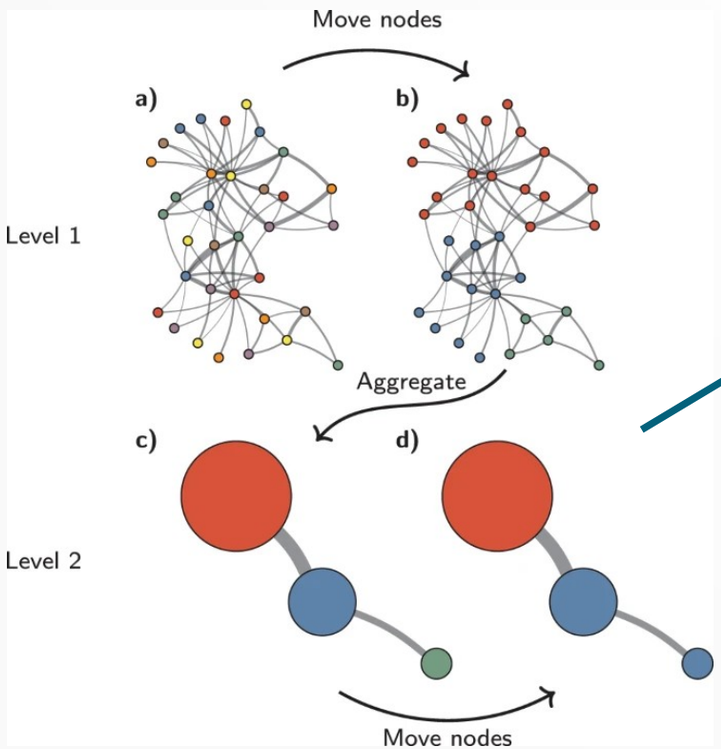
Visium D2-MDX

06/11/2023

Clustering vs Scoring

Louvain Clustering



https://doi.org/10.1038/s41598-019-41695-z

Optimize modularity in a similarity graph

UCell Scoring

$$U'_j = 1 - \frac{U_j - \sum_{i=1}^{n} r'_{ij} - \frac{n(n+1)}{2}}{n \cdot r_{max}}$$

Nonparametric test of the null hypothesis between groups' distribution

