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A discriminative feature selection approach for shape analysis: application to fetal brain cortical folding study

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Abstract

The development of post-processing reconstruction techniques has opened new possibilities for the study of in utero fetal brain MRI data. Recent cortical surface analysis have led to the computation of quantitative maps characterizing brain folding of the developing brain. In this paper, we describe a novel feature selection-based approach that can be used for studying the most discriminative brain folding patterns using in utero reconstructed fetal MR data. Results show that this temporal process related to brain maturation can be characterized by a small set of points, located in the main sulci.

Keywords: Structural MRI, Fetal imaging, Feature selection, Brain development

1. Introduction

Development of the central nervous system (CNS) is governed by a complex set of several spatio-temporal mechanisms. Understanding this sequence is fundamental for understanding perinatal neurology (Volpe, 2008). Many processes are involved in brain development at fetal and neonatal stages. These are asynchronous processes taking place at different locations in the brain. For instance, the main period of neural migration is 5 to 25 week post-menstrual age (PMA). Once neurons have been generated, they migrate through two different mechanisms (passive cell displacement and active cell migration). Axon and dendrite sprouting starts around 25 weeks PMA and declines around 1 year. The brain is also the scene of other major events such as synapse formation, glial cell proliferation, myelination, etc. (see de Graaf-Peters and Hadders-Algra (2006) for a recent review of the ontogeny of the human CNS).

As highlighted by de Graaf-Peters and Hadders-Algra (2006), the knowledge on the exact timeline of ontogenetic events occurring during human brain development will provide new insights on the influence of injuries appearing at a specific point in time during this important period of brain building. The modeling of this process timeline from in vivo data is of great importance for improving, for instance, neonatal care services. It is clear that fetal and neonatal periods are key steps of brain devel-

opment and a better understanding of the involved mechanisms is a corner stone in perinatal care.

Recent advances in ultrafast MRI sequences (such as half-Fourier turbo spin echo (HASTE) (Yamashita et al., 1997) or single shot fast spin echo (SSFSE) (Busse et al., 2000)) associated with the development of new techniques of image processing for retrospective motion correction (Rousseau et al., 2005) enabled to study *in vivo* fetal brain development. Since 2005, several two-step registration-based reconstruction techniques have been proposed to estimate a 3D high resolution image from sets of scattered T2-weighted slices (Jiang et al., 2007, Kim et al., 2010, Limperopoulos and Clouchoux, 2009, Rousseau et al., 2006). These reconstruction techniques have been further enhanced by including super-resolution framework (Gholipour et al., 2010, Kuklisova-Murgasova et al., 2012, Rousseau et al., 2010). Following these works on 3D fetal brain image reconstruction, several dedicated segmentation methods have been proposed (Caldairou et al., 2011, Dittrich et al., 2014, Gholipour et al., 2012, Habas et al., 2010b). See the work of Studholme (2011) for further reading on fetal MRI reconstruction and segmentation.

The development of these post-processing techniques had led to new ways to perform structural development studies of the fetal brain. Based on local volume changes using tensor-based morphometry techniques, maps of fetal brain growth patterns have been estimated leading to the detection of the emergence of sulci and gyri by differentiating between the changes in the cortical plate and the underlying cerebral mantle (Rajagopalan et al., 2011). This work has been extended to examine not only scalar expansion of tissue but the directional components of that

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1 expansion (Rajagopalan et al., 2012). The availability of 54
2 high resolution 3D images of the fetal brain with tissue 55
3 labelling enables also studies of tissue boundary shape 56
4 changes. This has led to the computation of quantita- 57
5 tive maps of brain folding further used for statistical de- 58
6 tecton of sulci and brain asymmetry emergence (Habas 59
7 et al., 2012). Cortical folding analysis has been also used 60
8 to predict physiological age (Wright et al., 2014). Such 61
9 brain folding studies are of great importance to improve 62
10 our understanding of malformation of the cortex. 63

11 In this work, we focus on the study of the evolution of 64
12 brain folding during later stages of intrauterine life. In- 65
13 stead of computing scalar features such as surface curva- 66
14 ture to provide global markers of brain development, we 67
15 have chosen to investigate the use of a data driven ap- 68
16 proach. The underlying question is: what is the smallest 69
17 most discriminative set of features reflecting fetal brain 70
18 folding? Following the work of Rajagopalan et al. (2012), 71
19 a deformation based morphometry approach is adopted to 72
20 capture directional growth information on the white mat- 73
21 ter / cortex interface. However, the voxel-based statistical 74
22 testing method applied in (Rajagopalan et al., 2012) does 75
23 not lead to easily interpretable results of growth patterns. 76
24 In this study, we have considered the use of feature selec- 77
25 tion techniques in order to extract the sparsest set of de- 78
26 formation fields describing the brain folding process. By 79
27 studying brain development as a shape modeling problem, 80
28 we are able to extract the most discriminative set of points 81
29 related to brain folding during in utero development. 82

30 2. Materials and Methods

31 2.1. Subjects and fetal MRI acquisition

32 This study has been conducted on a population of 22 86
33 fetus aged from 26 to 34 weeks of gestational age at scan 87
34 time. The data set includes 23 MRI T2 weighted images. 88
35 Fetal MRI images have been obtained on a 1.5 T Siemens 89
36 Avanto MRI Scanner (SIEMENS, Erlangen, Germany) us- 90
37 ing a 6-channel phased array coil combined to the spine 91
38 array positioned around the mother abdomen. The res- 92
39 olution of the T2 weighted HASTE sequence ($TE/TR =$ 93
40 $147/3190$ ms) is: $0.74 \times 0.74 \times 3.45$ mm. 94

41 2.2. Image reconstruction and segmentation

42 Raw dataset has been preprocessed using the "Baby 97
43 Brain Toolkit" (BTK) in order to increase image quality 98
44 without modifying the acquisition protocol used in rou- 99
45 tine (Rousseau et al., 2013). The retrospective motion 100
46 correction method is based on a registration refined com- 101
47 compounding of multiple sets of orthogonal fast 2D MRI slices 102
48 to address the problem of fetal motion. This is achieved 103
49 by first globally registering the low resolution images, and 104
50 then applying an iterative slice alignment scheme which 105
51 seeks to refine the 3D positioning of each slice to the cur- 106
52 rent combined high resolution volume. This is driven by 107
53 normalized mutual information to provide robustness to

contrast variation induced by motion of the fetal brain 108
with respect to the imaging coil in the magnet. More- 109
over, a super-resolution technique is applied in order to 110
remove the effects of the blurring convolution and to in- 111
crease the voxel grid density. The resolution of the recon- 112
structed images is: $0.74 \times 0.74 \times 0.74$ mm. A topological 113
based clustering technique is then applied on the motion- 114
compensated high-resolution images to provide segmen- 115
tation maps (ventricles, CSF, cortical plate, non-cortical 116
plate -including white matter, subplate, intermediate zone 117
and deep gray nuclei) (Caldairou et al., 2011). 118

