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Developments towards the slice-wise three-dimensional reconstruction of the distribution of the contrast perfusion in the myocardial muscle from biplane angiographic views

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Summary

In theory, radiographic myocardial perfusion imaging allows a quantitative assessment of the functional significance of a coronary stenosis. However, in the conventional two-dimensional projection images there does not exist a one-two-one relationship between a selected myocardial region of interest (ROI) and one particular coronary segment perfusing that area due to over-projection of myocardial regions in front of and behind the selected ROI perfused by other arterial segments, which may result in measurements which are difficult to interpret or even unreliable. To overcome these problems, we have developed two algorithms to determine the spatial distribution of perfusion levels in slices of the heart, selected approximately perpendicular to the left ventricular long axis, from two orthogonal angiographic views: the Segmental Reconstruction Technique (SRT) and the Network Programming Reconstruction Technique (NPRT). Both techniques require *a priori* geometric information about the myocardium, which can be obtained from the epicardial coronary tree (epicardial boundaries) and the left ventricular lumen (endocardial boundaries).

Using the SRT approach, pie-shaped segments are defined for each slice within the myocardial geometric constraints such that superimposition of these segments when projected in orthogonal biplane views is minimal. The reconstruction process uses a model with identical myocardial geometry and definition of segments. Each segment of the model is assigned a relative perfusion level with unit one if no other *a priori* information is available. In this case, the model contains geometric information only. In case *a priori* information about expected segmental perfusion levels is available, a level between zero and one is assigned to each segment. The *a priori* information on the myocardial perfusion levels can be extracted from either anatomic information about the location and severity of existing coronary arterial obstructions, or from a slice adjacent to the one under reconstruction.

Using the NPRT approach perfusion levels are computed for each volume picture element of a slice within the reconstructed myocardial geometry, thus resulting in a much higher spatial resolution than the SRT approach. *A priori* information of perfusion levels must be included in this approach, again based upon anatomical information, or upon the slice adjacent to the one under reconstruction. The very first slice of a myocardial study will be reconstructed by the SRT approach.

Extensive computer simulations for the SRT have proved that the mean difference between the actual and reconstructed segmental perfusion levels, on a scale from 0 to 1, is smaller than 0.45 (SEE = 0.0033, REE = 1.80) for various coronary artery disease states without the use of *a priori* information on expected perfusion levels. This error becomes smaller than 0.36 (SEE = 0.0026, REE = 1.42), if *a priori* information in the reconstruction technique is included. Similar computer simulations for the NPRT have proved that these mean differences, in geometric segments equal to those defined for the SRT, are smaller than 2.94 (SEE = 0.0308, REE = 0.77) on a scale from 0 to 16, without the use of *a priori* information on expected perfusion levels, and smaller than 1.72 (SEE = 0.0304, REE = 1.10) on the same scale when *a priori* information is included. Therefore, it may be concluded that slice-wise three-dimensional reconstruction of perfusion levels is feasible from biplane computer-simulated data, and that a similarity exists for mean perfusion levels in corresponding regions in the simulated and reconstructed slices, for various states of single coronary artery disease.

1. Introduction

Parametric X-ray imaging allows the assessment of the functional significance of a coronary stenosis expressed in terms of coronary flow reserve (CFR); this technique has been a subject of extensive research [1]. All approaches published in the international literature are based on some kind of volume parameter and time parameter. These spatially related parameters, 'volume of the myocardial region-of-interest' and 'contrast medium appearance time', or 'contrast medium transit time' [2, 3], however, should both be computed in three-dimensional space, rather than in a two-dimensional projection image. Two-dimensional projection images are hampered by superimposition of possibly normally and abnormally perfused myocardial regions-of-interest, if no super-selective administration of contrast medium was used.

To overcome these problems of superimposition, we have developed a technique for the three-dimensional reconstruction of the perfusion levels in myocardial slices selected at different levels along and approximately perpendicular to the long-axis of the left ventricle from two orthogonal views; our basic approaches have been described in detail in [4]. A diagram of the basic reconstruction process is given in Fig. 1.

Three-dimensional reconstruction from only two angiographic projections is an ill-posed problem, typically resulting in a very large number of feasible solutions or so called ambiguous reconstructions. Ambiguity, however, may be solved by including *a priori* information. Two types of *a priori* information will be introduced: 1) endocardial and epicardial descriptions of the reconstructed myocardial geometry obtained from the corresponding left ventricular and coronary angiograms, respectively, and; 2) the expected perfusion levels in the slice under reconstruction. The morphologic set of data will be used to restrict the set of feasible reconstructions, while the second set (expected perfusion levels) will be used to define an 'optimal feasible solution' within the limited set of feasible solutions. In this paper only the reconstruction of perfusion levels will be outlined; for reasons of simplicity the myocardial geometry of a particular slice will be defined by two concentric ellipses.

For the actual reconstruction process of the myocardial perfusion levels, we have developed two algorithms: the Segmental Reconstruction Technique (SRT), and the Network Programming Reconstruction Technique (NPRT). Both algorithms provide data on the spatial distribution of myocardial perfusion levels in slices selected approximately perpendicular to the left ventricular long axis [5], from biplane angiographic data acquired following a standard CFR acquisition protocol [6, 3]. As will be shown in the following paragraphs, good results can be obtained by reconstruction of the first slice of a study by the SRT-algorithm followed by NPRT for subsequent slices.

