




Two-Stage Deep Learning Pipeline for Prostate and Lesion Segmentation in MRI Scans

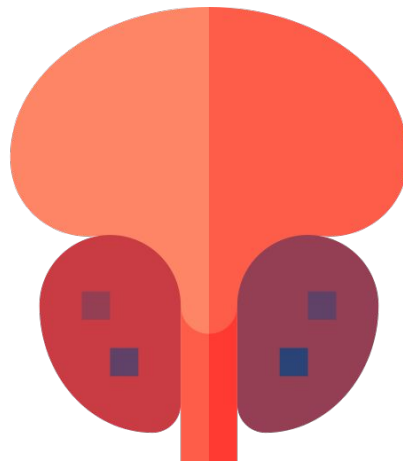


Ryan McGovern, Yoohyuk Chang,
Avery Kuo, Sujin Lee



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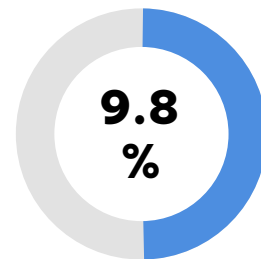
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Prostate Cancer Segmentation

1 in 44

Death among American men,
the 2nd leading causing death



Brachytherapy-treated men had
secondary malignancies, risk of
missing cancerous regions




Prostate Cancer Segmentation

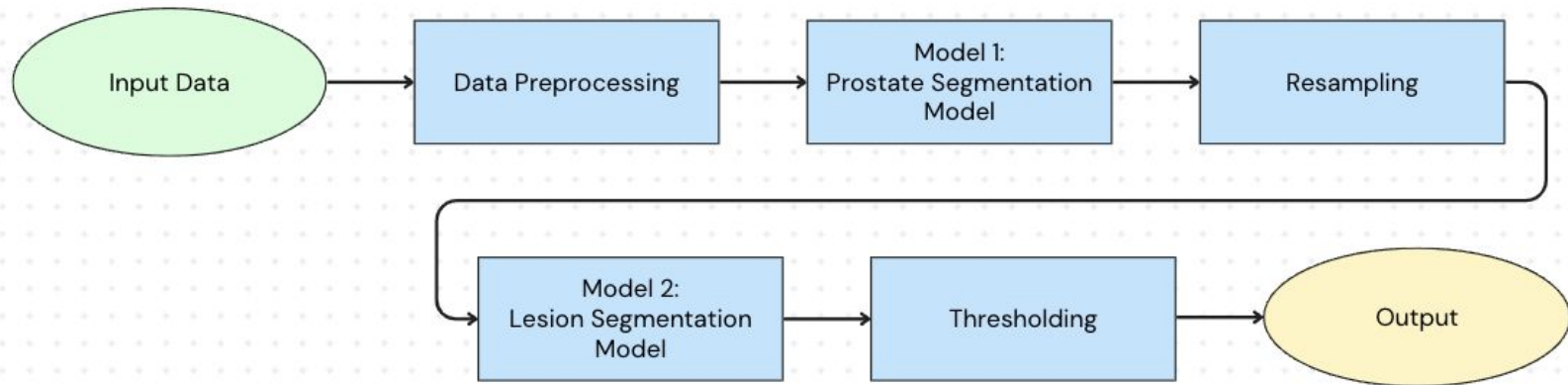
- **Challenges**

- **Variability** in prostate shapes, sizes
- **Low contrast** between the prostate lesions and surrounding tissues

