

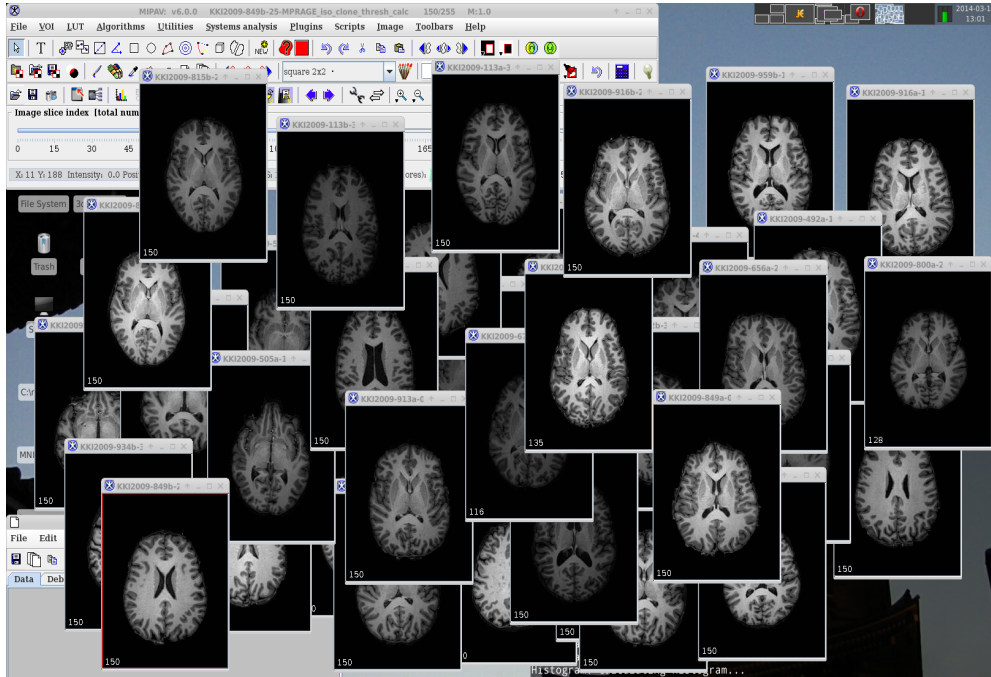
In-vivo analysis of brain anatomy at 7 Tesla

Pierre-Louis Bazin

Department of Neurophysics
and Department of Neurology

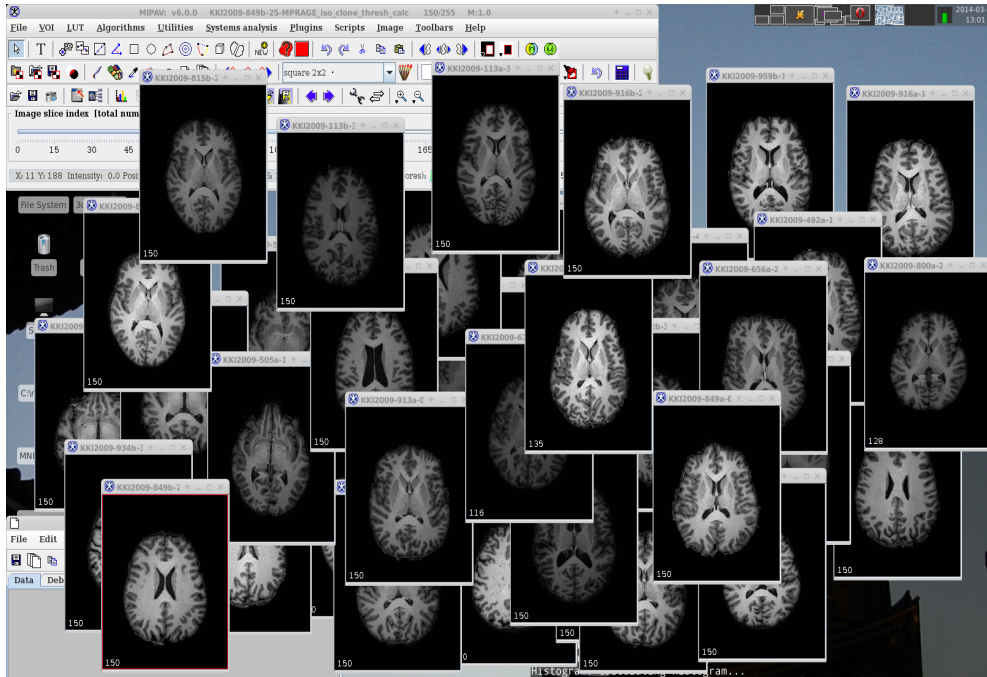
Max Planck Institute for Human Cognitive and Brain Sciences
Leipzig, Germany

Big Data in Neuroimaging



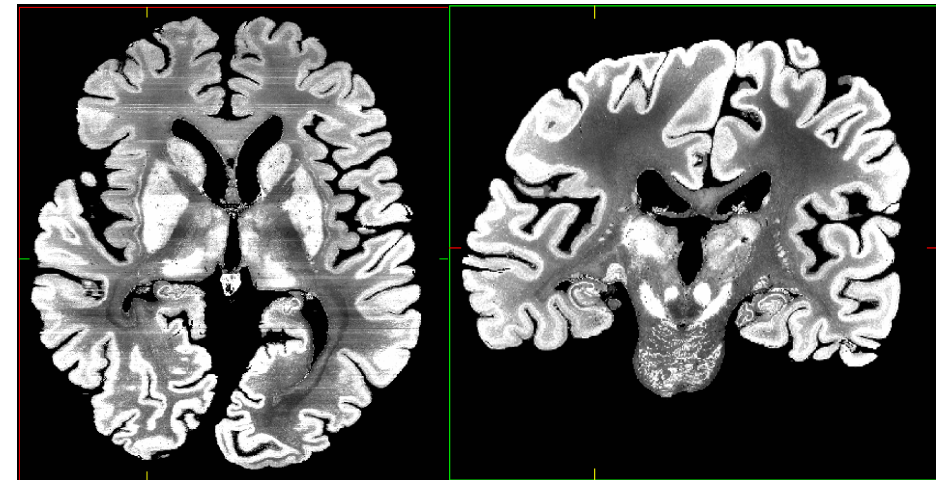
Large data sets

Big Data in Neuroimaging



Large data sets
Standard data

vs.

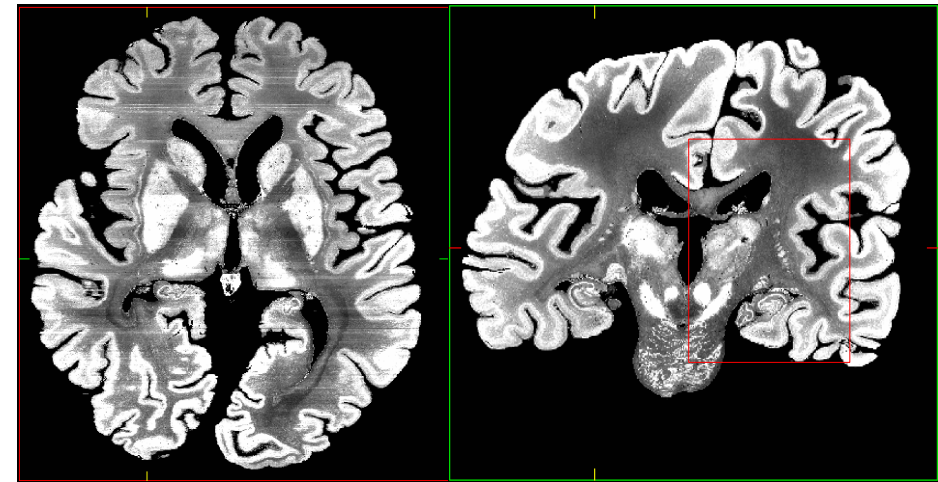
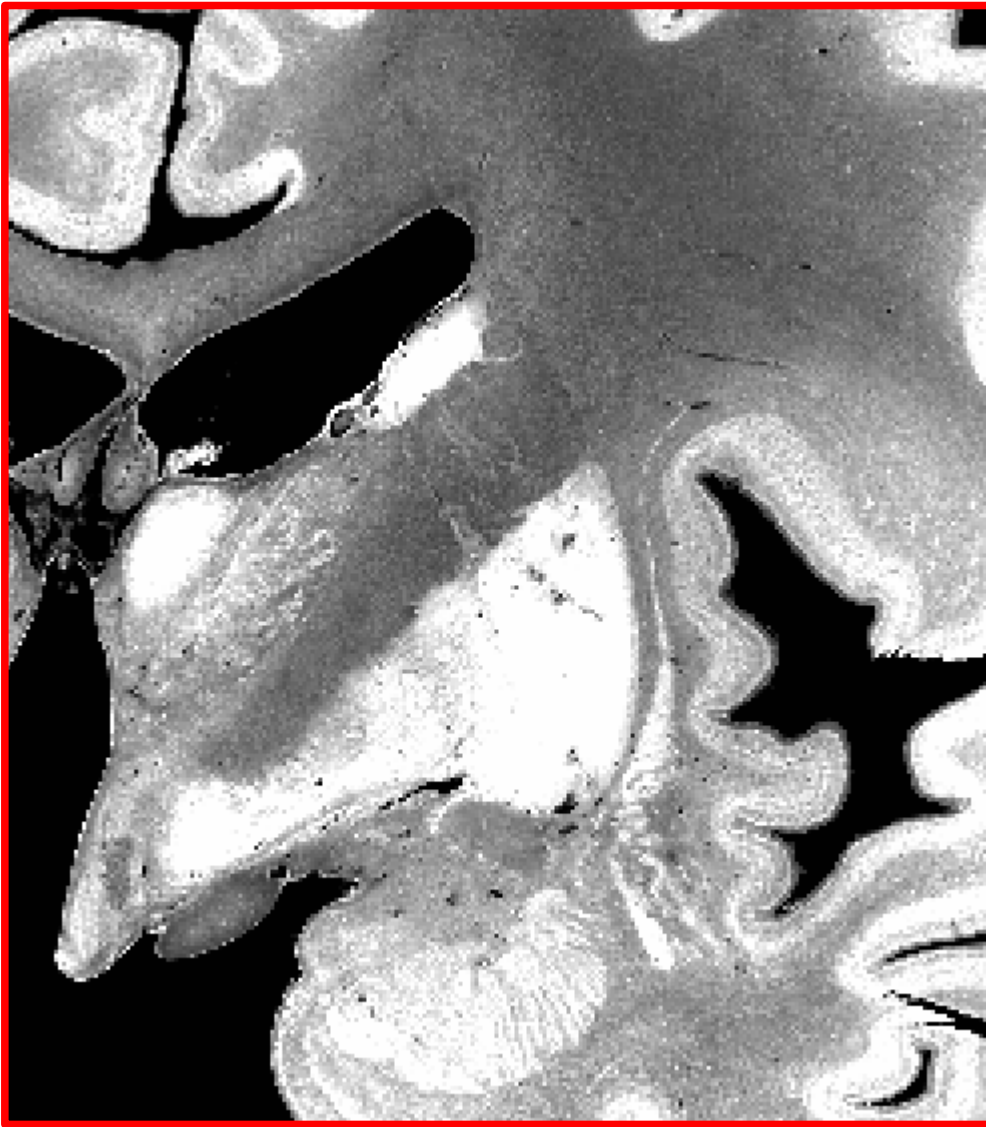


Large data

BigBrain: 3D cytoarchitecture
at 20 μ m isotropic resolution

[Amunts et al., Science 2013]

Big Data in Neuroimaging

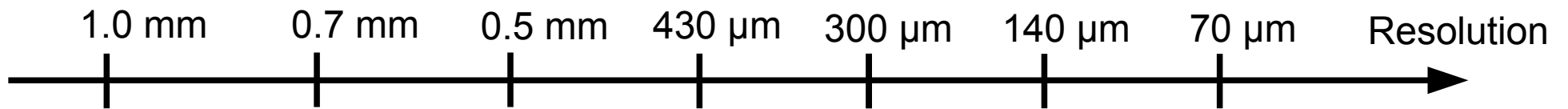
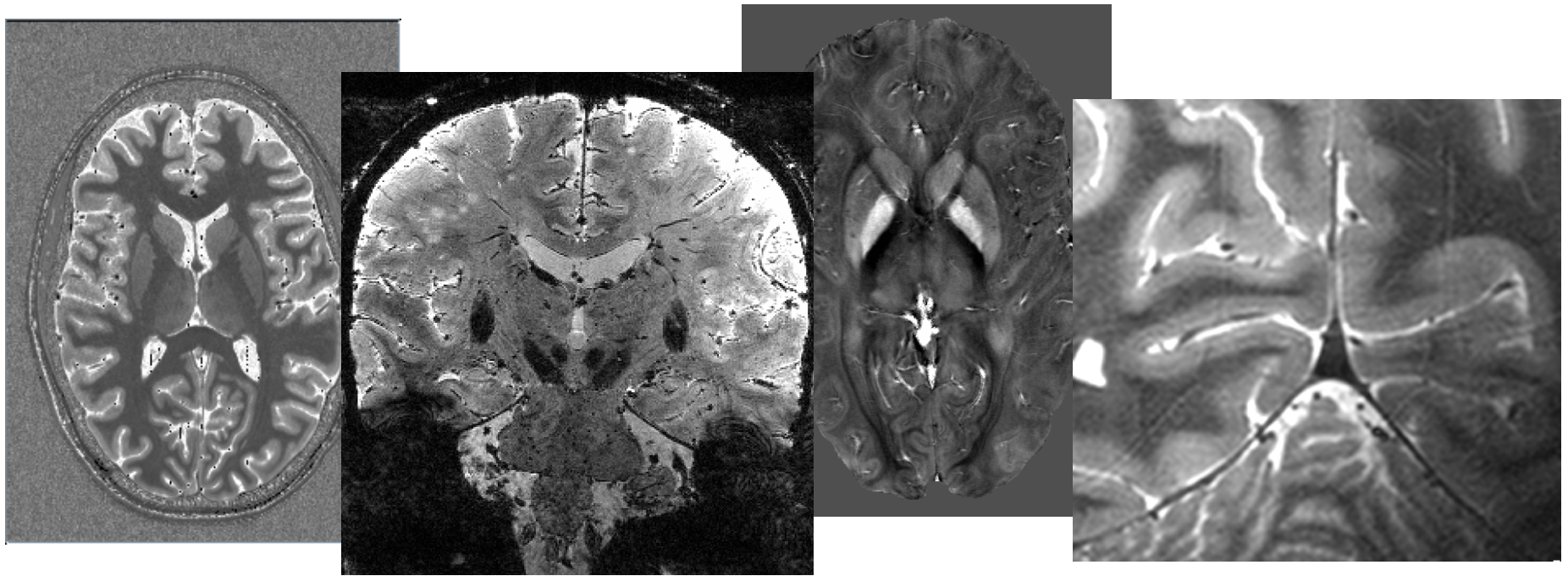


Large data

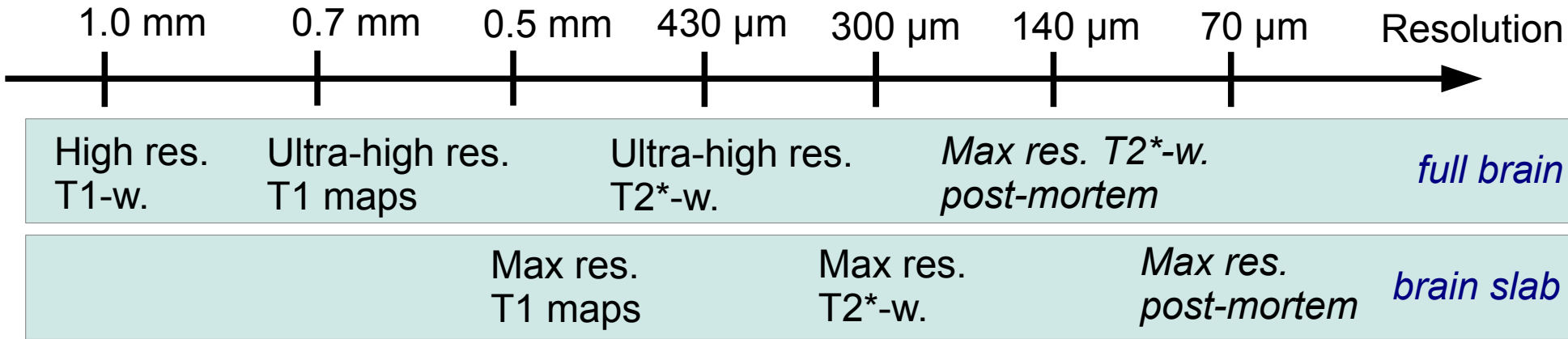
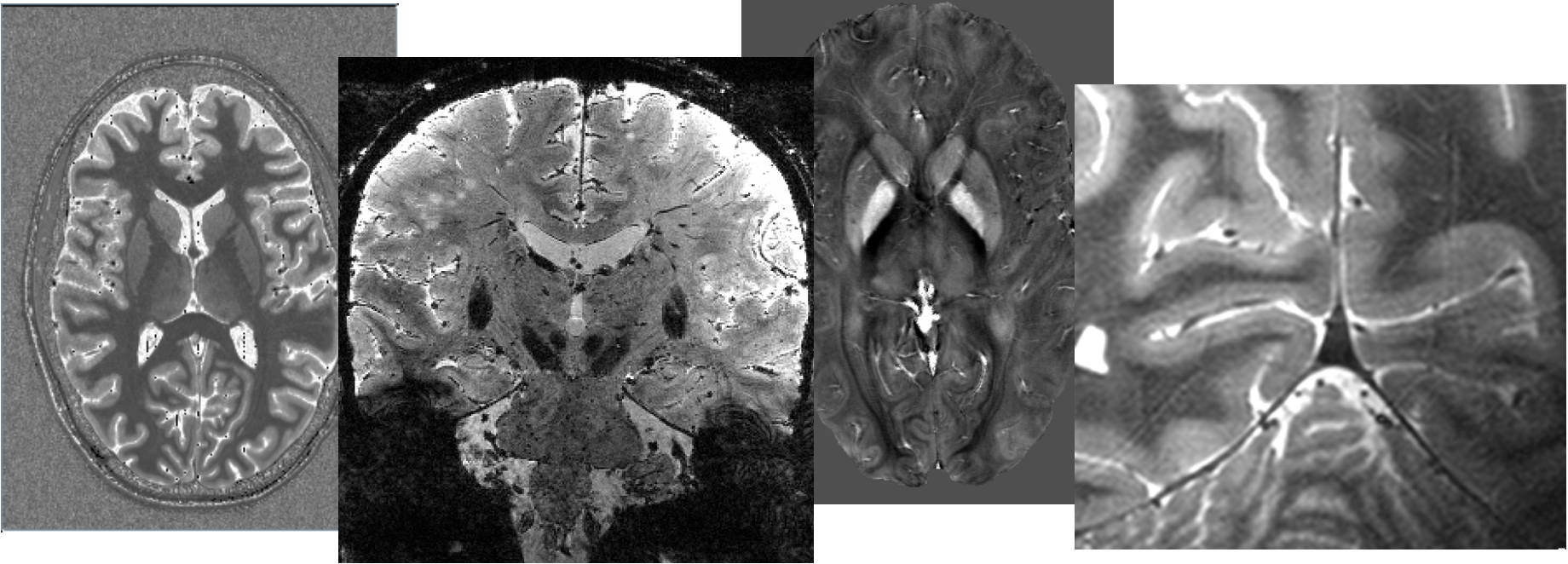
BigBrain: 3D cytoarchitecture
at 20 μ m isotropic resolution

[Amunts et al., Science 2013]

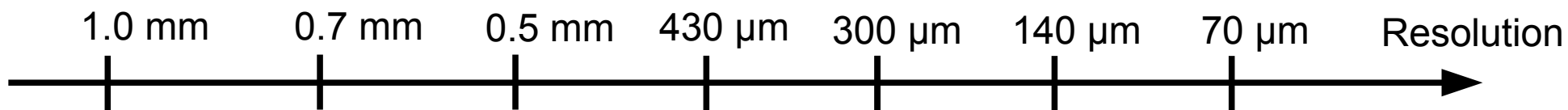
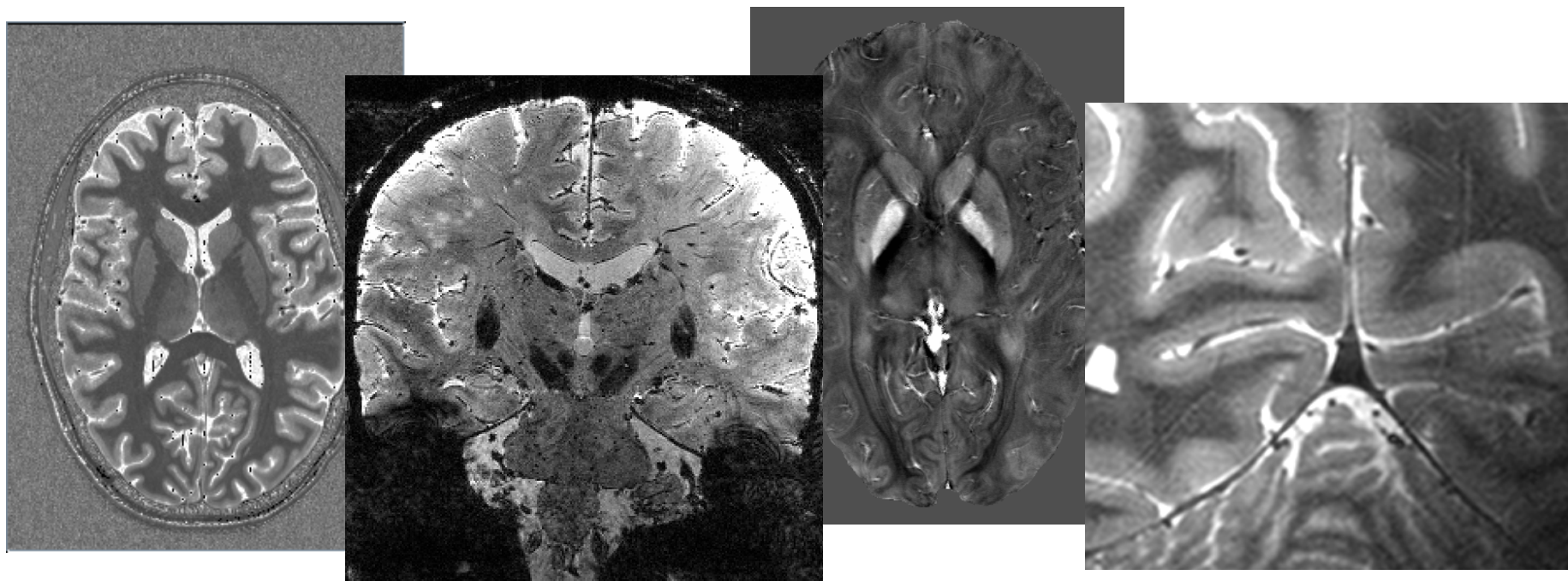
Current possibilities at 7 Tesla



Current possibilities at 7 Tesla

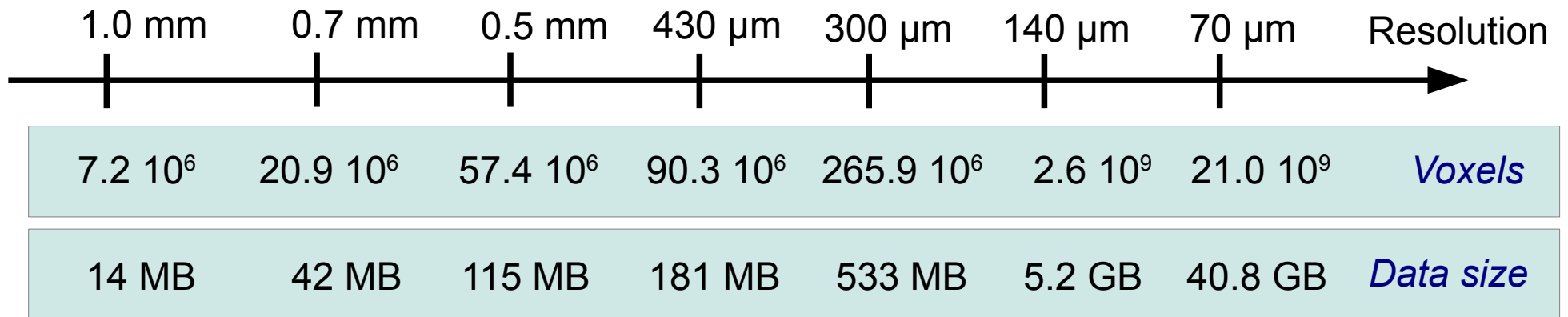
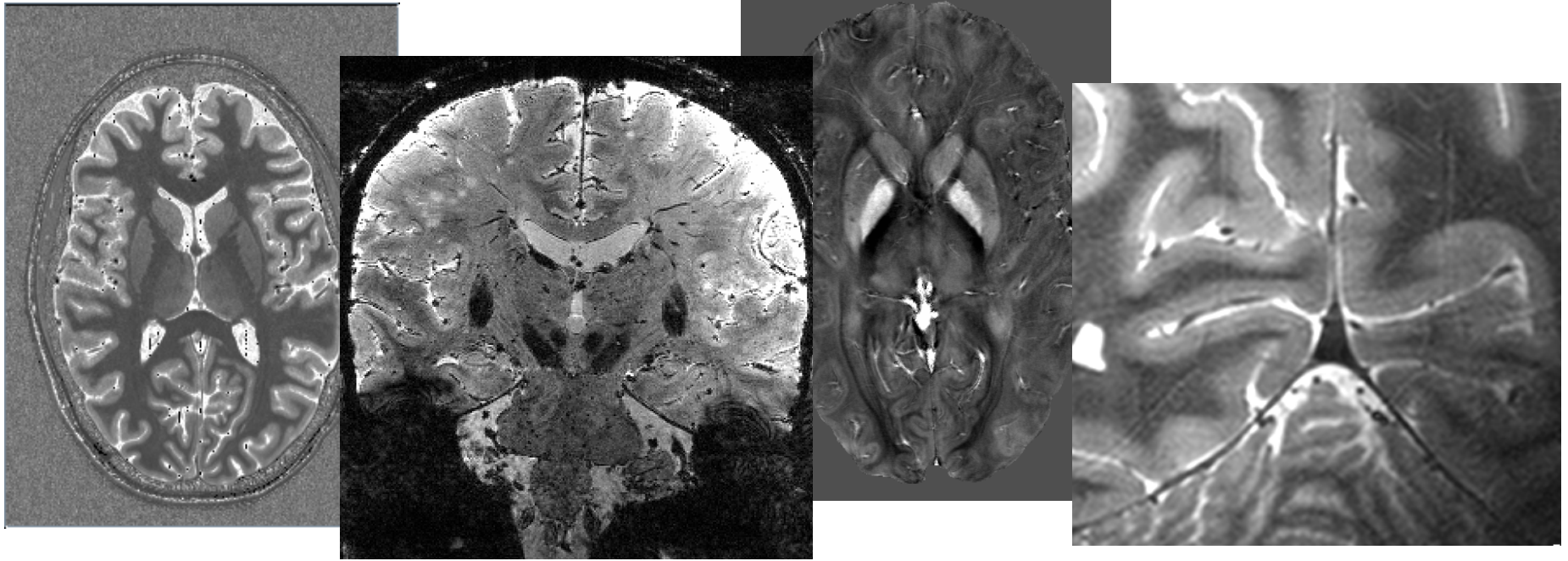


