An Animal Pipeline for FMRI in AFNI

from @animal_warper to afni_proc.py

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Overview

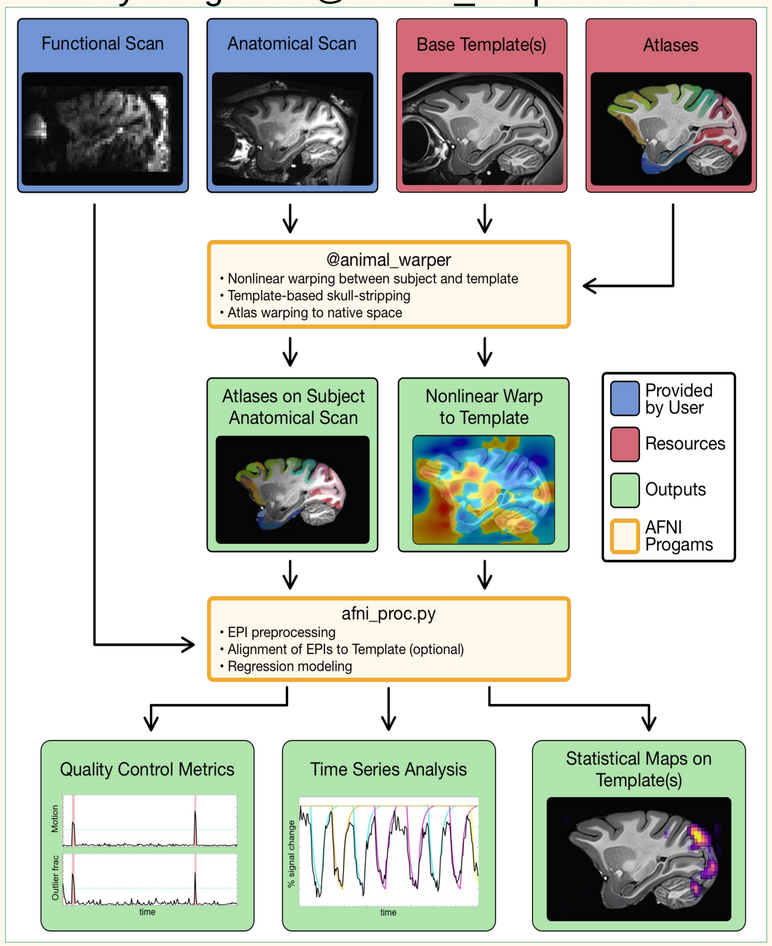
We present a full pipeline for processing and visualizing animal FMRI data in 2 easy steps:

1) @animal_warper

+ align anatomicals to a template
+ skull-strip the anatomical

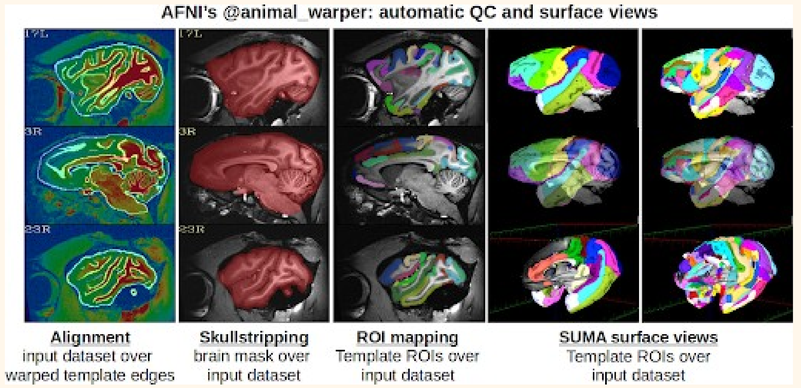
2) afni_proc.py

+ process (motion correction thru regression)
+ easily integrates @animal_warper results



@animal_warper

- Template or native space - your choice.
- Use atlases in native space.
- Validated with macaque templates/atlases (NMT, D99) and subjects (PRIME-DE).
- Skullstripping in native or template space
- Flexible spatial resolution (feature_size)
- QC - easy viewing alignment images



Install Demo data and scripts in AFNI with **@Install_MACAQUE_DEMO**

Links to demos in AFNI

https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/nonhuman/macaque/demo_task_fmri.html

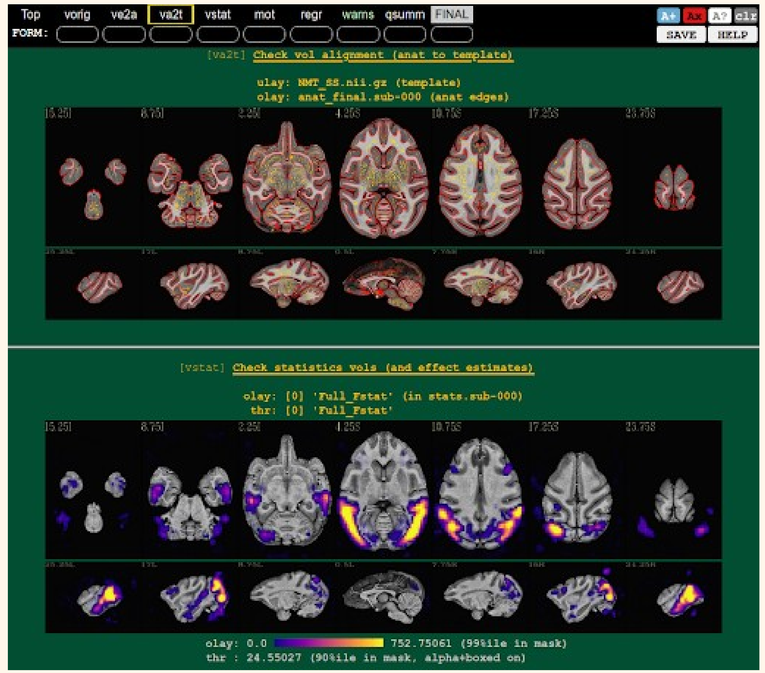
https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/nonhuman/macaque/demo_rest_fmri.html

References

Cox RW. 1996. Comput Biomed Res 29:162-173
Milham M, et al. 2018. Neuron 100, 61-74.e2.
Reveley C, et al. 2017. Cereb. Cortex 27, 4463–4477
Seidlitz J, et al. 2018. NeuroImage 170, 121–131

afni_proc.py

- Flexible and powerful FMRI pipeline
- Easy to script and generates its own shell script for robust and reproducible processing
- Paradigms: task, rest, naturalistic, ...
- Simple Block processing descriptions: *tshift align volreg blur scale regress*
- Takes @animal_warper alignment as input
- QC - browser HTML reports:



Acknowledgments

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