

# AnanseScanpy\_1.1.3\_PBMC\_vignette

November 4, 2022

## 1 AnanseScanpy vignette for multiomics PBMC dataset

PBMC multiomics datasets scanpy objects (anndata) generated from Seurat objects with Seurat-Disk

```
[1]: import scanpy as sc
      from anansescanpy import *

      sc.set_figure_params(figsize=(4, 4))
```

```
[2]: sc.logging.print_versions()
```

```
-----
anndata      0.8.0
scanpy       1.9.1
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PIL          9.2.0
anansescanpy 0.1.2
asttokens    NA
backcall     0.2.0
beta_ufunc   NA
binom_ufunc  NA
cffi         1.15.1
colorama     0.4.6
cyclor       0.10.0
cython_runtime NA
dateutil     2.8.2
debugpy      1.6.3
decorator    5.1.1
defusedxml   0.7.1
entrypoints  0.4
executing    1.2.0
h5py         3.7.0
hypergeom_ufunc NA
ipykernel    6.17.0
ipython_genutils 0.2.0
jedi         0.18.1
joblib       1.2.0
```

jupyter_server	1.21.0
kiwisolver	1.4.4
llvmlite	0.39.1
matplotlib	3.6.0
matplotlib_inline	0.1.6
mpl_toolkits	NA
natsort	8.2.0
nbinom_ufunc	NA
ncf_ufunc	NA
numba	0.56.3
numpy	1.23.4
packaging	21.3
pandas	1.5.1
parso	0.8.3
pexpect	4.8.0
pickleshare	0.7.5
pkg_resources	NA
prompt_toolkit	3.0.31
psutil	5.9.3
ptyprocess	0.7.0
pure_eval	0.2.2
pydev_ipython	NA
pydevconsole	NA
pydevd	2.8.0
pydevd_file_utils	NA
pydevd_plugins	NA
pydevd_tracing	NA
pygments	2.13.0
pyparsing	3.0.9
pytz	2022.6
scipy	1.9.3
session_info	1.0.0
setuptools	65.5.0
six	1.16.0
sklearn	1.1.3
sphinxcontrib	NA
stack_data	0.6.0
threadpoolctl	3.1.0
tornado	6.2
traitlets	5.5.0
typing_extensions	NA
wcwidth	0.2.5
zmq	24.0.1
zoneinfo	NA
-----	
IPython	8.6.0
jupyter_client	7.4.4
jupyter_core	4.11.1

```
jupyterlab      3.5.0
notebook        6.5.1
```

```
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Python 3.10.6 | packaged by conda-forge | (main, Aug 22 2022, 20:36:39) [GCC
10.4.0]
```

```
Linux-5.15.0-52-generic-x86_64-with-glibc2.31
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```

```
Session information updated at 2022-11-02 16:19
```

```
[3]: # Fill in the directories where the h5ad rna and atac objects are located
      atac_PBMC = sc.read("atac_PBMC.h5ad")
      rna_PBMC= sc.read("rna_diet_PBMC.h5ad")

      # Notes: the default assays for atac_PBMC and rna_PBMC are "peaks" and "counts"
      ↪ respectively

      # Nessesary pre-processing from converted Seurat object
      rna_PBMC.obs['predicted.id'] = rna_PBMC.obs['predicted.id'].str.replace(' ',
      ↪ '-')
      atac_PBMC.obs['predicted.id'] = atac_PBMC.obs['predicted.id'].str.replace(' ',
      ↪ '-')

```

```
[4]: # Run the functions in python:
      outputdir="/AnanseScanpy_outs/"
      contrasts=["B-naive_B-memory", "B-memory_B-naive", "B-naive_CD14-Mono"
      ↪ , "CD14-Mono_B-naive"]
      minimal=25
      export_CPM_scANANSE(anndata=rna_PBMC,min_cells=minimal,outputdir=outputdir
      ↪ ,cluster_id="predicted.id")
      export_ATA_scANANSE(anndata=atac_PBMC,min_cells=minimal,outputdir=outputdir
      ↪ ,cluster_id="predicted.id")
      config_scANANSE(anndata=rna_PBMC,min_cells=minimal,outputdir=outputdir,
      ↪ cluster_id="predicted.id",additional_contrasts=contrasts)
      DEGS_scANANSE(anndata=rna_PBMC,min_cells=minimal,outputdir=outputdir,
      ↪ cluster_id="predicted.id",additional_contrasts=contrasts)

```

