AnanseScanpy_Jupyter_PBMC_vignette-1.0.0

January 10, 2023

1 AnanseScanpy vignette for multiomics PBMC dataset

PBMC multiomics datasets scanpy objects (anndata) generated from Seurat objects with Seurat-Disk. This vignette includes the optional functions for Maelstrom (GimmeMotifs) analysis.

[1]:
```
import scanpy as sc
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import anansescanpy as asc

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

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

```
-----
anndata     0.8.0
scanpy      1.9.1
-----
PIL                 9.2.0
anansescanpy        0.2.4
asttokens           NA
backcall            0.2.0
beta_ufunc          NA
binom_ufunc         NA
cffi                1.15.1
colorama            0.4.6
cycler              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           6.17.1
```

```
ipython_genutils    0.2.0
jedi                0.18.1
joblib              1.2.0
jupyter_server      1.23.2
kiwisolver          1.4.4
llvmlite            0.39.1
matplotlib          3.6.2
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
platformdirs        2.5.2
prompt_toolkit      3.0.32
psutil              5.9.4
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
seaborn             0.12.1
session_info        1.0.0
setuptools          65.5.1
six                 1.16.0
sklearn             1.1.3
stack_data          0.6.1
statsmodels         0.13.5
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      7.4.7
jupyter_core        5.0.0
jupyterlab          3.5.0
notebook            6.5.2
-----
Python 3.10.6 | packaged by conda-forge | (main, Aug 22 2022, 20:36:39) [GCC
10.4.0]
Linux-5.15.0-56-generic-x86_64-with-glibc2.31
-----
Session information updated at 2023-01-10 11:21
```

[3]:
```python
# 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_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]:
```python
# Run the functions in python:
outputdir="AnanseScanpy_outs/"
contrasts=["B-naive_B-memory","B-memory_B-naive"]
minimal=25
asc.export_CPM_scANANSE(anndata=rna_PBMC,min_cells=minimal,outputdir=outputdir,
                        cluster_id="predicted.id"
)
asc.
 ↪export_ATAC_scANANSE(anndata=atac_PBMC,min_cells=minimal,outputdir=outputdir,
                         cluster_id="predicted.id"
)
asc.config_scANANSE(anndata=rna_PBMC,min_cells=minimal,outputdir=outputdir,
                    cluster_id="predicted.id",additional_contrasts=contrasts
)
asc.DEGS_scANANSE(anndata=rna_PBMC,min_cells=minimal,outputdir=outputdir,
                  cluster_id="predicted.id",additional_contrasts=contrasts
)
```

```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/anndata/_core/raw.py:139: FutureWarning: X.dtype being converted to
```

```
np.float32 from float64. In the next version of anndata (0.9) conversion will
not be automatic. Pass dtype explicitly to avoid this warning. Pass `AnnData(X,
dtype=X.dtype, …)` to get the future behaviour.
  return anndata.AnnData(

gather data from CD4-Naive with 1414 cells
gather data from CD4-TCM with 1592 cells
gather data from CD8-Naive with 1496 cells
gather data from CD16-Mono with 527 cells
gather data from NK with 492 cells
gather data from Treg with 160 cells
gather data from CD14-Mono with 3095 cells
gather data from CD8-TCM with 73 cells
gather data from B-intermediate with 351 cells
gather data from cDC2 with 168 cells
gather data from B-memory with 159 cells
gather data from CD4-TEM with 172 cells
gather data from MAIT with 121 cells
gather data from CD8-TEM with 664 cells
gather data from B-naive with 424 cells
gather data from gdT with 164 cells
gather data from pDC with 110 cells
gather data from HSPC with 26 cells
gather data from CD4-Naive with 1414 cells
gather data from CD4-TCM with 1592 cells
gather data from CD8-Naive with 1496 cells
gather data from CD16-Mono with 527 cells
gather data from NK with 492 cells
gather data from Treg with 160 cells
gather data from CD14-Mono with 3095 cells
gather data from CD8-TCM with 73 cells
gather data from B-intermediate with 351 cells
gather data from cDC2 with 168 cells
gather data from B-memory with 159 cells
gather data from CD4-TEM with 172 cells
gather data from MAIT with 121 cells
gather data from CD8-TEM with 664 cells
gather data from B-naive with 424 cells
gather data from gdT with 164 cells
gather data from pDC with 110 cells
gather data from HSPC 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_CD8-TCM_average
anansesnake_B-intermediate_average
anansesnake_cDC2_average
anansesnake_B-memory_average
anansesnake_CD4-TEM_average
anansesnake_MAIT_average
anansesnake_CD8-TEM_average
anansesnake_B-naive_average
anansesnake_gdT_average
anansesnake_pDC_average
anansesnake_HSPC_average
anansesnake_B-naive_B-memory
anansesnake_B-memory_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
skip
calculating DEGS for contrast anansesnake_CD8-TCM_average
skip
calculating DEGS for contrast anansesnake_B-intermediate_average
skip
calculating DEGS for contrast anansesnake_cDC2_average
skip
calculating DEGS for contrast anansesnake_B-memory_average
skip
calculating DEGS for contrast anansesnake_CD4-TEM_average
skip
calculating DEGS for contrast anansesnake_MAIT_average
skip
calculating DEGS for contrast anansesnake_CD8-TEM_average
skip
calculating DEGS for contrast anansesnake_B-naive_average
skip
calculating DEGS for contrast anansesnake_gdT_average
skip
calculating DEGS for contrast anansesnake_pDC_average
```

```
skip
calculating DEGS for contrast anansesnake_HSPC_average
skip
calculating DEGS for contrast anansesnake_B-naive_B-memory
skip
calculating DEGS for contrast anansesnake_B-memory_B-naive
skip
```