119 2.3. Brain image normalization

120 Adopting a standard approach for deformation based 121
morphometry to compare anatomies at different stages of 122
brain development, a mapping is estimated to bring every 123
subject's anatomy into correspondence within a common 124
coordinate system. This common space corresponds to 125
the average space of the subjects's anatomies. For this 126
purpose, an iterative registration approach proposed by 127
Guimond *et al.* (Guimond et al., 2000) has been used in 128
this work. The procedure to estimate a common space is 129
as following. First, a reference image is chosen among the 130
dataset and the non linear transformations from this refer- 131
ence to the remaining images of the dataset are estimated 132
using ANTS diffeomorphic registration technique (Avants 133
and Gee, 2004). Then, the choice of a reference induces 134
a bias that is corrected by using the average of all trans- 135
formations. Finally, this average transformation maps the 136
chosen reference to a new space which corresponds to the 137
average space of the subject's anatomies. The reference for 138
the next iteration will be this new space. These steps are 139
repeated iteratively, until convergence of the algorithm, 140
which usually occurs within a few iterations (Guimond 141
et al., 2000). 142

143 Parameters for ANTS registration are: cross correla- 144
tion as similarity measure, gaussian regularization with a 145
symmetric diffeomorphic transformation model. To avoid 146
any possibility of mis-registration due to brain tissue con- 147
trast changes, the similarity criterion used during the reg- 148
istration process is a weighted combination of image inten- 149
sities and tissue label maps (a similar strategy has been 150
proposed by Habas et al. (2010a)). Weights have been set 151
to 0.5 for each feature. 152

153 To assess the quality of the atlas building step based on 154
image registration, we have computed the average DICE 155
coefficient of the white matter maps between the estimated 156
template and the population. This average DICE coeffi- 157
cient is equal to 0.95 ± 0.06 , showing the validity of the 158
approach. 159

160 2.4. Feature selection

161 Our objective concerns the selection of the most dis- 162
criminative deformation-based features reflecting fetal brain 163
development. Please note that although we focus in this 164
work on brain folding, the proposed approach is versatile 165

and it could be used with any other kind of relevant features dedicated to brain anatomy study.

Let be $\mathcal{P} = \{I_1, I_2, \dots, I_N\}$ a set of N images. These images are normalized in an average space \bar{T} computed as described previously in section 2.3. The transformation \mathcal{T}_i that maps the average space \bar{T} to the image I_i is a composition of an affine transform and a non-linear deformation field. In order to capture local shape changes, we only consider the non linear components of the mappings $\{\mathcal{T}_i\}_{i=1, \dots, N}$.

Each of the N non linear deformation fields that maps voxels from average space to population space consists of M vectors of \mathbb{R}^3 (where M is the number of voxels considered in the region of interest). These 3D vectors are further arranged in a matrix $\mathbf{Y} \in \mathcal{M}_{M \times N}(\mathbb{R}^3)$ where the rows and columns correspond respectively to the features and the samples:

$$\mathbf{Y} = \begin{pmatrix} \vec{p}_{1,1} & \cdots & \vec{p}_{1,N} \\ \vdots & \ddots & \vdots \\ \vec{p}_{M,1} & \cdots & \vec{p}_{M,N} \end{pmatrix}, \quad (1)$$

where $\vec{p}_{i,j}$ is the 3D displacement vector of the voxel i in the deformation field of subject j . Since we focus in this study on brain folding, the analysis is restricted to the displacement vectors belonging to the cortical plate. The matrix \mathbf{Y} is the full set of features from which a sparse representation of brain folding is estimated. Instead of adopting a voxel-based approach, that is to say applying a statistical testing method to detect the most significant folding patterns, we propose a data driven approach aiming at extracting from the matrix \mathbf{Y} a small set of discriminative features.

Such a dimension reduction issue can be tackled with either feature extraction or feature selection techniques.

Feature extraction methods transform the high-dimensional data into a space of fewer dimensions. The main linear technique is the principal component analysis (PCA) which performs a linear mapping of the data to a lower-dimensional space in such a way that the variance in the low-dimensional representation is maximized and the covariance is minimized. Although PCA may be applied to study affine deformation, the linear assumption makes it less adapted for non linear deformations. Non-linear feature extraction techniques have been proposed by preserving local data structures. An important example of such non linear techniques is Isomap (Tenenbaum et al., 2000) (see Gerber et al. (2010) for an example of Isomap application to manifold modeling for MRI dataset analysis). However, the lower-dimensional space may not be easily interpretable, meaning that in our context, the extracted patterns do not correspond to displacement fields anymore. In this work, we investigate an alternate method by relying on a feature selection approach, aiming at computing a subset of the original variables.

Let Y_j be the j^{th} column of the matrix \mathbf{Y} and X_j a subset vector of Y_j ($X_j \subset Y_j$) of size $M' \leq M$. The key

assumption here is that the entire set of non linear deformations can be reconstructed using only a very small set of 3D displacement vectors. Within such a sparse framework, Y_j and X_j are linked by a reconstruction function f :

$$Y_j = f(X_j). \quad (2)$$

In this work, we chose to formulate the reconstruction function f using a Nadarya-Watson kernel regression function (Nadaraya, 1964):

$$\hat{f}(X, h) = \sum_{j=1}^N w_j(X, h) Y_j \quad (3)$$

where the weighting function w_j is written as

$$w_j(X, h) = \frac{K_h(X - X_j)}{\sum_{k=1}^N K_h(X - X_k)}. \quad (4)$$

The parameter h is the bandwidth of the kernel K_h acting on the subset X . The proposed sparsity-based approach relies on the assumption of redundant information in the original sample Y . Therefore, the relevant information is carried by a subset of parameters. Such a subset of M' parameters should minimize the following criterion:

$$\{\hat{\gamma}, \hat{h}\} = \arg \min_{\gamma, h} J(\gamma, h) \text{ s.t. } \|\gamma\|_0 \leq M', \quad (5)$$

where $\gamma \in \mathcal{M}_{p \times 1}(\{0, 1\})$ is a binary vector used to define the activated parameters and J is the reconstruction error defined as follows:

$$J(\gamma, h) = \sum_{j=1}^N \left\| Y_j - \hat{f}(\text{diag}(\gamma) \cdot Y_j, h) \right\|_2. \quad (6)$$

Optimization problems such as defined by equation (5) are NP-hard problems because of the use of L0 norm (Elad, 2010). In this work, we used an alternate optimization scheme, i.e. the two parameters of interest $\{\gamma, h\}$ are estimated alternatively. The estimation of the bandwidth parameter h is performed using a gradient descent technique within a leave-one-out strategy (Wand and Jones, 1995). The estimation of the activation vector γ is obtained using a greedy algorithm (Pudil et al., 1994) with a complexity of $\mathcal{O}(pM')$ cost function evaluations. The vector γ is first initialized to the null vector. Then, M' features at most are added iteratively. At each step, the feature added is the feature that maximizes the decrease of the reconstruction error. This procedure is detailed in algorithm 1.

The following convergence criterion have been defined for the proposed algorithm:

1. the maximal number of parameter to select M' is reached;
2. no parameter can be added without increasing the cost function;

1 3. the reconstruction error is lower than a predefined
2 error threshold \mathcal{E} .

The error criterion is the mean reconstruction error of parameters and is then expressed in mm:

$$\bar{\mathcal{E}}(\gamma, h) = \frac{1}{Np} \sum_{j=1}^N \sum_{i=1}^p \left\| Y_{i,i} - \hat{f}(\text{diag}(\gamma) \cdot Y_j, h)_i \right\|_2, \quad (7)$$

3 where $\hat{f}(\text{diag}(\gamma) \cdot Y_j, h)_i$ is the reconstruction of the i^{th}
4 displacement vector of the j^{th} subject.

