

# Enhanced Multi-resolution Peripheral Artery Tracking in CTA data

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## Abstract

Peripheral arterial diseases are among the most important public health problems in developed countries. Blood vessel analysis on medical images, that is, extraction of the center lines and corresponding local cylinder radii, is the basis for diagnosis and treatment of these diseases. The proposed method employs an already existing peripheral artery tracking method in a multi-resolution fashion. The multi-resolution approach intends to improve the execution time, but in the same time preserves accuracy and high recall of the tracked vessel tree. The new approach also aims to improve tracking of very small vessel structures (capillaries). The obtained results show 40% improvement of execution time, preserving the accuracy measure and losing 4% recall of tracked vessel tree, in comparison to an already existing single resolution vessel tracking framework. In addition, better capillary tracking performance of the proposed method is demonstrated.

**Keywords:** Vessel tracking, multi-resolution analysis, segmentation

## 1 Introduction

Peripheral arterial diseases (PAD) are among the most important public health problems in developed countries. They affect 12% of the adult population and 20% of individuals over the age of 70 [2]. Blood vessel analysis on medical images is the basis for diagnosis and treatment of these diseases and Computed Tomography Angiography (CTA) is extensively used for studying vascular diseases. CTA allows localization of peripheral arteries and related stenoses, occlusions or vessel wall calcifications. With the aid of robust vessel tracking algorithms, radiologists can evaluate the arteries more accurately.

Vessel segmentation is a challenging task, as segmentation methods should deal with different image modalities, application areas, degree of interactivity, types of output required, computational efficiency, etc. In fact, there is no general segmentation method that can extract vessels from every medical imaging modality. An overview of differ-

ent techniques on vessel tracking is given in [4] and [5]. Other existing reviews are dedicated to a limited amount of works and applications such as CT peripheral angiography [1].

Multi-resolution approaches perform segmentation on different image resolutions and aim to increase processing speed. After segmenting the large vessels at a low resolution, smaller vessels in the neighborhood of already segmented vessels can be segmented at higher resolutions with a higher level of precision. Wink et al. [7] introduce a multi-scale approach with an implicit scale selection mechanism which is also based on multi-scale vessel enhancement filtering. The vessel tracking method of Yang et al. [8] combines a 3D geometric moment operator with a multi-scale Hessian filter to estimate the vessel central axis location, its local diameter and orientation.

There are three methods which form the basis of the proposed method.

1. The model-based approach as proposed in [9], which combines appearance and geometric information in order to establish assumptions on the spatial appearance of a vessel.
2. The approach in [3] which is the improved version of [9] in terms of tracking and connecting the tracked vessels. This approach presents a new tree growing method which builds the vessel tree from tracked vessel segments using a rule-based anatomical heuristic, where each rule represents knowledge about a certain kind of connection. The tree growing phase is the only manual part of the algorithm where the user should select a desired vessel segment in order to build the vessel tree.
3. The peripheral vessel tracking in [6] which is a modified version of the other two approaches. The other two approaches are designed for tracking coronary arteries and needed many changes in order to track peripheral arteries. The changes range from the way the algorithm search for potential seed points of peripheral arteries to changing the parameters related to anatomy of peripheral arteries like the vessel minimum and maximum diameter or the gray value threshold for considering a voxel as potential vessel lumen. This approach from now on is referred to as the *base approach*.

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The scope of the work is extracting the centerline and corresponding radius of peripheral arteries in CTA data. Tracking of peripheral arteries mainly deals with relatively big datasets (with 700-1800 slices), covering half of the human body (from abdomen to foot). Therefore the algorithm requires substantial time and hardware resources to process the data. Finding a solution to accelerate vessel tracking algorithms would save a lot of time in everyday clinical life. A fast algorithm increases the usability and let the user interacts with the obtained result as soon as image acquisition is done.

The aim of this work is to propose an improved vessel tracking method by combining the strengths of an already existing peripheral vessel tracking method with a multi-resolution approach to achieve a faster processing performance while preserving a high recall and accuracy of the tracked peripheral arterial vessel tree. Also this work aims to investigate the possible improvement of the ability of the multi-resolution approach in tracking capillaries.