After running ANANSNAKE you can import back the results to the scanpy object and visualize a heatmap of the top factors with seaborn

[5]:
```
# Generate a UMAP if not performed already during pre-processing
adata=rna_PBMC
adata.raw = adata
sc.pp.normalize_total(adata, target_sum=1e4)
sc.pp.log1p(adata)
sc.pp.pca(adata)
sc.pp.neighbors(adata, n_neighbors=10, n_pcs=30)
sc.tl.umap(adata)
```

```
WARNING: adata.X seems to be already log-transformed.
```

```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/tqdm/auto.py:22: TqdmWarning: IProgress not found. Please update
jupyter and ipywidgets. See
https://ipywidgets.readthedocs.io/en/stable/user_install.html
  from .autonotebook import tqdm as notebook_tqdm
```

[6]:
```
# Import the Ananse results to the scanpy object and a separate dataframe as␣
 ↪well
df_influence=asc.import_scanpy_scANANSE(anndata=rna_PBMC,cluster_id="predicted.
 ↪id",
                        anansnake_inf_dir="AnanseScanpy_outs/influence/")
```

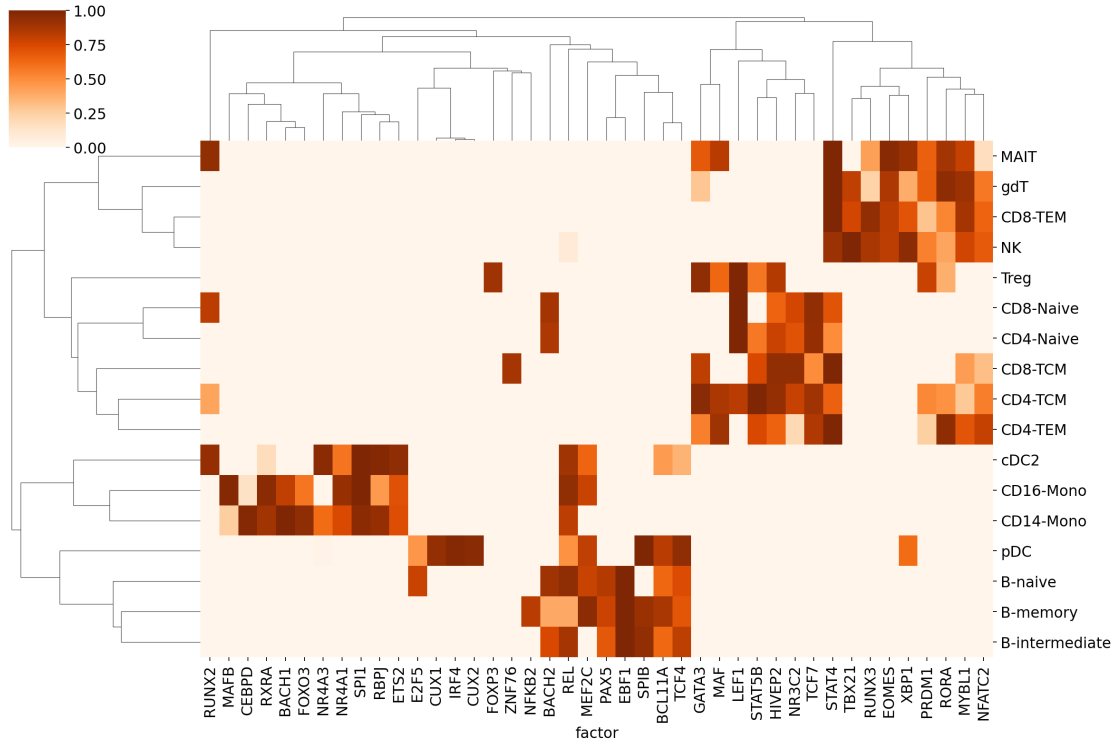
```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/anndata/_core/anndata.py:798: UserWarning:
AnnData expects .obs.index to contain strings, but got values like:
    [0, 1, 2, 3, 4]

    Inferred to be: integer

  value_idx = self._prep_dim_index(value.index, attr)
```

