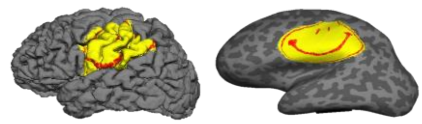
Surface-Based Brain Imaging Analysis and DPABISurf

Chao-Gan YAN, Ph.D.
严超赣

yancg@psych.ac.cn
http://rfmri.org
The R-fMRI Lab
Institute of Psychology, Chinese Academy of Sciences

Why Surface-based Analysis

- Function has surface-based organization
- Inter-subject registration: anatomy, not intensity
- Smoothing
- Clustering
- 2D ReHo other than 3D ReHo

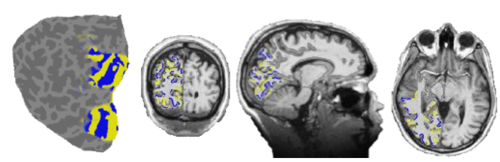


Exploratory Spatial Analysis

- Generally requires spatial smoothing of data to increase SNR
- For group analysis, requires that subjects' brains be aligned to each other on a voxelwise basis.
- Neither needed for an ROI analysis
- Smoothing and inter-subject registration can be performed in the volume or surface.

Why is a Model of the Cortical Surface Useful?

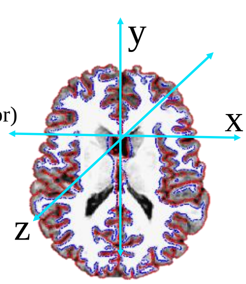
- Local functional organization of cortex is largely 2-dimensional! Eg, functional mapping of primary visual areas:



From (Sereno et al, 1995, Science).

Coordinate Systems: 3D (Volumetric)

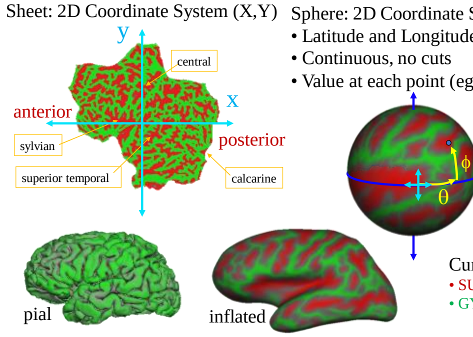
- 3D Coordinate System
  - XYZ
  - RAS (Right-Anterior-Superior)
  - CRS (Column-Row-Slice)
  - Origin (XYZ=0, eg, AC)
  - MR Intensity at each XYZ



Coordinate Systems: 2D (Surface)

Sheet: 2D Coordinate System (X,Y)

Sphere: 2D Coordinate System
- Latitude and Longitude (θ, ϕ)
- Continuous, no cuts
- Value at each point (eg, thickness)

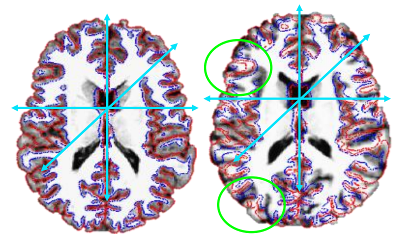


Curvature
- SULCUS (+)
- GYRUS (-)

Inter-subject Registration

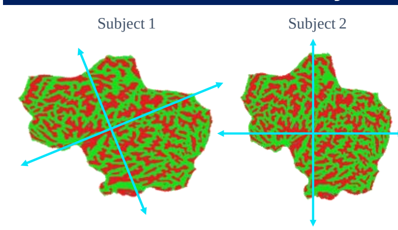
Volumetric Inter-subject Registration

- Affine/Linear
  - Translate
  - Rotate
  - Stretch
  - Shear
  - (12 DOF)



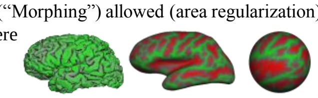
- Match Intensity, Voxel-by-Voxel
- Problems
- Can use nonlinear volumetric

