The Kapowski Chronicles: A Complete, Volumetric Cortical Thickness Open Source Pipeline with Evaluation on Public Data

Nicholas J. Tustison[†a,1], Brian B. Avants[†b], Philip A. Cook[b], Gang Song[b], Sandhitsu R. Das[b], Jeffrey R. Duda[b], Niels van Strien[c], James R. Stone[a], James C. Gee[b]

[a]*Department of Radiology and Medical Imaging, University of Virginia, Charlottesville, VA*
[b]*Penn Image Computing and Science Laboratory, University of Pennsylvania, Philadelphia, PA*
[c]*Department of Circulation and Medical Imaging, Norwegian University of Science and Technology, Trondheim, Norway*

Abstract

Numerous studies have explored the relationship between cortical structure and brain development, cognitive function and functional connectivity. The highly convoluted cortical topography makes manual measurements arduous and often impractical given the population sizes necessary for sufficient statistical power. Computational techniques have permitted large-scale studies as they provide robust and reliable localized measurements characterizing the cortex with little or no human intervention. Particularly useful to the neuroscience community are publicly available tools, such as the popular surface-based Freesurfer, which facilitate the testing and refinement of hypotheses. In this paper, we introduce the volume-based Advanced Normalization Tools (ANTs) cortical thickness automated pipeline comprising well-vetted components such as SyGN (multivariate template construction), SyN (image registration), N4 (bias correction), Atropos (*n*-tissue segmentation), and DiReCT (cortical thickness) all developed as part of the ANTs open science effort. Complementing the open source aspect of ANTs we investigate several hypotheses explored previously in the literature using four different publicly available data sets totaling approximately 1200 subjects. To further promote open science and use of the proposed tools, all scripts and templates used to produce the results are hosted on the Neuroimaging Informatics Tools and Resources Clearinghouse (NITRC) website.

Keywords: advanced normalization tools, cortical thickness, open science

1. Introduction

Historically rooted in the meticulous work of von Economo [22], imaging-based structural analysis of the brain plays a fundamental role in identifying the relationship between cortical morphology, disease and cognition. Quantitative cortical measures have been demonstrated in conditional abnormalities such as Huntington's disease [57, 56, 60], schizophrenia [50], bipolar disorder [45], Alzheimer's disease and frontotemporal dementia [21, 19], Parkinson's disease [36], Williams syndrome [70], multiple sclerosis [55], autism [12, 33], migraines [17], chronic smoking [41], alcoholism [29], cocaine addiction [48], Tourette syndrome in children [68], scoliosis in female adolescents [73], obsessive compulsive disorder [64], ADHD [1], obesity [54], and heritable [52] and elderly [8] depression. Cortical thickness also varies normally as a function of age [39], gender [44], untreated transsexuality [80], handedness [43, 2], intelligence [63], athletic ability [75], musical ability [9, 30], tendency toward criminality [53], and Tetris-playing ability in female adolescents [32]. Additionally, recent studies demonstrate possible functional connectivity relationships using cortical thickness measures [76, 42, 34]. Although these findings are subject to debate and interpretation [31], the availability of quantitative computational methods for extracting such information has proven invaluable for developing and refining fundamental neuroscience hypotheses.

Computational methods for analyzing the cortex may be broadly characterized as surface mesh-based or volumetric [58, 13]. Representative of the former is the Freesurfer[2] cortical modeling software package [15, 27, 25, 26, 28] which owes its popularity to public availability, excellent documentation, good performance, and integration with other toolkits, such as the extensive FMRIB software library (FSL) [67]. Similar to other surface approaches (e.g. [18, 47, 46, 37]), the pial and white matter surfaces from individual subject MR data are modeled with polygonal meshes which are then used to determine local cortical thickness based on a specified correspondence between the surface models.

Image volumetric (or meshless) techniques vary both in algorithmic terms as well as the underlying definition of cortical thickness. An early, foundational technique is the method of [35] in which the inner and outer surface geometry is used to determine the solution to Laplace's equation where thickness is measured by integrating along the tangents of the resulting field lines spanning the boundary surfaces. Subsequent contributions improved upon the original formulation. For example, in [77],

[1]Corresponding author: PO Box 801339, Charlottesville, VA 22908; T: 434-924-7730; email address: ntustison@virginia.edu.

†The first two authors contributed equally to this work.

