

Semiautomated Editing of Vessel Segmentation Masks

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Abstract

This thesis describes a technique for editing segmentation results of vessels, which should enhance usage and reduce work duration for physicians by using a simple and fast way of interaction. Moreover also a quick calculation of an accurate result was of primary interest. Since vascular structures are vulnerable to diseases, vessels are the main focus of this thesis. Nowadays, Image Analysis is able to facilitate the medical diagnosis procedure. Since stroke treatment is time-crucial, appropriate algorithms should be fast and enable an accurate depiction of the arteries to simplify the diagnostic process. However, because automatic segmentation is often quite inaccurate and manual segmentation is tedious, neither of these two methods alone is often adequate for usage. Because of this we suggest to combine the fast automatic segmentation and the exact manual editing done by clinical experts. To reduce effort and working time of the medical staff, this thesis describes different techniques, which were developed to modify and, more importantly, to improve the segmentation results. The segmentation mask can be altered as its components can be separately removed and independent elements can be connected. A framework was implemented, with which a user is able to perform these tasks interactively. The deletion process is supported by various metrics, which enable the search and removal of similar structures. Also this framework assists the reconnection of vessels by finding the most likely connection by the means of image intensities and their gradients. The main goal of this thesis was to facilitate and accelerate the editing process by implementing fast semi-automatic algorithms. Intuitive interaction methods also had a major impact on the design.

Kurzfassung

In dieser Bachelorarbeit werden Methoden zur Bearbeitung von Segmentierungsmasken von Gefäßen vorgestellt. Die Techniken sollen nicht nur die Bearbeitungsschritte für Kliniker erleichtern, sondern auch die allgemeine Arbeitszeit reduzieren. Diese Ziele sollen durch eine einfach zu kontrollierende Interaktionsmöglichkeit und eine schnelle Berechnung erreicht werden. Heutzutage kann eine geeignete Bildanalyse den Diagnoseprozess vereinfachen. Diese Segmentierungstechniken sollen aus schnellen Algorithmen bestehen, da Diagnosen oft, aufgrund hohen Zeitdrucks, schnell erstellt werden müssen. Aus diesem Grund sollen Algorithmen, die in diesem Gebiet eingesetzt werden, nicht nur die gesuchten Strukturen korrekt identifizieren, sondern auch eine schnelle Berechnung der Ergebnisse ermöglichen. Da das Erreichen von schnellen Berechnungszeiten oft fordert, die Genauigkeit der Berechnungen zu vernachlässigen, können fehlerbehaftete Ergebnisse entstehen. Diese Fehler werden dann manuell von klinischem Personal korrigiert, da Inkorrektheiten betreffend der Segmentierungsmaske zu fehlerhaften Schlussfolgerungen für die Diagnose führen können. Aufgrund des hohen Zeitaufwandes den diese Prozedur benötigt, werden in dieser Arbeit neue Methoden vorgestellt, um diesen Arbeitsschritt zu vereinfachen und zu beschleunigen. Die Segmentierungsmaske kann einerseits bearbeitet werden, indem Komponenten, die falsch klassifiziert wurden, entfernt werden. Außerdem können getrennte Elemente zusammengefügt werden. Ein Framework wurde implementiert, das dem Benutzer ermöglicht entweder mit der Maus oder der Tastatur diese Methoden auf einen geeigneten Datensatz anzuwenden. Der Löschvorgang wird durch einige Metriken unterstützt, die ein automatisches Löschen von ähnlichen Elementen ermöglicht. Außerdem unterstützt das Framework die Berechnung der korrekten Verbindung der Gefäße, indem Informationen wie Bildintensitäten und Gradienten miteinbezogen werden. Das Hauptziel dieser Arbeit war es den Bearbeitungsprozess zu vereinfachen und zu beschleunigen, indem schnelle halbautomatische Algorithmen entwickelt wurden. Auch intuitive Interaktionsmöglichkeiten wurden in den Designprozess miteinbezogen.

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CHAPTER

Introduction

1.1 Motivation

Many diseases, patients suffer from, occur because of a problem in their cardiovascular system. Since this system is in charge of vitally important tasks, issues respective to it are often fatal when not immediately identified by physicians. As analysed by the World Health Organization the most common causes of death include diseases regarding the cardiovascular system. Especially diseases affecting the vessels frequently occur [1]. As described by Benninghoff et al. [2] inside the brain one special vessel structure, called Circle of Willis, is located, which is particularly vulnerable and is often the origin of diseases' symptoms. Due to these facts this thesis focuses on improving a part of the diagnosis process of the vascular structure in the brain.

As time management plays an important role in the treatment planning of vascular diseases, fast diagnosis techniques must be available. To discover the origin of the symptoms the patient suffers from, imaging techniques like Computer Tomography (CT) or Magnetic Resonance Imaging (MRI) are used to generate a three dimensional image of the region of interest of the human body. As next step experts have to scan through the large number of images to find the problematic region. This process is very time consuming and small variations of the anatomy make this work laborious and exhausting. To simplify this process segmentation algorithms can be executed to presegment the anatomic structure and highlight the regions, where the origin of the symptoms is located. Time-saving algorithms are used to identify the sought tissue, which are known for often delivering slightly inaccurate results. Then a manual correction of the segmentation mask is necessary for experts to find the correct information, which is again complex and burdensome. The main goal of this thesis is to simplify the manual correction process by delivering a new semi-automatic editing technique.

The developed editing techniques can be separated into a computational part and an interactive part. The computational part includes the algorithms used to recognize new

target structures or to delete wrongly found components. Therefore not only image based information is essential, but also the anatomy of vessels is important. The interactive part of this technique consists of different interaction methods, provided for the user, to set parameters needed by the computational part. To determine the strengths and weaknesses of the implemented editing system, state-of-the-art characteristics were taken as reference.

1.2 Medical Background

1.2.1 Cardiovascular system

As discussed by the authors Welsch et al. [3] and by Benninghoff et al. [2], the cardiovascular system is composed of a body circulation and a pulmonary circulation. Both circulatory systems are driven by the pumps of the heart. The heart and blood vessels are the most important components of the cardiovascular system. One of the main functions of this system is the transport of oxygen, nutrients and hormones throughout the body.

1.2.2 Blood vessels

Blood vessels have a very important role in the transportation because through them all cells and tissues are provided with vital substances. For this reason vascular diseases, which disturb or interrupt the supply of the organs, can lead to a limitation or loss of organ functions [3]. The vascular system is also divided into a macro circulation consisting of arteries and veins and a micro circulation composed of capillaries, venules and arterioles. Arteries transport the blood away from the heart while the veins lead the blood to the heart. In general blood vessels are composed of different cells and of extracellular components. The extracellular components mostly consist of proteins together with flexible fibres and proteoglycans. These different types of cells and the extracellular components are specifically arranged in the wall of the vessel and form three layers. The first layer is called Tunica intima (Intima). This layer is lined with endothelial cells. Their function is to react to infections and attract antibodies to combat it. They also regulate the blood clotting when vascular damages occur. The second layer is called Tunica media, which is mostly built of smooth muscle cells and of extracellular components. It is responsible for the regulation of the diameter of the vessel and therefore also for the blood pressure. The third and last layer is referred to as Tunica adventitia. Its main purpose is to strengthen the vascular walls [3]. The described structure is shown in figure 1.3, which is taken from [2].

Circle of Willis (Circulus arteriosus cerebri)

A special characteristic of arteries is that they are able to connect with each other. This connection is called arterial anastomosis. A major benefit of anastomoses is becoming effective in the case of a failure of one vessel, because this structure is granting a collateral



Figure 1.1: This illustration, taken from [2], describes the structure of the vessels. The tunica adventitia is the outermost layer and is responsible for strengthening the walls. The layer in the middle is called Tunica media, which regulates the blood clotting and is therefore vulnerable for diseases. The most inner layer is the Tunica intima. There the production of antibodies takes place.

circulation. The other working vessel is, in case of an anastomosis, capable of supplying the tissue or organs, the malfunctioning vessel usually is responsible for. So it can be guaranteed that these tissues will not immediately die, due to the lack of blood circulation. Described by Benninghoff et al. [2] the Circulus arteriosus cerebri, also called Circle of Willis, is an important arterial anastomosis. This structure lies in the brain, more exact in the midbrain near the brain base. In this example the brain arteries connect in form of a ring. The Circle of Willis is formed through the anastomosis of the three cerebral arteries, the Arteria cerebri anterior, Arteria cerebri media and Arteria cerebri posterior.

