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# Protein Superimposition with Machine Learning and Deep Learning

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An abstract graphic on the left side of the slide, featuring a network of glowing blue nodes connected by thin lines, set against a dark teal background.

# INTRODUCTION

# Why this project?

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- The shape of a protein - an essential role in drug discovery
- Aligning proteins - function & relationships between proteins
- Increasing dataset - ANN model

- Use DL and ML to align 2 proteins
- Input: original protein + rotated one
- Output:
  - Rotation values or,
  - Zeal score

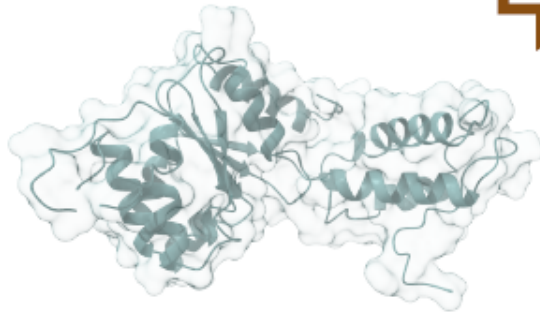
## Goal of the project

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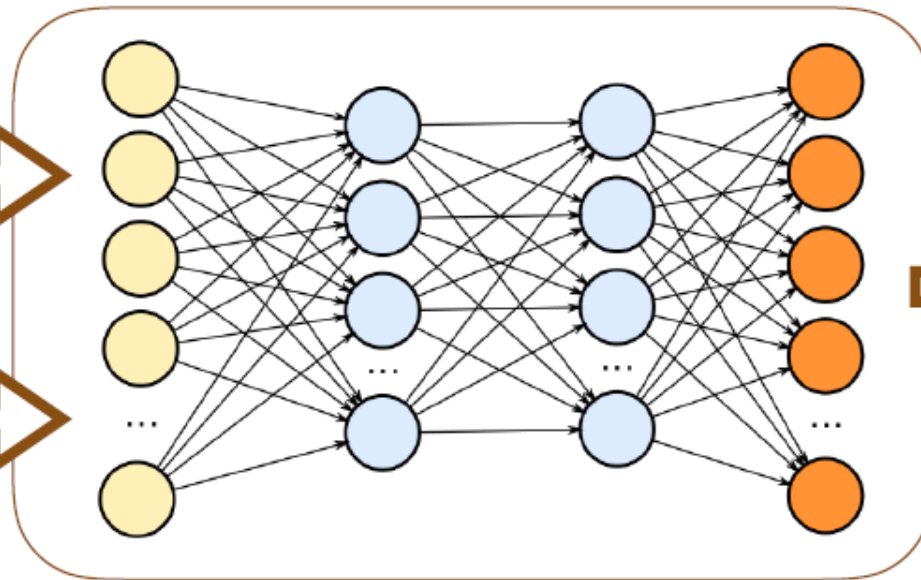
Input 1



