ADAPTIVE SCAN STRATEGIES FOR FETAL MRI IMAGING USING SLICE TO VOLUME TECHNIQUES

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ABSTRACT

In this paper several novel methods to account for fetal movements during fetal Magnetic Resonance Imaging (fetal MRI) are explored. We show how slice-to-volume reconstruction methods can be used to account for motion adaptively during the scan. Three candidate methods are tested for their feasibility and integrated into a computer simulation of fetal MRI. The first alters the main orientation of the stacks used for reconstruction, the second stops if too much motion occurs during slice acquisition and the third steers the orientation of each slice individually. Reconstruction informed adaptive scanning can provide a peak signal-to-noise ratio (PSNR) improvement of up to 2 dB after only two stacks of scanned slices and is more efficient with respect to the uncertainty of the final reconstruction.

1. INTRODUCTION

Fetal Magnetic Resonance Imaging (MRI) is increasingly used as a complementary diagnostic tool to sonography. It has been shown to be a useful tool for accurate prenatal diagnostics and to assess fetal development because of the increased field of view and contrast compared to ultrasound imaging. Currently, mainly the brain and the whole fetus appearance are qualitatively examined using MRI in clinical practice [1, 2]. Fetal motion and its unpredictable nature put high demand on radiologists and make an automatic evaluation of the scan challenging. The resulting images are usually corrupted by motion artifacts and often several scans have to be performed to acquire clinically useful data.

Malamateniou *et. al.* [3] classified motion compensation techniques for fetal and neonatal MRI into prospective and retrospective methods in addition to approaches to minimize motion artifacts by using fast imaging sequences. Prospective methods are usually navigator-based [4] or self-navigated sequences [5]. Navigators have been applied in the fetal brain. However, it increases the scanning time from $< 30s$ to approximately seven minutes and it is not always robust against extensive fetal movements [6]. Additionally, positioning of the navigator requires a pilot scan and at least one test scan, which further increases the total scanning time. Motion-robust spiral sequences [5] are useful for correcting in-plane motion, however, they often fail in cases of through plane motion [7] and many of those sequences take significantly longer than conventional scans.

Retrospective methods are applied after highly oversampled image data has been acquired. They have the disadvantage that they cannot fully correct through-plane motion because of the spin history effect [3] and that each step of the algorithms may require several hours to reconstruct the final volume. However, because of a short scan time and their non time critical post processing, they are currently popular for fetal image analysis. The most promising approaches use a combination of 2D/3D registration and robust statistics to exclude highly corrupted slices with regularized super-resolution [8, 9].

2. METHOD

It is possible to reconstruct a high resolution image X from a number of motion corrupted stacks of slice images denoted by $I_i, i \in 1...n$ using registration based super-resolution [9]. Therefore, the stacks are first roughly rigidly registered to each other in 3D and during several motion correction iterations the individual slices are continuously rigidly registered to the current reconstruction of X and reintegrated into X using iterative gradient decent super-resolution with robust statistics to exclude mis-registered slices. Hence, the updating equation for the super-resolution of a point x_i in volume X can be defined similar to [9] as

$$x_i^{(n+1)} = x_i^n + \alpha \sum_{jk} m_{ij}^k e_{jk}^n + \alpha\lambda \frac{\partial}{\partial x_i} R(X), \qquad (1)$$

where $m_{ij}^k \in 1...N$ defines the relationship between acquired slices and the reconstructed volume as spatially aligned discretized point spread function (PSF) for the acquisition of a voxel y_{jk} from volume X and e_{jk}^n the error between the acquired slices and an intensity corrected simulated slice from the current reconstructed volume X. The regularization term $\alpha\lambda \frac{\partial}{\partial x_i} R(X)$ can be implemented as edge preserving smoothing following each super-resolution step. Robust statistics is implemented within an expectation maximization (EM) framework, which weights or excludes each voxel in a

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slice according to its registration quality and difference to an according simulated voxel in a slice. To achieve a physical simulation of the image acquisition and a proper integration into X, slice voxels are modeled as discretized PSFs, which can be approximated by a full width at half maximum Gaussian function for computational efficiency, scaled by the dimensions of the voxels [10].

