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“Model-based segmentation of the left coronary artery from 2D angiograms”
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Abstract

This report is concerned with the segmentation of the coronary tree in 2D angiograms. The algorithm has to run during a cath-lab examination of a patient’s heart and thus needs to be fully automatic and real-time compatible.

We use a priori knowledge on the structure of interest as a way to perform a robust and accurate segmentation. More precisely, we resort to a generic 3D model of the Left Coronary Artery that is projected in the proper angulation to generate a skeleton of the expected 2D shape of the Left Coronary Artery in the considered image. The segmentation is performed in two steps: the Left Main Bifurcation is detected as a way to anchor the model, and the model is adapted in order to match the observed arteries.

The former is solved with an original method, described in details in this report. We derive from the projected skeleton an efficient and discriminating filter that allows the detection of the Left Main Bifurcation, while being robust to anatomical variations. To further improve its reliability, we explored an extension of the method that exploits not only the present angiography, but also the previous ones that were acquired in the course of the exam. This approach constrains very much the 3D geometry of the object of interest, while being completely transparent with the cath-lab workflow.

The bifurcation is then exploited to initialize a model-based segmentation of the whole coronary tree. The model is adjusted so that key points are properly positioned on the actual artery. A common fast-marching algorithm is used between each of these points to get the final segmentation of the vascular arch. The quality of the method is demonstrated over a large database of 123 angiography sequences from 15 patients.
Introduction

In the context of my last year at the ENSPS of Strasbourg, before obtaining an engineer degree as well as a master degree, I performed an internship in the Company Philips, in Suresnes (France). From the 1st March 2011 to the 31st August 2011, I joined the research team of Philips Healthcare, Medisys Research Lab, that works exclusively in the field of medical image processing. This internship met the conditions imposed by my institution since it took place in a company, and since I worked on a research topic.

Indeed, the vocation of my internship was to implement a new algorithm of image processing in cardiology. After a short presentation of the company and the research group, I will provide an overview of the clinical context and the activities of Medisys. Then, I will describe the state of the art in cardiac model-based segmentation, the already existing tools that I could lean on, and the objectives I was set up to fulfill. I will finally explain in details of the method I chose to implement and present numerous results.

1. Philips Healthcare / Suresnes

Royal Philips Electronics, most commonly known as Philips, is a multinational Dutch electronics company. Philips is one of the largest electronics companies in the world. In 2010, its sales were €25.42 billion. The company employs 119,000 people in more than 60 countries. Philips France has its headquarters in Suresnes, near Paris. The company employs over 3600 people nationwide. Philips is organized in a number of sectors: Philips Consumer Lifestyle, Philips Lighting and Philips Healthcare. The branch of Healthcare is further divided into healthcare informatics, imaging systems, diagnostic monitoring, patient monitoring and defibrillators. Several imaging modalities are assigned to the subbranch ‘imaging systems’: X-Ray / Computed Tomography (CT) / Fluoroscopy, Magnetic Resonance Imaging (MRI), Nuclear Medicine, PET (Position Emission Tomography) and Ultrasound.
2. Medisys Research Lab Activities

Medisys is a research group focusing on medical image processing and is affiliated with Philips Healthcare. Based in Suresnes (France), the group is working with numerous international Philips research and development groups. There are for example cooperations concerning X-Ray projects in Eindhoven (Holland), Ultrasound projects in Andover and Bothell (USA), CT projects in Cleveland (USA) and Haifa (Israel) and finally there is a collaboration with a group in Eindhoven on MRI.

Medisys develops and designs image processing solutions for a range of Philips Healthcare products. Medisys has a strong background in building software meeting the criteria of simplicity, reliability, processing speed optimized for clinical applications and improvements leading to high image quality. With its competencies, Medisys focuses on image enhancement, edge/surface detection, registration and segmentation. The latter is the main topic of this Master thesis. Medisys is contributing to Philips Healthcare by developing imaging software solutions that are directly compatible with Philips engineering products. Medisys also collaborates with several other research institutions not directly connected to Philips. Medisys employs about 30 research engineers and three PhD Students. Some research results are published in conference proceedings with peer-review or as a journal papers (sometimes in collaborations with external researchers or physicists).

Some key parts of Philips Healthcare imaging systems have been developed and patented by the Medisys group.
3. Model-Based Segmentation - State of the Art

This chapter will give an overview of the medical context of my internship. We will clarify the background and the circumstances that lead to a need for the segmentation of the coronary tree. Then we will present a short review of the state of the art, the different methods already used in the literature, and describe the method I have chosen to implement.

3.1 Clinical Context

According to data from the World Health Organization in 2009, ischemic heart diseases are the leading causes of death with 7.2 million deaths from coronary heart diseases (among 50 million deaths annually worldwide). In France, the prognosis remains serious because the myocardial infarction is responsible for 10 to 12% of the adults’ annual mortality. About 60,000 infarctions are treated annually. The hospital mortality is 7% before age 70, and much higher afterwards. 10% of the survivors die within 3 years after the infarction. The mortality due to myocardial infarction has decreased by 30% in 10 years in Western Europe and the United States. The prognosis has been improved through a series of advances: complementary techniques of angioplasty, better predictions of high risks patients at the beginning of an acute phase, as well as secondary prevention of relapses. These progresses are partially explained by the development of advanced image processing techniques: reconstruction tools, methods of detection and segmentation of vascular structures, etc.
Many algorithmic solutions have been implemented to assist the cardiologist in the diagnosis and the potential intervention that happens afterwards. A number of them involve a fine segmentation of some cardiac structures (chambers, arteries, veins), or of the tools used in the interventions (guides, catheter, stents, balloon). These segmentation algorithms must often meet demanding requirements regarding speed, robustness, accuracy, and workflow. In particular, many of need to be automatic since user interactions are not compatible with the clinical workflow.

The different methods of segmentation are based on a priori that characterize the object of interest, in a more or less formal way. They range from low-level features on the one hand, to methods using a prior acquisition of a 3D (or 4D) volume of the patient’s heart, thereby providing extremely strong a-priori on the geometry of the expected vasculature.

The internship I was offered positions itself between these two extremes. It is about building and exploiting a generic (as opposed to patient-specific) model of the structure of interest based on anatomical considerations. This strategy constrains very much the expected structure, while not requiring extra CT or IRM acquisitions. These strong constraints should hopefully allow the segmentation to be fast and robust, while staying accurate. The task I was assigned to was to choose the best formalism to gather these constraints, and to implement it. In a second step, I was asked to write a software prototype performing the segmentation of the structure of interest (in Matlab or C/C++), and evaluate its performance.

My internship focused on a particular structure of the heart commonly called the Coronary Tree. It is necessary to briefly present the anatomy of this structure before going into more details.

![ Coronary Tree diagram ](image)
Coronary Anatomy

The coronary arteries, whose name comes from their arrangement in crown around the heart, are the arteries covering the surface of the heart, and supplying the heart muscle with blood. The coronary tree is in fact made of two independent trees: the left and the right coronaries. Both arteries originate from the left side of the heart at the beginning of the aorta, immediately above the aortic valve.

The left coronary artery, abbreviated LCA and also known as the left main coronary artery (often abbreviated LMCA), arises from the aorta above the left cusp of the aortic valve. It typically runs for 1 to 25 mm and then bifurcates into the Left Anterior Descending Artery (LAD) and the Left Circumflex artery (LCX). The part that is between the aorta and the bifurcation is known as the left main artery (LM), while the term 'LCA' might refer to just the left main, or to the left main and all its eventual branches.

