Automatic labelling of the human cortical surface using sulcal basins

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Abstract

Human brain mapping aims at establishing correspondences between brain function and brain anatomy. One of the most intriguing problems in this field is the high interpersonal variability of human neuroanatomy which makes studies across many subjects very difficult. The cortical folds (‘sulci’) often serve as landmarks that help to establish correspondences between subjects. In this paper, we will present a method that automatically detects and attributes neuroanatomical names to the cortical folds using image analysis methods applied to magnetic resonance data of human brains. We claim that the cortical folds can be subdivided into a number of substructures which we call sulcal basins. The concept of sulcal basins allows us to establish a complete parcellation of the cortical surface into separate regions. These regions are neuroanatomically meaningful and can be identified from MR data sets across many subjects. Sulcal basins are segmented using a region growing approach. The automatic labelling is achieved by a model matching technique. © 2000 Elsevier Science B.V. All rights reserved.

Keywords: Medical image analysis; Cortical topography; Model matching

1. Introduction

The folding of the cortical surface of the human brain varies dramatically from person to person. However, the folding pattern is not completely arbitrary. In fact, the cortical folds (also called ‘sulci’) often serve as landmarks for referencing brain locations, and the more pronounced sulci have names that are well established in the neuroanatomical literature (Ono et al., 1990).

In this paper, we will present image analysis methods applied to T1-weighted magnetic resonance data sets that automatically segment and attribute neuroanatomical names to these folds. More precisely, we subdivide each fold into a number of substructures which we call sulcal basins, and attach labels to these substructures. The reason why we introduce the concept of a sulcal basin is that we believe that sulcal basins have a lower degree of interpersonal variability than entire sulci. Our belief is based on the findings of a twin study which showed that the deepest parts of the sulci are more strongly genetically predetermined than the more shallow ones (Lohmann and von Cramon, 1999a). The same study also shows that sulcal variability decreases with depth in the general population.

The work we present here is an extension of our earlier work (Lohmann and von Cramon, 1998a,b).

The method uses two stages. During the first stage, sulcal basins are segmented using morphological and region growing techniques. The second stage is a model matching procedure that automatically attributes neuroanatomical labels to the segmented basins. The model against which basins are matched is based on a volumetric shape representation of basins as well as on a model of spatial variation.

Our method is important in the context of human brain mapping. Human brain mapping aims at establishing correspondences between brain function and brain anatomy. One of the most intriguing problems in this field is the high interpersonal variability of human neuroanatomy which makes studies across many subjects difficult.
Most previous attempts at solving this problem are based on various methods of image registration where MR data sets are registered and warped onto a brain atlas (Mazziotta et al., 1995; Thompson and Toga, 1996; Thompson et al., 1997; Rizzo et al., 1997; Sandor and Leahy, 1997). A related approach is that by Guéziec and Ayache (1994) and also Declerck et al. (1995) who presented methods for extracting and matching lines in multiple MR data sets. New approaches to the problem of intersubject registration of sulcal patterns can be found in a number of references (Vaillant and Davatzikos, 1999; Caunce and Taylor, 1999; Goualher et al., 1999; Chui et al., 1999). Warping methods depend on establishing local correspondences between structures found in the image and in the atlas. Mismatches may lead to significant errors.

The approach presented in this paper allows interpersonnal comparisons without having to resort to image warping. Our concept of sulcal basins allows us to establish a complete parcellation of the cortical surface into separate regions. These regions are neuroanatomically meaningful and can be identified from MR data sets across many subjects. At the same time, the parcellation is detailed enough to be useful for brain mapping purposes.

The work closest in spirit to ours is that by Mangin et al. (1995), Manceaux-Demciau et al. (1997) and Regis et al. (1995) who also seek to obtain a structural description and generic model of the cortical topography. It differs from ours in a number of respects. Most importantly, their concept of ‘sulcal roots’ is based on a structural decomposition of sulcal skeletons. In contrast, our approach does not use sulcal skeletons but is based on a volumetric concept of sulcal indentations. This conceptual difference leads to different cortical parcellations. For instance, their parcellation would usually regard junctions between sulci as separations. However, sulcal junctions are often the deepest areas within sulci and are therefore at the heart of a basin in our model rather than at a boundary.