- **Importance**

- Improves **surgical precision** and **radiation therapy** outcomes
 - Reduces the **risk of recurrence** by targeting cancerous tissues
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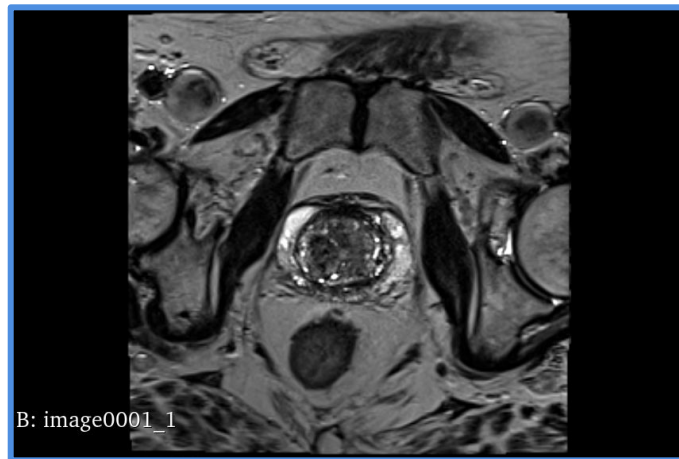
Objective



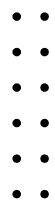
A pipeline of **data processing** and two **U-Net transformer models** that can output **prostate and legion segmentations**

Data Preprocessing: Input Data

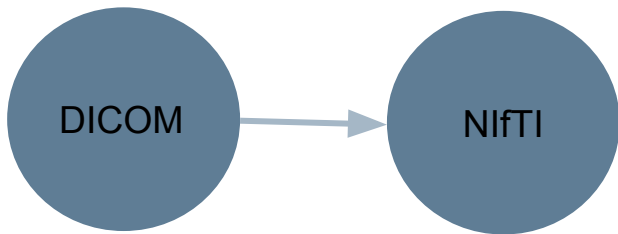
- **MRI scans of 1,152 patients** with prostate cancer from *The Cancer Imaging Archive (TCIA)*
- Downloaded corresponding Digital Imaging and Communications in Medicine (DICOM) annotations



Example MRI Scan Downloaded from TCIA



Data Preprocessing: Conversion to NIfTI



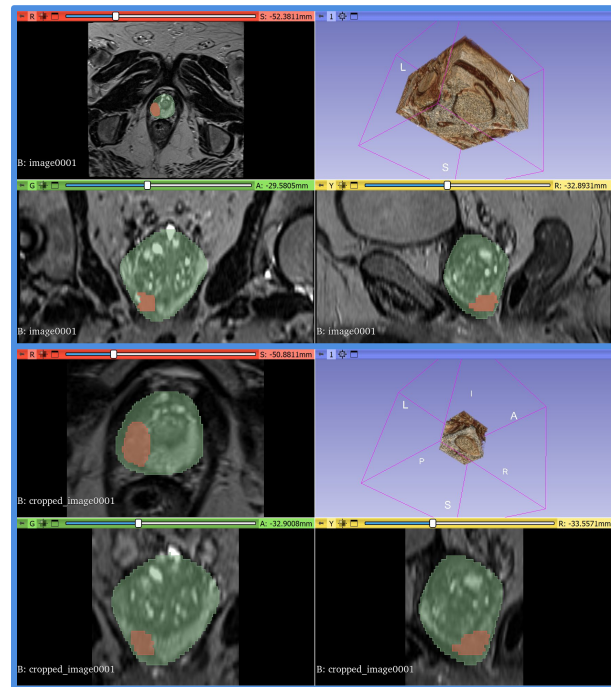
Used **NiBabel** and **Slicer Python** packages

- Easier integration of images and annotations with PyTorch training loops
- Facilitates handling of 3D slice information, affine transformations, and headers