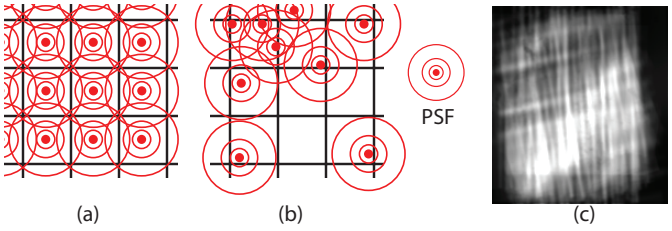


Fig. 1. 2D illustration of (a) regular sampling with approximate psf shown (red) of reconstructed voxels (black), (b) actual occurring sampling due to fetal motion, and (c) a slice from a real reconstruction showing the sampling density (the brighter the more samples).

The acquisition of many stacks, the displacement and rotation of the single slices because of fetal movements and their registration and the sampling of the PSF lead to an uneven quality reconstruction of X, which is illustrated in Fig. 1. Currently, the stacks are scanned parallel and perpendicular to the fetus' main axis, hoping, that the slices will cover all voxels of the target volume equally. However, fetal movements make this assumption very unlikely so that it is necessary to acquire multiple stacks of slices to ensure samples are sufficiently dense everywhere in the target anatomy. Therefore, we propose to determine the next scan orientation according to the current sampling density $\rho(X)$ based on an intermediate reconstruction for X. $\rho(X)$ can be calculated by $\rho_i = \sum_{jk} m_{ij}^k$, which encodes how often each voxel of X is visited during the reconstruction process. In this work we aim for $Var(\rho(X)) = 0$. However, this is not realistic because newly scanned slices will always add information to already sufficiently sampled voxels. Therefore, we try to maximize the minimally occurring sampling density, *i.e.*, we scan until $min(\rho(X)) > t$, and until we can be sure that every voxel in the reconstructed volume has been sampled at least t times. The main idea to achieve this is to align new scans along less sampled areas. After each stack acquisition, the registration of its slices, and their integration into X, the optimal next orientation can be defined by a plane that is as close as possible to a set of 3D points $(p_0, ..., p_n)$ within a region of interest (ROI) defining the least densely sampled areas. Sorting the coordinates according to their sampling density in ascending order yields a vector, whose 3D coordinates of the m lowest elements can be used to define the plane passing through the centroid c and normal vector $\vec{n}$, hence

$$\min_{c,\|\vec{n}\|=1} \sum_{i=0}^{m} ((p_i - c)^T \vec{n})^2. \qquad (2)$$

Solving this for c gives $c = \frac{1}{m}\sum_{i=0}^{m} p_i$ and allows to define the $m \times 3$ matrix $A = [p_1 - c, ..., p_n - c]$ and to change Eq. 2 to $\min_{\|\vec{n}\|=1} \|A^T n\|_2^2$. Using the singular value decomposition $A = USV^T$ results the plane normal $\vec{n}$ in the third row of U and the plane spanning vectors $\vec{v_1}$ and $\vec{v_2}$ in rows one and two, which can be used to define the next optimal scan orientation with the transformation matrix T_{new}.

Not all scanners and scan sequences allow to apply the above scheme in an optimal way, i.e., to determine T_{new} for each slice individually. Therefore, we propose three variations of our approach, which require gradually more integration effort into existing fetal MRI sequences. The region of interest for the reconstruction and optimal coverage can be defined from the first stack by using one of the currently available automatic reconstruction methods for, *e.g.*, the fetal brain [11].

The *'reorient-stack'* method: This approach is the most direct and easiest to implement application of our method and aims for finding an optimal orientation for subsequent stacks of slices. This means, that the basic *volumetric* acquisition of parallel slices per stack can remain untouched. The difference to the state-of-the-art scanning approach is that the acquired stacks are unlikely to be orthogonal for optimal sampling. An overview is given in Fig. 2.