[2]http://surfer.nmr.mgh.harvard.edu/

an Eulerian PDE approach was proposed to facilitate the computation of correspondence paths. Extending the surface-based work of [46], the hybrid approach of [37] uses the discrete Laplacian field to deform the white matter surface mesh towards the pial surface. Although the Laplacian-based approach has several advantages including generally lower computational times and non-crossing correspondence paths, direct correlative assessments with histology are potentially problematic as the quantified distances are not necessarily Euclidean. Other volumetric algorithms employ coupled level sets [78], model-free intelligent search strategies either normal to the gray-white matter interface [58] or using a min-max rule [72]. Most relevant to this work is the DiReCT (Diffeomorphic Registration-based Cortical Thickness) algorithm proposed in [16] where generated diffeomorphic mappings between the white and pial matter surfaces are used to propagate thickness values through the cortical gray matter. A unique benefit of DiReCT is that it naturally estimates the boundaries of buried sulci by employing a diffeomorphic constraint on the probabilistic estimate of the gray matter and cerebrospinal fluid interface.

Despite the variety of techniques for estimating cortical thickness from imaging data (of which only a fraction are cited), several common preprocessing components may be identified. The most fundamental of these include inhomogeneity correction, skull stripping, and *n*-tissue segmentation for differentiating the gray and white matter. For statistical analysis across large populations, construction of population-specific unbiased templates is also potentially beneficial [23]. In addition, intermediate steps might include a crucial registration component, e.g. propagating template-based tissue priors for improved segmentation.

The requisite additional components apart from the actual cortical thickness estimation, coupled with the general lack of availability of published algorithms [40], inhibits performing studies by external researchers and makes comparative evaluations difficult. For example, one recent evaluation study [13] compared Freesurfer (a surface-based method) with two volumetric methods [35, 16]. Whereas the entire Freesurfer processing pipeline has been made publicly available, tuned by the original authors in terms of implementation, and described in great detail (specifically in terms of suggested parameters); both volumetric methods were implemented solely by the authors of the evaluation (not the actual algorithmic developers) using unspecified parameters making the comparisons less than ideal. Further complicating comparisons is distinct processing domains between volumetric and surface-based techniques and the potential for the introduction of bias [38].

In this work, we describe our Insight Toolkit (ITK)-based cortical thickness pipeline which is freely available as part of the Advanced Normalization Tools (ANTs) software package. This includes all the necessary preprocessing steps consisting of well-vetted previously published algorithms for bias correction [71], brain extraction [4], *n*-tissue segmentation [6], template construction [7], and image normalization [5]. We also describe improvements made to the original DiReCT algorithm [16]. Equally as important, we provide explicit coordination between these pipeline components complete with a set of useful parameters which are employed to analyze the publicly available IXI data set. The full pipeline and parameter set is encapsulated in a well-documented shell script which is also available in ANTs. Furthermore, we provide all the derived image data and other processing scripts on the NITRC repository specifically meant for this publication. The availability of both the code and data permits the set of results described in this work to be fully reproducible. This permits other researchers to contrast their own results against this baseline processing and to adapt the given volumetric pipeline for measuring cortical thickness with their own datasets.

2. Methods and Materials

2.1. ANTs volumetric-based cortical thickness estimation pipeline

The ANTs-based cortical thickness estimation workflow is illustrated in Figure 1. The steps are as follows:

1. initial N4 bias correction on input anatomical MRI,
2. brain extraction using a hybrid segmentation/template-based strategy,
3. alternation between prior-based segmentation and white matter posterior probability weighted bias correction,
4. DiReCT-based cortical thickness estimation, and
5. optional normalization to specified template.

Each component, including both software and data, is briefly detailed below with the relevant references for additional information.

Additionally, the coordination of all the algorithmic components is encapsulated in the shell scripts `antsCorticalThickness.sh` with subcomponents delegated to `antsBrainExtraction.sh` and `antsAtroposN4.sh`. This includes optimal parameters for each of the algorithmic components which has worked well for our processing and which are used to acquire the results described in this work.

2.1.1. Anatomical template construction

Normalizing images to a standard coordinate system reduces intersubject variability in population studies. Various approaches exist for determining the normalized space such as the selection of a pre-existing template based on a single subject, e.g. the Talairach atlas [69], or a publicly available averaged group of subjects, e.g. the MNI [14] or ICBM [49] templates. Additionally, mean templates constructed from labeled data can be used to construct spatial priors for improving segmentation algorithms. The work of [7] explicitly models the geometric component of the normalized space during optimization to produce such mean templates. Coupling the intrinsic symmetry of SyN pairwise registration [5] and an optimized shape-based sharpening/averaging of the template appearance, Symmetric Group Normalization (SyGN) is a powerful framework for producing optimal population-specific templates [7].

