Joint Bayesian Cortical Sulci Recognition and Spatial Normalization

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Abstract. In this paper, we study the recognition of about 60 sulcal structures over a new T1 MRI database of 62 subjects. It continues our previous work [7] and more specifically extends the localization model of sulci (SPAM). This model is sensitive to the chosen common space during the group study. Thus, we focus the current work on refining this space using registration techniques. Nevertheless, we also benefit from the sulcuswise localization variability knowledge to constrain the normalization. So, we propose a consistent Bayesian framework to jointly identify and register sulci, with two complementary normalization techniques and their detailed integration in the model: a global rigid transformation followed by a piecewise rigid-one, sulcus after sulcus. Thereby, we have improved the sulci labeling quality to a global recognition rate of 86%, and moreover obtained a basic but robust registration technique.

Keywords: cortical folds labeling, sulci, registration, SPAM, EM.

1 Introduction

Group studies involve one of the most intriguing and challenging problem of brain imaging. Indeed, the human cortex is highly convoluted by series of intricated folds and vary strongly from one individual to another. Cortical anatomy, fibers of white matter and functional activity are known to be interwoven in some way still to be defined. Therefore, matching of anatomical structures is fundamental to hugely reduce the intersubject anatomo-functional variability.

Fortunately, some of the largest sulci are relatively stable either in their localization, their shape or according to their neighbouring folds [7]. Moreover, the deepest part of the main sulci are rather well-localized and organized [16,2]. Therefore, the major sulci are often used either to assess the quality of a normalization or as landmarks for co-registration. Indeed, sulci labels and brain normalization are interrelated. Most of the time, normalization and sulci labeling are two well-separated sequential steps. Either the first step [17] provides a

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common space to the second [7,6,15], or the second yields constraints to the first one [8]. We face here a kind of chicken-egg dilemma. Thus, most methods choose to break the loop and use a weaker approach to replace one of the two steps. They either use a normalization process based only on MRI intensities or geometrical features which can not disambiguate some folds, or use a poor common space to estimate sulci variability for labeling purpose. Nevertheless, we can go further and use the best of the two steps. In fact, iterative answers [19] can be build to overcome the dilemma to some extent. In the following, we propose such a method in a full Bayesian framework (close to the model proposed in [20]) to jointly find sulci labels and a robust registration to a well-defined common space.

This paper extends the sulcuswise localization models and the Bayesian framework introduced in our previous works [7]. Here, we kept aside the structural aspect of our works (in particular the study of neighbouring sulci relations [6]) to focus on the specific topic of joint sulci recognition and registration.

2 Database

The number of subjects in the learning database and the quality of the sulcal delineation across them is a crucial component to correctly guide the model design and enhance the performance of the recognition system. Beyond the largest folds, no ground truth exists. Indeed, the definition of the secondary and tertiary folds is a research subject in its own right. For that reason, many incoherences remained in the labeling of the database used previously [7]. Thus, an in-depth study of the cortical folds has been carried out. As a result, a difficult work, several months long, has been done in this direction to carefully question and correct our previous database, and extend it up to 62 subjects (all with left and right hemispheres). The first and third authors of this paper have jointly labeled the whole database and compared their opinions to justify their choices. Hence, manual sulci identification has been made as homogeneous and consistent as possible, based only on anatomical information extracted from T1 MRI. To that end, a set of 63 labels is used on the left hemisphere and 62 on the right one. The rules used to specify the labeling are based on the sulcal roots theory [2].

Several heterogeneous databases (our former database, a diffusion-dedicated database [3], a twins database [4] and some subjects from the ICBM database) were grouped from several sites: SHFJ, CHU La Pitié Salpêtrière, CHU La Timone, McGill (4 different 1.5T scanners with various spatial resolution). Most of the subjects are right-handed men, between 25 and 35 years old.

A collection of tools (released in the Brainvisa software [1]) has been developed to help the manual labeling, speed up the process and quickly compare many brains together.

We briefly remind here what we mean by sulcus. We used the Brainvisa [1] anatomical segmentation pipeline [5] to extract the cortical folds. We get a raw brain negative mold which is skeletonized and over-segmented according to depth, curvature and topological criteria. Thereby, we obtained a collection of elementary sulcal pieces to be labeled. Lastly, a sulcus is a set of such sulcal

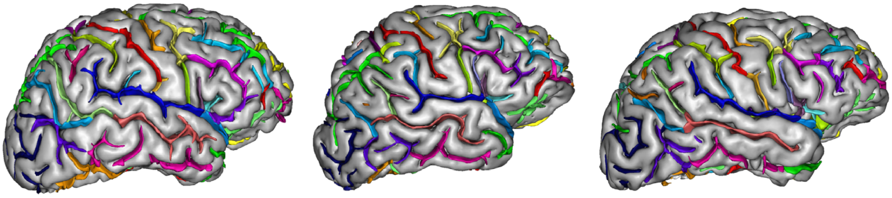

Fig. 1. Sulcal patterns variability: 3 manually labeled brains from our new database

pieces with the same label. Remember that the challenging part of sulci labeling is to stick the sulcal pieces together to give one sulcus, or to find the boundaries between sulci.

