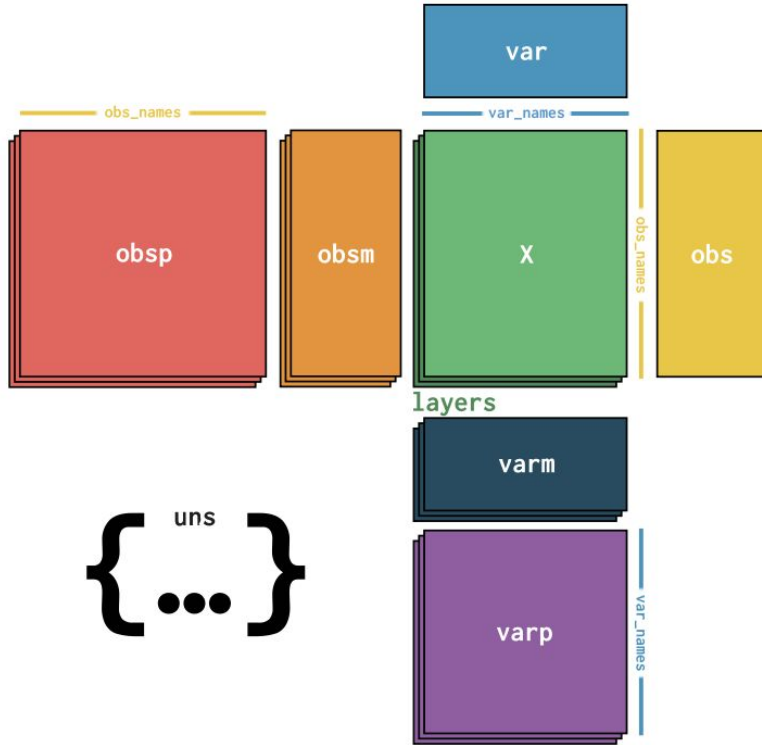


AnnData object



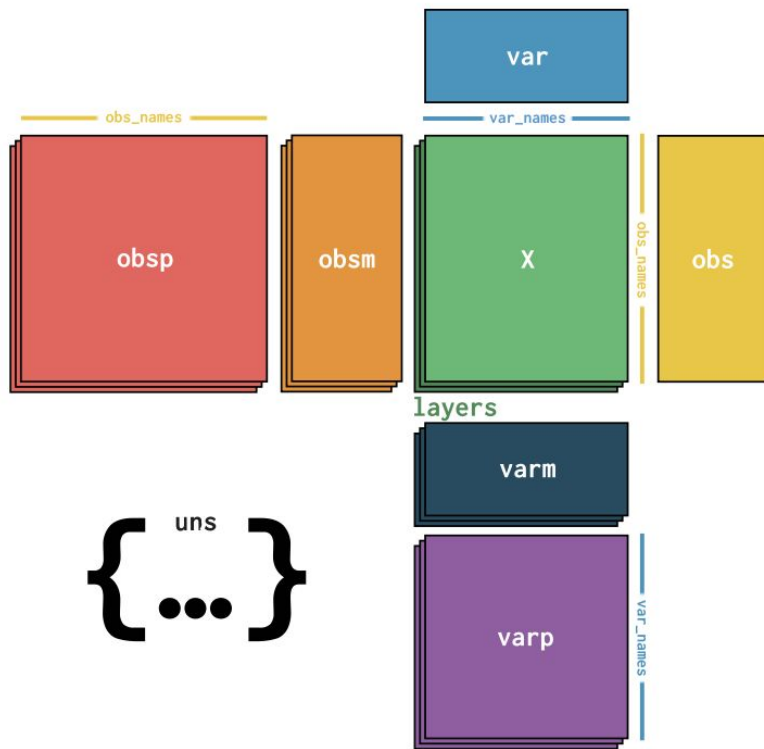
.h5ad object

Reading:

```
scanpy.read("filename.h5ad")
```

```
scanpy.write("filename.h5ad")
```