Visible anatomical features

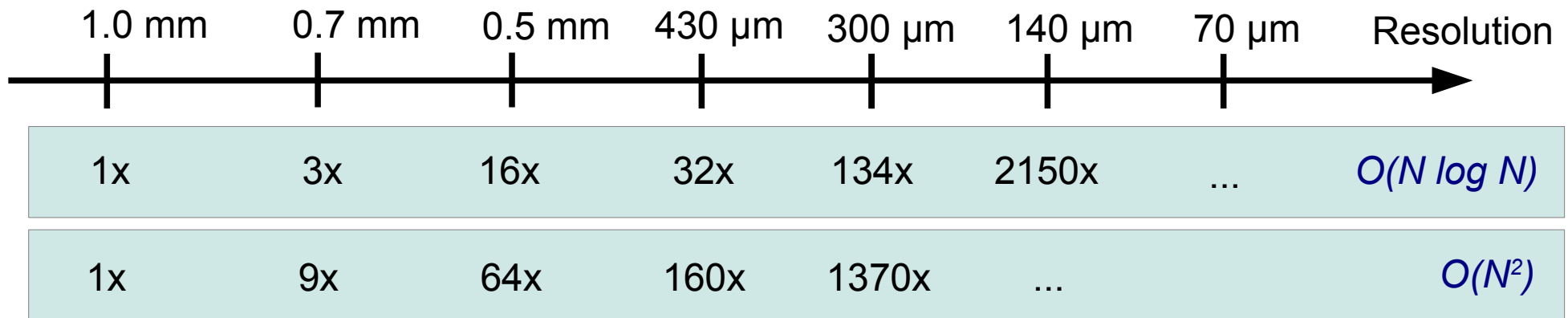
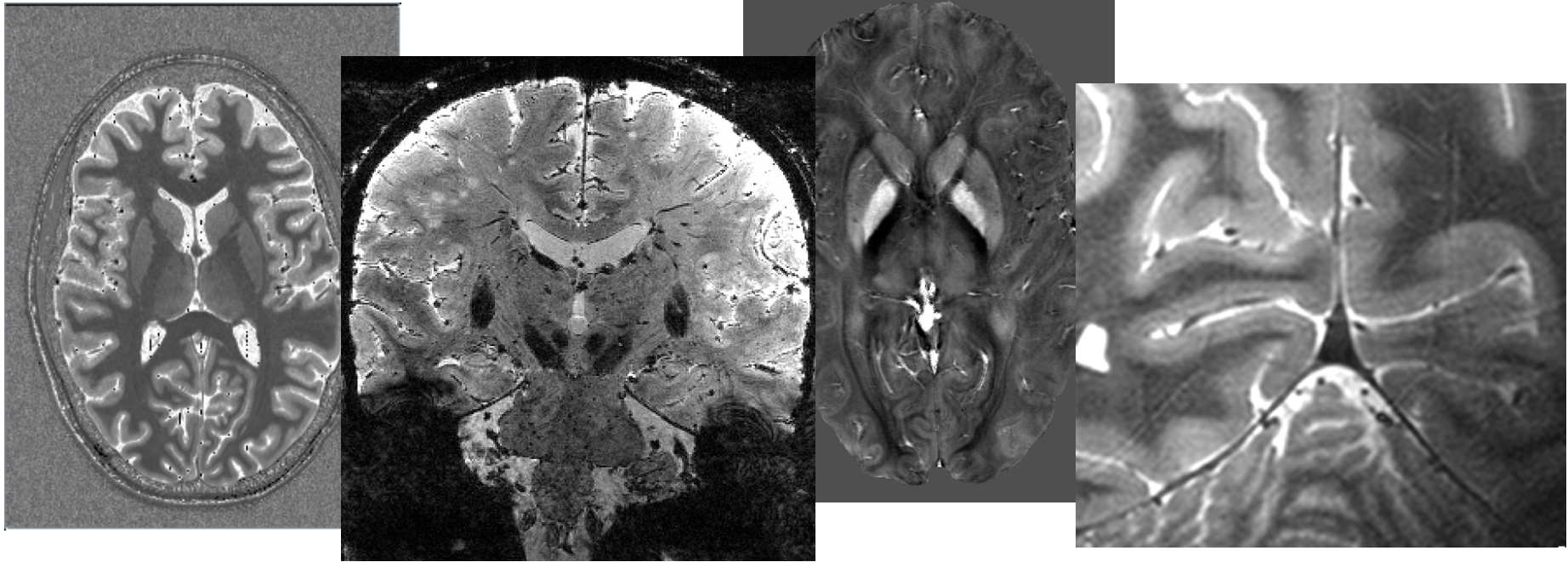


Myelin concentration	Bands of Baillarger	<i>anatomical features</i>
Cortical thickness	Multiple layers	
	Stria of Gennari	

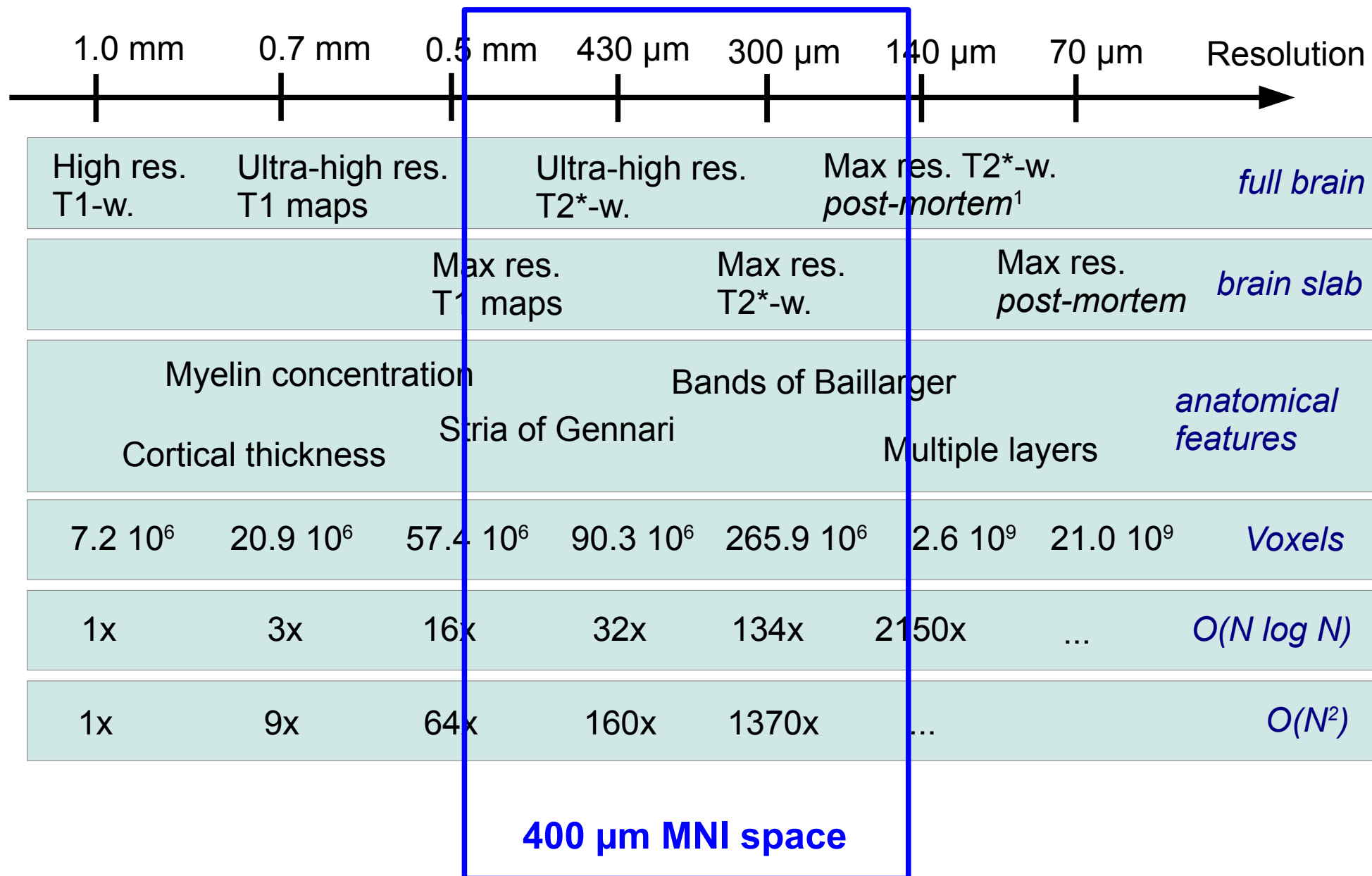
Data complexity



Algorithmic complexity



What resolution for analysis?



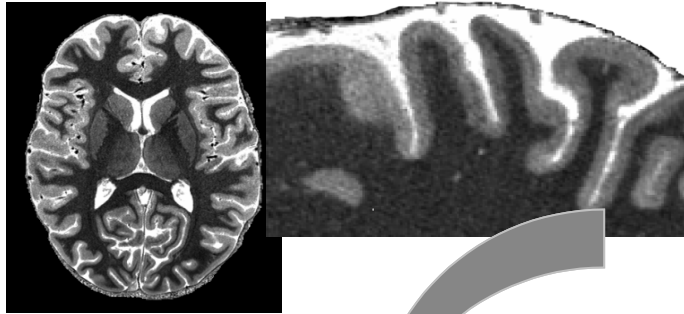
In-vivo analysis of cortical anatomy at 7 Tesla

1. High-resolution T1 mapping

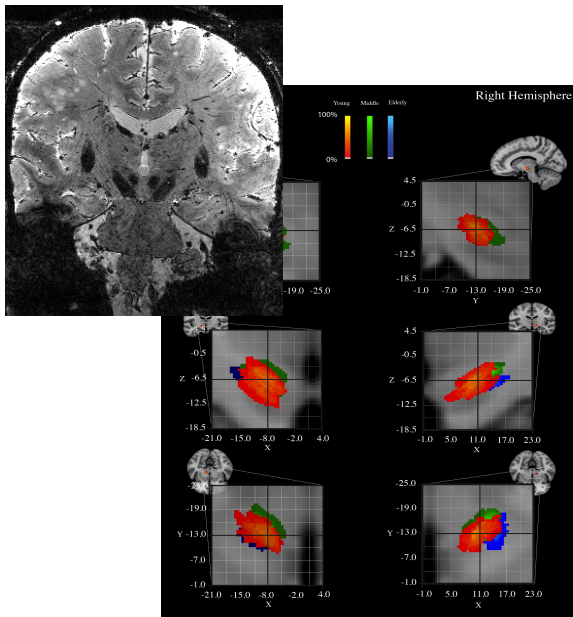


In-vivo analysis of cortical anatomy at 7 Tesla

1. High-resolution T1 mapping

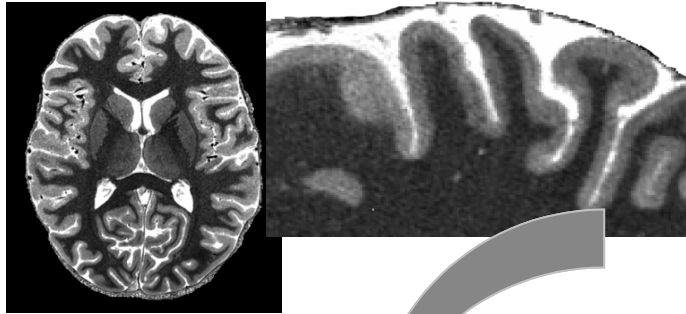


*Interlude 1:
Atlasing of the STh*

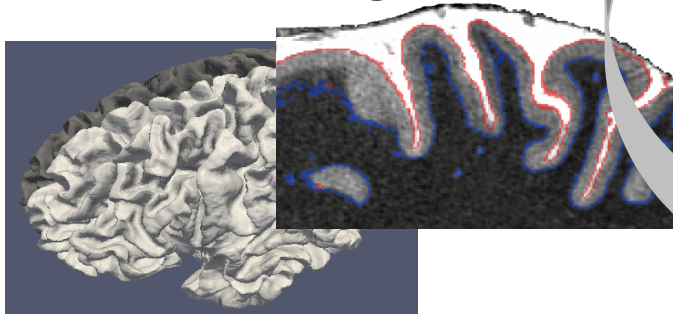


In-vivo analysis of cortical anatomy at 7 Tesla

1. High-resolution T1 mapping

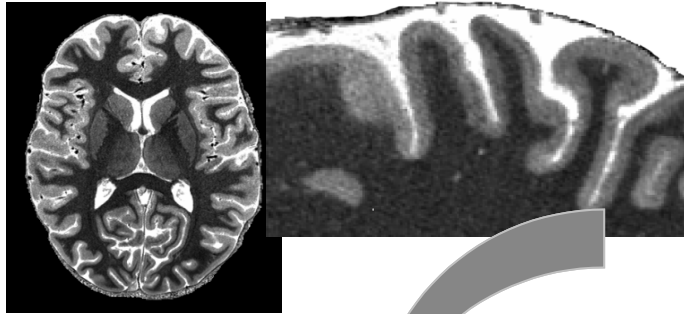


2. Cortical segmentation

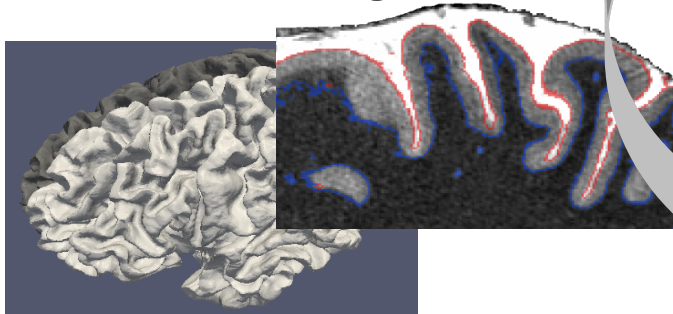


In-vivo analysis of cortical anatomy at 7 Tesla

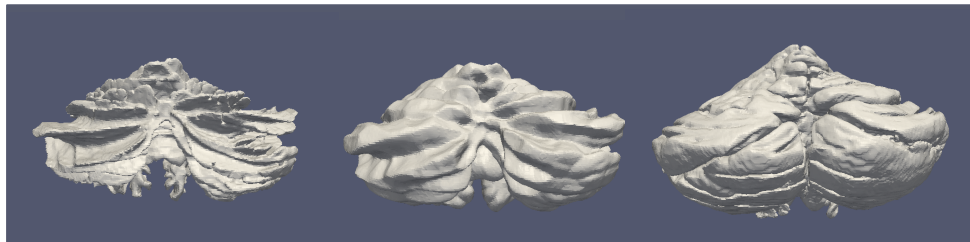
1. High-resolution T1 mapping



2. Cortical segmentation

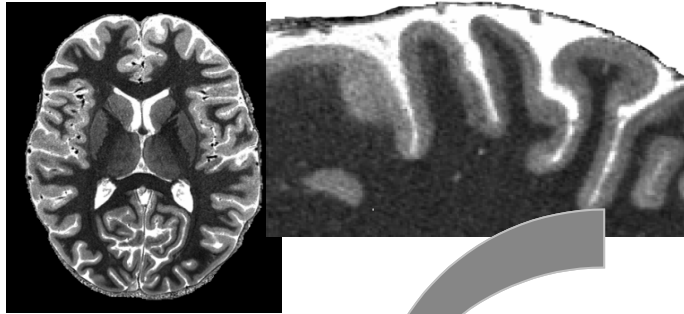


*Interlude 2:
Cerebellar cortical segmentation*

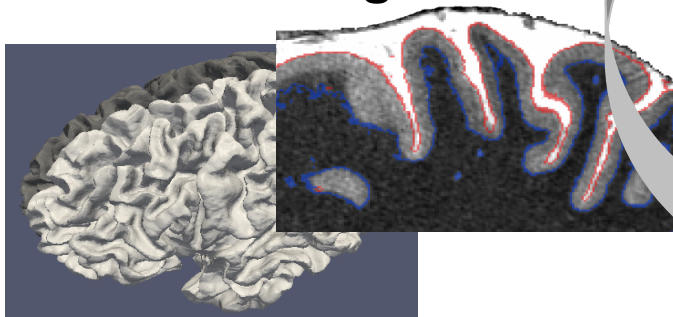


In-vivo analysis of cortical anatomy at 7 Tesla

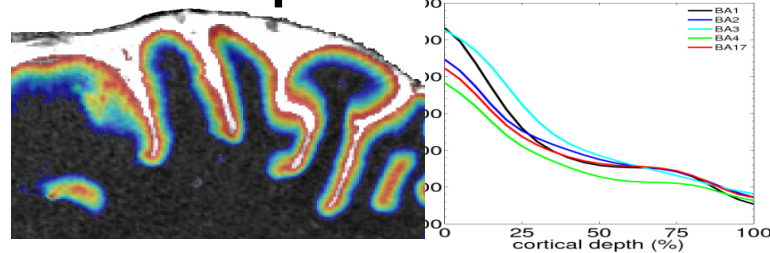
1. High-resolution T1 mapping



2. Cortical segmentation

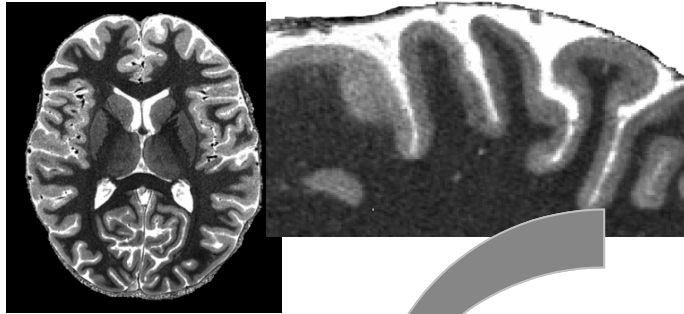


3. Laminae and profile estimation

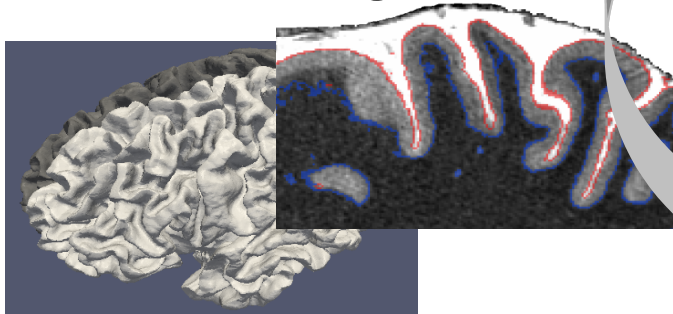


In-vivo analysis of cortical anatomy at 7 Tesla

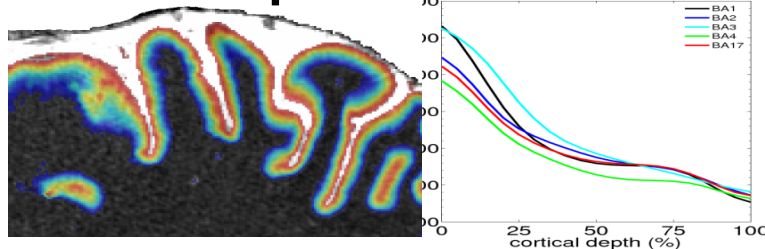
1. High-resolution T1 mapping



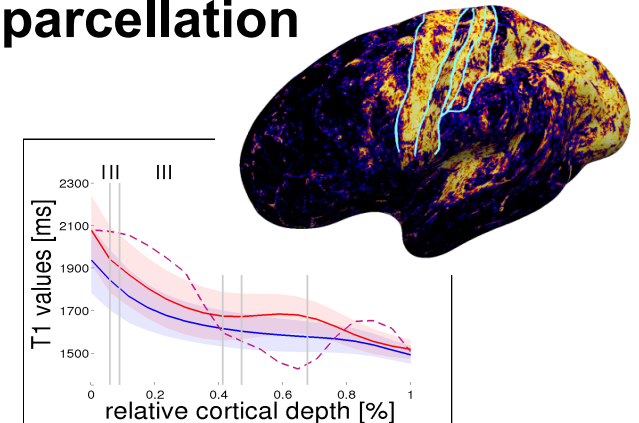
2. Cortical segmentation



3. Laminae and profile estimation

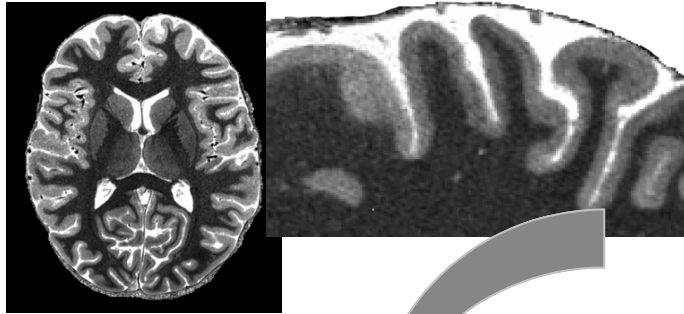


4. Cortical area modelling and parcellation

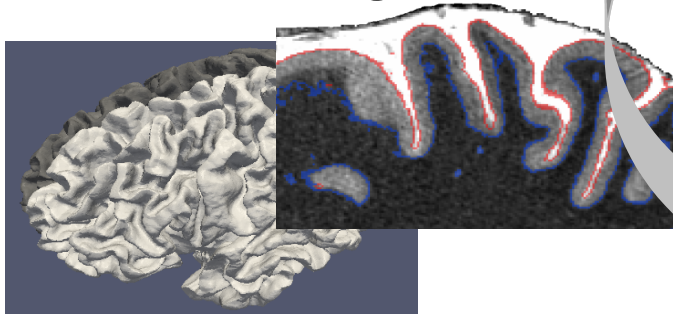


In-vivo analysis of cortical anatomy at 7 Tesla

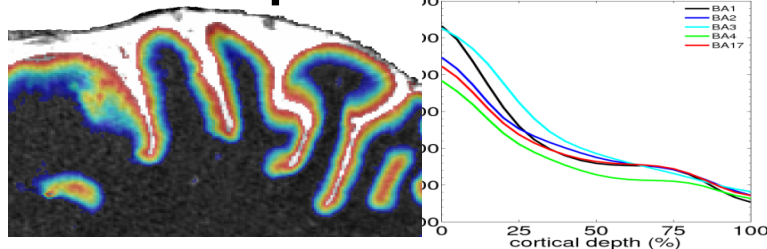
1. High-resolution T1 mapping



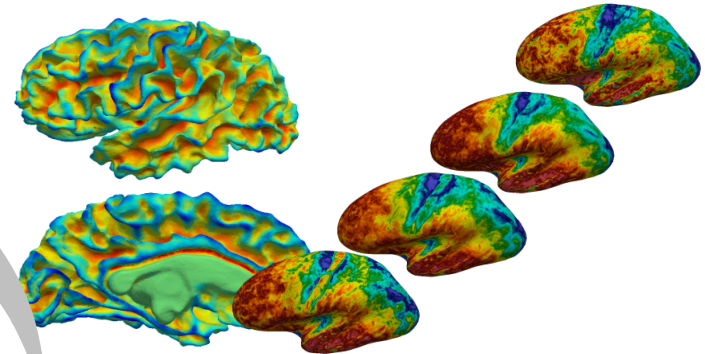
2. Cortical segmentation



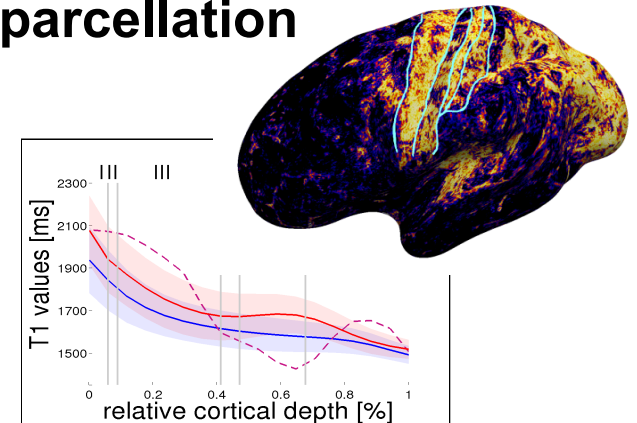
3. Laminae and profile estimation



5. Surface registration and group averaging

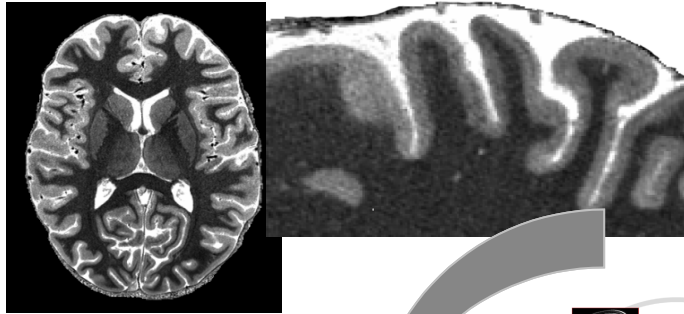


4. Cortical area modelling and parcellation

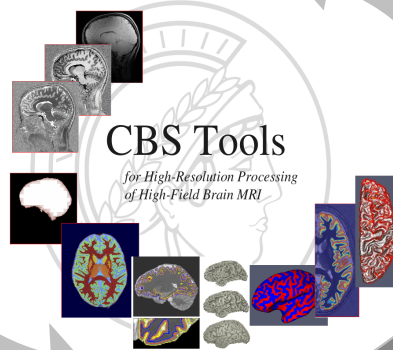
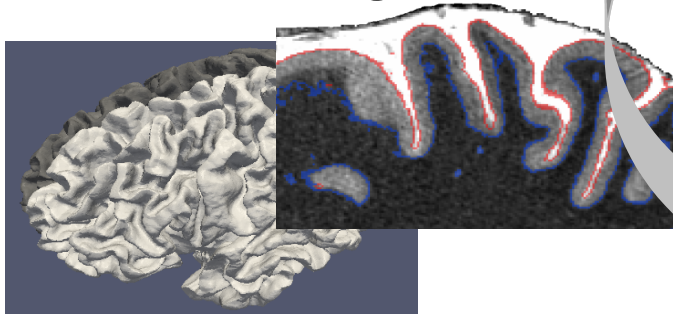