Ranking genes about gene expression measurements

Differences ?

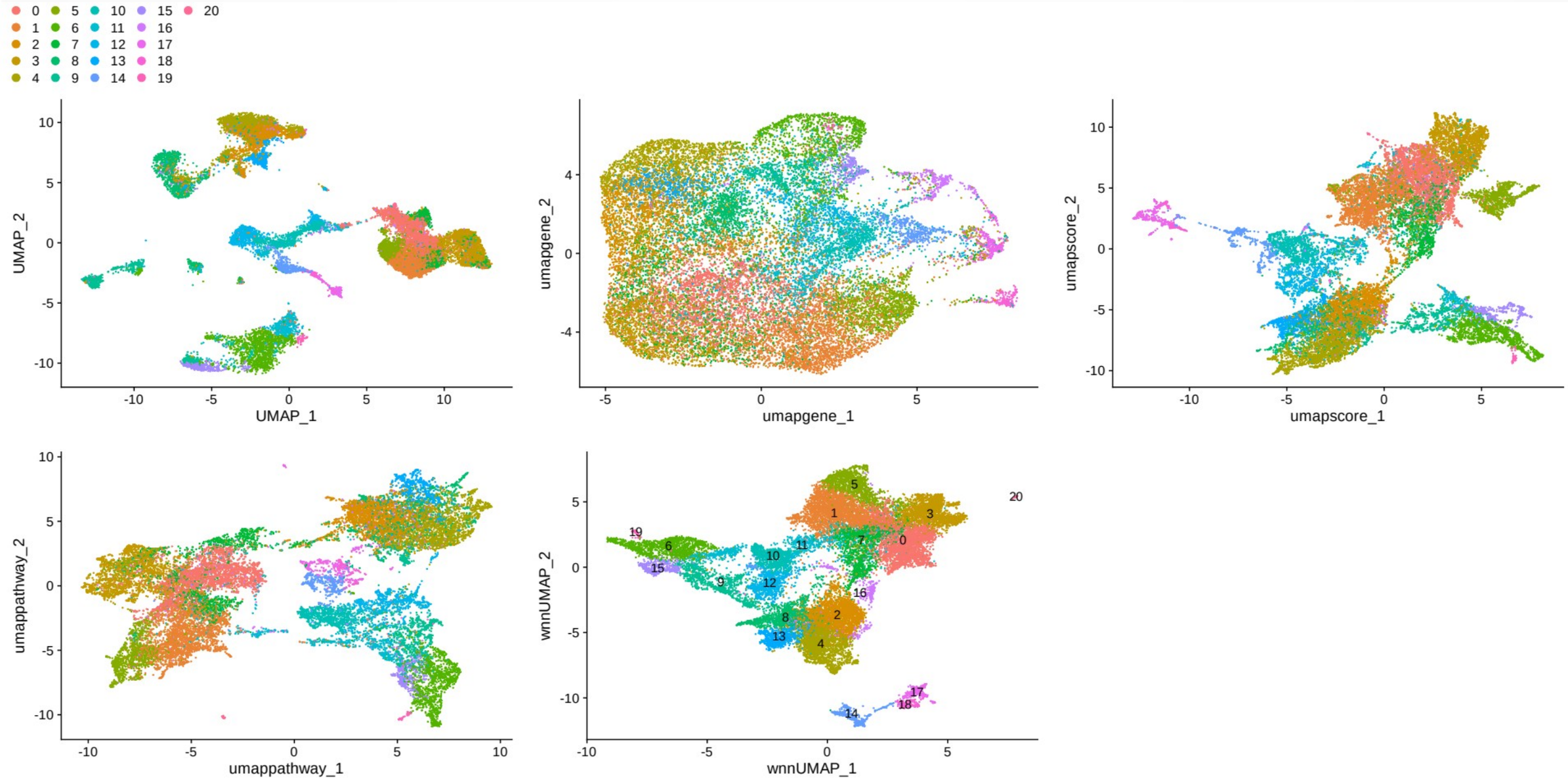
- Similarity between transcriptomics profils VS Difference transcriptomics profils on a selection of features
- Dependant to condition of experiment
- Sometimes : good correlation if features for the scoring are refined

