Unsupervised detection of cellular domains from spatial gene expression signatures by spage2vec

Gabriele Partel[1], Carolina Wählby[1]

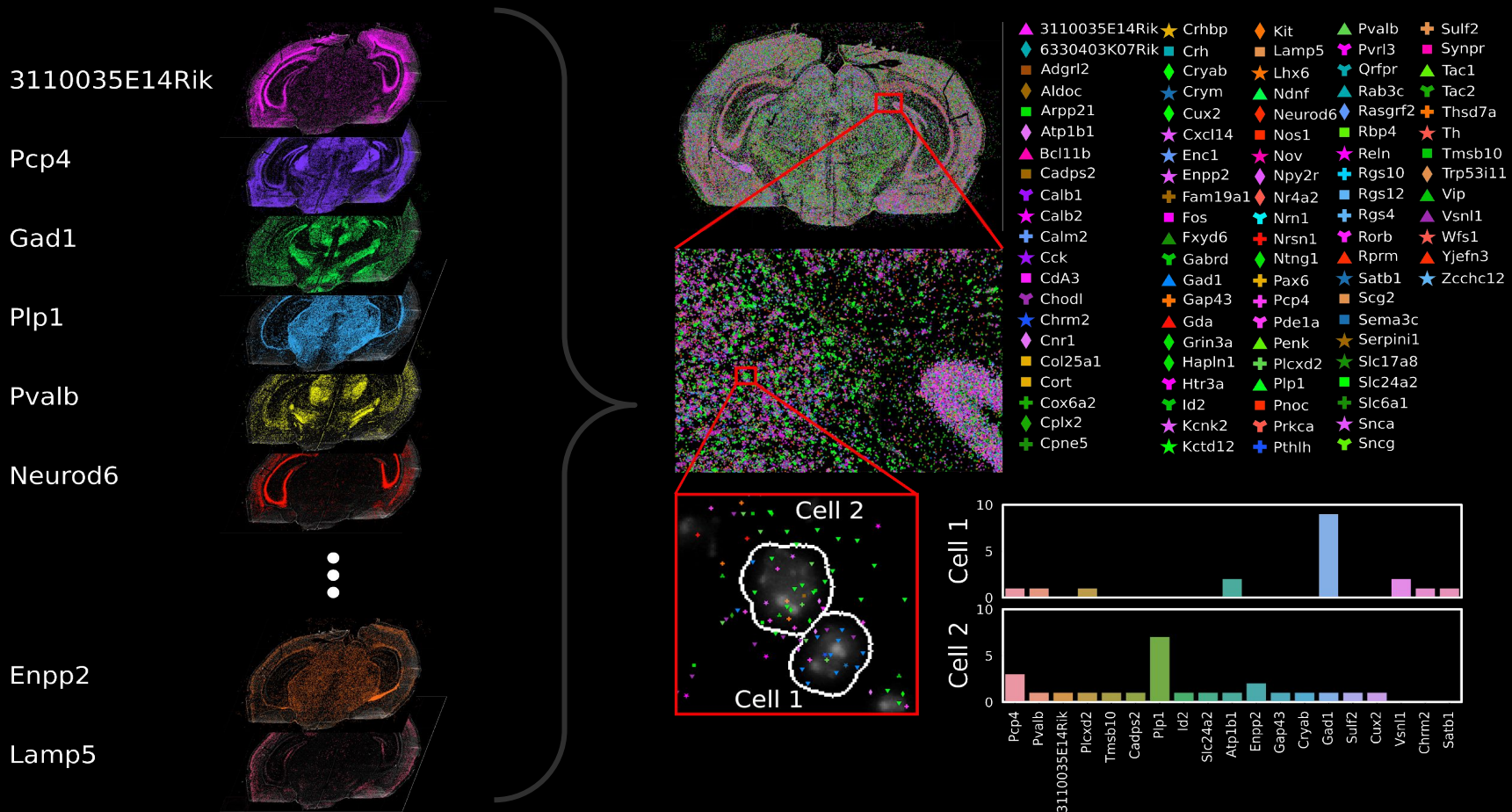[1] Division of Visual Information and Interaction, Department of Information Technology, and SciLifeLab, Uppsala University, Uppsala, Sweden
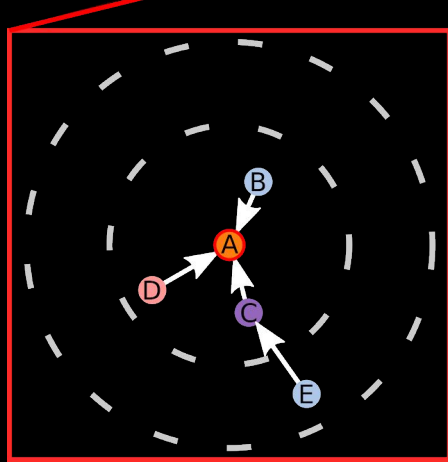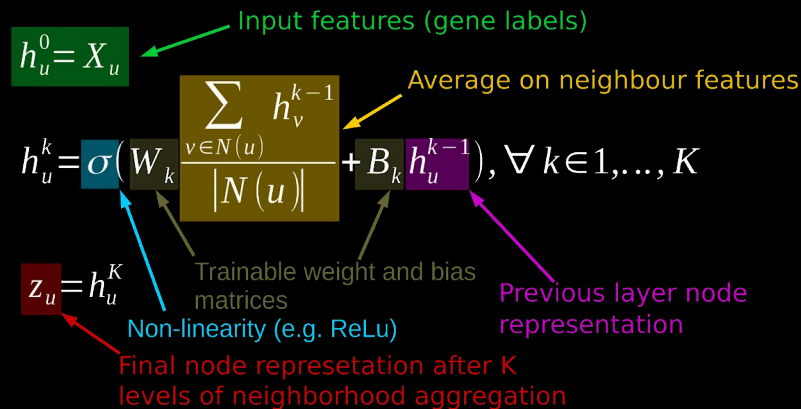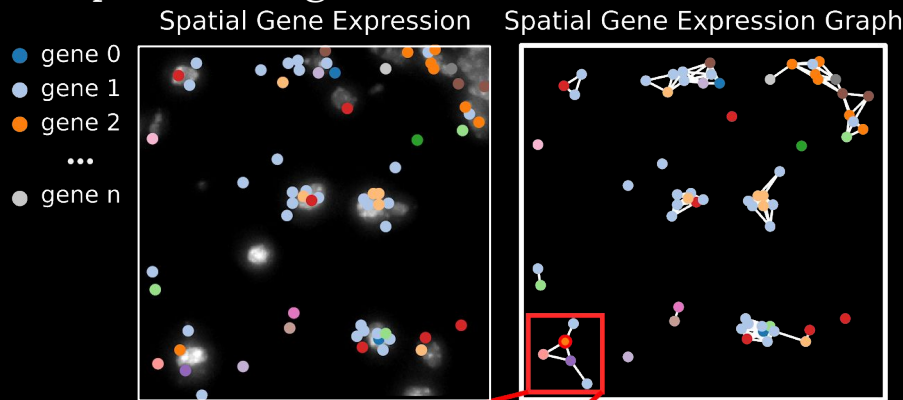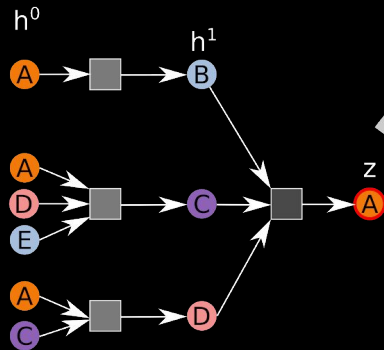
@gapartel