• Arteria cerebri anterior (ACA)

This artery is responsible for providing nutrients and oxygen for the anterior middle section of the cerebrum.

• Arteria cerebri media (ACM) The supply of the cerebrum is mostly dependent on this artery.

• Arteria cerebri posterior (ACP)

This artery is the counterpart to the ACA. Its main supply area is lying in the posterior middle section of the cerebrum.

The first two arteries are branches of the Arteria carotis interna (ACI), which is originally supplied by the aorta. The last one is a branch of the Arteria basilaris (AB). This

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artery reaches from the spinal cord to the brain stem. The short arteries, connecting the three arteries cerebri anterior, media and posterior in a ring-like form, are called Arteria communicans anterior (ACoA) and Arteria communicans posterior (ACoP). The illustration 1.2 schematically represents the blood-supply of arteries forming the Circle of Willis. All arteries described above are highlighted in red to contribute to the identification. Figure 1.3 represents the Circle of Willis segmented from a MRA image. A precise labelling of the associated vessels was made, to ensure a recognition in other segmented images in later chapters.



Figure 1.2: This illustration demonstrates the structure of the Circle of Willis. Also the arteries supplying this anastomosis are presented. The arteries, highlighted in red, form the Circulus arteriosus cerebri. This image is modified and taken from [2].



Figure 1.3: This image displays a segmentation of the Circle of Willis. All vessels, forming this structure, have been labelled to visualize the anatomical construction.

Diseases of the brain arteries

Diseases like aneurysm and thrombosis are widespread issues concerning the vascular structures, which can have life-threatening consequences. An aneurysm is a vascular dilation triggered by a high occurrence of enzymes, which degrade elastin and extracellular matrix. Also macrophages are involved in this process as well as the apoptosis of smooth muscle cells. Together this three components induce a sack-like bulge of the vascular walls, which imposes a rising tension to the vessel. This vascular dilation can lead to a formation of a thrombus, but also to a rupture of the vessel itself. Aneurysms often occur where the vascular wall is degraded. This degeneracy can for example be induced because of connective tissue disorders or can be promoted through former injuries. Usually humans, who suffer from aneurysms do not have any symptoms until the progression of the disease is in an advanced state. As a secondary disease of an aneurysm an arterial thrombosis can occur. A thrombosis can also have other causes like changes in blood composition. Also a slower blood flow can lead to a formation of a clot. Thereby a clot, also called thrombus, is originally formed by the fibrin mesh, thrombocytes and erythrocytes, but is

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changing over time on the basis of various chemical processes. The thrombus can block the blood flow partially or even as a whole. Because of this blocking an occlusion of the vessel emerges, which leads to damages or even death in the nearby tissue. In case of an occlusion of an artery in the brain, an ischemic stroke can be caused.

Apoplectic strokes, which describe an interruption of the blood supply of the brain, can have several causes like ischemic strokes or intracerebral bleedings. Ischemic strokes often happen because of a thrombosis, in contrast to intracerebral bleedings, which are a consequence of micro ruptures of the vessels. As quoted by Piper [4] the occurrence of an apoplectic stroke rises from 8 of 100.000 persons in the age group of 25 - 34 year olds from over 2000 per 100.000 persons, who are older than 85 years. This disease can have far-reaching consequences, which range from persistent neurologic defects to death. An apoplectic stroke is followed by symptoms like suffering from head ache, vomiting and loss of consciousness. The sooner a precise diagnosis can be found the better are the chances to survive and to minimize the remaining health damage. To clarify if the patient is suffering from an apoplectic stroke Computer Tomography (CT), Magnetic Resonance Imaging (MRI) or Magnetic Resonance Angiography (MRA) can be used. CTs can be advantageous to find bleedings. But with this technology ischemic strokes can only be determined 24 - 48 hours after their first emergence. In contrast, MRIs are capable of determining an ischemic stroke in all brain regions within an hour. Also bleedings can be recognized instantly. For these reasons MRIs should be preferred when an apoplectic stroke is assumed as explanation for the patient's symptoms. Also MRAs can be applied to find answers for the condition of the patient's brain arteries. Especially important is a MRA when a chronic vascular occlusion in one of the extracranial arteries happens. This process is one of a few methods, which can be used for examination of the patient, because in this case a very careful and gentle presentation of the Circle of Willis and his discharging arteries is necessary. This method is not only save for the patient, it is also precise enough to reveal multiple stenoses. When suffering from chronic vascular occlusions patients have symptoms like visual disturbances, feeling sick and dizzy. Just like an apoplectic stroke, chronic vascular occlusions can lead to death [4].

1.3 Medical Image Data Acquisition

As stated above, an early detection of an apoplectic stroke or a vascular occlusion can save a human's life. To discover the problematic area or respectively the affected vessel, Computer Tomography or Magnetic Resonance Imaging is used to create a visual representation of the body's interior. Below the processes of a CT and a MRI scan are explained and can be looked up more accurate in the reference book "Medical imaging technology" by Mikla et al. [5] and in the book "Visual Computing for Medicine: Theory, Algorithms, and Applications" by Preim et al. [6].

• Computer Tomography (CT)

As shortly stated above Computer Tomography is an imaging technique. At first

the patient is lain in a stationary computer tomograph, where an emitter-detector system rotates in a circular orbit around the patient, in a plane, perpendicular to the length-axis of the patient. An x-ray beam is generated by an emitter. Its thickness is adjustable so that it is wide enough to pass on both sides. These rays then pass through the patient and some energy is absorbed in the patient's tissue. The remaining radiation transpires through the body and is caught by a detector. The obtained intensity profiles, which represent the images, are sent to a computer, where a volumetric representation of the images can be calculated [5]. For better visibility of the vessels a contrast agent can be injected to the vascular system. Several seconds after the injection has been performed, it is possible to start the scan. The enhancement of the vessels is dependent on injection parameters like the quantity and how the medium was administered. One major drawback of Computer Tomography is the radiation dose a patient is exposed to. To gain higher resolution images usually the radiation dose is increased, which raises the risk of cancer [6]. As mentioned by Piper [4] a major disadvantage in case of an ischemic stroke is, that in a CT-image this disease is not visible until 24 hours after the onset of the symptoms. For this reason an MRI is often the preferred imaging technique when an occlusion in the brain arteries occurs.

• Magnetic Resonance Imaging (MRI)

This technology utilizes the fact that the human's body consists of 80% water. This substance is constructed out of hydrogen and oxygen atoms, which in turn consist partly of protons. These are positively charged and are able to spin around their axes. In addition they are randomly oriented so their magnetic field cancels out. In a Magnetic Resonance Tomograph a strong magnetic field is constructed and some protons in the patient's body will tend to align in the direction of the field, while the others will align opposite to it. When a radio frequency pulse signal, perpendicular to the field, is emitted, the energy content of the nuclei increases and a precession movement is performed. When the absorbed energy slowly dissipates the protons move back to their original alignment with the magnetic field. Meanwhile the emitted energy is recorded and used to represent the image. The final volume consists of intensity values, which are based on the specific tissue types [6]. One advantage of the MRI, compared to the CT, is the much higher detail of soft tissue. Furthermore the patient is not exposed to radiation and no other biological hazards, effecting the body, have been reported so far. However the scan is not allowed for patients with cardiac pacemakers or people, who have tattoos or other metal implants due to the strong magnetic field, which is constructed in the machine [5].

The images generated by the methods mentioned above are three-dimensional. Mostly these 3D images are represented as a sequential series of 2D slices. This representation has the advantage of lower computational complexity and less requirement of memory.

CHAPTER 2

Related Work

Via the images produced by CT, MRI or MRA doctors have to find out why the patients are suffering from their symptoms. A precise diagnosis, containing information, like the exact location of the origin of the symptoms and the source, that is inducing them, is essential to plan the next therapeutic steps. Therefore the radiologist has to be very precise, while looking through the MRI or CT images to find anomalies in the patient's body structure. This procedure can be very time-consuming because of the large dataset the medical staff has to go through. So valuable time to help the patient is lost.

