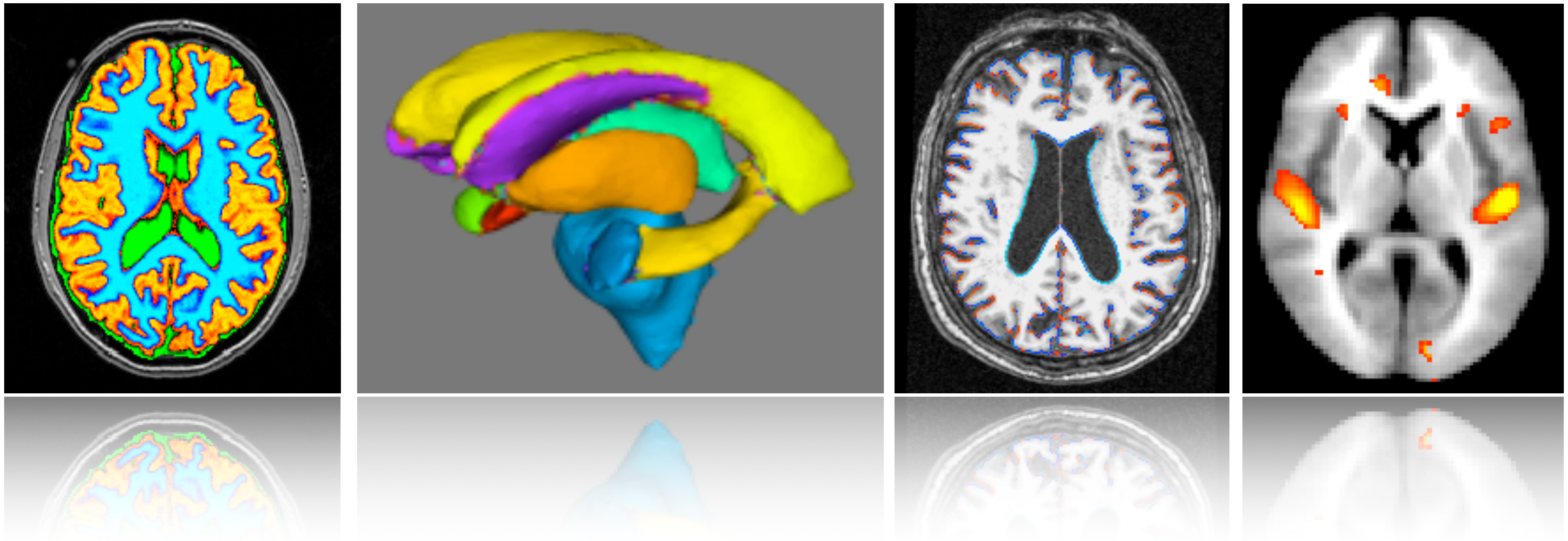
Structural Segmentation
结构分割

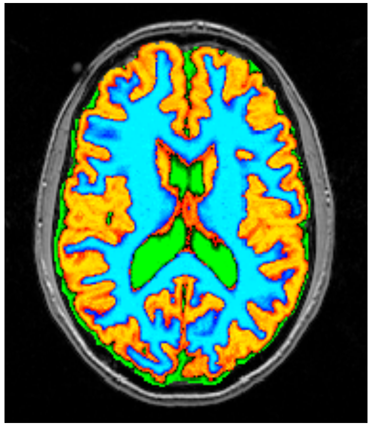


- FAST tissue-type segmentation 组织类型分割
- FIRST sub-cortical structure segmentation 皮层下结构分割
- BIANCA segmentation of white matter lesions 白质病灶分割
- FSL-VBM voxelwise grey-matter density analysis 体素灰质密度分析
- SIENA/SIENAX global atrophy estimation 全局萎缩估计

中文翻译：钟嘉慧 孔亚卓

FAST
FMRIB's Automated Segmentation Tool
FMRIB的自动分割工具
generic tissue-type segmentation and bias field correction
通用组织类型分割与偏置场校正

- Input: brain-extracted image(s)
  输入：提取大脑后的图像
- Segments into different tissue types
  将图像分割成不同的组织类型
- At the same time, estimate bias field
  与此同时估计偏置场
- Robust to noise, because each voxel looks at neighbours
  不受噪音的影响，因为每个体素以相邻体素为参考

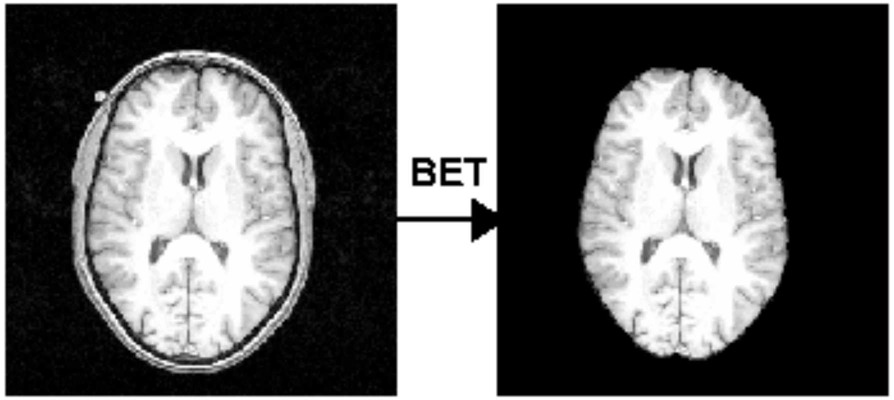


FAST: Input 输入

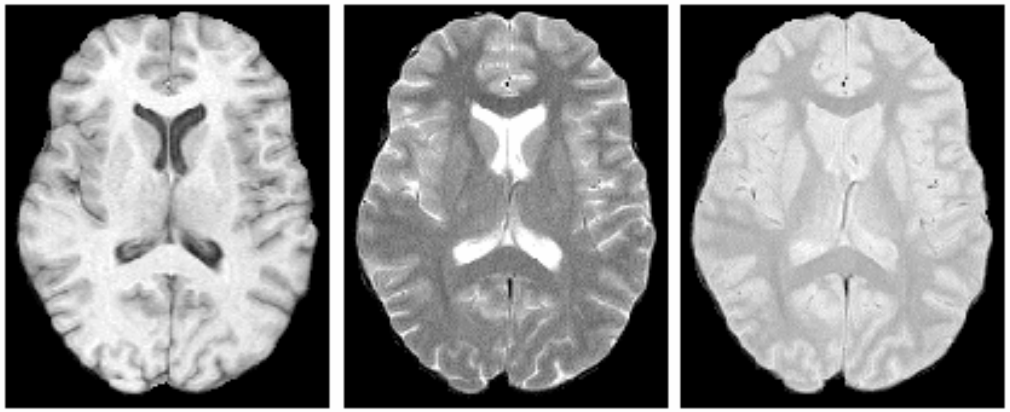
- First use BET to remove non-brain
  首先使用BET去除非脑组织

  All *volumetric* results are *highly sensitive* to errors here.
  所有体积结果都对此处的错误非常敏感

  For *bias-field correction alone* the errors do not matter that much
  对于单纯的偏置场校正而言，这里的错误影响不大

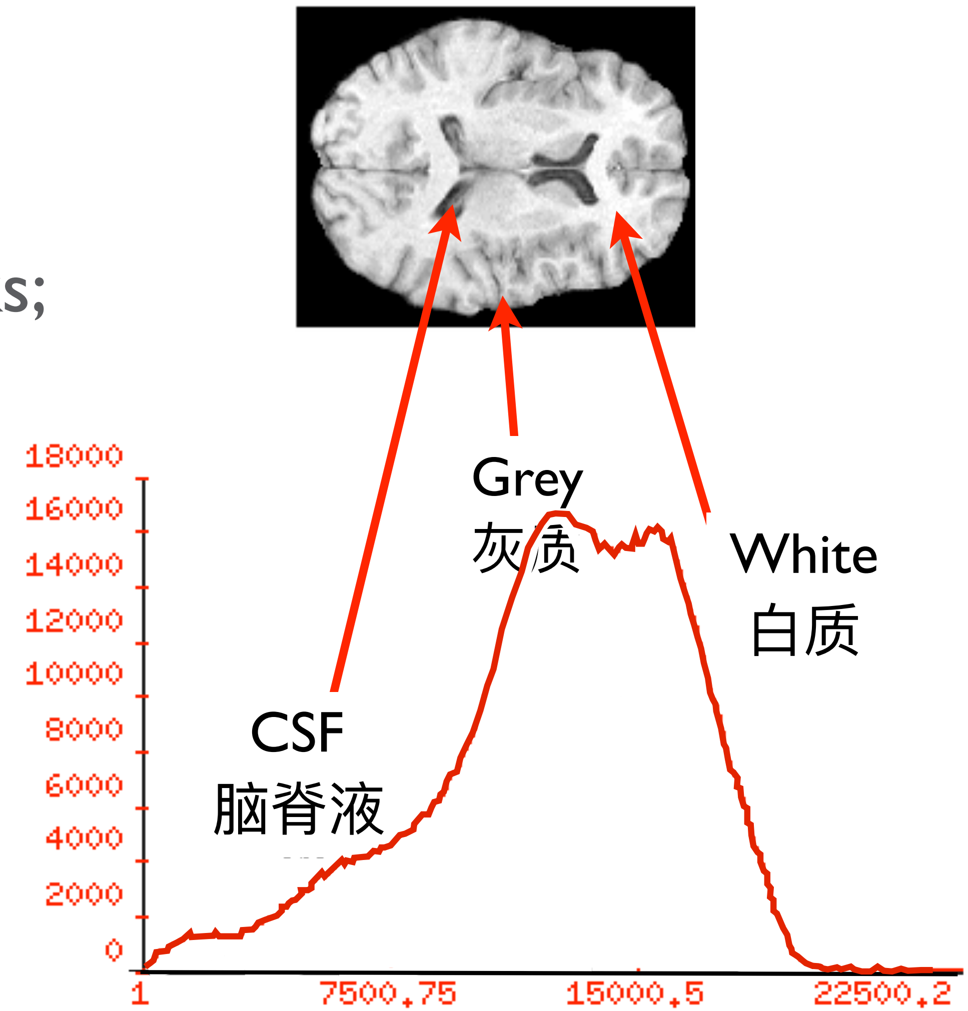


- Input is normally a single image (T1, T2, proton-density….)
  输入通常是单张图像（T1,T2,质子密度……）
- Or several inputs ("multichannel") 也可以输入多张图("多通道")
- For multi-channel, all must be pre-aligned (FLIRT) 要做"多通道"处理，图像必须先对齐（FLIRT）



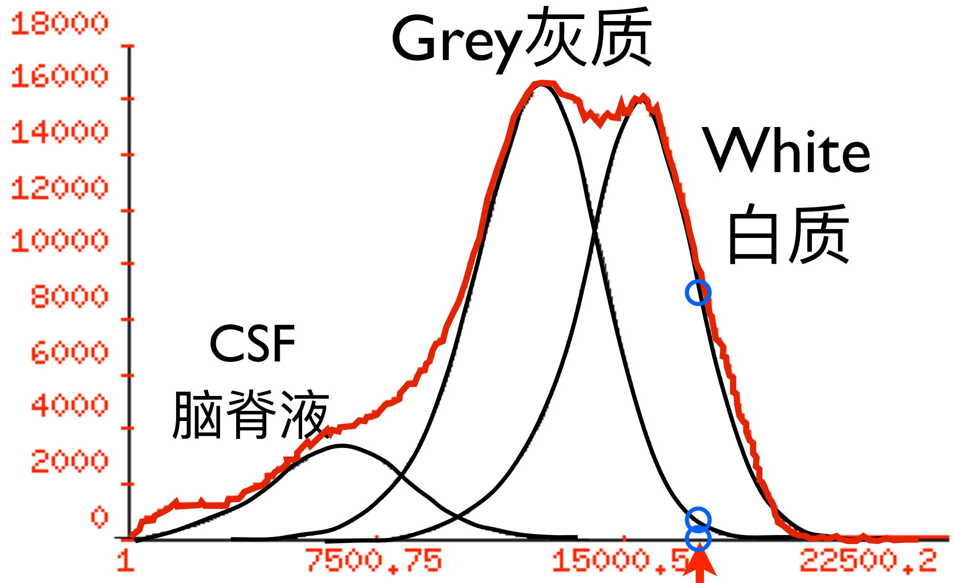
Intensity Model 强度模型
tissue intensity distributions 组织强度分布

- Histogram = voxel count vs. intensity
  直方图 = 体素计数与强度
- Model = mixture of Gaussians
  模型 = 高斯混合
- If well separated, have clear peaks; then segmentation easy
  如果分离良好，有明显的峰值，则容易分割
- Overlap worsened by 受以下因素影响:
  - Bias field 偏置场
  - Blurring 模糊
  - Low resolution 低分辨率
  - Head motion 头动
  - Noise 噪音



Probability Model 概率模型

- Histogram = voxel count vs. intensity
  直方图 = 体素计数与强度
- Model = mixture of Gaussians
  模型 = 高斯混合
- Probability determined for each tissue class
  确定每个组织类别的概率

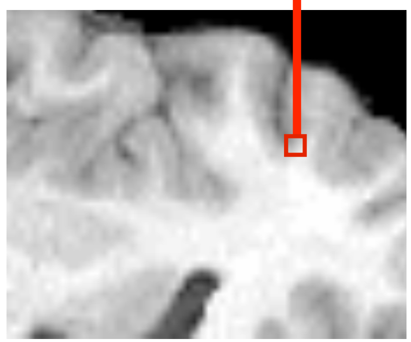


For example 例如:

Voxel near WM/GM border

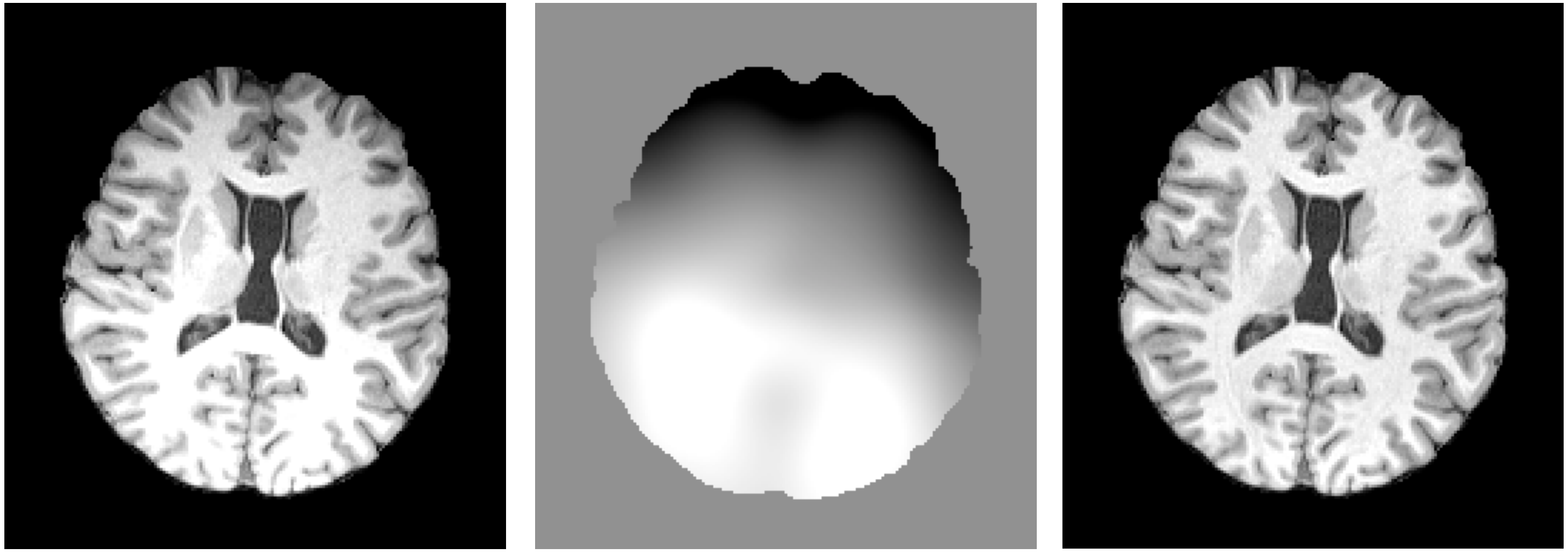
靠近白质/灰质边界的体素

Intensity强度 = 17203



P(CSF) near zero 接近0
P(GM) low 低
P(WM) moderate 中等

Bias Field Correction 偏置场校正



Original 原始 Bias 偏置场 Restored 校正后的

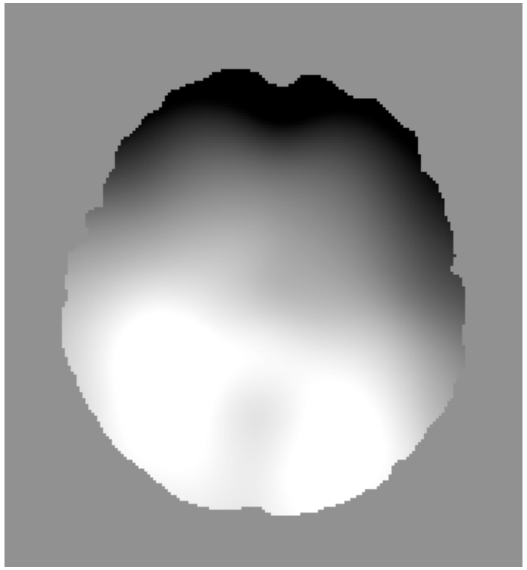
- MRI RF (radio-frequency field) inhomogeneity causes intensity variations across space MRI的射频场不均匀性会导致跨空间的强度变化
- Causes problems for segmentation 对分割造成影响
- Need to remove bias field before or during segmentation

  需要在分割之前或期间进行偏置场校正
- Becomes more common and problematic at high field

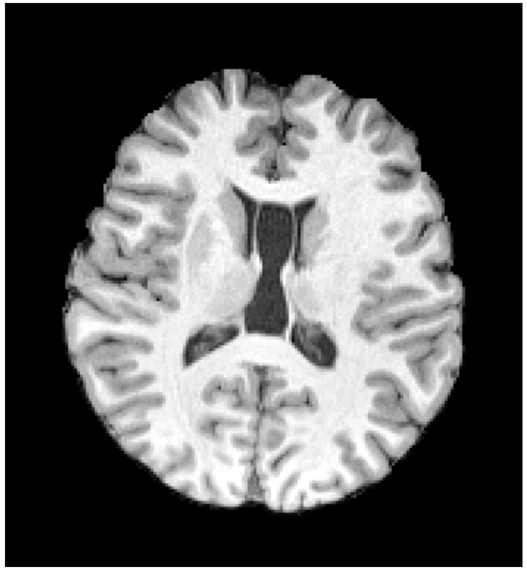
  这一问题在高强度磁场中更为常见和严重

Bias Field Correction 偏置场校正

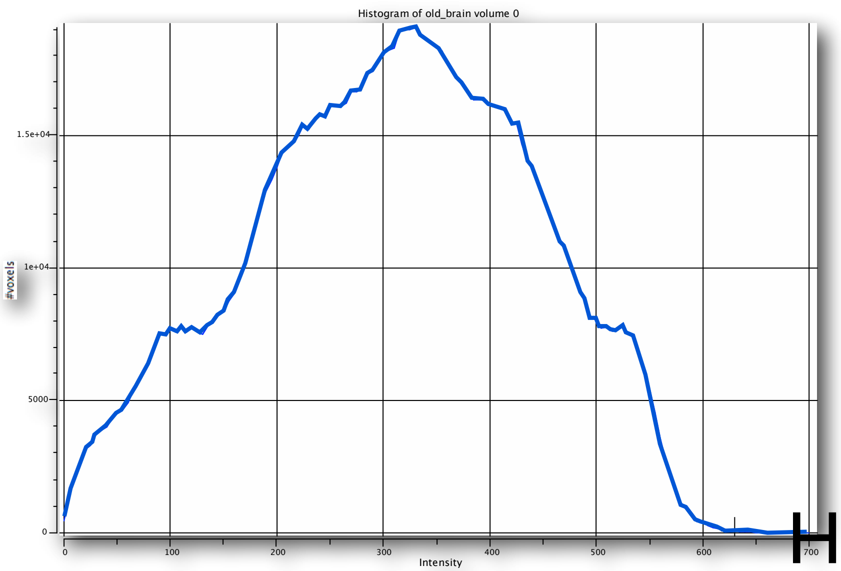
Original 原始

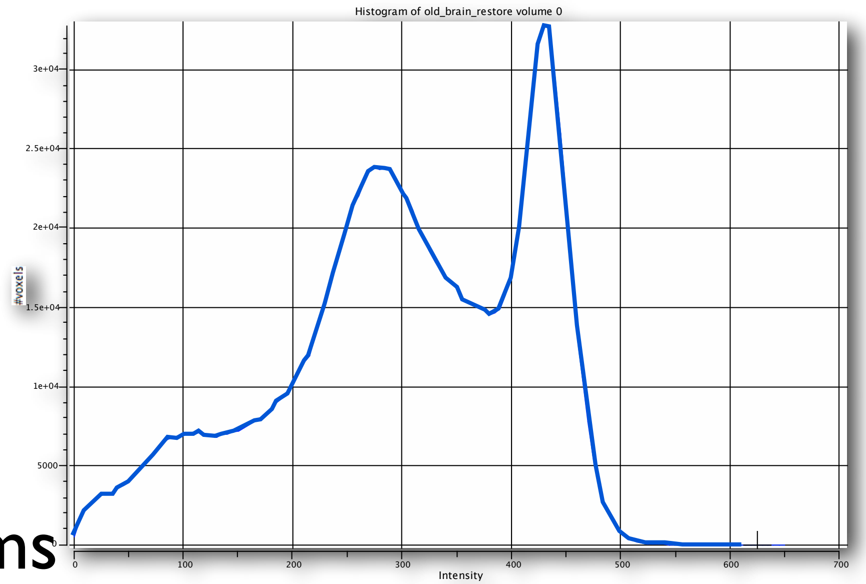


Bias 偏置场



Restored 校正后的

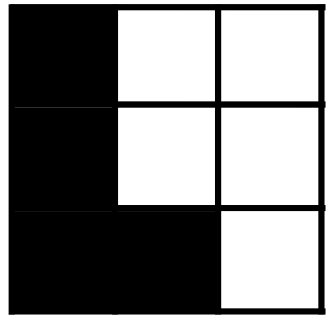




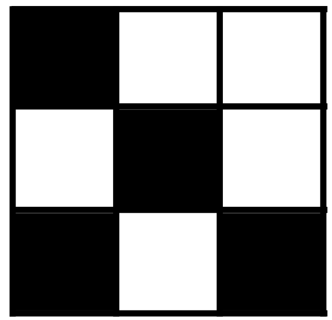
Histograms
直方图

Use Spatial Neighbourhood Information (MRF)
使用空间邻域信息(MRF)

