AAanalysis

Cheat Sheet

Sequence → physicochemical scales → interpretable features → explainable ML → biological mechanism

pip install aaanalysis · aaanalysis.readthedocs.io

AAanalysis is a Python framework for interpretable, sequence-based protein prediction. It turns sequences into physicochemical features (CPP), trains explainable models, and traces every prediction back to a residue × property × group comparison — robust for small datasets.

The Golden Workflow *canonical pipeline*

1. **LOAD** `load_dataset · load_scales` → **`df_seq · df_scales`**
2. **PARTS** `SequenceFeature.get_df_parts` → **`df_parts`**
3. **FEATURES** `CPP.run` → **`df_feat`**
4. **MODEL** `TreeModel.fit · dPULearn.fit` → **`feat_importance · labels_`**
5. **EXPLAIN** `CPPPlot.feature_map · ShapModel` → **`figure · feat_impact`**

Prediction Task Levels *task → setup*

Residue `AA_*` — positional
unit: sliding window (aa_window_size)
ref: non-site windows / shuffled background

Domain `DOM_*` — both
unit: part-set jmd_n · tmd · jmd_c (from tmd_start / tmd_stop)
ref: labelled A vs B groups

Protein `SEQ_*` — compositional
unit: whole chain (composition)
ref: labelled groups / composition-matched background

Sequence Anatomy *the TMD model*

TMD Target Middle Domain — the central segment of interest (e.g. transmembrane stretch, binding region).

JMD Juxta Middle Domain — the flanks adjoining the TMD (jmd_n on the N-side, jmd_c on the C-side).

JMD widths set globally: aa.options['jmd_n_len'] · ['jmd_c_len'].

1: positives · 0: rel-negatives · 2: unlabeled

Feature Ontology *Part × Split × Scale*

PART *where on the sequence*
tmd · jmd_n · jmd_c · tmd_jmd · jmd_n_tmd_n · tmd_c_jmd_c

SPLIT *how to read the part*
Segment — contiguous · Pattern — sparse pairs · PeriodicPattern — i, i+3/4

SCALE *which physicochemical property*
AAontology (~600 scales) · hydrophobicity · charge · helix propensity · shape

```
TMD × Segment × hydrophobicity → membrane insertion
JMD × Pattern × net charge → electrostatic recognition
TMD × PeriodicPattern × helix → α-helical interface
```

CPP Strategies *via split_kws*

Compositional ≈ sequence/protein-level

one whole-part average (composition-like, position-agnostic)

```
skw = sf.get_split_kws(
    split_types="Segment",
    n_split_min=1, n_split_max=1)
cpp = aa.CPP(df_parts=df_parts,
             split_kws=skw)
```

Positional ≈ residue-/region-level

sub-segments and/or patterns resolved to positions

```
skw = sf.get_split_kws(
    split_types=["Segment", "Pattern",
                 "PeriodicPattern"],
    n_split_max=5, steps_pattern=[3, 4],
    steps_periodicpattern=[3, 4])
cpp = aa.CPP(df_parts=df_parts,
             split_kws=skw)
```

Domain level uses both. → CPP strategies: see the CPP tutorial (docs).

