



HAL
open science

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

Simona Schiavi, Mario Ocampo-Pineda, Raphaël Truffet, Emmanuel Caruyer,
Alessandro Daducci, Marco Palombo

► **To cite this version:**

Simona Schiavi, Mario Ocampo-Pineda, Raphaël Truffet, Emmanuel Caruyer, Alessandro Daducci, et al.
SANDI-AMICO: an open-source toolbox for fast Soma And Neurite Density Imaging (SANDI) with AMICO.
27th annual meeting of the Organization for Human Brain Mapping (OHBM), Jun 2021, Virtual, Singapore.
<inserm-03783770>

HAL Id: inserm-03783770

<https://inserm.hal.science/inserm-03783770v1>

Submitted on 22 Sep 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



HAL Authorization

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

Poster No:

2139

Submission Type:

Abstract Submission

Authors:

Simona Schiavi¹, Mario Ocampo-Pineda¹, Michele Guerreri², Victor Montal³, Giulia Buizza⁴, Lisa Novello⁵, Sara Bosticardo¹, Jenna Hanmer⁶, Gabriel Ramos Llorde⁷, Chantal Tax^{8,9}, 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 - CIMeC, 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

DEIB, Politecnico di Milano

Milan, Italy

Lisa Novello

Center for Mind/Brain Sciences - CIMeC, University of Trento

Trento, Italy

Sara Bosticardo

Department of Computer Science, University of Verona

Verona, Italy

Jenna Hanmer

Sir Peter Mansfield Imaging Centre, School of Medicine, University of Nottingham

Nottingham, UK

Gabriel Ramos Llorde

Athinoula A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Harvard Medical

Boston, MA

Chantal Tax

CUBRIC, Cardiff University Image Sciences Institute, University Medical Center Utrecht

Cardiff, UK Utrecht, Netherlands

Andrada Ianus

Champalimaud Research, Champalimaud Centre for the Unknown

Lisbon, Portugal

Noam Shemesh

Champalimaud Research, Champalimaud Centre for the Unknown

Lisbon, Portugal

Emmanuel Caruyer

Univ Rennes, CNRS, Inria, Inserm

Rennes, France

Alessandro Daducci

Department of Computer Science, University of Verona

Verona, Italy

Marco Palombo

Centre for Medical Image Computing, University College London

London, UK

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 (S_{avg}) is:

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

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, $D_s = 3 \mu\text{m}^2/\text{ms}$, 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 $\text{SNR}=100$, 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: $\text{TE/TR} = 36.8/4000$ ms; $\delta/\Delta = 5.5/20$ ms; $b = 0, 1, 2.5, 4, 5.5, 7, 8.5, 10, 12.5$ $\text{ms}/\mu\text{m}^2$; 40 gradient directions each, resolution $0.12 \times 0.12 \times 0.4$ mm^3 .

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 f_s 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, f_n and f_s mirrored well the known myelo- and cyto-architecture of the mouse brain (Fig.1B).

The SANDI-AMICO f_n and f_s 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 f_s values over the midpoint cortical surface followed the expected cyto-architectonics of several Brodmann's areas (Fig.2B), confirming previous observations (3).

