



PROJECT 11, CNN MASTER

A study of morphometric patterns of brain development in premature infants

inDev Team, Inserm NeuroDiderot UMR1141 department. CEA Saclay, NeuroSpin center

Author : Marion Pavau
Supervisors : Jessica Dubois & Andrea Gondova
October 6, 2022

Contents

| | |
|---|-----------|
| List of Figures | ii |
| List of Tables | ii |
| Abstract | iii |
| Acknowledgments | iv |
| 1 Introduction | 1 |
| 2 Methods | 3 |
| 2.1 Objects of interest | 3 |
| 2.2 Data | 3 |
| 2.3 MSM method | 5 |
| 2.3.1 Theory | 5 |
| 2.3.2 sMSM and aMSM | 6 |
| 2.4 Projection of the parcellation from second session to first session | 7 |
| 2.5 Evaluation criteria | 7 |
| 2.5.1 Sørensen-Dice score | 7 |
| 2.5.2 Hausdorff distance | 8 |
| 2.5.3 Percentage area discrepancy | 8 |
| 3 Results | 9 |
| 3.1 Visual assessment | 9 |
| 3.2 Quantitative assessment over the whole brain | 10 |
| 3.3 Quantitative assessment per cortical region | 12 |
| 4 Discussion | 15 |
| 5 Conclusion | 16 |
| References | 17 |
| Attachments | 18 |

List of Figures

| | | |
|----|--|----|
| 2 | First and second session brain comparison | 4 |
| 3 | MSM registration principle | 5 |
| 4 | aMSM registration pipeline | 6 |
| 5 | Hausdorff distance on 2D geometrical figures | 8 |
| 6 | Visual parcellation comparison between methods. | 9 |
| 7 | Sørensen-Dice score comparison between methods. | 10 |
| 8 | Hausdorff distance comparison between methods. | 11 |
| 9 | Percentage area discrepancy comparison between methods. | 11 |
| 10 | Sørensen-Dice score data normal distribution test. | 12 |
| 11 | Cortical representations of the regions of interest in one hemisphere. | 13 |
| 12 | Regional dice score comparison between methods. | 13 |
| 13 | Regional Hausdorff distance comparison between methods. | 14 |
| 14 | Regional percentage area discrepancy comparison between methods. | 14 |

List of Tables

| | | |
|---|--|----|
| 1 | Average metrics per method. | 10 |
| 2 | Friedman test results for methods benchmark, default MSM, sMSM and aMSM and metrics Sørensen-Dice score, Hausdorff distance and Percentage area discrepancy. | 12 |

Abstract

Longitudinal studies allow to study brain development in premature infants, and are possible using Magnetic Resonance Imaging (MRI) [1]. They are enabling brain parcellation into regions of interest, which makes possible to compute micro-cortical measures, and structural and functional connectivity measures. This parcellation can be done using infants-specific tools. However, brain before the equivalent term age has not the same folding and complexity as equivalent term age brains and adults ones especially, which makes transferability of tools developed for later ages to very young infants difficult. In this study we want to test a multimodal surface matching (MSM) [2] method that already made it successful to show that regional growth across the cortical surface is linked with the emergence of new folds around the same region [3]. Unlike to a registration through template method [4], this method takes advantage of intra-subject matching to compute the registration. However inter-subject analysis has shown that using our configurations for MSM, the registration through template technique performed way better than direct MSM.

Acknowledgments

I would like to adress special thanks do Jessica Dubois and Andrea Gondova for creating this project and beeing a real support for me from the implementation of the method to the writing of this report. Thank you for making me feel comfortable with the project and the team all along those three months.

I am very grateful to Yann Leprince for his technical expertise, and to all the inDev team for their help and the great experience I had at the NeuroSpin center.

1 Introduction

During the last trimester of pregnancy and early postnatal period, large number of mechanisms involving genetic, epi-genetic and environmental factors impact the development of human brain. The white matter connects cortical and sub-cortical regions, and networks become functional. One of the most dramatic and apparent change in the cerebral cortex is surface expansion and folding. Birth is considered preterm when it happens before 37 weeks of gestation and prematurity has a profound long-term effect on brain development. Related white and grey matter abnormalities and altered cortical gyration have been described in preterm-born subjects across the lifespan with MRI [5, 6], which can be associated with difficulties in development that could conduct to sensory, motor, cognitive and emotional disorders.

Improved understanding of pre and postnatal critical period is thus crucial to the development of novel interventional and remediation strategies that could enhance the child care in the future.

Longitudinal studies allow to study brain development, and are possible using Magnetic Reasonance Imaging (MRI), a non-invasive technique that enable functional and structural analysis of the brain of premature infants, largely used today. The developing Human Connectome Project (dHCP) is a large initiative that aims to better understand the brain developing connectivity, and provide open source longitudinal data of preterm and term-born babies [1].

However, brain before the equivalent term age has not the same folding and complexity as equivalent term age brains and adults ones especially, which makes transferability of tools developed for later ages to very young infants (age superior to 28 days after birth) difficult.

For instance, parcellation of the cortex into regions, that consists in locating functional regions defined with features ranging from local properties of tissues to connectivity and functional patterns, is the first step of many analysis pipelines and often fails for the earliest scans (first session). Alternatively, longitudinal data of later scans (second session) can be parcellated with specific parcellation tools developed for near term-born infants.

We tried to register 15 subjects of the dHCP from the first session to the second session using a template. Yet, we think we can take advantage of the consistency between the first session scans, or earliest scans of one subject, and the second session scans, or later scans of the same subject, to parcellate the first session with the parcellation of the second session. Indeed, first session already presents developing primary folds that together with the general shape of the brain, makes it similar to the second session and enable the registration. The team of Robinson et al. has developped the multimodal surface matching method (MSM) capable of intra-subject matching.

For example, using anatomically constrained MSM on 30 preterm infants, scanned from two to four times during the 28 to 38 week of postmenstrual age (gestational age plus age after birth), it has been shown that regional growth across the cortical surface is linked with the emergence of new folds around the same region [3]. The anatomically constrained MSM (aMSM) has made possible this regional analysis that requires precise

matching of corresponding points between scans of one individual at different steps. It constitutes a great improvement with regards to other existing surface matching methods in terms of flexibility and has been shown to outperform competing methods for the alignment of multimodal data [2]. We are thus expecting MSM to give better results than the registration through template.

The goal of this project is to use the anatomically multimodal surface matching method to individually match surfaces of the first session to the second session, and to apply the parcellation already performed for the second session to the matched surface of the first one. The main steps of the project are first to implement the method to run on our data, second compare the registration through template technique with the non-anatomically constrained MSM and the aMSM technique using different metrics, and finally analyse and discuss the results.

2 Methods

In this section, we will look at the validity of the MSM method, and use different metrics to compare its performance with the registration through template technique on different configurations : the default configuration and the two configurations used for MSM in Garcia et al. paper [3], that are spherical MSM (sMSM) and anatomically constrained MSM (aMSM).

