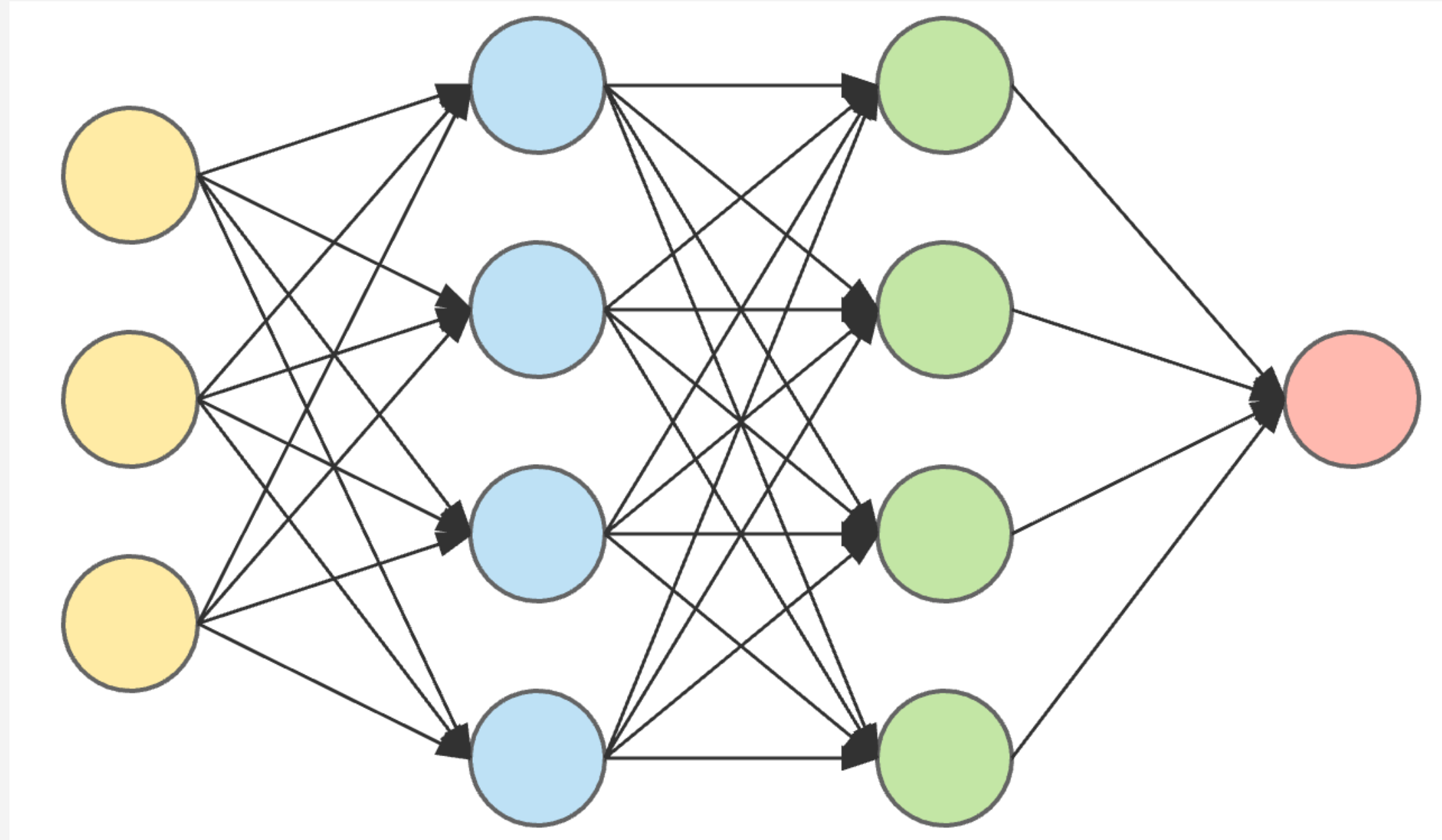


Application of Neural Networks to Common Carp Microbiome Classification

Marek Sztuka



Neuaraal Network



Data

- Sequencing of Common Carp gut microbiome (16s)
- 5 different experimental setups with various probiotic supplementation

Experimental setup	Control	1	2	3	4
Supplementation: Feed	NO	NO	EM	NO	EM
Enviromental	NO	EM farma	EM farma	EM	EM

