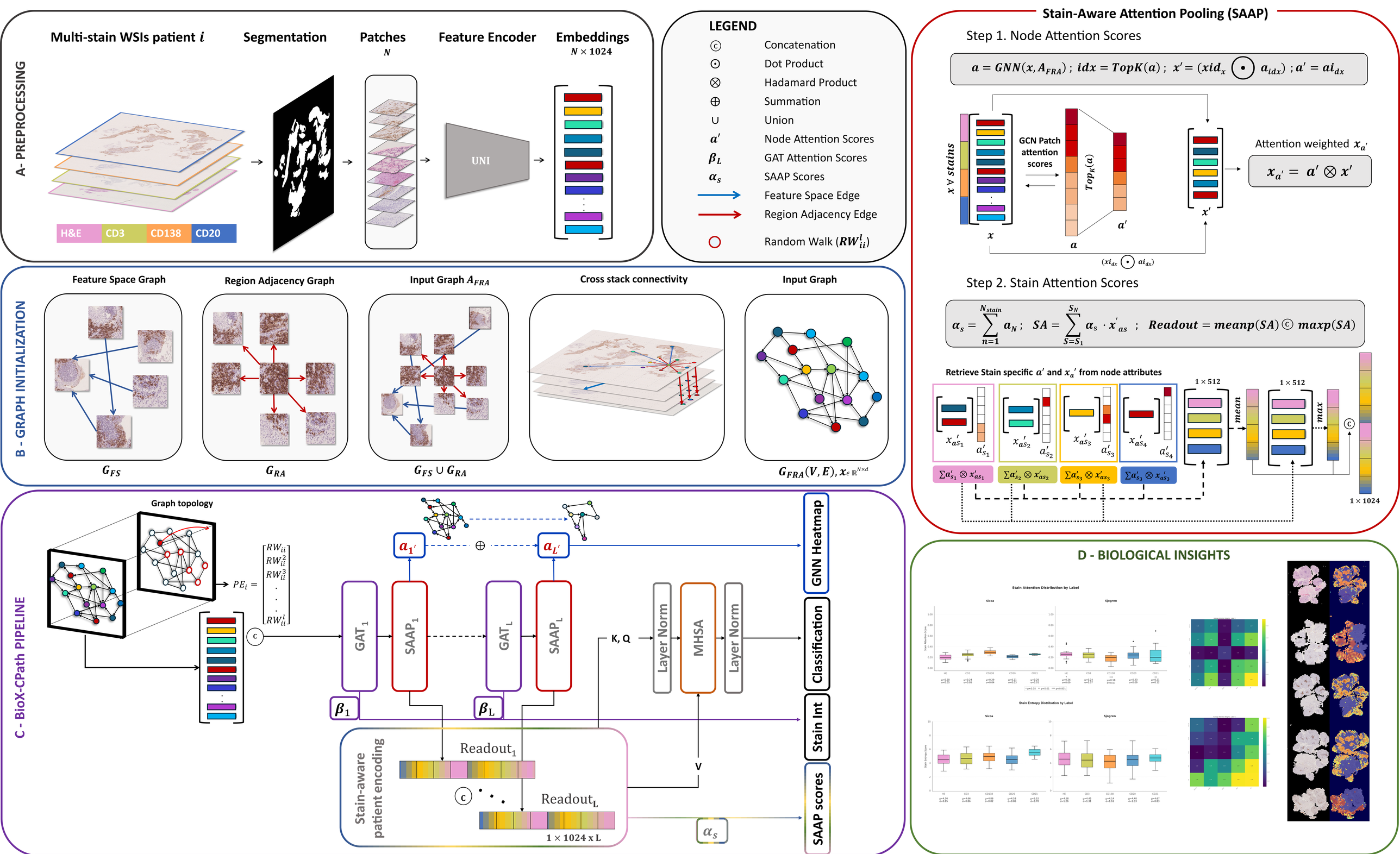
A- PREPROCESSING
Multi-stain WSIs patient i
Segmentation
Patches
N
Feature Encoder
Embeddings
$N \times 1024$
H&E
CD3
CD138
CD20
UNI
LEGEND
Concatenation
Dot Product
Hadamard Product
Summation
Union
a' Node Attention Scores
β_L GAT Attention Scores
α_s SAAP Scores
Feature Space Edge
Region Adjacency Edge
Random Walk (RW^l_{ii})
B - GRAPH INITIALIZATION
Feature Space Graph
Region Adjacency Graph
Input Graph A_{FRA}
Cross stack connectivity
Input Graph
G_{FS}
G_{RA}
$G_{FS} \cup G_{RA}$
$G_{FRA}(V,E), x_{\in} \mathbb{R}^{N \times d}$
C - BioX-CPath PIPELINE
Graph topology
$PE_i = \begin{bmatrix} RW_{ii} \\ RW^2_{ii} \\ RW^3_{ii} \\ \cdot \\ \cdot \\ \cdot \\ RW^l_{ii} \end{bmatrix}$
GAT$_1$
SAAP$_1$
GAT$_L$
SAAP$_L$
$a_{1'}$
$a_{L'}$
β_1
β_L
K, Q
V
Layer Norm
MHSA
Layer Norm
Stain-aware patient encoding
Readout$_1$
Readout$_L$
1×1024 x L
α_s
GNN Heatmap
Classification
Stain Int
SAAP scores
Stain-Aware Attention Pooling (SAAP)
Step 1. Node Attention Scores
$a = GNN(x, A_{FRA})$; $idx = TopK(a)$; $x' = (xid_x \odot a_{idx})$; $a' = ai_{dx}$
$x \forall stains$
GCN Patch attention scores
$Top_K(a)$
x
a
a'
x'
$(xi_{dx} \odot ai_{dx})$
Attention weighted $x_{a'}$
$x_{a'} = a' \otimes x'$
Step 2. Stain Attention Scores
$\alpha_s = \sum_{n=1}^{N_{stain}} a_N$; $SA = \sum_{S=S_1}^{S_N} \alpha_s \cdot x'_{as}$; $Readout = meanp(SA) \, © \, maxp(SA)$
Retrieve Stain specific a' and x_a' from node attributes
x'_{as_1} a'_{s_1}
x'_{as_2} a'_{s_2}
x'_{as_3} a'_{s_3}
x'_{as_4} a'_{s_4}
$\sum a'_{s_1} \otimes x'_{as_1}$
$\sum a'_{s_2} \otimes x'_{as_2}$
$\sum a'_{s_3} \otimes x'_{as_3}$
$\sum a'_{s_3} \otimes x'_{as_3}$
1×512
mean
1×512
max
1×1024
D - BIOLOGICAL INSIGHTS
Stain Attention Distribution by Label
Sicca
Sjogren
Stain Entropy Distribution by Label
Sicca
Sjogren