The paper is organized as follows. We begin by defining the concept of a sulcal basin and present an algorithm for extracting sulcal basins from MR images of the human brain. We then introduce a sulcal basin model and a matching procedure for identifying basins. Finally, we present some experiments.

2. Sulcal basins

2.1. Definition

We have previously introduced the notion of a sulcal basin (Lohmann and von Cramon, 1998a,b). In the following, we will summarize our definition and our method of extracting sulcal basins from MR images.

Fig. 1(a) shows a volume rendering of an MR data set depicting a top-right view of a healthy subject’s brain. The sulci are clearly visible as dark valleys. Fig. 1(b) shows the top part of the same brain. This time, however, we removed the grey matter so that the white matter surface becomes visible and the sulci become more pronounced. Corresponding locations in both images are indicated by labels.

Note that the fold labelled ‘sprc-sfs (superior precentral/superior frontal sulcus)’ which appears to consist of one large part in the volume rendering decomposes into three separate concave basins in Fig. 1(b). In fact, all sulci decompose into several such substructures, which we call ‘sulcal basins’.

More precisely, sulcal basins are defined to be concavities in the white matter surface which are bounded by convex ridges that separate one basin from the next so that adjacent sulcal basins meet at the top of the ridge. Fig. 1(c) illustrates this definition. The entire white matter surface is covered by such concavities so that a decomposition into sulcal basins yields a complete parcellation of the surface.

There are two principal advantages in introducing the concept of a sulcal basin. Firstly, in subdividing sulci we obtain a spatially more precise definition of brain loci. As we are ultimately interested in intersubject comparisons, this is an important consideration. Secondly, the high interpersonal variability in sulcal patterns can at least be partly attributed to different forms of groupings of sulcal basins. The two sets of sulcal basins below for instance can be easily matched, even though the two groups formed in each set cannot be matched:

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The postcentral sulcus, for instance, usually consists of

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two basins, a superior and an inferior basin. In some brains, these two basins are connected to form a continuous sulcus. In others, they are completely disconnected. Thus, sulcal basins may be much more useful as entities for matching than entire sulci.

2.2. Automatic detection of sulcal basins from MR data

In the following, we will describe our algorithm for extracting sulcal basins from MR images. Sulcal basins are concavities in the white matter surface, so that in principle it would be possible to detect sulcal basins by simply computing curvature properties of the white matter surface. However, the white matter surface is highly convoluted and the MR data sets have a limited spatial resolution, so that the computation of second-order differentials becomes quite inaccurate. As a consequence, we found that curvature computations are not feasible for our purpose.

Therefore, we use a different approach which is not based on curvature properties. The method consists of a sequence of image analysis steps which are illustrated in Fig. 2. The input data set [Fig. 2(a)] is first subjected to a white matter segmentation which separates white matter from other tissue classes [Fig. 2(b)]. This step helps to make the sulcal indentations more pronounced and thus more easily identifiable.

A large number of segmentation algorithms are known from the literature. Any suitable segmentation procedure can be used here. A general segmentation algorithm that produces satisfactory results for all types of input data does not exist at this point, so that the choice of a suitable algorithm and its parameters still very much depends on the type of data at hand. In our experiments, we used both simple thresholding techniques, as well as a new algorithm based on region growing (Lohmann, 1997).

We then close the sulci using a 3D morphological closing filter (Maragos and Schafer, 1990) to obtain an idealized smoothed surface [Fig. 2(c)]. We use a structuring element of spherical shape with a very large diameter. The exact size of the diameter is not critical as long as it is large enough. We subtract the white matter from the morphologically closed image so that only the sulcal interiors remain [Fig. 2(d)].

At this point in the procedure, the processed image contains the union of all sulcal basins. We now need to separate the individual basins by trying to find the ridges between them. These ridges can be viewed as ‘watersheds’ so that an approach reminiscent of a watershed segmentation is applicable.

