

# Quantification of Fetal Cortical Folding using Slice-to-Volume Reconstructed MRI and FreeSurfer

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## Institutions:

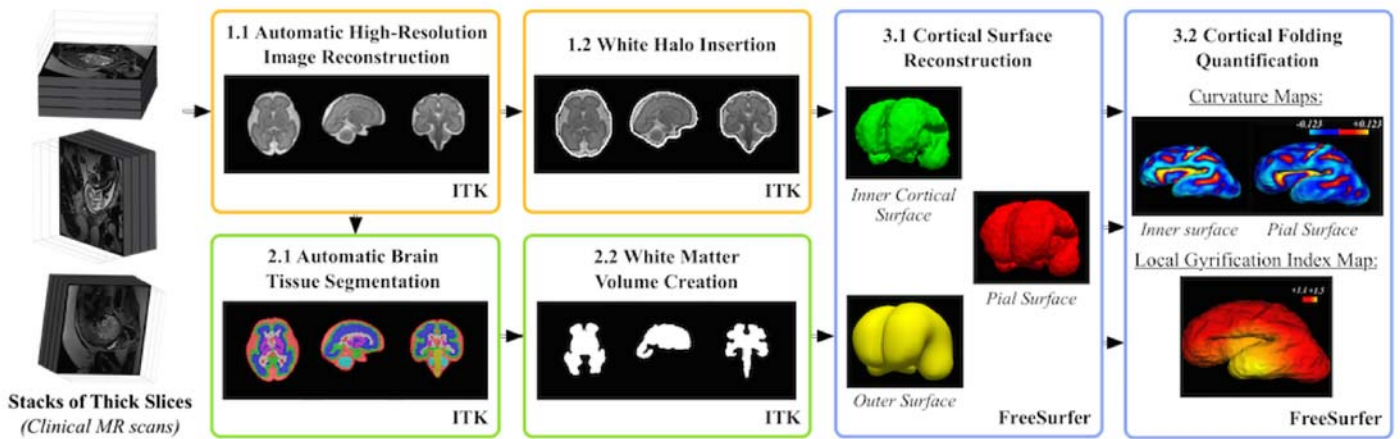
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## Introduction:

Recent advances in fetal T2w MRI and image analysis techniques offered new opportunities to analyze in vivo cortical folding, also known as gyrification, a good indicator of early brain maturation as it is one of the most dramatic structural changes happening during gestation. However, few studies have quantified the folding of the cerebral cortex in early development stage by developing new methods based either on spherical-mesh deformation [2012a, 2014] or using a topology-preserving marching cubes [2012b]. In this work, we explore for the first time the use FreeSurfer (<http://surfer.nmr.mgh.harvard.edu/>), an open-source brain imaging software, widely adopted in the neuroscientist community for analysis and visualization of adult brain MRI, for fetal brain analysis. Our approach aims to take advantage of the existing set of automated tools provided of the adult brain's cortical surface to 1) extract fetal cortical surfaces, 2) to compute brain maturation indicators, and 3) to render the results.

## Methods:

Our image processing framework (Fig. 1) consists of: 1) automatic reconstruction of a HR motion-corrected image where fetal brain is isolated (1.1 and 1.2 in Fig. 1), 2) automatic estimation of the white matter (WM) volume (2.1 and 2.2 in Fig. 1), and 3) automatic extraction of the cortical surface (3.1 in Fig. 1) and computation of folding measures (3.2 in Fig. 1). The HR image is obtained using an automatic image reconstruction pipeline [2015a,2015b]. Then, a white halo (width of 2 voxels) is added around the brain to create the initial image used by FreeSurfer (referred as T1.mgz). Inserting the halo reduces the risk of infinite evolution of the pial surface as the algorithm originally designed for adult brain, is looking for a bright region as a stopping criteria (not verified in fetal MRI). Then, 7 classes of tissue are segmented in the HR image using a multi-atlas multi-shape segmentation method [2012c]. Then, the initial WM volume used by FreeSurfer is created (referred as wm.mgz), by combining all tissue labels lying inside it. Finally, we use only the parts of the FreeSurfer recon-all pipeline that extract the cortical surfaces and compute the folding measures (Fig. 2): original surface triangle-based tessellation, removing topological defects, smoothing the surface edges, spherical-mesh deformation to obtain the pial surface, and computing at each point of the inner and pial surfaces the curvature and the local gyrification index.