The ANTs implementation of this technique is currently available as a shell script, `buildtemplateparallel.sh` (a multivariate version is also available as

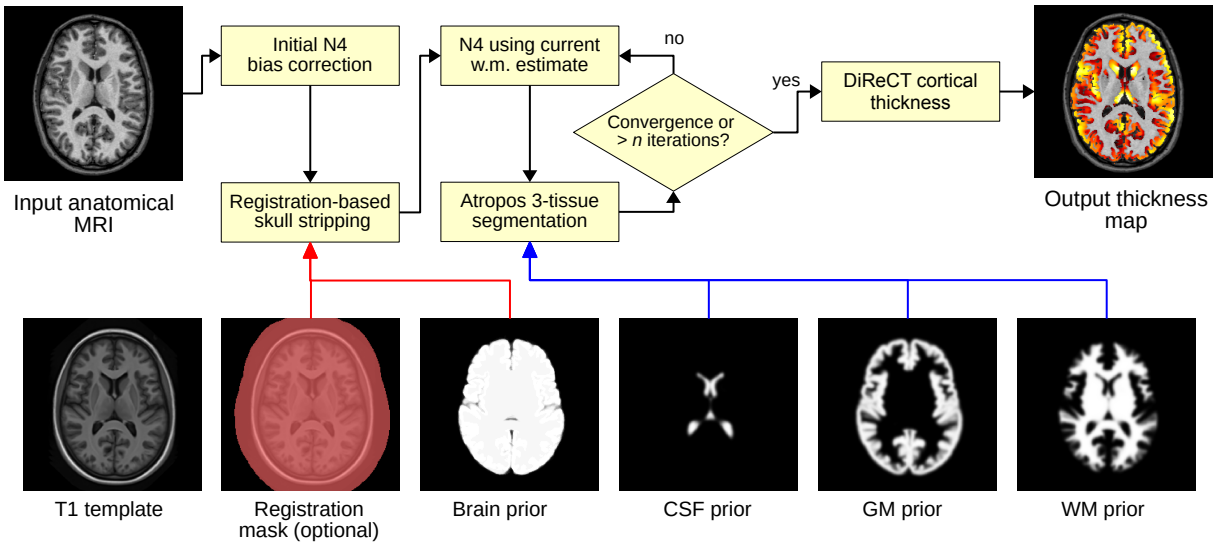

Figure 1: Illustration of the main components of the ANTs processing workflow containing all elements for determining cortical thickness. Not shown is the optional subject to template registration.

`antsMultivariateTemplateConstruction.sh`). Both scripts are distributed as part of the ANTs repository. The latter script permits the construction of multimodal templates (e.g. T1-weighted, T2-weighted, proton density MRI and fractional anisotropy). Both scripts accommodate a variety of computational resources for facilitating template construction. These computational resource possibilities include:

- serial processing on a single workstation,
- parallelized processing on a single workstation with multiple cores using `pexec`[3],
- parallelized processing using Apple's XGrid technology[4],
- parallelized processing using Sun Grid Engine for cluster-based systems[5], and
- parallelized processing using the Portable Batch System for cluster-based systems[6].

For this work, database-specific templates were used during cortical thickness pipeline processing for both brain extraction and brain segmentation steps. Multivariate templates were constructed from the multimodal data sets. However, their usage was based on the fact that they had been built previously for other work and not because they provide a discernible advantage over univariate templates (i.e. T1-only) for the proposed workflow.

[3] http://www.gnu.org/software/pexec/pexec.1.html
[4] https://developer.apple.com/hardwaredrivers/hpc/xgrid_intro.html
[5] http://www.oracle.com/technetwork/oem/grid-engine-166852.html
[6] http://www.pbsworks.com/

2.1.2. *N4 Bias field correction*

Critical to quantitative processing of MRI is the minimization of field inhomogeneity effects which causes artificial low frequency intensity variation across the image. Large-scale studies, such as the Alzheimer's Disease Neuroimaging Initiative (ADNI), employ perhaps the most widely used bias correction algorithm, N3 [65], as part of their standard protocol [10].

