
iCVMapp3r Documentation

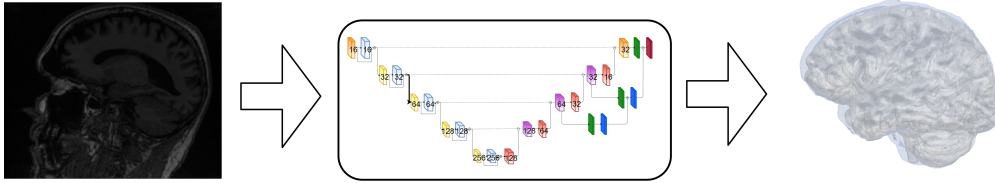
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iCVMapp3r (pronounced icvmapper) is a CNN-based segmentation technique of the intracranial volume (ICV) using MRI images from BrainLab. It can deal with brains with extensive atrophy and segments the ICV in seconds. It can segment the ICV with either T1-weighted image as the only input, or with different combinations involving a T1, T2, and FLAIR image.



BEFORE INSTALLING ICVMAPP3R

1.1 Acknowledging this work

If you wish to include results generated by iCVMapp3r in a publication, please include a line such as the following:

- Brain extraction was performing using the iCVMapp3r algorithm (*icvmapp3r.readthedocs.io*) based on a convolutional neural network.

1.2 Reference

- Ntiri, E. E., Holmes, M. F., Forooshani, P. M., Ramirez, J., Gao, F., Ozzoude, M., ... Goubran, M. (2021). Improved segmentation of the intracranial and ventricular volumes in populations with cerebrovascular lesions and atrophy using 3D CNNs. *Neuroinformatics*, 19, 597–618. <https://doi.org/10.1007/s12021-021-09510-1>

1.3 License

iCVMapp3r is licensed under the terms of the *GNU General Public License v3.0*.

iCVMapp3r 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 iCVMapp3r.

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

LOCAL INSTALL

2.1 Python

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

2.2 ANTs & Convert3D (c3d)

If either ANTs or c3d are not installed on your machine, run `install_depends.sh`, located in the project directory. The required software will be installed in the `depends` directory. If you are interested to install c3d on MacOS or Windows, you can download it from [this link](#).

2.3 Installing package and dependencies for iCVMapp3r locally

1. Clone repository

```
git clone https://github.com/AICONSLab/iCVMapp3r.git iCVMapp3r

(or install zip file and uncompress)

cd iCVMapp3r
```

If you want to create a virtual environment where iCVMapp3r can be run,

```
conda create -n icvmapper python=3.6 anaconda
conda activate icvmapper
```

To end the session,

```
conda deactivate
```

To remove the environment

```
conda env remove --name icvmapper
```

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 .[icvmapper_gpu]
```

If not:

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

3. Test the installation by running

