[ECCV 2024] Mew: Multiplexed Immunofluorescence Image Analysis through an Efficient Multiplex Network

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Mew: Multiplexed Immunofluorescence Image Analysis through an Efficient Multiplex Network

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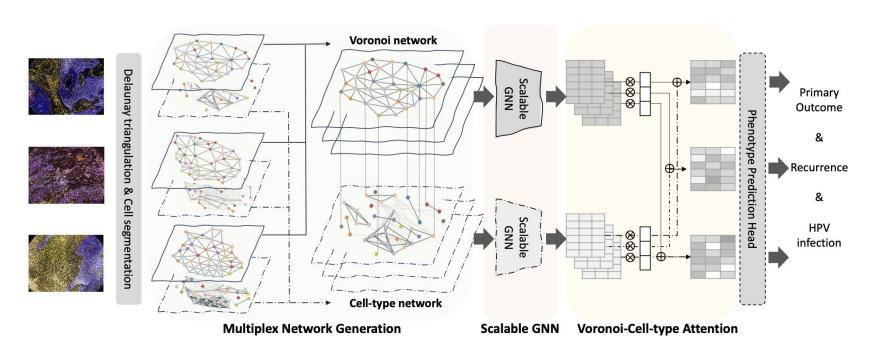
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Mew - In a nutshell,

[ECCV 2024] Mew: Multiplexed Immunofluorescence Image Analysis through an Efficient Multiplex Network

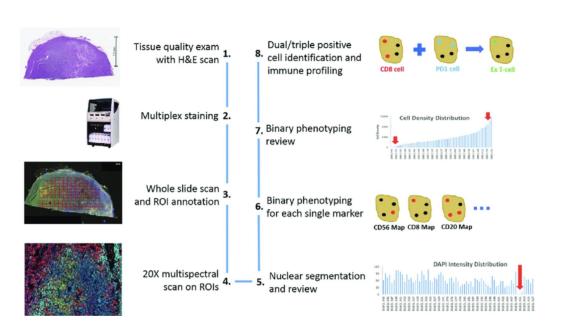
- Motivation: Can we alleviate 1) Cellular Heterogeneity 2) Scalability in mIF image analysis?
- Idea: Mew Multiplex Network + Efficient Graph Neural Networks

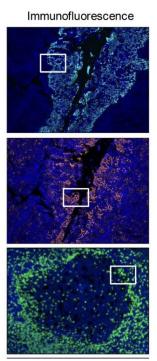


Mew - Background & Motivation

mIF image

- Multiplex immunofluorescence (mIF)
 - Technique uses <u>multiple fluorescent dyes</u> to label and visualize several target molecules <u>simultaneously</u> in a <u>single tissue</u> sample.
 - Allows for the detailed study of complex cellular interactions and the spatial relationships between different molecules





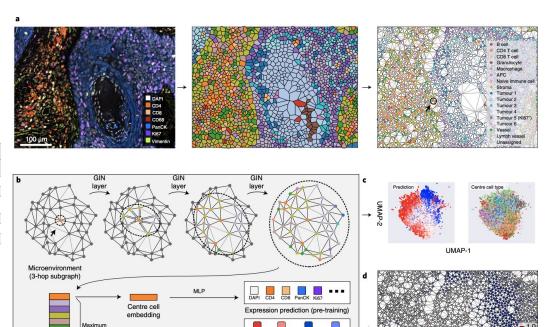
Mew - Background & Motivation

Graph ML in mIF image

- Recent advancements of Graph ML
 - [Nature BME 2023] SPACE-GM

Table 1 | Prediction performance on UPMC-HNC and DFCI-HNC tasks

Model	E	Binary classification	on (ROC-AUC)	Hazards model (C-index)	Generalization (ROC-AUC)	
	Primary outcome	Recurrence	Human papillomavirus (HPV) infection	Survival length	Primary outcome ^a	
Linear on composition (sample)	0.783	0.852	0.870	0.696	0.731	
MLP on composition (sample)	0.771	0.869	0.879	0.721	0.754	
Linear on composition (microenvironment)	0.774	0.823	0.864	0.700	0.799	
MLP on composition (microenvironment)	0.814	0.832	0.891	0.751	0.806	
SPACE-GM, no-pretraining	0.854	0.882	0.918	0.778	0.853	
SPACE-GM	0.867	0.883	0.926	0.799	0.873	



