

Random Forest Result #151 — Analysis Report

Generated 2026-09-21 02:38:55 · 1 run(s) · CAT-G Data Analyzer

1. random forest (#151)

2026-09-21 02:17:48 · random_forest · status: completed

The model explains 0.0% of the variance in the target — worse than simply predicting the mean; treat predictions as unreliable.

task_type	regression
r2_mean	-0.5783
r2_std	0.617272
mse_mean	3.519505
mse_std	1.086945

permutation importance

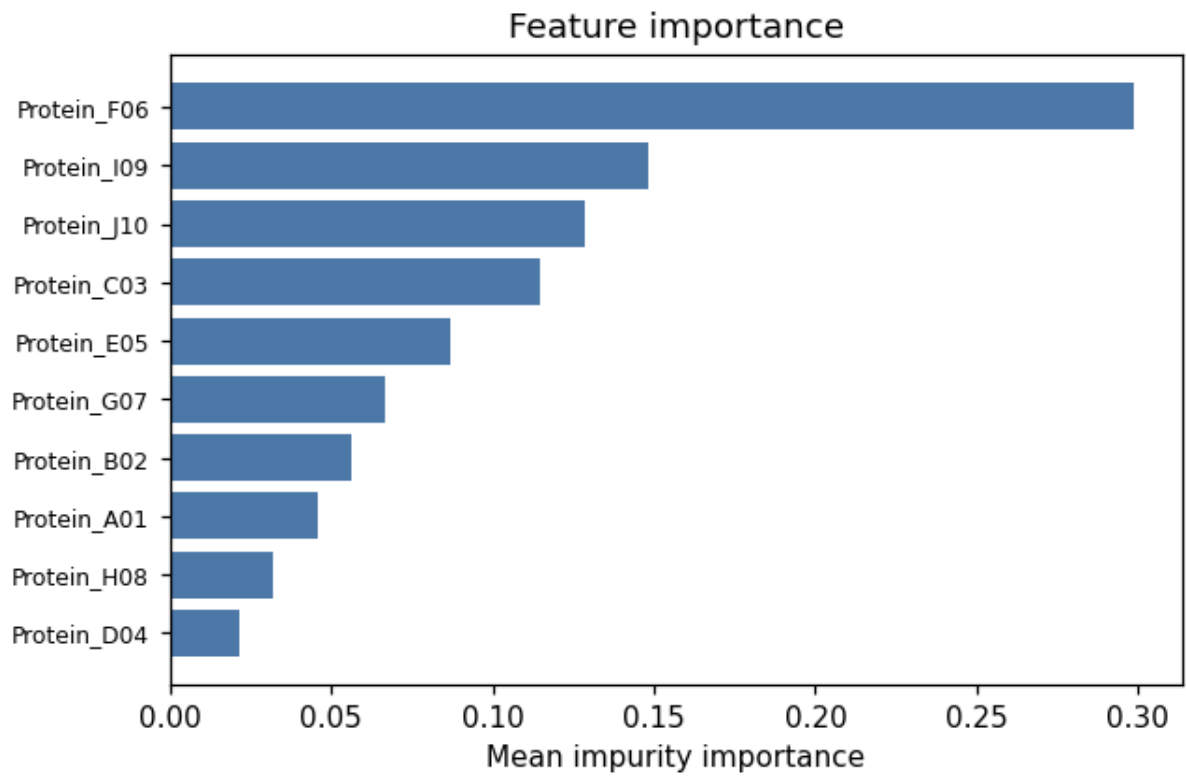
name	mean	std
Protein_A01	0.013745	0.033767
Protein_B02	-0.014693	0.036506
Protein_C03	0.168846	0.143659
Protein_D04	-0.01372	0.008411
Protein_E05	-0.082587	0.089068
Protein_F06	0.194496	0.264982
Protein_G07	0.114167	0.171214
Protein_H08	0.008102	0.009232
Protein_I09	0.192246	0.164957
Protein_J10	0.171206	0.182525

