Artificial Intelligence in Life Sciences - Challenge 1: QSAR

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Description

The aim is to predict a molecule's biological activity or toxicity based on its chemical structure. You are given a dataset of molecules together with activities, and you should train a machine-learning model to predict the activities of new molecules based on the selected model.

Notes:

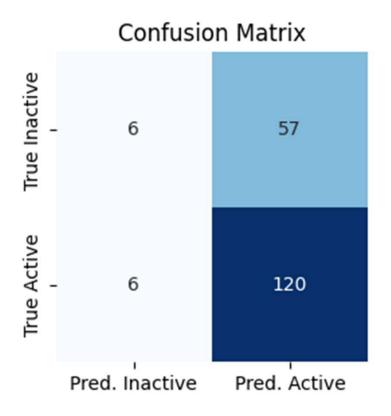
- In the training data: +1=active, 0=unknown, -1=inactive
- If you do any molecule standardization, make sure not to delete any test set molecules.

Workflow

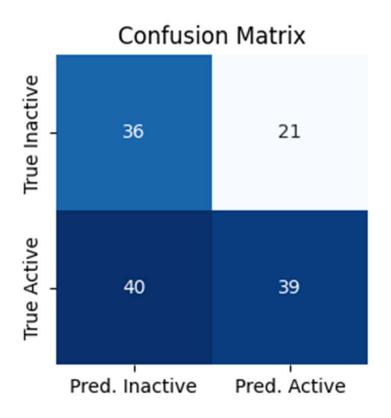
- Load dataset with SMILES representation of the biomolecules
- Determine their fingerprints
- Replace 0 with NaN values for unknown values
- Train test split
- Create prediction with Random Forest for every task
- Evaluate the results
 - Confusion matrix for each task
 - Classification metrics for each task
 - ROC Curve / AUC value
- Readjust the hyperparameters for the Random Forest

Final Hyperparameter setting for Random Forest

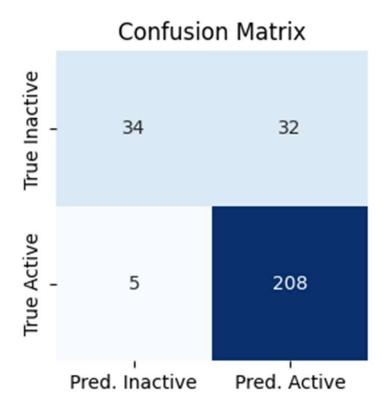
- n_estimators=500
- max_depth = 30
- min_samples_split=2
- min_samples_leaf=1
- max_features='log2'

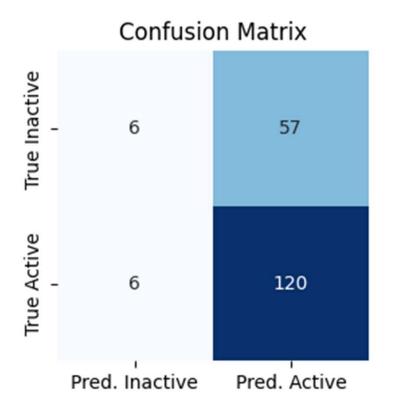


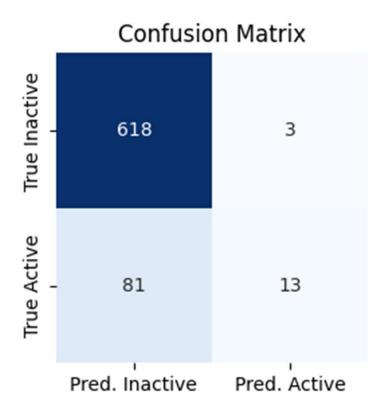
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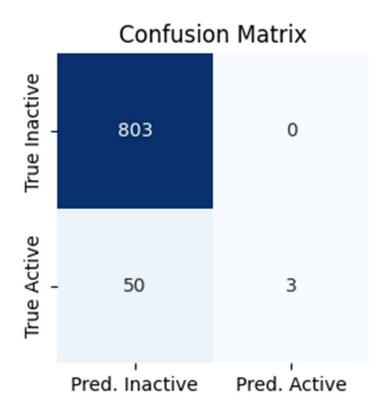