2.1 Objects of interest

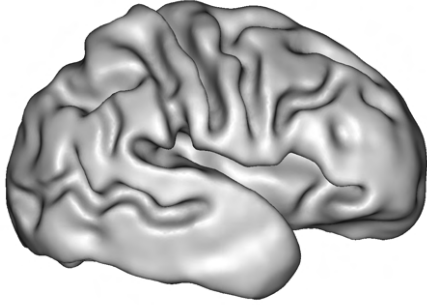
A surface is an object that can be physically represented in space. A mesh is a discretized representation of a surface, which points are called vertices. The inner surface is obtained when taking the border between white and gray matter (see figure 2a, 2b). It is the most commonly used as the folding strongly appears. The pial surface is the external surface of the cortex.

A texture file represents a biological or physical property like the thickness or curvature at each vertex of the mesh. When we fusion a mesh file with its corresponding texture file we get a 3D representation of the brain with the physical or biological properties associated with. We decided to use the curvature texture file because it is the most significant property regarding the increasing folding between the brains of the first and second group. The curvature property is thus supposed to give us relatively good registration.

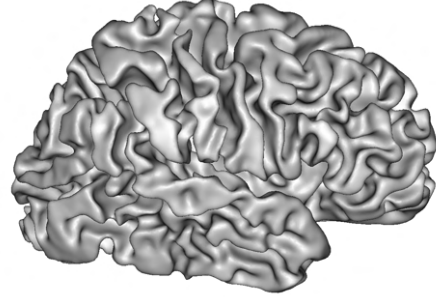
2.2 Data

Our MRI data are part of dHCP database [1]. Longitudinal data of pre-term neonates with the lowest ages at birth, imaged using a 32-channel head coil at 3 Tesla were selected. On our 15 subjects, the mean age at birth is 26.99 ± 1.54 (from 23.71 to 28.71) weeks, and the mean ages for first and second scan are 31.71 ± 2.29 (from 26.71 to 35.71) and 40.86 ± 1.52 (from 38.43 to 43.43) weeks respectively. The percentage of male and female was 53% and 47% respectively. The mean time difference between the first and second scan was 9.14 ± 2.63 (from 2.72 to 14.72) weeks.

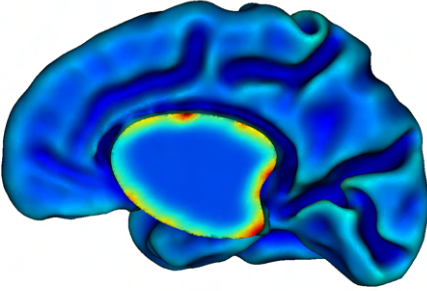
The inner surfaces for both sessions are extracted using cortical surface-based processing pipelines for the developing neonatal brain using T2-weighted images [7]. Inner cortical surfaces of the second session are parcellated into 36 bilateral regions using infant-specific M-CRIB-S tool [8].



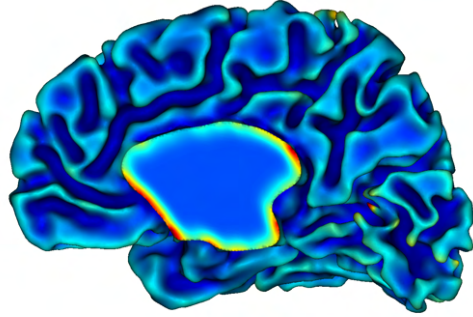
(a) Lateral view of the first session.



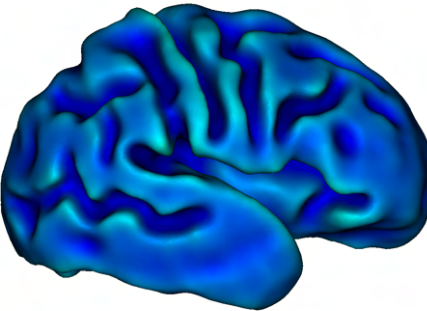
(b) Lateral view of the second session.



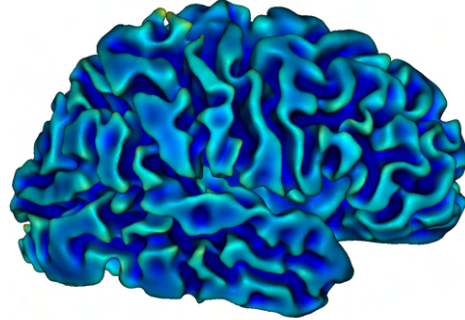
(c) Sagittal view of the first session fusionned with curvature texture file.



(d) Sagittal view of the second session fusionned with curvature texture file.



(e) Lateral of the first session fusionned with curvature texture file.



(f) Lateral view of the second session fusionned with curvature texture file.

Figure 2: First and second session brain comparison
Left hemisphere inner mesh. The age at birth was 31 weeks and the age at first and second scan were 33.29 and 44.86 weeks respectively.

2.3 MSM method

2.3.1 Theory

The Multimodal Surface Matching is a discrete optimization tool that allows accurate registration of surfaces and has reduced sensitivity to a local minima compared to other registration methods [2]. The method takes as input spherical meshes and textures. To transform our meshes into a sphere, inflation is performed using the structural processing pipeline from Makropoulos et al.

MSM uses Markov Random Field cost with penalization. Control points are chosen in the mesh, and at each step, a control point can "move" to another discrete point in its surrounding, inducing a deformation. The control point moves toward location, or rotates, which optimizes the cost function C , penalizing surface distortion.

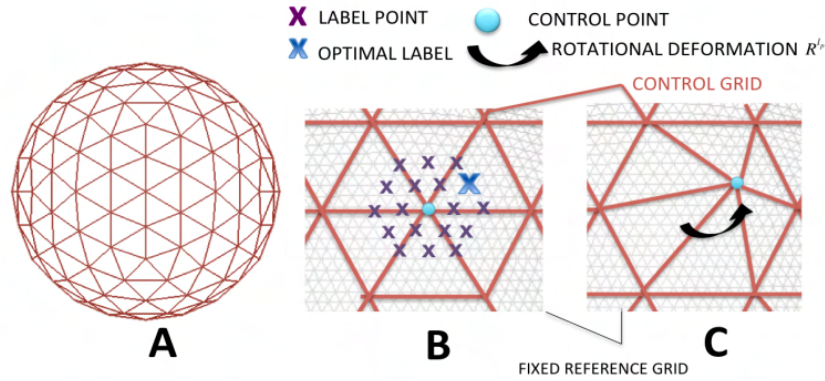


Figure 3: MSM registration principle.

Each control point of the control grid moves to one discrete location of the fixed reference grid.

Let $(G_D)_{D \in N}$ be the control-point grids and $p \in G_D$. R_p is the rotation associated with the control point p , $N(p)$ the control points neighbours of p and c a similarity function of R_p . The optimization problem solved by MSM is the following :

$$\min C = \sum_{p \in G_D} c(R_p) + \lambda \sum_{p \in G_D} \sum_{q \in N(p)} V(R_p, R_q)$$

λ is a penalization term that ensures trade off between accuracy and smoothness of the wrap. The regularization framework is said pair-wise as V has two inputs, that measures differences between proposed rotation matrices for neighbouring control points. This version of MSM is called PAIR MSM.