The basic idea is to first identify a locally deepest region at the bottom of each basin, and then to allow each such region to grow until all sulcal interiors are filled up.

We define sulcal depth using a 3D distance transform with respect to the morphologically closed image depicted in Fig. 2(c). The distance transform attaches a distance label to each white voxel in Fig. 2(c) which encodes its 3D Euclidean distance towards the nearest black voxel. In our application, we are only interested in the depth of each sulcal interior voxel. Note that this depth might sometimes be underestimated if measured along a path that traverses white matter. Therefore, we use a variation of the ordinary distance transform called ‘constrained distance transform’

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Fig. 2. The major steps of the algorithm.
(Verbeek et al., 1986; Verwer et al., 1989) which allows us to explicitly prohibit measuring the length of paths that lead through the white matter.

Once each voxel is depth-encoded, we search for locally deepest points by moving a search window of size \( n \times n \times n \) across the image where typically \( n = 7 \). Adjoining deepest points that are of almost equal depth and are close are merged into one larger patch so that perturbations due to noise are eliminated. In our experiments we used a 3D morphological closing filter with a sphere-shaped structuring element with a diameter of 3 voxels to achieve this.

We then let each initial island grow in a manner similar to region growing until a separating ridge is encountered. During region growing, successively higher levels are processed so that at each stage in the procedure, only voxels at the current depth level are added to a sulcal basin (Fig. 2(e)).

Note that the parcellation of the cortex induced by this algorithm is complete as each voxel in a sulcal interior is a member of some depth level and is therefore processed at some point and assigned to some basin. A pseudocode version of the region growing procedure is listed in Table 1.

This algorithm is used to segment the lateral sulcal basins. The Sylvian fissure cannot be well segmented by the algorithm described above because of its more complicated shape. Note that the ventricles are also cavities in the white matter and might therefore be falsely segmented as basins. However, the ventricles are very much deeper than the lateral sulci and can therefore be easily excluded by using a depth threshold, which in our experiments was set to 3 cm.

In a final postprocessing step, adjacent regions are merged if the ridge that separates them is not high enough. The height of a ridge is given through the depth encoding discussed earlier. More precisely, let \( \text{depth}(R) \) and \( \text{depth}(S) \) denote the depths of two basins \( R \) and \( S \), where the depth of a basin is defined as the depth of its deepest voxel. The depth of a ridge denoted by \( \text{depth}(R, S) \) is defined as the depth of the deepest voxel that is adjacent to both \( R \) and \( S \).

In our experiments, two basins \( R, S \) were merged if
\[
\text{depth}(R) - \text{depth}(R, S) < \text{threshold} \quad \text{and} \quad \text{depth}(S) - \text{depth}(R, S) < \text{threshold}
\]
where \( \text{threshold} \) was set to about 1 mm. The above considerations induce a concept of adjacency between basins that will be used again later on.

Fig. 3 shows a data flow diagram of the entire basin segmentation procedure. Fig. 4 shows the result of a segmentation. To allow a better view into the deepest parts of the sulci, several layers of depth are morphologically eroded.

### 3. Automatic labelling of sulcal basins

In the following, we will describe a method of automatically attaching neuroanatomical labels to the sulcal basins that have been segmented using the procedures described in the previous sections. It is based on a model matching procedure that employs a point distribution model for describing spatial variations as well as shape similarity measures.

#### 3.1. The shape model

Our anatomical model contains both a volumetric description of the ‘mean’ shape of each sulcal basin as well as a model which describes possible variations in the location of basins.

We identified 38 left-hemispheric basins that could be located across most subjects. Neuroanatomical labels for these 38 basins are listed in Appendix A.

The mean shape of these basins are obtained by averaging across a set of training images. More precisely, we segment basins from several MR images and manually attach anatomical labels to all basins found in each image. Basins for which no meaningful label can be found are given a special null label which by convention is set to \( k = 1 \).

