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## 2 Help on help

This is the PixelFlux help and User's Manual.

In PixelFlux, you access the help system with  or the corresponding item in the main menu of the **main module (Section 6.1)**, **analysis module (Section 7.1)** or **database module (Section 8.1)**. Usually, the help page corresponding to the current program situation will be shown, i.e. if you click at the help icon in the preset **tool window (Section 6.11.1)**, the description of **presets (Section 6.9.1)** will show up.

Moreover, PixelFlux contains a **direct help (Section 6.12.10)** that offers an introduction to the currently active mode (in the main module).

There is a table of contents with this help where the help topics are listed just as in a book. In addition, there is an index which lists the most important topics according to keywords and a [glossary](#) in which specific technical terminology is explained combined with the function to search these terms as well as a list of favorite topics. You can access these through the left part of the help.

The text highlighted in grey, for instance `File | Open`, refers to certain commands in PixelFlux. Elements shown as

 `Ctrl+Z`

indicate certain shortcuts you can use in PixelFlux to access those commands.

Please do not hesitate to give any kind of feedback. We look forward to receiving your **mail (Section 3.1)**. You can as well send us questions and suggestions referring to specific topics directly via the link "feedback" found in upper right part of this help.

## 3 General information about the software

### 3.1 Manufacturer Information and Contact



You can obtain the full versions of PixelFlux (Standard, Professional and Scientific) from the addresses listed below.

We are highly interested in feedback, criticism and new ideas. Please do not hesitate to send us a message via e-mail or via mail.

e-mail

[contact@chameleon-software.de](mailto:contact@chameleon-software.de)

Web site

[www.chameleon-software.de](http://www.chameleon-software.de)

Mail

Chameleon-Software GmbH  
Geschäftsführer: Dr. rer. nat. Jakob Scholbach  
Finkenstr. 66  
48147 Münster  
Germany

### 3.2 General information about the software

#### Contents

&nbsp;

- **Short description of the software**
- **Purpose**
- **User requirements**
- **User's manual in paper form**
- **Availability of this user's manual**
- **Further accompanying information**
- **Revision status of this user's manual**

#### Short description of the software

The software „PixelFlux“ is a software for treating color Doppler ultrasound videos according to the interpretation of the blood flow (perfusion) of vessels and tissues. The software is applied on a computer which is physically and timewise disconnected from the ultrasound examinar and the patient.

The work flow can be outlined as follows: the user opens an ultrasound video on the computer. (The videos are created using an appropriate ultrasound device and are transferred using an external data source or network to the computer. The acquisition, transfer and storage of the videos is not part of this software.) After the calibration of the video by setting the scale and the Doppler maximum velocity the user outlines a freely chosen area („Region of Interest“), which shall be interpreted according to the perfusion. The software translates image data into certain perfusion parameters referred to as velocity, area, and intensity. These parameters are displayed to the user and may be stored by the program.

#### Purpose

The software is intended to interpret image data stemming from color Doppler ultrasound images. The obtained results may serve the sonographically experienced user to support a diagnosis, which may subsequently lead to a refined diagnosis. However, the software itself does not suggest or formulate a diagnosis. Instead, the software solely performs a mathematical analysis of images or videos. The results of this analysis are referred to as perfusion parameters. In this sense, the software performs a perfusion-related image analysis. In the sequel, this process is referred to as a perfusion examination.

The software must only be used if a diagnosis obtained by different diagnostic means has already been obtained. Obtain a diagnosis or therapy recommendations solely from the results obtained with the software is a use which is not compliant with the purpose of this software. The information obtained with this software must always be used in context of other well established diagnostic means. In case of actual or perceived contradictions of the results obtained using the software and results of other diagnostic techniques, the results of the software must not solely be used to derive a decision concerning the patient.

The software interprets appropriate color Doppler ultrasound videos using mathematical methods. The video has to be recorded using a ultrasound device which - in the sense of the respective national regulations - is admissible for the use with patients. Furthermore, the quality requirements concerning the videos (see **Security advices for the use of the software (Section 3.4)**) have to be met. Videos which are not conform to these requirements must not be used in connection with this software.

The software has to be used physically and locally disconnected from the patient on a personal computer in a clinic or a medical practice. A medical contraindication for the use of the software does not exist, provided that the examination using Doppler ultrasound is possible.

## User requirements

The users which may use the software according to the purpose of the software is defined as follows: the acquisition of the ultrasound videos has to be conducted by a physician possessing the respective national certificates of medical ultrasound diagnosis for examining the organ in question. Moreover, it is necessary that the user knows the medical preconditions of the patient, in particular previous diseases etc.

The analysis of the ultrasound videos with the help of the software must also be conducted by a physician with the afore-mentioned abilities. Moreover, good computer handling abilities as well as language proficiency (German or English, depending on the used language of the software) are required.

## User's manual in paper form

This user's manual may be obtained from the manufacturer (see **Manufacturer Information and Contact (Section 3.1)**) free of charge within at most seven (7) days in paper form.

## Availability of this user's manual

This user's manual is part of the software and has to be kept ready for inspection by the user and the operator. If the user's manual is available electronically, only, the electronic access to the user's manual has to be always possible. Appropriate measures have to be taken by the user and the operator to ensure this requirement. In particular, an appropriate viewing software for the user's manual has to be installed.

## Further accompanying information

In addition to this user's manual a license agreement is ruling judicial and further usage conditions of the software. These contain in particular the usage time and licensation of the software.

## Revision status of this user's manual

Created the: 8th of December 2013

Last revision: 21.03.2018 21:54

## 3.3 Installation and system requirements

### Installation

The software has to be installed and used on a computer which is physically disconnected from the patient.

### System requirements concerning the used computer

The software runs on a computer with the following system requirements

- Operating system Windows (version Windows 7, Windows 8, or Windows 10)

- hard disk: free disk space of 30 MB for installing the program, additionally free disk space to save patient files and ultrasound videos (amount depending on intended usage frequency)
- RAM: 1 GB
- customary processor
- monitor: minimal resolution of 1024 x 768 pixels
- mouse
- keyboard
- device for data storage and recovery, e.g. a USB device or a DVD drive or a connection to the clinical network

### Further hardware requirements

If the software is used on a computer which is connected to an electronic archive (e.g. an archive for the ultrasound videos) or further comparable electronic devices, the computer needs to be separated from the archive or the respective electronic devices using a customary galvanic isolation (4kV).

If the videos are transferred from the ultrasound device to the computer using a frame grabber, the image rate of the frame grabber must be 15 images per second or higher and the resolution must be at least 1024 x 768 pixels.

### System requirements for transferring the ultrasound videos

A further requirement for using the software is the transfer of ultrasound videos or ultrasound DICOM files to the computer. The software and/or hardware needed to ensure this requirement are not part of the software and has to be ensured by using appropriate third party software and hardware. For example, this may be ensured using an appropriate PACS system. It has to be ensured that the direct and indirect transfer of the videos happens in a way that does not affect the integrity of the transferred files.

In particular,

- the files must not be damaged or corrupted during the transmission
- the files must be of a high quality, in particular as regards a possible image compression (e.g. when transferring the files using a frame grabber)

The software must only be used if this integrity is ensured. The responsibility for this lies with the operator and the user of the software.

### Installation and bringing into service

The software is installed on a computer with the above-mentioned system requirements. Depending on the local network architecture and rights management, the installation needs to be performed with the appropriate admin rights. The installation takes the following steps:

- download of the software from the manufacturer's website
- starting the installation wizard
- choosing the program destination (i.e., where the software is installed)
- running the installation using the installation wizard

The installation is complete if the message „PixelFlux was installed on your computer.“ is displayed.

The next step is the **activation (Section 11)**. This is the first step of bringing the software into service.

- starting the software (this may be done as the last step of the installation, see above)
- sending the shown computer code to the manufacturer, e.g. via email (see **Manufacturer Information and Contact (Section 3.1)**)
- after receipt of the activation code from the manufacturer: inserting the activation code
- the activation of the software is successful if the message „The activation was done successfully.“ is displayed.

Then, PixelFlux can be used. PixelFlux can be started using the start menu of Windows. This user's manual as well

as the help can also be reached using the start menu.

## Maintenance

The software does not require maintenance.

## Deinstallation and disposal

If a further use of the software is not intended or is the program installed on another computer, the software has to be deinstalled using the deinstall wizard. The wizard can be reached using the start menu.

## Dissemination of the software

If the software is left to third parties by the user or operator or if the software is passed in any other way, this user's manual has to be passed with it. Further conditions on the left over of the software or parts of it or other rights related to the software may apply according to the license agreement accompanying this user's manual.

## 3.4 Security advices for the use of the software

### Contents

&nbsp;

- **Quality requirements concerning the ultrasound videos**
- **Used file types**
- **Calibration**
- **Repeated measurements**
- **Angle correction**

### Quality requirements concerning the ultrasound videos



To ensure a reliable use of the software, the following requirements on the ultrasound videos and images have to be satisfied. If one or more of these requirements are not satisfied or in doubt, the ultrasound videos and images are not appropriate for the use in connection with the software and must therefore not be used together with the software.

The following requirements will be formulated below for an ultrasound video ("the video"), analogous requirements hold for ultrasound images.

- The video is of sufficiently high quality so that a medical assessment of the video at the ultrasound is possible. In particular, the organ / part of organ to be examined must be shown completely and with a good image resolution. Except for this requirement there is no a priori restriction on the organ / part of organ to be examined.
- The video was recorded obeying widely accepted standards of medical ultrasound diagnostics.
- The video is of good technical quality and has an image frequency of at least 20 images per second. This is also required from the transmission of the video using a frame grabber (if a frame grabber is used).
- The video has a high enough resolution. This also has to be ensured during the transmission of the video using a frame grabber (if a frame grabber is used). See **system requirements (Section 3.3)** for further details.
- Before, during or after the transmission of the video from the ultrasound device to the computer the video was not compressed in a way that compression artifacts (created because of a too strong compression) are created. In particular, the color scale of the video must not be distorted / changed because of a possible image compression. See **system requirements (Section 3.3)** for further details.
- The preset settings of the ultrasound device (for example the ultrasound transducer, color Doppler maximal velocity, color Doppler frequency, gain, etc.) are chosen in a way that the depiction of the examined organ is optimal from a medical and sonographical point of view. This requires in particular that aliasing (i.e., an oversteering of the color Doppler image due to an inappropriate maximum velocity setting) has to be avoided, the choice of an appropriate wall filter, the optimal ultrasound frequencies for B-image and Doppler image, and an appropriate choice of the transducer.

- The used color scale in the video displays a fine-grained distinction between low and high velocities or flows.
- The RGB data (color data) of the depictable image data are constant within the chosen preset of the ultrasound device.
- The preset settings of the ultrasound device are, in comparison to other videos of the same organ and the same patient, the same. The user has to define ultrasound presets which are specific to the examined organ and appropriate for the medical question at hand. If a similar / same examination is performed later, the same preset has to be used again. All measurements are only usable and comparable when referring to a concrete, current preset. In particular the gain of the ultrasound device must not be changed between examinations.

## Used file types

The software uses for the perfusion examination the following file types:

- image files (type .jpg)
- video files (type .avi)
- DICOM files (type .dcm or without file ending)

DICOM files have the advantage over image and video files that the patient data, in particular the patient name and date of birth can be saved in the DICOM file.



The use of DICOM files is strongly recommended.

When using other image or video files, there is a higher risk of a wrong assignment of the examination results with the examined patient, for example because of a wrong use of the software. This might eventually lead to attributing a diagnosis to the wrong patient.

perfusion examinations are, a priori, possible with image files and DICOM files containing only a single image (as opposed to a sequence consisting of multiple images).



It is strongly recommended to use video files or DICOM files containing at least three (3) complete heart cycles. In particular, it is strongly advised against using single images for the perfusion examinations.

When using videos which are too short or when using single images for the perfusion examination, there may be a risk of a wrong assessment of the perfusion. This risk may arise as the physiologically caused pulsation (periodic change) of the perfusion might not or not sufficiently be taken into account. A wrong assessment of the perfusion may eventually lead to a wrong diagnosis.



If files of the type .avi (video files) are used with the software, the video driver of the software must be installed and working.

If the video driver is not installed, or not working, there may be errors in the depiction of the videos. This may hinder the proper functioning of the software and may lead to wrong results of the perfusion examinations. The latter may eventually lead to a wrong diagnosis.

## Use of corrupt files



The integrity of the used DICOM, image or video files is fundamental for a factually correct perfusion examination. Therefore, prior to doing a perfusion examination, the integrity of the used image, video, or DICOM file has to be ensured. In addition, image, video or DICOM files which are corrupt or damaged or which are possibly corrupt or damaged must not be used for a perfusion examination.

