Motion compensated tomography reconstruction of coronary arteries in rotational angiography

Bousse Alexandre [1 2 3], **Zhou Jian** [1 2], **Yang Guanyu** [1 2 3], **Bellanger Jean-Jacques** [1 2], **Toumoulin Christine** [1 2 *]

[1] *LTSI, Laboratoire Traitement du Signal et de l'Image INSERM : U642, Université de Rennes I, Campus de Beaulieu, 263 Avenue du Général Leclerc - CS 74205 - 35042 Rennes Cedex,FR*

[2] *CRIBS, Centre de Recherche en Information Biomédicale sino-français INSERM : Laboratoire International Associé, Université de Rennes I, SouthEast University, Nankin,CN*

[3] *LIST, Laboratory of Image Science and Technology SouthEast University, Si Pai Lou 2, Nanjing, 210096,CN*

* Correspondence should be adressed to: Christine Toumoulin <christine.toumoulin@univ-rennes1.fr>

Abstract

This paper deals with the 3-D reconstruction of the coronary tree from a rotational X-ray projection sequence. It describes the following three stages: the reconstruction of the 3-D coronary tree at different phases of the cardiac cycle, the motion estimation, and the motion-compensated tomographic reconstruction of the 3-D coronary tree at one given phase using all the available projections. Our method is tested on a series of simulated images computed from the projection of a segmented dynamic volume sequence acquired in multislice computed tomography imaging. Performances are comparable to those obtained by reconstruction of a statical coronary tree using an algebraic reconstruction technique algorithm.

MESH Keywords Coronary Angiography ; methods ; Models, Cardiovascular ; Motion ; Radiographic Image Enhancement ; methods ; Tomography, X-Ray Computed

Author Keywords
Index Terms
Angiography ; B-spline interpolation ; deformable model ; inverse problem ; penalized least squares ; rotational X-ray

Introduction

Today, rotational X-ray angiography is commonly used for the diagnosis and treatment of coronary artery diseases. Analyzing 2-D X-ray projections, specialists can localize pathologies such as stenosis. For obvious reasons, 3-D reconstruction of the coronary tree is of major interest. This task falls within the field of 3-D tomographic reconstruction: from a projection data vector **g**, we wish to recover a volume image **f** such that

$$\mathbf{g} = \mathsf{P}\mathbf{f}$$

where

denotes the tomographic cone-beam projector. Unfortunately, due to heart motion, the full set of projections cannot be used directly: each projection corresponds to a different volume $\mathbf{f}_t$ and the direct reconstruction leads to inconsistencies in the inverse problem (1). Therefore, inverse problem (1) must be rewritten as

$$\mathbf{g}_t = \mathsf{P}_t W_t \mathbf{f}_1 \quad \forall\, t \in \mathsf{T}$$

where

$_t$ is the projection operator at time t, W_t is a motion operator that maps the first volume $\mathbf{f}_1$ to $\mathbf{f}_t$, and
is the set of considered time states.

If W_t is unknown, this difficulty can be overcome by considering a smaller part of the projections that correspond to the same heart phase (around four to six projections). In this situation, inverse problem (1) becomes strongly ill-posed, due to the small size of **g**. To compensate this, a suitable image prior must be included in the reconstruction algorithm [8], [4]. Another solution is to estimate the motion and the volume image simultaneously in a joint estimation algorithm. This approach has been applied in [5] in the case of positron emission tomography (which is time-consuming), and in [3] for filtered backprojection.

A third approach described here is to estimate motion prior to image volume reconstruction. Our aim is to demonstrate, through an idealized situation, which optimal performances can be expected. Our paper starts with the same assumptions used in [1]: we assume that a 3-D model of the coronary tree has been reconstructed at a reference time, and that the 2-D centerlines have been extracted from each projection.

In Section II, we present a deformable model of the coronary 3-D skeleton that yields an estimation of motion operator W_t using a B-spline model, by performing a quadratic minimization (instead of a nonquadratic minimization [1]). In Section III, we propose a

penalized least-squares reconstruction method, called reconstruction with motion compensation and vessel prior (RMCVP), which uses the set of all tomographic projections. Section IV presents our results on simulated data.