3 Models and Methods

Previously, we introduced a model to automatically identify sulci from localization information [7]. This labeling method and the model estimation are based on the strong assumption that all subjects (from training and testing databases) live in a common space. Hence, the more accurate the chosen data normalization process, the more efficient this model. We had used the well-known Talairach coordinate system [12]. This system is based on the alignement of the anterior and posterior commissures (AC-PC) and the interhemispheric plane, followed by the scaling of the brain boundaries along the three cardinal axes with the Talairach atlas.

In this paper, our main goal is still to infer a full labeling $L = \{L_i\}_{i \in \mathcal{E}}$ of brain folds. Namely, we have to find the label L_i of each elementary anatomical structure i to be labeled (in our application sulcal pieces: see section 2 for details). Here, $\mathcal{E}$ denotes the whole set of these structures. The labeling is based on localization information $D = \{D_i\}_{i \in \mathcal{E}}$ (in our case, D_i is the set of the 3D coordinates of the voxels of the structure i from the MRI data, but other information could be considered). These data are expressed in a common referential space (for instance the Talairach one) thanks to a transformation from the subject space and defined by the parameter Θ (equal to θ_{Tal} in the case of the Talairach space). Hence, the MAP (Maximum A Posteriori) formulation of labeling from our previous model can be rewriten as follows:

$$P(\mathbf{Labeling}|\mathbf{Data}) = P(L|D\Theta = \theta_{Tal}) \propto P(D|L\Theta = \theta_{Tal})P(L|\Theta = \theta_{Tal}) \quad (1)$$

In the same way, we can reconsider the formulation of the estimation of the localization model $\mathcal{M}$ (in this paper we use SPAM models, see section 3.4 for details) from a training database $\mathcal{A}$, by the introduction of normalization parameters (from subject space to the Talairach one): $\theta_{a,tal}$ for each subject $a \in \mathcal{A}$:

$$P(\mathbf{Model}|\mathbf{Training\ Set}) = P(\mathcal{M}|\{D_a L_a; \Theta_a = \theta_{a,tal}\}_{a \in \mathcal{A}}) \quad (2)$$

where each subscript a stands for data specific to the subject a.

In the following, we first introduce the general principles of a natural extension of this model which considers the re-estimation of normalization parameters (for global and sulcuswise rigid registration techniques). Then, the method details are given for the joint registration and labeling, and for the joint registration and model estimation. Finally, the method is derived for a specific sulcuswise localization model used in our experiments : the SPAM model.

3.1 Normalization and Registration

The Talairach coordinate system is really reliable only for the deepest anatomical structures (thalamus, putamen, caudate nucleus...) and quite inaccurate for the cortical folds. Besides, in the considered database (see section 2), AC-PC alignements have been done manually. In this paper, we propose to automatically define a better common space by transforming each subject using registration techniques with respect to our localization models. The pratical application of this idea is not straightforward and depends on the chosen normalization, since the registration is done between a subject and a probabilistic model rather than a mean subject or an atlas. In the following sections, we will state how to introduce the normalization step in a meaningful way to extend our previous model, estimate it from a training database, and use it to help the labeling process on a new unlabeled subject.

In this context, we choose to further study two specific complementary registration methods. The first one is rigid and defined by global parameters $\theta_g = (R_g, \boldsymbol{t}_g)$, where R_g is a rotation matrix and $\boldsymbol{t}_g$ a translation vector. It will provide a refined version of the Talairach space. Its optimization does not need any specific prior thanks to the strong constraints defined by the labelwise localization models. It also provides a good initialization for any second step non-linear registration.

To this end, many methods could be used and integrated in the considered model of this paper. Nevertheless, state of the art diffeomorphic registration techniques are extremely time consuming. Do not forget that our first goal is not to provide a perfect registration but to infer sulci labels. So we can afford the use of simpler methods if it is done with enough care.