The MSM method gives as output the transformation sphere of sphere input mesh registered to the sphere reference mesh. It has the same number of vertices as the input mesh. The output contains registration instructions on how to go from the input mesh to the space of the reference mesh.

2.3.2 sMSM and aMSM

As an improvement to MSM, sMSM and aMSM introduce a new regularization penalty that derives from physically relevant equations of deformation energy, and is inspired by the hyperelastic properties of brain tissues. We call it STRAIN MSM.

In opposition with the previous PAIR MSM, STRAIN MSM, similarity and regularization are computed using triangle of vertices or cliques. We refer to it as sMSM.

Let C_D be cliques ensemble used for estimation of the similarity term and C_R the one of regularisation. The optimization problem becomes:

$$\min C = \sum_{c_1 \in C_D} c(R_{c_1}) + \lambda \sum_{c_1 \in C_R} V(R_{c_2})$$

In addition aMSM constrains the registration to anatomical meshes. It thus takes in arguments the input anatomical mesh that is the white matter mesh of the first session, and the reference anatomical mesh that is the white matter mesh of the second session.

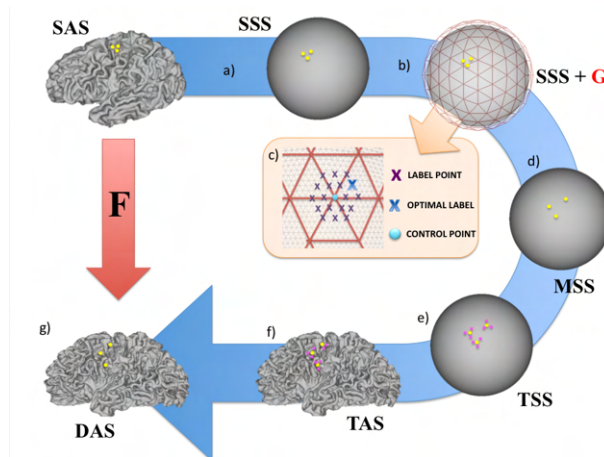


Figure 4: aMSM registration pipeline

aMSM infers a smoothed and regularized warp between source and target cortical anatomies, from Emma Robinson's web page on Advanced features of MSM

For each vertex of the mesh, the aMSM method transforms the input spherical surface into a spherical wrap that matches the reference surface. The method has the particularity to penalize anatomical deformation. We are thus expecting aMSM to perform better on our data compared to the default MSM or sMSM.

MSM has a large number of parameters that can be adapted to as specific use. In the Garcia and al. study, researchers developed two new configurations, STRAIN sMSM and STRAIN aMSM that are appropriate for young infants. As we use similar longitudinal data, we are expecting that those configurations perform well [3] [2].

2.4 Projection of the parcellation from second session to first session

Because we would like to apply the parcels that were assigned to the second session to the brains of the first session, and that the output of the MSM method does not change the number of vertices of the input mesh, we need to make either the output sphere mesh match the space of the parcel texture, or the parcel texture to match the new mesh.

Human Connectome software provides many functions for post-processing. We use the `-label-resample` function from the `workbench` command that resamples the second session parcellation texture to the first session mesh [9].

The registration through template method is a complete tool developed by Emma Robinson’s team that uses MSM registration through a reference and use then the `workbench` command to get the parcellations. This method does not direct intra-subject matching, but rather matches the first session and second session to a common template for 40 weeks brains. It uses midthickness which is the surface taken at mid-distance between the pial and inner surface as mesh and curvature, convexity/concavity maps, and myelin maps as texture files [7].

The templates are obtained by estimating a rotational transform between MNI space (volumetric standard) and HCP FS_LR space (standard HCP). The registration was made using MSM with the template that was the closest in age from the input mesh. The native surfaces and textures were then resampled into surface topology (FS_LR32k space) [4].

2.5 Evaluation criteria

To analyse the methods, we pass our parcellations to the FS_LR template for 40 weeks brains, assuming that the ”difference” from one subject to another should be equal to zero in case of perfect registration. Neglecting all other computational errors during pipeline that could induce a difference, for example the surfaces and textures extraction or the resampling, we can then infer that the difference is the error of the method. We base our evaluation on three metrics which define the difference from one subject’s parcellation to another: Sørensen-Dice score, Hausdorff distance and the percentage area discrepancy.

Those metrics are computed for each subject pair and each cortical region.

2.5.1 Sørensen-Dice score

The Sørensen-Dice score computes for a given parcel the overlap between two subjects.

Let A and B be two discrete ensembles.

$$Dice_score = \frac{2|A \cap B|}{|A| + |B|}$$

A perfect registration would give a Sørensen-Dice score of one.

2.5.2 Hausdorff distance

The Hausdorff distance measures the similarity between two different regions, by finding the maximum "non-overlapping" distance between those regions.

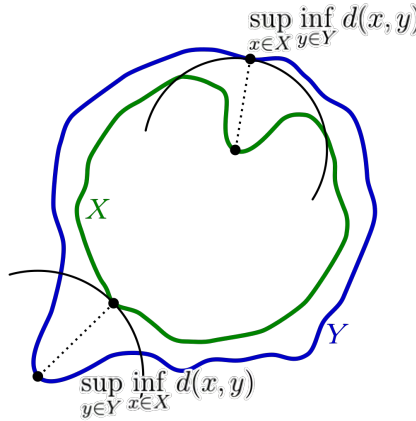


Figure 5: Hausdorff distance on 2D geometrical figures
From wikipedia page on Hausdorff distance

Let X and Y be two non-empty subsets of a metric space.

$$h(X, Y) = \max\left(\sup_{x \in X} \inf_{y \in Y} d(x, y), \sup_{y \in Y} \inf_{x \in X} d(x, y)\right)$$

Hausdorff distance is computed using scipy python package, version 1.2.3.

2.5.3 Percentage area discrepancy

Let A and B be two discrete regions.

$$\Delta A = \frac{|surface(A) - surface(B)|}{surface(B)}$$

In our case, a mesh is formed by a set of attached triangles. For each parcel, the polygons that are entirely belonging to the region are found, as well as their coordinates. Areas of cortical regions are computed using skimage python package, version 0.14.5 and soma python package, version 5.0.2.

3 Results

The mean run time for default MSM, sMSM, and aMSM were 613 ± 58 , 11431 ± 7805 , and 22127 ± 13665 seconds respectively.

