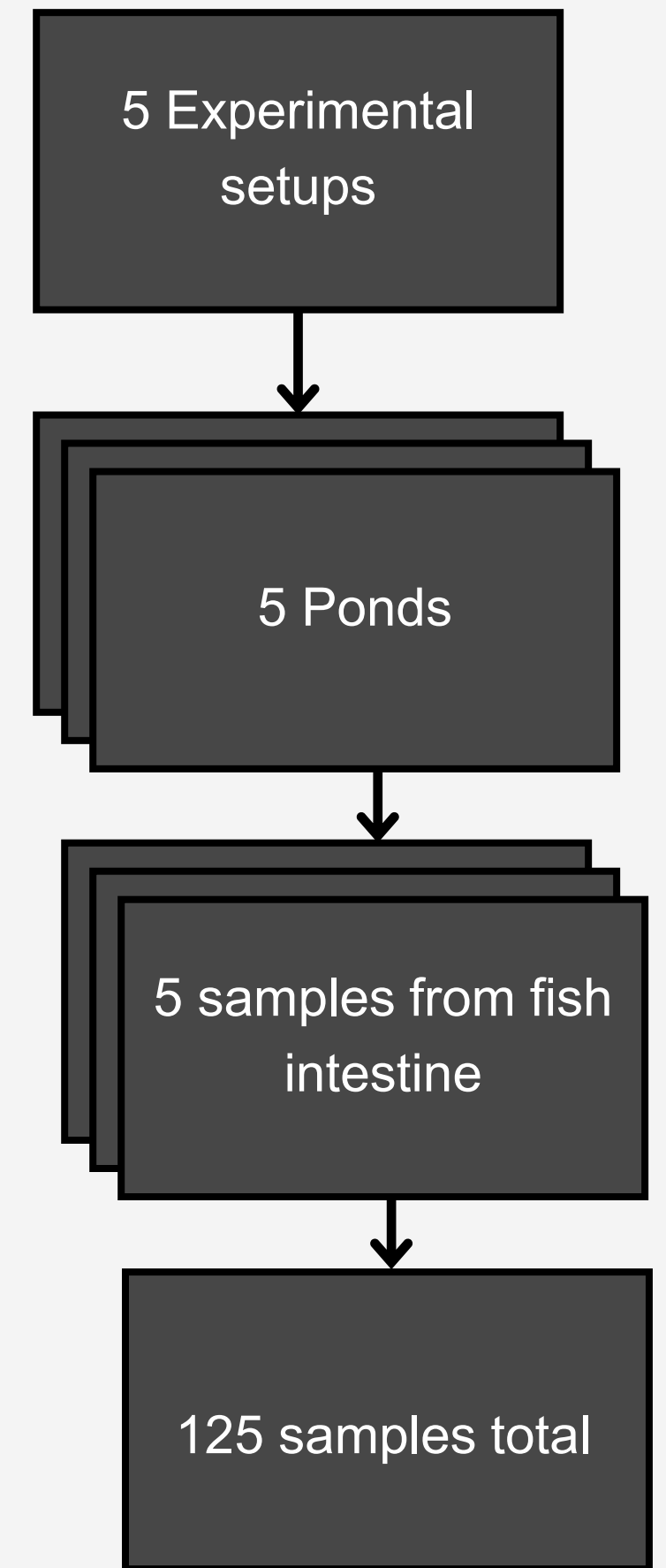
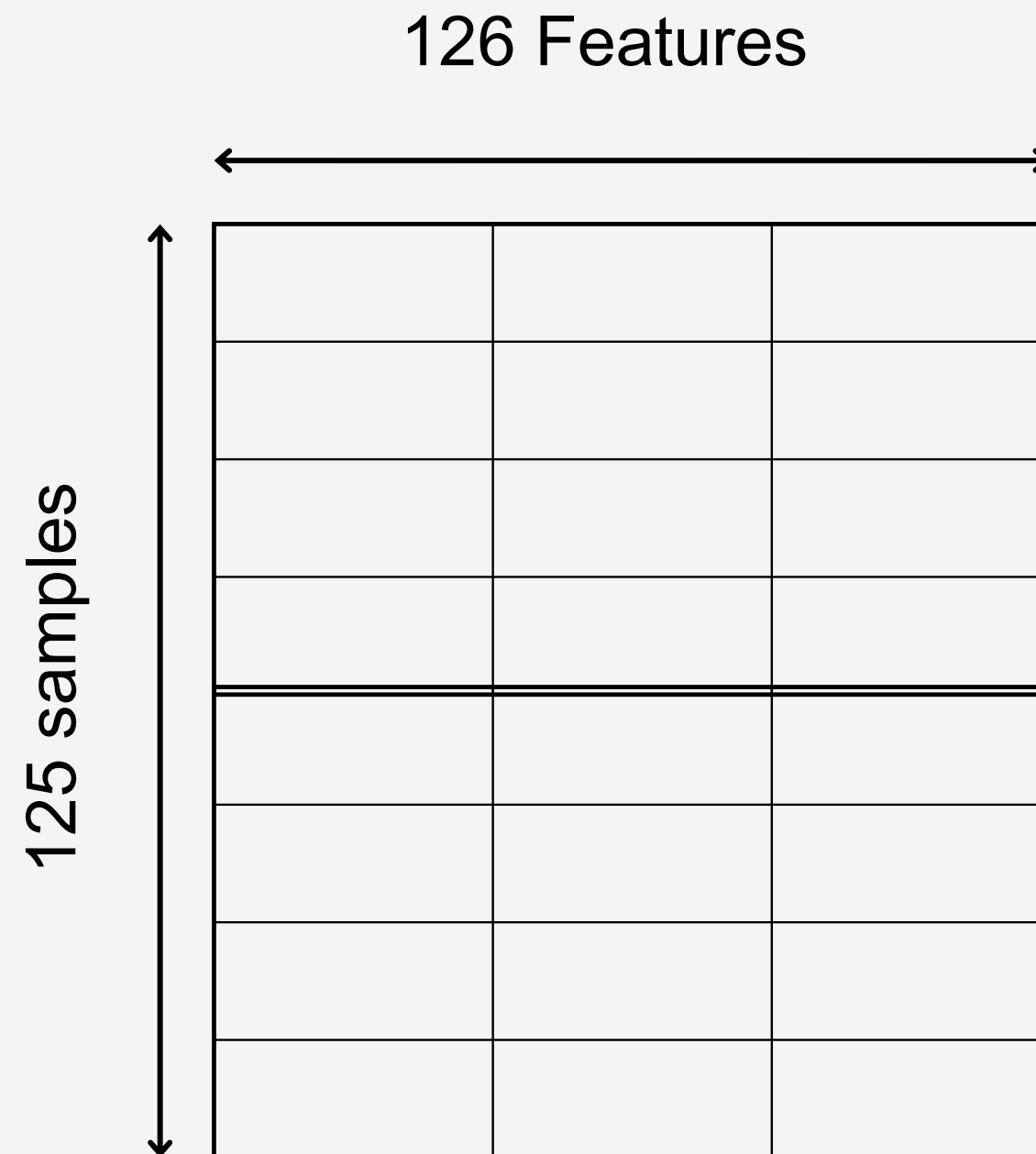
- Microbiome of fish intestine
- Sequenced reads of hypervariable regions of 16S rRNA gene
- 5 experimental setups, with different effective microorganism supplementation