As a second step, we suggest a simple non-linear registration method that extends naturally the global approach to a sulcuswise one. It is defined by a set of parameters $\theta_s = \{\theta_{s,l}\}_{l \in \mathcal{L}} = \{(R_{s,l}, \boldsymbol{t}_{s,l})\}_{l \in \mathcal{L}}$ with one rigid registration for each label l. Obviously, without constraints, some counterintuitive phenomena can occur because this registration is non-diffeomorphic. In fact, various structures could cross each other after registration and result in a poor local labeling. Besides, some neighbouring sulci have similar shapes and could be easily confused without strong enough constraints. This method has severe drawbacks that can be hugely reduced and controled with the use of a well chosen referential space for initialization and strong priors to control the range of available local transformations. To that end, we used independent priors for each label. The translations are estimated by a full-covariance 3D-Gaussian. For the rotations, we split their prior in 2 components based on the standard vector-rotation parametrization. We have chosen generalizations of multivariate Gaussian distributions: Von Mises distribution for the rotation angle, Kent or Bingham distributions for the direction of the rotation (see [11] for an overview). The local rigid transformations of a point $\boldsymbol{x}$ depends on the chosen reference point $\boldsymbol{g}$. Indeed, $R \cdot \boldsymbol{x} + \boldsymbol{t} = R \cdot (\boldsymbol{x} - \boldsymbol{g}) + (\boldsymbol{t} - R \cdot \boldsymbol{g} - \boldsymbol{g}) + \boldsymbol{g} = R \cdot \boldsymbol{x}_g + \boldsymbol{t}_g + \boldsymbol{g}$ with $\boldsymbol{x}_g$ and $\boldsymbol{t}_g$ expressed in the local coordinate system defined by $\boldsymbol{g}$. The case $\boldsymbol{g} = \mathbf{0}$ corresponds to the global arbitrary coordinates. To be as sharp as possible, the translation prior needs to be estimated from t_g with a well chosen reference $\boldsymbol{g}$. A natural choice, for a given label, is to use the gravity center of all sulci with this label over the database, with coordinates expressed in the normalized space of the model.

These approaches are quite well integrated in the following models and lead to drastic simplifications of the optimization scheme. They allow the use of a simplified model without any statistical dependency, which results in a fast and efficient optimization method (see eq. 9).

3.2 Joint Registration and Labeling

Here we suppose that the model $\mathcal{M}$ is known. Either, it may has been learned with (according to the method suggested in the section 3.3) or without (according to our previous work [7]) normalization refinement. Thereby, in this section, all probabilities $P(\cdot)$ are defined implicitely given $\mathcal{M}$. The following formula extends the equation 1 to find jointly the labels l and the registration parameters θ:

$$l^*, \theta^* = \underset{l,\theta}{\operatorname{argmax}}\, P(L = l\Theta = \theta | D) \tag{3}$$

Direct optimization of this quantity is difficult and time consuming. However, we can consider other quantities of interest as the marginal probabilities over Θ and L: $P(L|D)$ and $P(\Theta|D)$ respectively. According to our model design (independence assumptions and registration methods), it induces simplifications. Thus, we choose to first optimize the registration θ regarding L as hidden labels, and then optimize labels under the best θ^* previously obtained:

$$\begin{cases} \theta^* = \underset{\theta}{\operatorname{argmax}}\, P(\Theta = \theta | D) = \underset{\theta}{\operatorname{argmax}}\, P(\theta) \sum_{L=l} P(L = l | \theta) P(D | L = l; \theta) \\ l^* = \underset{l}{\operatorname{argmax}}\, P(L = l | D; \Theta = \theta^*) = \underset{l}{\operatorname{argmax}}\, P(D | L = l; \Theta = \theta^*) P(L = l | \Theta = \theta^*) \end{cases} \tag{4}$$

θ^* can be estimated by the iterative Expectation Maximization (EM) algorithm [9] which reaches a local optimum from a well-chosen initialization $\theta^{(0)}$:

$$\theta^{(n+1)} = \underset{\theta}{\operatorname{argmax}}\, Q\left(\theta \middle| \theta^{(n)}\right) \tag{5}$$

with

$$\begin{aligned} Q\left(\theta \middle| \theta^{(n)}\right) &= \mathbb{E}_L \left[log(P(DL\theta)) \middle| D\theta^{(n)} \right] \\ &= \sum_{L=l} P\left(L = l \middle| D\theta^{(n)}\right) log\left[P(D|L = l\theta) P(L = l|\theta) P(\theta)\right] \end{aligned} \tag{6}$$

where $\mathbb{E}_L\left[\cdot\right]$ stands for the expectation over L.

Currently, we will consider a widely spread assumption of conditional independence of all $\{D_i\}_{i\in\mathcal{E}}$ given L. Besides, the labels prior $P(L)$ does not depend on the transformation θ, and so we derive the above expression for global rigid registration:

$$Q_g\left(\theta_g\middle|\theta_g^{(n)}\right)=\sum_{l\in\mathcal{L}}\sum_{i\in\mathcal{E}}P\left(L_i=l_i\middle|D_i\theta_g^{(n)}\right)log\left[P(D_i|L_i\theta_g)P(L_i=l_i)P(\theta_g)\right] \tag{7}$$

The optimization of θ is now regarded as a standard parameter optimization within the framework of mixture models. Indeed, $P(L_i=l_i|\theta)$ is the prior of the model l_i defined by the likelihood $P(D_i|L_i=l_i\theta)$ (in our case these generative models are SPAM: see section 3.4). Finally, the $\{D_i\}_{i\in\mathcal{E}}$ are realizations of the mixture model.