AnnData object



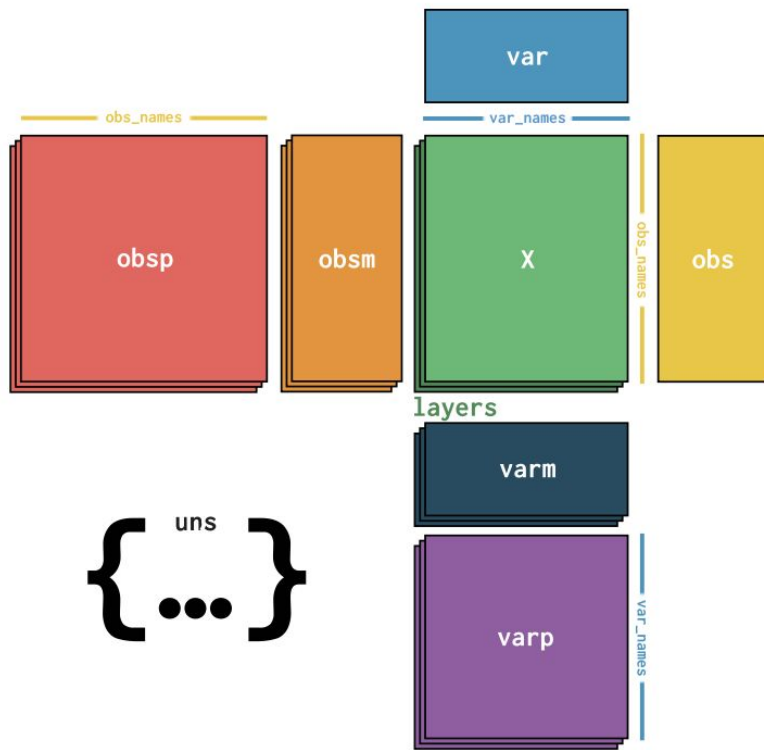
adata.X: Count matrix

Genes

	g1	g2	g3	g4
20	20	25	1	0
1	1	0	10	0
0	0	0	20	0

Cells

AnnData object



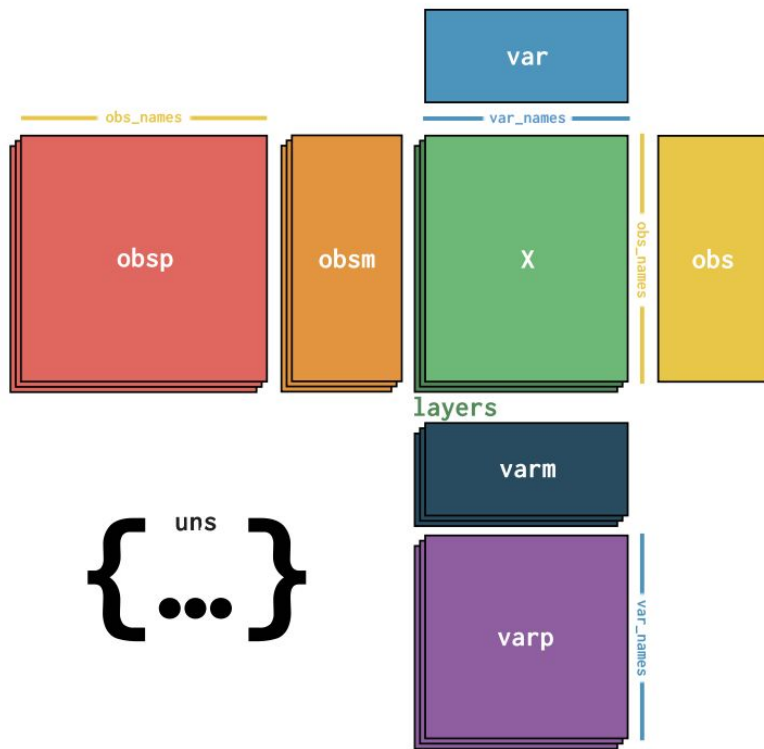
adata.var: gene level metadata

variables

Genes

mean	std	type	Highly variable
5.5	1.2	mt	True
10.2	0.01	rib	False
0	0	pc	False

AnnData object