In order to obtain a characterization of the mean shape for basins we simply perform a pixelwise average as

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**Table 1**

<table>
<thead>
<tr>
<th>Region growing algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>currentdepth ← maxdepth</td>
</tr>
<tr>
<td>while currentdepth &gt; 0 {</td>
</tr>
<tr>
<td>for each voxel v in sulcal interior {</td>
</tr>
<tr>
<td>if depth(v) &lt; currentdepth {</td>
</tr>
<tr>
<td>if v is not yet assigned to a region {</td>
</tr>
<tr>
<td>assign v to the region to which it is closest</td>
</tr>
<tr>
<td>}</td>
</tr>
<tr>
<td>}</td>
</tr>
<tr>
<td>currentdepth ← currentdepth − decrement</td>
</tr>
</tbody>
</table>
| }

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**Fig. 3. Flow diagram.**
follows. First we rotated and translated all data sets into a common coordinate system with AC (anterior commissure) at the origin of the system. We also performed a linear scaling along all three coordinate axes to compensate for differences in brain size.

Let $i = 1, \ldots, N$ denote the training images, and $k = 2, \ldots, n$ denote the basin labels, and let $x_i^k \in R^3$ denote the center of gravity of the $k$th basin in the $i$th data set. Then the mean location of basin $k$ is calculated as

$$m_k = \frac{1}{N} \sum_{i=1}^{N} x_i^k.$$

In order to correct for overall brain shape differences – in particular for variations in the locations of major sulci – we first shift each basin separately into its mean location as defined above. We do not, however, correct for rotational variations of sulci as the orientation is quite characteristic of sulci and should be preserved. At each pixel location in stereotactic space we record the number of images in which this pixel is occupied by each basin label. A voxel is defined to belong to the mean shape of basin $k$ if this number is larger than a given threshold. In our experiments, we used a threshold of $t = 5$ out of 15 training data sets.

The mean shape captures the average position as well as the average geometrical outline. Fig. 5(a) shows the resulting mean shapes for all 38 basins with the exception of basins belonging to the Sylvian fissure.

Note that the Procrustes mean shape as described in Goodall (1991) and Bookstein (1997) would not have been suitable in our context. The Procrustes mean shape does
not capture rotational and translational characteristics of the shape. However, in our domain, the orientation (i.e. rotation) and position are crucial aspects of the mean shape.

3.2. The spatial distribution model

In order to represent allowable variations in the location of sulcal basins we use the point distribution model as introduced by Cootes et al. (1995). Point distribution models (PDMs) require sets of landmark points as training data. In our application, the landmark data are entire volumetric objects, namely the sulcal basins that have been segmented and hand-labelled from MRI data.

In order to be able to employ the point distribution approach, we only use the centers of gravity of each basin as landmarks. Fig. 5(b) shows the location of these points. We can then estimate the average location of sulcal basins as well as variations in their location as follows (see also (Cootes et al., 1995)).

Let $N$ be the number of training data sets, and let $n$ be the number of basins contained in the model. Further, let $x_i \in \mathbb{R}^{3n}$ denote the locations of all $n$ basins in the $i$th data set. Then the mean location is calculated as

$$\bar{x} = \frac{1}{N} \sum_{i=1}^{N} x_i.$$ 

Note that this time the mean location is calculated across all basins and all training images. For each training set, the deviation from the mean location is calculated using

$$d_i = x_i - \bar{x},$$

with the $3n \times 3n$ covariance matrix given by

$$S = \frac{1}{N} \sum_{i=1}^{N} d_i d_i^T.$$ 

The main modes of variation in the location of the training points are determined by a principal component analysis such that the first eigenvector of the covariance matrix describes the most significant variation.

Each training instance $x$ can be recovered from the covariance matrix and the mean location vector as a linear combination of eigenvectors using

$$x = \bar{x} + Pb,$$

where $P = (p_1, \ldots, p_t)$ is the matrix of the first $t$ eigenvectors and $b = (b_1, \ldots, b_t)$ is a vector of weights. New instances of the model can be constructed by allowing the parameters $b_i$ to vary within acceptable ranges.