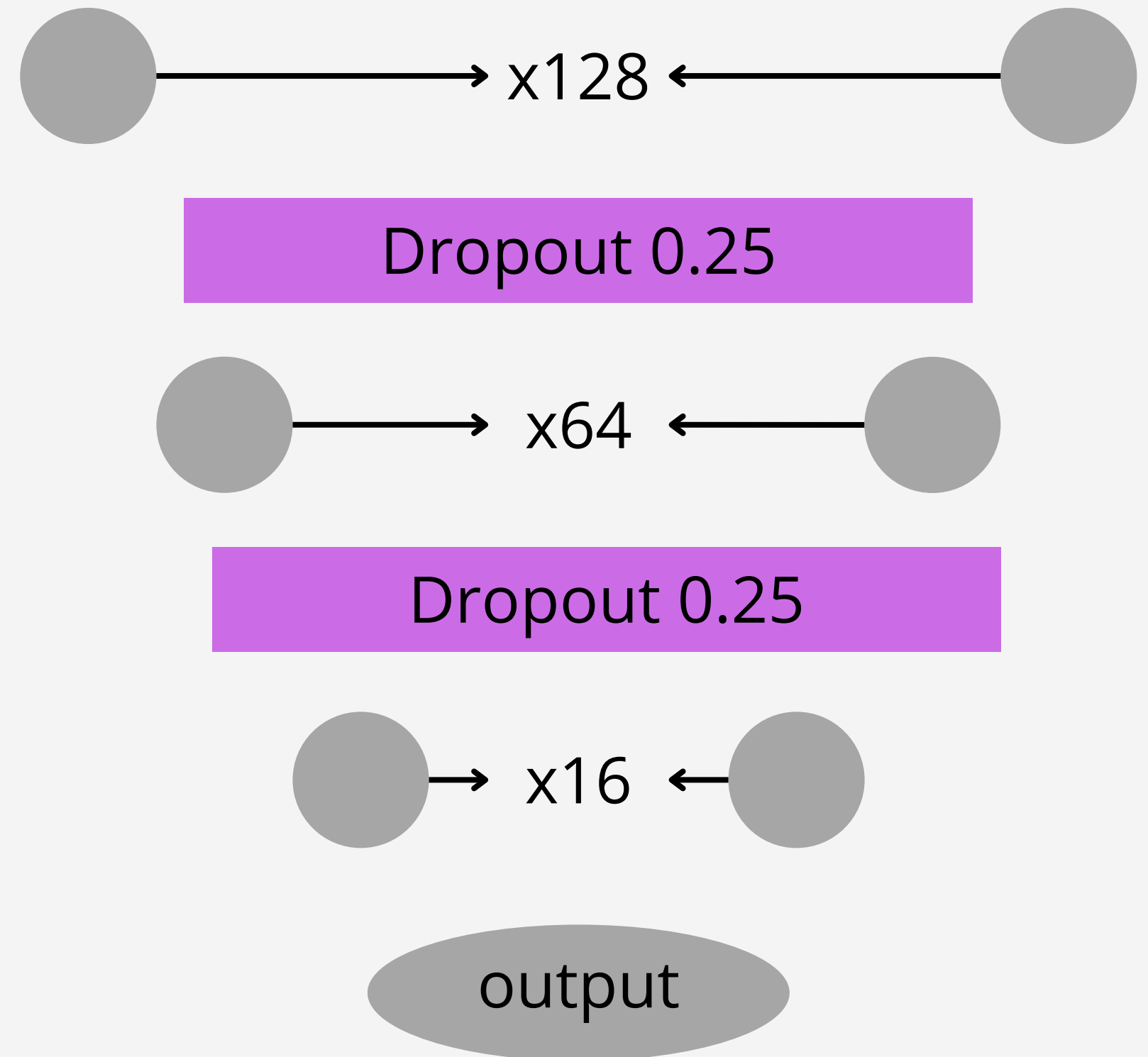
Goal

- Test different deep learning approaches to microbiome classification
- Create classifier differentiating experimental setups
- Search for differences used by classifier to assess importance of each family