The LAD branch divides itself on both sides in several septals and diagonals arteries, while the LCX branch yields several marginal branches.

The right coronary artery, abbreviated RCA draws a “C” in the anterior atroventricular groove, and divide itself in the Post Descending Artery (PDA) and a marginal artery. Following the relative importance of the right or left coronary artery, we refer to right dominant network or dominant left network, the latter being more common.
These vessels can be affected by atherosclerosis and can even end up blocked, causing angina or heart attack. The coronary arteries represent the only source of blood supply to the myocardium: there is very little redundant blood supply, which is why any blockage or even reduction of these vessels can be critical.

A **stenosis** is a partial narrowing of a coronary, and a **total occlusion** refers to the complete blocking of the vessel. They are both responsible for angina, chest pain, and sometimes myocardial infarction.

The coronary angiography is the most appropriate modality of imaging to visualize the coronary arteries. For this reason, angiography is an important tool for the diagnosis of heart failures, that enables to highlight an insufficient blood supply in the myocardium. Angiographies are performed with an X-Ray angiograph, along with the injection of a contrast product in the coronary artery (**Figure 5** and **6**).

The contrast agent is a solution of iodine that is injected in the lumen of a vessel with a catheter. The product mixes with blood so that the vasculature can become visible onto the angiographies.
As discussed above, we can sometimes notice a narrowing along an artery, which require a catheterization and the implantation of a stent to enlarge the artery diameter and restore the blood flow (Figure 7).

The segmentation algorithms are able to quantify these abnormalities (severity of the stenosis, estimations of blood flow...) while labeling the failing arteries and giving to doctor data that he needs in real time.

3.2 Segmentation and labeling of the Coronary artery

There are currently many methods to segment the coronary arteries. The most theoretically advanced are semi-automatic: they require the intervention of the doctor in the application to position points of interests in order to facilitate the segmentation. They are not real-time compatible, which is mandatory for many 2D applications\(^1\) (for instance for those that support the intervention.

In my internship, we consider fully automatic segmentation methods. A way to introduce geometrical a-priori for the detection of coronary arteries is to introduce 3D models of the coronary tree, based on manual measurements or computer-based learning. They allow to constrain the segmentation and to improve robustness. However, these models need to be flexible to handle the anatomical variability as well as the distortions induced by heartbeats.

\(^1\) For instance for those that support the intervention (tools navigation, stent deployement...) and need to be real-time, as opposed to those -supporting the diagnosis, that can be performed off-line.
State of the art

The segmentation of 2D coronary arteries is of practical interest for many industrial applications, but in the field of research there are few publications on this topic. The most efficient methods do not rely on advanced theories but rather on the pragmatic use and fine-tuning of low level methods. Therefore, they are the object of active research in the industry, but are of low interest for academical research and publications.

For the most part, the existing methods exploit low-level features. Typically, the contrast of arteries is enhanced with well-known filters as Vesselness or Coronariness that highlights the elongated shapes and reduces the contribution of background. Then the result is thresholded to get a coarse segmentation map. The thresholding methods, in particular, require a great practical expertise, but are not of great interest for scientific publications.

As an exemple, Frangi et al. [2] or L. Antiga [3] exploit vesselness filters to enhance the contrast of arteries, in 2D or 3D images. Some geometric parameters which define the shape of the object are calculated: \( R \) (geometric ratio), \( S \) (structureness), \( \lambda_1, \lambda_2, \lambda_3 \) (eigenvalues of the Hessian matrix).

\[
R_A = \frac{\text{Largest Cross Section Area}}{\pi} = \frac{\lambda_2}{\lambda_3}
\]

\[
R_B = \frac{\text{Volume}/(4\pi/3)}{\left(\frac{\text{Largest Cross Section Area}}{\pi}\right)^{3/2}} = \frac{|\lambda_1|}{\sqrt{|\lambda_2\lambda_3|}}
\]

\[
S = \|\mathcal{H}_f\|_F = \sqrt{\sum_{j \leq D} \lambda_j^2}
\]

We can then obtain the vesselness with the following formula:

2D Vesselness [2]:

\[
V_0(s) = \begin{cases} 
0 & \text{if } \lambda_2 > 0, \\
\exp\left(-\frac{R_A^2}{2\sigma^2}\right)(1 - \exp\left(-\frac{S^2}{2\sigma^2}\right)) & \text{if } \lambda_2 > 0 \text{ or } \lambda_3 > 0,
\end{cases}
\]

3D Vesselness [2]:

\[
V_0(s) = \begin{cases} 
0 & \text{if } \lambda_2 > 0, \\
(1 - \exp\left(-\frac{R_A^2}{2\sigma^2}\right))\exp\left(-\frac{R_B^2}{2\sigma^2}\right)(1 - \exp\left(-\frac{S^2}{2\sigma^2}\right)) & \text{if } \lambda_2 > 0 \text{ or } \lambda_3 > 0,
\end{cases}
\]
These measures are not identical but the goal is basically the same: the vesselness measures the probability for a pixel to be on a vessel. However, without prior knowledge, we cannot differentiate false positive (contrast-enhanced elongated structures such as sternal wires, outliers, and contrast abnormalities) from real arteries. Every company has its expertise to pragmatically get rid of these outliers, but there is not yet any unified formalism that allows to segment the 2D coronary arteries in a generic way.

On the contrary, many elegant methods dealing with coronary tree segmentation were published in 3D imaging. For instance, D. Lesage et al. use Bayesian approaches associated with a particle filter to perform the 3D segmentation of the coronary arteries [4].

In the context of 3D segmentation and labeling, some works are based on generic 3D models: the most popular are the model from Dodge [5], that will be presented later in 4.1.1, and the one from Sherknies [6] that integrates morphological variations.

Some groups have addressed the topic of 3D labeling. Lorenz [7] exploits Dodge’s model to register it with 3D centerline. In another paper, Lorentz et al. use surfaces models of heart chambers [8] to restrain the Dodge’s Model and fit the corresponding labels with CT angiographies.

Sherknies published another applications of Dodge’s model. He estimates the ventricular ejection fraction, by registering Dodge’s model with 2D angiograms for different state of the cardiac contraction [9].

S-Y James Chen et al. uses biplane imaging geometry from two projection images to reconstruct the whole arterial tree [10]. With five or more object points in both views, a constrained non linear optimization algorithm is applied to determine the best angulation from which the vasculature can be optimally observed.

In 2D, one work only has exploited Dodge’s model for labeling an already available 2D segmentation. In this method, the segmentation is already given, so that the goal boils down to identifying each of the vessel with a node of the tree. Chalopin [11] derives from the model a graph structure that represents the 2D coronary tree, with nodes, branches, and neighborhood relations (Figure 8). For each node, a set of parameters modeling the local shape of the vessel is given: the length of the branch, the diameter, the proximal and distal orientation, as well as the labels.
Geometric and topologic properties are evaluated on the current image and compared the results with the graph data. A full temporal sequence is exploited, in order to consolidate different independent labellings.

To conclude, little work has been published exploiting generic coronary models in 2D. My internship considered the original problem of segmenting the coronary tree in 2D angiograms.
3.3 Towards a Model Based Segmentation of the Left Coronary Artery

The 2D segmentation method that I chose to implement is introduced in this chapter. We resort to a 3D generic (as opposed to patient specific) model\(^2\) of the left coronary artery that is projected on the proper angulation onto the detector to gain a 2D skeleton. This skeleton is then registered with the current angiography, by exploiting several low level features (ridgeness, vesselness [4.2.1]...) to fit the vessel centerlines.