- Neighbourhood information: "if my neighbours are grey matter then I probably am too"
  邻域信息："如果我的邻居都是灰质，那我很可能也是。"
- Simple classifiers (like K-means) do not use spatial neighbourhood information
  简单的分类方法(如K-均值算法)不使用空间邻域信息
- More robust to noise 较不受噪音的影响
- Need the right balance between believing neighbours or intensity
  需要在信任邻域信息或强度值间作出平衡



Likely configuration 构造相似
High probability 高概率



Unlikely configuration 构造不相似
Low probability 概率低

Use Spatial Neighbourhood Information (MRF)
使用空间邻域信息(MRF)

Combine with probability based on
结合概率基于：

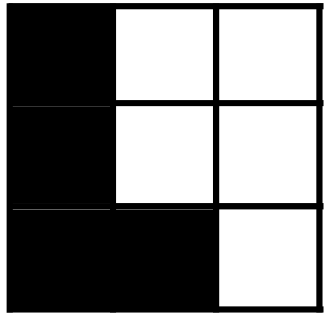
Gaussian Mixture Model

高斯混合模型:

Final log prob 最终对数概率 =
log p(intensity 强度值) + β log p(MRF)

Final result depends on β value
最终结果取决于β值

This is user-adjustable
这是用户可调节的



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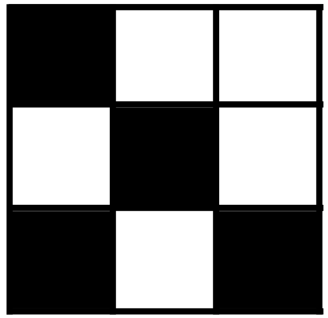
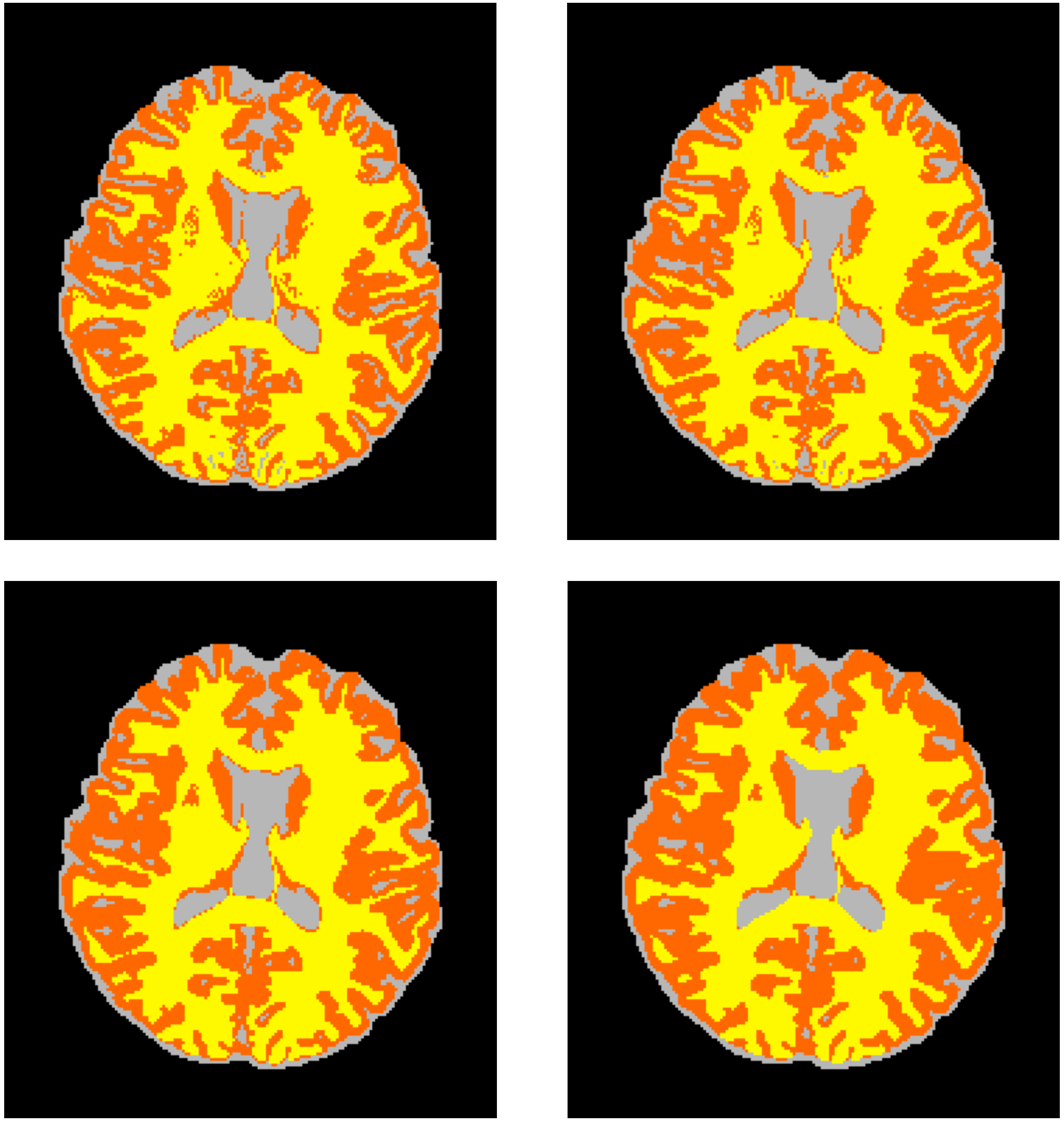
High probability 高概率



Unlikely configuration 构造不相似
Low probability 概率低

Effect of MRF Weighting

MRF加权的影响



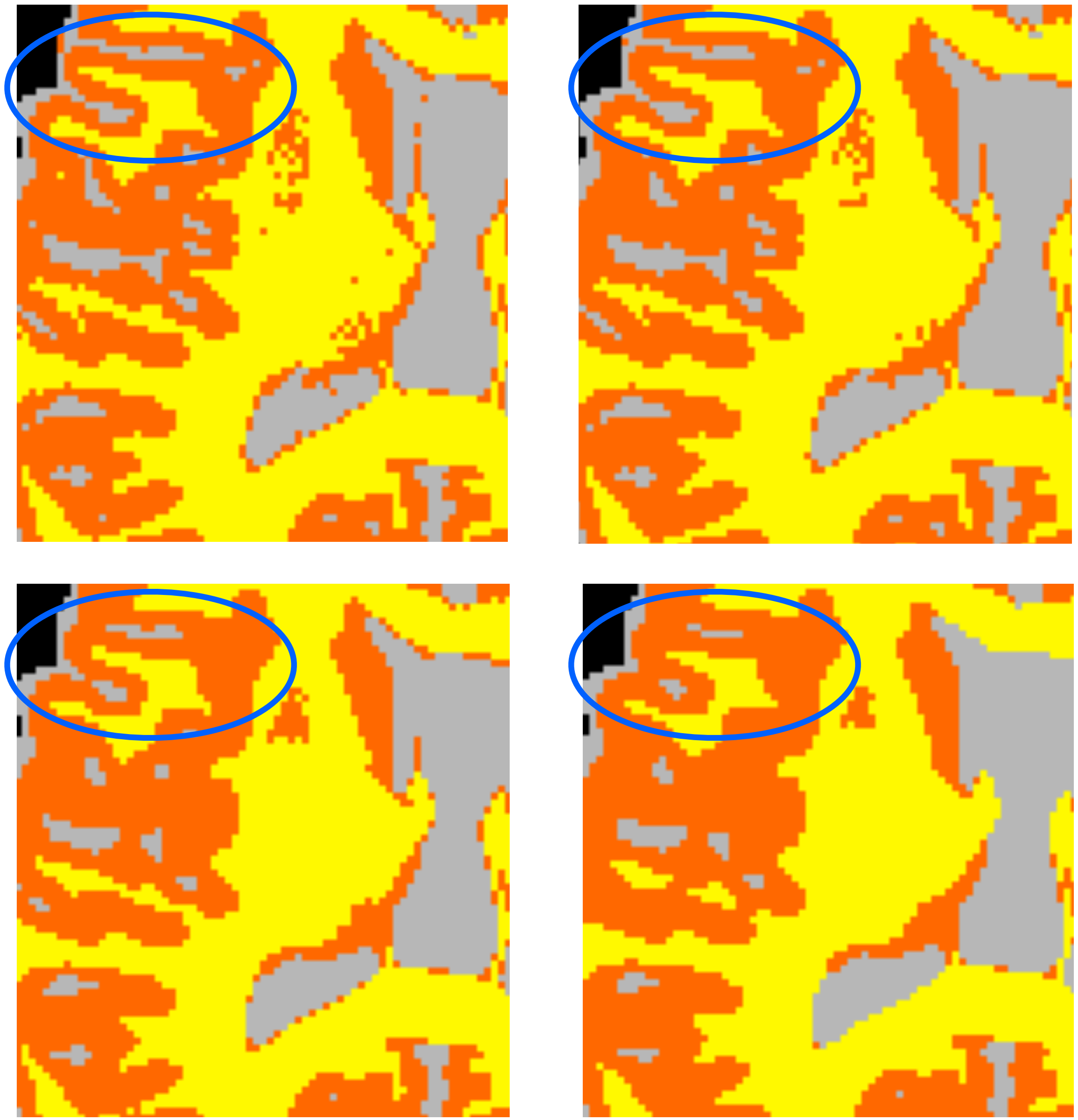
β=0

β=0.1

β=0.3

β=0.5

Effect of MRF Weighting
MRF加权的影响



β=0

β=0.1

β=0.3

β=0.5

Partial Volume Modelling 部分容积建模

- A better model is what fraction of each voxel is tissue X?
  每个体素的分数代表组织X就意味着这个模型更好吗?
- “partial volume” = fraction of CSF, GM or WM
  “部分容积”=脑脊液，灰质或白质的比例分数

PVE
部分容积效应

CSF, GM, WM
脑脊液，灰质，白质

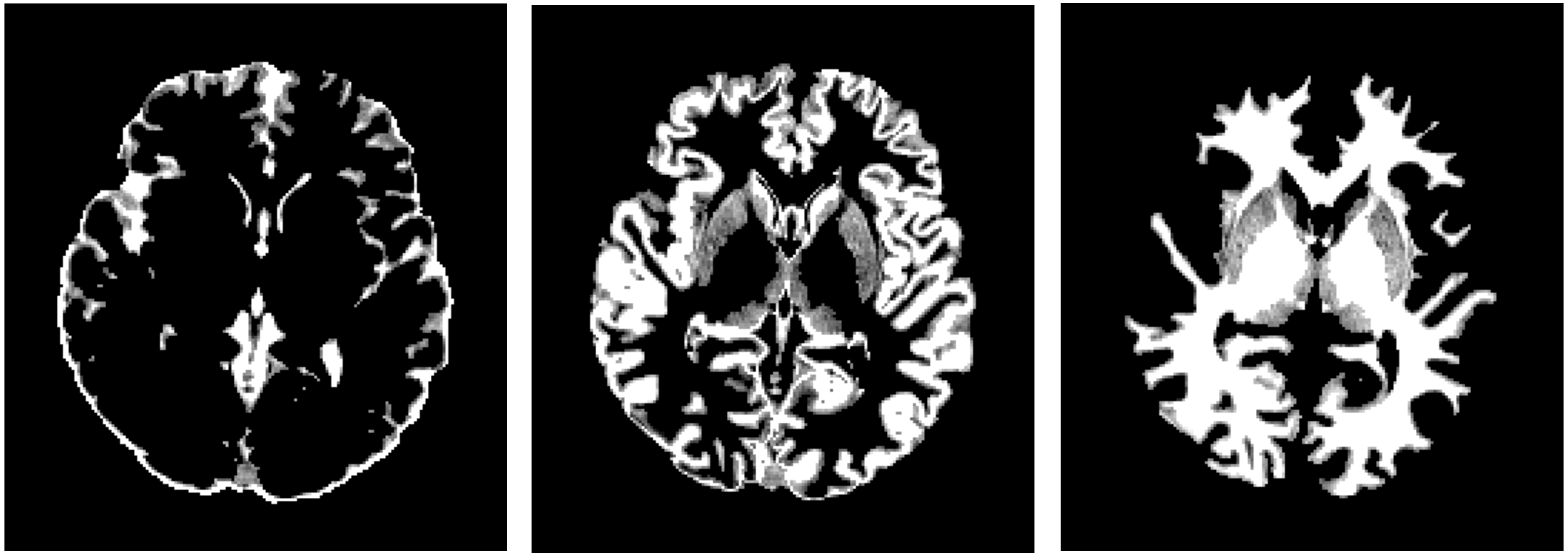


Image 图像

“Hard” Segmentation
强行分割

PVE (GM)
部分容积效应(白质)

- This substantially improves accuracy of volume estimation
- 这种方法大大的提高了容积估计的准确率

FAST - The Overview 概述

- Initial (approximate) segmentation 初始(粗略)分割
  - Tree-K-means 树状-K-均值算法
- Iterate 迭代
  - Estimate bias field 估计偏置场
  - Estimation segmentation; iterate 估计分割；迭代
    - Update segmentation (intensity + MRF) 更新分割（强度+MRF）
    - Update tissue class parameters 更新组织分类参数 (mean and standard deviation 均值与标准差)

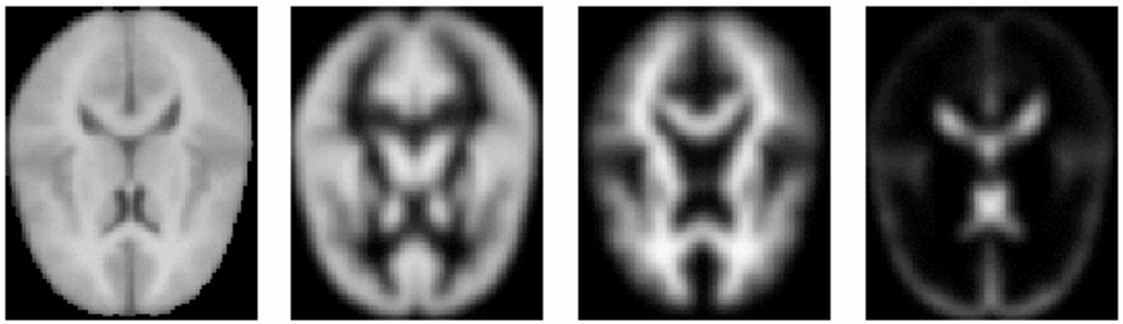
- Apply partial volume model 应用部分容积模型
  - MRF on mixel-type (how many tissues) 对混合型数据使用MRF
  - PV Estimation 部分容积估计

Optional Use of Priors (tissue probability maps)

选择性使用先验概率(组织概率图)

- Segmentation priors = average of many subjects' segmentations
  分割先验概率 = 多个被试分割的平均
- Can use priors to weight segmentation, but can skew results (e.g. due to misalignment)
  可以使用先验概率对分割进行加权，但这可能会导致结果偏差(例如由于错误的对齐)
- FAST does not use priors by default FAST默认不使用先验概率
- If bias field is very bad, priors can be turned on to help initial segmentation (alternatively, do more iterations)
  如果偏置场很严重，可以使用先验概率来帮助初始分割(或者进行多次迭代)
- Can also be turned on to feed into final segmentation (e.g. to aid segmentation of deep grey .... but see FIRST)
  也可以使用先验概率推进最终分割(例如，用于对深层灰质进行分割…但请参考FIRST)

Mean T_1-wt 平均的T1加权 | GM 灰质 | Priors 先验概率 WM 白质 | CSF 脑脊液



Other Options 其它选项

FAST:

- **Bias field smoothing (-l)** 偏置场平滑(-l)
  - vary spatial smoothing of the bias field
    改变偏置场的空间平滑度
- **MRF beta (-H)**
  - vary spatial smoothness of the segmentation
    改变分割的空间平滑度
- **Iterations (-I)** 迭代(-I)
  - vary number of main loop iterations
    改变主循环迭代次数

fsl_anat:

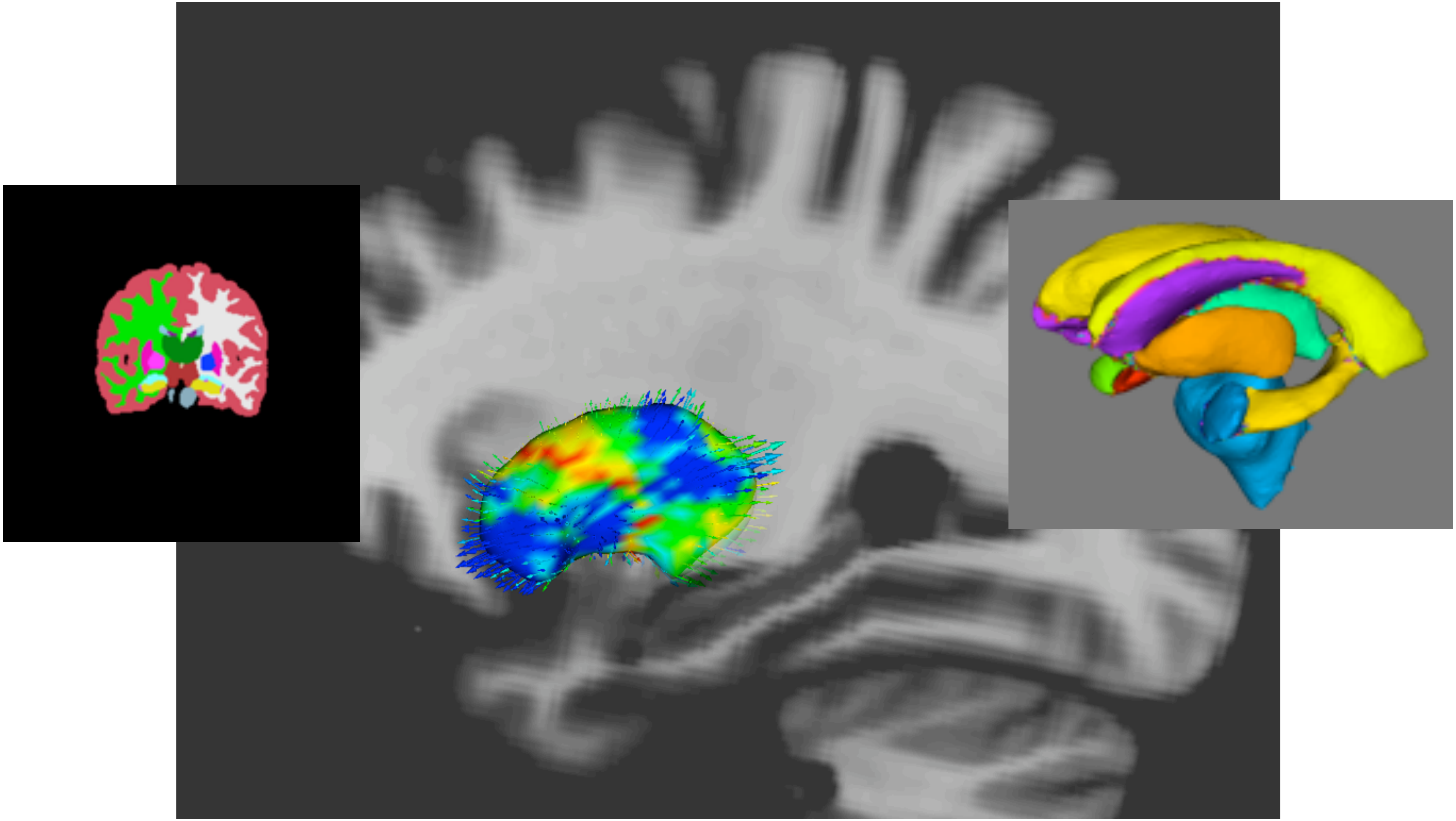
- This is a new, alternative tool that performs brain extraction and bias field correction (along with other things) in a different way and so is worth trying out too
  这是一个新的可供选择的工具，它以不同的方式实现大脑提取和偏置场校正(以及其他事情)，因此也值得尝试使用

FIRST

FMRIB's Integrated Registration & Segmentation Tool FMRIB的一体化配准与分割工具

Segmentation of subcortical brain structures

用于皮层下脑结构分割



Sub-Cortical Structure Models

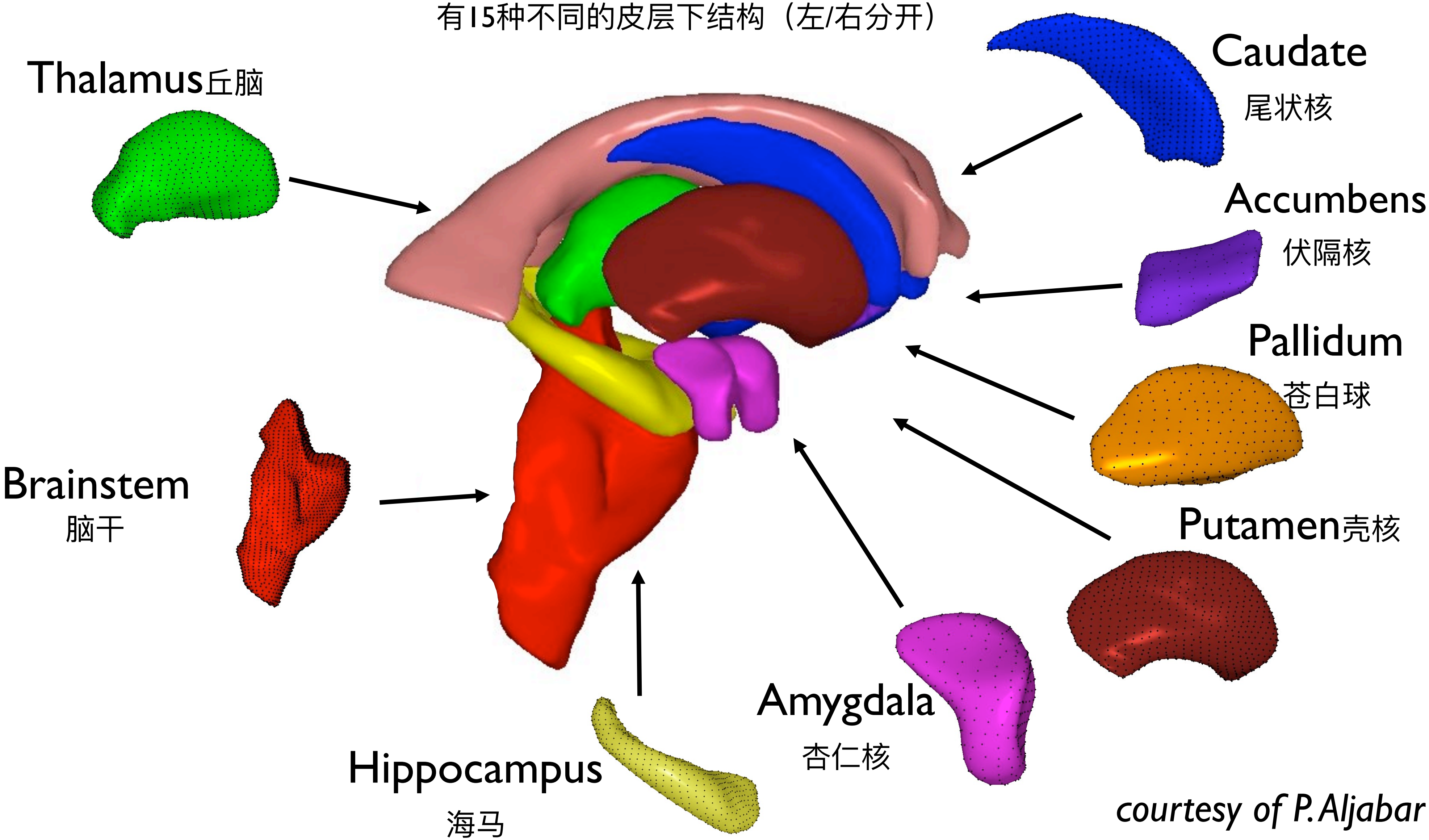
皮层下结构模型

Incorporate prior anatomical information via explicit shape models

通过显式形状模型整合先前的解剖学信息

Have 15 different sub-cortical structures (left/right separately)