In-vivo analysis of cortical anatomy at 7 Tesla

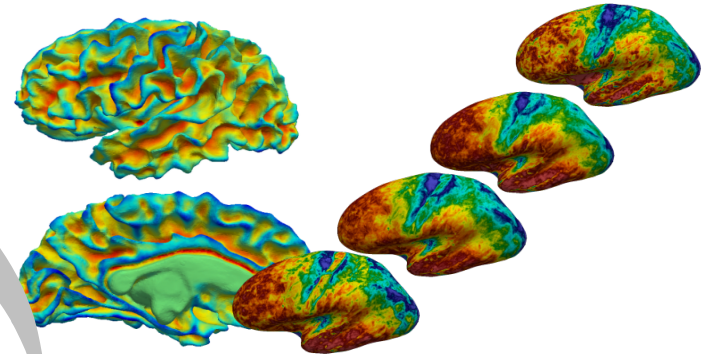
1. High-resolution T1 mapping



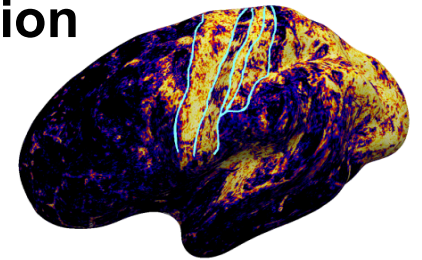
2. Cortical segmentation



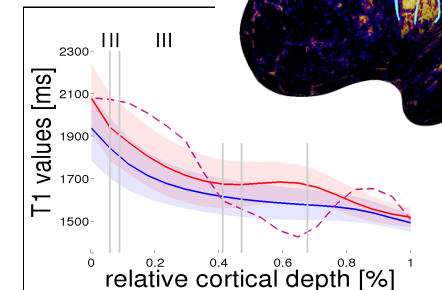
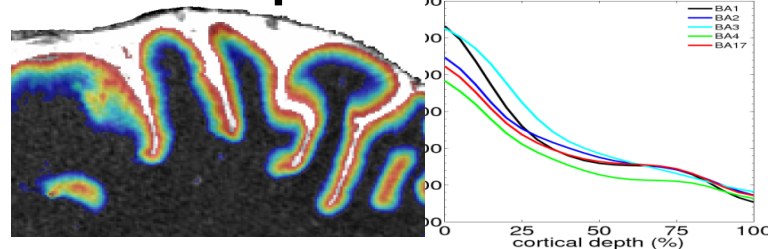
5. Surface registration and group averaging



4. Cortical area modelling and parcellation



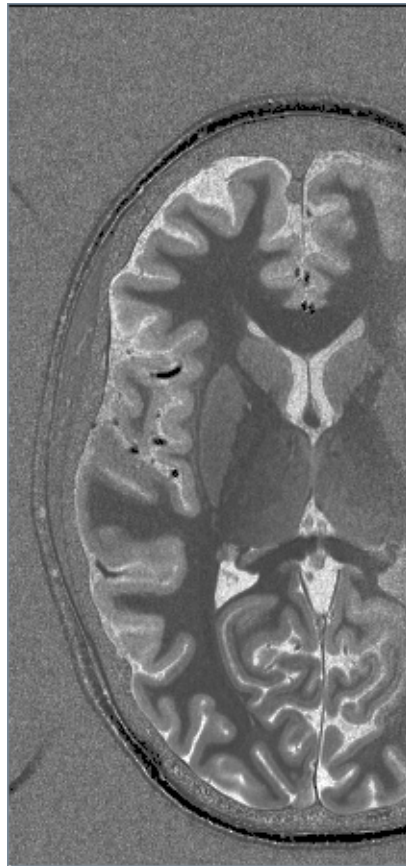
3. Laminae and profile estimation



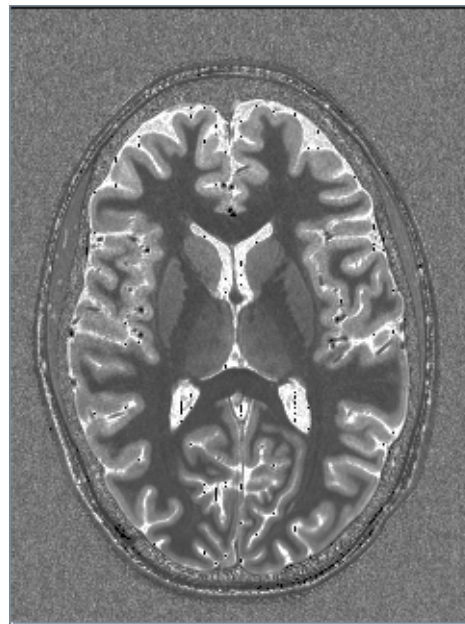
1. Ultra-high resolution T1 mapping at 0.5 mm

7T MP2RAGE (TR=5000 ms, T11=900 ms, T12=2750 ms):

- full brain at 0.7 mm isotropic resolution (with a GRAPPA acceleration factor of 2, 10:57 min)
- left and right hemisphere slabs at 0.5 mm isotropic resolution (no acceleration, 28:02 min)



0.5 mm slab



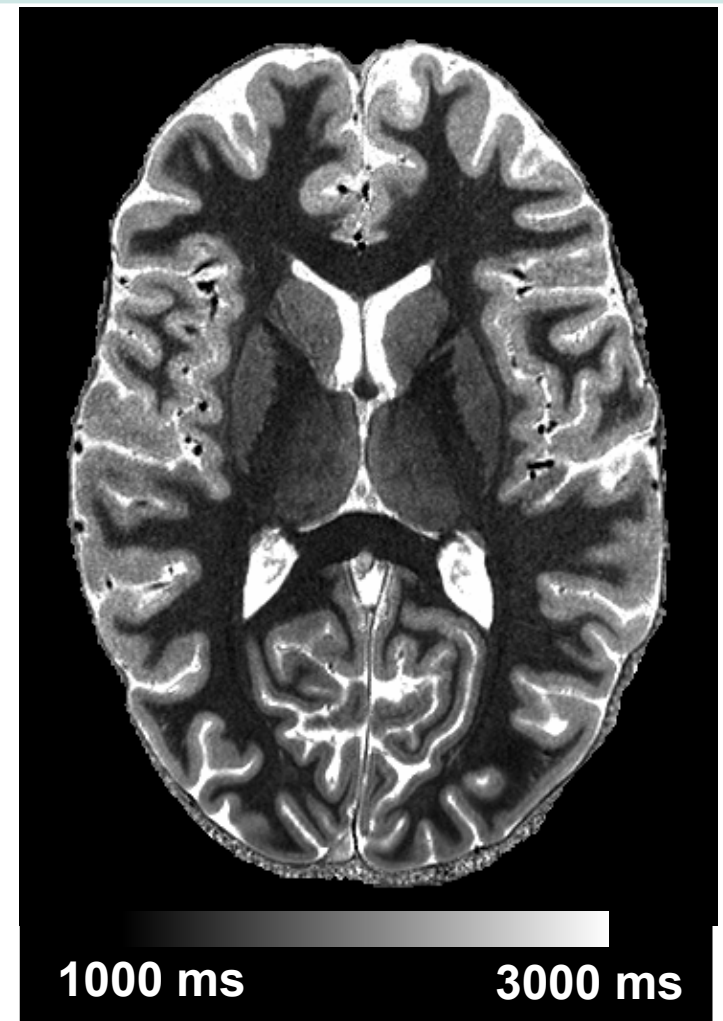
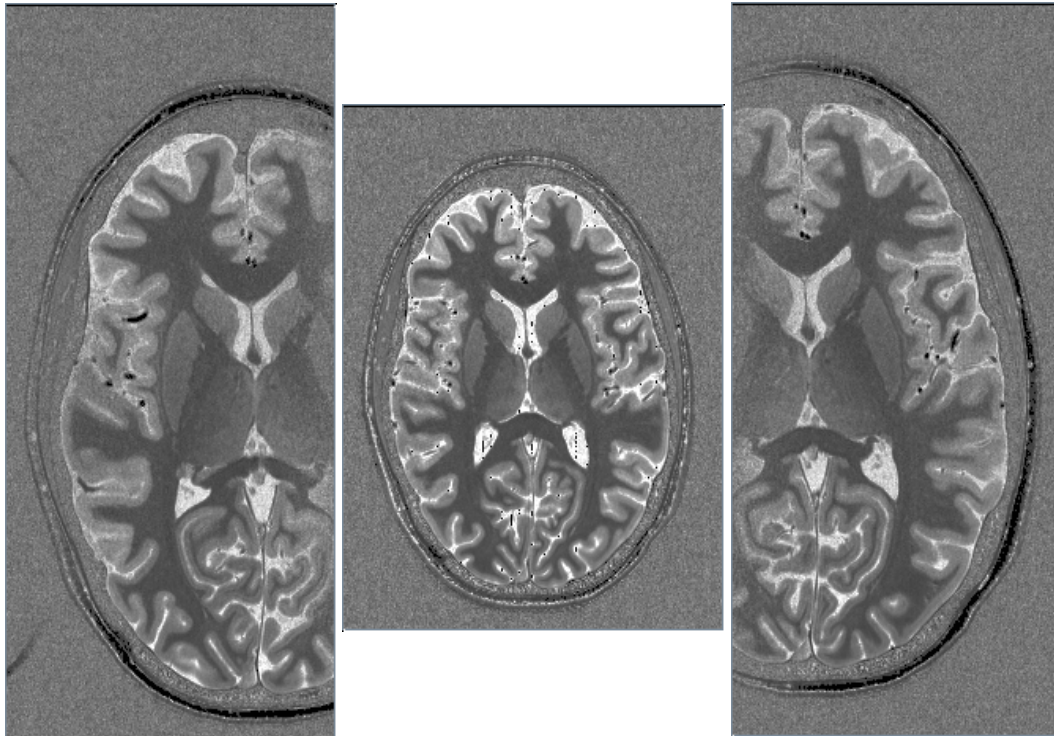
0.7 mm whole-brain



0.5 mm slab

[Marques et al., 2010]
[Hurley et al., 2010]

T1 slab fusion

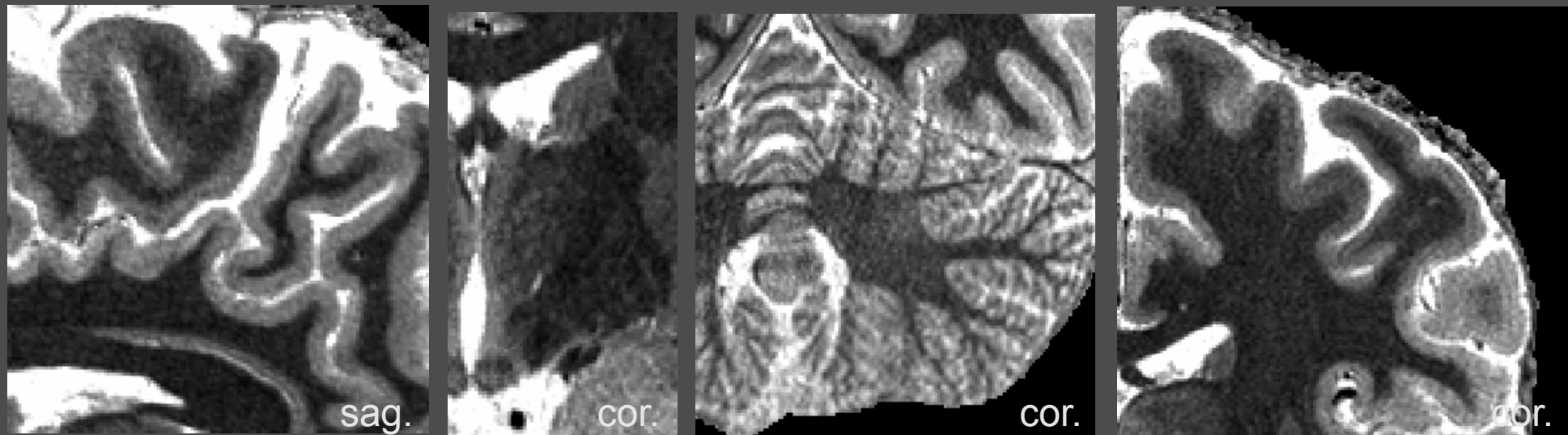


fused image
(interpolated to 0.4 mm)

Processing steps:

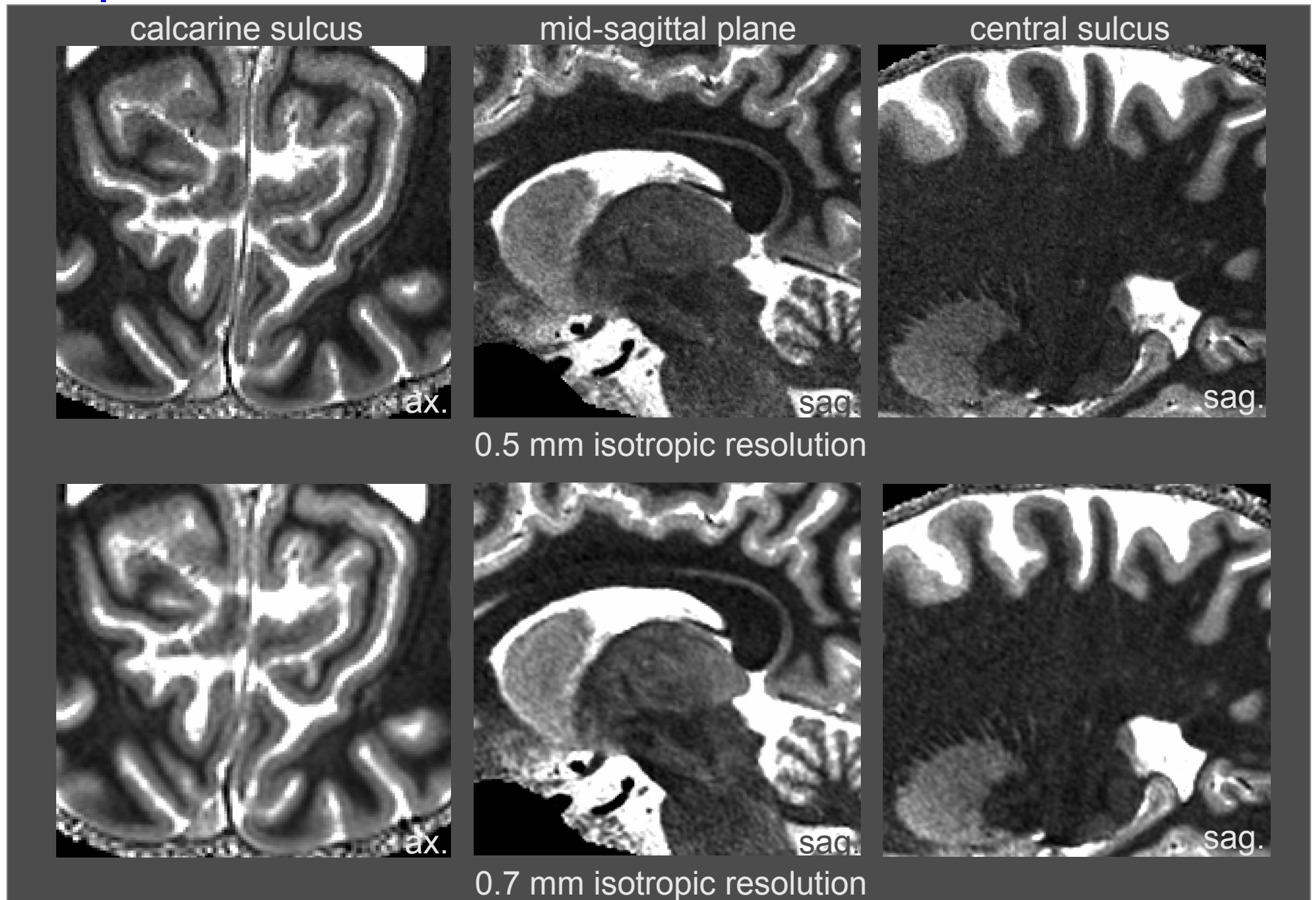
1. Normalize the whole-brain image into MNI @ 0.4 mm
2. Normalize slabs to whole-brain image
3. Skull-strip whole-brain MP2RAGE
4. Select T1 value from highest resolution and second inversion signal

Visible details of microanatomy at 0.5 mm

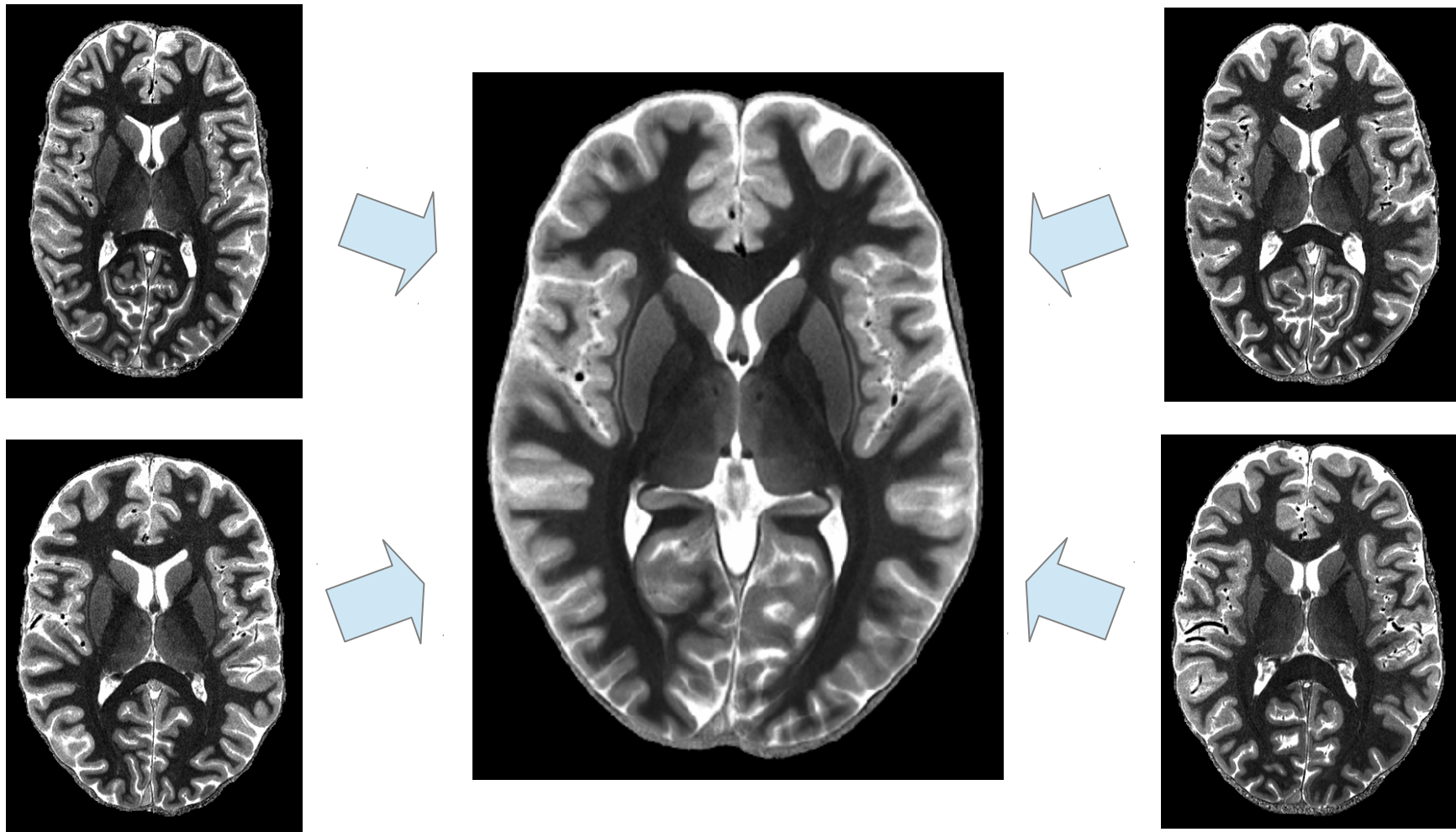


Individual subject

Comparison with 0.7 mm resolution



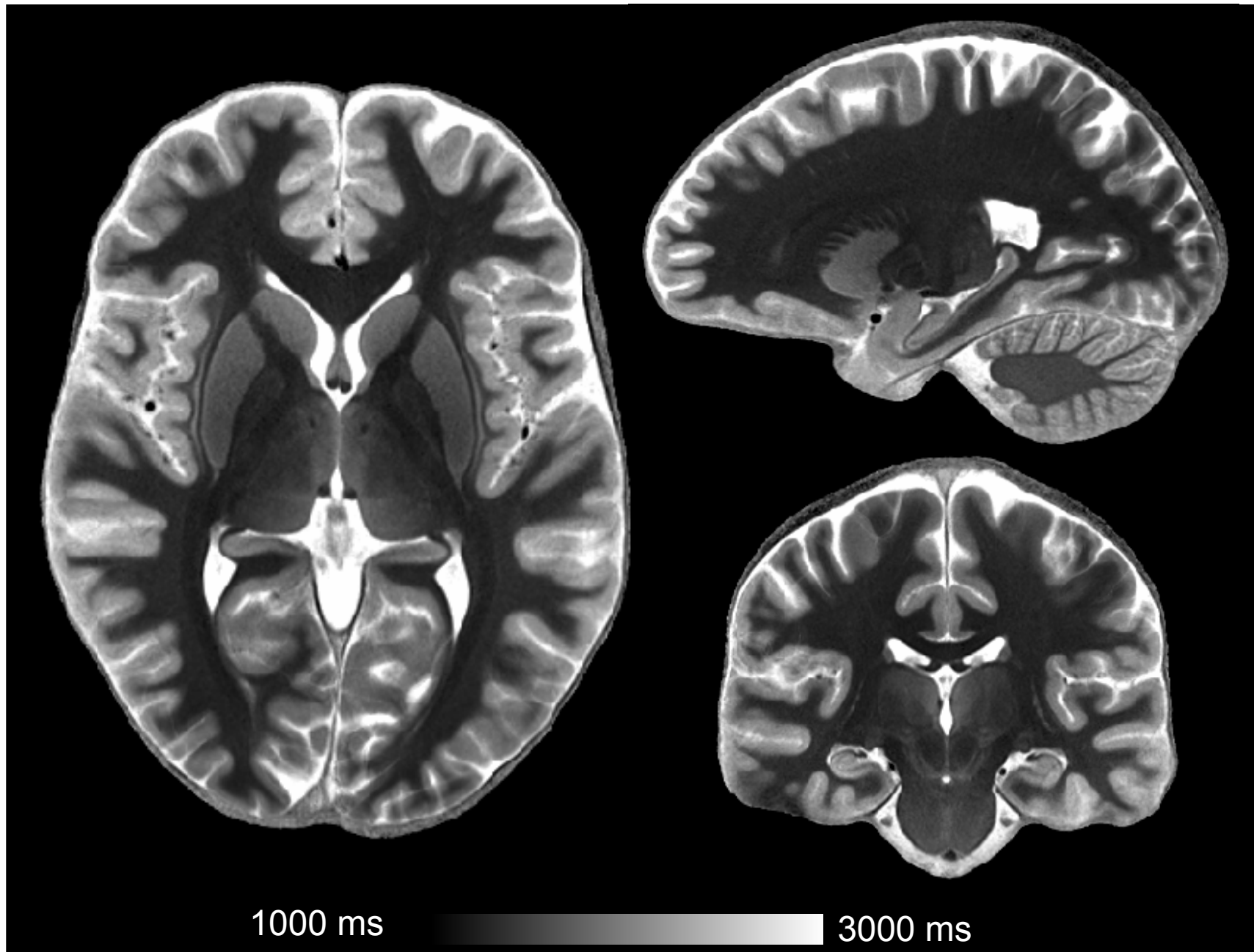
Average T1 Anatomical Atlas



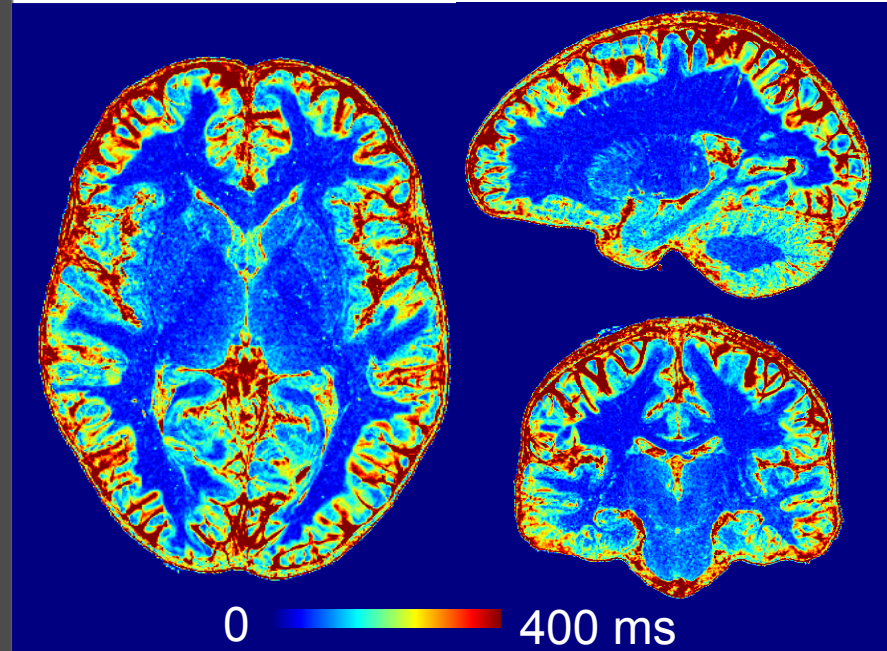
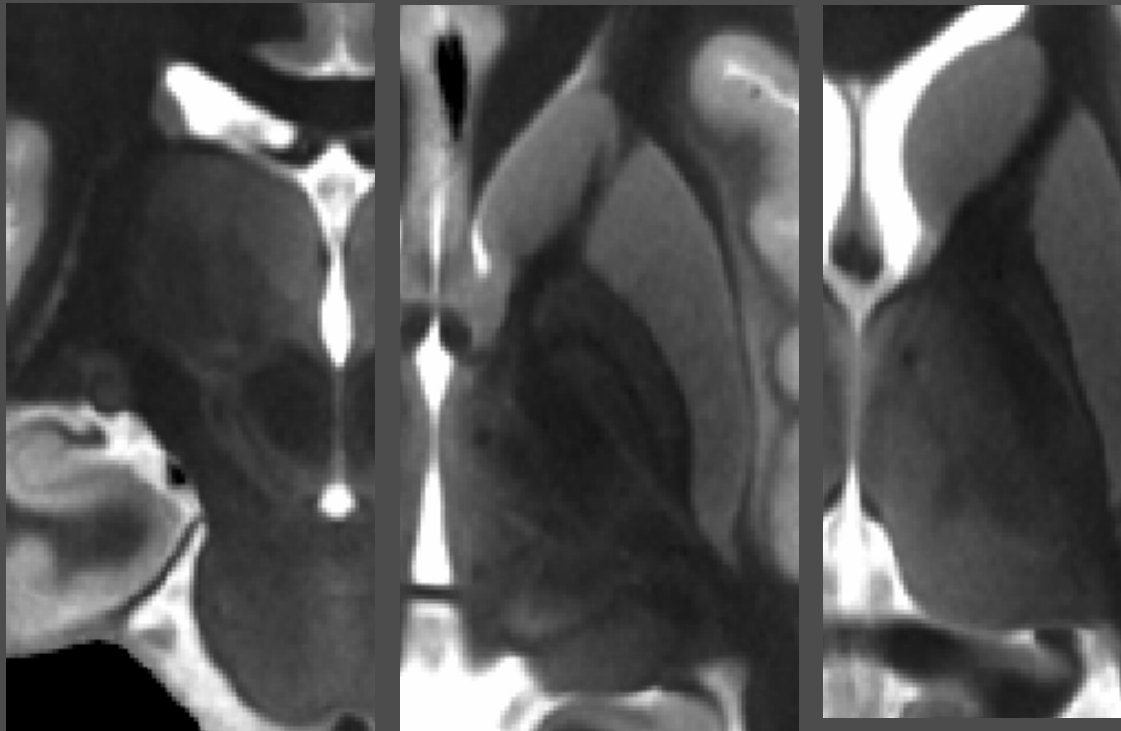
Groupwise average obtained with SyN (ANTs package):
12 subjects, symmetric diffeomorphisms, 25 steps