Which Module Should I Use? *intent → module*

Explore sequence patterns / composition → `AAlogo`

Discover discriminative physicochemical features → `CPP`

Reduce redundant amino-acid scales → `AAclust`

Train with positives + unlabelled data → `dPULearn`

Train an interpretable classifier → `TreeModel`

Explain a prediction (per feature / sample) → `ShapModel [pro]`

Visualize CPP features → `CPPPlot`

Data & Preparation *load · encode · clean*

Load benchmark sequences
`load_dataset(name) → df_seq`

Load AAontology scales
`load_scales() → df_scales`

Load precomputed features
`load_features(name) → df_feat`

Read / write FASTA
`read_fasta(file) → df_seq`

Encode sequences (one-hot / int)
`SequencePreprocessor().encode_*(seqs)`

Cluster redundant homologs
`filter_seq(df_seq) [pro]`

Feature Engineering *parts · CPP · scales*

Extract sequence parts
`get_df_parts(df_seq) → df_parts`

Discover discriminative features
`CPP(df_parts).run(labels) → df_feat ⋆`

Simplify → interpretable scales
`CPP.simplify(df_feat, labels)`

Build feature matrix X
`feature_matrix(df_feat, df_parts) → X`

Reduce redundant scales
`AAclust().fit(X) [Wrapper]`

Drop correlated features
`filter_correlation(X)`

Structural & Embedding *alternative feature sources*

Fetch AlphaFold + encode 3D/DSSP/PAE
`StructurePreprocessor().encode_dssp(df_seq)`

Encode protein-LM embeddings
`EmbeddingPreprocessor().encode(df_seq)`

Embeddings → pseudo-scales
`EmbeddingPreprocessor().build_scales(df_seq)`

Combine numeric feature dicts → CPP
`combine_dict_nums(dict_nums)`

Modeling & Explainability

Train + RFE + MC importance
`TreeModel().fit(X, labels) [Wrapper]`

Train with positives + unlabelled
`dPULearn().fit(X, labels) [Wrapper]`

Per-feature / sample SHAP impact
`ShapModel().fit(X, labels) [pro]`

Sequence Analysis *logos · motifs*

Position-specific logo
`AAlogo().get_df_logo(df_parts)`

Sample sequence windows
`AAWindowSampler().sample(df_seq)`

Pairwise sequence similarity
`comp_seq_sim(df_seq) [pro]`

Scan motifs (FIMO / MEME)
`scan_motif(df_seq, pwm) [pro]`

Metrics & Plotting *utilities*

Adjusted AUC (class imbalance)
`comp_auc_adjusted(X, labels)`

BIC score · KL divergence
`comp_bic_score(X, labels) · comp_kld`

Global plot style & fonts
`plot_settings(font_scale)`

Colours & standalone legend
`plot_get_clist(n) · plot_legend(ax)`

Protein Design (planned)

In-silico point mutations
`AAMut · AAMutPlot`

Sequence-design libraries
`SeqMut · SeqMutPlot`

AAanalysis · Worked Examples

tutorial-style code with the figure each call produces

Install · Import · Load

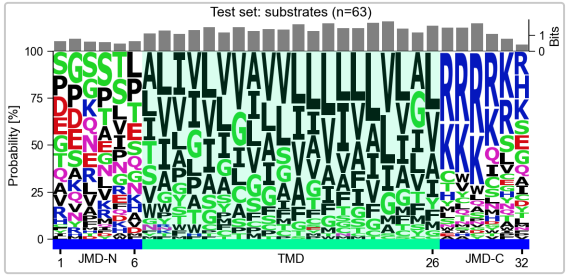
core + [pro]

```
# Python >= 3.11
pip install aaanalysis          # core
pip install 'aaanalysis[pro]'  # SHAP, FIMO, Bio

import numpy as np
import matplotlib.pyplot as plt
import aaanalysis as aa
df_seq = aa.load_dataset(name='DOM_GSEC')   # γ-secretase
labels = df_seq['label'].to_list()
df_scales = aa.load_scales()
# TMD model: 20-aa TMD, short JMD flanks
aa.options['jmd_n_len'] = 6
aa.options['jmd_c_len'] = 6
```

AAlogo — see the data

dataset at a glance

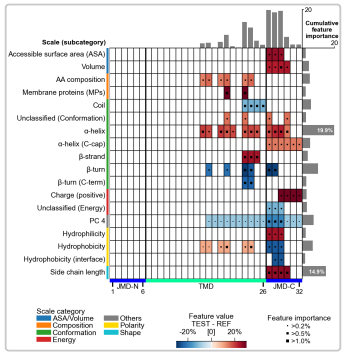
```
sf = aa.SequenceFeature()
df_parts = sf.get_df_parts(df_seq=df_seq,
    list_parts=['tmd', 'jmd_n', 'jmd_c'])

aal = aa.AAlogo()
df_logo = aal.get_df_logo(df_parts=df_parts,
    labels=labels, label_test=1, tmd_len=20)
df_info = aal.get_df_logo_info(df_parts=df_parts,
    labels=labels, label_test=1, tmd_len=20)
aa.plot_settings(font_scale=0.7)
aa.AAlogoPlot().single_logo(df_logo=df_logo,
    df_logo_info=df_info,        # bits bar on top
    name_data='Test set: substrates')
plt.tight_layout(); plt.show()
```



