

MultiResMIRegistration

This command line application demonstrates the use of ITK components for performing rigid multi-modal registration using mutual information.

What is Mutual Information?

Mutual information is a measure of how much information one random variable tells about another. The use of mutual information for medical image registration applications was independently introduced in 1995 by both Viola and Wells [1] and Collignon[2]. For two images, the mutual information is computed from the joint probability distribution of the images' intensity or gray-values. When two images are aligned, the joint probability distribution is "peaky" resulting in a high mutual information value. Mis-registration causes the distribution to disperse resulting in a low mutual information value.

One of the main advantages of using mutual information is than it can be used to align images of different modalities (e.g. CT to MR-T1, MR-T1 to PET etc).

More information on mutual information based registration can be found at the following web sites:

Paul Viola's homepage contains links to his Ph.D thesis, papers and pointers to other mutual information resources

 $http://www.\ ai\ .\ mi\ t.\ edu/peopl\ e/vi\ ol\ a/vi\ ol\ a.\ html$

Sebastien Gilles's web tutorial:

http://www-rocq.inria.fr/~gilles/IMMI/

This page from the Image Sciences Institute of Utrecht University has an animation of the effect of mis-registration on the joint probability distribution:

http://www.isi.uu.nl/Research/Registration/registration-project.html

Application overview:

This application reads in two 3D raw image volumes: the target volume and the reference volume. The application then iteratively estimates the rigid transform that will align the reference onto the target volume.

The application terminates after a completing a user-defined number of iterations. The estimated rigid transform is applied to the reference, the resulting registered image is then written out to file as a raw 3D image volume.

Optionally, each 2D slice form the target, reference and registered image volume can be written out as PGM files – facilitating viewing with simple 2D image viewers.

What components of ITK does this application use?

This application makes use of the ITK registration framework and ITK multi-resolution framework.

ITK Registration framework

The ITK registration framework is a generic framework for registering images and point sets. A registration algorithm is built from three components: a Transform, a Metric and an Optimizer. Standard component API's allows mixing and matching of the components.

The part of the registration framework used by this application are the itk::QuaternionRigidRegistrationTransform, the itk::MutualInformationImageToImageMetric and the itk::GradientDescentOptimizer.

ITK Multi-resolution Registration framework

Performing image registration using a multi-resolution strategy has been widely shown to improve speed, accuracy and robustness. The ITK Multi-resolution registration framework is a generic framework for defining a multi-resolution registration scheme. There are two major components in the framework: the underlying registration method and the down-sampling strategy.

Any RegistrationMethod that meets the minimal API requirements can plug into the multi-resolution framework. The down-sampling strategy is encapsulated in a MultiResolutionImagePyramid Object. A flexible schedule-based scheme allows the user to define the shrink factors at each level of the pyramid.

The multi-resolution scheme used in this application is define in itk:: MultiResolutionMutualInformationRigidRegistration.

How do I run the application?

The application takes one argument: the name of a parameter file. A valid parameter file contains 18 lines with the following format.

| Line | Parameter | Example |
|------|--|-------------------------------|
| 1 | Filename of the raw 3D target volume. | N:/ImageData/target.raw |
| 2 | Endian-ness of target. Zero represents little endian and a non- | 1 |
| | zero number represents big endian. | |
| 3 | Size of target volume in column-row-slice order | 256 256 26 |
| 4 | Target volume pixel spacing in column-row-slice order | 1. 25 1. 25 4. 0 |
| 5 | Filename of the raw 3D reference volume | N: /I mageData/reference. raw |
| 6 | Endian-ness of reference. Zero represents little endian and a | 1 |
| | non-zero number represents big endian. | |
| 7 | Size of reference volume in column-row-slice-order | 512 512 29 |
| 8 | Reference volume spacing in column-row-slice order | 0. 653595 0. 653595 4. 0 |
| 9 | Number of multi-resolution levels to be used. | 5 |
| 10 | The starting (zeroth) level shrink factor for the target volume. | 4 4 1 |
| 11 | The starting (zeroth) level shrink factor for the reference | 8 8 1 |
| | volume. | |
| 12 | The number of iterations to be performed at each resolution | 2500 2500 2500 2500 2500 |
| | level. | |
| 13 | The learning rate at each resolution level. | 1e-4 1e-5 5e-6 1e-6 5e-7 |
| 14 | The translation scale at each resolution level. | 320 320 320 320 320 |
| 15 | Output filename of the registered volume. | regi stered. raw |
| 16 | Endian-ness of the output volume. Zero represents little | 1 |
| | endian and a non zero number represents big endian | |
| 17 | PGM file dumping option. Zero represents "off" and a non- | 1 |
| | zero number represents "on". | |
| 18 | The output directory while the PGM files are to be written to. | pgmsdi r |
| | (NB. directory must already exists otherwise no images are | |
| | written out) | |

Both the target and reference volumes are assumed to be in binary (signed short) format. The patient is assumed to be in the same orientation in both the target and reference volumes.

