

A Fast Jump Move Graph Cut Reconstruction Algorithm for MR Parallel Imaging

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INTRODUCTION

Among recent parallel MR imaging reconstruction methods (e.g. [1]), a Bayesian method called Edge-preserving Parallel Imaging with GRAPh cut Minimization (EPIGRAM, [2]) demonstrated significantly improved SNR, edge preservation and visual quality over conventional regularized SENSE method. Unfortunately, EPIGRAM requires a large number of steps in proportion to the number of intensity labels in the image, making it computationally expensive for images with high dynamic range. Here a new jump-move based graph-cut algorithm is presented that provides a logarithmic reduction in reconstruction time (typically 25-50 times) while maintaining SNR reported by EPIGRAM. Preliminary *in-vivo* validation for coronary angiography and short axis cine at acceleration factors of 3 and 4 are reported. Our proposal constitutes a critical step towards real-time reconstruction of cardiac MRI using the EPIGRAM approach.

METHOD

Parallel imaging is converted to a Bayesian problem which reduces to the minimization of an energy function [2]

$$E(x) = \|y - Hx\|^2 + \sum_{(p,q) \in N} V(x_p, x_q)$$

Here V is a truncated linear penalty function that encodes edge preserving piecewise smooth priors, x is the target image, y are coil outputs and matrix H captures the sensitivities of different coils. In [2] graph mincut expansion move algorithm was used to minimize $E(x)$. Define \mathcal{L} as a set of all possible labels in the intensity range of an image. Define a new set of labels $S = [-2^{m-1}, -2^{m-2}, \dots, 2^{m-2}, 2^{m-1}]$ with $m = \log_2(|\mathcal{L}|)$. Here size of set S is $O(\log|\mathcal{L}|)$; clearly any label in \mathcal{L} can be reached by a combination of labels $d \in S$ (called a d -jump).

Given a jump $d \in S$ and initial labeling $\mathbf{x} = \{x_p \mid p \in P\}$, the energy

function above is converted into a binary energy function where each binary pixel b_p can be labeled either x_p or $x_p + d$. The binary decision for all the pixels to minimize the energy is made by finding a min-cut on the graph [4]. This leads to a new labeling $\mathbf{x} = \{x_p \mid p \in P\}$ where

$$x_p = \begin{cases} x_p & \text{iff } b_p = 0 \\ x_p + d & \text{iff } b_p = 1 \end{cases}$$

This process is repeated for each jump $d \in S$, reducing $E(x)$, until no d -jump can further reduce it. Note the number of proposed jump moves is logarithmic in the number of labels, compared to [2] whose computational complexity is linear.

Cine 2D SSFP cardiac short-axis images of six healthy volunteers were acquired at the mid-ventricular level on a 1.5T GE Excite 12 MR scanner with 8-element phased array cardiac coil.

RESULTS

Fig 1 shows recon time versus number of grayscale intensity labels of original EPIGRAM and proposed method. Fig 2 provides visual evidence of proposed method in comparison to conventional regularized SENSE [1, 4]. Over all 6 subjects, reconstructed SNR of SENSE was 36 ± 13 , and for Fast-EPIGRAM 72 ± 16 , around 2x gain - comparable to previously reported gains of EPIGRAM.

CONCLUSION

Reconstruction times are reduced by 25-50 times compared to original EPIGRAM - a critical step towards real-time reconstruction of cardiac MRI using graph based approaches. SNR numbers are comparable to previously reported values in [2], and continue to indicate almost 2x improvement over SENSE.

REFERENCES

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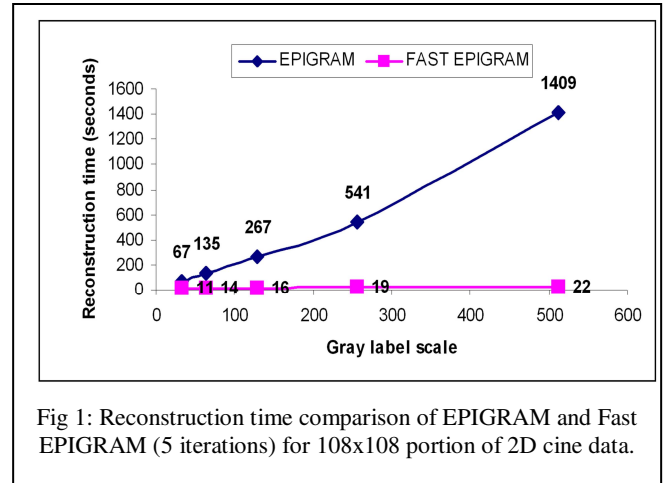


Fig 1: Reconstruction time comparison of EPIGRAM and Fast EPIGRAM (5 iterations) for 108x108 portion of 2D cine data.

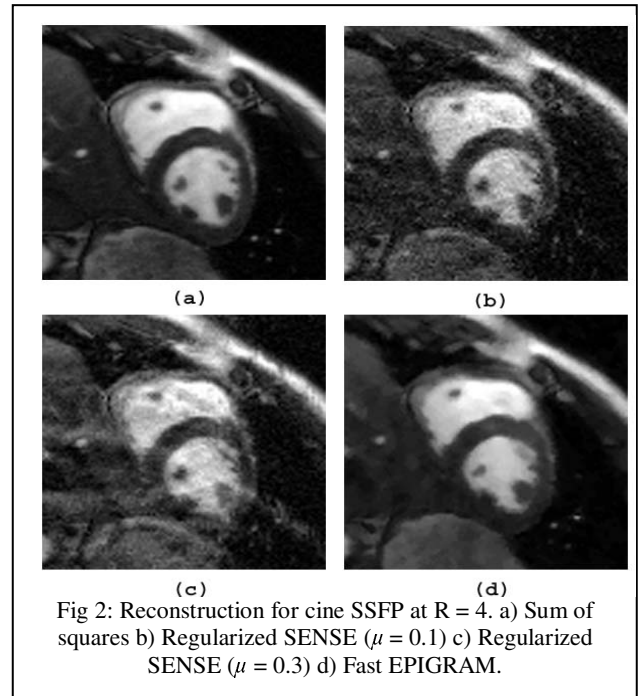


Fig 2: Reconstruction for cine SSFP at R = 4. a) Sum of squares b) Regularized SENSE ($\mu = 0.1$) c) Regularized SENSE ($\mu = 0.3$) d) Fast EPIGRAM.