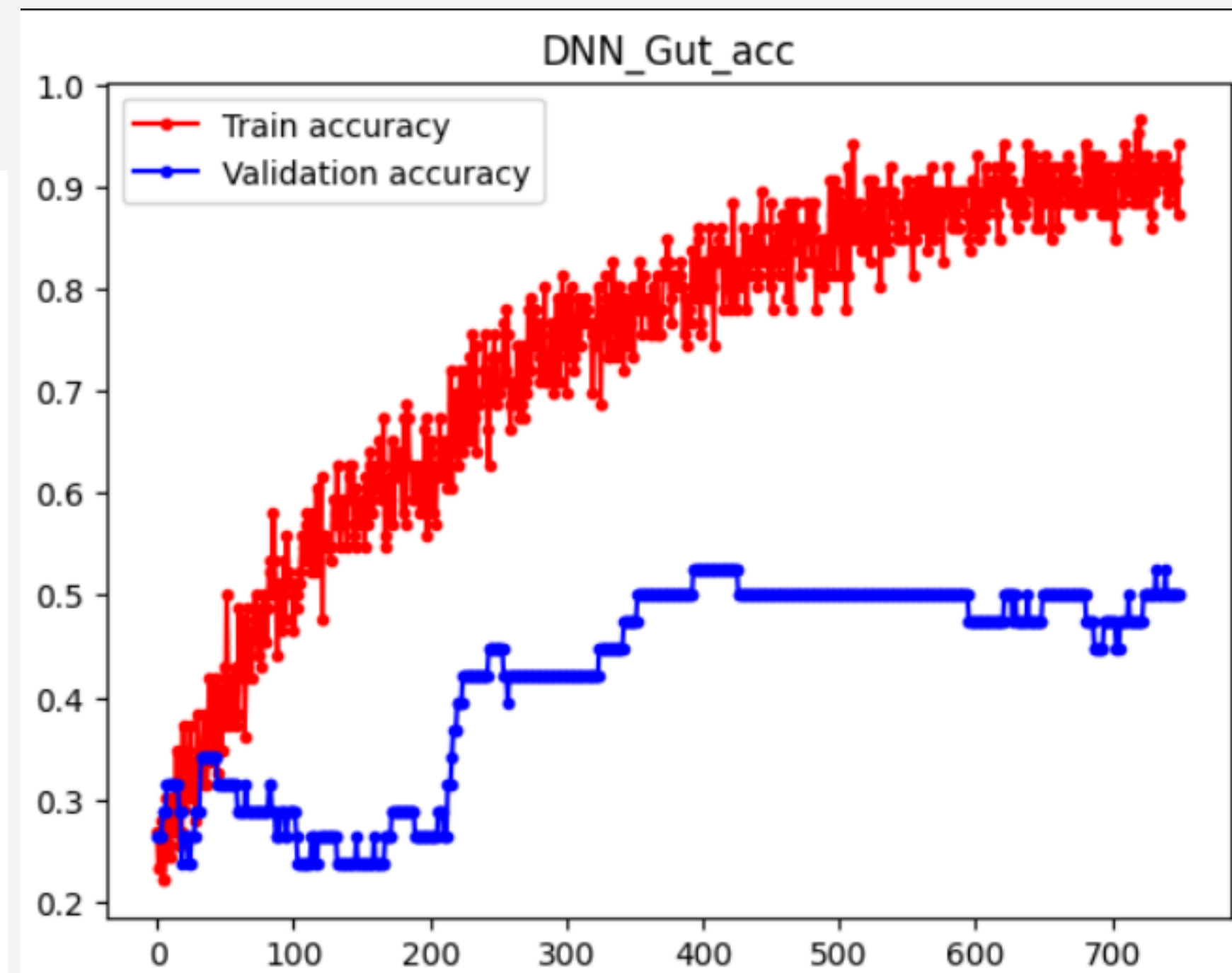