2.1 Image Segmentation

Segmentation techniques can be used to reduce the amount of time, spent by clinicians to go through every slice of the image. Segmentation creates a simplified representation by dividing an image into regions of foreground and background on the basis of similar properties like grev level, brightness or contrast. As stated by Falcão et al. [7] the whole segmentation process can be divided into two main tasks, namely recognition and delineation. Firstly recognition can be performed by an algorithm or manually by physicians. Thereby the rough determination, where the boundary of the target structure is located and the distinction from other object-like tissues, are of immediate importance. Secondly delineation describes the task of defining the spatial extent of the sought object. So the important aspects of this process are detecting relevant structures and specifying their borders. Thereby various techniques can be applied for identifying which voxel belongs to the target structure. Because of this characteristics the segmentation process can be used to identify regions of interest like blood vessels or other types of tissue [6, 8]. While algorithms sometimes deliver superior results in the delineation task, human users typically outperform automated software procedures in the recognition task. This is one of the reasons why there are no automatic segmentation techniques, that are able to correctly locate every sought tissue or vessel. As mentioned by Heckel et al. [9] other

causes for the inability of finding every type of body structure are, for example, noise, low contrast or biological variability. Another reason is described by Sharma et al. [8] and says that, "Automatic segmentation of medical images is a difficult task as medical images are complex in nature and rarely have any simple linear feature." In general a lot of different algorithms have been developed to overcome the shortness of having one universal software for finding all possible types of organs and tissues. Everyone has its own disadvantages and benefits and is often been intended to perform a clearly specified task like merely finding tumours or solely identifying vessels etc.

In this thesis the concept of automatic segmentation means algorithms, where the user does not have to specify parameters in any way, while the term user-steered segmentation stands for the active involvement of the user in the segmentation process. Thereby it is irrelevant whether the user has to set parameters for starting the algorithm for the first time or if he has to correct the result manually after a pre-segmentation was performed. In order to separate "good" automatic segmentation techniques from bad ones, four different requirements have been established. A suitable segmentation method should have following characteristics, as noted by Preim et al.[6].

• Robustness

The technique should be usable for a huge variety of cases. As discussed above, it is not possible to use one technique for all sorts of tissue, but there are also methods, which are adaptable for various types of structures as threshold-based algorithms.

• Accuracy

One very important characteristic is accuracy. This characteristic indicates the degree to which the delineation of the structure corresponds to the ground truth. Precise results should be delivered by a segmentation algorithm. Especially for an effective treatment of the patient's disease an exact diagnosis, which is highly dependable on an accurate result, is inevitable. Proving this characteristic is quite difficult. As stated by Olabarriaga et al. [10], accuracy can be assessed subjectively or objectively. For subjective evaluation an expert's knowledge is used to rank the generated results. Objective evaluation means comparing the result against the ground truth by using different distance measures.

• Reproducibility

Reproducibility means that an algorithm executed a few times on the same dataset should always produce the same result. Also different users should produce an identical outcome, when the same variables have been used. In contrast to accuracy, this feature is easy to prove, because no ground truth or professional expertise is essential.

• Speed

Medical image data is in many cases generated from patients, who currently find themselves in a life-threatening situation, for example in the case of an ischemic stroke. For saving a life or to minimize permanent damages, a final diagnosis must be performed as fast as possible. There might be algorithms that provide very precise and accurate images, but are extremely computationally demanding and take a long time to calculate the results. In such situations time is very costly and algorithms have to produce acceptable images as quickly as possible. Thereby minor details in images are neglected, to save time and increase the chance for the patient to survive. Obviously calculation time and a precise result must be in a balanced relation to each other. Also a too imprecise image, which is calculated in a short time, can be disastrous for the patient.

To distinguish between different segmentation techniques, they are divided on the basis of various criterions. These criterions are tested for all voxels in the image. If a voxel fulfils the selected criteria, it is stated to belong to the sought structure.

2.1.1 Threshold-based Segmentation

One type of segmentation techniques is called threshold-based segmentation. The goal of this type is to generate a binary image out of the original three dimensional MRI or CT image. This is done by selecting an interval of a lower and upper threshold. The interval is then applied to the image intensities. When the voxel has an intensity that lies between the interval's values, it is set to 1, otherwise it is set to 0 [6].

Generally threshold-based segmentation can be used to find different types of tissue. On the one hand this technique can be used to find bone in CT data. On the other hand it is also capable of finding vessels in MRA images. Figure 2.1 displays the resulting image of the threshold algorithm, implemented in our framework. As can be seen, the artery AB and other components, which have the same intensities as vascular structures, have been identified and are therefore displayed white.

The greatest benefit of all, gained from using this technique, is its reproducibility and its speed. No matter how often or by whom it is executed, with the same threshold always the same result is calculated. In addition the calculations are easy and quickly made, so the runtime of this algorithm is very short, mainly depending on the size of the image data. But it must be said that the accuracy of this segmentation method is restricted, because it is quite error-prone. On the one hand this problem is caused by the presence of artefacts in the image [8]. On the other hand only a correctly set interval is able to achieve a proper segmentation result, otherwise results are poor. Furthermore often a professional expertise is required to select a correct threshold. A meaningful threshold can also be generated with the use of histograms. Due to this central issue it is important to make a tool available for physicians, with which they are able to manipulate the calculated segmentation mask. So minor failures of the algorithms can be patched by manual interaction.



Figure 2.1: This figure displays the result of the threshold algorithm, implemented in our framework. The interval of the threshold was manually set to find vascular structures. As can be seen, the artery ACI was identified and is therefore coloured in white.

2.2 Interaction Techniques for Editing Segmentation Masks

The following classification is described by Olabarriaga et al. [10] and helps to understand the implications of the developed editing process. This user-steered segmentation process can be divided into four main components: the user, the computational part, the interactive part and the user interface.

The computational part describes the used algorithm, which is able to generate a delineation of the target structure from the background. The parameters needed for this calculation can be specified prior the execution, determined by the knowledge of the user or by hard-coding it into the programming code. For the description of the computational part the exact type of segmentation algorithm is irrelevant. The responsibilities of the interactive part include mediating information between the computational part and the user. More precisely specified, this component is translating the data input from the user into calculable parameters for computation. In addition it also visualizes the computed result in an understandable way. Then the user is able to interpret the visual feedback and can give a response, providing further information to the computational task. The concrete communication between computer and user takes place over input and output devices. In figure 2.2 the described structure of the process is visualized.

2.2.1 Characteristics of Interaction Techniques

The main goals of interactive interference in the segmentation process, are providing effective control for the user and minimizing the user's time, required to finish the process



Figure 2.2: This figure shows the design of the editing process. In this case of user-steered segmentation, the user interacts with the interactive part by using input and output devices. The delivered information is then forwarded to the computational part. From there the result is return to the user by the interactive part. This illustration was taken from [10], where this process is described in detail.

[7]. To achieve these aims, importance can be attached to firstly the input methods, controlling how data is set, and secondly if the input data has immediate impact on the segmentation result.

Three primary characteristics can be assigned to input methods, which help to recognize if these interaction techniques achieve the goals mentioned above. General requirements of manually performed segmentation are listed by Olabarriaga et al. [10] and by Falcão et al. [7]. These include inter alia speed, repeatability and accuracy.

• Speed

In some specialized literature, for example by Olabarriaga et al. [10] this evaluation criterion is also called Efficiency. Speed can be described separately for the computational and for the interactive part. For the computational part the same description, as used for automatic segmentation methods, is appropriate. It may be added that the computation should be fast enough to make interaction in real-time possible. In context of the interactive part it describes the extent of user involvement necessary to complete the segmentation process. This can be measured by the amount and nature of the user's intervention.

• Repeatability

Repeatability for user-steered segmentation expresses the variations in the calculated results caused by the subjective actions taken by the users. Not only the distinction in the expert's judgement, but also the difference among the operations implemented by the segmentation tools, is responsible for variable outcomes and must be taken into account when evaluating such methods.

• Accuracy

This characteristic has the same basic meaning as in terms of automatic segmentation but its impact on the resulting image is different. A 100 percent similarity of segmentation results with the true biological structure can not be guaranteed by automatic algorithms nor by manual segmentation. But manual recognition can be seen as a good approximation of correctly detecting target structures. Due to the poor repeatability of manual actions based on the subjective perspective of the user, also accuracy is not guaranteed after each interactive segmentation. Considering the problems defining this term, accuracy is often not taken into account when estimating the eligibility of interaction techniques used for user-steered segmentation.

2.2.2 Types of Input

In addition to the criteria used to evaluate the quality of the interaction techniques, also a classification on the basis of their input types can be made. In the following paragraphs the three different types of interaction inputs will be discussed and examples of existing interactive segmentation techniques will be given, which will be categorized according to this classification. Explained by Olabarriaga et al. [10] and Heckel et al. [9] the three main types of input are setting parameter values, making pictorial input on the image grid and selecting from a menu.

