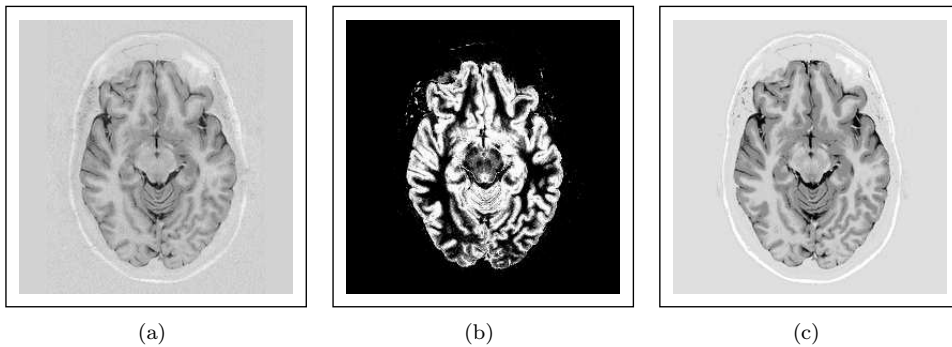


TINA Demo 003: The Medical Vision Tool

neil.thacker(at)manchester.ac.uk

Last updated
6 / 10 / 2008



Imaging Science and Biomedical Engineering Division,
Medical School, University of Manchester,
Stopford Building, Oxford Road,
Manchester, M13 9PT.

TINA Demo 003: The Medical Vision Tool

N.A. Thacker.
Dept. of Medical Biophysics
Imaging Science and Biomedical Engineering Division
Medical School, University of Manchester
Manchester, M13 9PT, UK
`neil.thacker(at)manchester.ac.uk`

1 Introduction

Several methods for automated analysis of MR data sets are demonstrated here via the use of replay macros to configure the TINA environment, followed by a minimum number of button presses for the key stages. The main intention is to provide working examples which illustrate results in published papers. The demonstrations provide specific examples of quantitative analysis of magnetic resonance images (MRI) data. This includes; multi-spectral image segmentation, data volume alignment, time curve fitting (so called “perfusion”), coil correction, and structure tracking. The software will run with a minimum of user interaction, in order to give a feel for what is possible and data quality.

2 Installation

In order to use the TINA stereo vision tool, you must already have compiled and installed the TINA libraries. See the TINA website

`http://www.tina-vision.net`

for instructions.

The TINA stereo vision tool project can be obtained either from the demos page of the TINA website or from the TINA CVS repository using the commands

```
cvs -d :pserver:anonymous@cvs.tina-vision.net:/home/tina/cvs login
(press enter when prompted for a password)
cvs -d :pserver:anonymous@cvs.tina-vision.net:/home/tina/cvs co tina-projects/medical_tool
```

This should check out the following files to the current directory

```
README: asci versions of this document.
Makefile: Executed project Makefile.
Makefile.linux  alternative linux Makefile.
Makefile.solaris: alternative solaris Makefile.
003_medical_tool.pdf: this document.
tinaTool.c: main tool specification software.
mrimages: subdirectory of example data.
replays: subdirectory of macros.
skeleton.c : code developers starting kit
???.cls : tina replay files (human readable asci)
```

In order to get started you must first build the tinaTool. Copy either the Linux or Solaris to alternative to Makefile (the default is already Solaris). This Makefile may require some manual editing: it assumes that you installed the TINA libraries in the `/usr/local/Tina5` directory, and that you are using the Xview widget set. Open the Makefile in an editor, set the TINA-X-GUI variable to specify the widget set you wish to use, and edit any paths that do not apply for your system. Finally, type “make” to build the tinaTool executable.

To run the vision tool you can type one of the following,

```
./tinaTool -f aorta
./tinaTool -f coil
./tinaTool -f coreg
./tinaTool -f fmri
./tinaTool -f mixseg
./tinaTool -f perf
```

which executes a series of button presses stored in associated “.cls” files. See below for details.

3 Usage

3.1 Graphics

Refer to the Tina Users Guide for information regarding installing and operating general purpose graphics panels (Tv’s). The TINA vision demonstration makes use of a variety of Tv’s for image display. These can be interchanges and replaced as necessary, for example; Click on “New Tvtool” in the top level tinaTool window to start a new Tvtool to display this graphics stream, then click on “left” in the Tv list of the Stereo tool, and finally “install” in the Tvtool window. The Tvtool will now display any “left” stereo images loaded into the Stereo tool. The macro’s will generally perform these steps for you.

