Longitudinal Alignment of Brain Cortical Anatomy using Strain-Constrained MSM

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Introduction: The Multimodal Surface Matching (MSM) method for spherical cortical surface registration[1] offers significant flexibility with regards to the types of brain imaging data that can be used to drive alignment[23]. However, because of the use of a spherical projection step, the warps cannot be interpreted or compared. Further, the smoothness of the original MSM warp is suboptimal due to the restrictions placed by the optimisation. In this work we address both these points by presenting a new version of MSM that warps cortical anatomies in a biologically constrained way.

Method:

Multimodal Surface Matching (MSM):

MSM is a discrete multi-resolution spherical alignment approach that uses a series of low resolution control point grids (Fig. 2B, red) to constrain the deformation of each moving sphere **y** (Fig 2a). At each iteration each control point (p) is offered a finite choice of possible displacements (Fig 2B orange box). Each displacement is given a label (l_p) and the impact of moving subsets or cliques of points (c_1, c_2) is assessed by balancing a data similarity term $c(\mathbf{l}_{c1})$ with a regularisation penalty $V(\mathbf{l}_{c2})$ that encourages smooth warps

$$\min C(\mathbf{l}) = \sum_{c_1 \in C_D} c(\mathbf{l}_{c_1}) + \sum_{c_2 \in C_R} \lambda(V(\mathbf{l}_{c_2}) \quad \text{Eq. 1}$$

MSM has demonstrated great versatility having been used to align a wide variety of different types of surface features[123]. However, any interpretation of MSM warps is limited, as the expansion resulting from projection of cortical anatomy onto a sphere is not even across the surface and is sensitive to brain shape and size

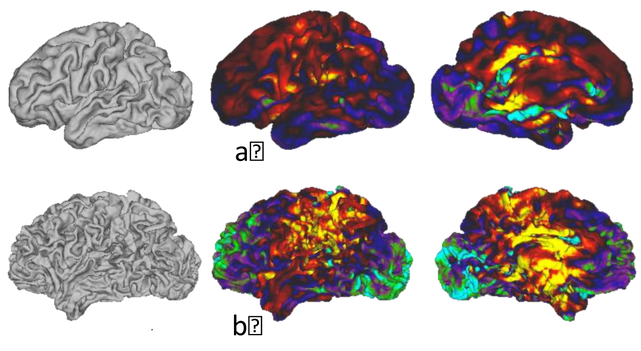


Fig 1. Metric distortions for the same subject show different patterns at two different time points a) 34 weeks PMA; b) 44 weeks PMA. Here metric distortions are measured as change in mesh face area

It is possible however to estimate an anatomical warp from MSM using the one-to-one vertex correspondence between each cortical surface and its respective sphere (Fig.2)

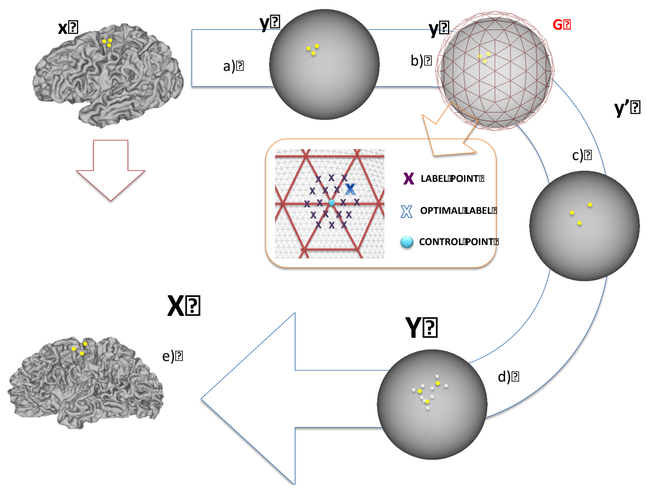


Fig 2. The anatomical surface of the moving mesh **x**, can be resampled onto the target anatomy **X** using correspondences found between the moving sphere **y'** and target sphere **Y.** Yellow dots show a triplet of points moving through the transformation: a) a triplet on **x** is also a triplet on **y**; b) The discrete optimisation offers a finite choice of possible displacements; c) triplet after choice of optimal displacement; d) Barycentric Resampling of points onto the moving sphere; Correspondences are learnt between **y'** and **Y** (white crosses) to allow barycentric d) barycentric weights are applied to target anatomy to generate a surface mesh with topology of **x** but shape of **X**

Anatomically constrained MSM (aMSM):

We therefore propose a new version of MSM that retains the simplicity and flexibility of the spherical framework but regularises the displacements of points on the sphere by taking into account the impact on the anatomical warp.

