

HViface tutorial

- 1- Compile 18 features for any two protein sequences (follow the “CoRNeA_tutorial.pdf”).
- 2- Load the trained model “._ANN_model_oversampling_15_04_2024_testing.keras” using “ANN_Oversampling_under_testing_final_18_06_2024-Copy1.ipynb”.
- 3- Predict the pairwise interactions using “ANN_Oversampling_under_testing_final_18_06_2024-Copy1.ipynb”.
- 4- Follow the CoRNeA tutorial for the “**Post processing for prediction results obtained from ANN prediction**”.
- 5- **Get the pairwise interaction in CSV format. You can sort the pairwise interactions with the convolution scores.**