·Figure 1: Image processing pipeline for in-vivo fetal cortical folding quantification taking advantage of the set of tools provided by FreeSurfer.

```

## Go into the Freesurfer 'subjects' directory
cd $SUBJECTS_DIR

## Creation of a new subject directory (XXX)
mksubjdirs XXX

#Go into the subject directory
cp XXX

## Copy your high-resolution reconstructed image and the white matter (WM) volume image
estimated into the 'orig' folder
cp "YOUR_HR_IMAGE_FULL_PATH" "orig/HR_halo_image.nii"
cp "YOUR_WHITE_MATTER_VOLUME_IMAGE_FULL_PATH" "orig/wm.nii"

## Convert images in the Freesurfer 'MGZ' format
## Flag 'cm' is very important for the WM volume image; if not set, mri_fill routine fails.
mri_convert orig/HR_halo_image.nii T1.mgz
mri_convert -cm orig/wm.nii wm.mgz

## Prepare the input images required by the Freesurfer routines (brain.mgz, norm.mgz,
brain.finalsurfs.mgz)
cp T1.mgz brain.mgz
cp T1.mgz norm.mgz
cp brain.mgz brain.finalsurfs.mgz

## Create the subcortical mass from which the orig surface is created. You need here to provide
the voxels coordinates of both the corpus callosum and the pons. They can be obtained using
"tkmedit" program.
mri_fill -PV 128 132 128 -CV 128 110 138 wm.mgz filled.mgz

## Normalize the original HR image
mri_normalize T1.mgz brain.mgz

## Estimate inner (pial) and outer cortical surface and compute average curvature
recon-all -tessellate -smooth1 -inflate1 -qsphere -fix -noaseg -white -smooth2 -inflate2 -sphere -
surfreg -jacobian_white -avgcurv -s XXX

## Create cortical surfaces
mris_make_surfaces -white NOWRITE -mgz -T1 brain -noaparcs -noaseg XXX lh
mris_make_surfaces -white NOWRITE -mgz -T1 brain -noaparcs -noaseg XXX rh

## Compute global/local gyrification indexes (GI/LGI)
recon-all -no-isrunning -s XXX -localGI

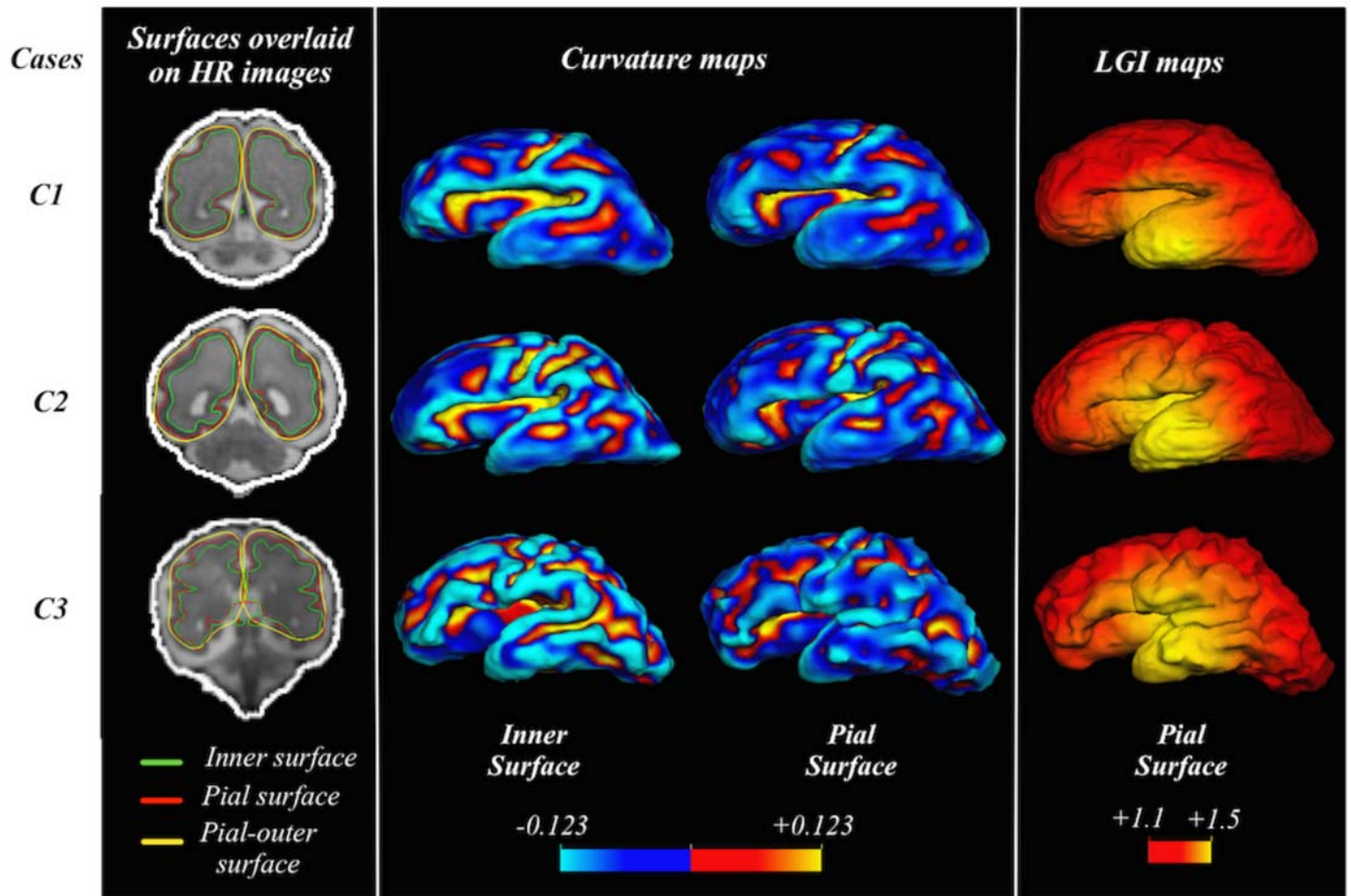
```