## 2 Methodology

The proposed method consists of the four phases of selection of the seed points, vessel segment tracking, mask creation around segments and building vessel tree.

1. *Seed selection:* The seed selection is based on the method in [9]. The algorithm uses local symmetry feature extraction and 3D image gradient in order to calculate potential seed points of peripheral arteries. For each voxel with position of  $\mathbf{p}$  in the data if the gradient is above a fixed threshold  $P_{gradient}$ , the voxel is regarded as the surface point of a vessel in the dataset. Then the intersection point  $\mathbf{p}'$  between the opposite side of the vessel profile and the scan line defined by position  $\mathbf{p}$  and the corresponding gradient vector is calculated by simple ray casting method. Once  $\mathbf{p}'$  is identified, the radius  $r_c$  and center point  $\mathbf{p}_c$  of the estimated vessel profile will be identified. For estimating the orientation  $\mathbf{d}_c$ , the algorithm generates a set of radial scan lines perpendicular to the vector  $\mathbf{pp}'$  and proceeds each scan line using the same ray casting approach and  $P_{gradient}$  as in the previous step, generating a set of points that intersects with the potential vessel surface. The intersection with minimal distance to the center point  $\mathbf{p}_c$  is denoted as  $\mathbf{p}''$ . The orientation vector  $\mathbf{d}_c$  is calculated as the cross product between  $\mathbf{pp}'$  and  $\mathbf{pp}''$ . Each of the calculated seed points is represented by position  $\mathbf{p}_c$ , radius  $r_c$  and the orientation vector  $\mathbf{d}_c$ , in the following referred to as seed set  $S_{seed}(\mathbf{p}_c, \mathbf{d}_c, r_c)$ .
2. *Vessel segment tracking:* For the calculated seed points, a curved cylindrical shape model is matched along the vessel structures for extracting the vessel segments of the peripheral arteries [9]. Similar to [3], the algorithm tracks the vessels in both directions

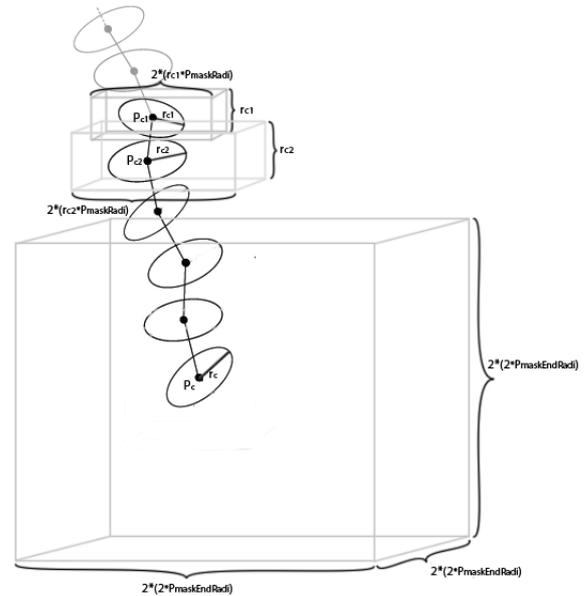


Figure 1: Mask creation scheme, vessel nodes are shown by black circles, created mask for each vessel node is shown by gray cube. Mask for end points of a vessel segment has relatively bigger size in comparison to other nodes.

of  $+\mathbf{d}_c$  (forward) and  $-\mathbf{d}_c$  (backward) of the seed set  $S_{seed}$ . This step is repeatedly carried out for all seed sets that are not located inside previously tracked vessel segment. The set of tracked vessel segments is denoted by  $V$ . End points of tracked vessel segments (denoted by  $EP$ ), play an important role in defining an efficient mask and respectively detecting new vessel segments. Extracting the mentioned end points is handled as a part of vessel segment tracking.

