Automatic Coronary Artery Tree Labeling in Coronary Computed Tomographic Angiography Datasets

Guanyu Yang[1,2], Alexander Broersen[1], Robert Petr[3], Pieter Kitslaar[1], Michiel A de Graaf[3], Jeroen J Bax[3], Johan HC Reiber[1], Jouke Dijkstra[1]

[1]Division of Image Processing, Dept. of Radiology, LUMC, Leiden, The Netherlands
[2]Lab of Image Science and Technology, Southeast University, Nanjing, China
[3]Dept. of Cardiology, LUMC, Leiden, The Netherlands

Abstract

In this paper, an automatic coronary tree labeling algorithm is developed for labeling the extracted branches with their anatomical names for CCTA datasets. A two-step matching algorithm is implemented by means of a statistical coronary tree model. The main branches are first identified in a registration step. Then all the segments including proximal, middle and distal parts of the main branches and all side-branches in the coronary tree are labeled. Additional clinical criteria are used to generate the final result. Fifty-eight CCTA datasets with right-dominant coronary trees were used for the evaluation. Compared with manually corrected results by an expert, 37 labels (4.76%) in the automatic results were needed to be changed or removed. For the remaining 741 labels obtained by the automatic method, the average overlap measurement between the expert reference and automatic results was 91.41%.

1. Introduction

Coronary computed tomographic angiography (CCTA) as a non-invasive imaging modality is widely adopted for the diagnosis of coronary artery disease [1]. According to the CCTA image guidelines for interpretation and reporting [2], radiologists and cardiologists usually report pathological findings, such as calcifications, stenoses and occlusions, per artery or per segment. Thus, an automatic coronary artery extraction and labeling algorithm is demanded which can extract coronary arteries and assign the anatomical labels to the extracted arteries. It facilitates the workflow for the radiologists and cardiologists. A number of methods have shown that the centerlines of coronary arteries in CCTA images can be extracted automatically [3]. Recently, we developed an automatic coronary tree centerline extraction algorithm to improve the centerline extraction ability and accuracy [4].

Several approaches [5, 6] focused on the coronary tree labeling in 2D X-ray angiography. But assigning the anatomical labels to coronary arteries in 3D CCTA images has different challenges. For instance, in CCTA images coronary arteries especially some tiny side-branches cannot be fully extracted because of the lower spatial resolution of CCTA images, motion artifacts and presence of calcification and stenoses. Therefore, coronary artery tree labeling in CCTA images should be studied. To the best of our knowledge, the literature on automatic coronary tree labeling in CCTA images is very limited. Recently, Akinyemi [7] presented an automatic labeling method which used geometric features of coronary arteries to train a multivariate Gaussian classifier. In this method, the large anatomical variation of the training datasets such as the size of the heart might decrease the accuracy the labeling results. Furthermore, vessel diameters were used as local features for training the classifier, which were difficult to be estimated accurately without any user-interactions because of the presence of the calcifications, stenoses etc.

In this paper, we focus on an automatic coronary artery tree labeling algorithm in CCTA images. This algorithm is mainly based on a 3D coronary tree model [8]. The main branches in the extracted coronary artery tree are firstly identified and then all the segments, i.e. the proximal, middle and distal parts of main branches and side branches, are labeled. Additional clinical criteria widely used by cardiologists are adopted to generate the final labeling results. In this preliminary study, fifty-eight clinical datasets with a right-dominant coronary artery tree were used to evaluate the algorithm.

2. Methodology

Fig. 1 displays the pipeline of our automatic coronary artery tree labeling algorithm which can be divided into two main steps. First, four main arteries, i.e., right coronary artery (RCA), left main (LM) artery, left anterior descending (LAD) artery and left circumflex (LCx) artery, will be identified by aligning them with the coronary tree model. Second, all the labels in the coronary tree model including the proximal, middle and distal parts of the main branches as well as the side-

branches are matched with their candidates in the extracted coronary artery tree to find the initial labeling result. After adjusting the initial labeling result according to clinical criteria, the final labeling result will be generated. These steps will be described in the following sections.
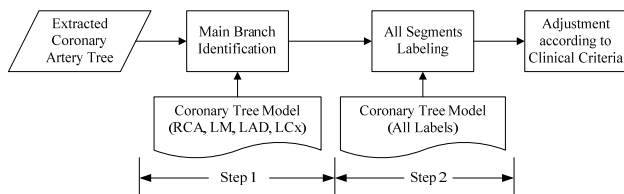

Fig. 1 Pipeline of coronary artery tree labeling.