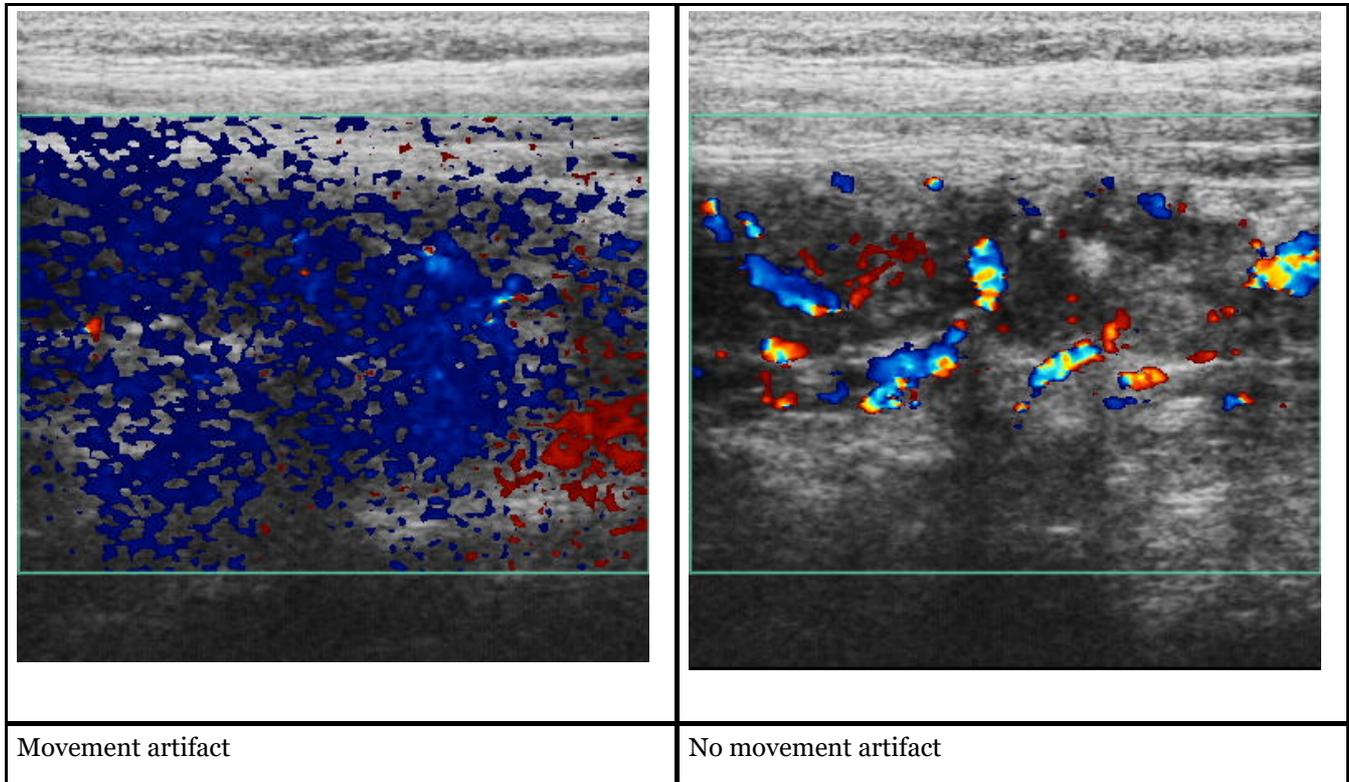
Using corrupt or damaged files may lead to wrong perfusion examination results and therefore eventually possibly to a wrong diagnosis.

## Movement artifacts

A movement artifact is a disruption of the ultrasound device caused by a quick movement of the transducer or of the patient (for example because of breathing). Such a movement of the transducer or the patient results in a wrong

image depiction which can be seen as large, monotonous area which is depicted as if it was a perfused area. This depiction, however, is by no means related to the presence or absence of the factually existing perfusion.

For example, the image at the left below shows a movement artifact, whereas the right image is taken from the same video sequence, but not containing an artifact.



 The perfusion examination must only be done with videos not containing any movement artifacts. To this end it must be ensured that the transducer is not moved during the examination. It must also be ensured that no breathing or other movements of the patients lead to movement artifacts.

Using videos with movement artifacts may lead to gross deviations of the examination results and therefore eventually possibly to a wrong diagnosis.

**Calibration**

The calibration of the ultrasound video contains three tasks:

- setting the cm (centimeter) scale
- setting the color scale
- setting the maximum velocity

The cm (centimeter) scale tells how long a centimeter (cm) is in the ultrasound image.

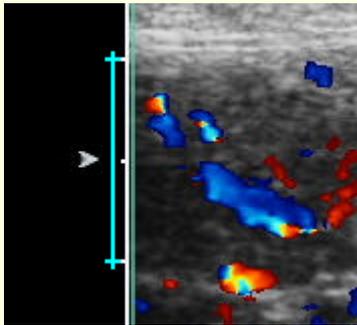
The color scale is the color scale shown by the ultrasound device. It encodes the movement of blood or possibly other moving parts using colors.

The maximum velocity refers to the color Doppler scale. It tells the velocity encoded by the color at the outer end of the color Doppler scale. (With many ultrasound presets this is also the most light color of the color scale).

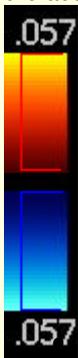
 The correct calibration is a basic requirement for the correct assessment of the perfusion. A wrong calibration may lead to seriously flawed measurement results and therefore may eventually lead to a wrong diagnosis.

In particular the following aspects have to be taken into account:

- Many ultrasound indicate show the cm scale by an axis with small ticks. Some ultrasound devices also show distances of .5 cm (as opposed to 1.0 cm). It is important to choose a distance of 1 cm in the image, as shown in the example below.



- Some ultrasound devices don't show the maximum velocity at the end of the color scale in cm/s (centimeter per second), but in m/s (meter per second). Before using the software with any ultrasound video the user's manual of the ultrasound device has to be reviewed or the ultrasound device manufacturer has to be asked which calibration convention is used by the ultrasound device. The software requires inputting the velocity using cm/s, i.e., in the following example a velocity of 5.7 cm/s has to be put in the corresponding input box.



The color scale has to be recognized completely. The recognition of the color scale by the program is displayed in the image by red and blue marks at the color scale, as shown above.

**Choice of the examination region (Region of Interest, ROI)**

The program allows to analyze the perfusion of an arbitrary examination region (ROI). The perfusion parameters refer to the ROI only.



The factually correct choice of the ROI (in relation to the examination context) is a basic requirement. For example, it is a crucial requirement, that the organ or part of organ to be examined is defined carefully and precisely.

A factually wrong choice of the ROI may lead to a wrong interpretation of the perfusion parameters by the user.



It is important that no further colored image components lie in the ROI, other than the vessels and vessel structures displayed by the ultrasound device. In particular, the ROI must not contain any colored labels.

If the ROI does contain further colored image parts (such as colored labels) which don't visualize vessels or vessel structures, the resulting perfusion examinations are factually incorrect and may therefore eventually lead to a wrong diagnosis.

**Repeated measurements**



Due to physiological changes, for example, it is always required to perform repeated examinations of the same organ or same part of organ with different videos.

Performing only a single examination without comparison and computation of averages with other examinations may lead to deviations of perfusion parameters and therefore may eventually lead to a wrong diagnosis.

## Angle correction

Taking into account the Doppler angle  $\alpha$  (angle between the direction of the blood flow in the examined vessel and the direction of the transducer) allows to compute the actual flow velocity of the examined vessel based on the velocity encoded by colored pixels depicting this vessel.



The factually correct angle correction is a basic requirement for the computation of the actual flow velocities and flow volumes. The following explanations are intended as a first introduction to this topic, only. They cannot replace a thorough education of the user about the topic of angle correction which is independently necessary.

A missing / wrong angle correction may lead to seriously flawed examination results and therefore eventually may lead to a wrong diagnosis.



In case the the angle correction is technically not possible, only the flow intensity can be computed. The clinical usage of the flow intensity requires observing a number of conditions. Essentially, these conditions consist in a standardized ultrasound device preset and the standardization of the anatomic situation during the image acquisition. Even though the comparability of the results of a given patient over time or between the same organ or vessels in different patients can be ensured by obeying these conditions, it has to be noted that the physiological and pathophysiological important total amount of blood flowing in a vessel can not be determined exactly.

To determine the amount of blood flow exactly the user has to use functions of the PixelFlux software which take the Doppler angle  $\alpha$  into account.

These are:

1. perfusion examinations in arterias with circle-shaped cross sections using a spectral analysis of the velocity spectrum and a longitudinal cut of the vessel
2. perfusion examinations in arterias with circle-shaped cross sections by standardized color duplex sonographic videos using an oblique section of the vessel
3. perfusion examinations in vessels with arbitrary cross section using three-dimensional (3D) standardized color duplex sonographic images and videos.

The angle correction in each of these three cases is now explained.

### Angle correction for longitudinal cuts

This kind of perfusion examination requires examining an arteria using a longitudinal cut of the arteria in the pulsed wave Doppler mode.

The required settings are done in the **Spectral envelope analysis (Section 6.9.7)** tool window. The required angle measurement is done using the tool **Angle measurement (Section 6.9.3)**.

### Angle correction for oblique cuts of the vessel in the frontal plane

If the vessel cannot be displayed in a longitudinal way, PixelFlux offers the computation of the flow volume based on the Doppler angle based on an oblique cut of the vessel. In this case, the vessel will be displayed with an elliptic shape by the ultrasound device. To this end, the angle correction has to be done with the usual 2D ultrasound image or video. Use the function **ROI in frontal plane (2D)** in the **examination tool window (Section 6.12.4)**. See there for further instructions.

The Doppler angle is computed automatically by the software from the individual angles of the vessel in the frontal and in the sagittal plane and is then applied to the computation of the flow volume.

### Angle correction in the 3D mode for images in the horizontal plane

When using standardized color duplex sonographical 3D-images or videos, the angle correction can be performed by the software as well. In this case the examination is done with an image in the horizontal plane (as opposed to the usual frontal plane). In this case the examination of the flow volume and the required angle correction can be done for vessels with arbitrary (not necessarily circle-shaped) cross sections using. Use the function **Tools | 3D angles** in the main window and **ROI in horizontal plane (3D)** in the **examination tool window (Section 6.12.4)**. See **Angle measurement (Section 6.9.3)** for a detailed explanation.

## 3.5 Warnings

For the safe use of the software, the software is issuing situation-based warnings, whenever necessary. The most important warnings from a safety point of view are listed below. See also **options - warnings (Section 6.10.8)** for an explanation / configuration of further warnings.

### Warning

The image file ... can not be opened.

The patient name could not be extracted from the file .... Therefore, please check that the examination is assigned to the right patient.

All perfusion parameters are identically zero. This perfusion examination is therefore probably invalid. Please double-check whether the examination was performed correctly and discard this examination, if necessary.

You are doing a perfusion examination with a single image only. To ensure the validity of the perfusion examination, it is strongly recommended to use a video with at least 3 complete cardiac cycles. Do you nonetheless want to perform this perfusion examination?

### Where, when

When a file could not be **opened (Section 6.2.1)**.

After opening a video or image file, or after opening a DICOM file whose header could not be analyzed.

After doing a perfusion examination whose results are identically zero. The warning is also shown in the analysis and database window.

When starting an examination with a single image only.

### Explanation, remedy

Either the file type is not supported or the file is corrupt.

Use DICOM files whose header can be analyzed.

See **Notifications and Warnings (Section 6.7)**.

Use videos for the perfusion examination if possible. See also **Security advices for the use of the software (Section 3.4)**.

## 4 Welcome

### **Welcome to the PixelFlux Help and User's Manual!**

PixelFlux is the first software in the world for dynamic perfusion analysis via colored Doppler videos.

This help is to facilitate the use of PixelFlux. Please read these first steps carefully: **Your first perfusion examination with PixelFlux (Section 5)**.

The documentation with the **Main form (Section 6.1)**, **Analysis module (Section 7.1)** and with the **Database (Section 8.1)**

contains all information on the three modules of PixelFlux.

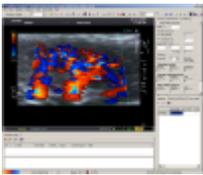
If there any questions on the software or on the help, do not hesitate to contact us. You can give feedback at the upper right of every page. We look forward to hearing from you!

## 5 Your first perfusion examination with PixelFlux

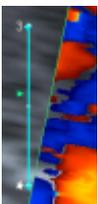
After you have installed and activated PixelFlux, start the program. PixelFlux **Main form (Section 6.1)** appears. This module serves for opening video files or DICOM files, and uses your input to start perfusion and other measurements.

**Open (Section 6.2.1)** a DICOM, video (.avi-) or image file by clicking on **File | Open** in the menu or .

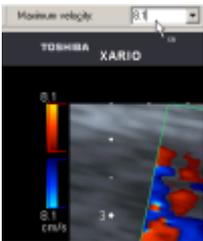
The first image of the video will be shown in the image area of the main form.



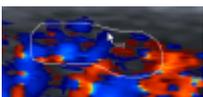
Then **calibrate (Section 6.3)** the image, i.e. specify scale and Doppler maximum velocity. For this, click on two points which have a distance of one centimeter from one another. The points are marked with a light blue cross and joined by a light blue line.



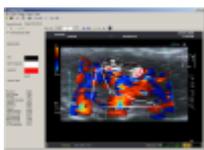
Then input the maximum velocity, which is usually depicted above the color scale by the ultrasound devices:



Finally outline the desired **Region of Interest (Section 6.5)** (ROI) with your mouse:



The perfusion examination now automatically starts and the **analysis window (Section 7.1)** displays the results of the measurement. You can view the ROI again, this time equipped with the **perfusion relief (Section 7.4)**, showing you the local distribution of perfusion in the ROI: red areas are highly perfused, white ones have medium perfusion and black ones have little to no perfusion. Along with this qualitative depiction, PixelFlux also shows quantitative values in charts: the velocity, perfused area and perfusion intensity are measured (**description of these entities (Section 7.2)**).



Now, you are able to perform your own perfusion examinations! PixelFlux is, however, much more than that. Learn more about the modes of the **analysis module (Section 7.1)** which manages the results of a single perfusion examination. Additionally, PixelFlux contains a **database (Section 8.1)** that stores your patient and examination data similarly to a PACS system.

## 6 Main module

### 6.1 Overview of the main module

The main module is the central module dealing with all image sources, and performing the perfusion and other examinations. Additionally, you access the two other modules, the  **database module (Section 8.1)** and the  **analysis module (Section 7.1)**.

- To get used to the basic features of PixelFlux,  **open (Section 6.2.1)** an image, a video or a DICOM file. Then, **calibrate (Section 6.3)** the image, i.e. specify scale and maximum velocity. Finally, choose a **region of interest (Section 6.5)** (ROI) and start the automatic perfusion examination.
- In addition to these basic functions, the software provides geometric tools allowing you to set up standardized ROIs (see **presets (Section 6.9.1)**) and to measure distances ( **ruler (Section 6.9.1)**),  **angles (Section 6.9.1)**,  **parallelograms (Section 6.9.1)**, and  **labels (Section 6.9.1)**. Of course you can also  **play (Section 9.2)** a video. You can  **copy (Section 9.1)** and  **save (Section 9.1)** the image. If necessary, it is possible to set up the position of the scale  **manually (Section 6.3)** or load the color scale of a different image (useful for 4D perfusion examinations).
- If you need to perform many examinations, PixelFlux allows you to save even more time by performing the examinations **automatically (Section 6.8)** (in your absence) after you have provided all details.
- Different **user profiles (Section 6.11.2)** make the work of several colleagues in your team easier. You can view all **information (Section 6.12.2)** of the currently opened file (in particular the DICOM header). **Options (Section 6.10.1)** handles complex operations which can be carried out by PixelFlux.
- You can open files **anonymized (Section 6.2.2)**, a useful feature for presenting videos with PixelFlux at conferences and other events.
- In addition to the classical perfusion examination PixelFlux has an extra tool for automatic analysis of  **spectral curves (Section 6.9.7)** and  **shape analysis (Section 6.12.8)**.
- You can use **tool windows (Section 6.11.1)** in order to easily manage the functions of PixelFlux.