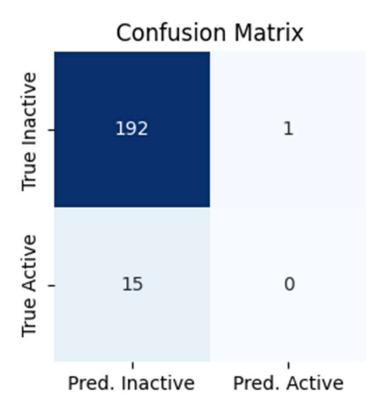
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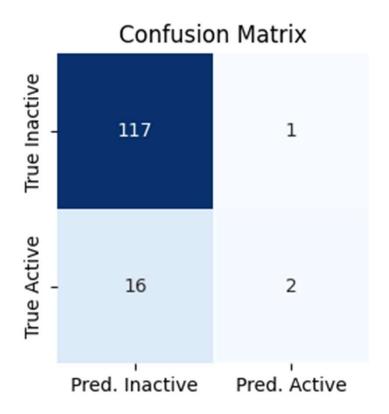


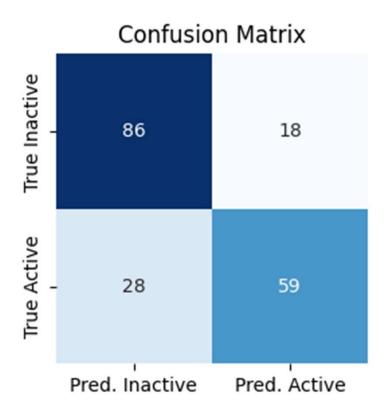


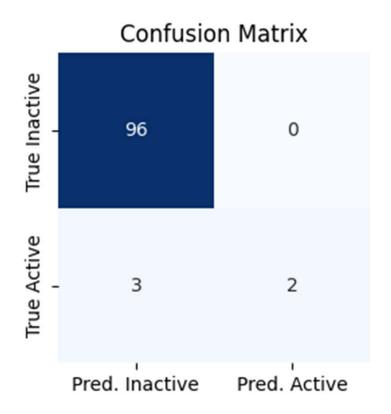


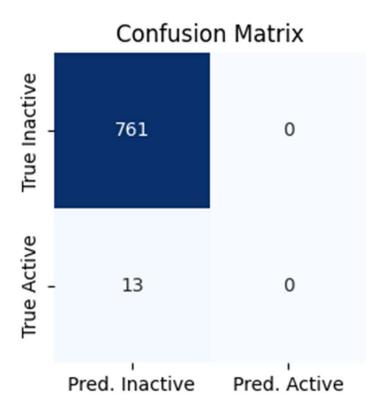












Classification Metrics for each task

	Accuracy	Precision	Recall	F1-Score	Balanced Accuracy	MCC
0	0.902913	0.5	0.05	0.090909	0.522312	0.134743
1	0.551471	0.65	0.493671	0.561151	0.562625	0.124465
2	0.867384	0.866667	0.976526	0.918322	0.745839	0.602565
3	0.666667	0.677966	0.952381	0.792079	0.52381	0.092057
4	0.882517	0.8125	0.138298	0.236364	0.566733	0.304919
5	0.941589	1.0	0.056604	0.107143	0.528302	0.230837
6	0.923077	0.0	0.0	0.0	0.497409	-0.019377
7	0.875	0.666667	0.111111	0.190476	0.551318	0.236806
8	0.759162	0.766234	0.678161	0.719512	0.752542	0.512793
9	0.970297	1.0	0.4	0.571429	0.7	0.622799
10	0.983204	0.0	0.0	0.0	0.5	0.0

ROC Curve/AUC