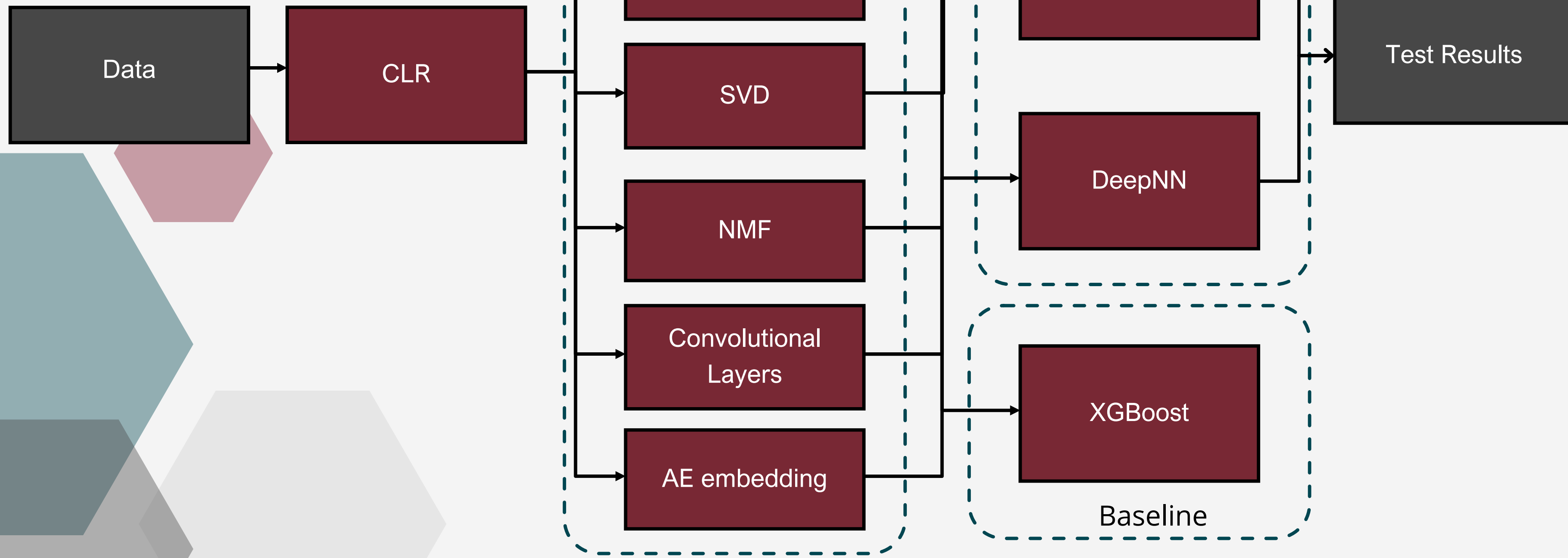
Materials

- Features - Bacteria families
- Samples - Individuals
- Cells - Bacteria abundance
- Sparse / zero inflated data

