Improving Pathological Structure Segmentation Via Transfer Learning Across Diseases

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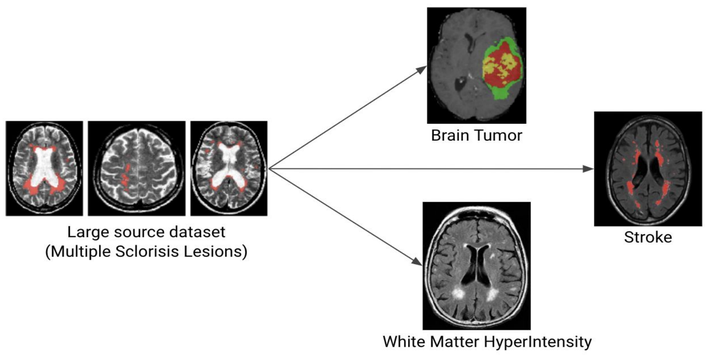
1. Motivation and Objective

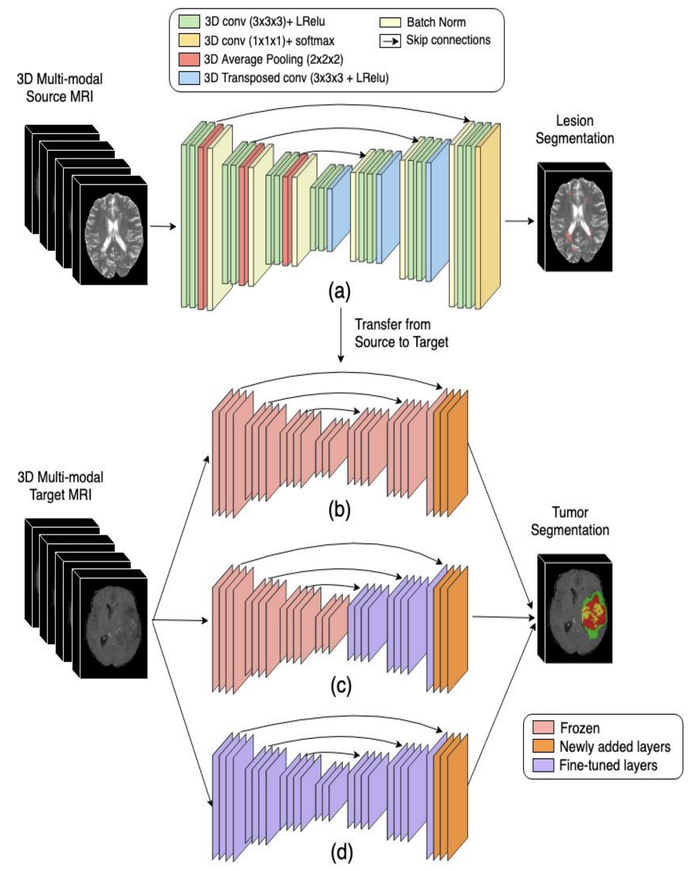
- Major challenges in pathology segmentation include:
  - Lack of access to large annotated datasets.
  - Existing small public datasets suffer from large class imbalance and inter-subject variability issues.
- State-of-art models are based on deep learning methods, which perform well when trained on large datasets[1].
- Leveraging models trained on large datasets in order to improve results on smaller dataset could be impactful.



  - We explore several fine-tuning strategies to best leverage source model for target dataset of varying sizes.

2. Proposed Method

- **First Phase:** Pretraining the UNet[1] with source MS dataset.
- **Second Phase**:
  - Replacing last three layers of the pre-trained MS network with **new layers**.
  - Fine-tuning with target brain tumor in three different ways:
    - **FT_LastThree**: only the newly added layers are re-trained.
    - **FT_Decoder**: only the decoder is fine-tuned.
    - **FT_All**: the whole network is fine-tuned.



