**Guide to Installing and Running NOMIS**

Paper: <https://www.biorxiv.org/content/10.1101/2021.01.25.428063v1>

Download: <https://github.com/medicslab/NOMIS>

Before you can use NOMIS, you need to install its dependencies (the external software that needs to be installed on your computer in order for NOMIS to work). NOMIS requires Python 3.7.4 or higher and several Python modules - argparse 1.1, nibabel 2.5.1, numpy 1.17.2, pandas 0.25.1, pickle 4.0, sklearn 0.21.3. To learn more about this process, see /02\_Extras/Software\_Guides/Python/Python\_For\_Beginners.docx

python $nomis -csv $csv -s $subjdir -o $output

Outputs:

* CNR
* Normative\_z\_scores
  + lh.aparc, rh.aparc, and aseg contain all of the fields found in the corresponding FS 5.3 norm app output csv except Cortex\_[L/R S/T/V] and entorhinal\_exvivo\_[L/R S/T/V]
* Raw\_scores – data directly pulled from Freesurfer output files