We take advantages of advances in discrete optimisation that allow for reduction of higher-order regularisation terms to pair-wise for solution for conventional pair-wise discrete solvers[4]. This allows us to apply a deformation strain-energy density penalty (W) inspired by[5]:

$$V_{STR}(l_p, l_q, l_r) := \gamma W^{\tau}_{pqr} = \gamma \frac{1}{2}(\mu(I_1^* - 3) + \kappa(J-1)^2)^{\tau}$$

$$I_1^* = I_1 I_3^{-1/3}$$

$$I_1 = trace(\mathbf{F}^T_{pqr}.\mathbf{F}_{pqr})$$

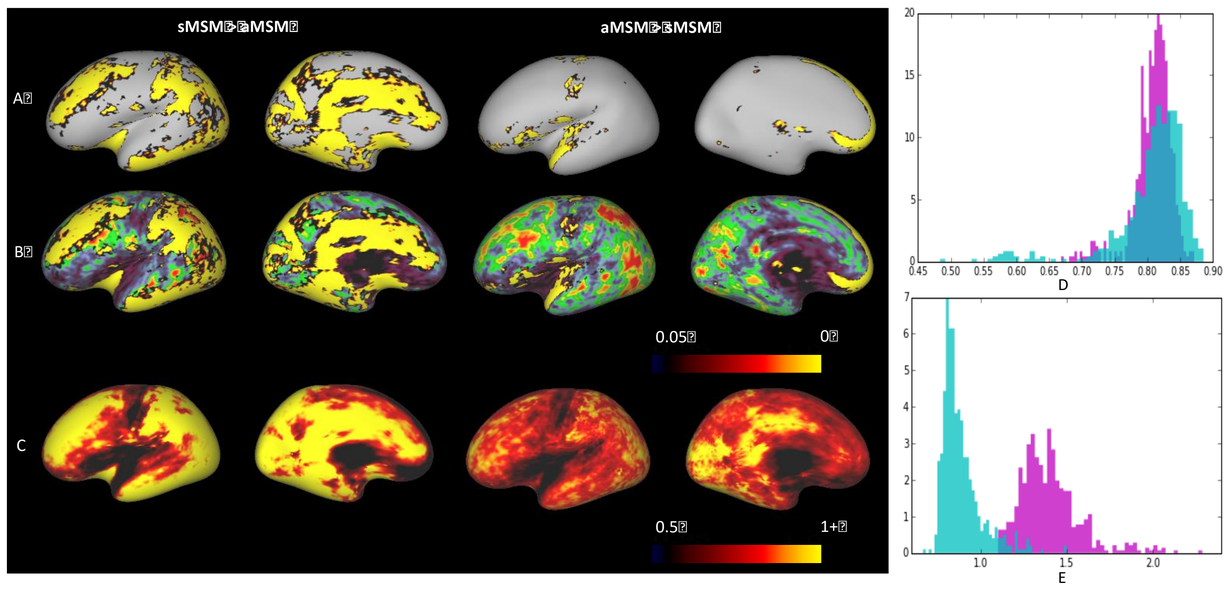
$$I_3 = J^2 = det(\mathbf{F}^T_{pqr}.\mathbf{F}_{pqr})$$

Here I^1 and I^3 are strain invariants estimated from affine transformations **F** for vertex triplets p,q,r on the anatomical mesh

Results:

The proposed anatomical registration framework has been tested for between subject longitudinal alignment of cortical folding patterns for 22 subjects at 38 weeks PMA to 27 subjects at 42 weeks PMA. All data has been collected as part of the developing Human Connectome Project[6].

Fig 3 compares the original spherical sMSM framework to the proposed aMSM. A) paired statistical significance tests performed with FSL's Randomise tool. These show a) areas where strain is significantly higher for sMSM relative to aMSM and vice versa. B) sMSM has significantly higher distortions in areas that overlap with areas of high folding variation (red = high variance across folding maps post registration) ; c) mean strain is significantly higher for sMSM(left) relative to aMSM (right); d) This is despite a slight increase in correlation of the sulcal depth maps after alignment (x axis correlation; y axis frequency;); e) Distribution of the 95th percentile of strain values across all registrations. aMSM (cyan) sMSM (magenta)



Conclusions:

Anatomically constrained MSM allows improved alignment with reduced distortions relative to spherical MSM. These improvements will allow us to build models of cortical development. In future the approach will be extended to alignment of function and cytoarchitecture.

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References: 1. E.C. Robinson et al. NeuroImage 2014. 2. R. Abdollahi NeuroImage 2014; 3. M.F Glasser et al Nature 2016; 4. H. Ishikawa CVPR 2014; 5. A.K. Knutsen J. Biomechanical Engineering 2010; 6 : http://www.developingconnectome.org/