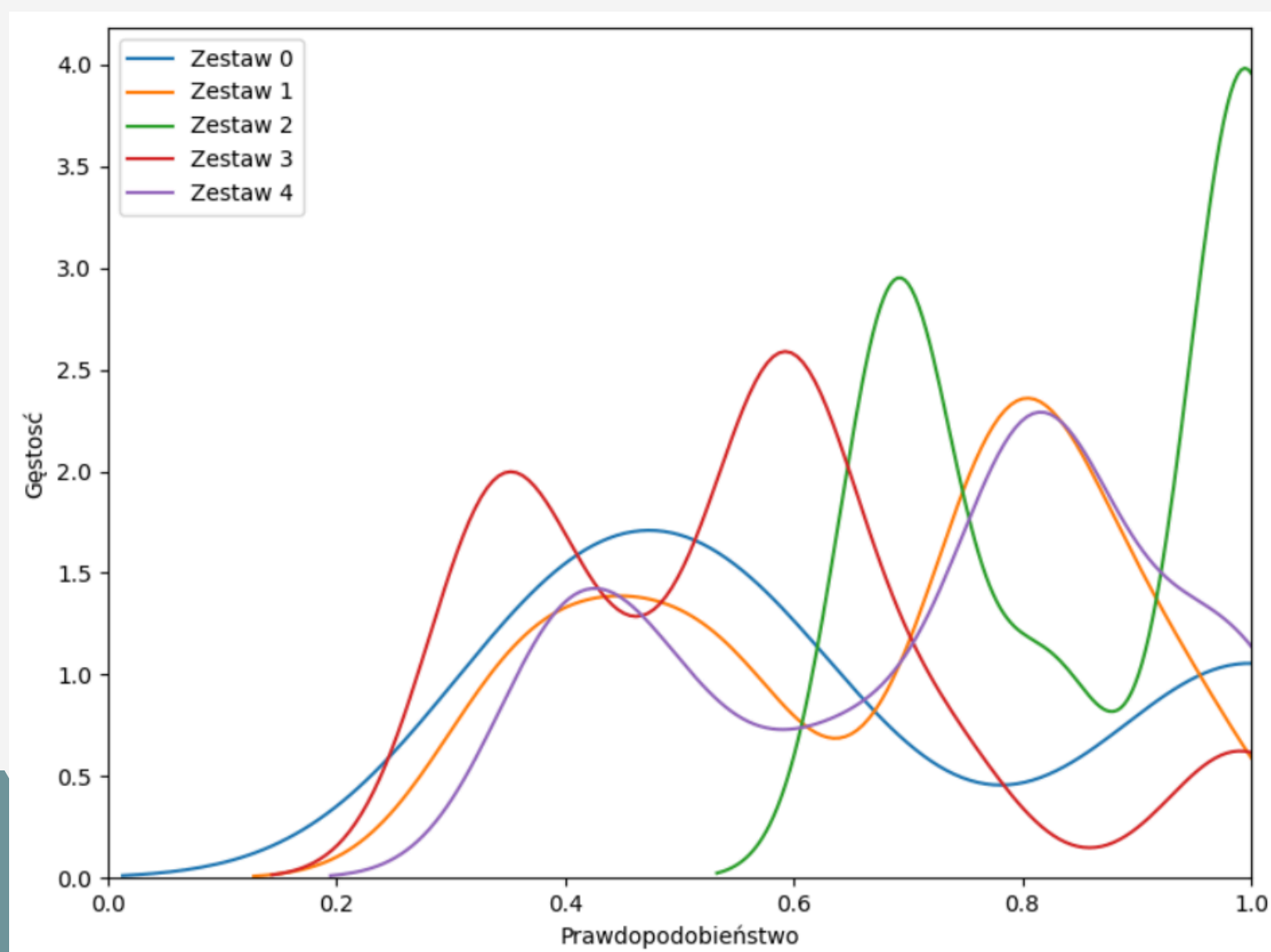