CPP — feature map

flagship · interpretability

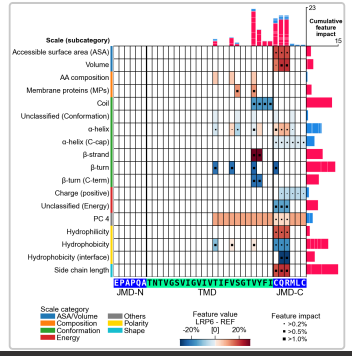
```
# extended parts -> default split grid applies
df_parts = sf.get_df_parts(df_seq=df_seq,
    list_parts=['tmd', 'jmd_n_tmd_n', 'tmd_c_jmd_c'])
cpp = aa.CPP(df_parts=df_parts, df_scales=df_scales)
df_feat = cpp.run(labels=labels, n_filter=40)
# swap scales for more interpretable correlated ones
df_feat = cpp.simplify(df_feat=df_feat, labels=labels)
X = sf.feature_matrix(features=df_feat['feature'],
                      df_parts=df_parts)
tm = aa.TreeModel(); tm.fit(X, labels=labels)
df_feat = tm.add_feat_importance(df_feat=df_feat)

cpp_plot = aa.CPPPlot()
aa.plot_settings(font_scale=0.65)
cpp_plot.feature_map(df_feat=df_feat)
plt.tight_layout(); plt.show()
```



ShapModel — explain a prediction

per-protein · [pro]

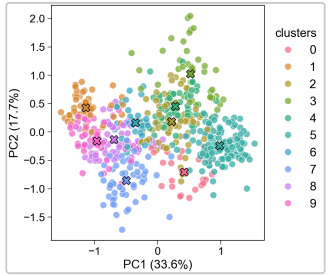
```
se = aa.ShapModel()
# fuzzy_labeling captures the true SHAP impact
se.fit(X, labels=labels, fuzzy_labeling=True)
# explain a borderline call — LRP6 (~60% substrate)
i = list(df_seq['entry']).index('O75581')
df_feat = se.add_feat_impact(df_feat=df_feat,
              sample_positions=i, names='LRP6')

cpp_plot.feature_map(df_feat=df_feat, shap_plot=True,
    col_imp='feat_impact_LRP6', name_test='LRP6',
    **args_seq)
plt.tight_layout(); plt.show()
```



AAclust — clusters

scale reduction · Wrapper

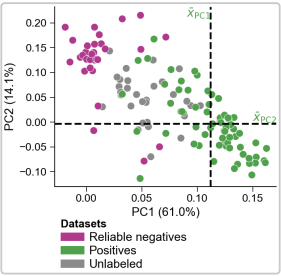
```
X = np.array(df_scales).T
aac = aa.AAclust()
aac.fit(X, names=list(df_scales), n_clusters=10)
aac.medoid_names_   # redundancy-reduced scales

aac_plot = aa.AAclustPlot()
aac_plot.centers(X, labels=aac.labels_)
plt.tight_layout(); plt.show()
```



dPULearn — PCA

reliable negatives · Wrapper

```
# labels: 1 = positive, 2 = unlabelled
dpul = aa.dPULearn()
dpul.fit(X=X, labels=labels, n_unl_to_neg=n_pos)
df_pu = dpul.df_pu_   # 1 pos · 0 rel-neg · 2 unl

dpul_plot = aa.dPULearnPlot()
dpul_plot.pca(df_pu=df_pu, labels=labels)
plt.tight_layout(); plt.show()
```



