

Author's Response To Reviewer Comments

Reviewer reports:

Reviewer #1: This Technical Note describes the Computational Anatomy Toolbox (CAT) software tool, which includes a Graphical User Interface (GUI) for the analysis of 3D MRI data. The CAT software tool is impressive, and enables voxel-based and surface-based morphometric analysis to be applied to these 3D imaging datasets. The authors helpfully illustrate the utility of the CAT software tool using brain images from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database.

This is an excellent, freely available tool for the Neuroimaging community and the authors are to be commended for developing it.

Thank you very much.

Minor comments

I first attempted to launch the CAT software tool on macOS 14.0 (Sonoma) with Apple M1 chip, and on the command line I received an error message. You should move it to the Bin.

I additionally tested the CAT software tool on macOS 12.6 (Monterey) with Intel chip, and I was able to run the CAT software tool successfully.

A: Thank you for testing CAT12. We are happy it ran smoothly on macOS 12.6. With respect to the error on macOS 14, please see the following issues. So, it could be that you got unlucky with the arm64 version. Apologies, this version is no longer available on the website. I have tested on my MacOS 14.4 Mac with M1 and M2 processors (it ran smoothly without any problems). If the problem on your system is not yet installed. Since your standalone version ran on another computer with an Intel chip, you should use the security system described here:

https://www.fil.ion.ucl.ac.uk/spm/docs/wikibooks/Installation_on_64bit_Mac_OS_%28Intel%29/#macos-catalina-big-sur-mojave

A minor criticism is that the installation instructions in the supporting Readme file for archive [CAT12.9_R2023b_MCR_Mac_arm64.zip] do not mention the SPM (Statistical Parametric Mapping) software tool. The CAT software tool needs to be downloaded separately and then the installation instructions are included in the supporting CAT software documentation (https://neuro-jena.github.io/cat12-help/#get_started).

A: The aforementioned CAT12 standalone version already contains everything (SPM12 and CAT12), and there is no need to install SPM12 and CAT12 separately (which is the default use), SPM12 and CAT12 have to be installed separately, which is also described in the supporting documentation.

With the issues I encountered in installation, I invite the authors to list the System Requirements - specifically the Operating System - in the manuscript and also in the supporting CAT software documentation.

A: Currently there are no system requirements and CAT12 runs successfully on a variety of different systems without any known potential bugs that may occur for some CAT12 versions and computer systems, which also allows us to fix these bugs in a timely manner. [#idSite=1&period=day&date=today](https://www.neuro.uni-jena.de/piwik/index.php?module=CoreHome&action=index&idSite=1&period=day&date=today)

In addition, it would be particularly helpful if the instructions on how to install CAT in the context of SPM were included in the supporting documentation archives.

A: The non-standalone versions contain such a file (README.md), which describes in detail the necessary steps to install CAT12. I have carefully checked the latest standalone versions (from March 20th) and the non-standalone version (from March 8th), and all versions are available on the website. I had a temporary version (i.e., CAT12.9_R2023b_MCR_Mac_arm64.zip) that I have already removed from the website.

Reviewer #2: Overall, I think the CAT software provides valuable tools to analyse morphometric differences in the brain and to visualise them. However, I think some clarifications would help the readers understand and evaluate the quality of the methods.

Thank you very much.

Comments:

Figure 2: Looking at the chart, I have a question regarding the pipeline. Is it required to run the whole pipeline using CAT? Or analysis or further?

A: No, it is not always required to run the whole pipeline using CAT. For example, we support the use of other segmentation provided by the reviewers, the spatial registration steps as implemented in CAT12 cannot be bypassed. However, it is possible to save these maps (i.e. gray and white matter segmentation) in the (native) space of the original input image.

Voxel-based Processing: The above question is quite important, seeing that the preprocessing uses rather old registration methods especially with clinical populations.

A: We understand the reviewer's concerns but believe that CAT12 uses up-to-date methods. More specifically, with particular reference to the registration step (Ashburner & Friston, 2011; <https://doi.org/10.1016/j.neuroimage.2010.12.049>) from the Shooting toolbox of SPM12 which includes an increasing number of iterations (increasing iterations). Shooting is the successor of the DARTEL registration from SPM12, which already showed quite good accuracy (Ashburner & Friston, 2008; <https://doi.org/10.1016/j.neuroimage.2008.12.037>), but uses smaller deformations to achieve the same or better accuracy compared to DARTEL.

Spatial Registration and Figure 3: For the registration, how is the registration performing with clinical populations (e.g. stroke patients) or specific disorders.