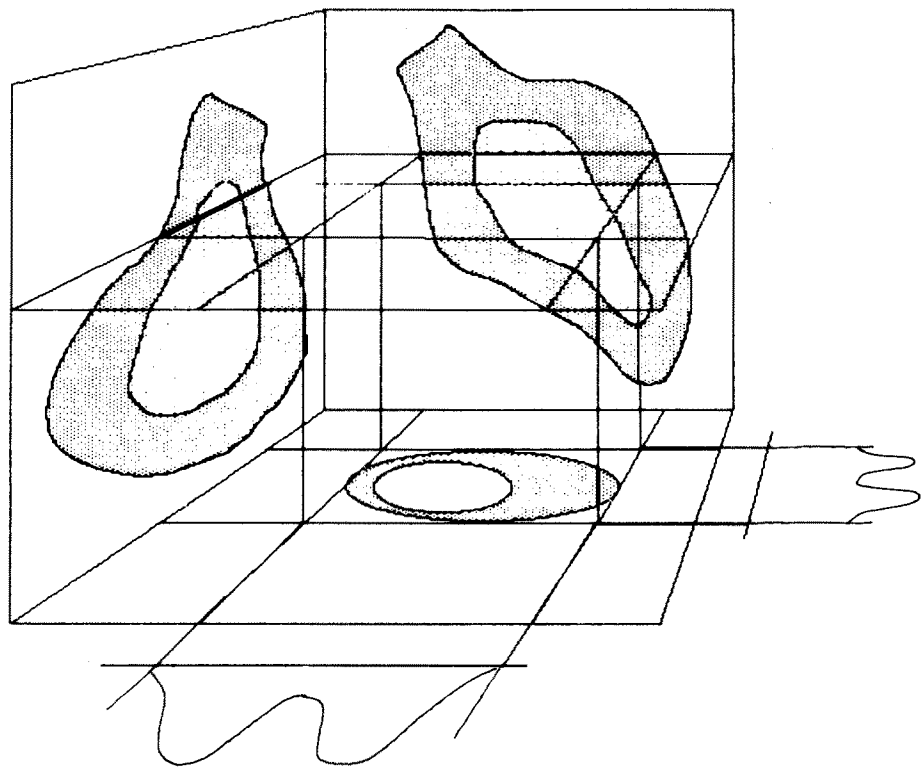

Fig. 1. The purpose of three-dimensional reconstruction from biplane orthogonal angiographic views is to obtain a stack of slices selected approximately perpendicular the left ventricular long axis.

2. Three-dimensional reconstruction of myocardial opacification

The basic algorithm for the three-dimensional reconstruction process is the so called Network Programming Reconstruction Technique, abbreviated by NPRT. It requires the myocardial geometry and expected myocardial values as *a priori* information, and allows the reconstruction of myocardial perfusion levels in slices selected approximately perpendicular to the left ventricular long axis from corresponding biplane scanlines. Each reconstructed slice will be used as a model for the perfusion distribution within the neighboring slice under reconstruction. Since such a perfusion model does not exist for the very first slice, the Segmental Reconstruction Technique, is used for the initial slice. Figure 2 illustrates how the various types of data are handled. Both reconstruction techniques will be discussed in some more detail in the next paragraphs.

2.1. The Segmental Reconstruction Technique (SRT)

A first spatial approximation of the myocardial opacification is obtained ty the SRT. The ultimate goal of this technique is to reconstruct the mean relative perfusion levels in eight pre-defined pie-shaped segments within the myocardial geometry, without using information of expected perfusion levels. This approach was first proposed by Onnasch et al. [7]. They compared the projected density profiles of a uniformly distributed model with the actual density profiles, in order to decide on the basis of these differences which segments were less opacified than indicated by the model. We adopted this idea and compute segmental ratios, indicative

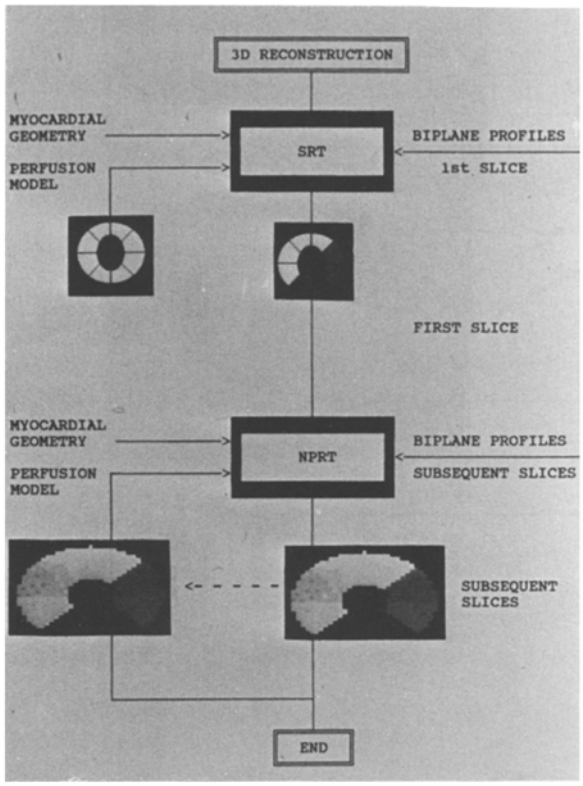

Fig. 2. The very first slice is reconstructed using the SRT; these results will be used as a model for the perfusion levels for the next slice, which is reconstructed by the NPRT approach. This result will be used a model for the next slice, etc., until all slices have been reconstructed. Only the reconstructed myocardial geometry is used as *a priori* information.

