Bias Correction for Improved Segmentation and Background Parenchymal Enhancement Calculation in Multi-Center Breast MRI Trials

Alex A Nguyen[1], Fredrik Strand[1,2], Nola M Hylton[1], and David C Newitt[1]

[1]Department of Radiology and Biomedical Imaging, University of California San Francisco, San Francisco, CA, United States, [2]Department of Oncology and Pathology, Karolinska Institutet, Stockholm, Sweden

Introduction

Dynamic contrast enhanced MR imaging (DCE-MRI) provides measurements reflecting the kinetics of tissue enhancement, which can be used to assess breast cancer risk.[1] In particular, background parenchymal enhancement (BPE) observed in breast fibroglandular tissue (FGT) has been shown to be associated with breast cancer risk as an imaging biomarker.[2,3] However, accurate FGT segmentation is a challenge when bias field inhomogeneity is present, especially in multi-center studies. For this retrospective study we compared a semi-automatic segmentation method with and without bias correction (BC) to a semi-manual method performed by a radiologist as our reference standard. We analyzed the accuracy and improvement of bias correction within a neoadjuvant treatment cohort in order to validate a more accurate response evaluation.

Methods

A cohort of 237 women undergoing MRI during neoadjuvant chemotherapy (NAC) treatment were scanned at 21 different centers on 1.5T and 3T scanners from 3 manufacturers. 237 DCE-MRI studies conducted before NAC (pre-treatment) and 213 studies after 12 weeks of taxane-based treatment (inter-regimen) were analyzed. We applied an in-house algorithm for semi-automatic segmentation using fuzzy c-means (FCM) clustering to identify FGT.[4] For semi-manual segmentation, a radiologist with two years of experience in breast MRI manually placed a mask around the parenchymal tissue and applied FCM clustering with fine tuning. All segmentations were performed on a single axial slice located at the nipple position of the contralateral breast. We applied the N4ITK algorithm to correct for the field inhomogeneity.[5] We calculated BPE as $(S_1\text{-}S_0)/S_0$, where S_0 is the pre-contrast signal intensity and S_1 is the early post-contrast signal intensity. Mean BPE was calculated to assess the segmentation agreement between methods. Pearson's linear correlation coefficient was calculated to compare the improvement gain of bias correction for BPE quantification. The Sørensen-Dice similarity coefficient was calculated to compare the accuracy of segmentation methods with regards to our reference standard.

Results

There was a 50% bias correction success rate at both pre-treatment and inter-regimen (119/237 cases and 107/213 cases, respectively). For successful cases, the Pearson's linear correlation coefficient, r, improved by 0.02 at pre-treatment and 0.04 at inter-regimen for mean BPE, $p<0.001$. With bias correction, half of the semi-automatic cases showed a higher agreement with the results from semi-manual method. Figure 1 shows a visual example where bias correction improved the semi-automatic segmentation method. The original image shows a bias field near the nipple and after bias correction, the semi-automatic segmentation included more FGT further away.

Conclusion

Use of bias correction before quantitative image analysis can effectively improve BPE quantification and reduce the overall variance. FCM clustering is not robust enough to account for bias field inhomogeneity and this was observed in many cases. For the cases where bias correction aided in providing more accurate segmentation and therefore more accurate BPE measurements, this preprocessing step allows measured BPE to be a better biomarker for assessing breast cancer risk. Future research will include optimizing the bias correction algorithm for breast MRIs and exploring machine learning techniques for more robust segmentation and reducing time for processing large datasets.

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References

1. Dontchos BN, Rahbar H, Partridge SC, Korde LA, Lam DL, Scheel JR, Peacock S, and Lehman CD. Are Qualitative Assessments of Background Parenchymal Enhancement, Amount of Fibroglandular Tissue on MR Images, and Mammographic Density Associated with Breast Cancer Risk? Radiology. 2015; 276(2), 371-380.

2. King V, Brooks JD, Bernstein JL, Reiner AS, Pike MC, Morris EA. Background Parenchymal Enhancement at Breast MR Imaging and Breast Cancer Risk. Radiology. 2011; 260(1), 50-60.

3. Chen JH, Yu HJ, Hsu C, Mehta RS, Carpenter PM, Su MY. Background Parenchymal Enhancement of the Contralateral Normal Breast: Association with Tumor Response in Breast Cancer Patients Receiving Neoadjuvant Chemotherapy. Translational oncology 2015; 8:204-9.

4. Klifa C, Carballido-Gamio J, Wilmes L, Laprie A, Lobo C, Demicco E, Watkins M, Shepherd J, Gibbs J, Hylton N. Quantification of breast tissue index from MR data using fuzzy clustering. Conf Proc IEEE Eng Med Biol Soc. 2004; 3:1667-70.

5. Tustison NJ, Avants BB, Cook PA, Zheng Y, Egan A, Yushkevich PA, Gee JC. N4ITK: Improved N3 Bias Correction. IEEE Trans Med Imaging. 2010; 29(6):1310–1320

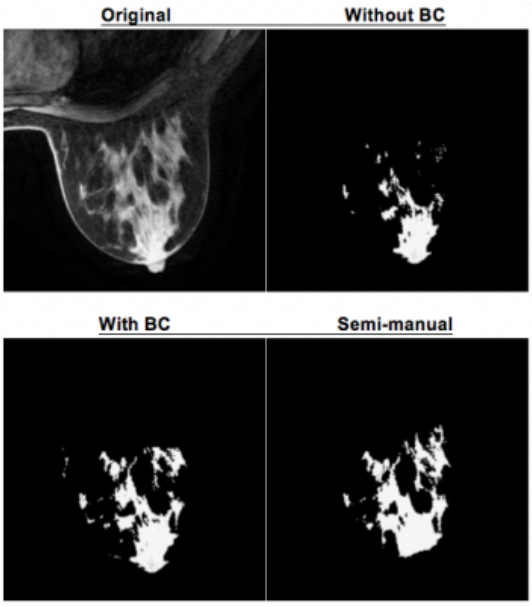

Figure 1: Successful example comparison of FCM segmentation between the semi-automatic method without bias correction, the semi-automatic method on bias corrected image, and semi-manual segmentation.