Deformable Tree Model and Motion Estimation

In order to solve inverse problem (2), the motion operator W_t must be estimated. In Section II-A, we propose a deformable tree model to estimate the 3-D skeletons of the coronary tree at each cardiac phase. In Section II-B, the motion operator W_t is constructed by mapping each of the reconstructed 3-D skeletons to the 3-D skeleton of the first cardiac phase.

Deformable Tree Model

Let us denote by $\mathbf{f}_t$ the volume vector at time $t \in [0, NT]$. We assume that the time-dependent volume $\mathbf{f}_t$ is T -periodical: for all $t \in [0, (N-1)T]$, $\mathbf{f}_{t+T} = \mathbf{f}_t$, T denoting the duration of a cardiac cycle and N the number of observed cardiac cycle. $\mathbf{f}_t$ is observed through a finite number of projections at regular instants $t_j = jT/S$, $j \in \{1,\ldots, NS\}$, where S is the number of projections in a cardiac cycle. Hence, the sequence $(\mathbf{f}_{t_j})_j$ is S-periodical, and we can rewrite $\mathbf{f}_{t_j} = \mathbf{f}_s$, with $s = j \bmod(S)$. $\mathbf{f}_s$ now denotes the volume at phase s of the cardiac cycle.

Let $\Theta_s = \{\vartheta_{1,s},\ldots,\vartheta_{N,s}\}$ be the device positions (angles) corresponding to a given phase s of the cycle and $P(\vartheta_{1,s}),\ldots, P(\vartheta_{N,s})$ be the corresponding projection planes containing the extracted vessels. The proposed method considers that a first 3-D skeleton of the coronary tree has been reconstructed at phase $s = 1$ [1]. Let us denote $V_1 = \{v_1^1, \ldots, v_L^1\} \subset \Omega$, the first 3-D coronary skeleton, where Ω is a bounded subset of $\mathbb{R}^3$. Our purpose is to estimate the 3-D skeleton V_s of each volume $\mathbf{f}_s$ from deformations of V_1. A topological structure on V_s is required to define a regularity cost to prevent its successive deformations to result in a degenerate tree. Two points are said to be neighbors if and only if they are consecutive points on a same branch. The estimation of V_s from V_{s-1} is performed via the minimization of a cost function that is composed of a data fidelity term and a regularization term. For each projection angle ϑ, let $P_\vartheta^{\text{geom}}(v) \in P(\vartheta)$ be the geometric cone-beam projection of the 3-D point v on the projection plane $P(\vartheta)$:

$$P_\vartheta^{\text{geom}}(v) = \frac{a}{b + v_x \cos(\vartheta) + v_y \sin(\vartheta)} \begin{bmatrix} v_x \sin(\vartheta) - v_y \cos(\vartheta) \\ v_z \end{bmatrix}$$

where a (respectively, b) is the distance of the X-ray source to the detector (respectively, the volume center). We can now define the data cost of a 3-D skeleton V with respect to the projections at phase s

$$E_s(V) = \frac{1}{N\,|V|} \sum_{v \in V} \sum_{n=1}^{N} D_{\vartheta_{n,s}}(P_{\vartheta_{n,s}}^{\text{geom}}(v))$$

