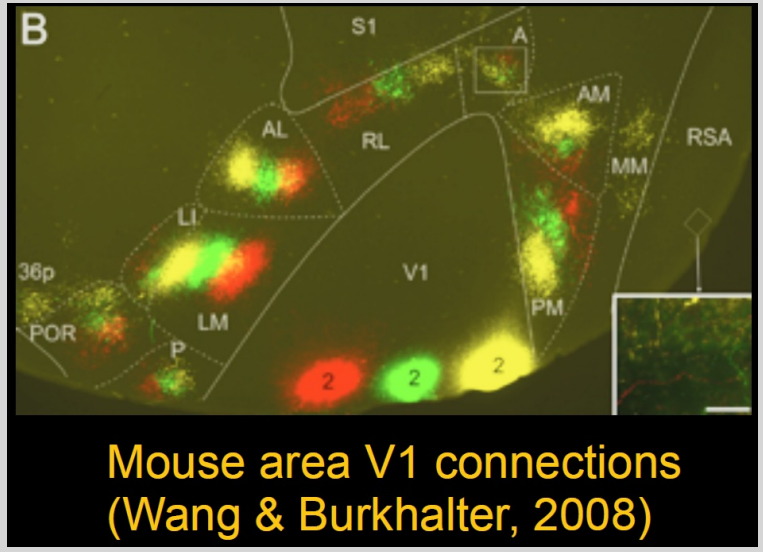
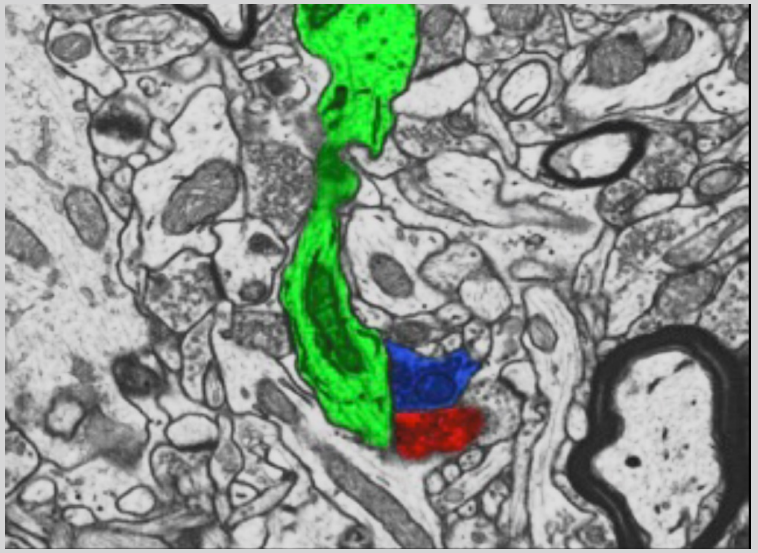
MRI Connectomics

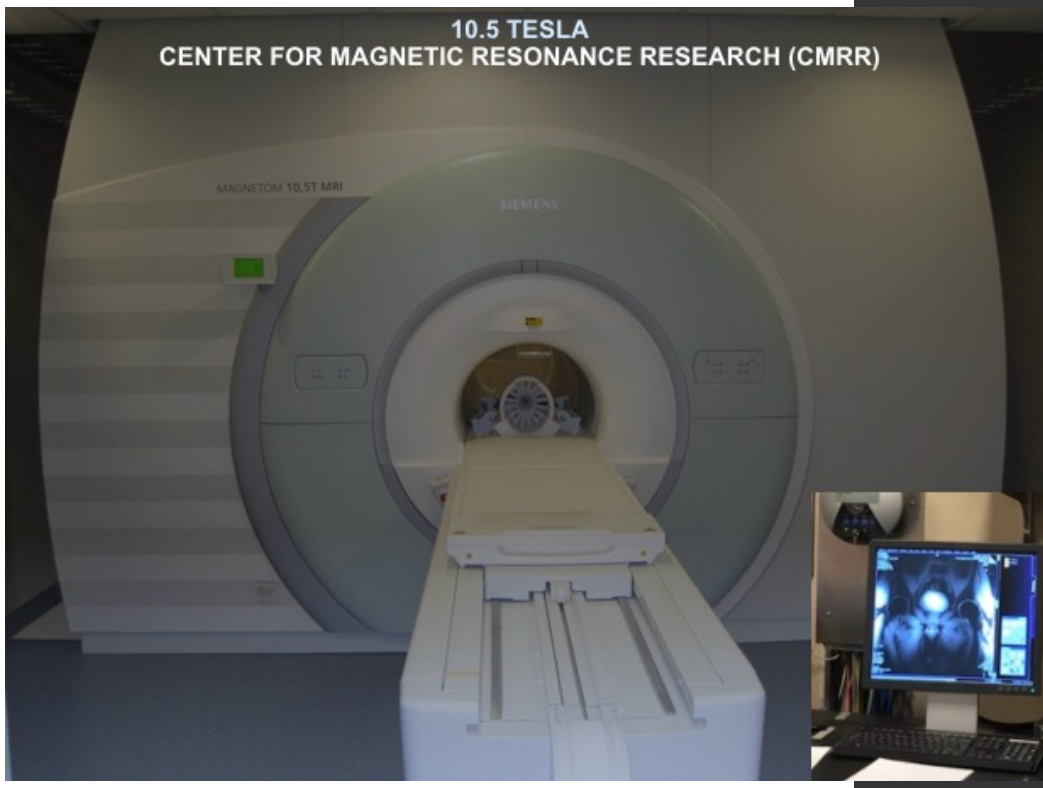
Pavel Filip, MD PhD MBA FEBN
Department of Neurology; First Faculty of Medicine, Charles University
Department of Cybernetics, Czech Technical University in Prague, Prague, Czech Republic
Center for Magnetic Resonance Research (CMRR), University of Minnesota, Minneapolis, USA

What is a connectome
or
Crash course on connectome and MRI

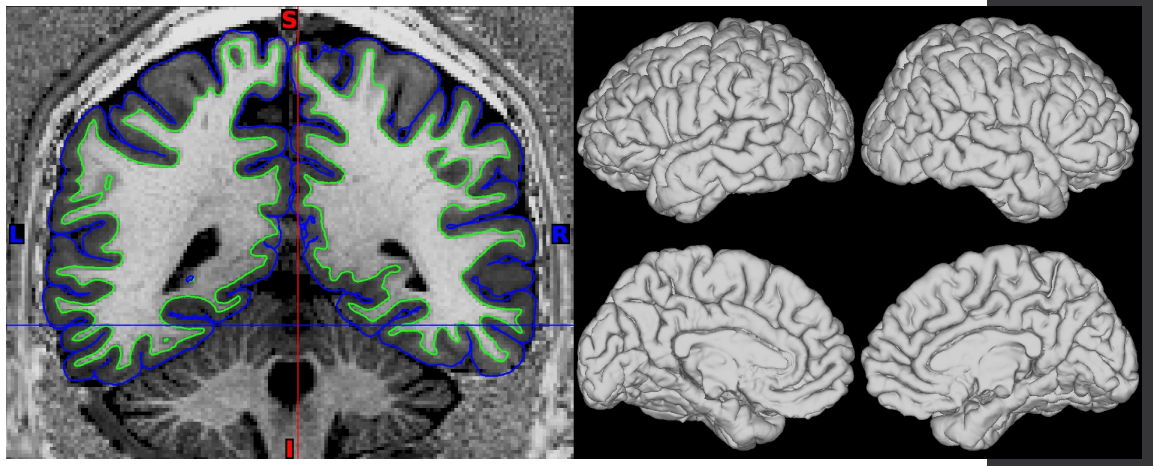
Macro-connectome brain level, long distance	**Meso-connectome** Cellular, long distance	**Micro-connectome** Synapses
	 Mouse area V1 connections (Wang & Burkhalter, 2008)	