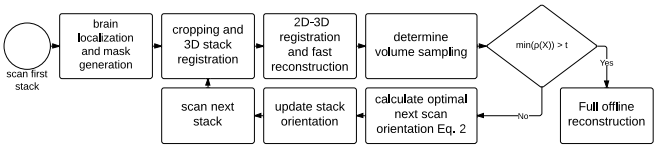


Fig. 2. Overview over the *'reorient-stack'* approach.

This approach can be used to *infuse* stacks gradually into X. Therefore, we compute for the first stack $x_i = \sum_{jk} m_{ij}^k y_{jk}$, register the slices of the first stack to this simple Gaussian weighted reconstruction and perform a few (usually 5–10) steps of Equation 1. Subsequently, the next stack can be scanned according to the orientation given by Equation 2. The new slices can then be registered to the current X and updated accordingly. This process is repeated until a predefined sampling quality threshold t has been reached, hence, $min(\rho(X)) < t$.

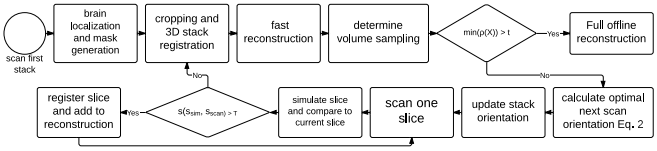


Fig. 3. Overview over the *'stop-if-motion'* approach.

The *'stop-if-motion'* method: The idea of this approach is to stop the scan and to calculate a new scan orientation according to Eq. 2 as soon as a scanned and registered slice is significantly different from an expected, simulated slice,

sampled from the so far available reconstructed volume X. Therefore, the scan orientation is reevaluated if the similarity $s(s_{sim}, s_{scan})$ is smaller than a predefined threshold T. We use *normalized cross correlation* as similarity measure and determined experimentally $T = 0.4$. An overview over this approach is given in Fig. 3.

The *'track-slices'* method: This approach tries to adjust the orientation of each new slice according to the motion trajectory of the fetus, which can be derived from the previous slice-to-volume registration results. We estimate the likely present motion trajectory from the last n orientation matrices of the most recently scanned slices and interpolate the most likely transformation θ of the fetus for the next stack. In practice $n = 3$ has been shown a good trade off between elapsed time and the accuracy of the actual fetal position. This process is continued until as many slices have been scanned as during the acquisition of the very first stack or if the new slice is fully outside the region of interest (*stack full* condition).

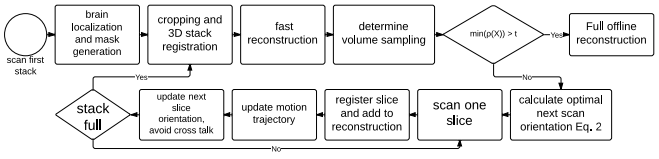


Fig. 4. Overview over the *'track-slices'* approach.

However, scanning individually oriented slices means that it is likely that the new slice will intersect the previous scanned locations and that the signal intensity is influenced by remaining magnetization for the overlapping voxels (cross talk). Therefore, we take a typical T_1 relaxation time for fetal brain of 1.5s for 1.5T and 2.5s for 3.0T [12] into account and keep track of the by new slices induced time t dependent magnetization with e^{-t/T_1} in a separate magnetization volume. This assumes all longitudinal magnetization is destroyed when a slice is excited, which is very likely to be true for single-shot fast spin echo (ssFSE) as we use it in practice. We then optimize and re-orient θ another time so that the remaining magnetization values in the anticipated slice are minimized and temporally adjacent slices overlap as little as possible. An overview over this approach is given in Fig. 4.

3. EVALUATION AND RESULTS

Scanner simulation: Because we aim for exploring of the potential benefits of the approaches prior to seeking ethical approval and reprogramming the scanner and to make our results comparable with known motion trajectories, we have build a computer simulation of a scanner and use previously reconstructed fetal brain scans as test data. From fetal cine sequences [13] we know that fetuses move their heads randomly in any direction combined with a small omni-directional jitter caused by the baby and by maternal movements (breathing, digestive movements, etc.). We have simulated these random movements and virtually move and rotate the available fetal reconstruction according to this motion trajectory. We sample it similarly to a real scanner (approximately 850 ms per slice).

