

GOING BEYOND VOXEL-WISE DECONVOLUTION IN PERFUSION MRI WITH stU-NET

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We present a deep learning method able to predict quantitative DSC-perfusion maps from raw sequences. The proposed stU-Net architecture originally combines a 3D encoder with a 2D decoder, and generalizes the architecture of [1].

1. METHOD: THE stU-NET ARCHITECTURE

Figure 1 summarizes the proposed stU-Net architecture, a hybrid 2/3D CNN that performs 3D convolutions with or without striding in its encoding part, and alternates between 2D transposed convolutions and regular 2D convolution in its decoding part. The encoder is fed with temporal sequences of 2D “strips”, i.e. rectangular 2D patches, extracted from raw perfusion sequences. The successive frames are stacked as a third dimension, homologous to the two spatial ones, allowing the network to naturally perform spatio-temporal convolutions. For dimensional consistency, the skip connections perform a max-pooling reduction in the temporal dimension of the intermediate (2+1)D feature maps computed by encoder.

2. RESULTS: COMPARISON WITH [1]’S METHOD

We evaluate the predictive performance of the stU-Net on a public data set containing 49 patients with brain tumors [2]*, that we randomly split into training, validation and test subsets respectively composed of 25, 12, and 12 subjects. We generate ground-truth quantitative CBV maps using the SVD pipeline of the freely available Verbena v4.0 software [3].

Figure 2 qualitatively plots the obtained results, for an arbitrarily-picked test case. The method of [1] seems unable to reconstruct the small-scale details of the Verbena map, and to over-estimate the CBV values in the tumour region. Quantitatively, the stU-Net achieves a superior average performance for both the $L1_{[\times 10^{-2}]}$ (17.58 ± 4.05 vs. 34.01 ± 5.49) and $L2_{[\times 10^{-2}]}$ metrics (8.38 ± 3.52 vs. 38.71 ± 15.06). This $L1$ performance for [1]’s method is in line with their published results on stroke data. The same conclusion holds when computing these metrics only in the tumor regions (16.52 ± 9.37 vs. 26.89 ± 21.51 for $L1_{[\times 10^{-2}]}$, and 5.93 ± 6.44 vs. 26.30 ± 67.29 for $L2_{[\times 10^{-2}]}$), or using SSIM ($82.08\% \pm 5.02$ vs. $63.16\% \pm 5.71$).

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*Data acquired in line with the principles of the Declaration of Helsinki.

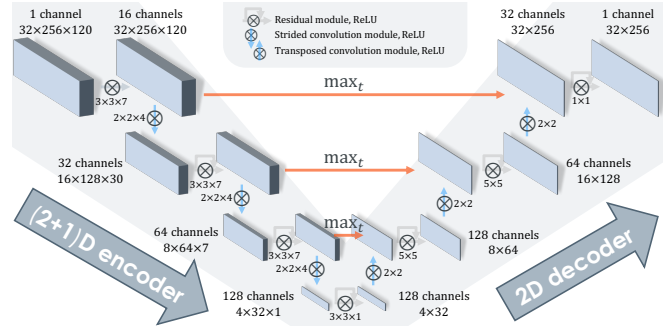


Fig. 1. Architecture of the spatio-temporal U-Net (stU-Net).

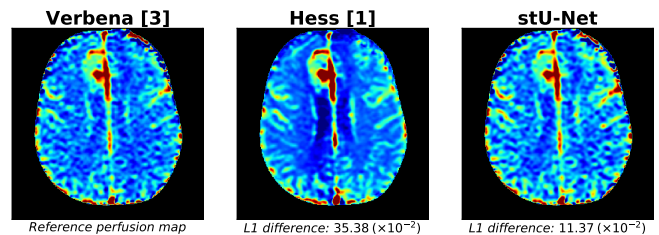


Fig. 2. CBV maps computed with the classical deconvolution approach of Verbena [3], the method of [1], and our stU-Net.

3. CONCLUSION

The spatio-temporal U-Net architecture, or stU-Net, showed superior performance to the current state-of-the-art on a public data set of patients with brain tumors.

4. REFERENCES

- [1] Hess et al., “Synthetic perfusion maps: imaging perfusion deficits in DSC-MRI with deep learning,” 2018.
- [2] Schmainda et al., “Glioma DSC-MRI perfusion data with standard imaging and ROIs,” 2016.
- [3] Mouridsen et al., “Bayesian estimation of cerebral perfusion using a physiological model of microvasculature,” *Neuroimage*, 2006.