For local registration, we supposed $P(\theta_s)=\prod_{l\in\mathcal{L}}P(\theta_{s,l})$, where each $\theta_{s,l}$ stands for sulcuswise local registration parameters.

$$Q_s\left(\theta_s\middle|\theta_s^{(n)}\right)=\sum_{l\in\mathcal{L}}\sum_{i\in\mathcal{E}}P\left(L_i=l\middle|D_i\theta_{s,l}^{(n)}\right)log\left[P(D_i|L_i\theta_{s,l})P(L_i)P(\theta_{s,l})\right] \tag{8}$$

$$\theta_s^*=\left\{\underset{\theta_{s,l}}{\operatorname{argmax}}\sum_{i\in\mathcal{E}}P\left(L_i=l\middle|D_i\theta_{s,l}^{(n)}\right)log\left[P(D_i|L_i\theta_{s,l})P(\theta_{s,l})\right]\right\}_{l\in\mathcal{L}} \tag{9}$$

Hence, the optimization of θ follows repeated sequences of local marginal posteriors $P(L_i|D_i\theta)$ estimations (E-step) which yields weights for the registrations optimizations (M-step). The weights can be read into links between structures to be labeled and the mixture model components. For the sulcuswise case, thanks to the independence assumption of the $\{\theta_{s,l}\}_{l\in\mathcal{L}}$, the registration optimization is done independently for each label l.

Lastly, a full labeling l^* is obtained by MAP as in our previous works [7] but after applying the transformation induced by the parameter θ^*:

$$l^*=\{l_i^*\}_{i\in\mathcal{E}}=\left\{\underset{l_i}{\operatorname{argmax}}\,P(D_i|L_i=l_i;\Theta=\theta^*)P(L_i=l_i|\Theta=\theta^*)\right\}_{i\in\mathcal{E}} \tag{10}$$

3.3 Joint Registration and Model Estimation

We are interested here by the supervised estimation of our model parameters $\mathcal{M}$. We supposed a training database $\mathcal{A}$ is avalaible (in this work, we use the database described in section 2) with one known label $L_{a,i}$ for each sulcal piece i and each subject $a\in\mathcal{A}$. Previously, the model estimation was built from the Talairach space. Now, we supposed that the registration parameters θ_a (that move each subject $a\in\mathcal{A}$ from the Talairach space to a new refined common space) are unknown and have to be computed at the same time as the model $\mathcal{M}$. To generalize the previous formulation (see equation 2), the ideal measure to optimize is then expressed as below:

$$m^*,\{\theta_a^*\}_{a\in\mathcal{A}}=\underset{m,\{\theta_a\}_{a\in\mathcal{A}}}{\operatorname{argmax}}\,P(\mathcal{M}=m\{\Theta_a=\theta_a\}_{a\in\mathcal{A}}|\{D_aL_a\}_{a\in\mathcal{A}}) \tag{11}$$

One way to approximate the maximization of this quantity is to alternate the optimization of the model parameters and that of the registration parameters:

$$\begin{cases} m^{(n)} &= \underset{m}{\operatorname{argmax}}\ P\left(\mathcal{M}=m \middle| \{D_aL_a\}_{a\in\mathcal{A}}; \left\{\Theta_a=\theta_a^{(n)}\right\}_{a\in\mathcal{A}}\right) \\ \left\{\theta_a^{(n+1)}\right\}_{a\in\mathcal{A}} &= \underset{\{\theta_a\}_{a\in\mathcal{A}}}{\operatorname{argmax}}\ P\left(\{\Theta_a=\theta_a\}_{a\in\mathcal{A}} | \{D_aL_a\}_{a\in\mathcal{A}}; \mathcal{M}=m^{(n)}\right) \end{cases} \tag{12}$$

Under the independence assumption of subjectwise registration parameters $\{\theta_a\}$ and those of sulcal pieces, the optimization becomes:

$$\begin{cases} m_l^{(n)} = \underset{m_l}{\operatorname{argmax}}\ P\left(\mathcal{M}_l=m_l \middle| \{D_{a,i}L_{a,i}=l\}_{\substack{a\in\mathcal{A} \\ i\in\mathcal{E}_{a,l}}}; \left\{\Theta_a=\theta_a^{(n)}\right\}_{a\in\mathcal{A}}\right) \\ \theta_a^{(n+1)} = \underset{\theta_a}{\operatorname{argmax}}\ P\left(D_a|L_a;\Theta_a=\theta_a\mathcal{M}=m^{(n)}\right) P\left(\Theta_a=\theta_a|L_a;\mathcal{M}=m^{(n)}\right) \end{cases} \tag{13}$$

with $\mathcal{M}=\{\mathcal{M}_l\}_{l\in\mathcal{L}}$, where $\mathcal{M}_l$ is the set of parameters monitoring the generative model of sulcus l, and $\mathcal{E}_{a,l}$ the set of sulcal pieces of subject a restricted to those with the label l.

