

# A construction of an averaged representation of human cortical gyri using non-linear principal component analysis



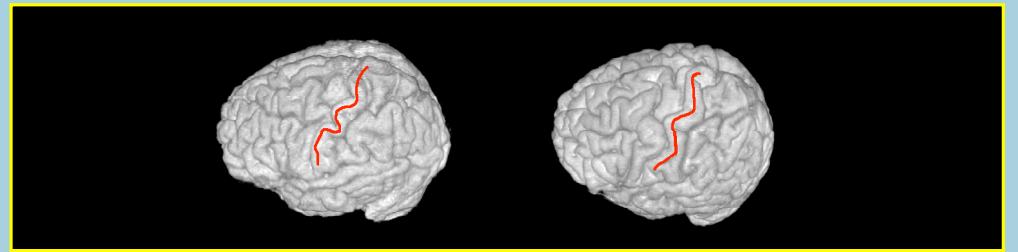
Gabriele Lohmann, D. Yves von Cramon & Alan C.F. Colchester\*

Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany,  
\*University of Kent at Canterbury, UK; email: lohmann@cbs.mpg.de

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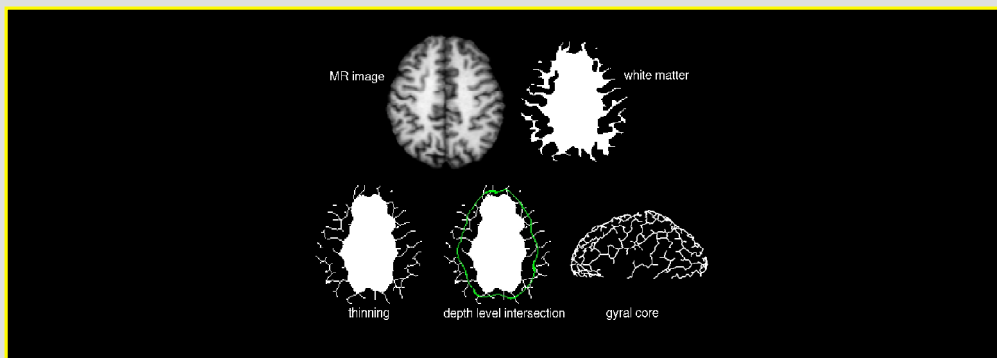
## Introduction

- Inter-subject registration requires a template onto which individual data set can be mapped.
- The template must be representative of the population.
- For a population with a high inter-subject variability, achieving representativeness is difficult.
- We propose to use non-linear PCA for this task.

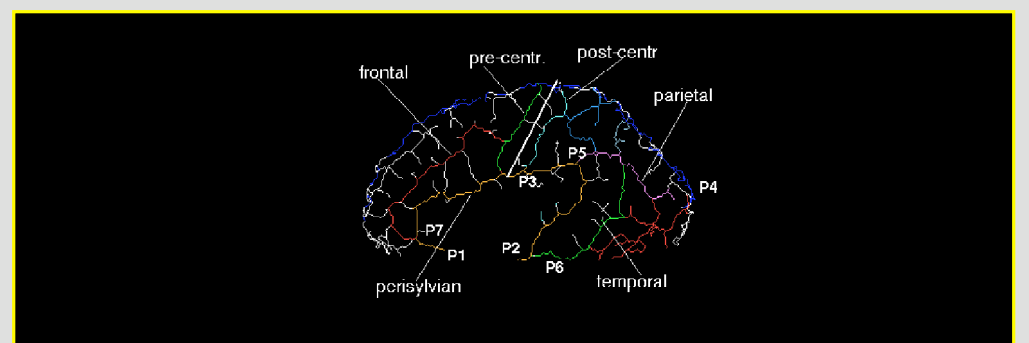


## Methods

- 1) Data:  
T1-weighted magnetic resonance data sets of 96 human volunteers acquired at a 3-Tesla Bruker Medspec 300 scanner, spatial resolution: 1 x 1 x 1.5 mm.
- 2) Gyral line representation:  
Cortical gyri are represented as 3D polygonal lines at eight different depth strata



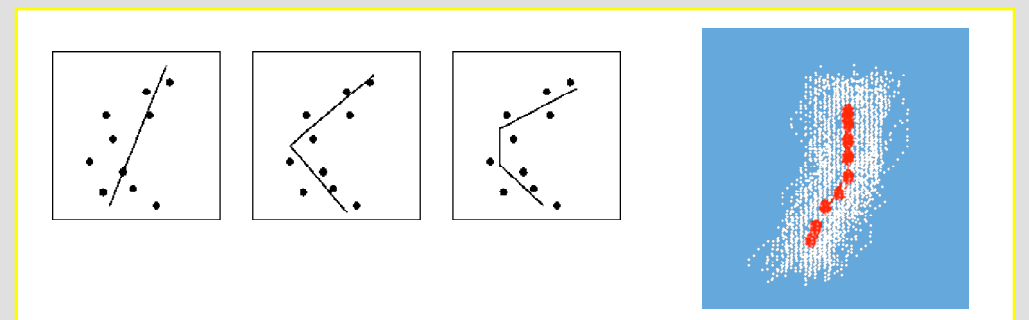
- 3) Gyral labelling:  
Gyral lines are semi-automatically labelled at their deepest level, using a set of heuristic rules. Dijkstra's algorithm for finding shortest paths in graphs is one of the key elements of our method. For instance, to identify the perisylvian core, we first identify the two anchor points P1 and P2 that mark the anterior and posterior ends of this core. We then apply Dijkstra's algorithm for finding the shortest path in the core graph that connects P1 to P2. P1 is defined as the most ventral point whose y-coordinate in the stereotactic Talairach system is less than -10. P2 is defined by a similar rationale.



