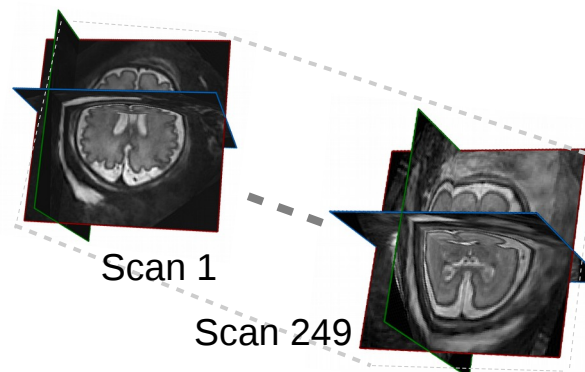


## dHCP fetal cohort, 3T

1

### Pre-processing:

Brain localization, slice alignment, registration, and reconstruction.



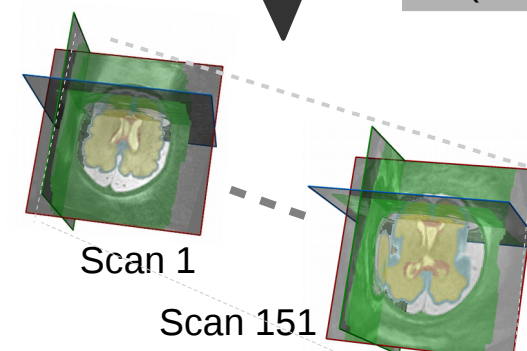
2

### Draw-EM:

Preliminary labels generated by leveraging a fetal brain atlas.

held-out-set-A  
(n=86, 3T)

held-out-set-B  
(n=12, 3T)

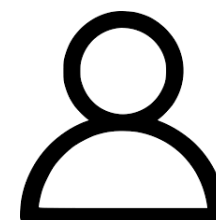


3

### Evaluation of preliminary labels:

A quality control step; only images that pass are used to train the deep segmentation network.

fail (n=59, 3T)



Researcher

pass (n=92, 3T)

model-development-set (n=49, 3T)

held-out-set-C (n=43, 3T)

4

### DeepMedic:

- A deep 9-class segmentation network (**SN1**) is trained, tuned, and assessed.
- It is also applied to scans that failed Draw-EM, for comparison.

6

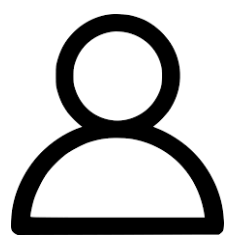
### DeepMedic (2):

- A deep cortical segmentation network (**SN2**) is trained, tuned, and assessed.

8

### Final evaluation:

The final cortical segmentation system was applied to the 86 volumes from held-out-set-A and 13 volumes from the independent 1.5 T dataset.



Expert  
Annotator

5

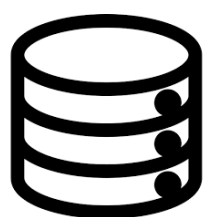
### Clinical refinement of output from SN1:

Segmentation maps of 283 slices, generated by SN1, are evaluated and refined by an experienced annotator.

7

### Fine-tuning the cortical segmentation network:

- Refined cortical gray matter labels on the dHCP 3T slices were fed back to SN2.
- 28 Volumes from an independent 1.5T clinical dataset were also incorporated.



## Independent clinical cohort, 1.5T