Phenotype prediction

Stroma-macrophage

Microenvironment cluster

microenvironment

Microenvironment

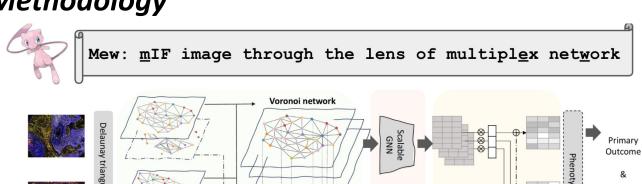
Node embeddings

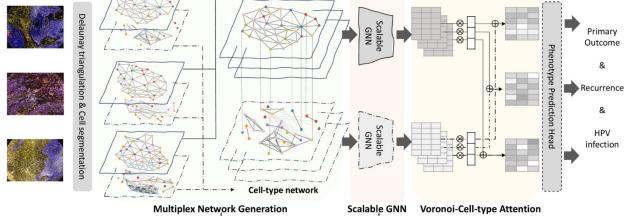
Dimensionality reduction

and clustering

Mew - Methodology

Mew

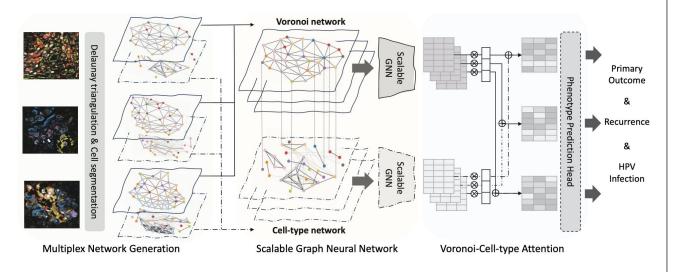




Mew - Methodology

Mew

- (1) Multiplex Network Generation
- (2) Scalable Graph Neural Network
- (3) Voronoi-Cell-type Attention



```
Algorithm 1 Pseudocode of the proposed algorithm
       Input: mpIF image I with its corresponding phenotype \mathcal{Y}^{I}
       Output: Pooled Prediction Matrix PI

    G<sup>I</sup> ← (V<sup>I</sup>, E<sup>I</sup>)

                                                                        \,\triangleright\, Voronoi network via preprocessing image I

 E'<sup>I</sup> ← Cell-type Edge Generater(C<sup>I</sup>, V<sup>I</sup>)

3: G'<sup>I</sup> ← (V<sup>I</sup>, E'<sup>I</sup>)
                                                                                                                      ▷ Cell-type network
4: \tilde{\mathcal{G}}^I \leftarrow (\mathcal{G}^I, \mathcal{G}'^I)
                                                                              Description > Multiplex Network: Voronoi + Cell-type
5: L ← PRECOMPUTER(A<sup>I</sup>, X<sup>I</sup>, K, stochastic=False)
 6: L' ← PRECOMPUTER(A'I, XI, K, stochastic=True)
7: while not converged do
            \mathbf{H}^{I} = \sigma([L[0]\mathbf{W}_{(0)}, L[1]\mathbf{W}_{(1)}, \dots, L[K]\mathbf{W}_{(K)})
             \mathbf{Z}^{I} = \xi(\mathbf{H}^{I}\mathbf{W}_{z})
             \mathbf{H}'^{I} = \sigma([L'[0]\mathbf{W}_{(0)}, L'[1]\mathbf{W}_{(1)}, \dots, L'[K]\mathbf{W}_{(K)})
            \mathbf{Z}^{I} = \xi(\mathbf{H}^{I}\mathbf{W}_{z})
             \tilde{\mathbf{Z}}^I \leftarrow \text{Voronoi-Cell-type Attention}(\mathbf{Z}^I, \mathbf{Z}'^I)
            \mathbf{P}^l \leftarrow MLP(\tilde{\mathbf{Z}}^l)
            \mathcal{L}_{ce} \leftarrow CE(Pool(\mathbf{P}^I), \mathcal{Y}^I)
15: end while
16: function Cell-type Edge Generater(C<sup>I</sup>, V<sup>I</sup>)
            \mathcal{E}^{I} = \{(\mathcal{V}_{i}^{I}, \mathcal{V}_{j}^{I}) \mid \mathcal{C}_{i}^{I} = \mathcal{C}_{i}^{I}, \forall i, j \in \{1, ..., |\mathcal{V}^{I}|\}, i \neq j\}
19: end function

    function Precomputer(A<sup>I</sup>, X<sup>I</sup>, K, stochastic=False)

