

retrain procedure:

- ① write_csv_train_new.sh → generate training and test CSVs (11 paths for all proteins dataset, no prediction)
model a:
- ② bash_training_greedy.sh
- ③ bash_predict_eval_greedy.sh → save protein a w/ params in results-greedy for all protein dataset
- ④ write_csv_evaluation_greedy.sh → generate evaluation CSVs (12 paths, no signal) for different params
- ⑤ bash_evaluate_greedy.sh → evaluate training set for all protein dataset for all p
- ⑥ bash_predict_optimal.sh → find the optimal p with best Exc/MSE and update the predictions of model a with best p model in results/3d directory for both train and test
- ⑦ bash_evaluate_greedy.sh → evaluate test set for all proteins dataset with optimal p

In the greedy training loop for each organelle:

- ① bash_training_greedy
- ② bash_predict_eval_greedy.
- ④ write_csv_evaluation_greedy.
- ⑤ bash_evaluate_greedy (for all p for training sets)
- ⑥ bash_predict_optimal. replace all the layer of model a in all datasets for all t
- ⑦ bash_evaluate_greedy. (for best p for test set)