Algorithm 1: Feature selection algorithm

Input:

- \mathbf{Y} Set of deformation fields
- P Maximum number of parameters to select
- \mathcal{E} Error threshold

Output:

- \mathbf{X} Selected features

$$\gamma := (0 \cdots 0)^T$$

Estimate parameter h

$$J_0 := J(\gamma, \hat{h})$$

$$k := 1$$

while $k \leq M'$ and $J(\gamma, \hat{h}) \leq \mathcal{E}$ **do**

$$J_k := J_{k-1}$$

foreach feature i such that $\gamma(i) = 0$ **do**

$$\gamma(i) := 1$$

if $J(\gamma, \hat{h}) < J_k$ **then**

$$J_k := J(\gamma, \hat{h})$$

$$i_k^{(+)} := i$$

end

$$\gamma(i) := 0$$

end

if one parameter to add is found **then**

$$\gamma(i_k^{(+)}) := 1$$

Estimate parameter h

$$k := k + 1$$

else

Stop the loop

end

end

$$\mathbf{X} := \text{diag}(\gamma) \cdot \mathbf{Y}$$

3. Results

6 Experiments have been conducted on both synthetic
7 and real datasets. In the first part, the behavior and the
8 performance of the algorithm are studied on the synthetic
9 dataset. Then, in a second part, the proposed method is
10 applied on in vivo fetal brain dataset.

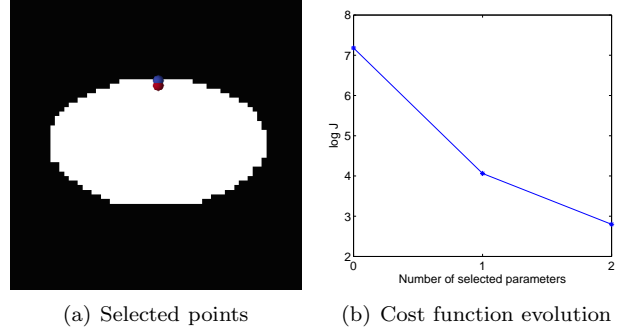


Figure 2: Selected points and cost function evolution of the proposed algorithm on a synthetic dataset. The colors reflect the energy of the parameters as a log scale. The first selected parameter (in red) is located on the border of the ellipse and on the varying axe of the dataset. The cost function decreases dramatically after one selected parameter and no parameter can be added without increasing the cost function after 2 iterations.

11 In each experiment, a Gaussian kernel is used within
12 the reconstruction function (see equation (3)) and the max-
13 imum number of parameter is set to $M' = 100$. The mean
14 parameter error threshold is set to $\mathcal{E} = 0.1$ mm for exper-
15 iments on brain MR images. For synthetic experiment only,
16 the threshold is set to $\mathcal{E} = 0$ mm in order to study
17 the convergence of the algorithm.

3.1. Synthetic dataset experiments

18 The synthetic dataset is composed of 20 two-dimensional
19 ellipses (rasterized to images of size 64×64 pixels) whose
20 shape varies according to the vertical axis (see Figure 1).
21 The first image of this dataset is then an elongated ellipse
22 while the last image is a circle. This dataset has been gen-
23 erated using only one degree of freedom (i.e. the length of
24 the vertical axis). On the first image, the vertical axis is
25 four times smaller than the horizontal one.

26 The results of the proposed algorithm on synthetic
27 dataset are depicted in Figure 2(a). Convergence is reached
28 in this experiment when only 2 features have been selected.
29 Indeed, adding more features do not make the cost func-
30 tion decrease. The evolution of the cost function is shown
31 in Figure 2(b) and suggests that the first selected point
32 captures the main variability of the dataset. Moreover,
33 it has to be noticed that the two selected points are lo-
34 cated on the vertical axis where the shape variability is
35 high. Due to the symmetric experimental setup, only one
36 selected point location should be necessary to describe the
37 growth pattern. This is confirmed by looking at the resid-
38 ual reconstruction error shown in Figure 3. The residual
39 errors (displayed in log scale) decrease dramatically after
40 the selection of the first parameter and are mainly located
41 on the borders of the vertical axis. Then, the decrease of
42 residual errors after the selection of the second point is
43 negligible.

44 The selected parameters are supposed to represent the
45 variability of the shapes. The set of 20 shapes shown in
46 figure 1 can be seen in two different ways: 1) as a set
47

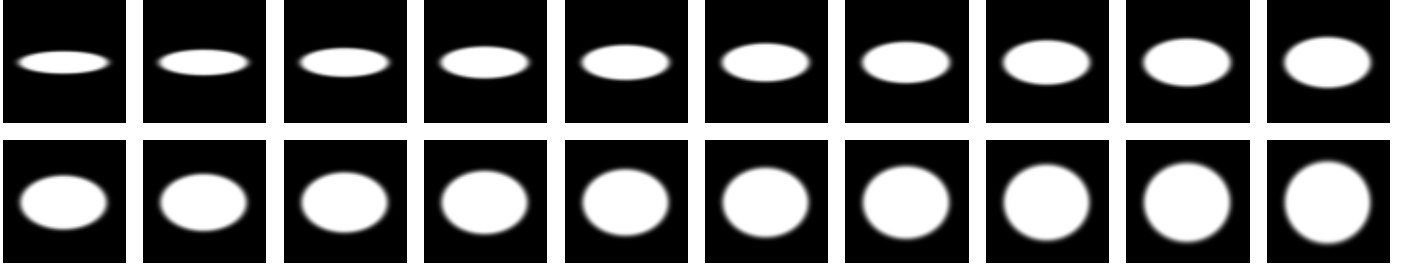


Figure 1: Dataset used in the synthetic experiment, composed of 20 images of size 64×64 pixels. The 2D shapes are varying according to the vertical axis.

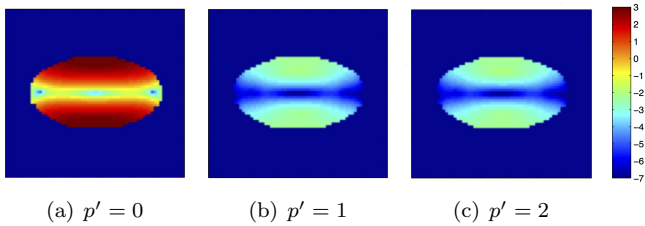


Figure 3: Residuals visualization on the synthetic dataset for 0, 1 and 2 selected parameters (displayed with a log scale). After one selected parameter, the residuals decrease dramatically.

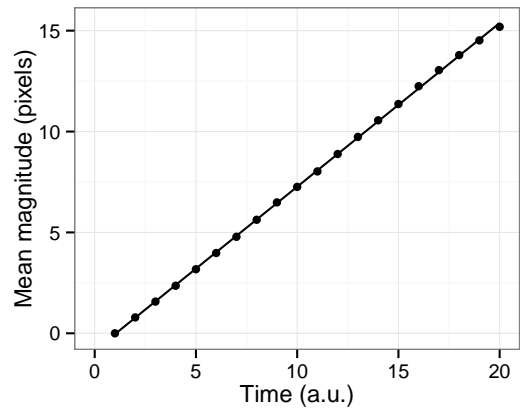


Figure 4: Analysis of the growth rate on the synthetical dataset. The plot shows the mean magnitude of selected vectors across time (in the reference space of the first image, $t = 1$). By studying the fit of a linear function, the growth rate can be estimated with the slope of the function. In this case, the estimated growth rate (0.812) is close the theoretical one (0.825).