A: Good point. However, due to space limitations, it was impossible to describe all available features of CAT12. However, for the registration step, we implemented customized approaches (as described in the manual; https://neuro-jena.github.io/cat12-help/#vox_proc) that were not included in the manual.

Stroke Lesion Correction (SLC)

To mitigate improper deformations during spatial registration in brains with stroke lesions, the CAT12 toolbox offers a Stroke Lesion Correction (SLC) flag (which can be used to correct for frequency) deformations during the Shooting registration step, which can occur due to the presence of lesions. To utilize this flag, the user should use the Manual Image Masking batch, where a lesion mask can be created. Subsequently, the SLC flag should be enabled in the command line. This flag excludes the lesion mask from the spatial registration, preventing large deformations that might otherwise arise when aligning the lesioned brain to the template. This approach results in a more accurate spatial alignment, particularly for clinical data involving stroke patients. This approach is essential for neuroimaging studies that require subsequent analysis.

White Matter Hyperintensity Correction (WMHC)

The accurate detection of white matter hyperintensities (WMHs) is crucial to prevent registration errors, such as the inappropriate registration of WMHs in close proximity to the cortex can lead to surface reconstruction issues by being misinterpreted as gray matter (GM). To address this issue, a WMHC technique (Ashburner & Friston, 2011) on the preliminary SPM segments to align the tissue probability map and the CAT12 atlas. WMHC corrections are conducted using region-growing and bottleneck algorithms (Dahnke et al., 2013). Within the individual segment, WMHs are detected and adjacent to the lateral ventricles that have high WM probability but GM-like intensity are classified as WMHs. These areas with WMHs are treated as a separate tissue class, depending on the WMH correction (WMHC) processing parameters.

Surface Registration and Figure 3: What type of noise is used to evaluate the accuracy? This can be important as not every noise is the same depending on the modality.

A: We have used the BrainWeb Phantom (<https://brainweb.bic.mni.mcgill.ca/brainweb>), which allows the simulation of Gaussian noise (and other segmentation). However, the implemented spatially adaptive non-local means (SANLM) denoising filter (Manjón et al., 2010) is used to reduce the noise.

Maybe having the letters of the figure panels referred to in the text would help the reader.

A: We have now added the letters of the figure panels to the text.

Performance of CAT: Although I see the advantage of using simulated data, I think it would require more explanation. First, how does it compare to real data? Second, is it only healthy data? In that case, the accuracy evaluation might not be relevant for the main purpose of the study.

A: For our evaluation, we used the BrainWeb Simulated Brain Database, which provides simulated data for normal brains as well as for brains with MS lesions. We used normal brains because our approach relies only on T1-weighted images, whereas the detection of MS lesions requires additional modalities. For the simulated data, we have used real clinical data from patients with Alzheimer's disease. This enabled us to evaluate the performance of the common neuroimaging tools.

Longitudinal Processing: Are VBM analyses sensitive enough to capture changes over days? I would be surprised, but I would like to see some results.

from it, I reckon).

A: Yes, definitely. VBM analyses are sensitive enough, and there are a number of studies that detected significant changes in detecting short-term changes after only a few hours! We have added the references (see below) to these latter studies to the

Taubert et al. 2016: Rapid and specific gray matter changes in M1 induced by balance training
<https://doi.org/10.1016/j.neuroimage.2016.03.017>

Broessner et al. 2021: Repetitive T1 Imaging Influences Gray Matter Volume Estimations in Structural Brain Imaging
<https://doi.org/10.3389/fneur.2021.755749>

Mapping onto the Cortical Surface: I am a bit confused about the interest in mapping functional or diffusion parameters to the surface. This would waste a lot of information from these parameters, but I am not familiar with this type of analysis. "Optionally, CAT also allows mapping of voxel values at multiple positions along the surface normal at each node". I do not understand

A: Yes, indeed, there are several papers that revolve around mapping onto the cortical surface (e.g., Brodoehl et al., 2020) that map different modalities onto the surface has several advantages, as described in detail in "Supplemental Note 5. Mapping onto the Cortical Surface" (see also in Supplemental Figure 7). Just to give one example: Mapping onto the surface allows for smoothing on the surface using geodesic distances, which is a typical smearing across anatomical boundaries that can occur in 3D (Euclidean) space. This, in turn, improves the ability to smooth the cortex but farther apart in the unfolded cortex.

Example application:

Is there a way to come back from the surface space to the volume space to compare the results? For example, VBM and SBM are not in the same space. Additionally, in the end, the surface representation is just that, a representation; most other methods do not translate the result on the surface back to the volume (if it is not already available).

