

Multomics Result Result #88 — Analysis Report

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1. cca (#88)

2026-09-21 02:18:24 · multiomics_result · status: completed

The first canonical variate correlates the two views at $r = 1.000$.

canonical correlations

Variate	Correlation
CV1	1.0
CV2	1.0
CV3	1.0

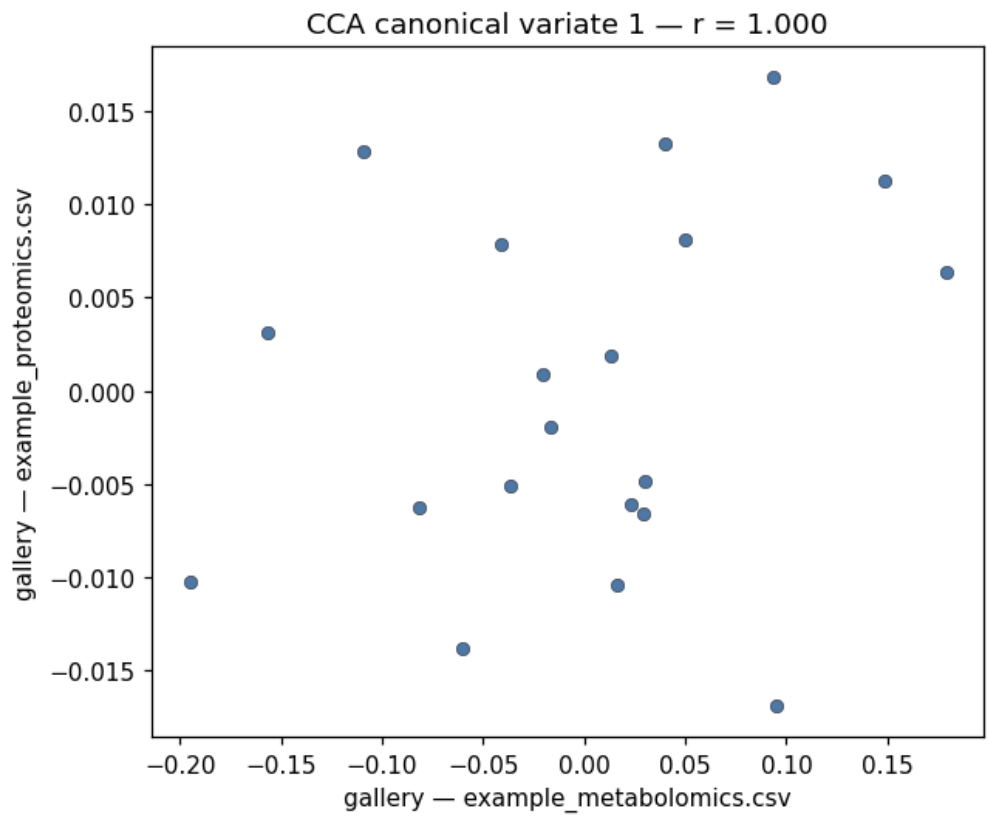
gallery — example metabolomics.csv top CV1 loadings

Feature	CV1 loading
Protein_content	-0.092203
Tryptophan	-0.004801
Valine	-0.004569
Serine	-0.004562
Leucine	-0.002716
Phenylalanine	0.002147
Threonine	0.001742
Isoleucine	-0.001573
Alanine	0.001427
Proline	-0.001098
Glycine	-0.000278

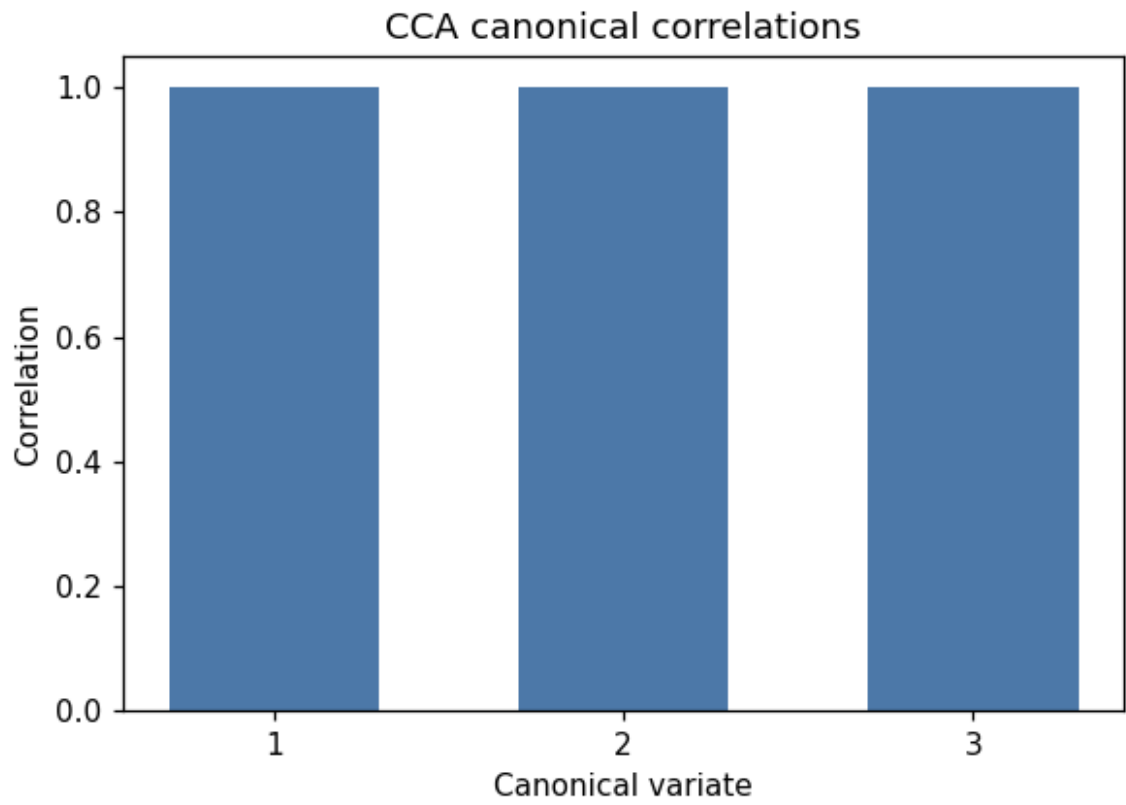
gallery — example proteomics.csv top CV1 loadings

