Segmentation of gliomas and prediction of patient overall survival: a simple and fast procedure.

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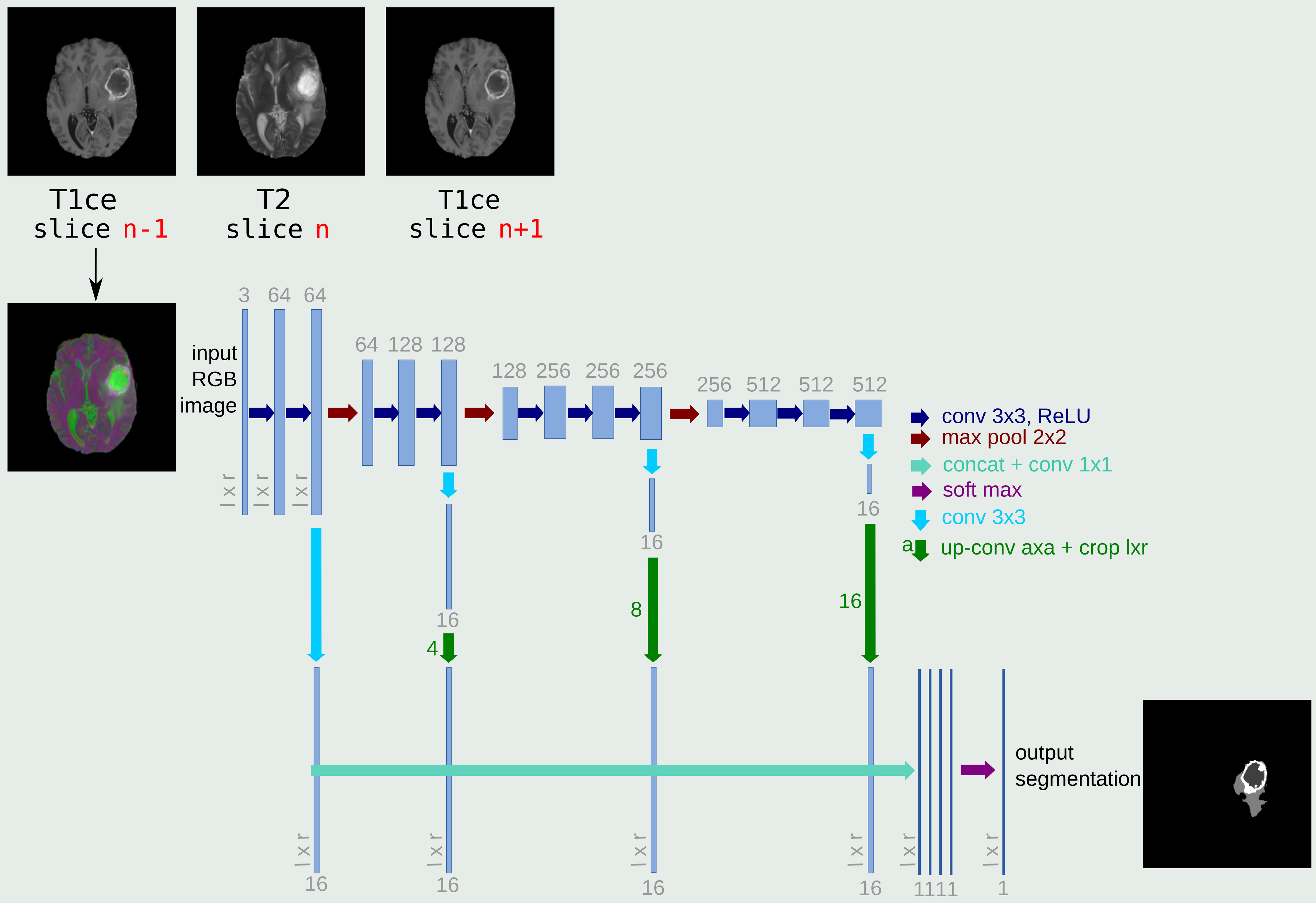
At a glance



Problem:

- We want a precise segmentation of glioma, and a survival prediction...
- ...and we want it quick!

Why our approach is interesting:

- It is simple, light, and versatile.

Conclusion:

- A novel approach to segment 3D volumes with 2D CNN [1, 2].
  → the *"3D-like"* approach using several modalities.
- Transfer learning works for medical image segmentation.
- Results... obtained in a few seconds.

Most important stuff

What people do:

- 3D patches at every voxel.
- 2,5D patches = 3 2D patches at every voxel.
  → that is heavy / slow.
- A dedicated network.
  → a large dataset for training is required.
- Classification from acquisition-dependant features.
  → not robust.

What we propose:

- Input a FCNN network with a series of 2D images.
  → 3 slices of a 3D volume = 1 color 2D image.
  ⇝ combination of two modalities (T1ce and T2).
- Reuse a fast and pre-trained base network (VGG-16).
  → transfer learning.
- Extract features only from segmentation.
  → no influence from the acquisition source.

And it's generic:

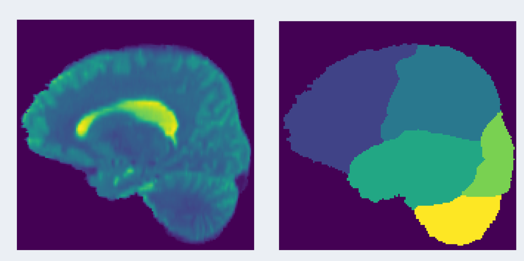
- Applied to *MRI brain volumes* for structures segmentation [1] (results on [3]) and for white matter hyperintensities segmentation [2].

Segmentation

- Tools: GNU/Linux, Keras over Tensorflow, NVIDIA GPU
- ADAM optimization procedure to minimize the loss.
- Parameters: learning rate = 0.002, $\beta_1 = 0.9, \beta_2 = 0.99, \epsilon = 0.001$
- Images are normalized.
- Network: trained in the 3 axis.
- For each slice n, a multimodality image composed of slices n of T1ce, $n-1$ and $n+1$ of T2 is created as 2D RGB input image for the network.
- Light post-processing: spacial regularization.

Survival prediction

10 defined features : patient age, relative size of necrosis, edema and active tumor wrt brain, (x, y, z)-normalized centroids of (necrosis+active tumor) and most infected area in brain atlas.



Training phase

For each patient in training set :

1. Retrieve all 10 features per patient.
2. Apply/learn PCA transformation on whole training set.
3. Train 50 RFs on scaled PCs.

Testing phase

For a patient to be tested :

1. Retrieve its 10 defined features.
2. Transform feature vector using learnt PCA parameters and scale it.
3. Predict class using 50 RFs and assign to most frequent class.

Related work

[1] Y. Xu, T. Géraud, and I. Bloch, "**From neonatal to adult brain MR image segmentation in a few seconds using 3D-like fully convolutional network and transfer learning**," in *ICIP*, pp. 4417–4421, 2017. ⇝ http://publications.lrde.epita.fr/xu.17.icip

[2] Y. Xu, É. Puybareau, T. Géraud, and J. Chazalon, "**White matter hyperintensities segmentation in a few seconds using fully convolutional network and transfer learning**," in *BrainLes (MICCAI 2017 competition)*, pp. 501–514, vol. 10670 of LNCS, Springer, 2018.

[3] A. M. Mendrik *et al.*, "**MRBrainS challenge: Online evaluation framework for brain image segmentation in 3T MRI scans**," *Computational Intelligence and Neuroscience*, 2015. ⇝ http://mrbrains13.isi.uu.nl/results.php