Once the 2D skeleton is obtained, it needs to be properly positioned, and then geometrically adapted, to fit the measured data. To solve the former task, many applications resort to a user interaction: the clinician manually selects a point of interest to properly position the skeleton in the angiography. In our case, this initialization has to be done automatically. We will take advantage from the generic model to find a “starting point” allowing to anchor the model on the angiography, as will be explained in 4.2.2.

More precisely, we rely on the Left Main Bifurcation to initialize the model as it is typical discriminative part of the LCA that presents little variability. The first step of our procedure

\(^2\) By that we mean that there exist one reference 3D model for every patient.
is to detect the Left Main Bifurcation and “fix” the model on this landmark, so that model and vasculature can be roughly overlaid.

![Left Main Bifurcation](image)

**Figure 10 - Left Main Bifurcation of LCA**

The second step is the vessel branch adaptation. We will first adapt the model to position the reference points of the model (that correspond to subbranches proximal, middle, or distal parts) at the proper position. Then, the centerline linking them will be extracted by a propagation method.

![LCA centerlines](image)

**Figure 11 - LCA centerlines**
(red : Left Main, light blue : LAD Artery, purple : LCx Artery)**
4. Internship work
4.1 Preliminary work

4.1.1. Model Selection and implementation

To begin the segmentation procedure, we first choose a 3D model of the coronary tree that already exists in the literature. The best known is the model from Dodge et al. [5].

4.1.1.1 Dodge’s Model Description

This 3D model of the coronary tree is represented by a "tree" made up of nodes (Figure 12): the bifurcation, the middle segment and the ends of the arteries. The coordinates of the points have been calculated with manual measurements: angiographic films have been projected on a wall from two orthogonal views and 3D distances were manually calculated. Each point is defined by its spherical coordinates $(r, \theta, \phi)$ from the ostium (entrance of the coronary artery) and the model was built in end-diastolic phase to avoid temporal variations. We have statistical data on twenty patients with averages and standard deviation of each point. There is also a study of the anatomical variations associated with different distributions (left dominant, right dominant ...) and gender.
4.1.1.2 Restriction to a simple 3D Tripod Skeleton

For the first step of the segmentation - the Left Main Bifurcation detection -, we keep only a small subpart of Dodge’s model (Figure 13). Actually, we don’t need the whole model to find the bifurcation. The beginnings of the three branches are sufficient to represent the local shape of the bifurcation. This simplified model, that we can call “tripod”, is made up of 6 nodes:

- The Ostium (O)
- The Left Main Middle segment (LM)
- The first proximal segment of Left Anterior Descending (L1 proximal)
- The first Middle segment of Left Anterior Descending Artery (L1 mid)
- The first proximal segment of the Circumflex Artery (C1 proximal)
- The first middle segment of the Circumflex Artery (C1 mid)

This tripod will be used later in this report to find the left main bifurcation. We will explain how to design a template from this set of point to match the bifurcation of the angiogram.

4.1.1.3 Bifurcation Computation

The Left Main Bifurcation wasn’t in the model of Dodge, so I had to estimate its position. I considered three segments (L1 mid-L1 proximal, Ostium-LMmid, C1 proximal-C1 mid) and I calculated the closest point to each of these 3D lines. A simple cross product yields the closest points between each line, the mean of this points giving the 3D position of the bifurcation. I added this 7th point to the simplified Model.
4.1.2 Projection in the proper geometry

The first step to obtain a generic 2D model is the projection of the 3D model. The projection angles are the physical angles of the system during the acquisition of the angiography. Given the divergent nature of X-ray beams, the projection is conic and it is necessary to take into account numerous parameters to calibrate the projection: SOD (source-to-object distance), SID (source-to-image distance), the pixel size, as well as the two projection angles of the C-arm, called respectively rotation and angulation. The angiographies I had come with a log file where those parameters were stored.

4.1.2.1 Radiologic convention

The rotation (P) occurs around the anterior oblique axis (RAO / LAO) and the angulation (C) around the craniocaudal axis. Standards for rotation are shown below (Figure 14) and [12].

![Figure 14 - C-arm standards](image)
4.1.2.2 Rotation, Translation and projection of the Model

An efficient way to compute on which pixel a 3D point is projected is to proceed in two steps. First a conic projection in the “camera” referential (ie, attached to the detector, Rcam), is performed, involving a projection matrix K. And second, a referential change from the Rcam to the “world” referential (ie, the patient table, Rworld) is applied. The latter involves two rotation matrixes corresponding to the rotation and angulation angles resulting in combined matrix R, followed by a translation T. The global projection reads:

\[
\begin{align*}
\text{Rotation and translation:} & \quad X_c \ Y_c \ Z_c = R \begin{bmatrix} X \ Y \ Z \end{bmatrix} + T = [R][T] \\
\text{Projection:} & \quad \begin{bmatrix} s-u \\ s-v \\ s \end{bmatrix} = \begin{bmatrix} \alpha & 0 & u_0 \\ 0 & \alpha & v_0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} X_c \\ Y_c \\ Z_c \end{bmatrix} = K \begin{bmatrix} X_c \\ Y_c \\ Z_c \end{bmatrix}
\end{align*}
\]

(6) (7)

After projecting the 3D model, we get 2D points that correspond to the 2D model of the coronary tree (Figure 16).
4.1.3 Validation of the Projection

I projected the tripod on a large database of 123 images. I positioned manually the 2D tripod on the Left Main Bifurcation and visually evaluated the whether the projected tripod matched the vasculature. In more than 95% of images, the 2D tripod was correctly overlaid the actual bifurcation.

![Figure 17 - tripod projections, positioned on the Left Main Bifurcation](image)

We can see below the quality of the projections for different angles of the C-arm

(green : excellent, yellow : correct, red : inaccurate)

![Figure 18 - quality of projections (angles in degrees)](image)

We can notice that the quality of the projection isn’t really affected by the position of the C-arm. It shows the robustness of the tripod towards the shifting of the X-Ray device. The outliers are generally due to unexpected shapes of bifurcation because of anatomical variability.
4.2 The detection of the Left Main Bifurcation

The goal here is to use the geometry of the tripod to find the Left Main Bifurcation. The orientations of the proximal part of the three main arteries bring a strong a priori on the overall appearance of the main bifurcation.

This a-priori is exploited to design a 2D filter that enhances the LMB. To do so, we build on classical vessel enhancement filters that are presented in the next subsection.

4.2.1 Presentation of a Vessel Enhancement Filter

In the previous chapters, we have mentioned filters meant to enhance vessels such as Vessellness or Coronariness filters. In my internship, we have considered a filter called Ridgeness, widely used for the enhancement and segmentation of vessels.

This filter consists of the computation of the second derivatives of the image in different directions, after a Gaussian prefiltering. The oriented ridge filter of the image $I$ in the direction $\theta$ and at the scale $\sigma$, reads at pixel $p$:

$$R^\theta_\sigma(p) = L_\theta * G_\sigma * I(p)$$  \hspace{1cm} (8)

where $G_\sigma$ is the Gaussian filtering with a kernel $\sigma$, and $L_\theta$ the second order derivative in the direction $\theta$. In Figure 19, we can observe the impulse response of the Ridge filter.