Surface-based Inter-subject Registration

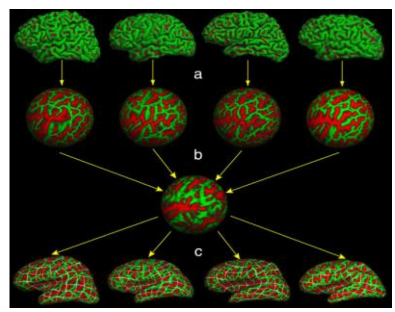


Curvature "Intensity"
- SULCUS (+)
- GYRUS (-)
- Codes folding pattern

- Translate, Rotate, Stretch, Shear (12 DOF)
- Match Curvature, Vertex-by-Vertex
- Nonlinear Stretching ("Morphing") allowed (area regularization)
- Actually done on sphere
- "Spherical Morph"

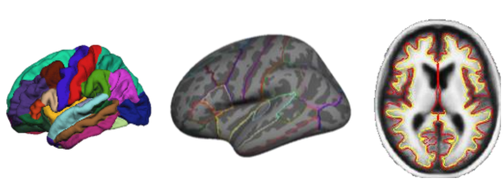


A Surface-Based Coordinate System



Common space for group analysis (like Talairach)

fsaverage



- Has "subject" folder like individual FS subjects
- "Buckner 40" subjects
- Default registration space
- MNI305 coordinates

?h.average.curvature.filled.buckner40.tif

Surface-based Inter-subject Registration

- Gray Matter-to-Gray Matter (it's all gray matter!)
- Gyrus-to-Gyrus and Sulcus-to-Sulcus
- Some minor folding patterns won't line up
- Fully automated, no landmarking needed
- Atlas registration is probabilistic, most variable regions get less weight.
- Done automatically in recon-all
- fsaverage

Spatial Smoothing

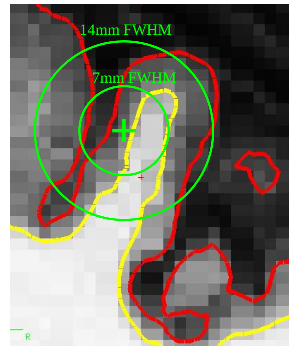
Why should you smooth?
- Might Improve CNR/SNR
- Improve intersubject registration

How much smoothing?
- Blob-size
- Typically 5-20 mm FWHM
- Surface smoothing more forgiving than volume-based

Based on Freesurfer Course

13

Volume-based Smoothing

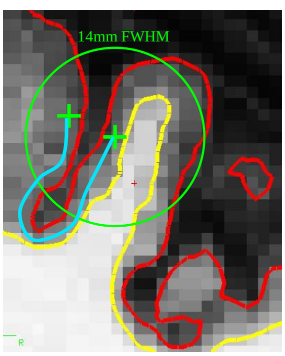


- Smoothing is averaging of “nearby” voxels

Based on Freesurfer Course

14

Volume-based Smoothing



- 5 mm apart in 3D
- 25 mm apart on surface!
- Kernel much larger
- Averaging with other tissue types (WM, CSF)
- Averaging with other functional areas

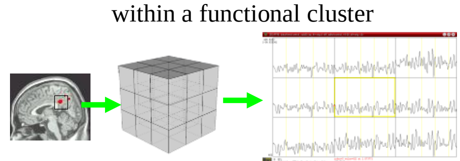
Based on Freesurfer Course

15

3D ReHo

Regional Homogeneity (ReHo)