A: In theory, interpolation may allow for the mapping of surface data back to 3D (volume) space, but this is not done in practice. In practice, surface mapping exists. The issue is further complicated by different measures. For example, vertex-wise cortical thickness is a measure of distance-based gray matter quantifies the local amount of tissue in a given voxel.

Evaluation of CAT12:

I was confused with Supplemental Figure 1 as it is not mentioned in the caption that it is the AD data and not the simulated data.

A: We have now added this information to the figure caption.

Regarding the reliability of CAT12, it seems to capture more things, but I struggle to see how we can be sure that this is "better" than manual tracing.

A: While we cannot fully eliminate the possibility of false positives, we have taken measures to minimize this risk. Specifically, we control the family-wise error (FWE) with a threshold of $p < 0.001$, which significantly reduces the likelihood of false positives. Furthermore, our hypotheses are based on well-established anatomical patterns of the disease.

We acknowledge that increased sensitivity can lead to concerns about specificity, but the larger effect sizes observed with CAT12 in Alzheimer's disease. Given this alignment with established patterns, we are confident that the larger effect sizes are not solely due to increased sensitivity.

"those achieved based on manual tracing and demonstrated that both approaches produced comparable hippocampal volumes. However, manual tracing could be misleading.

A: We acknowledge that comparable volumes do not always equate to identical accuracy. However, in neuroimaging research, the accuracy of automated segmentation methods. The study by Khlif et al. (2019) found that CAT12's automated segmentation method, through manual tracing, thereby providing a meaningful assessment of accuracy.

The primary goal of segmentation methods is to approximate the true anatomical volumes as closely as possible, and compare them to a high degree of accuracy. Additionally, manual tracing is inherently variable due to human error, while automated methods of segmentation estimates indicate that CAT12 performs well within this established standard of accuracy.

I think the multiple studies show that CAT12 is as valid as any other tool but I am not sure the argument that it is better is a valid one. A relevant morphological change is for a given disease.

A: We acknowledge that determining what constitutes a relevant morphological change for a given disease can be challenging. We have evaluated the sensitivity and accuracy in both real and simulated data, supporting our arguments.

1. Performance on Real Data: Multiple studies, including our own, have shown that CAT12 identifies consistent effects in clinical patterns of disease-related changes, indicating that CAT12 is sensitive to relevant morphological changes.

2. Validation with Simulated Data: In addition to real data, CAT12 has been tested on simulated datasets where the ground truth is known, showing accuracy, showing that CAT12 performs well under controlled conditions and is more robust against noise and intensity non-uniformity.

3. Consistency with Disease Patterns: The morphological changes detected by CAT12 are consistent with known disease patterns. While no tool is perfect, the evidence suggests that CAT12 offers improved sensitivity and accuracy, making it a robust choice for morphological analysis.

Methods:

Statistical Analysis: Why is the FWER correction used for the voxel-wise statistics (which perform many comparisons) and FDR would expect the opposite.

A: The choice of multiple comparison correction method depends on the specific analysis and its characteristics.

1. Voxel-wise Statistics:

- Voxel-wise analyses involve a large number of comparisons, making them prone to type I errors.
- The FWER correction (such as FWE) is conservative and controls the probability of making any type I error across all comparisons.
- This approach is suitable for voxel-wise analyses because it minimizes false positives across the many comparisons being made.

2. ROI-wise Statistics:

- ROI-based analyses involve fewer comparisons, typically related to specific anatomical regions of interest.
- The FDR correction controls the expected proportion of type I errors among the rejected hypotheses, which can be more appropriate for ROI-wise analyses.
- FDR provides a good balance between controlling for false positives and maintaining power, especially when the number of comparisons is smaller.

In short, voxel-wise analyses have a high potential for type I errors due to the large number of comparisons, warranting a more conservative correction. ROI-wise analyses involve fewer comparisons, making FDR a more suitable choice for balancing control of type I error and statistical power.

"The outcomes of the VBM and voxel-based ROI analyses were overlaid onto orthogonal sections of the mean brain created from the study sample (n=50)."

A: We have extended this sentence to "The outcomes of the VBM and voxel-based ROI analyses were overlaid onto orthogonal sections of the mean brain created from the T1-weighted images of the study sample (n=50)."

Reviewer #3: CAT has been around for a long time and is a well maintained toolbox - the paper describes all the features and I have commented on the pdf (uploaded) which I don't see has mandatory and thus 'accepted' the paper (and leave the authors to decide on the toolbox).

Dr Cyril Pernet

A: Many thanks for your helpful comments in the PDF, which we have considered in the manuscript.