Lines 9 to 11 specify the multi-resolution down-sampling schedule. Line 9 specifies the number of multi-resolution levels to be used. Line 10 and 11 respectively specify the starting (zeroth) level shrink factor for the target volume and reference volume. The shrink factors for all other levels are computed automatically by dividing the shrink factors of the previous level by a 2. All shrink factors less than 1 is rounded to a value of 1.

If the PGM option is turned on, line 18 specifies the directory where the output PGM files are to be written. Slices from the target volume are prefixed target then followed by the slice number starting from 000. Similarly, slices from the reference volume are prefixed reference and slices from the registered image are prefixed register.

Some example experiments

The Vanderbilt Retrospective Registration Evaluation Project contains multi-modal images (CT, MR-T1, MR-T2, MR-PD, PET) of ten patients. Please refer to the information at:

http://cswww.vuse.vanderbilt.edu/~image/registration/

The following results were produced using parameter file PracCTToT1.txt.

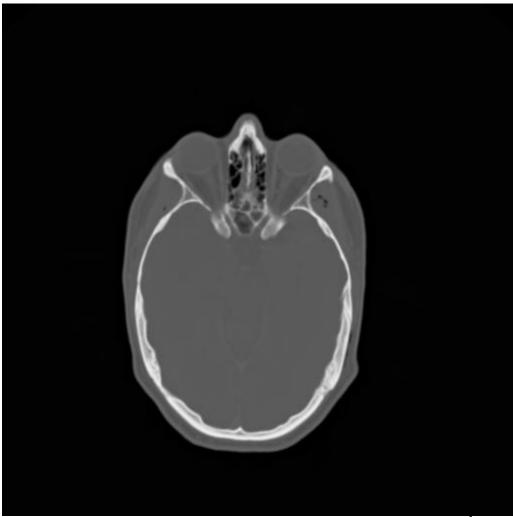


Fig 1: Slice 7 from the practice patient CT volume (the reference volume)¹

¹ The images were provided as part of the project, "Evaluation of Retrospective Image Registration", National Institutes of Health, Project Number 1 R01 NS33926-01, Principal Investigator, J. Michael Fitzpatrick, Vanderbilt University, Nashville, TN.

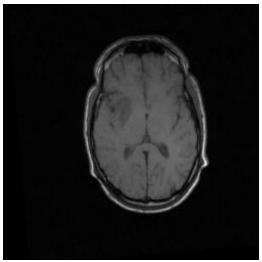


Fig 2: Slice 7 from the practice patient MR-T1 volume (the target volume)

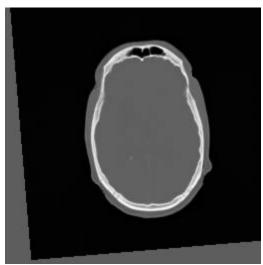


Fig 3: Slice 7 from the CT-to-MR-TI registered image

The following results were produced using parameter file PracPETToPD.txt.

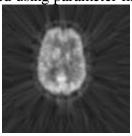


Fig 4: Slice 7 from the practice patient PET volume (the reference volume)

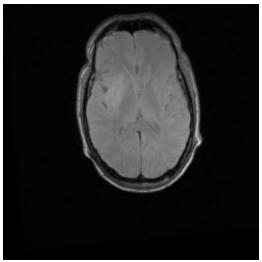


Fig 5: Slice 7 from the practice patient MR-PD volume (the target volume)

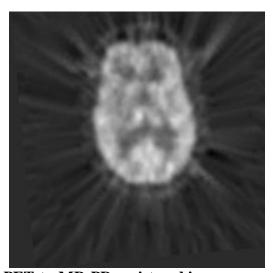


Fig 6: Slice 7 from the PET-to-MR-PD registered image

References

[1] P. Viola and W.M. Wells III, "Alignment by maximization of mutual information", *International Conference on Computer Vision* (E. Grimson, S. Shafer, A. Blake and K. Sugihara, eds.), IEEE Computer Society Press, Los Alamitos, CA, pp. 16-23, 1995.

[2] A. Collignon, F. Maes, D. Delaere, D. Vandermeulen, P. Suetens and G. Marchal, "Automated multimodality image registration based on information theory", *Information Processing in Medical Imaging* (Y. Bizais, C. Barillot and R. Di Paola, eds.), Kluwer Academic Publishers, Dordrecht, pp. 263-274, 1995.