The optimization of $\mathcal{M}$ reduces to normalizing each subject a based on their respective transformation θ_a and compute a standard model estimation in this reference space (see section 3.4 for SPAM estimation). For its part, the optimisation of the registration parameters θ_a boils down to find the best transformation to fit the data to the given model $\mathcal{M}=m^{(n)}$ constrainted by the prior $P\left(\Theta_a=\theta_a|L_a;\mathcal{M}=m^{(n)}\right)$.

3.4 SPAM and Registration

The model presented in this paper is based on a mixture of sulcuswise generative models based on localization data. So far, no assumption has been made on these models. In this section, we will show how to use a specific model to represent this information: the SPAM model (Statistical Probabilistic Anatomy Map [13]) already used in our previous work [7] and extending older sulci analysis of [14]. This model gives voxelwise probabilities. In our current context, the likelihood is defined through a transformation θ and for a given label l, the probability of finding one structure at the spatial position $\boldsymbol{x}$ is given by:

$$P_{SPAM}(\boldsymbol{x}|L=l\theta\mathcal{M}) = \frac{(K_\sigma * f_l)(\Phi_\theta(\boldsymbol{x}))}{\sum_{x\in\Omega}(K_\sigma * f_l)(\Phi_\theta(\boldsymbol{x}))} \tag{14}$$

with $K_\sigma * f$ standing for the convolution of f and K_σ which is a 3-dimensional spherical Gaussian kernel of covariance $\sigma^2 Id$, $f_l(\boldsymbol{x})$ is the frequency of appearance of label L at position $\boldsymbol{x}$ over the database (with $\{\{f_l(\boldsymbol{x})\}_{\boldsymbol{x}\in\Omega},\sigma\}\in\mathcal{M}$) and Φ_θ is a transformation function to transform $\boldsymbol{x}$ spatial coordinates from an initial reference space through the registration parameterized by θ. For a given sulcal piece i, its set of voxel coordinates $\mathcal{V}_i$, with voxelwise indepence assumption, the joint likelihood writes:

$$P_{SPAM}(\mathcal{V}_i|l\theta) = \prod_{x\in\mathcal{V}_i} P_{SPAM}(x|l\theta)^{\frac{1}{|\mathcal{V}_i|}} \tag{15}$$

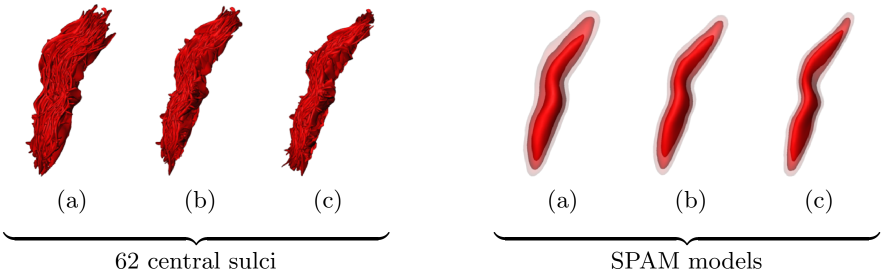

Fig. 2. Effects of constrained registration on SPAM model estimation: localization uncertainties are reduced from (a) to (c). Models are estimated from (a) Talairach space, (b) with global registration, (c) with local registration. SPAM models are represented conveniently by 3 nested isosurfaces of the probability corresponding to 30, 60 and 80% of the whole probability mass.

with $|\mathcal{V}_i|$ the number of voxels of the sulci which behaves like a normalization factor. Indeed, during the segmentation stage of folds, sulcal pieces of various size are obtained. Hence, this quantity erases size effects and gives comparable posteriors (used to weight the registration during the EM).

