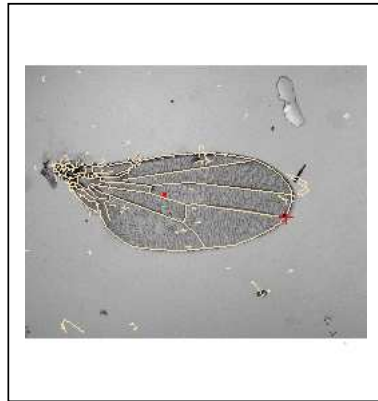


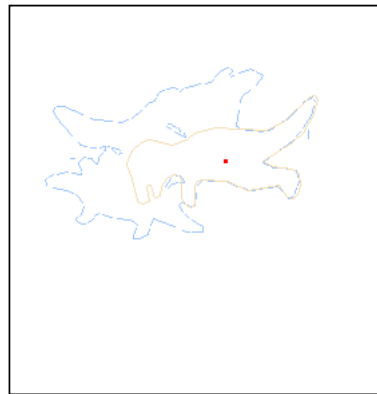
TINA Demo 004: The Pairwise Tool

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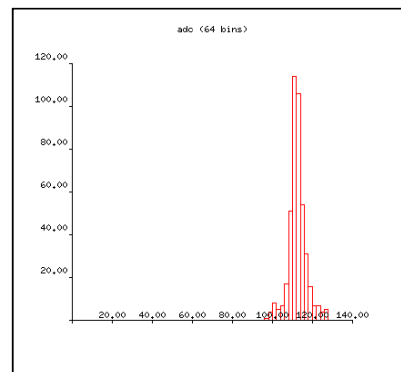
(a)



(b)



(c)



(d)



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TINA Demo 004: The Pairwise Tool

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1 Introduction

This set of demonstrations provides examples of the use of 2D recognition and location algorithms within the Tina vision libraries. The work shown is a summary of two decades of research which started with the development of a robust general representation of edge based shape [1][2][3][4]. The software and algorithms have been continuously developed and refined during this period [5][6][8], as these ideas were used for the specific applications of 2D shape analysis (morphometrics) [7] and MR data calibration (Diffusion) [9]. 3D versions are also available but beyond the current scope of this document.

2 Installation

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

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

for instructions. The TINA pairwise tool project can be obtained from the demos page of the TINA website.

One should check that the following files exist in the pairwise tool directory.

```
004_pairwise_tool.tex: text version of this document.
004_pairwise_tool.pdf: this document.
Makefile: the project Makefile.
Makefile.linux: alternative linux Makefile.
Makefile.solaris: alternative solaris Makefile.
phantom: subdirectory for DW-MR image data.
phantom_design: subdirectory for the current phantom design.
diffusion: subdirectory for DW-MR image data, etc.
flywing: subdirectory for fly wing 2D image data, etc.
dinosaur: subdirectory for dinosaur toy 2D image data, etc.
phantom.cls: macro file for DW-MR image data.
diffusion.cls: macro file for DW-MR image data.
flywing.cls: macro file for fly wing 2D image data.
dinosaur.cls: macro file for dinosaur toy 2D image data.
input_file\DataInfo.txt: example input text file for the phantom data provided.
output_files\IM_01b1_Results_Gold.txt: output file for the example phantom data provided.
tinaTool.c: main tool specification software.
pgh_tool.c: main tool specification software.
pgh_misc.c: contains a number of tool functions.
tlvisPdm_defs.h: contains structure definitions for TPS landmark data
```

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 Linux). This Makefile may require some manual editing: it assumes that you installed the TINA libraries in the `/usr/local/Tina6` directory. Open the Makefile in an editor and edit any paths that do not apply for your system. Finally, type “make” to build the tinaTool executable.

3 Usage

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

```
./tinaTool -f flywing  
./tinaTool -f dinosaur  
./tinaTool -f diffusion  
./tinaTool -f phantom
```

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

3.1 Dinosaur Data

What is the purpose?

To demonstrate the robust location of different 2D objects on a mixed partially occluded image of dinosaurs by matching the edge lines (boundaries).

How does it work?

By running “./tinaTool -f dinosaur” in the command line, the following tools and tv’s will open:

```
Pairwise Tool  
Pairwise Parameters  
Scale Parameters  
Hough Parameters  
Mono Tool  
mono tv
```

Next, an image of all dinosaurs overlaid on top of each other, which only contains the overall polygonal boundaries, is loaded to the mono tv (as_all_occ_hard). This is the image which will be matched to a reference image. Then, there are five poly files (as1, as2, as3, as4 and as5) corresponding to the reference shapes which may be added using the “add model” button of the “Pairwise Tool”. Default parameters are already set.

What to do next?

Press the “match lines” button followed by the “locate models” button to get the model matched and located on the mono image superimposed. Changing the model name (e.g. as1) and running “locate models” will locate the different objects.

