# SIMULATIONS OF SYNTHETIC DIFFUSION MRI DATA BASED ON BROWNIAN MOTION

**Radek Valla**

Master Degree Programme (2), FEEC BUT

E-mail: xvalla01@stud.feec.vutbr.cz

Supervised by: René Labounek

E-mail: labounek@phd.feec.vutbr.cz

**Abstract**: This study deals with the problem of bending and kissing fibers of axonal bundles in brain white matter. It describes new simulator of diffusion-weighted MRI (dMRI) data which is able to generate it based on random walk algorithm with geometrical constraints not only for crossing fiber geometry, but also as o novelty for bending and kissing fiber geometries. It means the simulator becomes a useful and essential tool for understanding and detection of differences between dMRI data coming from crossing, bending and kissing fibers.

**Keywords**: dMRI, simulations, Brownian motion, crossing, bending and kissing fibers

## 1. INTRODUCTION

Diffusion weighted MRI measures diffusion motion effect in the sample using gradient magnetic field. Diffusion motion in the sample causes a decrease in the dMRI signal. To measure diffusion profile in 3D space, it must be measured in different directions, usually hundreds of them. Taken data forms tensors in voxels that characterizes diffusion profile and paths of axon fibers can be tracked then throughout the voxels (brain respectively).

Basic and the first model for displaying diffusion profile from dMRI data, named diffusion tensor imaging (DTI), can calculate single tensor, considering that there is only one direction of anisotropic diffusion inside the voxel [1]. Although there are several methods considering more than one bundle of axons, they are able to detect crossing fibers (e.g. Q-ball imaging, diffusion spectrum imaging and ball and stick model) [2,3,4]or more advanced model can find out diffusion dispersion (e.g. ball and racket model, NODDI model) [5,6]. Methods able to detect crossing fibers fit well on kissing and bending fiber geometries. This can make false positive results in tractography and make precise tractography hard to achieve [7]. In Figure 1b, when crossing fiber geometry is fitted in the voxel but kissing is truly underlying, algorithm does not know how to continue in correct way, because 3 ways can be chosen while on kissing fiber geometry the direction is defined.

## 2. METHODS

### 2.1. PROBLEM DEFINITION

Imagine that we place group of water molecules in the middle of crossing or kissing in both systems. For crossing fibers, they can move in all four directions and move through the whole gradient field as it is shown in Figure 1a. For kissing fibers, molecules can move only in one fiber and be affected only by small range of gradient field. It applies similarly for second bended fiber.

With this simplified problem, magnetic spin phase distribution should differ for crossing and kissing fibers with similar angle geometry. Data taken from these two systems are assumed to differ. Simulator of diffusion motion in kissing or crossing fibers during turned on dMRI sequence should provide us information, if dMRI data can differ significantly or not.

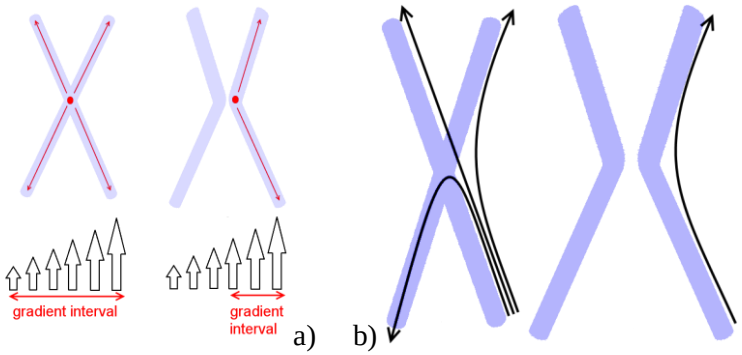


**Figure 1:** (a) Different gradient interval affecting crossing and kissing fibres (b) Tracking for crossing and kissing fibres

### 2.2. DIFFUSION MRI DATA SIMULATOR

In the simulator, data are computed based on water molecule diffusion move inside the fibers during turned on dMRI sequence. It generates synthetic dMRI data. Simulation begins with algorithm for simulation of Brownian motion that approximates isotropic diffusion of water molecules based on algorithm of random walk with Gaussian distribution in free space [8]. This algorithm was modified to our problem with anisotropic diffusion based on geometric constraints. For straight fiber, it is a straight cylinder whose surface does not allow water molecules to pass out of cylinder because of molecule reflection without energy loss from the surface. For kissing fibers, it is bended cylinder. Both geometric constrains are defined by leading points. These points are grouped into groups of three to make triangles on the surface. These triangles define planes, where reflection of the water molecules is calculated. This process simulates anisotropic diffusion inside fibers. Examples of reflection results you can see for both geometries in Figure 2.

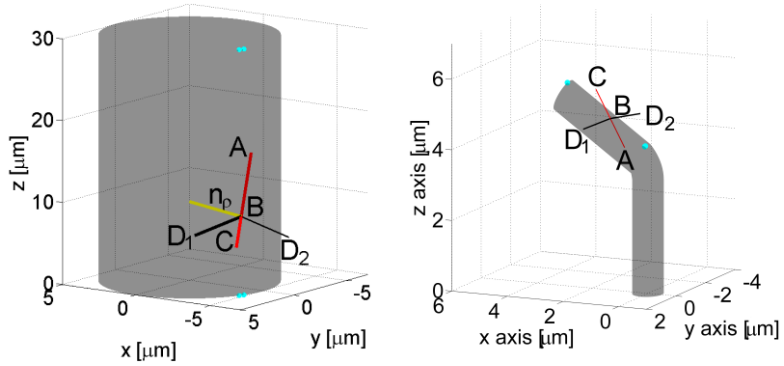


**Figure 2:** Reflection of water molecules in one step in straight and bended cylinders. Point A is starting point and C is final point of Brownian motion simulation without reflection. B is a common point of AC line segment and the cylinder. Points D1 and D2 are points after reflection, where D1 is the right solution. Dots on cylinders represent cylinder's control points of reflecting plane.

### 2.3. SIMULATION SETTING

Real data in dMRI measurements can be recorded with spatial resolution about 1mm isotropic voxel size. For this reason, cylinder's length was set to 1mm, its radius was 3μm, water molecule density was 1μm uniformly sampled. Gradient were measured from 30 directions with 3 gradient strengths. Angle between crossing fibres and of bended fibres was 60° [9] between 2 fibres. Each simulation was turned on 3 times to lower chance of random results. Because of high amount of water molecules it was necessary to parallelize the task, because one run took around 100 hours of CPU time for kissing fibres and 15 hours for crossing fibres.

## 3. RESULTS

Phase distribution of water molecule magnetic spins inside crossing fibers and kissing fibers after dMRI sequence show, that the results weren't random and can be used for comparison of dMRI data. Both crossing and kissing fibers final phase distribution are normal distributed. Thing of interest is difference between signal without molecule diffusion and with diffusion. Than we can compare dMRI data decrease in crossing and kissing fibers. For all runs in crossing fibers, data received after dMRI sequence was approximately 13,175% lower. In kissing fibers it was 13,603%.

## 4. CONCLUSION

The results showed that derived geometrical constraints can be used for synthetic dMRI data simulations. Although the constraints are one of crucial steps during genesis of synthetic dMRI data, the simulator has still many limitations which will be improved in future research. It will be especially the myelin sheath modelling, diffusion inside it and diffusion simulation in extracellular space. Simulation setting will place more fibers in voxel and make measurement in more gradient directions. Data received from simple simulation are not different enough to predict significant results in more complex simulations. Although, in all runs were dMRI data different by only 0,5% and it can improve with more gradient directions and strengths.

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