- "Comprehensive" map of neuronal connections

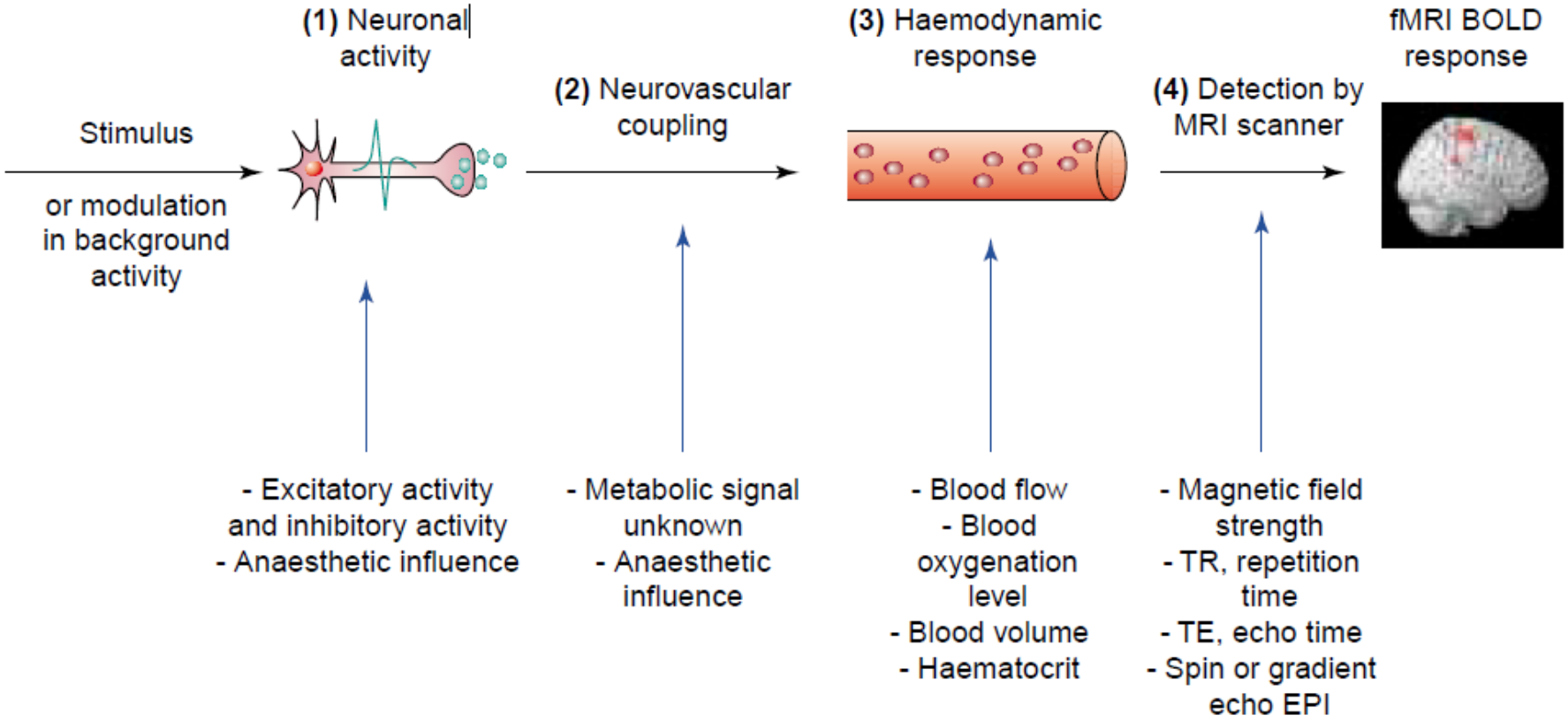
MRI as a method of measurement



- "Functional" connections – full/partial correlations
  - "Functional MRI" – **T2*-weighted BOLD**, SWIFT, ASL
  - But also EEG, MEG and many more
- "Structural connections" – track probabilities
  - **DWI**
- Structural data
  - Cortical thickness, cortical folding, volume/shape of structures…
- Microstructural data – "MRI histology"
  - Relaxation metrics (T1, T2, T1ρ, T2ρ, RAFF…) as markers of myelin, iron content
  - SWI
  - Multiple derived metrics as NODDI (water distribution, membrane integrity), T1w/T2w ratio ("myelin maps")



fMRI BOLD signal – what do we measure?



Arthurs and Boniface, 2002

Underlying neural activity

Dissociation/decoupling - regionality:

- vascular hypothesis
- local circuitry-based explanations
- regionality of HRF

- **gamma band power** of LFPs (nominally 40–100 Hz) most correlated with the subsequent vasodilation and/or increased oxygenation
- → Activity of interneurons as the primary driver of BOLD?

Effect	Metabolic signals and spike rate correlated	Metabolic signal and spike rate dissociated	Metabolic signal and LFP correlated	Metabolic signal and LFPs dissociated
Region				
Visual cortex	Rees et al., 2000; Logothetis et al., 2001; Kim et al., 2004; Shmuel et al., 2006; Goense and Logothetis, 2008;	Kayser et al. , 2004; Niessing et al., 2005; Maier et al., 2008; Rauch et al., 2008; Viswanathan, 2008; Sirotin and Das, 2009.	Logothetis et al., 2001; Moosmann et al., 2003; Niessing et al., 2005; Koch et al., 2006; Shmuel et al., 2006; Goense and Logothetis, 2008	Logothetis et al., 2001; Koch et al., 2006; **Maier et al., 2008; Sirotin and Das, 2009**
Primary auditory cortex	Mukamel et al., 2005; Nir et al., 2007.	Nir et al., 2007.	Mukamel et al., 2005; Nir et al., 2007.	
Neocortex (includes parietal and frontal cortex)	Smith et al., 2002; Hyder, 2004; Kida et al., 2006.	Devor et al., 2007.	Brinker et al., 1999; Goldman et al., 2002; Laufs et al., 2003a; Laufs et al., 2003b; Ureshi et al., 2004; Debener et al., 2005; Hewson-Stoate et al., 2005; Kida et al., 2006; Gsell et al., 2006; Martin et al., 2006; Devor et al., 2007 Masamoto et al., 2008; Huttunen et al., 2008; Scheeringa et al., 2009.	Hewson-Stoate et al., 2005; Masamoto et al., 2008; Meltzer et al., 2008
Hippocampal area	Englot et al., 2008; 2009.	Schridde et al., 2008; Ekstrom et al., 2009. Ojemann et al., 2009.	Canals et al., 2008; Englot et al., 2008; 2009; Ekstrom et al., 2009; Ojemann et al., 2009.	Sanchez-Arroyos et al., 1993; Uecker et al., 1997; **Schridde et al., 2008; Angenstein et al., 2009; Ekstrom et al., 2009.**
Cerebellum		Mathiessen et al., 1998; 2000. Caesar et al., 2003; Thomsen et al., 2004.	Mathiesen et al., 1998; 2000. Thomsen et al., 2004.	**Caesar et al., 2003.**

resting state fMRI

- Evoked neural activity and haemodynamic signals – R>0.9
- Spontaneous activity – R in the range of 0.0-0.3

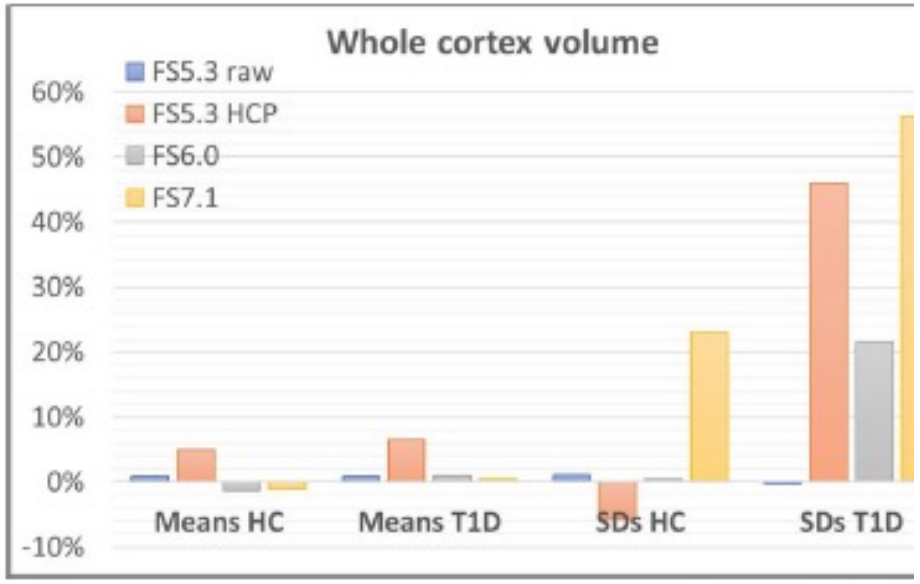
→**i.e. low correlations not caused by methodological issues**

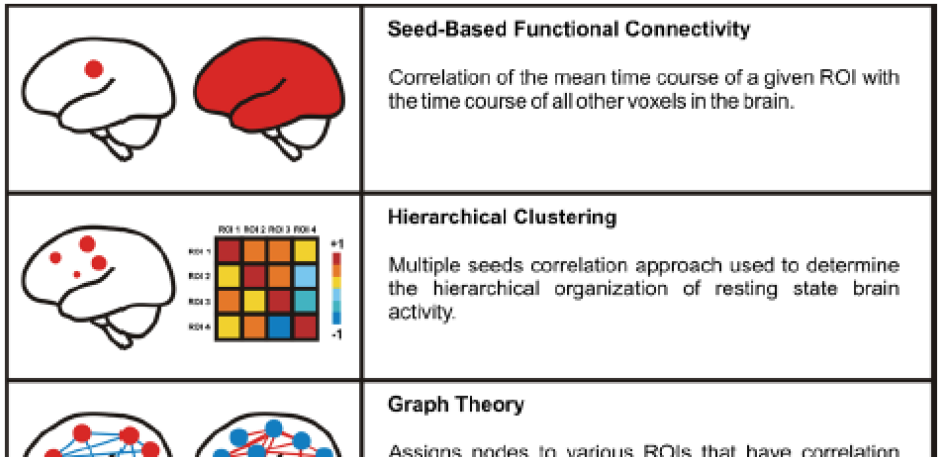
→**mismatch between observed BOLD dynamics and predicted dynamics from structural connectome**

- Vessel-autonomous oscillations (in mice persisting even after pharmacological blockage of glutamatergic transmission)
- Spontaneous movements – need for monitoring…

Data processing

- Multitude of options
  - Inferences?
  - Data dredging?