[7]:
```
# Show the top 5 transcription factors for each population
top=5

df_t = df_influence.transpose()
factors_topn = []
for i in df_t:
    df_sub=df_t[i]
    test = df_sub.sort_values(ascending=False)
    print(i,": ",list(test[0:top].index))
    factors_topn.append(list(test[0:top].index))

factors_topn=[j for i in factors_topn for j in i]
factors_topn=set(factors_topn)

selected_df = df_influence[list(factors_topn)]
```

```
cDC2 :  ['SPI1', 'RBPJ', 'NR4A3', 'ETS2', 'RUNX2']
CD8-Naive :  ['LEF1', 'TCF7', 'BACH2', 'RUNX2', 'NR3C2']
B-memory :  ['EBF1', 'MEF2C', 'SPIB', 'BCL11A', 'NFKB2']
B-naive :  ['EBF1', 'REL', 'BACH2', 'PAX5', 'E2F5']
Treg :  ['LEF1', 'GATA3', 'FOXP3', 'HIVEP2', 'PRDM1']
gdT :  ['STAT4', 'RORA', 'MYBL1', 'EOMES', 'TBX21']
CD8-TCM :  ['STAT4', 'NR3C2', 'HIVEP2', 'ZNF76', 'GATA3']
CD16-Mono :  ['SPI1', 'MAFB', 'RXRA', 'REL', 'NR4A1']
CD8-TEM :  ['STAT4', 'RUNX3', 'MYBL1', 'EOMES', 'TBX21']
NK :  ['TBX21', 'XBP1', 'STAT4', 'RUNX3', 'EOMES']
CD4-TCM :  ['STAT5B', 'GATA3', 'HIVEP2', 'TCF7', 'MAF']
MAIT :  ['STAT4', 'EOMES', 'RUNX2', 'XBP1', 'RORA']
CD4-TEM :  ['STAT4', 'RORA', 'MAF', 'TCF7', 'NFATC2']
pDC :  ['SPIB', 'IRF4', 'CUX2', 'TCF4', 'CUX1']
B-intermediate :  ['EBF1', 'SPIB', 'REL', 'TCF4', 'BACH2']
CD14-Mono :  ['BACH1', 'CEBPD', 'SPI1', 'FOXO3', 'RBPJ']
CD4-Naive :  ['LEF1', 'TCF7', 'BACH2', 'HIVEP2', 'NR3C2']
```

[8]:
```
# Plot the heatmap of the top 5
sns.clustermap(selected_df, annot=False, figsize=(15, 10),cmap="Oranges")
```

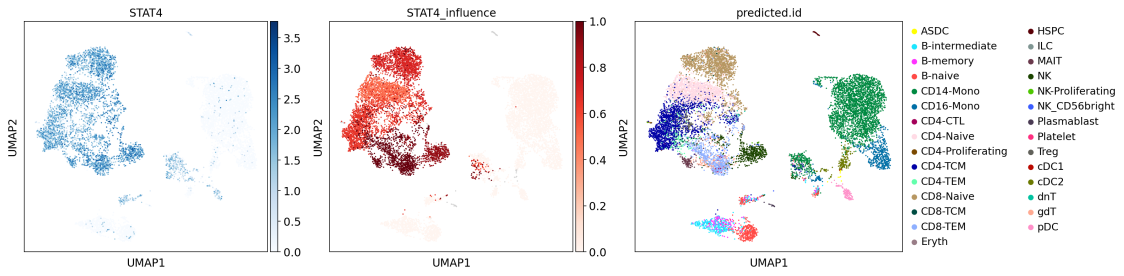
[8]:
```
<seaborn.matrix.ClusterGrid at 0x149eff7439d0>
```

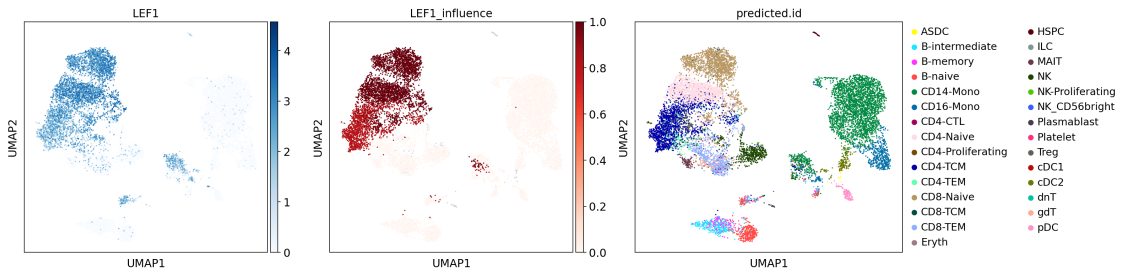


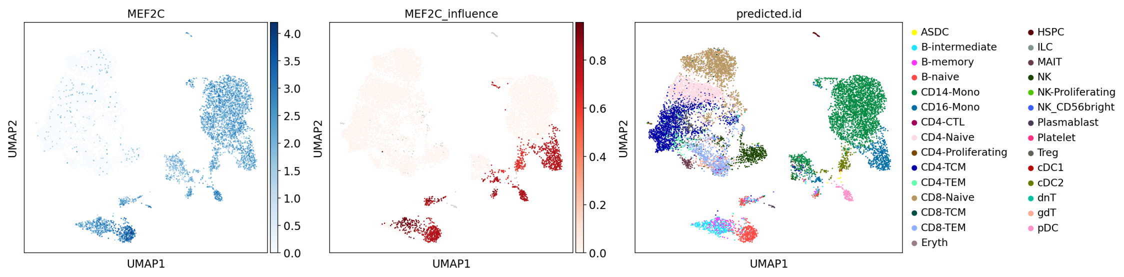
```
[9]: # Plot three TFs of interest upon the UMAP with expression and influence scores
for i in ["STAT4","LEF1","MEF2C"]:
    fig, axs = plt.subplots(1,3, figsize=(20,5))
    sc.pl.umap(adata, color=[i], cmap="Blues",
        show = False,
        ax = axs[0])
    sc.pl.umap(adata, color=[str(i+"_influence")], cmap="Reds",
        show = False,
        ax = axs[1])
    sc.pl.umap(adata, color=["predicted.id"],
        show = False,
        ax = axs[2])
    plt.tight_layout()
```

```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/scanpy/plotting/_tools/scatterplots.py:392: UserWarning: No data for
colormapping provided via 'c'. Parameters 'cmap' will be ignored
  cax = scatter(
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/scanpy/plotting/_tools/scatterplots.py:392: UserWarning: No data for
colormapping provided via 'c'. Parameters 'cmap' will be ignored
  cax = scatter(
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/scanpy/plotting/_tools/scatterplots.py:392: UserWarning: No data for
```

```
colormapping provided via 'c'. Parameters 'cmap' will be ignored
  cax = scatter(
```