Data Preprocessing: Bounding Boxes

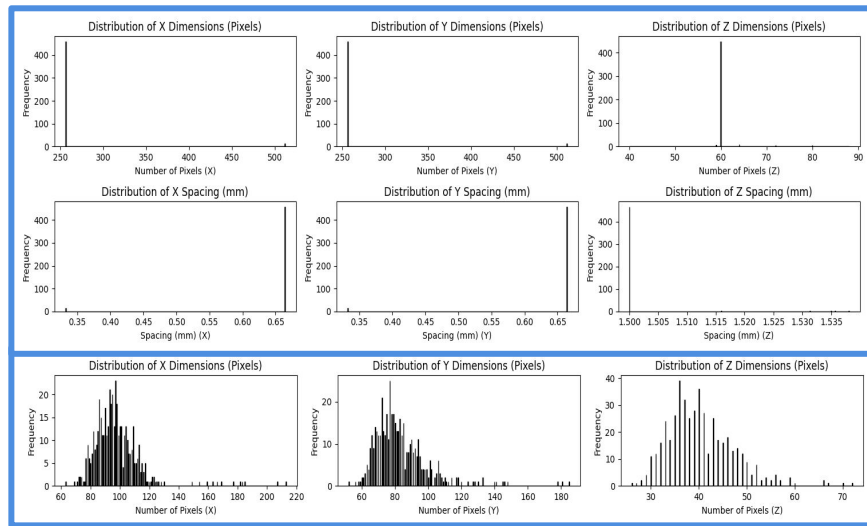
- Calculated minimum and maximum indices by converting original indices into **world coordinates** for consistency
- **Cropped** original image and segmentations according to **min/max indices** while **adding padding**



Comparison between original image and prostate/legion segmentations (top) and cropped image and prostate/legion segmentations (bottom)

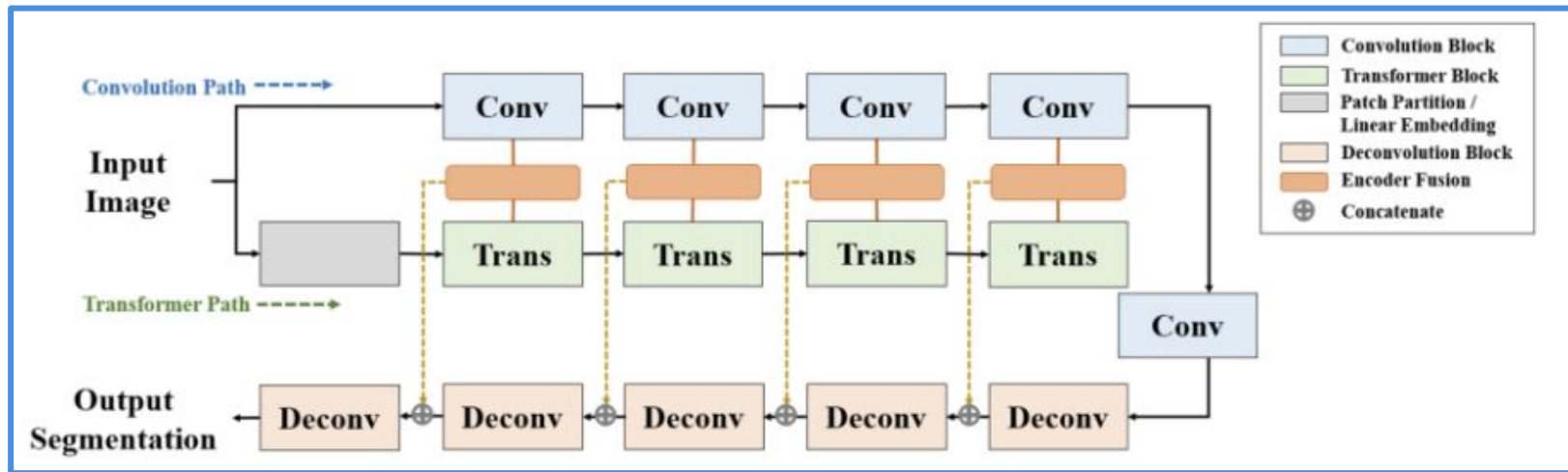
Data Preprocessing: Transformers

- Orient all input MRI images in the **same orientation** as CNNs are not rotationally invariant
- **Normalize intensity** within all input MRI data
- **Standardize size and spacing** for input data that goes into Model 1 and Model 2