- 4) Non-linear PCA:  
The anatomical labelling was applied to all 96 data sets. All labelled gyral cores were integrated into a common CA/CP-based coordinate frame. To obtain a gyral template, we applied nonlinear PCA to the resulting data clouds (Kegl et al. (2000)).

Principal curves are defined to be polygons which pass through the center of an n-dimensional data cloud. The data cloud is assumed to have an elongated shape so that a polygonal line can be considered to represent its most salient shape features.

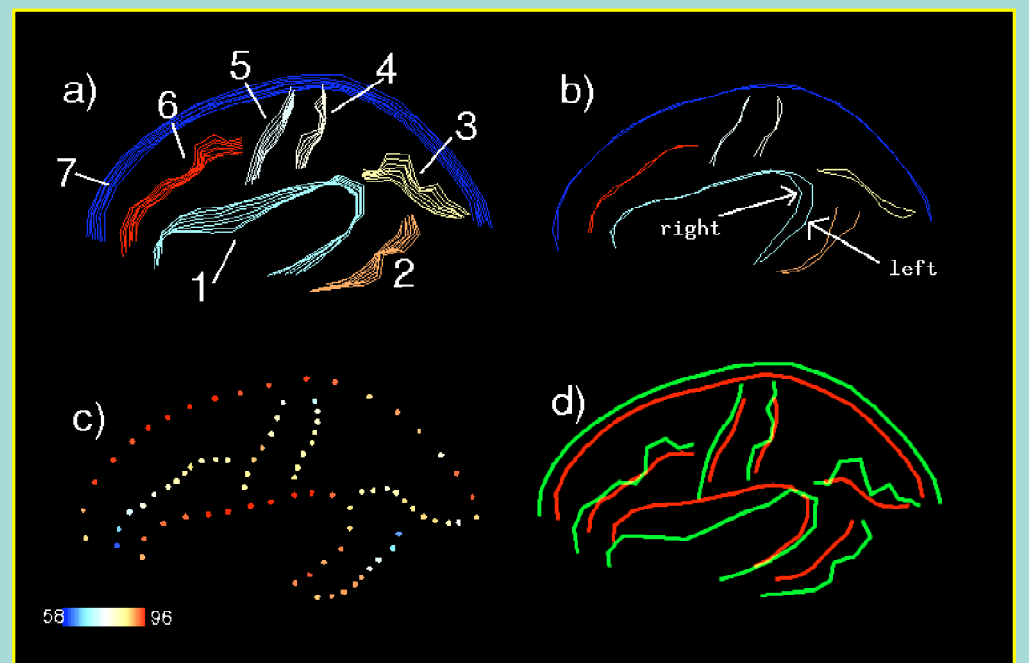
The algorithm starts with a straight line segment that is iteratively refined as new vertices are added.



## Results

The gyral model:

- a) the left hemisphere of the model in all its depth levels, 1:perisylvian, 2: inferior temporal, 3:parietal, 4:postcentral, 5:precentral, 6:frontal, 7:dorsal rim.
- b) an inter-hemispheric comparison where the right hemispheric model is flipped around the x-axis and superimposed onto the left hemisphere. The arrows indicate a region of inter-hemispheric differences in the vicinity of the planum temporale.
- c) the degree to which the model is representative of the population from which it was derived. Each node in the model graph has a label that indicates how many of the 96 individual labelled core graphs have a node of the same label within a 6 mm neighbourhood around the model node. Note that some segments of the model graph represent the data better than others. The anterior part of the middle frontal gyrus has low values indicating a high degree of inter-individual variability.
- d) compares the deepest depth level of the model (red) with the most shallow level (green). Note that the gyri at the shallow level are more convoluted than at the deepest level.



## Discussion

The model represents even quite subtle features of the cortical folding: for example, inter-hemispheric differences around the planum temporale are preserved. By comparing different strata of depth within the model, it is evident that the cortical gyri generally become smoother and less convoluted with depth. However, this appears not to hold for the precentral gyrus. The model also highlights areas of high inter-individual variability such as the anterior part of the middle frontal gyrus.

In addition to allowing study of gyral variability across individuals and between hemispheres, the representation provides a framework which can be used for future work on non-rigid registration.

## Reference:

Kegl, B., Krzyzak A., Linder, T., Zeger, K. (2000): "Learning and Design of principal curves", IEEE-PAMI, 22(3).