3.1 Visual assessment

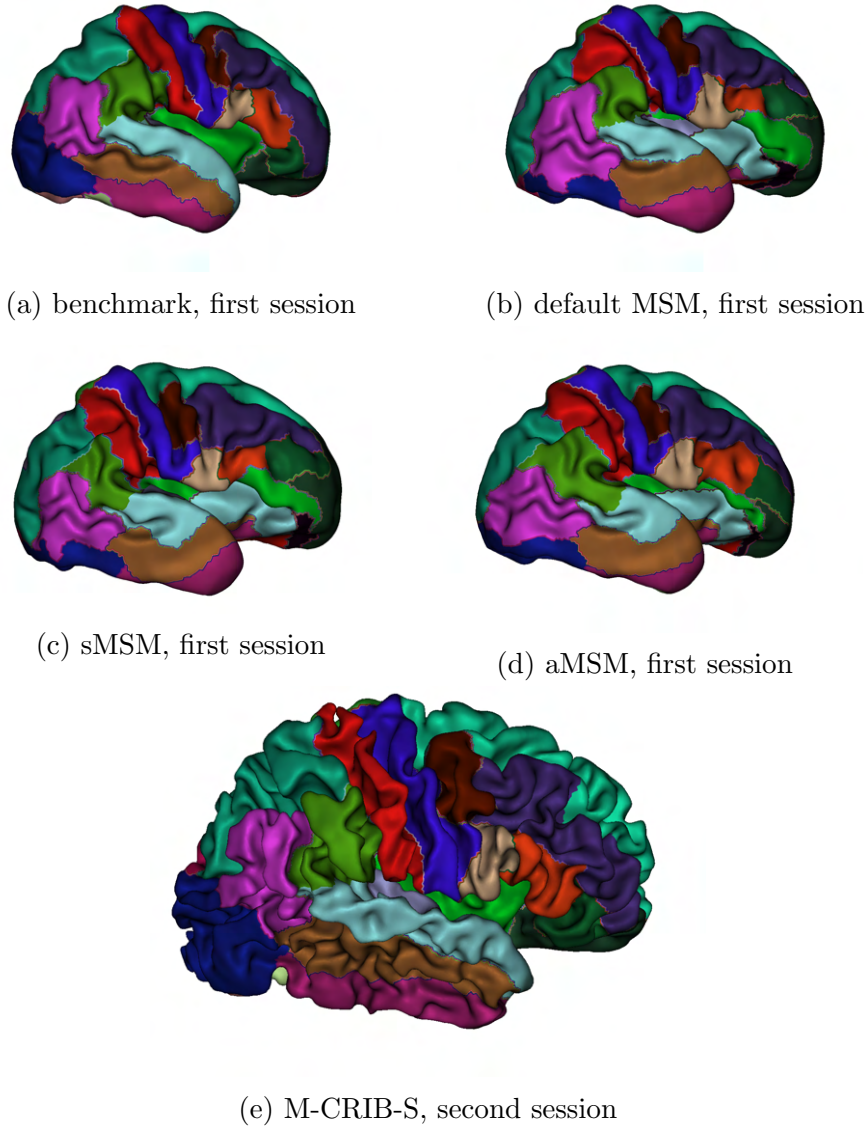


Figure 6: Visual parcellation comparison between methods.

Example left hemisphere inner surface lateral views of the first session fused with (a) benchmark, (b) default MSM, (c) sMSM and (d) aMSM label files. (e) is the inner surface with M-CRIB-S parcellation. The age at birth was 31 weeks and the age at first and second scan were 33.29 and 44.86 weeks respectively

Figure 6 exhibit a gap between the registration through template method and other methods in regions of the temporal lobe. On (a), the parcellation of included regions seems to follow the same shape and location as for (e). On the contrary, on (b), (c), and

(d), those regions does not have the same orientation and cross the lateral fissure which embodies the frontier between the temporal lobe and the frontal lobe. Qualitatively on this subject and lobe, the registration through template seems to perform way better than other direct MSM methods.

3.2 Quantitative assessment over the whole brain

A perfect registration method would give us a Sørensen Dice score equal to 1, and Hausdorff distance and Percentage of area change equal to 0. On table 1 we see the mean over label and over subject for the Sørensen Dice score, Hausdorff distance and Percentage area discrepancy for the different MSM methods. Given the mean, we can rank MSM through template method first. However the other methods vary in ranking depending on the metric we choose, and we would need to do further analysis to understand if those methods are significantly different.

| Method | Sørensen Dice score | Hausdorff distance | % area change |
|----------------------|---------------------|--------------------|---------------|
| sMSM | 0.463442 | 10.433042 | 0.369345 |
| default MSM | 0.532383 | 9.428009 | 0.365308 |
| aMSM | 0.462903 | 10.098797 | 0.307407 |
| MSM through template | 0.825698 | 3.753543 | 0.216952 |

Table 1: Average metrics per method.

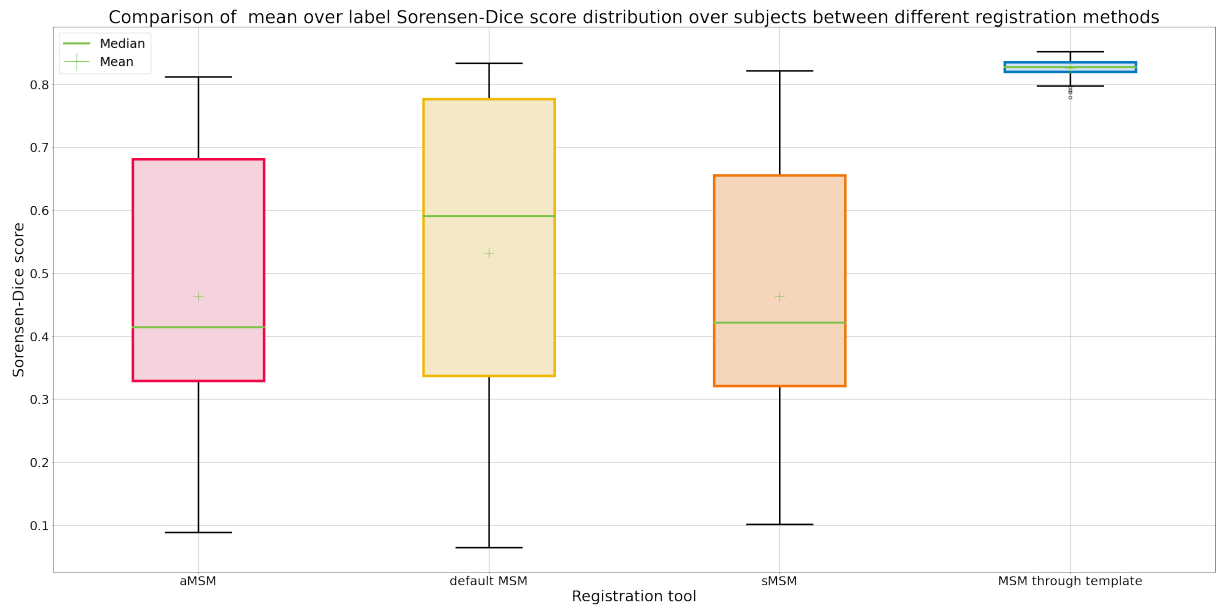


Figure 7: Sørensen-Dice score comparison between methods.

Box plot of mean Sørensen-Dice score over subject for benchmark, default MSM, sMSM and aMSM.