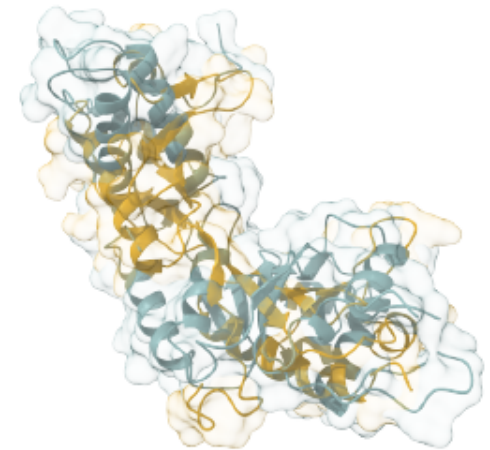
Input 2



**Deep Learning method**



Aligned  
Proteins

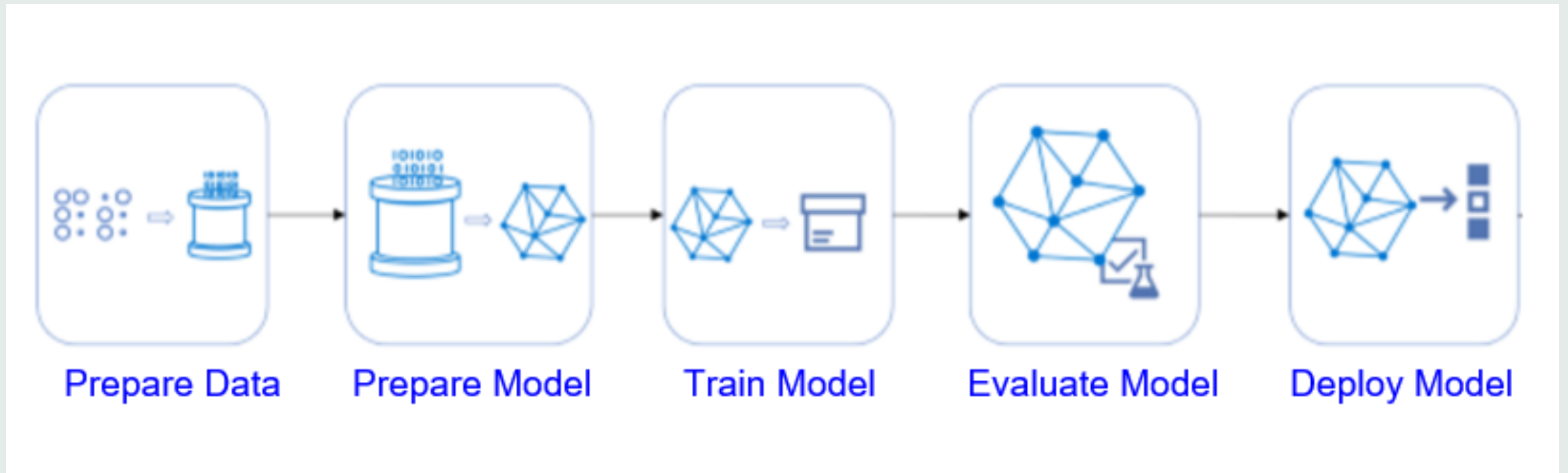


An abstract graphic on the left side of the slide, featuring a network of glowing blue nodes connected by thin lines, set against a dark teal background.