Fig. 6 illustrates the first two modes of variation applied to a sulcal line representation of one individual data set. Sulcal lines are polygonal representations of the cortical folding as described in (Lohmann, 1998).

3.3. Model matching

Matching the model to an individual data set requires us to find a vector $b$ of weights that yields a new instance $x$ of the PDM model that corresponds more closely to the individual data set. This task can be cast into an optimization problem.

The goal function that we seek to minimize is defined as follows. Consider the raster image shown in Fig. 2(d) containing the sulcal interiors. It is obtained by a subtraction of the white matter segmentation from the morphological closure as explained before. We now perform a 3D distance transform on this image (Borgefors, 1984; Saito and Toriwaki, 1994) such that each black voxel obtains a distance label that encodes its distance towards the nearest white voxel.

The goal function is obtained by adding all distance values which are covered by a non-zero voxel of the model basins. More precisely, let $j = 1, \ldots, m$ denote voxel sites in stereotactic space with $m$ being the number of voxel sites. For the individual data set whose basins we want to label, let $\text{dist}_j, j = 1, \ldots, m$, denote the distance of the voxel at position $j$ to the nearest white voxel where the distance is obtained as described above.

For the model image containing the model basins, let $\chi_j = 1$ iff the voxel at position $j$ in the model image belongs to some basin in the deformed model, and $\chi_j = 0$.

![Fig. 6. The two main modes of variation. The top row shows the variation pertaining to the first eigenvector. Its main anatomical characteristic appears to be a variation in the size of the frontal brain versus the posterior brain. The second row shows the variation pertaining to the second eigenvector. The variation ranges between $-\sqrt{\lambda_k}$ and $+\sqrt{\lambda_k}$ with eigenvalues $\lambda_k$, $k = 0,1$.](image-url)
if it does not belong to any basin. Then the quality of the match is defined as
\[
\sum_{j=1}^{m} \chi_{j}^{\text{dist}}.
\]

Thus, large discrepancies between the model image and the sulcal interior image are penalized.

The optimization process seeks to find a weight vector \( b = (b_1, \ldots, b_t) \) that generates an instance
\[
x = \hat{x} + Pb
\]
of the PDM model that minimizes the goal function where \( P = (p_1, \ldots, p_t) \) is the matrix of the first \( t \) eigenvectors of the PDM covariance matrix. Note that \( x \) defines new centers of gravity for all model basins. Thus, it describes translations of the model basins, their shape, however, is not altered.

We use Powell’s optimization method (Press et al., 1992) to solve this optimization problem. In order to avoid local minima, a number of different starting values are tested.

3.4. Assignment of labels

Once the model is deformed to an individual data set, we can use it to attribute anatomical labels to sulcal basins. However, this task is not trivial as the model basins will not completely overlap with the basins found in the individual data set. Therefore, we need a shape similarity measure for identifying the best match.

We use the Hausdorff distance metric (Huttenlocher et al., 1993) for this purpose. The Hausdorff metric is defined as follows. Let \( A = \{a_1, \ldots, a_n\} \) and \( B = \{b_1, \ldots, b_m\} \) be two sets of points in \( \mathbb{R}^3 \). Then the Hausdorff distance between \( A \) and \( B \) is defined as
\[
H(A,B) = \max(h(A,B),h(B,A)),
\]
where
\[
h(A,B) = \max_{a \in A} \min_{b \in B} \|a - b\|.
\]
The function \( h(A,B) \) ranks each point of \( A \) with respect to its distance to \( B \), and uses the largest distance as the result. Thus, it captures the degree of overlap between two shapes.

Using the Hausdorff metric we measure the distances between basins of the individual data set towards the shifted model basins. Thus, we obtain an assignment matrix \( X_{ik} \in \mathbb{R} \) where \( X_{ik} \) indicates the Hausdorff distance between basin \( i \) in the individual data set towards the shifted model basin \( k \). We can now simply attribute the label that has the smallest Hausdorff distance.

Occasionally, more than one match might be possible for some basin. In order to resolve such ambiguities we use Sinkhorn’s assignment procedure as described by Gold and Rangarajan (1996). This procedure amounts to an iterative update of the matching matrix until the match becomes unique.