3.2 Image Input

In order to use TINA with your own data , some knowledge of the image format is required. Generally you should be able to load DICOM images, or the commonly used analyze format. Derived image results should be stored as the Tina ”aiff” if you wish to maintain precision and store associated co-ordinate space details.

4 Multi-Spectral Partial Volume Brain Segmentation

The segmentation algorithms in TINA, although Bayesian in approach, avoids the use of spatial Bayesian priors during segmentation. Such priors can serve to bias the results towards what is expected rather than what is observed. The prior probabilities used come from a bootstrapped estimate of tissue proportion within a slice, which for large areas are asymptotically independent of the grey level noise. In addition the probabilities estimated correspond to the most likely partial volume tissue fraction rather than the probability of a label hypothesis (as generated in other packages such as SPM). This is achieved via the use of a linear model of the image formation process and explicit modelling of partial volume distributions. The result is partial volume estimates which can be integrated over regions and volumes to give genuine volumetric estimates of tissue proportion, even in thick data slices (see Tina memo 2001-009 and 2003-007).

operation:

- Configure the TINA system for by executing ‘tinatool -f mixseg’ from the UNIX command line. This will position the windows of the tool and automatically load a test dataset comprising four MRI sequences. A partial volume model file is also loaded and specified tissues listed in the main dialog window. This file is in a simple ASCII format for flexibility and specifies nominal mean grey level values and distributions for each tissue and a matrix of partial volume proportions.
- Select ‘roi’ in the Sequence Tv ‘mouse’ options to configure for region of interest selection. Using click and drag on the left mouse button select a region of the brain containing only tissues specified in the partial volume model file (other tissues can only be accounted for as outliers).
- Execute the ‘E-step’ function in the ‘NMR Segment Tool’, this will perform the expectation step of the EM algorithm.
- Execution of the ‘M-mean’, ‘M-cov’ and ‘M-prior’ routines will now re-estimate the parameters of the model.
- The current state of the model can be visualised using the EM plot routines, including 1 and 2D histogrammes and image reconstruction (using ‘model’) of the current MR image displayed in the Sequence Tv (model).

The basic model is also extended by the use of local image slope, this can be used by applying the ‘E-step grad’ and ‘M-k grad calc’, routines. These modify the most probable volume fraction using gradient information and re-estimate the gradient analysis parameters in an EM fashion (respectively). Re-fitting of the slope parameters results in a de-bug feature, which displays the slope data and fitted curve in the root window. Several iterations are generally required to achieve a good fit for these distributions. This analysis explicitly assumes homogenous tissue regions with distinct boundaries, and should not be used in areas of significant partial volume or its biological equivalent such as deep grey matter. The method is suitable for analysis of cortical grey matter.

Probability maps of tissue proportion can be computed by specifying the name of the required tissue type (as specified in the model file) and executing the ‘prob’ function. The partial volume probability image will be displayed in the ‘imcalc’ Tv.

These maps can be thresholded to provide binary region maps for masking using standard ‘Imcalc Tool’ processing, see the TINA ‘User’s Guide’ documentation for this and alternative segmentation algorithms.

5 Automated and Manual Co-registration

The co-registration routines within TINA are for rigid body alignment preferably of the same subject but across MR modalities (such as with data for the multi-spectral segmentation described above). This is achieved using a similarity metric which minimised distances between grey level boundaries. The limited number of parameters needed for a rigid alignment makes it possible to align using just three orthogonal projections through the centre of the data. This significantly increases the speed that alignments can be performed without significant loss of spatial accuracy. Alignments are still expected to be correct to within 0.1 voxels, which is the limit of the spatial rigidity of the MR acquisition and consistent with the accuracy of approaches which use the entire volume. The method is strictly not designed for between subject alignment, although this can be achieved at a crude level by convolving the images to reduce spatial resolution. Generally, accurate spatial correspondence between two brains is very difficult to obtain with an accuracy of greater than 5mm, due to structural variations in normal brain shape at the level of secondary sulci. Problems with local minima for such problems generally result in best results being obtained by manual method which is supported. High degrees of non-linear shape change can be obtained by regional alignment. We expect that this alignment technique will be adequate for the majority of scientifically meaningful analyses for the foreseeable future. This software was used in the analysis found in Tina memo 2004-001.

operation:

