

Brain Tumor Segmentation with Deep Neural Networks

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Introduction

Clinical Background:

- > 20.000 new brain cancer cases per year in the US
- MRI images as most common modality for tumor diagnosis
- Often difficult to localize (gliomas and glioblastomas)

Why Deep Learning?

- Voxel values in MR images are not standardized
- *Learning* features with CNNs (as opposed to classical machine learning)
- Improved diagnostics, growth rate prediction and treatment planning

Convolutional Neural Networks (CNNs)

- Deep Neural Networks adapted to image data
- Stanford University class: <http://cs231n.github.io/>

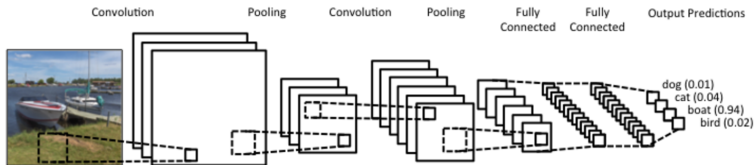


Figure: Schematic overview of a CNN architecture

(Image from <https://medium.com/@Aj.Cheng/convolutional-neural-network-d9f69e473feb>, 12.05.2018)

Convolution (in images)

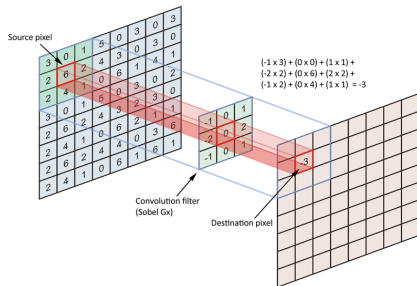


Figure: 2D-convolution: weighted sum over a local patch of data
(Image from <https://i.stack.imgur.com/YDusp.png>, 12.05.2018)

Architecture

- BraTS 2013 dataset
- Slice by slice segmentation due to bad depth resolution
- Different image modalities of the same structures

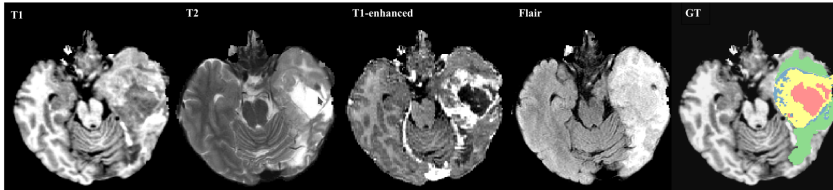


Figure: MRI sequences used as input channels and ground truth labels

Architecture

Two-pathway architecture:

- One smaller (7×7) and one larger (13×13) receptive field
- Prediction based on local region and larger context

Cascaded architectures:

- Goal: model dependencies between spatially close labels
- *Input concatenation*
- *Local pathway concatenation*
- *Pre-output concatenation*

Two-pathway architecture

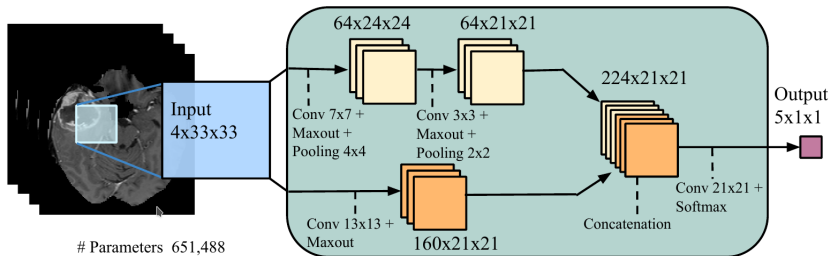


Figure: Two-pathway CNN architecture

Cascaded architecture

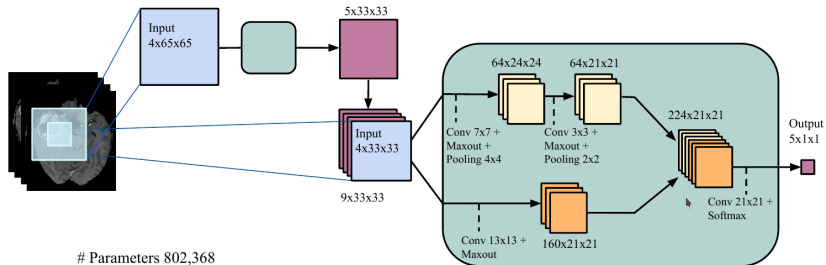


Figure: Cascaded architecture using input concatenation

Training

Gradient Descent:

- Forward propagation on a mini-batch of patches
- Compute label probabilities and deviation from ground truth
- Update the CNNs parameters

Two-phase training:

- Highly imbalanced data (98% healthy voxels)
- First: Pick patches such that all labels are equiprobable
- Then: Re-train output layer with original distribution

Regularization:

- Prevent overfitting by bounding kernel weights and modifying output probabilities

Two-pathway architecture

- Second phase and joint training of local and global path yields better performance
- Very fast, about 25s for a whole brain

Table: Quantitative results of the two-pathway architecture variations on the BRATS 2013 dataset

Rank	Method	Dice	Specifity	Sensitivity
4	TwoPathCNN*	0.85	0.93	0.80
9	LocalPathCNN*	0.85	0.91	0.80
10	AverageCNN*	0.84	0.95	0.77
14	GlobalPathCNN*	0.82	0.93	0.75
14	TwoPathCNN	0.78	0.67	0.96
15	LocalPathCNN	0.77	0.65	0.96

Cascaded architecture

- Fast, about 3 minutes for a whole brain
- Winner of the challenge takes about 100 minutes

Table: Quantitative results of the cascaded architecture variations on the BRATS 2013 dataset

Rank	Method	Dice	Specificity	Sensitivity
2	InputCascadeCNN*	0.88	0.89	0.87
4-a	MFCascadeCNN*	0.86	0.92	0.81
4-b	LocalCascadeCNN*	0.88	0.91	0.84

Cascaded architecture

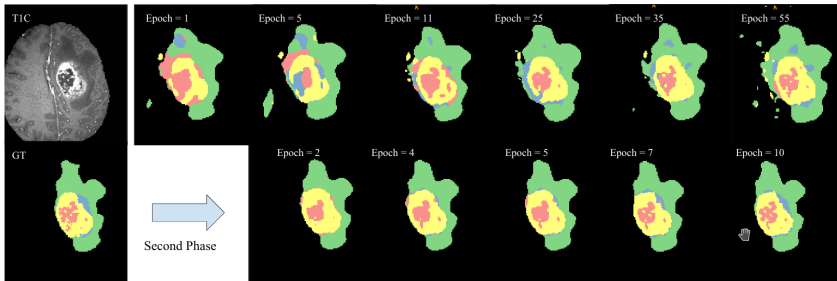


Figure: Progression of learning InputCascadeCNN*

Conclusion

- Automatic brain tumor segmentation based on deep learning (Convolutional Neural Networks)

Improve on currently published state-of-the-art methods

- Especially in speed (25s to 3m per brain)

Novel two-pathway architecture

- Local details and global context
- Model local dependencies of labels

Thank you for your attention!

Any questions?