

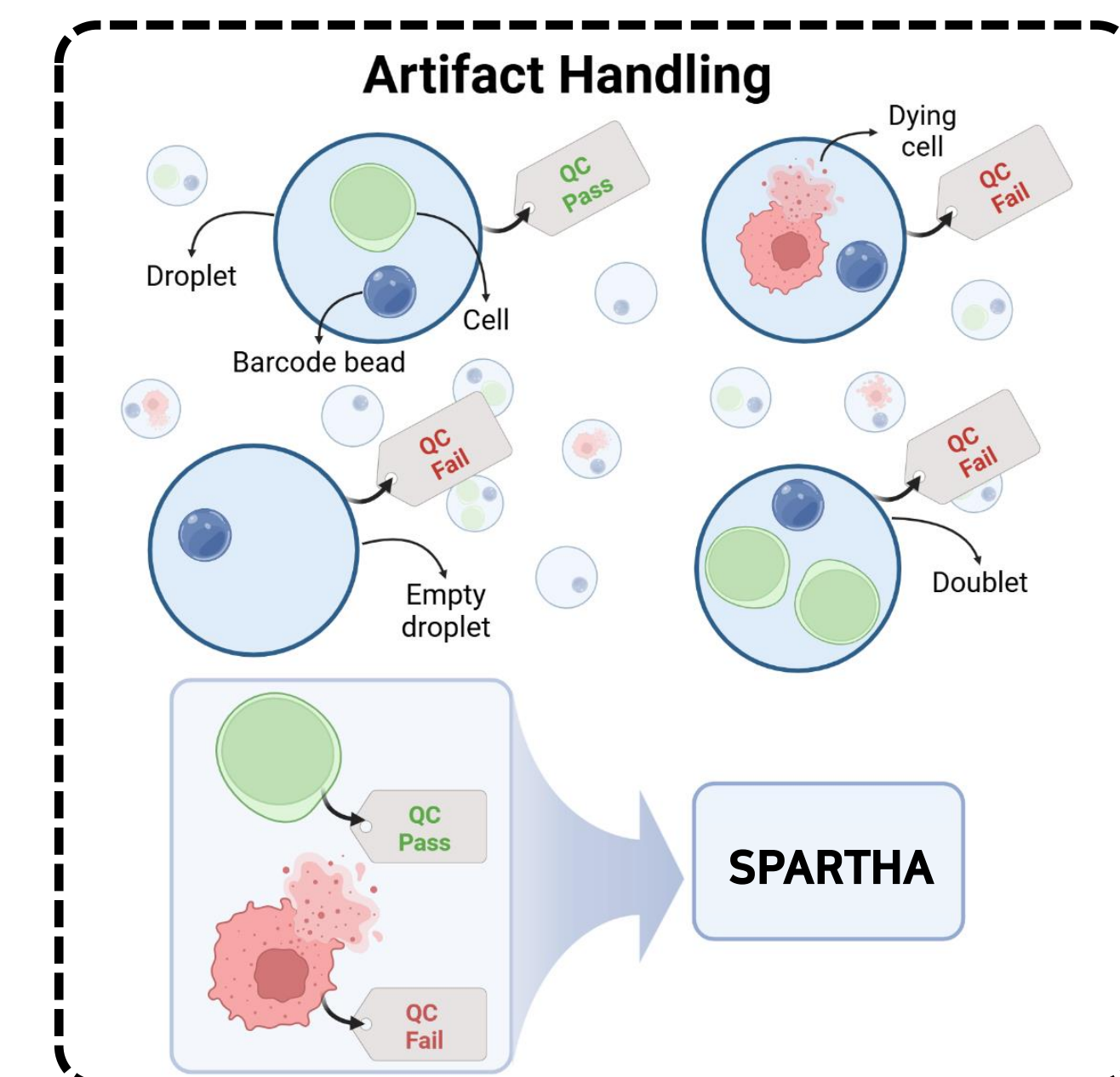
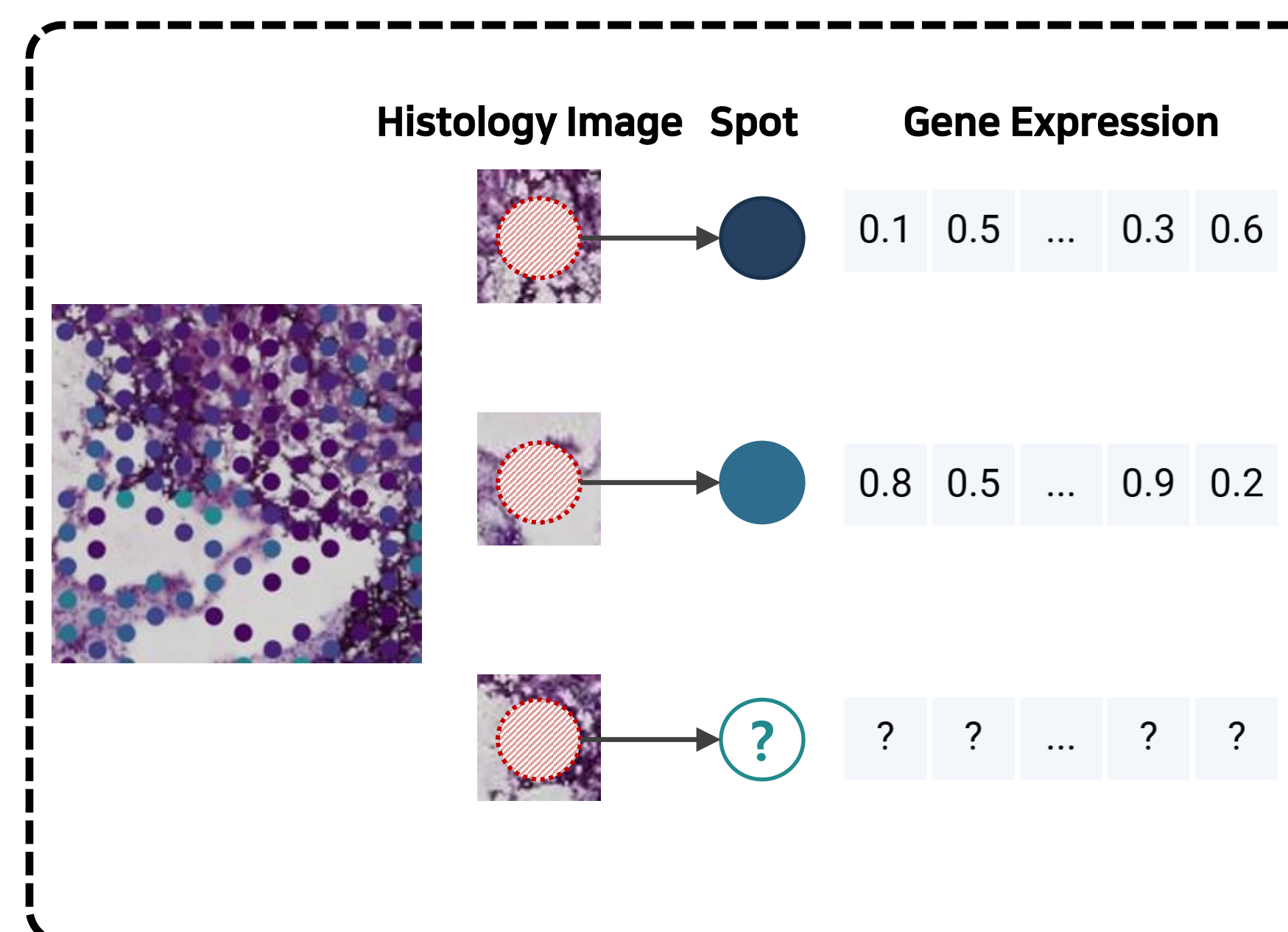
SPARTHA: Enhancing Spatial Gene Expression Prediction with Artifact Disentanglement from Histology Images