# WORKFLOW

# Workflow of the project

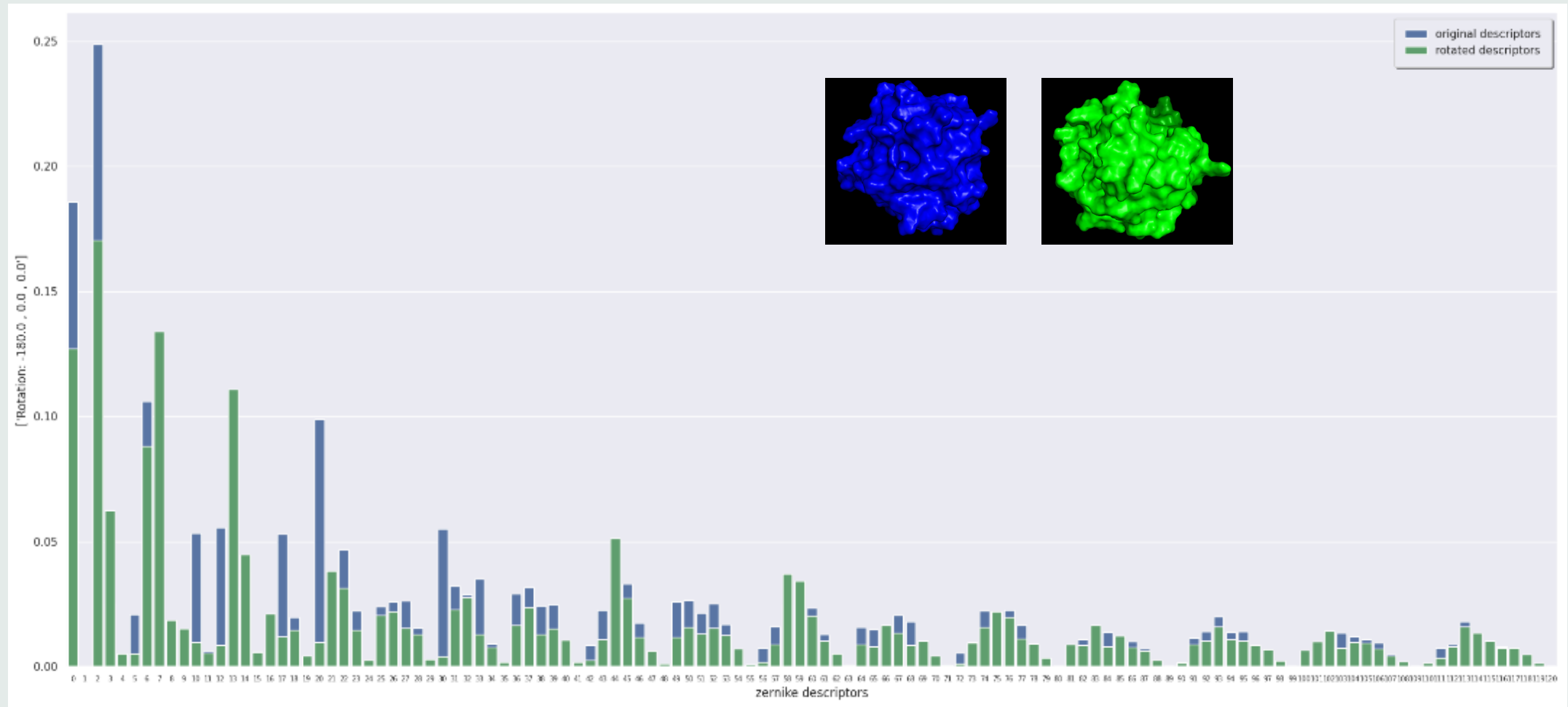
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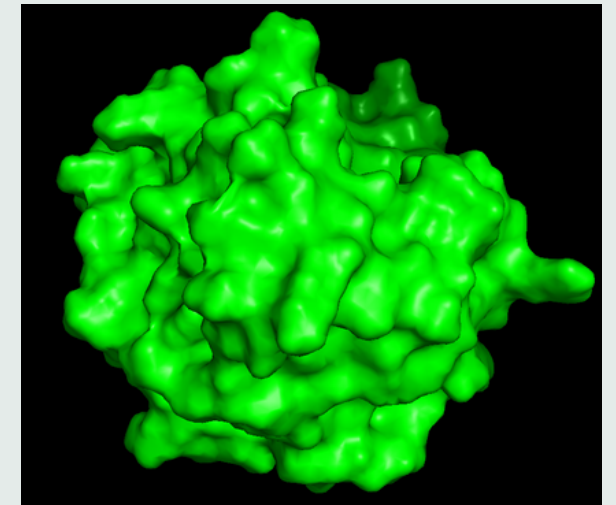
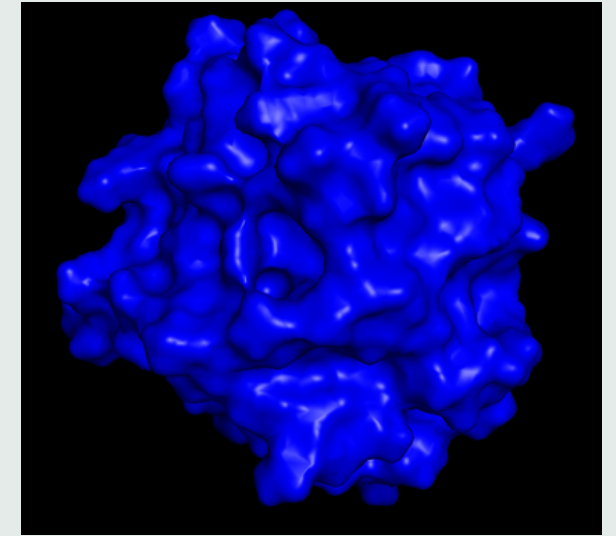
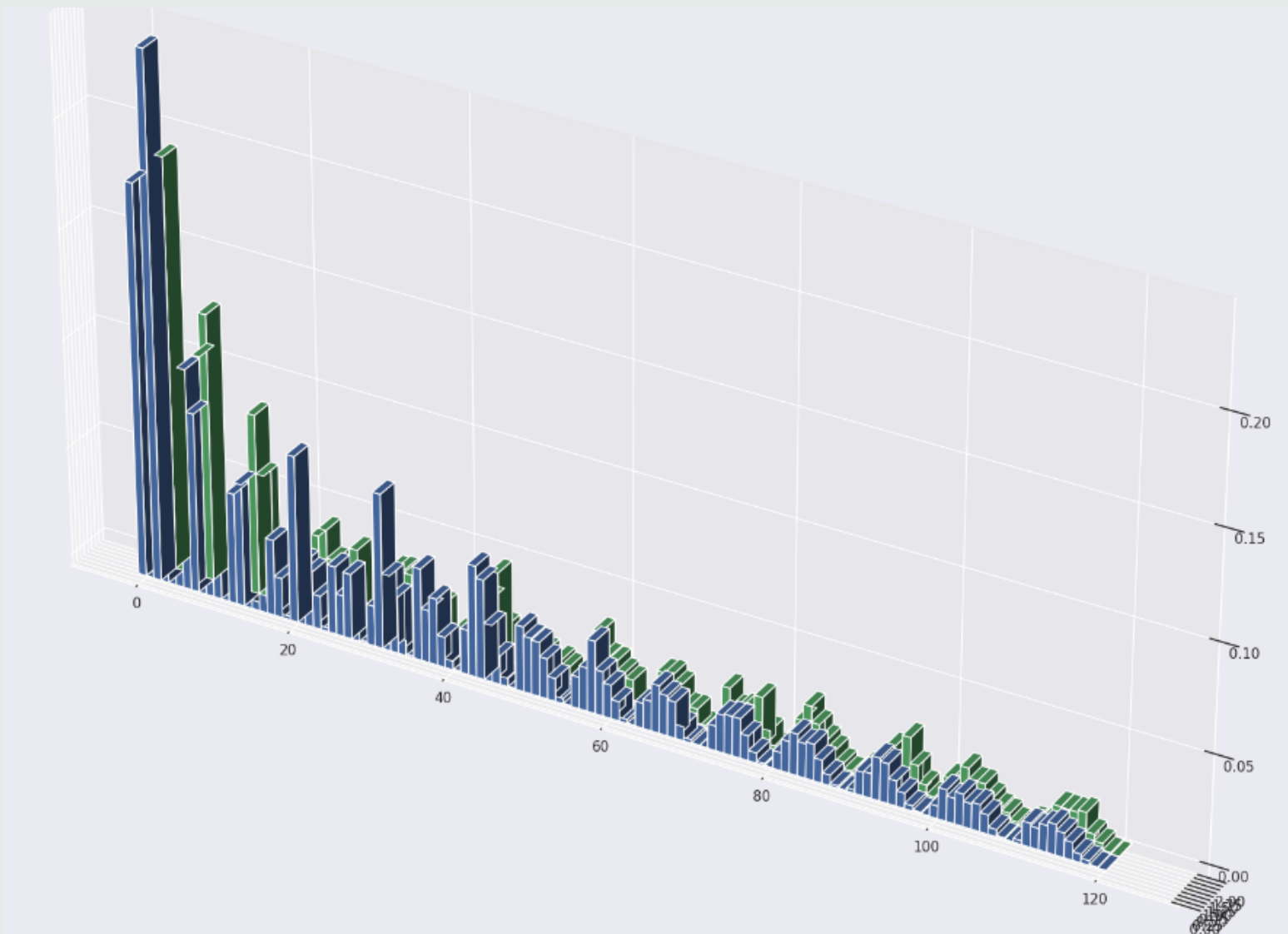
An abstract graphic on the left side of the slide, featuring a network of blue dots connected by thin lines, resembling a molecular structure or a data network, set against a dark teal background.

