White matter hyperintensities segmentation in a few seconds using fully convolutional network and transfer learning

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1. Context

2. Method

3. Experiments and results

4. Conclusion
1. Context

2. Method

3. Experiments and results

4. Conclusion
White matter hyperintensities (WMH)

WMH:
- are a manifestation of small vessel diseases,
- can be everywhere in white matter,
- play a key role in stroke, dementia and ageing.

Importance of WMH study:
- analysis (shape, volume, location) is needed for clinical research studies,
- associated with clinical symptoms, can help prognosis, diagnosis, treatment monitoring etc.

Problem: manual segmentation is time-consuming and observer-dependent.
Challenge MICCAI

- Segmentation of WMH

- Part of Brain Lesion (BrainLes) MICCAI 2017 Workshop

- Method submitted in a Docker container

- Test data was not released

http://wmh.isi.uu.nl/
Data

(a) FLAIR image  (b) T1 image  (c) Ground Truth
## Origin of the datasets

<table>
<thead>
<tr>
<th>Institute</th>
<th>Scanner</th>
<th>Train</th>
<th>Test</th>
</tr>
</thead>
<tbody>
<tr>
<td>UMC Utrecht</td>
<td>3T Philips Achieva</td>
<td>20</td>
<td>30</td>
</tr>
<tr>
<td>NUHS Singapore</td>
<td>3T Siemens TrioTim</td>
<td>20</td>
<td>30</td>
</tr>
<tr>
<td>VU Amsterdam (AMS)</td>
<td>3T GE Signa HDxt</td>
<td>20</td>
<td>30</td>
</tr>
<tr>
<td></td>
<td>1.5T GE Signa HDxt</td>
<td>0</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>3T Philips Ingenuity</td>
<td>0</td>
<td>10</td>
</tr>
</tbody>
</table>

Each volume is composed of about 45 slices used to generate the 2D input images for the network.
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Our WMH segmentation is inspired by our previous work\textsuperscript{1} on brain segmentation.

**Reminder:** VGG is a network:

- pretrained on ImageNet (database of hundreds of color natural images),
- dedicated to visual object detection in \textit{2D color images},
- including a \textit{base} network.

Previous work

A segmentation method based on VGG-16:

1. **Preprocessing:**
   preparation of a set of 2D RGB images from a 3D volume
   ~ pseudo-3D approach

2. **Learning:**
   transfer learning and modification of VGG-16 network

3. **Results:**
   inference on 2D color images, and reconstruction of 3D images

**Key idea:** A 2D color image encodes also 3D information.
Previous work

For each slice \( n \) do

3D volume

3D-like input
= 2D color image

segmentation of slice \( n \)
First experiment:
Use of the pseudo-3D approach with VGG-16 on WMH data.

Observation:
The network fails to detect small lesions.

Idea:
Help the network by enhancing these small lesions in the input data.
A morphological preprocessing

\[ \text{top-hat}(I) = I - \gamma(I), \]
where \( \gamma(I) \) is the morphological area opening of \( I \).

We apply this procedure for each slice of a FLAIR volume.
A morphological preprocessing

\[ \text{image } I \]
\[ \equiv \]
\[ \text{max-tree } T_{\text{max}}(I) \]
\[ \downarrow \]
\[ \equiv \]
\[ \text{opening } \gamma(I) \]
\[ \equiv \]
\[ \text{pruning of } T_{\text{max}}(I) \]
based on component area

The top-hat is the residue (difference) between \( I \) and \( \gamma(I) \).
Preprocessing: from 3D volumes to 2D images

For each slice $n$, do:

2 gray 3D volumes (FLAIR + T1) + 1 generated (top-hat) → a set of RGB 2D images

(It is not pseudo-3D anymore: each input 2D color image comes only from one slice.)
Network

← use of 2 modalities
+ small lesion enhancement

Experiments and results

Conclusion
Parameters

- Total number of iterations: 150k
- Learning rate:
  - $10^{-8}$ for the first 50k iterations
  - $10^{-10}$ for the last 100k
- Momentum:
  - 0.99 for the first 50k iterations
  - 0.999 for the next 100k
- Weight decay: 0.0005
- 4 stages only
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Training phase: development

- 30 patients for training/30 patients for testing (10 from each hospital).
- Augmentation of training data (with scale variations and rotations).
- Input images: a series (3D volume) of 2D color images.
Training phase: for the challenge

- Model trained on all the 60 "expanded" patients.
- For each patient in the test dataset:
  - pre-processing, centering, inference and reconstruction are fully automated
- Runtime on a 3D volume is less than 10 seconds on average.
Evaluation