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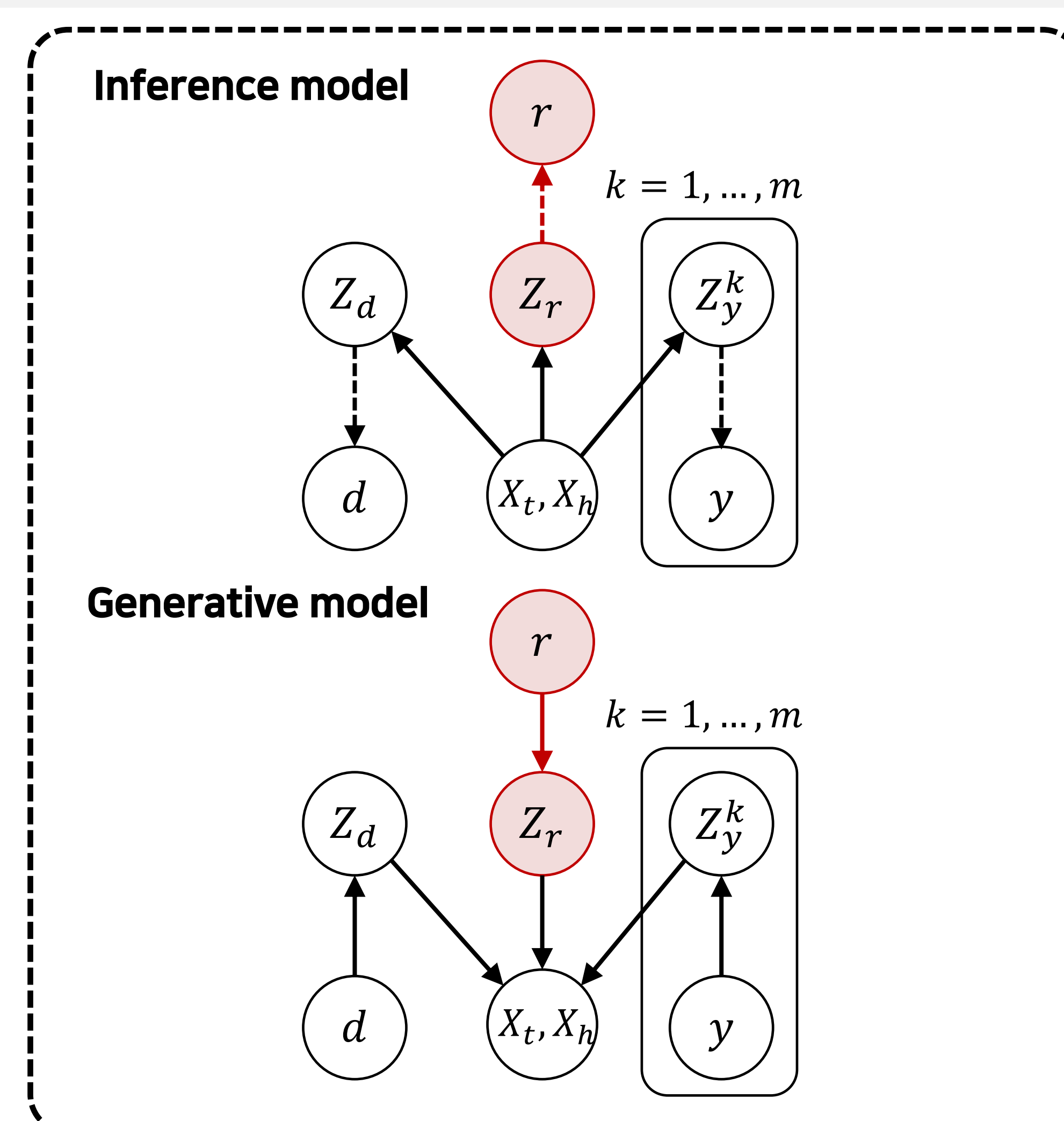
