

WROCŁAW UNIVERSITY OF ENVIRONMENTAL AND LIFE SCIENCES

Deep Learning in the bioinformatic modelling of taxonomically annotated microbial communities in aquaculture

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Goals:

DL approaches to classification of microbiome data Architectures (CNN, FNN) Dimensionality reduction

Development of DL model capable of classifing ponds which differed in probiotic supplementation

Materials

- Environmental microbiome of fish intestine
- Sequenced reads of 16S rRNA gene
- 5 experimental setups, with different probiotic supplementation





Materials

- Features Bacteria families
- Samples Individuals
- Cells Bacteria abundance
- Zero inflated data





samples

125





Input transformation

Centered log-ratio transformation





Baseline

Random class assignment
XGBoost

- Depth of the tree: 3
- eta: 0.1





Model Architecture - FNN

- Activation Relu
- Optimizer ADAM
- Loss categorical crossentropy
- Metric accuracy
- Weight regularizer L2 (0.01)



Model Architecture - CNN

- Activation Relu
- Optimizer ADAM
- Loss categorical crossentropy
- Metric accuracy
- Weight regularizer L2 (0.01)





Results 5 class



Results 3 class





Results 2 class



Conclusions Architectures

- Overall increase in accuracy when reducing No. classes
- Worse performance for CNN approaches due to non existent structural patterns
- FNN models proved to be slightly better than baseline xgboost
- Plain Convolution was the worst approach

Conclusions **Dimensionality reduction**

 Out of dimensionality reduction techniques embedding yield most satsfactionary results







THE BIOSTATISTIC GROUP

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Autoencoder Embedding