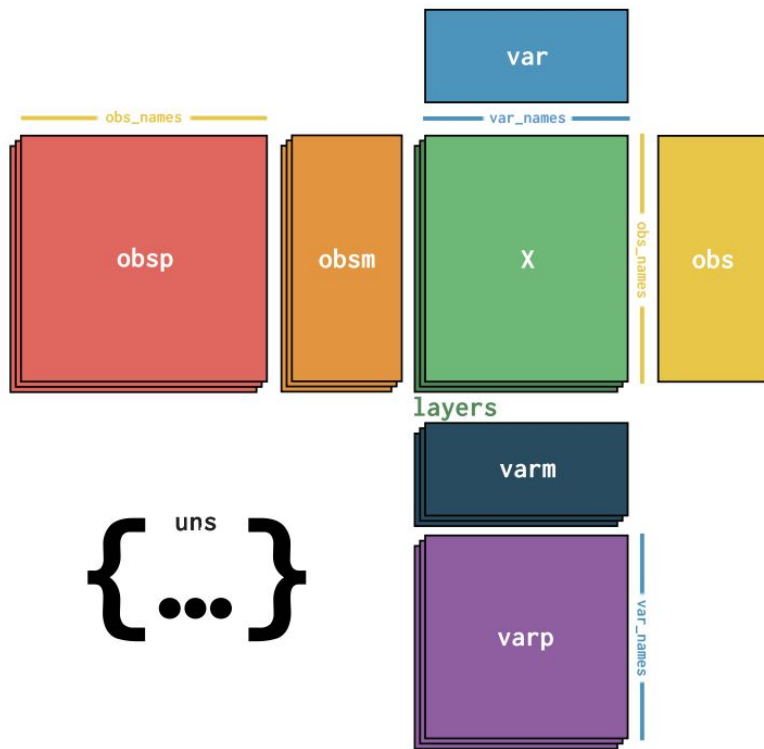
adata.obs: cell level metadata

variables

Cells

donor	batch	cell_type	Total count
P1	1	B cell	2000
P1	2	T cell	1200
P2	2	NK cell	3400

AnnData object



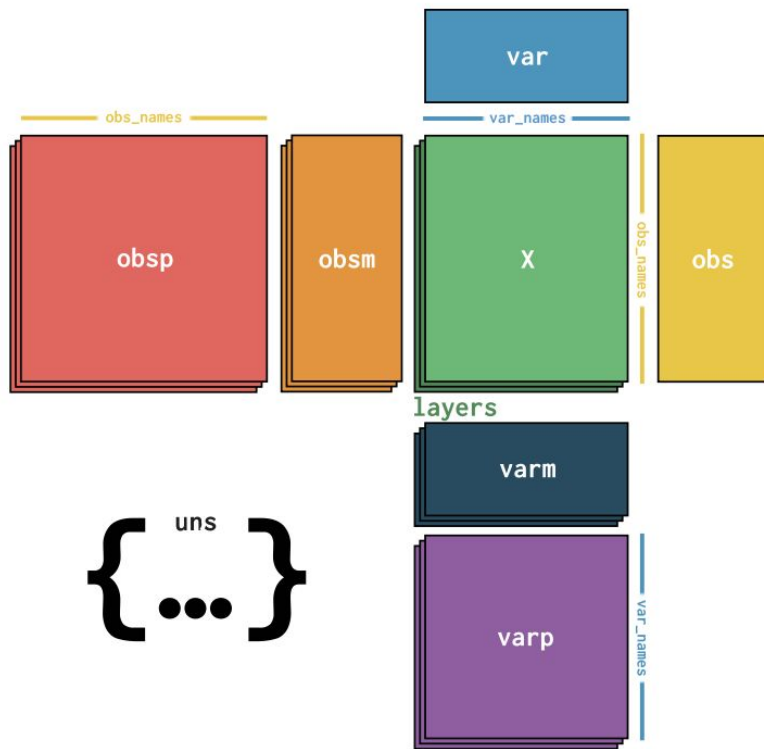
adata.obsm: observation level objects

`adata.obsm["X_pca"]` = Principal components

`adata.obsm["X_umap"]` = UMAP

...