```
icvmapper --help
```

To confirm that the command line function works, and

```
icvmapper
```

To launch the interactive GUI.

2.4 Download deep models

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

2.5 For tab completion

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

2.6 Updating iCVMapp3r

To update iCVMapp3r, navigate to the directory where iCVMapp3r 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)

GETTING STARTED

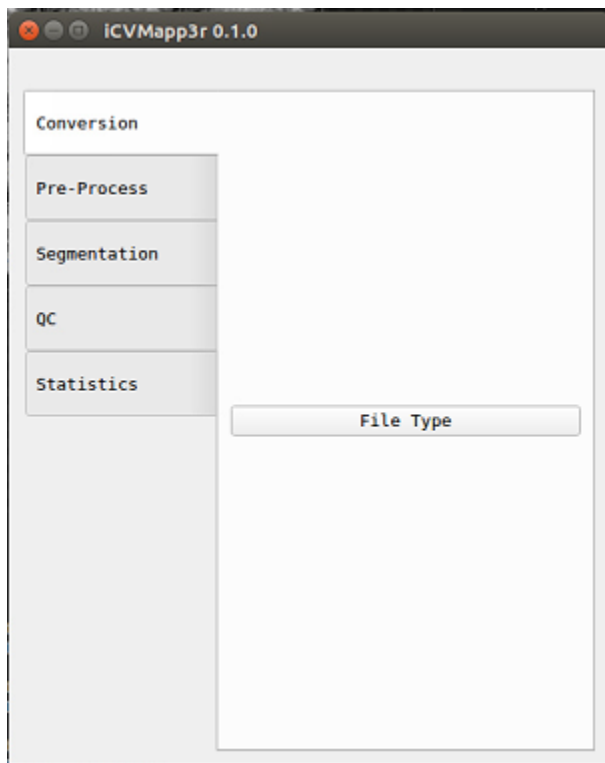
You can use iCVMap3r through the graphical user interface (GUI) or command line:

3.1 For GUI

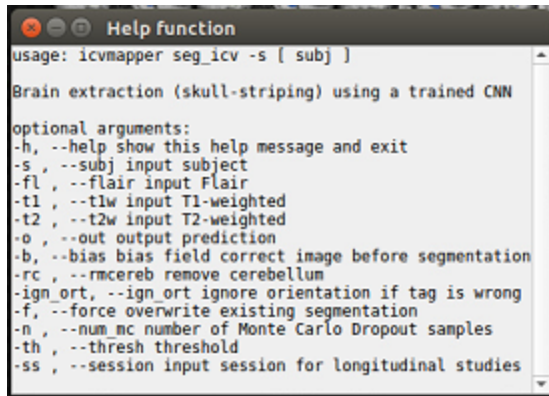
To start the GUI, type

```
icvmapper
```

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.



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



3.2 For Command Line

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

```
icvmapper -h
icvmapper --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`:

```
icvmapper seg_icv -h
icvmapper seg_icv --help
```

3.3 Intracranial volumes

To extract ICV use the GUI (Stats/ICV) or command line:

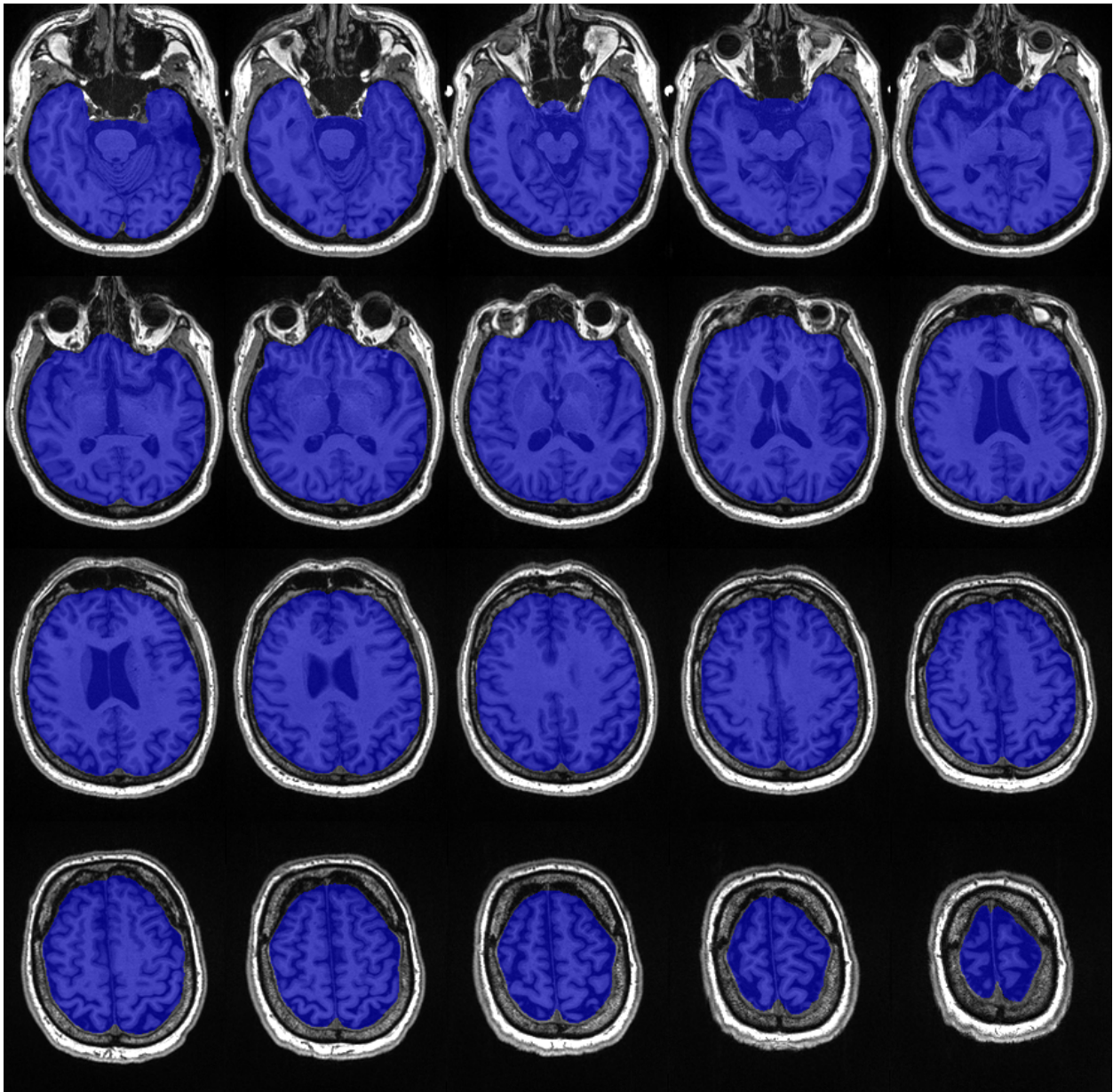
```
icvmapper stats_icv -h
```

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:

```
icvmapper seg_qc -h
```

The QC image should look like this:



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

Convert Analyze to Nifti (or vice versa)

```
icvmapper filetype
```

Required arguments:

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

Example:

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

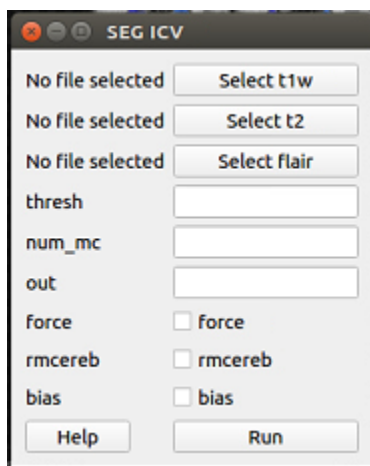
SEGMENTATION TUTORIALS

4.1 GUI

Watch this video tutorial:

Or follow the steps below:

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



Click “Select t1w” and choose your T1 image. Click either of “Select t2w” and “Select flair” (with respect to the sequences you have) and select the corresponding images. Click “Run”. Type your desired output name in the “out” box. If you want to overwrite the previous segmentation results, check the box beside “force” Check off “rmcereb” if you want to generate a segmentation with a removed cerebellum, and “bias” if you want to bias field correct the sequences using N4 Your output file will automatically appear in your t1w folder.

4.2 Command Line

```
icvmapper seg_icv
```

Optional arguments:

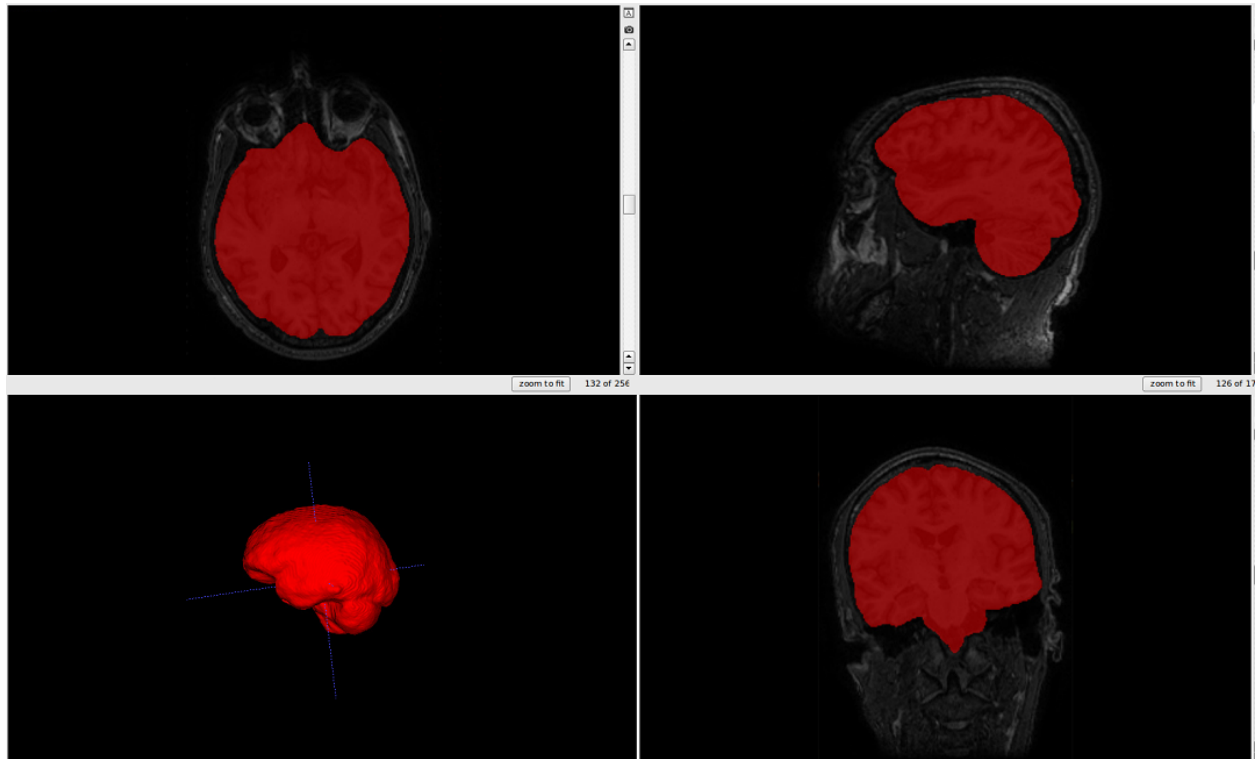
```
-h, --help          show this help message and exit
-s, --subj          input subject
-fl, --flair        input Flair
-t1, --t1w         input T1-weighted
-t2, --t2w         input T2-weighted
-o, --out           output prediction
-b, --bias          bias field correct image before segmentation
-rc, --rmcereb     remove cerebellum
-ign_ort, --ign_ort ignore orientation if tag is wrong
-f, --force         overwrite existing segmentation
-n, --num_mc        number of Monte Carlo Dropout samples
-th, --thresh       threshold
-ss, --session      input session for longitudinal studies
```

Examples:

```
icvmapper seg_icv -s subjectname -b
```

```
icvmapper seg_icv -t1 subject_T1_nu.nii.gz -o subject_icv.nii.gz
```

The output should look like this.:



CHAPTER
FIVE

ISSUES

DOCKER / SINGULARITY

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 ICVMapp3r

If you want to use Docker to run ICVMapp3r, 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 ICVMapp3r's Docker image

While you can download various Docker images, for the sake of this tutorial pull the ICVMpp3r image

```
docker pull mgoubran/icvmapper: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 ICVMapper can be run on your syste.

The simplest way to run the container is:

```
docker run -it mgoubran/icvmapper seg_icv -t1 /ICVMapp3r/data/test_case/mprage.nii.gz
```

6.4 Using ICVMapper 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 ICVMapper is stored as a Docker image, it can be built in singularity by calling:

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

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

```
singularity exec icvmapper.sif icvmapper --help
```

INDICES AND TABLES

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