Similarity or coherence of the time courses within a functional cluster

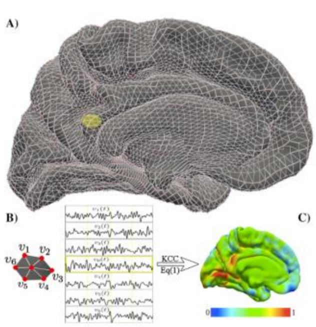


$$W = \frac{\Sigma(R_i)^2 - n(\bar{R})^2}{\frac{1}{12}K^2(n^3 - n)}$$

Zang et al., 2004. Neuroimage

16

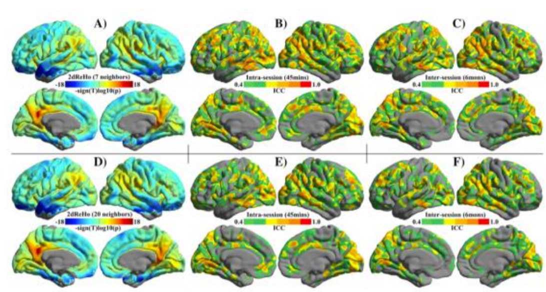
2D ReHo



Zuo et al., 2013. Neuroimage

17

2D ReHo

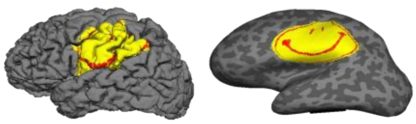


Zuo et al., 2013. Neuroimage

18

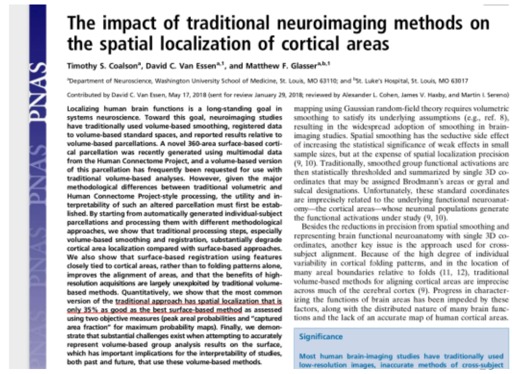
Why Surface-based Analysis

- Function has surface-based organization
- Inter-subject registration: anatomy, not intensity
- Smoothing
- Clustering
- 2D ReHo other than 3D ReHo



Based on Freesurfer Course

Why Surface-based Analysis



PNAS

The impact of traditional neuroimaging methods on the spatial localization of cortical areas

Timothy S. Coalson[a], David C. Van Essen[a,1], and Matthew F. Glasser[a,b,1]

[a]Department of Neuroscience, Washington University School of Medicine, St. Louis, MO 63110; and [b]St. Luke's Hospital, St. Louis, MO 63017

Contributed by David C. Van Essen, May 17, 2018 (sent for review January 29, 2018; reviewed by Alexander L. Cohen, James V. Haxby, and Martin I. Sereno)

Localizing human brain functions is a long-standing goal in systems neuroscience. Toward this goal, neuroimaging studies have traditionally used volume-based smoothing, registered data to volume-based standard spaces, and reported results relative to volume-based parcellations. A novel 360-area surface-based cortical parcellation was recently generated using multimodal data from the Human Connectome Project, and a volume-based version of this parcellation has frequently been requested for use with traditional volume-based analyses. However, given the major methodological differences between traditional volumetric and Human Connectome Project-style processing, the utility and interpretability of such an altered parcellation must first be established. By starting from automatically generated individual-subject parcellations and processing them with different methodological approaches, we show that traditional processing steps, especially volume-based smoothing and registration, substantially degrade cortical area localization compared with surface-based approaches. We also show that surface-based registration using features closely tied to cortical areas, rather than to folding patterns alone, improves the alignment of areas, and that the benefits of high-resolution acquisitions are largely unexploited by traditional volume-based methods. Quantitatively, we show that the most common version of the traditional approach has spatial localization that is only 35% as good as the best surface-based method as assessed using two objective measures (peak areal probabilities and "captured area fraction" for maximum probability maps). Finally, we demonstrate that substantial challenges exist when attempting to accurately represent volume-based group analysis results on the surface, which has important implications for the interpretability of studies, both past and future, that use these volume-based methods.

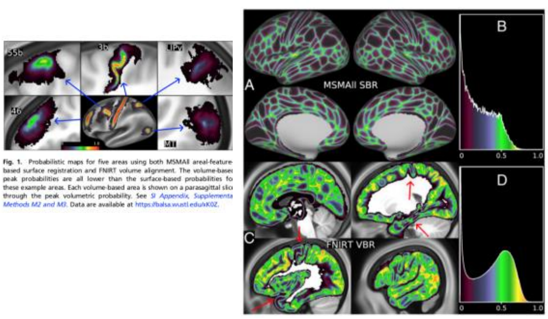
mapping using Gaussian random-field theory requires volumetric smoothing to satisfy its underlying assumptions (e.g., ref. 8), resulting in the widespread adoption of smoothing in brain-imaging studies. Spatial smoothing has the seductive side effect of increasing the statistical significance of weak effects in small sample sizes, but at the expense of spatial localization precision (9, 10). Traditionally, smoothed group functional activations are then statistically thresholded and summarized by single 3D coordinates that may be assigned Brodmann's areas or gyral and sulcal designations. Unfortunately, these standard coordinates are imprecisely related to the underlying functional neuroanatomy—the cortical areas—whose neuronal populations generate the functional activations under study (9, 10).