AnnData object

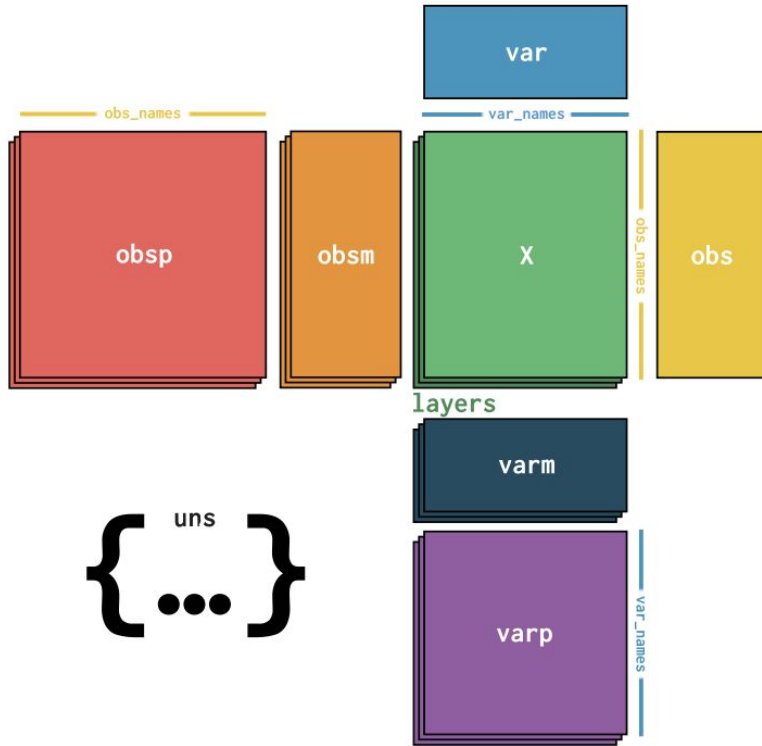


adata.obsp: observation level objects
(observations by observations)

adata.obsp[“affinity”] = pairwise cell distances

...

AnnData object

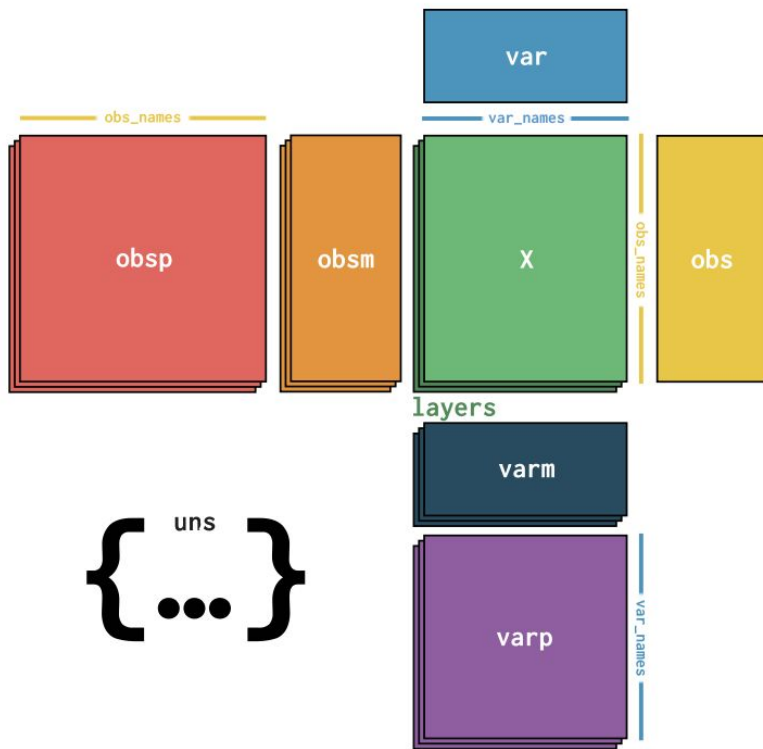


`adata.varm`: Gene level objects

`adata.obsm["PCs"]` = PC loadings

...