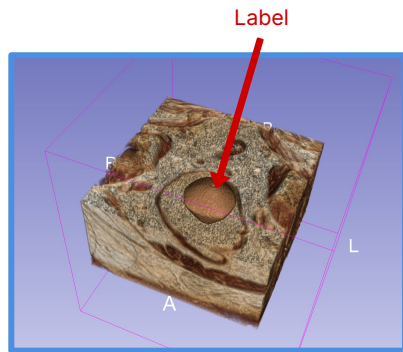


Distribution of image shapes (top), spacing (middle), and prostate shapes (bottom)

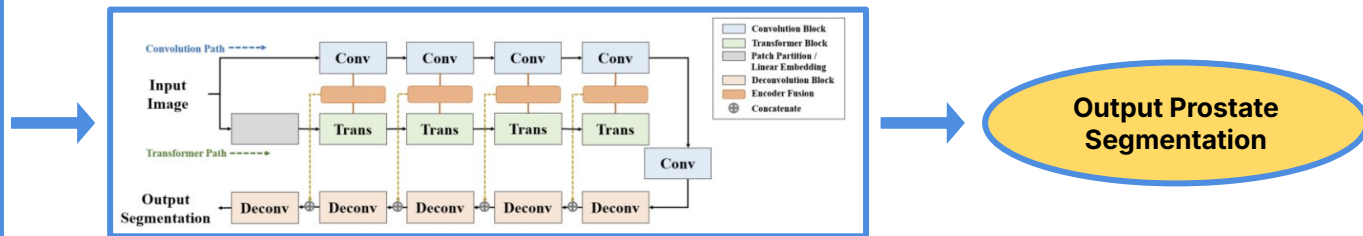
U-Net Transformer Model



Model 1: Prostate Segmentation Model



Input MRI Image



U-Net Transformer

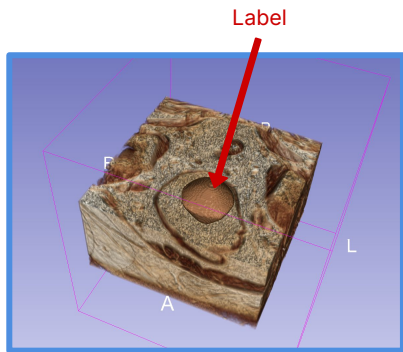
Conv

Trans

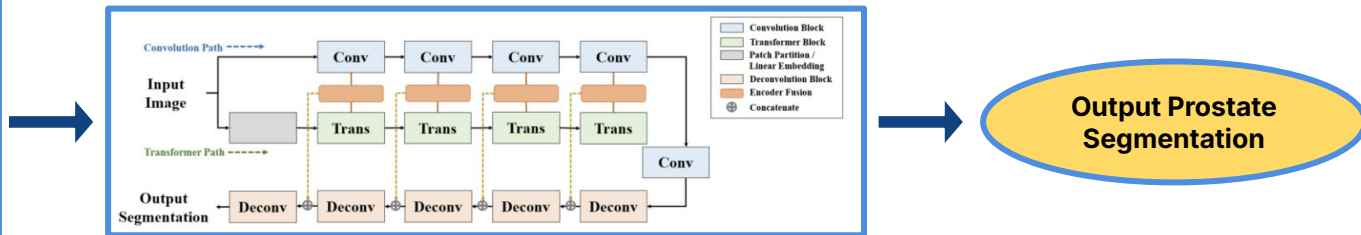
- Two sequential $3 \times 3 \times 3$ convolutions
- Dropout Probability = 0.2
- Parametric ReLU Activation

- 3D Tokenization and Windowed Self-Attention
- Global Context Learning
- Multi-Head Self-Attention and Multi-Layer Perceptron