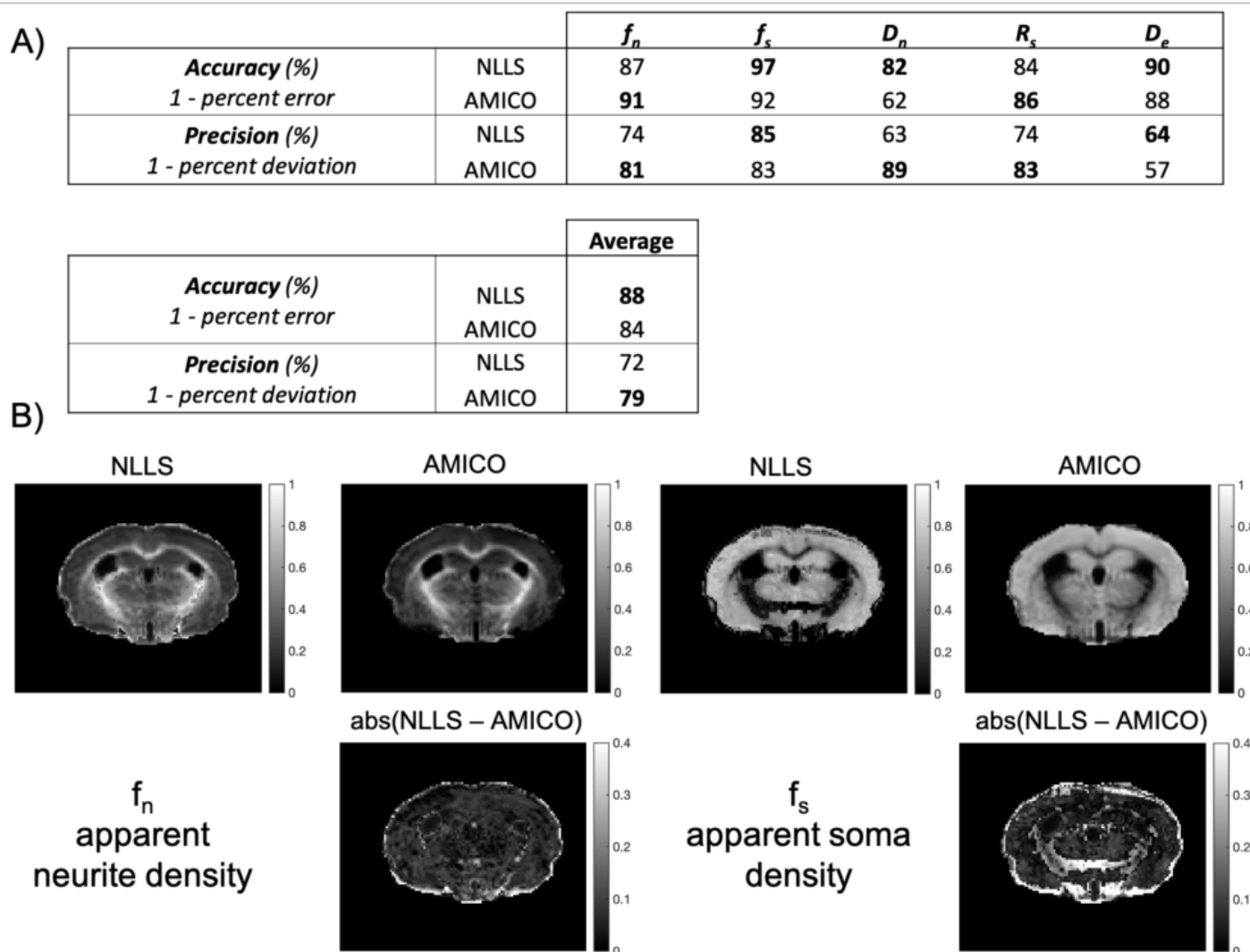
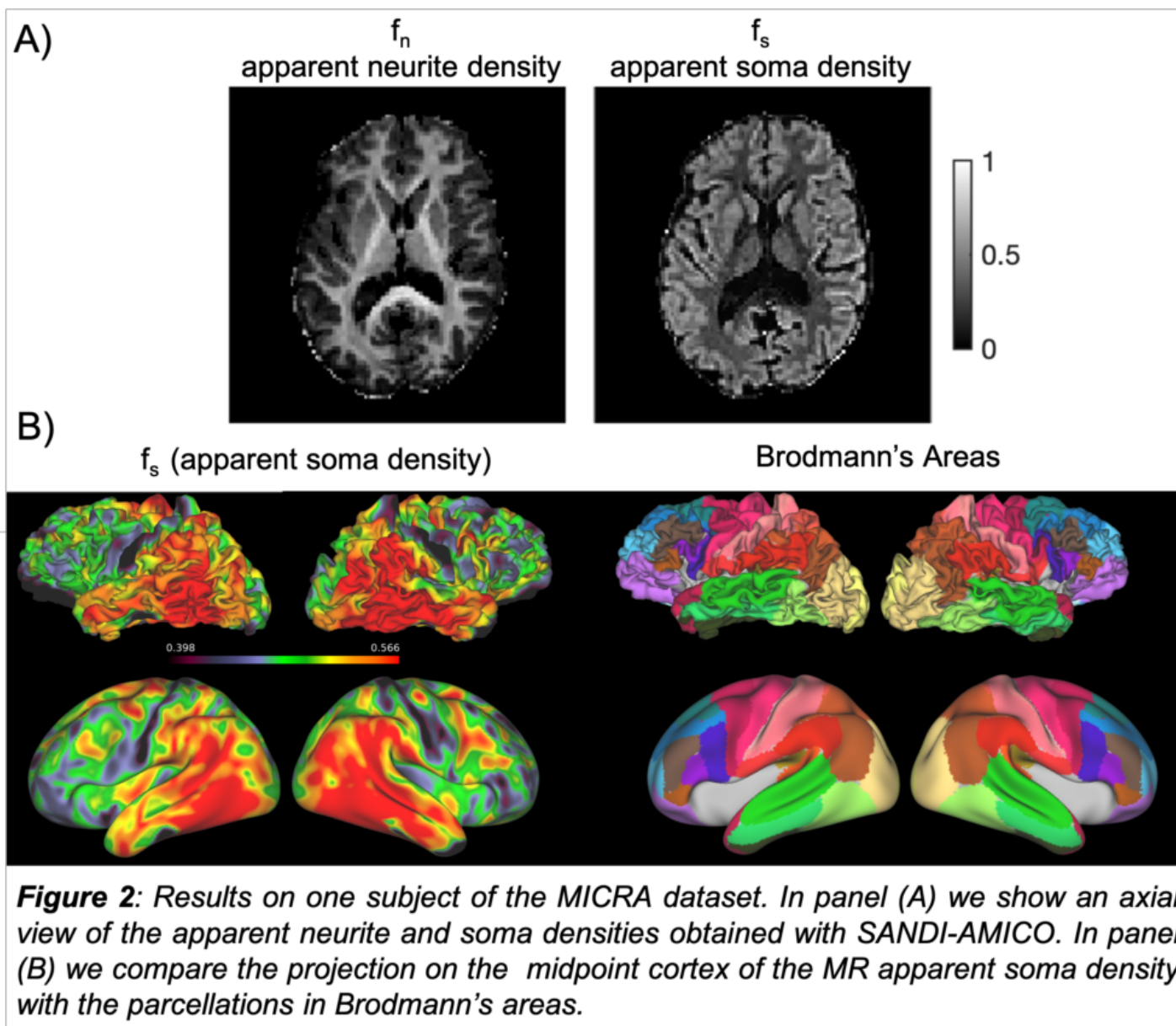