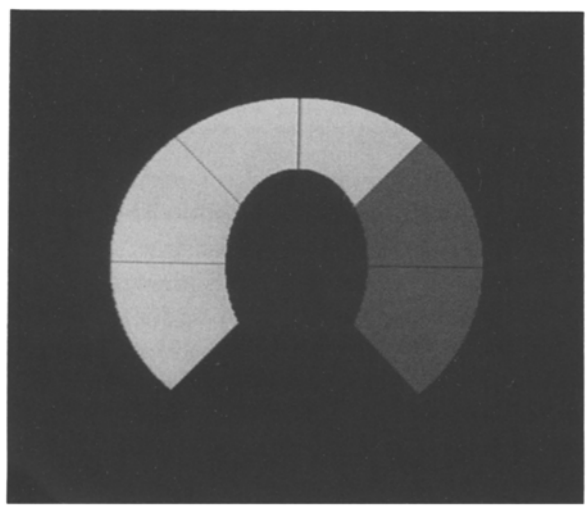

Fig. 4. A random realization of the model shown in Fig. 3.

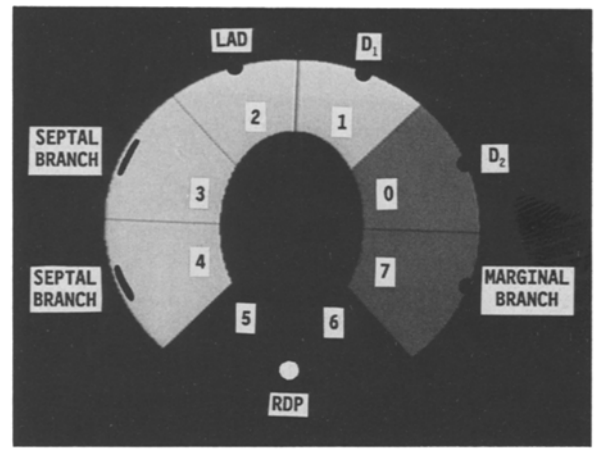

Fig. 3. An example of expected myocardial perfusion levels in a slice supposed to be distal to a 90% area stenosis in the Left Cirucumflex artery. The approximate positions of the intersection points of the three-dimensional coronary tree and the slice are indicated, as well as the segment numbers.

of the reduction in opacification as compared to the perfusion values in the model used, in a user-defined number of levels. In each of the biplane projections the actual density profile and the density profile of the projected model are divided into four intervals; a density level equal to the average value of the profile over that interval is assigned to the interval according to Onnasch [7]. The SRT pro-

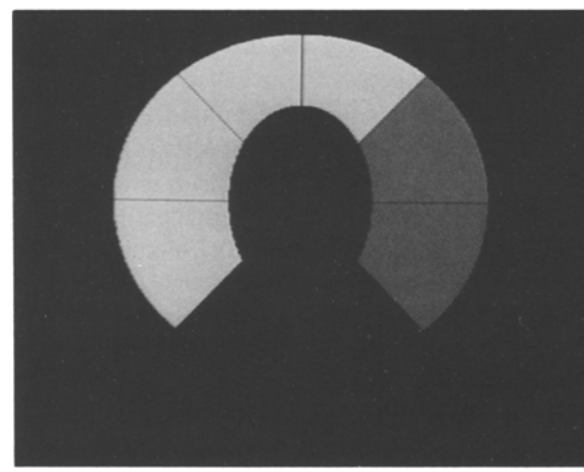

Fig. 5. The reconstructed result in case the orthogonal biplane density profiles of the computer-generated slice shown in Fig. 4 were reconstruced by the SRT, without use of any *a priori* information of expected perfusion levels.