Besides the reductions in precision from spatial smoothing and representing brain functional neuroanatomy with single 3D coordinates, another key issue is the approach used for cross-subject alignment. Because of the high degree of individual variability in cortical folding patterns, and in the location of many areal boundaries relative to folds (11, 12), traditional volume-based methods for aligning cortical areas are imprecise across much of the cerebral cortex (9). Progress in characterizing the functions of brain areas has been impeded by these factors, along with the distributed nature of many brain functions and the lack of an accurate map of human cortical areas.

Significance

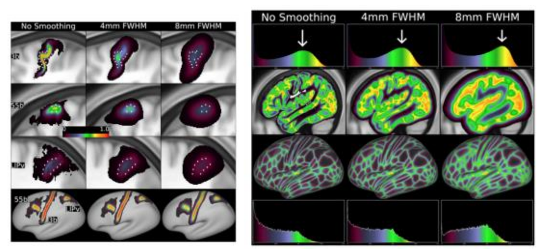
Most human brain-imaging studies have traditionally used low-resolution images, inaccurate methods of cross-subject

Why Surface-based Analysis



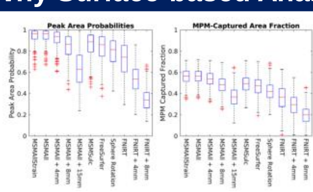
Coalson et al., 2018. PNAS

Why Surface-based Analysis



Coalson et al., 2018. PNAS

Why Surface-based Analysis



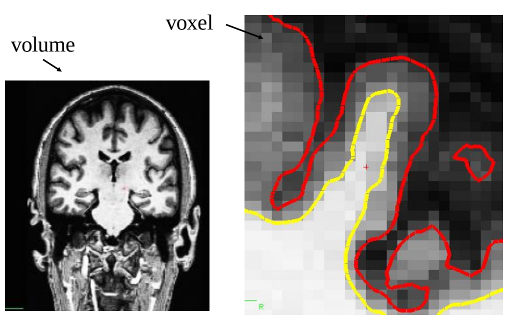
Widespread adoption of surface-based approaches has been slow: the desire to replicate or compare with existing studies that used the traditional volume-based approach; the relative lack of "turn-key" tools for running a surface-based analysis; the learning curve for adopting surface-based analysis methods; unawareness of the problems with traditional volume-based analysis; and uncertainty or even skepticism as to how much of a difference these methodological choices make.