1 of 20 different shapes (reflecting shape variability), or 2
 2 as a set of an evolving shape over time (i.e. temporal
 3 evolution of a shape). In later case, it is interesting to
 4 study time varying features that could reflect the growth
 5 rate for instance, such as length of the vertical axis.

6 Given the half-size d of the ellipse on the vertical axis
 7 and at $t = 1$, the half-size of the ellipse on the same axis
 8 and at $t = 20$ should be equal to $4d - d = 3d$, because
 9 the vertical axis on the first image is four time smaller
 10 than the same axis on the last image. Since there are 20
 11 images sampled over time, the growth rate should be equal
 12 to $\frac{3d}{20} = 0.15d$. In our case, the half-size of the vertical axis
 13 on the first image is 5.5 pixels. Therefore, the theoretical
 14 growth rate of the simulated dataset is 0.825 pixels per
 15 time unit.

16 Figure 4 shows the mean magnitude of vectors over
 17 time in the reference space of the first image ($t = 1$). The
 18 linear function fitted to the data has a slope of 0.812, which
 19 is close to the theoretical growth rate.

20 3.2. Application on fetal brain MRI dataset

21 Since our first objective is to study the geometrical
 22 changes of the cortical folding through in utero brain mat-
 23 uration, we define as region of interest the cortical gray
 24 matter. Moreover, average deformation fields (computed
 25 in the orthogonal direction of brain surface) along the
 26 cortical gray matter have been used in order to reduce the
 27 initial parameter set to a smaller set of 3D displacement
 28 vectors (Rajagopalan et al., 2012). Figure 5 shows five
 29 examples of deformation fields considered in this study.

30 3.2.1. Influence of the bandwidth parameter h

31 In this experiment, we evaluate the influence of the
 32 bandwidth parameter h over the selected points. Here, we
 33 applied the selection algorithm by setting manually this
 34 parameter $h \in \{0.5, 1, 1.5, 2, 3\}$. The results obtained ap-
 35 plying the algorithm on the temporal lobe for different
 36 values for h are displayed in figure 6. First, it can be
 37 easily seen that increasing the value of h makes the num-
 38 ber of selected points increase. Please note that h is a
 39 parameter that controls the smoothness of the non para-
 40 metric regression and therefore the value of h is related
 41 to the sparsity of the solution. Second, this experiment
 42 also shows the location stability of the selected features.
 43 It appears that the selected points are located in the main
 44 sulci (superior temporal sulcus, inferior temporal sulcus,
 45 lateral sulcus) in this region of interest, appearing during
 46 the considered period of age. This is a key point since it
 47 means that modifications of the bandwidth only influence
 48 the number of selected points, not their locations (i.e. the
 49 estimated growth pattern). The value of the bandwidth h
 50 does not modify the spatial pattern of the most discrim-
 51 inative selected points. Third, the experiment, restricted
 52 on the temporal lobe area, shows that growth variability

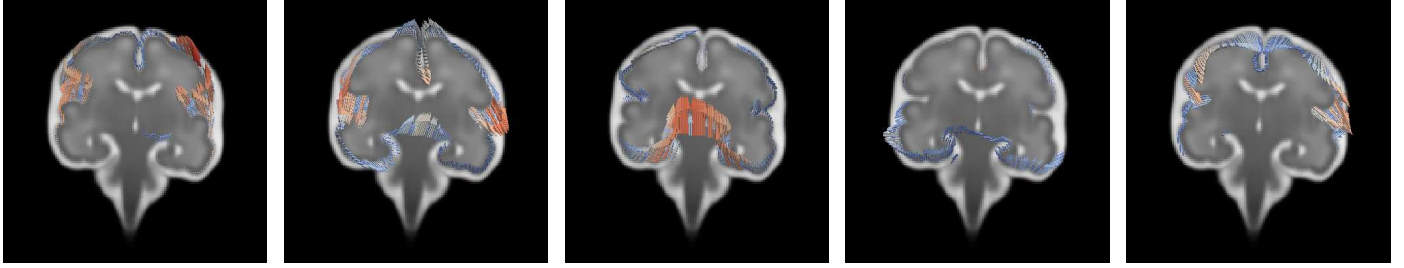


Figure 5: Five instances of the dataset used. The selection algorithm is applied on the cortical deformation fields mapping the reference space to population.

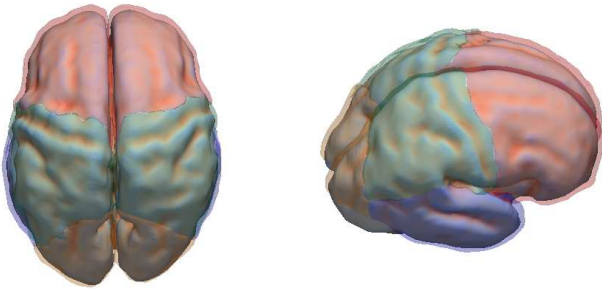


Figure 7: The regions of interest used with the feature selection algorithm. These regions corresponds approximately to the frontal (red), temporal (blue), parietal (green) and occipital (yellow) lobes.

can be captured by few points in the sulci of interest.

Please note that in the proposed algorithm, the bandwidth parameter h is estimated at each iteration using a leave-one-out strategy in order to minimize the variance of the regression function. For the next experiments, h is then computed automatically.

3.2.2. Points selection on fetal brain lobes

In this section, we propose to apply the feature selection algorithm onto 8 regions of interest (ROI) corresponding approximately to the frontal, temporal, parietal and occipital lobes of each hemisphere (see figure 7) in order to characterize spatial pattern of cortical folding for the considered period of age (26 to 34 weeks). Each of these ROI have been considered independently.

Experiments previously described have shown that the selected points tend to be in sulci valleys. Thus, the ROI defined here do not exactly match the anatomical lobes to avoid any bias of selected sulci. For instance, the central sulcus should define the boundary between the frontal and parietal lobes. However, we chose to associate the central sulcus with the parietal lobe, in order to give a chance to the algorithm to select cortical points of this sulcus.

The results of the selection algorithm on brain lobes are displayed in figures 8 and 9 respectively for lobes in left and right hemispheres. For each considered ROI, four types of results are provided : (a) selected points when the bandwidth h is set to 2, (b) selected points when h is automatically estimated, (c) a coronal view showing the location of

selected points and (d) the evolution of the cost function. While the first visualization (using $h = 2$) provides the main patterns of selected features, the second visualization (using automatic bandwidth computation) shows the sparsity of the reached solution of the algorithm. Only few features (up to 6) are required to discriminate the sets of images for each ROI. The coronal view confirms previous experiments (see Section 3.2.1): the selected points are located into sulci valleys.