Model 1: Prostate Segmentation Model



Input MRI Image



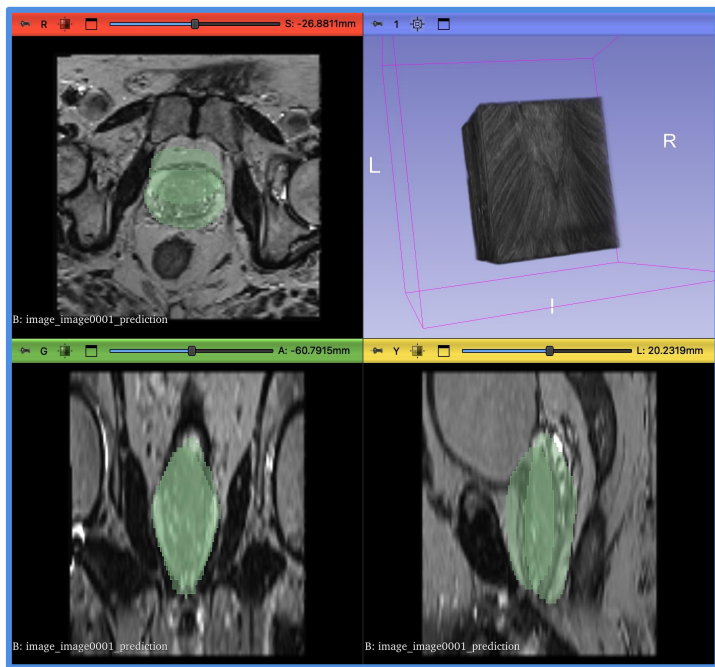
U-Net Transformer

Output Prostate Segmentation

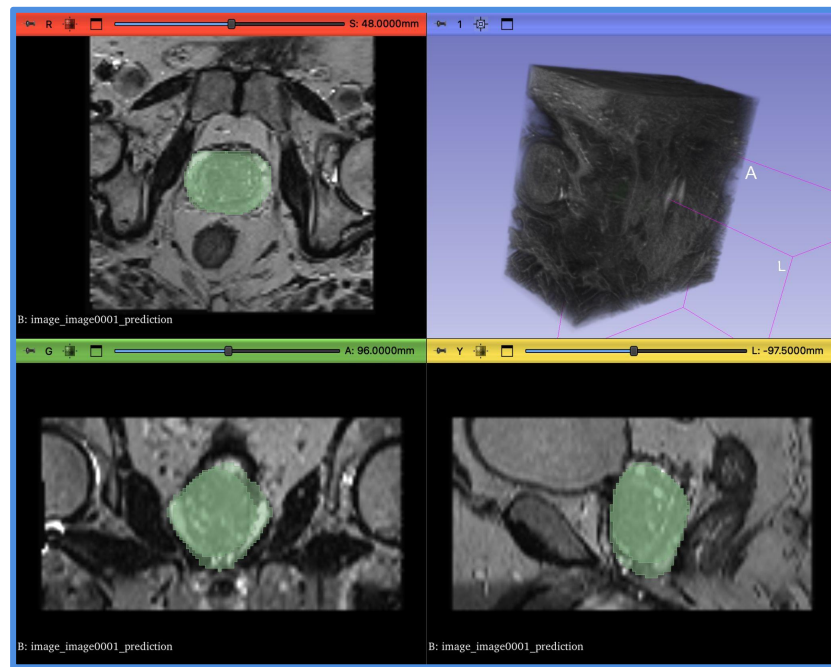
Deconv

- Downsampling in Encoder layers lose spatial information
- Deconv upsamples the feature maps back to the original image size
- Segmentation output must match the spatial resolution of the input

Model 1: Prostate Segmentation Model



Unaligned Orientations of the Segmented Prostate Region Generated from the Prostate Segmentation Model

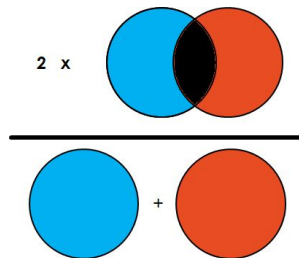


Aligned Orientations of the Segmented Prostate Region Generated from the Prostate Segmentation Model