**Dice:** Dice coefficient

**H95:** Hausdorff distance (modified, 95th percentile)

**AVD:** Average volume difference

**Recall:** Sensitivity for individual lesions

**F1:** \[
F1 = \frac{2PR}{(P + R)},
\]
where \(P\) and \(R\) are respectively the precision and recall for individual lesions:

\[
P = \frac{\text{true positives}}{\text{true positives} + \text{false positives}}
\]

\[
R = \frac{\text{true positives}}{\text{true positives} + \text{false negatives}}
\]
Validation of top-hat influence

<table>
<thead>
<tr>
<th>Type</th>
<th>Dice ↑</th>
<th>AVD ↓</th>
<th>Recall ↑</th>
<th>F1 ↑</th>
</tr>
</thead>
<tbody>
<tr>
<td>pseudo-3D</td>
<td>0.72</td>
<td>23.90</td>
<td>0.38</td>
<td>0.46</td>
</tr>
<tr>
<td>2D without top-hat</td>
<td>0.72</td>
<td>28.24</td>
<td>0.39</td>
<td>0.48</td>
</tr>
<tr>
<td>2D with top-hat</td>
<td>0.75</td>
<td>22.63</td>
<td>0.61</td>
<td>0.63</td>
</tr>
</tbody>
</table>

↑ means the higher the better / ↓ means the lower the better

Two conclusions:

- Pseudo-3D is useless here.
- Adding a morphological pre-processing gives much better results.
Quantitative results

Results of our method on the **challenge** dataset:

<table>
<thead>
<tr>
<th>Origin</th>
<th>Dice ↑</th>
<th>H95 ↓</th>
<th>AVD ↓</th>
<th>Recall ↑</th>
<th>F1 ↑</th>
</tr>
</thead>
<tbody>
<tr>
<td>UMC Utrecht</td>
<td>0.74</td>
<td>11.22</td>
<td>19.07</td>
<td>0.70</td>
<td>0.66</td>
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<tr>
<td>NUHS Singapore</td>
<td>0.77</td>
<td>8.28</td>
<td>17.64</td>
<td>0.61</td>
<td>0.68</td>
</tr>
<tr>
<td>AMS GE 3T</td>
<td>0.75</td>
<td>6.75</td>
<td>21.91</td>
<td>0.62</td>
<td>0.71</td>
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<tr>
<td>AMS GE 1.5T</td>
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<td>10.94</td>
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<td>AMS Philips 3T</td>
<td>0.50</td>
<td>70.27</td>
<td>46.33</td>
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<tr>
<td><strong>Weighted average</strong></td>
<td>0.73</td>
<td>14.54</td>
<td><strong>21.71</strong></td>
<td>0.63</td>
<td><strong>0.67</strong></td>
</tr>
</tbody>
</table>

Rank: 6\textsuperscript{th} place of the challenge (among 21 competitors).
Some qualitative results

(d) FLAIR image  (e) RGB input  (f) Our result vs GT
Some qualitative results: zoomed in

Yellow: true positives; Red: false positives; Green: false negatives
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Conclusions

- Fast, robust and automated method for WMH segmentation:
  - inspired from our *pseudo-3D* approach (ICIP’17)
  - *transfer learning* works for some med. image segmentation tasks

- Segmentation of a 3D volume **in less than 10 seconds**:
  - Benefits from merging modalities in a *color* image...
  - ...and using a simple 2D network

- Effective benefits of morphological preprocessing:
  - highly non-linear
  - helps the network to identify objects of interest

- Docker container downloadable on our website:
  - *reproducible research* is important...
Perspectives

- Improvement possible thanks to post-processing?

- Application to other segmentations, pathological or not

- Going further with predictions? (prediction of tumor proliferation score for breast cancer, prediction of patient overall survival from the study of brain lesions, etc.)
Supplementary materials and Docker file:
https://www.lrde.epita.fr/wiki/NeoBrainSeg

Thanks for your attention! Any questions?
Results of the methods of the challenge

Sorted by increasing AVD:

<table>
<thead>
<tr>
<th>Team</th>
<th>Dice ↑</th>
<th>H95 ↓</th>
<th>AVD ↓</th>
<th>Rec ↑</th>
<th>F1 ↑</th>
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<tbody>
<tr>
<td>nlp_logix</td>
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<td>LRDE</td>
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<td>14.54</td>
<td>21.71</td>
<td>0.63</td>
<td>0.67</td>
</tr>
<tr>
<td>...</td>
<td>0.68</td>
<td>14.55</td>
<td>34.34</td>
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<td>0.52</td>
</tr>
<tr>
<td>median</td>
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<td>...</td>
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