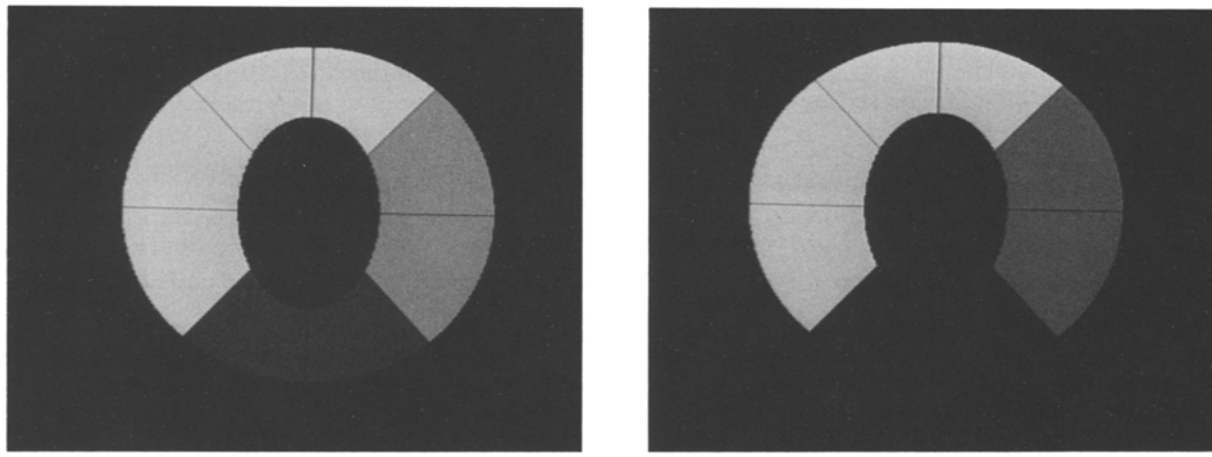

Fig. 6. The perfusion model (a) and the result (b), reconstructed from the density profiles of the slice shown in Fig. 4.

vides for each segment a ratio of reconstructed perfusion level to model perfusion level. These ratios are computed by iterative generalized inversion of the projection matrix for the eight segments and from the ratios of actual projection data to model projection data for each interval [8, 9].

2.2. The Network Programming Reconstruction Technique (NPRT)

The more complex NPRT approach allows the reconstruction of the perfusion levels for each volume pixel element within the reconstructed myocardial geometry, again in slices selected approximately perpendicular to the left ventricular long axis. Reconstruction by network programming techniques was first proposed by Gerbrands, Slump, and Reiber [10–12]. They reconstructed the shape of cross-sections of coronary arterial segments and of the left ventricular lumen; these were binary reconstructions of a presumed homogeneous contrast agent distribution. Our approach has been directed to a non-binary reconstruction of the inhomogeneous distribution of the contrast agent.

A network is defined as a set of nodes and arcs between pairs of nodes [13]. An arc is uniquely related to a pixel position, i.e. only arcs corresponding to pixel positions within the myocardial geometry are defined in the network. Each node is assigned a single density value extracted from one of the density profiles. All these density values are distributed over the network, such that all network constraints are satisfied and an objective cost function is optimized [4]. All network parameters are based upon the *a priori* expected perfusion levels.

3. Experimental results

Both the SRT approach and the NPRT approach have been validated by computer-stimulated experiments [14]. A cardiologist defined model slices supposed to be distal to a coronary obstruction in cases of single vessel disease by assigning relative perfusion levels to the eight segments, which were geometrically defined by the SRT approach. The range of relative perfusion levels was from zero to one; zero indicates that no perfusion at all was expected, while one indicates normal perfusion. An example of such a perfusion model is shown in Fig. 3, for a slice distal to a coronary obstruction of 90% area-stenosis in the proximal part of the Left Circumflex Artery. The approximate positions of the intersection points of the major coronary arteries within this slice are indicated, as well as the numbers of the segments. These intersection points and segment numbers were used in all computer-simulated validation studies.

In each study each segment of a selected model for the perfusion distribution was disturbed with random noise and as such used as the actual slice.

Table 1. The mean values, the standard error of the estimate (SEE) and random error of the estimate (REE) of the paired differences of segmental actual and reconstructed perfusion levels for the worst and best segments in each of the ten cases, reconstructed by the SRT approach without the use of *a priori* information. The mean values are defined in the relative interval from zero to one. Reconstructions were computed 3000 times for each case. The REE is defined as the square root of the number of experiments times the SEE, and reflects the sensitivity for noise.

Cases	Worst reconstructed segment			Best reconstructed segment		
	Mean	See	Ree	Mean	See	Ree
100% LCX prox	−0.36	0.0042	2.30	0.04	0.0022	1.20
100% LCX dist	−0.45	0.0033	1.80	−0.07	0.0021	1.15
90% LCX prox	−0.36	0.0037	2.02	−0.00	0.0023	1.25
90% LCX dist	−0.44	0.0033	1.80	−0.08	0.0021	1.15
100% LAD prox	−0.35	0.0043	2.36	0.00	0.0013	0.71
100% LAD mid	−0.35	0.0042	2.30	0.04	0.0021	1.15
100% LAD dist	−0.34	0.0041	2.24	0.02	0.0022	1.20
90% LAD prox	−0.35	0.0040	2.19	−0.00	0.0024	1.31
90% LAD mid	−0.35	0.0036	1.97	−0.01	0.0022	1.20
90% LAD dist	−0.39	0.0039	2.13	0.03	0.0022	1.20

Biplane orthogonal density profiles were computed from this actual slice, and used as input data for the reconstruction process. For each segment the reconstructed mean perfusion level was compared with the corresponding original (actual) mean perfusion level. Two cases were considered: 1) no use of *a priori* expected perfusion levels (uniformly distributed model), and; 2) use of the selected perfusion model. A total of 10 slices were defined, each of which was reconstructed 3000 times (number arbitrarily chosen); the variations in the 3000 cases were caused by the random noise generator.