# DATA PREPARATION & PREPROCESSING

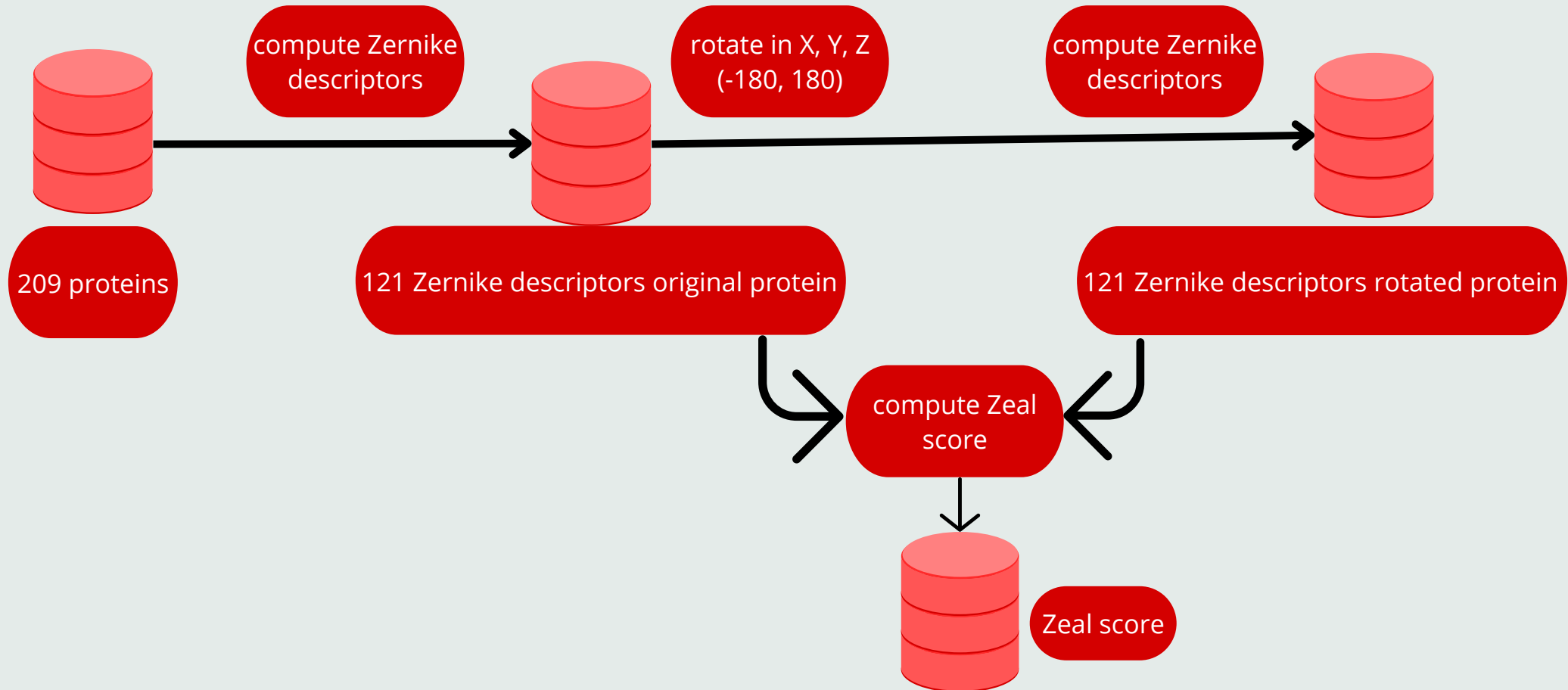
# Zernike descriptors



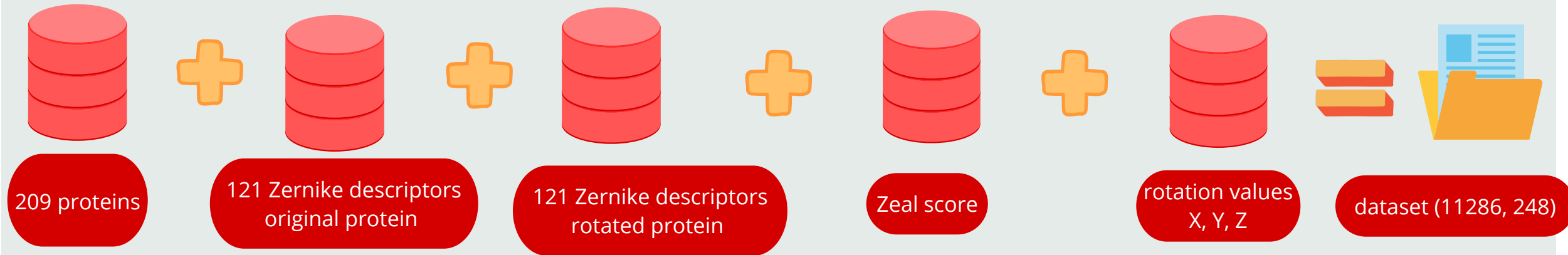




# Data preparation



# Data preparation



## Preprocessing:

- scale Zernike descriptors - MinMax scaler
- check null values

# Dataset

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| 0 | pdb_ID      | zd_I_0   | zd_I_1       | zd_I_2   | ... | zd_R_120 | r_0    | r_1    | r_2    | zeal     |
|---|-------------|----------|--------------|----------|-----|----------|--------|--------|--------|----------|
| 0 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000088 | -180.0 | 0.0    | 0.0    | 0.603379 |
| 1 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000042 | 0.0    | -180.0 | 0.0    | 0.719376 |
| 2 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000176 | 0.0    | 0.0    | -180.0 | 0.570384 |
| 3 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000083 | -160.0 | 0.0    | 0.0    | 0.643067 |
| 4 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000039 | 0.0    | -160.0 | 0.0    | 0.702196 |
| 5 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000157 | 0.0    | 0.0    | -160.0 | 0.583470 |
| 6 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000173 | -140.0 | 0.0    | 0.0    | 0.672413 |
