

Multionics Result Result #89 — Analysis Report

Generated 2026-09-21 02:39:14 · 1 run(s) · CAT-G Data Analyzer

1. nmf (#89)

2026-09-21 02:18:28 · multiomics_result · status: completed

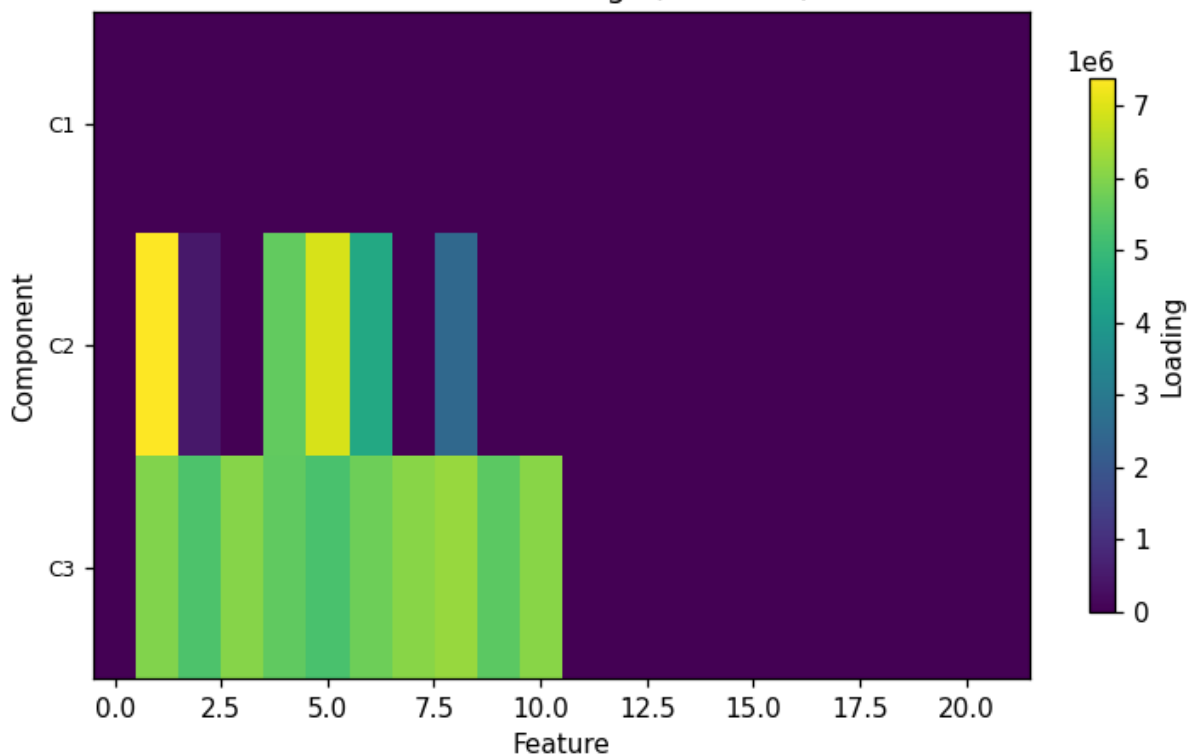
NMF decomposed the integrated matrix into latent factors.

reconstruction_error	12381233.822941
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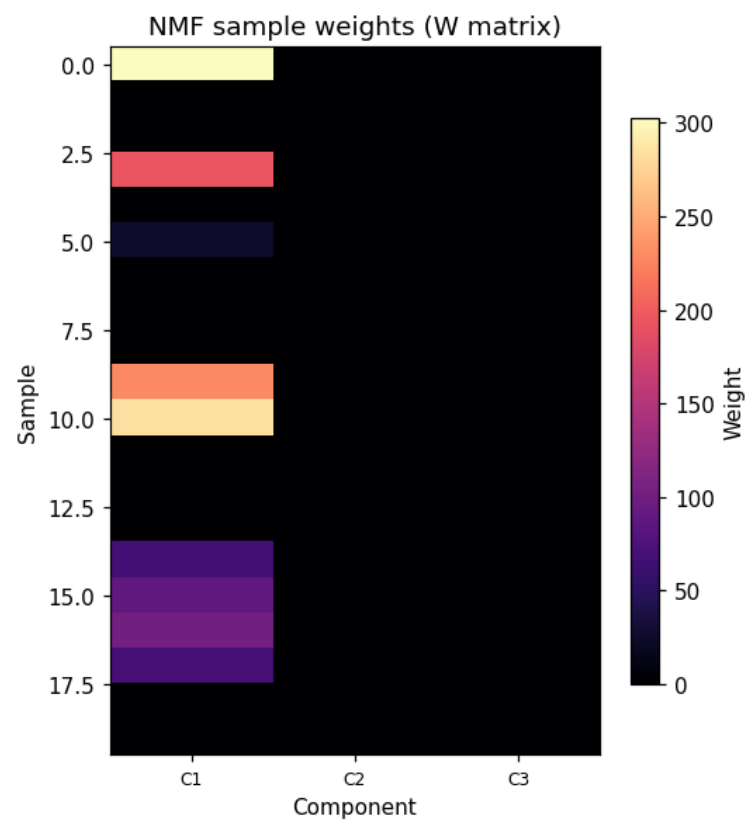
nmf top features

Component	Feature	Weight
Component 1	Threonine	6562.082156
Component 1	Tryptophan	5457.500878
Component 1	Glycine	5344.563369
Component 1	Valine	5181.768061
Component 1	Phenylalanine	4138.363356
Component 1	Serine	739.267238
Component 1	Proline	490.375805
Component 1	Alanine	63.395161
Component 1	Protein_H08	0.220272
Component 1	Protein_J10	0.097666

NMF feature loadings (H matrix)



nmf h heatmap



nmf w heatmap

Method & Provenance

method	Multi-omics — NMF
engine	Python · scikit-learn (NMF) 1.8.0
datasets	gallery — example_metabolomics.csv
started	2026-09-21 02:18:28.760895
permanent link	https://cat-g-omxpert.wishartlab.com/multiomics/results/by-token/3921b1b7149041ad98

Parameter	Value
dataset_ids	—
pipeline_type	nmf

Command history

```
# python
from sklearn.decomposition import NMF

# python
W = NMF(n_components=3).fit_transform(X)
```