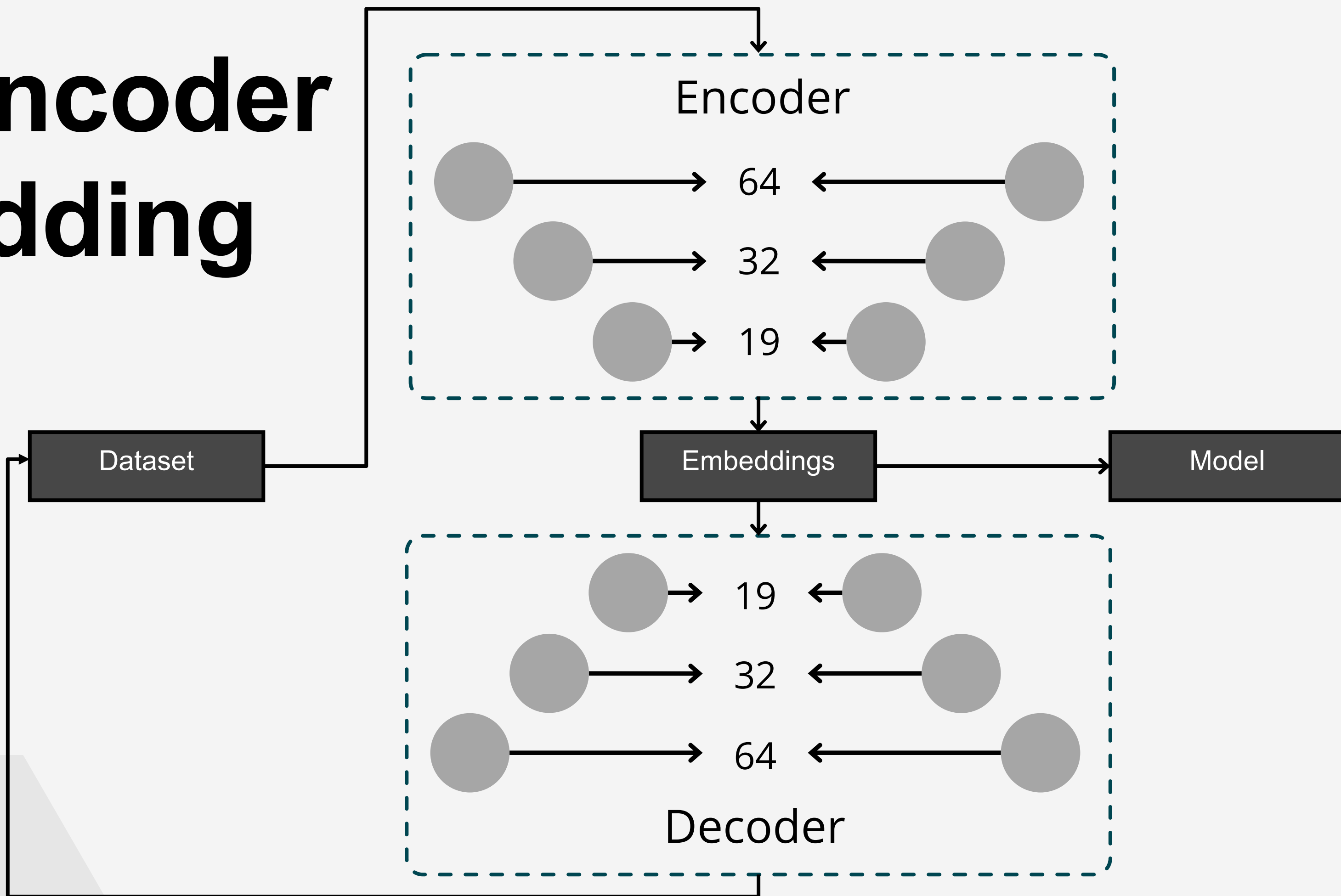
- CLR Transformed



Analysis Pipeline

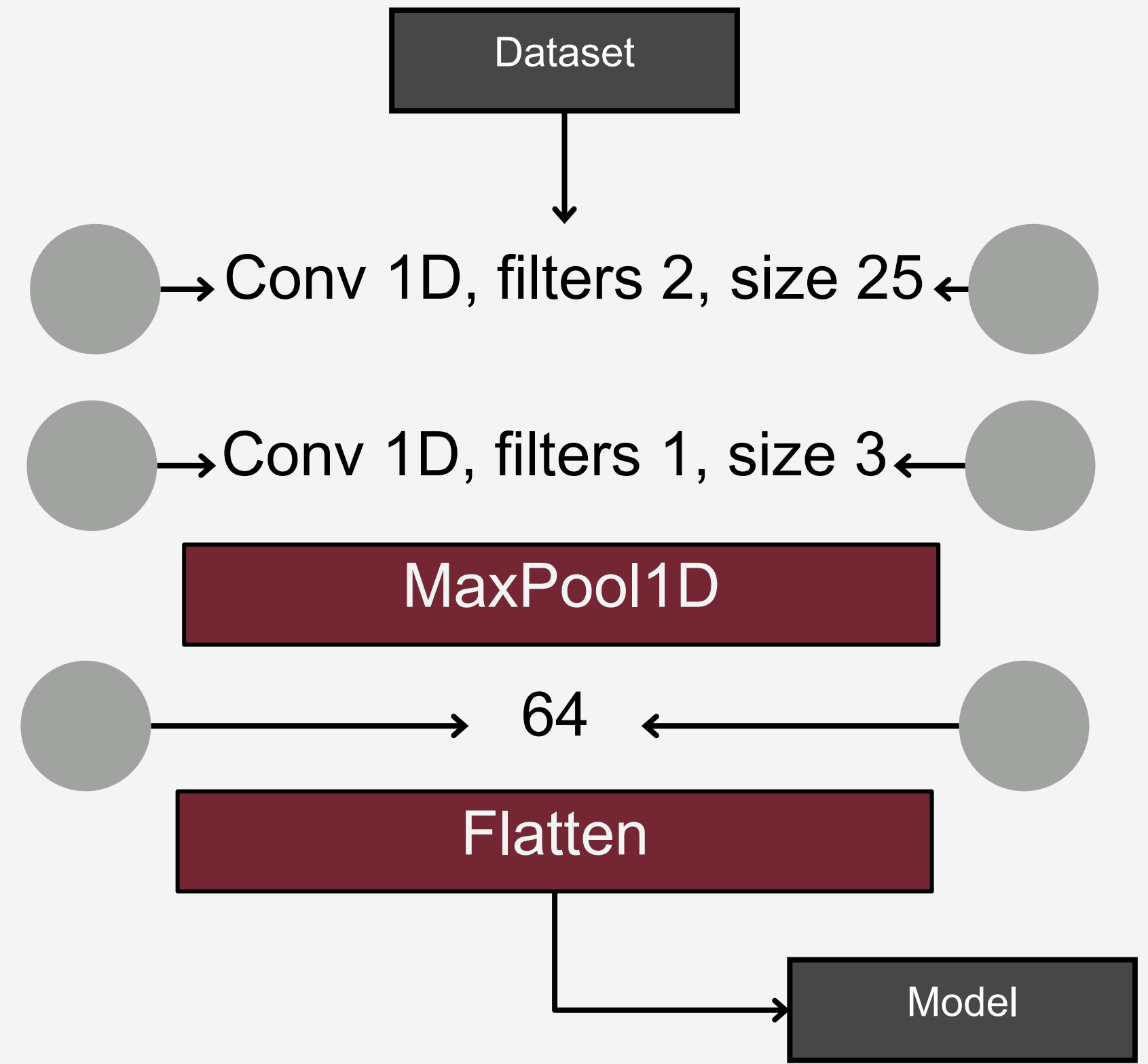


Autoencoder Embedding