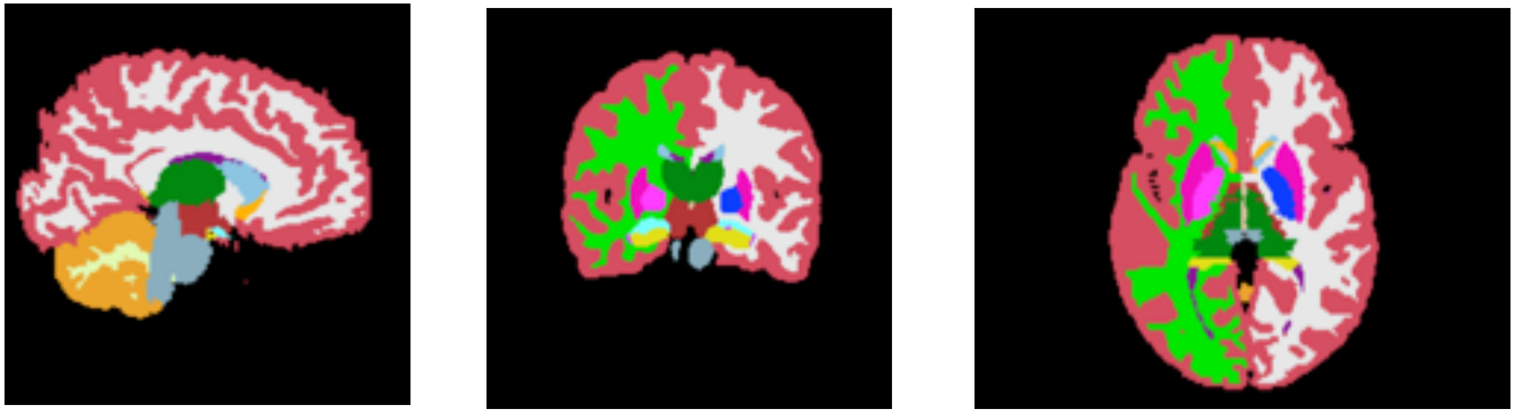
有15种不同的皮层下结构（左/右分开）



courtesy of P. Aljabar

Training Data 练习数据

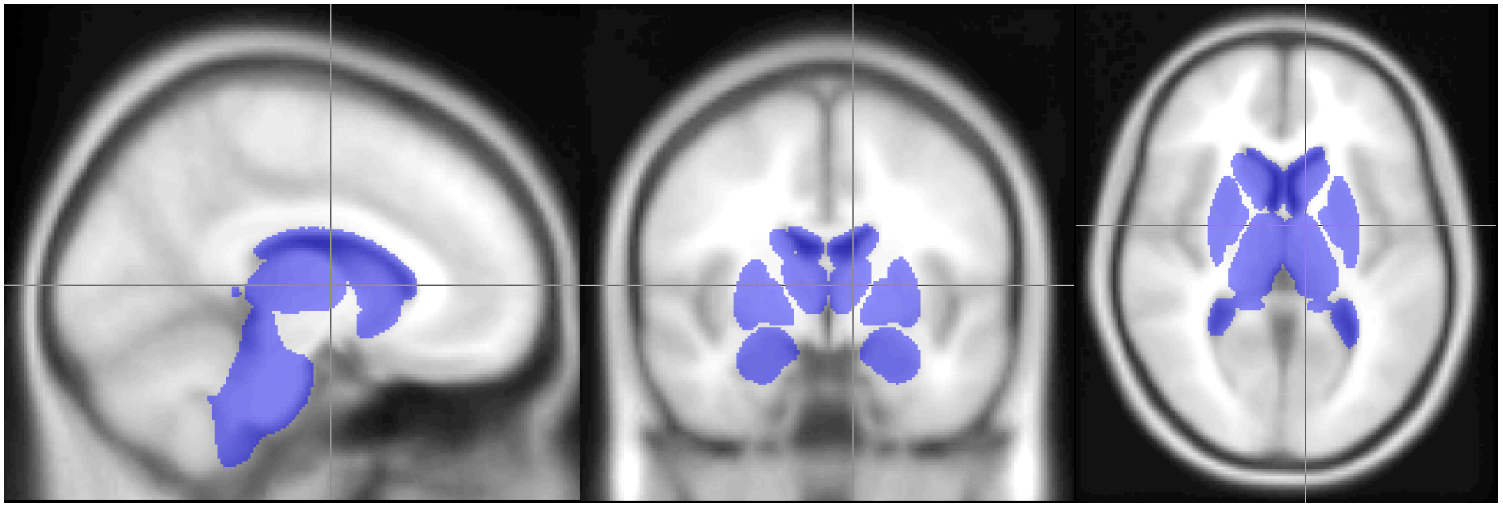
- Manual segmentations courtesy of David Kennedy, Center for Morphometric Analysis (CMA), Boston
  波士顿形态计量分析中心(CMA)David Kennedy提供的手动分割结果
- 336 complete data sets 336组完整的数据集
- T_1-weighted images only 只有T1加权图像
- Age range 4 to 87 年龄范围：4-87
  - Adults: Ages 18 to 87, Normal, schizophrenia, AD
    成年人：18-87岁，健康人，精神分裂症，阿兹海默症
  - Children: Ages 4 to 18, Normal, ADHD, BP, prenatal cocaine exposure, schizophrenia.
    儿童：4-18岁，健康人，多动症，BP，产前可卡因暴露，精神分裂症



Model Training 模拟练习：
Alignment to MNI152 space配准到MNI152空间

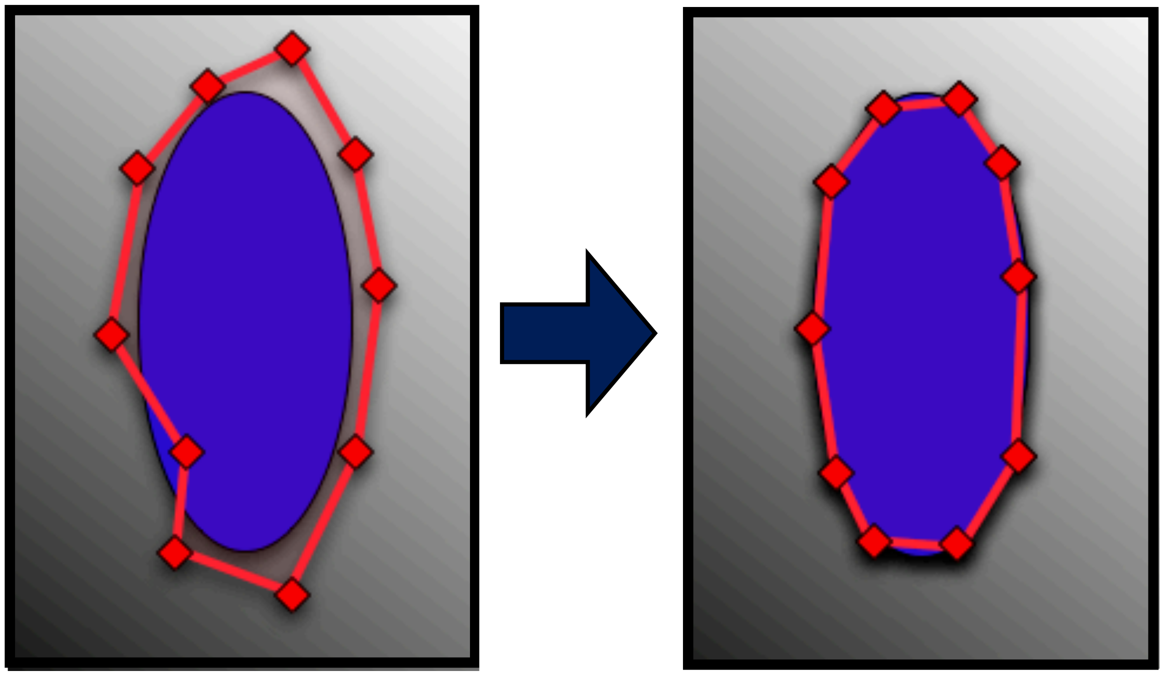
- All CMA data affine-registered to MNI152 space
  所有CMA数据通过仿射配准到MNI152空间
  - 1mm resolution, using FLIRT 使用FLIRT，分辨率1mm

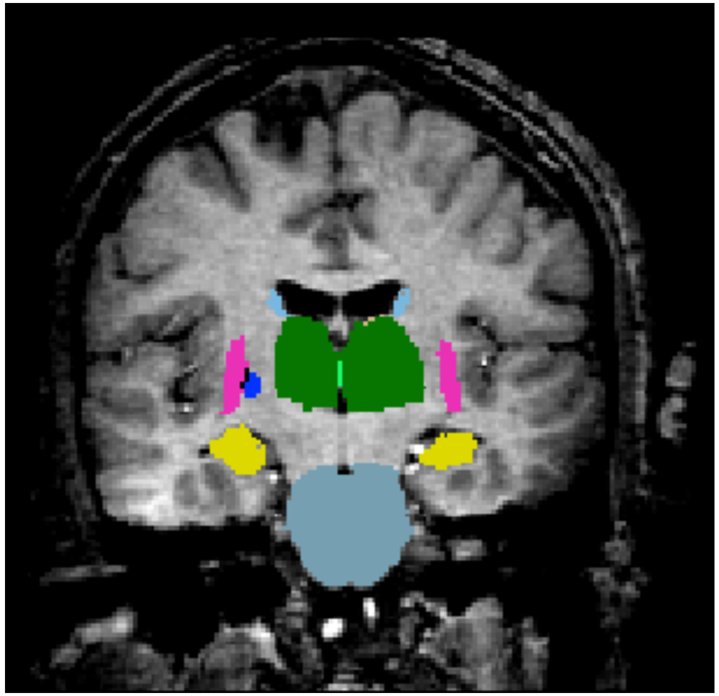
- 2-stage process 两步配准流程:
  - Whole head 12 DOF affine 全脑12自由度仿射
  - 12 DOF affine with MNI-space sub-cortical mask
    使用MNI空间皮层下掩板进行12自由度仿射



Deformable Models 可变形模型

- Model: 3D mesh 模型：3D网格
- Use anatomical info on shape & intensity (from training)
  使用(从训练数据)形状和强度信息
- Deformation: iterative displacement of vertices 变形：顶点的迭代位移
- Maintain point (vertex) correspondence across subjects
  维持不同被试间的顶点对应关系





The Model: Shape 模型：形状

- Model average shape (from vertex locations)
  建模 (顶点位置形成的)平均形状

- Also model/learn *likely variations* about this mean
  模拟/了解该均值有关的变量
  - modes of variation of the population; c.f. PCA
    人口变化的模式；参见PCA
  - also call eigenvectors 也称为特征向量

- Average shape and the modes of variation serve as prior information (known before seeing the new image that is to be segmented) 平均形状和变化模式用作先验信息（在查看要分割的新图像之前已知）
  - formally it uses a Bayesian formulation
    使用贝叶斯公式

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mean 均值

Singular values 奇异值

$$X = \mu_X + UDb_X$$

Eigenvectors (modes)
特征向量(模式)

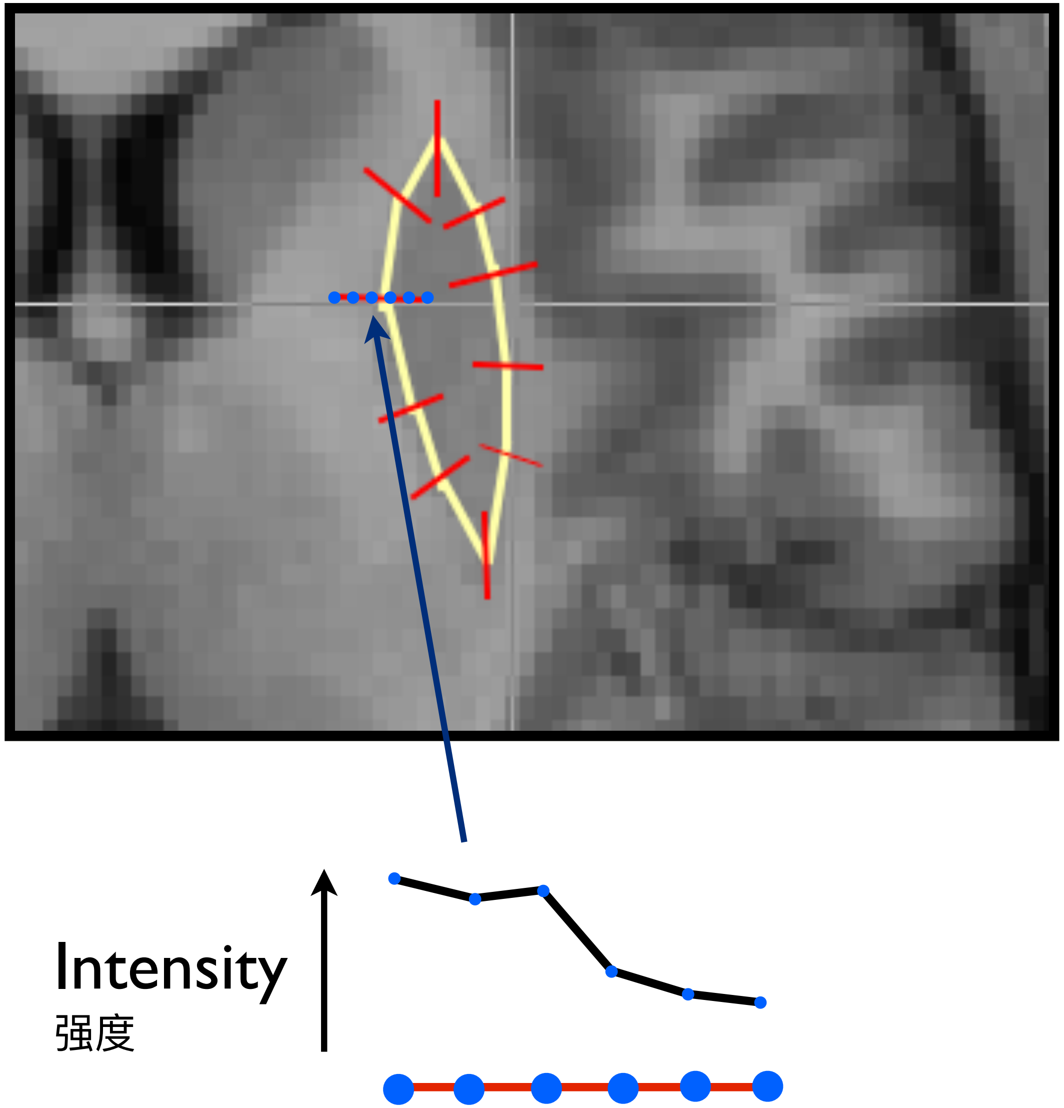
Shape parameters
形状参数

The Model: Intensity 模型：强度

- Intensity is then sampled along the surface normal and stored
  沿表面法线方向采样强度值并存储

- Learn average shape/intensity and “modes of variation” about both
  了解两者的平均形状/强度和“变化模式”

- Aside: the intensities are re-scaled to a common range and the mode of the intensities in the structure is subtracted
  另外：将强度重新调整到一个共同范围，并减去结构中的强度模式

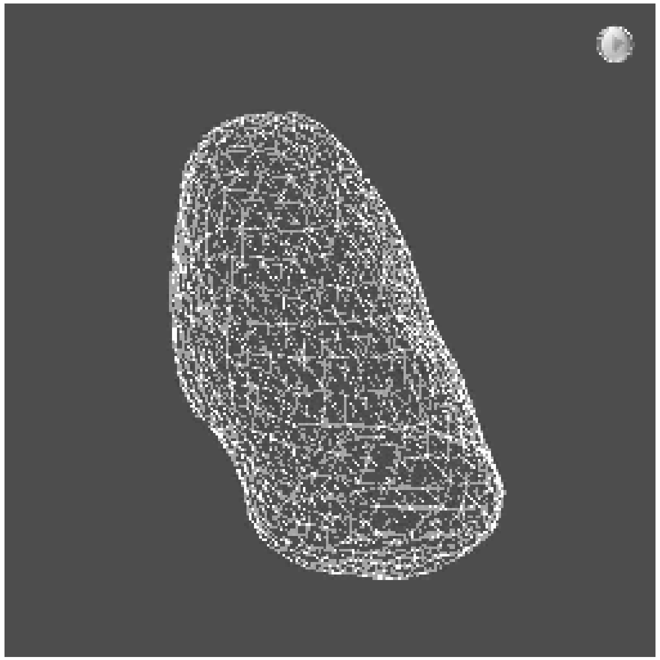


Fitting the Model 拟合模型

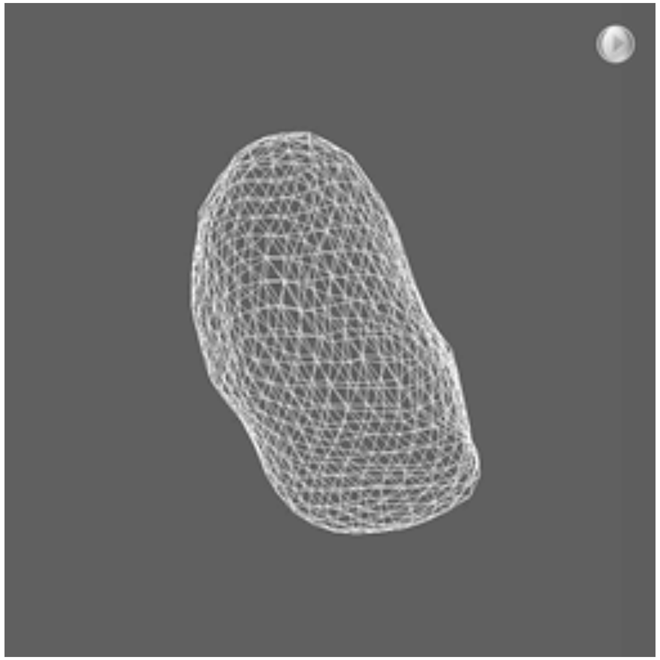
- Find the "best" shape by searching along *modes of variation*
  通过检索变化模式找到"最佳"形状
  - these efficiently describe the ways in which the structure's shape varies most typically over a population
    这些模式有效地描述了结构形状在人群中最为典型的变化方式

