# *Sharing is Caring*: Concurrent Interactive Segmentation and Model Training using a Joint Model

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## Classical Data Pipeline

The base supervised machine learning paradigm has three main steps: (1) data annotation, (2) target predictor training, (3) deployment.
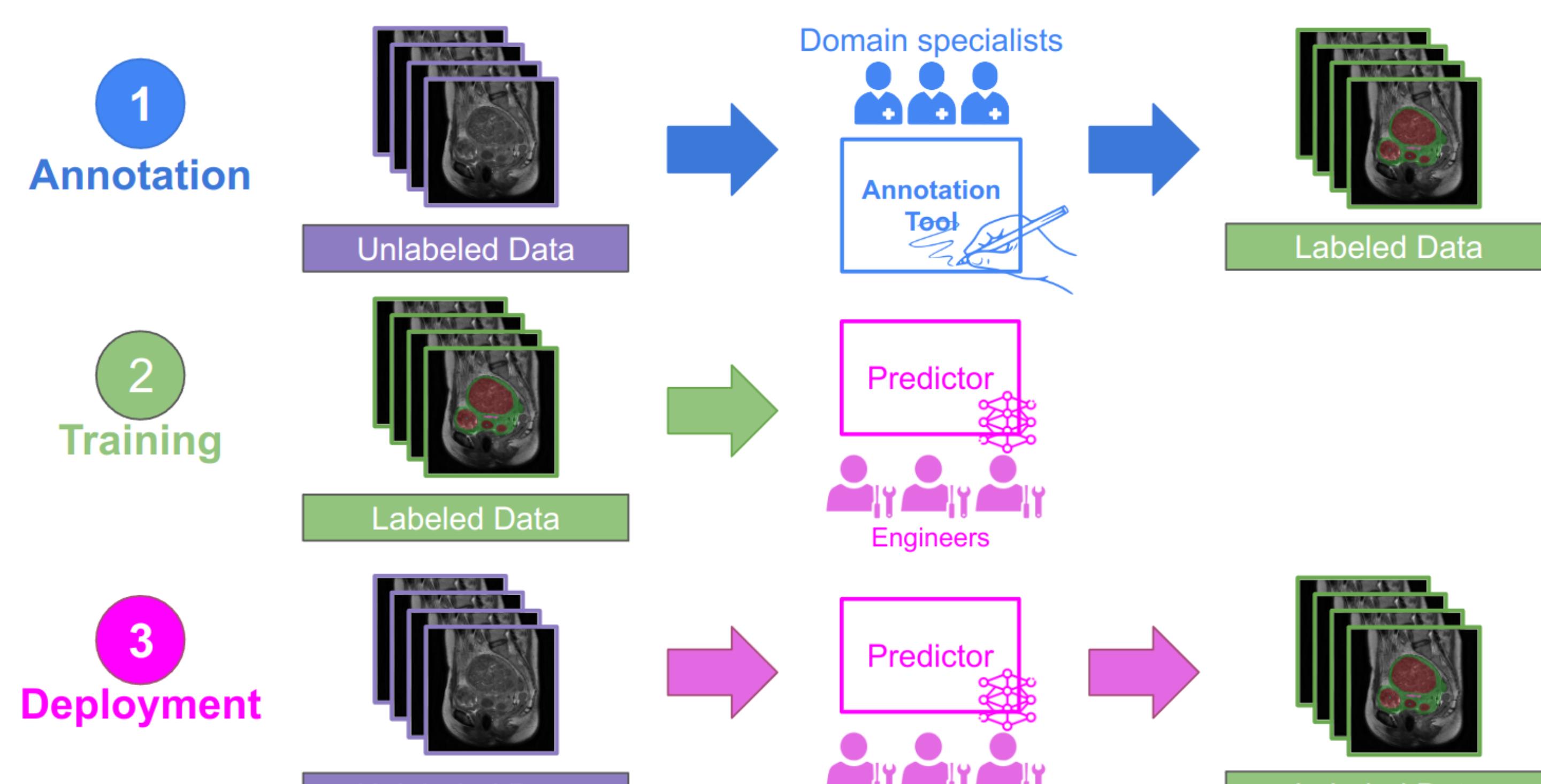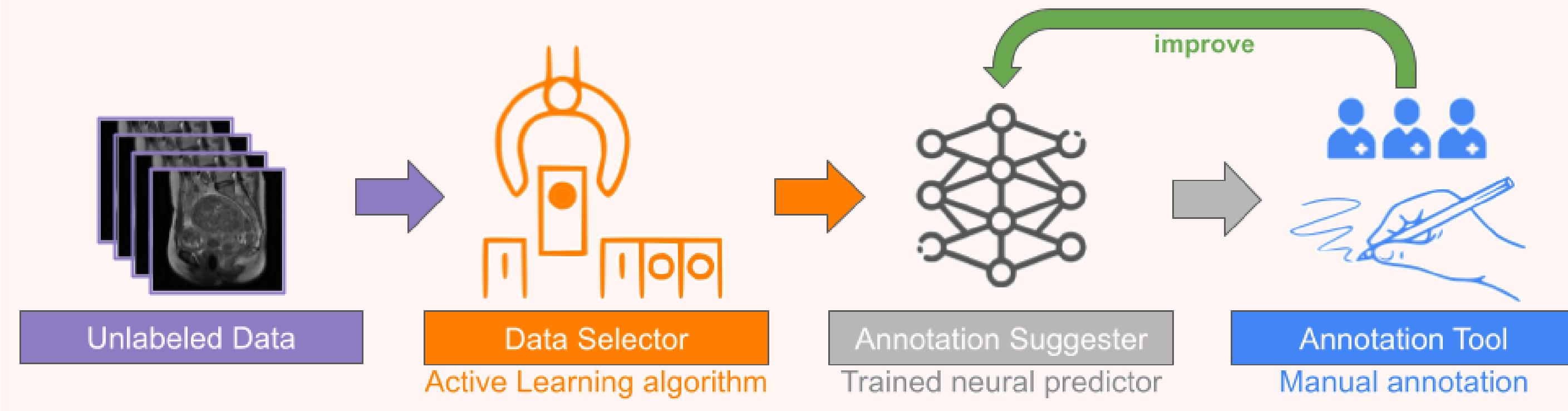


