



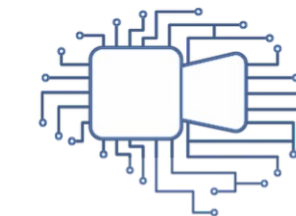
ISG: I can See Your Gene Expression

Yan Yang¹, LiYuan Pan², Liu Liu³, and Eric A Stone¹

¹BDSI, Australian National University, Australia

²BITSZ & School of CSAT, BIT, China

³Cyberverse Lab, China



PROBLEM OVERVIEW

Gene expression prediction from slide images:

- Slide images has a large resolution amounting to $10^5 \times 10^5$
- Features of slide images are sparse and non-uniformly distributed.

MOTIVATIONS

Common Pipelines:

Tile image into patches -> patch feature extraction -> gene expression prediction network.

Common Issues:

- Noisy patch selections.
- Fail to identify histology-related features
- Linear patch interactions for predictions.

Contributions:

We present an ISG framework with a Shannon Selection module, a Feature Extraction network and a Dual Attention network to address the above limitations

NETWORK ARCHITECTURE

Shannon Selection module

$$h(\mathbf{x}_i) = -\log \sum_{p: \mathcal{U}(p)=\mathbf{x}_i^*} 2^{-\|p\|_0} \approx -\log 2^{-K(\mathbf{x}_i)} = K(\mathbf{x}_i),$$

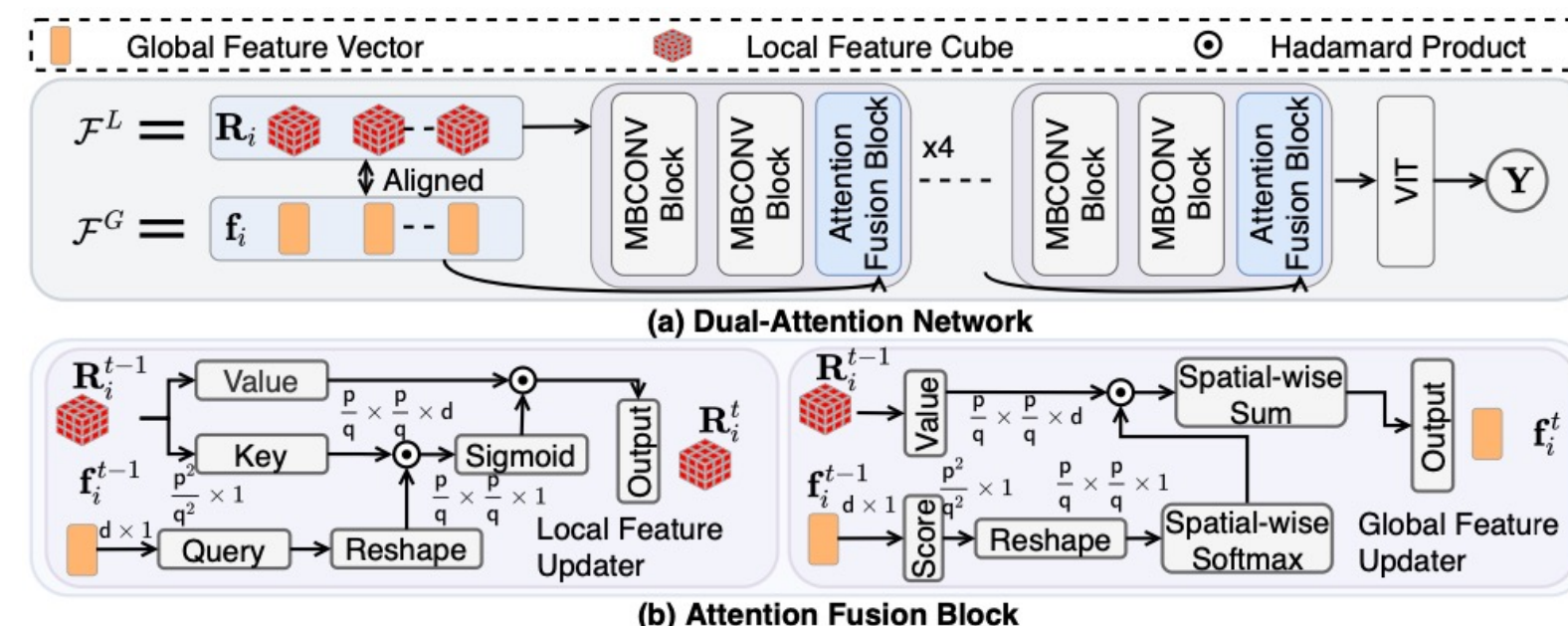
With a preset threshold, we select patches with abundant features.