Coalson et al., 2018. PNAS

25

26

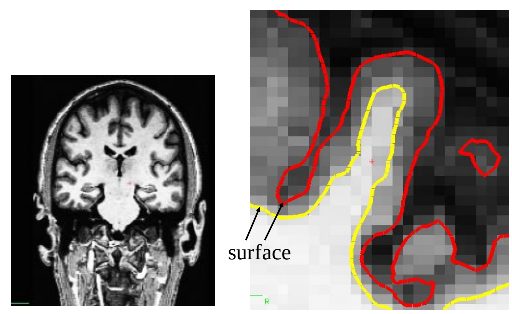
Jargon



Based on Freesurfer Course

27

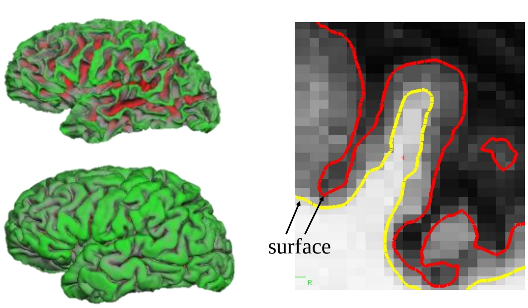
Jargon



Based on Freesurfer Course

28

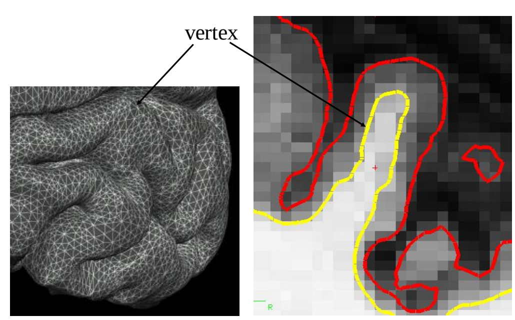
Jargon



Based on Freesurfer Course

29

Jargon

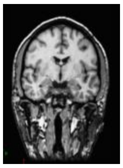


Based on Freesurfer Course

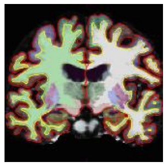
30

Call FreeSurfer…

FreeSurfer creates computerized models of the brain from MRI data.

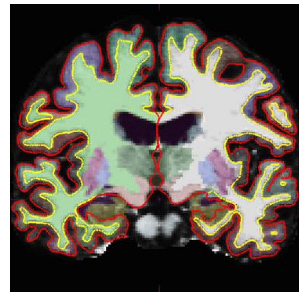


Input:
T1-weighted (MPRAGE)
1mm³ resolution
(.dcm)

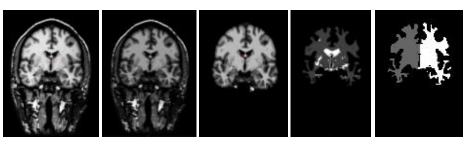


Output:
Segmented & parcellated conformed volume
(.mgz)

Recon



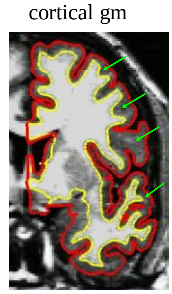
Volumes



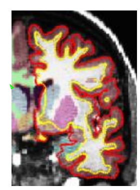
orig.mgz T1.mgz brainmask.mgz wm.mgz filled.mgz (Subcortical Mass)