		Cortex whole	Frontal lobe	Parietal lobe	Temporal lobe	Occipital lobe	Anterior cingulate	Posterior cingulate	Thalami	Hippocampi
FS5.3 with careful manual correction	HC (average [SD])	0.3313 [0.0235]	0.1207 [0.0093]	0.0805 [0.0066]	0.0752 [0.0049]	0.0315 [0.0037]	0.0034 [0.0004]	0.0034 [0.0004]	0.0105 [0.0010]	0.0059 [0.0004]
	T1D (average [SD])	0.3187 [0.0182]	0.1158 [0.0080]	0.0773 [0.0053]	0.0729 [0.0049]	0.0299 [0.0022]	0.0034 [0.0004]	0.0033 [0.0004]	0.0098 [0.0008]	0.0059 [0.0005]
	% inter-group dif.	**-3.80%**	**-4.05%**	**-4.01%**	**-3.12%**	**-5.10%**	**1.08%**	**-4.64%**	**-6.87%**	**-0.17%**
	p (uncorrected)	**0.0348**	**0.0467**	**0.0575**	**0.0927**	**0.0615**	0.7499	0.1674	**0.0052**	0.9405
FS5.3 raw	HC (average [SD])	0.3341 [0.0238]	0.1173 [0.0094]	0.0756 [0.0064]	0.0761 [0.0053]	0.0329 [0.0040]	0.0034 [0.0004]	0.0035 [0.0004]	0.0102 [0.0010]	0.0058 [0.0004]
	T1D (average [SD])	0.3214 [0.0181]	0.1133 [0.0070]	0.0722 [0.0050]	0.0740 [0.0052]	0.0312 [0.0022]	0.0035 [0.0004]	0.0034 [0.0004]	0.0095 [0.0007]	0.0057 [0.0005]
	% inter-group dif.	**-3.81%**	**-3.44%**	**-4.52%**	**-2.66%**	**-5.24%**	**1.85%**	**-3.82%**	**-6.79%**	**-0.53%**
	p (uncorrected)	**0.0355**	**0.0875**	**0.0376**	0.1741	**0.0599**	0.5817	0.2585	**0.0059**	0.8201
FS5.3 HCP	HC (average [SD])	0.3477 [0.0221]	0.1268 [0.0097]	0.0810 [0.0065]	0.0810 [0.0042]	0.0350 [0.0033]	0.0037 [0.0004]	0.0037 [0.0005]	0.0105 [0.0011]	0.0055 [0.0004]
	T1D (average [SD])	0.3394 [0.0265]	0.1243 [0.0112]	0.0780 [0.0068]	0.0791 [0.0069]	0.0335 [0.0024]	0.0037 [0.0005]	0.0035 [0.0004]	0.0098 [0.0010]	0.0056 [0.0005]
	% inter-group dif.	**-2.38%**	**-2.01%**	**-3.64%**	**-2.41%**	**-4.10%**	**0.62%**	**-4.66%**	**-6.82%**	**2.10%**
	p (uncorrected)	0.2351	0.3938	0.1221	0.2351	**0.0803**	0.8580	0.1784	**0.0179**	0.3695
FS6.0	HC (average [SD])	0.3271 [0.0236]	0.1173 [0.0098]	0.0754 [0.0064]	0.0755 [0.0047]	0.0341 [0.0045]	0.0032 [0.0004]	0.0035 [0.0004]	0.0104 [0.0011]	0.0054 [0.0004]
	T1D (average [SD])	0.3218 [0.0221]	0.1156 [0.0094]	0.0730 [0.0056]	0.0746 [0.0055]	0.0332 [0.0031]	0.0033 [0.0004]	0.0034 [0.0004]	0.0097 [0.0010]	0.0055 [0.0004]
	% inter-group dif.	**-1.62%**	**-1.50%**	**-3.27%**	**-1.25%**	**-2.51%**	**2.45%**	**-1.43%**	**-6.96%**	**1.22%**
	p (uncorrected)	0.4119	0.5162	0.1492	0.5135	0.4299	0.5152	0.6795	**0.0180**	0.5715
FS7.1	HC (average [SD])	0.3276 [0.0289]	0.1194 [0.0113]	0.0756 [0.0074]	0.0734 [0.0059]	0.0327 [0.0048]	0.0032 [0.0004]	0.0034 [0.0004]	0.0107 [0.0012]	0.0056 [0.0005]
	T1D (average [SD])	0.3202 [0.0284]	0.1163 [0.0117]	0.0735 [0.0066]	0.0718 [0.0069]	0.0316 [0.0035]	0.0032 [0.0005]	0.0033 [0.0004]	0.0102 [0.0011]	0.0057 [0.0006]
	% inter-group dif.	**-2.27%**	**-2.60%**	**-2.90%**	**-2.27%**	**-3.42%**	**1.86%**	**-1.32%**	**-4.61%**	**1.25%**
	p (uncorrected)	0.3582	0.3424	0.2695	0.3635	0.3432	0.6482	0.6909	0.1425	0.6396

Aftermath…

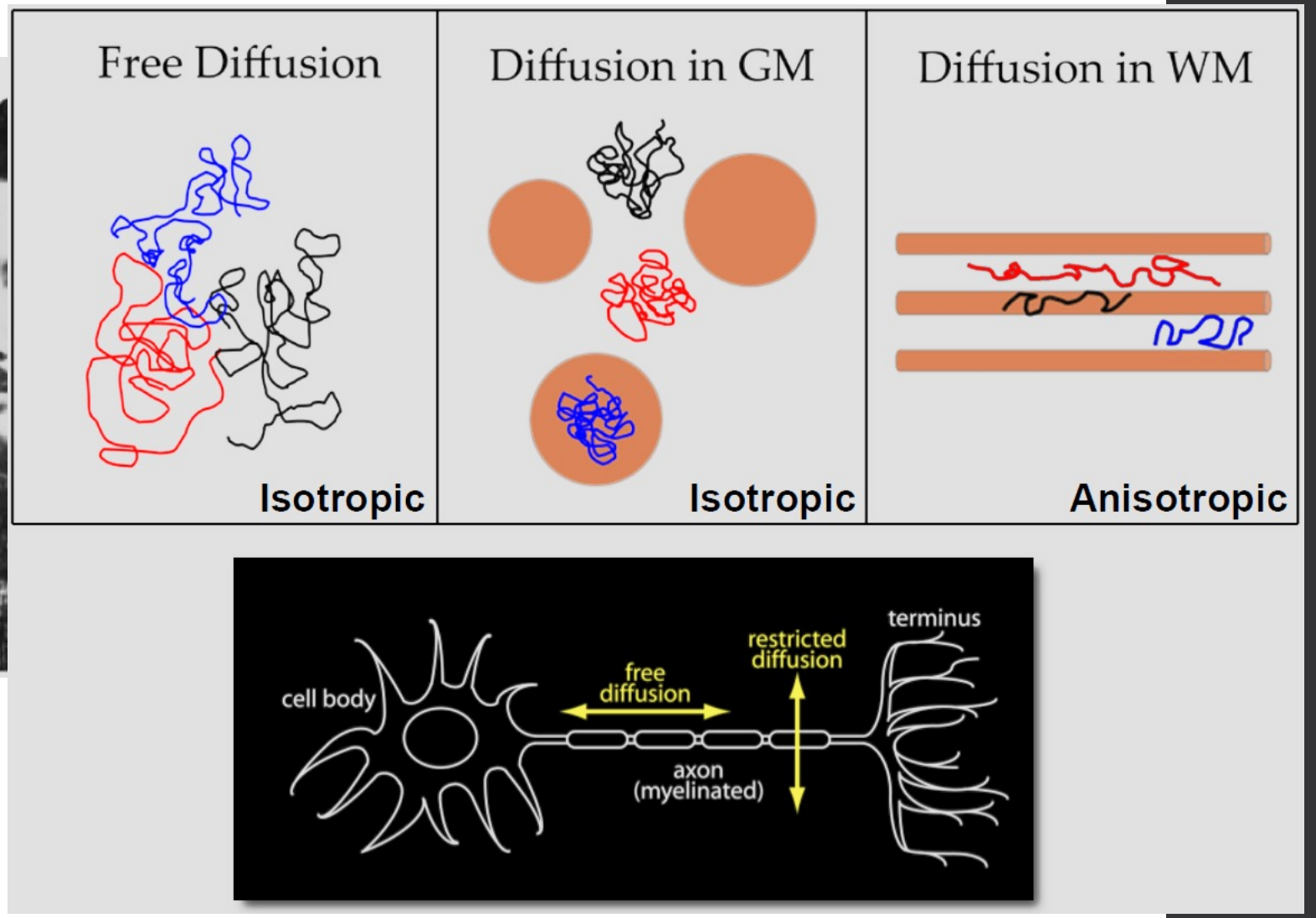
Editorial FREE

Dimitri M Kullmann

Brain, Volume 143, Issue 4, April 2020, Page 1045,
https://doi.org/10.1093/brain/awaa082
Published: 21 April 2020