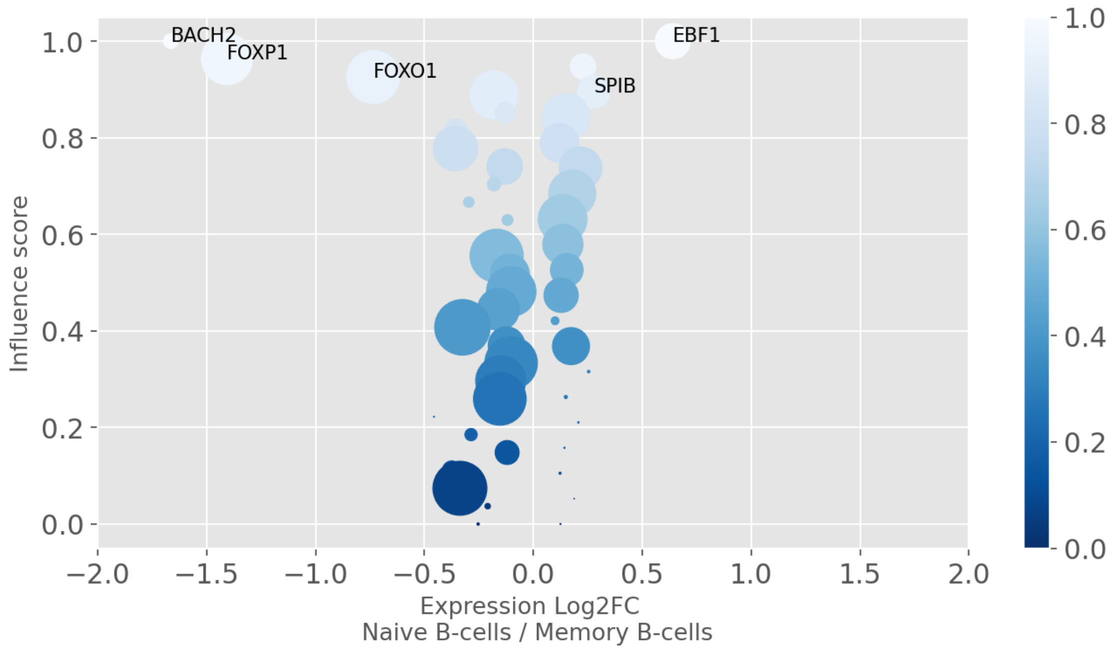




[10]:
```python
# Plot the direct cluster-to-cluster comparison
sc.set_figure_params(figsize=(10, 5))

MemoryInfluence = pd.read_csv('AnanseScanpy_outs/influence/
  ↪anansesnake_B-memory_B-naive.tsv',sep="\t",header=0)
NaiveInfluence = pd.read_csv('AnanseScanpy_outs/influence/
  ↪anansesnake_B-naive_B-memory.tsv',sep="\t",header=0)
NaiveInfluence["factor_fc"] = NaiveInfluence["factor_fc"]* -1
NaiveInfluence

B_comparison = pd.concat([NaiveInfluence,MemoryInfluence])
B_comparison=B_comparison.reset_index()
```

```
B_comparison

plt.style.use("ggplot")
plt.
↪scatter(B_comparison["factor_fc"],B_comparison["influence_score"],s=B_comparison["direct_ta
↪1,c=B_comparison["influence_score"], cmap='Blues_r')

# Naming and adding range to x-axis
plt.xlabel('Expression Log2FC \n Naive B-cells / Memory B-cells')
plt.ylabel('Influence score')
plt.xlim([-2, 2])
plt.colorbar()

# Add annotations
# Select factors with "factor_fc" > 0.26 and "factor_fc" < -0.5
selected_list= [i for i, x in enumerate(list(B_comparison["factor_fc"] > 0.26))␣
↪if x]+[i for i, x in enumerate(list(B_comparison["factor_fc"] < -0.5)) if x]

for i in selected_list:
    plt.annotate(B_comparison["factor"][int(i)],␣
↪(B_comparison["factor_fc"][int(i)], B_comparison["influence_score"][int(i)]))

plt.figure()
```

```
[10]: <Figure size 800x400 with 0 Axes>
```



```
<Figure size 800x400 with 0 Axes>
```