3.2.3. Evolution of deformation vector magnitude

We examine in this section the temporal evolution of magnitudes of selected deformation vectors. Once the most discriminant points are selected for each region of interest, we compute the set \mathcal{V} of deformation fields between each subject and the mean image estimated at 26 weeks: $\mathcal{V} = \{\vec{v}_{\mathbf{x}}(t_i)\}$ where \mathbf{x} is the location of each selected point and t_i is the time difference between the age of the subject i and 26 weeks. The evolution of the magnitudes of computed deformation fields at selected point locations is estimated using a temporal polynomial of degree 3 regression approach (see figure 10 for an instance of regression over time for one vector). Figure 11 shows (a) the time evolution of the mean magnitude for the eight considered ROI (corresponding to the left-right lobes), (b) the mean magnitude for the 4 ROI by fusing data from left and right hemispheres, and (c) the mean magnitude by considering only left vs right. It can be seen that mean magnitude at occipital lobe has a different temporal evolution from the three other anatomical regions. Moreover, temporal differences in left and right temporal evolution are also observed. Statistical testing on larger dataset has to be conducted in order to verify the significance of these observations.

3.3. Discussion

In this paper, we have shown that early cortical folding patterns occurring during fetal brain development can be expressed by a sparse representation using a feature selection approach. By using sparse non linear deformation fields, we have highlighted major cortical surface changes in the considered age interval. Such information extraction is important since sulci can be used to discriminate brain development stages. The period of age considered

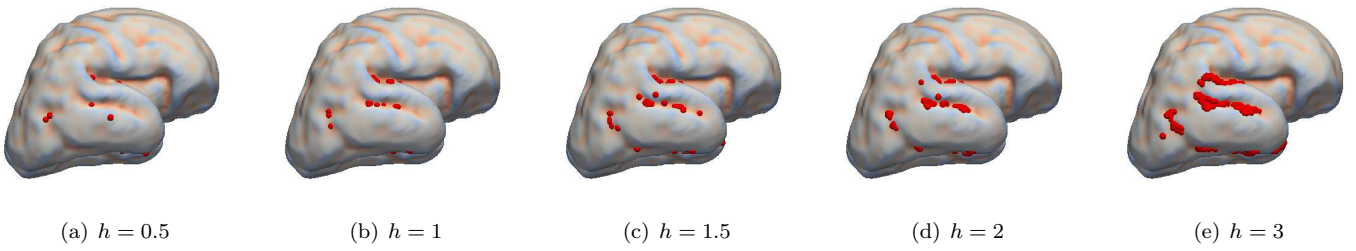


Figure 6: Study of the influence of the choice of the bandwidth parameter of the proposed algorithm. As the bandwidth increases, the number of selected parameters increases as well. An important property is the location stability of the solution with various bandwidth values.

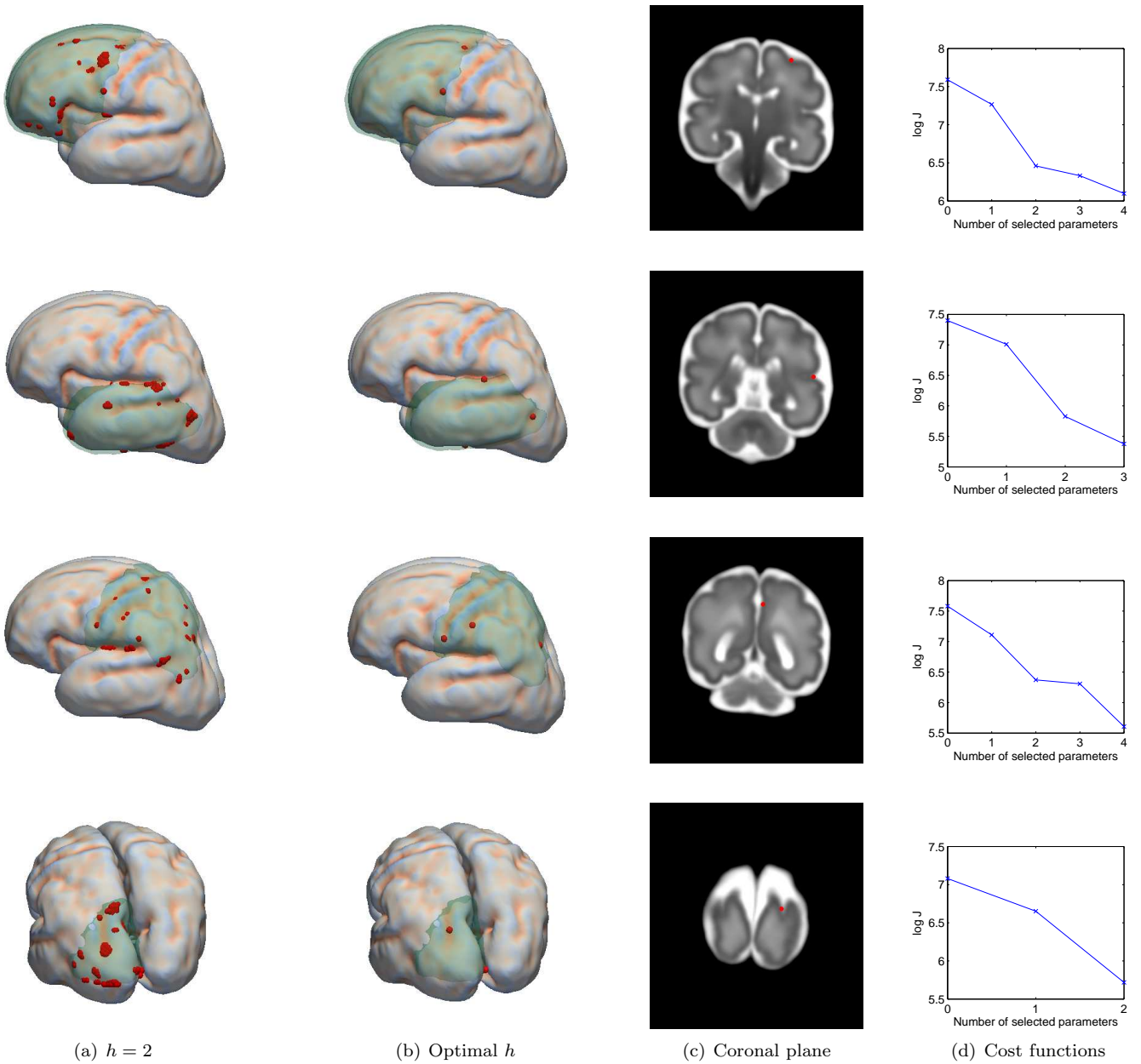


Figure 8: Selected cortical points on four lobe regions of the left hemisphere using the proposed algorithm. The left column shows the solution for a fixed bandwidth ($h = 2$). The other columns show the results for the optimal bandwidth. Top row: frontal lobe; second row: temporal lobe; third row: parietal lobe; last row: occipital lobe. The selected cortical points are depicted as red spheres. The color code in 3D mesh views maps the curvature of the cortical plate from blue color (positive curvature) to red color (negative curvature).