- Use intensity match to judge fitting success
  使用强度匹配来判断拟合是否成功

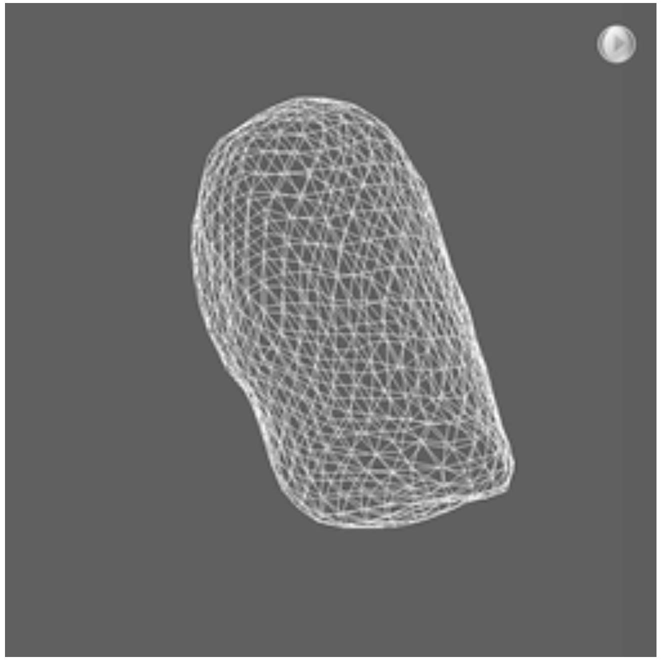
Average shape
平均形状



1st mode of variation
第一种变化模式

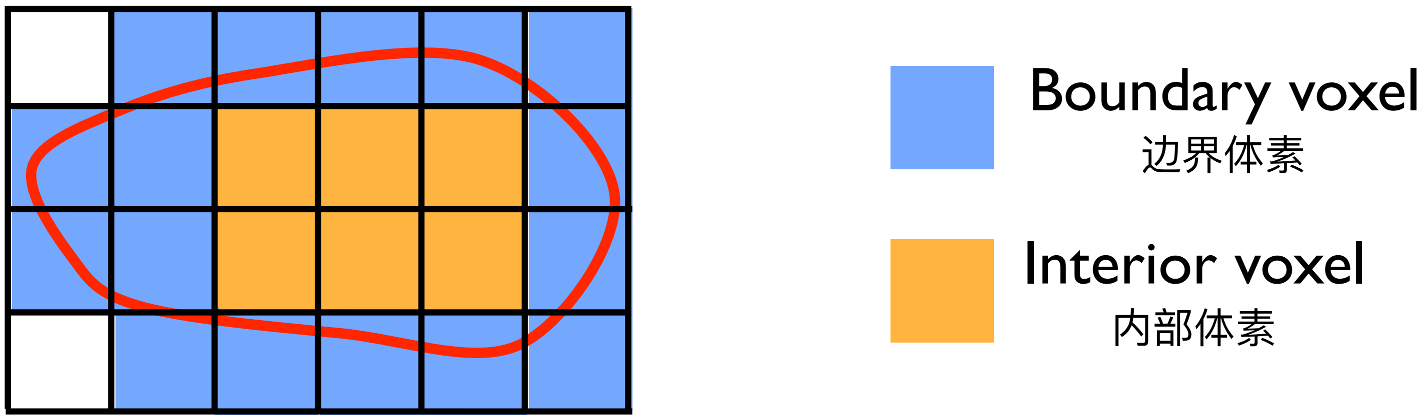


2nd mode of variation
第二种变化模式



Boundary Correction 边界校正

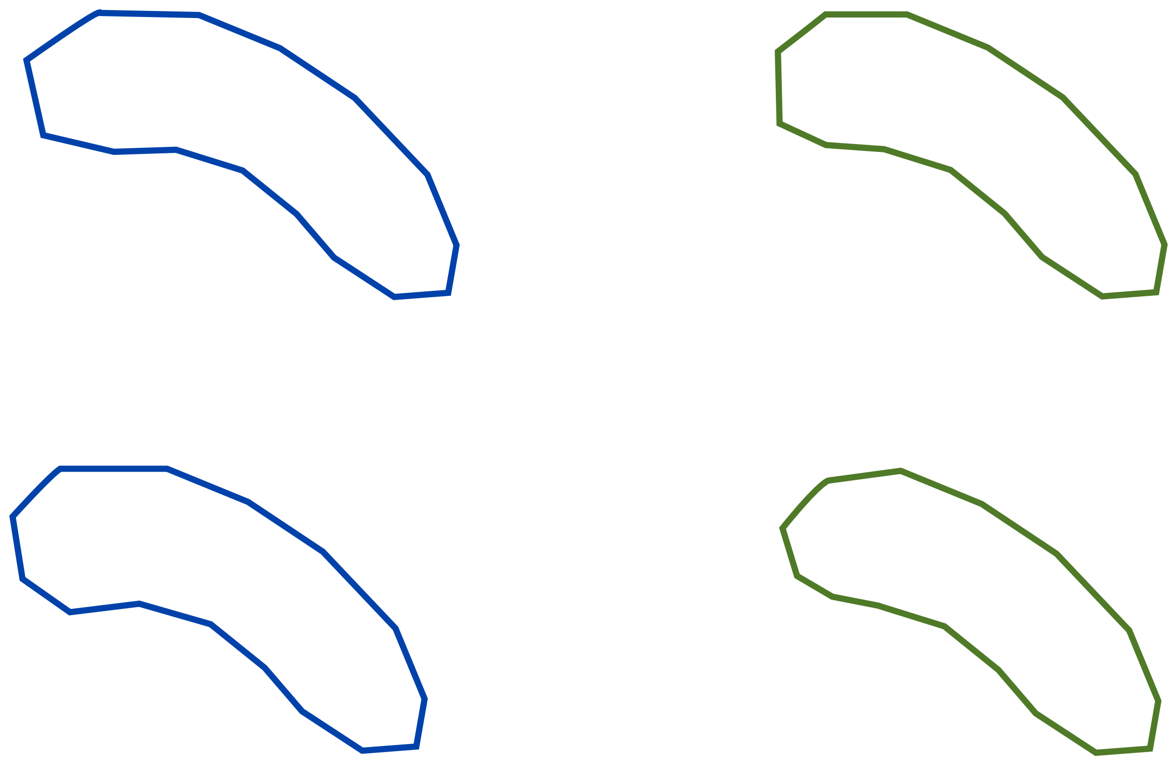
- FIRST models all structures by meshes FIRST通过网格模拟所有的结构
- Converting from meshes to images gives two types of voxels:
  由网格转换到图像会给出两种类型的体素：
  - boundary voxels 边界体素
  - interior voxels 内部体素
- Boundary correction is necessary to decide whether the boundary voxels should belong to the structure or not
  边界校正主要用于决定边界体素到底属不属于该结构的一部分
- Default correction uses FAST classification method and is run automatically (uncorrected image is also saved)
- 默认校正是通过FAST的分类方法进行的，并会自动运行(校正前的图像也会被保存下来)
  - ensures that neighbouring structures do not overlap 确保邻近的结构彼此没有重叠



Vertex Analysis 顶点分析

- Use a univariate test at each vertex to measure difference in location (e.g. between means of two groups of subjects)
  在每个顶点使用单变量检测来测量位置差异（例如，两组受试者的平均值之间的差异）

Controls 控制组 | Disease 病人组



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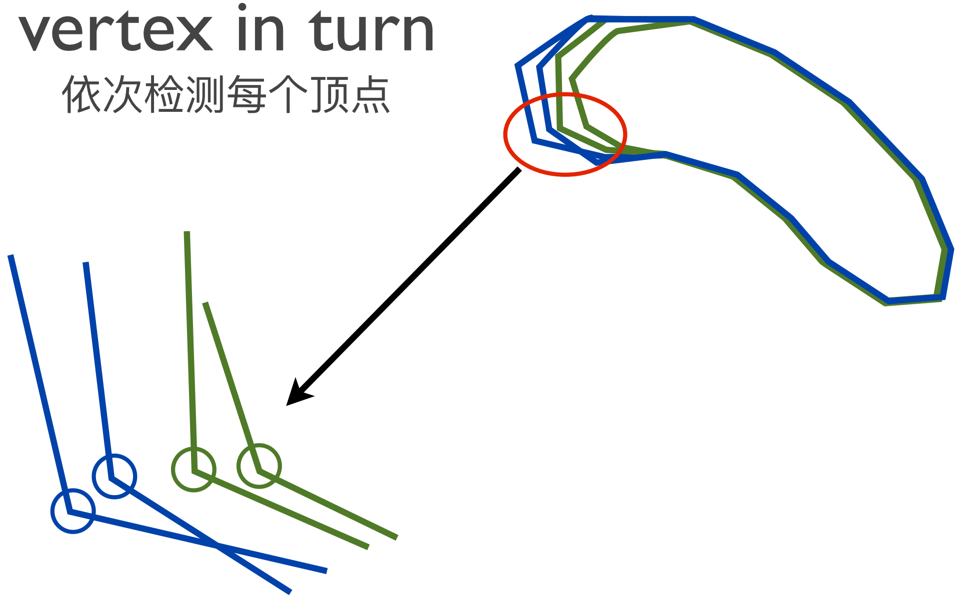
- Use a univariate test at each vertex to measure difference in location (e.g. between means of two groups of subjects)
  在每个顶点使用单变量检测来测量位置差异（例如，两组受试者的平均值之间的差异）

Controls 控制组　　　　Disease 病人组

Consider each vertex in turn
依次检测每个顶点



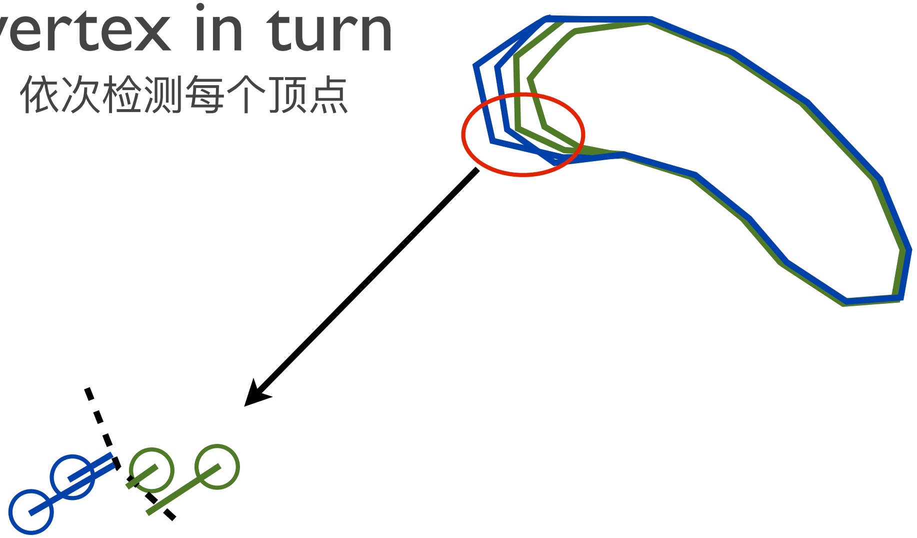
Vertex Analysis 顶点分析

- Use a univariate test at each vertex to measure difference in location (e.g. between means of two groups of subjects)
  在每个顶点使用单变量检测来测量位置差异（例如，两组受试者的平均值之间的差异）

Controls 控制组

Disease 病人组

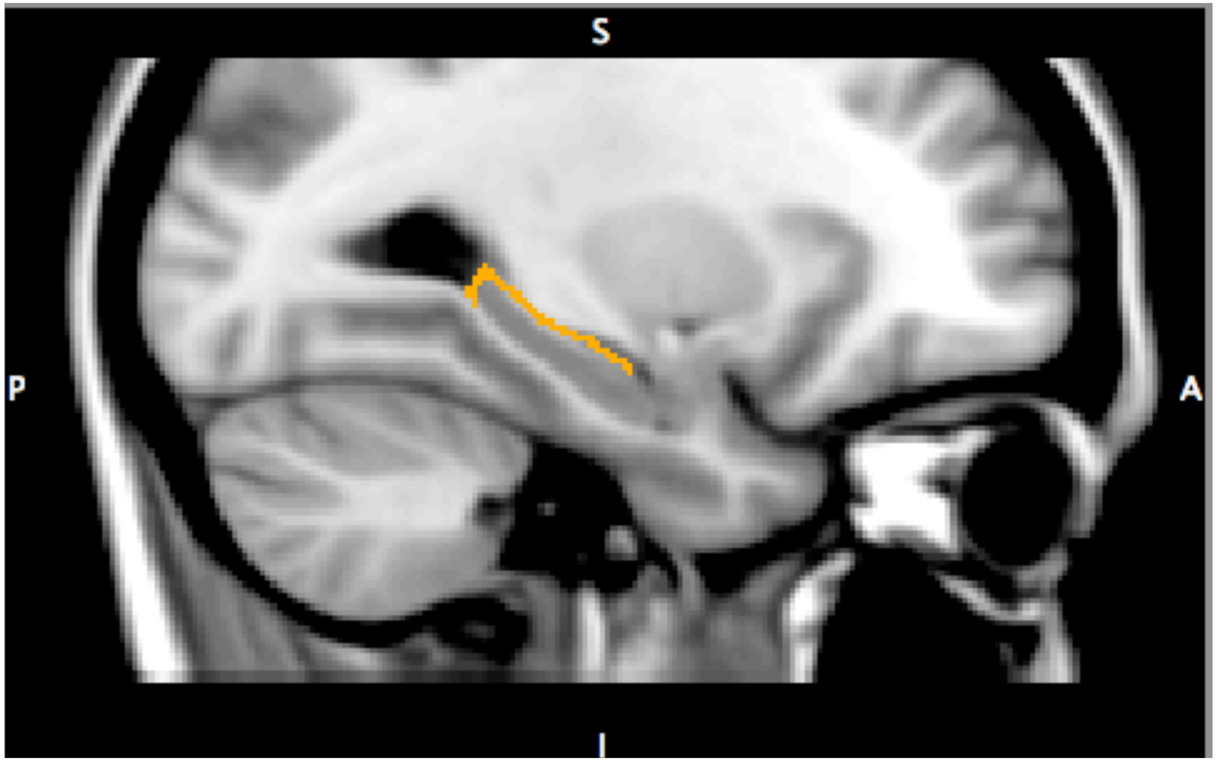
Consider each vertex in turn
依次检测每个顶点



Do a test on distance of these vertices to average shape
测试这些顶点到平均形状的距离

Vertex Analysis 顶点分析

- Use a univariate test at each vertex to measure difference in location (e.g. between means of two groups of subjects) using distance along surface normals
  在每个顶点使用单变量检测来测量位置差异(例如，两组受试者的平均值之间的差异),差异使用点到曲面的垂直距离来表示。
- Results are now given as ***images*** and statistics done with ***randomise***
  结果以图像形式给出，统计是以*randomise*程序完成



- Can do analysis in MNI space or native structural space
  可在MNI空间或结构空间中进行分析
- MNI space analysis ***normalises for brain size***
  MNI空间分析对大脑大小进行了标准化

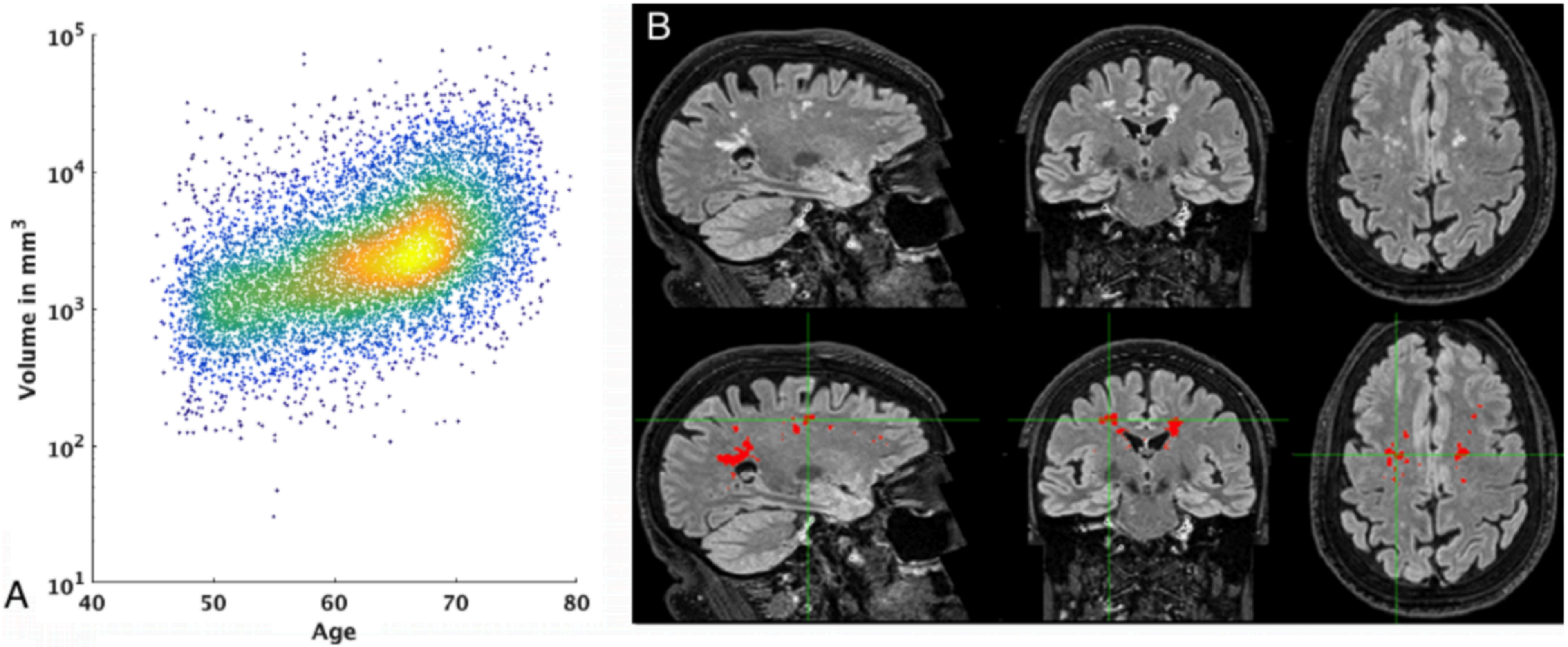
Running FIRST 运行FIRST

- Inputs: 输入:
  - T_1-weighted image T1加权图像
  - Model (built from training data) - provided with FSL
    模型(来自训练数据) - FSL软件自带
- Applying FIRST 应用FIRST
  - A single command: run_first_all 运行单一命令: run_first_all
    1. registers image to MNI152 1mm template
       将图像配准到MNI152 1mm模板
    2. fits structure models (meshes) to the image
       将结构模型(网格)拟合到图像上
    3. applies boundary correction (for volumetric output)
       应用边界校正(用于体积数据输出)
- Analysis: 分析:
  - Use command: first_utils 运行命令: first_utils
    - volumetric analysis (summary over whole structure)
      体积分析(整体结构的总结)
    - vertex analysis (localised change in shape and/or size)
      顶点分析(定位形状和/或大小的变化)
    - randomise (with multiple comparison correction) (多重比较校正)

BIANCA

Segmentation of White Matter Hyperintensities / Lesions

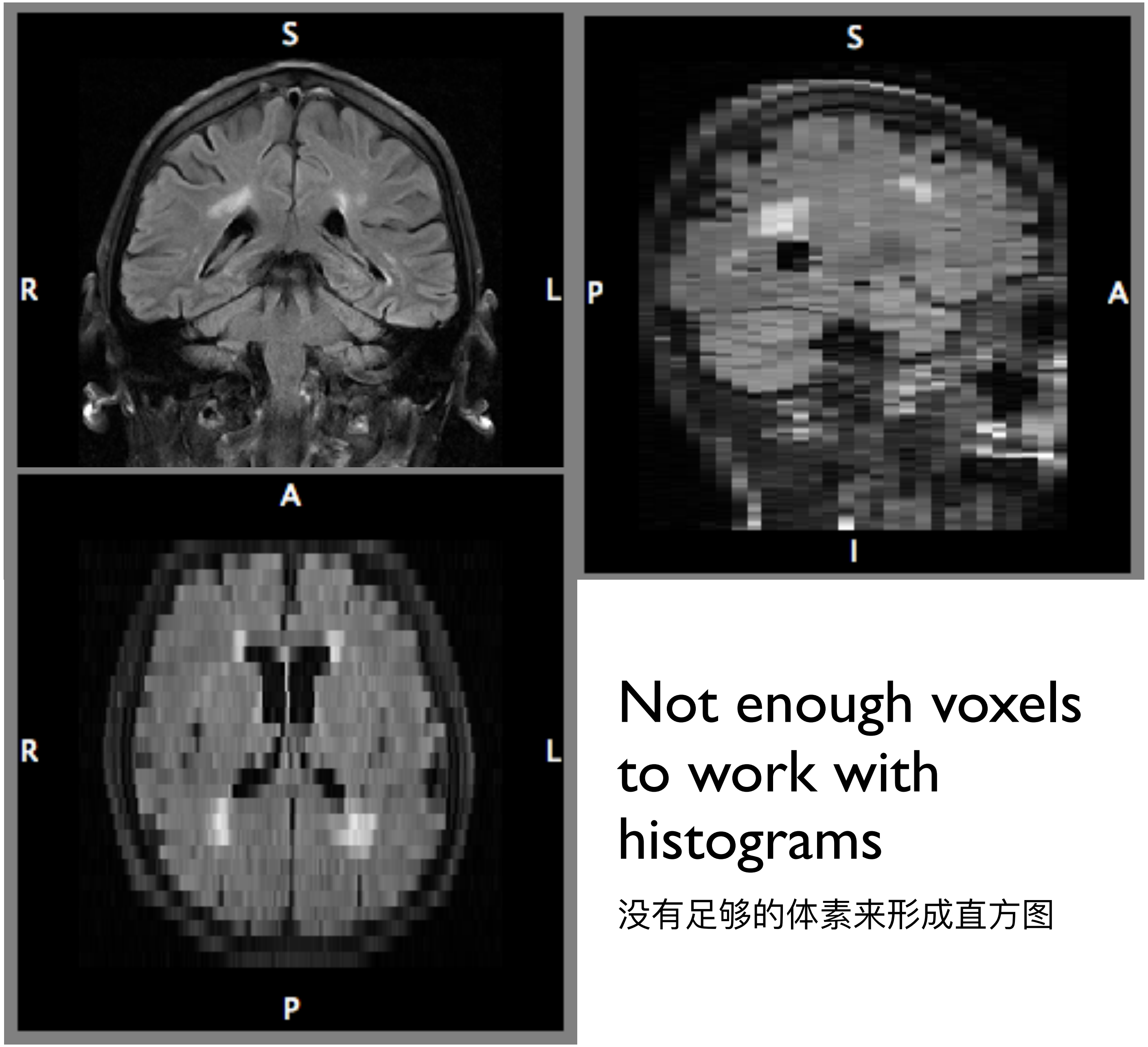
白质高信号区/病灶分割

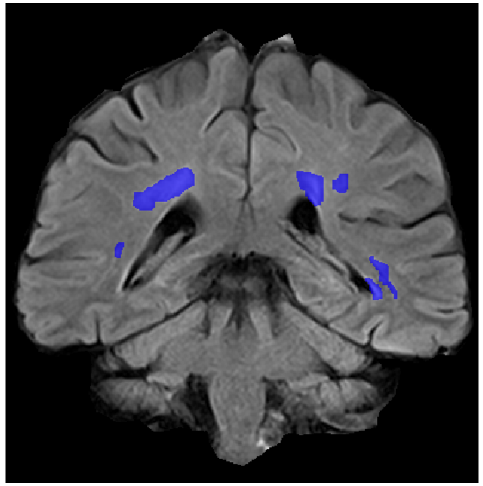


Lesion/WMH Segmentation 病灶/WMH分割

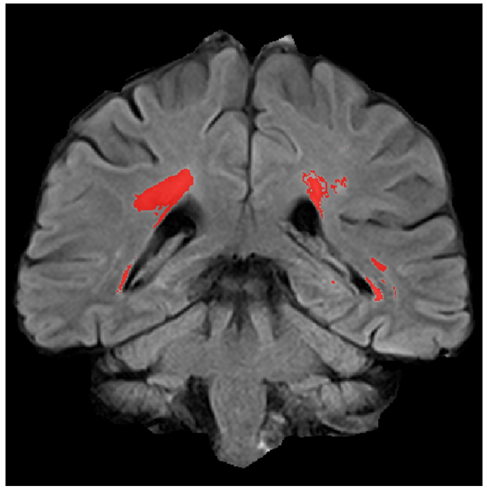
WMH = White Matter Hyperintensities (leukoaraiosis)