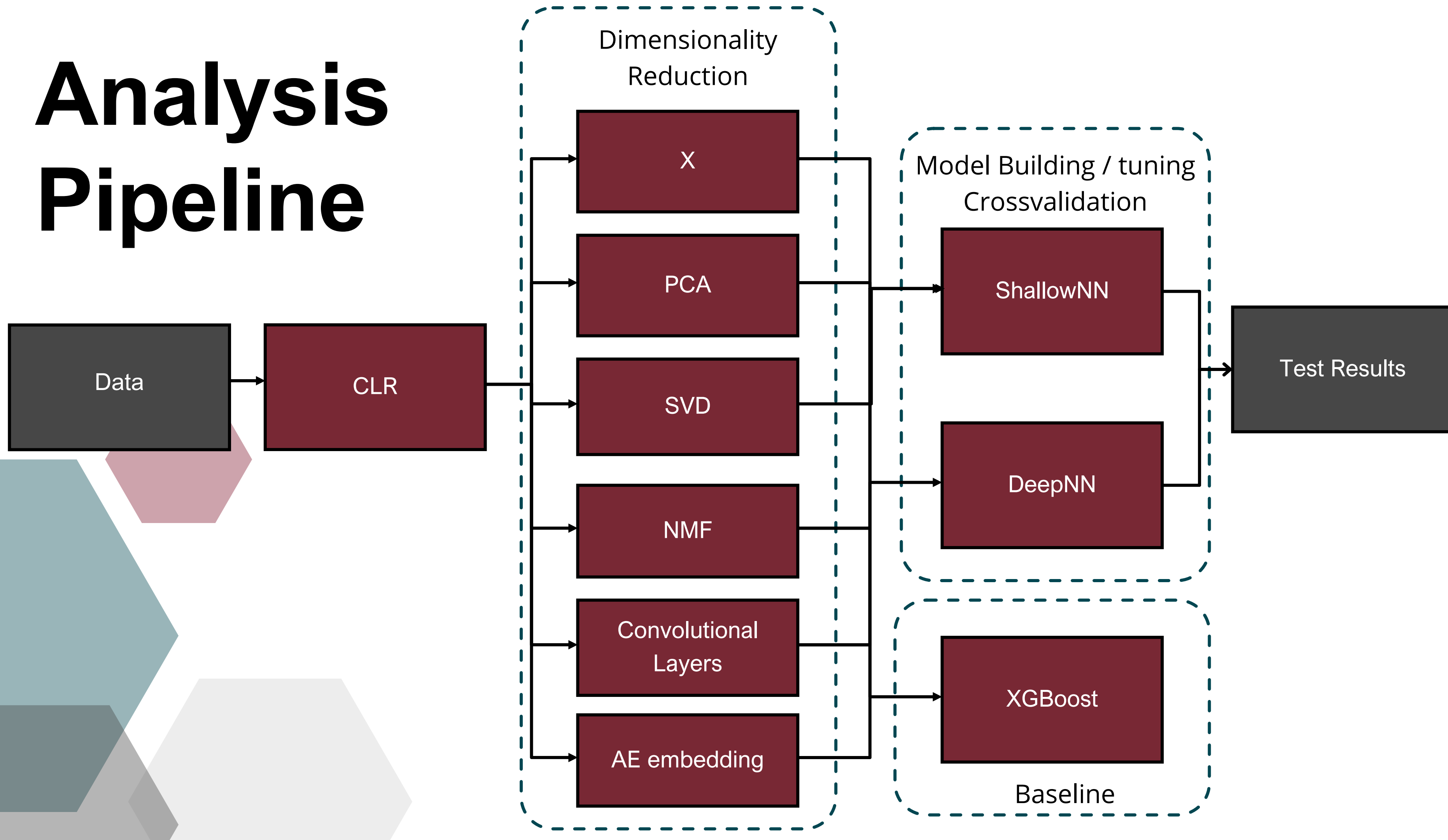


Convolution Layers

Fish - 1D Picture



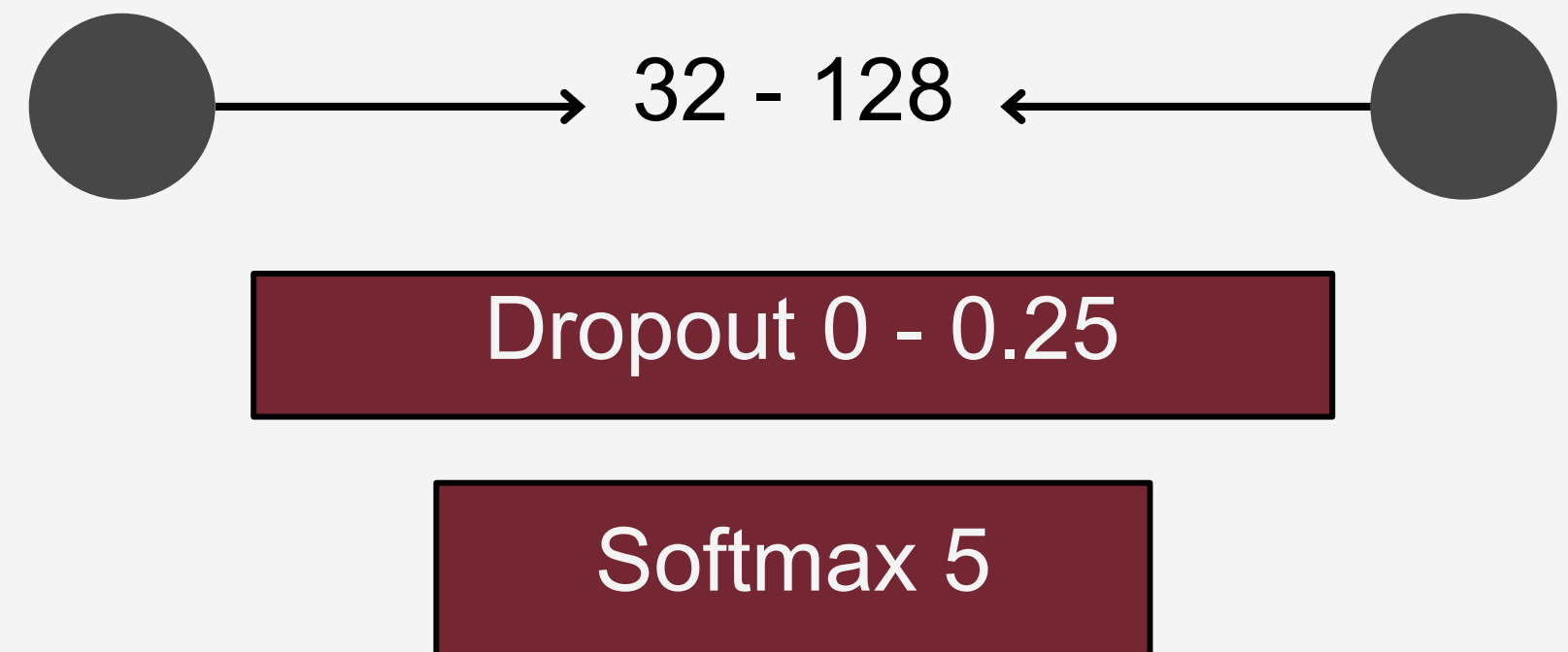
Analysis Pipeline



Model Architecture

- ShallowNN

