Multi-scaled image statistics with B-spline unbiased registration

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Introduction

Statistical analysis of imaging results is an essential step in abstracting the physiological information imbedded. However, in order to conduct statistical analysis on a pixel-by-pixel basis, spatial normalization through image registration is utilized. Currently, a pre-selected template is used as the target for all of the remaining data sets acquired from different subjects to be aligned to. This approach immediately raises two major questions: how to choose the template and how the final results will be affected by the choice of template. To overcome the subjectivity, Joshi et al have recently proposed an unbiased approach for template building [1]. In this approach, fluid dynamics based transformation [2] was utilized to drive the image deformation. However, as noted by Ashburner et al, fluid transformation is so flexible that it can warp any image to any other image. As a result, this high flexibility may remove the subtle structural differences between subjects, which some times are physiologically relevant information. Or in analysis of patient images, abnormal anatomies may be wiped out with this high flexibility approach. To better characterize the structural differences between subjects, we have modifies this technique by using B-spline models, which has the capability to adjust the flexibility of the transformation with its number of control points. Thus, group statistics can be obtained in multi-scales with different level of flexibility.

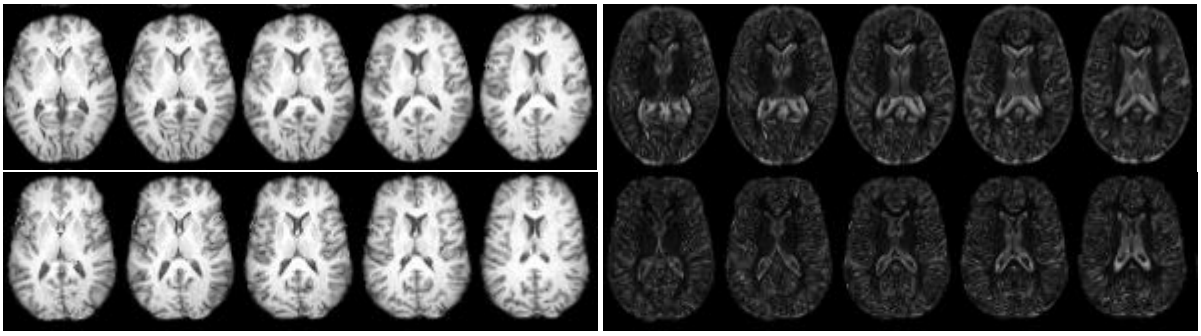
Materials and Methods

With the unbiased registration, the template is defined as the mean image (I_t) of all the data sets to be registered to. The mean image continues to be updated with the registration process. Image dissimilarity (C_I) is computed as the summation of the squared value between each data set with the mean image in both directions. C_c is to ensure the consistency of each forward and backward transformation pair ($M^i{}_f, M_b{}^i, i = 1...N$). The correct topology is preserved through the inclusion of C_T for all these transformations. Optimal transformation models $(M^1{}_f, M_b{}^1, ...M^N{}_f, M_b{}^N)^*$ can be obtained by minimizing a weighted sum of these cost terms. Finally, the B-spline model with different number of control points for unbiased registration achieves the multi-scaled group statistics (mean image and standard deviation map).

$$I_t(X_t) = \frac{1}{N}\sum_{i=1}^{N} I^i{}_s(M^i{}_b(X_t)) \qquad (M^1{}_f, M_b{}^1, ...M^N{}_f, M_b{}^N)^* = \text{argmin}(C_I + w_C C_c + w_t C_T)$$

Nine normal volunteers were recruited and a 3D MP-RAGE sequence was used to acquire T1 weighted images after obtaining written consent. The registration was initially performed with the 3D linear B-spline models with 2x2x2 control points, which is equivalent to tri-linear interpolation. In addition,, registration results were also obtained with 5x5x5 (piecewise tri-linear interpolation) control points to demonstrate the capability of generating multi-scaled group statistics for these 9 data sets.

Results



Upper panel shows the computed mean image (left) and the standard deviation (right) from these 9 data sets with the B-spline transformation model using 2x2x2 control points. The same results obtained from the models with 5x5x5 control points are given in lower panel. In both the mean images, the anatomical structures are well preserved without being blurred even with the tri-linear interpolation of 8 points. When comparing the SD maps, results obtained from 5x5x5 control points exhibit a much smaller SD when compared to that obtained using 2x2x2 control points. This is especially evident in ventricular regions.

Discussion

The proposed approach is an objective multi-scaled approach, allowing for pixel-by-pixel statistical comparisons across multiple sets of images. The technique is readily available for clinical applications and may offer a new means to establish templates free from biases of choosing the target. Furthermore, multi-scaled statistics could be utilized to reveal the variation in anatomy, which is not available in a single scale of flexibility.

References

[1] Joshi, et al. NeuroImage Aug. 2004. [2] Christensen, et al. IEEE-TMI Vol.5 1435-1447, 1996. [3] Ashbruner, et al. NeuroImage 9, 619-628, 1999.