Cortical vs. Subcortical GM

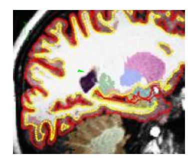
cortical gm



subcortical gm



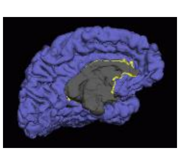
coronal

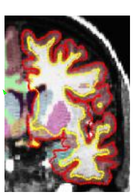


sagittal

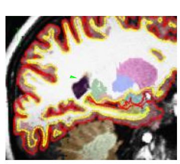
Cortical vs. Subcortical GM

subcortical gm





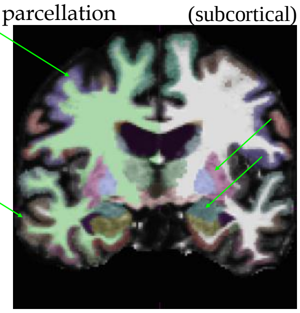
coronal



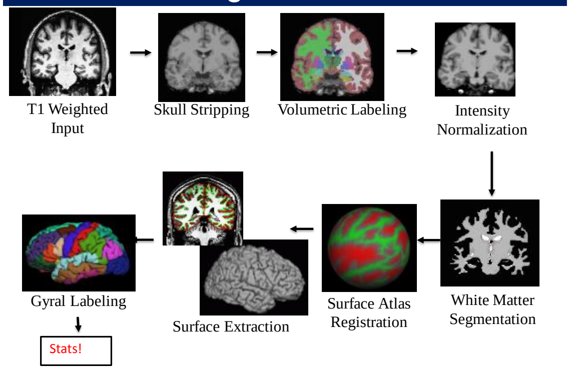
sagittal

Parcellation vs. Segmentation

(cortical) parcellation (subcortical) segmentation

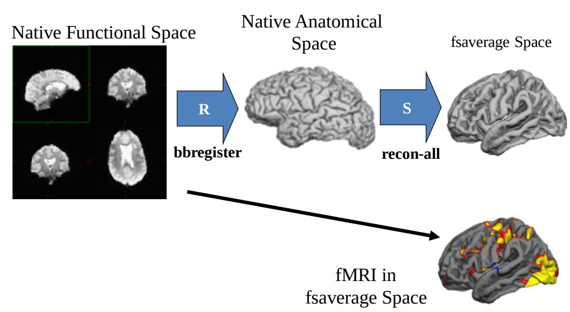


Processing Stream Overview



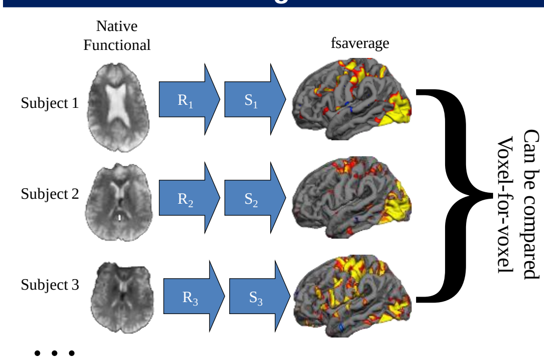
Based on Freesurfer Course

fMRI Registration

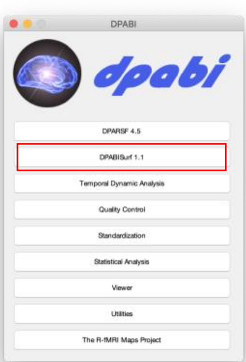


Based on Freesurfer Course

fMRI Registration

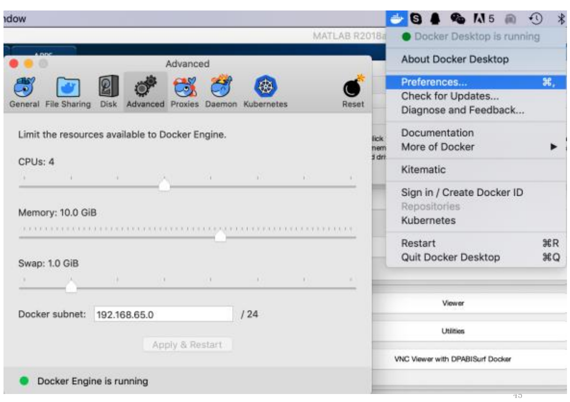


Based on Freesurfer Course

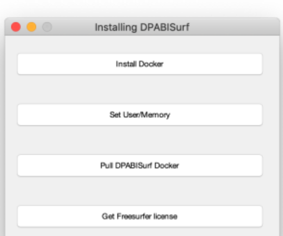


43

44

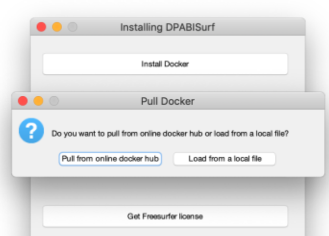


46

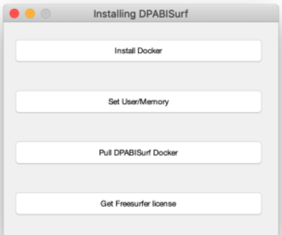


Linux: sudo groupadd docker
sudo usermod -aG docker $USER

47

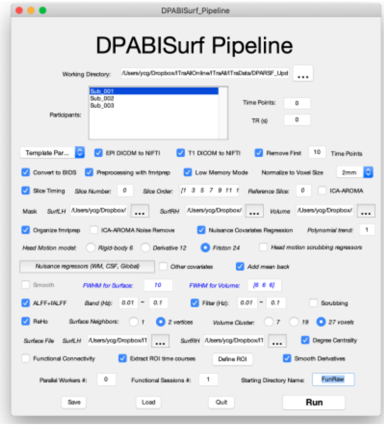


48



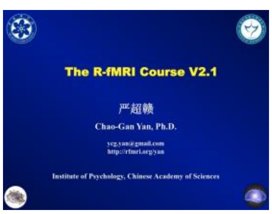
Please get Freesurfer license, and specify the license.txt you received in your email. Please visit:
https://surfer.nmr.mgh.harvard.edu/registration