3.4.1. Composite basins

In some cases, the basin segmentation procedure fails to detect a ridge between two basins. For instance in about 10% of the cases, the central sulcus was not segmented into two basins but into just one. Note, however, that the absence of a basin or the merger of two basins does not necessarily indicate a segmentation error. Such an event may also be due to anatomical variation. In order to distinguish between the two, we compute depth images such as the one shown in Fig. 4. An erroneous segmentation is present if two basins are segmented as one basin even though they appear separate in at least one depth level. In fact, a truly erroneous segmentation occurred in only one basin of one data set out of 37 data sets. In the remainder of the cases, the separating ridges were either not present or they were below the spatial resolution of our MRI data.

In order to deal with merged basins, we additionally use ‘composite’ basins which are composed of two or more model basins. At present we use four composite basins: a basin representing the central sulcus (composed of basins 2 and 3), a basin representing the postcentral sulcus (basins 17 and 19), and a basin representing the superior temporal sulcus (basins 22, 23 and 24).

These composite basins enter the assignment procedure just like any other basin. In cases where the segmentation was too coarse they provide a better match.

4. Experiments and results

Our input data consisted of 37 T1-weighted magnetic resonance images (MRI) of healthy volunteers. The spatial resolution between planes was approx. 1.5 mm and the within-plane resolution was set to approx. 0.95 mm. The images were subsequently resampled to obtain isotropic voxels of size 1 mm×1 mm×1 mm so that each data set contained 160 slices with 200×160 pixels in each slice. As noted before, all data sets were rotated into a standard stereotactic coordinate system and linearly scaled to a uniform size. In addition, we applied an automatic procedure to extract brain from non-brain material. For a more detailed description of our preprocessing procedure see (Kruggel and Lohmann, 1997).

Our basin segmentation method was applied to all 37 MR data sets. The model graph was acquired by hand-labelling the sulcal basins extracted from 15 of these data sets, and a PDM model was derived as described above.

The matching procedure was then applied to all remaining data sets. On average, about 1.5 basins received incorrect labels. Note that the number of basins varies across subjects. The assignment procedure prevented multiple matches. Only the null label was allowed to be
assigned to several basins. Large major basins never received a null label. The assignment of the null label to a small basin was not counted as an error because those assignments are problematic in any case.

Most errors occurred in areas where interindividual variability is largest. Particular problem areas were the intermediate frontal sulcus which was sometimes confused with either the superior or the inferior frontal sulcus. Most errors involved only small parts of secondary or tertiary sulci. In each case, the correctly labelled area equalled much more than 90% of the entire labelled area.

The Sylvian fissure and insula, however, cannot be adequately segmented with our present approach. This is due to the fact that the watershed mechanism does not really capture the complex shape of these structures. Therefore, the Sylvian fissure is not suitably represented in

Fig. 7. Results of the basin labelling procedure applied to two data sets. The top rows show the white matter segmentation with sulcal depth color-coded in shades of blue. The bottom rows show the labelling results. The colors correspond to nodes in the model graph. Note that corresponding basins can be identified in both brains. However, there are basins that appear in one data set, but not in the other (e.g. basin 5).
our basin model. We are currently in the process of developing methods that specifically address this problem.

The computation time for the basin segmentation was approximately 4:30 min on an SGI Unix workstation. The model matching algorithm also takes about 4:30 min per data set. Fig. 7 shows the result of the sulcal labelling applied to two data sets. The white matter segmentations are also shown to provide better visual clues.

5. Conclusion and future work

We have presented a method that automatically detects and attributes neuroanatomical names to substructures of the cortical folds which we call sulcal basins using magnetic resonance data of healthy human brains.

The labelling process is cast as a model matching process involving a point distribution model and a label assignment process using the Hausdorff distance metric and Sinkhorn’s assignment algorithm. The PDM model is used here in a somewhat unusual manner. Normally, PDM models are used to describe shape contours, whereas here we use it to model locations of volumetric objects. However, it is quite well suited for this task as it yields a spatial model that is specific enough to exclude illegal instances but general enough to permit all possible variations.