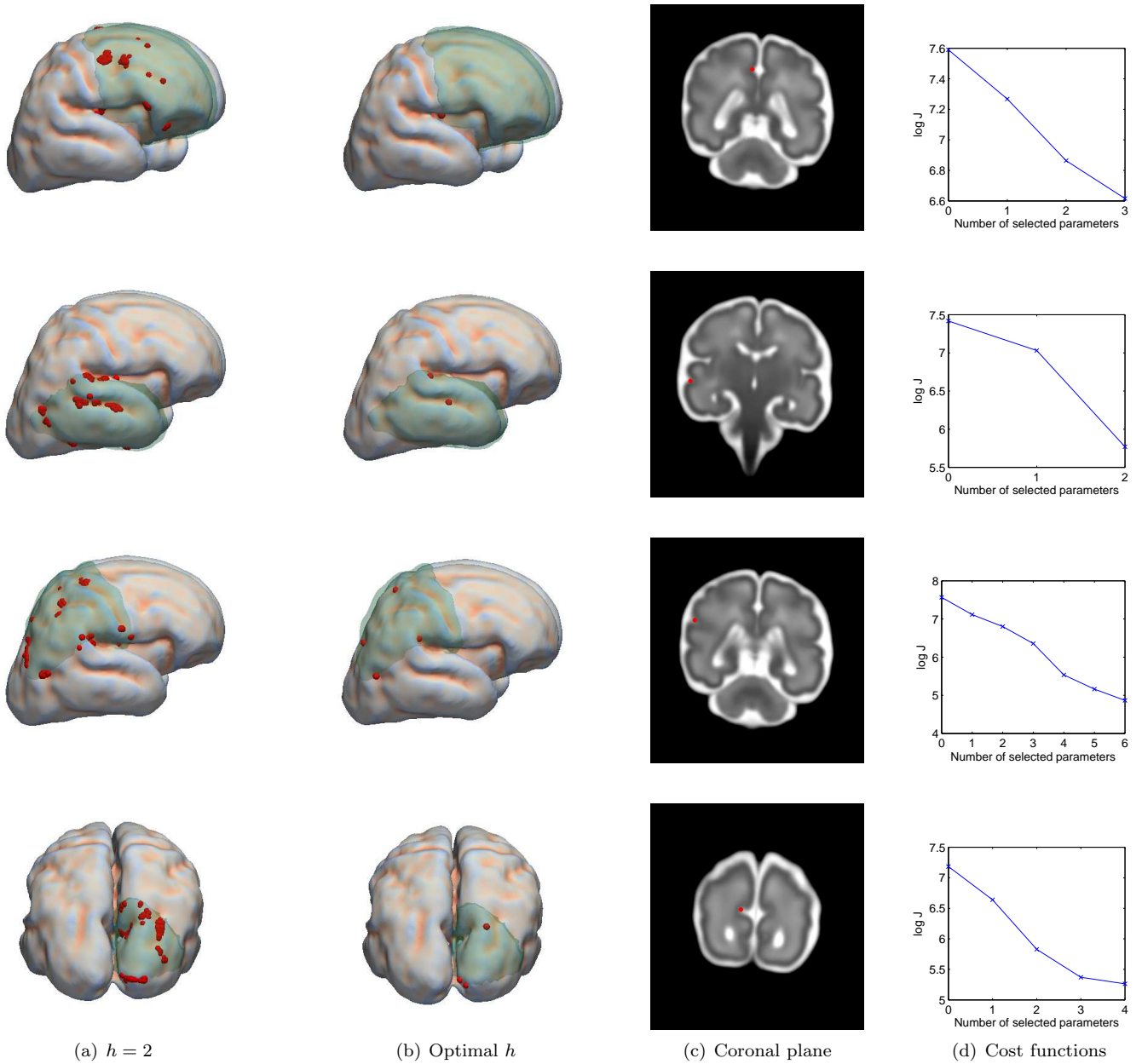


Figure 9: Selected cortical points of four lobe regions of the right hemisphere using the proposed algorithm. The left column shows the solution for a fixed bandwidth ($h = 2$). The other columns show the results for the optimal bandwidth. Top row: frontal lobe; second row: temporal lobe; third row: parietal lobe; last row: occipital lobe. The selected cortical points are depicted as red spheres. The color code in 3D mesh views maps the curvature of the cortical plate from blue color (positive curvature) to red color (negative curvature).

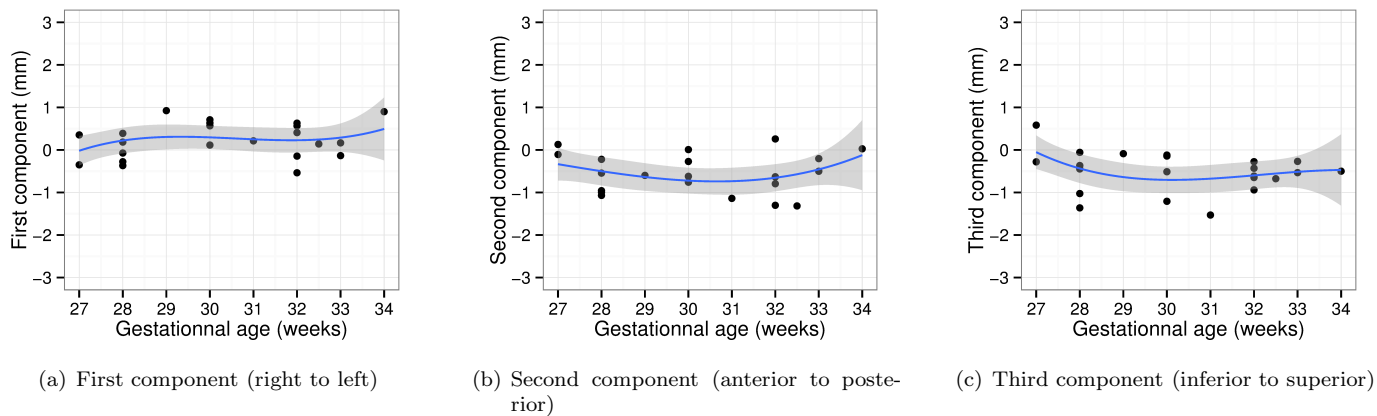


Figure 10: Example of polynomial regression over time (degree 3) for one selected vector of the right temporal lobe.

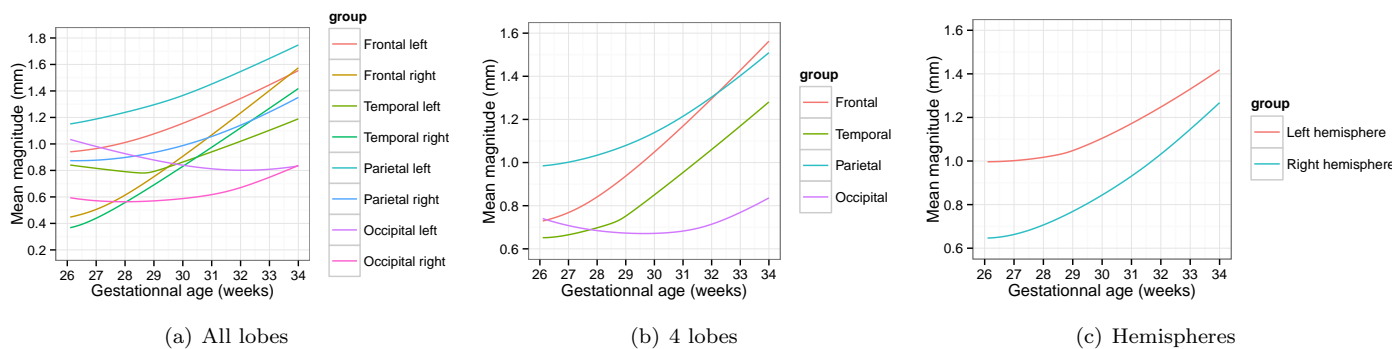


Figure 11: Mean magnitude of selected deformation vectors of lobes over time.

in this work (26 to 34 weeks) corresponds to a linear evolution of the surface curvature observed by Wright et al. (2014). Our experiments performed on mean magnitudes of deformation vectors tend to show the same trend.

