

# Improving skullstripping and nonlinear warping in AFNI: *sswarper2*



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## Introduction

Nonlinear alignment/registration is a common processing step in fMRI analysis. However, no alignment algorithm is perfect, and developers continue looking for ways to improve algorithms (subject to mathematical and practical constraints).

Here we describe *sswarper2*, a new nonlinear alignment program in AFNI<sup>1</sup> that both skullstrips (SS) a T1w volume and aligns (warps) it to a reference dataset. We show its improvements to predecessor *@SSwarper*, which had similar dual roles.

## Methods & Results

The primary nonlinear alignment program in AFNI is *3dQwarp*<sup>2</sup>. *@SSwarper* wraps around *3dQwarp* and also includes removal of nonbrain material ("skullstripping"), since warping and skullstripping are each complicated processes that improve when the other is done well. If the skull+nonbrain region of a subject's anatomical dataset has been exactly removed, alignment to a template is much easier; or if a dataset has been well aligned to a template, one can use the latter to "punch away" the skull of the former. *@SSwarper* makes use of this by iterating between these steps with increasing accuracy, improving each. During alignment, it uses a local Pearson cost to drive early stages of alignment<sup>3</sup>. It also saves snapshots of initial and final stages of overlap, to provide quality control (QC) checks.

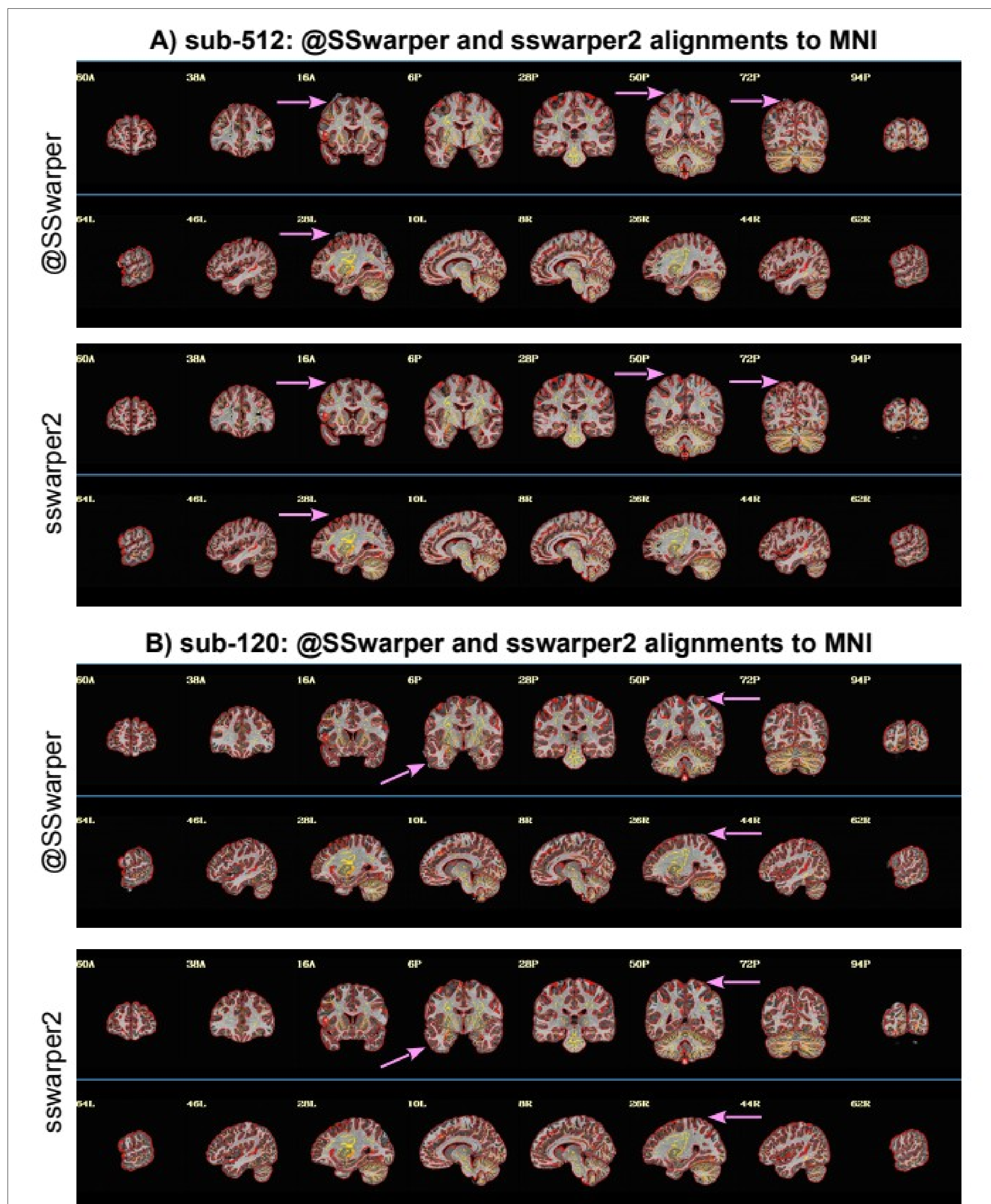
Similarly, *sswarper2* iterates between (local Pearson) alignment to a template and skullstripping, but it does so in smaller steps, more finely interleaved with skull removal, increasing stability. Additionally, *sswarper2* saves a detailed history of snapshots of intermediate processing steps, to facilitate any troubleshooting.