·Figure 2: Generic script that uses FreeSurfer to extract cortical surfaces and quantify cortical folding.

## Results:

We process 3 fetuses with normal brain, denoted as C1, C2 and C3. Acquisitions were performed at the Boston Children's Hospital respectively during the 27th (C1), the 30th (C2) and the 32th week of gestation. A Siemens Skyra 3T MR scanner with HASTE sequences

was used to acquire 5 (C1), 6 (C2) and 6 (C3) 3D orthogonal stacks of thick 2D T2w MR images (1.2x1.2x2mm<sup>3</sup>), with at least 1 stack per anatomical direction. Fig. 3 presents quantitative results, with extracted surfaces, curvature and local gyrification measures. Manual correction of the original WM volume were not performed in this study but would be required for an accurate quantification, which was beyond the scope of this work.



·Figure 3: Reconstructed cortical surfaces from fetal MRI and resulting quantitative maps of cortical folding for cases C1, C2 and C3 diagnosed with normal brains.

**Conclusions:**

We have shown for the first time there is a great promise in using FreeSurfer to extract and analyze fetal cortical surfaces from in-vivo MR images. However, there still exist few limitations. The surface extraction algorithm is based on image contrast assumptions, which differ between adult T1w and fetal T2w MRI. Thus, we can observe deformation towards the pial surface can fail in some areas.

**Imaging Methods:**

Anatomical MRI <sup>1</sup>

**Informatics:**

Workflows <sup>2</sup>

**Poster Session:**

Poster Session - Monday

**Keywords:**

Other - Fetal MRI, Cortical Folding Quantification, FreeSurfer

<sup>1</sup><sup>2</sup>Indicates the priority used for review

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Yes

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Not applicable

**Please indicate which methods were used in your research:**

Structural MRI

**For human MRI, what field strength scanner do you use?**

3.0T

**Which processing packages did you use for your study?**

Free Surfer

**Provide references in author date format**

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