Currently, our model covers the entire lateral surface of the left hemisphere where it provides a complete parcellation of the cortex. Future work will aim at expanding the model to include both hemispheres, as well as the medial and basal surfaces of the brain.

The experiments have shown that sulcal basins can indeed be segmented and labelled reliably and reproducibly. However, the correctness of a labelling cannot be easily assessed as even human experts do not always agree on the assignment of neuroanatomical labels. This is particularly true for small tertiary sulci for which no well-established anatomical names exist. But even some parts of secondary sulci such as the superior frontal sulcus are often difficult to identify visually. Therefore, quantitative assessments of the classification accuracy are somewhat dubious. The numbers given in the preceding section are based on visual inspection by a human expert.

Future work will include a refinement of the basin segmentation. So far, sulcal basins are rather large, and will have to be subdivided into smaller units.

The most important aspect of our future work will be however to provide a neuro-psychological validation for our concept of sulcal basins. Of particular interest are correlations between sulcal basin labellings and functional activations measured by functional magnetic resonance imaging (fMRI) studies. We expect to find that functional activations fall into equivalent basins across subjects. Some preliminary experiments indicate that this may indeed be the case (Lohmann and von Cramon, 1999b).

Appendix A

In Table 2 a list of neuroanatomical labels is given. The identification numbers correspond to the numbers given in Figs. 5 and 7.

<table>
<thead>
<tr>
<th>Id</th>
<th>Neuroanatomical name</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Unknown</td>
</tr>
<tr>
<td>2</td>
<td>Superior central sulcus</td>
</tr>
<tr>
<td>3</td>
<td>Inferior central sulcus</td>
</tr>
<tr>
<td>4</td>
<td>Superior precentral sulcus</td>
</tr>
<tr>
<td>5</td>
<td>Medial precentral sulcus</td>
</tr>
<tr>
<td>6</td>
<td>Inferior precentral sulcus</td>
</tr>
<tr>
<td>7</td>
<td>Superior frontal sulcus 1</td>
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<tr>
<td>8</td>
<td>Superior frontal sulcus 2</td>
</tr>
<tr>
<td>9</td>
<td>Superior frontal sulcus 3</td>
</tr>
<tr>
<td>10</td>
<td>Superior frontal sulcus 4 (anterior portion)</td>
</tr>
<tr>
<td>11</td>
<td>Intermediate frontal sulcus</td>
</tr>
<tr>
<td>12</td>
<td>Intermediate frontal sulcus</td>
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<tr>
<td>13</td>
<td>Intermediate frontal sulcus</td>
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<td>Marginal sup. basin (posterior)</td>
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<td>Inferior frontal sulcus</td>
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<td>Lateral orbital sulcus</td>
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<td>Superior postcentral sulcus</td>
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<td>Inferior postcentral sulcus</td>
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<td>Intraparietal sulcus (ascending branch)</td>
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<td>Intraparietal sulcus (descending branch)</td>
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<td>Superior temporal sulcus 4 (polar portion)</td>
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<td>Inferior temporal sulcus 3</td>
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<tr>
<td>30</td>
<td>Inferior temporal sulcus 4 (anterior portion)</td>
</tr>
<tr>
<td>31</td>
<td>Occipital basin</td>
</tr>
<tr>
<td>32</td>
<td>Inferior occipital sulcus</td>
</tr>
<tr>
<td>33</td>
<td>Transverse parietal basin</td>
</tr>
<tr>
<td>34</td>
<td>Sylvian fissure (anterior)</td>
</tr>
<tr>
<td>35</td>
<td>Sylvian fissure (medial)</td>
</tr>
<tr>
<td>36</td>
<td>Sylvian fissure (posterior)</td>
</tr>
<tr>
<td>37</td>
<td>Marginal sup.frontal basin</td>
</tr>
<tr>
<td>38</td>
<td>Marginal sup. frontal basin</td>
</tr>
<tr>
<td>39</td>
<td>Marginal sup. frontal basin</td>
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References