where $|V|$ denotes the cardinal of the set V, and $D_\vartheta : P(\vartheta) \to \mathbb{R}_+^*$ is a function calculating the distance to the extracted vessels, defined as follows. If v is a vessel endpoint, then $D_\vartheta(P_\vartheta^{\text{geom}}(v))$ is equal to the square distance between $P_\vartheta^{\text{geom}}(v)$ and the corresponding endpoint in the extracted vessel in $P(\vartheta)$. If υ is not an endpoint, then we calculate $D_\vartheta(P_\vartheta^{\text{geom}}(v)) = \Gamma(\vartheta)^{-1} \sum_{i=1}^{n_{\min}} \gamma_i(\vartheta) \| P_\vartheta^{\text{geom}}(v) - c_i \|^2$, where $\Gamma(\vartheta) = \sum_{i=1}^{n_{\min}} \gamma_i(\vartheta)$, $c_1,\ldots c_{n_{\min}}$ are the $n_{\min}$ closest points to $P_\vartheta^{\text{geom}}(v)$ in the extracted vessel in $P(\vartheta)$, and the $\gamma_i(\vartheta)$ coefficients are weights that take into consideration local properties of $P_\vartheta^{\text{geom}}(V)$, like the difference of directions between the projected vessel at point $P_\vartheta^{\text{geom}}(v)$ and the segmented vessel at point c_i. The regularization term $\mathbf{F}(V)$ corresponds to a deformation energy and is equal to the normalized sum of the square distances between two neighboring points (in the sense of the topological structure defined earlier):

$$F(V) = \frac{1}{\Upsilon(V)} \sum_{\ell \sim \ell'} \left\| v_\ell - v_{\ell'} \right\|^2$$

where $\Upsilon(V)$ denotes the number of cliques in V. Finally, for all $s \in \{2,\ldots, S\}$, the deformation energy $\mathbf{D}_s(V)$ for the estimation of V_s is

$$D_s(V) = E_s(V) + \kappa F(V)$$

where κ is a parameter that controls the elasticity of V. For $s = 2,\ldots, S$, the estimation of V_s from V_{s-1} is performed as follows: at iteration (q), points $v_\ell^{(q)}$ are displaced one by one in the gradient direction $\nabla_\ell E_s(V^{(q)})$ (∇_ℓ denotes the gradient with respect to υ_ℓ), with a time step $\delta_{q,\ell}$ equal to $N^{-1} \sum_{n=1}^{N} D_{\vartheta_{n,s}}(P_{\vartheta_{n,s}}^{\text{geom}}(v_\ell^{(q)}))$, in order to slow down the motion as $V^{(q)}$ approaches the solution.

Motion Parameters Estimation

Once we have an estimation of each 3-D coronary tree model V_s, the next step is to estimate the registration functions that compensate the motion in the tomographic reconstruction: for each $s \in \{2,\ldots, S\}$, we wish to build a function $\phi_s : \mathbb{R}^3 \to \mathbb{R}^3$ such that for each $\ell \in \{1,\ldots, L\}$, $\phi_t(v_\ell^s) \simeq v_\ell^1$. Let

be a grid of Ω centered on the voxels and $\mathcal{M}$ be a subgrid of

. A B-spline parametric model is chosen to represent $\phi_s = \phi_{\alpha_s} = (\phi_{\alpha_s}^X, \phi_{\alpha_s}^Y, \phi_{\alpha_s}^Z)$: for all $(c, C) \in \{x, y, z\} \times \{X, Y, Z\}$,

$$\phi^{C}_{\alpha_s}(x, y, z) = c + \sum_{m=1}^{|\mathcal{M}|} \alpha^{m}_{X,s} b_m(x, y, z)$$

where $b_m(x, y, z) = b(x - x_m)b(y - y_m)b(z - z_m)$ is a cubic B-spline function centered on $(x_m, y_m, z_m) \in \mathcal{M}$. The estimation of $\alpha_s = \{(\alpha^m_{X,s}, \alpha^m_{Y,s}, \alpha^m_{Z,s})\}_{m=1}^{|\mathcal{M}|}$ is carried out by minimizing a least-squares cost function

$$\psi(\alpha_s) = \sum_{\ell=1}^{L} \left\| \phi_{\alpha_s}(v^s_\ell) - v^1_\ell \right\|^2 + \mu \sum_{m \sim m'} \left\| \alpha^m_s - \alpha^{m'}_s \right\|^2 + \nu \|\alpha_s\|^2$$

where the second sum is taken over the neighboring points of $\mathcal{M}$, and μ and ν are regularization parameters. By convention, $\alpha_1 = 0$.