Model 1: Prostate Segmentation Model

- **Dice Score**

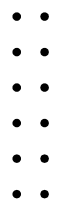
$$\frac{2 \cdot |A \cap B|}{|A| + |B|} = \frac{2 \cdot \text{TP}}{2 \cdot \text{TP} + \text{FP} + \text{FN}}$$



- **Hausdorff Distance**

$$H(A, B) = \max \left(\sup_{a \in A} \inf_{b \in B} d(a, b), \sup_{b \in B} \inf_{a \in A} d(a, b) \right)$$

- Measures the largest distance from any point in A to its closest point in B
- Measures the largest distance from any point in B to its closest point in A
- Takes the maximum of the two distances



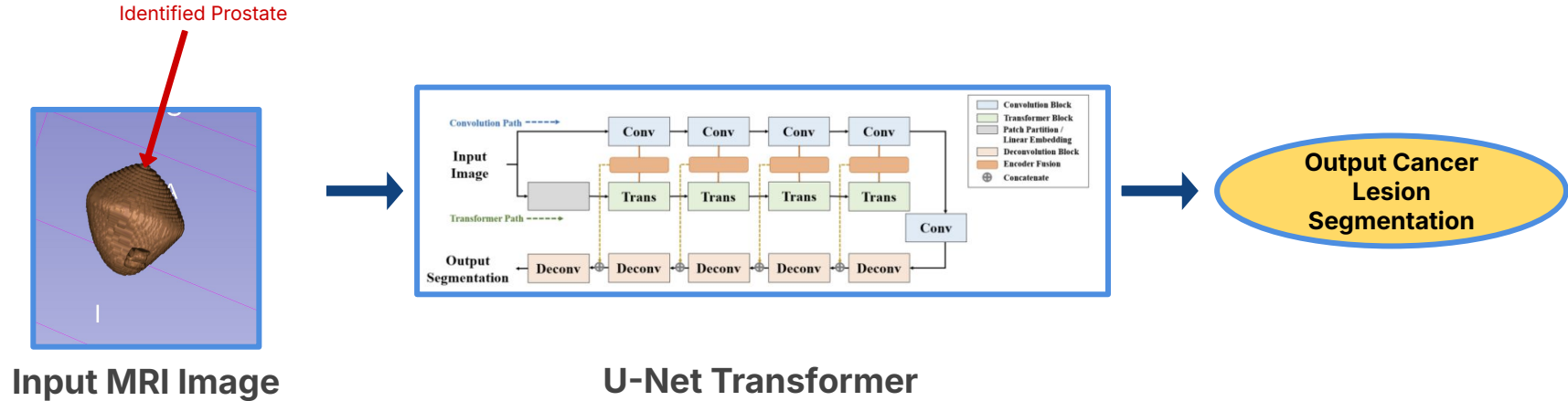
Model 1: Prostate Segmentation Model



- **Dice Metric:**
 - Score: 0.61
 - Standard Deviation: 0.22
- **Hausdorff Distance (95th Percentile):**
 - Mean: 9.44
 - Standard Deviation: 6.09

