

Mã»c Tiãu

- Há»c patient-level embeddings tá» 4 omics (mRNA, CNV, CpG, miRNA) trã»n ã» thã» dá» thã»f sinh há»c.
- Kã»t há»p ã» mã» thã»c theo bá»nh nhã»n bá»ng attention ã»f dã»ng cho downstream tasks (clustering, survival, v.v.).

Dã» Liã»t & ã» Thã»

- Node types: gene, cpg, mirna; Edge types: cpgã»gene (maps_to), mirnaã»gene (targets), tã»y chá»n geneã»gene (PPI).
- Mã»i bá»nh nhã»n = 1 HeteroData graph; topology cá» ã»nh, node features theo bá»nh nhã»n.

Kiã»n Trã»c

- heteroã»GNN encoder ã» node embeddings h cho tá»ng node type.
- Projection + Pooling:
- Gene: W_{mrna}, W_{cnv} ã» pool thã»nh z_{mrna}, z_{cnv} .
- CpG/miRNA: pool trá»c tiã»p ã» z_{cpg}, z_{mirna} .
- Fusion:
- Stage A: mean of modality embeddings (chá»% ã»f export, khã»ng ã»i vã»o loss).
- Stage B: attention fusion ã» fused embedding h_{fused} .

Stage A (Pretraining)

- Feature reconstruction (L_recon): decoders tã»i tá»o lá»i mRNA, CNV, CpG, miRNA tá» h.
- Edge reconstruction (L_edge): link prediction cho cã» quan há»t kiã»fu (cpg, maps_to, Tj 0-14 Td (gene), v.v.).
- Projection loss (L_proj, chá»% mRNA/CNV): z_{mrna}/z_{cnv} dá» ã»oã»n perã»patient mean; thã»m projection diversity (cosine) ã»f trã»nh z_{mrna} ã» z_{cnv} .
- Mã»c tiã»u: $L_A = L_{recon} + \hat{L}_{edge} \cdot L_{edge} + \hat{L}_{projection} \cdot L_{proj} + \hat{L}_{proj_reg} \cdot L_{diversity}$.

Stage B (Fusion & Finetuning)

- Khã»Yi tá»o bá»ng weights cá»sa Stage A, reã»encode lá»i graphs mã»i batch.
- Attention fusion trã»n $\{z_{mrna}, z_{cnv}, z_{cpg}, z_{mirna}\}$ ã» h_{fused} .
- Consistency loss (L_cons): kã»o h_{fused} gã»n tá»ng modality (thã»ã»ng ã» normalized L2).
- Entropy regularization (L_ent): maximize entropy cá»sa attention weights ã»f trã»nh singleã»modality collapse.
- Tiã»p tá»c L_{recon} vã» L_{edge} ã» m anchor ná»™i dung + cá»y trã»c.
- Mã»c tiã»u: $L_B = L_{recon} + \hat{L}_{edge} \cdot L_{edge} + \hat{L}_{cons} \cdot L_{cons} + \hat{L}_{ent} \cdot L_{ent}$. Khã»ng dã»ng projection losses á»Y Stage B.

Gradient Flow (quan trá»ng)

- Stage A: L_{recon}/L_{edge} ã» encoder; L_{proj}/L_{div} ã» projections (W_mrna/W_cnv) ã» encoder.
- Stage B: L_{cons} ã» attention ã» z_m ã» projections ã» encoder; L_{ent} ã» attention; L_{recon}/L_{edge} vã»n cá»p nhã»t encoder/decoders.

Cã»n Bá»ng Modality (CpG 450k vs miRNA 1k)

- Mean pooling vã» normalized consistency giã»m bias do sã» ã» ã»ng feature.
- Entropy regularization chá»ng attention quã» ã»peakyã».
- Thã»c hã»nh: chuã»n hã»a perã»modality, tune $\hat{L}_{cons}/\hat{L}_{ent}$ vã» attention temperature.

Knobs Quan Trá»ng \(\config\)

- Structure: $\hat{\theta}_{\text{edge}}$.
- Stage A: $\hat{\theta}_{\text{projection}}$, $\hat{\theta}_{\text{proj_reg}}$.
- Stage B: $\hat{\theta}_{\text{cons}}$, $\hat{\theta}_{\text{ent}}$, attention temperature.
- Perâ€™modality recon: $\hat{\theta}_{\text{recon_mrna/cnv/cpg/mirna}}$.

Outputs

- modality_embeddings \((z_{\text{mrna}}, z_{\text{cnv}}, z_{\text{cpg}}, z_{\text{mirna}})\), fused embedding \((\text{Stage B})\), attention weights, vÃ perâ€™term losses $\tilde{A}^{\prime\prime} \gg f$ theo dÃµi/tá»i $\mathcal{A}^{\circ}u$.