3. *Mask creation around segments:* For each vessel segment's node  $n_{node}(\mathbf{p}_c, \mathbf{d}_c, r_c) \in V$ , the algorithm creates a 3D mask based on the node's position  $\mathbf{p}_c$  and radius  $r_c$ . The size of the mask is equal in X and Y direction and is narrower in Z direction in order to maintain minimum overlap of the kernels in Z direction. The edge size of the 3D kernel for X and Y direction is  $P_{maskEdge} \cdot r_c$  and  $2 \cdot r_c$  for Z direction. Scaling the mask by radius  $r_c$  adapts the size of the mask to the enclosed segment and ensures that branches can be detected. After creating a mask for all nodes in vessel segments, the end points of tracked vessel segments need extra consideration. This extra treatment is required due to the possibility of finding potential seeds and consequently new vessel segments in distal nodes of a vessel segment. Therefore the mask size should be bigger in end points of a vessel segment than in the other parts. The kernel edge for end nodes is  $2 \cdot P_{maskEndEdge}$  for all X, Y and Z directions. Figure 1 presents the mask schematic (gray boxes) for vessel nodes (black circles). As it can be seen the

mask is created by concatenation of cuboids.

4. *Tree building*: The result of the tracking phase is a set of unconnected and unbranched vessel segments. The goal of this final phase is connecting tracked vessel segments based on the rule-based tree growing method in [3] which defines a connection path as the shortest path between a node and another node within the same vessel segment of a given size. The obtained result will be unify vessel tree due to this approach does not allow any disjoint vessel tree to be a part of final vessel tree.

The first three phases are performed in three different resolutions of the data:

- *Phase 1*: low resolution, where the data is 4-times down-sampled.
- *Phase 2*: mid-resolution, where the data is 2-times down-sampled.
- *Phase 3*: full resolution (original data).

The last phase is performed in full resolution after all possible vessel segments are tracked. Trilinear down-sampling is used to create the data in low and mid-resolutions. The proposed algorithm first selects seed points and tracks vessel segments in low resolution. If the amount of tracked vessel segments in low resolution is higher than a threshold, then the algorithm creates in mid-resolution a mask based on the tracked vessel segments in low resolution, selects seeds in the area limited to the mask and tracks again vessel segments. Otherwise, the algorithm discards the tracking results in low resolution and starts from scratch in mid-resolution. This means that the whole data is processed in mid-resolution in order to select see points and to track vessel segments based on them. In full resolution the algorithm defines a mask based on tracked vessel segments in mid-resolution and selects initial seed points in the area limited to the mask in order to track vessel segments in full resolution. Finally in the last step the algorithm builds vessel tree based on tracked vessel segments. The individual stages are explained in detail in the following sections.

## Low resolution

The objective in this resolution is finding the major arteries with a large diameter presented in the dataset. In this resolution seed selection is applied to the whole dataset resulting in certain amount of seed sets  $S_{seedLow}(\mathbf{p}_c, \mathbf{d}_c, r_c)$ . Based on the calculated seed point the algorithm tracks the vessel segments  $V_{Low}$  in this resolution. The minimum radius of the vessels  $P_{minRadiLow}$ , is assigned in a way that the algorithm tracks just vessels with big diameters. Due to the low accuracy of the obtained vessel segments in low resolution, these vessel segments are just used to create a

mask for mid- and full resolution and can not be considered as a part of the final vessel tree.

As the last step in low resolution, the quantity of tracked vessels is checked in order to evaluate vessel tracking performance in this resolution. Due to limiting the length and the radius of tracked vessel segments in this resolution, low quality datasets may result in no or very low amount of tracked vessel segments. If the total number of tracked nodes in low resolution  $N_{nodeLow}$  is higher than  $P_{minNodeLow}$ , the algorithm can proceed to the next level. Otherwise, the obtained results in low resolution are discarded and the algorithm starts from scratch in mid-resolution. Figure 2 depicts the schematic of the steps and Algorithm .1 presents the pseudo code in this resolution.