shap importance

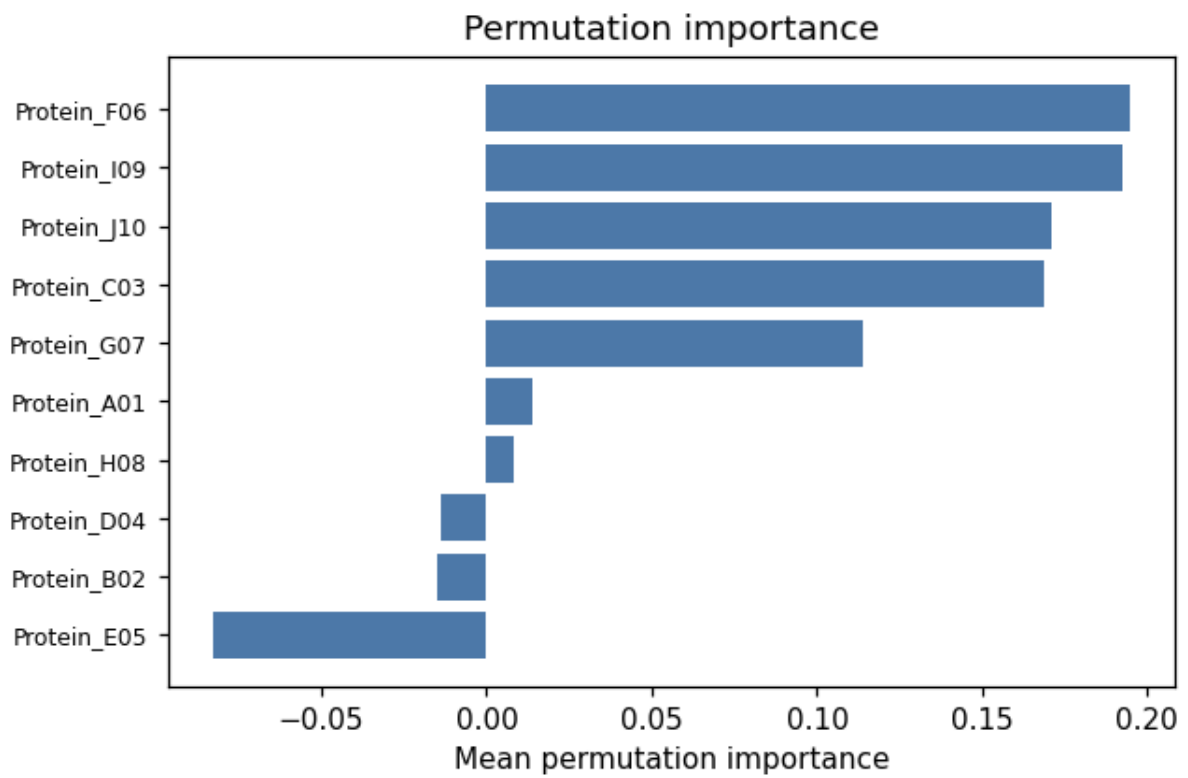
name	mean_abs
Protein_A01	0.104572
Protein_B02	0.036776
Protein_C03	0.247165
Protein_D04	0.018802
Protein_E05	0.030457
Protein_F06	0.434281
Protein_G07	0.218849
Protein_H08	0.023725
Protein_I09	0.248877
Protein_J10	0.263879

