MIA - A toolbox for Medical Image Analysis

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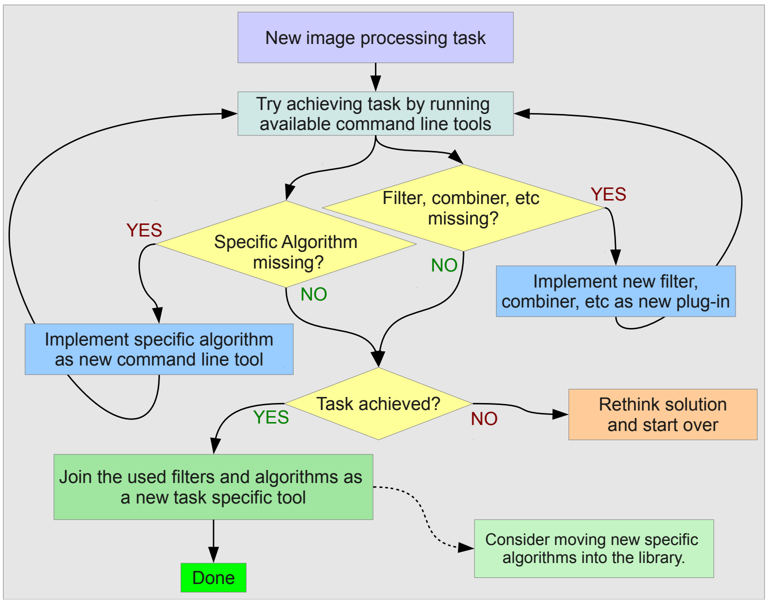
Description

MIA[1] is a general purpose image processing toolbox written in C++ that puts its focus on gray scale image processing. It consists of the following main building blocks: (1) libraries that provide infrastructure, basic data types, and generic algorithms, (2) plug-ins that handle image IO and implement specialized functionality like filters, cost functions, optimizers, (3) unit test for the implemented algorithms that ensure the reliability of the implementation, and (4) command line tools that work as drivers to the algorithms.


New image processing task

Try achieving task by running available command line tools

Filter, combiner, etc missing?

YES

Implement new filter, combiner, etc as new plug-in

NO

Specific Algorithm missing?

YES

Implement specific algorithm as new command line tool

NO

Task achieved?

NO

Rethink solution and start over

YES

Join the used filters and algorithms as a new task specific tool

Consider moving new specific algorithms into the library.

Done

The software is designed to accommodate a work-flow for the development of new algorithms as described in the diagram. The command lines tools provide a flexible means for algorithmic prototyping based on interactive execution of atomic image processing tasks and their combination in shell scripts.

If functionality is missing, like e.g, a filter, image combiner, or some specific algorithm, the design that is based on the combination of plug-in and task specific command line tools makes it easy to add this functionality without touching existing code. Hence, only little development overhead is required in the process of prototyping, and no additional testing is required to ensure that new code does not break existing functionality.

Then, moving from an algorithmic prototype defined as shell scripts to a C++ program is made easy, because the driving feature of most processing done by using MIA, that is, specifying how the functionality of certain plug-ins should be invoked, is very similar in both cases: Consider, for example, the filtering of a 2D image with a median filter of width 3 followed by a five class k-means classification: On the command line one will specify

```
mia-2dimagefilter -i image.png -o filtered.png median:w=3 kmeans:c=5
```

and within a C++ program one will write

```
auto filtered = run_filter_chain(image, {”median:w=3”, ”kmeans:c=5”});
```

Finally, the MIA provides the facilities for the automatic creation of an up-to-date user reference for the command line tools and the plug-ins that requires only little additional work from the developer.

Applications

The software has been used successfully for various image processing tasks, e.g the fluid dynamic registration algorithm[2] was applied in the assessment of bony changes in maxillo-facial surgery[3] , and 2D-t and 3D+t schemes were developed for motion compensation in myocardial[4] and prostate perfusion image series[5] by means of spline based non-linear registration.

Current development and future work

The current focus is laid on adding tutorials and documentation to make the software more accessible to third party users and developers. Future work includes providing an interface to SciPy, and adding more image registration methods, specifically to enable the fusion of 2D and 3D data, and to combine feature and voxel based registration approaches.

License

The software is published under the terms of the GNU General Public License version 3 or later.

[1] http://mia.sourceforge.net, Contact: gw.fossdev@gmail.com

[2] G Wollny, and F Kruggel, Comput. cost of non-rigid registration algorithms based on fluid dynamics, IEEE T Med Imaging, 2002

[3] G Wollny et al., Assessment, validation, and visualization of bony changes in crano-facial surgery, In Proc of VIIP’04, Spain, 2004

[4] G Wollny et al., Autom. Motion Comp. of Free Breathing acquired Myocardial Perfusion Data by using ICA, Med Img Anal, 2012

[5] G Wollny et al., Non-rigid motion compensation in MR prostate perfusion imaging, 18th Meeting of ISMRM-ESMRM, Sweden 2010

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