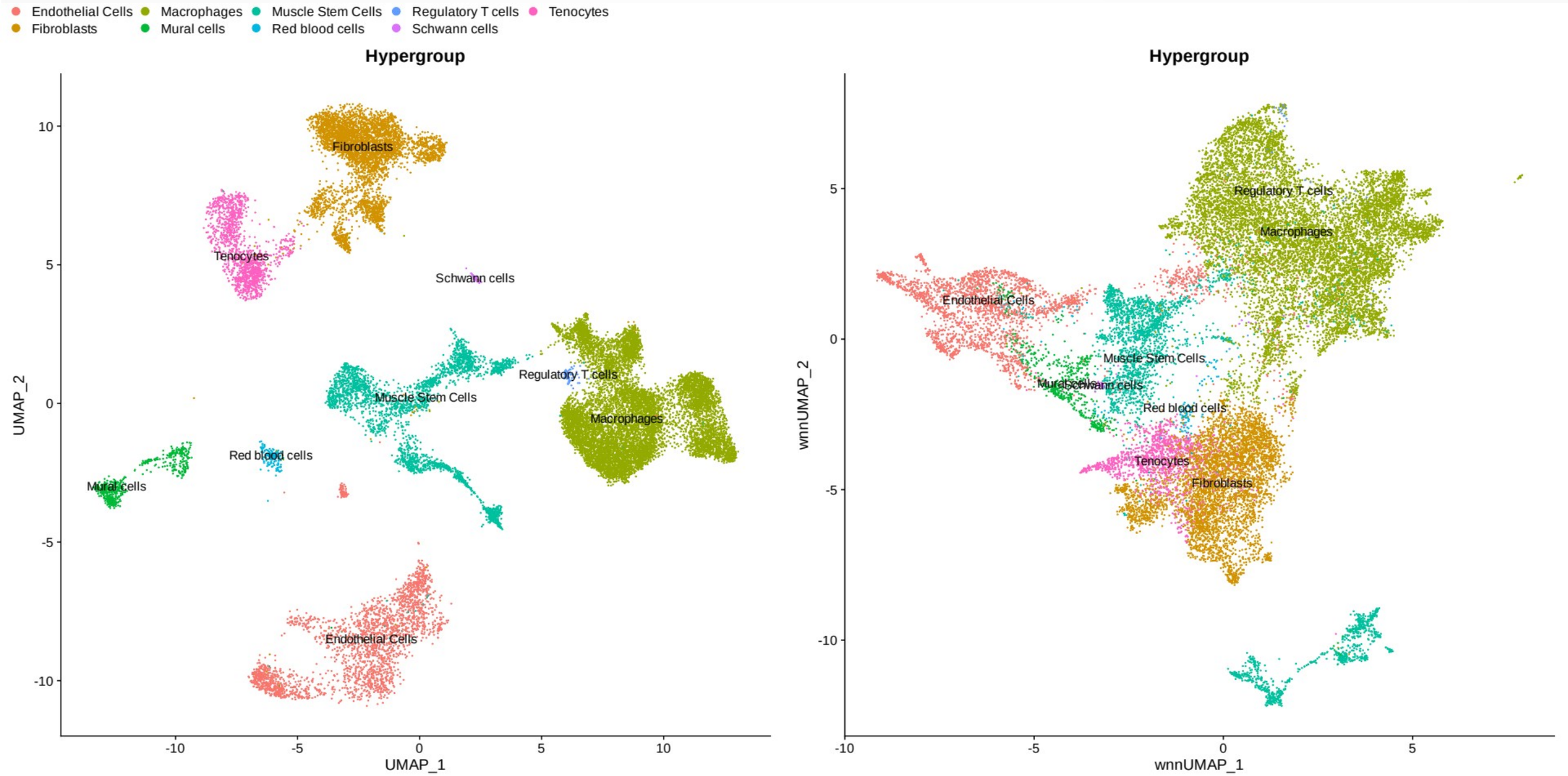
MultiModal Neighbors

- Modalities in single cell : RNA, ATAC, etc.
- Calculate Modalities Weights
- Create a new graph of nearest neighbors based on a weighted combination of two or more modalities

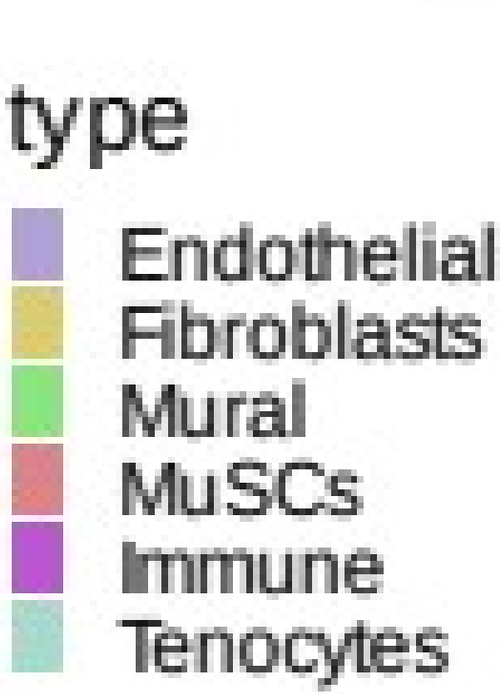
MultiModal Neighbors

- Alternative modality : response to a score from genelist.
- Use GO:BP & GO:MF, use best genelist score refined
- Isolate functionnal & gene expression clusters