![Figure 19 - First row: Ridge filter construction by convolution of a Gaussian with a rotating derivative filter. Second row: Three ridge filters for different scales $\sigma$](image)
In the literature of vessel filtering, the angle $\theta$ that maximizes the oriented ridge answer is selected. In that case $\theta$ corresponds to the vessel orientation:

$$R_{\sigma}^{\text{max}}(p) = \max_{\theta} R_{\sigma}^{\theta}(p)$$

(9)

One of the main reasons for the popularity of the ridge filters is that it is not necessary to explicitly compute every $R_{\sigma}^{\theta}$ to evaluate $R_{\sigma}^{\text{max}}$. It can be analytically expressed as a function of the eigenvalues of the hessian matrix, which ensures a fast computation.

The output of the filter significantly enhances the contrast of the vessels, whose pixels are bright, while background became dark, as shown in Figure 20.

![Figure 20 - Ridge filter output](image)

**4.2.2 First Approach: Linear Combination of Ridge filters**

To detect the LMB, we propose to compute the answer of the three expected branches to an oriented ridge filter, oriented in the direction given by the model. A straightforward implementation is to build a template of the bifurcation with the three oriented ridge responses corresponding to each branch.

![Figure 21 - Template of Ridge kernels designed with the model (second third images displays two scales of the template)](image)
This first implementation is a template matching: the cross-correlation between the template model and the angiography is computed. In addition, each branch is weighted with its length. Thus, a branch which is foreshortened because of perspective has a smaller contribution than other branches.

A variation of that first approach was to directly filter the image with an oriented ridge kernel, which is faster. The three branches are filtered separately, and a linear combination of each answer is computed. In practice, the ridges are oriented with the direction of each branch, and translated from the length of the current branch:

\[ F_{LMB}^1(p) = \sum_{i=1}^{3} \pi_i R_\sigma^{\theta_i} (p + \overrightarrow{P_0P_i}) \]  

Where $\pi_i$ is a weighted factor proportional to the length of the branch and $\theta_i$ the orientation of the vector $\overrightarrow{P_0P_i}$.

It became clear from our first tests on clinical data that this filter was not discriminative enough to detect the LMB. We do not actually enforce that all three branches respond to the filter. And indeed, the best answers arose from very contrasted portions of the vasculature, that corresponded to only 2, or even 1, of the three branches of the template. It turned out that the cumulated correlation was higher on vessel branches where one or two branches of the filter responded strongly (and the remaining branch(es) did not respond) than on the real bifurcation, where all three subbranches responded moderately.
4.2.3 Second Approach: Selection of Weakest Branch

To ensure that all three branches have a significant contribution to the filter, we now resort to the minimum answer of the three branches as the composite filter:

$$F_{LMB}^2(p) = \min_{i \in [1,3]} \left( R_\sigma^i \left( p + P_0^i \right) \right)$$  \hspace{1cm} (11)

The output of the filter yields a “bifurcation map” that will respond strongly only when all three branch of the model match with a vessel. In Figure 24 we can observe the overall appearance of this map. The three images correspond to three different scales of Ridges: the more we enlarge the Ridge Kernel, the more reduced the noise. The presence of bright “blobs” is typical for those kinds of filters. They nicely indicate potential LMB.

![Figure 24 - Bifurcation Map for 3 different scales](image)

We set the optimal scale of Ridge by testing exhaustively every value of $\sigma$. When the value is too small, there are too many peaks in the map, when the value is too high, the real peaks are attenuated by the background.

However, it turns out that this method is still not good enough. The connectivity between each branch is not taken into account. As a result, we get peaks that are situated in an area devoid of vessels, with three kernel meeting independent, random vessels (Figure 25).

![Figure 25 - unlinked vessels leading to false positive](image)
4.2.4 Third Approach: Elongation of the Ridge Kernel

Actually, we get better results by considering a series of aligned ridge filters for each branch, which is equivalent to elongating the ridge kernel. We divide each branch in three levels, and compute separately the filters, so that the vessel has to answer not only on the extremity of the subbranch, but to its completely path.

In practice, we decided to allow for the vessel not to exactly have the same trajectory than the model. This flexibility is an attempt to account for the anatomical variability of the LMB. We keep the median of the three filters so that one of the kernels can potentially stand out the vessel:

\[ F_{LMB}^3(p) = \min_{i \in [1,3]} \left( \text{median}_{j \in [1,3]} \left( R_{\sigma_l}(p + \alpha_j \overrightarrow{P_0P_1}) \right) \right) \]  (12)

where \( \alpha_j \) represents the different portions of the branch.

Subsequently, we get a more specific map of bifurcation, where peaks are more and more discriminative towards bifurcations:
But we observe in practice that, due to anatomical variability, the real LMB still does not always accurately match the skeleton, and thus can answer poorly to (11). Figure 28 shows a case of important vessel distortion where the model cannot account for all the real arteries.

Figure 28 - False positive caused by anatomical variability

**4.2.5 Fourth Approach: Handle Uncertainty on Vessel Orientation with a Cone-Shaped Template**

Finally, we take into account the uncertainty to the exact vessel angles in the last filter. We extend $F_{LMB}^3$ to explore variations around the expected vessel angle by positioning a series of ridge kernels parallel to the mean expected position (Figure 29).

Figure 29 - Structure of the final filter with a cone shape

The further away from the bifurcation, the larger the possible variations of the vessel, and the more kernels we introduce. This way, we handle variabilities that are of anatomical nature.
Once again, we compute separately each filter, for each sublevel of each branch (a total of 27 kernels). If at least one kernel of a sublevel meets a vessel, we consider that a vessel is detected. It means that we keep the maximum of each sublevel to optimize the detection:

$$F_{LMB}^4(p) = \min_{i \in [1,3]} \left( \text{median}_{j \in [1,3]} \left( \max_{k \in [-n_k, n_k]} \left( R_{\sigma}^0 (p + \alpha_j \overline{P_0 P_1} + k\beta_j \overline{P_0 P_1}^\ast) \right) \right) \right)$$

(13)

with $\overline{P_0 P_1}^\ast$ the vector orthogonal to $\overline{P_0 P_1}$.

In Figure 30, we can see how this cone shape template deals with tortuous arteries.

The filter is robust to variations due to the projection³, and changes of cardiac phases (Dodge’s model regards hearts in end diastole). Moreover, it can be efficiently computed. For each branch, the ridge-filtered image in one orientation only is needed. As a result, computing (12) boils down to filtering the original image with 3 ridge filters, and to discussing about their values (in practice, 27 samples per pixel), which is real-time compatible. The Figure 31 presents the input and the output of the bifurcation filter. We can see that one clear peak is observed, corresponding to the real bifurcation.

³ Indeed, we are not sure of its 3D position of the tripod, which can introduce some (second order) variations wrt. the real expected LMB skeleton.
Then, to detect the LMB, we simply select the maximum of $F_{LMB}^4$. Alternatively, we can select the $n$ candidates by keeping the $n$ maxima of $F_{LMB}^4$ after a non-maximum suppression (practically, we choose $n=3$), and identify the best one later in the algorithm (see 4.2.8).

On Figure 32, the tripod corresponding to the first 3 candidates is plotted. The tripod matches more or less accurately the local shape of the vessel (because of the build-in flexibility of the filter $F_{LMB}^4$):

4.2.6 Local Adjustment of the Tripod

A little adjustment can be performed on the tripod as a way to prepare the subsequent segmentation. Once positioned on the proper place, the tripod can be warped to better match LMB’s. We rotate the tripod in 2D (in the plane of the image, also called “Tilt motion”), and we adapt the angle between LAD and LCx.

---

*4 For instance, after having adapted $n$ complete coronary trees, we could select the one that best fits the data.*
Each of the new tripod will be filtered with $F_{LMB}^3$. This research is local, which allows for a slight translational adjustment of the bifurcation position.

