CONSTRUCTION OF A DYNAMIC 4D PROBABILISTIC ATLAS FOR THE DEVELOPING BRAIN

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INTRODUCTION

Probabilistic atlases have been established in the literature as a standard tool for enhancing the intensity-based classification of brain MRI. The rapidly growing neonatal brain requires an age-specific spatial probabilistic atlas to guide the segmentation process. In this paper we describe a method for dynamically creating a probabilistic atlas for any chosen stage of neonatal brain development. We present an atlas created from the segmentations of 153 subjects providing prior tissue probability maps for six structures - cortex, white matter, subcortical gray matter, brainstem and cerebellum, for ages of 29 to 44 weeks of gestation.

CREATING AGE-SPECIFIC PROBABILISTIC ATLASES

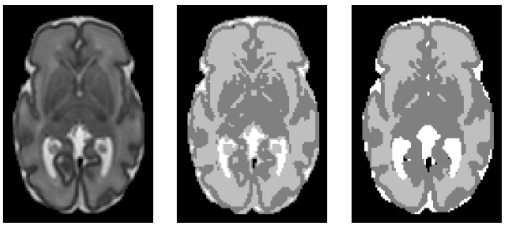
Traditionally, probabilistic atlases are created from a large number of manually segmented anatomical images I_1 ..., I_n. The images are typically registered into a single reference space via affine transformations $A_1,...,A_n$. The aligned images and corresponding segmentations are then averaged to produce a probabilistic atlas. However, such an atlas is biased towards the reference space and may not represent the average geometry of the population. Much of this bias can be removed if an average transformation is used to estimate the average space atlas. We represent affine transformations in 3D Euclidian space as 4 × 4 matrices acting on homogeneous coordinates. It is desired to average the affine transformations in relation to operation of composition. The group of transformations with the operation of composition does not form a vector space and linear average is therefore not defined. This can be overcome by estimating of the average for a set of affine matrices using matrix exponentials and logs, where the matrix exponential and logarithm are defined via Taylor expansion [1]. When building 4D atlas of the growing brain, we aim to create a continuous set of templates dependent on a parameter t which represents time, or in our case the age of the subjects. This can be achieved by kernel regression. Let $t_1,...,t_n$ be the gestational ages (GA) of the subjects at the time of scan. Then the average transformation $\bar{A}(t)$ at the age t and the average template image $\bar{I}(t)$ at the age t can be estimated using Gaussian weights as

$$\bar{A}(t) = \exp\left(\frac{\sum_{k=1}^{n} w(t_k,t)\log(A_k)}{\sum_{k=1}^{n} w(t_k,t)}\right) \quad w(t_k,t) = \frac{1}{\sigma\sqrt{2\pi}}\exp^{\frac{-(t_k-t)^2}{2\sigma^2}} \quad \bar{I}(t) = \frac{\sum_{k=1}^{n} w(t_k,t) I_k \circ A_k \circ \bar{A}(t)^{-1}}{\sum_{i=1}^{n} w(t_k,t)}$$

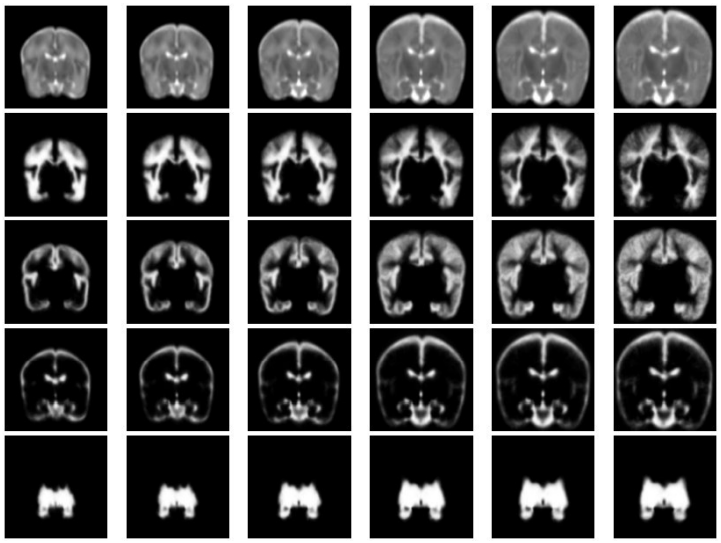
Average age-dependent probability maps for each tissue are estimated analogically from the segmentations of the original images.

SEGMENTATION OF TRAINING IMAGES

The following structures were used to create probabilistic atlases: Cerebro-spinal fluid (CSF), subcortical WM, cortical GM, subcortical GM, brainstem and cerebellum. The central brain structures (subcortical GM, brainstem and cerebellum) were segmented by atlas-based segmentation where an atlas is propagated to the training images using non-rigid registration [2]. We used manual segmentations of three reference subjects (31, 36 and 41 weeks GA) as deformable atlases and the training images were segmented using the atlas of the closest age. In contrast, the segmentation of cortical structures and CSF using atlas-based segmentation is problematic, as it is extremely difficult to establish correspondences across cortical surfaces. Therefore we segment the cortical region by fitting a mixture of Gaussians to the intensity histogram via Expectation-Maximization algorithm. The resulting segmentation in Fig. (b) shows considerable misclassifications due to the partial volume effect, resulting from the fact that intensities of voxels on the CSF-GM boundary are close to WM intensities. Similarly, the CSF-background boundary exhibits intensities of both GM and WM tissues. To correct the partial volume misclassifications, we reduce the prior probability of WM at each location, if both GM and CSF are present in the neighborhood (and similarly for CSF-background boundary), as suggested by Xue *et al.* [3]. We found that it is necessary to consider a 26-neighborhood to produce good results, as partial volume misclassifications can easily account for majority of voxels in a 6-neigbourhood of a voxel containing partial volume. An example of a segmentation using the above approach is shown in Fig. (c). Neonatal brains exhibit high variation of WM intensities, with darker corpus callosum, myelinated WM and "transitional fields" which are often misclassified as GM if only intensity information is used. Fortunately, these regions appear in the developing brain in predictable locations and we were therefore able to correct these misclassifications using atlas-based segmentations.



(a) (b) (c)



RESULTS

To create the 4D probabilistic atlas we used 153 T2-weighted fast spin echo images acquired on 3T Philips Intera system with MR sequence parameters TR = 1712ms, TE = 160ms, flip angle 90 deg, and voxel sizes 0.86×0.86×1mm. The age range at the time of scan was 26 to 47 weeks (GA), with mean and standard deviation of 36.5 ± 5 weeks. All subjects were born prematurely. The images were bias corrected by N3 method [4] where bias field was parameterized by a B-spline with a control point spacing of 15mm. The non-brain tissue was removed by propagating a mask with registration [1]. The resulting anatomical templates and probability maps for WM, cortical GM and subcortical GM are shown on the right.

CONCLUSION

In this paper we presented a 4D dynamic probabilistic atlas for neonatal brain between 29 and 44 weeks GA. The newly developed probabilistic atlas can serve as a basis for application of the methods such as those developed in [5] for segmentation of neonatal brain at term-equivalent age to neonatal brain scans at earlier time-points and possibly also fetal MRI.

REFERENCES

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