To compare overall robustness of the programs, we tested each on a set<sup>4</sup> of 169 anatomical T1w datasets from 8 different sites from 3 continents, with a wide subject age range (8-70 yrs), aligning to the MNI 2009c asymmetric template<sup>5</sup>. We compare individual and group-wide results both qualitatively and quantitatively.

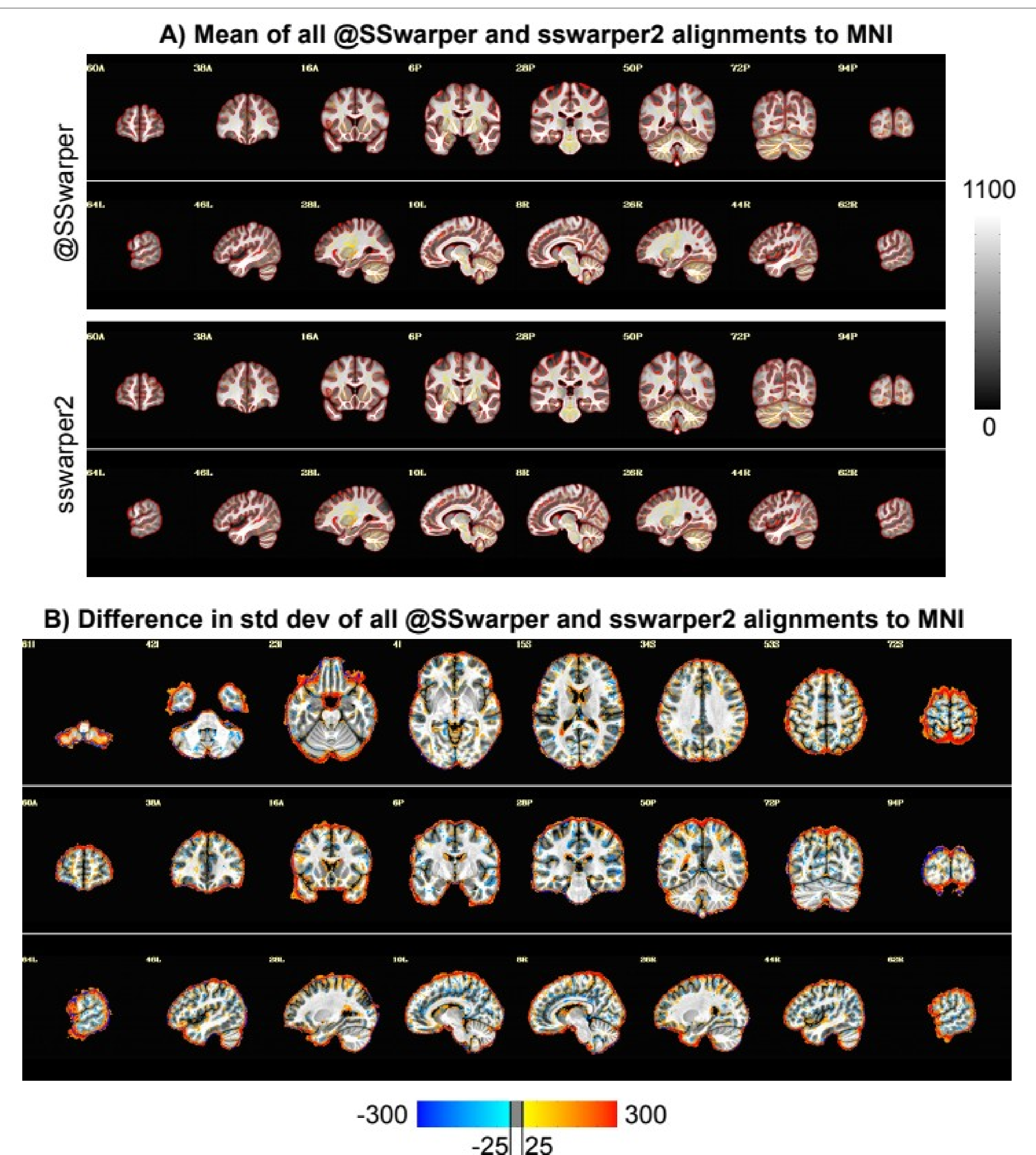
## Results

In many cases, *@SSwarper* and *sswarper2* yield quite similar results, providing accurate skullstripping and nonlinear registration to the MNI template. However, in a small number of cases, *@SSwarper* had inaccurate final skullstripping, resulting in localized misalignment. Fig 1 shows two examples of datasets in which the warped subject anatomy extends 2-3 mm outside the brain locally. In each case, *sswarper2* provides more accurate alignment and skullstripping.

Fig 2A shows the mean of all warped datasets (each had been unnormalized to similar brightness values per tissue class) for each program. There is overall good alignment to the template in both cases. Fig 2B shows the voxelwise standard deviation across the group for each program. Again, overall patterns are similar, but *sswarper2* results are uniformly more tightly aligned within the brain volume and at major tissue boundaries, while the effect of the small fraction of stretched *@SSwarper* results can be seen around the brain edge.



**Figure 1.** Examples of anatomical-to-template alignment for (old) *@SSwarper* and (new) *sswarper2*. The underlay (grayscale) is the warped anatomical volume, and the overlay shows the edges of the MNI template. Pink arrows highlight local misalignments from *@SSwarper* that are correctly provided by *sswarper2*. While *@SSwarper* typically produces good alignment, outlier misalignments such as shown occur in a small fraction of cases. The *sswarper2* program is much more robust against these kinds of errors.



**Figure 2.** Summary group results of alignment. A) The cross-group mean is shown for *@SSwarper* (top) and *sswarper2* (bottom); the edges of the reference MNI template are overlaid. In each case, the mean shows a fairly uniformly accurate alignment. B) The difference standard deviation (*@SSwarper* – *sswarper2*) of all warped anatomical datasets. Outside the brain, *@SSwarper* has higher values, since some alignments overstretched, while *sswarper2* tends to avoid such issues.

## Conclusions

While both alignment programs typically produce warped anatomicals that closely match the template structure, the new *sswarper2* provides more robust alignment across a broader range of datasets. AFNI's *sswarper2* results can also be integrated directly into *afni\_proc.py*<sup>6</sup> and other fMRI pipeline tools.

## Acknowledgments, References & QR Code

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