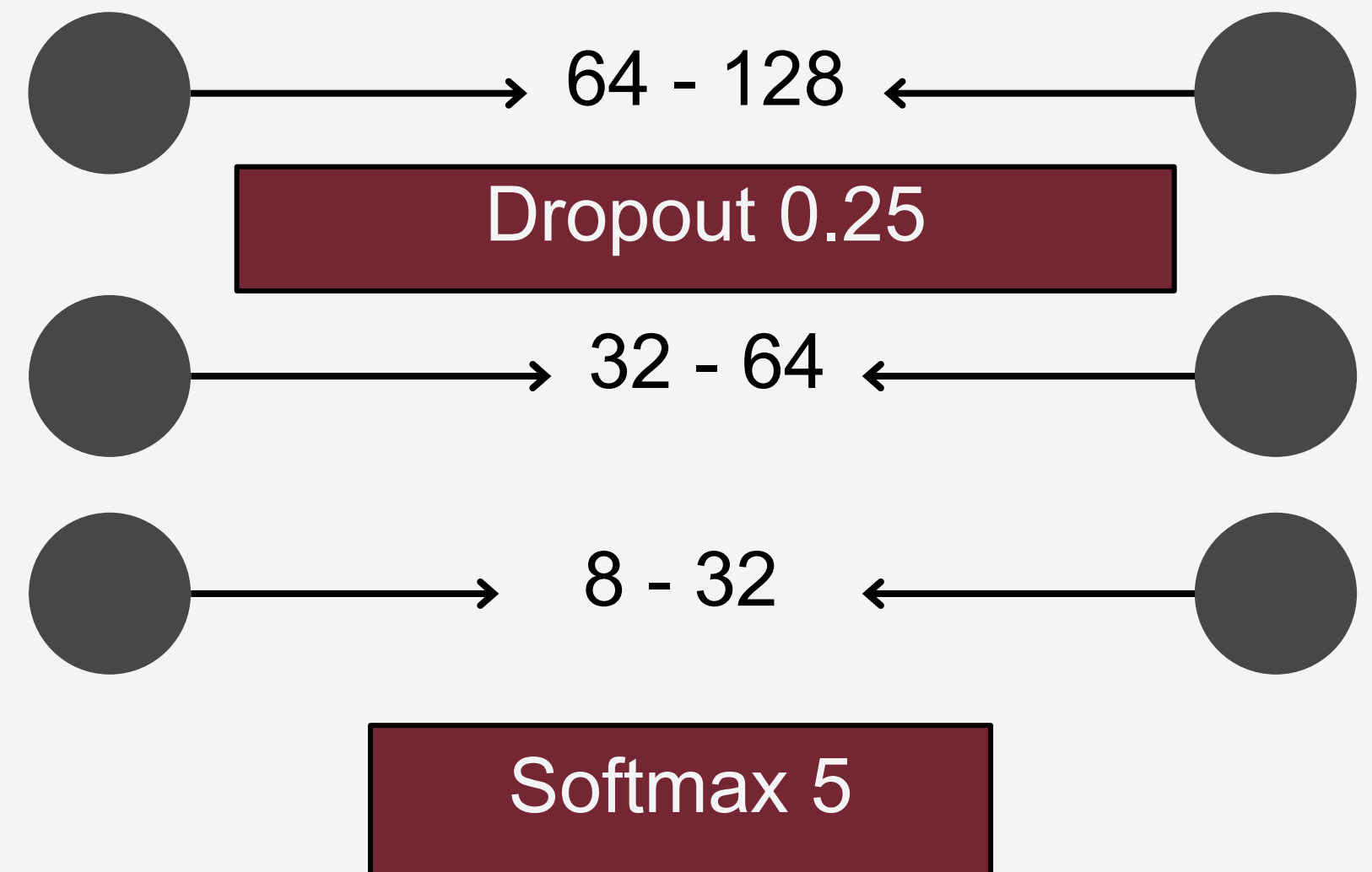
- Activation - ReLU
- Optimizer - ADAM
- Loss - Categorical Crossentropy
- Metric - Accuracy
- Weight regularizer - L2 (0.01)