split metrics

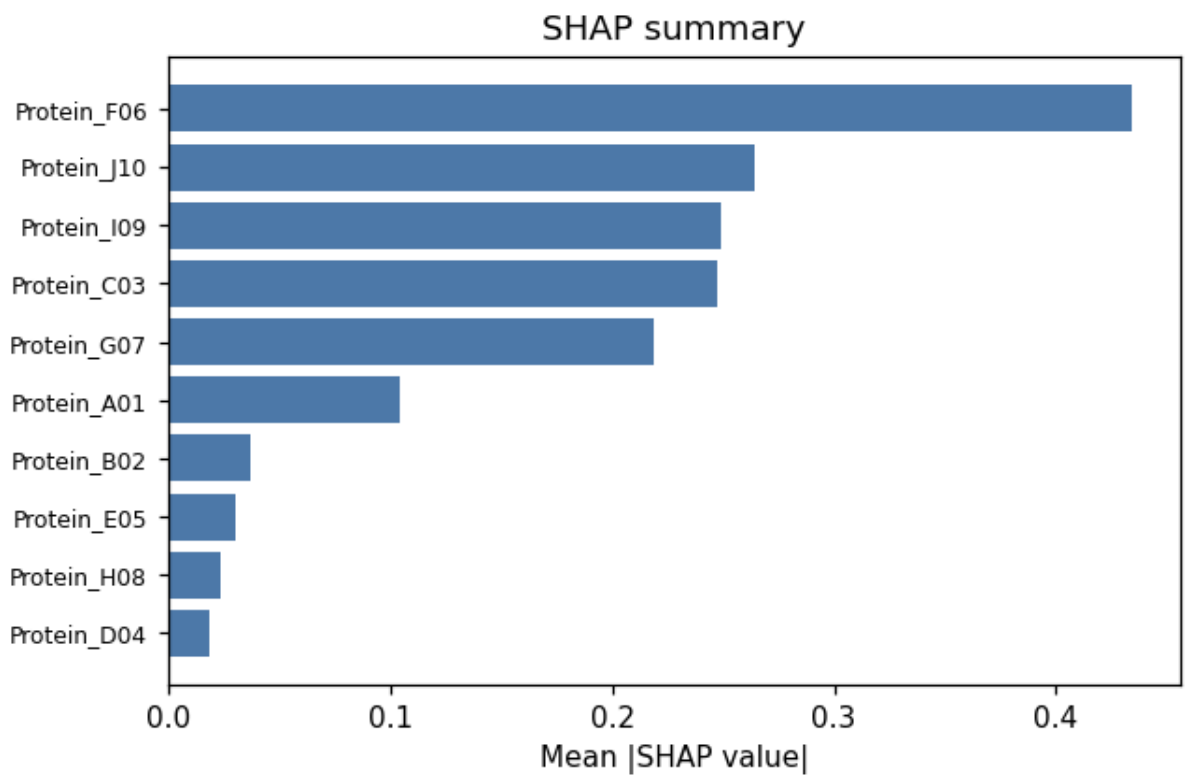
r2	mse
-0.958022	4.947417
0.292293	3.298471
-1.069172	2.312626