The handling of the several functions of PixelFlux are organized via **click modes (Section 6.11.3)**.

The above modes are available in the tool bar and the main menu at the top of the window. Click on an icon to receive further information on it.



## 6.2 Opening image sources

### 6.2.1 Opening video sources

PixelFlux is able to open image, video (avi) and DICOM files. In addition, you have several ways of choosing what file you want to open.

#### Content &nbsp;

- **Fundamentals**
- **Open next file, open previous file**
- **Drag files from the Windows Explorer to PixelFlux**

#### Fundamentals

You can choose between three different types of files:

1. image files
2. video files
3. DICOM files

You can open these files by clicking on  or **File | Open** . Select the file which you wish to open. Then, the first image of the video is shown. The file type (DICOM, video or image file) is automatically recognized.

When opening a file, PixelFlux automatically resets the **calibration (Section 6.3)**. PixelFlux automatically searches for the color scale and shows the result of the recognition process (see **image calibration (Section 6.3)**). When using 3D or 4D files, which often do not contain a color scale, it may be necessary to load the color scale from a different file. This is also possible (see **Load color scale from a different file (Section 6.3)**).

In many circumstances, your workflow might begin with opening a video or DICOM file when PixelFlux starts. There is an **option (Section 6.10.2)** to automatically show the open dialog when PixelFlux starts.

### Notes on DICOM files

DICOM is a digital image or video format designed for medical applications. In it, patient and examination information are included in addition to the image data. It is strongly recommended to use the DICOM format, if possible. See also the **Security advices for the use of the software (Section 3.4)**. The first advantage is, that there is no need of inserting the patients data later on. The second one is the correlation of video quality and video size which is superior most of the time. Additionally, PixelFlux is in most cases able to recognize the scale (see **image calibration (Section 6.3)**).

The PixelFlux DICOM reader has been tested with various DICOM dialects and is able to read not only ultrasound images or videos. If your files are not read, please **contact (Section 3.1)** us. To view the **header information (Section 6.12.2)** of a DICOM file, click on **File | Information ...** ().

### Open next file, open previous file

You can open the next file (according to the alphabetical order of the file name) in the current directory by clicking on **File | Open next file**. The open dialog will not appear. The file type (image, video or DICOM) will be recognized by PixelFlux. It is also possible to open the previous file (**File | Open previous file**).

### Drag files from the Windows Explorer to PixelFlux

You can open a file in PixelFlux by dragging it from the Windows Explorer to PixelFlux. To do so, move the windows of the Explorer and of PixelFlux so that you can see both at a time. Then, select the file in question with the left mouse button, but do not let the mouse button go. Drag the file symbol to PixelFlux and let go the mouse button.

## 6.2.2 Open files anonymized

You can open a video or DICOM file without displaying the patient's name.

If you do not wish to display the patient's name on the video screen of PixelFlux (for instance during a conference presentation), you may use the command **File | Open anonymously** in the main form. Then PixelFlux will open the file as usual, but will display a black bar to hide the patient's name (near the upper border of the image). Additionally, the patient information in DICOM files (which are normally used for the database) are anonymized.

This setting of an exam will be saved. This way, you can show the video in the database, too.

Please note that PixelFlux does not change the DICOM or video file. Therefore the patient's name will still be contained in the file, when you hand the file to another person. Before using this feature, please check whether the bar effectively hides the patient's name.

## 6.3 Image calibration

After opening and/or playing a video or DICOM file, the image needs to be calibrated to perform the perfusion examination, PixelFlux must be provided with the following calibration information:

1. *scale*
2. *maximum velocity*

3. (if necessary) the *position* of the color scale.

You can tell PixelFlux to *load the color scale from another file* than the one you are currently working with. This is useful for applying PixelFlux in the context of 4D perfusion examinations, as these videos do not display a color scale most of the time. Another option is to use *external scale profiles*.

### Content

- **Scale**
- **Maximum velocity**
- **Color scale position**
- **Load the color scale from another file**
- **Use external color scale profiles**
- **Use external calibration information**

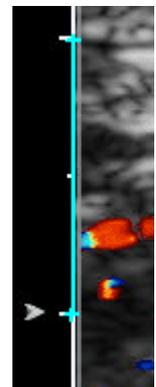
## Scale

To compute the perfused area you need to calibrate the image with respect to distance.

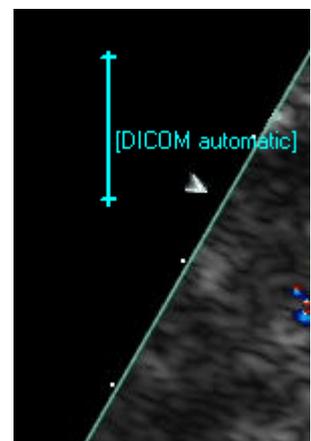
For the distance calibration, click on two points whose distance from one to another is one centimeter (cm) in reality. For this, every ultrasound device gives the scale (usually at the image margin).

The second point will automatically be placed exactly above or below the first point. If you want to disable this feature, uncheck the option `Only allow vertical cm points` (see **Options - calibration (Section 6.10.7)**).

To **undo (Section 6.4)** (and later redo) the calibration, click on  or `File | Reset`.



When you open a DICOM file, PixelFlux tries to recognize the scale using the DICOM header information. If the scale was successfully recognized, it is displayed in the image, too (see second image). Otherwise, it has to be calibrated manually as described above. The position of the cm-points are not recognized (as in the sample image below). However, only their distance is important.



Usually, the cm calibration of the previous video will be discarded when you open a new video or DICOM file. In order to keep the existing cm calibration, uncheck the checkbox `Reset cm calibration when opening files` in the **calibration tool window (Section 6.12.6)**.

The semi-automatic cm calibration can help you with the calibration by making minimal adjustments to the calibration points you clicked at: PixelFlux will try to find a light small spot near the point you clicked at and, if successful, will take this spot instead of the point you clicked at. You can disable this function in the **options (calibration) (Section 6.10.7)**.

The **magnifier (Section 6.12.7)** will be shown automatically if you calibrate the image manually. However, you can change this behavior in the **options (calibration) (Section 6.10.7)**.

### Maximum velocity

After you have clicked on the second "centimeter-point", you have to tell PixelFlux the maximum Doppler velocity, which is displayed at the top of the color scale by most ultrasound devices.



Please insert it in the input box in the upper left corner of the main form:

maximum velocity:

The velocity has to be in the unit cm/s, since all results are in the unit cm/s or cm<sup>3</sup>. Please note that some ultrasound devices (as in the sample image above) display the maximum velocity in m/s instead of cm/s (e.g. 0.086 m/s = 8.6 cm/s). See also the **Security advices for the use of the software (Section 3.4)**.

Alternatively to inserting the maximum velocity manually, you can use PixelFlux to recognize it automatically after having set up a few options (see **automatic velocity recognition (Section 6.10.4)**).

### Color scale position

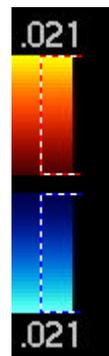
After opening a file, PixelFlux searches the colour scale. The result of this search is displayed in the image. PixelFlux draws red and blue lines at the red and blue Doppler range. Additionally, the colours are displayed in the status bar, at the bottom of the main window and in the **color scale toolwindow (Section 6.11.1)**:



In some cases (e.g. if the image quality is insufficient or if there is an unsuitable adjustment of the ultrasound device), it is possible that the scale is perceived or recognized in an incorrect way. If this happens, you have to set up the position of the scale manually.

To correct the position of the scale, first activate the corresponding mode by clicking on **Color scale | Position** (in the main menu) or  (in the main module tool bar). When viewing the status bar at the lower part of the main window, you see that the corresponding mode is activated.

To correct the color scale position, click on the color scale with the left mouse button (it is not important, whether you click on the upper or lower part, if there are two parts). PixelFlux searches for the color scale in the surrounding area and depicts the recognized scale with dotted lines, as shown in the sample image. The dotted lines indicate that the color scale was set up manually. This setting is also saved for the database. Alternatively, you can hold the  **Shift** button and then click on the scale.



There are also two older ways of manual setting, which should not be needed if you use the one described above. If you want to adjust the horizontal position (x) first click on **Color scale | Position (x)** or  and then click on the scale.

If you want to adjust the vertical position (y), first click on **Color scale | Position (y)** or  and then click close to the vertical end of either the upper or lower part of the scale.

In all three cases, then click on the button you first clicked on and continue calibrating the image.

If you want to undo the manual changes, click on **Color scale | Reset manual changes**. The automatic scale position will be refreshed.



The calibration is stored after having performed the perfusion examination. I.e. if you wish to perform a second examination with the same video, you can directly proceed to specify the new ROI. When you open a new video file, the calibration will usually be reset. However, you can tell PixelFlux not to reload the cm calibration (see above). You may also tell PixelFlux not to reload the color scale, when a new file is opened, which is particularly useful for 4D-examination. See below.

In addition, there are a number of **options (Section 6.10.1)** that may help PixelFlux finding the colour scale. If PixelFlux is unable to detect the colour scale, please **send (Section 3.1)** us a sample image. Thank you.

## Load the color scale from another file

If you use videos/images/DICOM files color scale, you can still quantify perfusion using these videos, if you have another video which displays a colour scale corresponding to the current video using the checkbox **Load color scale when opening file**. For details, see **here (Section 6.12.6)**.

## Use external color scale profiles

An option for videos and images without color scale is the use of predefined, external color scale profiles. This means that the color information corresponding to a scale are already stored in PixelFlux, so that you can use this information instead of the (non-existent) color scale of the image. To use such a profile, use **Use external color scale profiles**. For details, see **here (Section 6.12.6)**.

## Use external calibration information

You can also use the distance (cm) calibration from another file using the option **Reset cm calibration when opening files**. For details, see **here (Section 6.12.6)**.

## 6.4 Undoing the image calibration

If you made a mistake during the image calibration (wrong cm points ...), you can undo these settings before starting the computation of the perfusion.

For this, click on  or **File | Reset** ( **Ctrl + Z**).

All calibration information concerning the cm-distance, automatically recognized maximum velocities (if enabled), and the settings of tools (ruler, parallelogram, presets) will be deleted. PixelFlux stays in the current **mode (Section 6.11.3)** (calibration, color scale position, ruler, parallelogram). Later, you can redo the **image calibration (Section 6.3)** by clicking on the first point of a centimeter-distance.

## 6.5 Setting the region of interest

After you have completed the image calibration, you need to specify the region of interest. All Perfusion parameters refer to this region.

Set the ROI as follows:

1. **Press** the left button of your mouse and **hold** it pressed.
2. **Outline** the region by moving the mouse. The movement of the mouse will be drawn by a white line in the image area of the main form.
3. After you have finished, **release** the mouse button.

Then the perfusion examination starts. The program begins with the first image of the video file and considers up to 150 images.

When the perfusion examination is finished, the **analysis module (Section 7.1)** containing the perfusion

parameters is opened automatically.

💡 If you wish to abort the calculation, press  Esc.

💡 If you do not wish to start the perfusion examination instantly (for instance if you wish to add **presets (Section 6.9.1)**) outline the ROI with the right mouse button (instead of the left). Then add **presets (Section 6.9.1)** and start the measurement. Alternatively, you can avoid the immediate start of the measurement using the **examination tool window (Section 6.12.4)**.

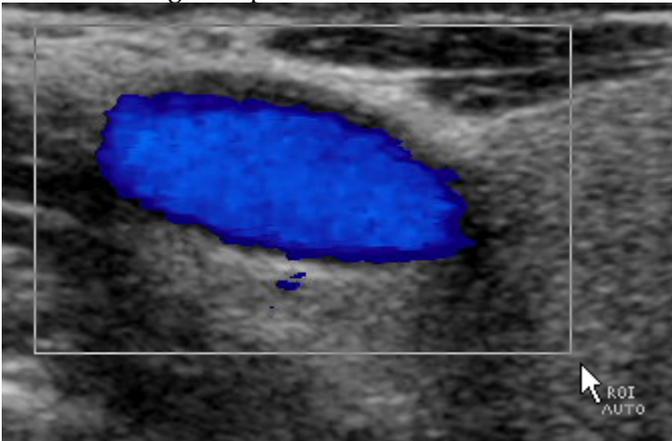
If you quantify the perfusion of a single vessel, you may also use the **automatic ROI recognition (Section 6.6)**.

## 6.6 Automatic ROI recognition

PixelFlux is able to automatically determine the ROI of a single vessel that is not connected to any other vessel. This mode only applies to perfusion measurements of *single vessels*, as opposed to measurements of more complex vessel structures.

To use this mode, activate the check box **Determine ROI automatically** in the **examination (Section 5)** tool window.

Unlike in the usual set up of the ROI, where you have to precisely encircle your ROI, you now simply define a rectangle that contains the single vessel. To do so, push the left mouse button, hold it and drag the mouse, as shown in the following example:

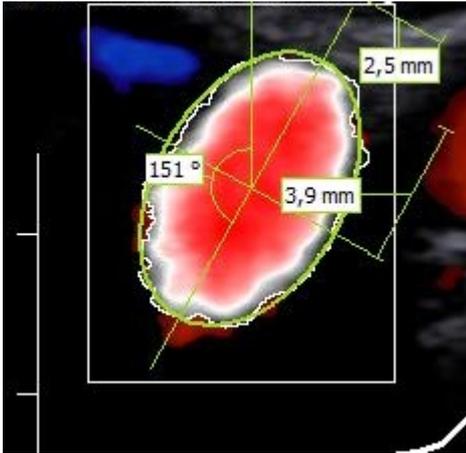


PixelFlux will then first search for the image where the vessel takes its biggest size.

After that, the single vessel, as it is shown in this image, is taken as the ROI for the examination. From this point on, the examination is performed as usual. It is strongly advisable to use this mode only when the single vessel in question is not moving. If it does move, parts of the vessel may, in some images, lie outside the automatically detected ROI.