gabriele.partel@it.uu.se

Spatially resolved transcriptomics map the expression of targeted genes in preserved tissue samples

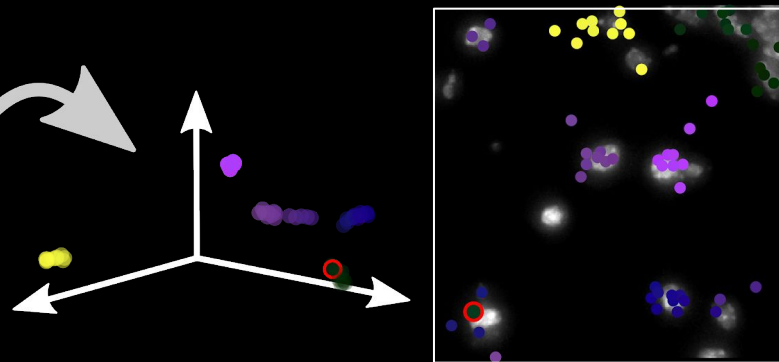# Spage2vec creates an unsupervised concise representation of localized spatial gene expression signatures

Spatial Gene Expression

Spatial Gene Expression Graph

gene 0
gene 1
gene 2
...
gene n

Input features (gene labels)

$$h_u^0 = X_u$$

Average on neighbour features

$$h_u^k = \sigma\left(W_k \frac{\sum_{v \in N(u)} h_v^{k-1}}{|N(u)|} + B_k h_u^{k-1}\right), \forall\, k \in 1, \ldots, K$$

$$z_u = h_u^K$$

Trainable weight and bias matrices

Non-linearity (e.g. ReLu)