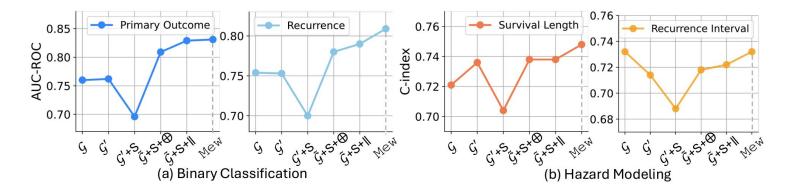
             Initialize empty list L = [
             Append X^I to L
             for k \leftarrow 1 to K + 1 do
                  if stochastic then
                                       1 if Bernoulli(\hat{\mathbf{P}}_{ij}^I) = 1
25:
26:
                   end if
27:
                  X^I \leftarrow A^I X
                   Append \mathbf{X}^I to L
28:
29:
             end for
30:
             return L
31: end function
32: function Voronoi-Cell-type Attention(Z<sup>I</sup>, Z<sup>I</sup>)
             for \ell \leftarrow 0 to |V^I| do
                  \alpha_{\ell, \text{Voronoi}} = \frac{\exp(\text{LeakyReLU}(\mathbf{a}^{\top} \mathbf{z}_{\ell}^{\ell}))}{\exp(\text{LeakyReLU}(\mathbf{a}^{\top} \mathbf{z}_{\ell}^{\prime})) + \exp(\text{LeakyReLU}(\mathbf{a}^{\top} \mathbf{z}_{\ell}^{\prime}))}
                  \alpha_{\ell, \text{Cell-type}} = \frac{\exp(\text{LeakyReLU}(\mathbf{a}^{\top}\mathbf{z}_{I}^{I}))}{\exp(\text{LeakyReLU}(\mathbf{a}^{\top}\mathbf{z}_{I}^{I})) + \exp(\text{LeakyReLU}(\mathbf{a}^{\top}\mathbf{z}_{I}^{I}))}
                   \tilde{\mathbf{z}}_{\ell}^{I} = \alpha_{\ell, \text{Voronoi}} \mathbf{z}_{\ell}^{I} + \alpha_{\ell, \text{Cell-type}} \mathbf{z'}_{\ell}^{I}
37:
             end for
            return \tilde{\mathbf{Z}}^{I}
39: end function
```

Mew - **Experiments**

Patient-level Phenotype Prediction & Ablation Study

	Binary Classification (BC)				Hazard Modeling Generalization		
	Primary Outcome	Recurrence	HPV infection	Average (BC)	Survival Length	Primary Outcome	
GCN [27]	0.687±0.052	0.751 ± 0.035	0.748 ± 0.064	0.729	0.693 ± 0.045	0.480	
GAT [58]	0.690 ± 0.072	$0.745{\pm0.009}$	$0.761 {\pm} 0.072$	0.732	0.705 ± 0.066	0.531	
GraphSAGE [22]	0.708 ± 0.063	$0.743 {\pm} 0.034$	$0.767 {\pm} 0.085$	0.739	0.708 ± 0.061	0.430	
SIGN [13]	0.715 ± 0.030	0.729 ± 0.030	$0.808 {\pm} 0.035$	0.751	0.701 ± 0.040	0.467	
ClusterGCN [7]	0.714 ± 0.042	0.678 ± 0.044	0.800 ± 0.023	0.731	0.707 ± 0.016	0.676	
FAGCN [3]	0.712 ± 0.024	$0.785 {\pm} 0.054$	0.773 ± 0.031	0.757	0.562 ± 0.056	0.524	
HDMI [26]	0.705 ± 0.050	$0.807 {\pm} 0.055$	0.797 ± 0.062	0.770	0.702 ± 0.041	0.585	
SPACE-GM [59]	0.716 ± 0.059	$0.767 {\pm} 0.036$	$0.778 {\pm} 0.052$	0.754	$0.600 {\pm} 0.129$	0.685	
Mew	0.737±0.060	0.832 ±0.065	0.813 ± 0.067	0.794	0.728 ± 0.044	0.743	