On figures 7, 8 and 9 we can see that MSM through template method has a better mean, better median and better variance because all data are contained in a very short interval. In addition, for default MSM, the size of the box is higher than for other methods, which state that 50% of data are much more dispersed around the mean. Having a specific

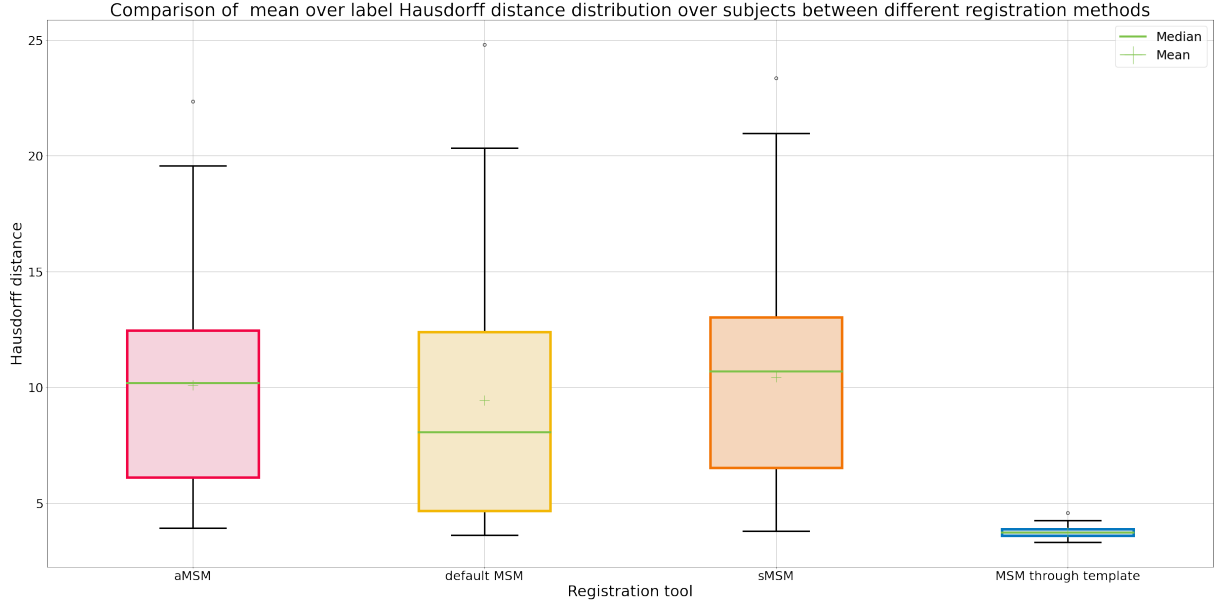


Figure 8: Hausdorff distance comparison between methods.
Box plot of mean Hausdorff distance over subject for benchmark, default MSM, sMSM and aMSM.

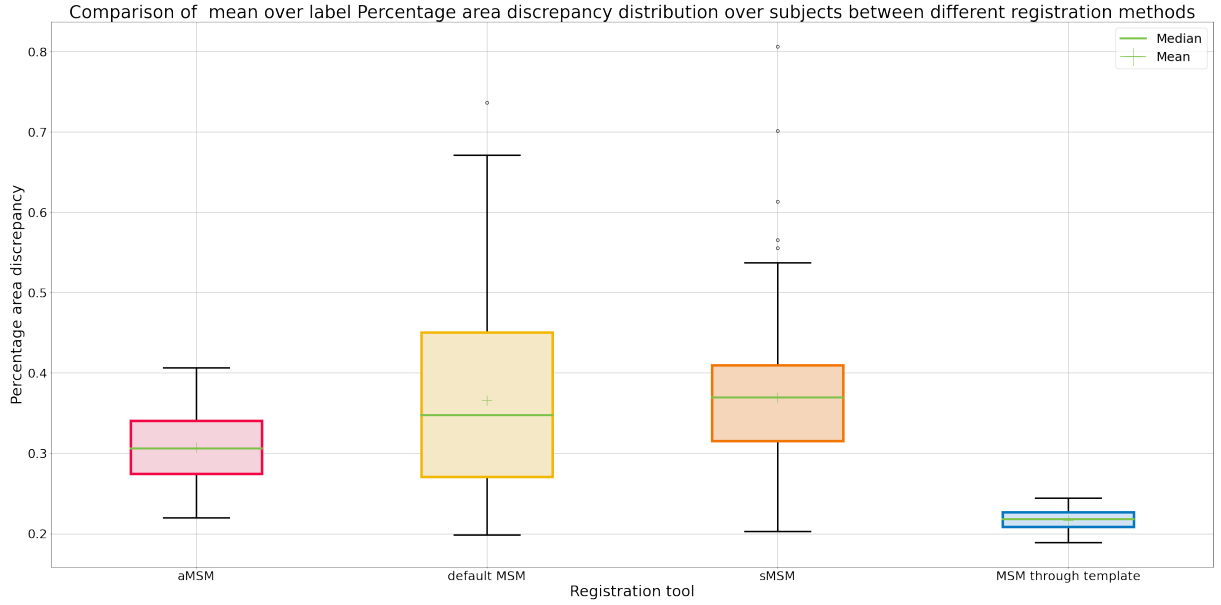


Figure 9: Percentage area discrepancy comparison between methods.
Box plot of mean Percentage area discrepancy over subject for benchmark, default MSM, sMSM and aMSM.

configuration dedicated to infants brains seems to then decrease the variability of the results.

Figure 10 shows that data for Sørensen Dice score does not follow a normal distribution. For this reason we use non-parametric tests to understand whether methods are statistically different from each other. Because the methods are correlated, we use Friedman test, that is a non-parametric version of the Repeated-Measures ANOVA, with the null-hypothesis that methods does not show statistically significant differences.

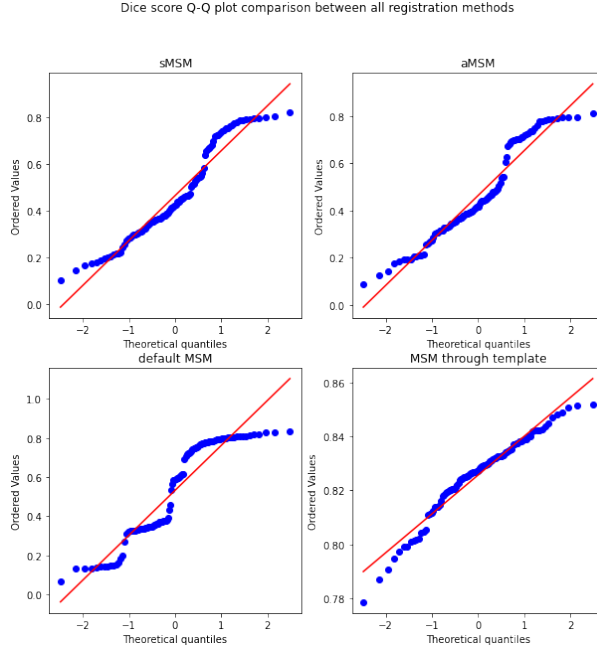


Figure 10: Sørensen-Dice score data normal distribution test.
Q-Q plot of mean area change per subject pair for benchmark, default MSM, sMSM and aMSM.