Optional: after running ANANSNAKE you can import back the maelstrom results to the scanpy object

```
[11]: # Import the maelstrom results into the scanpy object
      asc.import_scanpy_maelstrom(anndata=adata,cluster_id="predicted.id",
                                  maelstrom_dir="AnanseScanpy_outs/maelstrom/")
```

```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/anndata/_core/anndata.py:798: UserWarning:
AnnData expects .obs.index to contain strings, but got values like:
    [0, 1, 2, 3, 4]

    Inferred to be: integer

  value_idx = self._prep_dim_index(value.index, attr)
```

```
[12]: # Make a dataframe with the values per cluster from the scanpy object, like␣
      ↪df_mael above:
      df_maelstrom = asc.per_cluster_df(anndata=adata,assay="maelstrom",cluster_id =␣
      ↪"predicted.id")
      df_maelstrom.head()
```

```
[12]:            GM.5.0.GATA.0029_maelstrom  GM.5.0.T-box.0010_maelstrom  \
      CD4-Naive                    -3.158720                     0.987206
      CD4-TCM                      -2.779715                     1.403722
      CD8-Naive                    -3.666792                     0.658251
      CD16-Mono                     4.178187                    -1.309968
      NK                           -2.281777                     2.757341

                 GM.5.0.RFX.0007_maelstrom  GM.5.0.GATA.0018_maelstrom  \
      CD4-Naive                  -2.277142                   -2.157599
      CD4-TCM                    -1.754961                   -0.619564
      CD8-Naive                  -0.741593                   -0.943449
      CD16-Mono                   0.798259                    0.898081
      NK                         -0.058953                   -0.268780

                 GM.5.0.Homeodomain.0112_maelstrom  GM.5.0.C2H2_ZF.0240_maelstrom  \
      CD4-Naive                           0.899880                      -1.159911
      CD4-TCM                             0.363578                      -1.250483
      CD8-Naive                           0.527284                      -0.329431
      CD16-Mono                          -0.401259                      -1.429248
      NK                                 -0.263754                       3.122363

                 GM.5.0.C2H2_ZF.0081_maelstrom  GM.5.0.C2H2_ZF.0209_maelstrom  \
      CD4-Naive                      -1.746293                      -0.719396
      CD4-TCM                        -1.536671                       0.403295
```

```
CD8-Naive                          -0.719806                          -0.093785
CD16-Mono                           0.410906                           0.241499
NK                                  2.424381                          -1.519505

           GM.5.0.Unknown.0070_maelstrom  GM.5.0.C2H2_ZF.0003_maelstrom  …  \
CD4-Naive                           0.212972                           0.890589  …
CD4-TCM                             1.653069                           0.760212  …
CD8-Naive                           0.230939                          -0.407383  …
CD16-Mono                          -0.418713                          -0.746905  …
NK                                 -0.159066                          -0.230792  …

           GM.5.0.Homeodomain.0178_maelstrom  GM.5.0.C2H2_ZF.0024_maelstrom  \
CD4-Naive                               1.479400                       4.803352
CD4-TCM                                 0.604511                       5.277779
CD8-Naive                               1.216132                       4.953860
CD16-Mono                              -0.080583                      -4.045632
NK                                      0.173359                      -1.550070

           GM.5.0.C2H2_ZF.0149_maelstrom  GM.5.0.GATA.0004_maelstrom  \
CD4-Naive                          -0.168118                    2.045893
CD4-TCM                            -0.296064                    2.900595
CD8-Naive                          -0.612817                    1.811724
CD16-Mono                           1.540182                   -2.799684
NK                                  0.102610                    1.737805

           GM.5.0.Homeodomain.0119_maelstrom  \
CD4-Naive                               0.757803
CD4-TCM                                 0.326848
CD8-Naive                               2.425492
CD16-Mono                              -0.703423
NK                                     -1.272585

           GM.5.0.Homeodomain.0142_maelstrom  GM.5.0.C2H2_ZF.0259_maelstrom  \
CD4-Naive                               0.819696                       0.075058
CD4-TCM                                 1.297546                       0.713357
CD8-Naive                               1.613827                       1.050873
CD16-Mono                               0.506031                      -0.637716
NK                                     -0.620623                      -0.124345

           GM.5.0.Unknown.0191_maelstrom  GM.5.0.Mixed.0080_maelstrom  \
CD4-Naive                          -2.712276                     1.193752
CD4-TCM                            -0.849734                     0.984331
CD8-Naive                          -2.125865                     0.258764
CD16-Mono                           1.222093                    -0.247124
NK                                 -0.011337                     0.930425

           GM.5.0.Unknown.0124_maelstrom
```

```
CD4-Naive                     -0.678583
CD4-TCM                       -2.323999
CD8-Naive                     -0.404407
CD16-Mono                      1.905879
NK                            -0.624942

[5 rows x 245 columns]
```