Model architecture

- Optimizer - ADAM
- Metrics - Accuracy
- Loss function - categorical crossentropy
- Activation function - RELU
- Classification function - softmax



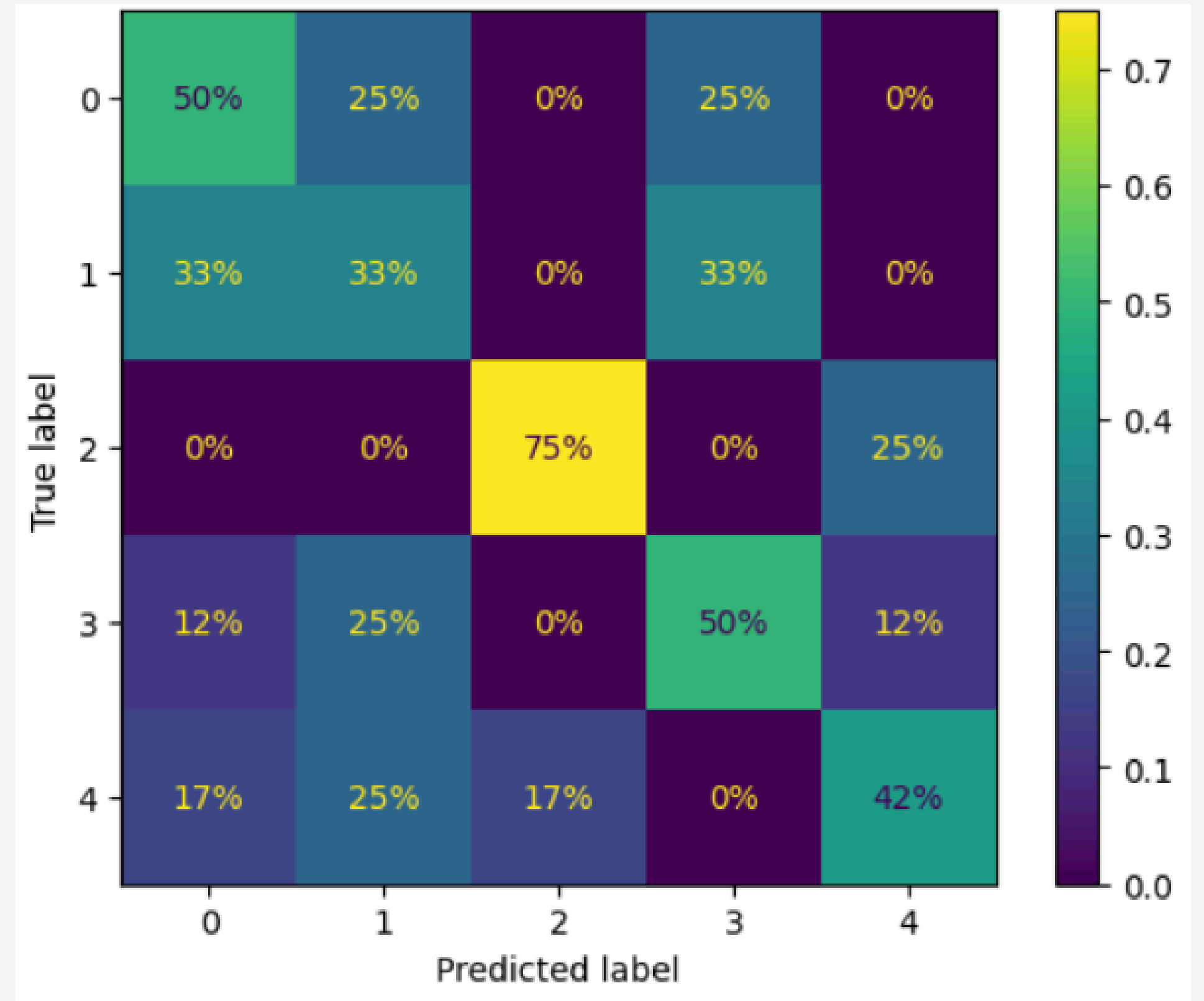
Results



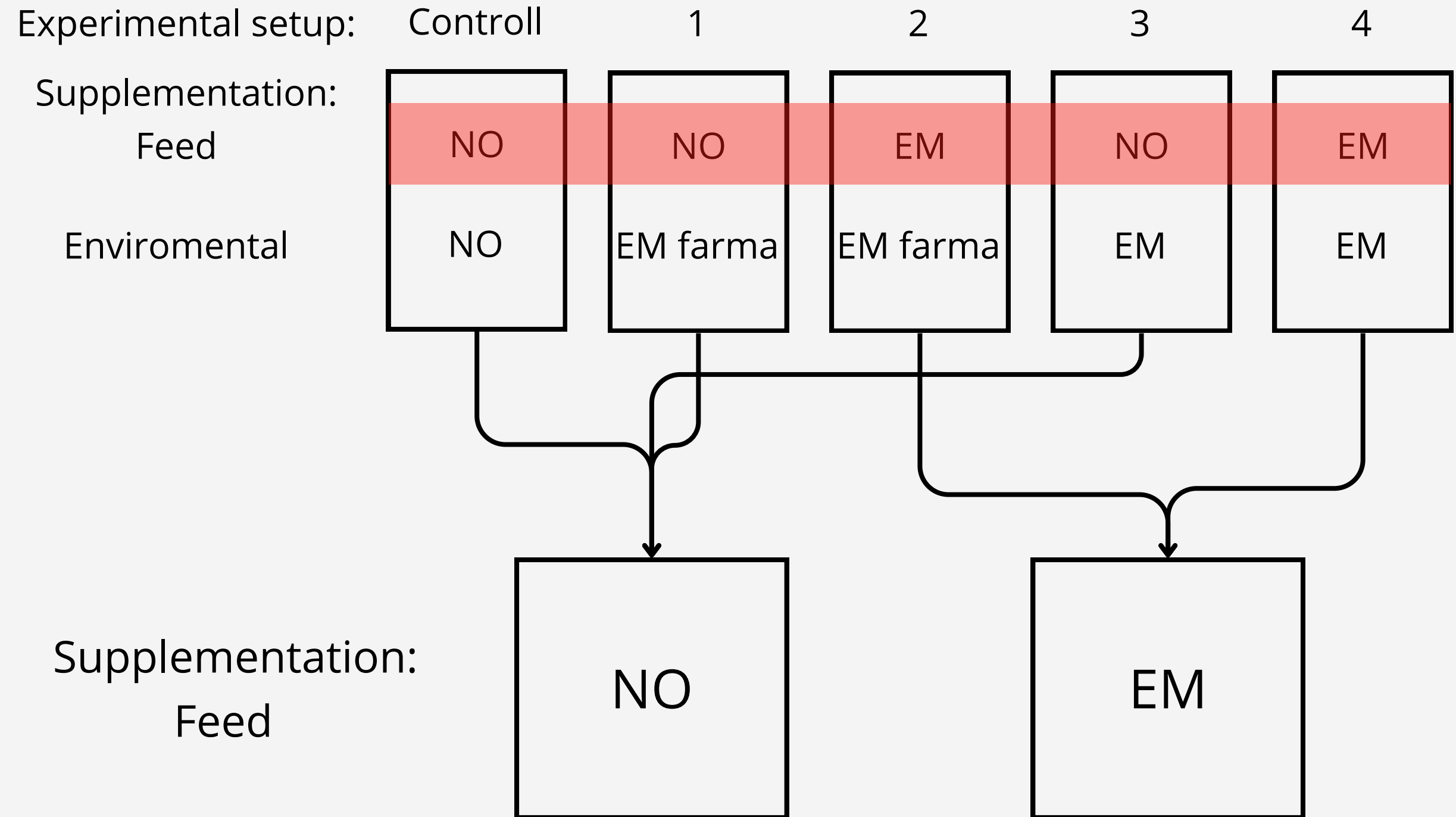
Results

Confusion matrix