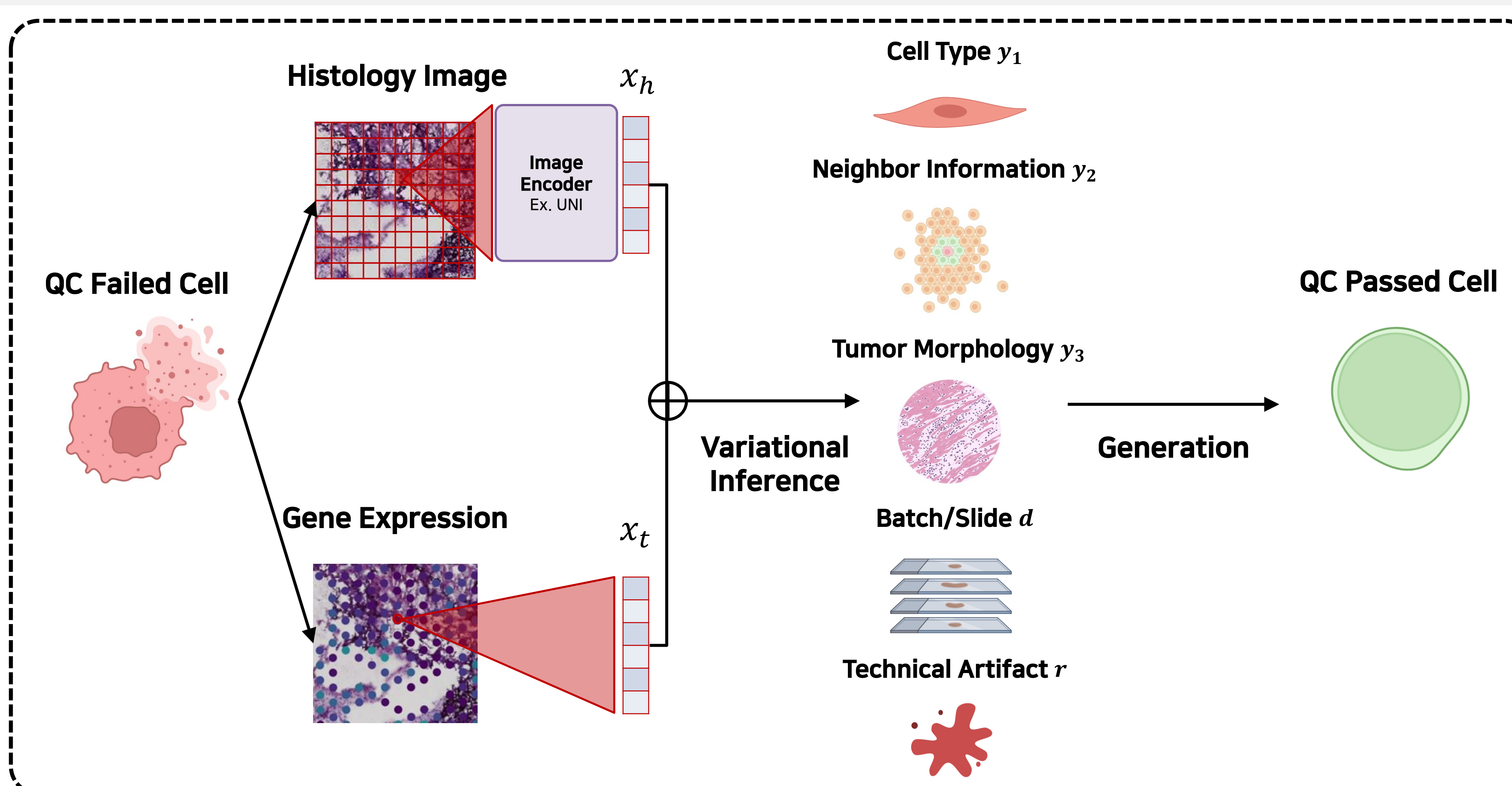
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INTRODUCTION