3. Data and Experimentation

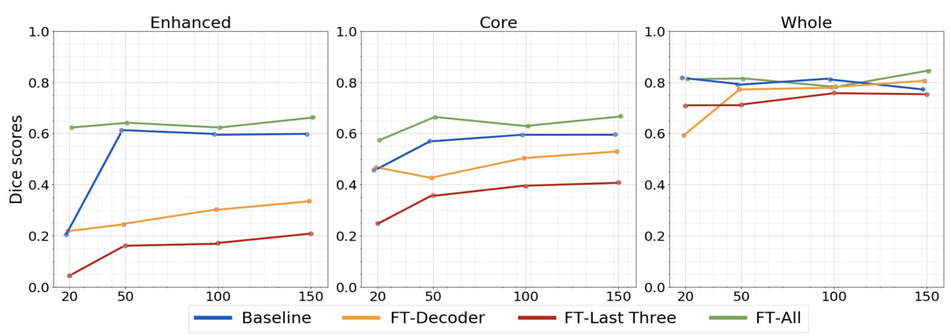
Source Data: Multiple Sclerosis (MS) dataset

- Proprietary, multi-modal, multi-site, multi-scanner clinical trial dataset.
- 3630 Multi-modal MRI (T1w, T2w, FLAIR, and T1 post-Gad).
- For our first phase, we use:
  - 80% of available data to train 3D UNet.
  - Remaining 20% of data to validate 3D UNet.
- Weighted Binary Cross Entropy loss.
- Evaluation metric: ROC curves for T2 lesion segmentation.
- An AUC of **0.77** is obtained on the validation set.

Target Data: Brain Tumor dataset (BraTS 2018 challenge[2])

- Multi-modal MRI (T1, T2, FLAIR, and T1ce).
- Registration to same space as source data using ANTs tool[3].
- For **20, 50, 100, 150** brain tumor samples (subset of BraTS 2018 training set):
  - **Transfer learning:** FT_LastThree, FT_Decoder, FT_All.
  - **Baseline**: Training from scratch with brain tumor MRI scans.
- Weighted Cross Entropy loss.
- Four-fold cross validation is performed.
- A **local validation set** of 50 samples is used to select operating point.

4. Quantitative Results

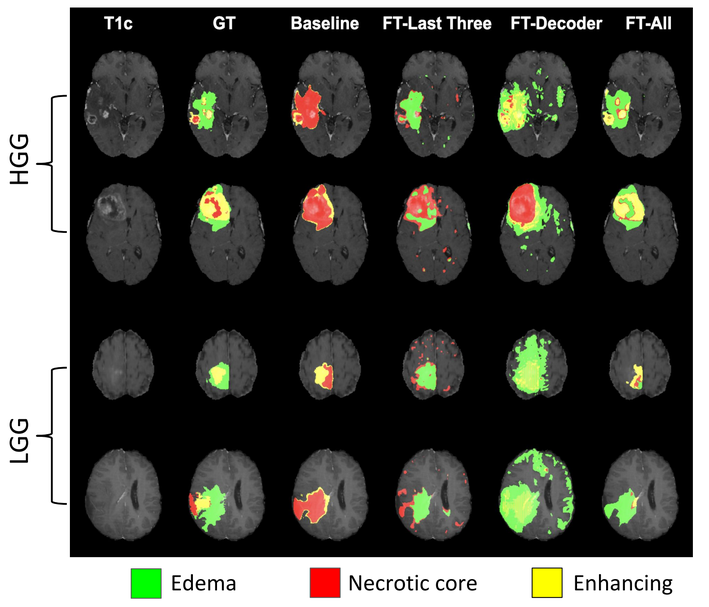


Dice scores obtained on the Brats 2018 Validation set used for testing.

- **FT-All outperforms** the baseline in almost every case.
- High gain when number of tumor cases is **extremely low,** i.e. 20.
- **Gain of FT-All over baseline diminishes** with more samples**.**

5. Qualitative Results (fine-tuning with 20 brain tumor samples)

- FT-All is able to capture sub-structures of tumor better than other methods.
- Performance is better on HGG cases over LGG, as more HGG cases are present in training set.



6. Conclusion

- We explored **different strategies for transfer learning** across diseases for the task of focal pathology segmentation.
- We observed that **fine-tuning the whole network** outperforms baseline and other fine-tuning methods, especially when very small target datasets are available, unlike in case of natural images where fine-tuning just last few layers helps.
- We encourage **public release of models** trained on large datasets.

References:
[1] Özgün Çiçek et al., 3D U-Net: Learning Dense Volumetric Segmentation from Sparse Annotation, MICCAI 2016.
[2] Menze et al., The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS), TMI 2015.
[3] Avants et al. A reproducible evaluation of ANTs similarity metric performance in brain image registration, Neuroimage 2011.

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