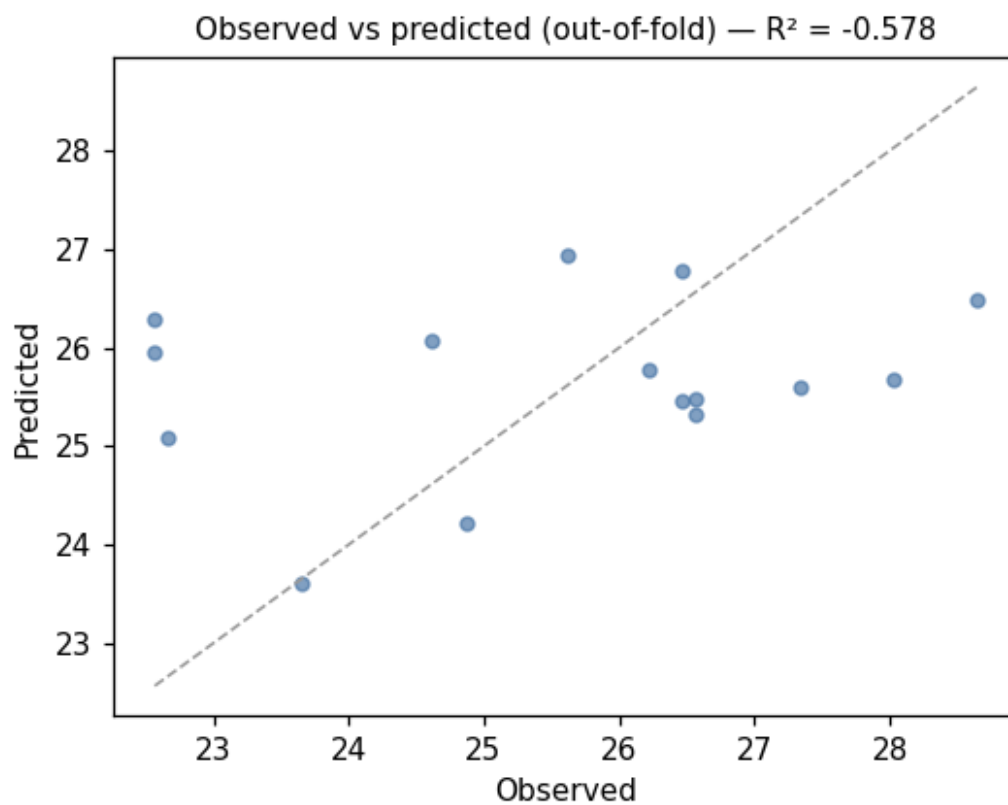
importance bar



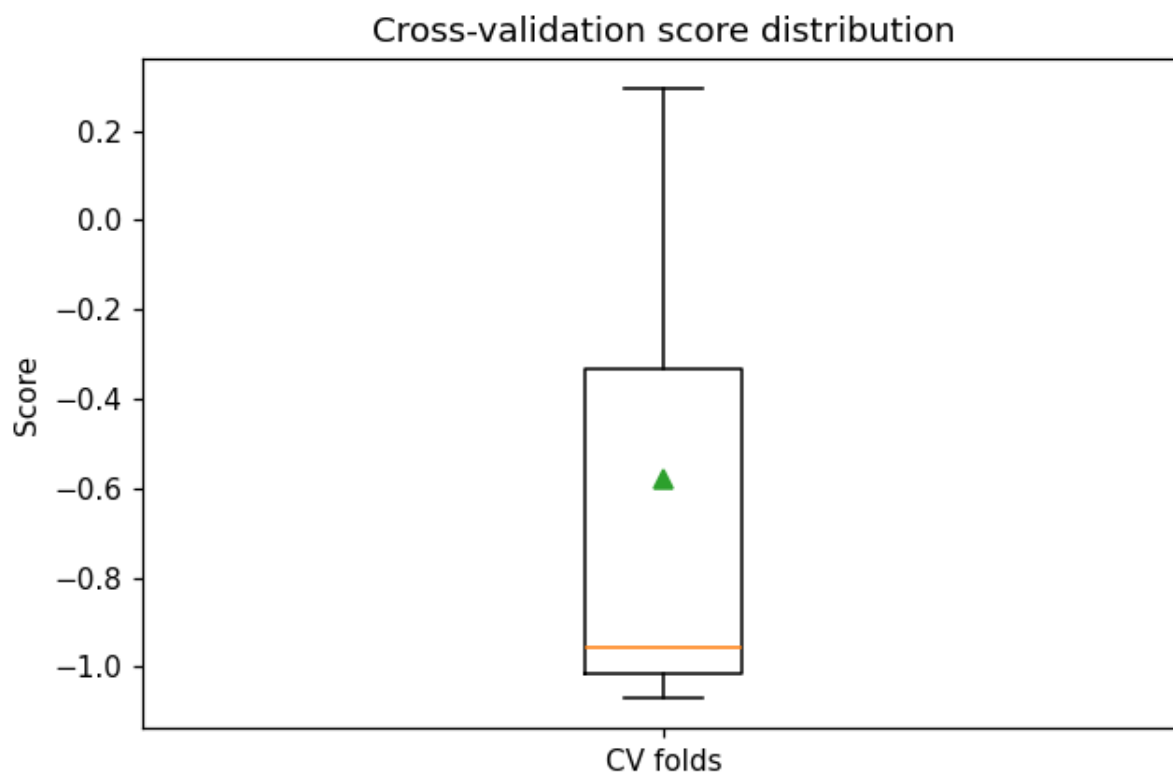
permutation bar



shap summary



pred vs obs



cv boxplot

Method & Provenance

method	Random Forest (Regression)
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engine	Python · scikit-learn 1.8.0
datasets	gallery — example_proteomics.csv
started	2026-09-21 02:17:48.827397
permanent link	https://cat-g-omxpert.wishartlab.com/results/by-token/a55dc899cd514343aea98c71dae

Parameter	Value
task_type	regression
model_type	regression
target_column	Protein_content
n_estimators	60
n_splits	3
test_size	0.25
run_univariate	True
run_permutation	True
run_shap	True
permutation_repeats	10
fdr_threshold	0.05

Command history

```
# python
from sklearn.ensemble import RandomForestRegressor

# python
model = RandomForestRegressor(n_estimators=60, random_state=42)

# python
scores = sklearn.model_selection.cross_val_score(model, X, y, cv=3)
```