Setting parameter values as input parameters often has an immediate effect on the computational method. Mostly data values are used directly as parameters for segmentation algorithms. As these highly influencing data is taken over unchanged for the computation, usually minor variations lead to major differences in the segmentation results. To effectively control the manual selection the user should bring prior knowledge of the underlying extraction techniques, otherwise this way of interaction is quite unintuitive. Therefore often a training of the expert is necessary. On the other hand setting parameter values is simple to implement. These techniques are usually realised as sliders or dial. Serving as example the authors Lifshitz and Pizer [11] and the authors Cabral et al. [12] used setting parameter values as part of their work. Altering the value of the threshold by using a slider was stated by Lifshitz and Pizer [11]. Cabral et al. [12] used the maximum number of iteration as input parameter to refine the process of region merging and splitting.

Making pictorial input on the screen is another technique to provide manual interaction for the user. Thereby the actor selects positions on the image grid, which represent spatial parameters for the underlying extraction algorithm. Depending on the information the computational part needs, a selected point can represent a point belonging to the target structure or can mean for example, that all similar points are located outside of the region. Also a higher number of input parameters can be selected, which together form the sought region of interest. To carry out this type of interaction input often pointing devices, as for example a mouse, is used. Furthermore the points or regions, selected by the user, are usually highlighted in real-time by, for instance, colour to give the users feedback about the marks they set. So the operators are able to get a deeper understanding of their actions and can verify the correctness of the input. The duration of this method is highly depending on the form of the implementation. If the user's task is to correctly identify the target structure by precisely tracing its contour, then the method can be quite time-consuming and demanding. When selecting a point, curve or structure with a few clicks is sufficient, the user may be able to make numerous changes in a short period of time. The live lane method by Falcão et al. [7] is one example, where precise and rough operations are balanced. In this method the user is able to trace edges, which are well-defined, fast and roughly, because the computational part can detect it automatically. The hardly separable areas can be drawn carefully and slowly, so the user can reflect about the next move.

Choosing from a menu is a further way of providing an algorithm with predefined parameters. In this case the users do not have to determine the required values themselves, but can choose from a range of parameters, calculated by the program beforehand. This input type can be very efficient and time-saving, because it minimizes the variety of choices. By guiding experts through the editing process, they can introduce their knowledge effectively without doing the required actions manually. The calculation effort needed to generate different choices can be very costly, which is why this strategy often can not be provided for the user. One example for this interaction strategy is described by Karimov et al. [13]. In this method structural information is extracted by a segmentation algorithm. Then the potential defects are detected automatically and displayed to the user. The identified segmentation failures can be selected by the expert and are corrected automatically by the method.

2.2.3 Direct and Indirect Data Input

As mentioned above, not only input methods influence effective controlling of the segmentation, but also whether the input data given has direct effect on the result or not. Approaches, where the input data has immediate impact on the calculated outcome, are called low-level tools. Procedures, where parameters must be interpreted first to be of use, thus used indirectly, are referred to as high-level tools.

Low-level tools typically require some basic knowledge about the algorithm used for segmentation and how exactly the provided data affects the output. As a result these methods are often less intuitive and time-consuming. Nevertheless these tools can be seen as general editing solution, adaptable for various segmentation problems, because for the implementation generally no special knowledge about human anatomy or other additional information is needed [9]. Kang et al. [14] describe three low-level tools for executing some basic three-dimensional corrections. The first tool was developed for filling holes. Thereby a seed point is needed to perform morphological closing. The second called point-bridging and the third, referred to as surface-dragging, were developed to correct wrongly labelled voxels and connect them with correctly found structures.

High-level tools in contrast do not urge their users to acquire knowledge about the underlying technical details. This is based on the fact that these tools try to conclude the intention of the user by gaining information from the performed editing. Since finding out about a person's plan is quite complex, these tools are often based on heuristics, making them more dependable on the anatomical structure in demand. The authors Kunert et al. [15] and Heimann et al. [16] proposed high-level tools, which prevent algorithms based on region growing from leaking into structures, that have been marked by the user.

CHAPTER 3

Methodology

The main steps performed in our program are the segmentation of an image, chosen by the user, and the correction of faults in the resulting segmentation mask. The framework, developed in the context of this thesis, can be divided into a segmentation stage and an editing stage. The focus of the segmentation process lies in finding vessels in the brain or more precise detecting the Circle of Willis. In the editing process correcting the falsely labelled regions is possible. Thereby the user is able to contribute his knowledge by manually giving information to the algorithms calculating the correction. Our approach is demonstrated on MRA images, as they are most commonly used for scanning stroke patients.

The segmentation stage implements the calculations needed to create a segmentation mask from a selected medical dataset. For this purpose a threshold algorithm is used, because it belongs to the basic types of segmentation techniques and is fast to calculate. A more detailed description about threshold-based algorithms is given in Chapter 2.1.1. Then a Connected Component Analysis is executed on the binary segmentation mask. Thereby a component is initialized with a primal voxel and the algorithm is looking for adjacent voxel. When found, these are added to the region. As soon as no more neighbouring voxels can be detected, a new component is initialized. This procedure is continued until all voxels have been visited and are assigned to a component [6]. The various components can be identified by different colours. So voxels, that have the same colour, belong to the same region. Finally a coloured segmentation mask is delivered to the editing part of the framework.

The editing stage contains the main functions of the framework. There the errorprone result of the threshold algorithm can be corrected by users with the support of semi-automatic algorithms. Methods, that can be used for correction, are the function, where a deletion of components is executed, and the procedure, where the connection of two different regions is found. Thereby each method can be divided into a computational part, an interactive part and a user part, as described in 2.2. The task of recognition, done by the user, is abstracted in the user part. The interactive part represents the interaction techniques, used to mediate parameters from the user to the computational part. The semi-automatic algorithms, implemented to delete components or find specific voxels, form the computational part.

3.1 Deletion of Components

One of the faults, made by segmentation algorithms, is the positive identification of voxels, which in truth do not belong to the target structure. This happens for example, when the selected intensity interval of the threshold algorithm is set too broad. Then voxels, which are not part of the vascular structure, are classified as corresponding to the vessel. Furthermore a distinction can be made between wrongly labelled individual voxels, lying adjacent to the true structures, and misclassified regions, located far away from real vessels. The deletion methods, proposed in this thesis, focus on correcting whole areas of falsely identified voxels. The editing process itself is independent from the segmentation algorithm, used to produce the segmentation mask.

3.1.1 Interactive Part

When the user wishes to remove a particular component he/she just has to click on it with the left mouse button. Then the selected area is removed from the segmentation mask. In this process all voxels belonging to this region, no matter if they are lying in the same slice, where the user has performed the action, or not, are deleted. Based on this fact the deletion process is executed in 3D. Removing one wrongly labelled component from the mask ensures that also minor changes can be made by the user.

In the case that an expert wants to remove several components at once, another technique can be used. To start this the mouse pointer can be positioned over a component, which should be deleted, and the character "d" may be pressed on the keyboard. Now not only the component selected is removed, but also other components, which do have a similar characteristic.

3.1.2 Computational Part

Removing a specific component can be done by one mouse click. The algorithm used for this task receives the exact position of the pixel as input parameter. In the segmentation stage all found components have been stored and are now available for calculation For every region a bounding box is calculated and the position value is tested whether it lies inside or not. When the voxel's location value fulfils this condition the actual component is removed. The approximated value of the runtime is O(n) because the more components are found in the segmentation mask, the more must be scanned for finding the area chosen by the user.

Deleting several regions at once is implemented in a function that is partially based on the algorithm described above. To find similar components a characteristic has been chosen that takes the anatomical structure of vessels into account. One assumption was made that vessels can be distinguished from other structures by their elongation. So when the user recognizes a very big stretched rectangular region, it is likely that this area does not represent a vessel. This component then can be picked and its elongation is used as reference to find other components, which do have the same or a longer extension. The elongation of a component is calculated from the ratio of the longest physical size of the area and the smallest physical size. It must be mentioned, that this characteristic is not robust and sensitive to rotation. Also this function receives the voxel's position as input variable. Firstly the component, which contains the voxel, is sought. Then its elongation value is stored and other components, with the same or a higher lengthening, are deleted. When the user chooses the right component, this method is able to remove many regions at once. Figure 3.1 shows an example for this deletion method. Here the user picked the orange component to be removed and to serve as reference for the ongoing process. The blue component had a similar or higher elongation value, which is why it was also deleted from the segmentation mask.



