Meeting - Week 3

Progress, Challenges & Next steps

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Questions? (1/3)

Should we train a separate model for each organ (e.g., liver, brain, prostate) to maximize specialization, or would a single model trained on all datasets generalize well across different organs? Alternatively, would pretraining on multiple organs and fine-tuning per organ be a better approach?

The LiTS preprocessing script resizes images to 320×320 and creates three-channel inputs using neighboring slices.

- Should we crop/resize our dataset to match this format, or can we keep the original resolution?
- How should we handle three-channel input if the number of slices is not a multiple of 3?
- Are there any strict formatting requirements we need to follow for U-Net 3+?

Questions? (2/3)

Handling 4D NIfTI Files in U-Net 3+

Some .nii files contain an extra dimension, making them 4D (e.g., 512×512×49×4).

- How should we handle the extra dimension? Should we select a specific channel, merge them, or treat them as separate inputs?
- If selecting a single channel, which one is most relevant for segmentation?
- Should we preprocess 4D files differently from standard 3D volumes?

How do we fairly compare this U-net 3+, with our multi-scaling approach if we need to crop images differently/more in U-net 3+, than our multi-scaling model approach, since then the different cropping seem to hold a big factor for the final score.

Questions? (3/3)

- It seems like we have test data with images and labels and then validation data without labels. Why is that? Is it, because we need to get the individual score of each of the segmentation and average it out as the average dice score of all images?
- We're unsure if we have to calculate the dice coefficient on the decoded segmentation and the mask? Since it doesn't seem like we have a mask in the validation part?