![Figure 33 - warping of the 2D tripod (only LAD and LCx are plotted)](image)

### 4.2.7 Results of Bifurcation Detection

To tackle the very general exam situation, we only make one simple assumption: the bifurcation need to be clearly visible in the image. In particular, all three proximal branches must reasonably lie in the field of view.

<table>
<thead>
<tr>
<th>Detection rate 123 images end diastole</th>
<th>2nd approach</th>
<th>3rd approach</th>
<th>4th approach</th>
<th>Tripod adjustment</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 candidate</td>
<td>40%</td>
<td>54%</td>
<td>62%</td>
<td>62%</td>
</tr>
<tr>
<td>3 candidates</td>
<td>50%</td>
<td>69%</td>
<td>88%</td>
<td>90%</td>
</tr>
</tbody>
</table>

The more sophisticated the method and the better the results. The 90% detection rate obtained with the last filter, with tripod adjustment shows the efficiency and the robustness of the method. It is to be compared to the visually assessed 95% of reasonable tripod projection (Figure 17). Given the numerous difficult configurations that were handled (pace-makers, sternal wires, stitches, electrodes, as well as low-contrast injection, and total occlusions – see Figure 35 to Figure 38 for some illustrations), my tutor considered it to be an excellent performance.
The validation is performed by using a ground truth manually plotted on each image around the bifurcation. If one or three of the 3 first candidates are found inside, the bifurcation is considered as detected.

![Figure 34 - ground truth used for bifurcation detection](image)

**Figure 34** and **Figure 35** and **Figure 36** show some results of detection with the first maximum.

![Figure 35 - detection with 1 candidate](image)

As seen in **Figure 36**, many angiographies refer to difficult configurations, with cases of pacemaker presence, low contrast injection, sternal wires and electrodes presence, and tortuous shapes...
In other images (Figure 37), the first candidate is caught by an electrode, a contrast problem or another shape close to bifurcation, but the 2nd or 3rd candidate manages to correctly find the bifurcation.

![Figure 37 - detection of LMB with candidate 2 or 3](image1)

The main causes of detection failures (10% - see Figure 38) are:

- Sternal wires (3.5%)
- Low contrast (1.7%)
- Tortuous shapes (3.3%)
- Other (1.6%)

![Figure 38 - False positives (green arrows on the real bifurcation)](image2)

To conclude, the bifurcation filter $F_{LMB}^4$ gives 90% of true detection with 3 candidates over 123 images, that is very satisfying considering the wide anatomical variability between patients and all the practical difficulties in routine angiographies (contrasted tools in the field of view, low injection, tortuous vessels, total occlusion).
4.2.8 Use of several 2D angiograms

4.2.8.1 Theory

The projection of a 3D model of the LMB allows to constrain very much the geometry of the sought bifurcation. However, it can happen that other structures exhibit the same local geometry in the considered angiography (Figure 37). To further improve the discriminative power of the method, we propose to exploit the previously acquired angiographies to better constrain the position and/or the geometry of the LMB. I had not enough time to finalize my work on this topic; I thus will present the ideas and some preliminary results.

A typical cath-lab examination indeed begins with a series of 5-10 angiographies, during which the clinician observes the vasculature from various perspectives to perform an accurate diagnosis. If no motion had occurred during this set of exams, the LMB in the different images would correspond to the same 3D space position. We could then position it jointly in the different angiographies (Figure 39).

![Image](https://example.com/image.png)

**Figure 39** - Unique 3D position of the LMB that leads to coherent 2D bifurcations in different images

A false alarm would be unlikely since it could only originate from a contrasted structure having by accident the same geometrical structure as the LMB in a series of angiographies acquired from different perspective.
**Breath translation**

Unfortunately, unknown breathing has occurred between each angiography. Moreover the clinician readjusts the position of the table during the sequence to improve the visualization. All this changes affect the 3D position of the bifurcation, and consequently remove the correlation between 2D projections (Figure 40).

![Figure 40 - Translation of the LMB during exam and influence on projection: the 3D LMB moves from green landmark (projected on the left plane) to the red landmark (projected on the right plane)](image)

However, global table motions can be compensated from the system data. It remains the uncertainty on breath translation.

To check the geometric compatibility between 2 candidates, we consider the interline distance of the 2 back-projected beams. If both rays are close, they can originate from one single 3D point (that has moved). On the contrary, if they are so far away from each other that they exceed the amplitude of breathing, it is impossible that they originate from the same 3D point. They cannot both correspond to the LMB.

To tackle the problem with little computations, we propose the following strategy: The \( n \) best answer from each 2D \( F_{LMB}^A \) filtering are selected. Each combination of candidates (one per angiography) is considered.
Then we compute from this combination a composite score based on the 2D $F_{LMB}^4$ score and the 3D coherence:

![Figure 41 - Score of a combination](image)

In **Figure 41**, we can see a triplet of candidates, with three energies $F_{LMB}^4 1, F_{LMB}^4 2, F_{LMB}^4 3$ and three corresponding beams d1, d2, d3. In this case the scores is the composition of two measures:

$$
Energy = \min(F_{LMB}^4 1, F_{LMB}^4 2, F_{LMB}^4 3)
$$

$$
Closeness = \min \left( \frac{D(d1,d2)}{D(d1,d3)}, \frac{D(d1,d3)}{D(d2,d3)} \right)
$$

where D is a binary distance (1 if dist(di, dj)<thresh, 0 otherwise). Finally the composite score is a function of the bifurcation energy, and of the spatial closeness:

$$
Score(triplet) = F(Energy(triplet), Closeness(triplet))
$$

### 4.2.8.2 The biplane configuration

During my internship, I actually only had time to consider the case of two angiographies. I considered a simple function (15) where:

- I assessed whether we were considering a physically possible pair. To do so, I computed the smallest possible 3D distance between the two candidates, and accepted the pairing if it was in the range of possible breathings [13], p.44.
• If the triplet was validated, the score was a linear combination of the different 2D energies. I ranged the 2D energies, and gave the smallest weight to encourage for a significant bifurcation answer in every 2D angiography.

• If the triplet was considered impossible physically, it was discarded.

While the table motion is known by the system, it was not recorded with the test sequences that I have. We thus decided to estimate it in the image by clicking on one feature that is visible on both angiographies, and computing the corresponding global translational motion.

Now, the only structure that is always clearly visible is the LMB itself! As a result, our table motion compensation actually ensures a perfect LMB motion compensation...

I therefore performed two series of tests:

• **A first series where the motion of the LMB has been perfectly compensated for.** This simulated the configuration where two C-arms simultaneously images the patient from different perspectives. This configuration exists on biplane systems. In that case, the distance separating two acceptable rays can be chosen very small (5mm)

![Figure 42 - A cardiology biplane system, with two C-arms simultaneously imaging the patient](image)

• **A second series of tests aimed at testing the general framework (with breathing).** We randomly picked some translational values with an amplitude typical from the motion that the heart undergoes due to breathing (standard deviation 0.4mm in the
X direction, 0.7mm if the Y direction), and applied that motion to the images. To still be able to pair the real bifurcations, we had to enlarge a lot the space search for acceptable pairs (15mm in X, 30 in Y).