This mode can be combined with the **angle correction according to the (elliptic) shape (Section 6.12.4)** of the vessel.

Then, on the one hand, the vessel will be recognized automatically, and, on the other hand, the angle correction will be performed according to the shape of the vessel, as the following example shows:



Only the largest connected vessel will be used as the ROI for the examination. Smaller vessels in the vicinity (such as the small vessel shown in blue at the upper left) are not counted as the ROI.

## 6.7 Notifications and Warnings

For each perfusion examinations, PixelFlux performs certain internal checks which are intended to help you spot potentially erroneous examinations, for example due to incorrect use of some functions of PixelFlux.

On the one hand, certain checks will be performed before the examination starts. On the other hand, after the examination has been done, other checks will be done. If certain conditions are met, a specific warning will be shown. These warnings may be a hint for you that some error occurred. In that case, you should double-check the examination and discard if the examination is indeed incorrect or in case of doubt. Finally, PixelFlux shows certain notifications that protocol what functions you have used to perform that examination.

### (Section 6.11.1)

#### Contents

- **Checks before the examination starts**
- **Notifications and warnings after the examination**

#### Checks before the examination starts

Before you start a perfusion examination, PixelFlux checks some settings and will warn you if necessary. You can then decide whether you want to ignore the warning and still do the examination or whether you don't perform the examination at that point.

##### Plausible maximum velocity

PixelFlux checks whether the maximum velocity that you have input is between 1 and 200 cm/s. If not, a warning is shown.

##### Sufficient image resolution

PixelFlux checks whether the resolution of your image or video is sufficiently good. If 1cm in the image takes less than 50 pixels a warning is shown. It is recommended to use only images with a resolution of at least 50 pixels per cm in order to ensure a sufficiently high accuracy. See also the **Security advices for the use of the software** (Section 3.4).

##### Minimum size of single vessel

If you are doing the perfusion examination of a single vessel using the automatic ROI recognition, PixelFlux checks whether the vessel is large enough. If the vessel is smaller than 1000 pixels, a warning is shown. The lower bound of

1000 pixels for the vessel area can be changed in the **options (Section 6.10.8)**.

### Color scale recognition

If you do a color perfusion examination PixelFlux checks whether the recognized color scale matches the color scales that have already been saved. This should help to ensure that the **color scale (Section 6.3)** (also see **Calibration toolwindow (Section 6.12.6)**) is recognized correctly.

If you use PixelFlux for the first time or use a new ultrasound machine etc., the color scale will not be in your stored list of color scales (even if it is recognized correctly). PixelFlux shows this by displaying an exclamation mark near the color scale . Then, PixelFlux asks before the examination starts whether the color scale was recognized properly. If you confirm this, the color scale is stored in your list of approved color scales. If you later do an examination with the same color scale, even in a different image, PixelFlux will recognize it and will not ask again. In this case, a check is shown . Once you do a perfusion examination using an image with a new color scale, PixelFlux will ask again etc.

You can disable this function at **options (calibration) (Section 6.10.7)**. In that case, PixelFlux will show a question mark: .

### Notifications and warnings after the examination

Once the perfusion examination is finished, PixelFlux runs a number of plausibility checks. These may help detecting whether the examination was done correctly. If one or multiple warnings occur, PixelFlux will show these immediately after the examination is finished. The warnings will only be issued for color examinations, but not for Area-only-measurements.

The warnings will also be issued when using the **Automode (Section 6.8)**. However, in this case, the warnings will not be shown after the examination is done, but will be displayed in the automode tool window. Moreover, for each warning, using the **options (Section 6.10.8)**, you can individually determine whether or not you want to store the examination in the database, should a warning occur.

Moreover, still in the options, you can disable or enable the warnings individually.

You see the issued warnings in the **Overview of the analysis module (Section 7.1)** and the **Overview of the database module (Section 8.1)** in the list **Notifications and Warnings**, together with an exclamation mark .

Moreover, you see a number of notifications (with ) that show you what settings you have used to perform the examination.

### Warning: perfusion identically zero

A warning occurs if the perfusion parameters in all images are constantly zero. If that is the case, you should check in particular whether the **color scale (Section 6.3)** was recognized correctly and whether the **ROI (Section 6.5)** was specified correctly. Also check whether the **examination mode (Section 6.12.4)** is set correctly.

### Artifact warning

A warning occurs if in an image the majority of the ROI is colored and if the PI of the area (red and blue) is high. These two conditions may be a sign of a movement artifact, i.e., that the patient has moved and therefore a large part of the ROI is colored without an actual perfusion being the reason thereof.

The threshold for the part of the ROI and the maximum PI can be changed in the options. The default values are 60% (of the ROI area) and a PI of 1.0.

### Warning: plausibility of the position of the ROI

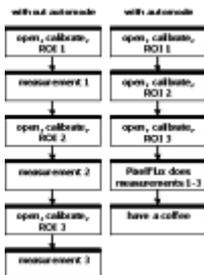
PixelFlux checks whether the position of the ROI is plausible: it checks whether the ROI lies partly or completely



## Overview

If you want to undertake many examinations, the automatic mode is very useful. By this, it is possible to tell PixelFlux which videos and regions of interest you wish to examine. After this, PixelFlux performs the perfusion calculation.

The automatic modus, or simply automode, works as follows:



## How to

Create a new automode file. This file contains all information about which examinations have to be processed later on. Click on **Auto mode | New** or  and select the file name of the automode file. PixelFlux creates an empty file. Now, the automatic mode is active. You will see that the title bar of the main form changes to "PixelFlux Scientific automatic mode" instead of "PixelFlux Scientific".

Alternatively, when you already have created an automode file and wish to continue working with that automode file later on, you can reopen it with **Auto mode | Open** or . (Likewise, you can close the automode file, if you wish to quit the automatic modus, by clicking on **Auto mode | Close**.)

To work with the automode, proceed as follows:

1. Open an image, video or DICOM as you usually do (see **open video sources (Section 6.2.1)**), perform the calibration as usual (see **calibration (Section 6.3)**). Outline the region of interest as usual (see **region of interest (Section 6.5)**). *Now*, the automodus begins to work: normally the perfusion examination would start immediately. But when the automode is active, the examination will not be performed. Instead, you have to specify the **examination data (Section 8.5.1)** and the information on the patient. Then, it may seem that PixelFlux does nothing. However, this is not true. PixelFlux stores the examination information in the automode file you specified in the first step. You can see the examinations in the automode file in the corresponding list in the automode tool window. PixelFlux shows the surname, the first name and the date of birth of the patient to be examined.
2. You may repeat the previous step, until all of your examinations are stored. If you wish to delete some examinations in the automode script, just select one or more items from the automode list (displayed in the **automode tool window (Section 6.11.1)**) and click on **Auto mode | Delete item**  **Ctrl + Del**.
3. When all your examinations are completed, start the automode and PixelFlux will perform the examinations. Click on **Auto mode | Start** or . PixelFlux will show all examinations with their details (surname, first name, patient's date of birth, organ, part of the organ, video file). PixelFlux begins to compute the perfusion parameters. The examination being processed, a blue arrow  appears. When an examination has been successfully processed, a green checkmark  appears. If a warning occurred, a yellow exclamation mark  is shown. If an error occurred, a red exclamation mark  appears. You can cancel the automode with **Auto mode | Pause** or by pressing  **Escape**.

The perfusion examinations are automatically stored in the file according to the patient you specified. When you use DICOM files, the patient information is taken from the DICOM header, so that you will not have to insert it.

PixelFlux will perform certain plausibility checks, see **Notifications and Warnings (Section 6.7)**. The resulting warnings will be displayed in the results list in the automode **tool window (Section 6.11.1)**. If one or more warnings are issued, the examination will not be stored to the database, unless you change the corresponding **option (Section 6.10.8)**.



When you use video or DICOM files from a CD, this CD has to be available when the automode script is executed.

## 6.9 Tools

### 6.9.1 Tools

There are many situations, in which it might be useful to select a defined region of interest. Using the tools ruler and parallelogram you can measure the image geometrically. Presets allow the relative positioning of a region of interest referring to the current parallelogram. You can use the following tools: ruler to measure lengths, angle measurements (also for purposes of 3D and 4D perfusion examinations), parallelogram, presets and labels.

You can **remove (Section 6.4)** all tools by clicking on **File | Reset** (  **Ctrl + Z**) or . This also resets all other image information, such as the **calibration (Section 6.3)**.

**(Section 6.4)(Section 6.4)(Section 6.4)(Section 6.4)**

1. **Ruler (Section 6.9.2)**
2. **Angle measurements (Section 6.9.3)**
3. **Parallelogram (Section 6.9.4)**
4. **Presets (Section 6.9.5)**
5. **Labels (Section 6.9.6)**

### 6.9.2 Ruler

To use the ruler, click at **Tools | Ruler** (  **F5**) or .

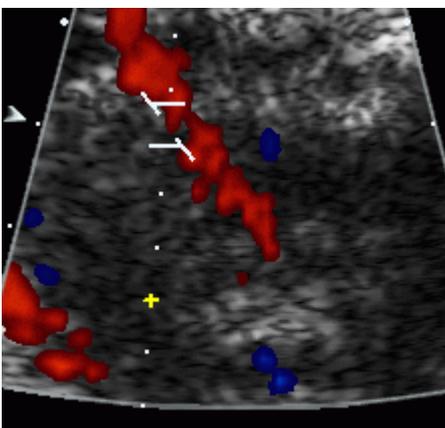
To use the ruler, click on two desired points of the ultrasound image. PixelFlux displays a green line connecting the points. The label indicates the length of the line. After you have calibrated the image, the unit will be in millimeter (mm), otherwise pixel.

The **mode**, which you currently use, is displayed in the status bar at the bottom of the main form. (E.g.  for ruler mode). The distance of the mouse pointer from the last ruler point will be displayed in the status bar, when using the ruler mode (in pixel resp. mm).

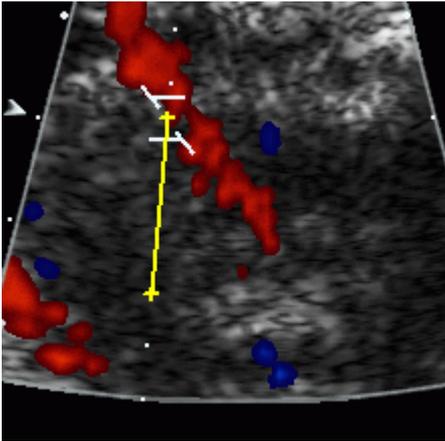
### 6.9.3 Angle measurement

PixelFlux enables you to measure user-defined angles in the image. Activate the angle mode by clicking on  or **Tools | Angle** (  **Shift+F5**). This activates the angle **click mode (Section 6.11.3)**.

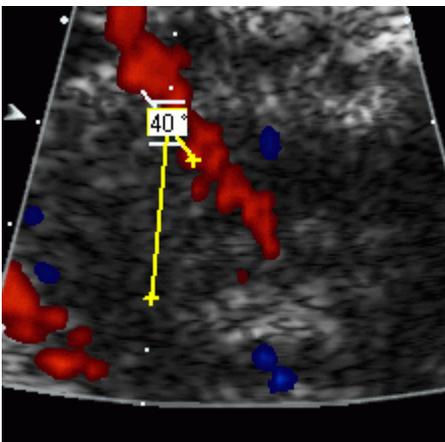
1st step: To measure an angle, click on a point lying on the first ray of the angle.



2nd step: Click on the vertex of the angle.



Third, click on the second ray. PixelFlux automatically shows the measured angle in the image (it always measures the acute or obtuse angle, respectively).



After you have performed an angle measurement, you can either perform another angle measurement by repeating the above steps or return to the perfusion examination or other modes. To return to the perfusion examination, click on the angle symbol again  (see above).

If you wish to assess the perfusion of single vessels using 3D or 4D measurement, it is usually necessary to measure the angle(s) of the vessel in the sagittal and in the frontal plane. See also the **Security advices for the use of the software (Section 3.4)**. PixelFlux has an option to facilitate this task: click on **Tools | 3D angles** (in the main menu or via right click on the image). Then, PixelFlux will activate the 3D angle **click mode (Section 6.11.3)**.

To measure the 3D angles, proceed as follows:

1. Click at the upper end of the vessel in the sagittal plane.
2. Click at the lower end of the vessel in the sagittal plane. (In contrast to the usual angle mode, you don't have to specify the second vertex of the angle, because it is supposed to be the vertical.)
3. Click at the upper end of the vessel in the frontal plane.
4. Finally, click at the lower end of the vessel in the frontal plane.

PixelFlux will automatically activate the angle correction (see **examination settings (Section 6.12.4)**) and copies the two angles in the appropriate input boxes. The corresponding 3D angle of the vessel will automatically be calculated and used for the subsequent examination.

## 6.9.4 Parallelogram

To use the parallelogram mode, switch to the parallelogram mode by clicking on **Tools | Parallelogram** or  or  or F6.

To set the parallelogram, click three times on the ultrasound image. This way you specify three vertices of the

parallelogram, the fourth vertex will be calculated and the parallelogram will be drawn. The lines will be labeled with their length (pixel or mm, see **ruler**). Similarly to the ruler, the distance of the current mouse position to the last specified parallelogram point is shown in the status bar. Additionally, you can use a **distance scheme (Section 6.10.6)** to define parallelograms with defined lengths of edges and angles.

You can modify the parallelogram by dragging the edges. Simply, place the mouse on one edge, press the left mouse button and move the edge accordingly. Likewise, move the entire rectangle by dragging the mouse in the center of the parallelogram.

## 6.9.5 Presets

Presets may help you to define the region of interest (ROI) of a perfusion examination in an objective manner. There are two kinds of presets:

1. parallelogram-based ones: either fixed or relative presets
2. ring-shaped presets based on a free ROI.

The presets are stored separately for each **user (Section 6.11.2)**.

**(Section 6.11.2)**

### Content

- **General use of presets**
- **Parallelogram-based presets**
- **Fixed parallelogram presets**
- **Relative parallelogram presets**

### General use of presets

The list of presets and the modes pertaining to them are located in the **tool window (Section 6.11.1)** "Presets".



To use the preset parallelogram for the region of interest, click on  or **Tools | Presets | Apply** (  F7). The perfusion examination will start automatically, provided the image calibration is completed.