Feature Extraction network

$$\mathcal{L}_{\text{total}} = \min_{D, E} \max_C \mathbb{E}_{\mathbf{x} \sim X} [\mathcal{L}_1 + \mathcal{L}_{\text{LPIPS}} + \mathcal{L}_C].$$

We extract low-dimensional patch-wise features by a style-based architecture as it can capture versatile feature representations.

Dual Attention network



We adaptively calibrate model attention to regions of interest.

EXPERIMENTAL RESULTS

Cancer Type	LIHC							COAD					PRAD			Avg.	
	Gene	CD3D	CD247	CD3E	CD3G	CD20	CD19	MK167	CD3D	CD247	CD3E	CD3G	CD20	CD19	TP63		KRT8
HE2RNA [29]	0.400	0.410	0.410	0.370	0.320	0.270	0.470	0.430	0.390	0.410	0.390	0.200	0.110	0.180	0.120	0.120	0.313
VIT-S [5]	0.193	0.252	0.256	0.279	0.258	0.187	0.189	0.260	0.291	0.312	0.300	0.314	0.280	0.065	0.153	0.151	0.234
VIT-MB[32]	0.337	0.388	0.378	0.345	0.360	0.361	0.464	0.351	0.379	0.382	0.370	0.379	0.383	0.207	0.154	0.165	0.338
CycleMLP[1]	0.343	0.364	0.396	0.374	0.353	0.352	0.348	0.320	0.347	0.378	0.377	0.372	0.378	0.203	0.140	0.187	0.327
MPViT[16]	0.365	0.358	0.377	0.350	0.379	0.356	0.491	0.311	0.361	0.371	0.352	0.374	0.413	0.205	0.142	0.199	0.338
ISG	0.486	0.498	0.533	0.524	0.425	0.440	0.597	0.415	0.470	0.468	0.445	0.385	0.432	0.235	0.264	0.348	0.435

(a) Comparison of gene expression predictions with SOTA methods

Cancer Type	LIHC							COAD					PRAD			Avg.	
	Gene	CD3D	CD247	CD3E	CD3G	CD20	CD19	MK167	CD3D	CD247	CD3E	CD3G	CD20	CD19	TP63		KRT8
ISG-IG	0.412	0.428	0.477	0.485	0.432	0.426	0.578	0.428	0.434	0.457	0.449	0.378	0.342	0.210	0.163	0.277	0.398
ISG-CANNY	0.473	0.445	0.511	0.484	0.373	0.396	0.583	0.400	0.436	0.436	0.438	0.340	0.341	0.190	0.249	0.318	0.401
ISG-Dex	0.436	0.437	0.503	0.493	0.428	0.433	0.576	0.386	0.423	0.442	0.427	0.338	0.362	0.189	0.245	0.315	0.402
ISG-DoG	0.468	0.431	0.490	0.457	0.411	0.414	0.591	0.382	0.431	0.422	0.421	0.350	0.351	0.209	0.273	0.343	0.403
ISG-LoG	0.338	0.293	0.316	0.337	0.305	0.323	0.354	0.181	0.235	0.216	0.207	0.243	0.199	0.136	0.155	0.202	0.253
ISG-Otsu	0.398	0.410	0.450	0.423	0.395	0.378	0.559	0.375	0.398	0.416	0.432	0.375	0.326	0.209	0.225	0.300	0.380
ISG	0.486	0.498	0.533	0.524	0.425	0.440	0.597	0.415	0.470	0.468	0.445	0.385	0.432	0.235	0.264	0.348	0.435

(b) Comparison of patch selection methods

Threshold (bits)	8×10^5	1.6×10^6	2.4×10^6
Avg PCC ↑	0.386	0.390	0.373
Avg \mathcal{L}_2 ↓	0.024	0.023	0.025

(c) Ablation of selection threshold

Dataset	ISG	HE2RNA [29]	MSIfromHE [12]
TCGA-CRC-DX	0.86	0.82	0.77
TCGA-CRC-KR	0.87	0.83	0.84
TCGA-STAD	0.78	0.76	0.81

(d) Clinic usage application.

SLIDE IMAGE SAMPLE

