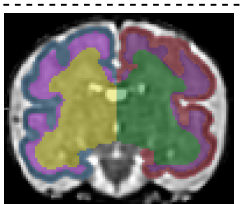


- Fetal MRI volume (GA < 32)



sp\_pred.sh

- Uses Sol's **SP** prediction model  
- [Github](#)

Segmentation  
correction

Automated segmentation correction scripts

fill\_holes.py

smooth.py

rm\_islands.py

sp\_surf.sh

- Activate **snakemake** env  
- Extract **inner** and **outer** surface

sp\_tidy.sh

- From **Snakemake's** folder structure to  
**MRI\_processing's** folder structure  
- Add **segmentation**  
- Add **recon**

01920

```
├─ lh.innersp.asc
├─ rh.innersp.asc
├─ lh.wm._81920.asc
├─ rh.wm._81920.asc
├─ 01920_nuc.nii
└─ 01920_nuc_deep_subj
```

**Environment package**

- MRI\_processing/milton.candela/pkgs/sp\_pkg

CP & SP surface