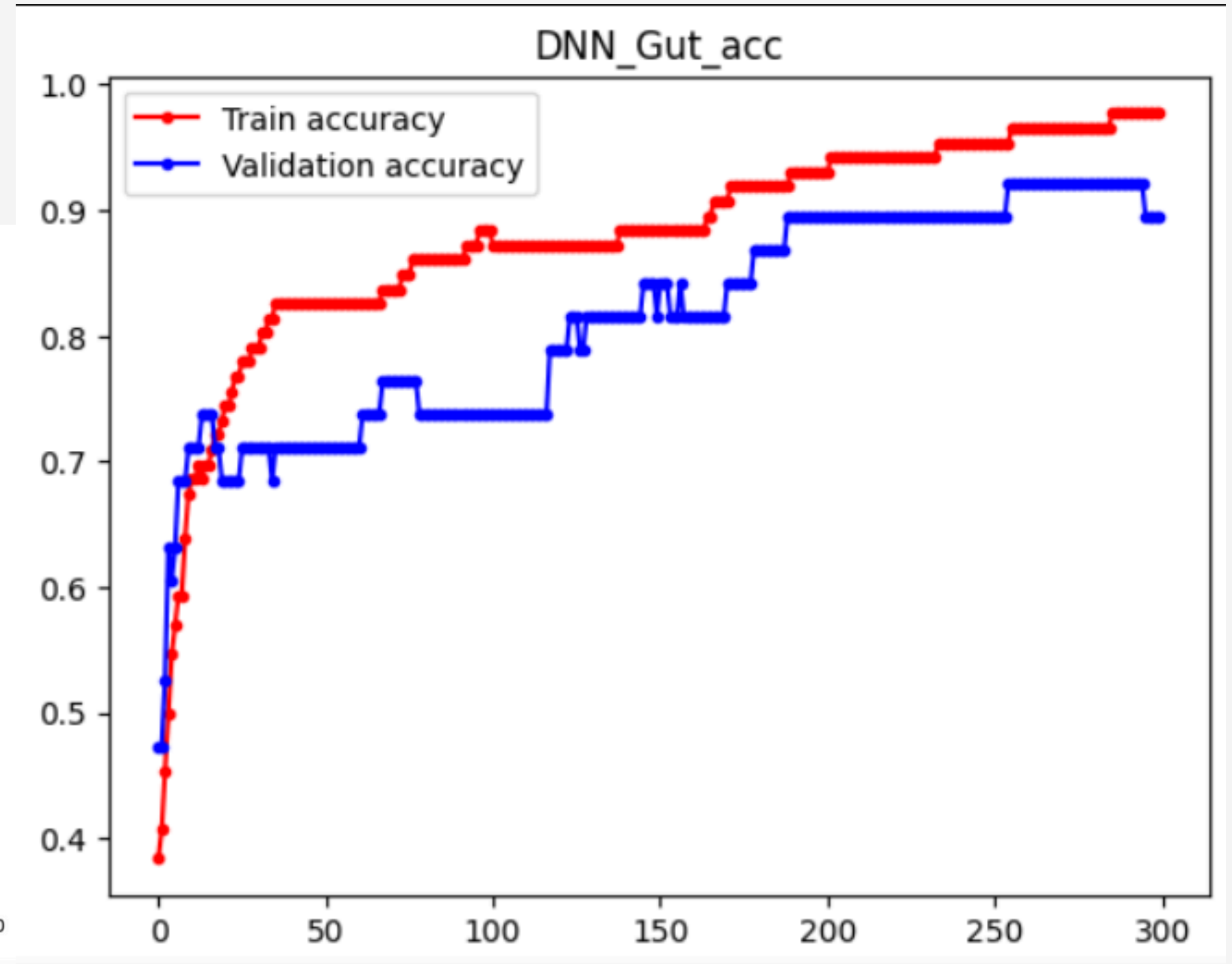
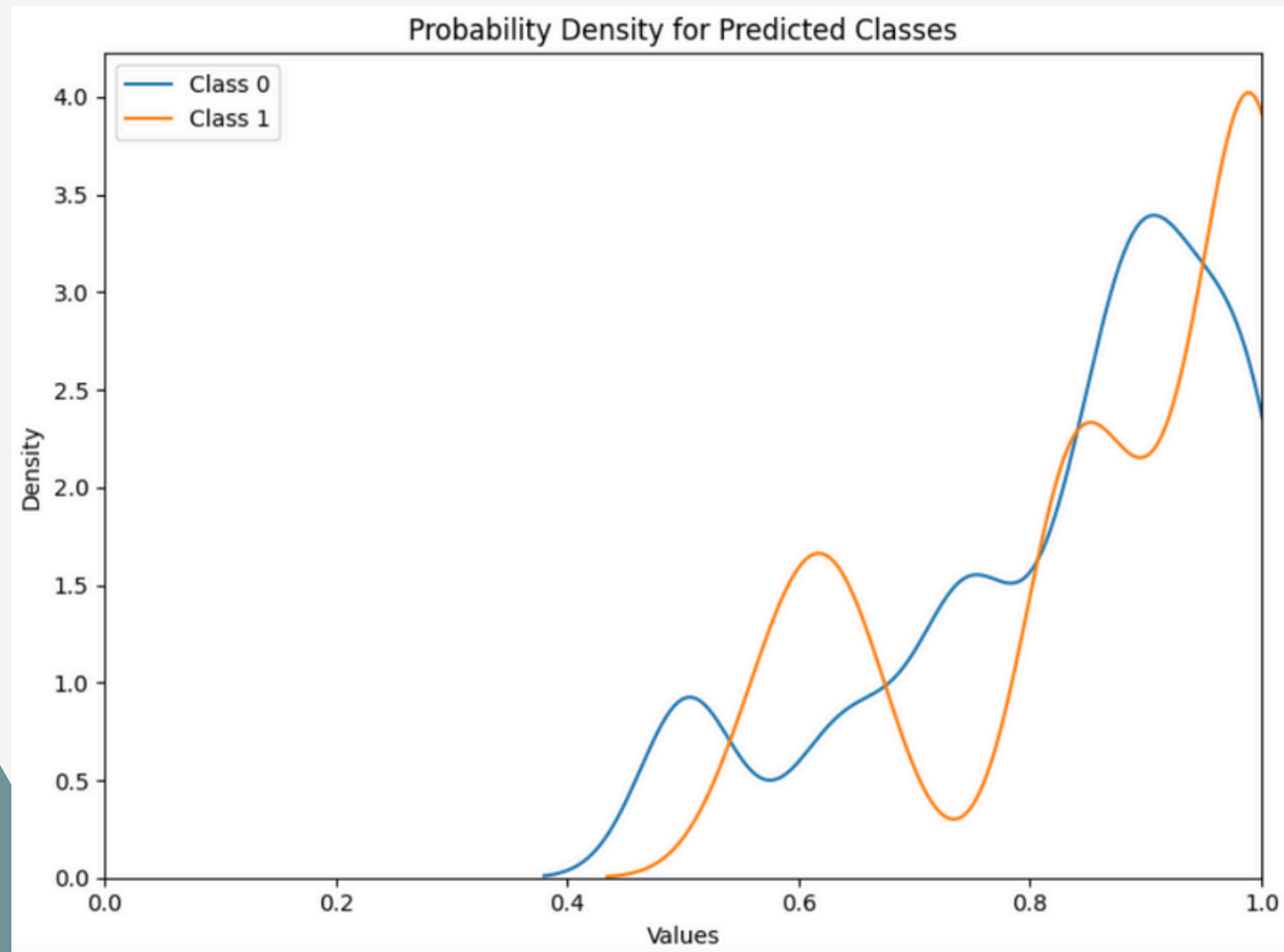
- Model is mismatching class 2 with 4 and 0 with 1, 3



