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Computer-aided detection of wall motion abnormalities in cardiac MRI

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4

DETECTING REGIONAL ABNORMAL CARDIAC CONTRACTION IN SHORT-AXIS MR IMAGES USING INDEPENDENT COMPONENT ANALYSIS

Abstract

Regional wall motion analysis is used in clinical routine to assess myocardial diseases such as infarction or hypertrophy. Physicians/radiologists can recognize abnormal cardiac motion because they have knowledge about normal heart contraction. This chapter explores the potential of Independent Component Analysis (ICA) to extract local myocardial contractility patterns and to use them for the automatic detection of regional abnormalities. A qualitative evaluation was performed using 42 healthy volunteers to train the ICA model and 6 infarct patients to test the detection and localization. By visual comparison, the experimental results show that automated detection of regional abnormal contraction correlate very well to hyperenhanced areas from delayed-enhancement MR images.

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You know, Donkey, sometimes things are more than they appear.

SHREK (2001)

IDENTIFICATION of reversible myocardial ischemic injury is a crucial assessment before coronary revascularization. Myocardial infarction is characterized by the presence of hypokinetic regions. Myocardial infarction can be assessed by using late contrast-enhanced MRI or known also as delayed-enhancement MRI [1].

In the previous chapter, the capability of Independent Component Analysis (ICA) to extract local shape abnormalities was investigated. In this chapter, ICA-based local shape feature detection is applied to automate the detection of abnormal cardiac motion from short-axis MR images. This is achieved by deriving a statistical model of normal heart contraction (*normokinetic model*) and its local contractility patterns. Hence, unlike the previous chapter, the ICA model is trained only from normokinetic heart images.

The objectives of this chapter is summarized as follows:

- A geometry-based sorting method of independent components is proposed, which provides an intuitive anatomical interpretation of the ICA modes.
- The potential of ICA in cardiac shape modeling to detect local contraction abnormalities in infarcted patients is investigated.
- A qualitative evaluation of the detection and localization of myocardial infarctions is presented. Results are visually compared with the corresponding delayed enhancement MRI images.

Section 4.1 describes shape modeling with ICA, the new sorting method for independent components and the method to detect local abnormalities. In Section 4.2, qualitative evaluation results are presented, followed by a discussion in Section 4.3.

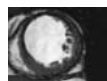
4.1 Methodology

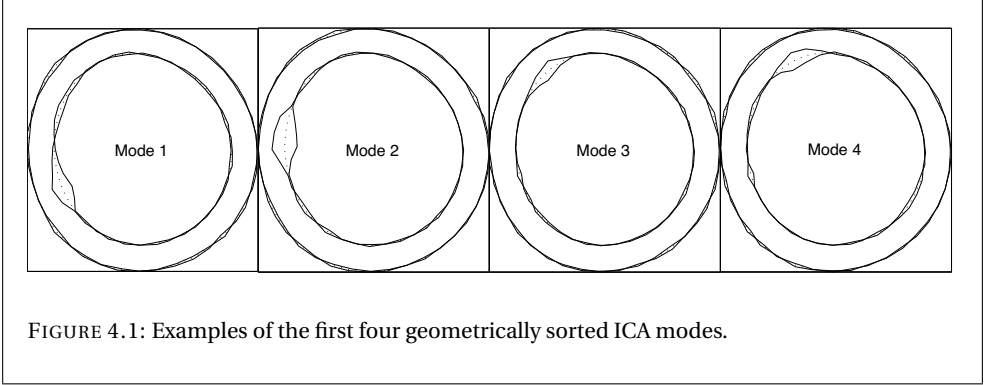
4.1.1 ICA modeling of the normal cardiac contraction

ICA is originally used for finding source signals from a mixture of unknown signals without prior knowledge other than the number of sources. In machine learning, ICA has been applied for feature extraction [2] and face recognition [3]. ICA can be applied to statistical shape modeling to extract independent components of the shape variation [4].