To delete the selected preset(s), click on  or **Tools | Presets | Delete preset** (  F10). In the **Automode (Section 6.8)** you can also select multiple presets: to select multiple presets in a row, hold  Shift pressed and mark the first and last preset to be selected. Moreover, you can combine single presets by holding pressed  Ctrl while selecting them.

### Parallelogram-based presets

These presets are based on a parallelogram. There are two types, fixed and relative presets.

#### Fixed parallelogram presets

A fixed parallelogram preset is set up by fixing its four vertices. These are positioned absolutely, i.e., not with respect to another parallelogram as with the relative parallelogram presets below. Therefore, you can choose a parallelogram whose position and size is fixed for each measurement.

To add a fixed parallelogram, proceed as follows: first add a parallelogram having the size and position you want

(see above). Then, click at **Add fixed parallelogram** in the tool window and input a name for this preset. The new preset shows up in the list of your presets. If necessary you can add further presets the same way. Then, select the preset in the list. Then, PixelFlux will add a parallelogram and the ROI according to this preset. Then you can start the perfusion examination with this ROI (see above).

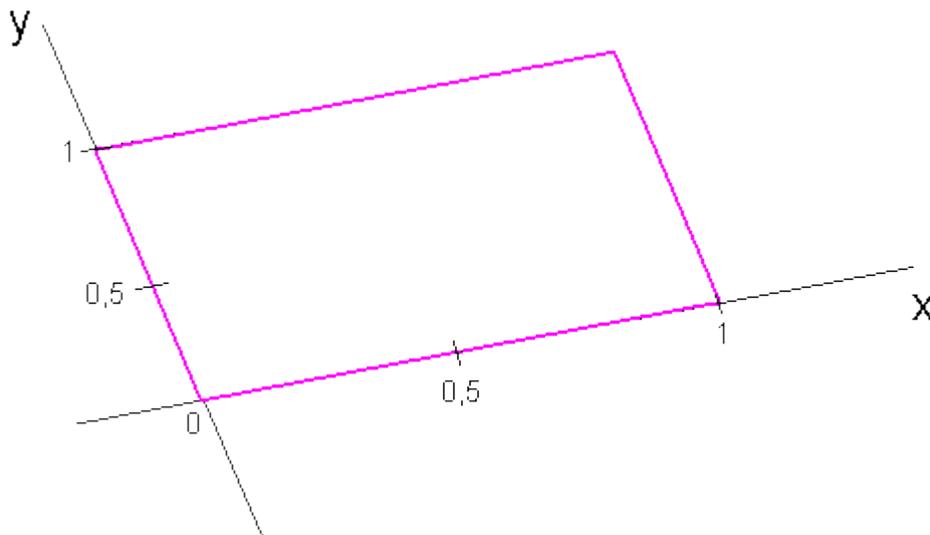
**Relative parallelogram presets**

This type of preset contains the following four values: height, width, movement in x-direction and movement in y-direction. These parameters specify another parallelogram which is called preset parallelogram (**pp**). The width parameter sets the width of the **pp** relatively to the width of the parallelogram (which you have set in the parallelogram mode). A width of 1 implies, that the **pp** is as wide as the parallelogram. 0.5 means that the **pp** is half as wide as the parallelogram etc. The height is referring to the height of the parallelogram.

The movement of the **pp** is defined this way: Each point of the image plane is defined by two coordinates:

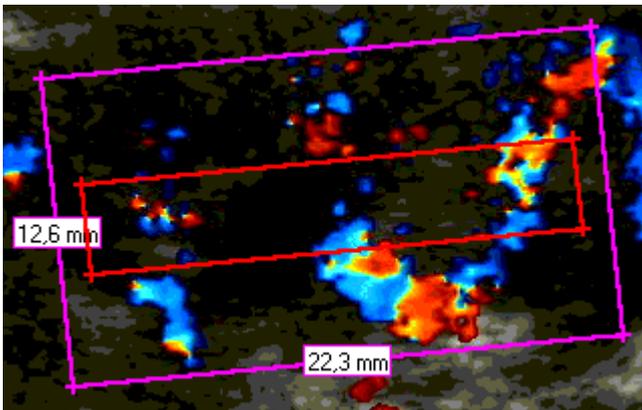
- left lower vertex of the parallelogram (x=0, y=0)
- left upper vertex of the parallelogram (x=0, y=1)
- right lower vertex of the parallelogram (x=1, y=0)
- right upper vertex of the parallelogram (x=1, y=1)

Therefore, each point of the image can be displayed with two coordinates via an appropriate stretching. The following image shows the parallelogram (violet) and the coordinates axes:

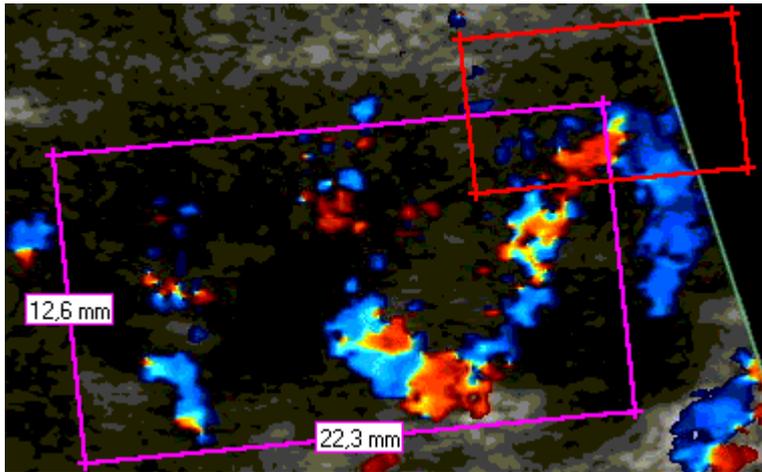


Now, the movement in x- and y-direction determines the center of the **pp**.

Here are some examples. Do not hesitate to "play" with the parameters to get a feeling for their meaning.



- width = 0.9
- height = 0.3
- movement in x-direction = 0.5
- movement in y-direction = 0.5, i.e. the center of the **pp** is just in the center of the parallelogram

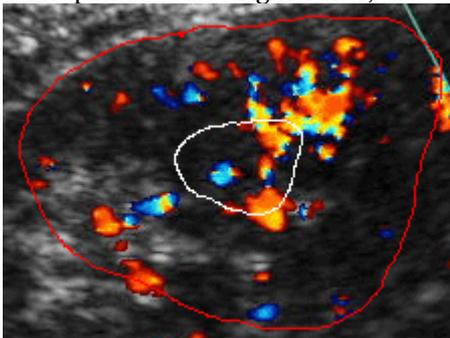


width = 0.5, i.e. the width of the **pp** is half the of width of the parallelogram  
 height = 0.5, i.e. the height of the **pp** is half the height of the parallelogram  
 movement in x-direction=1, movement in y-direction=1, i.e. the center of the **pp** is on the upper right edge of the parallelogram

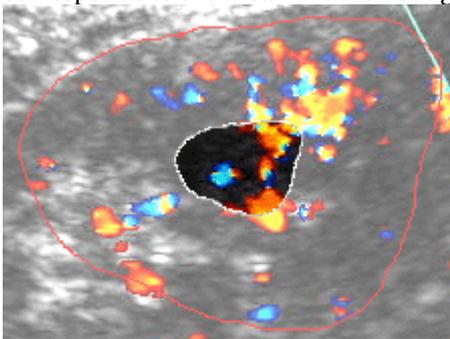
To add a preset, insert the desired values in the input boxes in the right part of the main window, then click on  or Tools | Presets | Add parallelogram (  F8). Each user can save their own presets.

**Free Presets**

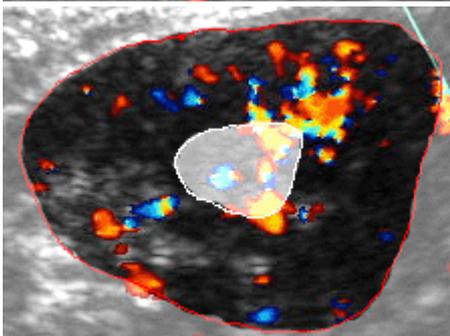
Starting from an user-defined ROI, define a new one via a stretching factor. In the sample images below the red line corresponds to the original ROI, the white line is (at the moment) an auxiliary line:



Now, you can select either the inner part or the rest ("ring") for the new ROI (in the sample images, the ROI corresponds to the area which is not lighter):



Inner part



Ring

The size of the new ROI (inner part or ring) is determined by the stretching factor. For example, if the stretching

factor is 0.5, the ROI is half the size (stretched from the center of the ROI) of the original one; 0.33 refers to a third... To add an "inner part"-preset, input the desired stretching factor and click on  or **Tools | Presets | Add inner preset** ( F9). To add a "ring"-preset, input the desired stretching factor and click on **Tools | Presets | Add ring** ( Shift+F9).

## 6.9.6 Label

You can add a label with an arrow in the image. This might be helpful for presenting your perfusion examinations etc. First, click at **Tools | label** ( Shift+F6) in the main menu or at the icon .

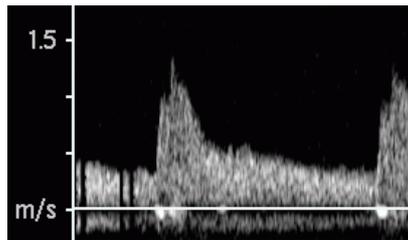
To add the label, click at the point you want to label, keep the mouse button pushed and move the mouse to where you want the end of the labelling arrow to be. Let the mouse button go and input the label in the edit box that appears. You can pick the last few labels you used earlier.

In order to move an existing label, repeat the above steps. In order to remove the label, click at  once again and remove the text in the edit box.

The label **click mode** (**Section 6.11.3**) will be deactivated automatically once you have added the label.

## 6.9.7 Spectral envelope analysis

PixelFlux has an integrated module for analyzing spectral curves of the following kind:



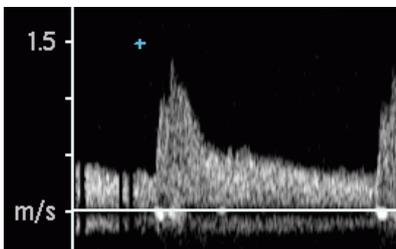
### Content

- [The spectral envelope analysis—Overview](#)
- [Results of the spectral envelope recognition](#)
- [Manual editing and correction of the curve](#)
- [Export the results](#)

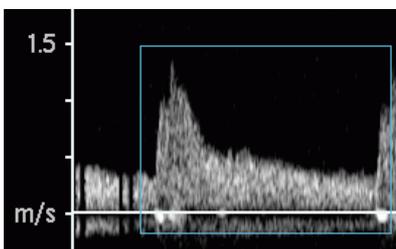
### The spectral envelope analysis—Overview

To analyze these curves, activate the envelope mode by clicking on  or **Tools | Envelope** ( F12).

1st step: first, you have to tell PixelFlux the area to be analyzed. Click on the **upper left corner** of a rectangle containing the desired area (x-coordinate: before the beginning of the wave, y-coordinate: above the maximum of the curve). The selected points will be marked with a light blue cross which appears after clicking.

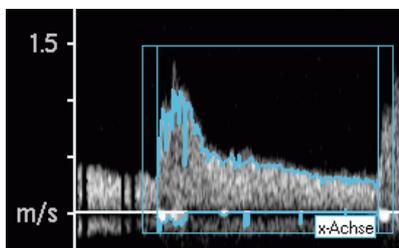


2nd step: click on the **lower right corner** (x-coordinate: *very close to the beginning of the systole of the next wave*, y-coordinate: below the (negative) maximum of the negative velocity). The area corresponding to these two points is marked with a light blue rectangle.



3rd step: click on the **x-axis (time axis)** of the chart. It is of no importance where exactly you click (i.e. the y-coordinate of the point is not important). As already noted PixelFlux shows the point with a small cross and with the caption "x-axis". Now, PixelFlux starts analyzing the envelope of the spectral curve. The spectral curves above and below the x-axis are analyzed (this step uses the contrast threshold, see **below**). PixelFlux shows the curves. They are used to determine which range of x-values (i.e. with respect to time) is really used for the analysis of the curve. First, the beginning is searched for after clicking on the point. Second, the end (i.e. the end of the diastole and the beginning of the new systole) is searched for and will be *very close* to the point you clicked on. Therefore, accuracy is particularly significant when clicking for the second time.

This range is depicted by two vertical lines (in the inner part of the rectangle). All further calculations refer to this range only.



Alternatively, you can specify the range which shall be analyzed manually. To do so, simply hold **Ctrl** pressed when clicking on the two points (of the first two steps).

4th step: Click on the **y-axis (velocity axis)** of the chart. It is recommended to click on a point of the scale which refers to a specific velocity (i.e. in the sample

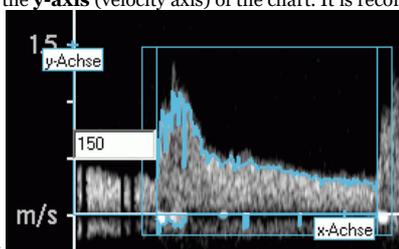


image at 1.5 m/s):

This point as well as the x- and y-axis are depicted. Then, input the velocity corresponding to the scale point of the 4th step. Use the *unit cm/s* in the sample image 150 cm/s (=1.5 m/s).

## Results of the spectral envelope recognition



The results are shown in the envelope window in different categories (labeled in bold letters)

**Velocities (cm/s):** You see the calculated (positive) maximal velocity and the minimal velocity. The latter is usually negative, but if there is no negative curve at all, PixelFlux shows the minimum positive velocity. Finally, you see the end-diastolic velocity.

**Average velocities (cm/s):** PixelFlux calculates the averages of the curves. The positive average refers to the positive curve and similarly for the negative one. The total average is just the sum of both.

**Flow volume (cm<sup>3</sup>/s):** When you input an area of ROI, the flow volume is calculated by multiplying the several average velocities by the area of the ROI. The unit of the volumes is cm<sup>3</sup>/s (=ml/s).