2.1. Coronary artery tree model

In our preliminary study, a 3D coronary artery tree model of right-dominant type is used to provide *a priori* knowledge which is based on the statistical results presented by Dodge et al. [8]. Fig. 2 demonstrates the centerlines of this 3D coronary artery tree model. This model is composed by a LM branch and three sub-trees which are defined in Table 1. This model is based on the 17-segments model defined by the American Heart

Fig. 2 3D model of coronary artery tree.

Association (AHA) [9] which is widely adopted in the clinical practice. In this model, the actual marginal branches derived from RCA are not included. In addition, the side-branches belonging to the left- or co-dominant types such as L-PDA are not included.
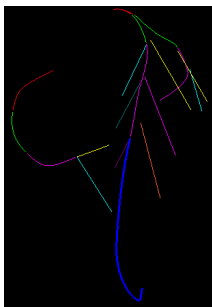
Table 1. Labels used in the coronary artery tree model (p = proximal, m = mid, d = distal)

Sub-tree	Main branch	Side-branches
RCA	pRCA, mRCA, dRCA	right posterior descending (R-PDA) artery, right posterior lateral (R-PLB) artery
LAD	pLAD, mLAD, dLAD	three septal (S1~S3) arteries, three diagonal arteries (D1~D3)
LCx	pLCx, LCx	two obtuse marginal (OM1, OM2) arteries

2.2. Main branch identification

Because the extracted coronary artery tree may have a different position, orientation and size as compared to the model, the local features such as vessel length, branch direction, etc. cannot be used to derive robust rules to detect the main branches. Thus, a centerline registration step is performed to align the patient coronary artery tree

with the 3D model. In a few cases, the side-branches cannot be extracted because of the motion artifacts or the partial volume effect. All of the side-branches except RPLB are removed from 3D model and registered with the extracted centerlines of coronary arteries using a point-set registration method [10]. The centerlines of both the extracted coronary artery tree and the model are normalized and re-sampled before the alignment. The maximum vessel lengths of left and right coronary artery trees in the extracted dataset, L_L and L_R, are calculated respectively. Then the distal parts of main branches in the model are cut to the same length as the L_L or L_R in order to avoid matching the long centerline in the model with a short one in the extracted tree when the main branches in the tree are not fully extracted.

The rigid transformation between the extracted tree and model centerlines is estimated. Because extracted centerlines normally include main branches and some side-branches, we ensure that the main branches in the model are attracted by the main branches in the extracted data. Therefore, the points along the centerlines in the extracted data are assigned to different weighting factors in the registration which are equal to the number of child end points. Since side-branches are derived from main branches, the points along the main branches have higher weighting factors as displayed in Fig 3(a). After registration, the distances between each pathline (from the ostium point to an end point) in the extracted tree and aligned main branches in the model are computed. The pathline with the minimal distance to the main branch in the model is assigned to the corresponding label. As shown in Fig. 3(b), three green pathlines are identified as RCA, LAD and LCx because they have minimal distances to the corresponding aligned main branches (blue centerlines). The distal part of identified main branch could be a side-branch of the real main branch. Thus, in the next section, an iterative algorithm is presented to find the optimal correspondence with the model.
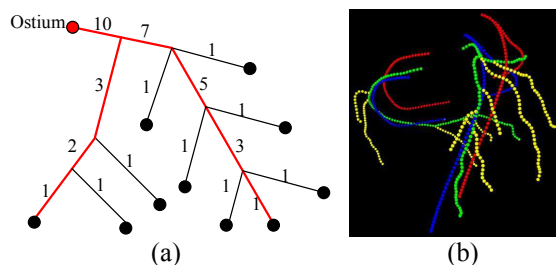

(a)   (b)

Fig. 3 (a) Illustration of weighting factors assigned for each point along the extracted left coronary tree. Black points are the end points of arteries. Red lines are main branches. (b) An example of centerline registration. Red: initial centerlines of model, yellow: extracted coronary artery tree, blue: aligned model, green: identified main branches.

2.3. All segments labeling

Once the main branches have been identified, the overlapping part of the detected LAD and LCx is labeled as LM and the side-branches derived from LAD-LCx bifurcation are labeled as ramus intermedius (RI) arteries. As shown in Fig. 4(a), the remaining parts of the coronary artery tree can be separated into three sub-trees, each of them is composed by the identified main branch and several side-branches. The short side-branches (less than 1cm) and the side-branches that have a sharp angle at the bifurcations are removed before the labeling. Subsequently, the three extracted sub-trees are matched with the corresponding sub-trees in the model, as shown in Fig. 4(b).

An iterative algorithm is performed to find the best labeling result from all of the possible labeling results, by minimizing a cost function. The rigid transformation obtained in the previous step is used to deform the model with its side-branches. Both 3D model and extracted tree are re-sampled with the same re-sampling interval. After that, the following steps are performed:

(1) Choose one pathline from the sub-tree in the model and assume it corresponds to the identified main branch. According to the labels along the pathline from the model, the identified main branch is separated into several parts whose lengths are the same as the corresponding segment in the model. Considering the extracted centerline could be tortuous, the length is defined by the line between start and end points of each part. The cost for this match is computed simultaneously.