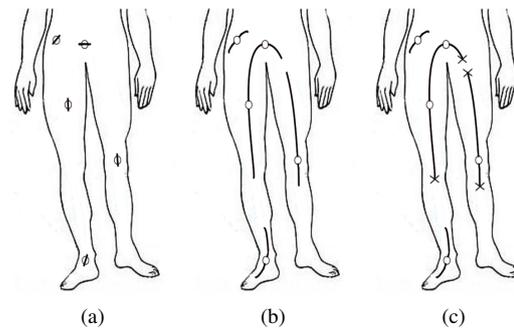


Figure 2: Seed selection and vessel tracking in low resolution. (a) calculated seed points (b) tracked vessel segments (c) identified end nodes of the tracked vessel segments with the length larger than  $P_{vesselEndLow}$ .

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input :  $\Delta = 4$  down-sampled version of volumetric
         dataset
output: Set  $V_{Low}$  of estimated vessel segments

1 for each voxel with position  $\mathbf{p}$  in  $\Delta = 4$  down-sampled
  version of volumetric dataset do
2   if  $\text{gradient}(\mathbf{p}) \geq P_{gradientLow}$  then
3     Calculate the set of  $S_{seedLow}$  ;
4   end
5 end
6 for each seed set  $s_{seed}(\mathbf{p}_c, \mathbf{d}_c, r_c) \in S_{seedLow}$  do
7   Find the set of  $V_{Low}$  and  $EP_{Low}$ ;
8   if (total number of nodes inside  $V_{Low}$ )
      $\leq P_{minNodeLow}$  then
9     Proceed to one level higher based on
     Algorithm .2 ;
10  end
11 end

```

**Algorithm .1**: Pseudo code of steps in low resolution

## Mid resolution

The objective in this resolution is creating a mask based on the tracked vessel segments in the low resolution, performing seed selection in the area defined by the created mask and afterward tracking vessel segments based on the selected seeds.

After defining the mask based on  $V_{Low}$ , the seed selection phase is applied. But as it can be seen in figure 3b, this phase is applied just in the area defined by the masks. Note that the mask is shown as consistent cuboids for reasons of simplicity. The obtained seed points  $S_{seedMid}(\mathbf{p}_c, \mathbf{d}_c, r_c)$ , are used for the vessel tracking phase in this resolution. Tracked vessel segments  $V_{Mid}$  are more accurate than the one in low resolution. Figure 3 depicts the steps and Algorithm .2 presents the pseudo code.

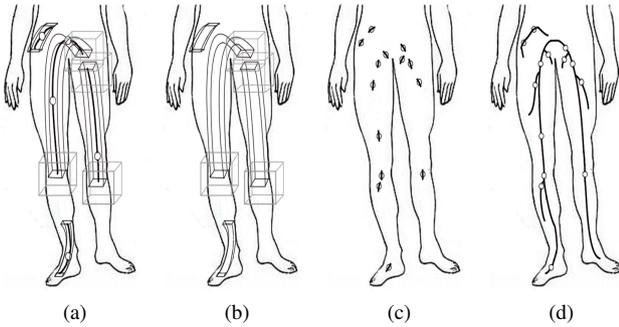


Figure 3: Algorithm's performance in mid-resolution. (a) created mask for tracked vessel segments in low resolution (b) area in mid-resolution data that seed selection should be performed (c) calculated seed points (d) tracked vessel segments

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input :  $\Delta = 2$  down-sampled version of volumetric
          dataset
input : Set  $V_{Low}$  of estimated vessel segments
output: Set  $V_{Mid}$  of estimated vessel segments
1 for each vessel segment's node  $n_{nodes}(\mathbf{p}_c, \mathbf{d}_c, r_c)$ 
   $\in V_{Low}$  do
2   | Create  $Mask_{Mid}$ ;
3 end
4 for each voxel with position  $\mathbf{p}$  inside  $Mask_{Mid} \in \Delta = 2$ 
  down-sampled version of volumetric dataset do
5   | if  $gradient(\mathbf{p}) \geq P_{gradientMid}$  then
6     | | Calculate the set of  $S_{seedMid}$ ;
7     | end
8 end
9 for each seed configuration  $s_{seed}(\mathbf{p}_c, \mathbf{d}_c, r_c) \in S_{seedMid}$ 
  do
10  | Find the set of  $V_{Mid}$  and  $EP_{Mid}$ ;
11 end