[Avants et al., 2008]

Average T1 Anatomical Atlas

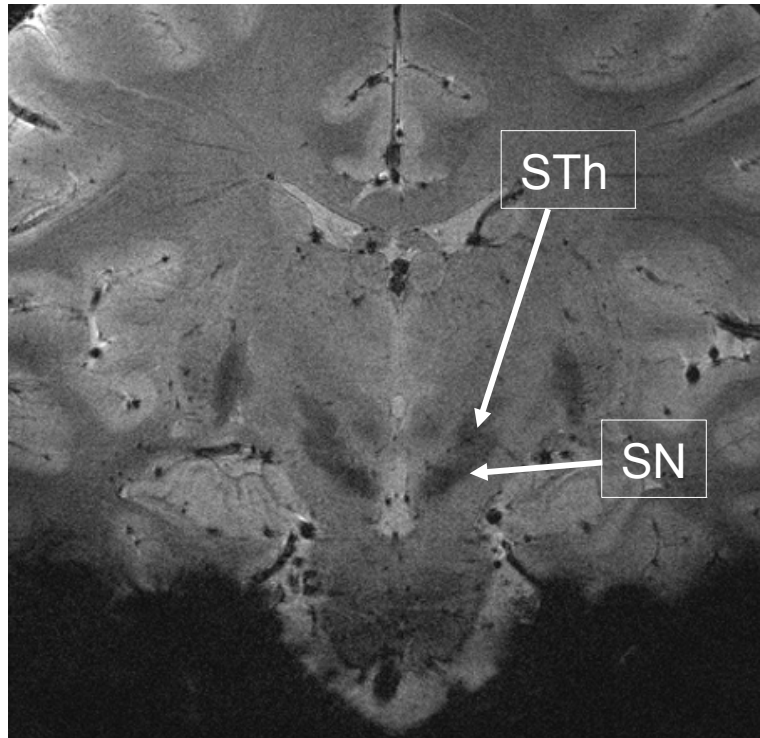


Groupwise T1 anatomical details and variability



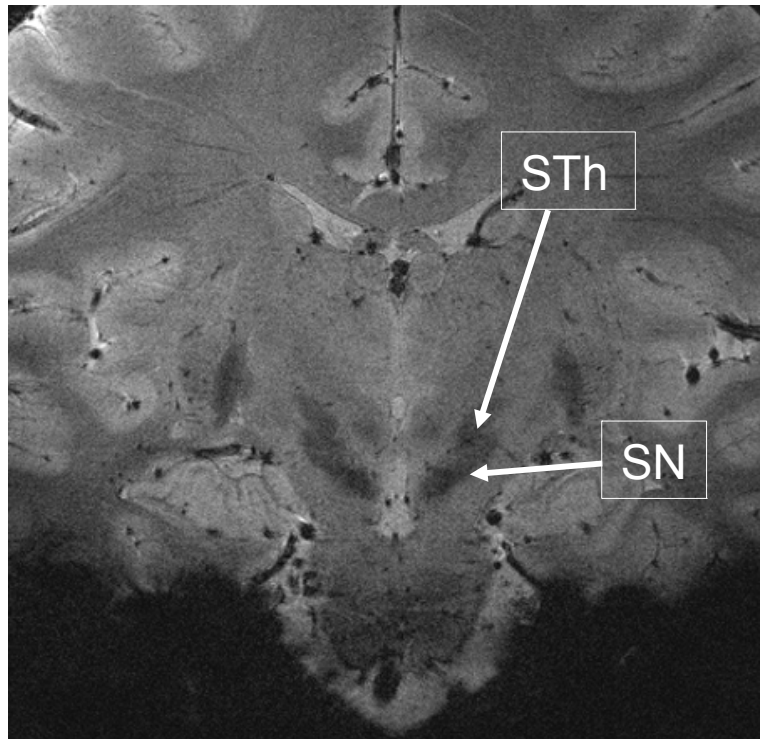
Standard deviation of T1
for the 12 subjects

Interlude: Atlas of the Sub-thalamic nucleus



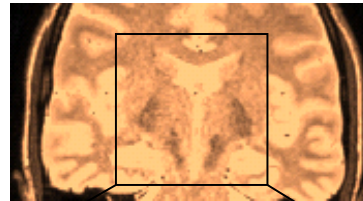
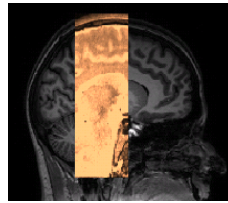
Sth: major target for
Deep Brain Stimulation
(Parkinson's disease)

Interlude: Atlas of the Sub-thalamic nucleus



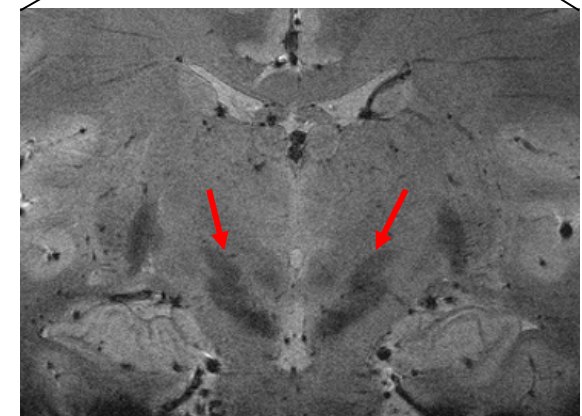
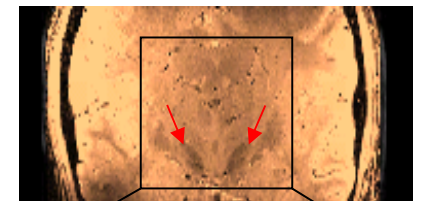
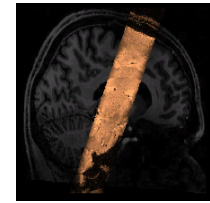
Sth: major target for Deep Brain Stimulation (Parkinson's disease)

3T structural MRI
(0.8 x 0.8 x 0.8 mm)



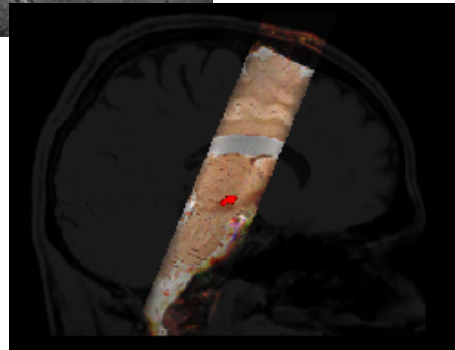
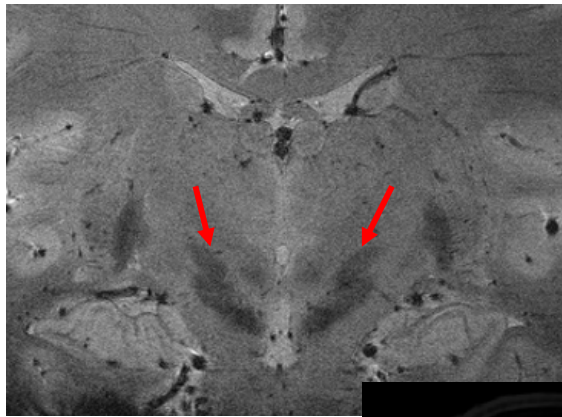
T2*-weighted

7T structural MRI
(0.5 x 0.5 x 0.5 mm)



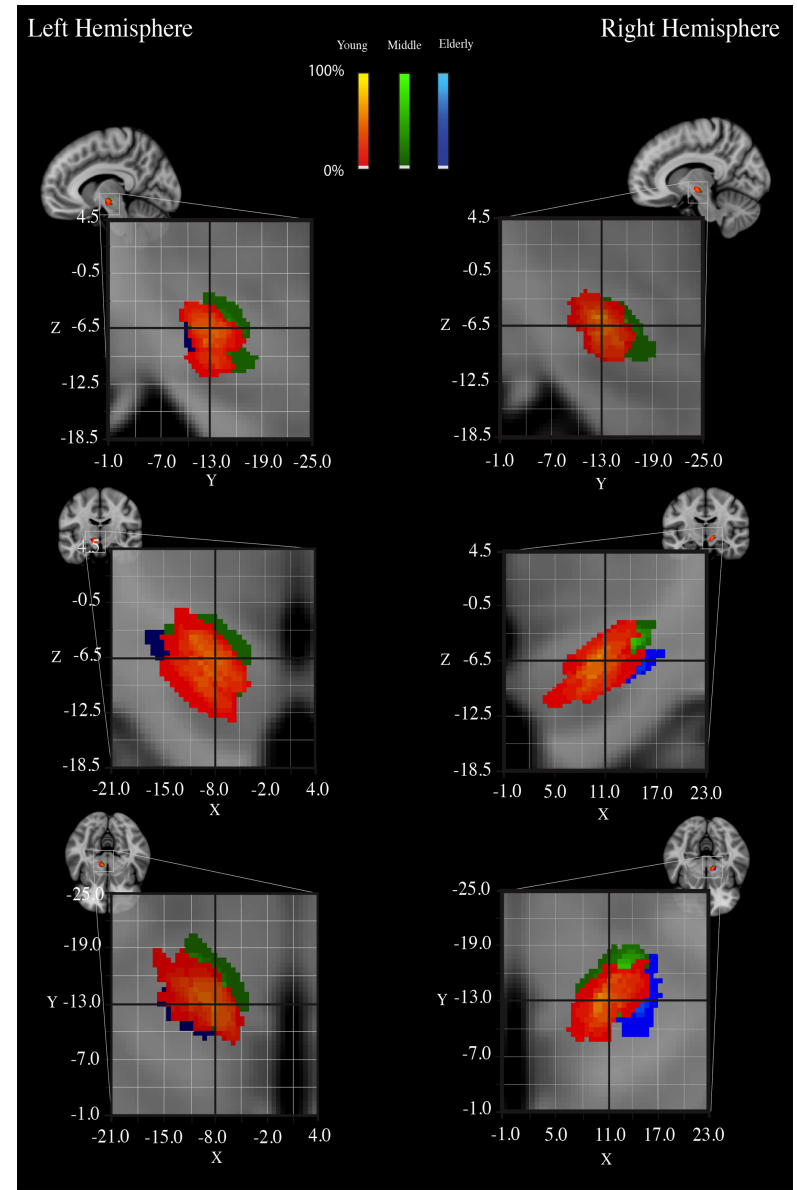
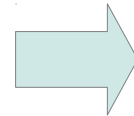
T2*-weighted

Interlude: Atlas of the Sub-thalamic nucleus



Manual
delineations

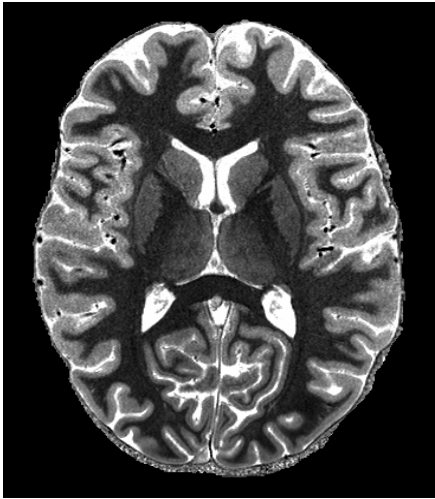
Inter-rater reliability
Cohen's kappa = 0.86



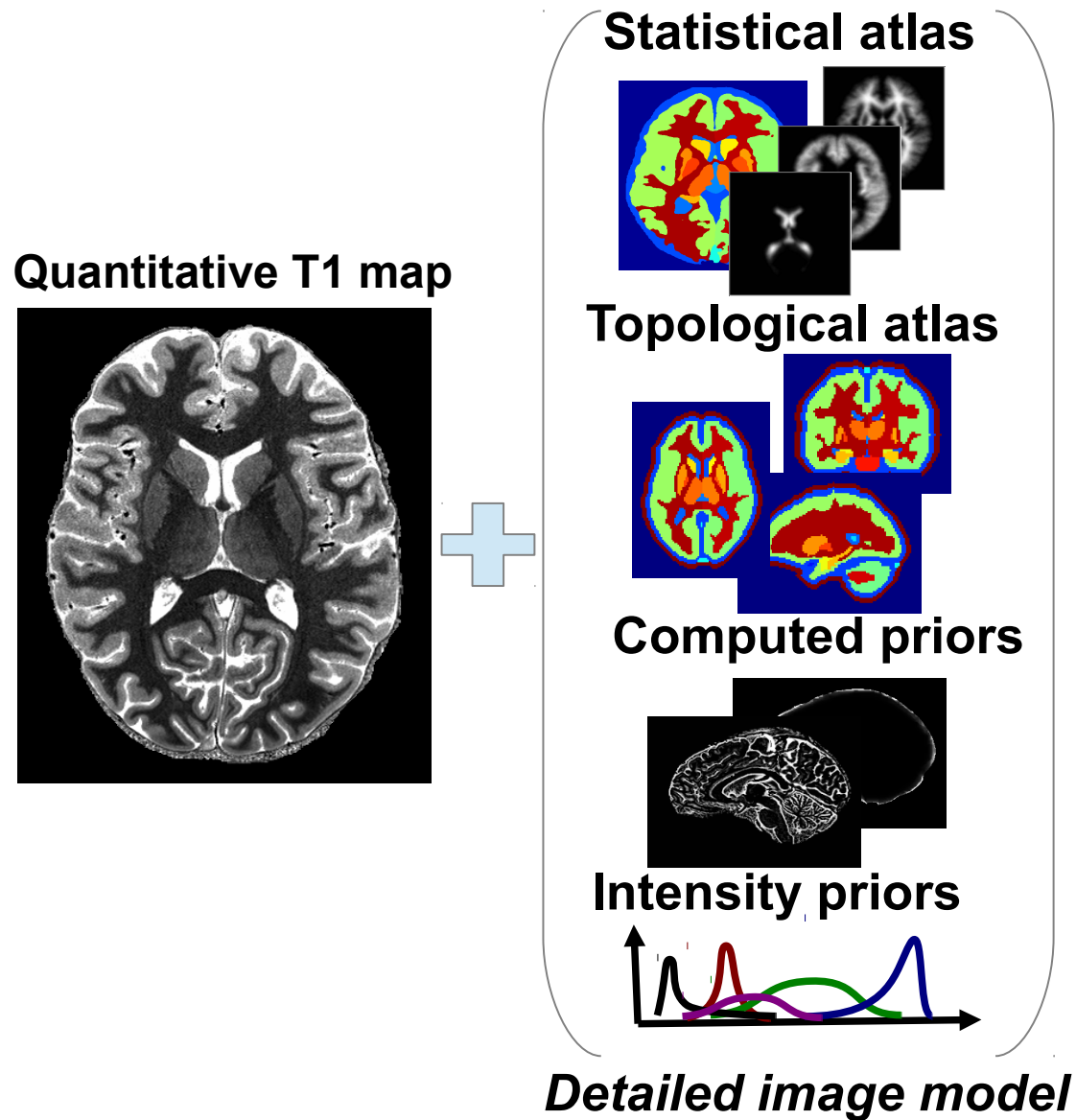
[Keuken et al., JoN 2013]

2. 7T Brain Segmentation and Cortex Extraction

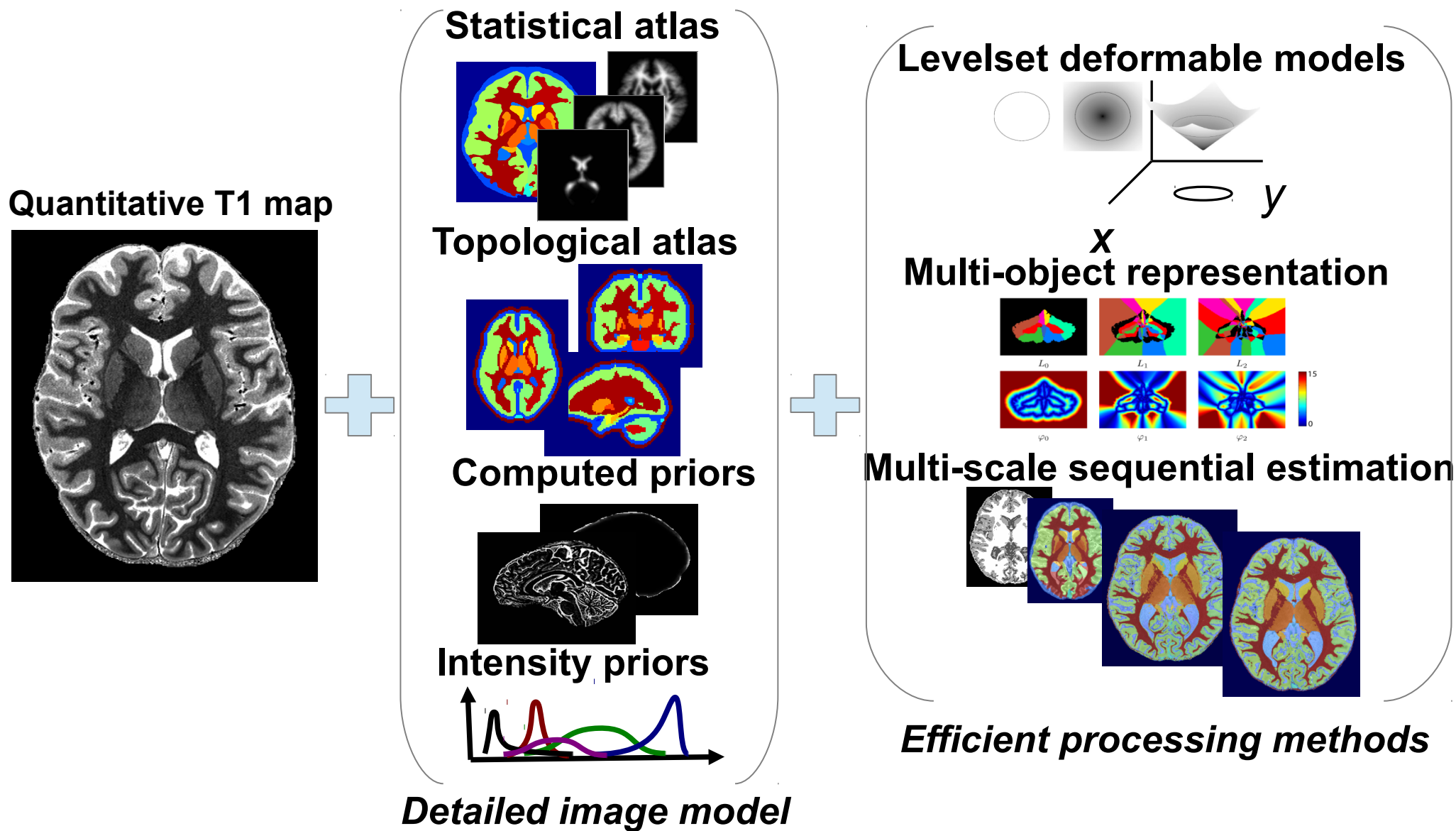
Quantitative T1 map



2. 7T Brain Segmentation and Cortex Extraction



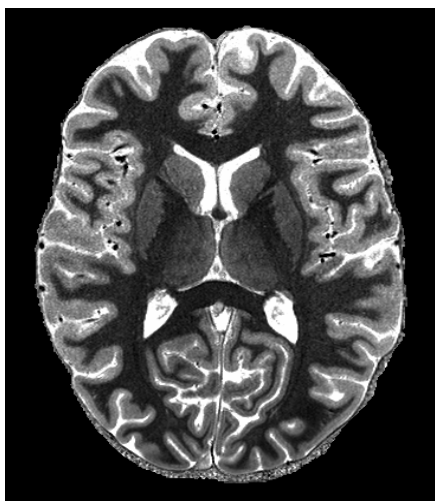
2. 7T Brain Segmentation and Cortex Extraction



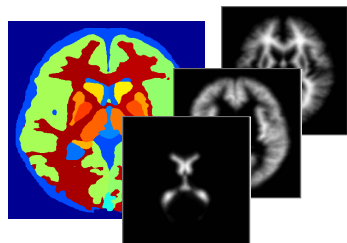
[Bazin et al., Neuroimage 2013]

2. 7T Brain Segmentation and Cortex Extraction

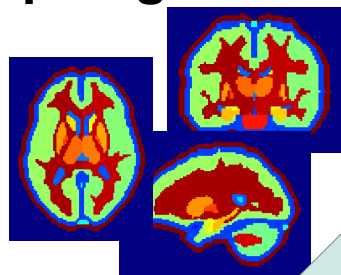
Quantitative T1 map



Statistical atlas



Topological atlas



Computed

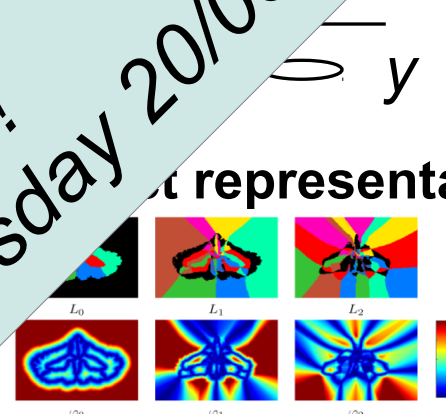


In

All will be revealed!
Technical seminar, Thursday 20/03

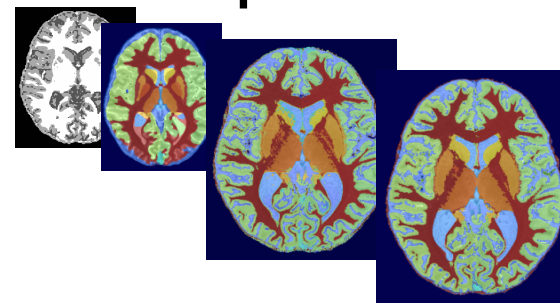
Detail image model

Levelset of image models



Multi-scale sequential estimation

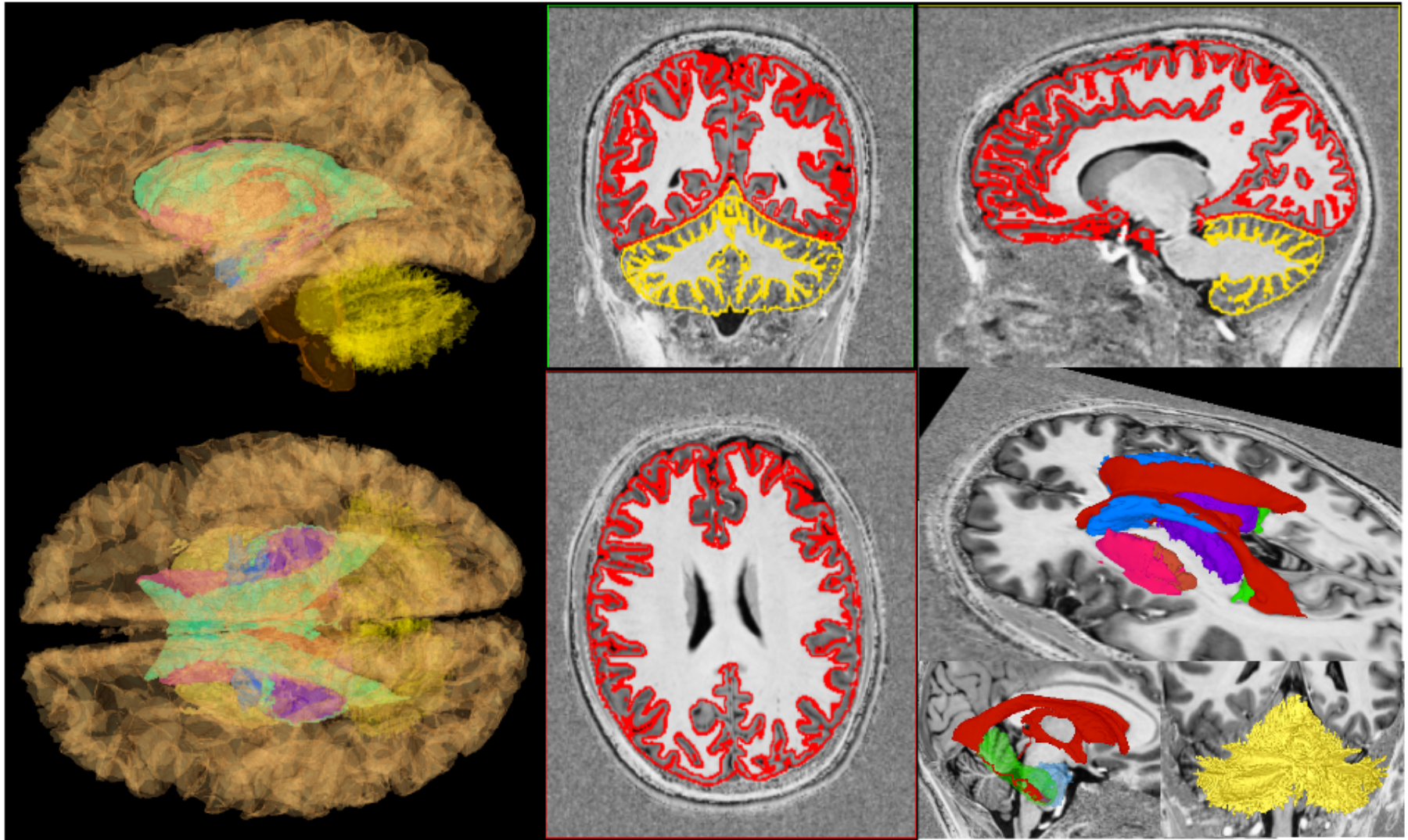
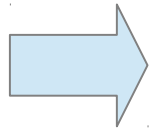
Efficient processing methods