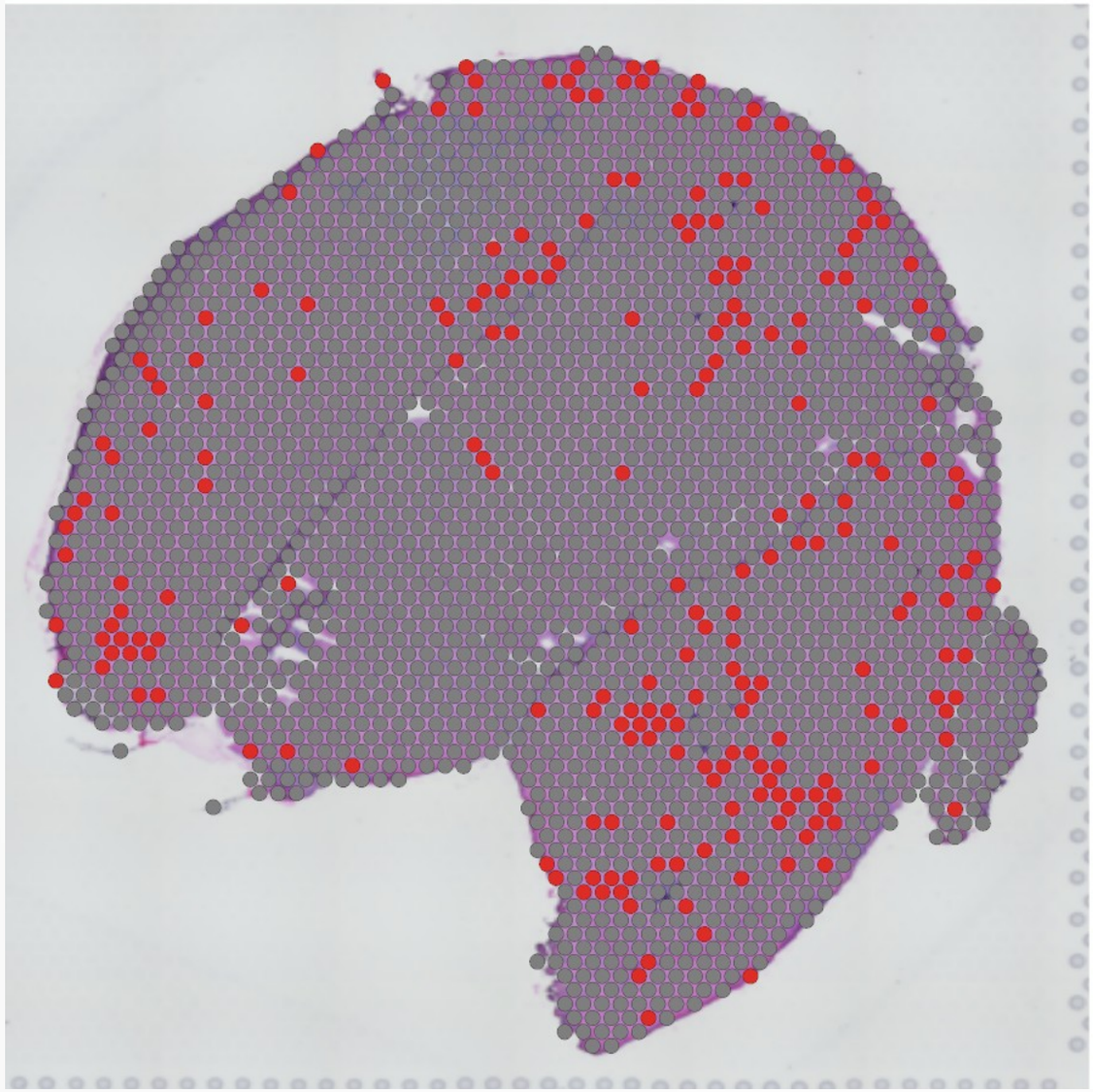

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
UMAP_2
UMAP_1
umapgene_2
umapgene_1
umapscore_2
umapscore_1
umappathway_2
umappathway_1
wnnUMAP_2
wnnUMAP_1


Endothelial Cells
Fibroblasts
Macrophages
Mural cells
Muscle Stem Cells
Red blood cells
Regulatory T cells
Schwann cells
Tenocytes
Hypergroup
UMAP_1
UMAP_2
wnnUMAP_1
wnnUMAP_2