Figure 1. General classical deep learning data annotation and model deployment pipeline.

## Archetypical Framework

Archetypical state-of-the-art systems do two preparatory steps to expedite the annotation process: (1) data selection to reduce the quantity of data to annotate; (2) usage of an improvable annotation suggester to pre-annotate the data. They still use classical manual tools for corrections.



Figure 2. Archetypical state of the art framework.

## Limitations of the Classical Data Pipeline

Existing systems are suboptimal: (1) annotations are required to produce annotations, - predictor is trained only once a sufficient amount of data has been annotated; (2) data annotation, data selection and target predictor training require different isolated methods and expertise to achieve the same goal - produce annotations; (3) the annotation tools do not improve as more data is annotated.
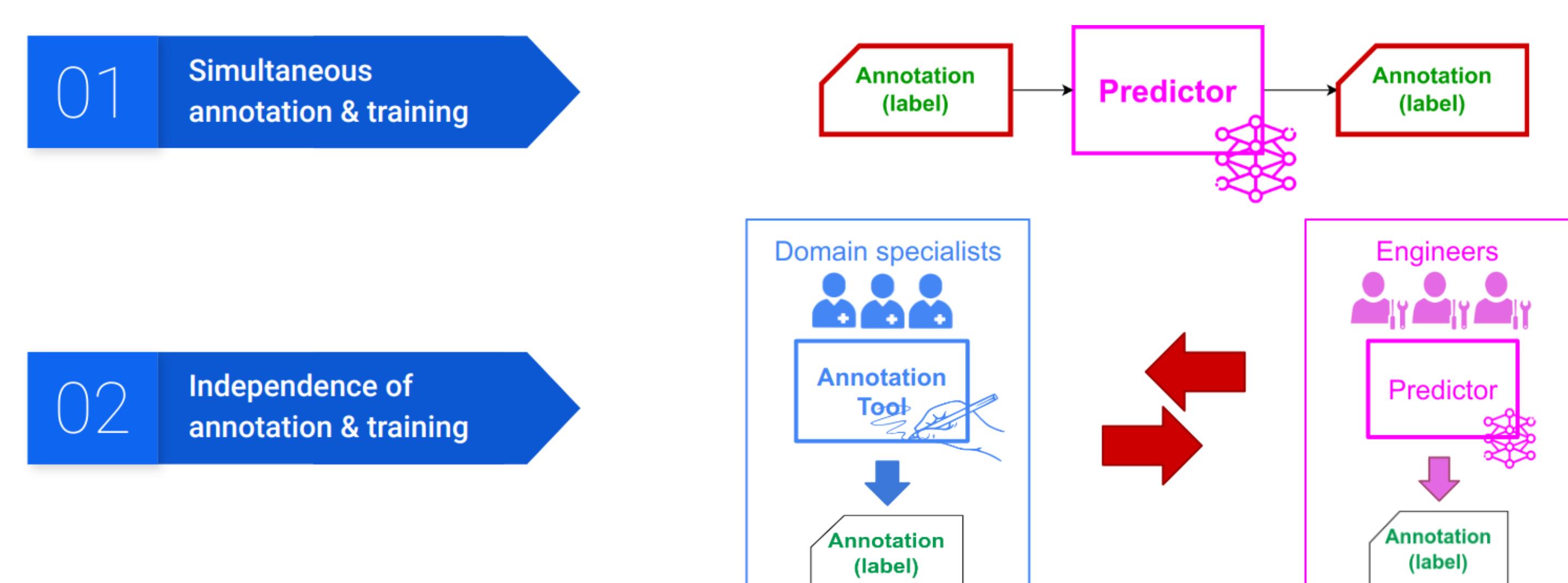


Figure 3. Two main limitations of the classical data annotation and model training pipeline.