In [71], we introduced an improvement of N3, denoted as "N4", which demonstrates a significant increase in performance and convergence behavior on a variety of data. This improvement is a result of an enhanced fitting routine (which includes multi-resolution capabilities) and a modified optimization formulation. For our workflow, the additional possibility of specifying a weighted mask in N4 permits the use of a "pure tissue" probability map (described below) calculated during the segmentation pipeline for further improvement of bias field estimation. In addition to its public availability through ANTs and the Insight Toolkit, it has also been included in the popular open source Slicer software package for visualization and medical image computing [24].

N4 is used in two places during the individual subject processing (cf. Figure 1). Following conversion of the raw dicom T1-weighted image to Nifti format using our related `Neuropipedream` set of raw image conversion and organization tools[7], N4 is used to generate an initial bias corrected image for use in brain extraction. The input mask is created by adaptively thresholding the background from the foreground using Otsu's algorithm [51]. Following brain extraction, three-tissue segmentation involves iterating between bias field correction using the current pure tissue probability map as a weight mask

[7] http://sourceforge.net/projects/neuropipedream/

and then using that bias corrected image as input to the Atropos segmentation step (described in the next section).

2.1.3. Atropos 3-tissue segmentation

In [6] we presented an open source n-tissue segmentation software tool (which we denote as "Atropos") attempting to distill 20+ years of active research in this area particularly some of its most seminal work (e.g. [79, 3]). Specification of prior probabilities includes spatially varying Markov Random Field modeling, prior label maps, and prior probability maps typically derived from our template building process. Additional capabilities include handling of multivariate data, partial volume modeling [62], a memory-minimization mode, label propagation, a plug-n-play architecture for incorporation of novel likelihood models which includes both parametric and non-parametric models for both scalar and tensorial images, and alternative posterior formulations for different segmentation tasks.

Due to the important interplay between segmentation and bias correction, we perform multiple N4 $\Leftrightarrow$ Atropos iterations. In order to better integrate Atropos and N4, we use a pure tissue probability weight mask generated from the posterior probabilities generated from the segmentation process. Given N labels and the corresponding N posterior probability maps $\{P_1, \ldots, P_N\}$ produced during the segmentation process, the N4 weight mask is created at each N4 $\Leftrightarrow$ Atropos iteration from

$$P_{pure\ tissue}(\mathbf{x}) = \sum_{i=1}^{N} P_i(\mathbf{x}) \prod_{j=1, j\neq i}^{N} \Big(1 - P_j(\mathbf{x})\Big). \qquad (1)$$

One of the key insights of the original N3 algorithm is the observation that inhomogeneities cause the intensity values of pure tissue peaks to spread in the intensity histogram as if convolved with a Gaussian. A core contribution of N3 is the proposed corrective of deconvolving the intensity histogram to accentuate the tissue peaks coupled with a spatial smoothing constraint. The pure tissue probability weight mask weights more heavily the voxels corresponding to pure tissue types during the deconvolution process while minimizing the contribution of regions such as the gray/white matter interface where it is unclear as to which peak they belong.

2.1.4. Brain extraction

Brain extraction using ANTs combines template building, high-performance brain image registration [5], and Atropos with topological refinements. An optimal template for brain extraction is generated offline using labeled brain data. For example, in this work we use the LPBA40 data for generating a brain extraction template and a corresponding brain probability mask which is available on the website associated with this submission.

The warped template probability map is thresholded at 0.5 and the resulting mask is dilated with a radius of 2. Atropos is used to generate an initial 3-tissue segmentation estimate within the mask region. Each of the three tissue masks undergo specific morphological operations which are then combined to create a brain extraction mask for use in the rest of the cortical thickness workflow. does there need to be a bit more technical detail here? while you can refer to the script, why perform these operations? there are numerous references, most germane probably some recent stuff from J Prince (i think) and the freesurfer watershed approach which came from ... i forget ... maybe one of the french groups.

A comparison using open access brain data with publicly available brain extraction algorithms including AFNI's `3dIntracranial` [74], FSL's `BET2` [66], Freesurfer's `mri_watershed` [59], and BrainSuite [20] demonstrated that our combined registration/segmentation approach [4] performs at the top level alongside BrainSuite (tuned) and FreeSurfer. ok you have the segonne ref here ...

