

Multomics Result Result #91 — Analysis Report

Generated 2026-09-21 02:39:18 · 1 run(s) · CAT-G Data Analyzer

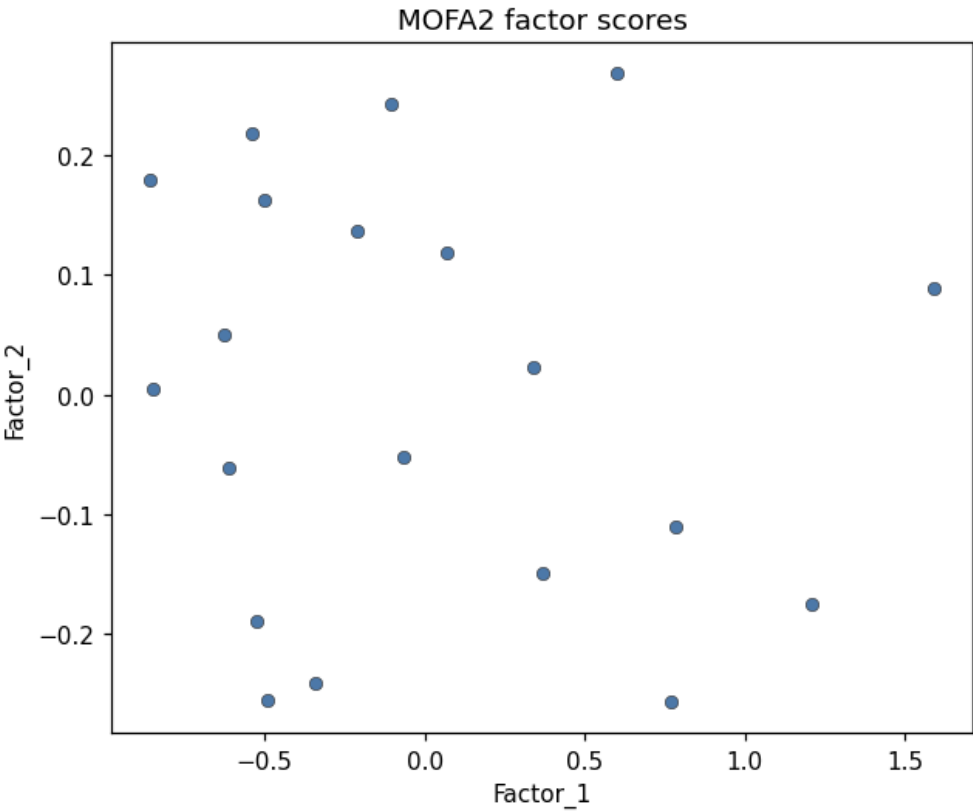
1. mofa2 (#91)

2026-09-21 02:18:34 · multiomics_result · status: completed

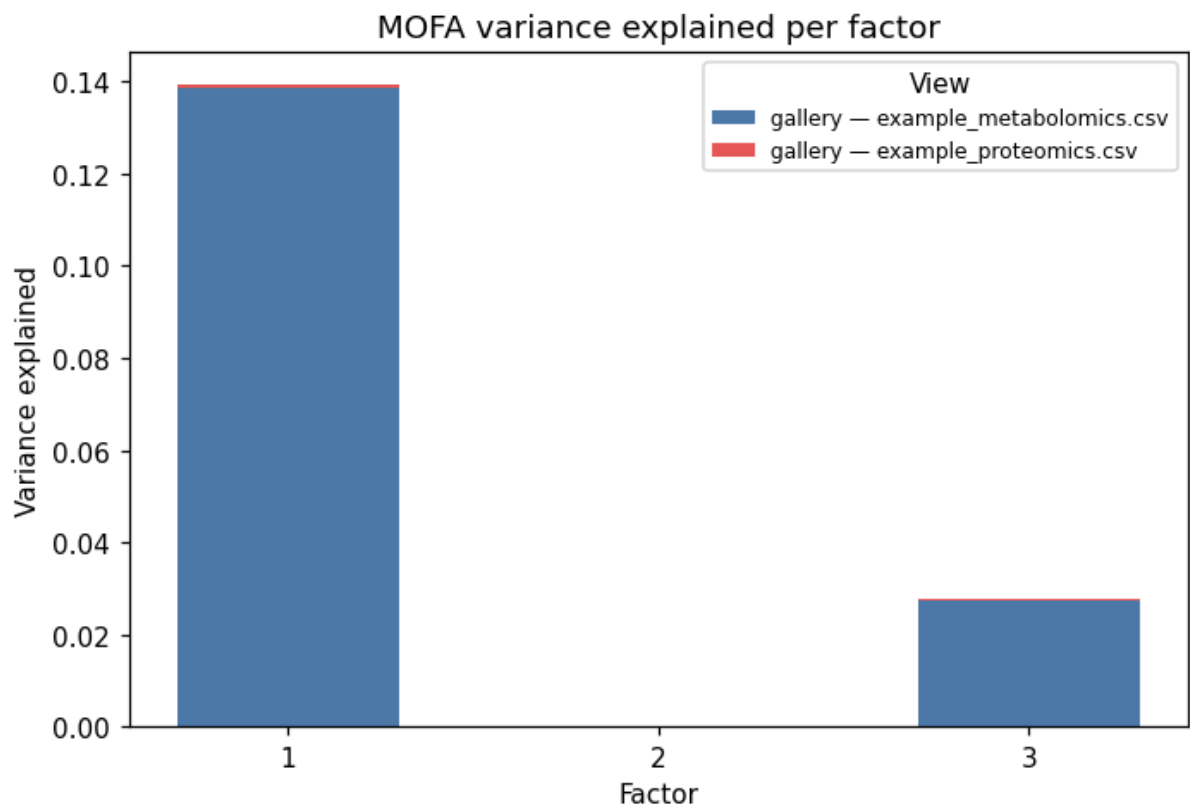
MOFA factor analysis completed across the input views.

mofa variance explained

View	Factor	R ²
gallery — example_metabolomics.csv	Factor 1	0.138522
gallery — example_metabolomics.csv	Factor 2	0.0
gallery — example_metabolomics.csv	Factor 3	0.027202
gallery — example_proteomics.csv	Factor 1	0.000944
gallery — example_proteomics.csv	Factor 2	0.0
gallery — example_proteomics.csv	Factor 3	0.000339



mofa factor scatter



mofo variance bar

Method & Provenance

method	Multi-omics — MOFA2
engine	Python · mofapy2 0.7.5
datasets	gallery — example_metabolomics.csv
started	2026-09-21 02:18:34.569473
completed	2026-09-21 02:18:35.258126
permanent link	https://cat-g-omxpert.wishartlab.com/multiomics/results/by-token/cea42a29cdd8490685

Parameter	Value
dataset_ids	—
pipeline_type	mofa2

Command history

```
# python
from mofapy2.run.entry_point import entry_point

# python
ent = entry_point()

# python
ent.set_data_options(scale_views=True)

# python
ent.set_model_options(factors=10)

# python
ent.set_train_options(iter=1000, convergence_mode='fast', seed=42)

# python
```

```
ent.build()
```

```
# python  
ent.run()
```