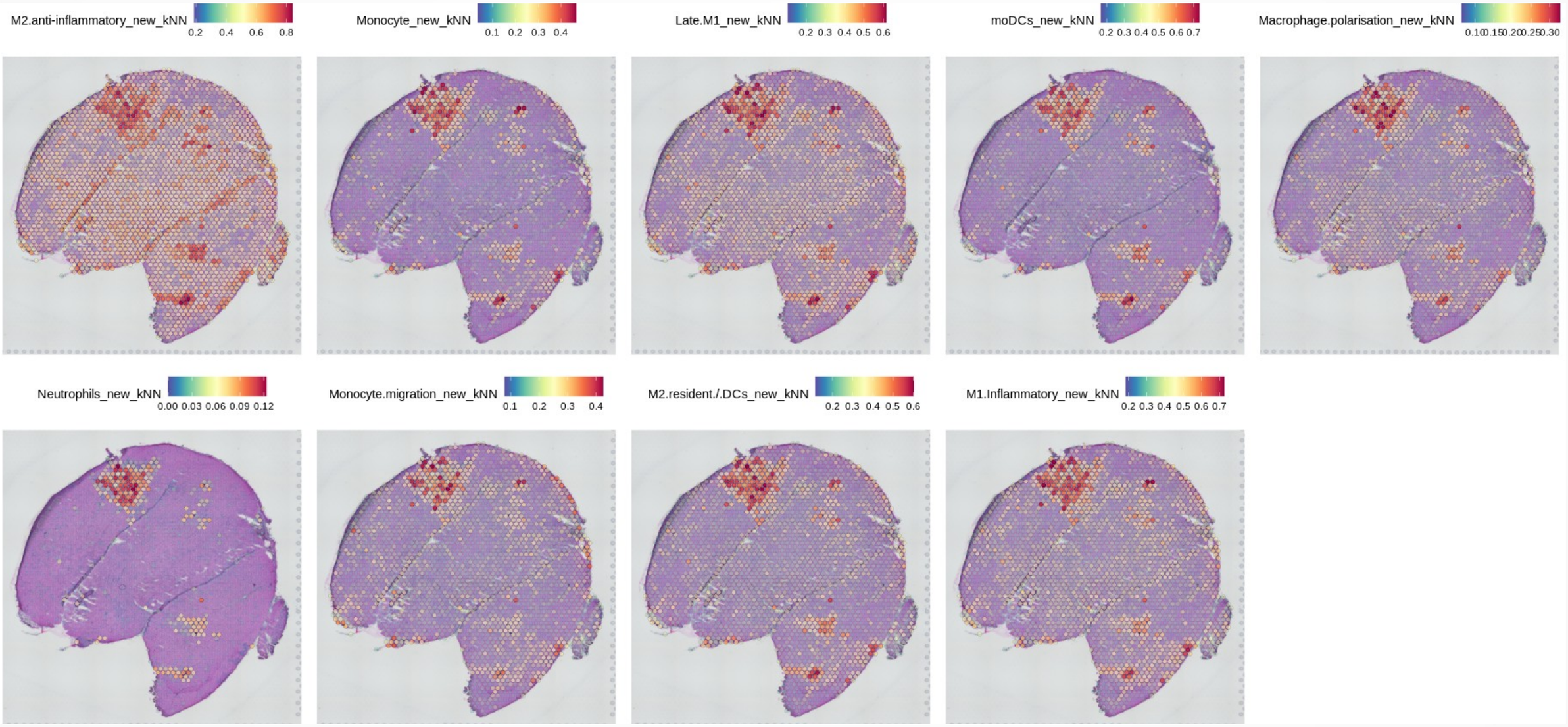
Application on Visium

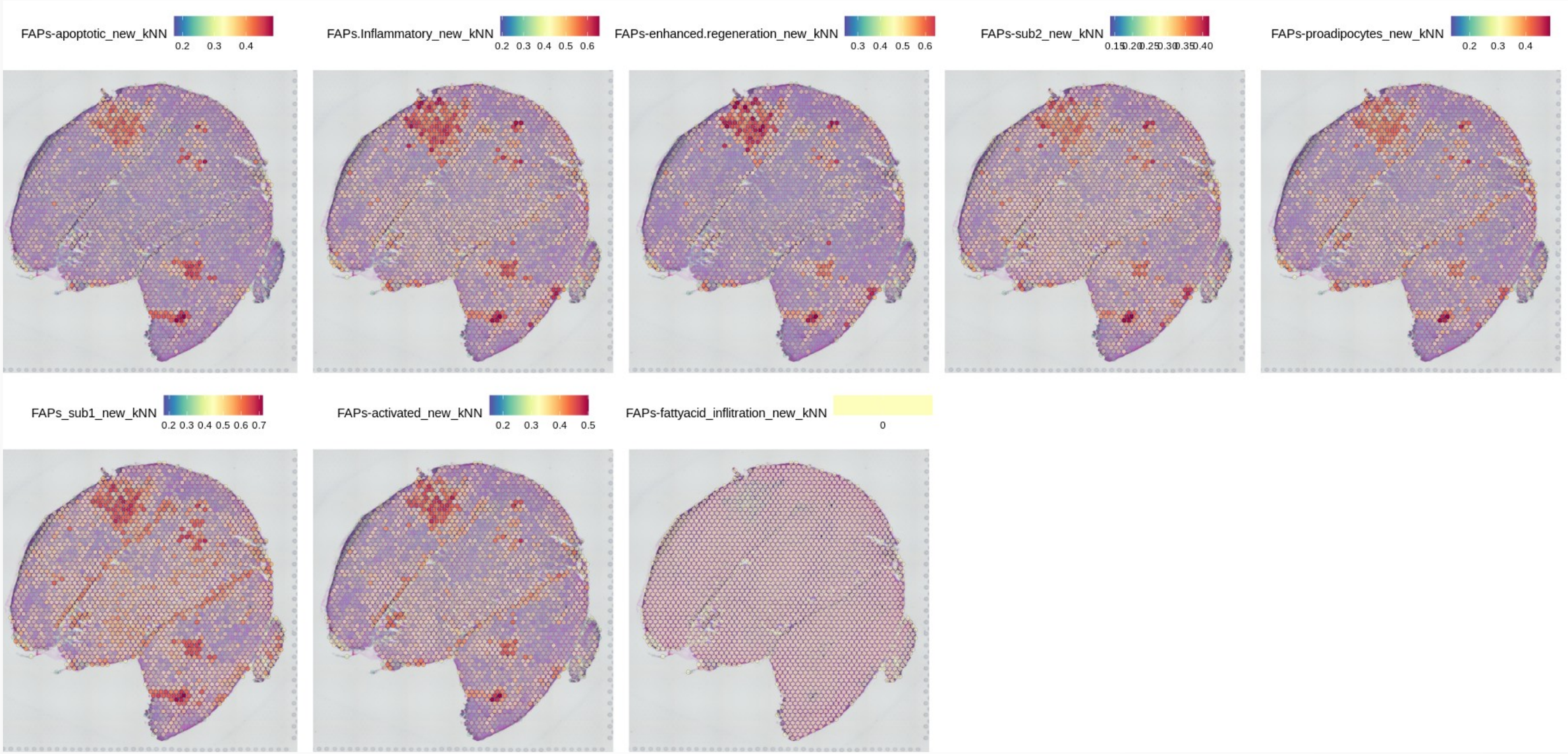


2

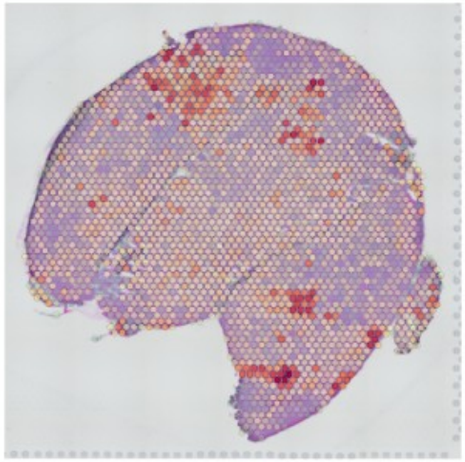


3

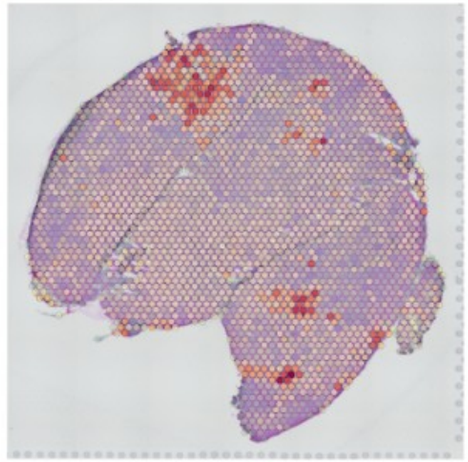

M2.anti-inflammatory_new_kNN
0.2 0.4 0.6 0.8
Monocyte_new_kNN
0.1 0.2 0.3 0.4
Late.M1_new_kNN
0.2 0.3 0.4 0.5 0.6
moDCs_new_kNN
0.2 0.3 0.4 0.5 0.6 0.7
Macrophage.polarisation_new_kNN
0.10 0.15 0.20 0.25 0.30
Neutrophils_new_kNN
0.00 0.03 0.06 0.09 0.12
Monocyte.migration_new_kNN
0.1 0.2 0.3 0.4
M2.resident./.DCs_new_kNN
0.2 0.3 0.4 0.5 0.6
M1.Inflammatory_new_kNN
0.2 0.3 0.4 0.5 0.6 0.7


FAPs-apoptotic_new_kNN
0.2 0.3 0.4
FAPs.Inflammatory_new_kNN
0.2 0.3 0.4 0.5 0.6
FAPs-enhanced.regeneration_new_kNN
0.3 0.4 0.5 0.6
FAPs-sub2_new_kNN
0.15 0.20 0.25 0.30 0.35 0.40
FAPs-proadipocytes_new_kNN
0.2 0.3 0.4
FAPs_sub1_new_kNN
0.2 0.3 0.4 0.5 0.6 0.7
FAPs-activated_new_kNN
0.2 0.3 0.4 0.5
FAPs-fattyacid_inflitration_new_kNN
0

