LOCAL INTERPRETABLE MODEL-AGNOSTIC EXPLANATIONS FOR MEDICAL IMAGE SEGMENTATION

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INTRODUCTION

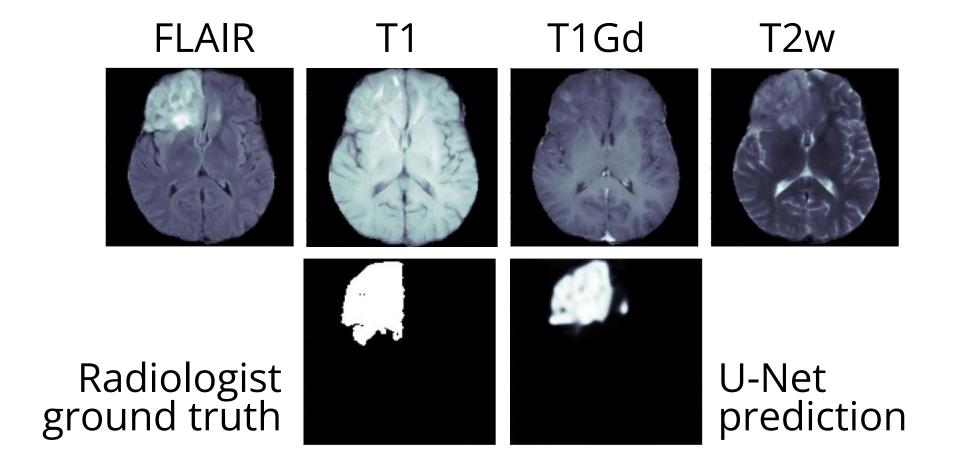
- The field of **eXplainable Artificial Intelligence** (XAI) attempts to address the AI black-box problem by uncovering unknown mechanisms and limitations of complex models.
- Existing XAI frameworks often have narrow compatibility and cannot be applied to medical image segmentation tasks.
- Local Interpretable Model-Agnostic Explanations (LIME) is an explainability framework intended to accommodate a vast array of black-box models.

We modified LIME to work with multiple MRI sequences for slice-wise tumor segmentation.

MATERIALS

Dataset

- MRI scans via The Cancer Genome Atlas
- 144 slices × 144 pixels × 144 pixels × 4 sequences
- Patient of Interest: 'TCGA-HT-7874,' slice 75



U-Net

- Convolutional neural network architecture
- Performs 2D slice-wise tumor segmentation with multisequence MRI input

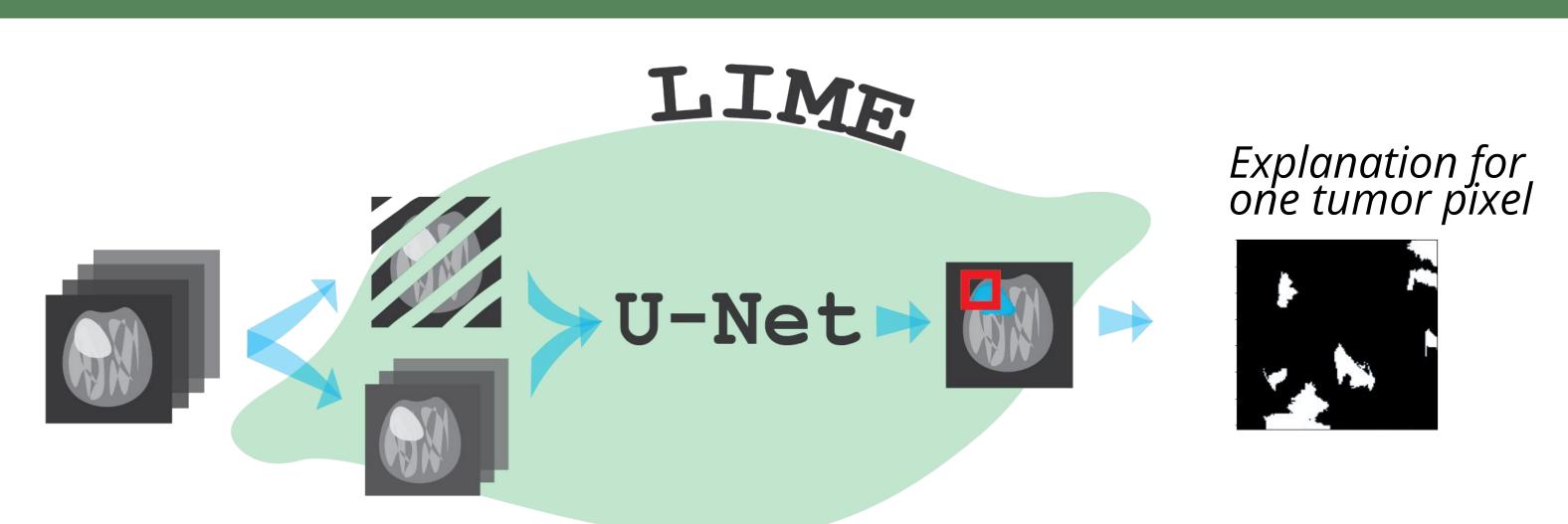
LIME

Identifies important features for individual predictions

Local: investigates specific instance/prediction Interpretable: linear, sparse surrogate model Model-agnostic: perturbations around a local input allow compatibility across classifiers Explanations: surrogate model feature weights approximate model behavior

$$egin{aligned} \xi(x) &= \operatorname{argmin}_{g \in G} \ \mathcal{L}(f,g,\Pi_x) + \Omega(g) \ \mathcal{L}(f,g,\Pi_x) &= \sum_{z,z' \in \mathcal{Z}} \Pi_x(z) \left(f(z) - g(z')
ight)^2 \end{aligned}$$