[13]:
```
# Link motifs to transcription factors specified with "combine_motifs"␣
  ↪parameter.
# Here, the maximum correlation of all motifs will be used (other options␣
  ↪include: max_var and max_cor; see help)

adata=asc.Maelstrom_Motif2TF(anndata=adata,
                     cluster_id = 'predicted.id',
                     maelstrom_dir= "AnanseScanpy_outs/maelstrom/
  ↪",combine_motifs="max_cor",
                      save_output= True
)

# Note: if you already have a dataframe from maelstrom as input, the function␣
  ↪will run faster
```

```
loading maelstrom values from maelstrom assay using the cluster identifier
predicted.id
```

```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/anndata/_core/raw.py:139: FutureWarning: X.dtype being converted to
np.float32 from float64. In the next version of anndata (0.9) conversion will
not be automatic. Pass dtype explicitly to avoid this warning. Pass `AnnData(X,
dtype=X.dtype, …)` to get the future behaviour.
  return anndata.AnnData(
```

```
Seurat NormalizeData with default settings will be run on all the genes
Only keep motif-TF combinations with an R > 0.3
total length m2f_df_unique 625
Selecting correlating TFs
total m2f: 343
Motif best (absolute)correlated to expression is selected per TF
Selecting anticorrelating TFs
total m2f: 282
Motif best (absolute)correlated to expression is selected per TF
```

```
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/anndata/_core/anndata.py:798: UserWarning:
AnnData expects .obs.index to contain strings, but got values like:
    [0, 1, 2, 3, 4]

    Inferred to be: integer
```

```
  value_idx = self._prep_dim_index(value.index, attr)
/vol/mbconda/julian/envs/AnanseScanpy/lib/python3.10/site-
packages/anndata/_core/anndata.py:798: UserWarning:
AnnData expects .obs.index to contain strings, but got values like:
    [0, 1, 2, 3, 4]

    Inferred to be: integer

  value_idx = self._prep_dim_index(value.index, attr)
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packages/anndata/_core/anndata.py:798: UserWarning:
AnnData expects .obs.index to contain strings, but got values like:
    [0, 1, 2, 3, 4]

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packages/anndata/_core/anndata.py:798: UserWarning:
AnnData expects .obs.index to contain strings, but got values like:
    [0, 1, 2, 3, 4]

    Inferred to be: integer

  value_idx = self._prep_dim_index(value.index, attr)
```
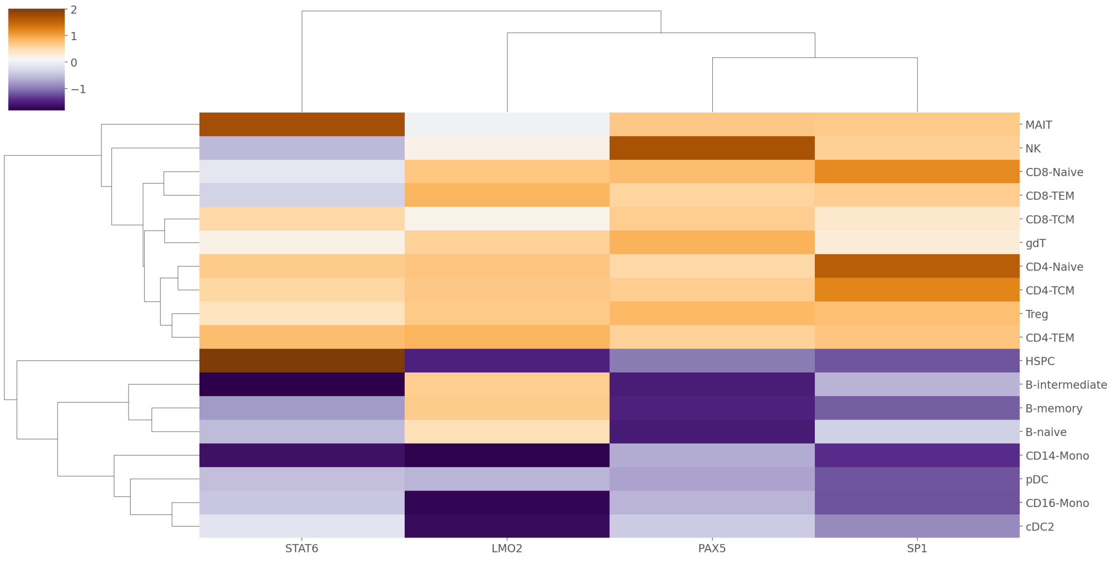
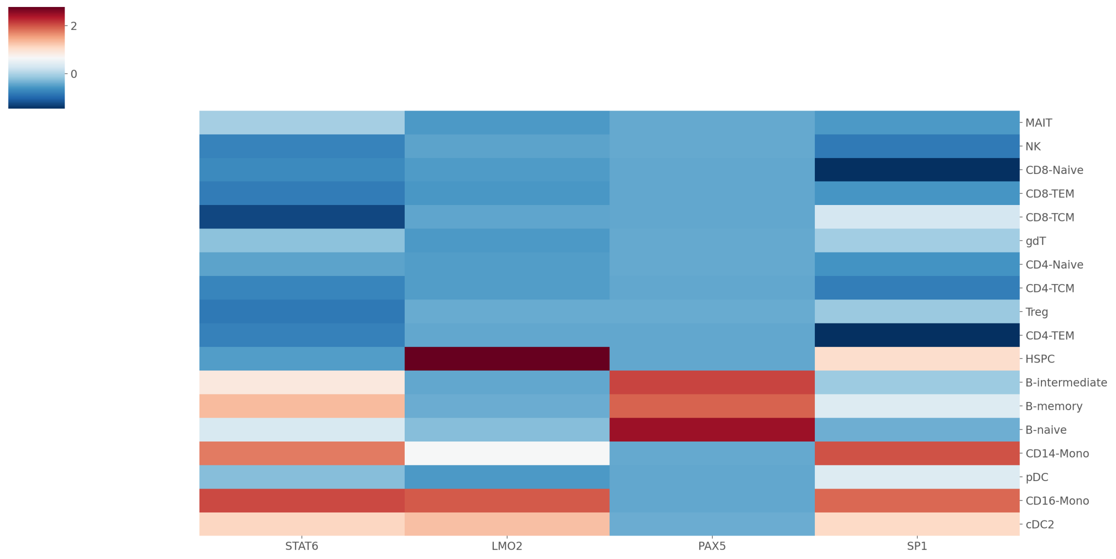

