

Statistical analysis of cortical surfaces

K.J. Worsley, D. MacDonald, J. Cao, Kh. Shafie, and A. C. Evans
Montreal Neurological Institute and McGill University, Montreal, Canada

Introduction Cortical surfaces can now be extracted from MRI images by surface segmentation and matching using 3D deformations (1). In this abstract we present methods for the statistical analysis of these surfaces that can be used to detect abnormal deformations in an individual or between groups, or the effect of any general linear regression of surfaces on explanatory variables.

Methods Model-based segmentation is achieved automatically by deforming a 3D polyhedral mesh (8192 polygons, 4.5mm average internode distance) through minimization of a cost function, initially presented in (1). We model the (x, y, z) coordinates at a single node by a 3-variate normal distribution with an arbitrary variance matrix that allows for correlation between the coordinates. The statistical problem in its simplest form is to detect differences in node coordinates between two groups of n and m surfaces. We use the standard Hotelling's T^2 statistic, equal to the Mahalanobis distance between the two group means divided by $1/n + 1/m$, to detect differences in coordinates. This is then transformed to an F statistic by $F = T^2(n + m - D - 1)/((n + m - 2)D)$ where $D = 3$ is the number of dimensions. Under the null hypothesis of no group differences, F has an F -distribution with D and $n + m - D - 1$ degrees of freedom. If the coordinates follow a stationary multivariate Gaussian random field then it can be shown that F follows a stationary F -field. We now apply generalisations of standard methods for searching for deformations over the whole cortical surface. The first is based on peaks of the F -field (2), and the second is based on some recent work in progress on the extent of clusters of supra-threshold voxels (or nodes in this case) from F -fields (Cao, in preparation).

The effective full width at half maximum (FWHM) of the component Gaussian fields is obtained from the variance of the derivative of the coordinates, approximated by the difference in the coordinate at neighbouring nodes divided by the inter-node distance. The inter-node distance was measured on the average surface, obtained by averaging the coordinates of the nodes over all surfaces. If we define Q as the trace of the within-group variance of the derivatives multiplied by the inverse of the within-group variance of the coordinates, averaged over all nodes, then $\text{FWHM} = \sqrt{\{4 \log_e 2\} / [(Q/D)(n + m - D - 3)/(n + m - 2)]}$. This estimate is based on the assumption that the normalised coordinates are isotropic. The RESELS are then defined as the area of the search surface (measured on the average surface) divided by FWHM^{D-1} .

It may be desirable to smooth the images before analysis to improve the sensitivity to more extensive deformations. As in the case of PET and fMRI images, the size of the smoothing kernel should match the extent of the deformation to be detected. The coordinates were smoothed using a 3D Gaussian kernel smoother, with distance defined as the Euclidean distance between nodes on the average surface. The smoothing was applied to all surfaces and the above analysis repeated.

Results The algorithm was applied to 47 normal MR images. Without smoothing, the effective FWHM was 11.0mm, the surface area was 71593mm², giving RESELS=596. No differences were found using the maximum F when the surfaces were divided randomly into two groups of $n = 23, m = 24$ ($P = 0.272$), nor for detecting a difference between males ($n = 25$) and females ($m = 22$) ($P = 0.384$), even after 20mm FWHM smoothing ($P = 0.165$). For detecting deformations on an individual ($n = 1$), one surface was chosen at random and a Gaussian deformation of 20mm FWHM was applied to the x coordinate in the left temporal region. This deformation was first detected ($P < 0.05$) by the maximum F statistic when the amplitude of the deformation reached 6mm.

Conclusions The methods presented here are quite general. They can be used to detect differences between a single individual and a group of normals. It is straightforward to generalise the method to detect the effect of an explanatory variable in a linear model; group differences can be viewed as the effect of a contrast between group means in a simple analysis of variance model.

References

1. MacDonald JD, Avis D, Evans AC. *Proceedings Visualization in Biomedical Computing*. 1994: 160–169.
2. Worsley KJ, Marrett S, Neelin P, Vandal AC, Friston KJ, Evans AC. *Human Brain Mapping*. 1996, accepted.