Figure 1: Comparison between AMICO and the standard NLLS fitting of SANDI model in simulations (A) and in-vivo mouse data (B). In the tables (A), we report the accuracy and precision of both methods on synthetic data with SNR=100. Overall, our AMICO implementation results ~10% higher in precision while losing only <5% in accuracy. In panel (B) we show the MR apparent neurite (left) and soma (right) densities recovered by both methods and the absolute difference between them. AMICO is ~50 times faster than NLLS and the recovered maps appears smoother.

(https://files.aievolution.com/prd/hbm2101/abstracts/abs_2028/Figure1_v5.png)

·Figure 1



(https://files.aievolution.com/prd/hbm2101/abstracts/abs_2028/Figure2_v3.png)

·Figure 2

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 ¹

Neuroanatomy, Physiology, Metabolism and Neurotransmission:

Cortical Anatomy and Brain Mapping

Cortical Cyto- and Myeloarchitecture ²

Novel Imaging Acquisition Methods:

Diffusion MRI

Keywords:

Computational Neuroscience

Cortex

Informatics

Modeling

MRI

Open-Source Code

Structures

WHITE MATTER IMAGING - DTI, HARDI, DSI, ETC

Other - Grey Matter, SANDI, AMICO

^{1|2}Indicates the priority used for review

My abstract is being submitted as a Software Demonstration.

Yes

Please indicate below if your study was a "resting state" or "task-activation" study.

Other

Healthy subjects only or patients (note that patient studies may also involve healthy subjects):

Healthy subjects

Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.

Yes

Was any animal research approved by the relevant IACUC or other animal research panel? NOTE: Any animal studies without IACUC approval will be automatically rejected.

Yes

Please indicate which methods were used in your research:

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

- (1) Novikov DS, Fieremans E, Jespersen SN, Kiselev VG. Quantifying brain microstructure with diffusion MRI: Theory and parameter estimation. *NMR Biomed.* 2019;32(4):e3998. doi:10.1002/nbm.3998
- (2) Alexander DC, Dyrby TB, Nilsson M, Zhang H. Imaging brain microstructure with diffusion MRI: practicality and applications. *NMR Biomed.* 2019;32(4):e3841. doi:10.1002/nbm.3841
- (3) Palombo M, Ianus A, Guerreri M, et al. SANDI: A compartment-based model for non-invasive apparent soma and neurite imaging by diffusion MRI. *Neuroimage.* 2020;215:116835. doi:<https://doi.org/10.1016/j.neuroimage.2020.116835>
- (4) Afzali M, Nilsson M, Palombo M, Jones DK. SPHERIOUSLY? The challenges of estimating spherical pore size non-invasively in the human brain from diffusion MRI. *bioRxiv.* 2020. doi:10.1101/2020.11.06.371740
- (5) Daducci A, Canales-Rodríguez EJ, Zhang H, Dyrby TB, Alexander DC, Thiran J-P. Accelerated Microstructure Imaging via Convex Optimization (AMICO) from diffusion MRI data. *Neuroimage.* 2015;105:32-44. doi:<http://dx.doi.org/10.1016/j.neuroimage.2014.10.026>
- (6) Koller K, Rudrapatna U, Chamberland M, et al. MICRA: Microstructural image compilation with repeated acquisitions. *Neuroimage.* 2021;225:117406. doi:<https://doi.org/10.1016/j.neuroimage.2020.117406>
- (7) Fischl B, Salat DH, Busa E, et al. Whole brain segmentation: automated labeling of neuroanatomical structures in the human brain. *Neuron.* 2002;33:341-355. doi:10.1016/s0896-6273(02)00569-x