Our results are presented in the following Table for 108 images:

<table>
<thead>
<tr>
<th>Detection rate of the LMB</th>
<th>$F_{LMB}^4$</th>
<th>$F_{LMB}^4$ with biplane (no breathing)</th>
<th>$F_{LMB}^4$ with two angiographies (simulated breathing)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 candidate</td>
<td>60%</td>
<td>68%</td>
<td>61%</td>
</tr>
<tr>
<td>2 candidates</td>
<td>79%</td>
<td>85%</td>
<td>79%</td>
</tr>
<tr>
<td>3 candidates</td>
<td>90%</td>
<td>92%</td>
<td>91%</td>
</tr>
</tbody>
</table>

Results of biplane for 1, 2 and 3 candidates

The results in the biplane configuration are interesting. The detection rates are improved, but still imperfect. Indeed, wrong candidates with high energies (sternal wire, stitches, electrodes) can sometime be matched geometrically with another real LMB.

On the other hand, virtually no improvement was observed in the general case where breathing is allowed. It turns out that the acceptable distance between two rays is so large that we can practically match every candidate from both angiographies, so that the results remain practically unchanged.

The impact of the dramatic research range enlargement is illustrated on Figure 43 and Figure 44.

---

5 There are less sequences than for the monoplane case, because we discarded angiographies that were too close from each other geometrically.
Left and right are presented two angiographies of the same patient. Top row: the crosses figure the candidates, in red the 1st candidate, green the 2nd, blue the 3rd, and other seven candidates are plotted in yellow. The colored lines are the epipolar lines. For instance, the red line in the top left quadrant shows the positions that correspond to the red cross on the right. The acceptable pairings with the considered cross lie closely to that epipolar line. They are circled in red, and do not meet the best answer in that image. Bottom line: the squares correspond to the best three pairs (same color code: 1st in red, 2nd in green and 3rd in blue). We can observe in that case that the LMB on the right cannot be paired with the candidates 1 and 3 on the pacemaker on the left. As a result, the LMB that was ranked 2nd on the right is now ranked 1st.
Left and right are presented two angiographies of the same patient. Top row: the crosses figure the candidates, in red the 1st candidate, green the 2nd, blue the 3rd, and other seven candidates are plotted in yellow. The colored lines are the epipolar lines. For instance, the red line in the top left quadrant shows the positions that correspond to the red cross on the right. The acceptable pairings with the considered cross lie closely to that epipolar line. They are circled in red. This time, many candidates are acceptable, including the first one on the pacemaker. Bottom line: the squares correspond to the best three pairs (same color code: 1st in red, 2nd in green and 3rd in blue). We cannot observe any improvement in that case.

We still believe, however, that there is some information that can be extracted from the previous angiographies of the same patient. Experiments are currently carried out with a different approach: we try to adjust the tripod in the 3D space, so that it correctly fits simultaneously on different angiographies. Hopefully, this will help to discard outliers having a shape incompatible with the other angiograms.
4.3 Extension of the model

Now that the LMB has been successfully positioned on the angiography, it can serve as an anchor to the whole LCA model. The next step is to adapt the model so that it matches the observed vessels. Actually, this task is quite difficult as the generic model of the LCA turns out to be far away from the vasculature. The poor compatibility of the projected generic model with the angiography has two main reasons:

- **The anatomical variability.** While anatomical variability was a limited problem when we only considered the LMB, it produces larger differences further away in the coronary tree.
- **A practical problem concerning my data: the scale was not well known.** A projection parameter was missing in the data that I had, so that I could not accurately assess the scale of the image.

Furthermore, let me mention that I could not devote much time to exploring that last part of my internship (a couple of weeks). As a result, I can only elaborate on preliminary results.

We considered a simplified model of the LCA to reduce the deviation of the model with the actual clinical sequences. It is made of the tripod used previously with four extra segments on the LAD and LCx branches:

- L2 mid
- L3mid
- C2mid
- C3mid

![Figure 45 - projection of the simplified model (LAD branch in blue, LCx branch in purple)](image-url)
We present on **Figure 45** an image showing a large difference in the third segment of the circumflex artery.

A way to control the anatomical variability is to use data from the Dodge’s Model we did not exploit yet: the variance of the control points.

### 4.3.1 The Variance Model

In 4.1.1.1, we mentioned that model of Dodge contains information about the variance of every control point around its mean position [5]. Then, three standard deviations can be exploited:

- Standard deviation on radii
- Standard deviation on rotations
- Standard deviation on angulations

For each point, the area of uncertainty is represented by an ellipsoid, as illustrated in **Figure 46**:

![Figure 46 - Ellipsoid model in world referential](image)

### 4.3.3 Model-Based detection of the LAD and LCx artery

The next step is obvious (**Figure 47**): we project the control points and the associated variances in the current angiography. We then obtain 2D points surrounded by an ellipse (the calculation of the ellipsoid projection is detailed in [14]).
In these uncertainty areas, we compute the oriented ridge answer in the direction given by the model. The strongest answer in the research area is selected. This way, we exploited both the model position and orientation to find the local corresponding vessel.

![Figure 47 - Projection of the L2 and L3 variance, combined with a Ridge descriptor](image)

On Figure 47, we show the projection of L2 and C2 ellipsoids on the left, and the oriented ridge filter inside the ellipses with the orientations $\overline{C1mid - C2mid}$ and $\overline{L1mid - L2mid}$ on the right.

**4.3.4 Results of the LAD and LCx detection**

The method used suffers from the wide variability of arteries.

![Figure 48- Success for LAD and LCx points detection](image)

**Figure 48**, the points L2, L3, C2,C3 are correctly detected, as the model projected match the vasculature quite well.

On the contrary, the influence of variability is shown on **Figure 49**. We have selected two angiographies obtained under the same angulations, but the circumflex arteries looks very
different. On the left image, the Circumflex artery has a trajectory that is far from the model, while the right image matches quite well to the model.

![Figure 49 - Influence of anatomical variability towards the model matching method (images with same angulations)](image)

We finally get the following results:

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<td>LAD2</td>
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<tr>
<td>Detection rate (best candidate – 123 images)</td>
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While the positioning of the segments L2 and Cx2 is still interesting, the performance of the detection of the third segments is poor.

To conclude, this method of model matching is not efficient enough on the whole model as such. The procedure implemented is probably not flexible enough, but this work did not fit any more in my internship since I spent the most important part of my time to implement the LMB filter.

Maybe an iterative positioning of the model would have been judicious to get closer to arteries. Instead of adapting the whole model in one step, we should position the segments LAD2 and Cx2 first, and then rely on them to detect the segments LAD3 and Cx3. This way, we would hopefully avoid a propagation (and cumulation) of the uncertainty.
4.4 Segmentation of the vascular arch

This last part of the report illustrates some results of segmentation concerning the beginning of the three LCA branches. We assume that the model control points are correctly positioned. The segmentation of the arteries consists then in the computation of the centerlines of the vessel.

4.4.1 Computation of Vessel Centerlines

In 2D, a centerline is a line that bisects a vessel into 2 equal parts. The centerline is supposed to answer the best to a ridge filter.

We resort to front propagation algorithms. They are well-known to efficiently find the optimal path between two points, in our case the path joining two control points while staying on maximum ridges (see below for more details). I implemented and used Dijkstra’s algorithm [15] to perform that task.

The principle is the following:

- We compute a potential map, with low values where the path has to go through (i.e. the vessel). This potential (Figure 51) is commonly a ‘negative’ of the Ridge map:

\[
P(p) = R^\text{max} - R_\sigma(p)
\]
We select a control point as a front starting point ('seed').

Then we build a distance map with Dijkstra’s algorithm. The seed has the minimum distance value (0), and we propagate through every possible neighbor, while penalizing with the Euclidean distance and the cumulated potential value. This algorithm is detailed in the appendix [15].