(2) Given the labeling result of main branch in (1), calculate the cost to match it with all the possible labeling results of side-branches.

(3) Go back to step (1) until all the pathlines in the sub-tree of model have been selected.

(4) Find the global optimal labeling result with the minimal matching cost from all of the labeling results obtained in the step (2).

In the step (2), the side-branch labeling should satisfy two criteria: **A** the hierarchical relationship defined in Table 1. For example, any side-branch does not allow having another side-branch. And **B** *a priori* knowledge provided by the model. For instance, a branch which runs in the area usually supplied by diagonal branches cannot be labeled as a septal branch. If the segment cannot have a valid label, it will be marked with "NoLabel". Let $L = \{(P_1, Q_1), (P_2, Q_2), ..., (P_Z, Q_Z)\}$ denote one labeling result which is composed by a correspondence list between segments P in the extracted data and Q in the model. Any segment marked with "NoLabel" will not be included in L. Given $P = \{p_0, p_1, ..., p_N\}$ and $Q = \{q_0, q_1, ..., q_M\}$ denote the centerline points in the segments (N and M are the numbers of points), their matching cost is defined as follows,

$$c = \sum_{k=1}^{\min(N,M)} \left\| p_{a_k} - q_{b_k} \right\|, \begin{cases} a_k = k, b_k = \lfloor kM/N \rfloor, \text{if } M > N \\ a_k = \lfloor kN/M \rfloor, b_k = k, \text{if } M \le N \end{cases} \quad (1)$$

$\lfloor \cdot \rfloor$ represents the floor function. The matching cost for labeling result L and the final optimal matching cost C_g can be defined as:

$$C_L = \sum_{z=1}^{Z} \frac{c_z}{N_z} \cdot e^{-\alpha(\sum_{z=1}^{Z} N_z / Sum\_N_{\min} - 1)}, \quad C_g = \min_L C_L \quad (2)$$

in which $Sum\_N_{\min}$ is the minimal summation of number of points who have been labeled in the extracted data for all the L's. Since the improper assumption to label the identified main branches in the step (1) may lead to some side-branches marked with "NoLabel", an exponential function is introduced into matching cost C_L to penalize the labeling results with a lot of "NoLabel" side-branches and it is controlled by parameter α ($0 < \alpha < 1$). In this paper, we used $\alpha=0.4$.
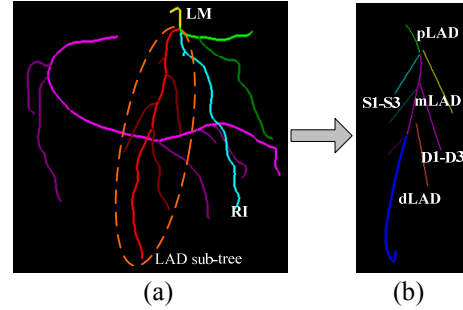

(a)   (b)

Fig. 4 (a) Coronary artery tree is divided into three sub-trees, i.e. RCA (purple), LAD (red) and LCx (green) sub-trees. LM and RI branches are in yellow and cyan respectively. (b) The extracted LAD sub-tree is matched to the LAD sub-tree in the 3D model.

2.4. Clinical criteria

In the clinical practice, the proximal, middle and distal parts of RCA, LAD and LCx are separated at the bifurcations of the specific side-branches. Therefore, we defined some additional criteria to adjust the initial labeling obtained from the statistical model. The criteria are defined as follows,

(1) Use D1 and D2 to separate pLAD and mLAD. The mLAD should be longer than 1cm. If the D1 is present but the D2 is not or the segment between their openings is shorter than 1cm, the length of the mLAD is fixed at 3cm.

(2) Use the OM1 bifurcation to separate the pCx and the LCx.

(3) Define the p-, m-, and dRCA using 1/3 of the length of the RCA (from right ostium to the RPDA-RPLB bifurcation).

If these side-branches mentioned in the above criteria are not present in the labeling results, the initial labeling result will not be changed.
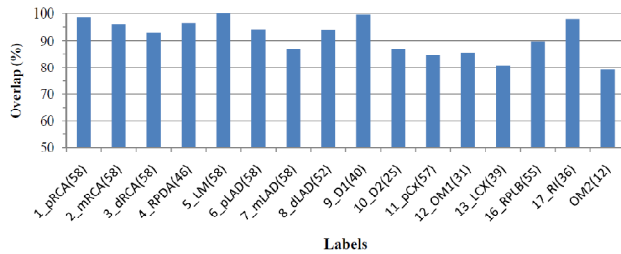
Fig. 5 Overlap measures between automatic and expert labeling results. The numbers in the brackets are the number of datasets.
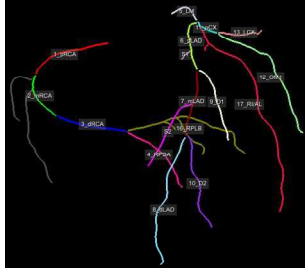

Fig. 6 Coronary artery tree labeling result.