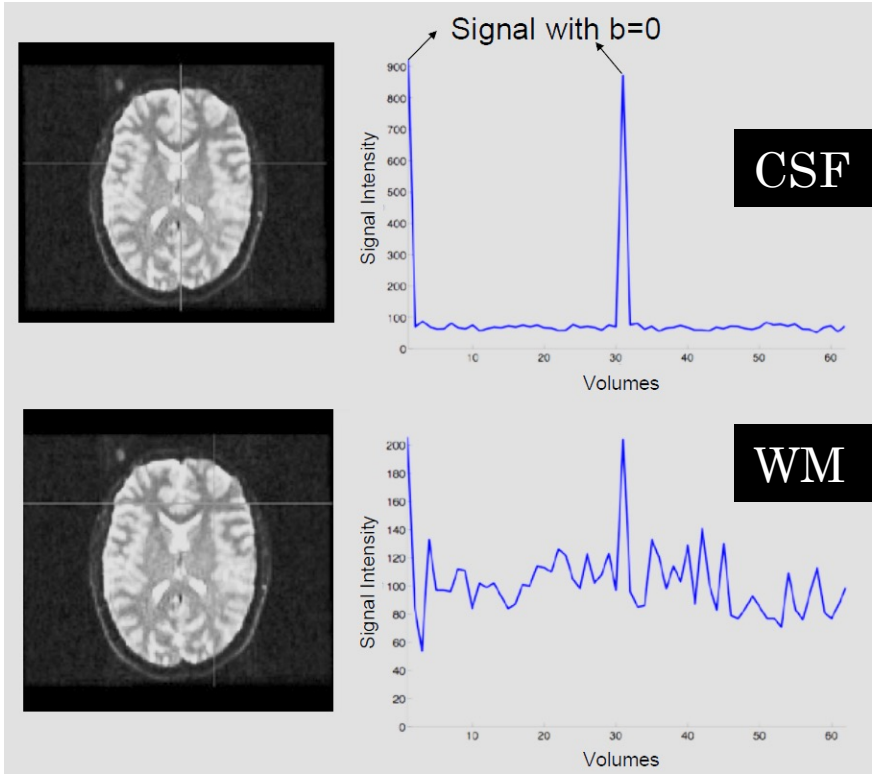
Brain receives far more manuscript submissions than can reasonably be sent for formal peer review. Although the reasons for editorial rejection are diverse and include such factors as under-powered study design, limited conceptual novelty or remoteness from clinical translation, the motivation behind the authors' work is rarely in doubt. Nevertheless, there remains a small number of submissions where the route to clinical application or to improved understanding of disease mechanisms is very difficult to infer, leaving one asking, 'Why did the authors undertake this work in the first place?' Such manuscripts disproportionately report on functional MRI in groups of patients without a discernible hypothesis. Showing that activation patterns or functional connectivity motifs differ significantly is, on its own, insufficient justification to occupy space in *Brain*. Given that functional MRI is ~30 years old and continues to divert many talented young researchers from careers in other fields of translational neuroscience, it is worth reiterating two of the most troubling limitations of the method (and these are not the notorious pitfalls such as failure to correct for multiple comparisons or circular inference). First, the fundamental relationship between the blood oxygenation level-dependent (BOLD) signal and neuronal computations remains a complete mystery. As a direct consequence, it is extremely difficult to conclude that functional connectivity as measured by functional MRI genuinely measures information exchange between brain regions. Second, effect sizes are quasi-impossible to infer, leading to an anomaly in science where statistical significance remains the only metric reported. A

DWI


Free Diffusion
Isotropic
Diffusion in GM
Isotropic
Diffusion in WM
Anisotropic
cell body
free diffusion
restricted diffusion
terminus
axon (myelinated)

DWI

- Diffusion weighting is modulated by:
  - Gradient strength
  - Diffusion time
  - Gradient orientation

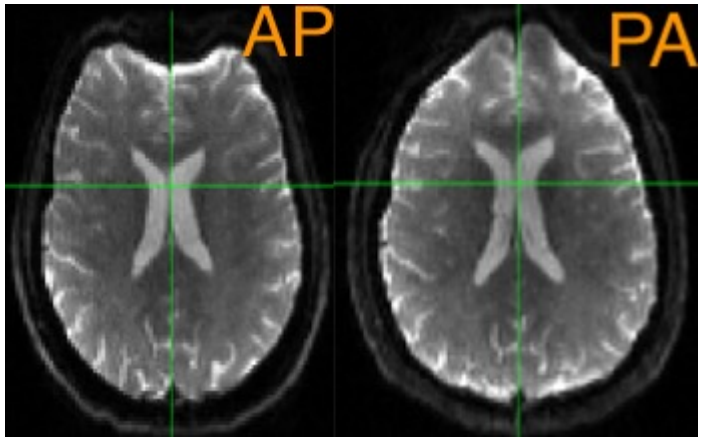


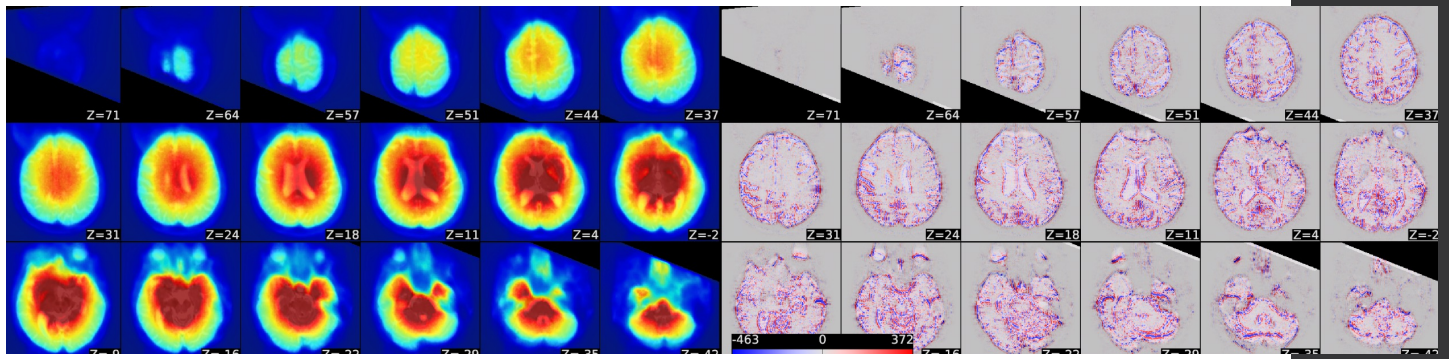
- Images acquired with a gradient along x have contrast sensitive to the diffusion of water molecules along x.

- Utilisation
  - DTI
  - Kurtosis
  - NODDI
  - Fiber orientation distribution / density
  - Tractography
  - ….

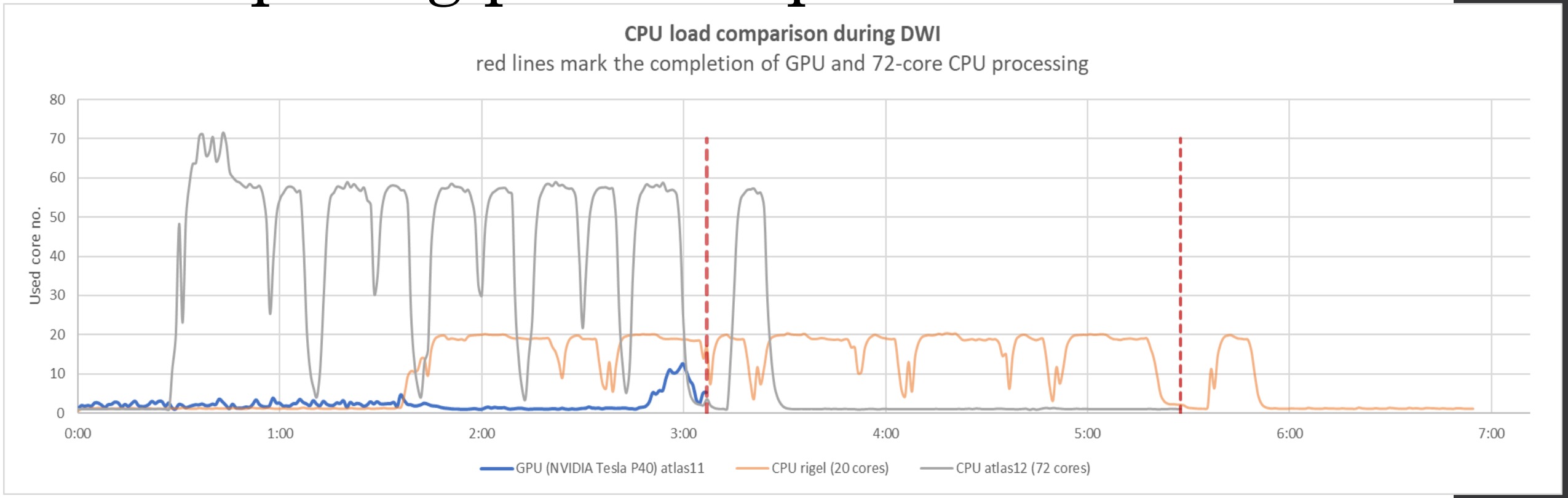
Problems with MRI data

- Noise, artifacts (Gibbs ringing, standing waves, chemical shifts, magic angle…)
- Gradient non-linearities
- Distortions
  - Susceptibility-induced
  - Eddy current-induced
- Subject movement
  - Gross movement
  - Intra-volume movement
  - i.e. movement within the bias field and changes of the susceptibility field
- Intra-volume temporal differences
- Signal dropouts
- Cardiac and respiratory cycle
- Blood and CSF flow