```

**Algorithm .2:** Pseudo code of steps in the mid-resolution

## Full resolution

The algorithm in full resolution aims to maximally grow the vessel network by tracking smaller vessels. Creating the mask for this resolution is slightly different than the one for mid-resolution. The straightforward procedure would be creating a mask for all tracked vessel segments  $V_{Mid}$ . But in full resolution, the more efficient way is creating the mask for the difference of tracked vessel segments in mid- and low resolution. This modification in creating the mask forces the algorithm to focus mainly on the areas around new vessel segments tracked in mid-resolution in order to find their possible arborization in full resolution. After this subtraction, for any remaining nodes in mid-resolution  $n_{NodeMid}(\mathbf{p}_c, \mathbf{d}_c, r_c) \in (V_{Mid} - V_{Low})$ , the algorithm creates the mask with the tuned parameters for full resolution. As explained before, the two parameters of  $P_{maskEdgeFull}$  and  $P_{maskEndEdgeFull}$  respectively define the mask size for vessel segments and end points of the vessel segments. Figure 4a shows the mask creation scheme in full resolutions. In this step, as it shown in Figure 4b, the seed selection phase is applied on the original input data after the full resolution mask has been defined. The obtained seed points  $S_{seedFull}(\mathbf{p}_c, \mathbf{d}_c, r_c)$  are used for the vessel tracking phase in this resolution. As mainly thin vessels are the tracking target in this resolution,  $P_{maxRadiFull}$  is reduced. Finally the tracked vessel segments plus the vessel segments obtained in mid-resolution form the final tracked vessel segments and are used in the tree growing phase to create the peripheral vessel tree.

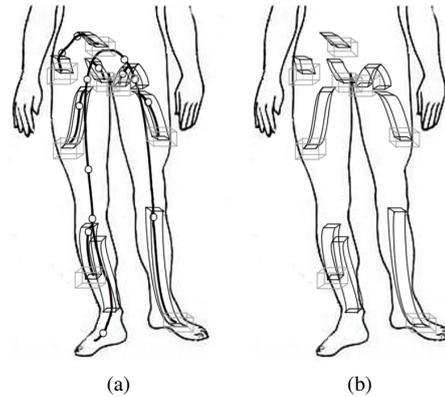


Figure 4: Mask creation scheme for full resolution. (a) created mask for new tracked vessel segments in mid-resolution (b) area in full resolution in which seed selection is performed.

## 3 Results

Evaluation was done based on 9 randomly selected CTA datasets which vary widely in terms of image quality and

**input** : Original version of volumetric dataset  
**input** : Sets of  $V_{Low}$  and  $V_{Mid}$  of detected vessel segments  
**output**: Set  $V_{Full}$  of estimated vessel segments