- Configure the TINA system for by executing ‘tinatool -f coreg’ from the UNIX command line. This will position the windows of the tool and automatically load a test dataset.
- The data can be rotated manually using the mouse within any of the three co-registration Tv panels.
- Any slice of the data can be stored for later processing using a variety of interpolation techniques from the ‘Reslice’ menu by ‘push’ing from the ‘Coreg Tool’ into the ‘imcalc’ Tv for the selected Tv panel.
- Any set of three views can be ‘Latch’ed and a new data set aligned to this one using manual or ‘auto’ automatic co-registration via selection of one of the alternative display options.
- To demonstrate this on the current data set select ‘anaglyph’, rotate the data and press ‘auto’ to correct the alignment. Execution time is of the order of a minute depending upon your machine and the technique should work for anything up to 5 pixel shifts (typical).
- For more accurate results select the ‘linear’ reslice option and re-run the ‘auto’ alignment.

See the TINA ‘User’s Guide’ documentation for more details on algorithms and functionality.

6 BOLD Data Analysis

From our investigations into BOLD analysis with data from our Phillips scanner, we have concluded that the main anomalies in BOLD analysis come from three sources, inappropriate phase shift for the assumed stimulus curve, base-line drift of the scanner and motion correction. Other effects, such as temporal and spatial correlation and the specific shape of the stimulus curve (eg: convolution with the expected haemodynamic response) are far

less significant. The TINA software therefore contains methods to test the success of motion correction (which is done using the co-registration software described above), a model independent base-line drift estimation (which calculates the relative normalisation in each slice of data) and a shifted correlation approach to find the most significant correlation around the expected position. Other significant steps in analysis are corrected by Monte-Carlo to generate meaningful P values.

operation:

- Configure the TINA system for by executing ‘tinatool -f fmri’ from the UNIX command line. This will position the windows of the tool and automatically load a test dataset.
- The ‘Stimulus’ correlation function can be ‘plot’ed in the ‘imcalc graph’ by pressing the appropriate button. This also sets the curve used for subsequent analysis (the ‘compare’ function will not run until one is selected).
- Equivalent statistical measures to many used in the literature can be selected from the ‘Sequence’ menu and used to ‘compare’ the temporal data behaviour. Results are displayed in the ‘imcalc’ Tv panel. Select each in turn and visually compare the results.
- Statistical distributions can be displayed for selected regions of the ‘imcalc’ Tv using click and drag on the left mouse button.

The affects of motion on each of these measures can be investigated using the ‘replays/mcorr’ replays (1,2 and 3) which can be executed by ‘run’ning the appropriate ‘Macro File’ from the ‘Sequence Tool’. The resulting plots of correlation score vs edge gradient are displayed in the ‘imcalc’ Tv panel but may need to be resized for viewing (‘init’). The plot shows correlation score against local image slope (see Tina memo 2001-002). Motion artifact can be attributed to broadening of the central distribution for mid to high gradient values.

7 MR Perfusion Analysis

The estimation of blood flow in the brain is done in TINA using a method which varies considerably from that found commonly in the literature. From our experiments and observations of real data we have concluded that techniques based upon deconvolution with an arterial input function are dominated by flow heterogeneity. We therefore developed an approach for quantitative analysis of the “perfusion data” based upon the spatial differentiation of the time of arrival of the injected bolus. Final stages of this calculation are generally carried out in the image calculator. This new method does not require the estimation of an arterial input function and is fully quantitative. As both blood volume and net-transit times can be calibrated absolutely from the available data. As the method is sensitive to bulk movements of the contrast agent the it estimates net-flow rather than true perfusion. Any random (non-directional) component of flow across the voxel is potentially lost. However, agreement with values from the literature would appear to suggest that the non-directional component is negligible (see Tina memo 2001-003).

operation:

- Configure TINA with the command ‘tinatool -f perf’. Click ‘push’ in Sequence Tool to push the top image onto the image stack, making it visible in the ‘Imcalc’ Tv window. Select ‘flow/t’ from the ‘plot’ menu options, select a pixel with the left button in the ‘Imcalc’ Tv and the time course behaviour is displayed. Try again with ‘conc/t’ for the concentration time graphs, and again for ‘gamma’ fitted conc/t graphs.
- Temporal correlations in the images can be used to identify regions of flow. Using the ‘mouse’ menu, select a ‘roi’ on the first image. Select the roi to include a region with some known flow. Click ‘ROI’ in the segment tool and then ‘plot’. This shows the average activation within this region. Click ‘compare’ to see a map of the correlations between this region and the others in the image.