WMH = 白质高信号区(脑白质疏松症)





manual 手动



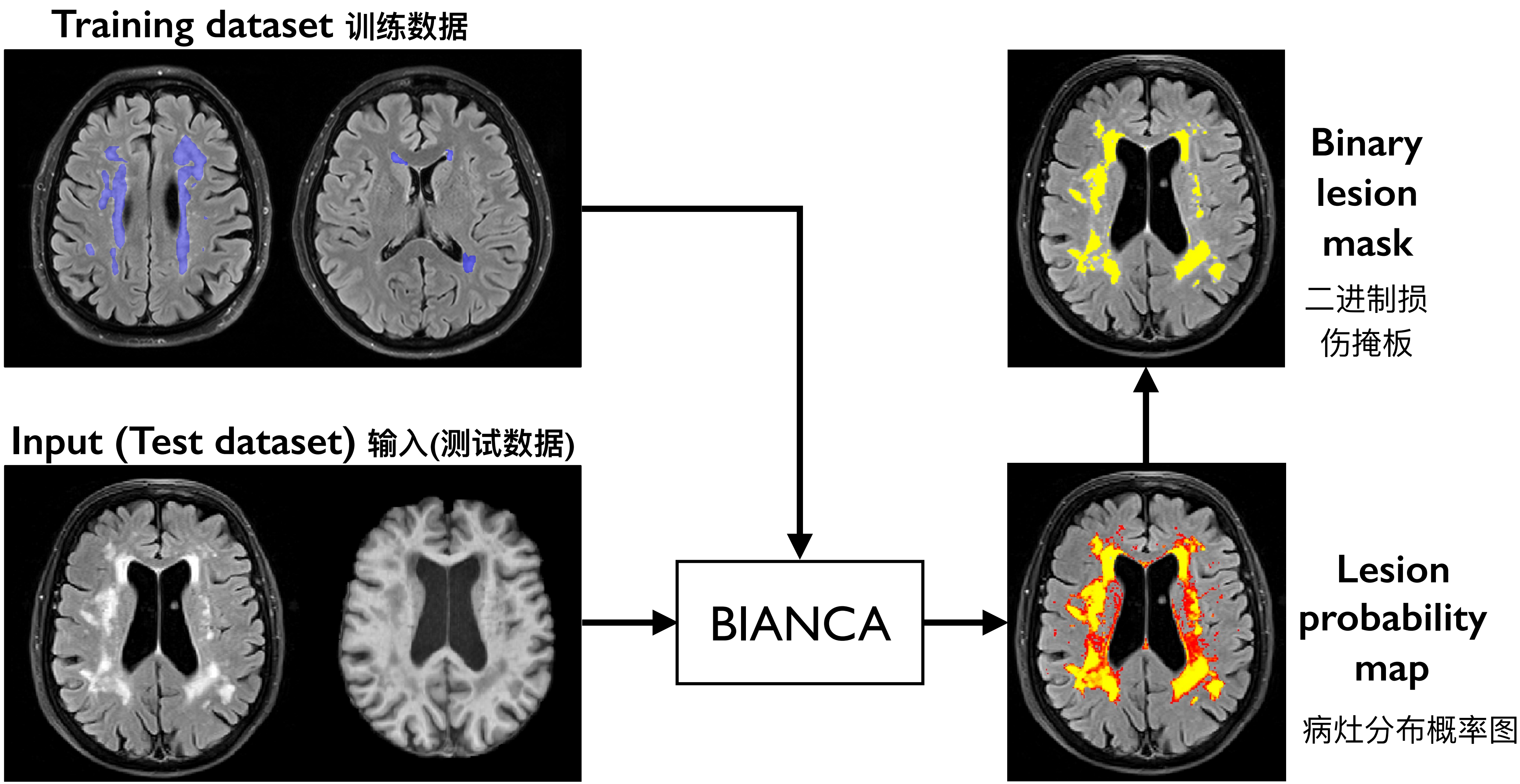
automated 自动化

Not enough voxels to work with histograms

没有足够的体素来形成直方图

Lesion/WMH Segmentation 病灶/WMH分割

Brain Intensity AbNormalities Classification Algorithm (BIANCA)
大脑强度异常分类算法



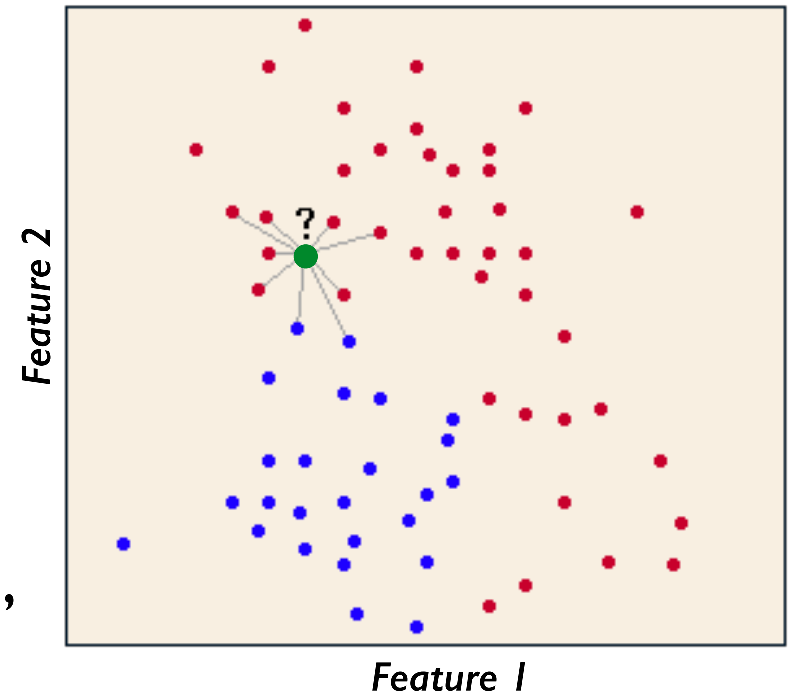
Griffanti et al., NeuroImage 2016

Methodology 方法学

- kNN method kNN方法
  - Anbeek et al, 2004, 2008
  - Steenwijk et al, 2013

- Each point is from one voxel in a training image (labelled positive or **negative**)
  每个点都来自一张训练图像中的一个体素(并被标记为正性或负性)

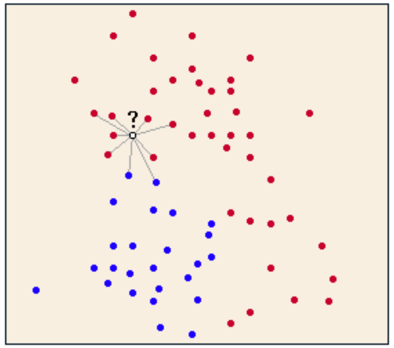
- Data at each point comprises intensities, coordinates, local averages, etc. (***features***)
  每个点的数据包括强度、坐标、局部平均值等(特征值)



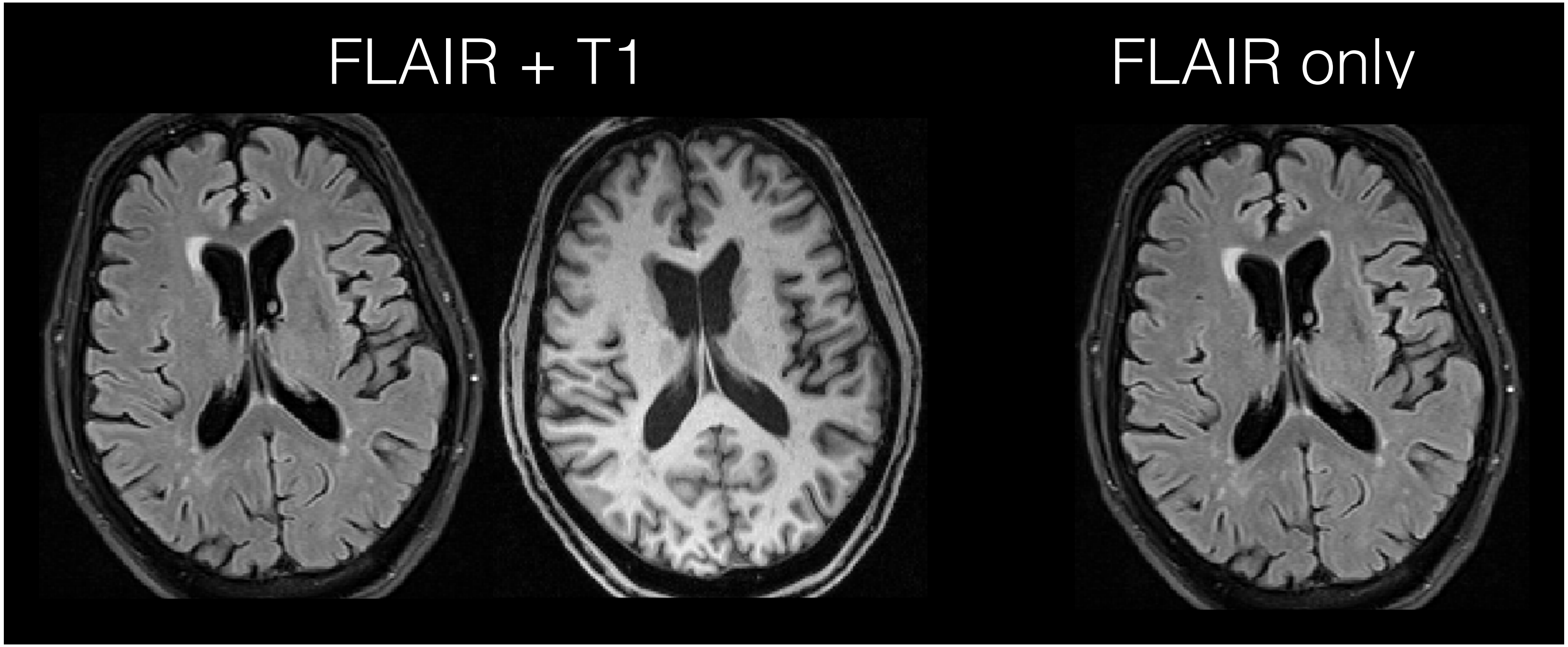
k=9; p(positive正性)=7/9=0.78

- **New data point**: kNN picks k nearest neighbours for a voxel of interest and calculates the ratio of positively and negatively labelled ones ➜ **probability** of being positive (e.g. lesion)
  新的数据点：kNN选择感兴趣的体素的k个最近邻近点并计算它们被标记为正/负性的比例 → 该点为正性的概率(如病灶)

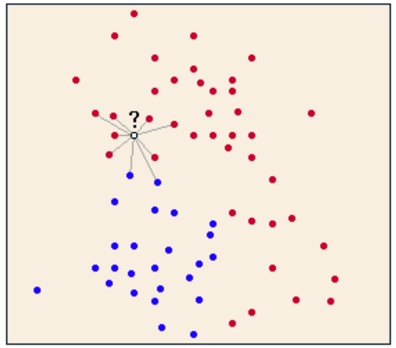
Methodology - options 方法学-选项



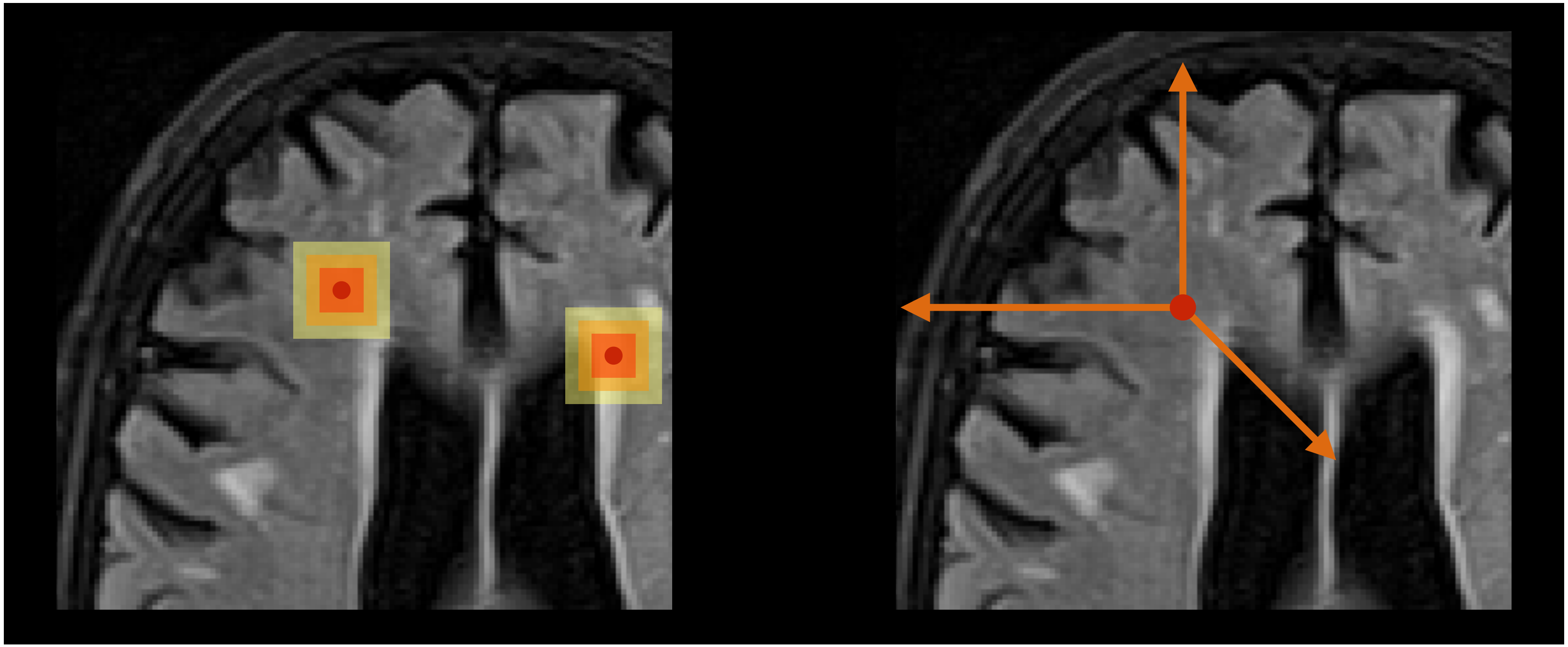
- Many options exist: 有多种选项:
  - **modalities** (e.g. FLAIR, T2w, T1w) 模态(如FLAIR,T2加权,T1加权)



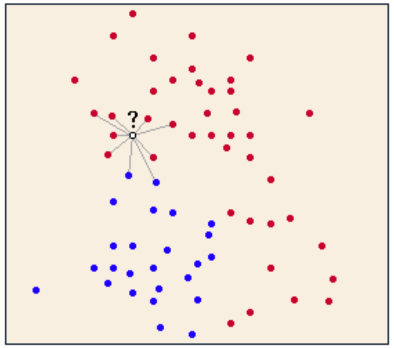
Methodology - options 方法学-选项



- Many options exist: 有多种选项:
  - modalities (e.g. FLAIR, T2w, T1w) 模态(如FLAIR, T2加权, T1加权)
  - **features** (e.g. local averages, MNI coordinates) 特征(如局部均值, MNI坐标)



Methodology - options 方法学-选项



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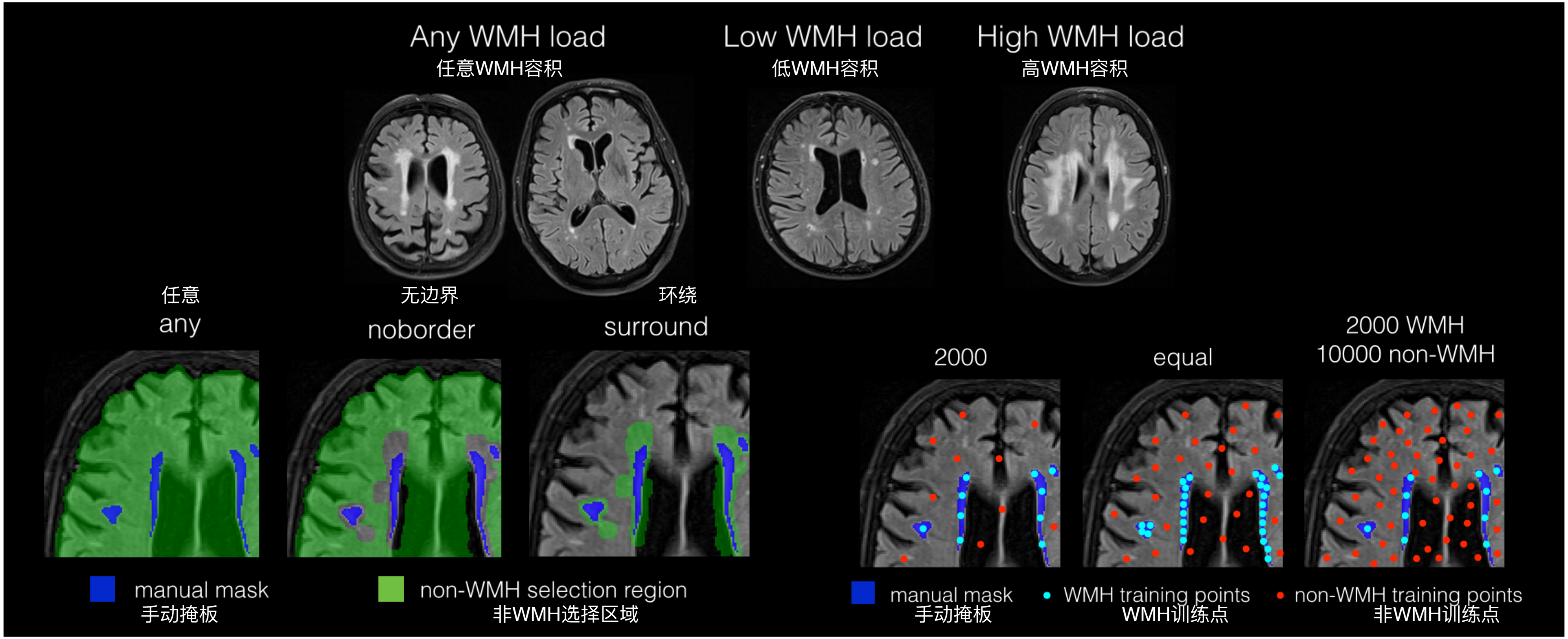
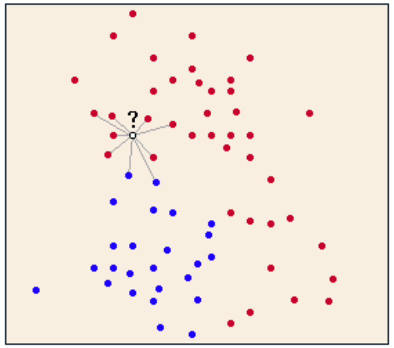
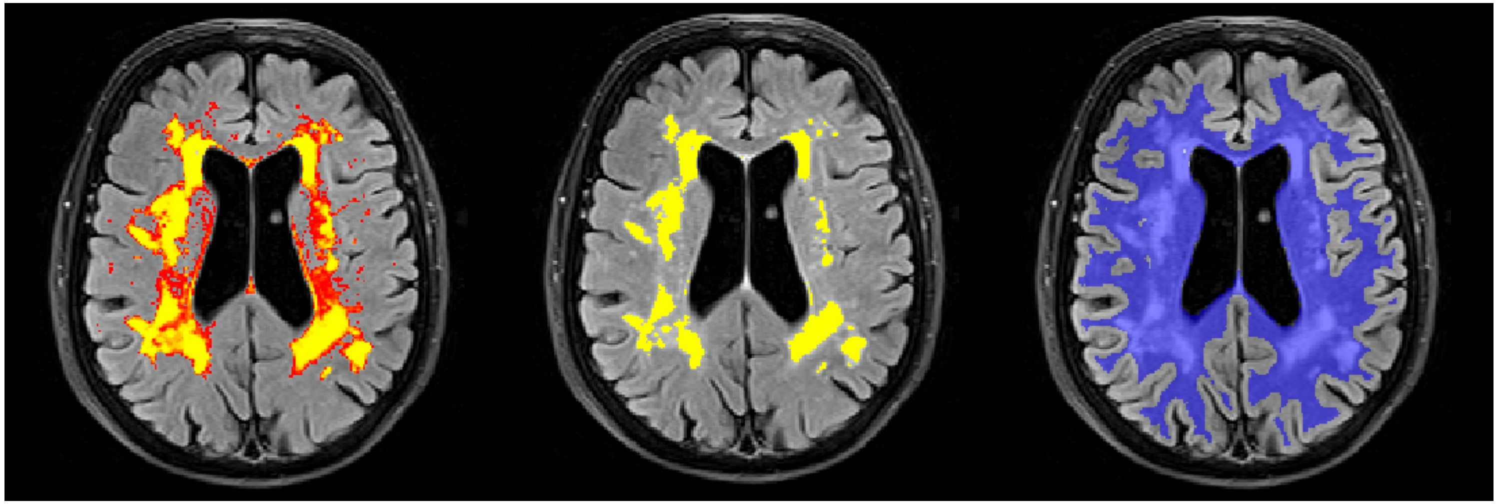
  - modalities (e.g. FLAIR, T2w, T1w) 模态(如FLAIR,T2加权,T1加权)
  - features (e.g. local averages, MNI coordinates) 特征(如局部均值, MNI坐标)
  - **training** (e.g. type of scans, no. voxels, locations sampled)
    训练(如扫描类型,体素数量,采样位置)



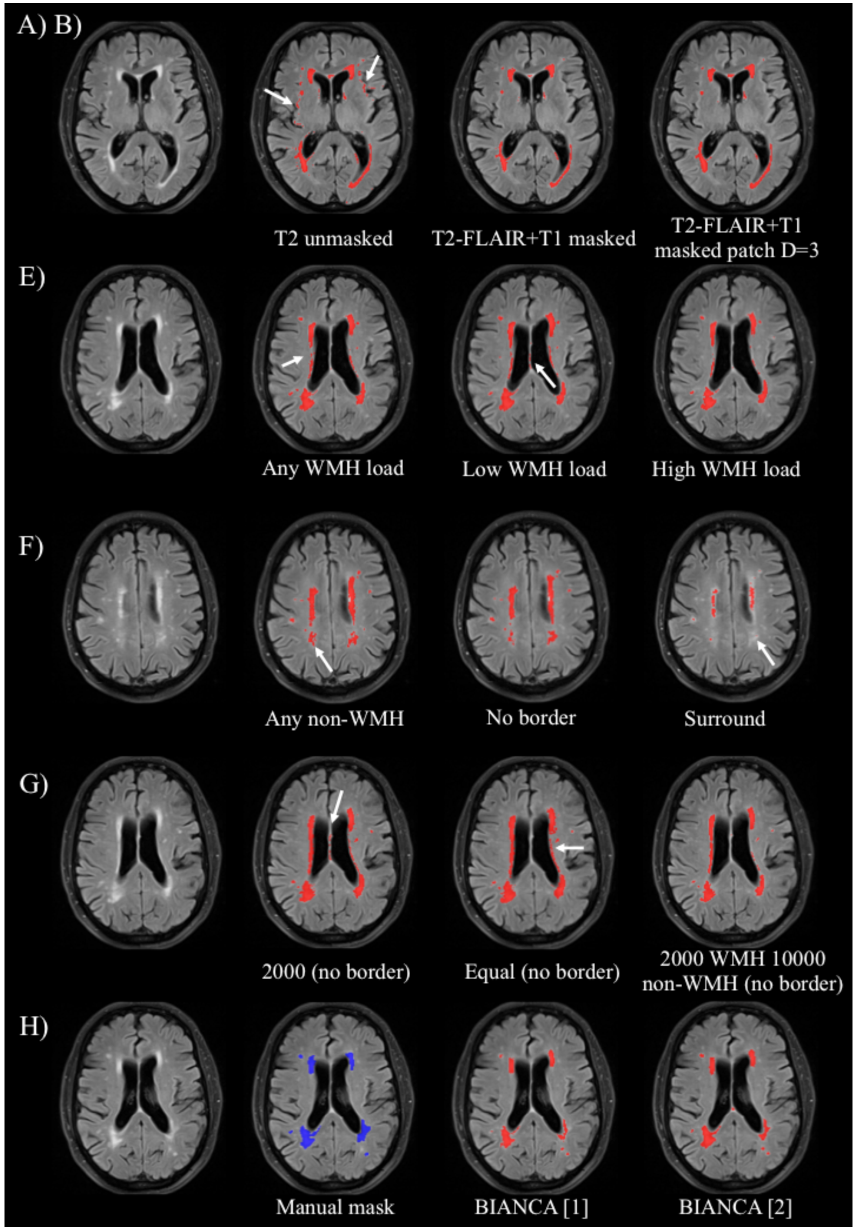
Methodology - options 方法学-选项



- Many options exist: 有多种选项:
  - modalities (e.g. FLAIR, T2w, T1w) 模态(如FLAIR,T2加权,T1加权)
  - features (e.g. local averages, MNI coordinates) 特征值(如局部均值, MNI坐标)
  - training (e.g. type of scans, no. voxels, locations sampled)
    训练(如扫描类型,体素数量,采样位置)
  - **post-processing** (Thresholding and Masking cerebellum, thalamus, inferior deep and cortex masked out)
    后处理 (重设阈值和制作掩板: 小脑，丘脑，内部深层灰质和皮层都被标记出来了)