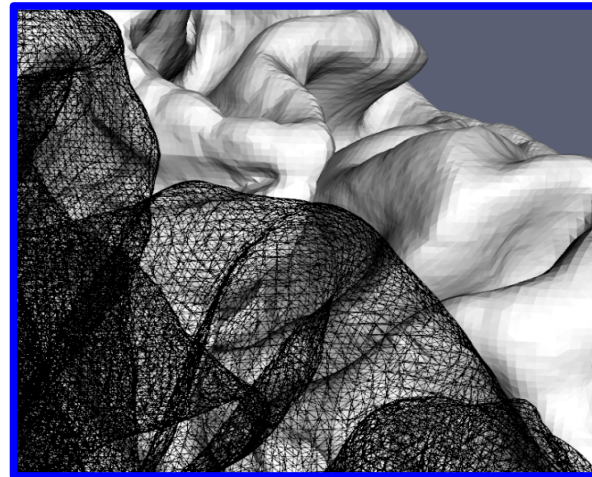
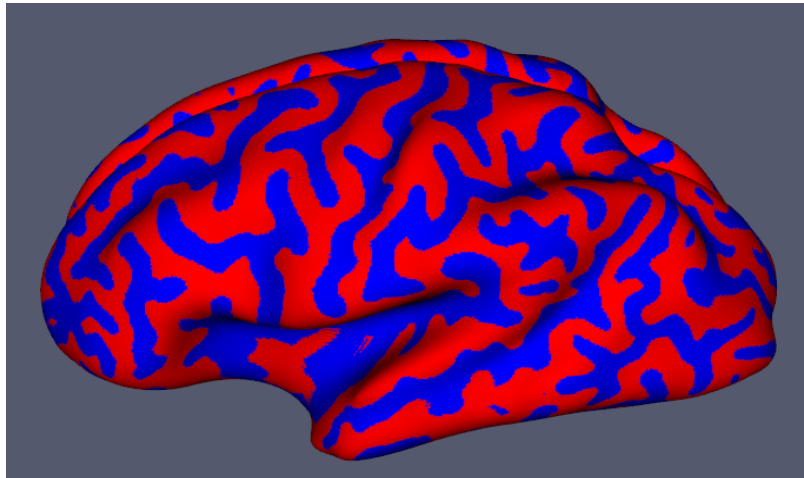
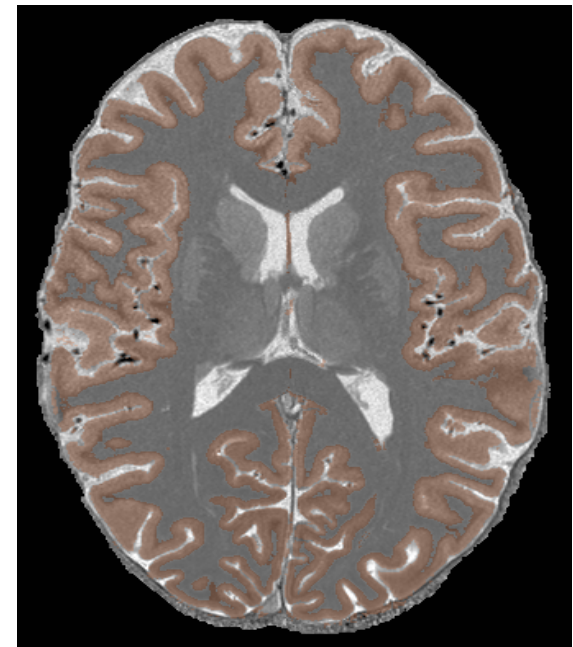
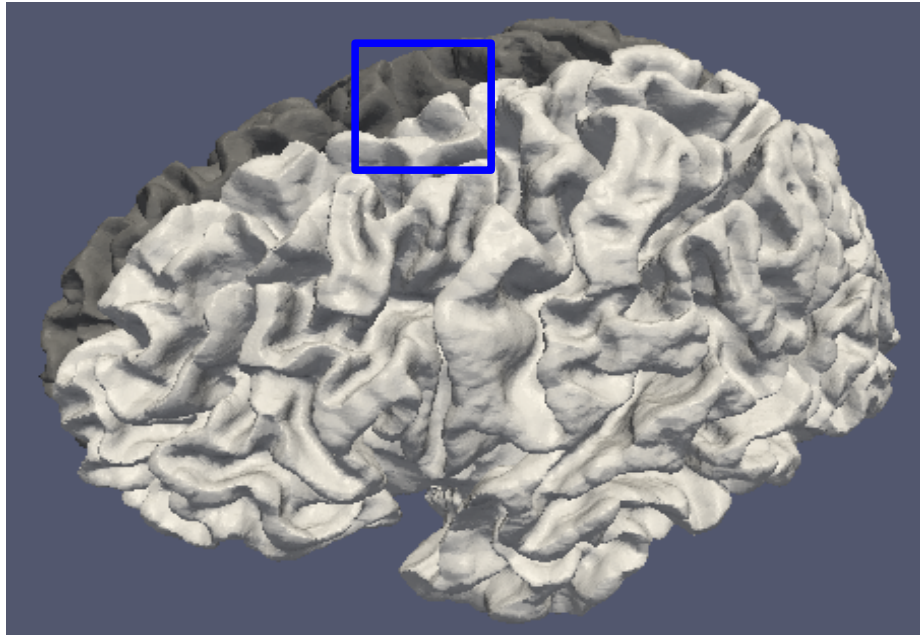
Efficient processing methods

[Bazin et al., Neuroimage 2013]

2. 7T Brain Segmentation and Cortex Extraction



Cortical surfaces at 400 μ m scale

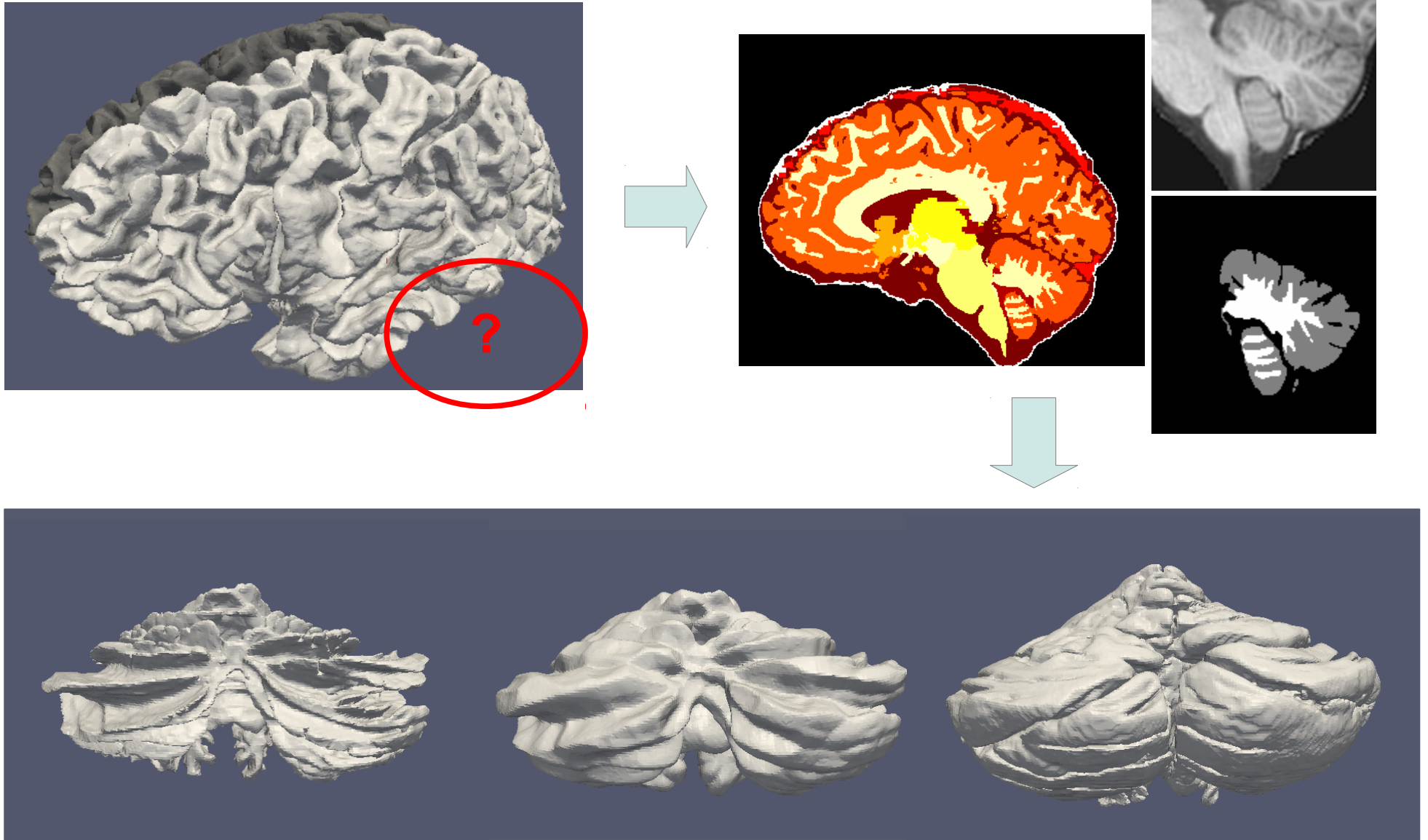


**Mesh complexity:
750,000 points,
1.5 millions triangles**

Interlude 2: cerebellar cortical mapping

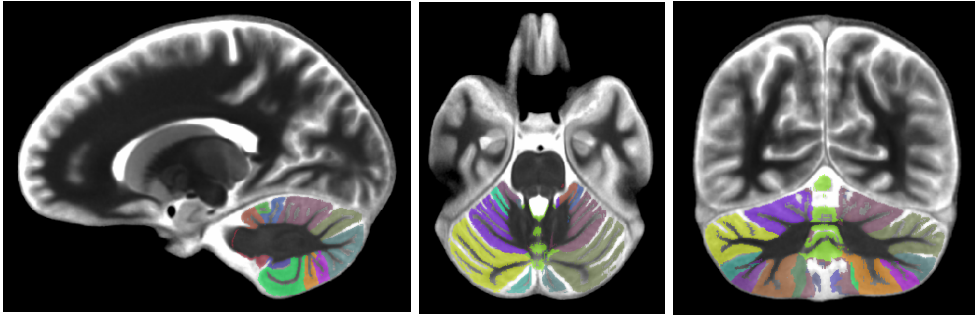


Interlude 2: cerebellar cortical mapping

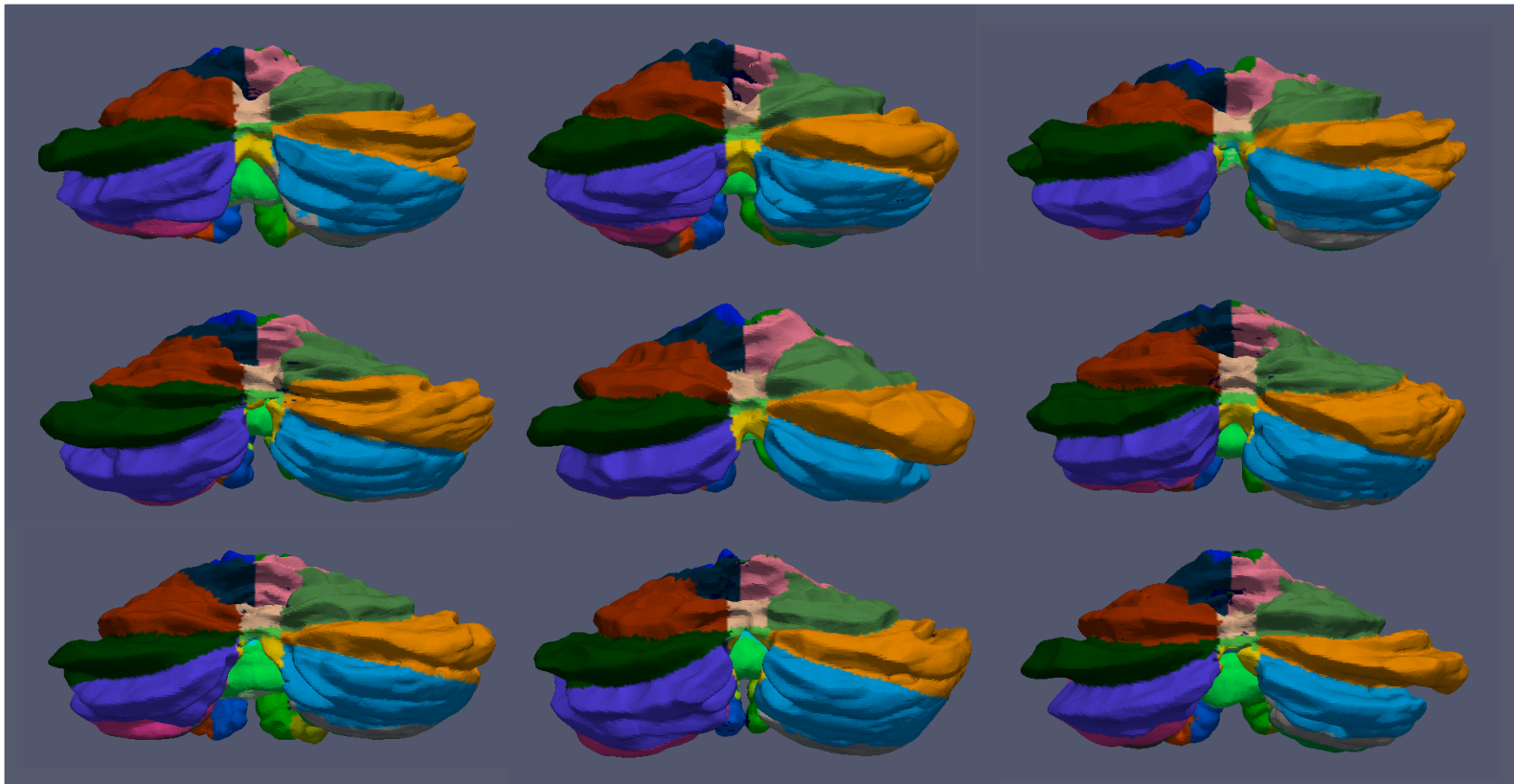


Same methods employed for cerebral and cerebellar cortices

Interlude 2: cerebellar cortical mapping



7T group template



Automatic lobule labelling

Interlude 2: cerebellar cortical mapping

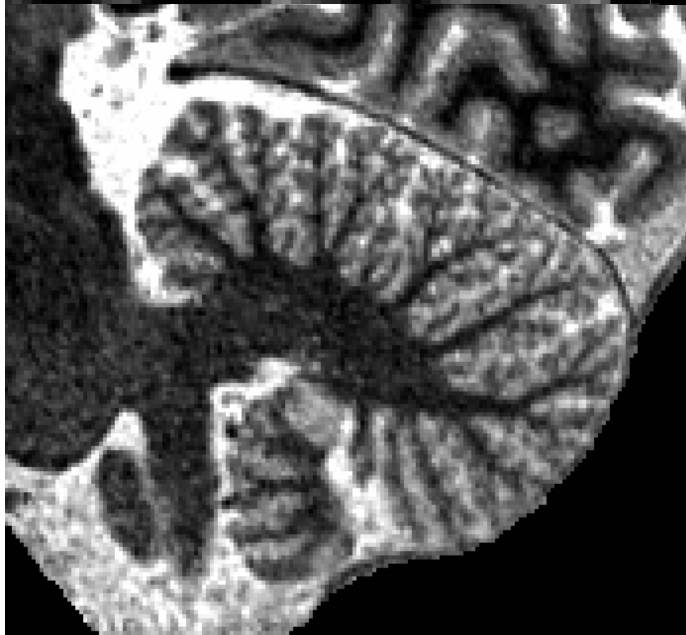
3T MRI
1 mm



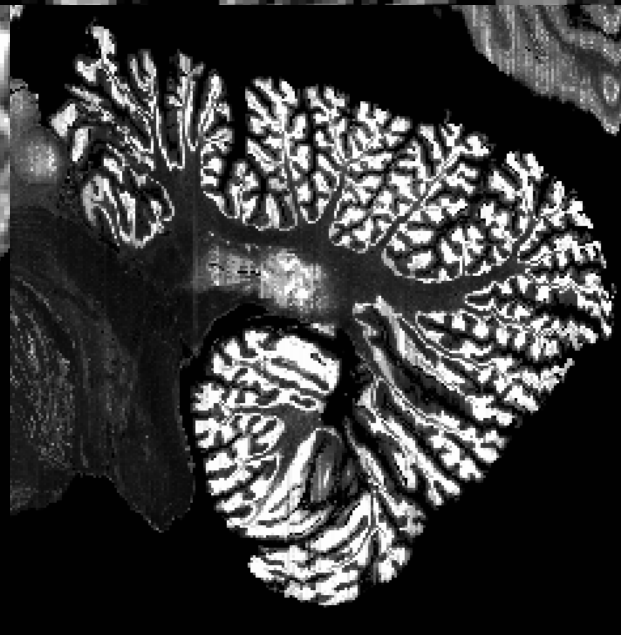
3T MRI
0.7 mm
(HCP)



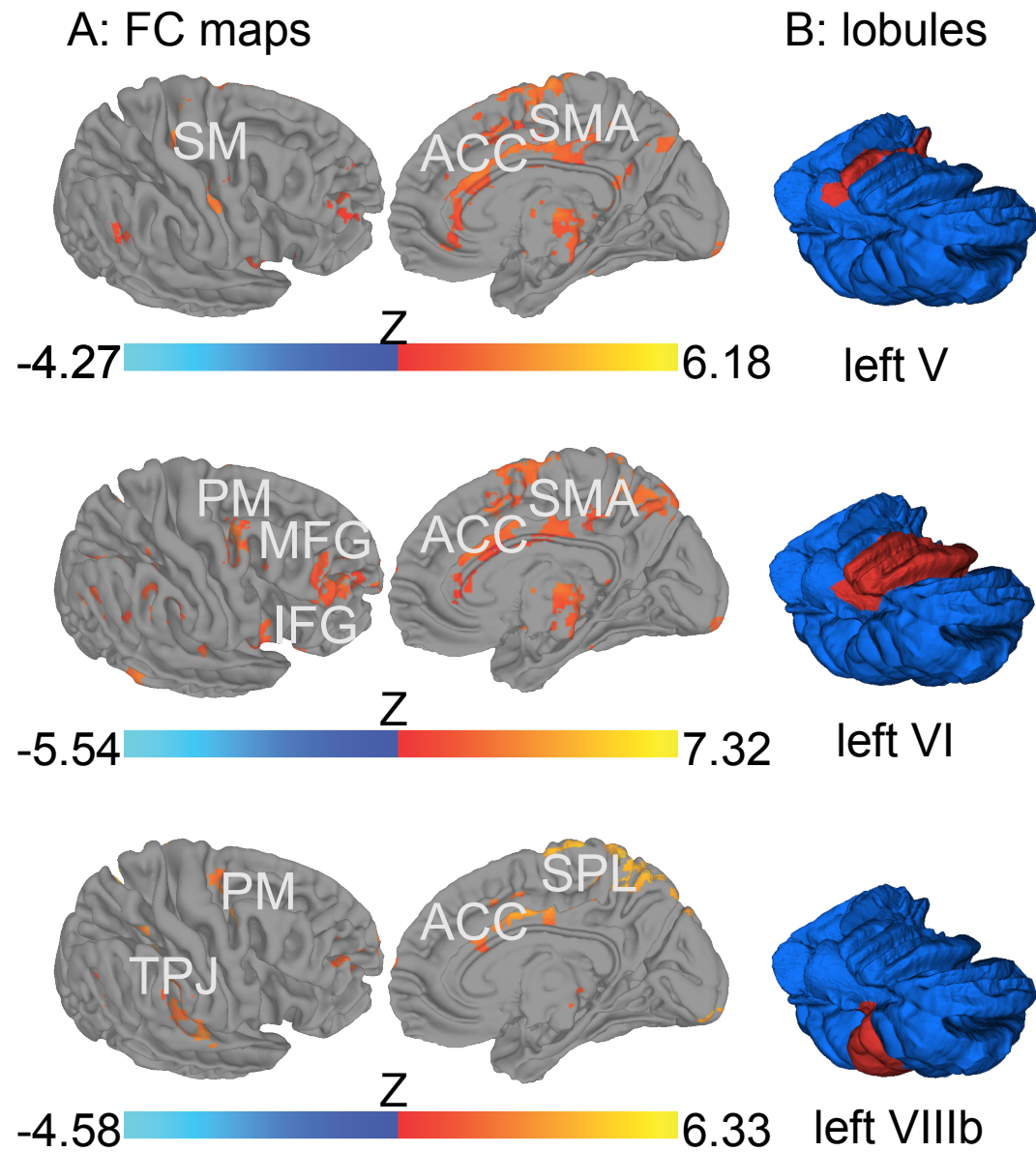
7T MRI
0.5 mm



BigBrain
(histology)



Interlude 2: cerebellar cortical mapping



Study of cerebelar-cerebral functional connectivity

3. Cortical Laminae Modelling

The **bending** of cortical layer changes their relative thickness in order to **preserve** their respective local **volume**

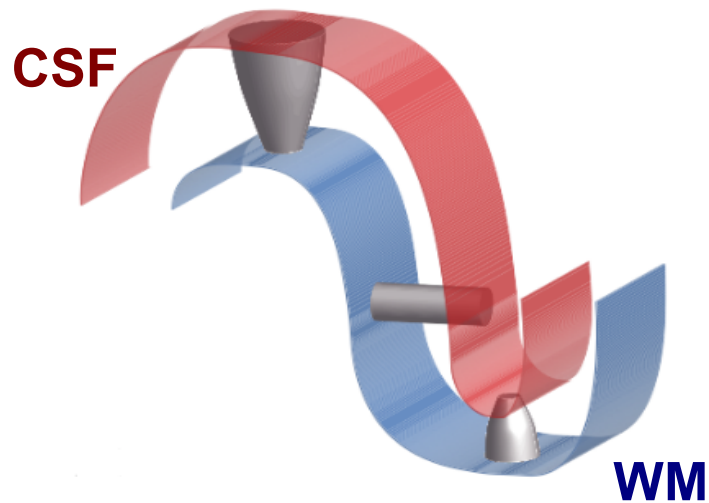
[Bok, Z. ges. Neurol. Psychiat., 1929]

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Volume-preserving lamination:

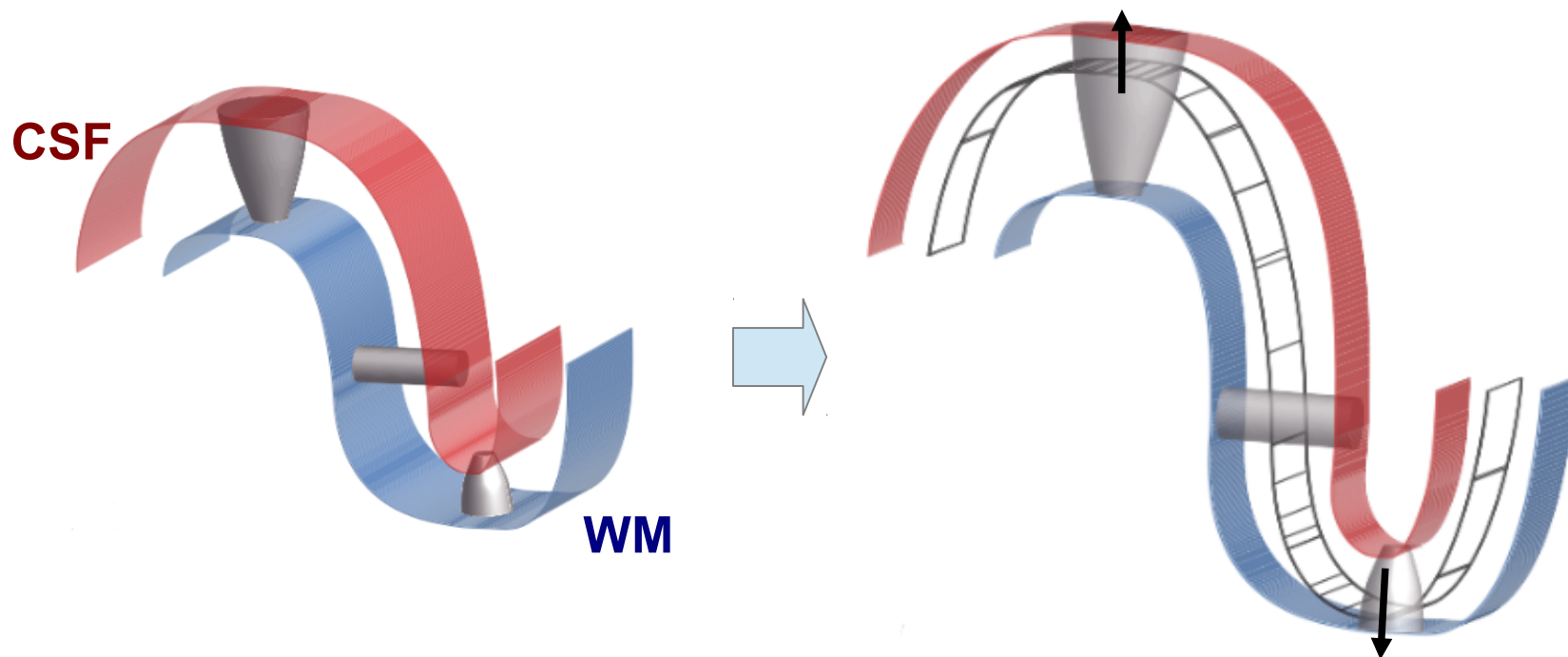


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Volume-preserving lamination:

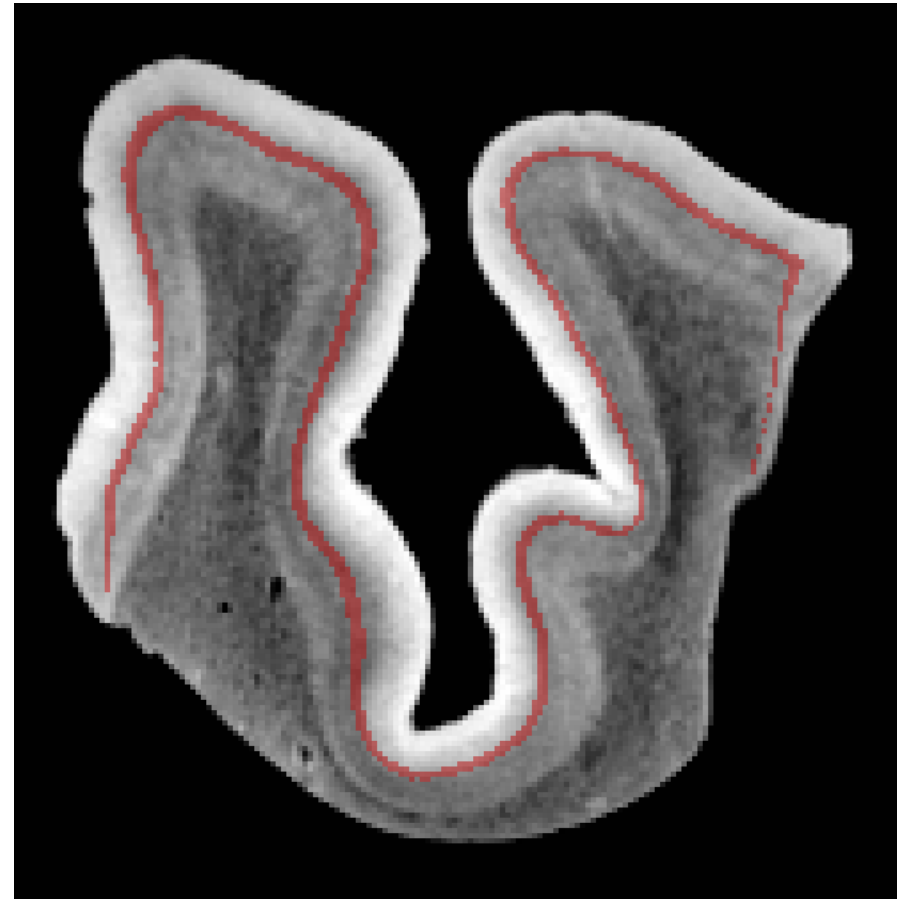
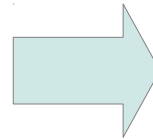
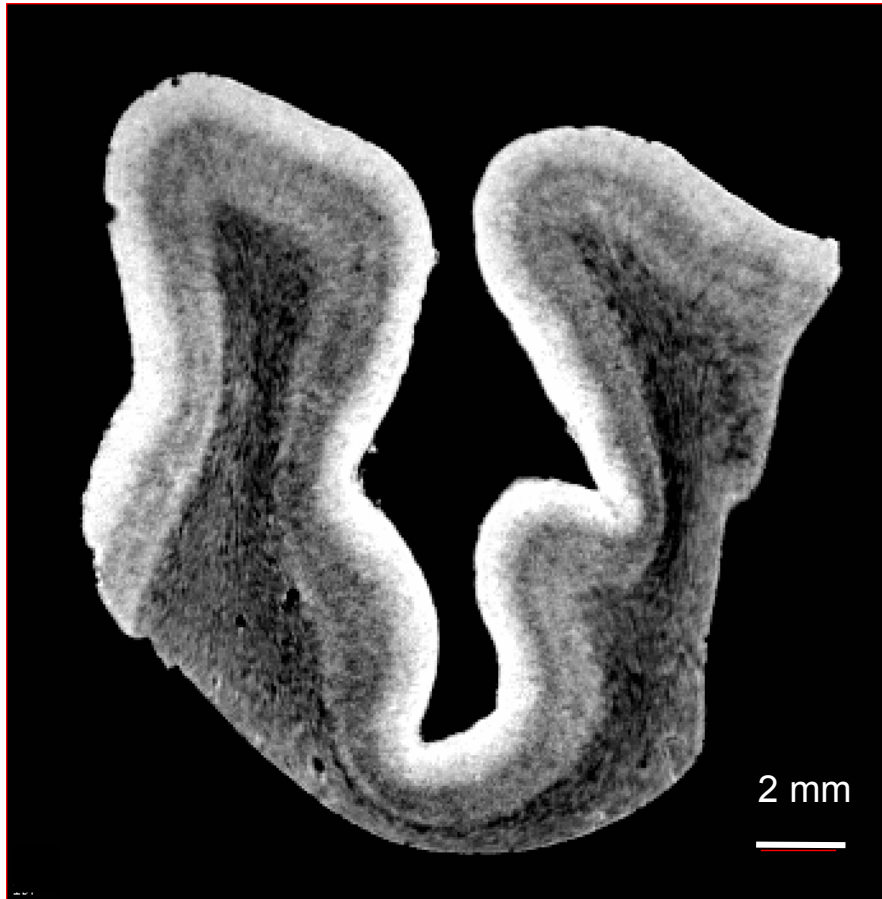


Place intra-cortical laminae of equal depth to maintain volume ratios

[Waehnert et al., NeuroImage 2013]

Validation on post-mortem data

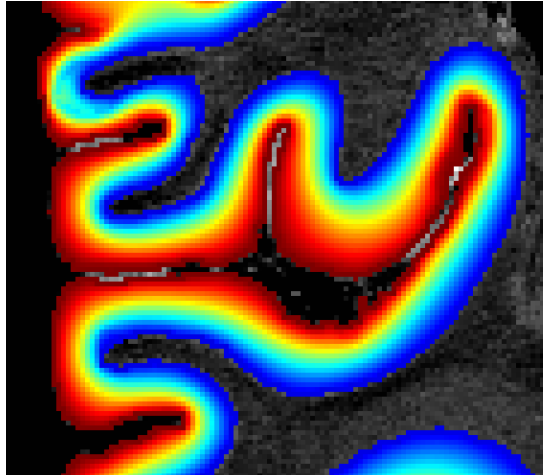
T2* weighted image of
pre- and postcentral gyrus,
(resolution: 70 μm)



volume-preserving model

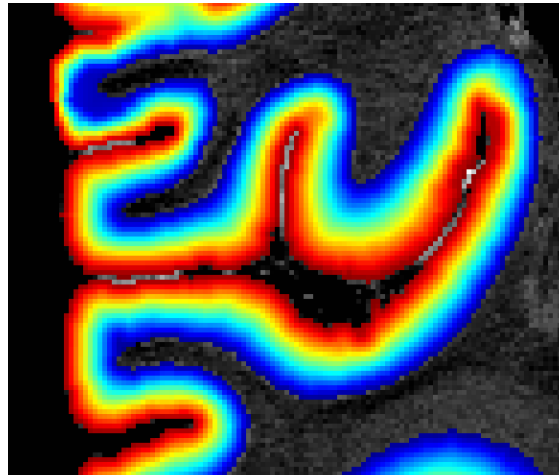
Comparison with previous models

**Ex-vivo sample of the occipital pole
(T2*-weighted, 150 μ m resolution)**



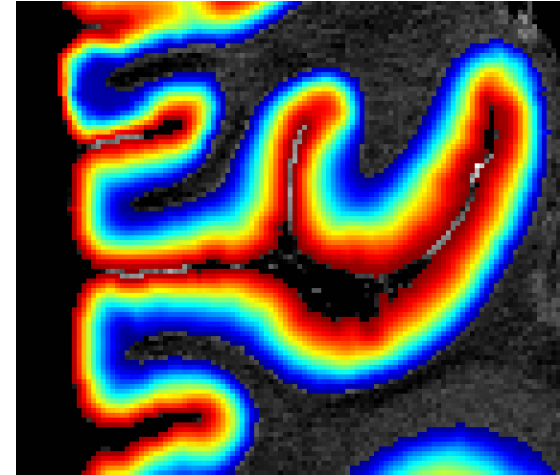
Laplace

Solution of Laplace equation between cortical boundaries



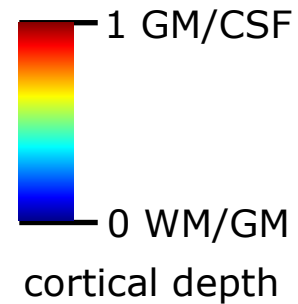
equidistant

Constant distance fraction between the lamina and the boundary



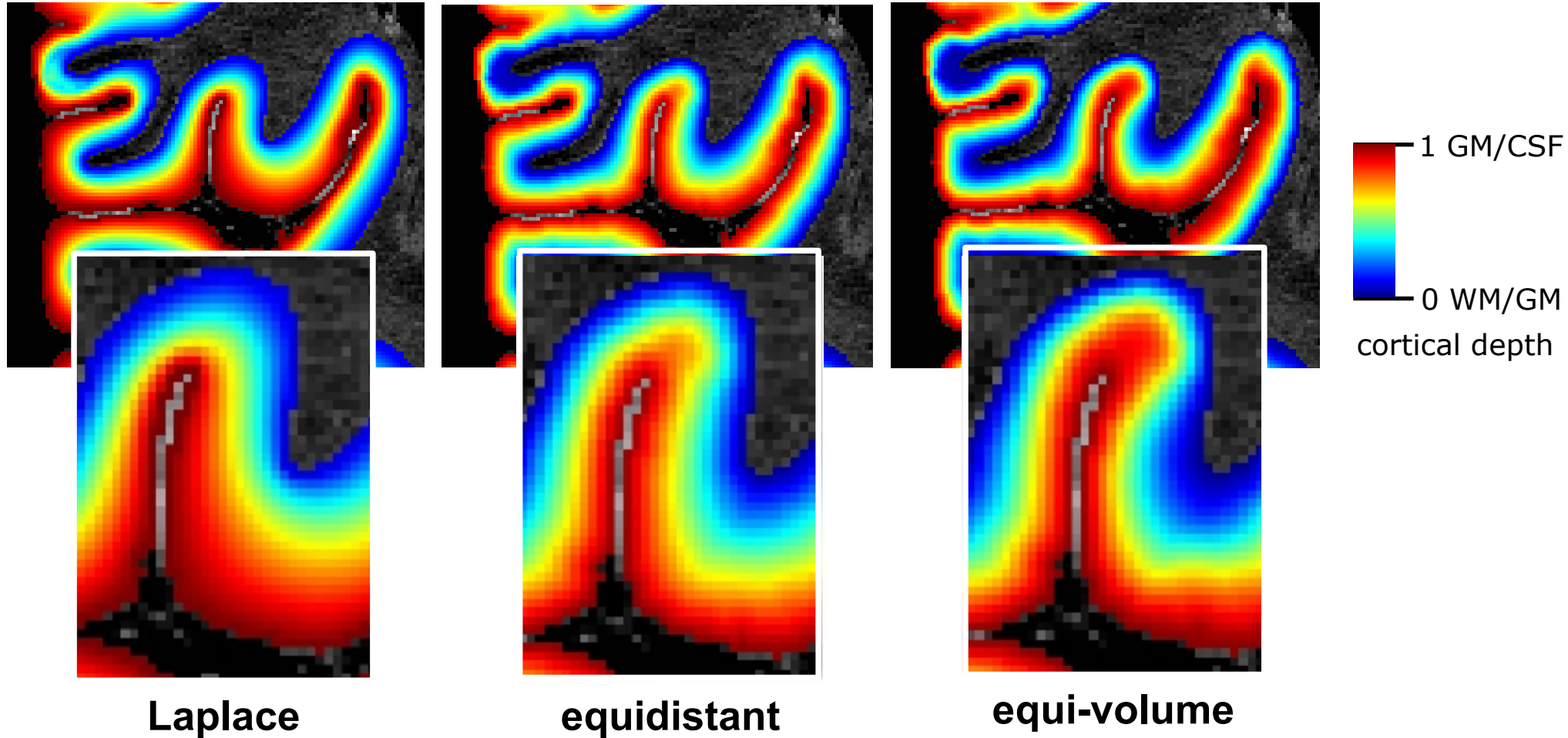
equi-volume

Constant volume fraction between the lamina and the boundary



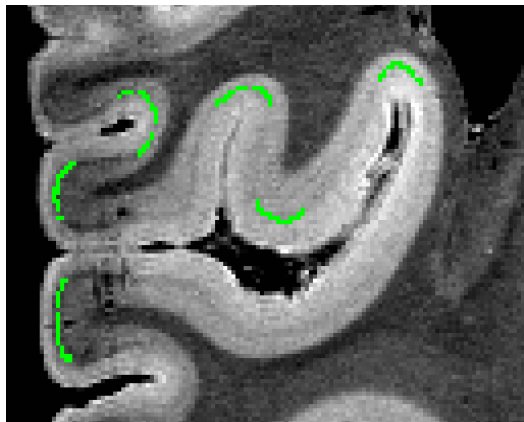
Comparison with previous models

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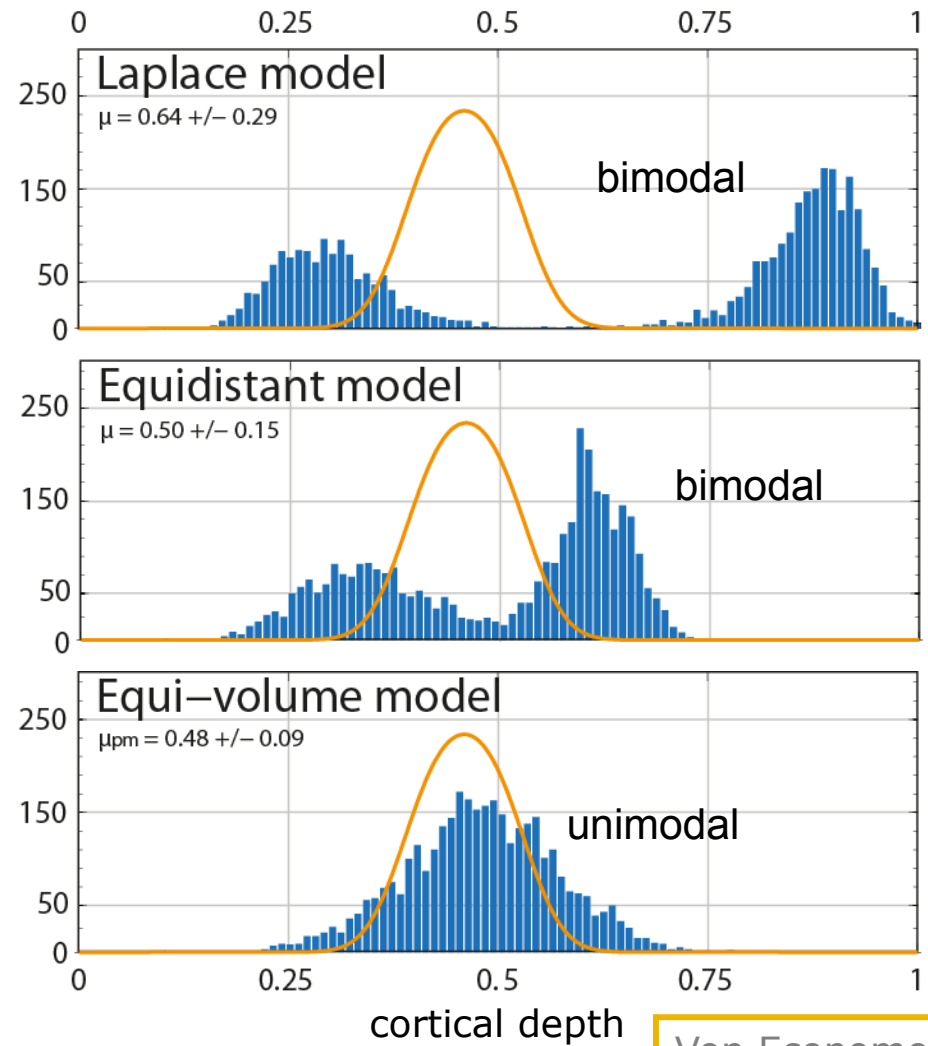
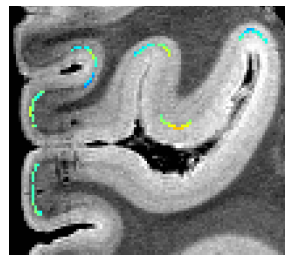
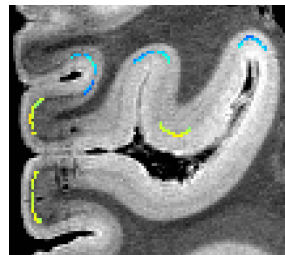
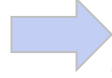
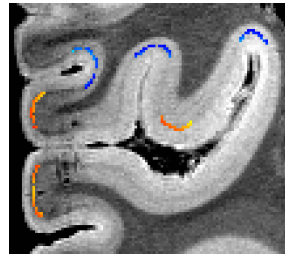
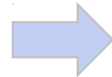


Comparison with previous models

Estimation of the depth of the stria of Gennari

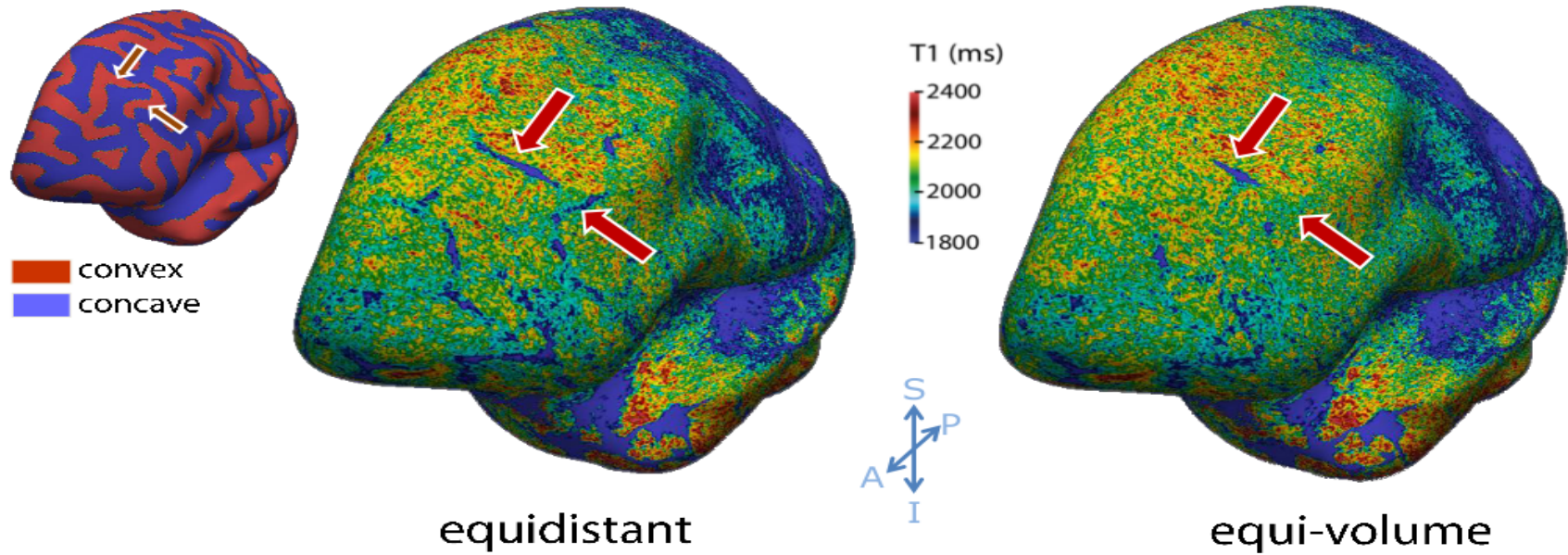


Manual labels on curved parts of the stria of Gennari

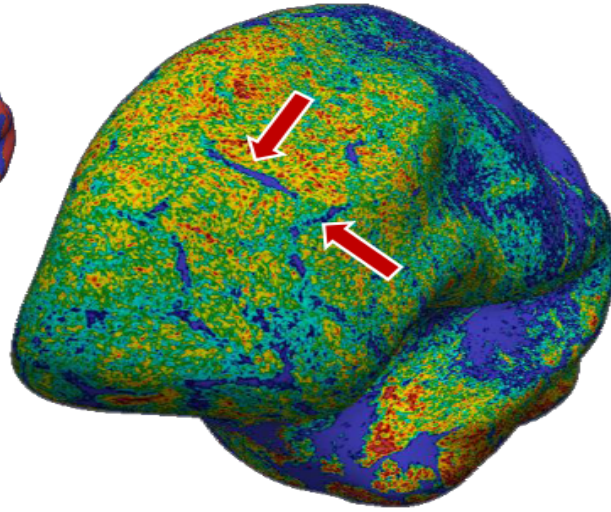
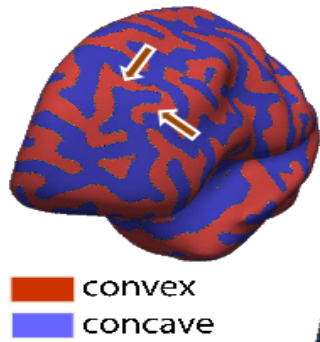


Von Economo 1925

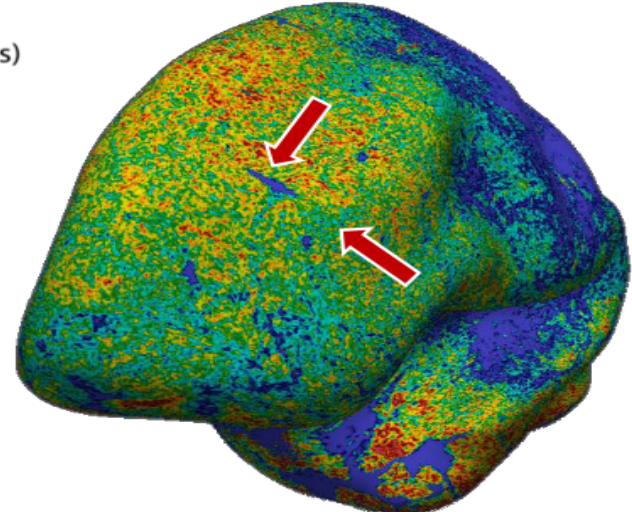
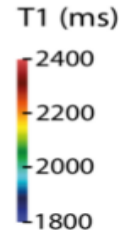
Effects of curvature and resolution



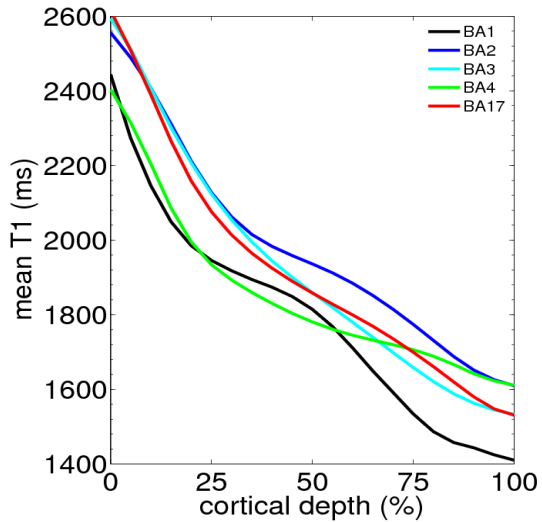
Effects of curvature and resolution



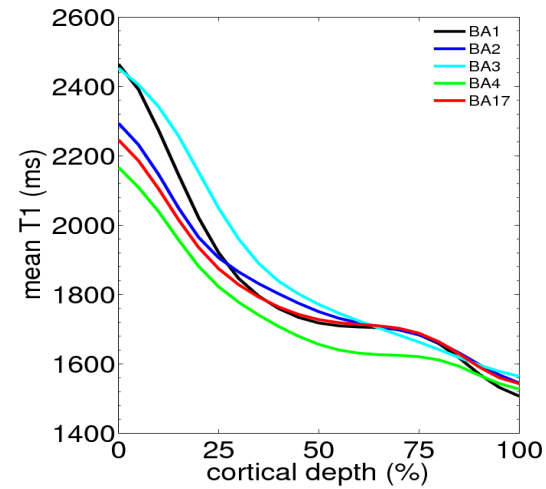
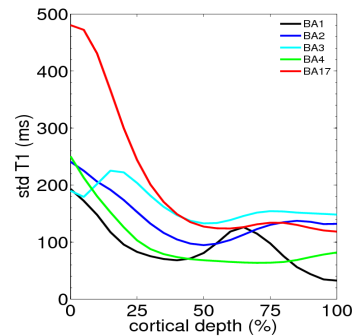
equidistant