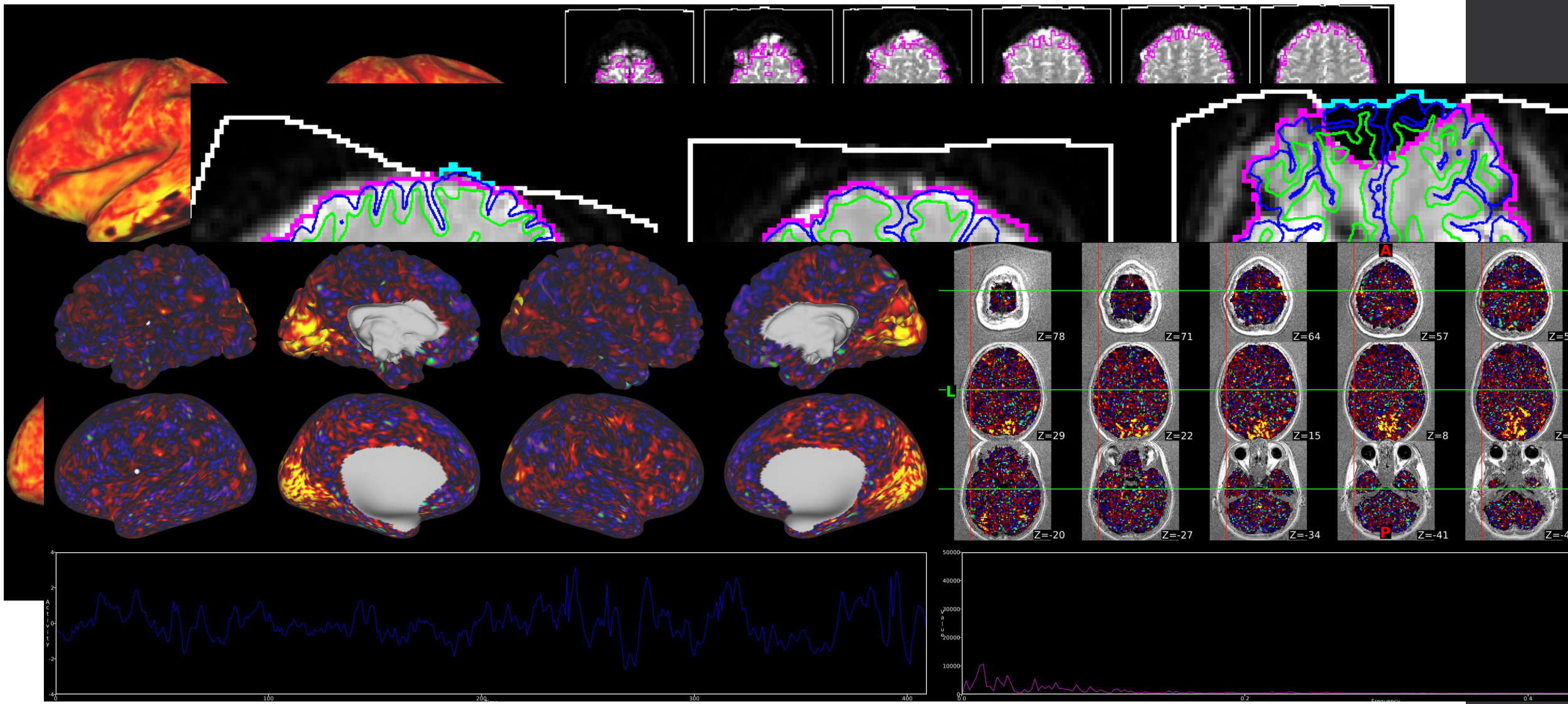




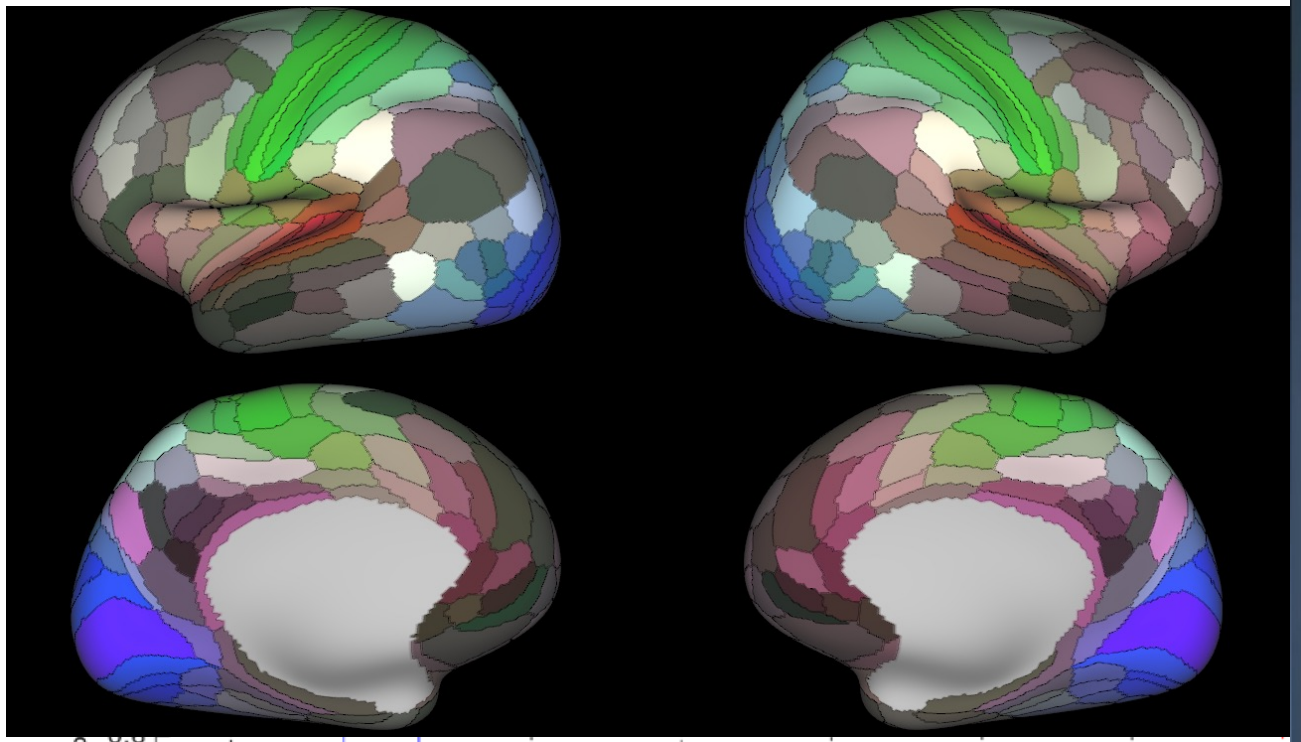
Computing power requirements

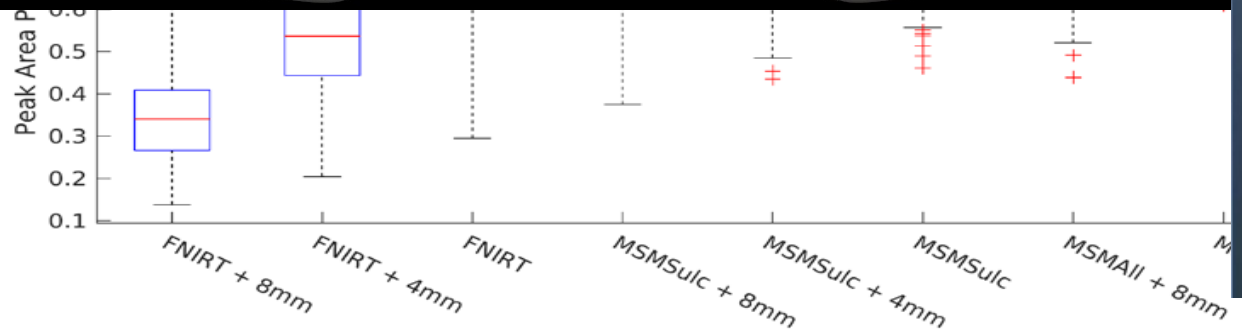


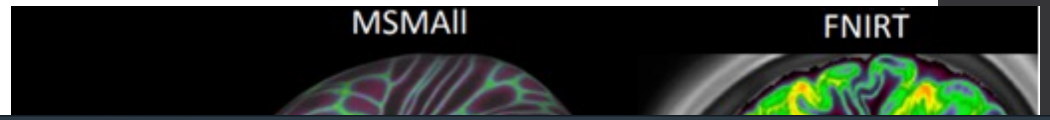
Quality control



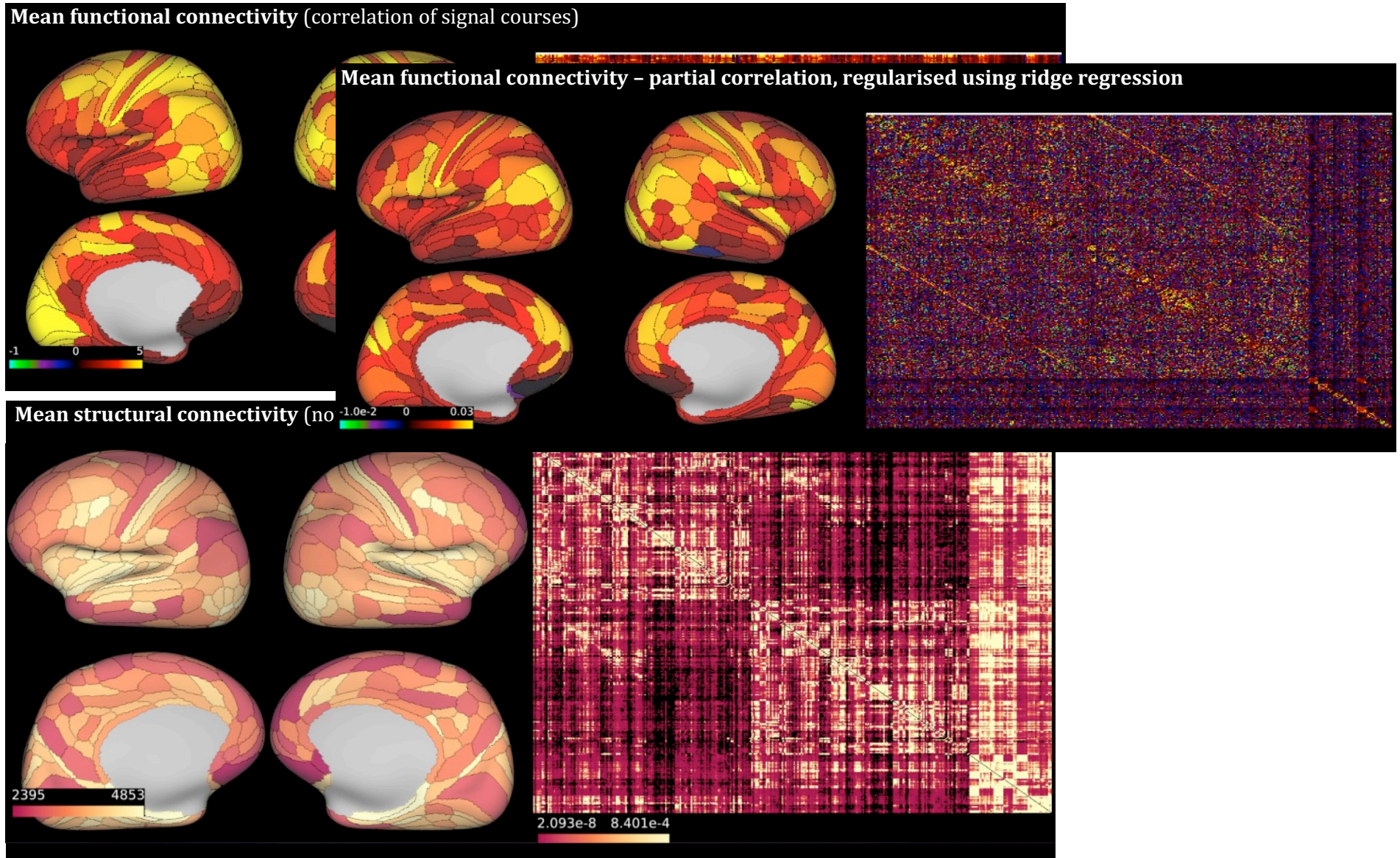
Group analysis and brain parcellation







Connectome matrices



Utilisation in real studies
Structural connectome of tremor

Parkinsonism and Related Disorders 95 (2022) 28–34

Contents lists available at ScienceDirect

Parkinsonism and Related Disorders

journal homepage: www.elsevier.com/locate/parkreldis

Tremor associated with similar structural networks in Parkinson's disease and essential tremor

Pavel Filip [a,b,*], Kristína Burdová [a], Zdeněk Valenta [c], Robert Jech [a], Viktória Kokošová [d], Marek Baláž [e], Silvia Mangia [b], Shalom Michaeli [b], Martin Bareš [e,f], Lubomír Vojtíšek [g]