| Metric | sMSM, aMSM, default MSM stat | All methods stat |
|-----------------------------|------------------------------|------------------|
| Sørensen-Dice score | 27.2 | 196 |
| Hausdorff distance | 23.4 | 194 |
| Percentage area discrepancy | 29.6 | 188 |

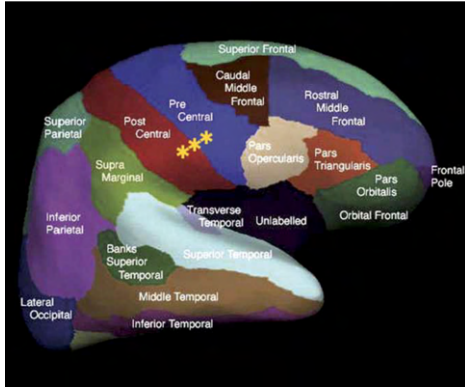
Table 2: Friedman test results for methods benchmark, default MSM, sMSM and aMSM and metrics Sørensen-Dice score, Hausdorff distance and Percentage area discrepancy.

Friedman test reject the null-hypothesis if $statistic \geq 5.99$ and $statistic \geq 7.8$ with a confidence of 95% for two and three degrees of freedom respectively. According to the Friedman test, sMSM, aMSM and default MSM does not show the same data distribution with at least 95% of confidence. This is also the case while comparing with the registration through template.

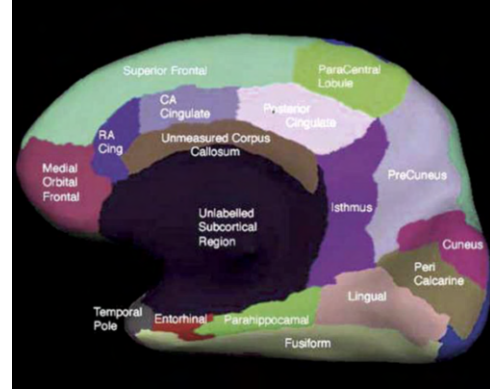
3.3 Quantitative assessment per cortical region

Figures 12, 13 and 14 show the distribution of the label’s mean score over subject. We directly see that the computation gave non-values for regions 1, 4, 32 and 33 (among Frontal Pole, Temporal Pole, Banks Superior Temporal, and Unmeasured Corpus Callosum) on all metrics and all subjects. Regions 0, 2 (CA cingulate), 3 (Caudal Middle Frontal), 5 (Cuneus), 31 (Supra Marginal) and 34 (Transverse Temporal) nearby have also less succeeded. In fact, regions 1, 4, 32 and 33 does not appear in the parcellation of the second session, which may be cause by the developing gyrification of the brain.

The difference between registration on left and right hemisphere is to noticed, although one cannot say one side performed better than the other.



(a) Lateral view



(b) Sagittal view

Figure 11: Cortical representations of the regions of interest in one hemisphere. Pial surfaces. From [10]

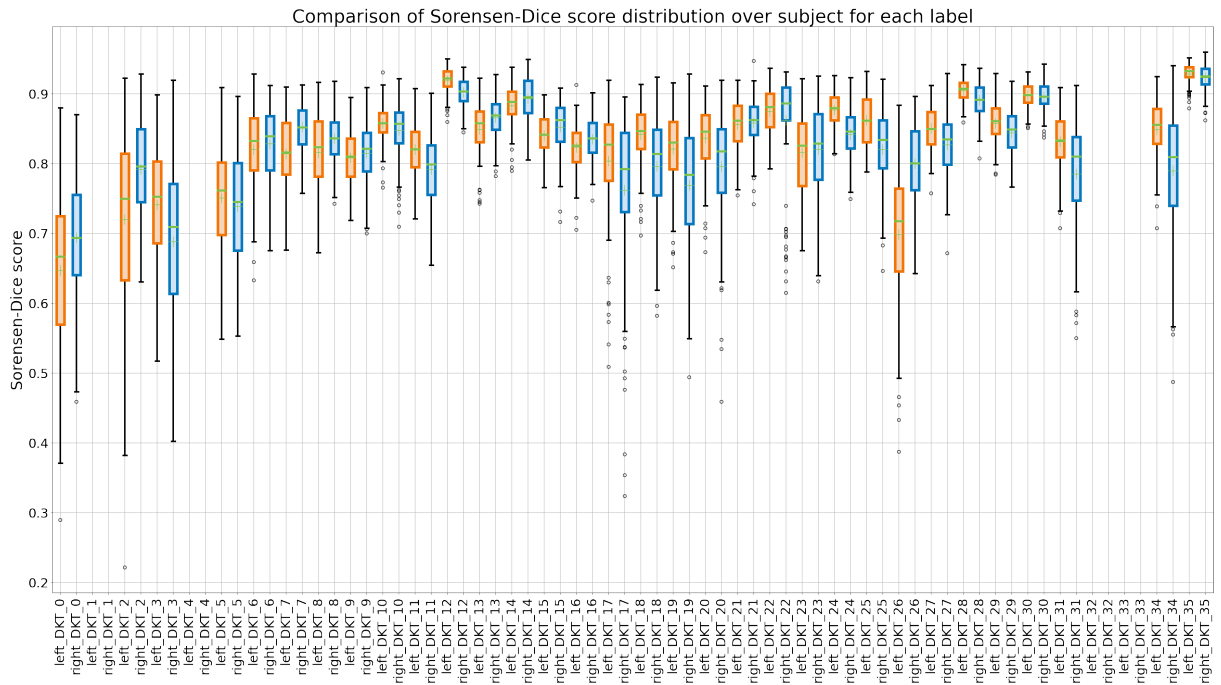


Figure 12: Regional dice score comparison between methods .
Box plot of mean dice score over label for benchmark, default MSM, sMSM and aMSM.

However, given the results and the run time, the default MSM is the most computationally efficient method.

