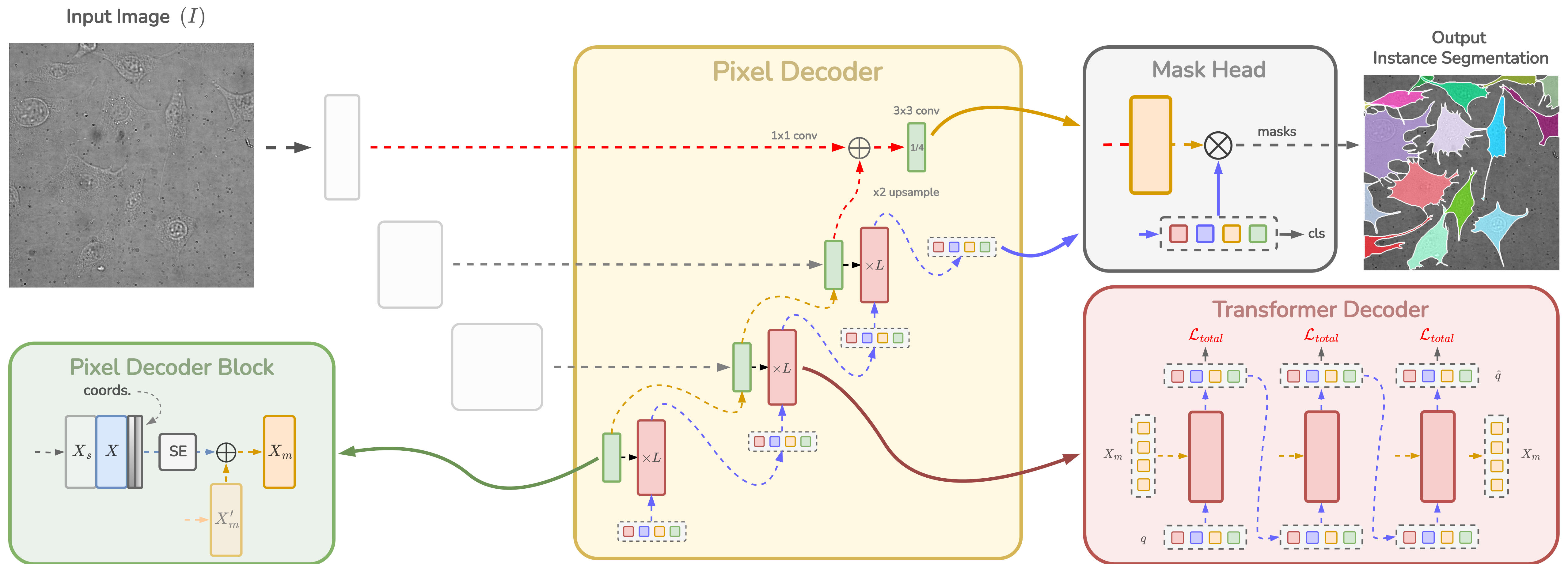


# IAUNet: Instance-Aware U-Net

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**Figure 1. Model overview.** IAUNet consists of a Pixel decoder and a Transformer decoder. The encoder extracts multi-scale features used as skip connections in the Pixel decoder. Each decoder block combines these features with CoordConv-based positional encodings and applies stacked depth-wise convolutions followed by a Squeeze-and-Excitation (SE) block to produce refined mask features. The Transformer decoder then refines learnable queries over multiple layers using these mask features with deep supervision.

## Abstract

Instance segmentation is critical in biomedical imaging to distinguish individual objects like cells, which often overlap and vary in size. We propose IAUNet, a novel query-based U-Net architecture that retains the full U-Net design and adds a lightweight convolutional Pixel decoder for efficient multi-scale feature aggregation. To enhance instance segmentation, we incorporate a Transformer decoder with deep supervision that refines object queries across layers. We also introduce Revvity-25, a new 2025 dataset with detailed annotations of overlapping cell cytoplasm in brightfield images. IAUNet achieves strong results, outperforming existing convolutional, transformer-based, and query-based models.