[a] Department of Neurology, Charles University, First Faculty of Medicine and General University Hospital, Prague, Czech Republic
[b] Center for Magnetic Resonance Research (CMRR), University of Minnesota, Minneapolis, MN, USA
[c] Department of Statistical Modelling, Institute of Computer Science of the Czech Academy of Sciences, Prague, Czech Republic
[d] Department of Neurology, Faculty of Medicine, Masaryk University and University Hospital Brno, Brno, Czech Republic
[e] First Department of Neurology, Faculty of Medicine, Masaryk University and University Hospital of St. Anne, Brno, Czech Republic
[f] Department of Neurology, School of Medicine, University of Minnesota, Minneapolis, MN, USA
[g] Central European Institute of Technology (CEITEC), Masaryk University, Neuroscience Centre, Brno, Czech Republic

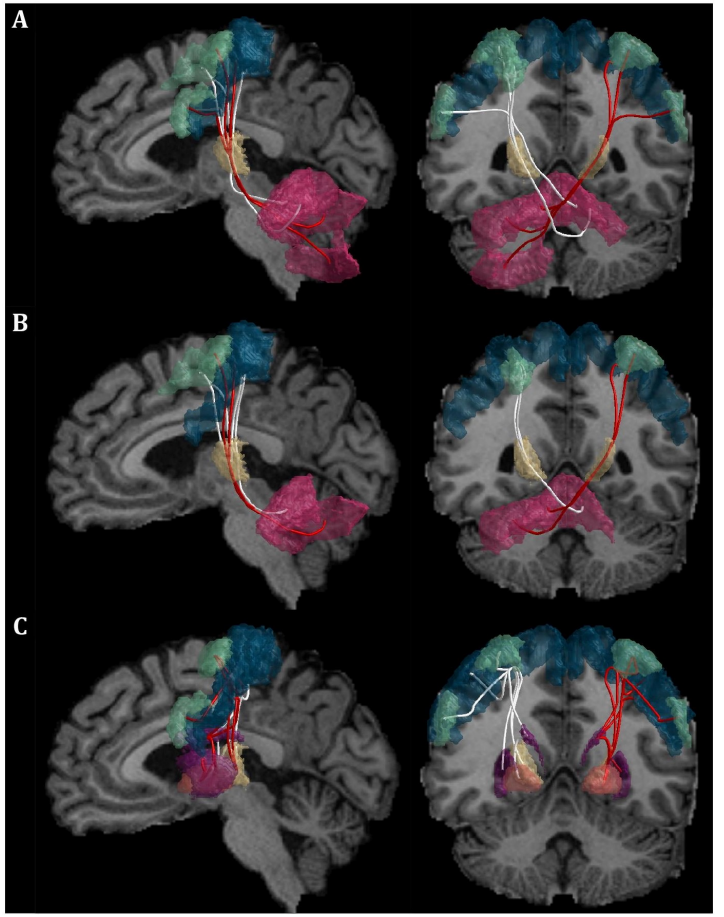
ARTICLE INFO

Keywords:
Tremor
Probabilistic tractography
Structural connectome
Parkinson's disease
Essential tremor