Figure 3.1: This figure shows the results before and after the deletion of several regions. The left image represents the mask before the process. The finished result is displayed at the right side. In this case the orange component was picked to be removed. As can be seen also the blue component was deleted, because its elongation value was similar or higher.

An automatic deletion of components, which can be eliminated to be part of the vascular structure, is performed by the framework after the editing process has been started. The removal is applied to all regions, that only have a depth of one slice. This slice-based elimination is automatically executed without the user's intervention after the first editing step. In figure 3.2 the difference between the segmentation mask before

3. Methodology

and after the deletion process is shown. The affected components have been highlighted to emphasize that many small artefacts have been removed. The unaffected regions are usually larger in size and in depth, so they remain untouched. By removing these artefacts a more transparent mask is produced, to make the task of refocusing on the vessels simpler.



Figure 3.2: This figure shows the results before and after the automatic deletion was executed. The left image represents the segmentation mask before the deletion process. The finished result is displayed at the right side. In this figure the components, that are removed, have been highlighted to demonstrate that mostly small artifacts are affected by this method.

3.2 Connection of two different Regions

During the recording of medical images the patient is supposed to stay in a steady position. Even tiny movements can have an impact on the intensities measured in the process. Therefore voxels, which in truth belong to the vascular structure, can have small differences in their intensities, in contrast to the other classified voxels. When the threshold is set narrowly, it may happen that a voxel is falsely excluded. As a result a disruption in the artery can be seen. For this thesis a method was developed to close these interruptions by joining two separate components. A connection will be calculated on the slice, where the editing process has been started. Therefore this method operates in 2D. Figure 3.3 shows disruptions of the arteries marked by arrows. The blue components of the segmentation mask represent the arteries blended with the original MRA image. In this example the intensity values are too low to be identified as vascular structure. When taking a closer look, the distances between the components are slightly brighter than the surrounding black background. So with the use of the blended MRA image, in some cases it is possible to see the real connection between the fragments of the arteries. All following images, describing the linking, are produced while executing the framework. Figure 3.4 shows the region, which is used to visually demonstrate the procedure.



Figure 3.3: This figure is composed of the coloured segmentation mask and the original MRA image. The blue components, representing the found arteries, are interrupted, which is indicated by the arrows. The disruptions were caused by the voxels located in between the components. Their intensity values were too low to be included into the segmentation mask and were therefore not coloured.

3.2.1 Interactive Part

In contrast to the deletion methods, this process depends on more than one seed point, delivered by the user. The computational part of this function needs four key points, that automatically form an area. For the computation of the true connection, the area chosen by the user should contain two segments of the ends of the arteries. In figure 3.4 an example area, that could be selected by a user, is presented. The choice of an input region is cruical for the computation. Because of this the user should consider to pick the key points wisely. On the one hand the area should contain an appropriate amount of the vessels, which shall be connected. On the other hand the image is ought not to be too large, to avoid other bright structures to be part of, since this would cause serious errors during the computation.

3.2.2 Computational Part

To compute a connection between the separated components, a path is created, which is merged with the end-points of the two segments at the end of the process. This path is



Figure 3.4: In this figure an example of an area selected by an user is shown. The white points indicate the spots, which were picked to form the region. As can be seen two segments of the component's endings, which ought to be connected, should be inside the area, to improve the chances of a correct result.

lying in between the borders of the vessels and its width can be adjusted by the user. In some cases a perfect path is found, which is automatically connecting the segments. When an automatic linking is not possible, an algorithm is used for the joining process. The following steps describe the procedure in more detail.

Region Selection and Calculating End-Points

Firstly a square is spanned over the region of interest by the four key points, representing coordinates. This rectangle contains the information of the MRA image in the region of the picked positions. In this area the whole computation takes place. As next step the end-points of the components are sought. For this calculation it was important to seek points, that lie to each other as closely as possible. This increases the possibility, that the shortest connection between the vessel artefacts can be found.

Creating a Gradient Magnitude Image

The path connecting the components, has some characteristics, which had to be considered. Often the anatomically correct segment, connecting the parts of the artery, runs curvy

and not in a linear way. In addition the calculated path should be located in the center of the vessel, and not on the border. This is important, because when in a later step the user is allowed to broaden the path, it should still correctly represent the location, where the true anatomical structure lies and not be shifted in any direction. To ensure a centered location of the path, a gradient magnitude image is calculated. Since gradient magnitudes emphasizes boundaries, these technique is used to localize the walls of the vessel. In this context a gradient describes the directional alteration of the image intensities. This value is represented by a two-dimensional vector, storing the derivatives in the vertical and horizontal direction. The gradient has a direction, which is pointing to the most significant change of the intensities [6]. For finding the correct connection between the arteries a gradient magnitude image is computed. The gradient magnitude describes the length of the gradient vector and is calculated at each pixel of the image region. Due to the discrete image data, the gradients are approximated by the differences of the adjacent neighbours. The resulting gradient magnitude image consists of grey-values. The higher the gradient magnitude is, the higher the pixel value and vice versa. In figure 3.5 the region, shown in figure 3.4, was used to calculate a gradient magnitude image. For this paper a light editing was performed on the image to enhance the visibility of the gradient magnitudes for the reader. In this image the borders of the vessel are displayed as white areas. As can be seen in the middle of the figure, the bright structures nearly vanish, because there the intensities are very similar and no exact boundary can be found.



Figure 3.5: This illustration displays a gradient magnitude image. For an increased visibility of the magnitudes the image was slightly brightened The higher the intensity of a pixel, the greater is the value of the gradient magnitude. In this figure the white areas represent the walls of the vessels. In the center of the image the intensities are less bright, because of the low intensity changes in this region.

Creating a Centralized Path

For calculating a correct located path, the region within the borders of the vessel is needed. Because of this, the gradient magnitude image is transformed in a binary image.

3. Methodology

Therefore a threshold-filter was used. An interval was defined, which converted the high-level intensities to white and the very dark pixel values to black. Figure 3.6a shows the resulting image of the transformation. The form of the vessel is clearly evident. Through the thresholding a clear separation of the structure from the background was achieved. The hole in the middle of the vessel is caused because of the low intensities representing that no value alterations and therefore no borders have been found. In some cases when the borders of the vessel are only weakly pronounced, the chosen interval of the threshold-filter must be modified. If no adjustment is carried out, voxels are falsely classified as background. Also when the boundaries are well defined the interval must be adapted, otherwise voxels belonging to the background are identified as target structure. In this method the alteration of the interval is done automatically. Since a homogenous



(a) The result received after thresholding. (b) The result received after hole-filling.

Figure 3.6: (a) displays the resulting image received by thresholding the gradient magnitude image. The values having a distinct gradient magnitude were coloured white, while the others were set to black. (b) represents the outcome of the image taken from (a) after a binary-hole-filling filter was applied to it.

region is required to calculate the final centred path, the hole in the middle must be filled. This is done by using a binary-hole-filling filter on the thresholded image. The filter applied in this method only closes holes, which are not connected to the image border. Therefore morphological reconstruction techniques are used, which are based on dilation and erosion. The result of applying a binary-hole-filling filter is shown in figure 3.6b. Here the borders of the vessel have not been changed and a homogenous region has been created.

The white region, which has been computed so far, indicates where the vessel is approximately located. Now a path can be calculated by using a binary-thinning algorithm, which is based on erosion. Applying this technique ensures that the path is located quite centralized, as can be seen in figure 3.7b. The resulting path is the skeleton of the region and has a width of one voxel. A more detailed description is given by Preim [6]. Figure 3.7a displays the outcoming path, which is used for further calculations.



(a) The resulting path of the skeletonization (b) The illustration, which voxels represent algorithm. the path.

Figure 3.7: (a) displays the path computed by the binary-thinning algorithm. (b) is an illustration showing which voxels remain after the erosion process. As can be seen the path is centered inside the vessel's borders.

Connecting the Path with the End-Points

In some cases the computed path is not automatically connecting the end-points of the separated vessel. Thus small gaps, in the scale of a few voxels, can occur. Figure 3.8 displays a schematic overview of the described situation. In this illustration can be seen, that the red path is a few voxels too short to connect the blue segments. Therefore an algorithm was developed to close these holes by calculating a linear bridge.