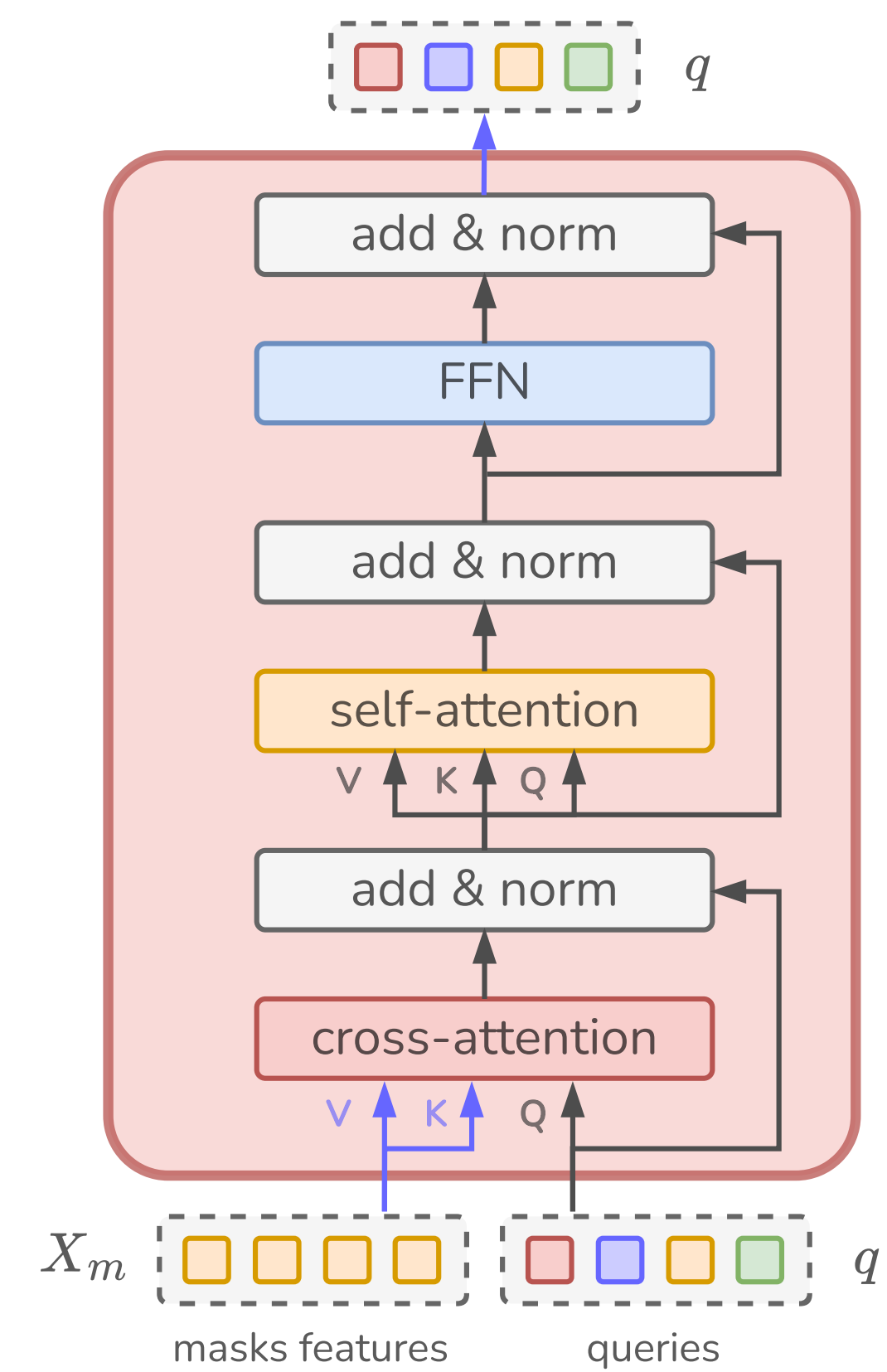
## Design

### Pixel Decoder

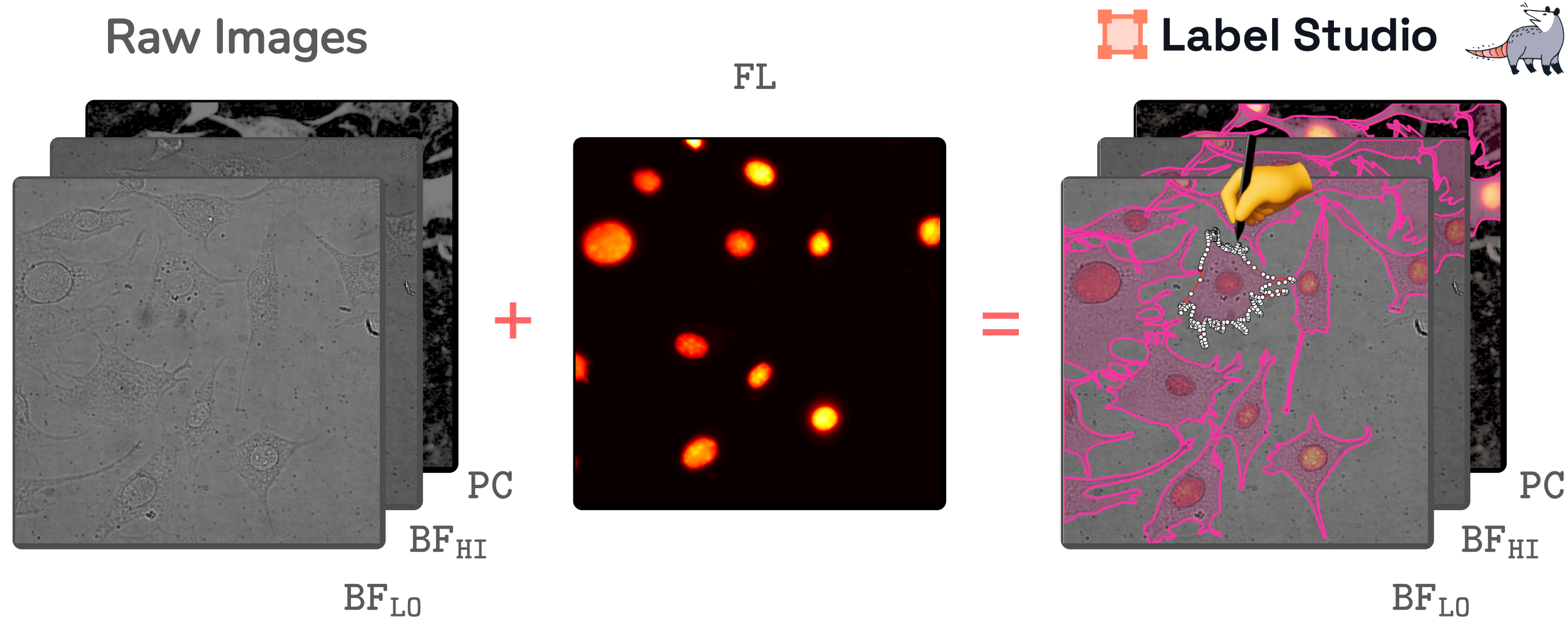
- A lightweight Pixel decoder is designed to refine multi-scale features.
- Features are processed through lightweight depth-wise convolutions.
- CoordConv injects explicit positional information into the decoder without increasing computational complexity.
- Squeeze-and-Excitation (SE) block enhances feature refinement for better instance separation.

### Transformer Decoder

- Transformer decoder learns instance-level representations.
- Uses learnable queries for potential objects.
- Queries attend to mask features via cross- and self-attention.
- Three blocks per layer refine semantic and spatial content.