Split into 2 classes



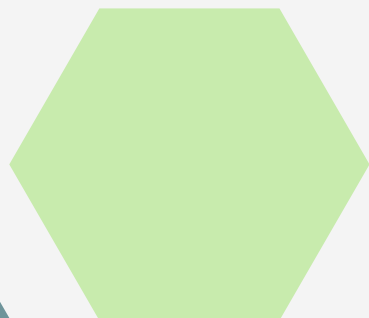
Results - 2 classes



Feature importance

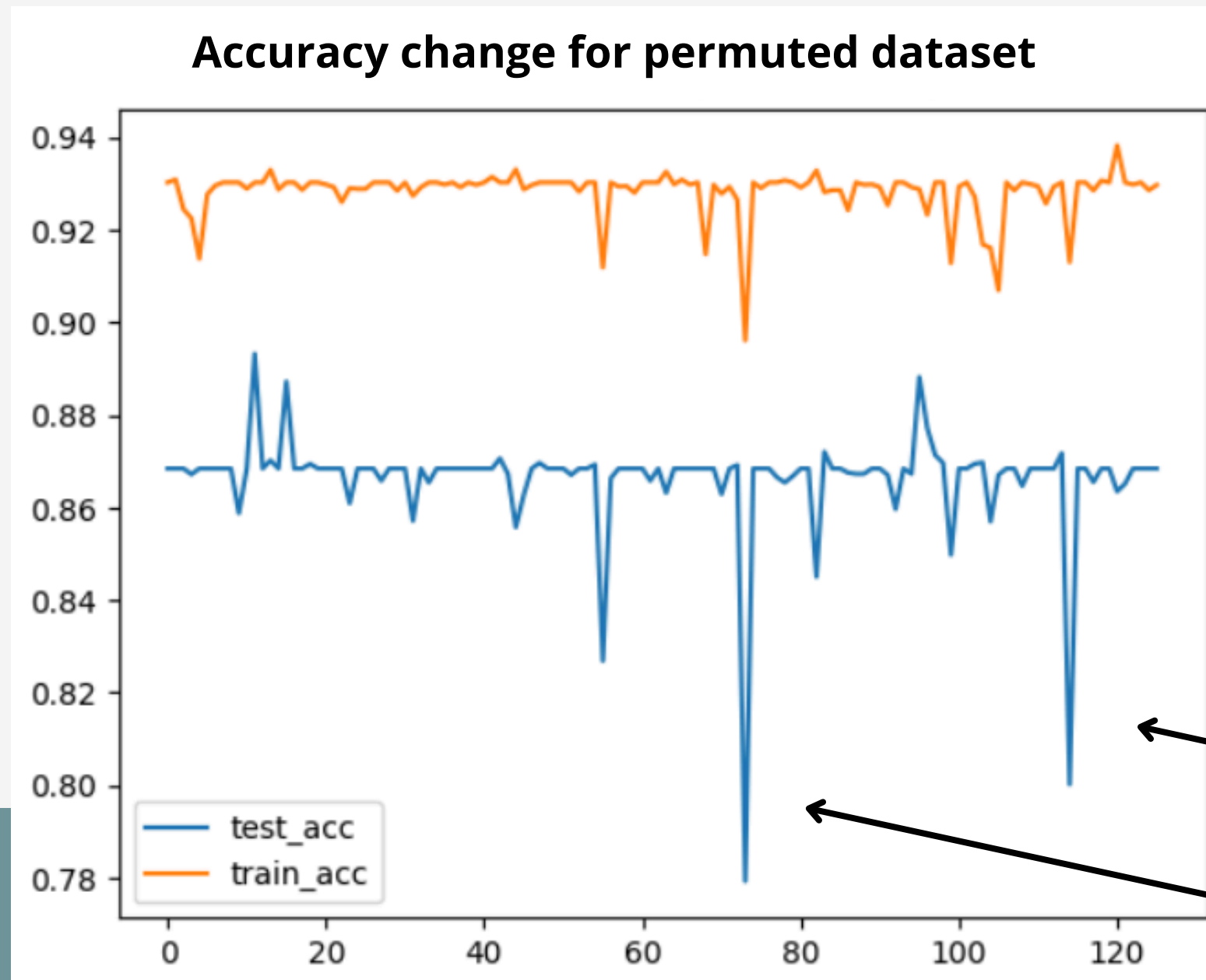
Methods:

- 1- Permute or replace values for random ones in one column
- 2 - Evaluate model on altered dataset
- 3 - Calculate change in metrics and loss function between base and altered dataset
- 4 - Repeat procedure N steps



Feature importance

Results



- Bacteroidota Cyclobacteriaceae
- Proteobacteria Halieaceae

Feature importance

Results

Accuracy change for randomly generated column