ICA is a linear generative model, where every training shape can be approximated by a linear combination of its components. Let $\mathbf{x} = (x_1, y_1, \dots, x_m, y_m)^T$ be a shape vector, consisting of m pairs of (x, y) coordinates of landmark points. The linear generative model is formulated as follows:

$$\mathbf{x} \approx \bar{\mathbf{x}} + \Phi \mathbf{b} . \quad (4.1)$$





The matrix $\Phi \in \mathbb{R}^{2m \times p}$ defines the independent components (ICs) and $\mathbf{b} \in \mathbb{R}^p$ is the weight coefficient vector. The mean shape, $\bar{\mathbf{x}}$, is defined by

$$\bar{\mathbf{x}} = \frac{1}{n} \sum_{i=1}^n \mathbf{x}_i . \quad (4.2)$$

where n is the number of shapes and p is the number of retained components.

The goal of ICA is to find a matrix, Ψ , such that

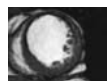
$$\mathbf{b} = \Psi (\mathbf{x} - \bar{\mathbf{x}}) \quad (4.3)$$

with a constraint that columns of Ψ correspond to statistically independent directions. Thus the independent components are given by $\Phi = \Psi^{-1}$. The matrix Ψ is estimated by an optimisation algorithm (see [5] for survey of ICA).

Some pre-processing steps are necessarily performed before the ICA computation. The training shapes must be aligned, such that all shapes are invariant under Euclidean similarity transformations (rotation, translation and scaling). Procrustes analysis [6] is used for the shape alignment. Point correspondence between shapes is usually obtained by taking landmark points with the same anatomical interpretation. The resulting training shapes are zero mean, unit variance and all points are registered between shapes.

In this application, the observed data are left ventricular (LV) myocardial contours from short-axis cardiac MR images at end-diastole (ED) and end-systole (ES) phases. To model the contractility pattern, contours for each subject are combined serially into one shape vector in the following order: endocardium contour at ED, epicardium contour at ED, endocardium contour at ES and epicardium contour at ES.

Figure 4.1 shows examples of ICA derived modes of shape variation sorted geometrically. For comparison, the first mode of shape variation with PCA from the same data is shown in Figure 3.2(b). ICA modes have a general shape of a local "bump", whereas the remainder of the shape is unaffected. This is an important property of ICA, which can be used to detect local shape anomalies. In contrast, PCA modes give global shape variations, distributed over the entire contour. A comparison study of ICA and PCA in cardiac shape modeling is given in [4].



The same geometry-based sorting of independent components described in Chapter 3 is used. Figure 4.1 shows an example of the first four ICA modes after the sorting process. Note that the local shape variations are ordered clockwise.

4.1.2 Determining the number of independent components

One important parameter to determine is the number of independent components to estimate during the computation of ICA. Predicting this number with PCA may not always be a good idea, because PCA has a risk to eliminate "weak" ICs in the reduced data [7]. In shape modeling, this parameter affects appearance of the shape variations. As the number of computed ICs increases, the components represent more localized shape variations. If this parameter is too small, then the component gives global shape variation, much like PCA modes.

The determination of the optimal number of computed ICs is task-specific. In this application to detect local abnormalities, we need sufficient regional segments. Too few segments will give an inaccurate localization. More segments will improve the detection resolution, but this is constrained by the computation time and the number of available shapes to avoid overlearning [8]. Figure 4.2 shows the number of segments as a function of the number of computed ICs from 42 shapes of normal hearts.