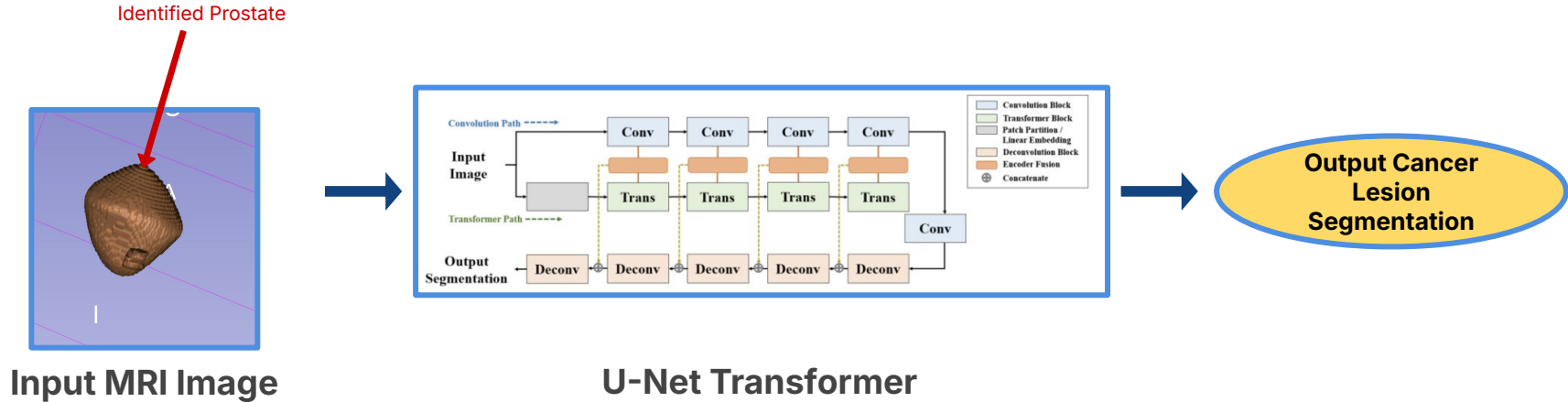


Model 2: Lesion Segmentation Model



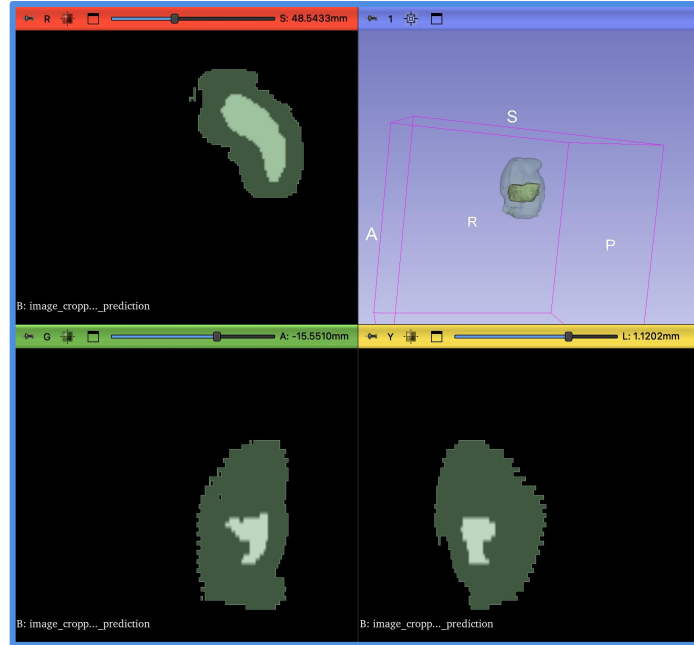
- Utilizes same model that we implemented for Model 1 except with different transforms that we calculated during the training loop.
- Transform for Model 2 is of higher resolution to segment smaller lesions

Model 2: Lesion Segmentation Model



- Utilizes same model that we implemented for Model 1 except with different transforms that we calculated during the training loop.
- Transform for Model 2 is of higher resolution to segment smaller lesions


Model 2: Lesion Segmentation Model



Unaligned Orientations of the Segmented Prostate Region Generated from the Prostate Segmentation Model



Model 2: Lesion Segmentation Model

- **Dice Metric:**
 - Score: 0.04
 - Standard Deviation: 0.08
 - **Hausdorff Distance (95th Percentile):**
 - Mean: 43.26
 - Standard Deviation: 20.21
- 



Conclusion




- **Summary**

Developed two **Transformer-U-Net models** for accurate **prostate and lesion segmentation**

- **Implications of Our Results/Models**

Enables **faster, more accurate prostate cancer detection** to support **diagnosis and treatment** for clinicians

- **Future Work**

- **Explore using the first model's predicted prostate region** for training the second model to compare it with our current second model
 - Research ways to **invert transforms** given cropped and padded data
 - Apply our models to **other organs** in the human body as it can be indicative of potential diseases
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