Previous layer node representation

Final node represetation after K levels of neighborhood aggregation

Local gene expression aggregation from node's neighborhood
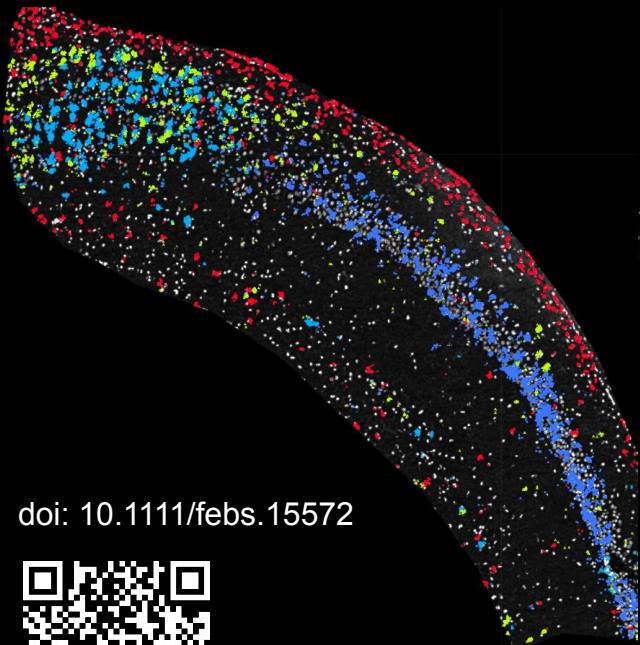
h^0

h^1

z

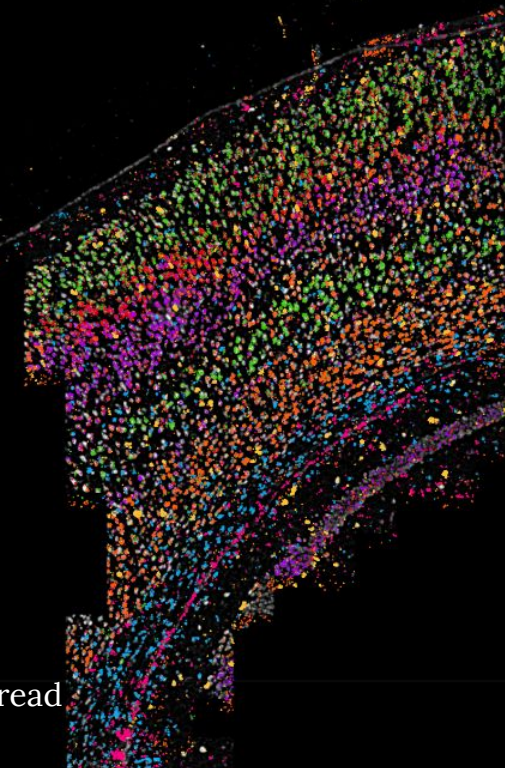Spage2vec representation of spatial gene expression

Spage2vec representation of the spatial gene expression can be used to identify cell-type signatures by clustering analysis
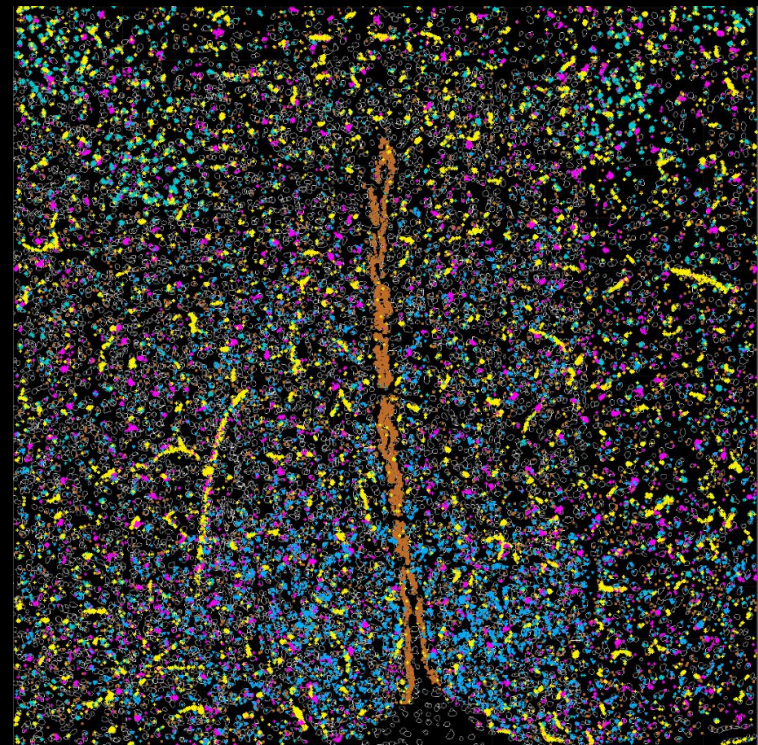
ISS - Qian et al. (2019)

osmFISH - Codeluppi et al. (2018)

MERFISH - Moffitt et al. (2018)

Explore by yourself or read the publication!