Tomographic Reconstruction

In order to import the motion in an algebraic formula, we must compute a motion matrix $W(\alpha_s)$ that maps the volume vector at phase $s = 1$ to the volume vector at phase s, for each $s \in \{2,\ldots, S\}$. The volume vectors $\mathbf{f}_1, \ldots, \mathbf{f}_S$ must be redefined: let $f_1: \Omega \subset \mathbb{R}^3 \to \mathbb{R}$ be the 3-D volume function at phase $s = 1$. We assume that f_1 can be written as the sum of B-spline functions $w_p(x, y, z) = w(x - x_p)\, w(y - y_p)w(z - z_p)$ centered on the voxel grid

: $f_1(x, y, z) = \sum_{p=1}^{|G|} u_p w_p(x, y, z)$. The transformation f_s of the image f_1 from the motion ϕ_{α_s} is a result of the composition1 $f_s(x, y, z) = f_1(\phi_{\alpha_s}(x, y, z)) = \sum_{p=1}^{|G|} u_p w_p(\phi_{\alpha_s}(x, y, z))$. Let us denote $\mathbf{f}_s = (f_s(x_1, y_1, z_1), \ldots, f_s(x_{|}$

$_{|}, y_{|}$

$_{|}, z_{|}$

$_{|}))^T$, with $(x_j, y_j, z_j) \in$

for all $j \in \{1,\ldots, |$

$|\}$. Thus, we have the matrix formulation $\mathbf{f}_s = W(\alpha_s)\mathbf{u}$, where $\mathbf{u} = (u_1, \ldots, u_{|}$

$_{|})^T$ and $(W(\alpha_s))_{j,p} = w_p(\phi_{\alpha_s}(x_j, y_j, z_j))$. Our aim is now to estimate $\mathbf{u}$ by solving the least-squares problem

$$\text{minimize} \sum_{s=1}^{S} \left\| P_{\Theta_s} W(\alpha_s)\mathbf{u} - \mathbf{g}_s \right\|^2 + \varrho Pr(\mathbf{u})$$

such that $\forall p \in \{1,\ldots, |$

$|\}$, $u_p \geq 0$. Here,

Θ_S denotes the tomographic cone beam projector at angles $\Theta_s = \{\vartheta_{1,s}, \ldots, \vartheta_{N,s}\}$ (please note that

Θ_S is different from

$^{geom})$ and $\mathbf{g}_s$ the corresponding observed projections. Pr(**u**) is a vessel prior cost on **u** defined as follows: for all $p = 1,\ldots, |$

$|$, let $\Delta_p = \min\{d^2((x_p, y_p, z_p), v^1_\ell),\ \ell = 1, \ldots, L\}$ be the square distance of voxel p to V_1. We define Pr(**u**) as

$$\Pr(\mathbf{u}) = \sum_{p=1}^{|G|} \Delta_p \, |u_p|^{\beta}$$

where $\beta > 0$. This function penalizes high values for voxels that are located far from the centrelines. A similar prior has been used in [4].

Results

We simulated 3-D volumes of a coronary tree at 20 different cardiac phases, using 3-D centrelines $V_1, \ldots, V_{20}$ that had been extracted previously from a 3-D dynamic sequence acquired on a 64 slice general electric (GE) light-speed computed tomography (CT) coronary angiography [7]. This sequence included 20 volumes reconstructed at every 5% of the RR interval. The simulated dynamic volume is a sequence of binary functions $\mathbf{f}_s$:

$\to \{0, 1\}$, such that $\mathbf{f}_s(\upsilon) = 1$ if υ is located in a tube centered on the 3-D centerlines V_s and $\mathbf{f}_s(\upsilon) = 0$ in the opposite case. A Gaussian white noise with a standard deviation $\sigma = 0.05$ was added to the 2-D extracted centrelines coordinates, in order to simulate gating and 2-D centrelines extraction errors. The dimension of the voxel grid

is 192 × 192 × 192.

is included in a cube Ω whose vertex coordinates are (±0.5,±0.5,±0.5). The number of cycles is 4 with a total of 80 projections uniformly distributed from 0° to 120°. Each volume $\mathbf{f}_s$ is projected four times during the acquisition. The projection operator

Θ_S has been computed following [6].