The operational sequences of this method will be described, regarding the illustration 3.8. Since every bridge is calculated separately, the following explanation will focus on the calculation of *Bridge A*. As can be seen *Bridge A* is the link between the end-point of the vessel segment A and the voxel of the path, which lies nearest to it. For the computation of this connection the coordinates of these two voxels are used. Since the calculation proceeds from the vessel to the path, the end-point of the vessel segment will be called "start point". The voxel of the path, nearest to the vessel segment A, will be referred to as "final point". Firstly the direction, in which the bridge should be built, must be calculated. For this purpose a subtraction is made between the start point and the final point, resulting in a distance vector. The signs of the x- and the y- coordinate stands for the horizontal direction, in which the bridge will run. The sign of the x-coordinate states, if the bridge runs upwards or downwards in the image. The values of the distance vector specify the amount of voxels needed for the construction of the bridge.



Figure 3.8: This figure shows a schematic illustration how the centered path is connected to the vessel segments by bridges. Bridge A is calculated using the end-point of Vessel Segment A and the nearest voxel of the path. The end-point of Vessel Segment B and the voxel of the path nearest to it, are needed to compute Bridge B.

Now the building process can be started. Beginning on the start point the direct neighbours are compared respective to their intensity values. Vessels do have quite high intensity values in MRA images, which is why in this method voxels, with a higher intensity value, have a higher probability to belong to a vascular structure. Therefore the neighbouring pixel, that has the higher intensity, is added to the bridge. Not all four direct neighbours are compared to each other. Only two voxels are selected, according to the sign of the x- and the y-coordinate. For the x-value a positive sign means, that the neighbour located on the right side will be used for comparison. A negative sign indicates to choose the left adjacent voxel. When the sign of the y-value is negative, the voxel located upwards is used, otherwise the neighbour downwards will be selected. In figure 3.9 an example is shown. When considering the start point, which is marked blue, only the voxels with the value 0,4 and 0,3 will be compared. The distance between the start point and the end point is resulting in the vector (6, 3). So the x- and y-coordinate are positive, which specifies that always only the right and the below neighbours will be included in the calculation.

After the comparison of the two voxels, one is added to the region of the bridge. Depending on the included voxel, the distance vector is modified. When the voxel represented by the x-coordinate was selected, then the value of x will be affected, otherwise the y-coordinate

0,1	0,5					
S	0,4	0,3	0,36			
0,3	0,7	0,7	0,6			
0,4	0,8	0,5	0,5	0,7	0,7	0,6
	0,3	0,4	0,5	0,8	0,7	F
		0,3	0,5	0,1	0,2	0,5

Figure 3.9: This figure shows the computation of the bridge. It is used to connect the end-point of one vessel segment (blue) with the voxel of the path, nearest to this segment (red). Here the exact path of the bridge is displayed, which would be calculated by the developed algorithm. Beginning at the start point (S) always two neighbours are compared. The voxel with the higher intensity is added to the path of the bridge. This procedure is repeated for every voxel until the final point (F) is reached.

will be altered. How the coordinate of the distance vector is changed depends on the sign of the affected coordinate. When it is negative, the value will be increased by one. Otherwise when the coordinate is positive, it will be reduced by the same factor. Referring to the example shown in figure 3.9 for the first comparison of the voxel at the start point, the x-coordinate would be decreased. The whole procedure is then repeated for the newly added voxel. This algorithm is executed until a distance vector of (0,0) is reached. Then the computation of the bridge has been finished.

The same procedure is then executed for the second gap located between the centralized path and the *vessel segment B*, shown in figure 3.8. After the two gaps have been closed, a continuous connection, with the width of one voxel, has been computed between the two vessel components.

Enlarging the Computed Connection

As last step the user is able to enlarge the connection, so that its width is suitable to the width of the segments. A slider bar can be used for the adaption. For every broadening step a region growing filter is applied to the path. The region growing is performed by a dilation with a structuring element. For various widths, the size of the structure element is changed. Figure 3.10 shows three cases of broadening the connection. In 3.10a no region growing was performed and the link is only one voxel wide. Such thin paths can be of use when narrow arteries ought to be connected. The width of the connection in

figure 3.10b is appropriate to link the vessel segments. In the image shown in 3.10c the connection is too broad. Furthermore it can be seen that with a increasing width, the connection becomes slightly more rectangular That is happening because the broadest width possible, is to fill out the region, in which the calculation took place.



(a) The connection with a widht (b) The connection having the of one voxel. same width as the vessel segments.



(c) The width of the connection is too broad.

Figure 3.10: This figure shows examples how the width of the connection can be broadened In (a) the breadth is only one voxel. The slider has not been dragged so far, so no region growing was applied. (b) shows the connection having a width, matching with the width of the vessel segments. In (c) a structuring element, which is too large has been used, so the connection is too broad.

3.3 Implementation

The framework developed for this thesis utilizes three different toolkits. For the visualization process the Visualization Toolkit (VTK 7.0) and the open-source version of Qt (5.7) were used. The Insight Segmentation and Registration Toolkit (ITK 4.10) was important for delivering various methods for processing medical datasets. The development environment, chosen for developing this framework, was the 32 Bit version of Microsoft Visual Studio 2013.

CHAPTER 4

Results and Discussion

In this chapter we focus on demonstrating the results of the techniques, described in chapter 3. However not only the resulting images themselves will be displayed, but also an evaluation of the interaction techniques and the automated algorithms will be made by the means of state-of-the-art methods. These have been described in chapter 2. Seven different datasets have been used to test the effectiveness of the developed editing process. These datasets have been evaluated by experts, who examined whether the patients had a complete Circle of Willis or if arteries, belonging to this structure, were missing from birth. This information was essential for the evaluation step, since the editing methods were also used to find whole arteries, which were not part of the segmentation mask. By having the knowledge about the existence of these arteries, it was possible to test whether the algorithm could find them, or not.

4.1 Visualization of Results

The results of the editing process are shown on one dataset, to simplify a precise analysis of the impact of these methods. Three different scenarios will be given to deliver a detailed description of their potential. At first an overview of the effects will be given, by applying both editing functions to one specific slice. The computed results are shown and examined in the section 4.1.1. For presenting the whole implications of the deletion and connection functions, these are analysed in separate test cases, described in section 4.1.2 and 4.1.3.

4.1.1 General Overview

In this section the modifications done by the implemented methods, are shown for one specific slice. Since the user operates in this slice-based view, this presentation demonstrates how the user perceives the editing process. To emphasize the difference



(a) The segmentation mask before the edit-(b) The segmentation mask after the editing process.

Figure 4.1: This figure shows the difference before and after a deletion and a connection of different components was performed. (a) represents the segmentation mask, which was computed by the threshold algorithm. (b) displays the segmentation mask after a deletion and a connection of components was applied to correct wrongly labeld segments. As can be seen, components of all sizes were removed. In addition omitted vessel segments have been added, so that a continuous ACM was created.

between the segmentation mask, shown in 4.1a, and the result, displayed in 4.1b, both images were placed side by side. A clear difference can be seen, concerning the distracting artefacts and the corrected vessel flow. In image 4.1b the procedure of connecting was applied on five different locations, resulting in an continuous artery ACM. Furthermore a lot of small components, which were supposed to not belong to the vascular structure, have been removed. This was done by using the method of removing several components and picking the largest dark blue component as reference segment. This component had a big elongation value, so that most of the coloured artefacts were deleted in one step. The remaining segments were separately removed by picking each individually.

4.1.2 Impact of the Deletion Process

The deletion process plays a crucial role in editing the segmentation mask. Many segmentation results suffer from oversegmentation, which complicates the task of correctly interpreting the anatomical structure. When oversegmentation occurs, many large and small artefacts are classified as artery segments, which in truth are not part of this structure. On the one hand when quickly scrolling through the slices, these can easily be misinterpreted as important and can lead to false conclusions made by the user. On the other hand the components prevent a clear sight on the important target structure in a three-dimensional view and should therefore be removed.