In this paper we consider only rigid transformations: a global one with $\Phi_{g\theta}(\boldsymbol{x}) = R_g \cdot \boldsymbol{x} + \boldsymbol{t_g}$ and local ones with $\Phi_{s,l\theta}(\boldsymbol{x}) = R_{s,l} \cdot \boldsymbol{x} + \boldsymbol{t}_{s,l}$, for each label l. During the registration stage, we have to optimize the parameter set θ. A SPAM model is non-parametric and currently represented as a 3D-volume of probabilities. Thus, analytical optimization is not easy. In this paper, we choose to use the well-known Powell's method [10] to cover the 6-parameter space made up of $\boldsymbol{w}$ (vector-rotation parametrization of R) and the translation $\boldsymbol{t}$ to maximize the matching. See figure 2 to notice the refinement of the raw SPAM model (fig. 2 (a)) by the use of registration techniques.

Lastly, the SPAM model is introduced in our joint labeling and registration framework, replacing $P(D_i = d_i | L_i = l_i; \theta)$ by $P_{SPAM}(\mathcal{V}_i | L = l_i; \theta)$ with $\mathcal{V}_i = d_i$.

4 Results and Discussion

The following results are based on the new database of 62 subjects: left and right hemispheres (versus only 26 right hemispheres before) presented in section 2. All estimations are obtained from a leave-one-out scheme. Namely, for each subject a full model estimation (SPAM, variability estimation of registration parameters: rotations and translations, label priors) is computed from all subjects but the tested one. Then, the unseen subject is labeled from its related model. Thereby, the following results are much more reliable than our previous ones [7].

In the following, we consider three error rates (see equation 16) ranging between 0 and 100%. The two first rates are global error measures where each sulcuswise contribution is weighted by its size. The first E_{mass} is kept here for comparison purposes with our old results [7]. The second one E_{SI} draws inspiration from the measure called similarity index (SI [18]). It is more comprehensive

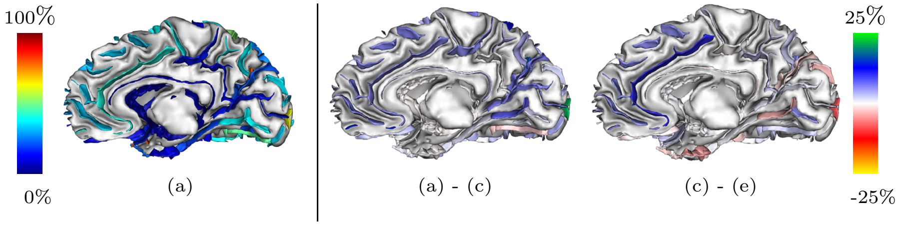

Fig. 3. Left: Leave-one-out mean local error rates E_{local} of a model (a) ranging between 0 and 100%. Right: Leave-one-out mean local error rates differences between two models named by a letter (begining of section 4) to highlight the enhancements. (a) - (c) shows improvements due to a full use of global registration with labeling according to model (a). (c) - (e) shows improvements of the best local registration with labeling according to model (c).

than the first one only based on false positive errors. It also removes errors shared by several sulci (extra or missing sulcal pieces) by counting them only once. Quite on the contrary, the last $E_{local}(l)$ is local and rather draconian. It takes all errors involving a given label l into account (false positive and true negative) without redundancy correction:

$$E_{mass}=\frac{\sum_{l\in\mathcal{L}} FP(l)}{\sum_{l\in\mathcal{L}} FP(l)+TP(l)} \qquad E_{SI}=\sum_{l\in\mathcal{L}} w_l \frac{FP(l)+FN(l)}{FP(l)+FN(l)+2*TP(l)} \qquad E_{local}(l)=\frac{FP(l)+FN(l)}{FP(l)+FN(l)+TP(l)} \tag{16}$$

where w_l is the true size of the sulcus l normalized by the sum of the sizes of all sulci, $FP(l)$, $FN(l)$ and $TP(l)$ stands respectively for false postive, false negative and true positive errors of label l. Each of these measures is computed comparing the manual labels to the automatic ones, and weighted so that each sulcal piece counts as much as its size.

In the following, five models will be discussed and named by letters for a better understanding. (a) basic SPAM model estimated from Talairach, with independent labeling from Talairach (eq. 2). (b) basic SPAM model estimated from Talairach, with joint labeling and global rigid registration from Talairach (eq. 7). (c) globally refined SPAM model (eq. 13) from Talairach, with joint labeling and global rigid registration from Talairach (eq. 7). (d) locally refined SPAM model (eq. 13) from Talairach, with joint labeling and local rigid registration from Talairach (eq. 9). (e) is like (d) but the reference space is not Talairach but the one estimated by a first model estimation or labeling with model (c) (see section 3.1).

The basic SPAM model (a) already gives low error rates. Since, the labeling is done for each sulcal piece independently, severe errors remain (huge sulci parts missing, double outlines). We have tested previously [7] and with some success the use of a Markov field [6] to fix these issues, but this is beyond the scope of the current paper. We suggest here that some of these errors can be considered as registration errors or referential inadequacy between the subject and the model.