In this work, we have considered non linear deformation fields providing voxel correspondence between each subject. Feature selection technique has been applied on these dense deformation fields in order to compute the smallest discriminative set of features characterizing the cortical folding process during fetal brain development. In this study, the registration step and the feature selection are independent. An alternative approach could have been to develop a registration technique incorporating a sparsity prior on the deformation fields. This kind of generative approach is related to the work of Durrleman *et al.* (Durrleman et al., 2012) in which a new parametrization of deformations is proposed in order to capture the variability in image ensembles. The key idea in their work is to select the most relevant control points and to estimate their positions in a template domain. A major difference between these two works is that control points may not belong to the shape under study. Thus, measuring the variability through the distribution of control points may not be easily interpretable with respect to the studied temporal process. By separating the registration step and the shape variability study, we can focus on shape deformation locally related to cortical folding.

Our work is also related to the recent study of growth seeds performed by Lefèvre et al. (2009), where an analysis of depth maps of cortical surface based on the Helmholtz decomposition of the deformation fields. In the work of Lefèvre et al. (2009), which is also related to the works of Cuzol et al. (2005) and Grenander et al. (2007), the main idea relies in that a decomposition is used to make the physical interpretation of the deformation fields (capturing the brain maturation process) easier. Our approach is complementary to these techniques in the sense that the relevant (i.e. most discriminative) displacement vectors are selected using a non-parametric approach. Further work would consist in analyzing the impact of the deformation model on the selected features.

As shown in our experiments, the most discriminative points lie in deep sulcal regions. These specific locations could be used as consistent shape features in further studies. Future work will consist in analyzing these patterns with regard to previous related works on sulcal root (Régis et al., 2005) and sulcal pit (Lohmann et al., 2008). It has been shown that deepest parts of sulci generally show less interindividual variability than superficial parts (Lohmann et al., 2008). The study of local fluctuations of these cortical patterns using a clustering approach such as in (Sun et al., 2009) could provide complementary insights on brain folding to gyrification index measurements (Clouchoux et al., 2011). The spatial distribution of deep sulcal landmarks (Im et al., 2010), especially over time (Meng et al., 2014), may help to set up new early markers of later functional development (Dubois et al., 2008) or particular

cortical malformation (such as polymicrogyria) that might be difficult to detect and quantify visually.

4. Conclusion

In this paper, we have used a feature selection approach to characterize cortical folding patterns occurring during fetal brain development with a sparse representation.

The use of such a feature selection technique is not restricted to only fetal brain development studies. It could be used to define biomarkers, shape representation, diffusion / fiber tracts, etc.

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References

- Avants, B., Gee, J., 2004. Geodesic estimation for large deformation anatomical shape averaging and interpolation. *NeuroImage* 23, supplement 1, 139–150.
- Busse, R. F., Riederer, S. J., Fletcher, J. G., Bharucha, A. E., Brandt, K. R., Sep. 2000. Interactive fast spin-echo imaging. *Magnetic Resonance in Medicine* 44 (3), 339–348.
- Caldairou, B., Passat, N., Habas, P. A., Studholme, C., Koob, M., Dietemann, J.-L., Rousseau, F., 2011. Segmentation of the cortex in fetal MRI using a topological model. In: *Biomedical Imaging: From Nano to Macro*, 2011 IEEE International Symposium on. pp. 2045–2048.
- Clouchoux, C., Kudelski, D., Gholipour, A., Warfield, S. K., Viseur, S., Bouyssi-Kobar, M., Mari, J.-L., Evans, A. C., du Plessis, A. J., Limperopoulos, C., May 2011. Quantitative in vivo MRI measurement of cortical development in the fetus. *Brain Structure and Function* 217 (1), 127–139.
- Cuzol, A., Hellier, P., Mémin, E., 2005. A novel parametric method for non-rigid image registration. *Information processing in medical imaging : proceedings of the ... conference* 19, 456–467.
- de Graaf-Peters, V. B., Hadders-Algra, M., Apr. 2006. Ontogeny of the human central nervous system: What is happening when? *Early Human Development* 82 (4), 257–266.
- Dittrich, E., Riklin Raviv, T., Kasprian, G., Donner, R., Brugger, P. C., Prayer, D., Langs, G., Jan. 2014. A spatio-temporal latent atlas for semi-supervised learning of fetal brain segmentations and morphological age estimation. *Medical Image Analysis* 18 (1), 9–21.
- Dubois, J., Benders, M., Borradori-Tolsa, C., Cachia, A., Lazeyras, F., Ha-Vinh Leuchter, R., Sizonenko, S. V., Warfield, S. K., Mangin, J. F., Hüppi, P. S., Jan. 2008. Primary cortical folding in the human newborn: an early marker of later functional development. *Brain* 131 (8), 2028–2041.
- Durrleman, S., Allasonnière, S., Joshi, S., Aug. 2012. Sparse Adaptive Parameterization of Variability in Image Ensembles. *International Journal of Computer Vision* () 101 (1), 161–183.
- Elad, M., 2010. *Sparse and redundant representations: from theory to applications in signal and image processing*. Springer.
- Gerber, S., Tasdizen, T., Fletcher, P., Joshi, S., Whitaker, R., 2010. Manifold modeling for brain population analysis. *Medical Image Analysis* 14 (5), 64–653.
- Gholipour, A., Akhondi-Asl, A., Estroff, J. A., Warfield, S. K., Apr. 2012. Multi-atlas multi-shape segmentation of fetal brain MRI for volumetric and morphometric analysis of ventriculomegaly. *NeuroImage* 60 (3), 1819–1831.