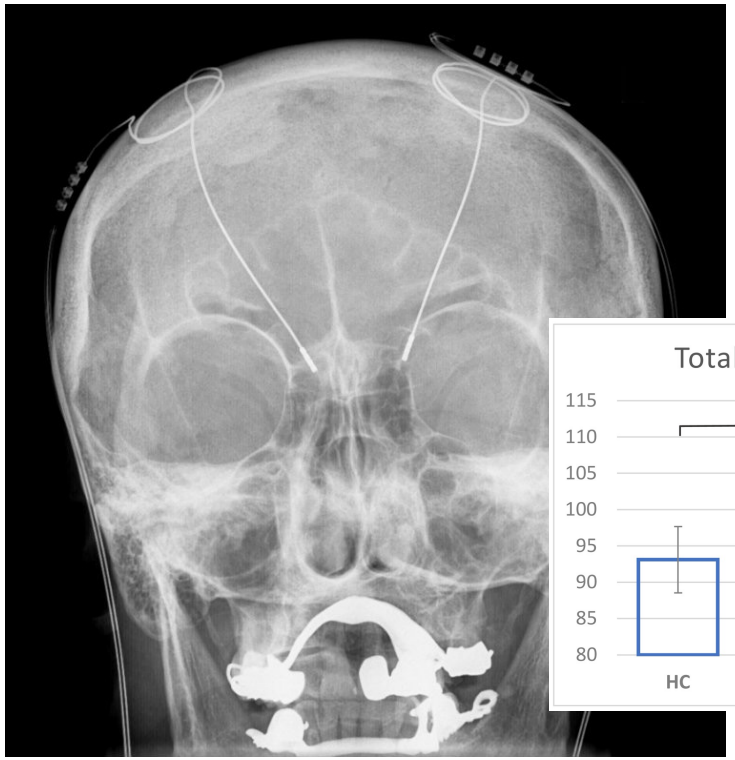
ABSTRACT

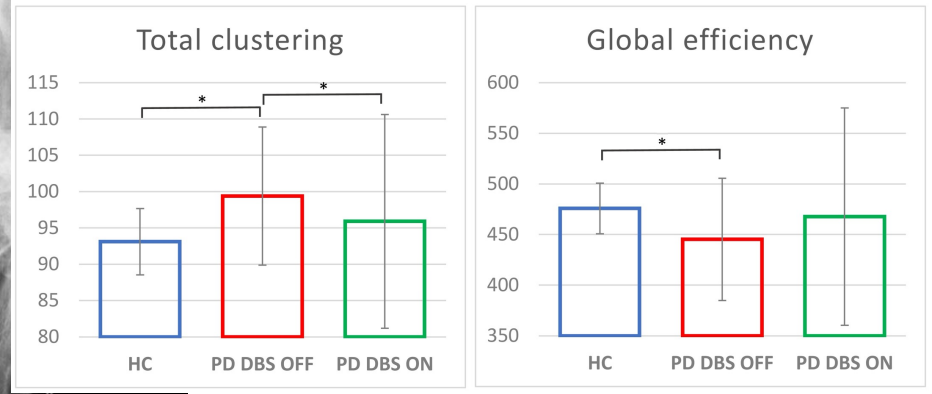
Introduction: Despite substantial clinical and pathophysiological differences, the characteristics of tremor in Parkinson's disease (PD) and essential tremor (ET) patients bear certain similarities. The presented study delineates tremor-related structural networks in these two disorders.

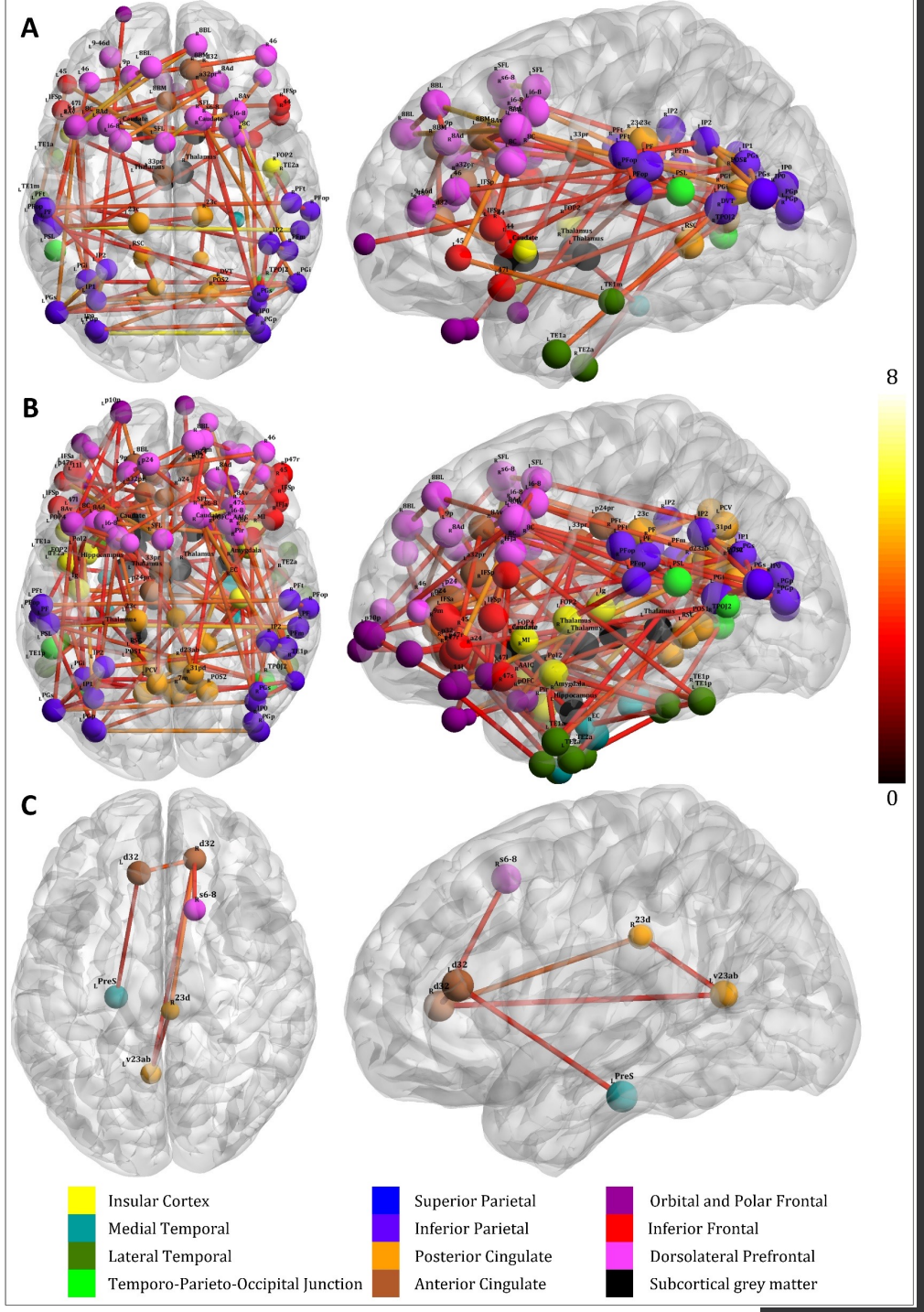
Methods: 42 non-advanced PD patients (18 tremor-dominant, 24 without substantial tremor), 17 ET, and 45 healthy controls underwent high-angular resolution diffusion-weighted imaging acquisition to reconstruct their structural motor connectomes as a proxy of the anatomical interconnections between motor network regions, implementing state-of-the-art globally optimised probabilistic tractography.



Utilisation in real studies
Functional connectome of DBS effect







SUMMARY

MRI connectomics

Major brain functions are network-based, not focal

“Soft-science” problem

Still distinguishing between macro / meso / micro-connectome

Further literature…

NeuroImage 80 (2013) 105–124

Contents lists a

journal homepage:

The minimal preprocessing pipelines

Matthew F. Glasser [a,*], Stamatios N. Sotiropoul
Bruce Fischl [d,e], Jesper L. Andersson [b], Junqian
Jonathan R. Polimeni [d], David C. Van Essen [a], M

[a] Department of Anatomy and Neurobiology, Washington University Medical Sch
[b] Centre for Functional Magnetic Resonance Imaging of the Brain (FMRIB), Unive
[c] Mallinckrodt Institute of Radiology, Washington University Medical School, USA
[d] Athinoula A Martinos Center for Biomedical Imaging, Department of Radiology,
[e] Computer Science and AI Lab, Mass. Institute of Technology, Cambridge, MA, US
[f] Center for Magnetic Resonance Research, University of Minnesota Medical Scho
[g] Translational and Molecular Imaging Institute, Icahn School of Medicine at Mou

ARTICLE INFO

Article history:
Accepted 30 April 2013
Available online 11 May 2013

Keywords:
Human Connectome Project
Image analysis pipeline
Surface-based analysis
CIFTI
Grayordinates
Multi-modal data integration

ABSTRACT

The Human Connec
imaging (MRI) moc
of subjects. The MRI
scanners and often
pipelines for structu
level tasks, includin
ment to standard sp
the HCP. The final
grayordinate spatial
ses while reducing t
we provide the min
ditional advice for ir
Finally, we discuss s

Introduction and rationale

The Washington University–University of Minnesota H
Connectome Project Consortium (WU–Minn HCP) (D. Van Esser
2012) is charged with bringing data from the major MRI neuroir
modalities, structural, functional, and diffusion, together into a co
framework to enable cross-subject comparisons and multi-
analysis of brain architecture, connectivity, and function. Speci
the imaging modalities include T1-weighted (T1w) and T2-we
(T2w) structural scans, resting-state and task-based functiona
scans, and diffusion-weighted MRI scans. Additionally, the HCP i
mitted to making these complex datasets publicly available and