| 7 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000034 | 0.0    | -140.0 | 0.0    | 0.691126 |
| 8 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000158 | 0.0    | 0.0    | -140.0 | 0.590590 |
| 9 | d3fv3g_.ent | 0.180773 | 3.328894e-17 | 0.242312 | ... | 0.000226 | -120.0 | 0.0    | 0.0    | 0.707422 |

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# MODELS

# Models

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- 80% training + 20% testing
- First approach
  - Input: zernike descriptors original protein + zernike descriptors rotated protein
  - Output: rotation values
- Second approach
  - Input: zernike descriptors original protein + zernike descriptors rotated protein + rotation values
  - Output: zeal score

# Models

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- Considered models:
  - Multioutput Random Forest Regressor
  - Multioutput MLP Regressor
  - CNN Regressor (three outputs)

# Multiooutput Random Forest

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Multiooutput Random Forest Regressor - output - rotation values:

- 100 trees
- MSE: 0.0426



# Models - Multioutput MLP Regressor

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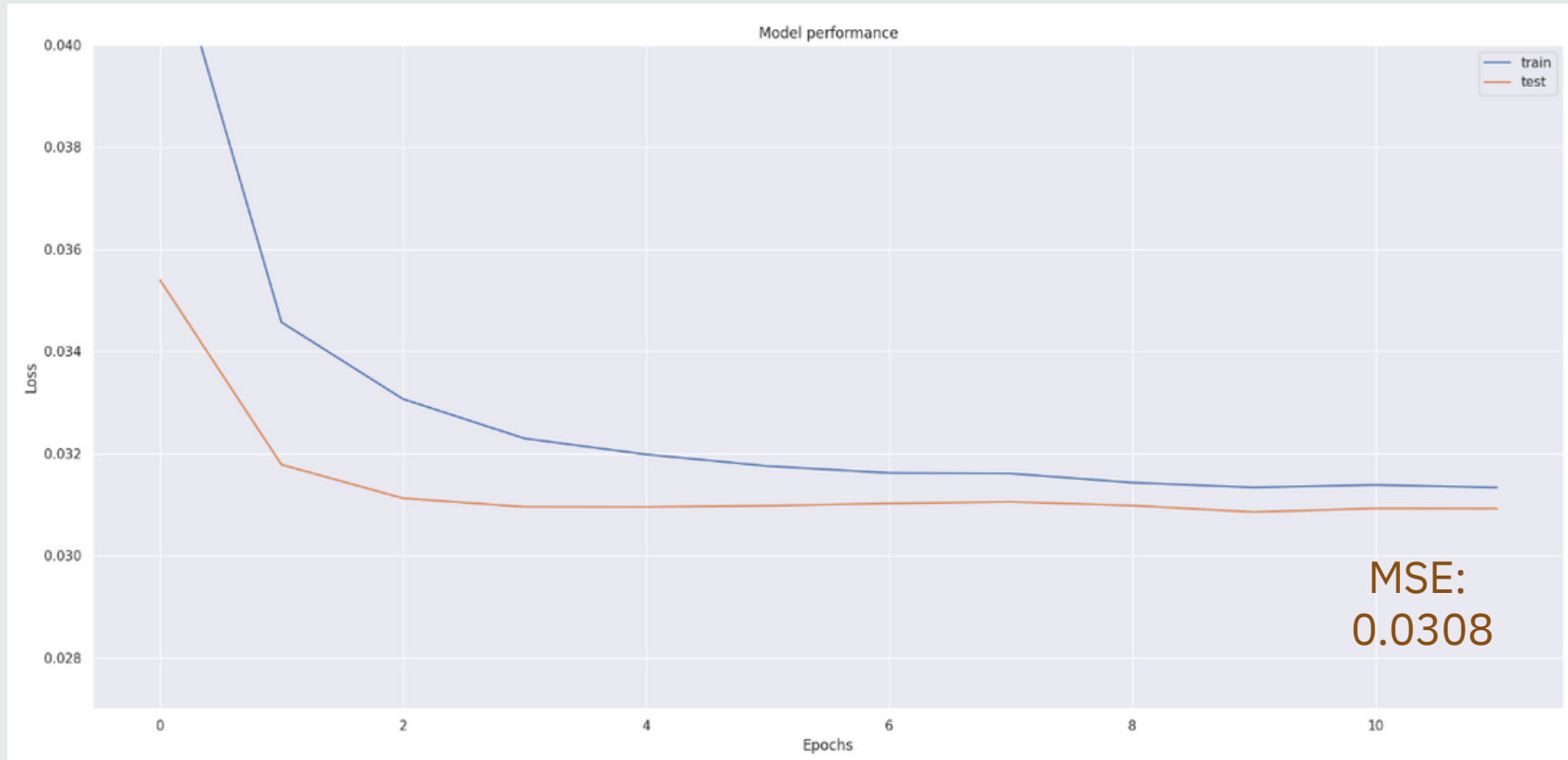
- Multioutput MLP Regressor - output - rotation values
  - 43 hidden layers
  - 200 max iterations
  - Early stopping
- MSE: 0.0325