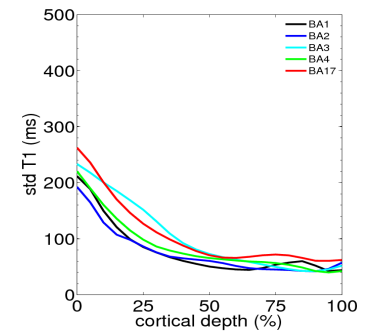
equi-volume



0.7 mm resolution

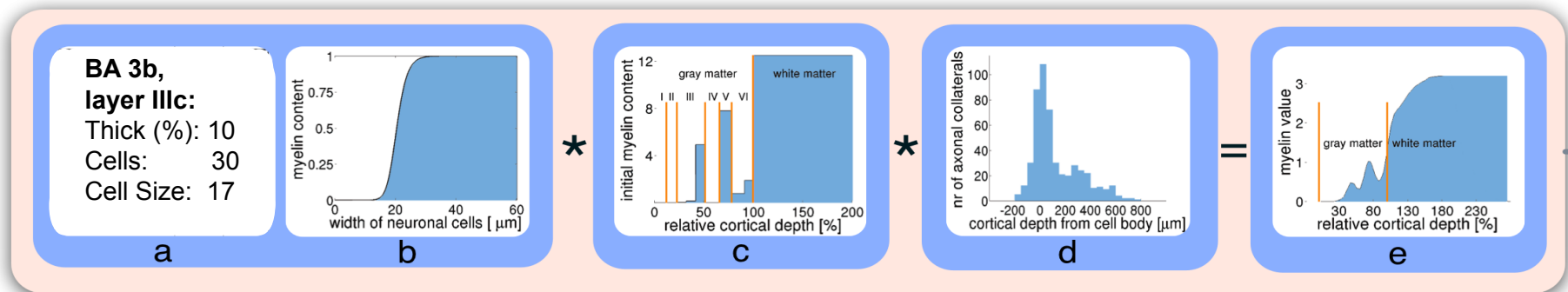


0.5 mm resolution



4. Histology-based modelling and parcellation

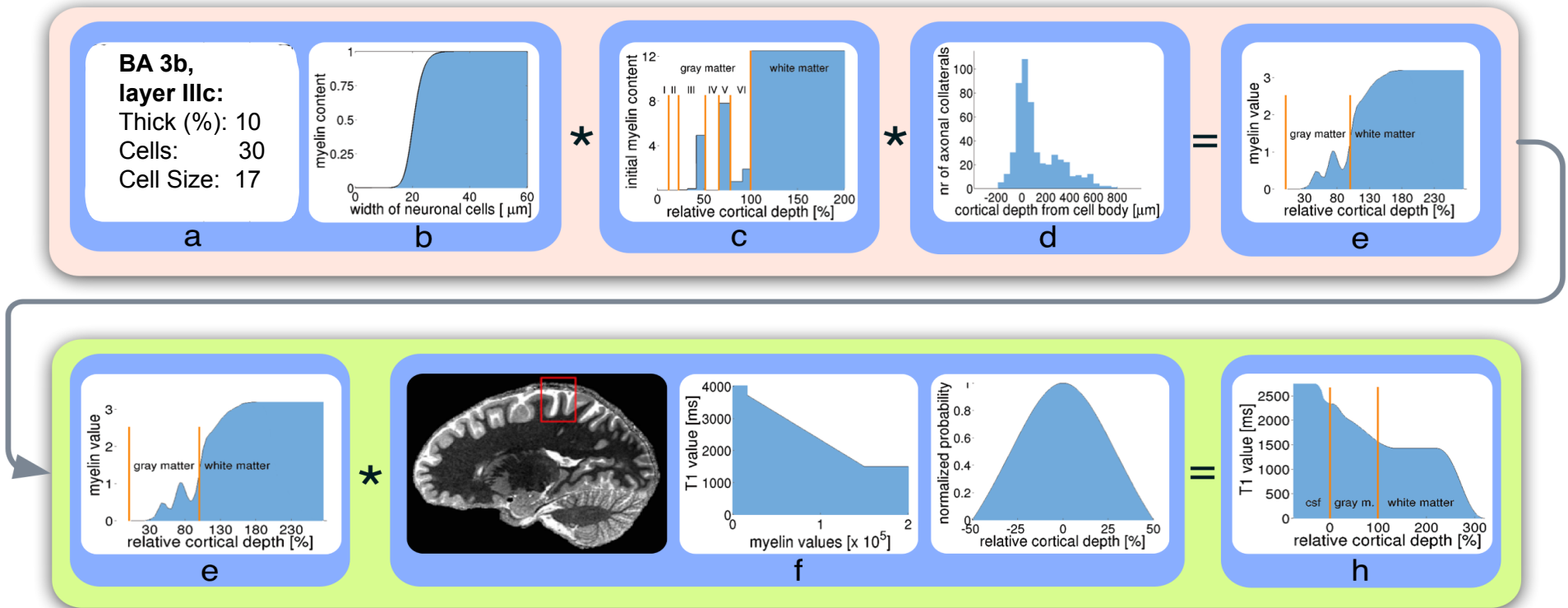
Myelin density profiles



[Hellwig, J. Hirnforschung 1993]

4. Histology-based modelling and parcellation

Myelin density profiles

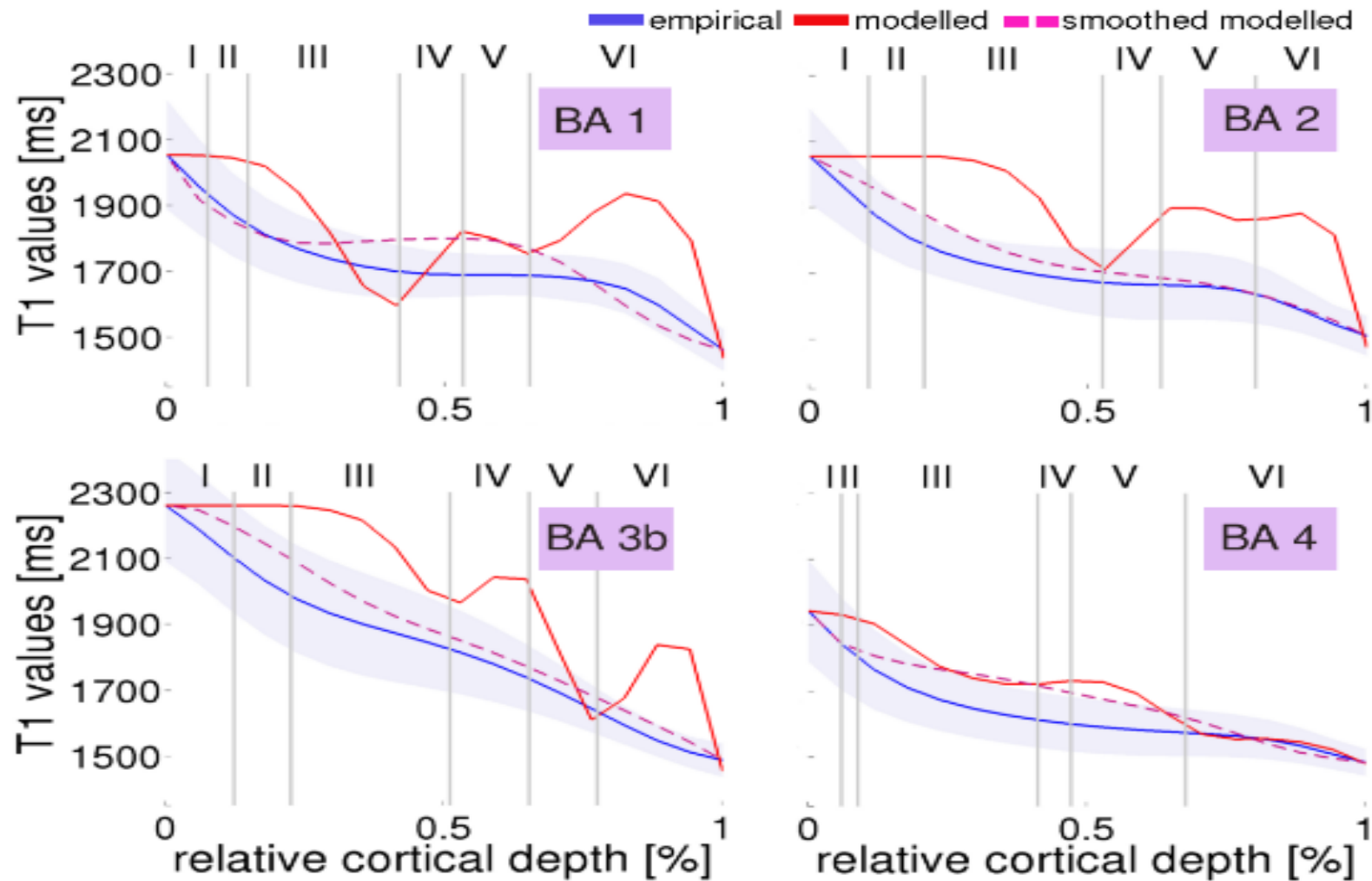


Quantitative T1 intensity profiles

[Dinse et al., MICCAI 2013]

Cytoarchitecture-derived MR profiles

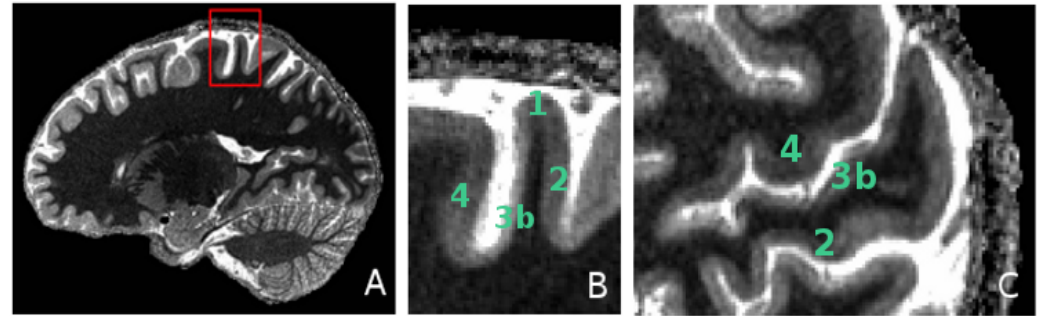
Comparison of empirical and model-based profiles from cytoarchitecture



[Dinse et al., MICCAI 2013]

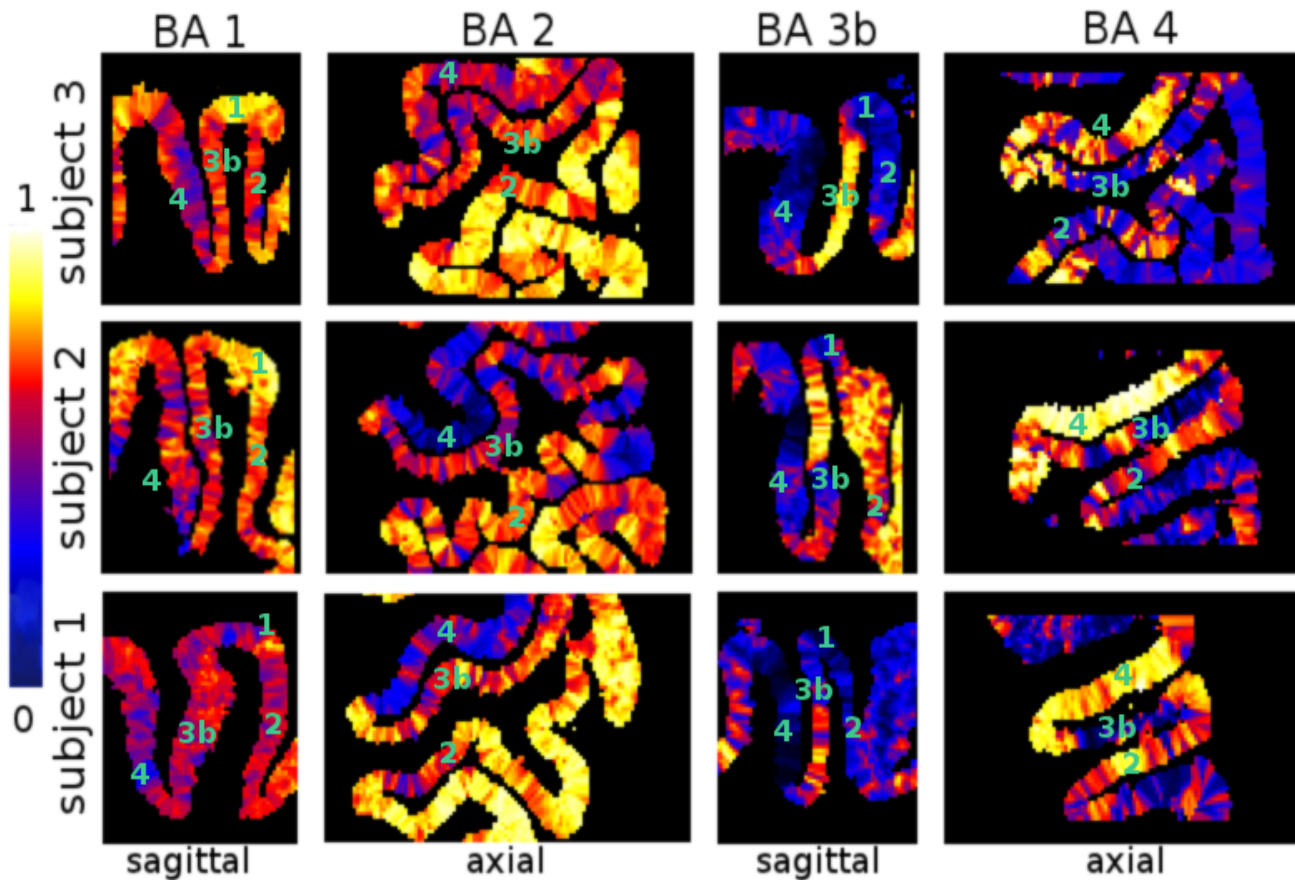
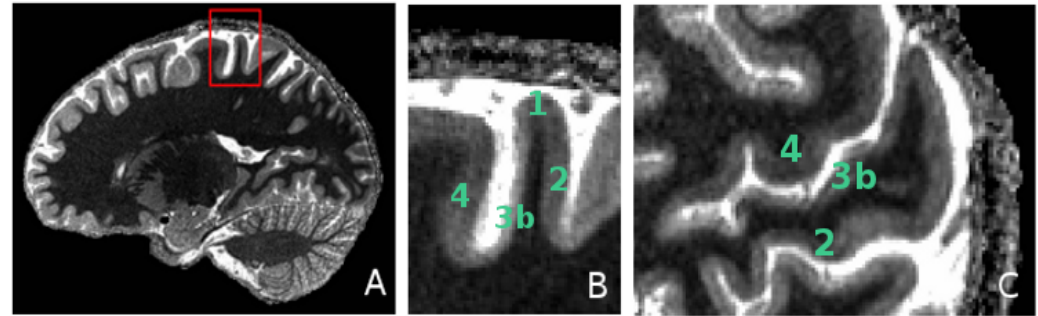
Model-based Brodmann area parcellation

BAs 4, 3b, 1 and 2:
neighboring areas



Model-based Brodmann area parcellation

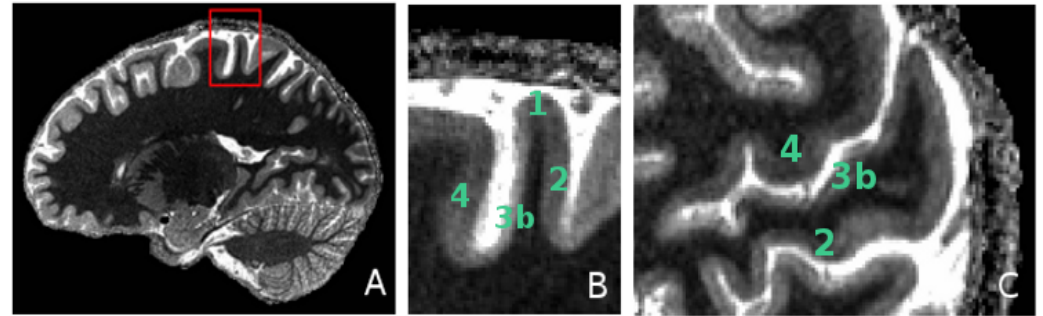
BAs 4, 3b, 1 and 2:
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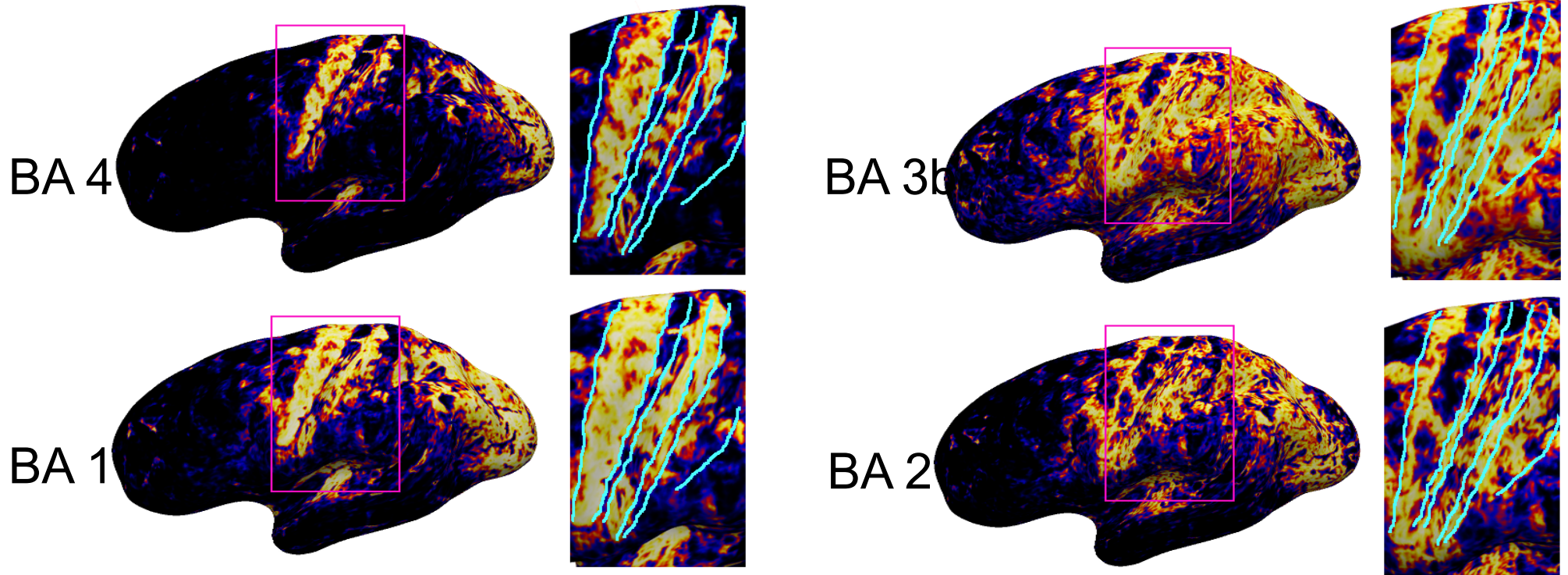
Model-based
probability maps
in individual subjects

Model-based Brodmann area parcellation

BAs 4, 3b, 1 and 2:
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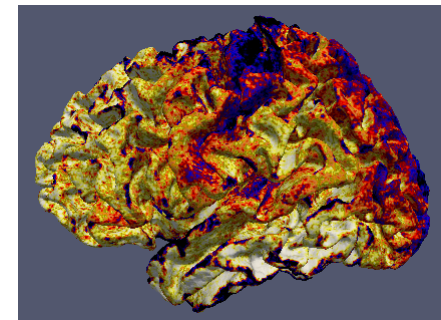
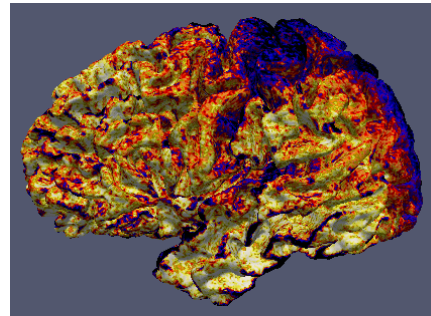
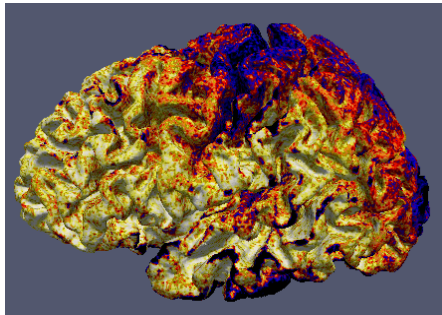
Model-based probability maps for an individual subject



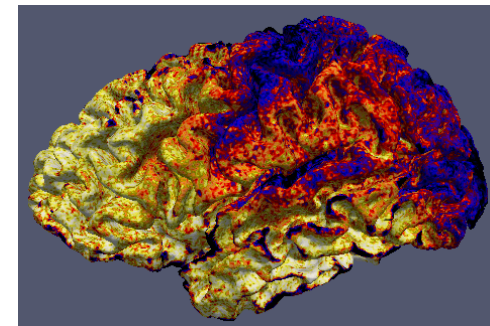
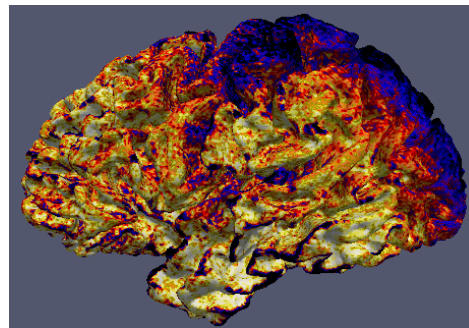
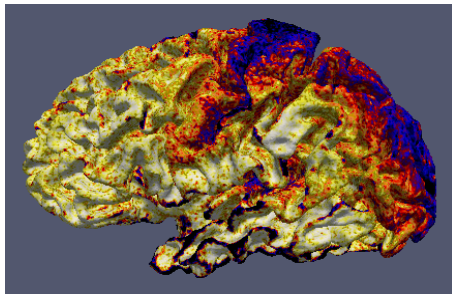
[Dinse et al., under review]

5. Multi-contrast Multi-scale Surface Registration

Rationale: aligning cortical regions based on common architecture

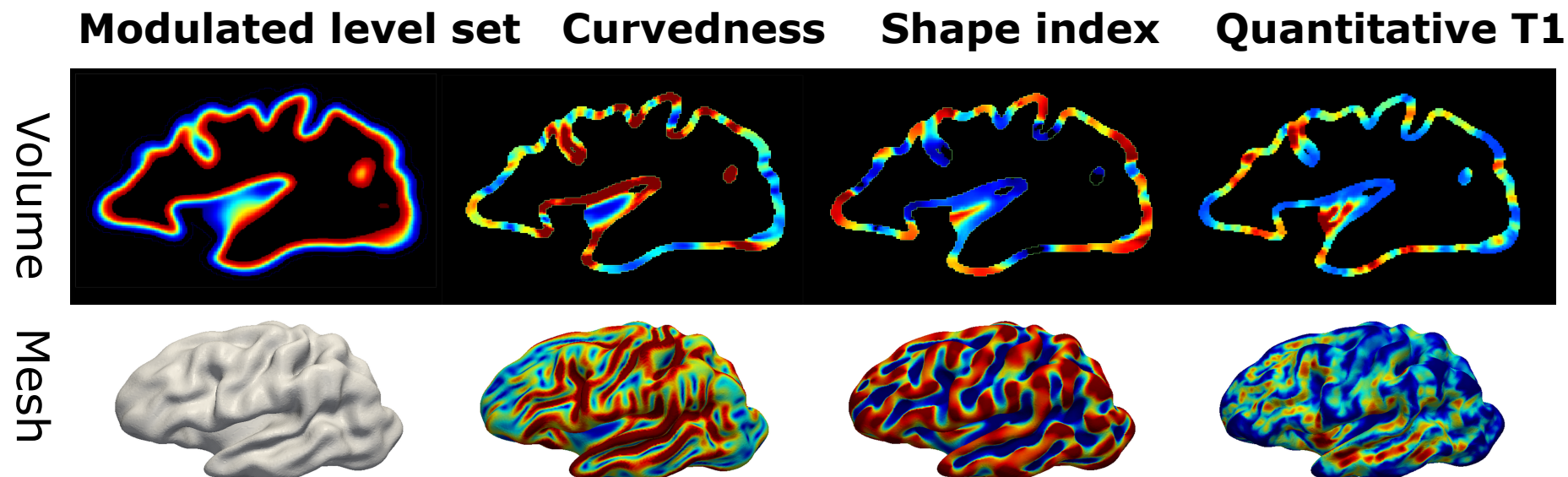


Average T1?