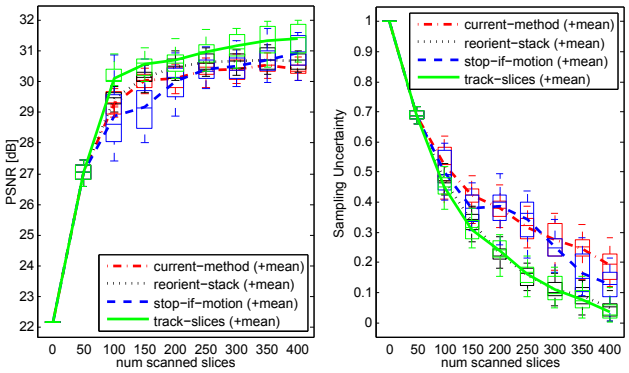
Results: We have implemented our framework on an Intel Xeon E5-2643 system with 16 GB RAM. To evaluate the candidate methods we use different motion trajectories and compare a full reconstruction to the state-of-the-art sampling method every time a stack of images is ready. Therefore, we use the difference of the peak signal-to-noise ratio ($\Delta PSNR$) between the currently in practice used scan method and the proposed approaches. Another valuable information is to test how many slices are required for each approach until a minimum sampling density per voxel is reached and how the non regular sampling decreases with every new slice. Therefore, we define the *sampling uncertainty* as the number of voxels that have no direct correspondence to an actually scanned voxel divided by the overall number of voxels within the region of interest.

We compare the three candidate methods (*reorient-stack*, *stop-if-motion*, and *track-slices*) to the currently used scanning approach (*current-method*), i.e. acquiring stacks orthogonal and parallel to the fetal main axis, and show their performance in Fig. 5. We performed experiments on ten different random motion trajectories of two different fetal brain reconstructions of gestational age of 24 and 37 weeks. The motion includes random small jitter and a turn (i.e. rotation) with varying speed in a random direction for overall up to 90° but not faster than 5° per second. A small random translation component is added to the motion trajectory, which is overall less than 2 cm for the whole simulation. On average we simulated approximately 50 slices per stack for the *current-method* and the *reorient-stack* method. The *stop-if-motion* and *track-slices* methods have been evaluated every 50 slices. Fig. 5 compares the performance of the these approaches.

Runtime: This is a crucial factor for certain parts of the methods because scan time is limited. Registration and determining a new scan orientation are the non-neglectable parts of the evaluated methods. One slice to volume registration needs to take less than $0.2s$ for a success of the *track-slices* approach. Calculating a new optimal scan orientation between subsequent stacks of images takes on average less than $0.2s$, which is together with the time for each intermediate reconstruction the main overhead for the other methods.

4. DISCUSSION AND CONCLUSION

In this paper we have explored the feasibility and potential benefits of three different methods to improve pre-natal MRI when fetal motion corrupts the scan. While equalizing the sampling density leads to minor improvements of the final result, accounting for motion leads to better scan results in a shorter time when considering a global image quality measurement. It is likely that a local measure of the PSNR – i.e., worst PSNR over a region of interest swept over the full image volume – reveals higher benefits of reconstruction informed adaptive scanning. Currently, the adaptive approaches are



(a) (b)

Fig. 5. The tested approaches are compared in terms of improving reconstruction quality per added stack $PSNR$ (a) and in terms of *sampling uncertainty* (b). While the *track-slices* method allows a better reconstruction result, it also shows a higher variance of the *sampling uncertainty* than minimizing only this uncertainty as done with the *reorient-stack* method. The *stop-if-motion* method shows a high variance in both graphs, which is due to the missing data if the fetus moves too much.

limited by the speed and extent of the fetal motion and their computational overhead. For very quick and wide movements the investigated approaches show a similar performance as the standard approach. It is possible to use all three methods with a real scanner, however, the efforts for sequence adaption and integration increase for each of the three. Furthermore, a fast implementation of the motion compensation and super-resolution reconstruction is required. The in this paper explored methods show evidence that fast adaptive scanning approaches have great potential to improve the final scan result or to reduce the required scan time of fetal MRI in the future.