Applications 应用

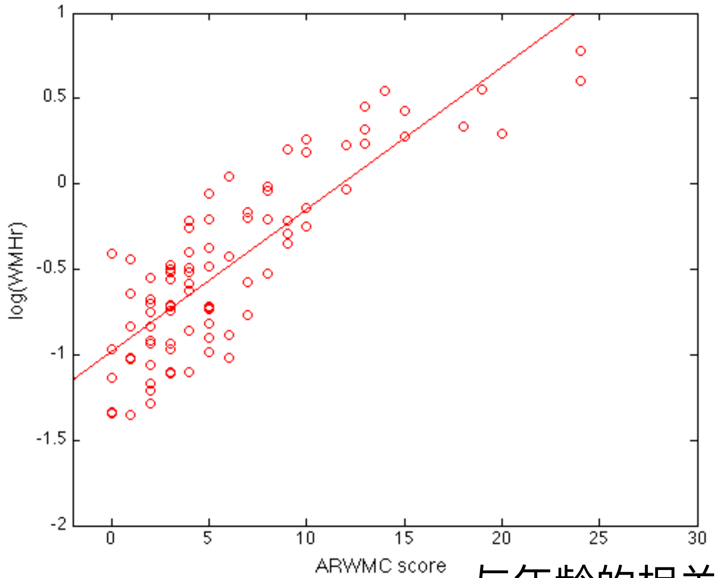


Algorithm optimisation 算法优化

SI = 0.76 ICC = 0.99

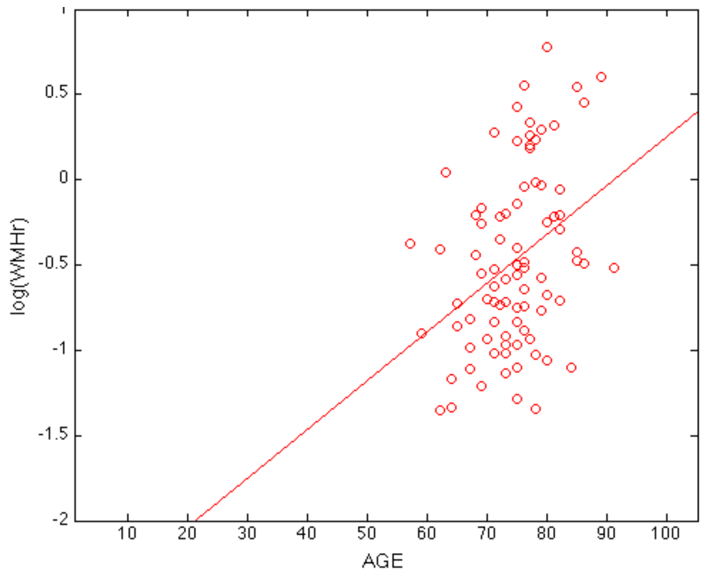
与视觉评分的相关性

Correlation with visual ratings



与年龄的相关性

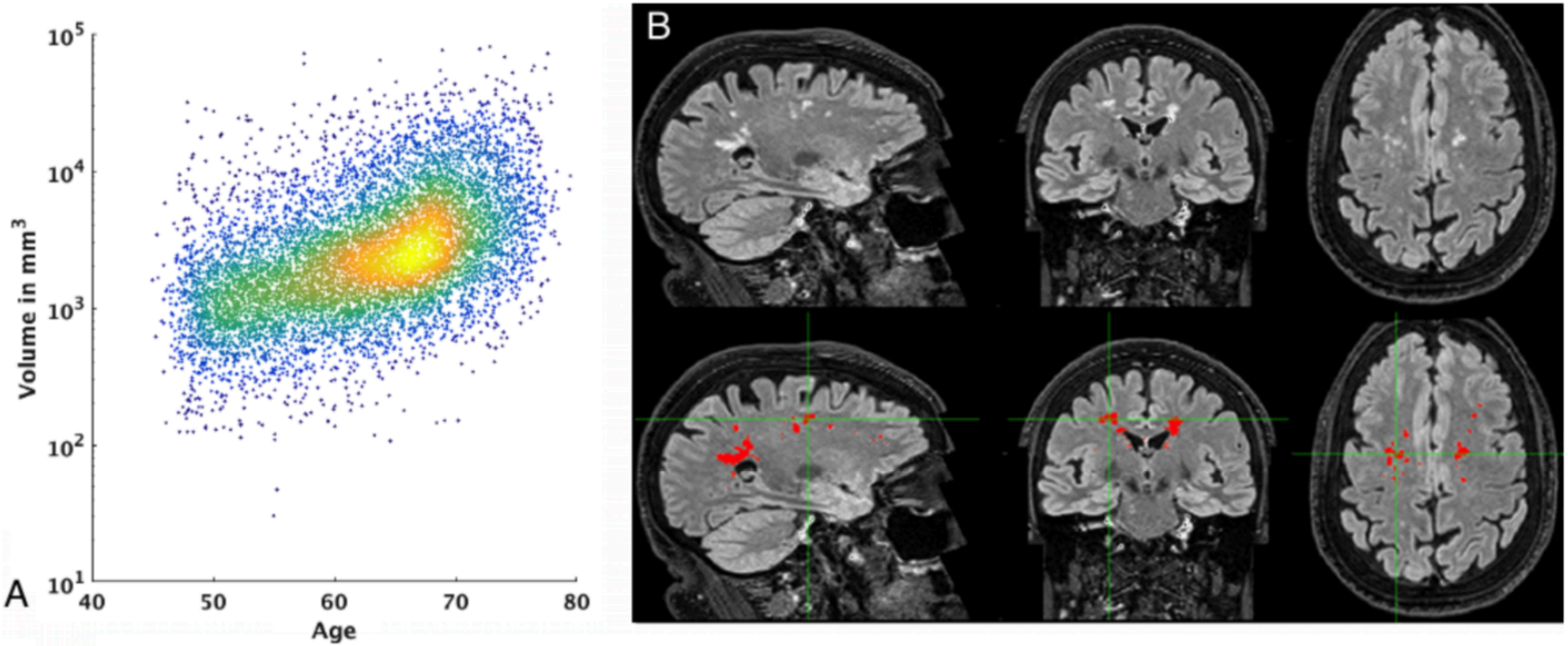
Correlation with age



Griffanti, et al., NeuroImage 2016

Applications 应用

UK Biobank - 10,000 subjects 被试



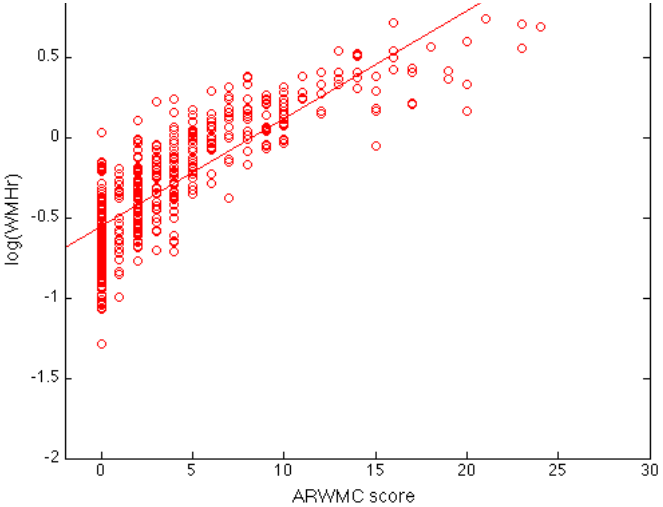
Significant correlations with: 显著相关的有:

- systolic blood pressure 收缩压($r=0.13$, $p<10^{-20}$)
- diastolic blood pressure 舒张压($r=0.11$, $p<10^{-15}$)

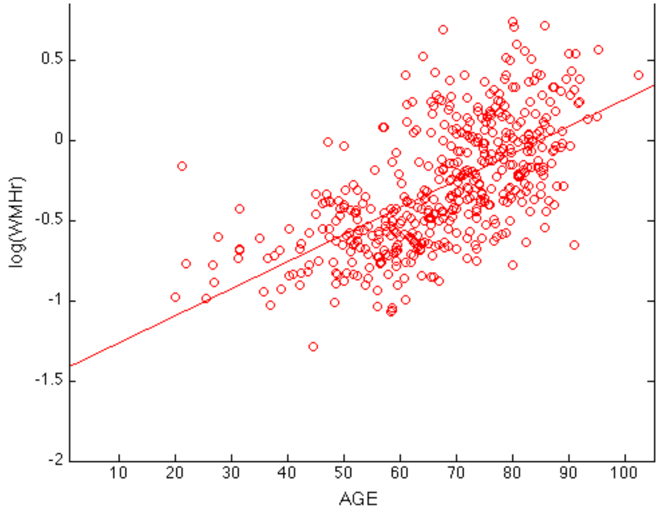
Alfaro-Almagro, et al., NeuroImage 2017

Applications 应用

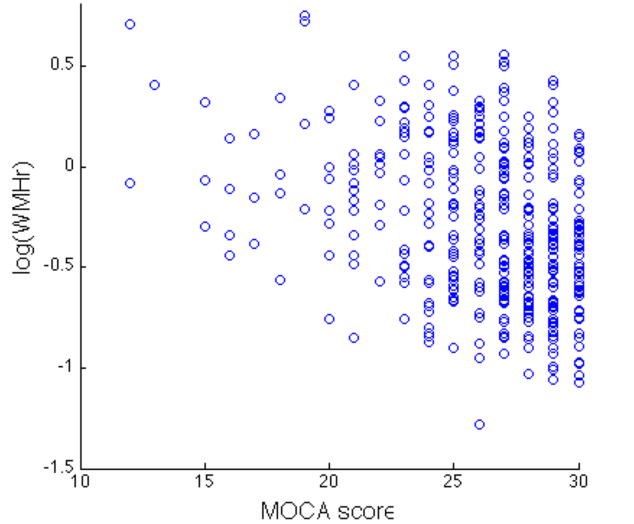
Correlation with visual ratings
与视觉评分的相关关系



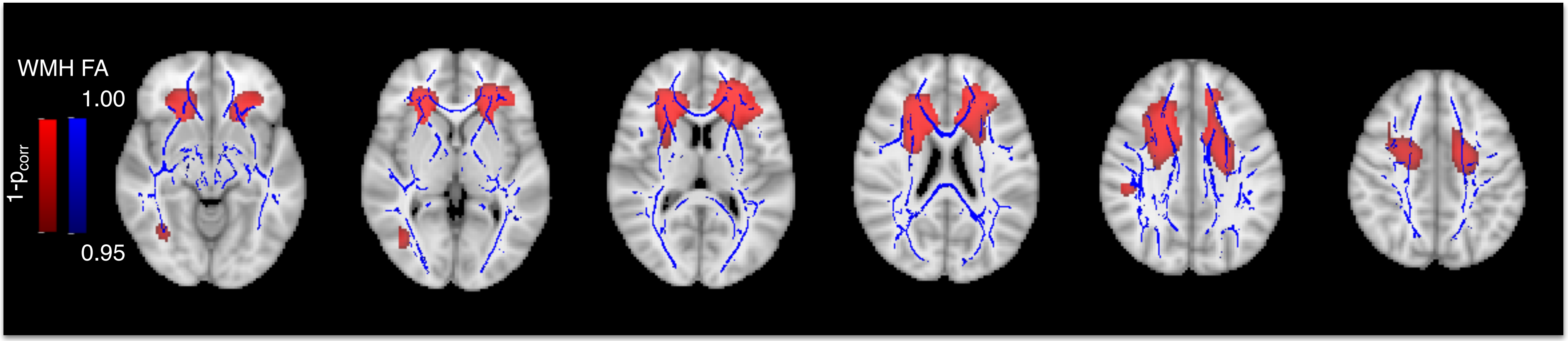
Correlation with age
与年龄的相关关系



Correlation with cognitive score
与认知得分的相关关系



VOXEL-WISE ANALYSIS 体素分析



Vascular cohort - Higher WMH and lower FA in subjects with cognitive impairment (CI) according to both MMSE and MoCA vs subjects with no CI.

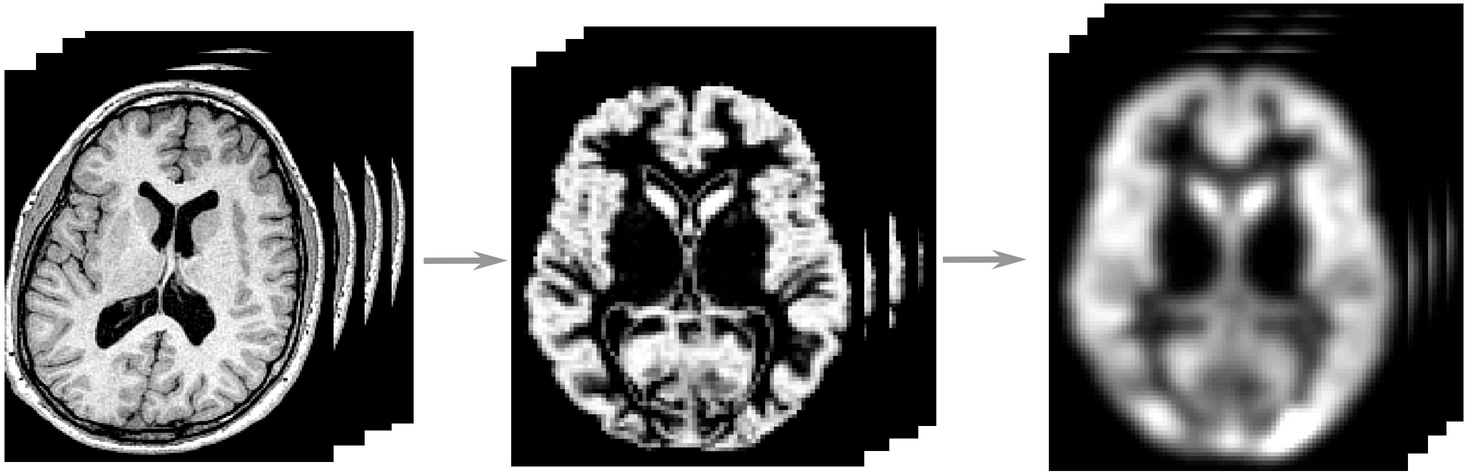
血管队列- 与没有认知损伤的被试相比，认知损伤(判断基于MMSE和MoCA)的被试有较高的WMH和较低的分数各向异性。

Zamboni, et al., Stroke 2017

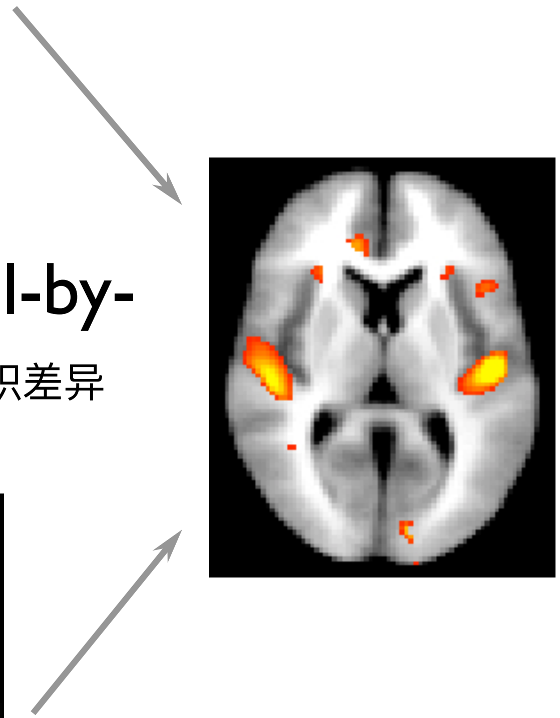
FSL-VBM

Voxel-Based Morphometry with FSL tools

使用FSL工具进行的基于体素的形态测量



To investigate GM volume differences voxel-by-voxel across subjects 基于体素研究不同被试间的灰质体积差异



Voxel-based analysis of local GM volume
基于体素的局部灰质体积分析

- Somewhat controversial approach 有点争议的方法
  (e.g. what exactly is it "looking at"?) 它关注的究竟是什么?

- BUT - it gives some clues for: 但是-它还是能提供一些有用的信息:
  - volume/gyrification differences between populations
    不同人群之间脑容积和脑沟回差异
  - correlations with (e.g.) clinical score 例如与临床评分之间的关系
  - fMRI/PET results "caused" by structural changes
    解释由结构变化导致的fMRI/PET结果

- Currently it is very widely used, although some other alternatives exist 目前该方法的使用还是很广泛的，尽管还有其他替代方法的存在
  (e.g. surface-based thickness analysis, 例如基于表面的皮层厚度分析
  tensor/deformation-based morphometry) 基于张量/变形的形态测量法

Voxel-based analysis of local GM volume
基于体素的局部灰质体积分析

- No a priori required = whole-brain unbiased analysis
  无需先验 = 全脑无偏分析
- Automated = Reproducible intra/inter-rater
  自动化的 = 可重复的评估者组内组间结果
- Quick 快速

- Localisation of the GM differences across subjects
  定位不同被试间的灰质差异

  ⇒ non-linear registration 非线性校正

- Trade-off: 权衡:
  - not enough non-linear = no correspondence 非线性不足=没有对应关系
  - too much non-linear = no difference (in intensities)
    非线性过多=(强度上)没有差异

Voxel-based analysis of local GM volume
基于体素的局部灰质体积分析

- Optimised protocol (Good et al., 2001) 优化范式
  1) Segmentation: BET then FAST to get GM partial volume estimate 分割：先用BET再用FAST来获得灰质部分体积估计

Voxel-based analysis of local GM volume

基于体素的局部灰质体积分析

- Optimised protocol (Good et al., 2001) 优化范式

  2) Make a study-specific template 制造特定于研究的模板

  & non-linearly register all images to it (FNIRT)

  将所有图像非线性配准到模板上(FNIRT)

Make template by iteratively registering images together, starting with a standard template

从标准模板开始，通过反复地将图像配准到一起来创建模板

Want equal numbers of patients and controls

需要病人组和控制组的数量相等

X patients病人

X controls 控制组

Voxel-based analysis of local GM volume

基于体素的局部灰质体积分析

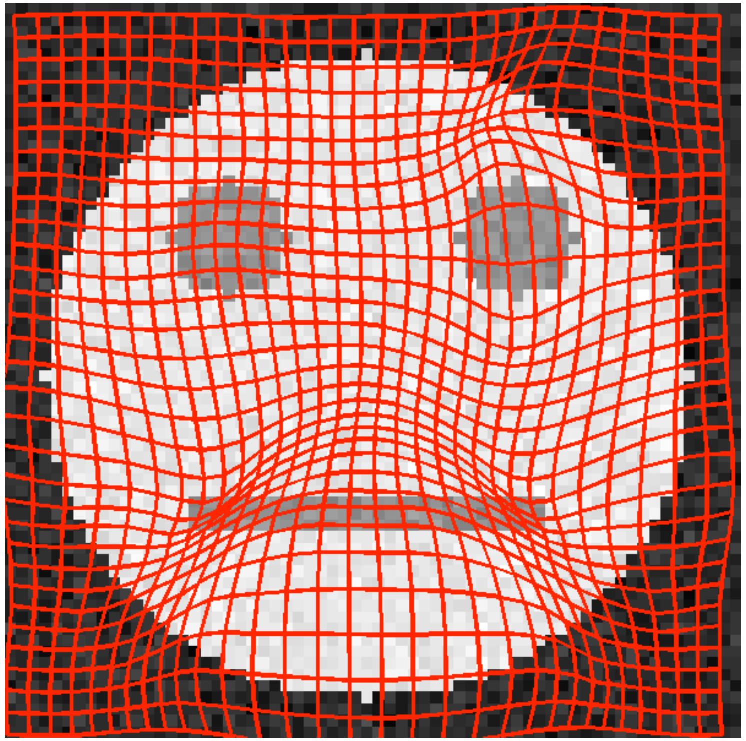
- Optimised protocol (Good et al., 2001) 优化范式

  3) "Modulation": compensates tissue volume for the non-linear part of the registration (FNIRT)

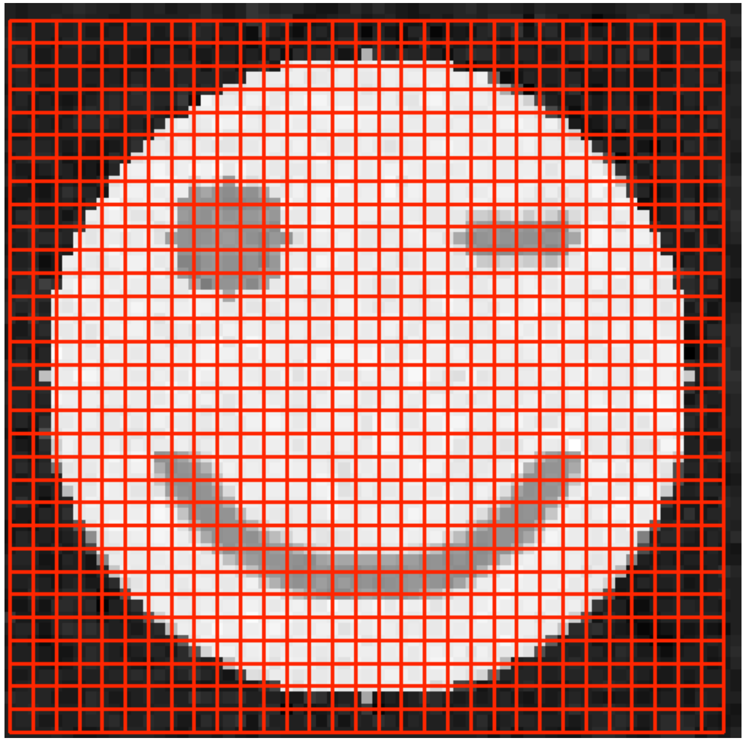
     "调整"：补偿配准非线性部分的组织体积(FNIRT)

