

# Weakly Supervised Brain Tumor Segmentation

Florentin Bieder, Robin Sandkühler and Philippe C. Cattin Center for medical Image Analysis & Navigation



## WHAT IS WEAK SUPERVISION?

In Deep Learning the power of a model largely depends on the amount and quality of data it is trained on. Supervised models usually need a target *label* for each datapoint for training. This allows the model to capture the relationship between input and output. We distinguish between following types of supervision:

### **Full Supervision:**

label

#### Weak Supervision:





Image source: MICCAI BRATS 2015

# EXAMPLES OF DOMAIN TRANSLATION MODELS

Andermatt et al. proposed PathoGAN[1] for weakly supervised image segmentation, an extension of the seminal unpaired image-to-image translation model CycleGAN[2].



Fig. 2: A complete cycle in *CycleGAN*.

## WHY WEAK SUPERVISION?

Advantages and challenges of weak supervision:

- + Producing weakly labelled data is cheap, or even already available, while full segmentations require an expert labelling each pixel.
- + Weak supervision does not have to deal with the noise and bias of the expert labels.
- + A model trained using weak supervision might potentially detect new symptoms of a known disease.
- It is not obvious how to build a model that can be trained using only weak supervision.
- The state-of-the-art weakly supervised methods are still outperformed by fully supervised methods.

#### PAIRED VS. UNPAIRED DOMAIN TRANSLATION

When we consider the task of domain translation we distinguish two settings: *paired* and *unpaired* translation. In the paired setting we have images with the same content in both domains (e.g. T1 and T2 MRIs of the same object) while in the unpaired setting we have no corresponding images across the domains (e.g. healthy and diseased organs). Instead of the standard generators used in CycleGAN (see fig 2), a more sophisticated model was used which includes a skip connection (see Fig. 3) to pass the information about the pathology around the pseudo healthy domain.





Fig. 1: Paired vs. unpaired data We can also consider weakly labeled data as unpaired data, and try to apply unpaired domain translation models. **Fig. 3:** One pass through the  $P \rightarrow H \rightarrow P$ -cycle in the *PathoGAN* model proposed by Andermatt et al.[1].

Xia et al.[3] proposed a model (see Fig. 4) intended for the generation of healthy looking images from images that contain pathologies as a means of augmenting training data for training other models or for the use in education.



Fig. 4: Translation including segmentation and reconstruction in the model proposed by Xia et al.[3].

Vorontsov et al.[4] tried to use both fully- and weakly-labelled data to perform segmentation. To include weakly labelled data they also proposed a domain translation approach (see Fig. 5).



Image source: MICCAI BRATS 2015

#### References

- [1] Andermatt et al., "Pathology Segmentation Using Distributional Differences to Images of Healthy Origin" *MICCAI*, 2018
- [2] Zhu et al. "Unpaired Image-to-Image Translationusing Cycle-Consistent Adversarial Networks" *ICCV*, 2017
- [3] Xia et al. "Adversarial Pseudo Healthy Synthesis Needs Pathology Factorization"  $MIDL,\ 2019$
- [4] Vorontsov et al. "Boosting segmentation with weak supervision from image-to-image translation" arXiv preprint, 2019
- [5] Chu et al. "CycleGAN, a Master of Steganography" NIPS, 2017



Fig. 5: One forward pass of an image from the P-domain in the model proposed by Vorontsov et al.[4].
■ pathological ■ pseudo-path. ■ pseudo-healthy ■ deep networks Image source: Vorontsov et al.[4].