49



50

Further Help



http://rfmri.org/Course

http://rfmri.org/wiki

The R-fMRI Journal Club

Official Account: RFMRILab

51

DPABI特训营与DPABISurf加强营

定期举办，请关注http://rfmri.org

52

深度特训与数据分析

DEEP BRAIN

静息态功能磁共振成像数据处理深度特训

从您见到这条消息开始，您便将有机会与 The R-fMRI Lab 的静息态功能磁共振专家团队共同探索大脑的奥秘！深度跟组特训期间，您将会亲身体验：

- 数据处理 专家指导下高效学习静息态功能磁共振成像数据处理
- 思路设计 与国际知名专家讨论形成研究思路
- 论文撰写 系统的 SCI 论文写作训练

http://deepbrain.com

DEEP BRAIN

静息态功能磁共振成像深度数据分析

功能磁共振成像越来越成为一种主流的科研手段，然而功能磁共振的数据分析却是一项具有高度挑战性的工作。海量的原始数据，繁多的分析步骤，复杂的分析方法都让研究者们无所适从。恰当的分析方法可以从普通的数据中挖掘出富有创新性的结果，而不适当的分析则可能让精心收集的数据黯然失色。深度大脑公司联合 The R-fMRI Lab 的专业脑功能成像研究团队推出一站式功能磁共振数据分析解决方案，助您从容应对功能磁共振数据带来的挑战。

DPABISurf工作站

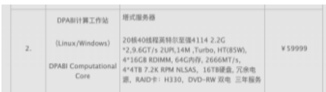
DPABI工作站

序号	名称	参数	市场指导价
1	DPABI教育工作站（Windows） DPABI Educational Core Windows	14英寸轻薄窄边框商务办公笔记本电脑 八代四核八线程i5-8250U, 16G内存, 256G固态硬盘+1T机械硬盘, PCIe, 独立显卡, 指纹识别	￥8999
2.	DPABI计算工作站 (Linux/Windows) DPABI Computational Core	塔式服务器 20核40线程英特尔至强4114 2.2G *2,9.6GT/s 2UPI,14M ,Turbo, HT(85W), 4*16GB RDIMM, 64G内存, 2666MT/s, 4*4TB 7.2K RPM NLSAS，16TB硬盘，冗余电源，RAID卡：H330，DVD-RW 双电 三年服务	￥59999
3.	DPABI移动工作站 （Windows） DPABI Mobile Core Windows	15.6英寸移动图形工作站 八代六核十二线程i7-8750H, 16G内存, 256G固态硬盘+1T机械硬盘, P1000 4G独立显卡	￥24999
4.	DPABI计算工作站 (Mac) DPABI Computational Core Mac	iMac Pro 14核28线程Intel Xeon W 处理器，2.5GHz Turbo Boost 最高可达 4.3GHz, 64G内存 2666MHz DDR4 ECC, 1TB 固态硬盘, Radeon Pro Vega 56 图形处理器 8G HBM2 显存	￥84999
5.	DPABI移动工作站 (Mac) DPABI Mobile Core Mac	15 英寸 MacBook Pro 八代六核十二线程Intel Core i7 处理器, Turbo Boost 最高可达 4.3GHz, 16G内存 2400MHz DDR4，512G固态硬盘, Radeon Pro 560X 图形处理器，配备 4G GDDR5 显存，采用原彩显示技术的视网膜显示屏，触控栏和触控 ID, 四个雷雳 3 端口	￥32999
6.	DPABI定制工作站	如果您有更充足的预算，需要更为强大的性能，请联系我们按需定制服务器	定制

http://deepbrain.com/DPABICore

54

DPABI计算工作站



2.	DPABI计算工作站 (Linux/Windows) DPABI Computational Core	塔式服务器 20核40线程英特尔至强4114 2.2G *2,9.6GT/s 2UPI,14M ,Turbo, HT(85W), 4*16GB RDIMM, 64G内存, 2666MT/s, 4*4TB 7.2K RPM NLSAS, 16TB硬盘, 冗余电源, RAID卡: H330, DVD-RW 双电 三年服务	¥59999

http://deepbrain.com/DPABICore

DPABISurf 并行计算:

每天完成 **20** 个被试的皮层计算!!!

55

The R-fMRI Lab

WeChat Official Account: RFMRILab

Acknowledgments

Chinese Academy of Sciences
Xi-Nian Zuo
Hangzhou Normal University
Yu-Feng Zang
NYU Child Study Center
F. Xavier Castellanos
Child Mind Institute
Michael P. Milham

Funding
- National Natural Science Foundation of China
- National Key R&D Program of China
- Chinese Academy of Sciences

57

Thanks for your attention!

58