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1 for each vessel segment's node
   $n_{nodes}(p_c, d_c, r_c) \in (V_{Mid} - V_{Low})$  do
2   | Create  $Mask_{Full}$ ;
3 end
4 for each voxel with position  $p$  inside  $Mask_{Full}$  in
  original version of volumetric dataset do
5   | if  $gradient(p) \geq P_{gradientFull}$  then
6     | Calculate the set of  $S_{seedFull}$ ;
7   end
8 end
9 for each seed configuration  $s_{seed}(p_c, d_c, r_c) \in S_{seedFull}$ 
  do
10  | Find the set of  $V_{Full}$ ;
11 end
12  $V_{Total} = V_{Mid} + V_{Full}$ ;

```

**Algorithm .3:** Pseudo code of steps in the full resolution

Parameter	Low	Mid	Full
$P_{gradient}$	1025 G/S	1100 G/S	1100 G/S
$P_{maskEdge}$	-	2 voxel	6 voxel
$P_{maskEndEdge}$	-	8 voxel	10 voxel
$P_{vesselEnd}$	13 mm	10 mm	-
$P_{minRadi}$	4 mm	1 mm	1 mm
$P_{maxRadi}$	12.5 mm	11.5 mm	9 mm

Table 1: Summary of assigned values for parameters used in the proposed multi-resolution approach.

degree of disease. For each dataset the centerlines of peripheral arteries were annotated by a trained observer.

The parameters used for the multi-resolution approach can be found in Table 1. The tests have been carried out on a workstation running Windows 7 professional (64-bit) with an Intel Core i7 Processor (2.67 GHz) and 12 GB RAM.

The measured average accuracy is 0.77 mm, which is an increase of 0.02 mm in comparison to the base approach (0.75 mm). Due to the fact that parts of vessel segments are tracked in a down-sampled version of the data, average accuracy loss was expected. The measured average recall R (reflects how much of clinically relevant vessels are tracked) is 86%, which represents 4% reduction compared to the base approach (90%). The measured average precision PR (reflects how much of tracked vessels are clinically relevant) is 75%, which shows 5% improvement in comparison to the base approach(70%). The total execution time for all 9 datasets is 2371 seconds which represents a 40% improvement in comparison to base approach (3854 seconds). The comparison of the evaluated measures between the presented method and the base approach is shown in Figure 5.