5. REFERENCES

[1] M. Rutherford, S. Jiang, J. Allsop, L. Perkins, L. Srinivasan, T. Hayat, S. Kumar, and J. Hajnal, "MR imaging methods for assessing fetal brain development," *Dev Neurobiol*, vol. 68, no. 6, pp. 700–11, 2008.

[2] C. Limperopoulos and C. Clouchoux, "Advancing fetal brain MRI: targets for the future," *Seminars in perinatology*, vol. 33, no. 4, pp. 289–298, Aug. 2009.

[3] C Malamateniou, S J Malik, S J Counsell, J M Allsop, A K McGuinness, T Hayat, K Broadhouse, R G Nunes, A M Ederies, J V Hajnal, and M A Rutherford, "Motion-Compensation Techniques in Neonatal and Fetal MR Imaging.," *AJNR American journal of neuroradiology*, vol. 6, pp. 1124–36, May 2012.

[4] N. White, C. Roddey, A. Shankaranarayanan, E. Han, D. Rettmann, J. Santos, J. Kuperman, and A. Dale, "PROMO: Real-time prospective motion correction in MRI using image-based tracking," *MR in Medicine*, vol. 63, no. 1, pp. 91–105, 2010.

[5] J. G. Pipe, "Motion correction with PROPELLER MRI: Application to head motion and free-breathing cardiac imaging," *Magn. Reson. Med.*, vol. 42, no. 5, pp. 963–969, 1999.

[6] H Bonel, K A Frei, L Raio, M Meyer-Wittkopf, L Remonda, and R Wiest, "Prospective navigator-echo-based real-time triggering of fetal head movement for the reduction of artifacts.," *European radiology*, vol. 18, no. 4, pp. 822–829, Apr. 2008.

[7] K. P. Forbes, J. G. Pipe, J. P. Karis, V. Farthing, and J. E. Heiserman, "Brain Imaging in the Unsedated Pediatric Patient: Comparison of Periodically Rotated Overlapping Parallel Lines with Enhanced Reconstruction and Single-Shot Fast Spin-Echo Sequences," *American Journal of Neuroradiology*, vol. 24, no. 5, pp. 794–798, 2003.

[8] A. Gholipour, J. A. Estroff, C. E. Barnewolt, S. A. Connolly, and S. K. Warfield, "Fetal brain volumetry through MRI volumetric reconstruction and segmentation," *IJ Computer Assisted Radiology and Surgery*, vol. 6, no. 3, pp. 329–339, 2011.

[9] M. Kuklisova-Murgasova, G. Quaghebeur, M. A. Rutherford, J. V. Hajnal, and J. A. Schnabel, "Reconstruction of fetal brain MRI with intensity matching and complete outlier removal," *Medical Image Analysis*, vol. 16, no. 8, pp. 1550–1564, 2012.

[10] S. Jiang, H. Xue, A. Glover, M. Rutherford, D. Rueckert, and J. V. Hajnal, "MRI of moving subjects using multislice snapshot images with volume reconstruction (SVR): application to fetal, neonatal, and adult brain studies.," *Trans. IEEE medical imaging*, vol. 26, no. 7, pp. 967–980, July 2007.

[11] K. Keraudren, V. Kyriakopoulou, M. Rutherford, J.V. Hajnal, and D. Rueckert, "Localisation of the Brain in Fetal MRI Using Bundled SIFT Features," in *MICCAI'13*. 2013, LNCS, pp. 582–589, Springer.

[12] L.-A. Williams, N. Gelman, P. A. Picot, D. S. Lee, J. R. Ewing, V. K. Han, and R. T. Thompson, "Neonatal brain: regional variability of in vivo MR imaging relaxation rates at 3.0 T–initial experience.," *Radiology*, vol. 235, no. 2, pp. 595–603, 2005.

[13] T. T. A. Hayat, A. Nihat, M. Martinez-Biarge, A. McGuinness, J. M. Allsop, J. V. Hajnal, and M. A. Rutherford, "Optimization and initial experience of a multisection balanced steady-state free precession cine sequence for the assessment of fetal behavior in utero.," *AJNR Am J Neuroradiol*, vol. 32, no. 2, pp. 331–8, 2011.