**Flow indices:** Finally, PixelFlux calculates RI (resistance index), PI (pulsatility index) and PPI (peak pulsatility index) according to the following formulae:

$$RI = \frac{v_{\max} - v_{\min}}{v_{\max}}, \quad PI = \frac{v_{\max} - v_{\min}}{\bar{v}}, \quad PPI = \frac{v_{\max} - v_{\text{end-diast.}}}{\bar{v}}$$

Here,  $v_{\max}$  denotes the maximum velocity,  $v_{\min}$  the minimum velocity,  $\bar{v}$  average maximum velocity (average of the maximal velocities at each point within the period) and  $v_{\text{end-diast.}}$  end-diastolic velocity. The last is taken from the positive curve, if the corresponding value is not too close to zero, otherwise from the negative curve.

### Further parameters

**Area of ROI (cm<sup>2</sup>):** To calculate flow volumes, input an area of the ROI. PixelFlux offers several possibilities: you can outline a ROI manually. (To stop the perfusion calculation, which normally starts automatically, click on [Windows | Examination details | Do not start examination yet](#) (F11), see [here \(Section 6.12.4\)](#)). When you have outlined a ROI, its area is automatically copied to [ROI \(active\)](#). If you have a circular vessel, you can input its diameter in cm and PixelFlux calculates the area of the vessel.

Additionally, you can input up to three additional values. This is necessary to eliminate deviations of the vessel size (for example because of potential inaccuracies in the image acquisition) by taking the average over several measurements. may be useful, if you have slightly oscillating vessel sizes or other difficulties in image acquisition. See also the **Security advices for the use of the software (Section 3.4)**. All areas which you may specify are used, and PixelFlux calculates the average of these areas. If you do not wish to consider the area of the ROI which was manually outlined, uncheck [ROI \(active\)](#). The average of all areas will be shown. Only this average will be used to calculate flow volumina (see above).

**Angle correction (°):** PixelFlux allows to easily correct the values by an angle correction. This is necessary to obtain the correct values if the vessel which you analyze is not perpendicular to the transducer surface. You can specify the angle between the vessel and the vertical. PixelFlux automatically calculates the

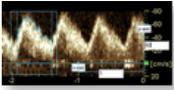
corrected values using the formula  $v = \frac{v_0}{\cos(\alpha)}$ , where  $v$  is the corrected velocity,  $v_0$  the uncorrected velocity resulting from the analysis of the spectral envelope and  $\alpha$  is the angle between the vessel and the vertical.



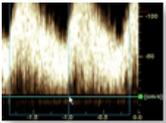
Some ultrasound devices show the vessel angle. Alternatively, you can measure [angles](#) with PixelFlux.

 If an angle correction was performed with the ultrasound device during or after the image acquisition, the angle correction must not be performed in PixelFlux.

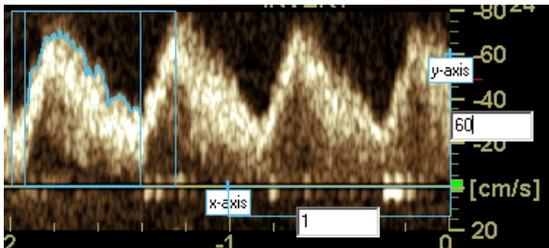
**Pulsation rate:** Optionally you can let PixelFlux calculate the pulsation rate, if the image you are using displays the time scale at the x-axis, such as in the following sample image:



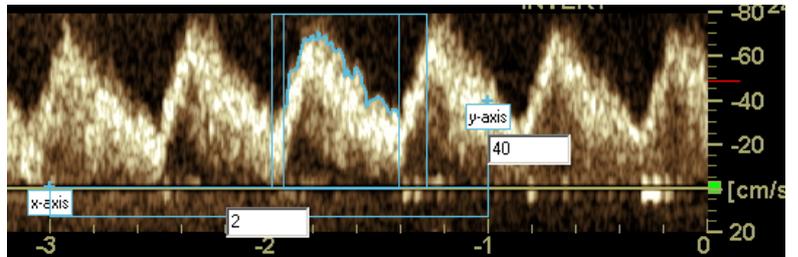
To do so, activate the check box **Calculate pulsation frequency** in the envelope tool window. Then, proceed as follows: do the first to steps as usual (see above). However, be sure to select only *one single cycle* (not multiple ones). In the third step, you will have to consider two requirements: firstly, the point you click at has to lie on the x-axis. Secondly, the point should be located above some point showing a tick mark of the time scale:



The cross-hair moving with the mouse pointer helps you positioning the point: move the mouse such that the horizontal line is at the x-axis while the vertical line hits a tick mark of the time scale (the tick marks are usually depicted under the scale). In the above sample the point was selected at -1 sec. In the fourth step click at a point that is located (with respect to its vertical or y-coordinate) at the height of some tick mark of the y-axis (velocity axis) and, with respect to its horizontal or x-coordinate) above some tick mark of the x-axis. Many manufacturers display the y-axis (usually at the right side of the chart) labelled with 0 seconds (or similarly), so that you can click at the y-axis in that case. The points you have clicked at are labelled with "x-axis" and "y-axis", as described above. Now, you input the velocity value in the input box at the y-axis (as described above). Finally, you input the *difference* of the two x-values (as seen from the two tick marks the points lie over) into the input box beneath the x-axis. The following two examples illustrate the procedure:



At the y-axis the tick mark 40 cm/s was clicked at. At the x-axis it was clicked at the point -1 second. Thus, the input boxes contain the value 60 (y-axis; i.e., 60 cm/s) and 1 (x-axis, i.e., 1 second).



In this sample the third point was put at the x-axis, at the point -3 seconds. The fourth point was (mainly for illustrating purposes here) chosen at the x-value -1 second, the y-value is 40 cm/s. (The point lies at the height of the tick mark 40 cm/s). Thus the input boxes have to be filled with 40 (cm/s) and 2 (x-axis, that is 2 seconds).

After inputting these data the envelope tool window displays the pulsation rate in 1 per minute, that is, "80" signifies a pulsation rate of 80 per minute. The setting, whether you want to let PixelFlux compute the pulsation rate will be saved when you shut down PixelFlux, so that you find the same setting when restarting the program. In order to deactivate the calculation of the pulsation rate, uncheck the checkbox **Calculate pulsation frequency** in the envelope tool window.

### Manual editing and correction of the curve

**Contrast threshold** The setting of the contrast threshold allows you to analyze images with different image brightnesses and qualities. The spectral envelope recognition works as follows: points in the image which are brighter than the threshold are considered to belong to the spectral curve, the darker ones are considered not to belong to the curve. Therefore, the threshold affects the result of the analysis. If the threshold is lower, more pixels are considered to belong to the curve.

The default value of the threshold is 50. We recommend not to change the threshold during a scientific study etc., as this may affect your results.



contrast threshold 50.  
(100 corresponds to white, 0 corresponds to black)



contrast threshold 30

### Correcting the curve manually

You can correct the automatic recognition of the curve manually. Proceed as follows: Press the **Ctrl** key, hold it down and outline the part of the curve (with the left mouse button pressed) which you wish to correct. When releasing the mouse button, the positive curve will be corrected. When you use the right mouse button, the negative curve will be corrected. When you additionally press Shift, the curve (positive or negative according to the mouse button) is interpolated linearly, i.e. only start and end point of your mouse movement are taken and between them a linear interpolation is done. In all cases, the corrected curve will be shown and all results are recalculated automatically.

### Export the results

You can export the results of the envelope analysis to the clipboard by clicking on **Export | Export current examination**. By clicking on **Export | Export settings** you may specify which items of the current exam shall be exported. See **Exporting data (Section 9.5)** for further information. The values are separated by tabs, so that you can edit them easily in software such as Microsoft Excel or OpenOffice.

Alternatively, you can click on  to save the examination in the database.

## 6.10 Options

## 6.10.1 Options - overview

You can customize PixelFlux in various ways in order to obtain the best performance you need personally. To access the options, click on **File | Options ...** in the main menu of the **main window (Section 6.1)**.

**(Section 6.1)(Section 6.1)(Section 6.1)(Section 6.1)**

The options are divided in the following sections. You will find these options on the corresponding tab sheets.

1. **General options (Section 6.10.2)** (program startup, log file, further options including use for veterinary purposes)
2. **Automatic recognition (Section 6.10.4)** of the maximum velocity
3. **Settings concerning the perfusion relief (Section 6.10.5)**
4. **Position help for the parallelogram (Section 6.10.6)**
5. **Settings concerning image calibration (Section 6.10.7)** (color scale and semi-automatic cm calibration)
6. **Warnings (Section 6.10.8)**

## 6.10.2 General options

There are a number of general **options (Section 6.10.1)** that influence the general program flow of PixelFlux.

### Contents

- **Show DICOM-open-dialog when PixelFlux starts**
- **Do not show user dialog automatically**
- **Create a log file**
- **Use PixelFlux in veterinary medicine (without dates of birth)**
- **Do not analyze huge DICOM headers**
- **Use non-standard routine for bmp files**

### Show DICOM-open-dialog when PixelFlux starts

Activate this option to start PixelFlux with the usual dialog to open a DICOM file. This way, you will not have to click on **File | Open**.

### Do not show user dialog automatically

This option is useful, if you have only one user. Check this option, if you do not wish that PixelFlux shows the user dialog when PixelFlux starts. Then, you can change the user with **File | User ...**.

### Create a log file

If PixelFlux does not work as expected, you can help facilitate the analysis of PixelFlux. Check the third item in the options list. Now, if an error occurs, please **send (Section 3.1)** us the file "[installation directory]/User/[user name]/log.txt". ([installation directory] refers to the directory where PixelFlux is installed, often "C:/Programs/PixelFlux", [user name] is the name of the current user). Only internal information concerning PixelFlux is stored in this file. The entries in the file have the following format:

[date]-[time]-[identification no. of the process]-[parameter]

Please click **here (Section 6.10.3)** to receive further information on these topics.

PixelFlux automatically deletes entries which are older than one week. Alternatively, you may empty the log file manually. Simply click on **Empty log file** at the **Other options** tabsheet.

### Use PixelFlux in veterinary medicine (without dates of birth)

This option is to facilitate the use of PixelFlux in veterinary medicine. Activate the option if you do not know the date of birth of the patients or if you do not wish to specify it. Then, PixelFlux will not ask you for the date of birth (esp. not in the database). Instead of the patient's name you can specify an animal number or other numeric value.

### Do not analyze huge DICOM headers

Some ultrasound manufacturers make huge DICOM header appendices. As the analyzing of these huge appendices takes PixelFlux much time, you can deactivate it. The normal DICOM contents (image data, patient data etc.) will not be affected by this option. It is recommended that you enable this option.

### Use non-standard routine for bmp files

This option is for unusual bmp formats. Please do not use this option, unless Chameleon Software specifically recommends it.

## 6.10.3 Log file

An entry of the form

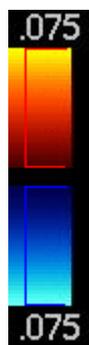
05/02/12-14:53:40-[procedure]-[parameter list]

means, that PixelFlux did the mentioned procedure on 05/02/12 at 14:53:40. The meaning of the parameters may change (depending on the procedure).

## 6.10.4 Automatic maximum velocity recognition

This **option (Section 6.10.1)** allows to use a procedure which recognizes the **maximum Doppler velocity (Section 6.3)** of your DICOM or video files. To use this option, proceed as follows:

1. Check the checkbox **Use automatic velocity recognition** in the tab sheet **Automatic maximum velocity recognition** to activate this mode.
2. To configure this mode, click the button **Open file** and open a **typical** file (video or DICOM file). The file will be displayed in the left part of the register card. Make sure that the color scale is detected properly. If it is not, please **send (Section 3.1)** us this file and try again with another file.

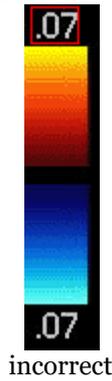


Now, specify the rectangle which depicts the maximum velocity: Press the left mouse button in the upper left corner, move the mouse to the lower right corner and release the mouse button. The rectangle will be displayed in the image (see sample below).

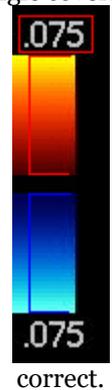
If you mis-click, simply try again.

The position of this rectangle is relative to the color scale. It is important that the rectangle contains the whole text.

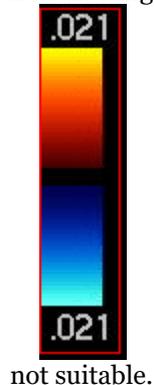
Avoid a rectangle being too narrow, especially in the horizontal direction.



The first image (subtitled "incorrect") will give incorrect results, if there are any images like the following. PixelFlux will read the image as 7 cm/s, since the narrow rectangle covers only the "0.7", but not the "5".

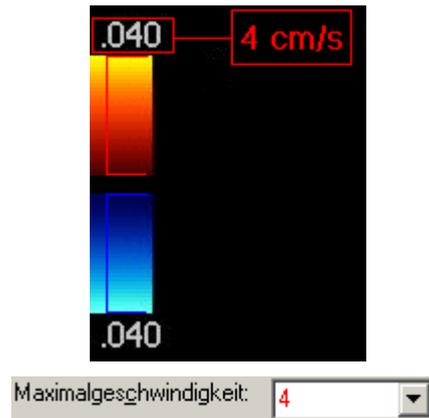


PixelFlux supposes that the maximal velocity of the red and the blue part of the color scale are equal, i.e., it is sufficient to recognize only one of them. Therefore, the following setting is not suitable:



- The two tolerances allow PixelFlux to accept images which are slightly different from the existing ones. It is highly recommended to change the default values (1st tolerance = 30, 2nd tolerance = 5) only after consulting Chameleon Software.

The recognition mechanism is based on the principle that PixelFlux tries to recognize the velocity, whenever you open a DICOM or video file. If this is successful, it will be displayed in the image and in the velocity input box (in red):



If the recognition is not successful, simply calibrate the image as usual (i.e. input the velocity in the velocity input box). When performing a measurement, PixelFlux registers the combination of image (the specified small rectangle) and the velocity and uses this combination for further recognitions. Therefore, it is important that you input the correct velocity when using the option . If your velocity input was incorrect, you may delete the incorrect combination (which would be used otherwise for future perfusion examinations): click on the corresponding item in the third register card **Recognized velocities** and press **Del** to delete it.

<b>5.0</b>	<b>10.0</b>	<b>2.1</b>
5	10	2,7

Here, the first two items are correct, the third is incorrect. Additionally, you can edit the corresponding velocity. Simply mark the item if you wish to correct, press **F2** and input the correct velocity.