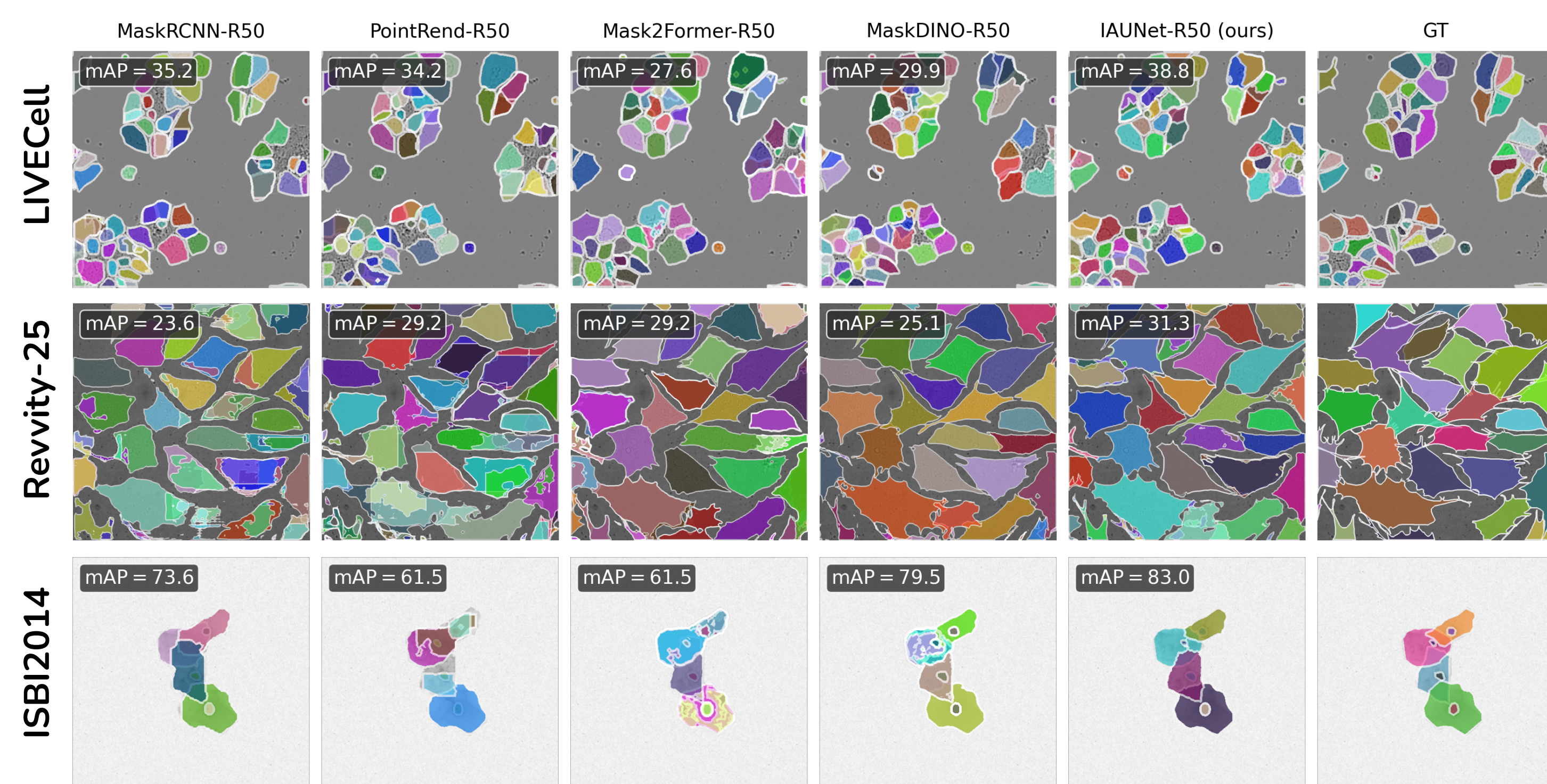


## Revvity-25



**Figure 2.** Multimodal annotation workflow for the Revvity-25 dataset.

Revvity-25 comprises 110 brightfield images with 2,937 expert-validated cell instances, each labeled with high-fidelity polygon masks averaging 60 points per cell (up to 400). It is the first public dataset to pair high-resolution brightfield images with precise instance-level annotations of overlapping cells.



**Figure 3.** Visualization of instance segmentation predictions across different state-of-the-art models (using ResNet50 backbone). We also report per-image AP score.