## Experimental Results: Metrics

Evaluation: **three emulated** and **one real** annotation scenarios.
**Emulated scenarios:** (1) in female pelvis MRI segmentation on our dataset; (2) in Liver and (3) in Pancreas CT segmentation on decathlon datasets. **Emulated setup:** (a) completely annotated datasets; (b) user interaction simulation in order to generate annotations.
**Real scenario:** kidney MRI segmentation on the AMOS dataset. **Real setup:** (c) mostly non-annotated data; (d) medical expert via a developed GUI.
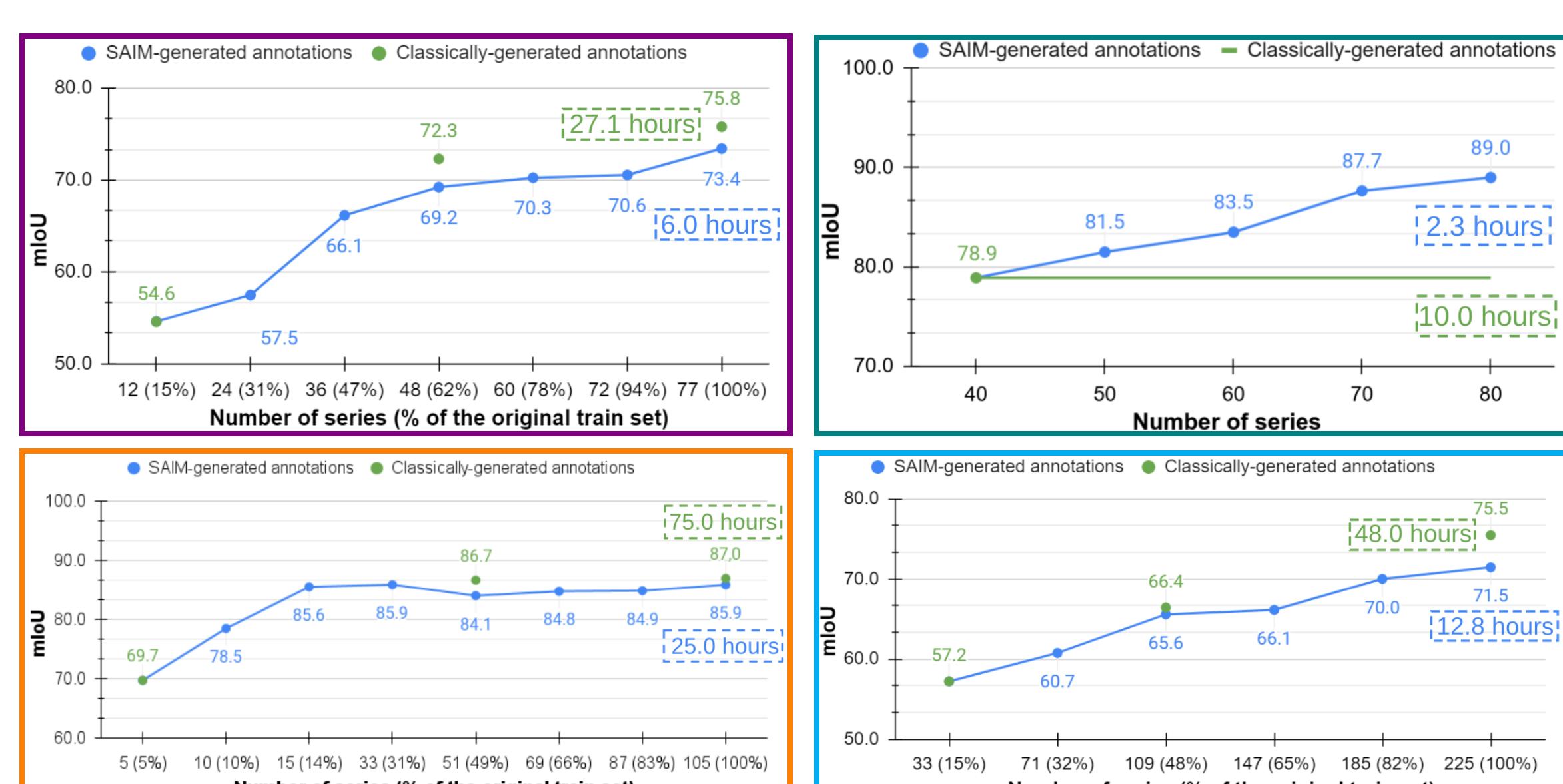


Figure 4. **SAIM** experimental evaluation results given as mIoU at each iteration, where: green - performance using annotations created in 3D Slicer and MITK, blue - performance using **SAIM**-created annotations. Dataset color code: Female pelvis MRI, AMOS Kidney MRI, Decathlon Liver CT, Decathlon Pancreas CT.