By thresholding the correlation image using ‘thres’ in the image calculator and then changing the image type to ‘BIN’ then ‘CHAR’ the resulting mask can be used to region analyse flow. The region flow functions are, ‘flow/t’, ‘conc/t’ and ‘gamma’ respectively.

8 Coil Correction

All surface coils and some head coil systems (particularly on high field systems) produce significant signal strength variation across an image. Correcting for such spatially varying anomaly is often referred to as coil correction.

This artefact is generally corrected during tissue segmentation by allowing extra parameters to describe the signal strength variation during the optimisation of model parameters. However, such approaches require a tissue model and can potentially force distinct tissue regions to have an anomalous single grey level value. The approach taken here uses a robust statistical approach to estimate the smooth variation in coil artefact from local estimates of image slope. As the technique does not require a tissue model it will work on a broad variety of images. The method works best for images with good signal to noise and small quantities of partial voluming (ie: isotropic voxels) (see Tina memo 2000-004 and 2007-003).

operation:

- Configure TINA with the command ‘tinatool -f coil’. This will automatically load an image of an orbit (eye) into the ‘Mono Tool’ and push it into the ‘Imcalc Tool’ for processing.
- In order to process this image press the ‘xy norm’ function in the ‘Imcalc Tool’. This will generate a multiplicative map of the coil artifact.
- Correct the original image by multiplying using the ‘*’ button in the ‘Imcalc Tool’.

Other data sets are available in the same directory for ; shoulder, spine, skin, ear and brain (proton density) MR data. Each of these can be loaded into the software via the ‘Mono Tool’ ‘input’ function. They will require noise estimation via the ‘Imcalc Tool’ ‘noise’ function before computation of the multiplicative map. The smoothing kernel for this algorithm needs to be adjusted according to image size and the expected rate of change of the local coil effect. Smoother coil maps can be determined with more precision. As coil inhomogeneity is something which is fixed by the geometry of the scanner the coil smoothing parameter needs to be adjusted for image size. Generally, in our data, a ‘sigma’ of 10 is suitable for small images (256x256) and 20 for larger images.

This correction process is designed specifically for MR images, which do not require estimation of an additional measurement offset, as found in other image data. The process generates only a first order correction to the image which can be interpreted as attempting to minimise the local grey level slope away from edge data. The optimal correction of the correction process is computed as a polynomial power of the linear estimate. The best value is chosen as that which minimises the a robust measure of local image gradient. The result of this process is summarised by the “scale factor %f = %f” report in the main Tina dialog box. The first number is the polynomial power for optimal correction and the second term is effectively a chi-square per degree of freedom. This second term should converge to a value around 1 on repeated application of the correction.

The process can be iterated, however, as the definition of what constitutes a significant edge structure is based upon a statistical analysis of local image gradient this may not be stable beyond 2 steps. The method will also not work for data which has significant through plane partial volume effects (due to thick voxels for example).

9 Aorta Tracking (smartROI tool)

Tina contains a tool for automatic identification of boundaries using a simple linear grey level appearance model (AAM).

operation:

- Configure TINA with the command ‘tinatool -f aorta’. This will automatically load an aortic image sequence into the ‘Sequence Tool’ and prepare a model of the aorta ready to be loaded into TINA for feature tracking. Load the mean aorta shape ‘Model’ into the ‘smartROI Tool’ by adding a ‘.mml’ to the filename in the ‘smartROI Tool’ thus;
”./models/test.mml”
and clicking ‘input’.
- Open the ‘smartROI params’ to view the current setup and click on ‘show’ to overlay the current mean model on the data.
- Load a PCA by removing the filename extension (.mml) and click ‘input pca’. A set of numbers will appear in the top tinatool. In the ‘smartROI params’ change the number of model modes to 5 and the number of profile modes to 3 thus;
”mdl modes 5” ”prf modes 3”
Click ‘show’ to update this information.

- To search the solution click 'search'. After a few seconds the outline will have found the minimum.
- This outline may be converted to a polygonal ROI using 'outer2roi' which may then be adjusted further or used in any way a roi is used.

Zoom onto the ascending aorta as necessary (using the standard Tv zoom facility). Any temporal slice can be selected in the Sequence Tool and the aorta located. The region obtained can be used to extract the enclosed data from this or any other co-registered image by 'push'ing the image into the 'Imcalc Tool' and applying the 'roi' function.