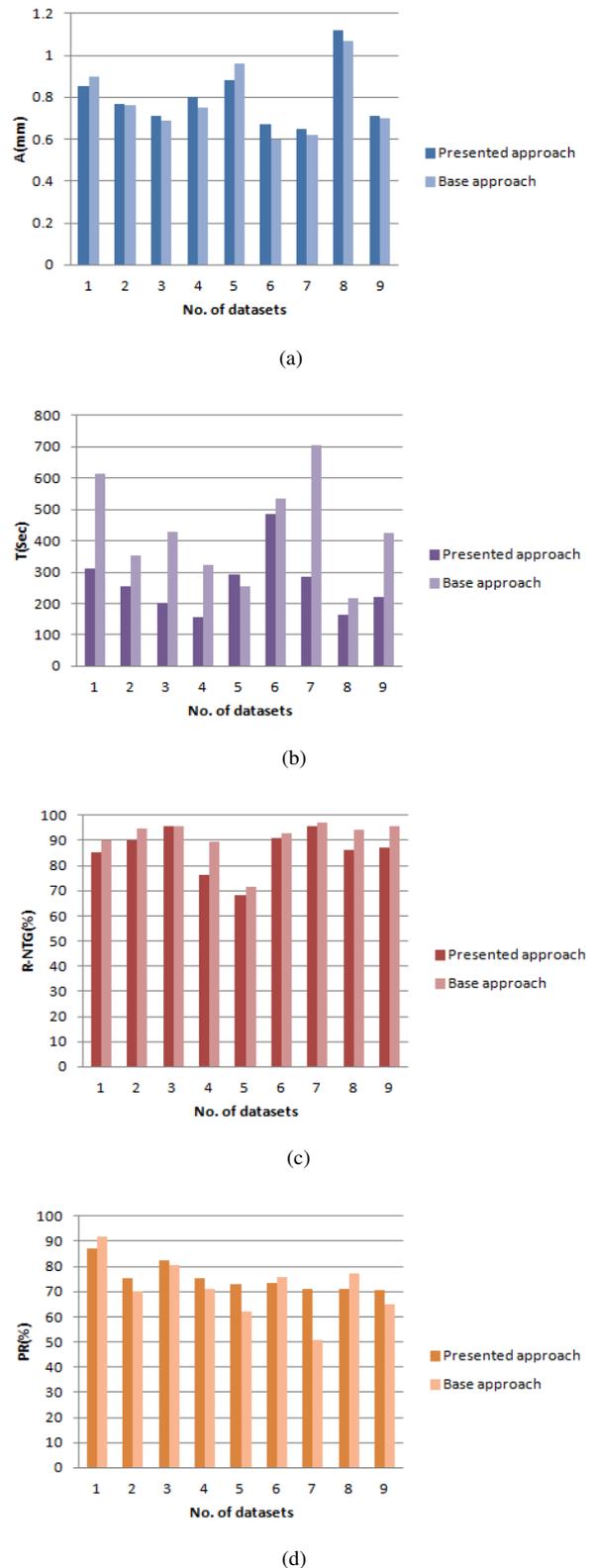


Figure 5: The comparison of evaluation measures between the presented method and the base approach of the 9 training datasets: (a) accuracy (A), (b) execution time (T), (c) recall (R), (d) precision (PR).

In order to analyze the capability of the algorithm to track capillaries a new dataset with high spatial resolution contain 1651 slices is chosen (each of the other 9 test data has around 350 slices). The highlight is the fact that the base approach needs 1644 seconds in order to track the vessels with capillaries, whereas the proposed approach tracks the same vessels with capillaries in just 442 seconds. It means almost 75% faster than the base approach. This is one of the biggest advantages of multi-resolution tracking approach.

In addition, extra tracked capillary for dataset 3 is shown in Figure 6. As it can be seen on the right side of the figure, tracking of the deep femoral artery continues from the point it stopped in the base approach (the vessel segment on left side).

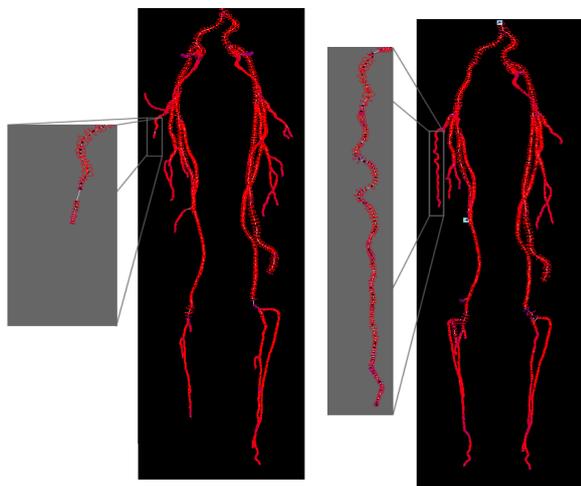


Figure 6: Extra tracking of capillaries. Left part shows the uncompleted tracked deep femoral artery in the base approach and the right part shows the continuation of deep femoral artery in proposed approach for dataset 3.

Figure 7 shows progress of the algorithm in detail for dataset 1.

## 4 Conclusion

In this paper an approach for accelerating the segmentation of the peripheral arteries was discussed. It was shown that the multi-resolution approach can reduce execution time significantly and keep the accuracy almost untouched. The only drawback is a slightly negative impact on the recall quality. Furthermore, the proposed algorithm performs better in tracking capillaries.