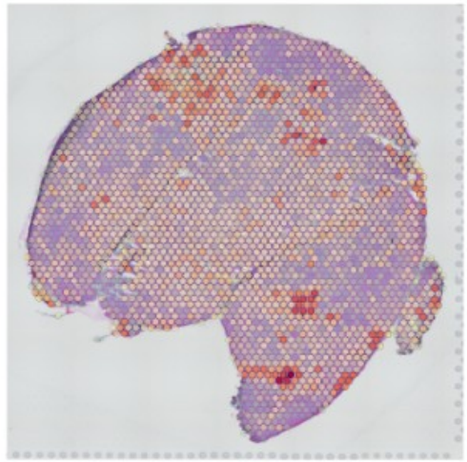
EC.migration.leucocyte_new_kNN 0.2 0.3 0.4 0.5



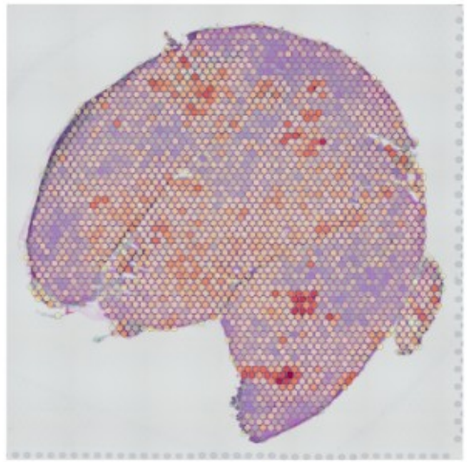
EC.angiogenesis_new_kNN 0.200.250.300.350.40



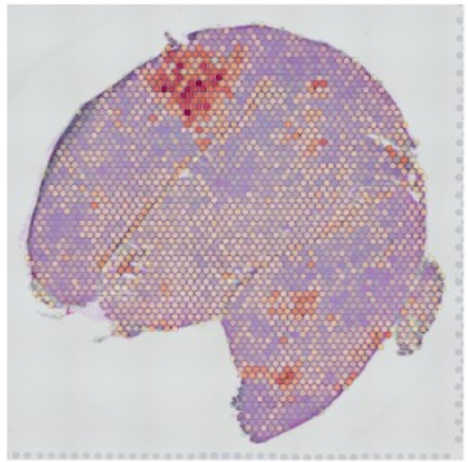
EC.ECM_new_kNN 0.2 0.3 0.4



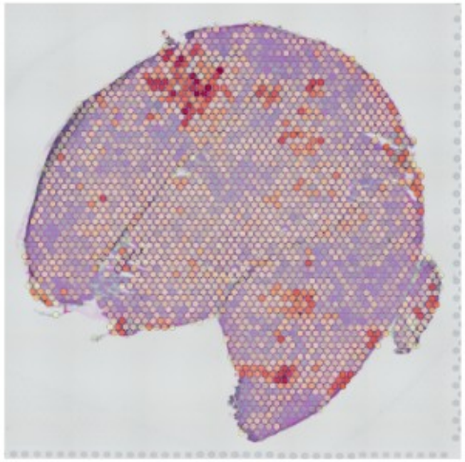
EC.stimulation.inflammation_new_kNN 0.080.120.160.200.24



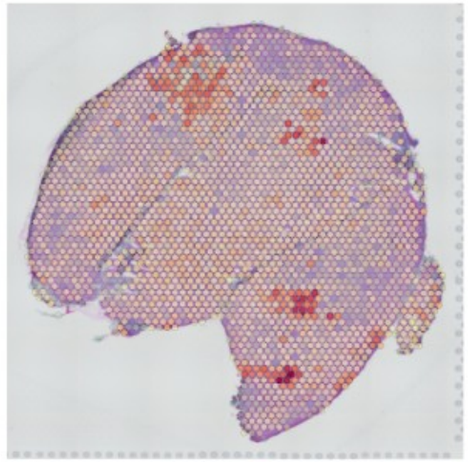
EC.sprouting.angiogenesis_new_kNN 0.05 0.10 0.15 0.2