3.1 The validation of the Segmental Reconstruction Technique

An anatomically relevant model of a slice, for instance one selected distal to a 90% area stenosis in the proximal part of the Left Circumflex artery,

Table 2. The mean values, the standard error of the estimate (SEE) and random error of the estimate (REE) of the paired differences of segmental actual and reconstructed perfusion levels for the worst and best segments in each of the ten cases, reconstructed by the SRT approach without the use of *a priori* information. The mean values are defined in the relative interval from zero to one. Reconstructions were computed 3000 times for each case.

Cases	Worst reconstructed segment			Best reconstructed segment		
	Mean	See	Ree	Mean	See	Ree
100% LCX prox	−0.26	0.0026	1.42	−0.07	0.0016	0.87
100% LCX dist	−0.24	0.0068	1.74	−0.07	0.0016	0.87
90% LCX prox	−0.13	0.0033	1.80	−0.03	0.0023	1.25
90% LCX dist	−0.18	0.0034	1.86	0.05	0.0014	0.76
100% LAD prox	−0.36	0.0026	1.42	−0.08	0.0015	0.82
100% LAD mid	−0.28	0.0029	1.58	−0.07	0.0016	0.87
100% LAD dist	−0.13	0.0033	1.81	−0.02	0.0015	0.82
90% LAD prox	−0.12	0.0034	1.86	−0.01	0.0017	0.93
90% LAD mid	−0.13	0.0034	1.86	−0.02	0.0016	0.87
90% LAD dist	−0.13	0.0029	1.58	−0.06	0.0017	0.93

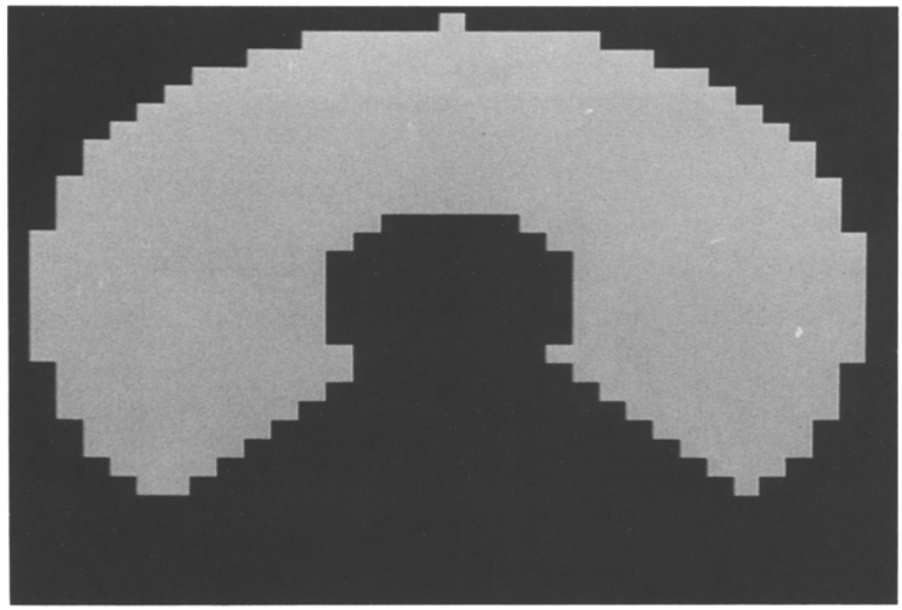

Fig. 7. The perfusion model representing only that the Left Main Coronary artery was injected with contrast agent.

was defined by assigning a perfusion level to each of the eight segments. The actual slice was defined by disturbing the segmental perfusion levels of the model slice with random noise. An example is shown in Fig. 4. Figure 5 shows the reconstructed result in case no *a priori* information of expected perfusion values was used. In this case the selected model was only used to generate a random realization as an actual slice. To show the influence of the model upon the reconstruction result this experiment was repeated with use of the model shown in Fig. 6a. The reconstruction result is shown in Fig. 6b. The close similarity between the model slice and the reconstructed slice demonstrates the strong influence of the model on the reconstructed result.

The results of the ten experiments of the reconstruction without the use of expected perfusion values (no *a priori* information) with various clinically relevant settings are summarized in Table 1. The results of similar experiments performed by incorporating expected perfusion levels (with *a priori* information) are shown in Table 2. Thes tables show only the results of those segments for which the difference between the mean actual segmental perfusion levels and the mean reconstructed segmental perfusion levels were largest (worst reconstructed segments) and, those wiht the smallest differences or reconstruction errors (best reconstructed segments). The mean values indicate the paired differences between the actual segmental perfusion levels and the corresponding reconstructed segmental perfusion levels, calculated over 3000 cases (arbitrarily chosen). All levels are defined in the relative interval from zero to one. The reconstruction errors in the worst cases improved slightly by including *a priori* information into the reconstruction technique. (Compare Table 2 to Table 1).