Test Case 1

For solving the problems mentioned above, the three-dimensional deletion process has been developed. In this test case the consequences of this method are described and visualized in figure 4.2. Figure 4.2a shows the original state of the segmentation mask of slice 121. As can be seen, a lot of coloured small artefacts were found. But also bigger structures have been falsely identified. These are, for example, displayed on top of this image coloured in violet and orange. Even though also very tiny components were separately removed, the whole slice was completely edited under 45 seconds. In the image 4.2b the result of the deletion process of slice 121 can be seen. There the big structures as well as all small artefacts have been deleted. Figure 4.2d displays the slice 122, which is located directly underneath. Although the deletion was only performed in slice 121, also in slice 122 the majority of falsely classified components has been removed. Here the implication of the three-dimensional deletion can be observed. Figure 4.2c shows the initial condition of slice 122. When comparing this image with the edited, the deleted components can be easily identified. The figures 4.2e and 4.2f show the slice with the number 136. Although 15 slices are located between slice 121 and 136, the deletion process, applied in 121, still has an impact on it. Obviously new components have been found in slice 136, but the big components initially removed in the slice above, have also been deleted here. When comparing the original state of slice 136 with the modified one. a considerable difference can be noticed.

Test Case 2

In a slice-based view the three-dimensional deletion can not be observed at first sight. The impact does not become evident until a scrolling is performed. For presenting the reach of the implications all at once, a three-dimensional view will now be used for a more precise visualization. Figure 4.3 shows the original segmentation mask on the left side and the edited result on right. For this MRA the threshold algorithm computed a segmentation mask consisting of 3876 separate components. The segmentation result is shown in 4.3a. For generating figure 4.3b, at first 2288 objects have been removed automatically by the deletion method. These components had a depth of one slice and were therefore deleted after the editing process had been started. Then 40 large objects were removed by picking one long component. Its elongation value was taken as reference for deleting 39 other similar or longer segments. From the remaining 1548 components a few have been deleted by separately selecting them. In the resulting image now the Circle of Willis can be easier identified, since the big structures have been removed. Also the absence of the 2288 components, deleted in the first step, makes the mask much more transparent, because the little barriers do not longer block the view on the target structure. This phenomenon can be seen especially well on the top of the image 4.3a, where the ACA is overlapped by many small artefacts. In the edited result this artery can be recognized more easily.



(e) Slice 136 before editing.

(f) Slice 136 after the editing of slice 121.

Figure 4.2: This figure visualizes the three-dimensional deletion process. The figures (a), (c) and (e) are presenting the different slices before the editing of slice 121 took place. (b) represents the result of slice 121 after applying the deletion methods on the wrongly classified components. (d) displays the modifications of slice 122 caused by the editing process in slice 121. (f) shows the changes produced by this event for slice 136. As can be seen the modification of one slice has an impact on all the other slices, where the deleted components would also have been located.



(a) The 3D presentation of the original seg- (b) The 3D presentation of the edited segmentation mask.

Figure 4.3: This figure visualizes the difference between the segmentation mask (a) calculated by a threshold algorithm and the mask (b) after the deletion method was applied. For generating (b) firstly all components with a depth of one slice have been removed. Then the biggest components were deleted. As a result only the small artefacts and the target structure remain in the image.

4.1.3 Impact of Connection Process

In this section we will focus on the effectiveness of the connection method. Because of minor differences between the intensity values of neighbouring voxels, sometimes gaps occur in vessel segments. These can distract the user from finding real vessel occlusions. Therefore a closure should be possible to correct the segmentation mask, according to the true biological structure.

Test Case 1

In this test case we demonstrate how a gap of the ACP is filled. Overall this artery was correctly identified by the segmentation algorithm, which is why it is connected in other slices. Only a small section of the segmentation is error-prone and will now be corrected. In figure 4.4 the editing process of the ACP is demonstrated. Image 4.4a shows the fragmentary identification of this structure. The image 4.4b presents the repaired artery. As can be seen, the connection algorithm is not only able to connect the endings of the vessel linearly, but also in a curvy way. This is possible, because the connection method follows the higher intensity values, that indicate the direction of the true path. As a result the calculated track mostly corresponds to the real vascular structure. The correction of the ACP is also shown in figure 4.5. Here the whole procedure is visualized

in a three-dimensional view. An overview, where the process is performed, is given in 4.5a. The two images 4.5b and 4.5c demonstrate the modification done by the connection method. As can be seen originally the artery was only identified in one slice at this position. After the proposed algorithm was applied in another slice, a further connection was built on this location. So the diameter of the vessel was increased.



(a) A gap in the middle of the ACP. (b) The closed gap of the ACP.

Figure 4.4: This figure shows the difference of the segmentation mask, computed by the threshold algorithm, and the resulting image, received after the editing process. The connection method creates a path, that follows the highest intensity values. This kind of calculation ensures that the track follows the true anatomical structure.

Test Case 2

In the example above a gap of an existing artery was filled. But the connection method is also able to find vascular segments, which have been totally ignored by a segmentation algorithm. The threshold algorithm, used in our framework, could not find the ACoA. Figure 4.6 shows the right segment and a part of the left segment of the ACA. These two should be connected through the ACoA. As confirmed by experts, in this dataset the sought artery is existing. Thus the segmentation algorithm was not able to identify it, but our developed method is. Figure 4.6a shows the unprocessed segmentation mask. In the image 4.6b the result of the connection method is shown. Not only the gap in the ACA was filled, also the ACoA could be correctly identified. To enhance the presentation of the slice-based editing, we visualized the process in 3D in figure 4.7. The edited Circle of Willis is shown in the image 4.7. The red rectangle marks the location, where the identified artery is connecting the left and the right ACA. The images 4.7b and 4.7c demonstrate in detail, which voxels have been added to the segmentation mask to form the ACoA. Although the computation of the connection method is two-dimensional, the results can also be significant for the display in 3D. Figure 4.8 visualizes the computed path on voxel-level in 2D and 3D. The green components present the pre-segmented components. The blue voxels illustrate the newly found paths. In 4.8b the total amount of blue voxels is less, because the voxels of higher slices cover the newly added path, which is located beneath them.



(a) The Circle of Willis shown in a 3D view. The red rectangle marks the position of the ACP, where the computation takes place.



(b) The ACP is only connected in one slice. (c) The surface of the ACP was repaired. Therefore the diameter of the vessel is only The diameter at this position was increased one slice. to three slices.

Figure 4.5: This figure shows the connection of the segments of the ACP. In (a) the location, where the modification is executed, is marked by a red rectangle. (b) represents the position, where the connection will be calculated. As can be seen the whole artery is only linked by one slice at this position, although six slices, displayed on the side of the image, initially form the artery. The fifth slice is connected in (c). So the diameter at this spot is increased to three slices.



(a) The original segmentation mask showing the ACA and the missing ACoA.



(b) The segmentation mask before the con-(c) The segmentation mask after the connecnection methods was applied. tion methods was applied.

Figure 4.6: (a) shows the initial segmentation mask. Here the incomplete ACA and the missing ACoA can be seen. The yellow arrow indicates the location where the absent artery should be displayed. In (b) the zoomed in location is displayed. Here a brighter path between the segments can be seen, where the true connection should have lain. (c) visualizes the resulting image after the connection method linked the ACA and found the ACoA.



(a) The location of the ACoA in 3D.



(b) The segmentation mask, which did not (c) The segmentation mask with the added find the artery.

Figure 4.7: This figure demonstrates the impact of the connection method. Although the computation of the connection method is two-dimensional, the results can also be significant for the display in 3D. The red rectangle, displayed in (a), shows the location, where the search for the ACoA is executed (b) demonstrates the initial state of the segmentation mask. (c) shows the detected ACoA.



(a) Detailed 2D view of the connection. (b) 3

(b) 3D overview over the computed path.

Figure 4.8: In (a) the detected paths are visualized in detail. Therefore the pre-existent segments are marked green, while the newly added voxels are coloured blue. (b) represents the segmentation mask, visualized in 3D. Here the total amount of blue voxels, representing the new path, is less than in (a). This is because the slices above cover the slice, in which the connection was executed.

4.2 Discussion of Results

The framework developed in this thesis was aimed to design methods for semi-automatically editing segmentation masks. Thereby the focus lay on fast calculations and simple controlling for the users. For measuring if we have reached our targets, our methods will be evaluated on the basis of state-fo-the-art characteristics, which were described in chapter 2. As mentioned in chapter 3 the structure of the framework is constructed of a computational part and an interactive part. Through the interactive part the user is providing essential parameters for the computational part. Thus the main role of the user is to guide the computational part to find correct solutions, by offering an assumption of the delineation. The interactive part was designed to effectively provide information, that was collected by the user. A precise evaluation of the interactive part is given in 4.2.1. For calculating a correct result also the structure of the computational part is essential. Thus a detailed description of the benefits and disadvantages can be found in 4.2.2.