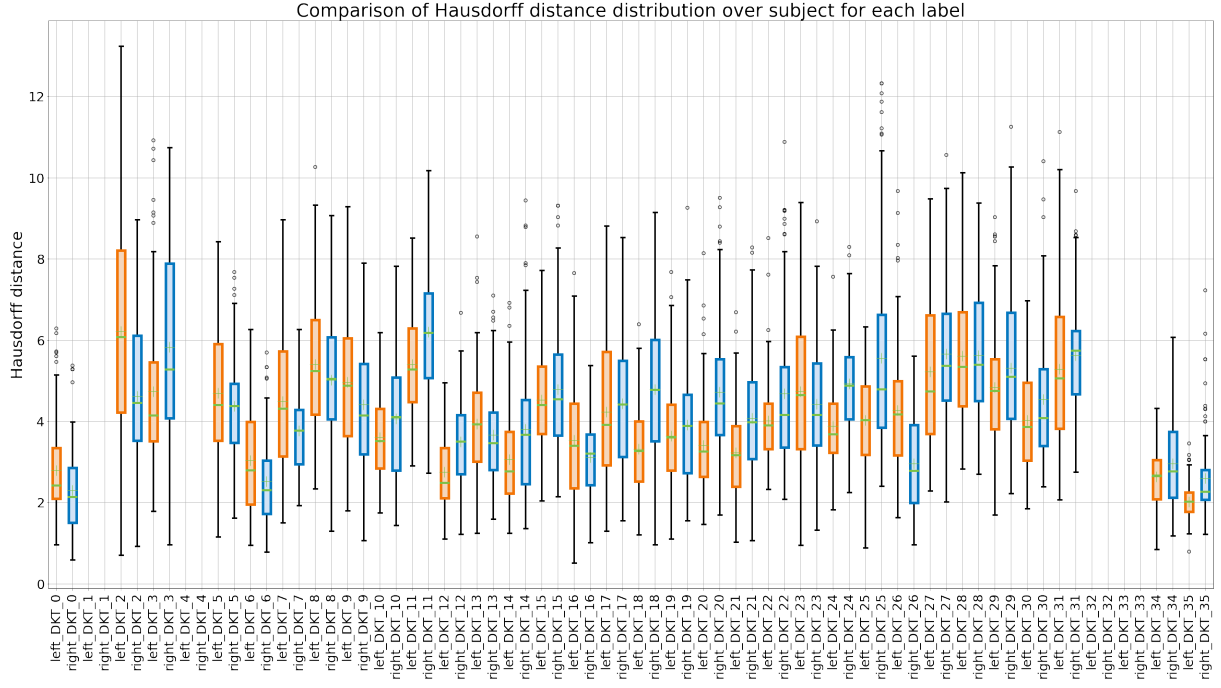


Figure 13: Regional Hausdorff distance comparison between methods.
Box plot of mean Hausdorff distance over label for benchmark, default MSM, sMSM and aMSM.

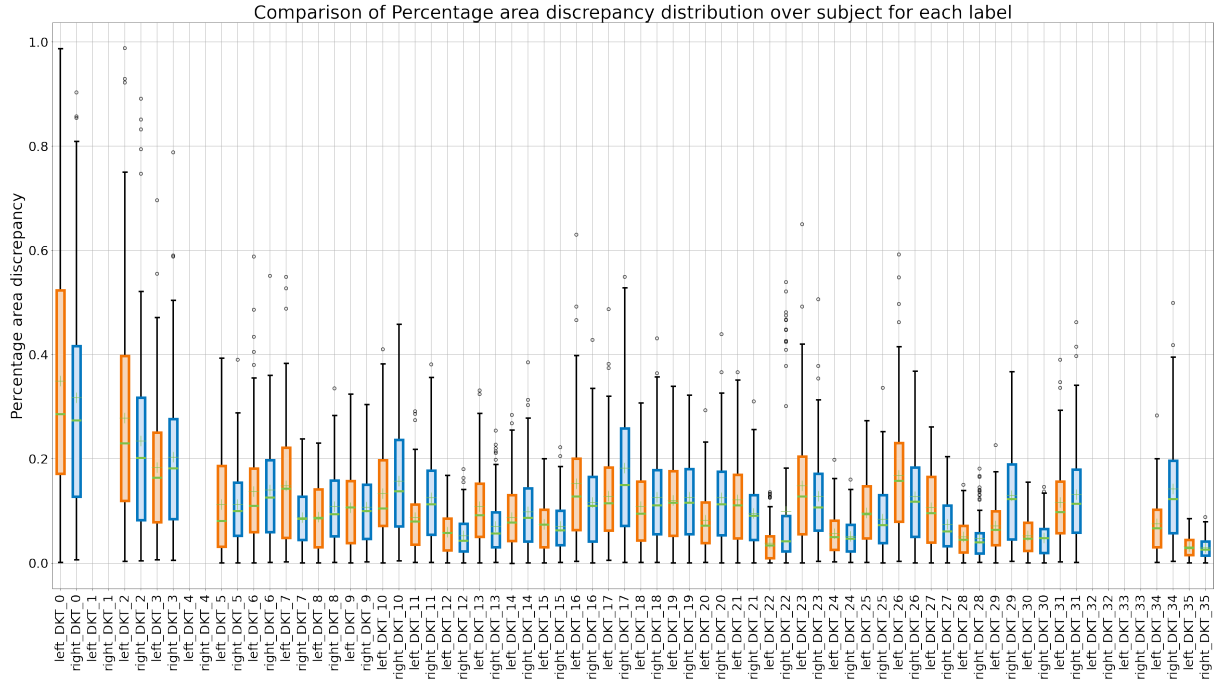


Figure 14: Regional percentage area discrepancy comparison between methods.
Box plot of mean area change over label for benchmark, default MSM, sMSM and aMSM.

4 Discussion

According to the three used metrics, Hausdorff distance, Sørensen Dice score and Percentage of area discrepancy we have seen that the registration through template method has a much lower error and variance compared to default MSM, sMSM and aMSM. However we do not take advantage of the similarity between the two subjects, but rather the method computes the registration by passing the first and second session to a template.

In this method, the subjects are registered through a template corresponding to the same age at scan. The averaging that induces the template could decrease the noise and deviation of the surface registration. On the other hand, inter-individual positioning changes between regions should not be respected with such technique.

We were however expecting aMSM to perform better than MSM, sMSM and registration through template. This was only slightly the case for sMSM. However brains of first and second session, scanned in average 10 weeks apart, present large discrepancies, that could have made the registration too difficult.

Because we would like to take advantage of intra-subject matching and take into account inter-subject variability, and that the results of the registration through template are not sufficient for micro-cortical measures, and structural, functional connectivity measures, a further investigation is needed to try to improve direct intra-subject matching with MSM.

First, we had to reverse the registered sphere to get it to the second session to run the workbench command. The underlying motivation is that we assumed that the results would be better when registering from the first session to the second session, because the brains of the second session present more folding and complexity. However, this reversed operation is adding a step in the pipeline that could decrease performance. It may then be worth to register surfaces from the second session to the first session to use the workbench directly.

Secondly, because curvature is following the increasing gyrification between the first and second session, we assume it would improve the registration. However, the myelin rate is also a property that changes fast during the last trimester of pregnancy and early post-natal age. We could then compare the error rate given by metrics for the registration with curvature texture and the one with myelin rate texture. Moreover, MSM has the advantage to take any type of data file for the registration and to allow multi-data registration. Using curvature, texture and myelin maps would add more information to the registration.

Midthickness is the surface taken half distance between pial surface and white-matter surface. We could also compare the accuracy of the method using midthickness and white-matter surface as it allows to reduce variability [2].

5 Conclusion

The Multimodal Surface Matching is a discrete optimization tool with penalization, that is able to perform spherical registration. This method demonstrated improved performance compared to other registration methods and is very flexible. Furthermore, a newer version of MSM, STRAIN MSM uses physically and biologically plausible properties of tissues to penalize surface deformations, and uses triangles for penalization. The anatomically constrained MSM takes spherical and anatomical surfaces to penalize slightly differently anatomical deformation.