# Models - CNN Regressor

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- CNN Regressor - output - rotation values
  - 2 1D convolutional layers
  - Flatten layer
  - Dense layer
  - Output layer
  - 200 max epochs
  - Early stopping

# CNN Regressor



Loss function (MSE) for the CNN Regressor (output rotation values)

Model: "sequential"

| Layer (type)                   | Output Shape    | Param # |
|--------------------------------|-----------------|---------|
| reshape (Reshape)              | (None, 242, 1)  | 0       |
| conv1d (Conv1D)                | (None, 238, 64) | 384     |
| max_pooling1d (MaxPooling1D)   | (None, 79, 64)  | 0       |
| dropout (Dropout)              | (None, 79, 64)  | 0       |
| conv1d_1 (Conv1D)              | (None, 77, 32)  | 6176    |
| max_pooling1d_1 (MaxPooling1D) | (None, 25, 32)  | 0       |
| dropout_1 (Dropout)            | (None, 25, 32)  | 0       |
| flatten (Flatten)              | (None, 800)     | 0       |
| dense (Dense)                  | (None, 64)      | 51264   |
| dropout_2 (Dropout)            | (None, 64)      | 0       |
| dense_1 (Dense)                | (None, 3)       | 195     |
| Total params: 58,019           |                 |         |
| Trainable params: 58,019       |                 |         |
| Non-trainable params: 0        |                 |         |

## Models - CNN Regressor

CNN Regressor (output: rotation values) model  
configuration

# Models

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- Considered models:
  - Random Forest Regressor
  - MLP Regressor
  - CNN Regressor (one output)

# Random Forest

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Random Forest Regressor - output - Zeal score:

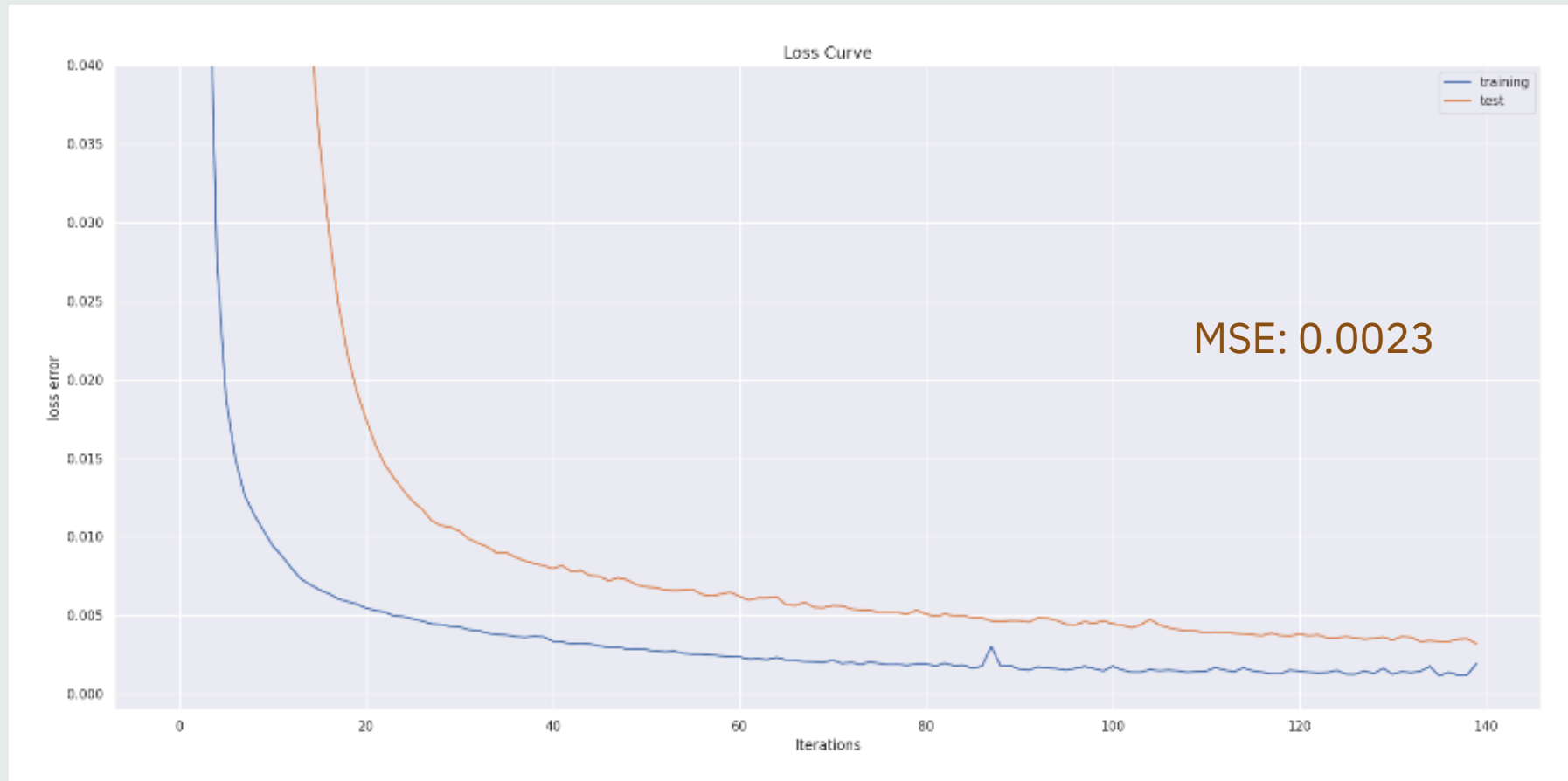
- 100 trees
- MSE: 0.0016

# Models - MLP Regressor

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- MLP Regressor - output -Zeal score
  - 43 hidden layers
  - 200 max iterations
  - Early stopping

# MLP Regressor



Loss function (MSE) for the MLP Regressor (output Zeal score)



# Models - CNN Regressor

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- CNN Regressor - output - Zeal score
  - 3 1D convolutional layers
  - Flatten layer
  - Dense layer
  - Output layer
  - 100 max epochs
  - Early stopping

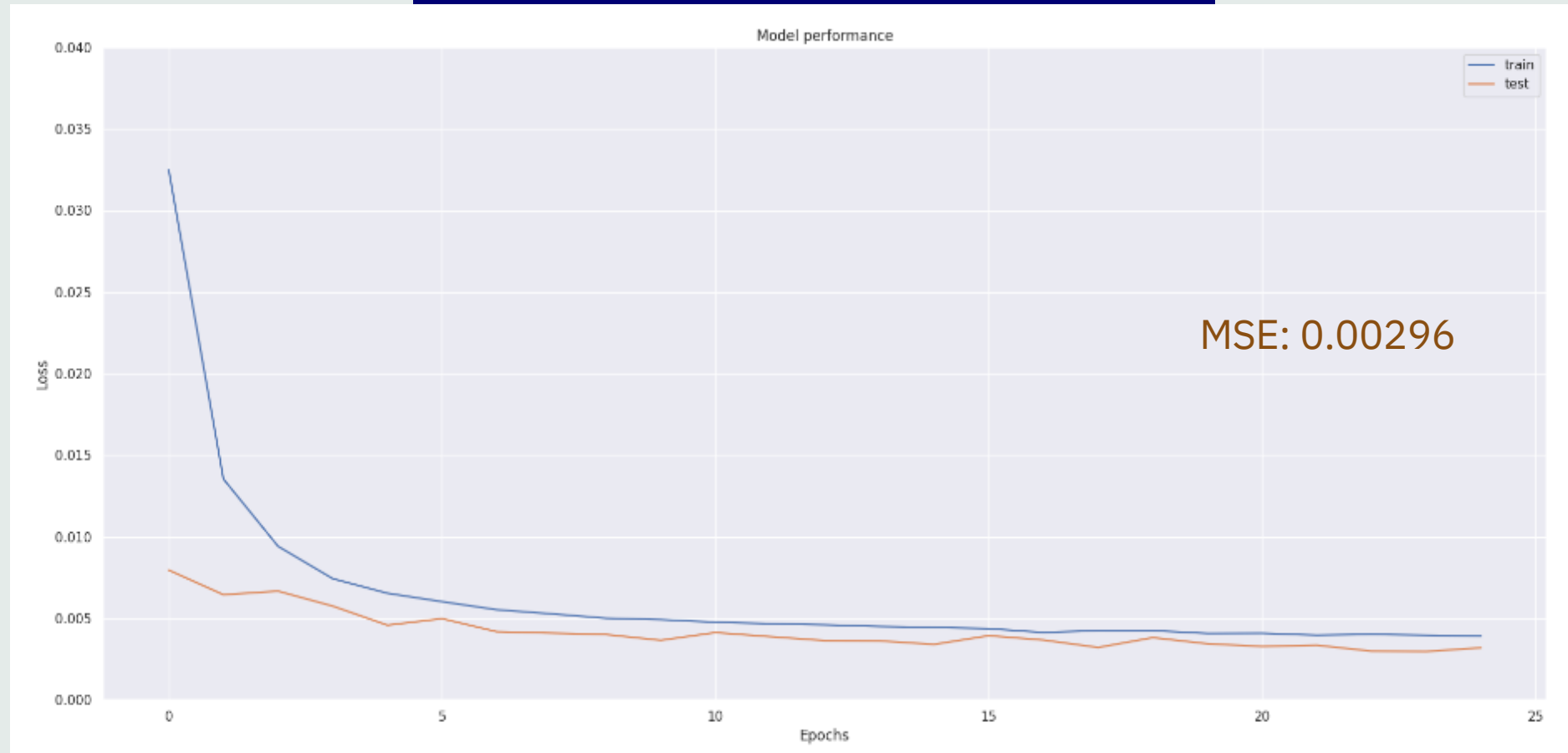
Model: "sequential"

