
VentMapp3r Documentation

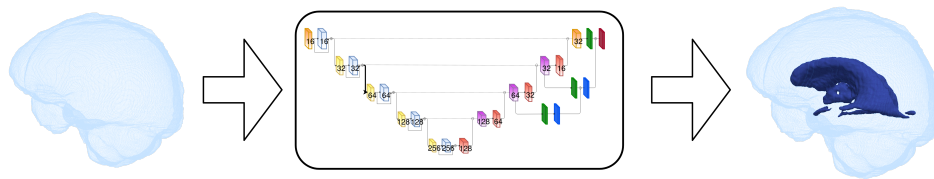
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Jan 06, 2022

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VentMapp3r (pronounced ventmapper) is a CNN-based segmentation technique of the ventricular system using MRI images from BrainLab. It can deal with brains with extensive atrophy and segments the ventricles in seconds. It can segment the ICV with either T1-weighted image as the only input, or with different combinations involving a T1, T2, and FLAIR image.



Before installing VentMapp3r

1.1 Acknowledging this work

If you wish to include results generated by VentMapp3r in a publication, please include a line such as the following:

- Ventricular segmentation was performing using the VentMapp3r algorithm (ventmapp3r.readthedocs.io) based on a convolutional neural network.

1.2 Reference

- The paper is currently in preparation. The citation will be provided upon publication.

1.3 License

VentMapp3r is licensed under the terms of the *GNU General Public License v3.0*.

VentMapp3r is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. You should have received a copy of GNU General Public License v3.0 along with VentMapp3r.

The code is released for academic research use only. For commercial use, please contact maged.goubran@sri.utoronto.ca.

2.1 Python

For the main required Python packages (numpy, scipy, etc.) we recommend using [Anaconda for Python 3.6](#)

2.2 Installing package and dependencies for VentMapp3r locally

1. Clone repository

```
git clone https://github.com/mgoubran/VentMapp3r.git VentMapp3r  
  
(or install zip file and unzip)  
  
cd VentMapp3r
```

If you want to create a virtual environment where VentMapp3r can be run,

```
conda create -n ventmapper python=3.6 anaconda  
source activate ventmapper
```

To end the session,

```
source deactivate
```

To remove the environment

```
conda env remove --name ventmapper
```

2. Install dependencies

```
pip install git+https://www.github.com/keras-team/keras-contrib.git
```

If the computer you are using has a GPU:

```
pip install -e .[ventmapper_gpu]
```

If not:

```
pip install -e .[ventmapper]
```

3. Test the installation by running

```
ventmapper --help
```

To confirm that the command line function works, and

```
ventmapper
```

To launch the interactive GUI.

2.3 Download deep models

Download the models from [this link](#) and place them in the “models” directory

2.4 For tab completion

```
pip3 install argcomplete  
activate-global-python-argcomplete
```

2.5 Updating VentMapp3r

To update VentMapp3r, navigate to the directory where VentMapp3r was cloned and run

```
git pull  
pip install -e .[option] -process-dependency-links
```

where “option” is dependent on whether or not you have a GPU (see package installation steps above)

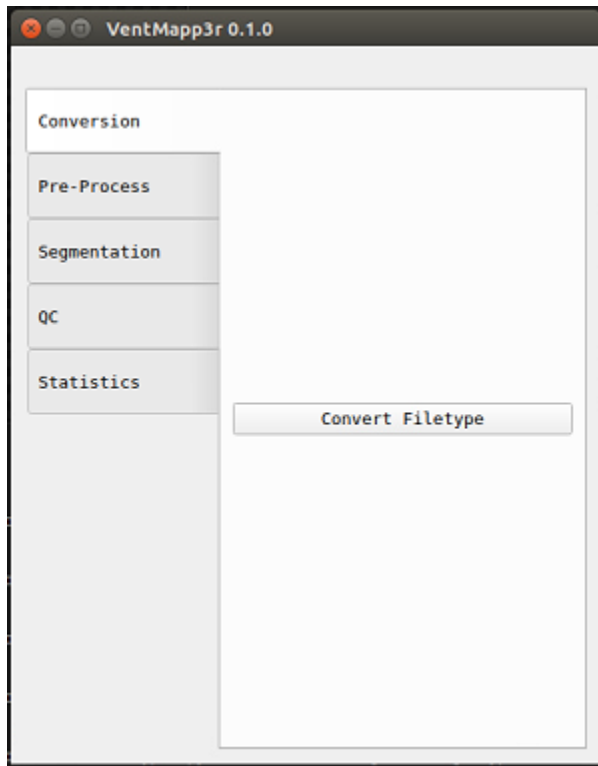
You can use VentMapp3r through the graphical user interface (GUI) or command line:

3.1 For GUI

To start the GUI, type

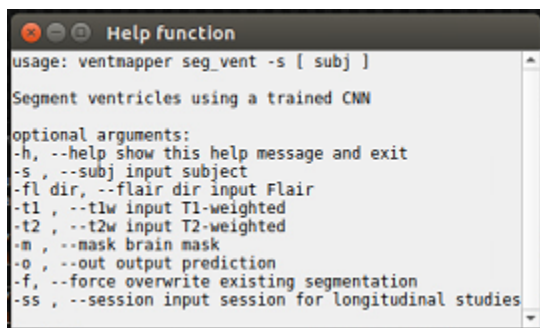
```
ventmapper
```

A GUI that looks like the image below should appear. You can hover any of buttons in the GUI to see a brief description of the command.



Graphical user interface for the VentMapper application

You can get the command usage info by click the “Help” box on any of the pop-up windows.



Help screen for graphical user interface for Dasher application

3.2 For Command Line

You can see all the ventmapper commands by typing either of the following lines:

```
ventmapper -h
ventmapper --help
```

Once you know the command you want to know from the list, you can see more information about the command. For example, to learn more about seg_hfb:

```
ventmapper seg_vent -h
ventmapper seg_vent --help
```

3.3 Ventricular volumes

To extract ventricular volumes use the GUI (Stats/ventricular Volumes) or command line:

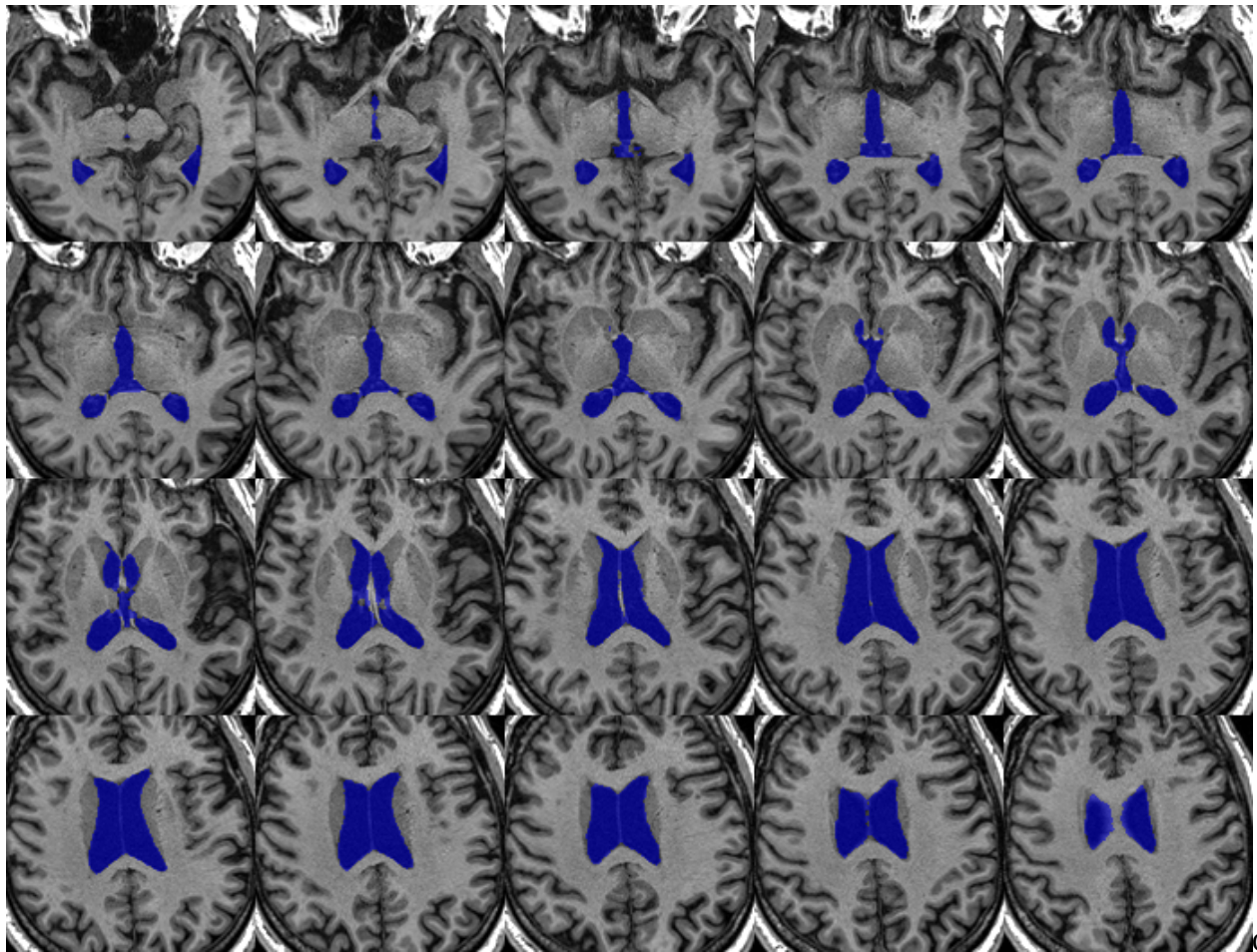
```
ventmapper stats_vent -h
```

3.4 QC

QC files are automatically generated in a sub-folder within the subject folder. They are .png images that show a series of slices in the brain to help you quickly evaluate if your command worked successfully, especially if you have run multiple subjects. They can also be created through the GUI or command line:

```
ventmapper seg_qc -h
```

The QC image should look like this:



control image for ventricular segmentation

Quality

3.5 Logs

Log files are automatically generated in a sub-folder within the subject folder. They are .txt files that contain information regarding the command and can be useful if something did not work successfully.

3.6 File conversion

To convert from one filetype to another (namely Analyze to Nifti, or vice versa)

```
ventmapper filetype
```

Required arguments:

```
-i , --in_img    input image, ex:MM.img  
-o , --out_img   output image, ex:MM.nii
```

Example:

```
ventmapper filetype --in_img subject_T1.img --out_img subject_T1.nii.gz
```

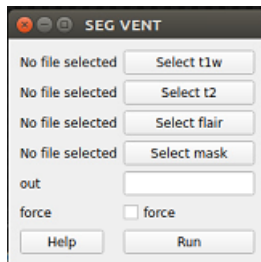
4.1 GUI

Watch this video tutorial:

IMAGE ALT TEXT

Or follow the steps below:

After opening the VentMapp3r GUI, click “Ventricle” under the “Segmentation” tab. Wait for a new pop-up window to appear. The window should look like the image below.



ventricle pop up window

Click “Select t1w” and chose your T1 image. Click “Run”. Click either or both “Select t2w” and “Select flair” (with respect to the sequences you have) and select the corresponding images. Type your desired output name in the “out” box. Check the box next to “force” if you want to overwrite a previous output. Click “Run”. Your output file will automatically appear in your t1w folder.

4.2 Command Line

```
ventmapper seg_vent
```

Optional arguments:

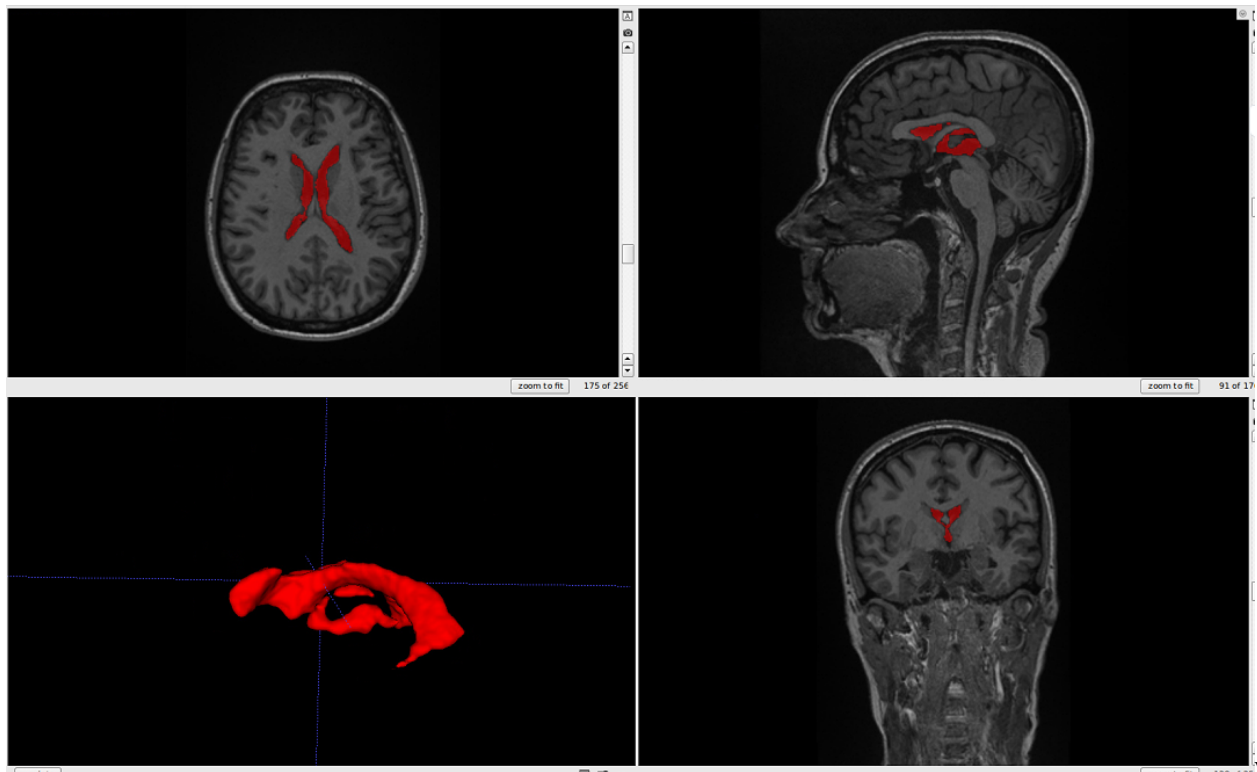
```
-h, --help          show this help message and exit
-s, --subj          input subject
-fl, --flair         input Flair
-t1, --t1w          input T1-weighted
-t2, --t2w          input T2-weighted
-m, --mask          brain mask
-o, --out            output prediction
-f, --force         overwrite existing segmentation
-ss, --session      input session for longitudinal studies
```

Examples:

```
ventmapper seg_vent -s subjectname -b
```

```
ventmapper seg_vent -t1 subject_T1_nu.nii.gz -o subject_vent.nii.gz
```

The output should look like this.:



segmentation

ventricle

CHAPTER 5

Issues

If you intend to use Singularity, scroll down to the Singularity section. Otherwise, the steps to use the image in Docker can be found below.

6.1 Before using Docker image for VentMapp3r

If you want to use Docker to run VentMapp3r, you must first install Docker on your system. While the installation method differs per system, instructions can be found for the following:

- [Ubuntu](#)
- [Windows](#)
- [Mac](#)

Once Docker is installed, open the docker terminal and test it with the command

```
docker run hello-world
```

6.2 Pulling VentMapp3r's Docker image

While you can download various Docker images, for the sake of this tutorial pull the VentMpp3r image

```
docker pull mgoubran/ventmapper:latest
```

Verify that the image was pulled successfully by checking all images on your system

```
docker images
```

6.3 Running the Docker image

If you have installed Docker for the first time, and have verified that the `hello-world` image was running, then VentMapper can be run on your system.

The simplest way to run the container is:

```
docker run -it mgoubran/ventmapper seg_vent -t1 /VentMapp3r/data/test_case/mprage.nii.  
↪ gz
```

6.4 Using VentMapper on Singularity

Docker images can still be used on Singularity. This is especially good if you are processing images using Compute Canada clusters. The following instructions are based on the steps provided on the [Compute Canada wiki](#).

Load the specific Singularity module you would like to use.

```
module load singularity/3.5
```

Although VentMapper is stored as a Docker image, it can be built in singularity by calling:

```
singularity build ventmapper.sif docker://mgoubran/ventmapper
```

To ensure that the Docker image has been built in Singularity, run

```
singularity exec ventmapper.sif ventmapper --help
```

CHAPTER 7

Indices and tables

- `genindex`
- `modindex`
- `search`