GENERATING EXPLANATIONS



Perturb one sequence \rightarrow pass all four to U-Net \rightarrow explain one pixel's prediction Repeat binary classification (pixel = tumor/non-tumor) to simulate segmentation

Superpixel Generation Algorithm Comparison

quick shift

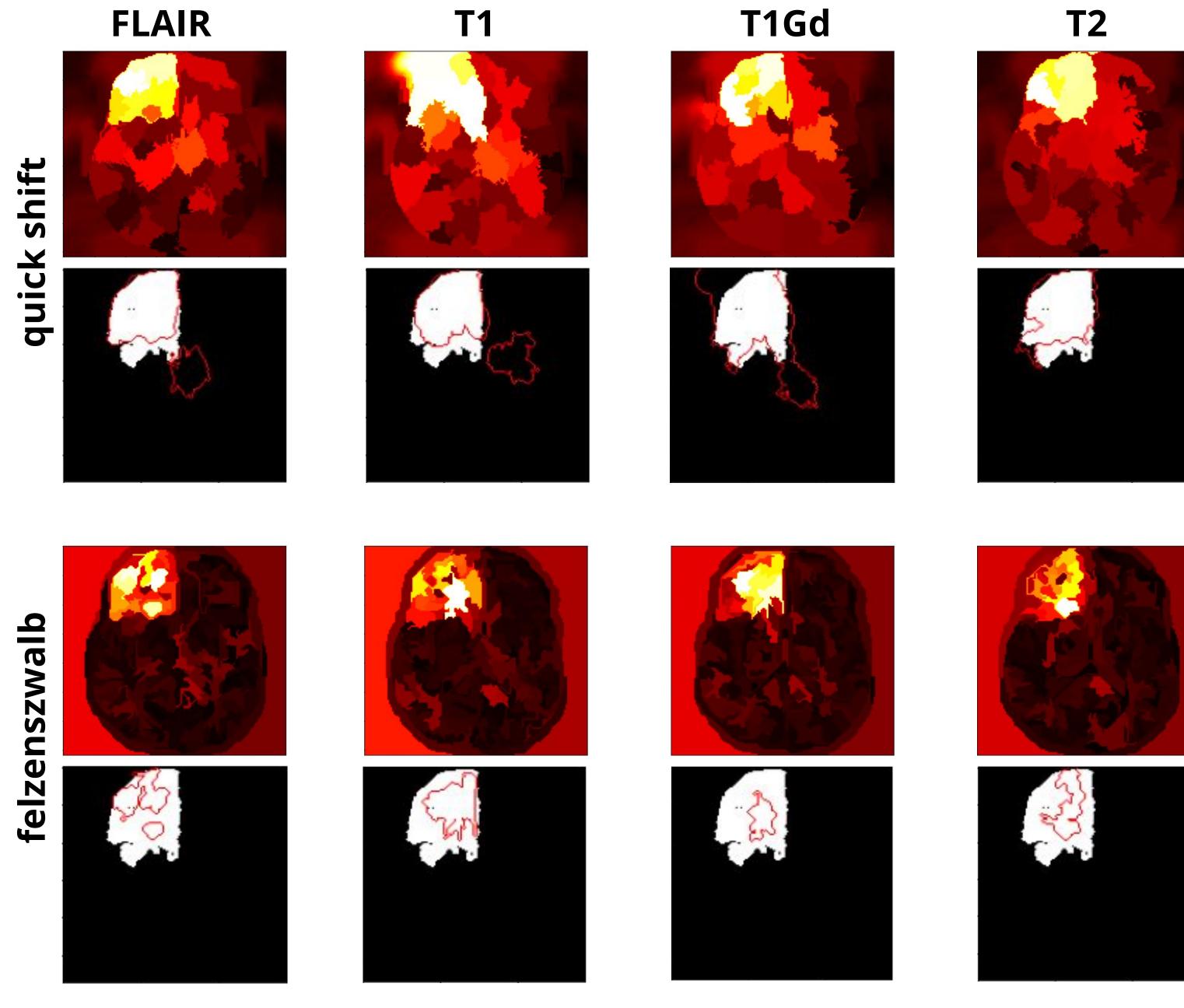
- Forms a tree of density-dependent links to nearest neighboring pixel
- Superpixel clusters occupy joint spatial and color dimensions

felzenszwalb

- Graph-based segmentation approach
- Pixels-as-vertices representation, connecting edges
- Segmentation based on vertex-wise affinity

RESULTS

Explaining U-Net: LIME-determined important features



	FLAIR	T1	T1Gd	T2
quick shift	74.9%	72.0%	89.7%	74.9%
felzenszwalb	26.1%	34.1%	12.8%	22.2%

Table: Percentage of tumor pixels included in explanations when threshold = 0.5

CONCLUSION

Takeaways

- Modified LIME to accommodate segmentation tasks by simulating binary classification problems.
 Allowed for inputs of multisequence imaging data types with limitations.
- Quick shift-segmented explanatory regions for tumor-identified pixels incorporate a larger percentage of total tumor pixels relative to felzenszwalb.

Future Endeavors

- Explore the merits of *slic* segmentation algorithm, which utilizes the LAB color space as opposed to RGB.
- Train U-Net on contextual information (e.g. clinical observations) as opposed to lone ground truth segmentations and tumor vs. non-tumor labeling.
- Develop metrics for assessing U-Net accuracy and determine if particular MRI sequences result in more optimal diagnoses.
- Attempt global explanation using a set of local instances.

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