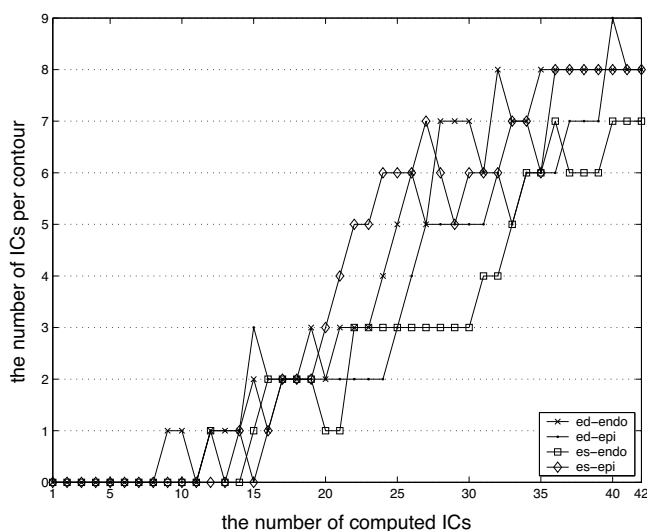


FIGURE 4.2: A plot of the number of ICs per contour as a function of the number of computed ICs. Note that small number of computed ICs produced zero number of ICs per contour because all ICs were detected as noise components, i.e., their shape variation width is larger than the largest Gaussian filter (see Chapter 3).

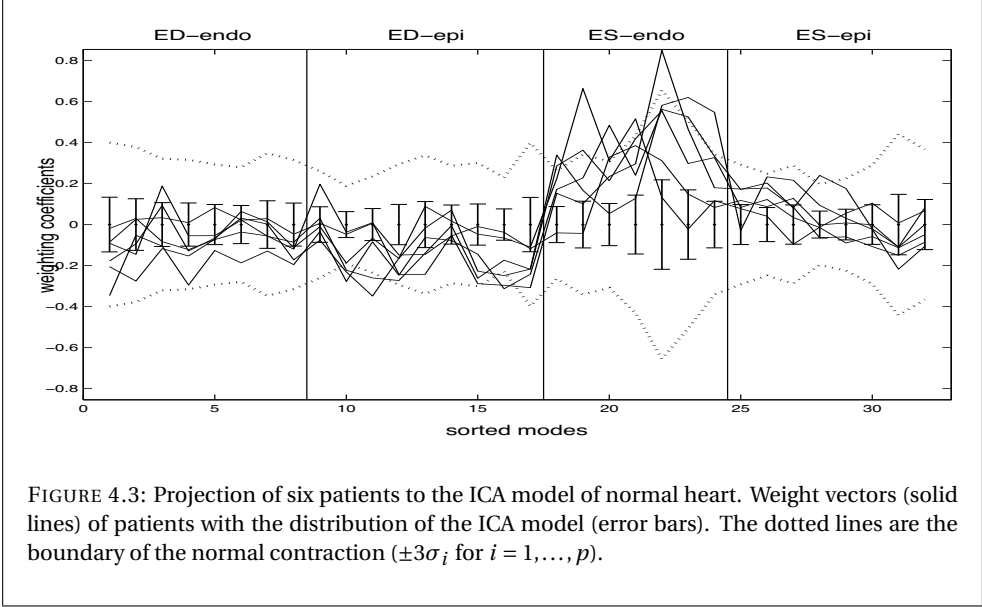


FIGURE 4.3: Projection of six patients to the ICA model of normal heart. Weight vectors (solid lines) of patients with the distribution of the ICA model (error bars). The dotted lines are the boundary of the normal contraction ($\pm 3\sigma_i$ for $i = 1, \dots, p$).

4.1.3 Detection of abnormal contractility patterns

Let $\mathbf{y} \in \mathbb{R}^{2m}$ be a shape vector, fitted onto the mean shape of the model using the Procrustes fit [6]. The weight vector of the sample \mathbf{y} is given by