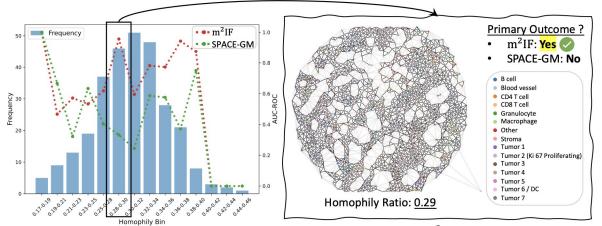
	Binary Classification (BC)			Hazard Modeling (HM)		
	Primary Outcome	Recurrence	Average (BC)	Survival Length	Recurrence Interval	Average (HM)
GCN [27]	0.579 ± 0.036	$0.630 {\pm} 0.098$	0.605	0.571 ± 0.079	$0.568 {\pm} 0.087$	0.570
GAT [58]	0.539 ± 0.022	$0.524{\pm}0.043$	0.532	0.603 ± 0.012	0.567 ± 0.037	0.585
GraphSAGE [22]	0.540 ± 0.110	$0.572 {\pm} 0.093$	0.556	0.578 ± 0.068	0.507 ± 0.055	0.543
SIGN [13]	$0.522{\pm0.008}$	$0.466 {\pm} 0.076$	0.494	0.541 ± 0.096	$0.553 {\pm} 0.082$	0.547
ClusterGCN [7]	0.545 ± 0.059	$0.531 {\pm} 0.060$	0.538	0.473 ± 0.136	$0.484{\pm}0.047$	0.479
FAGCN [3]	0.584 ± 0.092	0.498 ± 0.081	0.541	0.567 ± 0.037	0.502 ± 0.021	0.535
HDMI [26]	0.499 ± 0.026	$0.483{\pm}0.028$	0.491	0.565 ± 0.076	0.572 ± 0.033	0.569
SPACE-GM [59]	0.563 ± 0.035	$0.524{\pm}0.041$	0.544	0.492 ± 0.059	$0.577{\pm0.043}$	0.535
Mew	0.658 ±0.030	0.660 ±0.047	0.659	0.631 ±0.048	$0.597 {\pm 0.083}$	0.614



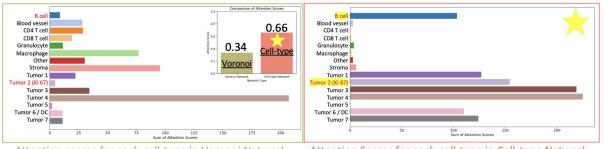
Mew - **Experiments**

In-depth Analysis & Scalability

	Mew		
Preprocessing ($ \mathcal{G} = 308$) Training ($ \mathcal{G} = 16$) Evaluation ($ \mathcal{G} = 53$)	$5345.12s$ $7.03s (\bar{\mathcal{V}} = 1,071)$ $60.28s$	20.45s $(\bar{\mathcal{V}} = 1,071)$ 156.18s	75.60s 36.01s ($ \bar{\mathcal{V}} = 117,974$) 0.53s



(a) AUC-ROC with Homophily frequency in comparison with m²IF and SPACE-GM



Attention scores for each cell-type in Voronoi Network

Attention Scores for each cell-type in Cell-type Network