We select a destination. Then the optimal path has to come from the seed to the destination, while scoring the minimum distance (composition of the geometrical distance and the cumulated potential).

The optimal path is obtained by performing a gradient descent from the destination (L3 in Figure 53).
In practice, we consider 2 consecutive points of the model for the seed and destination, and we repeat iteratively the method.

### 4.4.7 Results of Front Propagation

We implemented the front propagation algorithm on the simplified model, but removed L3 and C3 points as their detection rate was too low. We computed the following optimal paths:

- LMB-LM
- LMB-L1 and L1-L2
- LMB-C1 and C1-C2

The results are not mature enough yet to compute success rates. I had not enough time at the end of my internship to carefully parametrize the front propagation in such a way that shortcuts, in particular for long paths, are avoided. But we can however show some illustrations, with a good and a failed segmentation Figure 54.
Conclusion

During this internship, I had to deal with a topic of medical image processing that is of great practical interest for industrial applications, and that is still widely studied by research groups. The 2D segmentation and labeling of arteries presents numerous difficulties related with 2D images: superposition, foreshortening, and intersections. Actually, few articles have been published on this topic and there is a need to find generic, robust methods. My research topic was to explore the use of a 3D generic model of the Left Coronary Artery to perform segmentation and a labeling of 2D angiographies. This original approach was never mentioned in the literature.

The whole segmentation and labeling was an ambitious project that wasn’t really completed. The success of my internship was to implement a new efficient and specific filter that detects the Left Main Bifurcation. Moreover, we can improve its efficiency by using several angiographies of the same exam. The database of angiographies that I had to handle presented a large intra-patient variability concerning the shapes of the vasculatures. The LMB filter is robust to all these difficulties and is usable as such for future algorithms of LCA segmentation. This part of my internship will result in a submission to the ISBI’2012 conference.

Finally these six months spent in Philips Company, and Medisys Research Lab gave me a great overview of some aspects in corporate life as well as the functioning of a research laboratory. I also acquired a kind of autonomy in my work that, for example, could be useful in a PhD.
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Résumé en Français

Ce rapport décrit le travail fourni durant mon stage de fin d’étude effectué chez Philips Healthcare dans le domaine du traitement d’images médicales. Pendant une durée de 6 mois, du 1er Mars au 31 août 2011, j’ai été intégré dans l’équipe de recherche et développement du laboratoire de recherche Medisys Research Lab.

Présentation du stage

J’ai été amené à travailler sur le sujet de la segmentation 2D de l’arbre coronaire en angiographie cardiaque. L’angiographie est une modalité d’imagerie par rayons X qui permet de visualiser les artères coronaires. C’est donc un outil majeur dans le diagnostic des insuffisances cardiaques qui permet notamment de mettre en évidence des sténoses (i.e le rétrécissement partiel du diamètre d’une artère), voire une occlusion totale pouvant entraîner un infarctus du myocarde. Ces types d’anomalies sont traitées par des angioplasties, qui consistent à insérer un stent dans l’artère coronaire par le biais d’un cathéter afin de rélargir le diamètre de l’artère et rétablir la circulation sanguine. L’insertion du stent dans la bonne artère est délicate et des techniques de segmentation, d’étiquetage et de quantification aident fortement le clinicien à se repérer pendant l’intervention.

Mon stage traitait plus précisément de la segmentation et de l’étiquetage de l’artère coronaire gauche. Cette artère est composée de 3 branches principales : l’artère coronaire gauche principale (LM), l’artère interventriculaire antérieure (LAD), et l’artère circonflexe (LCx). Les deux dernières possèdent un bon nombre de ramifications, mais qui ne seront pas prises en compte dans mon travail.

Pour segmenter l’arbre coronaire gauche, on fait intervenir des connaissances à priori sur la structure d’intérêt de manière à rendre la segmentation aussi précise et robuste que possible. En pratique, on s’aide d’un modèle générique 3D de l’artère coronaire gauche qui, projeté sous l’angle adéquat, fournit le squelette 2D de l’arbre coronaire de l’angiographie 2D considérée. La segmentation est effectuée en deux étapes : la détection de la bifurcation principale qui permet d’initialiser la position du modèle 2D, puis le calcul du squelette de l’arbre vasculaire. Dans ce rapport, on insiste sur la première étape qui constitue l’originalité de la méthode.
Etat de l’art

Un état de l’art dans le sujet indique que peu de travaux ont été publiés dans le domaine de l’étiquetage 2D des artères coronaires, voir aucun en segmentation 2D. Les méthodes de rehaussement de contrastes des vaisseaux sont nombreuses. Frangi et al. Et L’Antiga publient des articles très intéressants sur des filtres spécifiquement construits pour mettre en évidence les artères : la Vesselness, et la Coronariness, qui reposent sur des mesures géométriques. Cependant ces filtres ne sont pas très robustes à la présence d’autres objets. En pratique, dans le monde industriel chacun possède son expertise permettant de se débarrasser des outils gênants comme les pace-maker, les agraphes, les électrodes et autres cathéters. Mais il manque toujours un formalisme global aux méthodes actuelles qui permettrait d’effectuer une segmentation en un temps, sans post-traitement.

En revanche, en segmentation 3D, les méthodes sont beaucoup mieux formalisées. David Lesage et al utilise une approche Bayésienne associée à des filtres particulaires pour segmenter l’arbre coronaire avec des images de CT.

En général, les segmentations sont basées sur des modèles 3D, génériques ou spécifiques à un patient. Les modèles de Dodge et Sherknies sont souvent utilisés dans la littérature. L’étiquetage est aussi un sujet beaucoup mieux maîtrisé en 3D avec Lorenz qui effectue un recalage avec les centerlines d’images CT et s’aide aussi d’un modèle des chambres cardiaques afin contraindre plus fortement le positionnement des artères. Chen S-Y James et al. s’appuie sur la géométrie épipolaire pour reconstruire à partir d’images biplan l’arbre vasculaire. Ceci permet de trouver les meilleurs angles de vues pour observer l’arbre coronaire. Enfin, le seul article intéressant en 2D est celui de Chalopin en étiquetage. Celle-ci travaille avec une structure en forme de graphe pour définir les artères coronaires avec des nœuds, des branches et des relations de voisinage. La segmentation est déjà donnée et on cherche à calculer les propriétés géométriques et topologiques des centerlines pour identifier des nœuds précis du graphe et attribuer une étiquette.
Méthode envisagée

La méthode que j'ai finalement choisie est basée sur un modèle 3D, celui de Dodge. Ce modèle est constitué de 23 points, qui correspondent à des bifurcations, des milieux de branches et des extrémités. Ce modèle est projeté dans les mêmes conditions que celles d'un examen : avec les angles de l'arceau de l'angiographe. On obtient suite à cette projection un modèle 2D qui est plus à même d'être exploité pour se recaler aux squelettes réels de l'arbre vasculaire. Ce modèle 2D doit être superposé aux artères correspondantes sur l'image. Le positionnement initial est très important. Celui-ci peut être fait manuellement par le clinicien qui utilise l'application, mais cela fait perdre du temps, surtout pendant un examen. C'est pourquoi on cherche à initialiser le modèle automatiquement. On choisit la bifurcation principale de l'artère coronaire gauche comme point d'accroche. C'est en effet le point le plus caractéristique et qui présente le moins de variabilité anatomique. La méthode d'initialisation est le point le plus important de ce rapport.

