

# Ensemble of Prior-guided Expert Graph Models for Survival Prediction in Digital Pathology (Supplementary Material)

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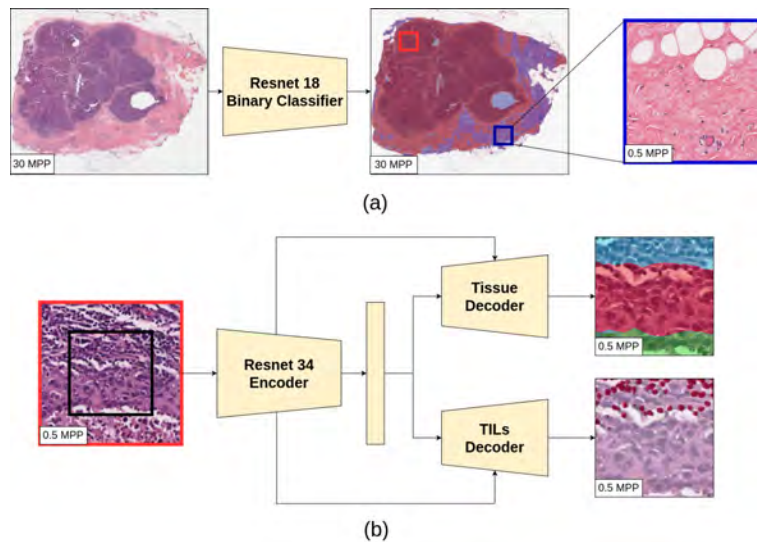


Fig. 1: Segmentation prior: (a) A coarse tissue binary classifier filters out *irrelevant* patches (blue) and passes the *relevant* patches (red) to the segmentation network. (b) It is a biheaded MA-UNet with a ResNet34 encoder, performing simultaneous tissue and TILs segmentation. The network takes  $512 \times 512$  patches as input at 0.5 MPP (Microns per pixel) and outputs  $256 \times 256$  tissue and TILs segmentations at the input center. The tissue decoder segments into tumor (red), tumor-associated stroma (blue), and other tissues (green). The TILs decoder segments into TILs vs. no TILs, shown in red.”

\* Equal contributions

Methods	BRCA	COAD&READ	STAD	UCEC	Overall
TransMIL	0.659 ± 0.071	0.533 ± 0.083	0.519 ± 0.061	0.660 ± 0.095	0.593
Tumor-Stroma TransMIL	<b>0.663 ± 0.049</b>	0.554 ± 0.085	0.535 ± 0.065	0.635 ± 0.099	0.597
Tumor-Other TransMIL	0.648 ± 0.053	<b>0.571 ± 0.053</b>	<b>0.538 ± 0.060</b>	<b>0.667 ± 0.099</b>	<b>0.606</b>
Stroma-Other TransMIL	0.655 ± 0.0469	0.523 ± 0.105	0.511 ± 0.057	0.627 ± 0.089	0.579

Table 1: Survival prediction C-Index scores of TransMIL on different tissue subsets across 4 cancer types. We observe individual experts on different tissue subsets, consistently beat the TransMIL on complete set across all the datasets

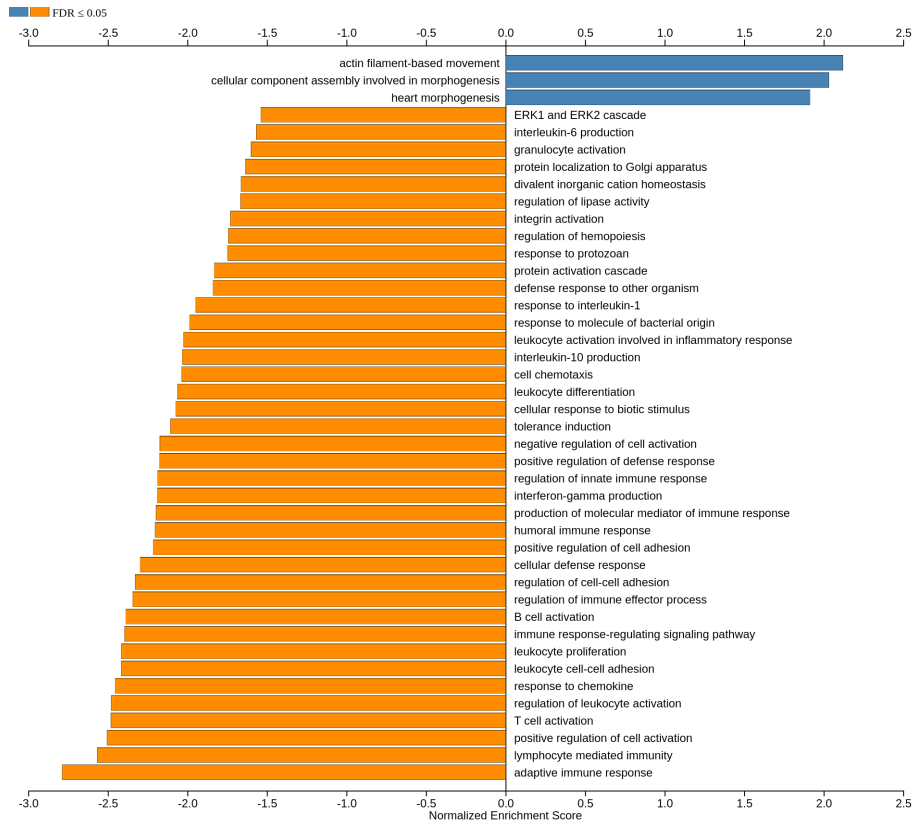


Fig. 2: Gene Ontology (GO) terms significantly ( $FDR \leq 0.05$ ) up or down regulated across the high and low risk patient groups identified using **complete-graph D-GNN** on TCGA-BRCA. Orange bars shows up regulation of GO terms in low risk groups compared to high risk groups and vice versa for blue bars.

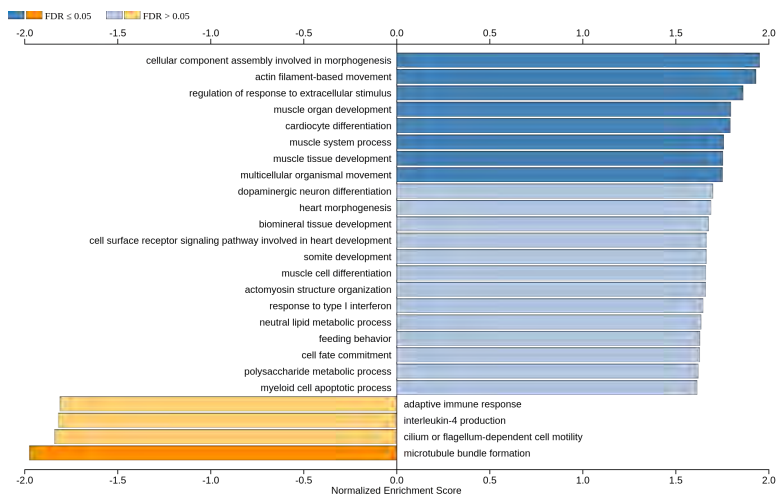


Fig. 3: Gene Ontology (GO) terms significantly up or down regulated across the high and low risk patient groups identified using **GTN** on TCGA-BRCA. We show all the significant GO terms, with different FDRs marked with different shades of colors. Orange bars shows up regulation of GO terms in low risk groups compared to high risk groups and vice versa for blue bars