| Layer (type)                   | Output Shape    | Param # |
|--------------------------------|-----------------|---------|
| reshape (Reshape)              | (None, 245, 1)  | 0       |
| conv1d (Conv1D)                | (None, 241, 64) | 384     |
| max_pooling1d (MaxPooling1D)   | (None, 80, 64)  | 0       |
| dropout (Dropout)              | (None, 80, 64)  | 0       |
| conv1d_1 (Conv1D)              | (None, 78, 32)  | 6176    |
| max_pooling1d_1 (MaxPooling1D) | (None, 26, 32)  | 0       |
| dropout_1 (Dropout)            | (None, 26, 32)  | 0       |
| conv1d_2 (Conv1D)              | (None, 24, 16)  | 1552    |
| flatten (Flatten)              | (None, 384)     | 0       |
| dense (Dense)                  | (None, 64)      | 24640   |
| dropout_2 (Dropout)            | (None, 64)      | 0       |
| dense_1 (Dense)                | (None, 1)       | 65      |
| Total params: 32,817           |                 |         |
| Trainable params: 32,817       |                 |         |
| Non-trainable params: 0        |                 |         |

## Models - CNN Regressor

CNN Regressor (output: Zeal score) model configuration

# CNN Regressor

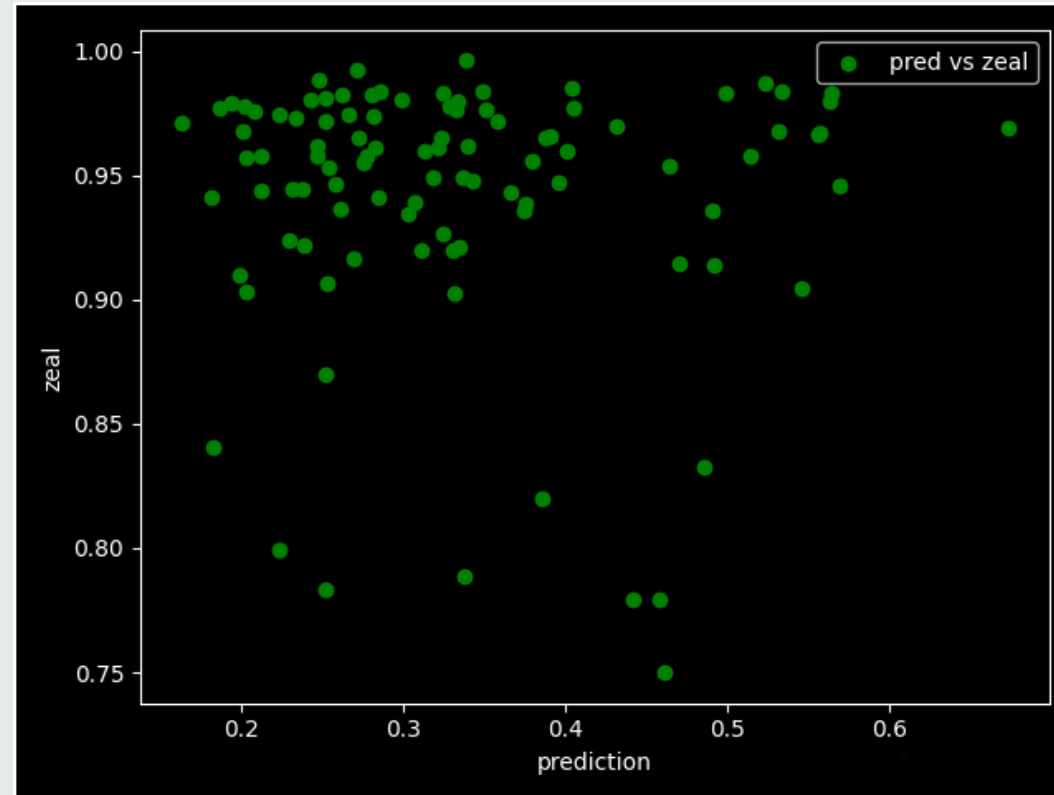


Loss function (MSE) for the CNN Regressor (output Zeal score)

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# DEPLOYMENT

# Validating in real case



Performance of the models with real data

An abstract graphic on the left side of the slide, featuring a network of glowing blue nodes connected by thin lines, resembling a molecular structure or a digital network. The background of the slide is a solid dark teal color.

# CONCLUSIONS

# Conclusions

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- data generation - computational expensive, tedious process
- more data is needed
- the models outputting the Zeal score work better
- 2D convolutional layers - possible improvement

THANK  
you





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