"Dictionary Learning Based Super-Resolution Reconstruction Algorithm for Biomedical Images"

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Abstract -*High resolution 3D cardiac MRI is difficult to achieve due to the relative speed of motion occurring during acquisition. The lack of suitable reconstruction techniques that handle non-rigid motion means that cardiac image enhancement is still often attained by simple interpolation. In this paper, we explore the use of example-based super-resolution, to enable high fidelity patch-based reconstruction, using training data that does not need to be accurately aligned with the target data. By moving to a patch scale, we are able to exploit the data redundancy present in cardiac image sequences, without the need for registration. To do this, dictionaries of high-resolution and low-resolution patches are co-trained on high-resolution sequences, in order to enforce a common relationship between high- and low-resolution patch representations. These dictionaries are then used to reconstruct from a low-resolution view of the same anatomy. We demonstrate marked improvements of the reconstruction algorithm over standard interpolation.*

Key Words: training set, patch-based construction, reconstruction algorithm.........

INTRODUCTION

The speed of cardiac and respiratory motion present during Magnetic Resonance Imaging (MRI) of the heart makes the acquisition of high-resolution 3D cardiac image volumes a difficult task. Instead, Super-resolution image reconstruction is a very important task in many computer vision and image processing applications. The goal of image super-resolution (SR) is to generate a high-resolution (HR) image from one or more low-resolution (LR) images.

In this paper the high resolutions in 2D planar image formed by slices or form an image quality in photographic objects .improving the resolution of each image is an important in cardiac image visualisation and analysis. Improve the resolution image are carried out either improving speed of image or in post processing stage to achieve supper-resolution. The supper-resolution algorithm can classified into three main categories that means interpolation-based algorithm, learning based algorithm and reconstruction algorithm. The interpolation based algorithms are fast but result not fine. In learning based algorithms are need to careful selection of training set, the reconstruction algorithm with dictionary learning apply smoothness and HR image should reproduced LR image. in highly non-rigid motion present in MRI imaging with low resolution image make accurate registration difficult achieve, like wise reconstruction technique use in brain imaging which provide only rigid motion for this reason upsampling of to cardiac image via interpolation scheme such as bi-cubic are commonly used in MRI imaging. We have to perform that the idea of upsampling acquired data through the example-based-super resolution using image patches. Aur aim to exploit the data redundancy at patch level across the sequence of image. The basic idea behind that low resolution (LR) image find super-resolution (SR)in database of high resolution(HR)image pair. the corresponding HR pair used to upsampled using relation between images. In previous work the database of image patches of the same anatomy. These case works on the assumption that the same relation between the construction of the HR and LR patches actually exits. In this paper the development of sparse representation and dictionary learning for single image reconstruction which applied to brain imaging such that LR patch based sparsity with respect to LR dictionary as corresponding to HR patch has to HR dictionary . We should use reconstruct HR image with upto 8 time upsampling without any registration.

2. METHOD

We aim to reconstruct a LR orientation (the through-plane view of a 2D slice stack) sequence, from frames of a HR sequence of the corresponding anatomy. To ease explanation, we assume in the following a LR SA stack sequence and single slice HR LA sequences. However, the same methods equally apply to any pair of orthogonal views that yield HR in-plane. By using orthogonal views of the same anatomy, we eliminate the need for affine registration

2.1. Training

Our training data consists of frames from a HR LA sequence YH $= \{y_h\}$,and corresponding LR sequences obtained through blurring and downsampling according to Eq. By using training data that covers the whole cardiac cycle, pk = Rk y, where Rk is an operator to extract a patch of size of size n × m from location k. These patches are used to co-train the HR and LR dictionaries.

2.2 Patch pairs construction

To focus the training on the relationship between LR patches and high-frequency information (edges and textures), patches are extracted from a LR image, y L , and a difference image given by y E= $Y_H - Y_L$. For the LR patches, features containing high frequency information are extracted from y L by convolving with 2D Gaussian / Laplacian filters: $p_k^L = f_k \times y_l$. Finally, Principal Component Analysis is used to reduce the feature vector extracted p_k^L = Cp_k^L, where C is a projection operator that transforms p_k^L to a low-dimensional subspace preserving 99.9% of its average energy. Image intensities are used for the HR patches p_k^H = $R_k \times y_l$ This gives pairs of co-occurring patches at each location k, P = $\{p_k^L, p_k^H\}$ k .

2.3 Correlated dictionary learning :

Correlated dictionaries ensure that a HR patch and its LR counterpart have the same sparse representations in their respective dictionaries. We also need to ensure that the LR patches can be encoded sparsely and in the same way for both train and test data. When reconstructing a LR test patch, we find the sparse representation of that patch in terms of the LR dictionary only. The LR dictionary D L is therefore also constructed using LR patches only

$$\mathbf{D}^L, \alpha = \min_{\mathbf{D}^L, \alpha_k} \sum_L \|\mathbf{p}_k^L - \mathbf{D}^L \alpha_k\|_2^2 \text{ subject to } \|\alpha\|_0 < \lambda$$

where λ denotes the desired sparsity of the reconstruction weights vector α. This standard dictionary learning equation is solved sequentially for D L and α using the method. The resulting sparse code αk for each patch k, is then used to solve for the HR dictionary by minimizing

$$\mathbf{D}^H = \min_{D_H} \sum \|\mathbf{p}_k^H - \mathbf{D}^H \alpha_k\|_2^2 = \min_{\mathbf{D}^H} \|\mathbf{P}^H - \mathbf{D}^H \mathbf{A}\|_F^2$$

where columns of P are formed by the HR training patches, p H k and columns of A are formed by the atoms α. Denoting A + as the Pseudo-Inverse of A, the solution is given by

$$\mathbf{D}^H = \mathbf{P}^H A^+ = \mathbf{P}^H \mathbf{A}^T (\mathbf{A}\mathbf{A}^T)^{-1}$$

resulting in correlated dictionaries, D H and D L .