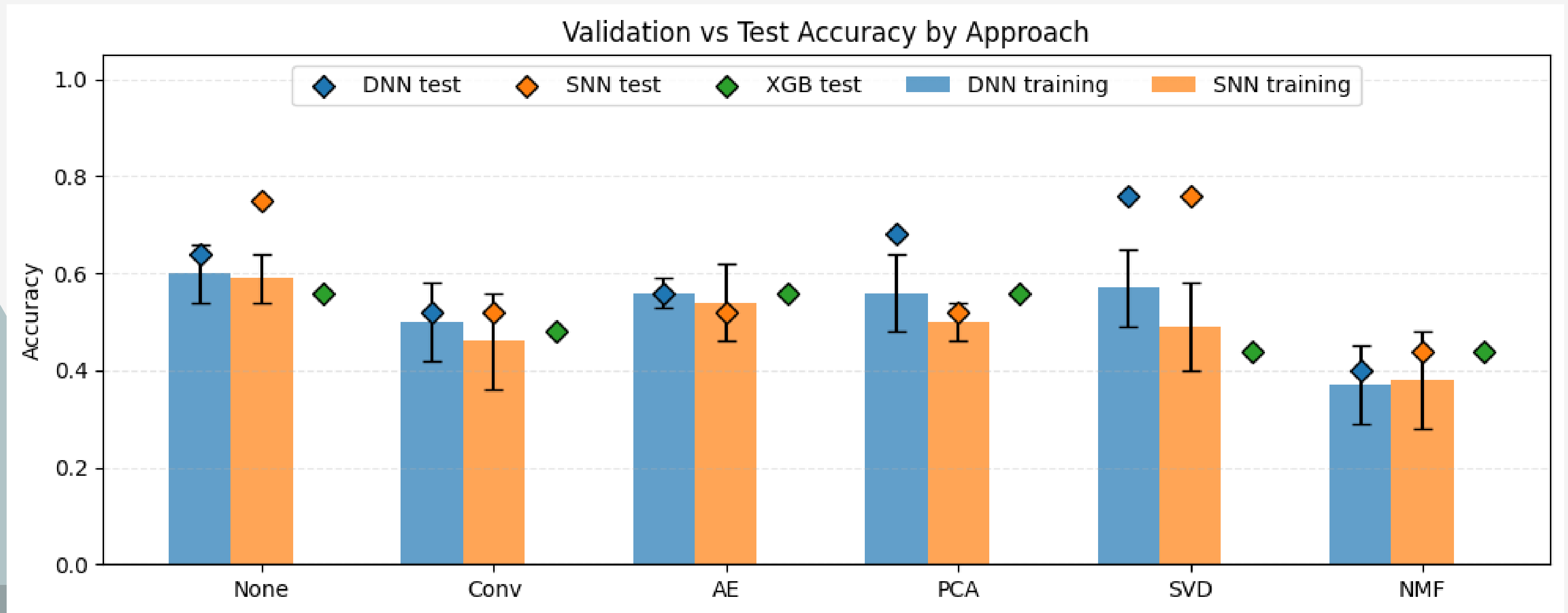
Model Architecture

- *DeepNN

- Activation - ReLU
- Optimizer - ADAM
- Loss - Categorical Crossentropy
- Metric - Accuracy
- Weight regularizer - L2 (0.01)



Results



Simulation

Based on CLR transformed data

- Same shape
- Normal Distribution $N(0 + S, \sigma)$

Two parameters:

- S - mean shift
- P_s - columns with shifted mean

$$5 \xleftarrow{P_s} 125$$

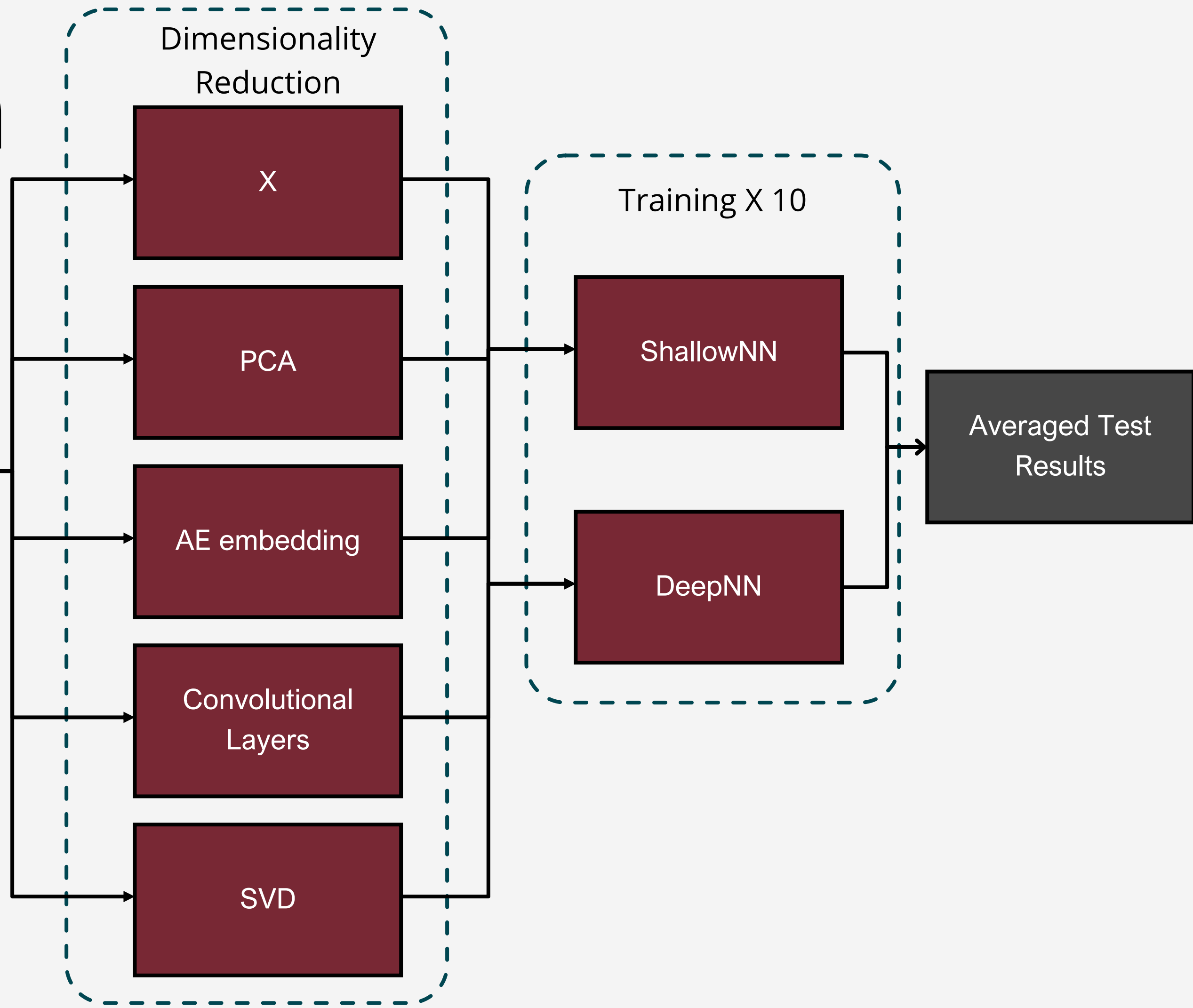
$$0.1 \xleftarrow{S} 2.0$$

$\times 10$

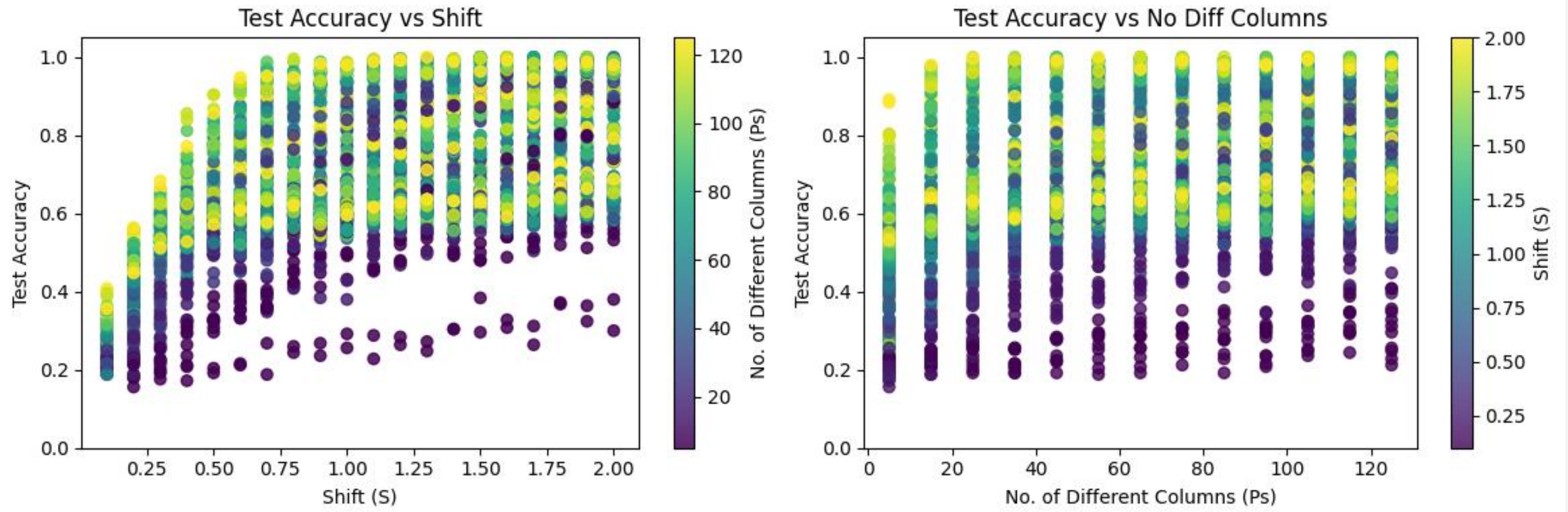


Simulation Pipeline

Simulated Data

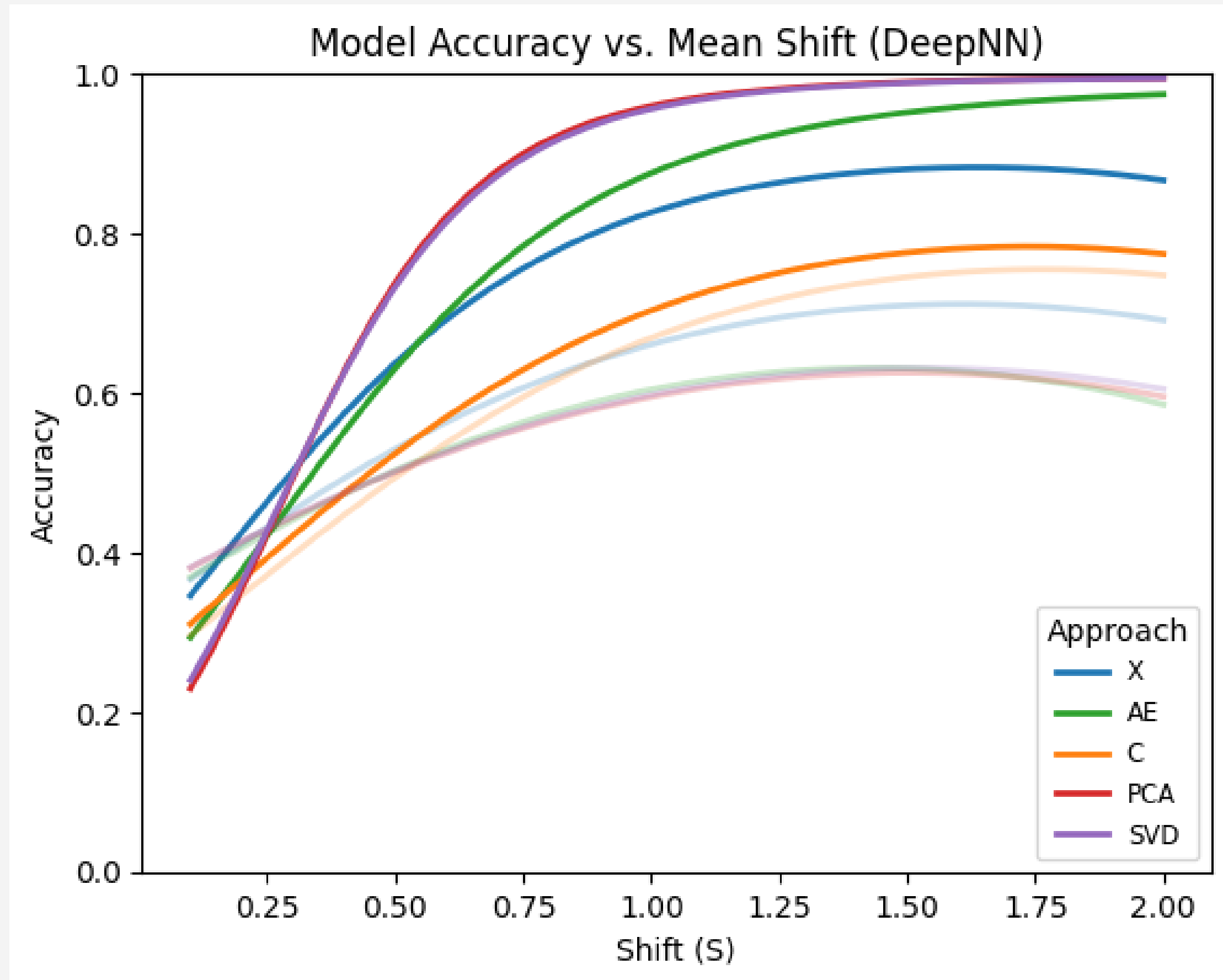


Results - Simulation



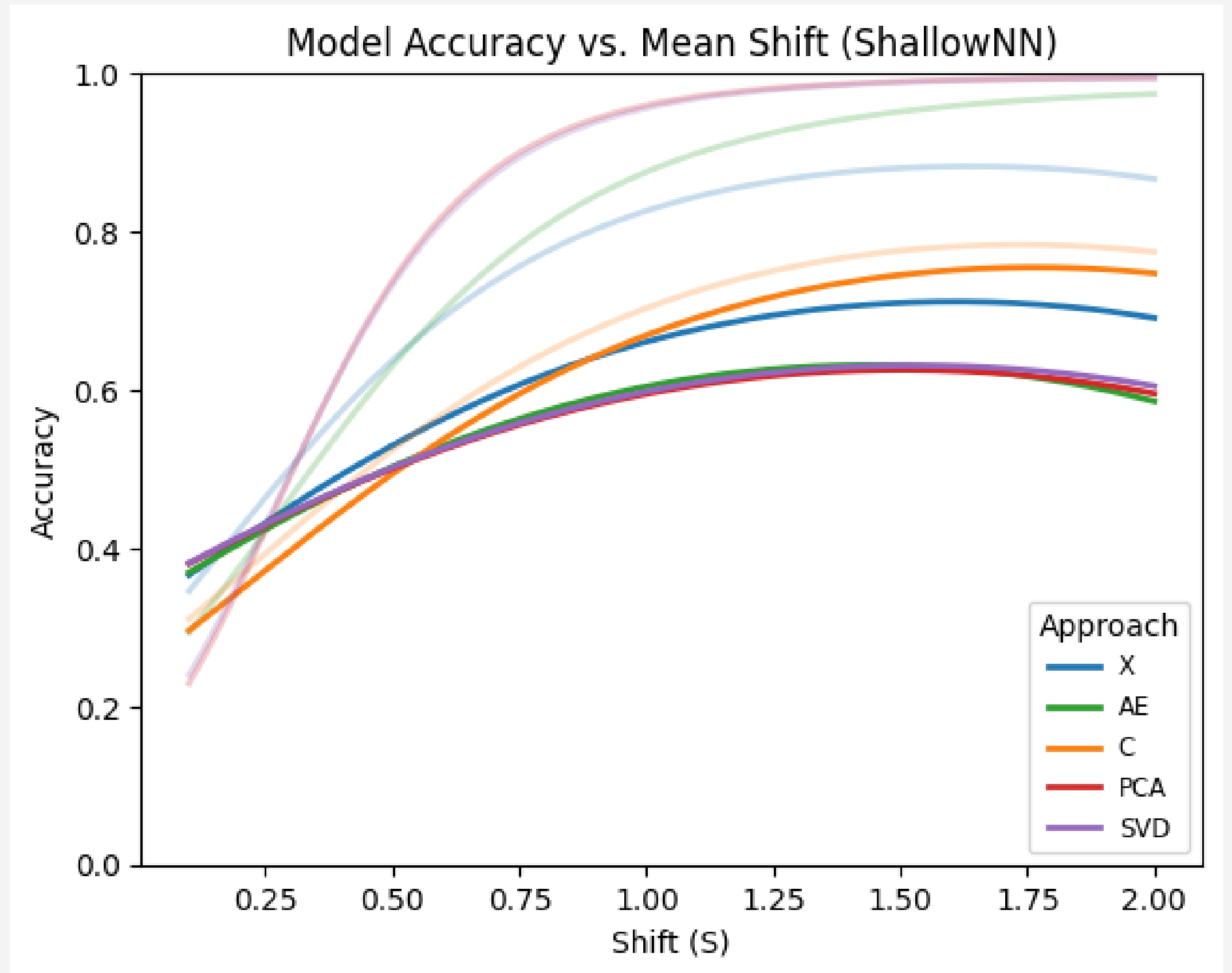
Results

- Simulation



Results

- Simulation



Conclusions

- NMF and Conv didn't perform
- PCA and SVD perform the best
- DeepNN's >> ShallowNN's
- Dimensionality Reduction improves classification accuracy
- Tuned NN's perform slightly better than XGBoost
- Shift correlates with classification accuracy

Thank you !

FiN

Simulation

- Based on case data
- Normal Distribution $N(\mu, \sigma)$
- S - mean shift
- P_s - columns with shifted mean
- P_0 - columns with mean 0



$\mu = S * 1$

$\mu = S * 2$

$\mu = S * -1$

$\mu = S * -2$