Loading Data:

Press the “clear” button, then type “as1” in the Model Name space followed by the “add model” button, then type “as2” followed by the “add model” button, until all poly files are added. Now type in the Model Name space one of these five models. Alternative data sets are available, in particular the ‘as_all_occ_hard25’ file shows the robustness of the methods to missing edge data.

3.2 Fly Wing Data

What is the purpose?

The automatic estimation of anatomical landmarks, using previously marked up examples, for use in morphometric studies of genetic shape variation.

How does it work?

By running “./tinaTool -f flywing” in the command line, the following tools and tv’s will open:

```
Pairwise Tool  
Pairwise Parameters  
Hough Parameters  
Scale Parameters  
Imcalc Tool  
imcalc tv
```

Mono Tool
mono tv

Next, the reference flywing image (c0001d01f05r2) is loaded and pushed to the imcalc tool (visible in the Imcalc tv), while another similar flywing image is loaded in the mono tool and displayed in the mono tv (c0001d01f01r2). This is the image which will be matched to the reference image. Hence, there is a poly file corresponding to the reference image which is added in the “add model” part of the “Pairwise Tool”. The optimum parameters are already set.

What to do next?

By pressing the “match lines” button, the edge lines from the mono tv are matched to the reference ones corresponding to the reference image on the imcalc tv. Now if “landmark” is -1, by pressing the “locate models” button, all the landmarks are located as a whole. However, if “landmark” is a number between 0 and 14 (one of the 15 flywing landmarks), the software attempts to locate that specific landmark. This gives a first set of values for the transformation parameters. Once this is done, pressing the “refine landmark” button provides further refinement of the landmark using the correlation of local structures. This gives a second set of values for the transformation parameters. Now remove the top image from the stack by pressing the “c” button on the Imcalc Tool. Then by pressing the “transform image” button the total transformation parameters are used to transform the reference image. Next by pushing the mono image to the stack and pressing the “flp” button on the Imcalc Tool, one can observe how well the images are matched based about the specific landmark selected. The last two coordinates written on the Tina Tool (trans_point and refined_point) refer to the reference landmark point in the mono tv coordinate system and the final refined point matched to it.

Loading Data:

Using the “scan” button browse the computer to load the required reference image into the mono tool and push it into the imalc tool. Find the TPS file corresponding to the reference image (e.g. landmarks5r2.TPS), then press load landmarks. A message on Tina tool confirms this action: “e.g. 15 landmarks were loaded”. Now on the “Pairwise Tool”, press “RidgesOnly” button to apply a suitable edge detector, then press “Line Geom2” button to prepare appropriate edge lines for the matching process. Also press “clear” and then “add model” to make sure that the reference lines corresponding to the reference image are loaded to match to. Processing can now continue as above.

4 Phantom Data

4.1 Object Recognition and Diffusion Measurement

What is the purpose?

This macro and the corresponding code have been prepared for the purpose of one-click execution, where the DW-MR image data specified in the “DataInfo.txt” text file are used to produce the results which are written out in the “xxx_Results.txt” text file together with a number of image files (aiff format), where xxx is replaced by the name of the first image slice corresponding to the smallest b value provided. In the “null-graphics” (command line only) version of the software, two arguments must be given after the name of the executable. These are firstly the path for the “DataInfo.txt” file, and secondly the path where the output files are expected to be written by the software. The executable which is currently generated for the “null-graphics” version is “./phantomTool” (rather than ./tinaTool). In the “full-graphics” version of the software (with full graphics functionality) these two directories are known by default. These default directories are “./input_file” and “./output_files”.

Here is the example content of the current “DataInfo.txt” file:

```
./phantom
4
0.0
100.0
500.0
900.0
IM_01b1
IM_01b2
IM_01b3
IM_01b4
```

Marsden

The content for this example is described as follows.

Line 1: the path for the directory where the DW-MRI input data exist.

Line 2: the number of b values for which DW-MR images are available (integer).

Line 3-6: the amounts of b values in increasing order from the top to the bottom (float numbers). The example numbers correspond to the example data acquired using the Marsden phantom in the IMI project.

Line 7-10: the names of the DW-MR image slices corresponding to the b values just listed and in the same order (i.e. the corresponding b values increase from the top to the bottom). These names can be the original names (and so the dicom files do not need any renaming in advance). The first file name (Line 7) is used as the prefix for all the output file names.

Line 11: the name of the phantom design, for instance “Marsden” which refers to the first phantom designed in the IMI project.

There are some files specific to the phantom under study (named in Line 11) which will be used in both localisation and diffusion measurement tasks. These are kept in a default directory called “./phantom_design” and are described as follows.

“phantom-sim.TPS”: the name of the TPS file containing the reference landmarks (to be used for refinement after locating the corresponding tubes). These landmarks are fixed (centre of the tubes) and should not be altered for the existing phantom.

“sim.poly”: the poly file used for localisation, which is available for the existing phantom and should not be altered.

