Model A: RNA to situ relationship

Identify location based on maximal convolution between the RNA-seq data and in-situ data (similar to the max(MCC) approach but relying on more RNA-seq genes).

Requires checking 3039 options for locations for each cell.

Model B: Spatial location approximation

Dimension reduction of the geometry data using manifold learning.

(x,y,z)->(a,b)->reconstruction (x,y,z)

Then learn a model

b.csv + d.csv -> (a,b)

Model C: Combining the two models.