If you should temporarily change the size of the recognition rectangle (see above), any previously recorded velocity recognition patterns are no longer usable. In this case, a note shall appear in the list of velocity patterns.

### 6.10.5 Options - perfusion relief

A very useful feature of PixelFlux is the **perfusion relief (Section 7.4)**. It allows you to get a quick visual impression of the perfusion of the ROI. In the **options (Section 6.10.1)**, in the tab sheet **Perfusion relief**, you can specify the colors which are used for the representation of the relief. There are three colors to specify. The first is the color which will be used if the perfusion parameter at the corresponding point is zero. The second corresponds to the half of the maximum. The third is the color corresponding to the maximum.

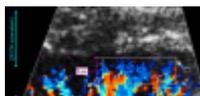
It is recommended to select a dark color (e.g. black) for the first one, because normally large parts of the ROI are only little perfused. The second is by default white and the third red.

You can change the colors by clicking on the coloured panels.

### 6.10.6 Position help for parallelogramm

When you use the **parallelogram tool (Section 6.9.1)**, PixelFlux can help you set up parallelograms with defined lengths of edges and angles. To do so, activate the **option (Section 6.10.1) Use position help for parallelogram**.

When you define a parallelogram, PixelFlux will then highlight those points in the image such that the resulting parallelogram will have defined lengths of edges and angles with respect to the horizontal line.



In this example the first edge of the parallelogram has already been fixed. The minimum distance of the next (third) vertex to the reference vertex (the last one that has been set) is 5 millimeter, the maximum distance is 40 millimeter, the step width is 5 mm. This means that points having a distance of 5, 10, 15, 20, 25, 30, 35, or 40 millimeter shall be shown. Moreover, the angle step width was 90 degrees, which implies that only points are shown that are either vertically above or below the reference point or horizontally right or left to it.

The default values of minimum distance etc. can be changed in the register card **Position help for parallelogramm**.

Moreover, you can tell PixelFlux to allow only edges having these specified lengths and angles. To do so, activate the checkbox `allow parallelograms with these values only`.

## 6.10.7 Options - calibration

The calibration **options (Section 6.10.1)** are at your disposal to simplify the image calibration, especially what concerns the color scale and the cm/distance calibration. These options are located in the tab sheet `Calibration`.

### (Section 6.10.1)

#### Content

- **Check color scale**
- **Color scale recognition**
- **Special scale recognition algorithm**
- **Position of the color scale**
- **Color settings for color scale recognition**
- **Semi-automatic cm calibration**

### Check color scale

You can specify whether the color scale shall be checked when you start a perfusion examination. If you do not wish that, uncheck the checkbox `Check color scale using the existing color scale profiles`. Moreover, you can delete the list of currently saved color scale profiles. Click **here (Section 6.7)** for further information concerning this mode.

### Color scale recognition

There are a number of settings that refine the color scale search. In general, you should not need to change any one these values. If in doubt, **send us (Section 3.1)** sample videos to help you determine the optimal values.

### Special scale recognition algorithm

This option is for videos whose scale is extremely difficult to recognize. You can tell PixelFlux to use a different algorithm to detect the color scale. Please use this option only with specific recommendation by Chameleon Software.

### Position of the color scale

`Color tolerance` is intended for fine tuning of PixelFlux' internal color scale recognition algorithm. Do not modify this value without specific recommendation by Chameleon Software. The default value is 50 and this will work for videos generated by most ultrasound devices. The lower the value, the more colors that will be eligible to be "colorful", (i.e. potentially carrying a perfusion information) as opposed to those pixels which are more or less gray. Changing the value out of a reasonable range will strongly affect the results. Changing the value within reasonable bounds may slightly change the outcomes, therefore be advised not to change this setting once you have found a working setting. See also the **Security advices for the use of the software (Section 3.4)**.

`Look for color scale at both image borders`, `Look for color scale at left image border only`, and `Look for color scale at right image border only` allow to restrict the search of the color scale at the left or right border of the image. By default, the first option is activated, that is to say, PixelFlux searches the scale both at the left and the right border.

`margin to upper image border (pixel)` allows to exclude the upper part of the image for the purposes of the color scale recognition. Many manufacturers display a (sometimes slightly coloured) bar at the very top of the image. In order to tell PixelFlux to skip that upper section, you can set this value. The default value is 40. The color scale will only be searched underneath this y-coordinate. Thus, if your images do not have such a colored bar at the top of the image, and the color scale is situated closely to the upper border of the image, the value may be changed to 0.

`margin to lateral image border (pixel)` has a similar effect: it excludes a given margin from the right and left border of

the image. The default value is 5, that is, by default the color scale is only searched 5 pixels (or more) right to the left image border and conversely at the right image border.

### Color settings for color scale recognition

If you check the option **Admit all colors for measurement**, pixels not closely matching the colors of the color scale will also be admitted to the perfusion examination. In this case, the color of the color scale that is closest to the color of the pixel in question will be associated to this pixel. You can set up a maximal distance that must not be exceeded using **Maximal color distance**. These options should only be used after explicit recommendation by Chameleon Software. You can also monitor the assignment of colors in the image with the ones in the color scale using the **color scale tool window (Section 6.12.6)**.

### Semi-automatic cm calibration

You can specify whether the semi-automatic cm/distance calibration is used. Please click **here (Section 6.3)** for further information on this function.

## 6.10.8 Options - warnings

These **options (Section 6.10.1)** allow you to set which checks will be performed by PixelFlux to ensure the validity of your perfusion examinations.

For each type of warning you can disable the corresponding check. Moreover, in the context of an examination using **automode (Section 6.8)**, you can determine whether an examination with a warning should or should not be stored in the database.

For a detailed description of how the various warnings work and further options concerning these options, please click **here (Section 6.7)**.

## 6.11 Program handling

### 6.11.1 Overview of the tool windows

The tool windows allow you to use the functions of the **Overview of the main module (Section 6.1)** of PixelFlux in an easy way.

#### Content

- **List**
- **Handling**

#### List

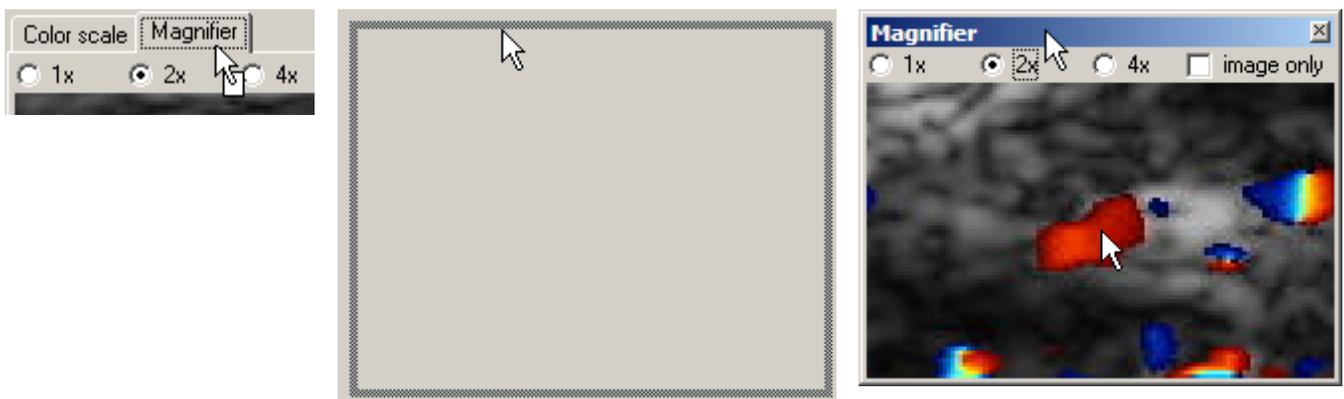
There are the following tool windows:

1.  **Presets (Section 6.9.1)** for adding, managing and applying presets
2.  **File information (Section 6.12.2)** (concerning the video file in general and DICOM header, if applicable)
3.  **Automode (Section 6.8)** displays a list of the examinations in the current automode script (if the automode is active)
4.  **Examination details (Section 6.12.4)** enables you to choose what is examined and to specify further examination settings such as angle correction
5.  **Envelope (Section 6.9.7)** for spectral analysis of curves

6.  **Calibration settings (Section 6.12.6)** for settings concerning the color scale and the distance calibration
7.  **Magnifier (Section 6.12.7)**
8.  **Shape analysis (Section 6.12.8)**
9.  **Direct help (Section 6.12.10)**
10.  **Quickview (Section 6.12.9)** (summary of the last few measurements)

## Handling

By default, these windows are aligned to the docking areas in the right and lower part of the main window. To move them, press the left mouse button on the corresponding register card. Keep the mouse button pressed and drag the window anywhere on the screen, including the other docking stations.



To show or hide a window, click on **Windows | Presets visible** or the corresponding other menu items. Of course, you can also hide a window by clicking on the small cross at the upper right border of the windows.

The positions and docking positions, i.e. the position where the windows are docked (if they are) are saved, when you quit PixelFlux. Therefore, you will find your PixelFlux desktop unchanged, when you restart PixelFlux later on.

## 6.11.2 User profiles

You can set up different user profiles. This way, you can easily handle different users of PixelFlux in a network... When first starting PixelFlux, a new default user profile will be created automatically.

The user profile includes the following information:

- user name
- directory of patient files: all patient files created by the user (.ppp) are stored in this directory.
- presets. **Presets (Section 6.9.1)** allow pre-defined settings, reproducible ROI's.
- directory of video, DICOM and analysis files. When you open a video or DICOM file or a analysis file, PixelFlux updates the corresponding path. Therefore, when PixelFlux shows an open dialog, it always shows the directory of the file you used most recently.

You can change the current user by clicking on **File | User ...** (**Ctrl + U**) in the main menu of the **main module (Section 6.1)**.

To add a new user, click on **New**, input the user's name and choose the patient directory. The default directory is *X/Patienten*, where *X* is the directory where PixelFlux is installed. **Delete** removes the selected user, **Edit** allow to change the user's name or the patient directory.

 To avoid that the user dialog appears every time you start PixelFlux, use the **corresponding option (Section 6.10.2)**.

## 6.11.3 Click mode

The handling of the main module of PixelFlux is organized by click modi. This means that the action, which PixelFlux will perform after you have clicked on the image, depends on the currently active mode. For example, if the angle mode is active, the click will be recognized for the specification of the angle measurement.

The following modes exist:

-  distance calibration - This mode will be activated after opening a file, to help you to calibrate the image. See **image calibration (Section 6.3)**.
-  ROI - This is the mode for the specification of the region of interest. See **specification of ROI (Section 6.5)**.
-  Set the color scale position manually. Helps you to specify the position of the color scale **manually (Section 6.3)**, in case PixelFlux did not recognize it properly.
-  Ruler - for measuring of **distances (Section 6.9.1)** in the image.
-  Angle - for measuring of **angles (Section 6.9.1)**, e.g. for later angle correction.
-  Parallelogram - for the use of **parallelograms (Section 6.9.1)** and later use of parallelogram-based **presets (Section 6.9.1)**.
-  Envelope - for the analysis of **spektral curves (Section 6.9.7)**.
-  Copy (part of) image - for **copying (Section 9.1)** the whole image or rectangular parts of the image.
-  **Shape analysis (Section 6.12.8)** - for analyzing the curvature and related entities of shapes.

You can see the currently active mode in the status bar on the lower border of the main form. To activate a particular mode, click on the corresponding menu item or button (see the corresponding descriptions above). The ROI mode is active by default.

## 6.12 Tool windows

### 6.12.1 Overview of the tool windows

The tool windows allow you to use the functions of the **Overview of the main module (Section 6.1)** of PixelFlux in an easy way.

#### Content

- **List**
- **Handling**

#### List

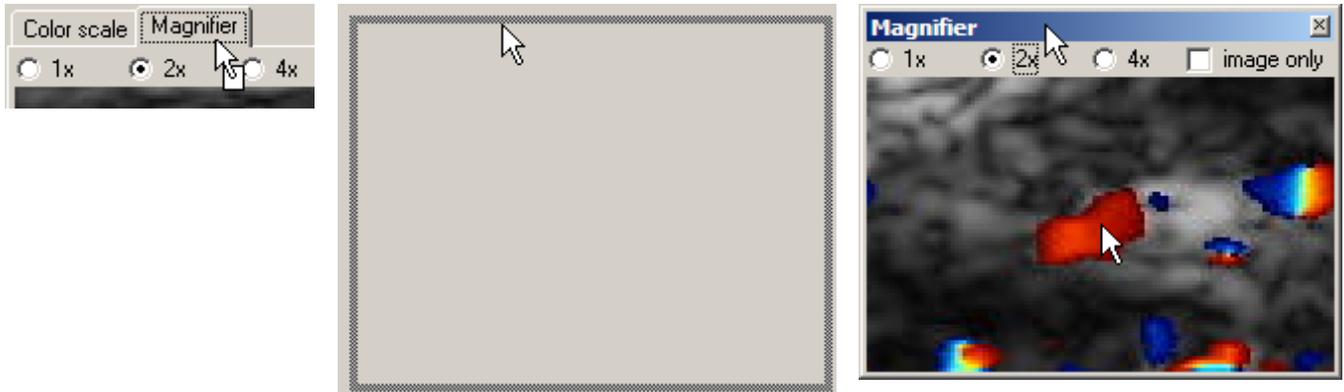
There are the following tool windows:

1.  **Presets (Section 6.9.1)** for adding, managing and applying presets
2.  **File information (Section 6.12.2)** (concerning the video file in general and DICOM header, if applicable)
3.  **Automode (Section 6.8)** displays a list of the examinations in the current automode script (if the automode is active)
4.  **Examination details (Section 6.12.4)** enables you to choose what is examined and to specify further examination settings such as angle correction
5.  **Envelope (Section 6.9.7)** for spectral analysis of curves
6.  **Calibration settings (Section 6.12.6)** for settings concerning the color scale and the distance calibration
7.  **Magnifier (Section 6.12.7)**
8.  **Shape analysis (Section 6.12.8)**
9.  **Direct help (Section 6.12.10)**

10.  **Quickview (Section 6.12.9)** (summary of the last few measurements)

## Handling

By default, these windows are aligned to the docking areas in the right and lower part of the main window. To move them, press the left mouse button on the corresponding areas register card. Keep the mouse button pressed and drag the window anywhere on the screen, including the other docking stations.