[14]:
```
# Plotting the motif score heatmaps and the relative expression of top negative␣
 ↪correlating motifs
df_anticor = asc.
 ↪per_cluster_df(anndata=adata,assay="TFanticor_score",cluster_id = "predicted.
 ↪id")

# Take a number of factors of interest or otherwise a top n factors:
factors_topn = ["PAX5","STAT6","LMO2","SP1"]
factors_topn2=[str(s) + '_TFanticor_score' for s in factors_topn]
selected_df=df_anticor[factors_topn2]
selected_df.columns = (s.removesuffix("_TFanticor_score") for s in selected_df.
 ↪columns)

df_expression = asc.
 ↪per_cluster_df(anndata=adata,assay="TFanticor_expression_score",cluster_id =␣
 ↪"predicted.id")

factors_topn3=[str(s) + '_TFanticor_expression_score' for s in factors_topn]

selected_df2 = df_expression[factors_topn3]
```

```
# Remove assay suffixes from scanpy objects
selected_df2.columns = (s.removesuffix("_TFanticor_expression_score") for s in␣
↪selected_df2.columns)

# Plot the relative motif score map
res=sns.clustermap(selected_df, annot=False, figsize=(20, 10),cmap="PuOr_r")

# reorder heatmaps according to the other one above
selected_df2=selected_df2[list(selected_df.columns[res.dendrogram_col.
↪reordered_ind])]
selected_df2=selected_df2.reindex(list(selected_df.index[res.dendrogram_row.
↪reordered_ind]))

# Plot the relative expression score map
sns.clustermap(selected_df2, annot=False, figsize=(20,␣
↪10),col_cluster=False,row_cluster=False,cmap="RdBu_r")

# Note: the ETS1 motif shows high repression score for CD8 like cell types,␣
↪like on the UMAP above

# Note: PAX5 is an important repressive factor in B-cells, also indiciated in␣
↪our heatmap
# Source: Delogu A, Schebesta A, Sun Q, Aschenbrenner K, Perlot T, Busslinger M.
↪
# Gene repression by Pax5 in B cells is essential for blood cell homeostasis␣
↪and is reversed in plasma cells.
# Immunity. 2006 Mar;24(3):269-81. doi: 10.1016/j.immuni.2006.01.012. PMID:␣
↪16546096
```

```
[14]: <seaborn.matrix.ClusterGrid at 0x149efaecee90>
```