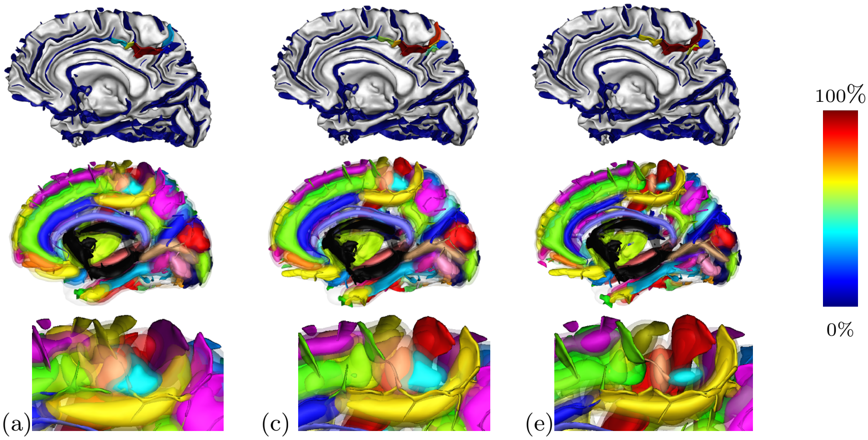

Fig. 4. Some effects of joint labeling and registration on an arbitrary subject which gives bad recognition of the posterior cingulate fissure label (post.C.F) with model (a). Top: local posterior probabilities of the post.C.F mapped on each sulcal piece of the subject. Middle: estimated SPAM models mixed with their respective automatic and registred sulci of the considered subject: look at the enhancement on the post.C.F (yellow color). Bottom: zoomed and cropped version of the previous row. Letters denote models fully described at the begining of section 4: (a) basic SPAM models, (c) with global registration and (e) with local registration. Note that the labeling are almost the same between (c) and (e), but with model (e) the matching is better.

In fact, global error rates are significantly reduced by using the joint labeling and global registration (see table 1 (b)). Moreover, the errors decrease again, with the use of the globally refined SPAM models (c). The enhancements are quite uniformly distributed over the brain (see figure 3). Thus, the two joint approaches at learning and testing stages are effective. In the case of the non-linear transformation, each local registration is constrainted independently. So the more the referential space is reliable, the stronger the constraints are. As expected, initializing the local methods (model estimation and labeling) with the registration result of the global one (e) gives sharper and stronger constraints

Table 1. Leave-one-out mean (over 62 subjects) percentage of global SI and mass error rates (and their standard deviations between parenthesis) for all models listed at the begining of section 4

		No registration	Global registration		local registration	
		(a)	(b)	(c)	(d)	(e)
E_{SI}	Left	17.55 (5.93)	15.27 (2.74)	14.59 (2.88)	16.79 (4.35)	14.22 (2.96)
	Right	16.83 (3.77)	14.70 (3.09)	13.97 (2.91)	15.61 (3.72)	13.48 (3.13)
E_{mass}	Left	16.64 (3.69)	14.56 (2.54)	14.01 (2.62)	16.61 (4.17)	14.11 (2.79)
	Right	15.96 (3.66)	13.95 (2.98)	13.37 (2.82)	15.29 (3.51)	13.30 (2.99)

than the direct use of the Talairach space (d) which actually worsen the results. Unfortunately, this step does not bring about any global significant improvement (see table 1 (c) versus (e)), but rather some local ones at the medial frontal part of the brain for instance (see figure 3). Indeed, the labeling quality is nearly the same, but its reliability is enhanced since the local posteriors probabilities $P(L_i|D_i\Theta)$ better fits the true labeling (see figure 4, top row). Namely, the model is more confident in the given labeling (see figure 4, bottom row).

5 Conclusion and Perspectives

In this paper, we have proposed new models extending our previous works [7] coupling sulci labeling and constrainted registration in a common framework. We have presented two complementary rigid-based registration techniques: one to reduce global localization uncertainties, and another with one local transformation per sulcus. The proposed methods give significant improvements. Their resulting labelings are almost the same but the local approach yields more reliable posterior probabilities which may be helpful for further processings (morphometry studies for instance). Originally, we were interested in the labeling enhancement. Finally, our models also provide a registration method constrainted by reliable anatomical landmarks: the sulci. On the contrary of most landmark-based normalization methods, in our case no labeling is needed to set the constraints: the process is fully automatic. It would be interesting to compare the registration capacities of these methods with standard ones.

Many statistical independence assumptions have been made during the model design, so there is still room for improvement. In fact, the labeling of a sulcal piece should be done in relation with its neighbourhood: a Markov field can do the job (as in our previous work [7] [6], but registration has now to be included). We can also consider registration methods constrainted so that the local anatomical organization of folds are preserved in some way. Nevertheless, more complicated models may need adapted approximations to run properly. These extensions are partially complementary and may benefit from each other.