```
gather data from CD4-Naive with 3095 cells
gather data from CD4-TCM with 1592 cells
gather data from CD8-Naive with 1496 cells
gather data from CD16-Mono with 1414 cells
gather data from NK with 664 cells
gather data from Treg with 527 cells
gather data from CD14-Mono with 492 cells
gather data from NK-Proliferating with 424 cells
gather data from CD8-TCM with 351 cells
gather data from B-intermediate with 172 cells
gather data from cDC2 with 168 cells
gather data from B-memory with 164 cells
```

gather data from Plasmablast with 160 cells  
gather data from CD4-TEM with 159 cells  
gather data from MAIT with 121 cells  
gather data from CD8-TEM with 110 cells  
gather data from dnT with 73 cells  
gather data from B-naive with 26 cells  
gather data from CD4-Naive with 3095 cells  
gather data from CD4-TCM with 1592 cells  
gather data from CD8-Naive with 1496 cells  
gather data from CD16-Mono with 1414 cells  
gather data from NK with 664 cells  
gather data from Treg with 527 cells  
gather data from CD14-Mono with 492 cells  
gather data from NK-Proliferating with 424 cells  
gather data from CD8-TCM with 351 cells  
gather data from B-intermediate with 172 cells  
gather data from cDC2 with 168 cells  
gather data from B-memory with 164 cells  
gather data from Plasmablast with 160 cells  
gather data from CD4-TEM with 159 cells  
gather data from MAIT with 121 cells  
gather data from CD8-TEM with 110 cells  
gather data from dnT with 73 cells  
gather data from B-naive with 26 cells  
adding additional contrasts  
anansesnake\_CD4-Naive\_average  
anansesnake\_CD4-TCM\_average  
anansesnake\_CD8-Naive\_average  
anansesnake\_CD16-Mono\_average  
anansesnake\_NK\_average  
anansesnake\_Treg\_average  
anansesnake\_CD14-Mono\_average  
anansesnake\_NK-Proliferating\_average  
anansesnake\_CD8-TCM\_average  
anansesnake\_B-intermediate\_average  
anansesnake\_cDC2\_average  
anansesnake\_B-memory\_average  
anansesnake\_Plasmablast\_average  
anansesnake\_CD4-TEM\_average  
anansesnake\_MAIT\_average  
anansesnake\_CD8-TEM\_average  
anansesnake\_dnT\_average  
anansesnake\_B-naive\_average  
anansesnake\_B-naive\_B-memory  
anansesnake\_B-memory\_B-naive  
anansesnake\_B-naive\_CD14-Mono  
anansesnake\_CD14-Mono\_B-naive  
adding additional contrasts

calculating DEGS for contrast anansesnake\_CD4-Naive\_average  
skip  
calculating DEGS for contrast anansesnake\_CD4-TCM\_average  
skip  
calculating DEGS for contrast anansesnake\_CD8-Naive\_average  
skip  
calculating DEGS for contrast anansesnake\_CD16-Mono\_average  
skip  
calculating DEGS for contrast anansesnake\_NK\_average  
skip  
calculating DEGS for contrast anansesnake\_Treg\_average  
skip  
calculating DEGS for contrast anansesnake\_CD14-Mono\_average  
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calculating DEGS for contrast anansesnake\_NK-Proliferating\_average  
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calculating DEGS for contrast anansesnake\_CD8-TCM\_average  
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calculating DEGS for contrast anansesnake\_B-intermediate\_average  
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calculating DEGS for contrast anansesnake\_cDC2\_average  
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calculating DEGS for contrast anansesnake\_B-memory\_average  
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calculating DEGS for contrast anansesnake\_Plasmablast\_average  
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calculating DEGS for contrast anansesnake\_CD4-TEM\_average  
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calculating DEGS for contrast anansesnake\_MAIT\_average  
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calculating DEGS for contrast anansesnake\_CD8-TEM\_average  
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calculating DEGS for contrast anansesnake\_dnT\_average  
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calculating DEGS for contrast anansesnake\_B-naive\_average  
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calculating DEGS for contrast anansesnake\_B-naive\_B-memory  
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calculating DEGS for contrast anansesnake\_B-memory\_B-naive  
skip  
calculating DEGS for contrast anansesnake\_B-naive\_CD14-Mono  
skip  
calculating DEGS for contrast anansesnake\_CD14-Mono\_B-naive  
skip