4.2.1 Interactive Part

As described in 2.2.1 three different characteristics can be used to describe the effectiveness of interaction techniques: speed, repeatability and accuracy On the basis of these properties the interaction techniques, used for the deletion and for the connection method, will be evaluated.

The deletion method is started by picking a position with the mouse. When this position lies in a specific component, this structure will be removed. So by selecting only one seed point, the calculation can be executed. Also the deletion mode, where several components are removed at once, requires just one seed point for starting its calculations. For this reason it can be said, that very little user interaction is required to remove one or several big segments. For deleting many very small artefacts this method is quite time-consuming. This is because our solution is not adapted for very tiny components, since this would exceed the scope of this work. To sum up, the speed of the user interaction, required to start the deletion method, is varying depending on the task. When removing big segments the interaction can be performed with a few clicks, while small artefacts are laborious to get rid of.

A big advantage of this interaction technique is its repeatability For repeating the deletion of a specific component, it is not even necessary to select exactly the same voxel in the component. Any voxel inside the component is sufficient

The accuracy of this method is difficult to define. Actually the deletion is used to remove wrongly classified components from the segmentation result. Therefore it is adapting the segmentation mask to the true biological structure. For this task the user has to perform the recognition of structures, whether the component is really a vessel or not. However the user is limited by the interaction strategy and can not delete individual voxels. As stated by Olabarriaga et al. "a method is potentially accurate when it provides full control to the user to generate any desired result [10]." Since this is not the case, the interaction techniques, used for the deletion method, can not be defined as accurate. This statement does not automatically indicate, that the generated result, in terms of the true biological structure, is also inaccurate.

The connection method needs four points, picked by the user, to be activated. The interaction, needed for defining this region, requires more points than the deletion method. Thus the speed of the connection task is not as fast as the deletion, but is still very simple and can be made swiftly.

The repeatability of this interaction technique is not only dependent on picking almost the same position for every execution, but is also highly reliant on the judgement of the user. When different experts use this method the selection of the region is inherently subjective and can not be standardized. Because every expert picks slightly different points the results can vary. This issue is difficult to minimize without violating the scope of interaction. Therefore this method demands carefully chosen interactions, which can be trained quickly when repeated frequently.

The accuracy of this method is highly dependable on the selected area. In order to increase the probability of an accurate result, the chosen region should contain the following information: On the one hand enough voxels of the vessel segments should be contained to enable a connection. On the other hand not too many voxels of the segments should be included, because this would slightly distort the centerline of the connected path. In addition the region, constructed of the higher intensity values, should be contained. Since this bright way represents the true linking in the original MRA, this information is vital for the algorithm. The interaction technique used for this method was designed to give the user as much freedom as possible, while delivering all information needed for the computational part. Therefore the algorithm limits the interaction possibilities that the user may need to construct a desired result. For this reason the interaction technique is not providing an accuracy of 100 percent, but enables a computation of sufficiently good results.

4.2.2 Computational Part

In chapter 2.1 the effectiveness of image segmentation algorithms was described based on various characteristics. These will now be used for evaluating the semi-automatic algorithms, developed for this thesis. Thus the properties speed, reproducability, accuracy and robustness will be discussed for each algorithm.

The deletion method was designed for deleting individual components quickly. To ensure a fast access to the components, every segment is stored separately with its attributes. For finding a specific segment or several with similar properties, they are scanned through one by one. Thus the worst runtime of the algorithm is O(n), where "n" is the amount of components.

When executing the deletion algorithm on the same component in several sessions, the results will always look identical. As the position of the component is received as input argument, the algorithm knows the exact coordinates, where the element is located. Since the same component is always located at the same area in the image, precisely this segment is removed every time. Due to this the developed algorithm is repeatable. In addition the components, which are deleted without the user's intervention, are also always the same. This is because the algorithm checks their properties, which are always identical in each session.

The deletion method can also be defined as robust. This statement can be made, because the exact shape of the component is unimportant for this method. Every type of segment, irrelevant which anatomical structure it represents, can be removed.

The characteristic accuracy can not be defined for this method. This is because the function of this algorithm is not to segment an image, but to edit a segmentation mask. Although it enhances the degree to which the segmentation corresponds to the true anatomical structure, this does not improve the accuracy of the segmentation algorithm, used to compute the mask.

The connection method can be described as image segmentation algorithm applied to a restricted image region. Although a lot of filters are used to compute the final result, every connection is calculated within a maximum of two seconds. Choosing the size of the calculated connection is more time-consuming. Every change of its width takes less than one second. Thus good results can be computed in a matter of seconds.

Also the characteristic reproducibility is fulfilled by this method. When receiving the same input region in each session, the same result is computed every time. This is because

the filters, used to create the final result, are all reproducible As a consequence also the output image of the whole algorithm is always the same.

In contrast to the deletion method, this algorithm is not robust, since only vascular structures can be connected. For calculating these links prior knowledge of image modalities is used. Thereby the specific presentation format of different anatomical structures is exploited. For finding the true path of the arteries, high intensity values are important. These are caused by the presence of vessels. Therefore only structures, that produce high intensities in grey-value images, can be connected correctly.

The accuracy of the connection method can vary according to the input parameters. When regions have been selected, where the crucial information can be clearly identified, good result will be calculated, otherwise wrong connections will be created.

4.3 Limitations and Future Work

One weakness of the deletion algorithm, is caused by using the bounding box of the components to determine, whether the picked voxel lies inside or outside. As mentioned above, the user picks a voxel inside an element to indicate that this one should be removed. The problem of this concept emerges when a vascular structure is quite long and broad. Then also its bounding box is quite large, which can sometimes lead to false deletions. When a small element is closely located to the vessel's bounding box, it may happen that not the element is deleted, but the vessel. This may occur when the picked voxel is located inside the bounding box of the element and inside the bounding box of the vessel. The component, which is found first, will be removed. A possibility to solve this problem would be to order the components, according to their size. So the smallest elements could be examined first.

In addition the deletion method could be expanded by an approach for deleting many tiny artefacts at once. Currently removing this type of segments is quite time-consuming, since reducing very tiny artefacts, was not the main focus of this thesis. As the intention lay on enabling a clear view on the Circle of Willis, so removing big covering segments had priority.

The approach, developed to connect two interrupted vessel segments, delivers very good results, when the input region was chosen well by the user. Selecting this area is a subjective task, not easily made by humans, since the information needed for the algorithm is not always visible at the first sight. To simplify this choice, a prefiltering of the surrounding area could be developed. A fast filter could find the best region for the connection algorithm and therefore increase the possibility of calculating a good result.

CHAPTER 5

Conclusion

This thesis described the development of a semi-automatic editing process applicable on segmentation masks. Since vascular structures, especially those located in the brain, are vulnerable to diseases, these were the structures put into focus for the editing task. It is crucial to quickly find a diagnosis for patients, suffering from this life-threatening conditions. For this reason the interaction techniques, used for the editing process, were designed to be of simple and fast control. Also the calculation of an accurate result and the quick response of the computation of the used algorithms, were of primary interest. In the framework firstly a presegmentation was performed on a MRA image by a threshold algorithm. The resulting segmentation mask could then be modified by the user with the developed editing methods. By removing falsely classified components, the more important structures, as the arteries of the Circle of Willis, were easier to identify. Due to errors made during the image recording or because of inappropriate values of the segmentation algorithm, gaps can occur in healthy continuous arteries. To close these holes an algorithm was developed to calculate connections, which should follow the true biological vessel track. For reviewing the effectiveness of the created methods, an evaluation was made according to state-of-the-art characteristics of image segmentation algorithms. Also the implemented interaction techniques have been discussed on the basis of cutting-edge properties like speed, repeatability and accuracy.

All in all, the developed editing methods yield accurate results in a short period of time. Certainly the proposed approaches are not perfect and do have a few limitations, but the discussions demonstrated that the intended goals have been satisfactorily achieved.

Acronyms

 $\mathbf{ACA}\,$ Arteria cerebri anterior

 ${\bf ACM}\,$ Arteria cerebri media

 $\mathbf{ACP}~\operatorname{Arteria}$ cerebri posterior

 $\mathbf{ACoA}\;$ Arteria communicans anterior

 ${\bf ACoP}\,$ Arteria communicans posterior

 $\mathbf{ACI}\,$ Arteria carotis interna

 ${\bf AB}\,$ Arteria basilaris

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