## *SAIM* (Single Active Interactive Model): Key Pieces
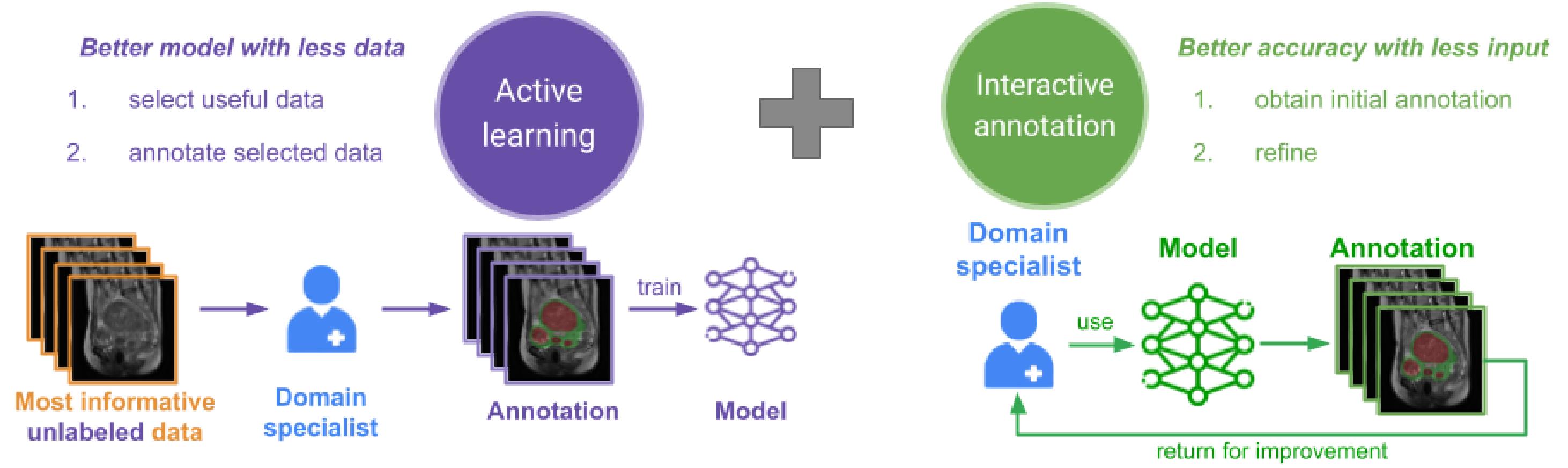


Figure 5. Two key existing ideas required to realise **SAIM**.
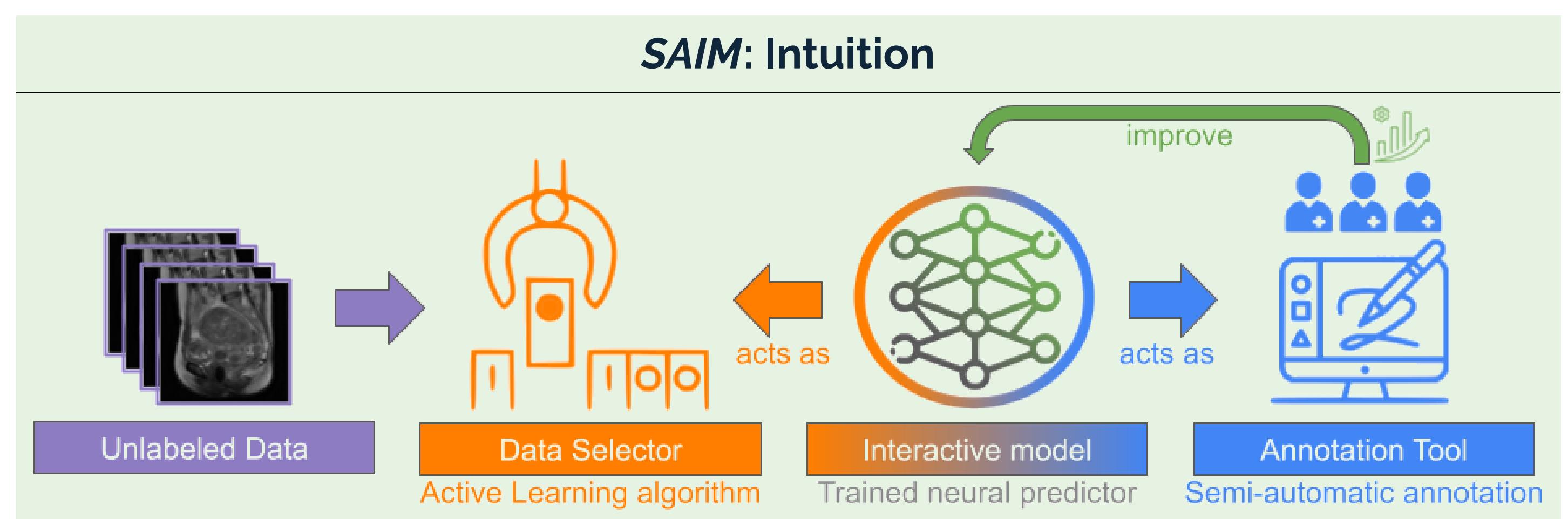
## *SAIM*: Intuition



Figure 6. The intuition behind **SAIM**: use of deep interactive annotation with the shared model and the use of active learning for efficient data selection using the shared model. The shared model improves at each iteration.