- **Task:** Predicting RNA expression from correlated histopathology images.
- **Challenges:** While histology images are cost-effective, spatial transcriptomics experiments are expensive, leading to limited data availability.
- **Limitations of Previous Approaches:** Strict preprocessing may discard useful signals, batch effects across samples and platforms confound results, and filtering for highly variable genes reduces throughput.
- **Motivation:** Maximizing the use of all available data and throughput (number of samples and genes) while preserving potentially valuable information.



METHODS



- **Data Preprocessing:** Instead of filtering out low-quality data, we annotate the data based on widely used quality criteria, classifying it as “pass” or “fail”.
- **Modeling Class specific features :** Our goal is to model the underlying biological variation across spatial transcriptomics (ST) and histology modalities, while removing confounding domain effects. We achieve this through causal latent variable modeling, disentangling **biological signals** (e.g., cell-type, tissue morphology) from confounders (e.g., batch, artifacts).
- **Modeling Domain specific feature:** We explicitly model **confounders** (e.g., batch, slide) in a separate latent space, ensuring that biological signals remain invariant to such factors.
- **Modeling Artifacts:** The key idea is to model **artifacts** as **residual**, orthogonal to biological signals. We treat artifacts as a hidden nuisance variable and learn a dedicated latent space to capture artifact-induced variation. To guide learning, we incorporate an artifact classification objective to encourage separability between QC pass/fail patterns.

- **ELBO Loss:**
$$\mathcal{L}_{ELBO}(\theta, \phi) = \mathbb{E}_{q_\phi(Z_y, Z_d, Z_r | X_t, X_h)} [\log p_\theta(X_t | Z_y, Z_d, Z_r) + \log p_\theta(X_h | Z_y, Z_d, Z_r)] - \sum_{k=1}^m \text{KL}(q_\phi(Z_y^k | X_t, X_h) \| p_\theta(Z_y^k | L^k)) - \text{KL}(q_\phi(Z_d | X_t, X_h) \| p_\theta(Z_d | L_d)) - \text{KL}(q_\phi(Z_r | X_t, X_h) \| p_\theta(Z_r | L_r))$$
 - Z_y : Class specific latent (cell type, spatial context, morphology)
 - Z_d : Batch/Slide latent
 - Z_r : Artifact latent
- **Auxiliary Classification Loss:** KL Divergence for artifact distribution
$$\mathcal{L}_{cls} = \sum_{k=1}^m \mathbb{E}_{q_\phi(Z_y^k)} [\log q_\psi(L_y^k | Z_y^k)] + \mathbb{E}_{q_\phi(Z_d)} [\log q_\psi(L_d | Z_d)] + \mathbb{E}_{q_\phi(Z_r)} [\log q_\psi(L_r | Z_r)]$$
 - L_y : Domain-Invariant labels (cell type, spatial context, morphology)
 - L_d : Batch/Slide label
 - $L_r = y_{qc} \in \{0,1\}$: Artifact label

