SANDI-AMICO: an open-source toolbox for fast Soma And Neurite Density Imaging (SANDI) with AMICO
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SANDI-AMICO: an open-source toolbox for fast Soma And Neurite Density Imaging (SANDI) with AMICO

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Authors:

Simona Schiavi¹, Mario Ocampo-Pineda¹, Michele Guerreri², Victor Montal³, Giulia Buizza⁴, Lisa Novello⁵, Sara Bosticardo¹, Jenna Hanmer⁶, Gabriel Ramos Llorde⁷, Chantal Tax⁸,⁹, Andrada Ianus¹⁰, Noam Shemesh¹⁰, Emmanuel Caruyer¹¹, Alessandro Daducci¹, Marco Palombo²

Institutions:

¹Department of Computer Science, University of Verona, Verona, Italy, ²Centre for Medical Image Computing, University College London, London, UK, ³Sant Pau Memory Unit, Department of Neurology, Hospital de la Santa Creu i Sant Pau, Biomedical Rese, Barcelona, Spain, ⁴DEIB, Politecnico di Milano, Milan, Italy, ⁵Center for Mind/Brain Sciences - CIME, University of Trento, Trento, Italy, ⁶Sir Peter Mansfield Imaging Centre, School of Medicine, University of Nottingham, Nottingham, UK, ⁷Athinoula A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Harvard Medical, Boston, MA, ⁸CUBRIC, Cardiff University, Cardiff, UK, ⁹Image Sciences Institute, University Medical Center Utrecht, Utrecht, Netherlands, ¹⁰Champalimaud Research, Champalimaud Centre for the Unknown, Lisbon, Portugal, ¹¹Univ Rennes, CNRS, Inria, Inserm, Rennes, France

First Author:

Simona Schiavi
Department of Computer Science, University of Verona
Verona, Italy

Co-Author(s):

Mario Ocampo-Pineda
Department of Computer Science, University of Verona
Verona, Italy
Michele Guerreri
Centre for Medical Image Computing, University College London
London, UK
Victor Montal
Sant Pau Memory Unit, Department of Neurology, Hospital de la Santa Creu i Sant Pau, Biomedical Rese
Barcelona, Spain
Giulia Buizza
Introduction:

Over the last decades, many techniques have been proposed to infer brain tissue microstructure from the diffusion-weighted MRI (dMRI) signal (1). Most of them assume geometrical configurations that are specific to white matter and are widely used also in clinical applications (2). Recently, the Soma And Neurite Density Imaging (SANDI) (3) has been proposed to estimate MR apparent neurite and soma density in grey matter. However, the estimation of these parameters from dMRI measurements is challenging (4) and time consuming when using conventional fitting methods based on non-linear least square (NLLS) minimization.

Here, we overcome these limitations by proposing SANDI-AMICO: a new implementation of SANDI inside the Accelerated Microstructure Imaging via Convex Optimization (AMICO) framework (5). We demonstrate the performance of SANDI-AMICO in simulations and in vivo data from mouse and human brains. The SANDI-AMICO toolbox is available at https://github.com/daducci/AMICO.
Methods:

SANDI assumes that soma (cell bodies) and neurites can be approximated as two non-exchanging compartments, modeled as spheres of certain size and cylinders of zero radius ("sticks"), respectively. Under these assumptions, the normalized direction-averaged dMRI signal (Savg) is:

\[ \frac{S_{\text{avg}}(b)}{S(0)} = f_n S_n(b,D_n) + f_s S_s(b,D_s,R_s) + (1-f_n-f_s) S_e(b,D_e) \]  

where \( f_n \) is the neurite signal fraction, \( D_n \) the intra-neurite diffusivity; \( f_s \) the soma signal fraction, \( R_s \) the apparent soma radius, \( D_s = 3 \ \mu m^2/\mu s \), and \( D_e \) the extra-cellular diffusivity (3). \( S_n, S_s \) and \( S_e \) are computed as in (3).

SANDI-AMICO rewrites eq.[1] as linear system \( Ax = y \), where \( A \) is a matrix containing simulated signals of each compartment, \( y \) the vector of measured signals, and \( x \) the unknown contributions. To build \( A \), we searched for the combination of sphere radii and diffusivities that produced sufficiently different signals according to the specific acquisition protocol. The elements of \( x \) are then estimated using a non-negative least square with Tikhonov regularization.

We used analytical simulations to compare the performance of AMICO and NLLS estimations under controlled conditions. We generated 2,500 different synthetic signals using random combinations of the SANDI model parameters and eq.[1], according to the mouse data protocol and adding Gaussian noise with SNR=100, similar to the data. We assessed the accuracy and precision of both AMICO and NLLS implementations by comparing the percent error and deviation of the estimated model parameters with the ground-truth values, known by design.

The in-vivo dMRI data from one healthy mouse brain was acquired with a PGSE-EPI sequence at 9.4T (Bruker/Biospec) with: TE/TR= 36.8/4000 ms; \( \delta/\Delta = 5.5/20 \) ms; \( b=0,1,2,5,4,5,5,7,8,5,10,12.5 \) ms/\( \mu m^2 \); 40 gradient directions each, resolution 0.12x0.12x0.4 mm³.

We tested the quality of the fitting also using one human subject from the MICRA dataset, acquired at 3T (Siemens/Connectom). Acquisition details can be found in (6). We used Freesurfer (7) to project the SANDI-AMICO fs map onto the midpoint cortical surface.

Results:

From the simulation study, we found that AMICO outperformed NLLS in terms of precision (~10% higher), showing higher robustness to noise with only minimal loss in accuracy (<5%) (Fig.1A).

On the mouse data, the AMICO fit was much faster than NLLS (23 s vs 943 s) and the estimated parametric maps of much higher quality (Fig.2B). In particular, fn and fs mirrored well the known myelo- and cyto-architecture of the mouse brain (Fig.1B).

The SANDI-AMICO fn and fs maps from the human data showed a remarkable contrast, matching the expected myelo- and cyto-architecture of the human brain (Fig.2A). Furthermore, the variations of fs values over the midpoint cortical surface followed the expected cyto-architectonics of several Brodmann's areas (Fig.2B), confirming previous observations (3).
Table A shows the accuracy and precision of the NLLS and AMICO methods with different error metrics. The average accuracy and precision are also provided in the table. Figure 1 compares the AMICO and NLLS methods by showing the apparent neurite and soma density maps. AMICO appears to offer a smoother recovery while maintaining high precision and accuracy.
Conclusions:

We presented SANDI-AMICO: an open-source toolbox for the fast and robust fitting of the SANDI model.

Modeling and Analysis Methods:

Diffusion MRI Modeling and Analysis

Neuroanatomy, Physiology, Metabolism and Neurotransmission:

Cortical Anatomy and Brain Mapping
Cortical Cyto- and Myeloarchitecture

Novel Imaging Acquisition Methods:

Diffusion MRI
Keywords:

- Computational Neuroscience
- Cortex
- Informatics
- Modeling
- MRI
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- WHITE MATTER IMAGING - DTI, HARDI, DSI, ETC
- Other - Grey Matter, SANDI, AMICO

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- Diffusion MRI
- Computational modeling

For human MRI, what field strength scanner do you use?

3.0T

Which processing packages did you use for your study?

- FSL
- Free Surfer
Provide references using author date format