Jacobian modulation

雅克比调整

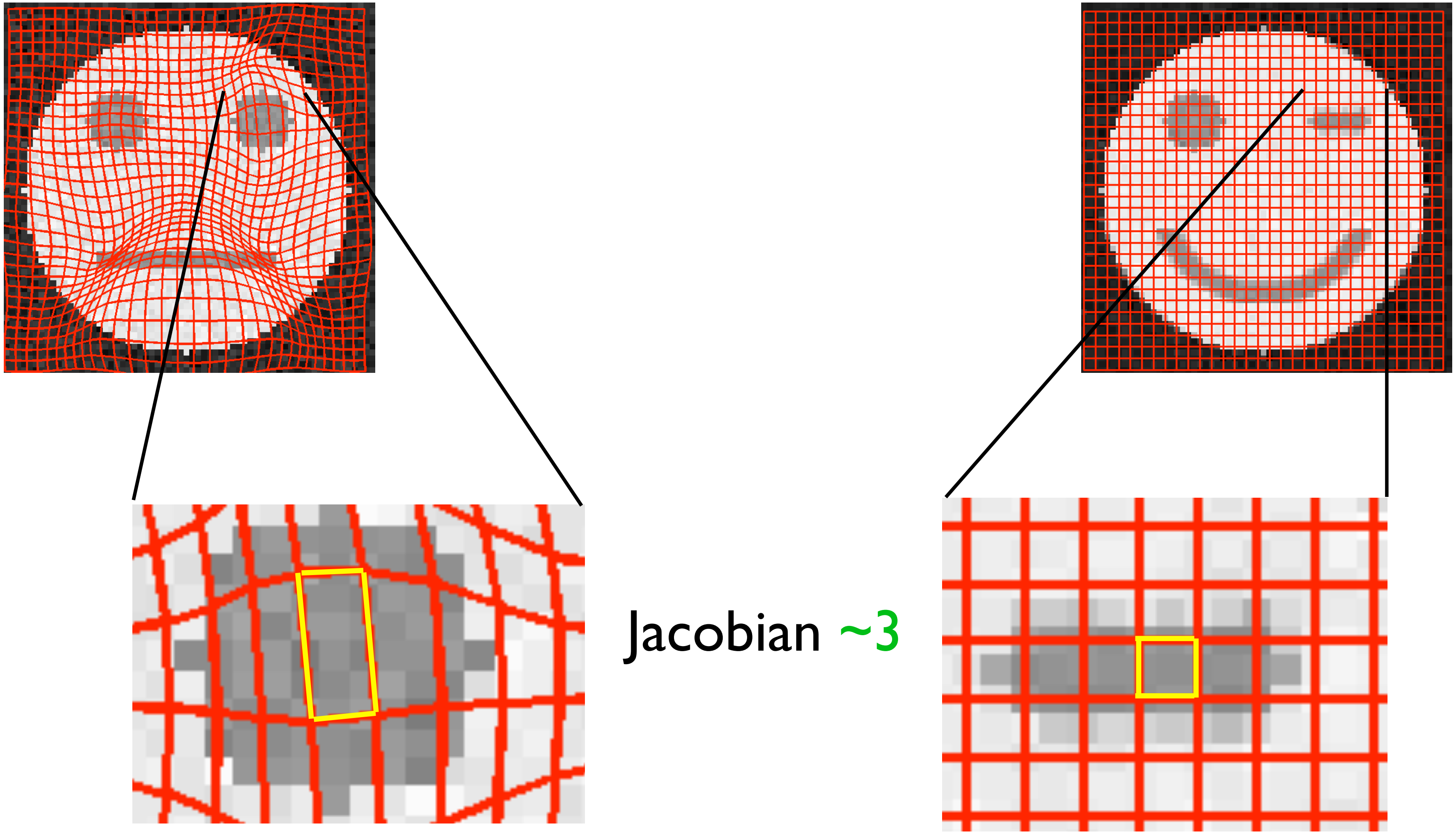


Jacobian modulation
雅克比调整



Jacobian modulation

雅克比调整



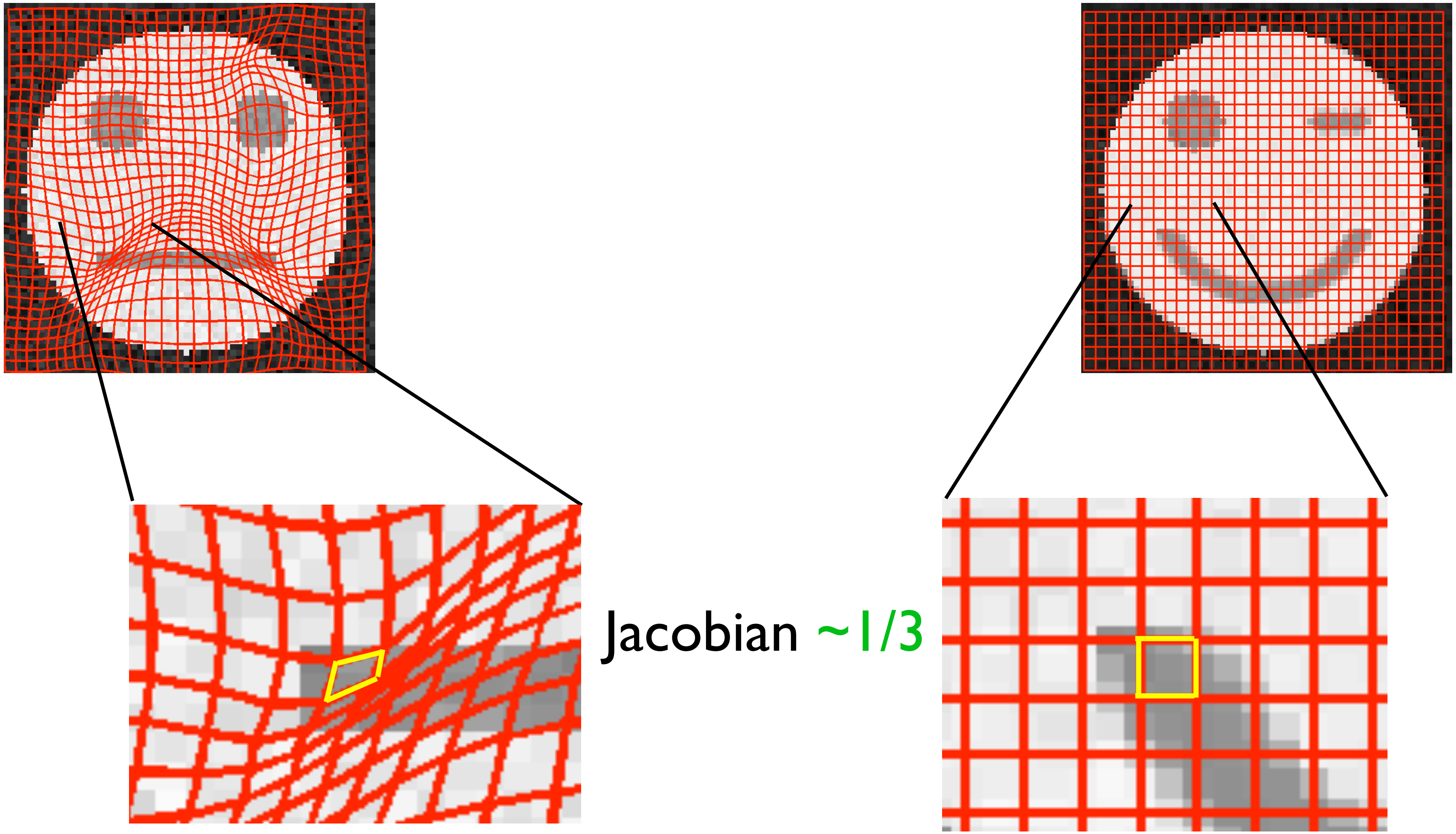
~3mm^2 in original space

原始空间中~3mm^2

1mm^2 in warped space

变换后的空间中为1mm^2

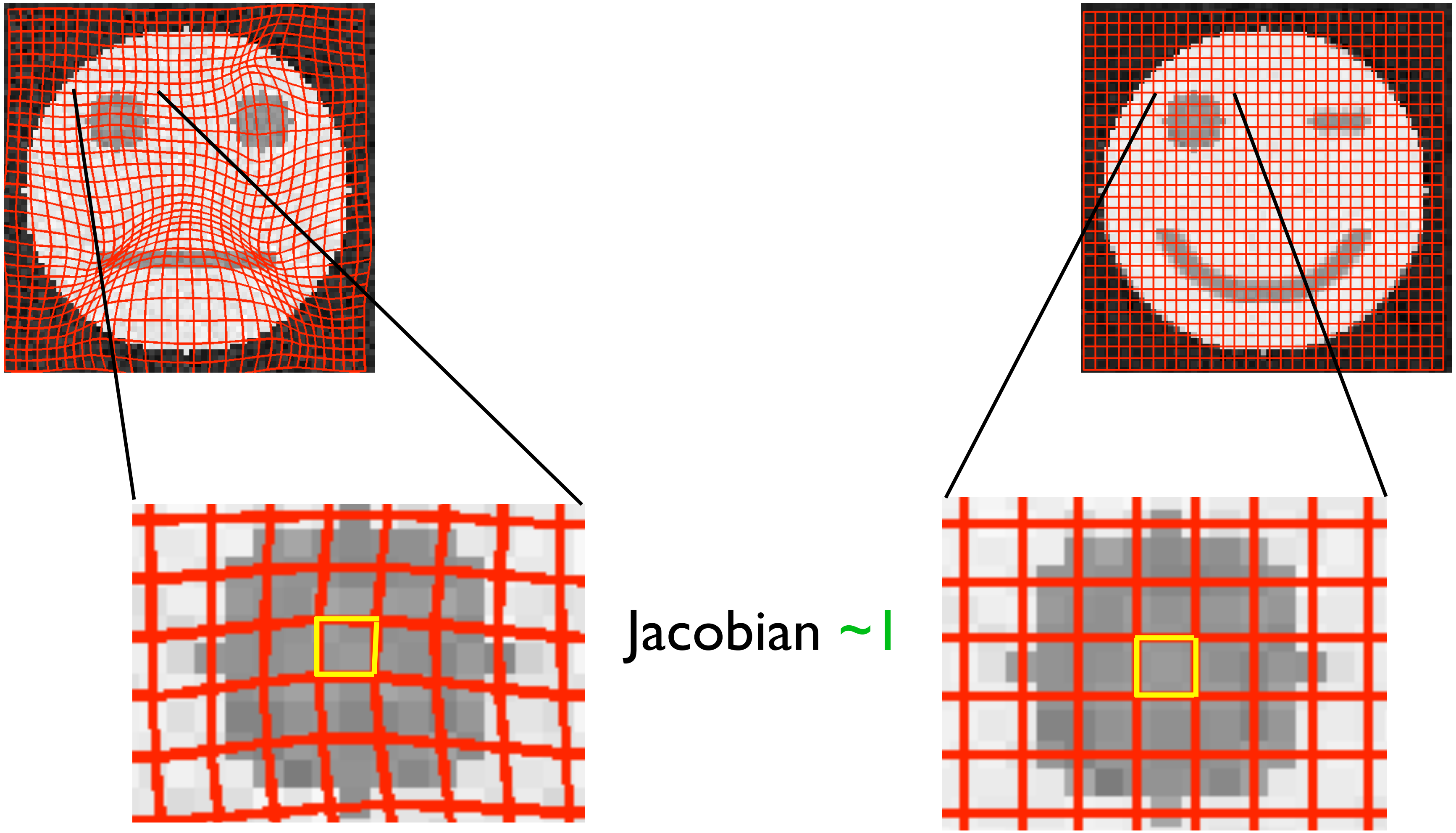
Jacobian modulation
雅克比调整



~1/3mm² in original space
原始空间中~1/3mm²

1mm² in warped space
在变换后的空间中为1mm²

Jacobian modulation
雅克比调整



~1mm² in original space
原始空间中~1mm²

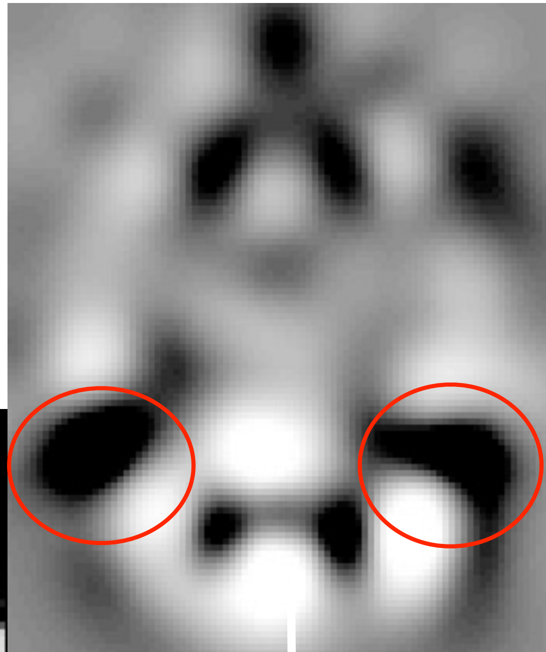
1mm² in warped space
在变换后的空间中为1mm²

Voxel-based analysis of local GM volume

基于体素的局部灰质体积分析

Jacobian map: correction for local expansion/contraction

雅克比图：用于局部扩张/收缩校正

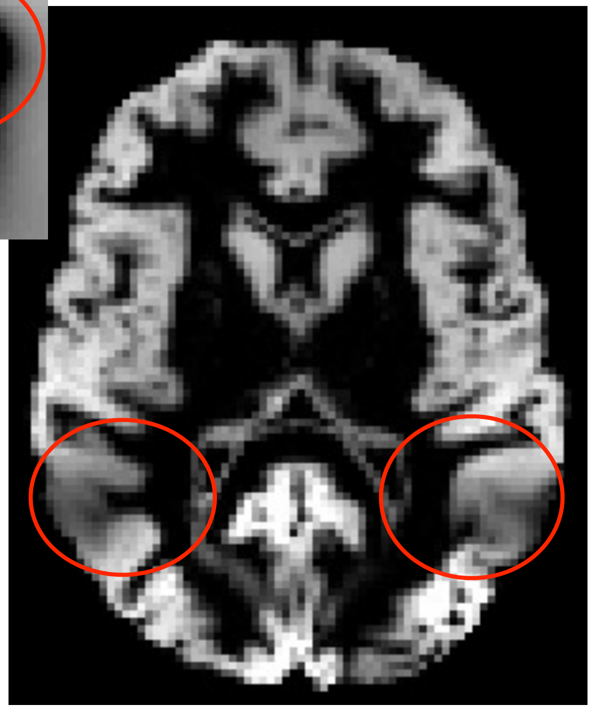


Uncorrected GM results

未校正的灰质结果

Results in "correct" amount of local GM

校正后的结果



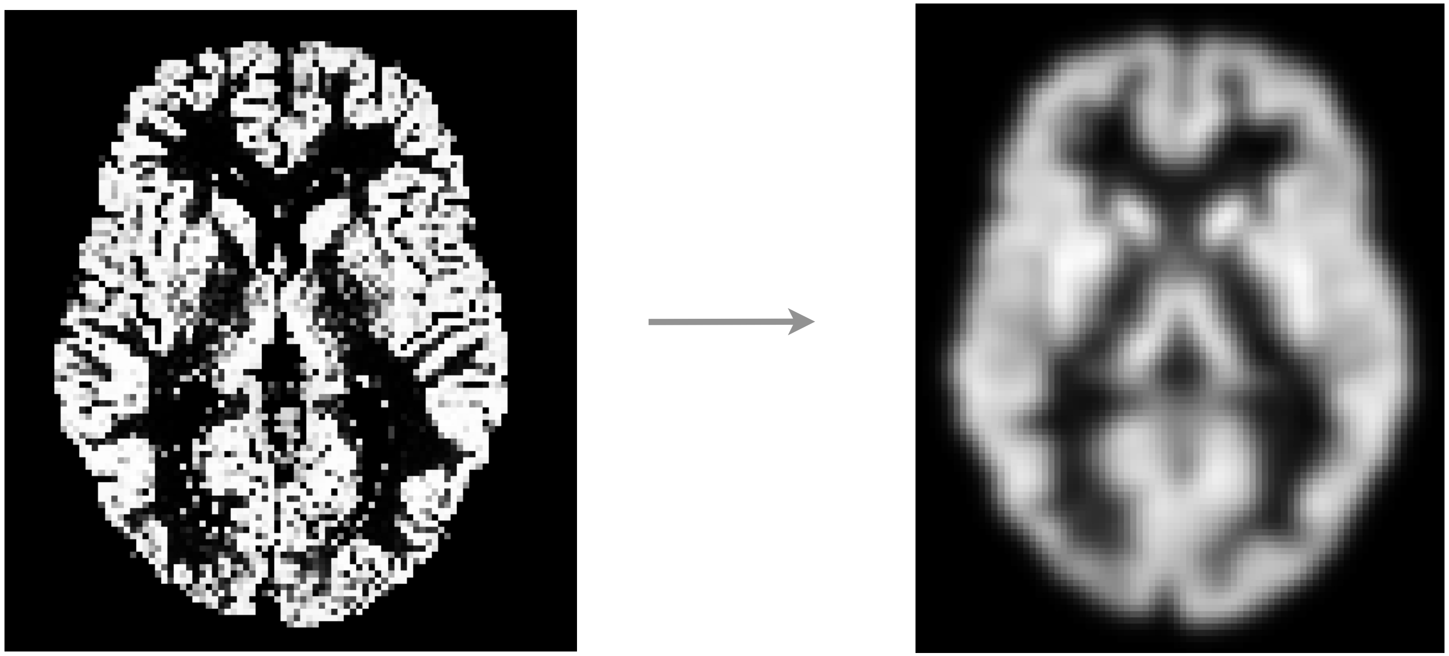
Voxel-based analysis of local GM volume

基于体素的局部灰质体积分析

- Optimised protocol (Good et al., 2001) 优化范式

  4) Smooth with a Gaussian filter

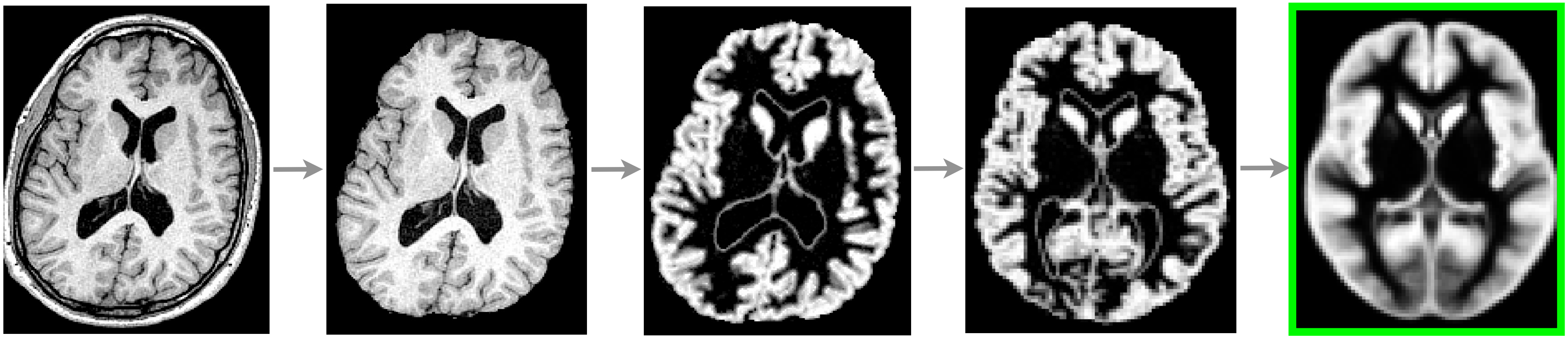
  使用高斯过滤进行平滑处理



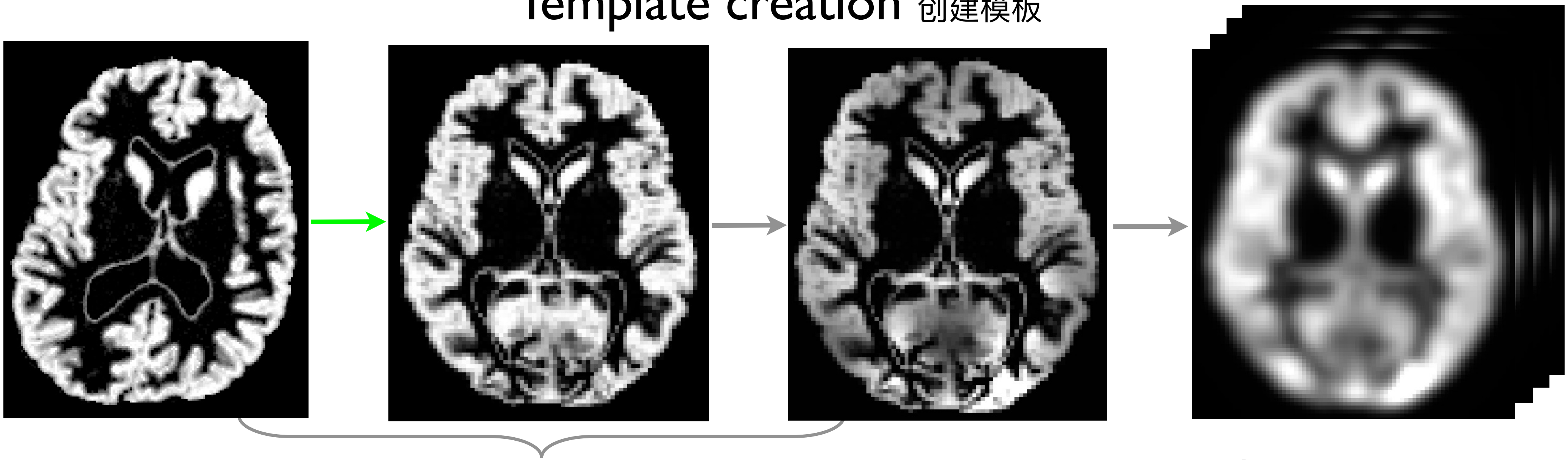
Voxel-based analysis of local GM volume

基于体素的局部灰质体积分析

- Optimised protocol (Good et al., 2001) 优化范式



Template creation 创建模板

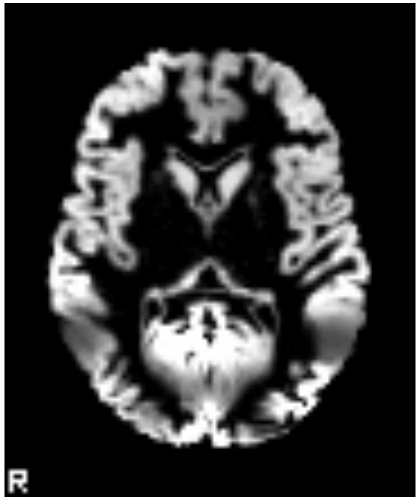


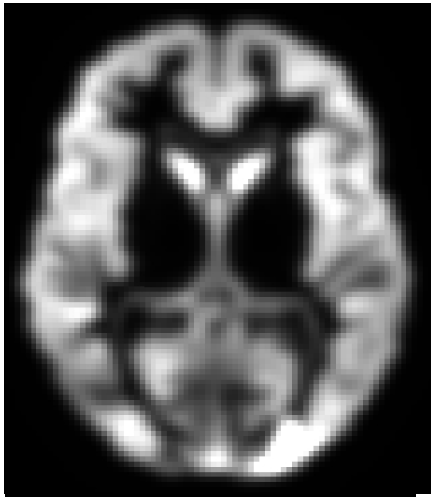
Processing steps 处理步骤

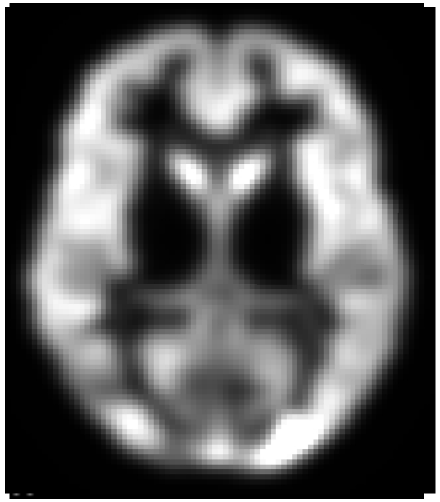
Analysis 分析

Voxel-based analysis of local GM volume

基于体素的局部灰质体积分析

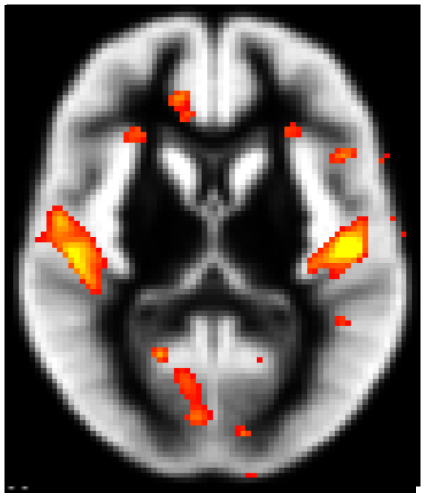


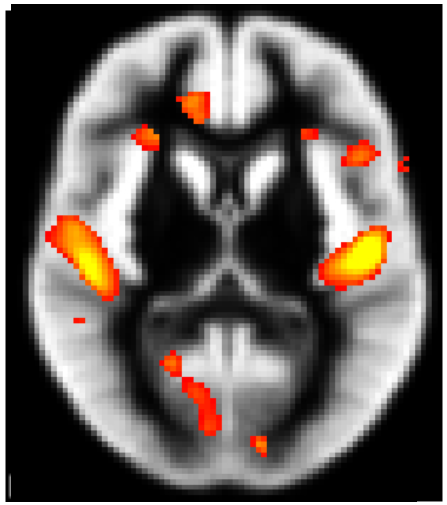




smooth平滑=5mm

smooth平滑=8mm

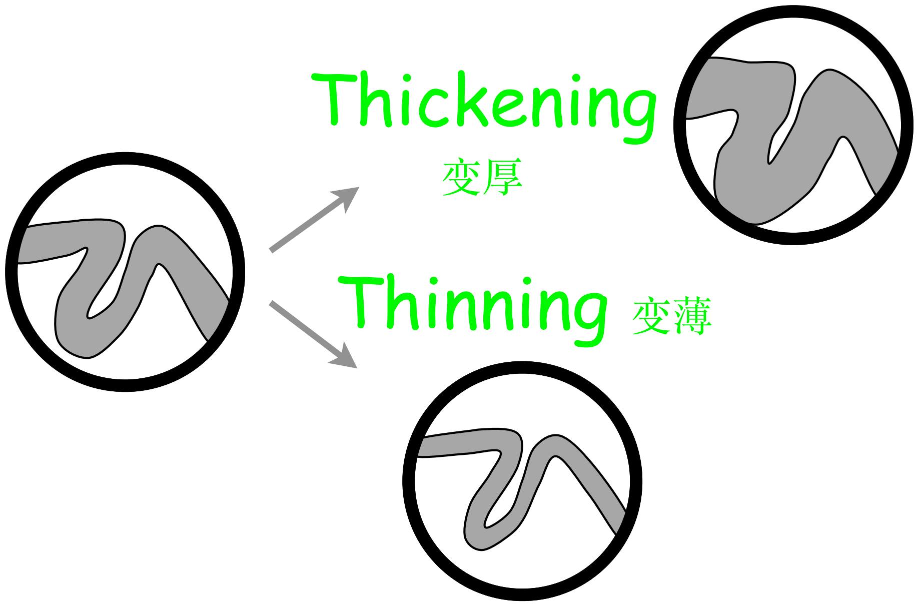




Voxel-based analysis of local GM volume
基于体素的局部灰质体积分析

- Controversial approach - back to the issues: 存在争议的方法-回到问题本身:

1) Interpretation of the results - real loss/increase of volume?
   对结果的解释 - 真的是体积减少/增加了吗?



Courtesy of
John Ashburner
John Ashburner的结果

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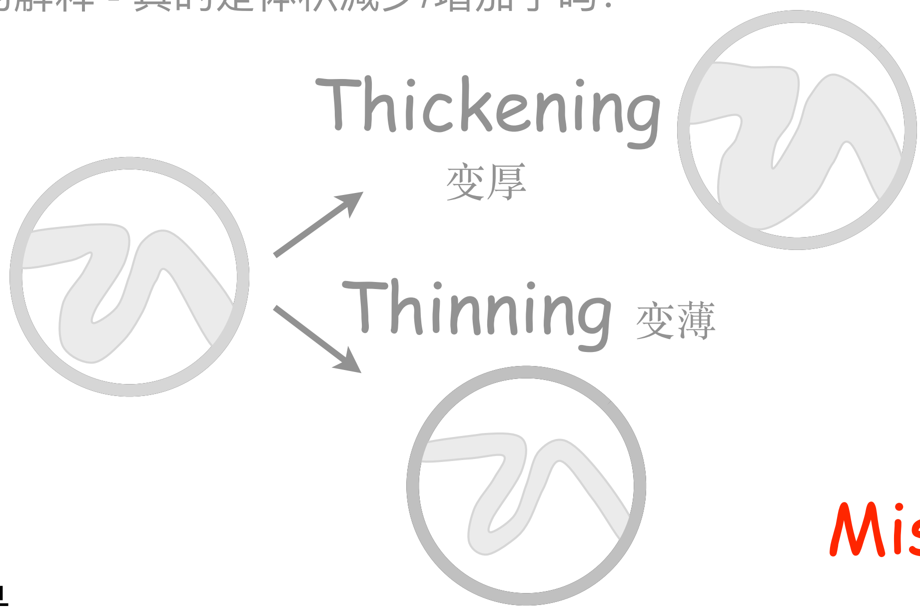

Courtesy of
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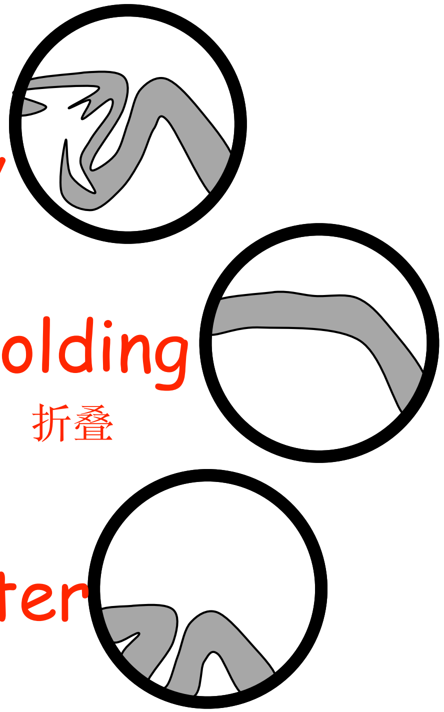
Or 或是...

- Difference in the contrast? 对比的不同?
- Difference in gyrification pattern? 皮层皱褶模式不同?
- Problem with registration? 配准导致的问题?



Mis-classify
错误分类

Folding
折叠

Mis-register
错误配准

Voxel-based analysis of local GM volume

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- Controversial approach - back to the issues: 存在争议的方法-回到问题本身:

1) Interpretation of the results - real loss of volume?

对结果的解释-真的是体积增加/减少了吗?

- Difference in the contrast? 对比导致的差异?
- Different in gyrification pattern (developmental)?
  皮层折叠模式(发育导致的)差异
- Problem with registration (Bookstein 2001) 配准导致的问题?