## *SAIM*: Complete
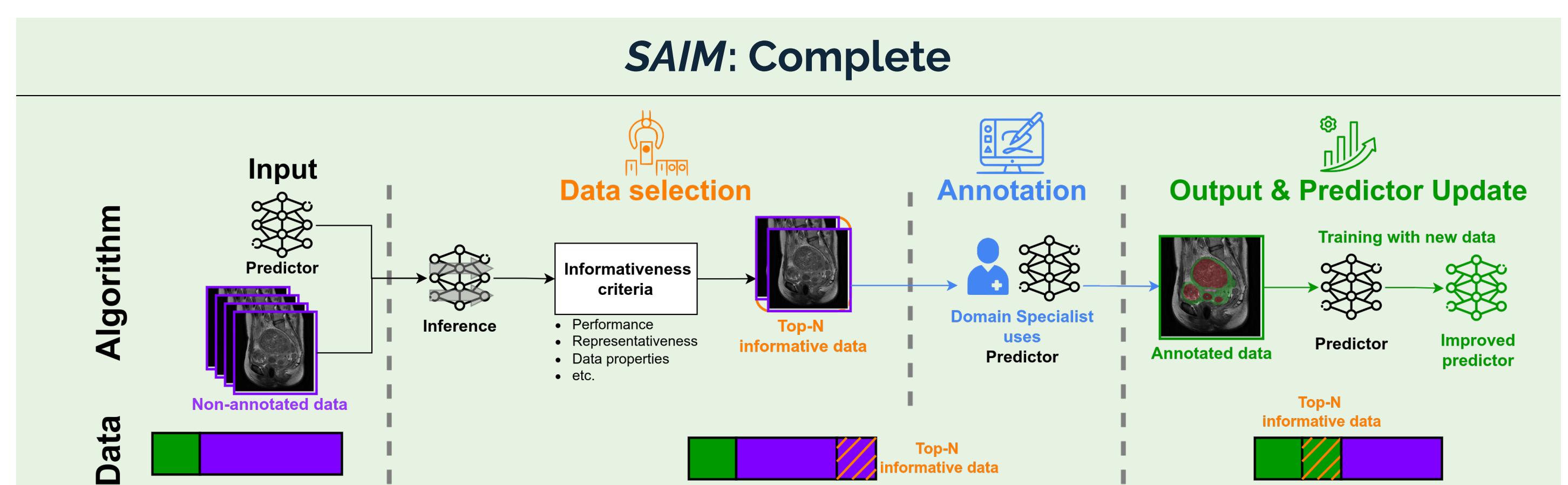


Figure 7. Detailed **SAIM** schematic: a single iteration is shown, only the input changes between iterations.