3.2 The validation of the Network Programming Reconstruction Technique

All experiments performed with the SRT approach were also performed with the NPRT approach. The actual slice was defined by disturbing every perfusion level within each segment of the model slice with random noise. An example for a slice selected distal to a 90% area stenosis in the proximal part of the LAD is shown in Fig. 8a. The uniformly distributed model, which only reflects

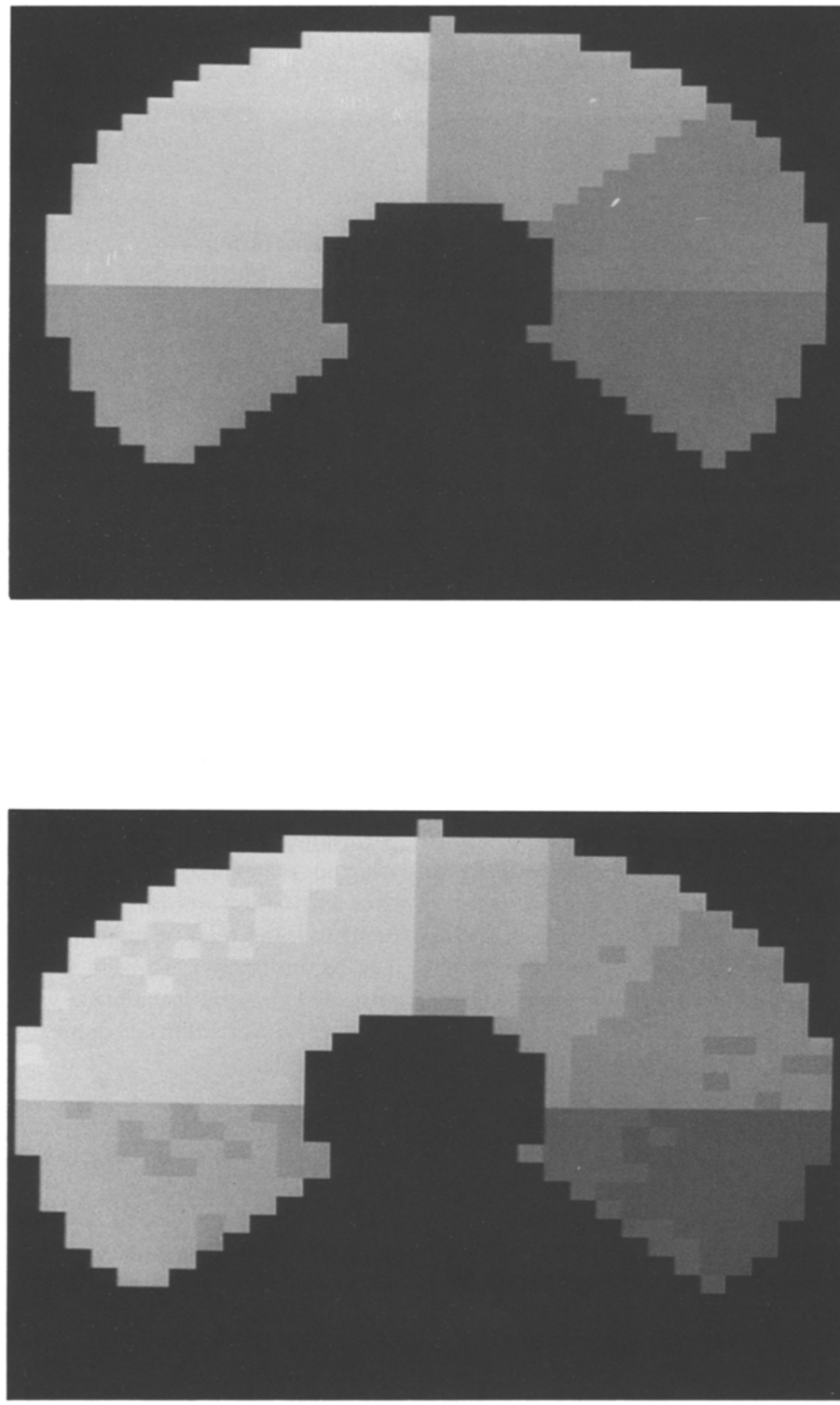

Fig. 8. The perfusion level of each segment in a model similar to the slice shown in Fig. 3 is randomized, to create an actual slice (a). The density profiles of (a) are reconstructed with knowledge of the model shown in Fig. 7. The result is shown in (b).

Table 3. The mean values, the standard error of the estimate (SEE) and random error of the estimate (REE) of the paired differences of segmental actual and reconstructed perfusion levels for the worst and best segments in each of the ten cases, reconstructed by the NPRT approach without the use of *a priori* information. The mean values are defined in the relative interval from zero to sixteen. Reconstructions were computed 3000 times for each case.

Cases	Worst reconstructed segment			Best reconstructed segment		
	Mean	See	Ree	Mean	See	Ree
100% LCX prox	2.94	0.0308	0.77	−0.01	0.0137	0.34
100% LCX dist	3.63	0.0206	1.11	−0.06	0.0063	0.33
90% LCX prox	0.98	0.0173	0.90	−0.09	0.0170	0.89
90% LCX dist	2.09	0.0353	1.00	−0.01	0.0070	0.20
100% LAD prox	3.05	0.0206	0.58	−0.13	0.0329	0.92
100% LAD mid	2.23	0.0275	0.57	0.15	0.0178	0.37
100% LAD dist	1.92	0.0781	2.10	−0.11	0.0452	1.20
90% LAD prox	0.49	0.0169	1.00	−0.01	0.0121	0.74
90% LAD mid	−0.78	0.0392	1.20	−0.02	0.0315	0.96
90% LAD dist	−1.40	0.0259	0.71	−0.02	0.0113	0.60

the fact that a left coronary arteriography was performed, is shown in Fig. 7; no perfusion is expected in segments 5 and 6, which are supposed to be related to the Right Coronary Artery. In Fig. 8b the reconstruction results are presented. Streaks, known for backprojections from a limited number of views, are visible. This experiment shows that the actually uniformly distributed segments remain, though visually judged, rather uniformly distributed.