3. Evaluation results and discussion

Fifty-eight CCTA datasets acquired by a 320-slice CT scanner (Toshiba Aquilion One) and a 64-slice CT scanner (Toshiba Aquilion 64) were used to evaluate our algorithm. The datasets in which the coronary arteries could not be extracted because of severe lesions at the proximal parts of the main branches, were not included in these datasets. The centerlines of the coronary artery trees in these datasets were extracted automatically using the method presented by Yang et al. [4]. After extraction, the centerlines were used directly as the inputs for this labeling pipeline. The identification of the main branch succeeded in all of the 58 CCTA datasets. The labeling results were checked by an expert in cardiac CT and corrected manually if necessary. S1, S2, S3 and D3 were not included in the manual correction since they have no clinical relevance. A total number of 778 segments were checked. The expert changed or removed the label of 37 (4.76%) segments. For the other 741 segments, we calculated the overlap between the automatic and expert results. The average overlap of the 17 labels and the number of the datasets that contain a label are displayed in Fig. 5. The overall overlap of all of 741 segments is 91.41%. Fig. 6 shows an automatic labeling result in one dataset. All segments including proximal, middle and distal parts as well as side-branches were labeled correctly. Labeling is used to denote the location of the lesion. This is an important aspect for defining the clinical relevance of the lesion [11].

4. Conclusion

In conclusion, we developed an automatic labeling algorithm for coronary arteries in CCTA images. It is based on a two-step method to find the optimal labeling result of a coronary artery tree. A preliminary evaluation showed a high accuracy of the computed labeling results as compared to the clinical expert labels.

Acknowledgements

References

[1] Mowatt G, Cook J, Hillis G, Walker S, Fraser C, Jia X, Waugh N. 64-Slice computed tomography angiography in the diagnosis and assessment of coronary artery disease: systematic review and meta-analysis. Heart 2008; 94:1386-93.

[2] Raff GL, Abidov A, Achenbach S, Berman DS, Boxt LM, Budoff MJ, et al. SCCT guidelines for the interpretation and reporting of coronary computed tomographic angiography. J Cardiovasc Comput Tomogr 2009; 3(2):122-36

[3] Schaap M, Metz C, et al. Standardized evaluation methodology and reference database for evaluating coronary artery centerline extraction algorithms. Med Image Anal 2009; 13(5):701-14

[4] Yang G, Kitslaar P, Frenay M, Broersen A, Boogers MJ, Bax JJ, Reiber JHC, Jouke D. Automatic centerline extraction of coronary arteries in coronary computed tomographic angiography. Int J Cardiovasc Imaging. In press.

[5] Ezquerra N, Capell S, Klein L, Duijves P. Model guided labeling of coronary structure. IEEE Trans Med Imaging 1998; 17(3): 429-41.

[6] Haris K, Efstratiadis SN, Maglaveras N, Pappas C, Gourassas J, Louridas G. Automatic labelling of the coronary tree using a three dimensional reference prior model. IEEE Trans Med Imaging 1999; 18: 1003-15.

[7] Akinyemi A, Murphy S, Poole I, Roberts C. Automatic labeling of coronary arteries. In: 17th European Signal Processing Conference 2009; 1562-66.

[8] Dodge JT, Brown G, Bolson E, Dodge HT. Intrathoracic spatial location of specified coronary segments of the normal human heart. Circulation 1988; 78(1): 1167–80.

[9] Austen WG, Edwards JE, Frye RL, Gensini GG, Gott VL, Griffith LS, et al. A reporting system on patients evaluated for coronary artery disease. Report of the Ad Hoc Committee for Grading of Coronary Artery Disease, Council on Cardiovascular Surgery, American Heart Association. Circulation. 1975; 51: 5-40.

[10] Myronenko, A. and Song, X. Point-Set Registration: Coherent Point Drift. IEEE Trans Pattern Anal 2010; 32(12): 2262-75.

[11] Leaman DM, Brower RW, Meester GT, Serruys P, van den Brand M. Coronary artery atherosclerosis: severity of the disease, severity of angina pectoris and compromised left ventricular function. Circulation. 1981; 63(2): 285-99

Address for correspondence.
Guanyu Yang, Lab of image science and technology, Dept. of computer science, Southeast University, 210096, nanjing, China