Feature	CV1 loading
Protein_content	-0.009469
Protein_E05	0.0
Protein_H08	0.0
Protein_F06	-0.0
Protein_A01	0.0
Protein_D04	0.0
Protein_C03	-0.0
Protein_I09	-0.0

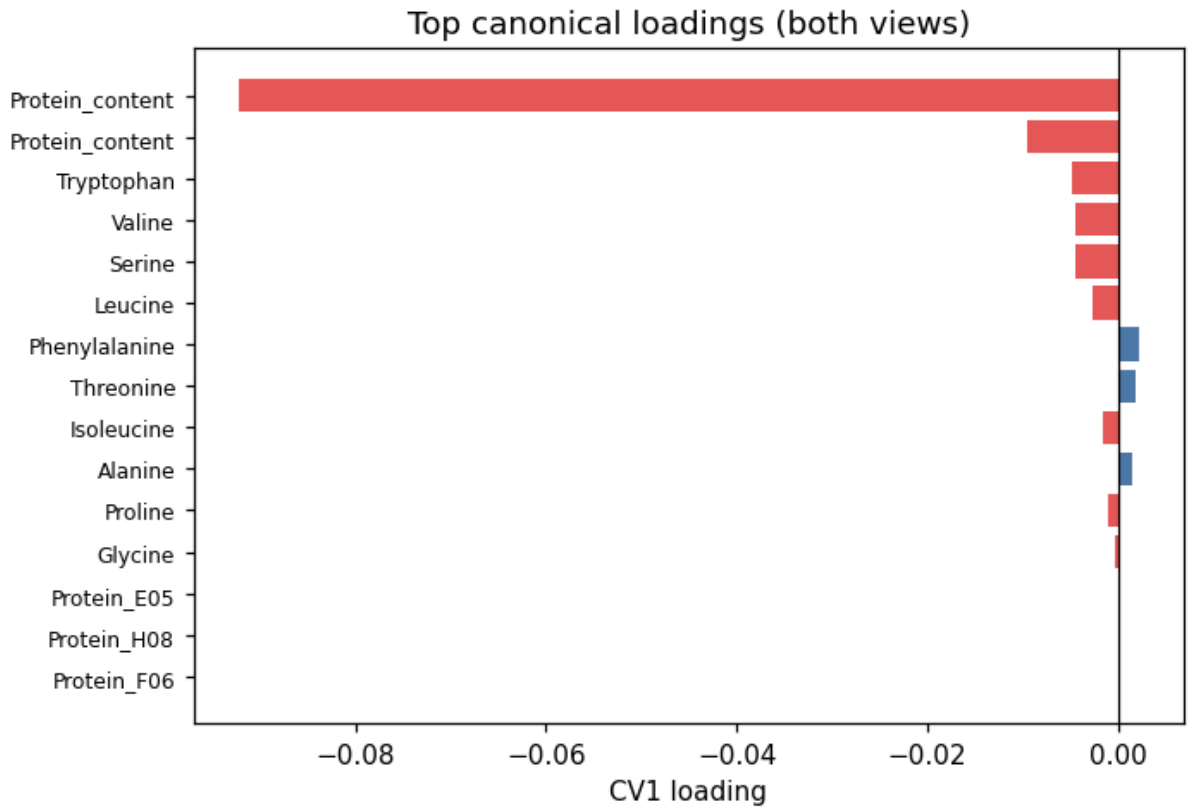
Protein_J10	-0.0
Protein_G07	0.0
Protein_B02	-0.0



cca variate scatter



cca correlation bar



cca loadings bar

Warnings

- All canonical correlations are at or near 1.0. With 20 samples and 3 components the model is almost certainly overfit; interpret the correlations as a description of this dataset only, not as evidence of real cross-omics structure.

Method & Provenance

method	Multi-omics — Canonical Correlation Analysis
engine	Python · statsmodels (CanCorr) 0.14.6
datasets	gallery — example_metabolomics.csv
started	2026-09-21 02:18:24.618760
permanent link	https://cat-g-omxpert.wishartlab.com/multiomics/results/by-token/21244bc41b924556a8

Parameter	Value
dataset_ids	—
pipeline_type	cca

Command history

```
# python
from statsmodels.multivariate.cancorr import CanCorr

# python
cca = CanCorr(X_block, Y_block).fit()
```