Figure 9 demonstrates both the influence of the model on the reconstruction result, and the conservation of the non-uniform distribution of perfusion levels. The perfusion model of Fig. 9a was chosen such that in segment 0 normal perfusion was expected, which did not correspond with the generated actual slice. To generate this slice, each voxel was assigned a random perfusion level. The mean perfusion level for each segment was identical to the corresponding segment in Fig. 8a. From this actual slice the density profiles were computed and reconstructed with knowledge of the model shown

Table 4. The mean values, the standard error of the estimate (SEE) and random error of the estimate (REE) of the paired differences of segmental actual and reconstructed perfusion levels for the worst and best segments in each of the ten cases, reconstructed by the NPRT approach without the use of *a priori* information. The mean values are defined in the relative interval from zero to sixteen. Reconstructions were computed 3000 times for each case.

Cases	Worst reconstructed segment			Best reconstructed segment		
	Mean	See	Ree	Mean	See	Ree
100% LCX prox	0.88	0.0204	0.65	0.07	0.0093	0.29
100% LCX dist	1.08	0.0200	0.61	0.01	0.0204	0.73
90% LCX prox	0.35	0.0208	1.10	−0.00	0.0133	0.68
90% LCX dist	1.72	0.0304	1.10	−0.00	0.0051	0.18
100% LAD prox	0.66	0.0162	0.52	0.02	0.0122	0.39
100% LAD mid	1.41	0.0945	3.00	0.08	0.0151	0.48
100% LAD dist	0.30	0.0191	0.60	0.02	0.0178	0.56
90% LAD prox	0.45	0.0343	1.00	−0.00	0.0268	0.81
90% LAD mid	0.95	0.0184	1.00	−0.00	0.0037	0.21
90% LAD dist	0.29	0.0187	0.71	0.00	0.0144	0.54