AnnData object

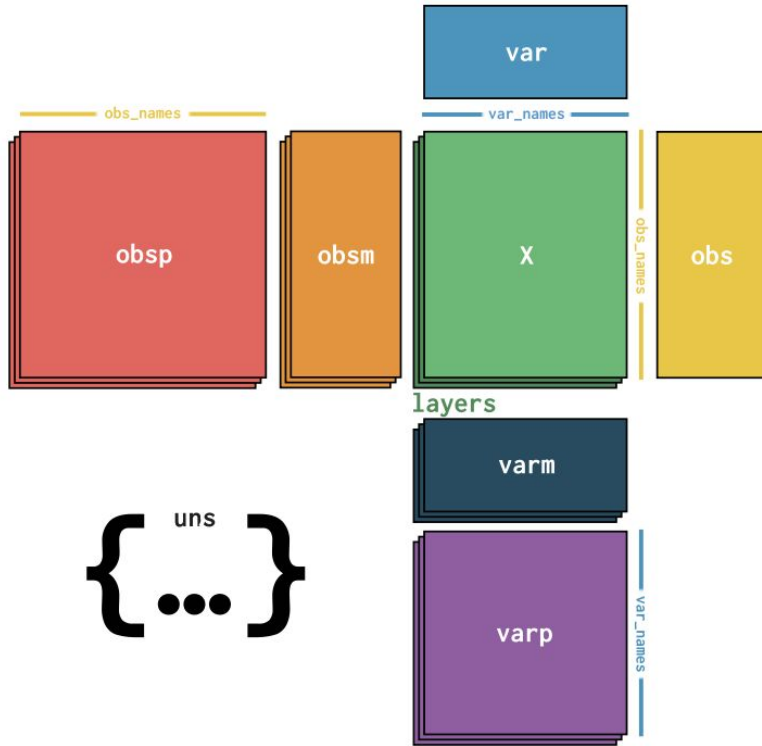


adata.varp: Gene level objects
(genes by genes)

```
adata.varp["interact"] = gene-gene interaction values
```

■ ■ ■

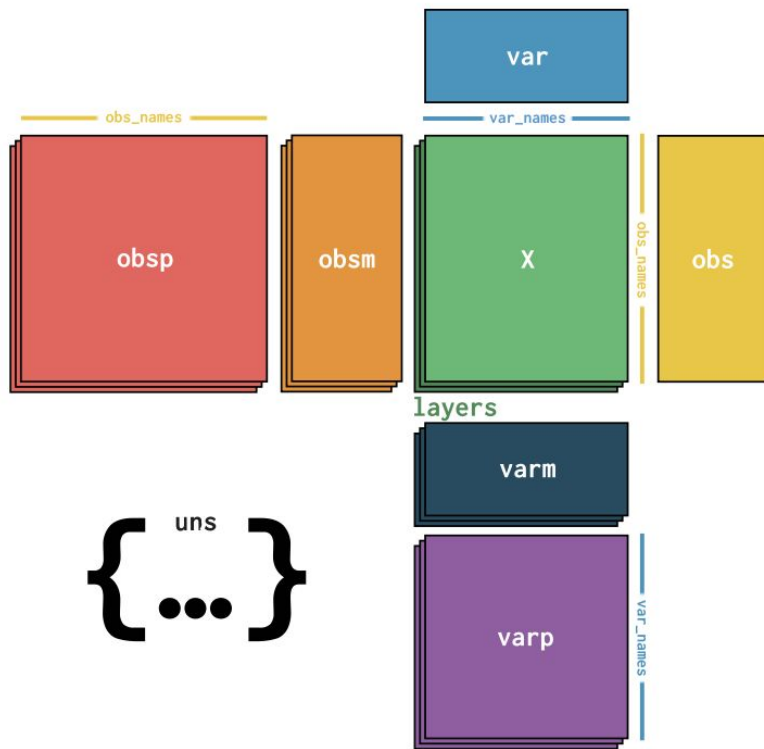
AnnData object



adata.uns: Unstructured objects

`adata.uns["hires_image"]` = high resolution image array
`adata.uns["lowres_image"]` = low resolution image array
`Adata.uns["cell_type_colors"]` = lists of color codes

AnnData object



[Complete documentation](https://anndata.readthedocs.io/en/latest/index.html)

<https://anndata.readthedocs.io/en/latest/index.html>