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References

1. `http://brainvisa.info`
2. Régis, J., Mangin, J.-F., Ochiai, T., Frouin, V., Rivière, D., Cachia, A., Tamura, M., Samson, Y.: Sulcal root generic model: a hypothesis to overcome the variability of the human cortex folding patterns. Neurol. Med. Chir. 45, 1–17 (2005)
3. Poupon, C., Poupon, F., Allirol, L., Mangin, J.-F.: A database dedicated to anatomo-functional study of human brain connectivity. In: 12th Ann. Meet. Org. Human Brain Mapping (2006)

4. Pinel, P., Thirion, B., Meriaux, S., Jobert, A., Serres, J., Bihan, D.L., Poline, J.-B., Dehaene, S.: Fast reproducible identification and large-scale databasing of individual functional cognitive networks. BMC Neurosci. 8, 91 (2007)
5. Mangin, J.-F., Frouin, V., Bloch, I., Régis, J., Lopez-Krahe, J.: From 3D Magnetic Resonance Images to Structural Representations of the Cortex Topography Using Topology Preserving Deformations. Journal of Mathematical Imaging and Vision 5, 297–318 (1995)
6. Rivière, D., Mangin, J.-F., Papadopoulos-Orfanos, D., Martinez, J.-M., Frouin, V., Régis, J.: Automatic Recognition of Cortical Sulci Using a Congregation of Neural Networks. MIA 6, 77–92 (2002)
7. Perrot, M., Rivière, D., Mangin, J.-F.: Identifying cortical sulci from localization, shape and local organization. In: ISBI, pp. 420–423 (2008)
8. Cathier, P., Mangin, J.-F., Pennec, X., Rivière, D., Papadopoulos-Orfanos, D., Régis, J., Ayache, N.: Multisubject non-rigid registration of brain MRI using intensity and geometric features. In: Niessen, W.J., Viergever, M.A. (eds.) MICCAI 2001. LNCS, vol. 2208, pp. 734–742. Springer, Heidelberg (2001)
9. Dempster, A., Laird, N., Rubin, D.: Maximum likelihood from incomplete data via the em algorithm. Journal of the Royal Statistical Society, Series B 39(1), 1–38 (1977)
10. Powell, M.J.D.: An Efficient Method for Finding the Minimum of a Function of Several Variables Without Calculating Derivatives. Computer Journal 7, 155–162 (1964)
11. Mardia, K.V., Jupp, P.: Directional Statistics, 2nd edn. John Wiley and Sons Ltd., Chichester (2000)
12. Talairach, J., Tournoux, P.: Co-planar Stereotaxic Atlas of the Human Brain. Georg Thieme Verlag, Stuttgart (1988)
13. Evans, A.C., Collins, D.L., Neelin, P., MacDonald, D., Kamber, M., Marrett, T.S.: Three-Dimensional Correlative Imaging: Applications in Human Brain Mapping. Functional Neuroimaging 14, 145–161 (1994)
14. Le Goualher, G., Collins, D.L., Barillot, C., Evans, A.C.: Automatic Identification of Cortical Sulci Using a 3D Probabilistic Atlas. In: Wells, W.M., Colchester, A.C.F., Delp, S.L. (eds.) MICCAI 1998. LNCS, vol. 1496, pp. 509–518. Springer, Heidelberg (1998)
15. Lohmann, G., von Cramon, D.Y.: Automatic labelling of the human cortical surface using sulcal basins. Medical image analysis 4(3), 179–188 (2000)
16. Lohmann, G., von Cramon, D.Y., Colchester, A.C.F.: Deep Sulcal Landmarks Provide an Organizing Framework for Human Cortical Folding. Cerebral Cortex 18(6), 1415–1420 (2008)
17. Tosun, D., Prince, J.L.: A Geometry-Driven Optical Flow Warping for Spatial Normalization of Cortical Surfaces. TMI 27(12), 1739–1753 (2008)
18. Yang, F., Kruggel, F.: Optimization Algorithms for Labeling Brain Sulci Based on Graph Matching. In: ICCV, pp. 1–7 (2007)
19. Vaillant, M., Davatzikos, C.: Hierarchical Matching of Cortical Features for Deformable Brain Image Registration. In: Kuba, A., Sámal, M., Todd-Pokropek, A. (eds.) IPMI 1999. LNCS, vol. 1613, pp. 182–195. Springer, Heidelberg (1999)
20. Yeo, B., Sabuncu, M., Desikan, R., Fischl, B., Golland, P.: Effects of registration regularization and atlas sharpness on segmentation accuracy. Med. Image Anal. 12(5), 603–615 (2008)