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Revvity-25										
Models	backbones	num_queries	AP	AP <sub>50</sub>	AP <sub>75</sub>	AP <sub>S</sub>	AP <sub>M</sub>	AP <sub>L</sub>	#params.	FLOPs
<b>Models with Convolution-Based Backbones</b>										
Mask R-CNN [14]	R50	100	39.7	77.2	37.4	0.6	19.0	44.6	44M	115G
PointRend [34]	R50	100	42.2	79.4	40.9	0.4	21.7	47.3	56M	66G
Mask2Former [19]	R50	100	<u>46.4</u>	79.8	<u>49.9</u>	<u>0.7</u>	<u>25.7</u>	<u>52.8</u>	44M	67G
MaskDINO [20]	R50	100	45.6	80.4	48.2	<b>1.8</b>	22.3	51.8	44M	64G
<b>IAUNet (ours)</b>	R50	100	<b>49.7</b>	<b>82.1</b>	<b>54.8</b>	0.6	<b>27.3</b>	<b>56.0</b>	39M	49G
Mask R-CNN [14]	R101	100	40.7	77.5	39.9	0.4	20.1	45.8	63M	134G
PointRend [34]	R101	100	42.9	79.3	42.5	0.0	18.4	48.9	75M	86G
Mask2Former [19]	R101	100	47.2	80.1	<u>51.8</u>	<b>1.7</b>	<u>25.7</u>	53.3	63M	86G
MaskDINO [20]	R101	100	<u>47.3</u>	<u>81.0</u>	50.4	<u>0.9</u>	23.0	<u>53.5</u>	63M	84G
<b>IAUNet (ours)</b>	R101	100	<b>51.5</b>	<b>84.7</b>	<b>56.1</b>	<b>1.7</b>	<b>29.2</b>	<b>57.8</b>	58M	69G
<b>Models with Transformer-Based Backbones</b>										
Mask R-CNN [14]	Swin-S	100	24.7	63.4	12.5	0.0	7.3	28.9	69M	141G
PointRend [34]	Swin-S	100	43.6	80.0	43.0	0.5	21.5	48.9	81M	93G
Mask2Former [19]	Swin-S	100	51.2	83.3	56.4	2.7	27.7	58.0	69M	93G
MaskDINO [20]	Swin-S	100	50.3	83.2	53.9	<b>4.7</b>	27.6	56.1	71M	181G
MaskDINO [20]	Swin-S	300	49.4	83.6	53.3	<u>2.9</u>	25.8	55.3	71M	187G
<b>IAUNet (ours)</b>	Swin-S	100	<u>53.0</u>	<u>85.7</u>	<u>57.0</u>	1.3	<b>29.7</b>	<u>59.1</u>	64M	76G
<b>IAUNet (ours)</b>	Swin-S	300	<b>53.3</b>	<b>86.0</b>	<b>59.6</b>	1.6	<u>29.4</u>	<b>59.8</b>	64M	87G
Mask R-CNN [14]	Swin-B	100	27.1	64.9	17.2	0.1	9.7	31.2	107M	186G
PointRend [34]	Swin-B	100	45.2	80.1	47.9	0.1	23.0	50.9	119M	137G
Mask2Former [19]	Swin-B	100	52.0	83.6	<u>58.4</u>	<u>1.1</u>	27.8	59.0	107M	138G
MaskDINO [20]	Swin-B	100	50.5	83.5	54.9	<b>2.0</b>	27.1	56.4	110M	226G
MaskDINO [20]	Swin-B	300	50.4	84.3	54.8	0.8	26.3	56.6	110M	232G
<b>IAUNet (ours)</b>	Swin-B	100	<u>53.5</u>	<u>86.1</u>	<u>59.4</u>	0.8	<b>30.5</b>	<u>59.7</u>	102M	120G
<b>IAUNet (ours)</b>	Swin-B	300	<b>53.7</b>	<b>86.5</b>	<b>59.4</b>	1.0	<u>30.0</u>	<b>60.3</b>	102M	132G

**Table 1. Instance segmentation on our Revvity-25 dataset.** IAUNet outperforms strong query-based baselines as well as other state-of-the-art models when training with fewer parameters

## Conclusions

We introduce IAUNet, a query-based U-Net with a lightweight Pixel decoder and a Transformer decoder for efficient cell instance segmentation. IAUNet achieves strong performance with low computational cost. We also present Revvity-25, a high-resolution microscopy dataset with expert-labeled cell masks for modal and amodal segmentation. This work sets a strong baseline for future research and will be presented at CVPR 2025 at the CVMI Workshop in Nashville.