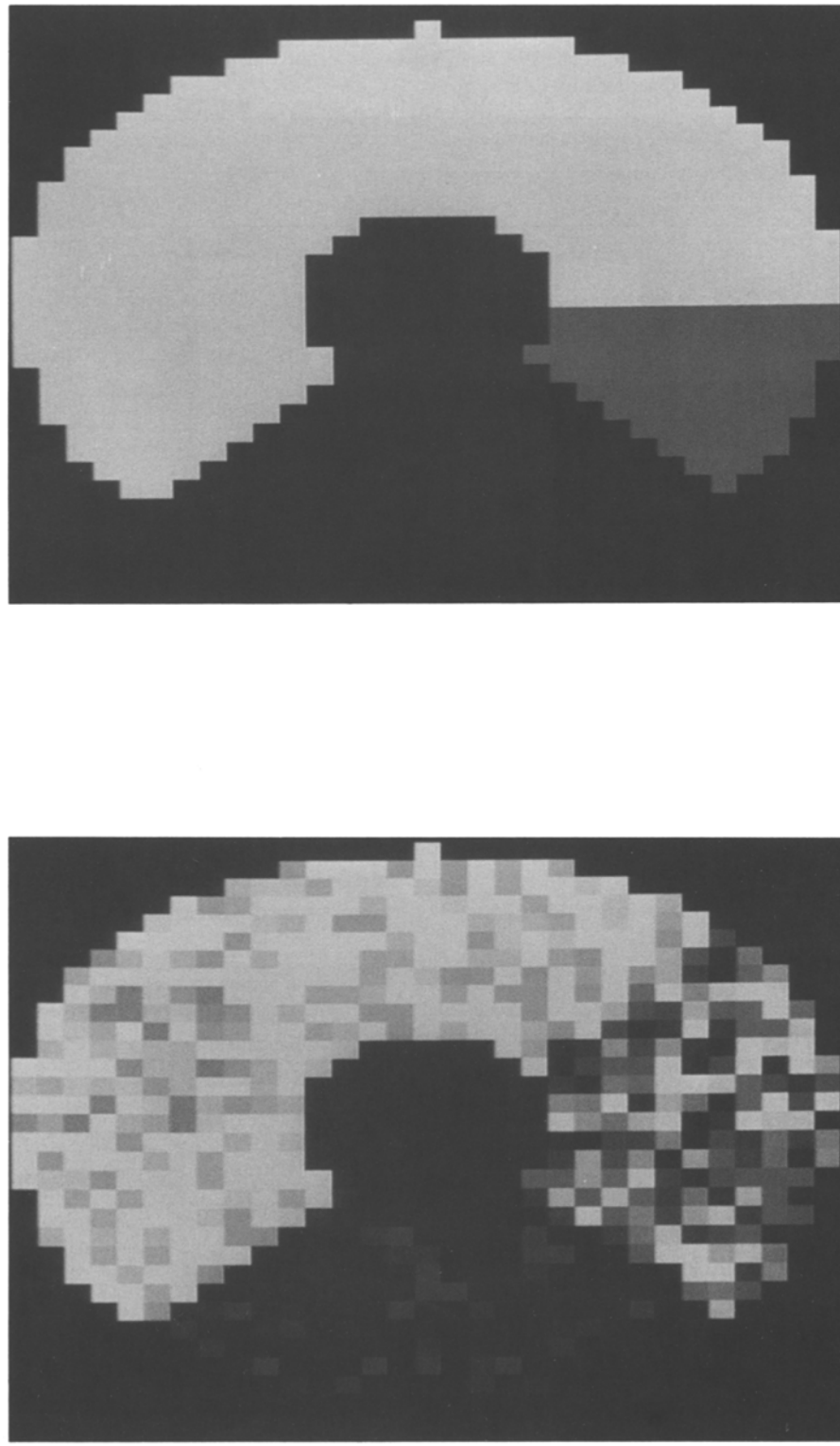

Fig. 9a & b.

in Fig. 9a. The reconstruction result is shown in Fig. 9c. It is clear that the incorrectly expected perfusion levels in segment 7 tends to attract low perfusion levels.

The results of the experiments of the NPRT reconstruction without the use of *a priori* information for the same ten cases as used in the Tables 1 and 2 are summarized in Table 3. The results of similar experiments including *a priori* information are presented in Table 4. Again only the results of the worst and best reconstructed segments are shown. All levels are now defined in the interval from zero to sixteen. It is clear that the worst cases improved by including *a priori* perfusion levels into the reconstruction technique.

4. Conclusions

Though both the SRT and the NPRT are still under development and were only validated with computer-generated data, we may conclude the following from the results obtained so far:

(1) The SRT performs well as a low spatial resolution technique;
(2) The SRT requires *only a priori* information of the myocardial geometry;
(3) The SRT will provide the very first slice under reconstruction;
(4) The NPRT performs well as a medium spatial resolution reconstruction technique;
(5) The NPRT requires *a priori* information of the myocardial geometry;
(6)The NPRT performs better when applying the slice adjacent to the one under reconstruction as a model.

The SRT was implemented in the C-programming language and uses approximately one second of processing time per slice on a Compaq 386 AT compatible Personal Computer. The NPRT was implemented in the Pascal programming language and uses less then 30 seconds of processing time per slice on the same machine. No special efforts were made towards the implementation of run-time efficient code. So far the resolution of the NPRT slices was limited by the hardware to $32 \times 32 \times 16$ pixels. Developments are directed towards a resolution of

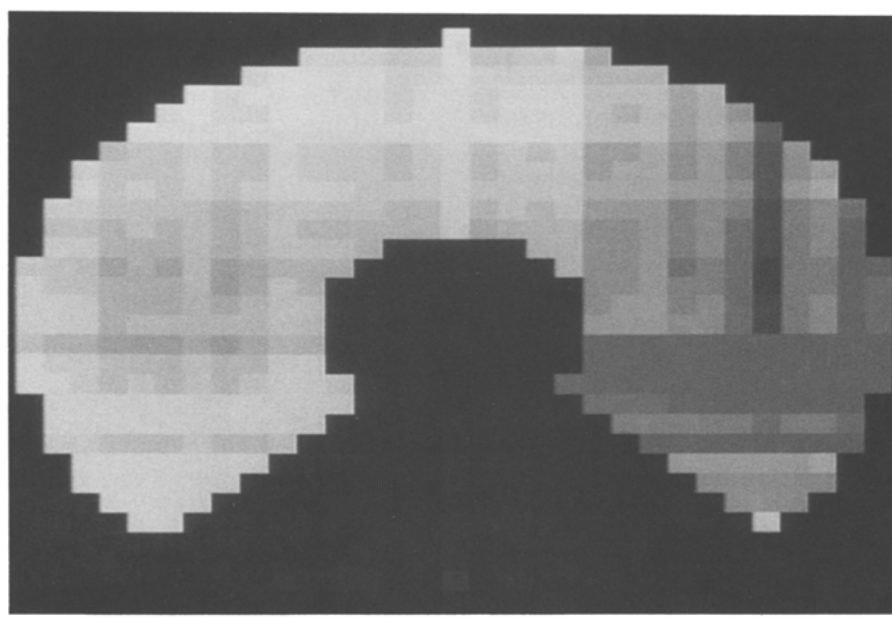

Fig. 9. The perfusion level of each voxel is randomized to define an actual slice (b). An incorrectly chosen model (a) is used to reconstruct the density profiles of (b). The result, with visual resemblance to the model is shown in (c).

128 × 128 × 32 pixels, in order to obtain slices comparable to those obtained by Thallium-201 tomography.

Computer-simulated experiments will be further extented with a sensitivity measure for deviations in myocardial geometry. Both reconstruction techniques will also be validated with patient studies of dual plane coronary flow reserve analysis and Thallium-201 tomography in the near future.

Acknowledgements

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