# Baby Brain Toolkit

### Fbrain ERC project: Computational Anatomy of Fetal Brain

# February 1, 2011

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# 1 Introduction

BTK stands for Baby Brain Toolkit. This toolkit is developed in the context of the Fbrain ERC project: "Computational Anatomy of Fetal Brain" <sup>1</sup>. Studies about brain maturation aim at providing a better understanding of brain development and links between brain changes and cognitive development. Such studies are of great interest for diagnosis help and clinical course of development and treatment of illnesses. Several teams have begun to make 3D maps of developing brain structures from children to young adults. However, working out the development of fetal and neonatal brain remains an open issue. This project aims at jumping over several theoretical and practical barriers and at going beyond the formal description of the brain maturation thanks to the development of a realistic numerical model of brain aging.

# 1.1 Copyright

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 $<sup>^{1} \</sup>rm http://lsiit\text{-}miv.u\text{-}strasbg.fr/miv/index.php?contenu=erc}$ 



Figure 1: Example of an anatomical reconstruction of a fetal brain by using btkImageReconstruction. (a) axial, (b) coronal, and (c) sagital view.

# 1.2 Dependencies and Compilation

Baby Brain Toolkit (BTK) depends on:

- The most recent version of the Insight ToolKit (ITK) www.itk.org.
- Tclap library: this library can be installed for debian-based distribution using the following command line: apt-get install libtclap-dev
- OpenMP library: this library can be installed for debian-based distribution using the following command line: apt-get install libgomp1

# 2 Applications

# 2.1 Denoising

btkNLMDenoising This program applies a non-local mean filter to a 3D image for denoising purpose. Usage: -i input\_image\_filename -o output\_image\_filename. The best results are usually obtained by using a mask (or a padding value).

btkNLMDenoising4DImage This program applies a non-local mean filter to each 3D image of a 4D image, for denoising purpose. Usage: -i input\_image\_filename -o output\_image\_filename. The best results are usually obtained by using a mask (or a padding value).

#### 2.2 Anatomical reconstruction

**btkImageReconstruction** This program allows to obtain a high-resolution image from a set of low-resolution images, typically axial, coronal, and sagital acquisitions [2].

 $\label{eq:minimal usage} \mbox{Minimal usage: btkImageReconstruction -i image1} \mbox{ $\cdots$ -i imageN -o output.}$ 

Recommended usage: btkImageReconstruction -i image1  $\cdots$  -i imageN -m mask1  $\cdots$  -m maskN -o output --mask. The use of a mask provide better results since it allows an accurately estimation of the initial transform, and constrains the registration to the region of interest.

The full list of optional parameters of the method can be obtained by  ${\tt btkImageReconstruction}$  --help

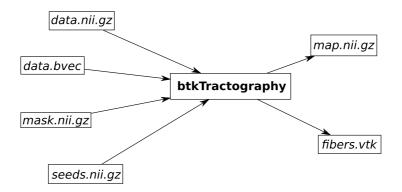


Figure 2: Standard pipeline of the btkTractography program.

# 2.3 Tractography

### Standard usage

Suppose you want to perform a tractography on a diffusion weighted MRI dataset. You should have a dwi image, the corresponding gradient vectors' coordinates, a mask of the brain white matter and a label image of the seeds. Assume this data is stored in files named repsectively for instance data.nii.gz, data.bvec, mask.nii.gz and seeds.nii.gz. The tractography is accomplished by the command below.

When the program terminates its task, the probability connection map and the fibers estimation are saved in files respectively named map.nii.gz and fibers.vtk. The connection map is a volume image of probability intensities (i.e. intensities between 0 and 1) with the same origin, orientation and spacing as the diffusion weighted image. The fibers are polygonal data of VTK library in world coordinates. The standard pipeline of the program is shown in Fig. 2.

#### Advanced usage

In addition to standard arguments of btkTractography program, there are some other parameters that let you to alter algorithm's behaviour. These options can be classified into three groups: model's options, constraints on trajectory and filter's options. The first group options allow you to tweak the model (for more details about it, please refer to [1]). The second group options let you to control the particle's trajectory. These options provide prior informations to the algorithm. The last group options are dedicated to the particle filter control.

Since the default parameters values may work in the most of cases, they are optional. A list is of optional features is available by using the command

and program's arguments are much more described below.

#### Model's order

The model's order (i.e. the spherical harmonics' order) can be specified by the option

```
--model-order <n>,
```

for  $n \in \{2, 4, 6, 8\}$ . The default value is 4. For more details, please refer to [1].

#### Model's regularization

A Laplace-Beltrami regularization coefficient is used to assume a better estimation of the model. This coefficient can by manually modified by the option

```
--model-regularization <r>,
```

for  $r \in \mathbb{R}$ . The default value is set as 0.006. For more details, please refer to [1].

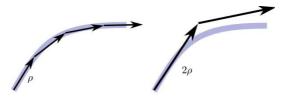


Figure 3: Effect of the step size option on a particle's trajectory. With a large step size (right), the particle may overshoot the trajectory of the ground truth.

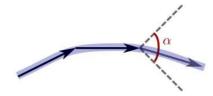


Figure 4: An angle threshold allows the algorithm to sample successive direction only in the cone defined by this angle. This illustration show the principle in two dimensions.

#### Displacement step size

The displacement step size of a moving particle can ben adjusted as you want by using the option

--step-size <r>,

where  $\mathbf{r} \in \mathbb{R}_{+}^{*}$ . Note that this option is expressed in the voxel unit. The default is fixed at 0.5 voxel.

By setting a big step size, the particles will move quickly. So the biger is the step, the faster the algorithm will finish, but as shown by Fig. 3, some informations may be missed and the particle's trajectories may overshoot the ground truth, resulting in a bad estimation.

#### Angular threshold

An angular threshold prevent a particle to return back. This option has to be expressed in radian and can bet set by

--angular-threshold <a>,

where  $a \in ]0, 2\pi[$ . The default value is set as a  $\frac{\pi}{3}$  angle.

As illustrated in two dimensions in Fig. 4, an angle threshold is used to define an allowed area for successive sampled directions. This can be seen as a global curvature parameters on trajectories. A small angle defines trajectories with a small curvature.

# Rigidity

The rigidity option controls how much you want the particles to have straight trajectory. You can adjust it by

--curve-constraint <r>,

where  $\mathbf{r} \in \mathbb{R}_{+}^{*}$ .

#### Number of particles

The number of particles in the system is set by the option

--number-of-particles <n>,

where  $n \in \mathbb{N}^*$ . By default, the algorithm will use 1000 particles.

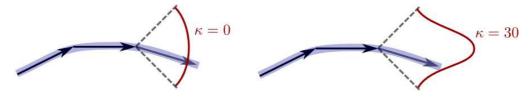


Figure 5:

#### Resampling threshold

This option modify the resampling threshold of the system. When the number of effective particles in the system falls below this resampling threshold, the particles are resampled according a multinomial resampling. It can be adjust by

--resampling-threshold <r>,

where  $\mathbf{r} \in [0,1]$  is the percent of minimal effective particles in the system.

# 3 Utilities

btkModifyImageUsingLookUpTable This program modifies one image using a look up table defined in a ascii file (2 columns, one for the original values, one for the final values). Usage: -i input\_image\_filename -t input\_table\_filename -o output\_image\_filename

# Acknowledgment

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# References

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