3-D Centerlines and Motion Estimation

The motion grid $\mathcal{M}$ is an 8 × 8 × 8 uniform grid of Ω. The 2-D centrelines at each phase s have been drawn by performing geometric projections of each 3-D centrelines V_2,..., V_{20} on the projection planes $P(\vartheta_{1,s})$, ..., $P(\vartheta_{N,s})$. We chose κ = 1.5 for the model deformation algorithm, μ = 0.1 and ν = 0.005 for the estimation of α_s. In Fig. 1, the two selected cardiac states correspond to the end diastolic and systolic phases, respectively, in order to test the robustness of the method for the largest movements. In most cases, the algorithm for the construction of a coronary tree at a given cardiac phase has converged after less than 30 iterations.

Tomographic Reconstruction

Because we strive to obtain the 3-D spatial support of the vessels (and not the density distribution inside the vessels that reflects only the contrast medium), we decided to threshold the reconstructed data in order to get a binary object equivalent to the original set and then to compare their binary supports. The threshold value has been varied to demonstrate its influence. We calculated the reconstruction error as follows: the reconstructed volume $\mathbf{f}$ was binarized using a threshold ς and compared with the original binary volume $\mathbf{f}_1$ at phase s = 1, according to the formula

$$\epsilon_{\varsigma}(\hat{\mathbf{f}}, \mathbf{f}_1) = 1 - \frac{|\mathrm{Supp}(\mathrm{bin}_{\varsigma}(\hat{\mathbf{f}})) \cap \mathrm{Supp}(\mathbf{f}_1)|}{|\mathrm{Supp}(\mathbf{f}_1)|}$$

where $\mathrm{bin}_{\varsigma}(\mathbf{f})$ denotes the binarized transformation of $\mathbf{f}$ with threshold ς and Supp($\mathrm{bin}_{\varsigma}(\mathbf{f})$) (respectively, Supp($\mathbf{f}_1$)) denotes the set of voxels, such that $\mathrm{bin}_{\varsigma}(\mathbf{f})$ (respectively, $\mathbf{f}_1$) is equal to 1. Two projections of the simulated volume $\mathbf{f}_1$ at the first cardiac phase can be seen in Fig. 2. We used a gradient-based method to solve the least-squares problem (4) with ϱ = 1.5 and β = 1. Results obtained with our method (RMCVP) are displayed in Fig. 2. We compared our results with two other methods: the reconstruction with no MCVP (RNMCVP) method and the gated reconstruction with vessel prior (GRVP) method. The RNMCVP method is a penalized least-squares reconstruction method using all of the 80 projections by minimizing (4) with no motion compensation (i.e., $W(\alpha_s)\mathbf{u}$ is replaced by $\mathbf{f}_1$ and the minimization is performed with respect to $\mathbf{f}_1$). The GRVP is a penalized least-squares reconstruction method also based on the minimization of (4) where the projection operator

performs only four projections that are taken at the same cardiac phase. This method also includes the image prior (5). A reference score is obtained by solving the inverse problem (1) where volume $\mathbf{f}$ remains static throughout the 80 projections, using an algebraic reconstruction technique (ART) algorithm [2]. This method is supposed to represent an ideal case. All algorithms have converged within less than 50 iterations. Results are presented in Table I. In terms of performances, RMCVP is comparable to statical ART reconstruction. In terms of results, RMCVP is better than GRVP, suggesting that as long as motion is well compensated, reconstruction is more efficient when all projections are used instead of only four gated projections.