RESULTS

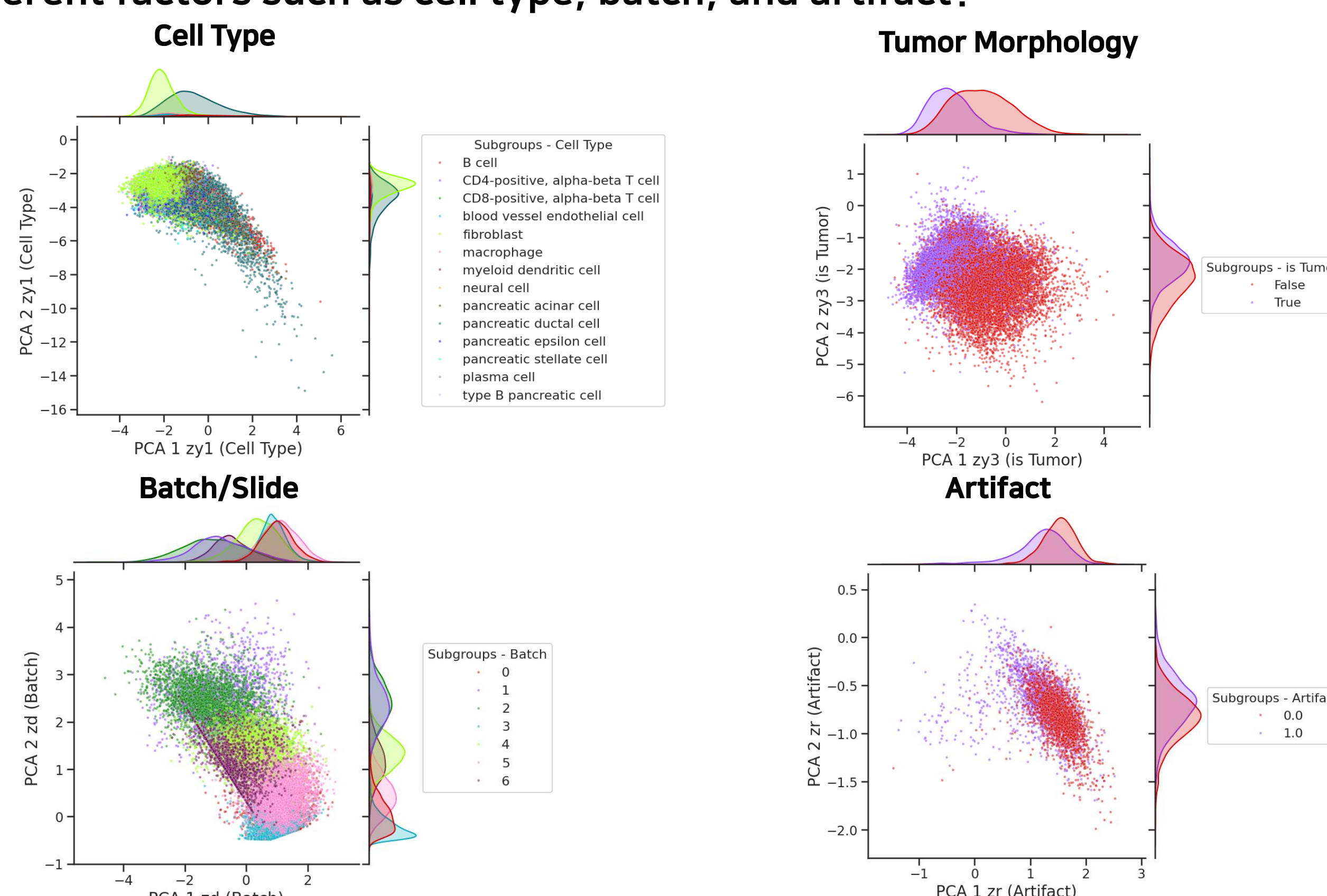
Q: Did the generated data quality improve along with the prediction performance?

All	PCC ↑	R ² ↑	MAE ↓	MSE ↓
HisToGene	0.0803	-43.570	0.7914	1.0144
SpatialDIVA	0.7171	0.4479	0.1302	0.1387
Ours	0.7209	0.4618	0.1335	0.1352

HVG	PCC ↑	R ² ↑	MAE ↓	MSE ↓
HisToGene	0.0317	17.645	0.7989	1.0250
SpatialDIVA	0.6271	0.3815	0.2587	0.3752
Ours	0.6289	0.3875	0.2677	0.3716

QCPR	QCPR3 ↑	QCPR4 ↑	QCPR5 ↑
SpatialDIVA	0.6683	0.8415	0.9521
Ours	0.795	0.9306	0.9831

Q: Does the model successfully disentangle the embeddings corresponding to different factors such as cell type, batch, and artifact?



Information

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Poster

