AUTOMATIC RESPIRATORY SELF-NAVIGATION PROCESSING (ASAP) FOR CORONARY MRA USING PRINCIPAL COMPONENT ANALYSIS

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Target Audience: Researchers developing self-navigation techniques for coronary MRA and other MR applications.

Purpose: Respiratory self-navigation (SN) is an alternative technique to the conventional diaphragm navigator (NAV) to detect respiratory motion in coronary MRA (CMRA) [1]. Compared with NAV, SN does not need to be set up and is capable of directly detecting superior-inferior (SI) translational motion of the heart. However, the SN readout, transformed into image space, is essentially a projection of the imaging volume onto the SI axis. Hence, it usually lacks outstanding features, such as the lung-liver interface in NAV, to allow robust and automatic motion detection. Previous methods include center-of-mass (COM) [1] and cross-correlation (CC) based methods [2]. COM is often inaccurate and unreliable, and CC usually relies on the manual selection of part of the projection profile as a template, requiring user intervention, although an automatic method has been recently proposed [3]. In this work we propose an alternative strategy for automatic template selection based on principal component analysis (PCA) of the SN profiles. The sliding CC method is subsequently used to determine the translation for each profile, defined as the relative shift between the template and the projection profile that yields the maximum CC value.

Methods: The M SN profiles with a base resolution of N can be regarded as M vectors in $\mathbb{R}^N$. Therefore, the first component in the PCA of the M vectors represents the coefficients of the linear combination of the pixels that yields the largest variance across the different M SN profiles. In other words, the larger the coefficient, the more likely the corresponding pixel being part of the underlying moving structure, in this case, the heart. Therefore, simple thresholding on the coefficients creates a mask which contains the relevant pixels that make up the moving structure, defined as the template to be used subsequently in the sliding CC processing. Numerical simulation is performed in MATLAB (The Mathworks, Natick, MA) with a 3D Shepp-Logan numerical phantom and random Gaussian noise added into the projection profile (peak SNR = 100). For further validation, the proposed method is also tested on five in vivo CMRA datasets obtained using a self-navigated 3D radial bSSFP sequence on a 1.5T clinical scanner (MAGNETOM Avanto, Siemens AG Healthcare, Erlangen, Germany) [4]. The detected motion using the proposed method is compared with the true motion in simulation and those using manual template selection for the in vivo datasets by calculating correlation and normalized root mean error (NMSE). The motion information is subsequently used for SI translational motion correction by phase modulation in k-space. The chest coil element is used for signal reception to maximize the sensitivity to heart region.

Results: In the simulation, the detected translational motion matches exactly with the true motion with correlation = 0.9998 and NMSE = 0.0079. For the in vivo cases, between the motion detected by the proposed method and by manual template selection, correlation is 0.9730±0.0190, and NMSE is 0.07476±0.04304. Visually, the respiratory motion detected by the proposed method also matches well with the SN profiles, shown in Fig. 1(a). The subsequent translational motion correction using this information results in better coronary artery visualization compared with uncorrected image, as shown in Fig. 2.

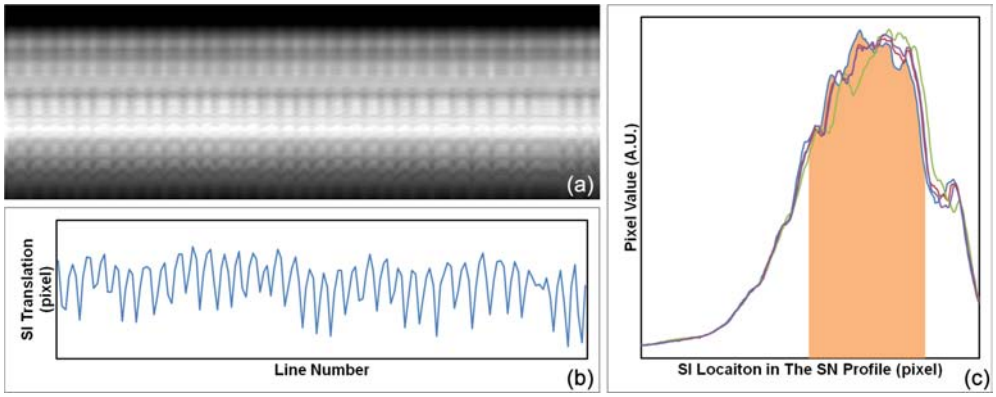

Figure 1: In vivo results: (a) acquired SN profiles; (b) detected translational motion of the heart; (c) different SN profiles and the calculated template mask (in orange);

Discussion and Conclusion: We have demonstrated a novel automatic algorithm based on PCA and CC to detect translational motion from respiratory self-navigation projections without user intervention. Promising results are shown in both simulation and in vivo datasets. The detected motion can be used to directly correct for translational motion and/or for data binning for image-based motion correction [4]. Further investigation is needed to test the robustness and accuracy of the proposed method. Upon further validation, the proposed method will improve the reliability of free-breathing whole-heart CMRA where consistent respiratory motion correction plays a key role in patient studies. Also, it is desirable to extend the proposed method for other applications, such as abdominal imaging, and cardiac and respiratory self-navigated cine MRI.

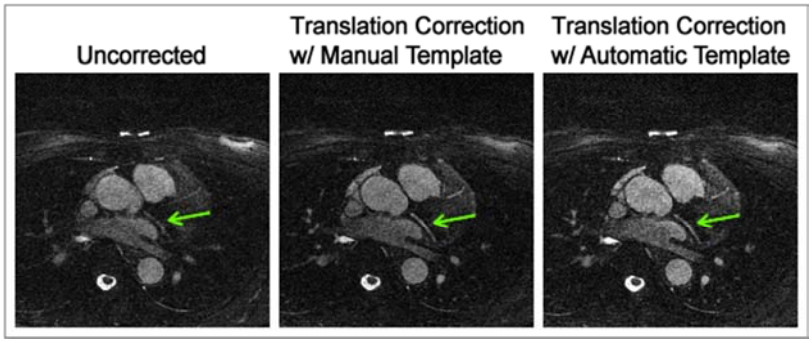

Figure 2: SI translation correction with motion detected with manual template selection and the proposed method. Similar improvements in image quality can be observed.

References: [1]Stehning et al MRM 2005;54:476 [2]Lai et al JMRI 2008;28:612 [3]Piccini et al MRM 2012;68:571 [4]Pang et al ISMRM 20(2012)

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