Discussion and Conclusion

We briefly introduced in this paper in progress an algebraic reconstruction method for the reconstruction of coronary arteries from a full sequence of X-ray rotational projections. The evaluation of the method has been carried out on simulated data. The aim of our simulation was to demonstrate which performance can be expected when the motion (or deformation) is estimated prior to the reconstruction, using assumptions done in [1]. The parameter spaces, intrinsic to the method, were systematically explored in order to evaluate their impact on result quality. Thus, a too large κ value will lead to an incorrect estimation since it will introduce a large variation in the shape of the vessel. Conversely, if κ is too small, irregular matching may appear along the vessels. Its value has been chosen to involve a smooth deformation of the 3-D coronary model. The respective values of μ, ν, and ϱ have a much smaller impact, allowing relatively large ranges: [0.01, 1] for μ, [0.0001, 1] for ν, and [0.5, 20] for ϱ. A β-value larger than 2 tends to favor a smooth reconstruction.

Several key issues remain to be analyzed. Any volume reconstruction method including a motion prior is submitted to time computation and memory constraints, which requires special attention. We have used a volume of 192 × 192 × 192, and our method requires 15 min on a standard computer (Processor Intel Core2 CPU, clock speed: 2.66 GHz, Memory size: 4 GB) (67% for the centreline estimation, 33% for reconstruction). It is also critical to take into account all the errors that can be made during the process in clinical setting. Vessel segmentation in the projections (no detection or false detection), background effects, and inaccuracies in motion estimation are among the major ones and must be further examined. The complexity (i.e., number of branches) of the object and the presence of abnormal patterns (stenoses and thin or tortuous vessels for instance) are another important issue.

Ackowledgements:

The authors are indebted to J.-L. Coatrieux for having constantly advised us on this research project.

Footnotes:

1

In theory, we should use a diffeomorphism ϕ_{α_s} that maps V_1 to V_s and perform the composition

$I_1 \circ \varphi_{\alpha_s}^{-1}$

. Because our B-spline model is not “exactly” invertible, we used a function ϕ_{α_s} that approximately maps V_s to V_1.

References:

- 1. Blondel C , Malandain G , Vaillant R , Ayache N Reconstruction of coronary arteries from a single rotational x-ray projection sequence. IEEE Trans Med Imag. 25: (5) 653 - 663 May 2006;
- 2. Grangeat P La Tomographie : Fondements Mathématiques, Imagerie Microscopique et Imagerie Industrielle. Paris, France Lavoisier; 2002; 287-
- 3. Grangeat P , Koenig A , Rodet T , Bonnet S Theoretical framework for a dynamic cone-beam reconstruction algorithm based on a dynamic particle model. Phys Med Biol. 47: (15) 2611- 2625 Jul 2002;
- 4. Hansis E , Schäfer D , Grass M , Dössel O An iterative method for the reconstruction of the coronary arteries from rotational x-ray angiography. Proc SPIE Med Imag. 2007 ; 6510: 651026-1- 651026-10
- 5. Jacobson MW Approaches to motion-corrected PET image reconstruction from respiratory gated projection data. PhD dissertation. Univ. Michigan; Ann Arbor, MI 2006;
- 6. Man BD , Basu S Distance-driven projection and backprojection in three dimensions. Phys Med Biol. 49: 2463- 2475 May 2004;
- 7. Yang G , Bousse A , Toumoulin C , Shu H A multiscale tracking algorithm for the coronary extraction in MSCT angiography. Proc Eng Med Biol Soc (EMBS). 2006; 1: 3066- 3069
- 8. Zhou J , Bousse A , Yang G , Bellanger J , Luo L , Toumoulin C , Coatrieux J A blob-based tomographic reconstruction of 3d coronary tree from rotational x-ray angiography. Proc SPIE Med Imag. 2008; 69132N-1- 69132N-12

Fig. 1

Result of the deformation algorithm between end of systole and end of diastole.