- 1 Gholipour, A., Estroff, J. A., Warfield, S. K., Oct. 2010. Robust
2 super-resolution volume reconstruction from slice acquisitions: ap-
3 plication to fetal brain MRI. *IEEE Transactions on Medical Imag-*
4 *ing* 29 (10), 1739–1758. 74
- 5 Grenander, U., Srivastava, A., Saini, S., May 2007. A Pattern-
6 Theoretic Characterization of Biological Growth. *IEEE Transac-*
7 *tions on Medical Imaging* 26 (5), 648–659. 78
- 8 Guimond, A., Meunier, J., Thirion, J.-P., 2000. Average brain mod-
9 els: A convergence study. *Computer Vision and Image Under-*
10 *standing* 77 (2), 192–210. 81
- 11 Habas, P., Kim, K., Corbett-Detig, J., Rousseau, F., Glenn, O.,
12 Barkovich, A., Studholme, C., 2010a. A spatiotemporal atlas of
13 mr intensity, tissue probability and shape of the fetal brain with
14 application to segmentation. *NeuroImage* 53 (2), 460–470. 85
- 15 Habas, P. A., Kim, K., Rousseau, F., Glenn, O. A., Barkovich, A. J.,
16 Studholme, C., Aug. 2010b. Atlas-based segmentation of devel-
17 oping tissues in the human brain with quantitative validation in
18 young fetuses. *Human Brain Mapping* 31 (9), 1348–1358. 89
- 19 Habas, P. A., Scott, J. A., Roosta, A., Rajagopalan, V., Kim, K.,
20 Rousseau, F., Barkovich, A. J., Glenn, O. A., Studholme, C., Jan.
21 2012. Early Folding Patterns and Asymmetries of the Normal Hu-
22 man Brain Detected from in Utero MRI. *Cerebral Cortex* 22 (1),
23 13–25. 94
- 24 Im, K., Jo, H. J., Mangin, J. F., Evans, A. C., Kim, S. I., Lee,
25 J. M., Feb. 2010. Spatial Distribution of Deep Sulcal Landmarks
26 and Hemispherical Asymmetry on the Cortical Surface. *Cerebral*
27 *Cortex* 20 (3), 602–611. 98
- 28 Jiang, S., Xue, H., Glover, A., Rutherford, M., Rueckert, D., Hajnal,
29 J. V., Jul. 2007. MRI of moving subjects using multislice snapshot
30 images with volume reconstruction (SVR): application to fetal,
31 neonatal, and adult brain studies. *IEEE Transactions on Medical*
32 *Imaging* 26 (7), 967–980. 103
- 33 Kim, K., Habas, P. A., Rousseau, F., Glenn, O. A., Barkovich, A. J.,
34 Studholme, C., Jan. 2010. Intersection Based Motion Correction
35 of Multislice MRI for 3-D in Utero Fetal Brain Image Formation.
36 *IEEE Transactions on Medical Imaging* 29 (1), 146–158. 107
- 37 Kuklisova-Murgasova, M., Quaghebeur, G., Rutherford, M. A., Ha-
38 jnal, J. V., Schnabel, J. A., 2012. Reconstruction of fetal brain
39 MRI with intensity matching and complete outlier removal. *Med-*
40 *ical Image Analysis* 16 (8), 1550–1564. 111
- 41 Lefèvre, J., Leroy, F., Khan, S., Dubois, J., Hüppi, P. S., Baillet, S.,
42 Mangin, J.-F., 2009. Identification of growth seeds in the neonate
43 brain through surfacic Helmholtz decomposition. *Information pro-*
44 *cessing in medical imaging : proceedings of the ... conference* 21,
45 252–263. 115
- 46 Limperopoulos, C., Clouchoux, C., Aug. 2009. Advancing fetal brain
47 MRI: targets for the future. *Seminars in perinatology* 33 (4), 289–
48 298.
- 49 Lohmann, G., von Cramon, D. Y., Colchester, A. C. F., May 2008.
50 Deep Sulcal Landmarks Provide an Organizing Framework for Hu-
51 man Cortical Folding. *Cerebral Cortex* 18 (6), 1415–1420.
- 52 Meng, Y., Li, G., Lin, W., Gilmore, J. H., Shen, D., Oct. 2014.
53 Spatial distribution and longitudinal development of deep cortical
54 sulcal landmarks in infants. *NeuroImage* 100 (C), 206–218.
- 55 Nadaraya, E., 1964. On estimating regression. *Theory of Probability*
56 *and its Application* 10, 186–190.
- 57 Pudil, P., Novovicova, J., Kittler, J., 1994. Floating search methods
58 in feature selection. *Pattern Recognition Letters* 15 (11), 1119–
59 1125.
- 60 Rajagopalan, V., Scott, J., Habas, P., Kim, K., Rousseau, F., Glenn,
61 O., B., A., Studholme, C., 2012. Mapping directionality specific
62 volume changes using tensor based morphometry: An application
63 to the study of gyrogenesis and lateralization of the human fetal
64 brain. *NeuroImage* 63 (2), 947–958.
- 65 Rajagopalan, V., Scott, J. A., Habas, P. A., Kim, K., Corbett-Detig,
66 J. M., Rousseau, F., Barkovich, A. J., Glenn, O. A., Studholme,
67 C., Feb. 2011. Local Tissue Growth Patterns Underlying Normal
68 Fetal Human Brain Gyrfication Quantified In Utero. *Journal of*
69 *Neuroscience* 31 (8), 2878–2887.
- 70 Régis, J., Mangin, J.-F., Ochiai, T., Frouin, V., Rivière, D., Cachia,
71 A., Tamura, M., Samson, Y., 2005. “Sulcal root” generic model: a
hypothesis to overcome the variability of the human cortex folding
patterns. *Neurologia medico-chirurgica* 45 (1), 1–17.
- Rousseau, F., Glenn, O. A., Iordanova, B., Rodriguez-Carranza, C.,
Vigneron, D., Barkovich, A. J., Studholme, C., 2005. A novel
approach to high resolution fetal brain MR imaging. *International*
Conference on Medical Image Computing and Computer-Assisted
Intervention: MICCAI 8 (Pt 1), 548–555.
- Rousseau, F., Glenn, O. A., Iordanova, B., Rodriguez-Carranza,
C., Vigneron, D. B., Barkovich, A. J., Studholme, C., Sep.
2006. Registration-Based Approach for Reconstruction of High-
Resolution In Utero Fetal MR Brain Images. *Academic Radiology*
13 (9), 1072–1081.
- Rousseau, F., Kim, K., Studholme, C., Koob, M., Dietemann, J.-
L., 2010. On super-resolution for fetal brain MRI. *International*
Conference on Medical Image Computing and Computer-Assisted
Intervention: MICCAI 13 (Pt 2), 355–362.
- Rousseau, F., Oubel, E., Pontabry, J., Schweitzer, M., Studholme,
C., Koob, M., Dietemann, J.-L., 2013. Btk: An open-source
toolkit for fetal brain mr image processing. *Computer Methods*
and Programs in Biomedicine 109 (1), 65–73.
- Studholme, C., Aug. 2011. Mapping Fetal Brain Development In
Utero Using Magnetic Resonance Imaging: The Big Bang of Brain
Mapping. *Annual Review of Biomedical Engineering* 13 (1), 345–
368.
- Sun, Z. Y., Perrot, M., Tucholka, A., Rivière, D., Mangin, J.-
F., 2009. Constructing a dictionary of human brain folding pat-
terns. *International Conference on Medical Image Computing and*
Computer-Assisted Intervention: MICCAI 12 (Pt 2), 117–124.
- Tenenbaum, J., de Silva, V., Langford, J., 2000. A global geo-
metric framework for nonlinear dimensionality reduction. *Science*
290 (5500), 2319–2323.
- Volpe, J. J., 2008. *Neurology of the Newborn*. Elsevier Health Sci-
ences.
- Wand, M., Jones, M., 1995. Kernel Smoothing. No. 60 in *Chapman &*
Hall CRC Monographs on Statistics & Applied Probability. Chap-
man & Hall.
- Wright, R., Kyriakopoulou, V., Ledig, C., Rutherford, M. A., Hajnal,
J. V., Rueckert, D., Aljabar, P., May 2014. Automatic quantifi-
cation of normal cortical folding patterns from fetal brain MRI.
NeuroImage 91, 21–32.
- Yamashita, Y., Namimoto, T., Abe, Y., Takahashi, M., Iwamasa, J.,
Miyazaki, K., Okamura, H., Feb. 1997. MR imaging of the fetus by
a HASTE sequence. *American Journal of Roentgenology* 168 (2),
513–519.