## Experimental Results: Images
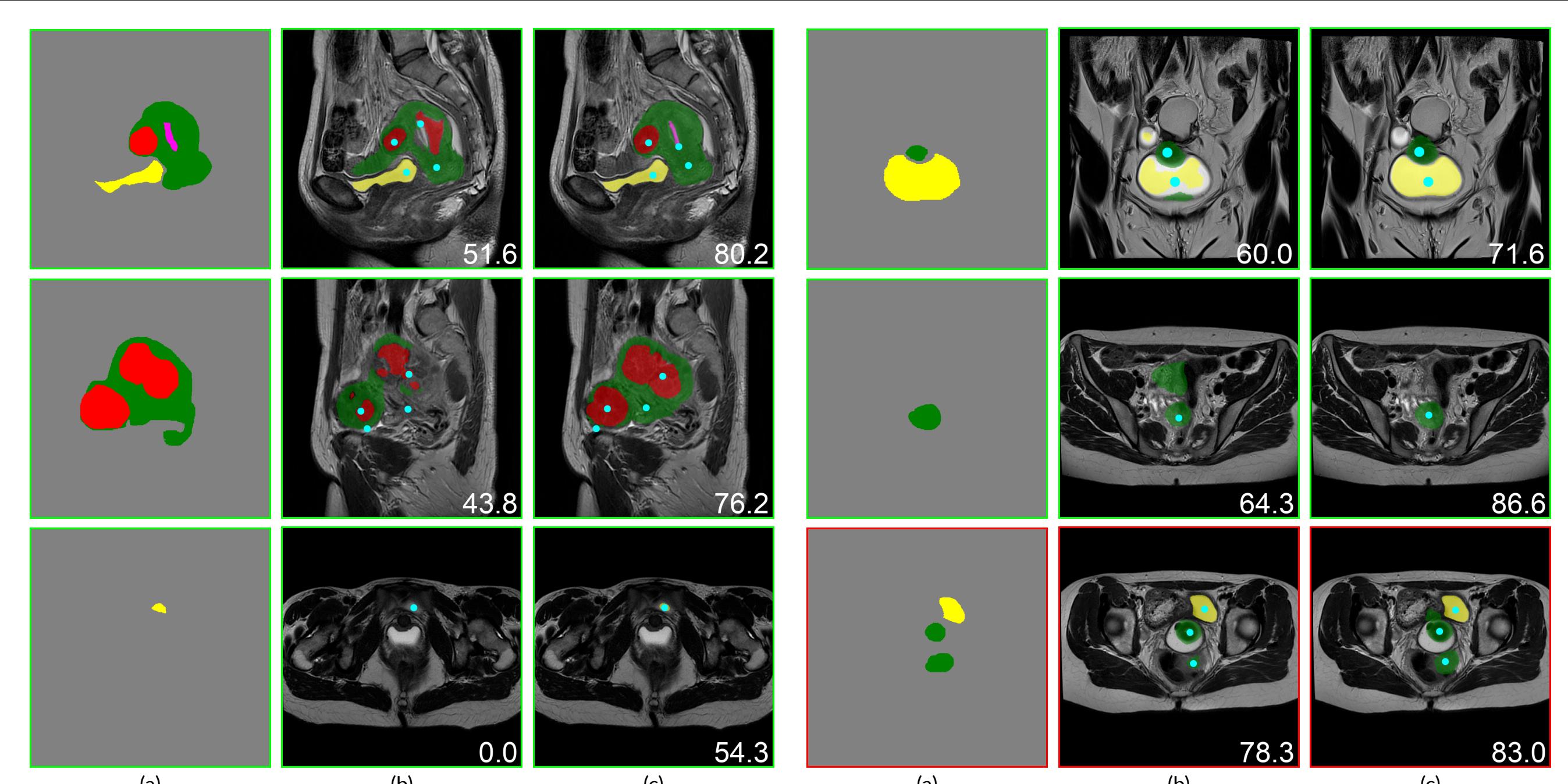


Figure 8. **SAIM** segmentation results in a emulated annotation scenario for female pelvis MRI segmentation dataset, where `uterus` - green, `bladder` - yellow, `tumours` - red, uterine `cavity` - pink, and user clicks are in cyan: (a) ground truth; (b) interactive predictor pre-trained on 15% (12 out of 77 series) of the complete training set (c) the same interactive predictor using the complete training set (77 series), but with the remaining 85% (65 out of 77 series) annotated as a part of **SAIM**. Performance-wise: rows in green (1-5) - improvement, row in red (6) - considered a degradation despite overall higher IoU due to the false positive for `uterus`. IoU is given in the bottom right corner.