2) Continuum of results, depending on: 结果的连续性取决于:

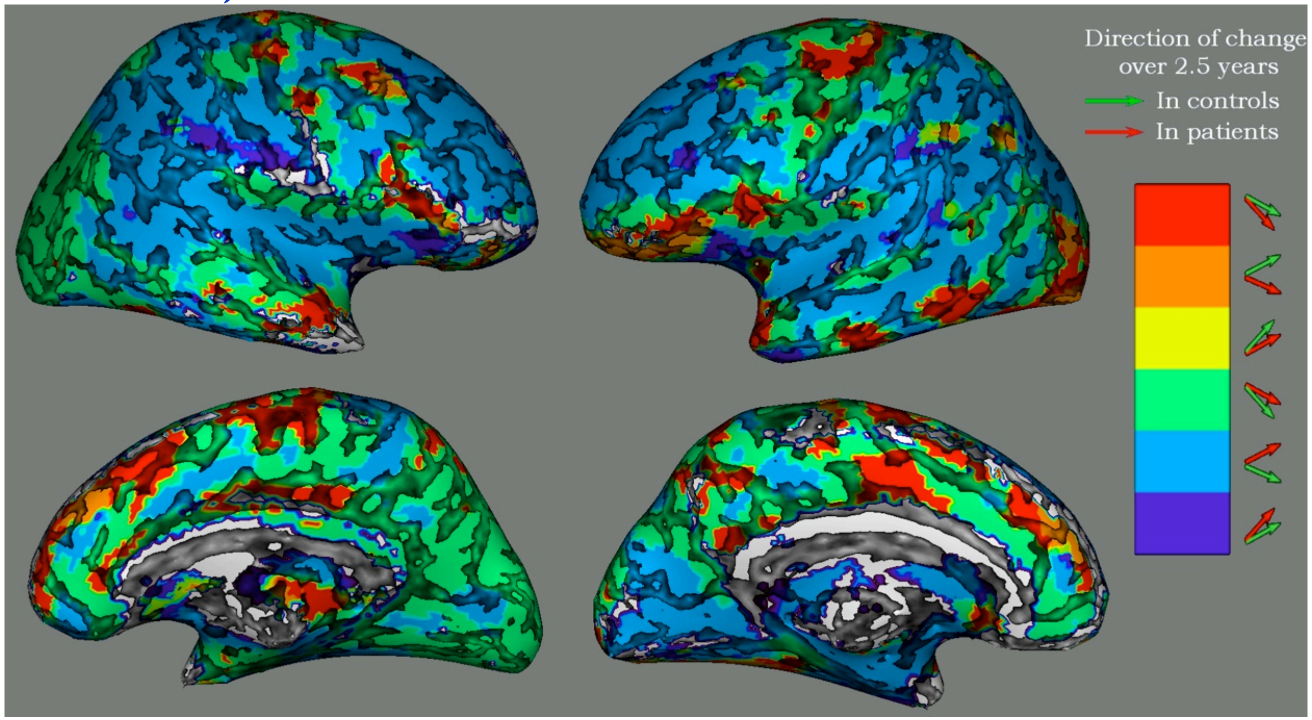
- Smoothness (Jones 2005) 平滑度
- DOF of the nonlinear registration (Crum 2003) 非线性配准的自由度
- Template? 模板?
- Software? 软件?

→ See Ridgway et al., NeuroImage 2008 for best practice

最佳操作请参见Ridgway et al., NeuroImage 2008

Voxel-based analysis of GM volume
基于体素的灰质体积分析

- Useful literature/examples: 有用的文献/实例:
  - Longitudinal protocol in FSL: FSL中的纵向范式:
    Douaud et al., Brain 2009



- - Comparisons of longitudinal protocols and softwares:
  不同纵向范式与软件间的比较
  Thomas et al., NeuroImage 2009

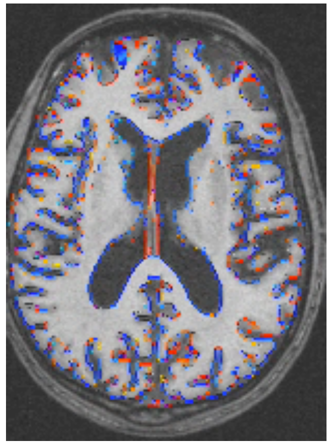
SIENA
Structural Image Evaluation (with Normalisation) of Atrophy

萎缩的结构像评估(包括标准化)

Multiple- and single-timepoint analysis of brain change

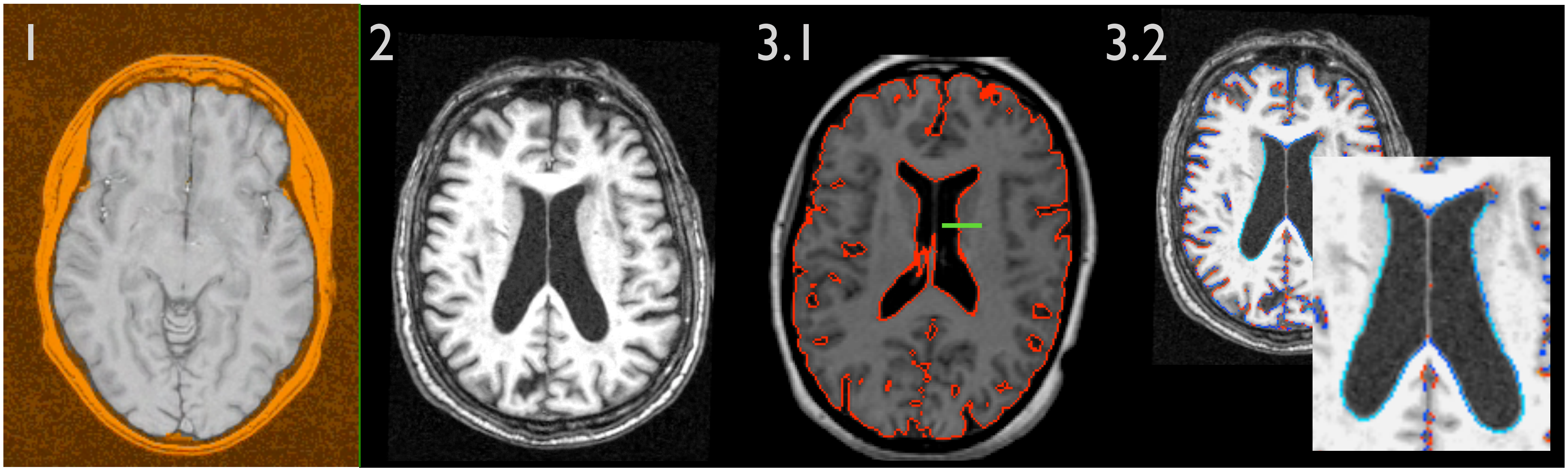
大脑变化的多时间点和单时间点分析

	original global-only estimation 仅对全局进行的原始估计	voxelwise local-only estimation 仅对局部进行的体素估计
two timepoints (atrophy *rate*) 两时间点(萎缩率)	SIENA	Longitudinal FSL-VBM 纵向FSL-VBM
single timepoint (atrophy *state*) 单时间点(萎缩状态)	SIENAX	FSL-VBM



SIENA Longitudinal atrophy estimation 纵向萎缩评估

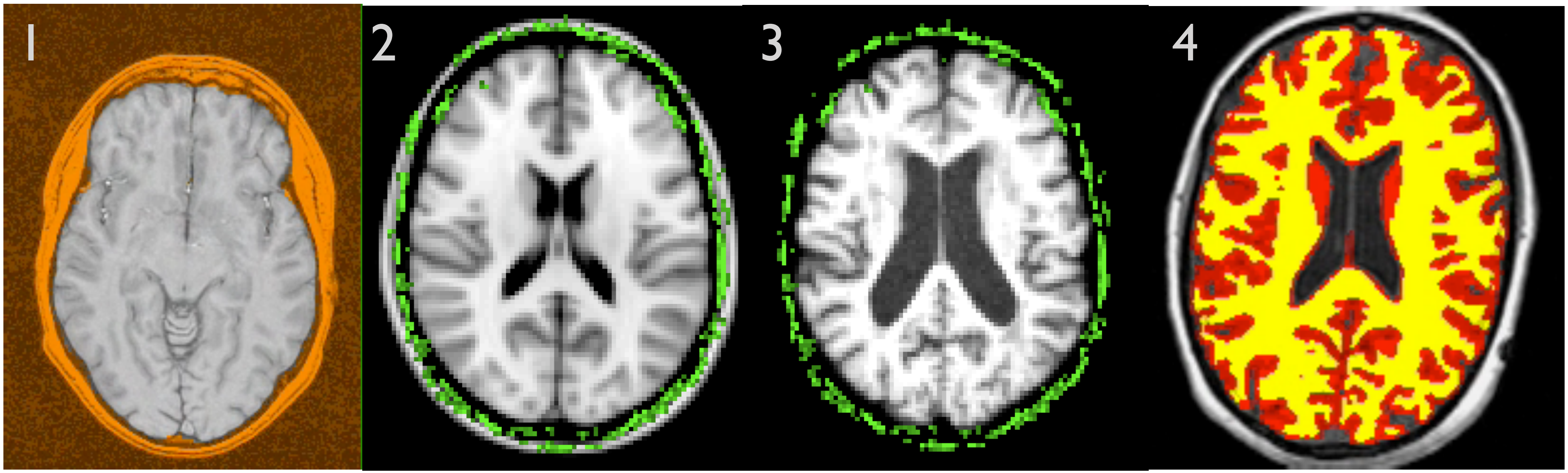
1. BET: find brain and skull - applied to both time points 找到大脑和颅骨-应用于两个时间点上
2. FLIRT: register to half-way space (similar interpolation for 2 points)
   FLIRT: 将图像配准到中间空间(两个时间点采用相似的插值法)
3. Atrophy estimation using edge motion 使用边缘运动估计萎缩
   3.1. Run FAST, then sample normal profile of brain-non brain boundary
   运行FAST,然后采样脑与非脑组织边界的正常轮廓
   3.2. Take derivative of both time points' profiles and calculate shift for each boundary point: blue=atrophy, red="growth"
   取两个时间点的轮廓的倒数病计算每一个边界点的位移：蓝色=萎缩, 红色="增长"
4. Average over all edge points and conversion to % brain volume change (PBVC)
   计算所有边界点的位移平均值，并将其转换成大脑体积变化百分比%(PBVC)



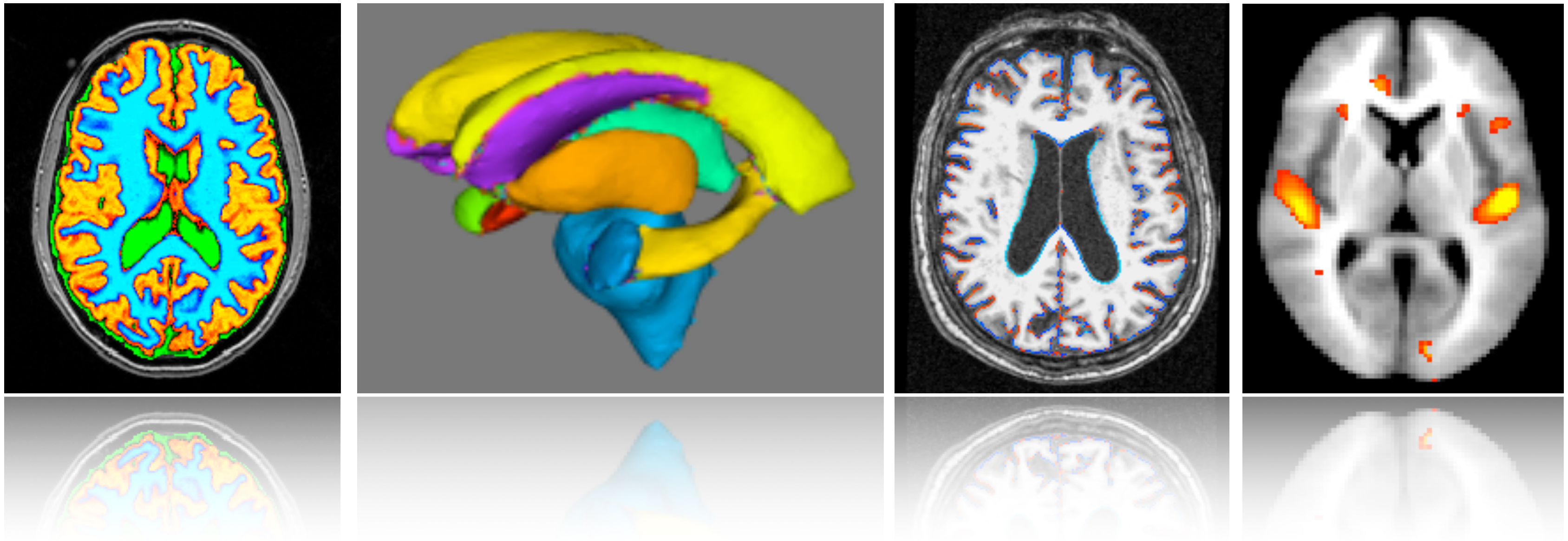
SIENAX Cross-sectional atrophy estimation 横向萎缩估计

1. BET : find brain and skull 找到大脑与颅骨
2. FLIRT : register to standard space using skull for scaling
   FLIRT :将图像配准到标准空间，基于头骨进行缩放
3. Use standard-space masking to remove residual eyes/optic nerve
   使用标准空间掩板来去除残留的眼神/视神经
4. FAST : partial volume segmentation of tissues 对组织进行部分体积分割
5. Output : normalised brain volume (NBV) 标准化的大脑体积

Note: NBV is useful for including as a *head/brain-size covariate* in other structural analyses (e.g. FIRST, VBM, etc.) NBV
可用于在其他结构分析（例如FIRST，VBM等）中将其作为头部/大脑大小的协变量



The End 结束



- FAST tissue-type segmentation 组织类型分割
- FIRST sub-cortical structure segmentation 皮层下结构分割
- BIANCA segmentation of white matter lesions 白质病灶分割
- FSL-VBM voxelwise grey-matter density analysis 体素灰质密度分析
- SIENA/SIENAX global atrophy estimation 全局萎缩估计