NeuroImage 80 (2013) 144–168

Contents lists available at SciVerse ScienceDirect

NeuroImag

journal homepage: www.elsevier

Resting-state fMRI in the Human Connectome I

Stephen M. Smith [a,*], Christian F. Beckmann [c], Jesper Anderss
Gwenaëlle Douaud [a], Eugene Duff [a], David A. Feinberg [d], Lud
Michael Kelly [a], Timothy Laumann [f], Karla L. Miller [a], Steen M
Gholamreza Salimi-Khorshidi [a], Abraham Z. Snyder [f], An T. V
Essa Yacoub [b], Kamil Uğurbil [b], David C. Van Essen [f], Matthew

[a] FMRIB (Oxford Centre for Functional MRI of the Brain), Oxford University, Oxford, UK
[b] Center for Magnetic Resonance Research, University of Minnesota Medical School, Minneapolis, MN, U
[c] Donders Institute for Brain, Cognition and Behaviour, Radboud University, Nijmegen, The Netherlands
University of Twente, Enschede, The Netherlands
[d] Helen Wills Institute for Neuroscience, University of California, Berkeley, CA, USA
[e] Department of Electronics, Information and Bioengineering, Politecnico di Milano, Milan, Italy & MR L
[f] Washington University School of Medicine, Washington University, St. Louis, MO, USA
[g] OHBA (Oxford Centre for Human Brain Activity), Oxford University, Oxford, UK
[h] Translational and Molecular Imaging Institute, Icahn School of Medicine at Mount Sinai, New York, NY

ARTICLE INFO

Article history:
Accepted 6 May 2013
Available online 20 May 2013

ABSTRACT

Resting-state functional magnetic reson
brain by acquiring fMRI data while subje
functionally related brain regions spont
being acquired for the Human Connecto
a detailed in vivo mapping of functional
to make these datasets freely available
total of 1 h of whole-brain rfMRI data at
of 0.7 s, capitalizing on recent developm
of the cohort at higher field strength an
decisions taken regarding the rfMRI da
initial results showing data quality and

Introduction

The term "connectome" (Sporns et al., 2005) refers to the mapping of connectivity throughout the brain using such imaging modalities as resting-state functional magnetic resonance imaging (rfMRI) and diffusion MRI. rfMRI is used to study connectivity in the brain by acquiring fMRI data from a subject lying "at rest" in the scanner, and utilising the fact that the spontaneous timeseries from functionally related brain regions are correlated (Biswal et al., 1995; De Luca et al., 2005; Fox and Raichle, 2007; Fox et al., 2005; Greicius et al.,

of cor
allow
althou
(and, i
dent c
al., 200
estima
level o
ever, r
indirec

ARTICLE

A multi-modal parcellatic cerebral cortex

Matthew F. Glasser[1], Timothy S. Coalson[1*], Emma C. Robinson[2,3*], Carl D. Hacke
Kamil Ugurbil[5], Jesper Andersson[2], Christian F. Beckmann[6,7], Mark Jenkinson[2], S

Understanding the amazingly complex human cerebral cortex requires a ma
known as cortical areas. Making an accurate areal map has been a century-
modal magnetic resonance images from the Human Connectome Projec
neuroanatomical approach, we delineated 180 areas per hemisphere bounde
function, connectivity, and/or topography in a precisely aligned group
characterized 97 new areas and 83 areas previously reported using post-mo
specific approaches. To enable automated delineation and identification of t
studies, we trained a machine-learning classifier to recognize the multi-m
classifier detected the presence of 96.6% of the cortical areas in new subj
could correctly locate areas in individuals with atypical parcellations. Th
will enable substantially improved neuroanatomical precision for studies o
of human cerebral cortex and its variation across individuals and in develop

Neuroscientists have long sought to subdivide the human brain into a mosaic of anatomically and functionally distinct, spatially contiguous areas (cortical areas and subcortical nuclei), as a prerequisite for understanding how the brain works. Areas differ from their neighbours in microstructural architecture, functional specialization, connectivity with other areas, and/or orderly intra-area topographic organization (for example, the map of visual space in visual cortical areas)[1–3]. Accurate parcellation provides a map of where we are in the brain, enabling efficient comparison of results across studies and communication among investigators; as a foundation for illuminating the functional and structural organization of the brain; and as a means to reduce data complexity while improving statistical sensitivity and power for many neuroimaging studies.

The human cerebral cortex has been estimated to contain anywhere from ~50 (ref. 1) to ~200 (refs 3, 4) areas per hemisphere. However, attaining a consensus whole-cortex parcellation has been difficult because of practical and technical challenges that we address here.

Most previous parcellations were based on only one neurobiological property (such as architecture, function, connectivity or topography), and many cover only part of the cortex. Combining multiple properties provides complementary as well as confirmatory information, as different properties distinguish different sets of areal boundaries, and more confidence can be placed in boundaries that are consistent

derived from T1
images[5,9,10]. Cort
(tfMRI) contras
(rfMRI) revealed
topographic orga

Previous par
algorithmic ap
neuroanatomica
areal borders, dc
consulting prior
the initial parcell
semi-automate
mortem architec
We used an algo
in two or more
neuroanatomist
documenting a
extant neuroana
algorithmic app
delineate and ic
on multi-modal
replicated in new

Prior parcella
or group average

NeuroImage 183 (2018) 972–984

Contents lists available at ScienceDirect

NeuroImage

journal homepage: www.elsevier.com/locate/neuroimage

Extending the Human Connectome Project across ages: Imaging protocols for the Lifespan Development and Aging projects

Michael P. Harms [a,*,1], Leah H. Somerville [f,g,1], Beau M. Ances [b], Jesper Andersson [h], Deanna M. Barch [a,c,e], Matteo Bastiani [h], Susan Y. Bookheimer [k], Timothy B. Brown [c], Randy L. Buckner [f,g,m,n], Gregory C. Burgess [a], Timothy S. Coalson [d], Michael A. Chappell [h,i], Mirella Dapretto [k], Gwenaëlle Douaud [h], Bruce Fischl [m,o], Matthew F. Glasser [c,d,p], Douglas N. Greve [m], Cynthia Hodge [a], Keith W. Jamison [q], Saad Jbabdi [h], Sridhar Kandala [a], Xiufeng Li [r], Ross W. Mair [g,m], Silvia Mangia [r], Daniel Marcus [c], Daniele Mascali [t], Steen Moeller [r], Thomas E. Nichols [h,j,u], Emma C. Robinson [v], David H. Salat [m], Stephen M. Smith [h], Stamatios N. Sotiropoulos [h,w], Melissa Terpstra [r], Kathleen M. Thomas [s], M. Dylan Tisdall [x], Kamil Ugurbil [r], Andre van der Kouwe [m,n], Roger P. Woods [k,l], Lilla Zöllei [m], David C. Van Essen [d], Essa Yacoub [r]

[a] Department of Psychiatry, Washington University School of Medicine, St. Louis, MO, USA
[b] Department of Neurology, Washington University School of Medicine, St. Louis, MO, USA
[c] Department of Radiology, Washington University School of Medicine, St. Louis, MO, USA
[d] Department of Neuroscience, Washington University School of Medicine, St. Louis, MO, USA
[e] Department of Psychological and Brain Sciences, Washington University in St. Louis, St. Louis, MO, USA
[f] Department of Psychology, Harvard University, Cambridge, MA, USA
[g] Center for Brain Science, Harvard University, Cambridge, MA, USA
[h] Wellcome Centre for Integrative Neuroimaging, Oxford Centre for Functional Magnetic Resonance Imaging of the Brain (FMRIB), Nuffield Department of Clinical Neurosciences, University of Oxford, Oxford, UK
[i] Institute of Biomedical Engineering, Department of Engineering Science, University of Oxford, Oxford, UK
[j] Oxford Big Data Institute, Li Ka Shing Centre for Health Information and Discovery, Nuffield Department of Population Health, University of Oxford, Oxford, UK
[k] Department of Psychiatry and Biobehavioral Sciences, David Geffen School of Medicine at UCLA, University of California, Los Angeles, CA, USA
[l] Department of Neurology, David Geffen School of Medicine at UCLA, University of California, Los Angeles, CA, USA
[m] Athinoula A. Martinos Center for Biomedical Imaging, Department of Radiology, Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA
[n] Department of Psychiatry, Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA
[o] Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, Cambridge, MA, USA
[p] St. Luke's Hospital, St. Louis, MO, USA
[q] Department of Radiology, Weill Cornell Medical College, New York, NY, USA
[r] Center for Magnetic Resonance Research, University of Minnesota, Minneapolis, MN, USA
[s] Institute of Child Development, University of Minnesota, Minneapolis, MN, USA
[t] Centro Fermi - Museo Storico della Fisica e Centro Studi e Ricerche "Enrico Fermi", Rome, Italy
[u] Department of Statistics, University of Warwick, Coventry, UK
[v] Department of Biomedical Engineering, King's College London, London, UK
[w] Sir Peter Mansfield Imaging Centre, School of Medicine, University of Nottingham, Nottingham, UK
[x] Department of Radiology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA

ARTICLE INFO

ABSTRACT