**Links**

* [Data](http://medicaldecathlon.com/) (pancreas only)
* [Results on challenge with nnU-NET](https://arxiv.org/abs/1809.10486)
* [DeepMind U-NET architecture](https://arxiv.org/abs/1809.04430) (with top-k loss for class imbalance)
* [Focal loss paper](https://arxiv.org/abs/1708.02002)
* [Usefull tutorial for processing data in PyTorch](https://pytorch.org/tutorials/beginner/data_loading_tutorial.html)
* [Loading .nii.gz files with python](https://nipy.org/nibabel/gettingstarted.html)

**Messages from Nikita**

April 17:

The task will be Pancreas segmentation (go to http://medicaldecathlon.com/, then go to the data folder). You need to know how to work with basic Unet (Python + DL library of your choice, my preference is PyTorch since this is what I am most experienced with). Additionally, you might wanna check https://arxiv.org/abs/1809.10486 for some nice results on this challenge. Finally, you might want to have a look at the attached article for a very recent 3d Unet architecture from DeepMind, in particular, take note of the Top-k loss they are using, which is useful when dealing with class imbalance.

April 19

Hi team,

Some additional comments, instructions and code which you can find helpful. The pancreas train data varies in shape: from 37 in z-dimension up to 751, while xy dimensions stay the same and equal 512x512. Thus taking patches of dimension 128 in z is too much, you can try patch size from nnUnet (96x160x128) as a first guess if you want to go for a typical 3D Unet and choose not implement the DM-Unet. If you pick DM-Unet, you feed in 21x512x512 patches.

Additionally, the voxel spacing varies as well. This means that you have to resample the images to the same voxel size. I would propose to use SimpleITK for image loading and basic operations such as resampling. For the resampling code, use this

https://github.com/deepmedic/SimpleITK-examples/blob/master/examples/resample\_isotropically.py

You need to resample both the data and the labels. Resample data with linear interpolator. Your labels are integers indicate if the voxel is background, pancreas or tumor, and you should use nearest interpolator for labels. I don't think you need to make any additional labels for mask here.

Here are some statistics for you which you may need to do your work:

1. Median spacing: (2.5, 0.80, 0.80), that is, we have poorer resolution in z. You can resample anisotropically to this size.
2. Median foreground percentage (pancreas+cancer / whole volume): 0.2 %
3. Median cancer percentage (cancer / whole volume): 0.01 %

Given the class imbalance, I would also propose to use a WeightedRandomSampler and sample in such a way that 30-50% of your training patches contain a non-background class. Finally, you should of course be aware of the fact that loading whole volumes from the disk each time you sample patches is rather slow compared to loading just the patches you require.

Good luck.

Regards,

Nikita

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NOTES TAKEN IN THE FIRST MEETING

* Weighted crossentropy
* There a lot of imbalance data, we need to do around 16 patches per samples. And then
* Load images itk library.
* Check data augmentations.
* Patching we want to sample
* The labels in the data set, 0 background, 1 pancreas, 2 cancer. 30% contain pancreas 30% no pancreas .
* Multiclass segmentation problem.

NOTES TAKEN MAY 10th

- Depending on the loss function we maybe dont have to use the softmax function.

- normalize with the whole patch collection using mean and standard deviation. we need to clip the values (-200,+200)

- anisotropic reshamping (try if it works)

- weighted cross entropy for the imbalance of the classes