## References

- [1] P. Felkel, R. Wegenkittl, and A. Kanitsar. Vessel tracking in peripheral CTA datasets - an overview. In *Proc. Spring Conf. Comput. Graph.*, pages 269 – 278, 2001.

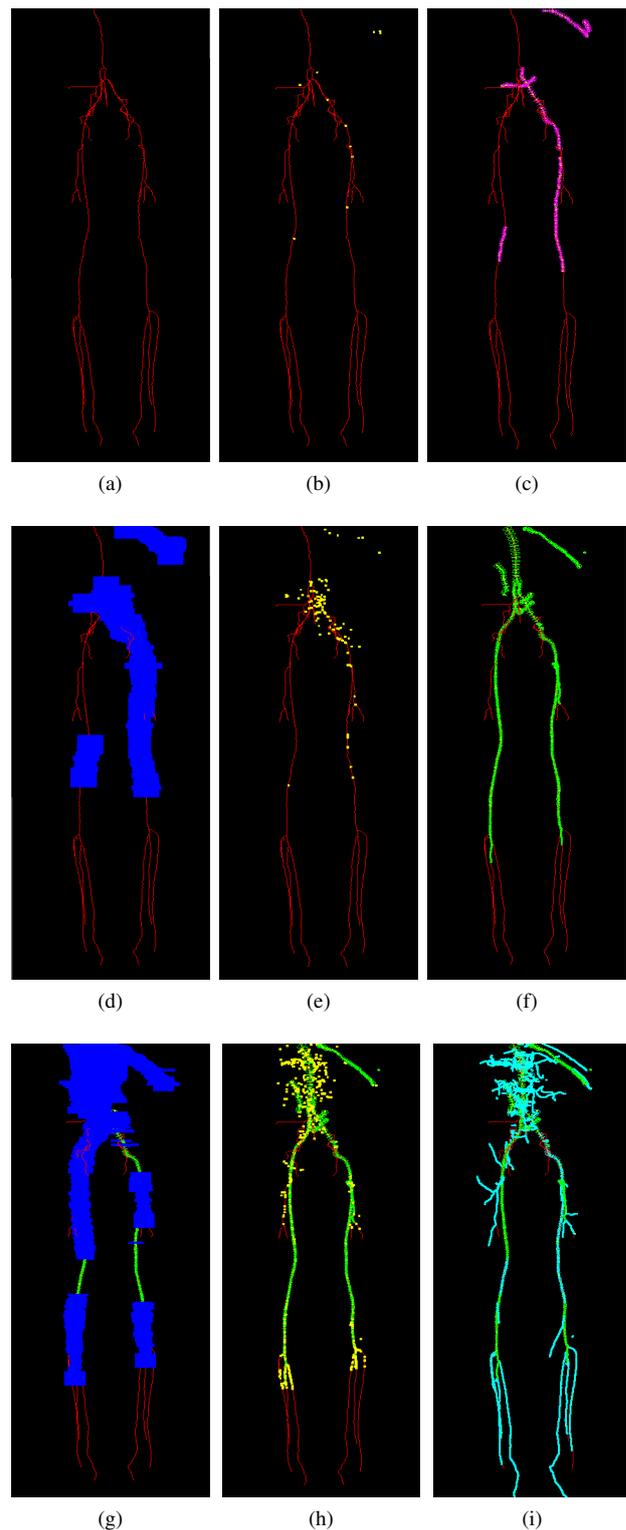


Figure 7: Visualization of different steps of algorithm: (a) reference vessel (b) calculated seeds in low resolution (c) tracked vessel segments in low resolution (d) mask in mid-resolution (e) seeds in mid-resolution (f) tracked vessel segments in mid-resolution (g) mask in full resolution (h) seeds in full resolution (i) tracked vessel segments in full resolution.

- [2] B. A. Golomb, T. T. Dang, and M. H. Criqui. Peripheral arterial disease : Morbidity and mortality implication. *Circulation*, 114:688 – 699, 2006.
- [3] A. Grünauer. Coronary artery tracking with rule-based gap closing. In *proc. of bildversarbeitung hier die medizin*, pages 269 – 273, 2011.
- [4] C. Kirbas and F. Quek. A review of vessel extraction techniques and algorithms. *ACM Comput. Surv.*, 36:81 – 121, June 2004.
- [5] D. Lesage, E. D. Angelini, I. Bloch, and G. Funka-Lea. A review of 3D vessel lumen segmentation techniques: Models, features and extraction schemes. *Medical Image Analysis*, 13(6):819 – 845, 2009.
- [6] E. Vučini, A. Grünauer, M. Trapp, and K. Bühler. A client-server architecture for semi-automatic segmentation of peripheral vessels in CTA data. *Abstract ECR 2013*.
- [7] O. Wink, W. J. Niessen, and M. A. Viergever. Multi-scale vessel tracking. *IEEE Transactions on Medical Imaging*, 23(1):130 – 133, 2004.
- [8] G. Yang, A. Bousse, C. Toumoulin, and H. Shu. Multi-scale tracking algorithm for the coronary extraction in MSCT angiography. *28th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBS '06)*, (1):3066 – 3069, 2006.
- [9] S. Zambal, J. Hladuvka, A. Kanitsar, and K. Bühler. Shape and appearance models for automatic coronary artery tracking. *Midas Journal, MICCAI Workshop - Grand Challenge Coronary Artery Tracking*, Aug. 2008.