2.4 Reconstruction:

Patches from a LR test image are extracted in the same way as for the LR training images. The sparse code for each patch with respect to the LR dictionary, DL, is found

$$\alpha_k = \arg\min_{\alpha_k} \sum_k \|p_k^L - \mathbf{D}^L \alpha_k\|_2^2 \text{ subject to } \|\alpha_k\|_0 < \lambda$$

again. Crucially, this is the same sparse coding equation as in the training phase. The reconstruction weights vector αk for each test patch are used to approximate HR patches by $\{p_k^H\}$ k = $\{D_{\alpha_k}^H\}$ k . To create a smooth overall reconstruction, overlapping patches are used, and the upsampled image give by their average reconstruction. The final HR image is given by adding the LR interpolated approximation

$$\tilde{\mathbf{y}}_H = \mathbf{y}_L + \left(\sum_{k\in\Omega} \mathbf{R}_k^T \mathbf{R}_k\right)^{-1} \sum_{k\in\Omega} \mathbf{R}_k^T \tilde{\mathbf{p}}_k^H .$$

3.FMRI EXPERIMENTAL ANALYSIS

The functional Magnetic Resonance Imaging (fMRI) is a powerful imaging tool that can be used to perform brain activation studies non-invasively in vivo while subjects are engaged in meaningful behavioral task. Before the emergence of fMRI, radioisotope based techniques, such as positron emission tomography (PET) which measures regional cerebral blood flow (rCBF), were widely used for mapping the brain function. However, these techniques are invasive and have a low spatial and temporal resolution. Developing successful fMRI experiments requires careful attention to experimental design, data acquisition techniques, and data analysis. The experimental design is at the heart of any cognitive neuroscience investigation.

3.1 Analysis of Imaging Data:- Data analysis mainly consists of motion correction, corcgistration, normalization to a template (if required), smoothing, estimation of parameters of a statistical model (statistical modeling), and statistical inference to determine significant areas of brain activation. The fMRI images are prcprocessed and a General Linear Model would be setup to investigate the candidate brain regions that arc activated preferentially by the sequence tasks. This section outlines the analysis procedure used for image analysis The major steps of data analysis include:

• Data Acquisition

• Preprocessing

• Model Setup and Estimation

• Statistical inference (Results assessment)

SPM stands for Statistical Parametric Mapping(SPM), which is the main output of the software. Statistical Parametric Mapping refers to the construction and assessment, of spatially extended statistical process used to test hypotheses about [neuro] imaging data obtained from PET (Positron Emission Tomography) and fMRI. The parameterized value is generally some form of Student's t-test estimating the likelihood that a comparison of two image groups matches a given model that explains their possible differences.

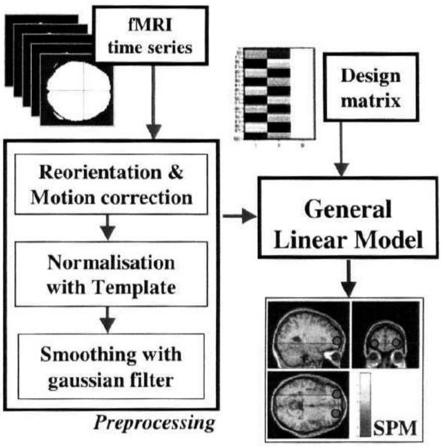

Figure 3.1: Data Processing Steps in SPM

3.2 Data Acquisition:-Issues of data acquisition are included here because it is crucial that the data are acquired in a way that the experimental hypothesis can be addressed. This includes the experimental design as well as technical questions of modality, acquisition parameters, and reconstruction. The most important consideration is the actual design of the experiment. In conducting a hypothesis-based experiment, we wish to be able to attribute any observed effects to experimentally manipulated conditions. This can be guaranteed only if conditions are randomly allocated to a presentation order for each subject in a sensible manner. Further, this randomization should be appropriately balanced, both across and within subjects.

3.3Preprocessing: This stage includes several steps, all of which are aimed at massaging the data so that it is suitable to be statistically analyzed by SPM99. In our experiment, the scanner was operated continuously for a session. Two additional scans acquired at the beginning of each session were discarded to account for the transients in the magnetic field of the scanner. Further, one scan at the beginning of every block that corresponded to the block instruction was also discarded from analysis.

3.4 Smoothing:The normalized functional images are spatially smoothed with a gaussian filter using a suitable full width half maximum (FWHM of 6mm in our case i.e., double the voxel size). The smoothing process not only increases the signal to noise ratio (SNR), but also validates the underlying gaussian assumption for the BOLD activity that is in turn used in the statistical inference step.

4. CONCLUSION

We have demonstrated how we can already achieve marked improvement over bicubic interpolation on real MRI data. Extensive validation of real cardiac datasets is difficult due to the lack of ground truth and is the subject of ongoing work.

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