AAanalysis · Reference

5-minute example · options · class ↔ plot · glossary · citations

The 5-Minute Example

copy-paste this

```
import matplotlib.pyplot as plt
import aaanalysis as aa
df_seq = aa.load_dataset(name='DOM_GSEC')
labels = df_seq['label'].to_list()
sf = aa.SequenceFeature()
df_parts = sf.get_df_parts(df_seq=df_seq)
cpp = aa.CPP(df_parts=df_parts)
df_feat = cpp.run(labels=labels)
X = sf.feature_matrix(features=df_feat['feature'],
                      df_parts=df_parts)
tm = aa.TreeModel(); tm.fit(X, labels=labels)
df_feat = tm.add_feat_importance(df_feat=df_feat)
cpp_plot = aa.CPPPlot()
aa.plot_settings()
cpp_plot.feature_map(df_feat=df_feat)
plt.tight_layout(); plt.show()
```

aa.options

system-level settings

```
aa.options['random_state'] = 42
aa.options['verbose'] = True
aa.options['allow_multiprocessing'] = True

# TMD model – JMD flank widths
aa.options['jmd_n_len'] = 10
aa.options['jmd_c_len'] = 10

# plot labels & system-level scales
aa.options['name_tmd'] = 'TMD'
aa.options['df_scales'] = my_scales
```

Class ↔ Plot Class

mirrored API

CPP	CPPPlot	
AAclust	AAclustPlot	Wrapper
AAlogo	AAlogoPlot	
dPULearn	dPULearnPlot	Wrapper
TreeModel	–	Wrapper
ShapModel [pro]	–	Wrapper
AAMut	AAMutPlot	planned
SeqMut	SeqMutPlot	planned
AAWindowSampler	–	
SequenceFeature	–	
NumericalFeature	–	
SequencePreprocessor	–	

How to Cite

if you use AAanalysis

AAclust [Breimann24a]

Breimann & Frishman (2024a), AAclust: k-optimized clustering for selecting redundancy-reduced sets of amino acid scales
Bioinformatics Advances

AAontology [Breimann24b]

Breimann et al. (2024b), AAontology: An ontology of amino acid scales for interpretable machine learning
Journal of Molecular Biology

CPP & dPULearn [Breimann25a]

Breimann & Kamp et al. (2025), Charting γ-secretase substrates by explainable AI
Nature Communications

Design Principles

- Explicit over implicit — DataFrames everywhere
- Wrappers (.fit / .predict / .eval) set trailing *_ attributes after fit
- Biological interpretability is first-class
- Small-data robust and reproducible (layered seeds)

Glossary

canonical vocabulary · CONTEXT.md

Prediction level — Residue (AA_*) · Domain (DOM_*) · Protein (SEQ_*) — the unit a task predicts at; sets the dataset, the part, and the reference.

Part — Named segment used as feature input: tmd, jmd_n, jmd_c, tmd_jmd, jmd_n_tmd_n, tmd_c_jmd_c.

Split — How a scale is read across a part: Segment (contiguous), Pattern (sparse), PeriodicPattern (i, i+3/4).

Scale — AA → ℝ mapping. AAontology ships ~600 curated scales in two-level categories.

Feature — (Part × Split × Scale) — the atomic, residue-grounded, interpretable unit of CPP.

Compositional vs positional — How split_kws resolves locality: a whole-part average (compositional) vs sub-region/position-resolved (positional).

df_seq — Sequence table: entry, sequence, label, TMD bounds (tmd_start, tmd_stop).

df_parts — Wide table — one column per part (tmd, jmd_n, jmd_c, …).

df_feat — Ranked features: feature, abs_auc, mean_dif, p_val, positions, scale, category.

Wrapper — sklearn-style class — .fit / .predict / .eval, sets trailing *_ attributes after fit.

Plot class — *Plot mirror of an analytical class — same arguments, visualization only.

PU labels — dPULearn input: 1 = positive, 2 = unlabelled. Output: 1 / 0 (reliable-negative) / 2.

CPP — Comparative Physicochemical Profiling — discovers ranked Part × Split × Scale features.

AAontology — Two-level scale taxonomy; CPP uses its categories to organize and rank features.