“sim_ref.aiff”: the reference file used for the correlation matching task (localisation refinement), which is available for the existing phantom and should not be altered.

“float_mask#.aiff”: the name of the mask files where the last letter (#) is a number referring to each specific tube in the phantom. For instance, for the Marsden phantom this number varies between 0 and 4 (as there are one tube in the centre and 4 surrounding tubes. These aiff files are available for the existing phantom and should not be altered.

In the case of this example, the output text file is called “IM_01b1_Results.txt”. Also, there are five image files produced for the adc maps corresponding to the five tubes, called “IM_01b1_adc_tube_0.aiff”, “IM_01b1_adc_tube_1.aiff”, “IM_01b1_adc_tube_2.aiff”, “IM_01b1_adc_tube_3.aiff” and “IM_01b1_adc_tube_4.aiff”. Similarly, there are another five image files corresponding to the s0 maps, called “IM_01b1_s0_tube_0.aiff”, “IM_01b1_s0_tube_1.aiff”, “IM_01b1_s0_tube_2.aiff”, “IM_01b1_s0_tube_3.aiff” and “IM_01b1_s0_tube_4.aiff”. Here, tube_0 refers to the central tube while tubes numbered 1 to 4 refer to tubes with clockwise order where tube 1 refers to that located just after (clockwise) the marker on the phantom. Finally, all five adc maps are placed together in one image file called “IM_01b1_adc_all_tubes.aiff”, and similarly for the s0 maps, the total image is “IM_01b1_s0_all_tubes.aiff”.

How does it work?

In the full-graphics version, by running “./tinaTool -f phantom” in the command line, the following tools and tv’s will open:

```
DW-MR Phantom Tool
Pairwise Tool
Imcalc Tool
imcalc tv
Mono Tool
mono tv
```

These are only some of the tools and tv’s which are actually used while the code runs.

The local Makefile can be amended to produce an executable that does not use any graphics (using the null version of gdk2 codes at `/tina-tools/tinatool/gphx/null` and `gtk2` at `/tina-tools/tinatool/wdgt/null/`). This version of the

software runs using command line only, and does exactly what the version with graphics does, generating the same output file. This mechanism is designed for command line execution of library components.

In the null-graphics version, the command to run is `“./phantomTool <path for the input file> <path for the output files>”`.

What to do next?

By clicking on the “measure regional adc” button on the Paiwise Tool (or just running the command line for the null-graphics version), the software goes through the process of reading the input data and writing the output results. During this process, “landmark” is varied between 0 and 4 as corresponding masks for the five tubes are used. The “degree of rotational symmetry” is fixed at 4 for the phantom. This parameter is usually set to 1 for images of asymmetrical objects such as flying and dinosaur data.

Once the process ends, one can study the output files, especially the output text file, for the analysis of the results produced.

4.2 Diffusion Measurement Only

What is the purpose?

To demonstrate regional extraction of quantitative measurements, in this case Apparent Diffusion Coefficients (ADC) for MRI data. It is assumed that the mask images used will have been generated using the object localisation and image transformation methods shown in the other demonstrations.

How does it work?

By running `“./tinaTool -f diffusion”` in the command line, the following tools and tv’s will open:

```
NMR Analysis Tool
Sequence Tool
sequence tv
Imcalc Tool
imcalc tv
imcals graph tv
Mono Tool
mono tv
```

There are four image slices loaded to the sequence tv. Example image slices which are currently located at “diff_macro” directory are: “IM-0112-00b1.dcm”, “IM-0112-00b2.dcm”, “IM-0112-00b3.dcm” and “IM-0112-00b4.dcm”, which correspond to the b values: b1=0, b2=100, b3=500 and b4=900 respectively. Then, the top image slice has been pushed to the imcalc tv and a mask image has been loaded to the mono tv. The sample mask image currently is “my_mask_0_fit” (AIFF file) which masks the central tube in the phantom image data.

What to do next?

The first functionality is to click on the “Plot” selection in the NMR Analysis Tool and select “diff fit”. Now by clicking on each pixel of the existing image on the imcalc tv, the four corresponding pixels on the four existing image slices on the sequence tv are used to fit a mono exponential which is plotted on the imcalc graph tv.

The second functionality is to push the mask image from the mono tv to the imcalc tv (stack). Now by clicking on the “ADC” button and then the “DW-MR fit” button on the NMR Analysis Tool, a new image appears on the imcalc tv which is the ADC map of the area identified by the mask image. By clicking on the “S0” button, one can also get the S0 map for the mask area shown on the imcalc tv. Mask image must be a binary image (the same size as the DW-MR image slices) which is stored as floating point where white is the area of interest.

By pressing the “Histograms” button on the tina tool, and pressing “graph TV” on the Histogram Tool, one can view the histograms corresponding to the ADC (150-155) and S0 (170-175) by entering the number (or using “<” and “>” buttons) and pressing the “plot hist” button.

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