Our study was made on very young preterm infants with a mean age of at birth of 29.70 ± 10.76 weeks, and the mean ages for first and second scan of 31.71 ± 2.29 and 40.86 ± 1.52 weeks. We compared the performance of the default MSM, sMSM and aMSM with the registration through template technique that does not take advantage of the direct similarity between the two sessions.

The results have shown that the registration through template technique was outperforming the other MSM techniques. However, further studies could be conducted where another surface or texture is used to test the registration's performance.

This study gives an insight on performance of different registration methods on very young preterm infants, that will allow to study the brain development in more detail, which understanding is crucial for the development of new interventional and remediation strategies.

References

1. Hughes, E. J. *et al.* A dedicated neonatal brain imaging system. *Magnetic Resonance in Medicine* **78**, 794–804 (2017).
2. Robinson, E. C. *et al.* Multimodal surface matching with higher-order smoothness constraints. *NeuroImage* **167**, 453–465. ISSN: 1053-8119 (2018).
3. Garcia, K. E. *et al.* Dynamic patterns of cortical expansion during folding of the preterm human brain. *Proceedings of the National Academy of Sciences* **115**, 3156–3161. ISSN: 0027-8424 (2018).
4. Robinson, E. C. *dHCP template alignment* version 1.0. Last accessed 14 December 2021. 2021. https://github.com/ecr05/dHCP_template_alignment.
5. Parikh, N. A. Advanced neuroimaging and its role in predicting neurodevelopmental outcomes in very preterm infants. *Seminars in Perinatology* **40**. Outcomes of High-Risk Infants, 530–541. ISSN: 0146-0005 (2016).
6. Hadaya, L. & Nosarti, C. The neurobiological correlates of cognitive outcomes in adolescence and adulthood following very preterm birth. *Seminars in Fetal and Neonatal Medicine* **25**. Long term outcomes following very preterm birth, 101117. ISSN: 1744-165X (2020).
7. Makropoulos, A. *et al.* The developing human connectome project: A minimal processing pipeline for neonatal cortical surface reconstruction. *NeuroImage* **173**, 88–112. ISSN: 1053-8119 (2018).
8. Adamson *et al.* Parcellation of the neonatal cortex using Surface-based Melbourne Children’s Regional Infant Brain atlases (M-CRIB-S). *Scientific Reports* (2020).
9. Software, H. C. *Workbench Command* Last accessed 18 February 2021. 2021. <https://humanconnectome.org/software/workbench-command/-label-resample>.
10. Desikan, R. S. *et al.* An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest. *NeuroImage* **31**, 968–980. ISSN: 1053-8119 (2006).

Attachments

```
1 def label_2_binaries(subject_label):
2     #function that takes as input an array of labels which length is the
    number
3     #of vertices
4     #and returns a binary array containing the binary information for
    each label
5     nb_label = np.max(subject_label) + 1
6     label_binaries = np.zeros((len(subject_label),nb_label))
7     for i in range(nb_label):
8         label_binaries[:,i] = np.where(subject_label[:,0] == i, 1, 0)
9     return label_binaries
```

```
1 def dice_score(subject_label_1, subject_label_2):
2     #get the label in binaries
3     binaries_1 = label_2_binaries(subject_label_1).astype(int)
4     binaries_2 = label_2_binaries(subject_label_2).astype(int)
5     #compute dice score
6     dice_scores = []
7     k = 1
8     for i in range(binaries_1.shape[1]):
9         if np.all(binaries_1[:,i] == 0) or np.all(binaries_2[:,i] == 0):
10             dice = np.nan
11         else:
12             intersection = np.sum(binaries_1[binaries_2[:,i]==k,i]) *
2.0
13             dice = intersection / (np.sum(binaries_1[:,i]) + np.sum(
    binaries_2[:,i]))
14             dice_scores.append(dice)
15     return np.array(dice_scores)
```

```
1 def label_2_coordinates(subject):
2     #function that takes as input an array of labels and coordinates
    which
3     #length is the number of vertices
4     #and returns for each label the coordinates of associated vertices
5     nb_label = int(np.max(subject[:,0])) + 1
6     label_coordinates = []
7     for i in range(nb_label):
8         data = np.copy(subject[:,1:])
9         data = np.delete(data,np.where(subject[:,0] != i), axis = 0)
10        label_coordinates.append(data)
11    return label_coordinates
```

```
1 def hausdorff_dist(subject_1,subject_2):
2     label_coordinates_1 = label_2_coordinates(subject_1)
3     label_coordinates_2 = label_2_coordinates(subject_2)
4
5     hausdorff = np.zeros(len(label_coordinates_1), dtype = float)
6     #set to NaN if does not exist
7     for i in range(len(label_coordinates_1)):
8         hausdorff[i] = float(distance.directed_hausdorff(
    label_coordinates_1[i], label_coordinates_2[i])[0])
9     return hausdorff
```

```
1 def label_2_indices(subject):
2     nb_label = int(np.max(subject[:,0])) + 1
```

```

3     label_indices = []
4     for i in range(nb_label):
5         data = np.where(subject[:,0] == i)
6         data = data[0]
7         label_indices.append(data)
8     return label_indices

1 def area_change(polygon, subject_1, subject_2):
2     label_indices_1 = label_2_indices(subject_1)
3     label_indices_2 = label_2_indices(subject_2)
4
5     label_coordinates_1 = label_2_coordinates(subject_1)
6     label_coordinates_2 = label_2_coordinates(subject_2)
7
8     area_change = []
9     for i in range(len(label_coordinates_1)):
10         label_polygons_1 = []
11         label_polygons_2 = []
12         for x in polygon:
13             if x[0] in label_indices_1[i] and x[1] in label_indices_1[i]
14             and x[2] in label_indices_1[i]:
15                 new_x = [int(np.where(label_indices_1[i] == x[0])[0]),
16                 int(np.where(label_indices_1[i] == x[1])[0]), int(np.where(
17                 label_indices_1[i] == x[2])[0])] #list of indices corresponding to
18                 label_coordinates
19                 label_polygons_1.append(new_x)
20                 if x[0] in label_indices_2[i] and x[1] in label_indices_2[i]
21                 and x[2] in label_indices_2[i]:
22                     new_x = [int(np.where(label_indices_2[i] == x[0])[0]),
23                     int(np.where(label_indices_2[i] == x[1])[0]), int(np.where(
24                     label_indices_2[i] == x[2])[0])] #list of indices corresponding to
25                     label_coordinates
26                     label_polygons_2.append(new_x)
27
28             if (label_coordinates_1[i].size == 0 or label_coordinates_2[i].
29             size == 0):
30                 area_change.append(1)
31             else :
32                 try :
33                     surf_subject_1 = skimage.measure.mesh_surface_area(
34                     label_coordinates_1[i], label_polygons_1)
35                     surf_subject_2 = skimage.measure.mesh_surface_area(
36                     label_coordinates_2[i], label_polygons_2)
37                     area_change.append(abs(surf_subject_1 - surf_subject_2)/
38                     surf_subject_2)
39                 except :
40                     area_change.append(1)
41
42     area_change = np.array(area_change)
43
44     return area_change

```