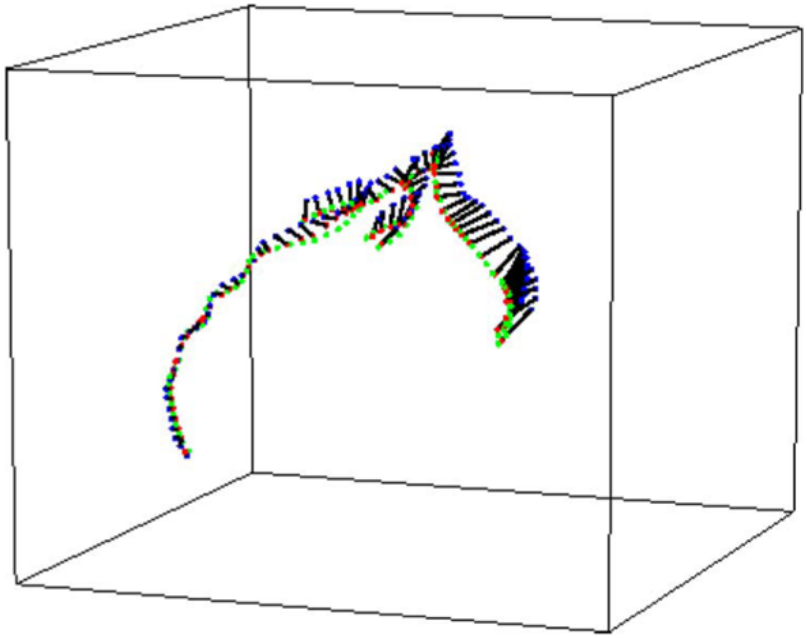

Fig. 2

First row: projection data of the coronary tree at phase s = 1. Second row: projections of the reconstructed volume using the RMCVP method.

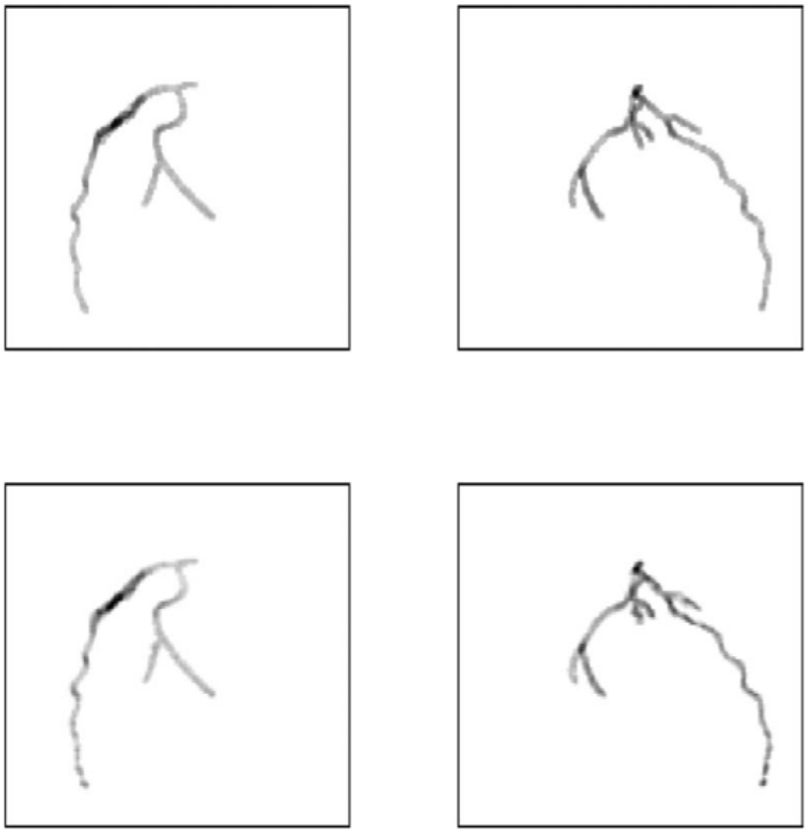

TABLE I

Reconstruction Error of the Four Methods

Method	RNMCVP	GRVP	RMCVP (σ = 0 / σ = 0.05)	Static ART
ς = 0.1	79%	25%	11/14%	8%
ς = 0.3	66%	21%	6/7%	5%
ς = 0.7	81%	24%	10//12%	8%