2.1.5. DiReCT (aka KellySlater/KellyKapowski) Cortical Thickness Estimation

DiReCT was introduced in [16] and made available in ANTs with the program `KellySlater`. Since then several improvements have been made and incorporated into the program `KellyKapowski`.[8] Among the most significant advancements is that the more recent implementation is multi-threaded, written in rigorous ITK coding style, and has been made publicly available through ANTs complete with a unique user interface design developed specifically for ANTs tools.

2.2. Public Data Resources

2.2.1. NIREP Data for Cortical Labels

The Nonrigid Image Registration Evaluation Project (NIREP[9]) is an ongoing framework for evaluating image registration algorithms [11]. The initial data set introduced into the project consists of 16 (8 male and 8 female) high resolution skull-stripped brain data with 32 cortical labels (cf. Table 1) manually drawn using a published protocol.

2.2.2. Data for Pipeline Evaluation

IXI. The IXI data[10] used for the evaluation consists of 577 healthy subjects imaged at three sites using several modalities (T1-weighted, T2-weighted, proton density, magnetic resonance angiography, and diffusion tensor imaging). The database also consists of demographic information such as age, weight, height, ethnicity, occupation category, educational level, and marital status. The number of subjects spanning a range of demographic characteristics makes this a rich data set for validating and exploring correlations with cortical thickness measured using the ANTs pipeline.

Oasis.

[8] Traditional academic discourse encountered in the published literature rarely contextualizes peculiarities such as algorithmic nomenclature. We briefly mention that this was the source of a rare disagreement between the first two authors based, as many disagreements are, on a simple misunderstanding and not an affronting existential statement concerning a certain favorite sitcom of the author's youth.

[9] http://www.nirep.org/

[10] http://biomedic.doc.ic.ac.uk/brain-development/

1) L occipital lobe	2) R occipital lobe
3) L cingulate gyrus	4) R cingulate gyrus
5) L insula gyrus	6) R insula gyrus
7) L temporal lobe	8) R temporal lobe
9) L superior temporal gyr.	10) R superior temporal gyr.
11) L infero temporal region	12) R infero temporal region
13) L parahippocampal gyr.	14) R parahippocampal gyr.
15) L frontal pole	16) R frontal pole
17) L superior frontal gyrus	18) R superior frontal gyrus
19) L middle frontal gyrus	20) R middle frontal gyrus
21) L inferior gyrus	22) R inferior gyrus
23) L orbital frontal gyrus	24) R orbital frontal gyrus
25) L precentral gyrus	26) R precentral gyrus
27) L superior parietal lobule	28) R superior parietal lobule
29) L inferior parietal lobule	30) R inferior parietal lobule
31) L postcentral gyrus	32) R postcentral gyrus

Table 1: The 32 cortical NIREP labels.

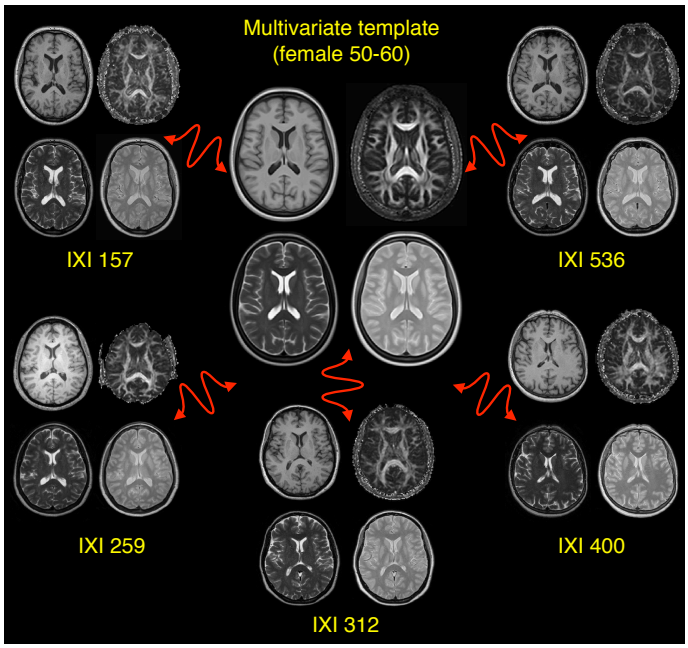

Figure 2: Sample multivariate template constructed from a subset of the IXI data (female, age 50–60). Axial slices of five of the 37 total subjects from this cohort are shown.

3. Discussion and Conclusions

Acknowledgments

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