5. Multi-contrast Multi-scale Surface Registration

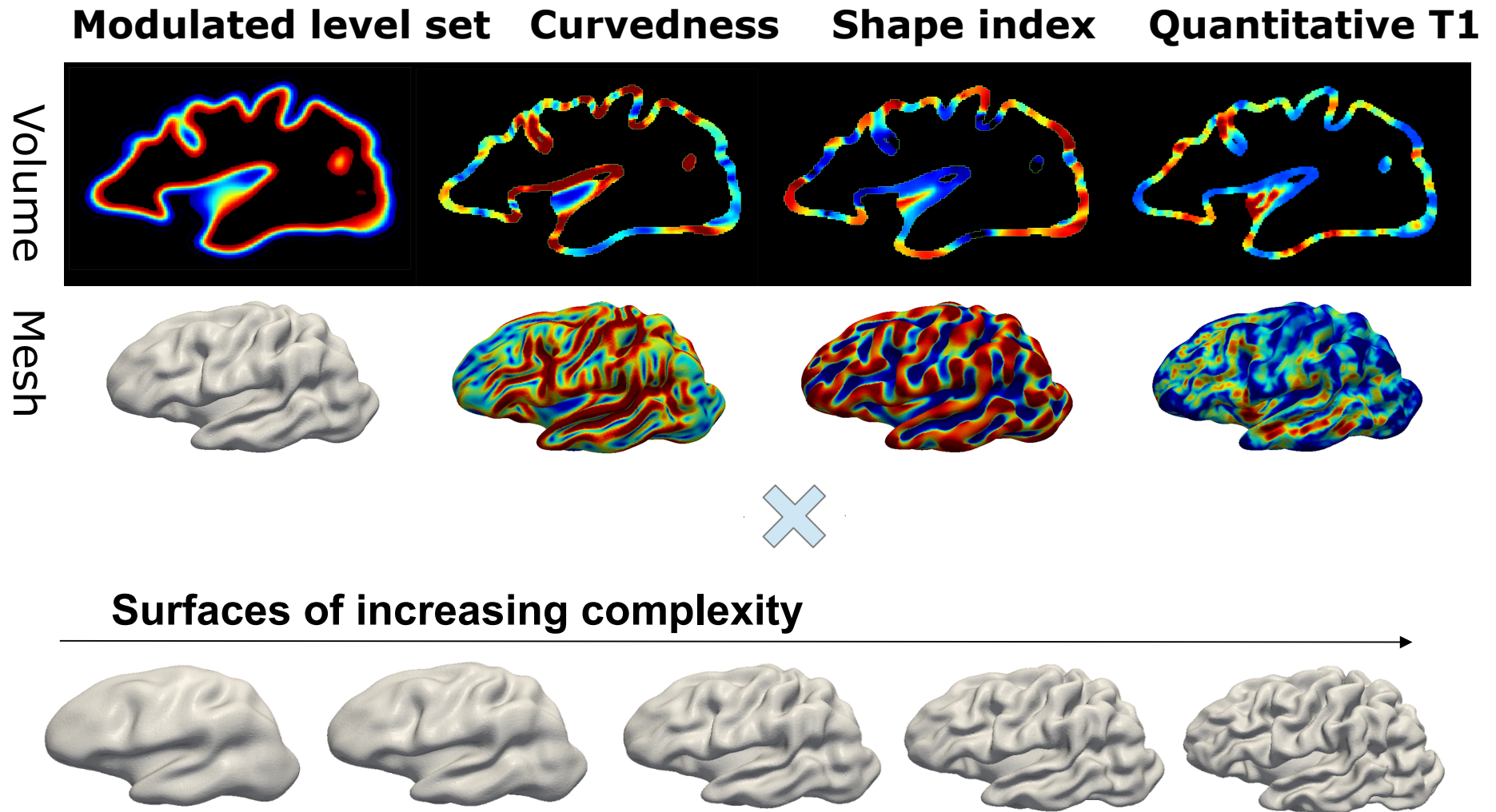
Radial and tangential contrasts



[Tardif et al., MBIA 2013]

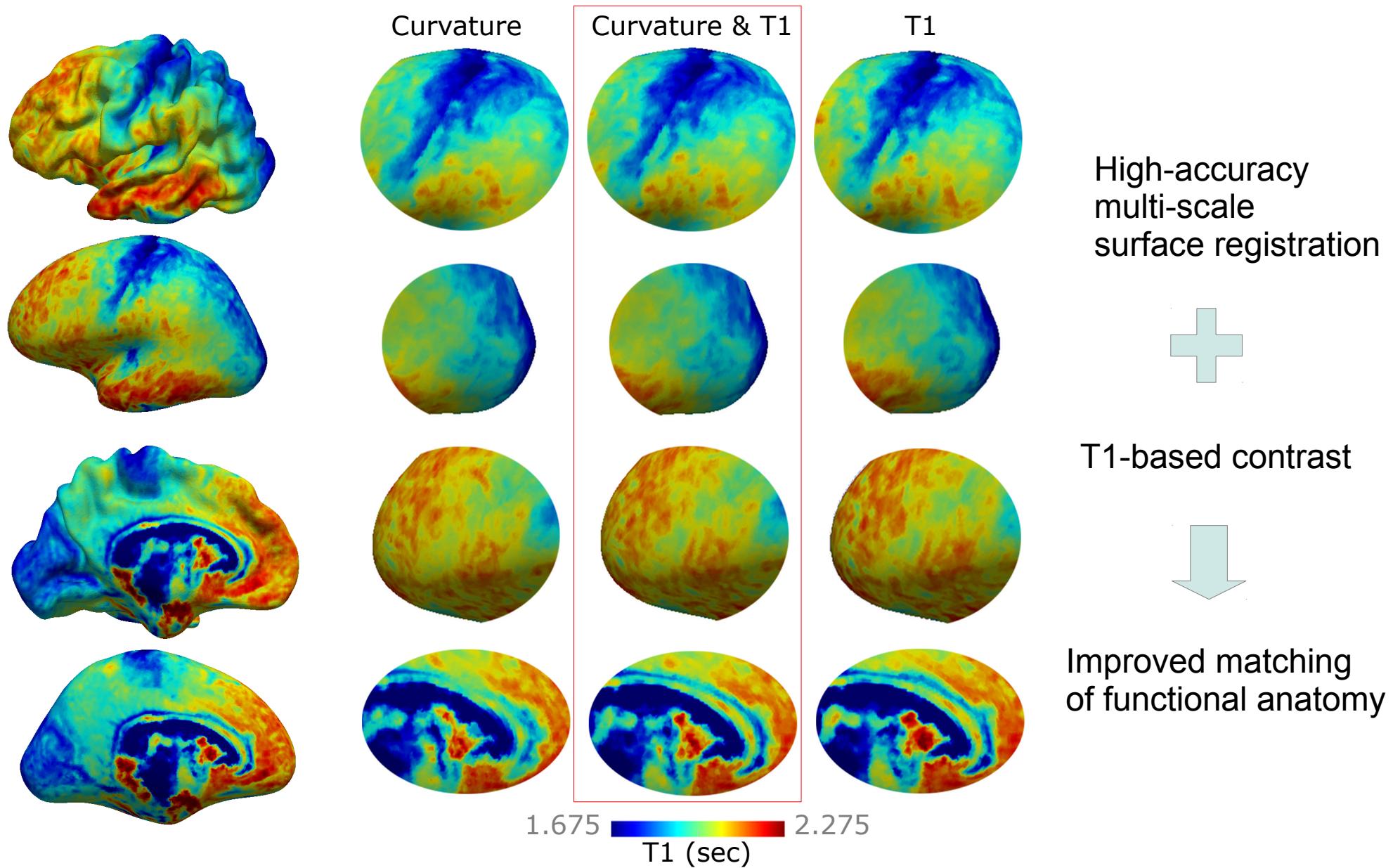
5. Multi-contrast Multi-scale Surface Registration

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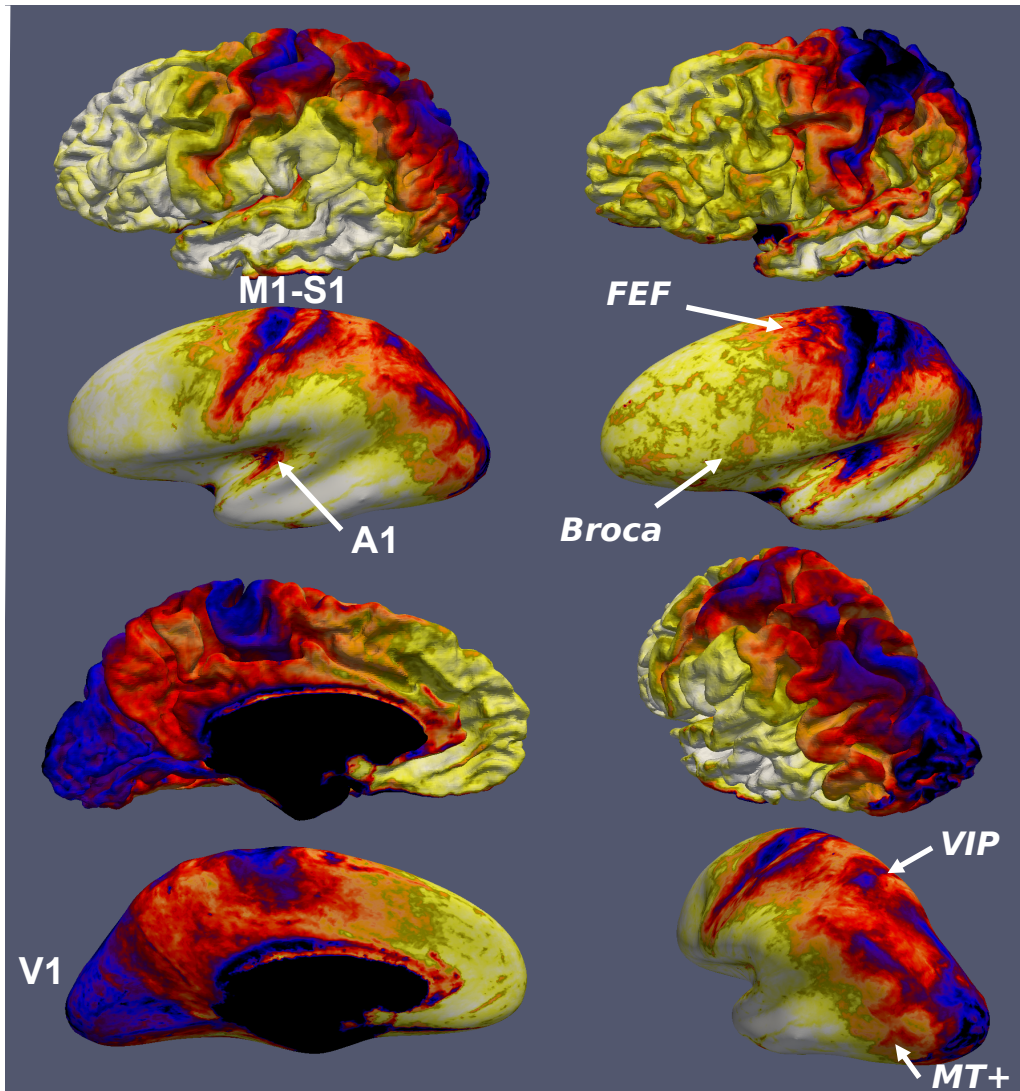
[Tardif et al., MBIA 2013]

High-resolution group averages of cortical anatomy



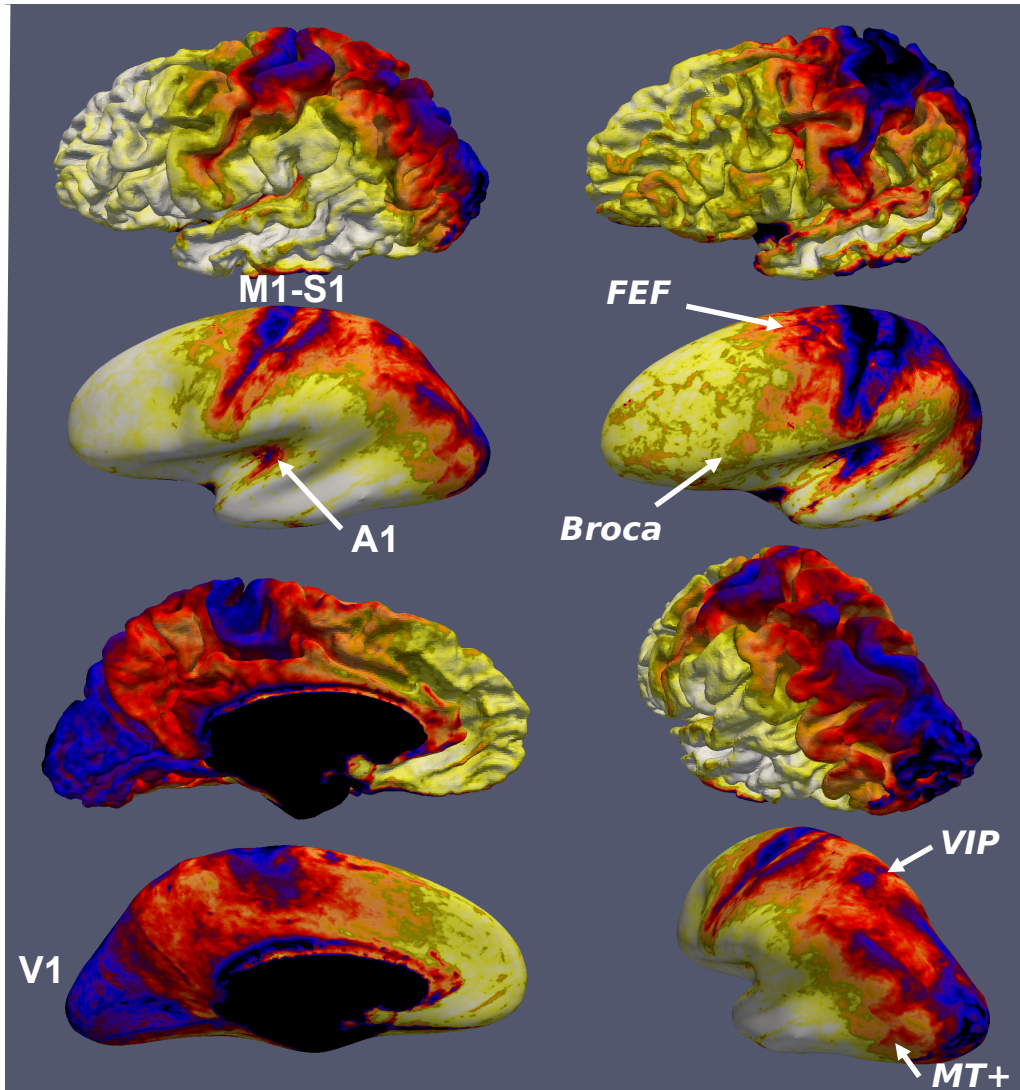
[Tardif et al., MBIA 2013]

Group average maps of T1



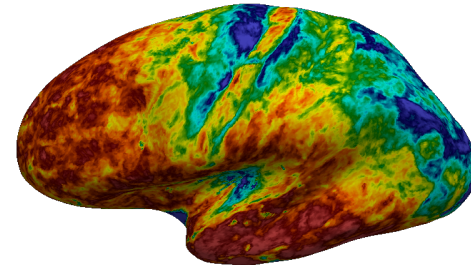
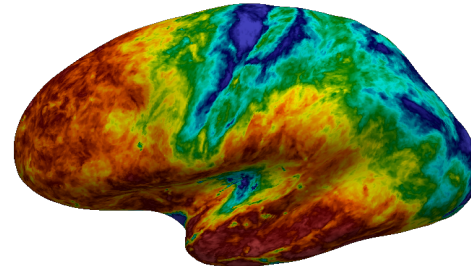
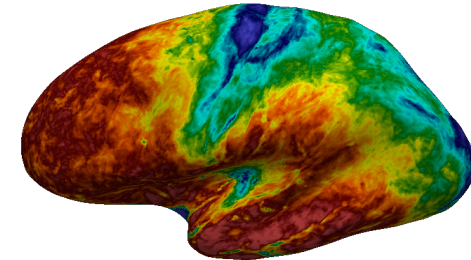
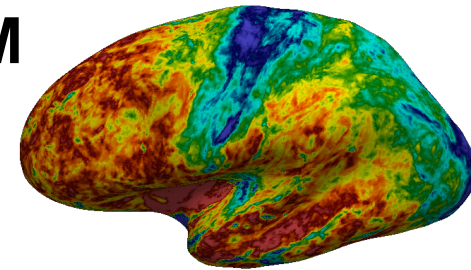
Average over central 50% of T1 profile

Group average maps of T1



Average over central 50% of T1 profile

WM



CSF

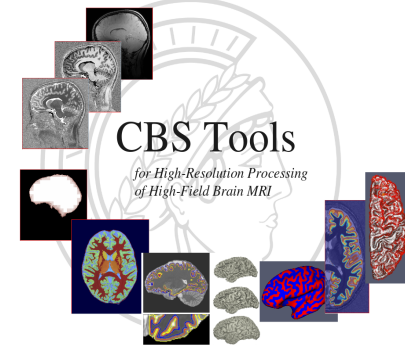
Depth-specific T1 contrast

Cortical depth



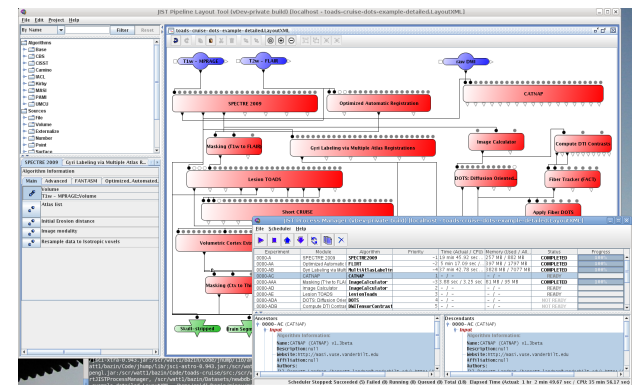
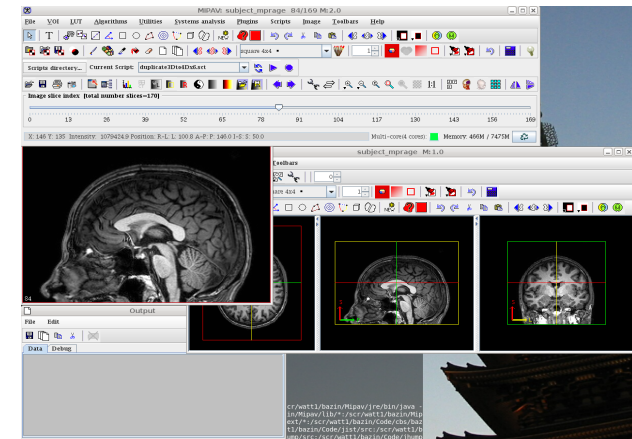
Software: the CBS Tools

<http://www.cbs.mpg.de/institute/software/cbs-hrt/>
<http://www.nitrc.org/projects/cbs-tools/>



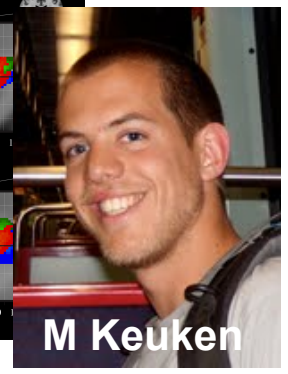
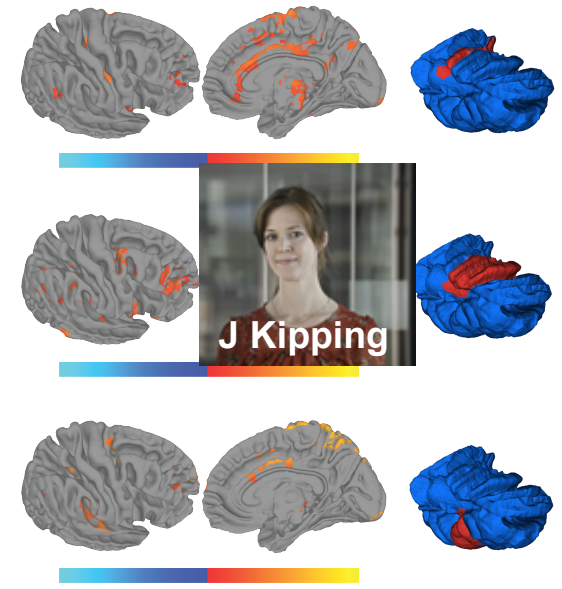
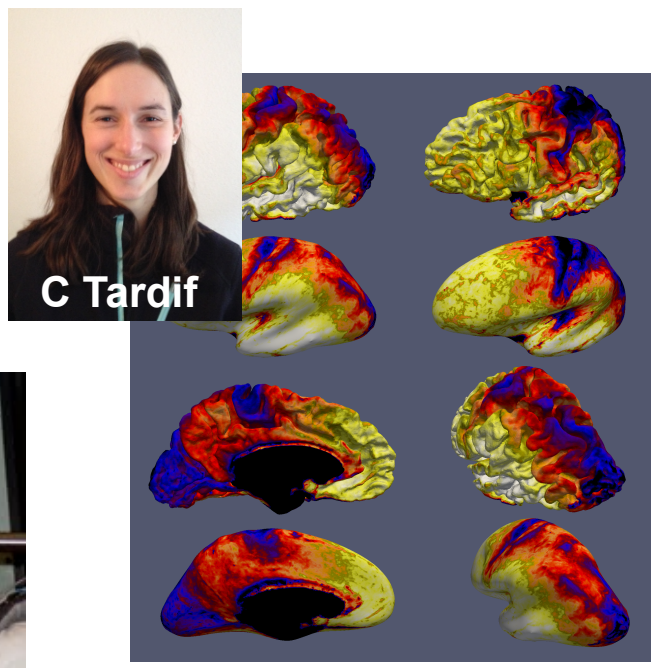
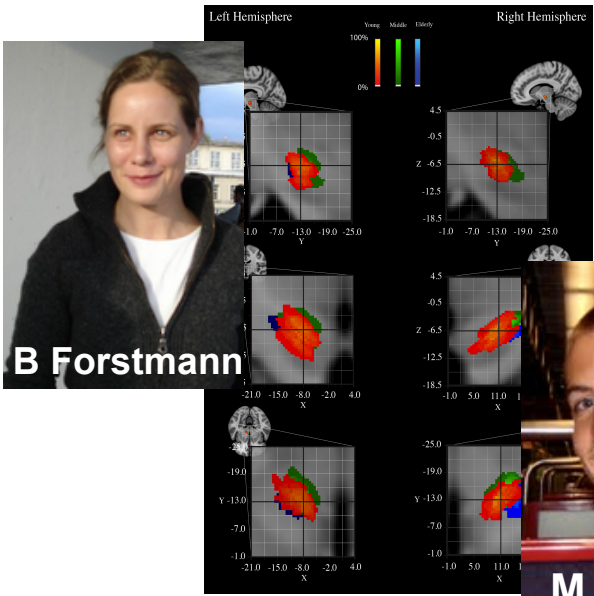
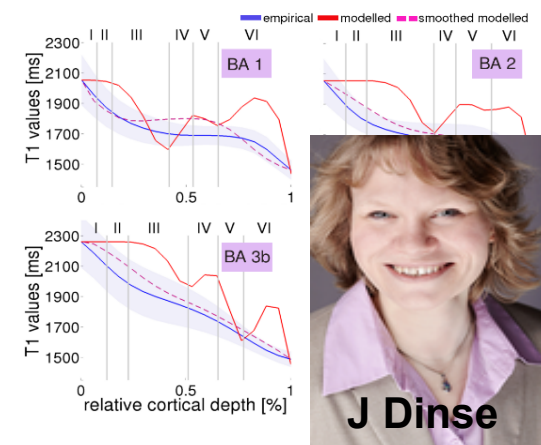
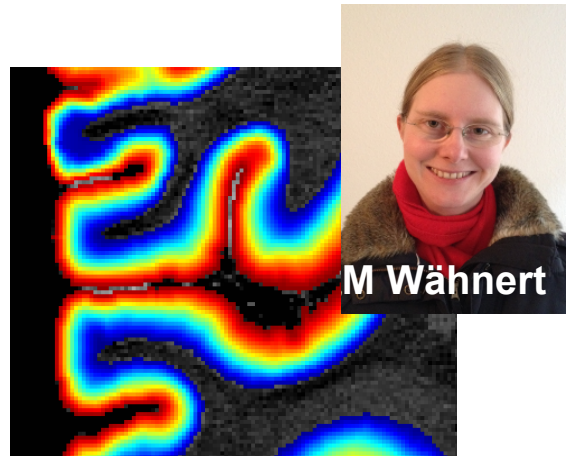
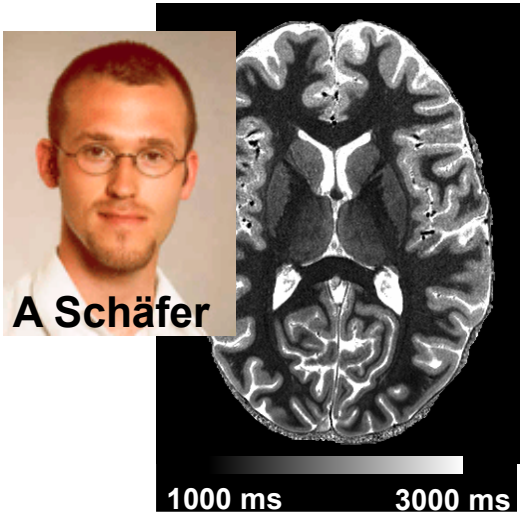
- Integrates all the developed algorithms
- Freely available, integrated in MIPAV and JIST
- Handles MP2RAGE and many other contrasts at 3T and 7T
- Normalization to MNI space routinely at 0.4 mm
- Advanced pipeline environment

Version 3.0 to be released in 05/14



[McAuliffe et al., CBMS 2001]
[Lucas et al., Neuroinf. 2010]

Main contributors



Acknowledgments

Miriam Waehnert
Juliane Dinse
Marcel Weiss
Christoph Leuze
Bibek Dhital

Dr. Andreas Schäfer
Dr. Christine Tardif
Dr. Robert Trampel
PD Dr. Stefan Geyer
PD Dr. Gabriele Lohmann

our Neurophysics team
the Max Planck Institute

Prof. Robert Turner

This work is partially supported by a
Marie Curie International Reintegration Grant
from the European Research Commission

John Bogovic
Xian Fan
Aaron Carass
Prof. Jerry Prince

Max Keuken
Dr. Birte Forstmann

Evan McCreedy
William Gandler
Dr. Matthew McAuliffe

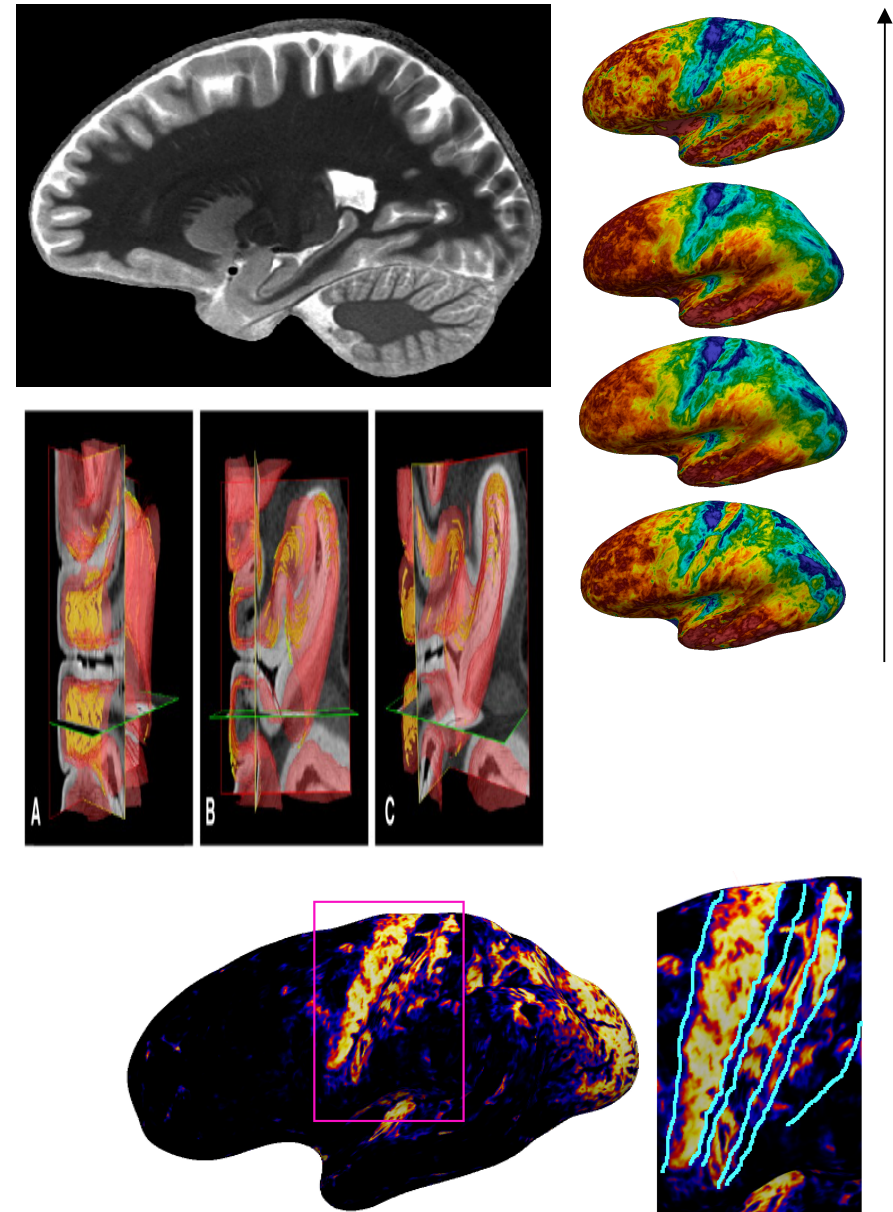
Dr. Bennett Landman

Judy Kipping
Dr. Daniel Margulies



Conclusions

- Ultra-high resolution imaging has matured
- Resolutions, contrasts call for improved image processing methods
- Cortical processing at 0.5 mm reveals fine details of myeloarchitecture
- Volume-preserving cortical lamination is needed to respect layer anatomy
- Cyto-architecture modeling can parcellate cortical areas in-vivo
- Multi-contrast surface alignment improves group averages of myelination



Thank you for your attention!

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