Travail préliminaire

Tout d'abord, nous avons observé en pratique que le modèle de Dodge ne correspondait pas toujours précisément à la forme de l’arbre coronaire. Un paramètre d’échelle n’était pas fourni dans mes données, j'avais donc à utiliser une valeur arbitraire conseillée par mon maître de stage. Mais la cause la plus probable était la variabilité anatomique de ma base d’image : deux angiographies acquises sous le même angle de projection peuvent contenir deux mêmes artères de forme radicalement différentes. Nous avons tout de même remarqué que cette variabilité était fortement réduite pour ce qui était de la bifurcation principale et de la naissance des 3 artères qui l’entourent.

Nous avons donc pensé à modéliser le comportement global de cette bifurcation avec le modèle de Dodge duquel nous gardons seulement 7 points avoisinants la bifurcation. Ce petit modèle local est appelé trépied de part son nombre de branches. Sa projection donnait une forme qui, dans 95% des cas correspondait à la forme réelle de la bifurcation.
Détection de la bifurcation principale

La méthode utilisée pour trouver la bifurcation principale est également basée sur un modèle, qui est le trépied évoqué précédemment. On combine en fait le trépied 2D à des caractéristiques bas niveau tels que les Ridges de l’angiographie. Les filtres de Ridge sont connus pour mettre en évidence les artères, de la même manière que la Vesselness. Grâce à eux il est possible de savoir si un pixel se situe ou non sur une artère.

A partir du squelette 2D de la bifurcation, on élaboré un filtre qui permet la détection de la bifurcation principale de manière spécifique et efficace, tout en tolérant les variations anatomiques. A fur et à mesure de mon avancement dans le stage, j’ai cherché à élaborer et améliorer pas à pas ce filtre de bifurcation. Le premier utilisait une version simple de template matching entre le trépied et l’angiographie. Le template étant un ensemble de kernel Hessiens disposés autour de chaque point du trépied avec l’orientation des branches.

La deuxième méthode filtre séparément les 3 branches du trépied et retiens le minimum de chaque réponse de façon à privilégier les zones de l’image ou au moins les 3 branches répondent. Puis la 3è méthode introduit des kernels supplémentaires de façon à allonger la zone de détection d’une branche et donner plus de cohérence à la forme de la bifurcation.

La dernière méthode, qui sera retenue utilise un filtre en forme de cône qui intègre une incertitude angulaire au niveau de chacune des 3 branches pour prévenir les variabilités anatomiques. Ce filtre a été testé et répond très favorablement aux bifurcations dans 90% des cas sur une base de 123 images : on conserve les 3 premiers maxima de la réponse du filtre, et si un de ces 3 maxima se situe dans la zone de vérité-terrain délimitée manuellement, la bifurcation est considérée comme détectée. Les résultats sont un peu moins bons si l’on ne retient que le premier candidat (62%), mais l’on considère que d’autres à priori peuvent être utilisés ensuite pour sélectionner le meilleur des 3 candidats parmi les 3 potentiels.
Cette détection de bifurcation est très efficace car elle tolère la présence d’outils chirurgicaux comme les pace-maker, les cathéters, les électrodes mais aussi des images très peu contrastées, avec des degrés d’injection très faible et des artères tortueuses. Ces difficultés génèrent seulement 10% de faux positifs, ce qui est très satisfaisant.

**Utilisation de plusieurs angiogrammes**

Pour améliorer encore la fiabilité du filtre, on propose une extension de cette méthode qui exploite non seulement l’angiographie courante, mais aussi toutes celles qui ont été acquises précédemment durant l’examen. Cette approche permet de contraindre au maximum la géométrie de l’objet d’intérêt, tout en étant transparente du point de vue du médecin. J’ai pu y travailler quelques semaines sans pour autant avoir eu le temps de finaliser des résultats significatifs. La méthode méritait quand même de figurer dans le rapport compte tenu de son originalité.

En effet, en considérant l’unicité de la position 3D de la bifurcation, les projections résultantes sous plusieurs angulations donneront également des positions uniques bien définies sur les images 2D. Ainsi il existe une cohérence entre les position des bifurcations qui doit être vérifiée. Par exemple deux candidats d’angiographies différentes peuvent être appariés, et ainsi exclure ceux qui ne correspondent pas géométriquement. Nous avons donc un critère basé modèle sur la forme de la bifurcation, et un critère sur la géométrie 3D. Cela devrait réduire encore plus le nombre de faux positifs.

Malheureusement, divers mouvements interviennent pendant des acquisitions et entre les acquisitions : déplacement de la table par le médecin, respiration et contraction du cœur. Ceux-ci viennent « brouiller » la position 3D de la bifurcation. Pour régler ce problème, on peut tout d’abord compenser sur les angiographies le mouvement de la table, enregistré pendant l’examen. Pour le reste on utilise une zone d’incertitude, dans laquelle se situe la bifurcation 3D.

Pour utiliser cette cohérence spatiale, on rétroprojette les candidats 2D à la bifurcation, avec leur géométrie respective (angulation, distance à la source, etc).

On compare ensuite les faisceaux rétro projetés. Si leur distance est inférieure à un certain seuil, alors les deux candidats correspondants sont compatibles et on regarde à ce moment leur énergie de bifurcation.
Cette méthode a été testée avec et sans phénomènes de respiration. Dans le cas optimal (sans respiration) l'appariement géométrique est discriminant et élimine bien les mauvais candidats. Les pourcentages de détection avec un seul candidat s'améliorent significativement. En revanche, avec une respiration, la situation se complique. La zone d'incertitude résultante sur l'image devient trop grande. De ce fait, presque tous les candidats peuvent être appariés, entre bons candidats, comme entre mauvais, et le pourcentage de détection ne s'améliore pas vraiment.

Nous n'avons pas encore épuisé toutes les potentialités de cette approche. Il est encore possible d'effectuer un ajustement du trépied en 3D simultanément sur plusieurs angiographies, ce qui ajoute encore une contrainte de cohérence géométrique supplémentaire.

Segmentation basée-modèle

Cette localisation de la bifurcation permet d'initialiser la segmentation basée-modèle de l'arbre coronaire, comme expliqué dans la deuxième partie du rapport. L'association du modèle et de caractéristiques locales bas-niveau de l'image fournit des points caractéristiques bien positionnés sur l'artère.

Le modèle générique s'éloigne parfois des artères, chez certains patients, c'est pourquoi on utilise des informations sur la variance du modèle. On a autour de chaque point une ellipsoïde qui définit le volume d'incertitude. Ce volume projeté, on obtient des ellipses sur l'image. Les segments d'artères correspondants sont ainsi pour la plupart dans cette zone de recherche. Des caractéristiques bas niveaux telles que des Ridges orientés permettent de retrouver la position correspondante aux points du modèle.

Un algorithme classique de front propagation est enfin utilisé entre chacun de ces points afin d'obtenir la segmentation finale de l'arbre vasculaire. Les centerlines sont ainsi tracées sur les artères et constituent le résultat de la segmentation. De plus les étiquettes présentes dans le modèle 3D se transmettent au modèle 2D, et sont finalement intégrées directement dans la segmentation.
**Résultats**

Les résultats finaux de segmentation ne sont pas encore assez matures pour les mentionner. Les calculs de centerlines ont constitués une petite partie de mon stage (2 semaines) et je n'ai pas eu le temps de paramétrer consciencieusement l'algorithme de front propagation. En revanche, le filtre de bifurcation a démontré son efficacité au travers d'une grande base de 123 séquences d'angiographies provenant de 15 patients. Il est de plus améliorable en utilisant plusieurs angiographies. Cette méthode sera proposée au symposium d'imagerie médicale ISBI 2012 afin d'être publiée dans un article.