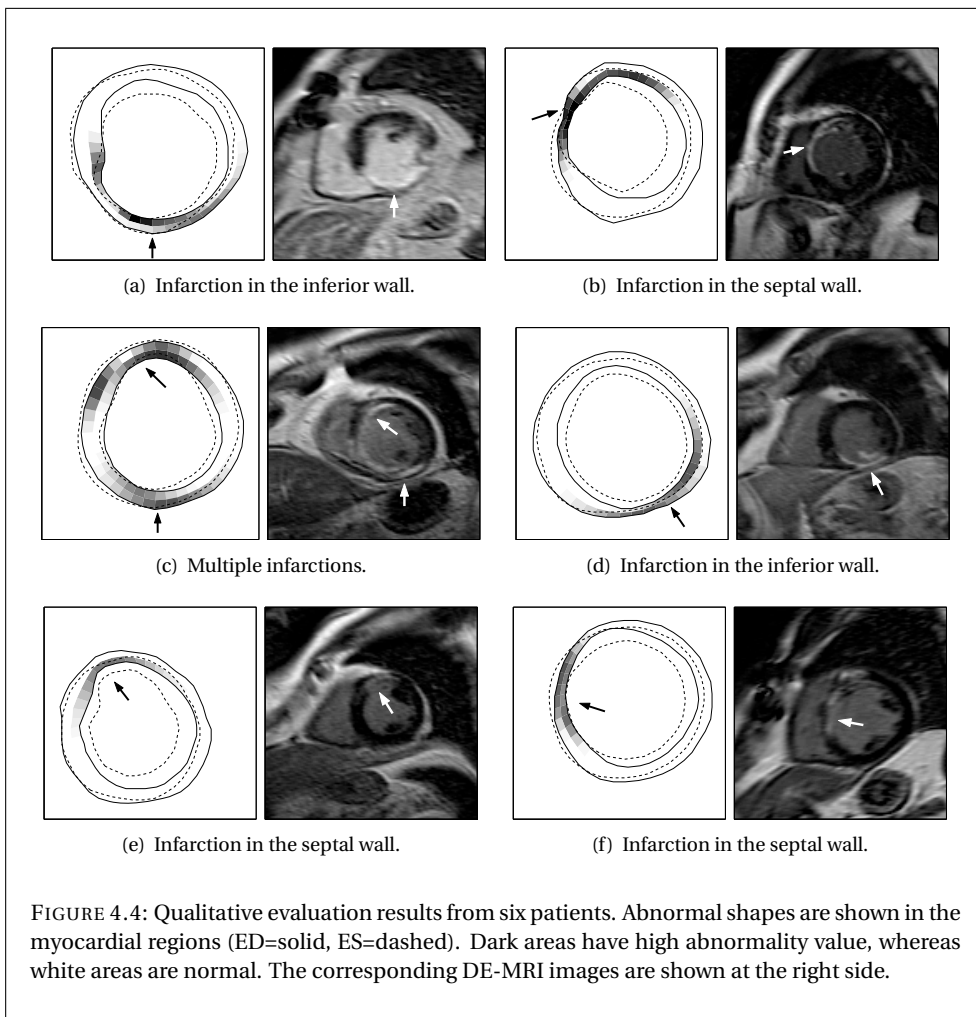
$$\mathbf{b}_y = \Phi^{-1}(\mathbf{y} - \bar{\mathbf{x}}) \quad (4.4)$$

which represents the parameters approximating the patient shape. Patient anomalies are estimated by elements in the weight vector that lie outside the distribution of parameters of the ICA model.

An *anomaly* at the i -th component $q_y^{(i)}$ is defined as a value that falls beyond $\pm 3\sigma_i$ (99.7%), to make sure that the anomaly is an outlier. Thus the *anomaly vector* q_y is defined by taking the outlier components, normalized by their standard deviation. Each element of q_y is defined by

$$q_y^{(i)} = \begin{cases} 0 & \text{if } -3\sigma_i \leq b_y^{(i)} \leq 3\sigma_i \\ \frac{b_y^{(i)}}{\sigma_i} & \text{otherwise} \end{cases} \quad \text{for } i = 1, \dots, p \quad (4.5)$$

The anomaly vector (4.5) is mapped to a shape vector to facilitate a more intuitive regional interpretation. From the sorted ICs, the corresponding Gaussian filters giving the maximum responses for each IC are known. These Gaussian filters are generated to model the local bumps, resulting in a mixture of Gaussian functions. The regional sum of the Gaussian mixture gives a shape vector that indicates regional abnormal heart contraction of a patient.