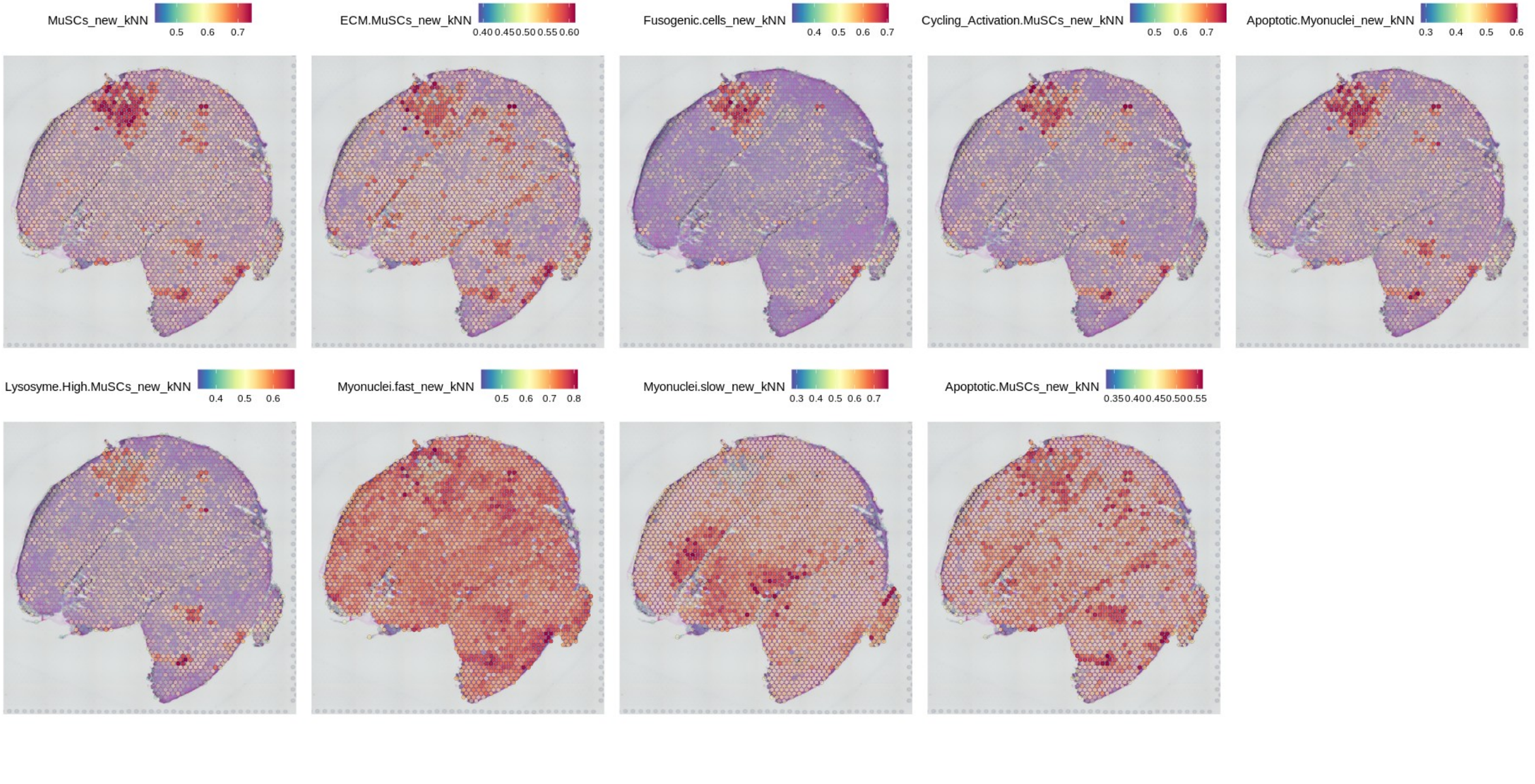


EC.chimiotactism_new_kNN 0.2 0.3 0.4 0.5



EC.stress.ROS_new_kNN 0.300.350.400.45




MuSCs_new_kNN
0.5 0.6 0.7
ECM.MuSCs_new_kNN
0.40 0.45 0.50 0.55 0.60
Fusogenic.cells_new_kNN
0.4 0.5 0.6 0.7
Cycling_Activation.MuSCs_new_kNN
0.5 0.6 0.7
Apoptotic.Myonuclei_new_kNN
0.3 0.4 0.5 0.6
Lysosyme.High.MuSCs_new_kNN
0.4 0.5 0.6
Myonuclei.fast_new_kNN
0.5 0.6 0.7 0.8
Myonuclei.slow_new_kNN
0.3 0.4 0.5 0.6 0.7
Apoptotic.MuSCs_new_kNN
0.35 0.40 0.45 0.50 0.55

Perspective

- Spatial Trajectories : https://themilolab.github.io/SPATA2/articles/spata-v2-spatial-trajectories.html
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