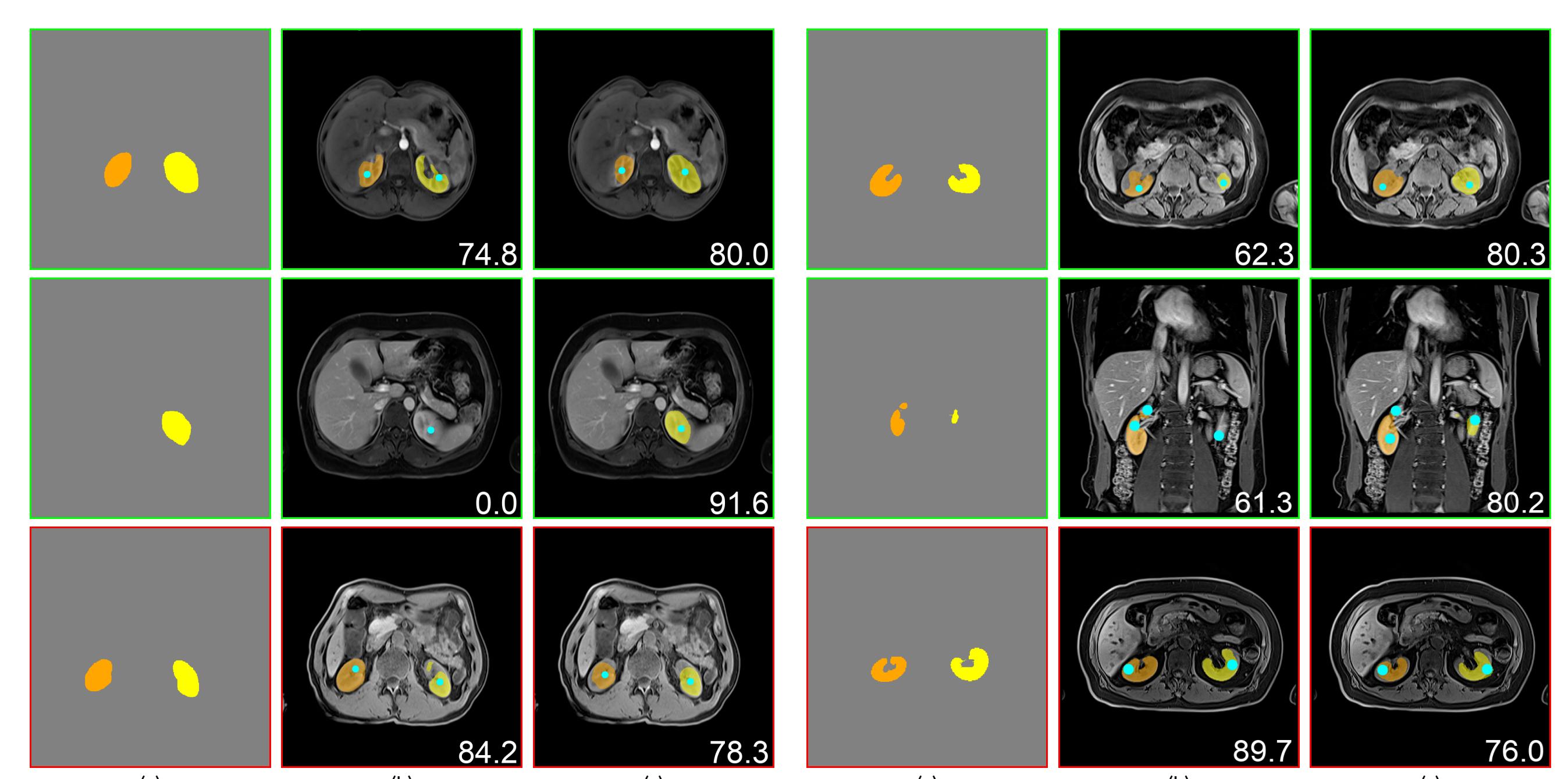


Figure 9. **SAIM** segmentation results in a real annotation scenario for kidney MRI segmentation on the AMOS dataset, where `right kidney` and `left kidney` are orange and yellow respectively with user clicks in cyan: (a) ground truth; (b) interactive predictor pre-trained on original AMOS training set (40 series) (c) the same interactive predictor after doubling the training set as a part of **SAIM** (80 series). Performance-wise: rows in green (1-4) - improvement, rows in red (5-6) - degradation. IoU is given in the bottom right corner.