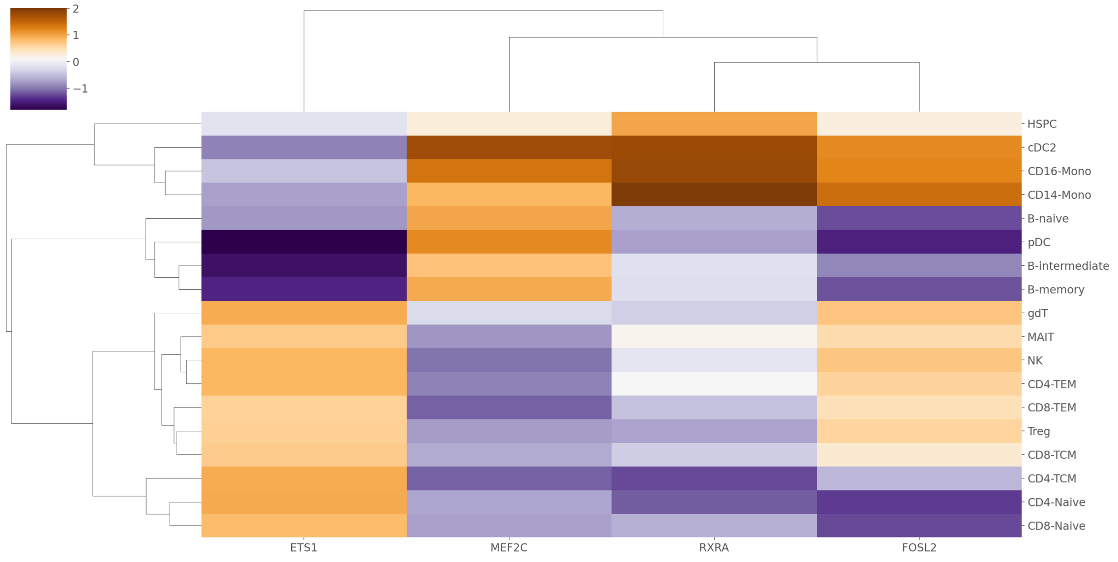


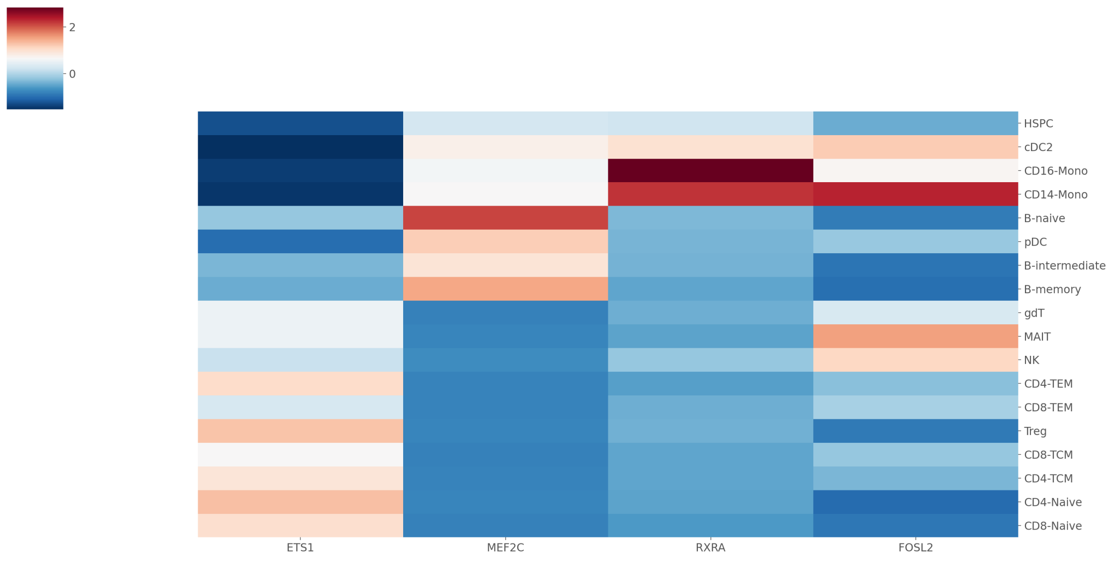
[15]:
```
# Plotting the motif score heatmaps and the relative expression of top positive␣
↪correlating motifs
df_cor = asc.per_cluster_df(anndata=adata,assay="TFcor_score",cluster_id =␣
↪"predicted.id")

# Take a number of factors of interest or otherwise a top n factors:
factors_topn = ["MEF2C","ETS1","RXRA","FOSL2"]
factors_topn2=[str(s) + '_TFcor_score' for s in factors_topn]
selected_df=df_cor[factors_topn2]
```

```
selected_df.columns = (s.removesuffix("_TFcor_score") for s in selected_df.
  ↪columns)

df_expression = asc.
  ↪per_cluster_df(anndata=adata,assay="TFcor_expression_score",cluster_id =␣
  ↪"predicted.id")

factors_topn3=[str(s) + '_TFcor_expression_score' for s in factors_topn]

selected_df2 = df_expression[factors_topn3]

# Remove assay suffixes from scanpy objects
selected_df2.columns = (s.removesuffix("_TFcor_expression_score") for s in␣
  ↪selected_df2.columns)

# Plot the relative motif score map
res=sns.clustermap(selected_df, annot=False, figsize=(20, 10),cmap="PuOr_r")

# reorder heatmaps according to the other one above
selected_df2=selected_df2[list(selected_df.columns[res.dendrogram_col.
  ↪reordered_ind])]
selected_df2=selected_df2.reindex(list(selected_df.index[res.dendrogram_row.
  ↪reordered_ind]))

# Plot the relative expression score map
sns.clustermap(selected_df2, annot=False, figsize=(20,␣
  ↪10),col_cluster=False,row_cluster=False,cmap="RdBu_r")
```

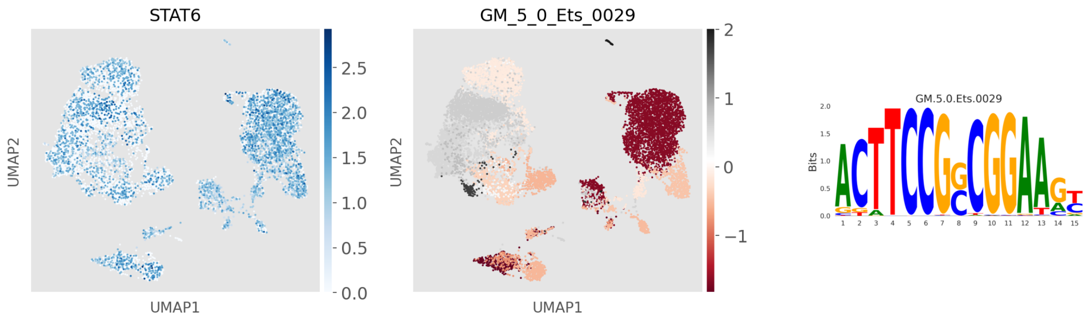
[15]:

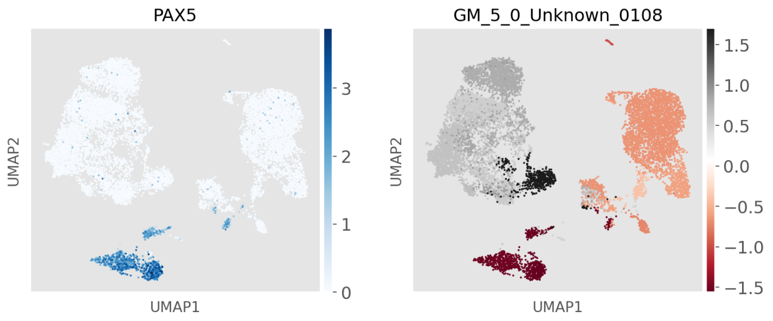
```
<seaborn.matrix.ClusterGrid at 0x149effc030d0>
```

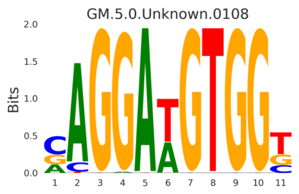




[16]:
```
# Showing the negative correlating factors of interest with "max_cor" as the␣
↪default "combine_motifs" parameter

TF_list = ["STAT6","PAX5"]
asc.Factor_Motif_Plot(adata,factor_list=TF_list,logo_dir='AnanseScanpy_outs/
↪maelstrom/logos/',assay_maelstrom = 'TFanticor')
```




PAX5
UMAP2
UMAP1
0
1
2
3
GM_5_0_Unknown_0108
UMAP2
UMAP1
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5


GM.5.0.Unknown.0108
Bits
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11