4.2 Experimental Results

An ICA model was constructed from 42 healthy volunteers. The mid-ventricular level from short-axis MRI was taken from each subject. Contours were drawn manually and resampled to 40 landmarks defined by equi-angular sampling, starting from the intersection between left and right ventricle. The calculation of ICA was performed using the JADE algorithm [9], implemented in Matlab. The optimal number of computed ICs with minimum of 7 segments per contour is 40 (see Figure 4.2).

To evaluate the infarct detection and localization of the method, MRI data of 6 patients with all necrotic infarcts were investigated. Mid-ventricular short-axis (SA) MRI

images and the corresponding delayed-enhancement (DE) MRI images with the same orientation and the distance only < 1 mm were acquired. Regional abnormal contraction was compared visually with the corresponding DE-MRI. The myocardial infarct regions in the DE-MRI are demonstrated by signal hyperenhancement, corresponding to myocardial necrosis [1].

Six representative evaluation results are presented in Figure 4.4. The anomaly vectors of patients were projected to the corresponding myocardial regions. The contraction patterns are also shown in the plot of ED contours (solid line) and ES contours (dashed line). It is clearly seen from Figure 4.4, that the dark areas have a reduced contraction. The corresponding DE-MRI are given in the right side where the infarction regions are depicted by hyperintensity regions.

4.3 Discussion

This chapter shows the potential of ICA as an analysis tool for extracting local shape deformation. Using ICA to train a model of normal cardiac contraction, both global and regional motions are captured. To this end, the method can automatically distinguish between abnormal and healthy cardiac motion.

An intuitive anatomical interpretation of the normal contraction model is achieved by ordering the ICs of the model geometrically along the whole contour. From this, anatomical shape information can be inferred, providing a method to localize the motion abnormalities.

In the qualitative comparison for 6 patients, the hypokinetic regions show an excellent correspondence to the hyperintensity regions of the "gold standard" DE-MRI. This demonstrates that the ICA-based infarct detection and localization from short-axis MRI images is a promising technique for computer aided infarct localization.

4.4 References

- [1] R. J. Kim, E. Wu, A. Rafael, E. L. Chen, M. A. Parker, O. Simonetti, F. J. Klocke, R. O. Bonow, and R. M. Judd, "The use of contrast-enhanced magnetic resonance imaging to identify reversible myocardial dysfunction," *N Engl J Med*, vol. 343, no. 20, pp. 1445–53, Nov 2000.
- [2] P. O. Hoyer and A. Hyvärinen, "Independent component analysis applied to feature extraction from colour and stereo images," *Network: Computation in Neural System*, vol. 11, no. 3, pp. 191–210, 2000.
- [3] M. S. Bartlett, J. R. Movellan, and T. J. Sejnowski, "Face recognition by Independent Component Analysis," *IEEE Trans. on Neural Networks*, vol. 13, no. 6, pp. 1450–1464, Nov. 2002.
- [4] M. Üzümcü, A. F. Frangi, J. H. Reiber, and B. P. Lelieveldt, "Independent Component Analysis in statistical shape models," in *Proc. of SPIE*, M. Sonka and J. M. Fitzpatrick, Eds., vol. 5032, May 2003, pp. 375–383.
- [5] A. Hyvärinen, "Survey on independent component analysis," *Neural Computing Surveys*, vol. 2, pp. 94–128, 1999.

- [6] I. L. Dryden and K. V. Mardia, *Statistical Shape Analysis*. John Wiley & Sons, 2002.
- [7] J.-P. Nadal, E. Korutcheva, and F. Aires, "Blind source separation in the presence of weak sources," *Neural Networks*, vol. 13, no. 6, pp. 589–596, 2000.
- [8] A. Hyvärinen, J. Särelä, and R. Vígario, "Bumps and spikes: artifacts generated by independent component analysis with insufficient sample size," in *Proc. Int. Workshop on ICA and BSS*, 1999, pp. 425–249.
- [9] J. Cardoso and A. Souloumiac, "Blind beamforming for non Gaussian signals," *IEEE Proceedings-F*, vol. 140, pp. 362–370, 1993.