To show or hide a window, click on **Windows | Presets visible** or the corresponding other menu items. Of course, you can also hide a window by clicking on the small cross at the upper right border of the windows.

The positions and docking positions, i.e. the position where the windows are docked (if they are) are saved, when you quit PixelFlux. Therefore, you will find your PixelFlux desktop unchanged, when you restart PixelFlux later on.

## 6.12.2 File information

The **tool window (Section 6.11.1)** concerning file and examination information displays some pieces of information related to the currently opened video or DICOM file in the **main module (Section 6.1)**. As with other tool windows, it can be displayed and hidden using the menu item in the menu **Windows**.

The tool window shows the patient information (name, first name, date of birth) and examination information (date of examination, and possibly color frequency, automatically recognised scale). These can only be retrieved from DICOM headers, but not from video (avi) files. Moreover, you see some general file information (file name, file type etc.), as well as the complete content of the DICOM header. The table contains all header information of the file which are coherent to the DICOM standard 3.0.

You can save the content of the DICOM header, as it is shown in the list, in a text file by clicking at **Save**.

 The patient and examination information from the DICOM header are taken automatically to the database if you create a new patients. See also the **Security advices for the use of the software (Section 3.4)**.

### Exporting DICOM header information into the database

You can tell PixelFlux to export DICOM header information into the patient files that are stored in the **database (Section 8.1)**. To do so, check the box next to those fields that you want to export. For example, to save the field describing the modality of your ultrasound device is stored in the field [0008, 0060], according to the DICOM 3.0 protocol. Thus, open the tree at the item [0008] DICOM header section (if present) and in there, click at the node [0060] Modality. Now, whenever you do a measurement, the content of this modality field will be overtaken in your patient file. Finally, you can **export (Section 9.5)** these (and other settings) to a third-party application, such as a spreadsheet calculator.

 The DICOM header information will only be present in the patient file if the setting was set before the examination was done. In other words, it is not possible to extract the DICOM header information from the DICOM file to the patient file a posteriori.

## 6.12.3 Automode

The automatic mode or, for brevity "Automode" helps you saving time by performing the perfusion examinations in your absence.

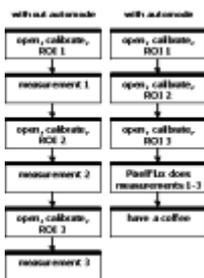
## Content &nbsp;

- [Overview](#)
- [How to](#)

## Overview

If you want to undertake many examinations, the automatic mode is very useful. By this, it is possible to tell PixelFlux which videos and regions of interest you wish to examine. After this, PixelFlux performs the perfusion calculation.

The automatic modus, or simply automode, works as follows:



## How to

Create a new automode file. This file contains all information about which examinations have to be processed later on. Click on [Auto mode | New](#) or  and select the file name of the automode file. PixelFlux creates an empty file. Now, the automatic mode is active. You will see that the title bar of the main form changes to "PixelFlux Scientific automatic mode" instead of "PixelFlux Scientific".

Alternatively, when you already have created an automode file and wish to continue working with that automode file later on, you can reopen it with [Auto mode | Open](#) or . (Likewise, you can close the automode file, if you wish to quit the automatic modus, by clicking on [Auto mode | Close](#).)

To work with the automode, proceed as follows:

1. Open an image, video or DICOM as you usually do (see [open video sources \(Section 6.2.1\)](#)), perform the calibration as usual (see [calibration \(Section 6.3\)](#)). Outline the region of interest as usual (see [region of interest \(Section 6.5\)](#)). Now, the automodus begins to work: normally the perfusion examination would start immediately. But when the automode is active, the examination will not be performed. Instead, you have to specify the **examination data (Section 8.5.1)** and the information on the patient. Then, it may seem that PixelFlux does nothing. However, this is not true. PixelFlux stores the examination information in the automode file you specified in the first step. You can see the examinations in the automode file in the corresponding list in the automode tool window. PixelFlux shows the surname, the first name and the date of birth of the patient to be examined.
2. You may repeat the previous step, until all of your examinations are stored. If you wish to delete some examinations in the automode script, just select one or more items from the automode list (displayed in the **automode tool window (Section 6.11.1)**) and click on [Auto mode | Delete item](#)  **Ctrl + Del**.
3. When all your examinations are completed, start the automode and PixelFlux will perform the examinations. Click on [Auto mode | Start](#) or . PixelFlux will show all examinations with their details (surname, first name, patient's date of birth, organ, part of the organ, video file). PixelFlux begins to compute the perfusion parameters. The examination being processed, a blue arrow  appears. When an examination has been successfully processed, a green checkmark  appears. If a warning occurred, a yellow exclamation mark  is shown. If an error occurred, a red exclamation mark  appears. You can cancel the automode with [Auto mode | Pause](#) or by pressing  **Escape**.

The perfusion examinations are automatically stored in the file according to the patient you specified. When you use DICOM files, the patient information is taken from the DICOM header, so that you will not have to insert it.

PixelFlux will perform certain plausibility checks, see **Notifications and Warnings (Section 6.7)**. The resulting warnings will be displayed in the results list in the automode **tool window (Section 6.11.1)**. If one or more warnings are issued, the examination will not be stored to the database, unless you change the corresponding **option (Section 6.10.8)**.



When you use video or DICOM files from a CD, this CD has to be available when the automode script is executed.

## 6.12.4 Examination settings

PixelFlux allows the use of certain settings influencing the perfusion examinations. You find these settings in the examination **tool window (Section 6.11.1)**.

You can specify what quantity PixelFlux is supposed to measure. Moreover, there are various ways of doing an angle correction for perfusion examinations of single vessels. Also for single vessels, you can let PixelFlux compute the ROI automatically. Finally, you can ignore the period and do not let the examination start directly after specifying the ROI.

**(Section 6.11.1)(Section 6.11.1)(Section 6.11.1)(Section 6.11.1)**

### Inhalt

- **Examination**
- **Angle correction**
- **Angle correction in frontal plane**
- **Automatically determining sagittal and frontal angles by the shape of the vessel**
- **Angle correction for ROI in horizontal plane (in 3D mode)**
- **Automatically determining the single vessel ROI**
- **Ignore period**
- **Cancel normal examination**

### Examination

There are several quantities PixelFlux can examine.

First of all, the standard perfusion examination by analyzing the colored parts of every single image. This includes the pulsed wave (also called power-mode) and the color duplex. Second, there is a grayscale mode, which considers each point in the ROI according to their brightness. Third, there is a mode which simply measures areas of user-defined ROIs.

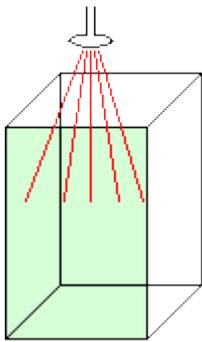
You can choose the currently active mode in the examination **tool window (Section 6.11.1)**. If this tool window is invisible, activate it by clicking on **Windows | Examination details** (in the main menu). There you can choose the corresponding mode by using the icons  (color mode),  (grayscale mode), or  (area measurement).

The currently active mode is shown in the status bar at the bottom of the main form. In the color mode, depending on whether PixelFlux detects a color scale consisting of one or two parts, the power mode icon  or the color duplex icon  appears. In both color modes the color scale has to be detected. In most videos this is automatically carried out by PixelFlux when you **open (Section 6.2.1)** the video file. However, you can set the **color scale (Section 6.3)** manually.

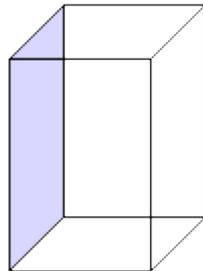
### Angle correction

The angle correction has to be employed if you want to perform a perfusion examination of a single vessel whose direction is not perpendicular to the transducer. An angle correction is not possible when you do perfusion examinations of multiple vessels or branched or chaotic vessel structures. Also see the **Security advices for the use of the software (Section 3.4)**.

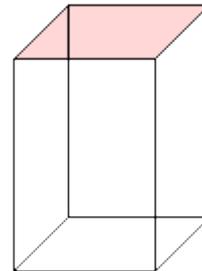
Before explaining the various ways you can do an angle correction, we explain a few fundamental facts concerning the various planes you might encounter in 2D and 3D ultrasound.



frontal plane (light green) with rays emanating from the transducer (red)



sagittal plane



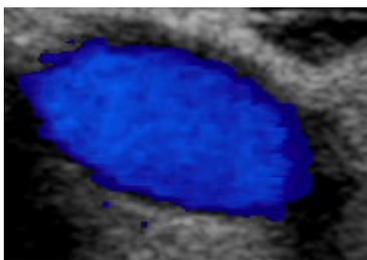
horizontal plane

The frontal plane is the one that you see in usual 2D ultrasound, i.e., the plane consisting of the rays emanating from the transducer. The sagittal plane and the horizontal plane are both perpendicular to the frontal plane. The horizontal plane can be described as the one lying parallel to the surface of the transducer. 3D ultrasound devices (as opposed to the usual 2D) will depict all these three planes. The angle correction depends in what plane you do the perfusion examination. There are two fundamentally different situations: firstly, your ROI lies in the **frontal plane**, as is always the case in 2D ultrasound. To do an angle correction for a ROI in the frontal plane, check **ROI in frontal plane (2D)**. Secondly, your ROI can be taken in the **horizontal plane** (which is only possible with 3D ultrasound devices). In this case, check **ROI in horizontal plane (3D)**. No angle correction is done when you check **no angle correction**.

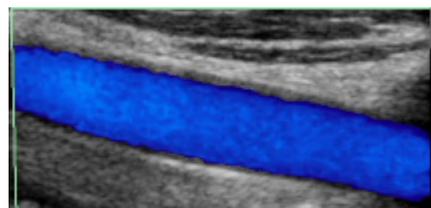
### Angle correction in frontal plane

In order to apply the angle correction in the frontal plane, two requirements have to be met:

1. The three-dimensional shape of the single vessel needs to be a *cylinder*. In particular, it is not possible to use this mode when the vessel is distorted from the natural cylindrical shape, for example due to external pressure onto the vessel.
2. The shape of the vessel, as you see it in your frontal plane ultrasound image needs to be an *ellipse*, as opposed to a longitudinal cut, where in the transducer image the vessel is shown as a an (approximately) rectangular shape.



A typical elliptic cut of a single vessel. Angle correction is possible.

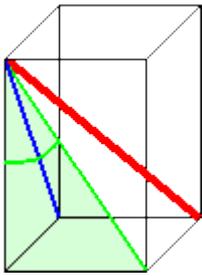


A longitudinal cut of a single vessel. Angle correction is not possible.

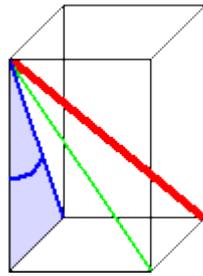


Whenever possible, it is advisable to position the transducer such that the resulting sagittal and frontal angles are small. The sagittal angle is small if the ellipse you are seeing is eccentric (as opposed to a circle, where the two semi-axes have equal length). The frontal angle is small if the direction of the longer semi-axis is close to the vertical. Angle corrections with high angles tend to be more susceptible for deviations of the resulting perfusion parameters.

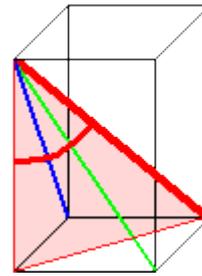
In order to perform an angle for single vessels in the frontal plane correction, you need to input the sagittal angle and the frontal angle of the vessel towards the transducer. These two angles are used by PixelFlux to calculate the total angle. The following schematic depictions explains these three angles: the red ray is the blood vessel, the light green plane is the frontal plane featuring the frontal angle, while the light blue plane is the sagittal plane, the sagittal angle is shown in dark blue. The transducer points vertically from top to bottom:



frontal plane (light green) with frontal angle (dark green)



sagittal plane (light blue) with sagittal angle (dark blue)



total angle between vessel (red thick diagonal line) and transducer ray (left frontal vertical edge of the box)

Input the frontal and sagittal angles in the edit boxes `angle in frontal plane (°)` and `angle in sagittal plane (°)`, respectively. The unit is °, i.e. 0° represents a vertical vessel (i.e., running directly towards the transducer), whereas 90° is a horizontal vessel. PixelFlux will automatically calculate the total angle for you and will display it at `Angle of the vessel (°)`.

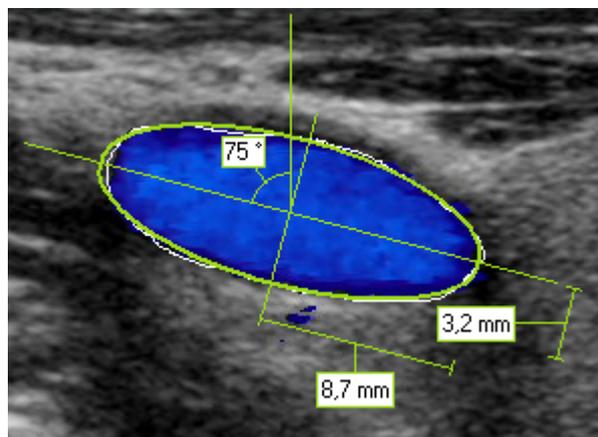
To obtain the frontal and the sagittal angle, proceed as follows: create an image in the frontal plane and another one in the sagittal plane (of the same vessel). First, open the image in the sagittal plane and measure the angle of the vessel with respect to the vertical line. For this, you can use the **angle tool (Section 6.9.1)**. Now, open the image in the frontal plane. Again, measure the angle (which is now the frontal angle) and input it. PixelFlux automatically calculates the total angle from these two angles. Then, start your perfusion examination in the usual way.

 The velocity and intensity will be corrected by dividing the (uncorrected) velocity by the cosine of the total angle of the vessel with the vertical axis. The area (both the colored area and the total area of the ROI) will be multiplied by the sine of the sagittal angle. (See **here (Section 7.2)** for the definition of velocity, area, intensity, and volume.)

It is recommended to perform perfusion examinations only for vessels with small angles.

### Automatically determining sagittal and frontal angles by the shape of the vessel

Since the manual measurement of the frontal and sagittal angles as described above can be time-consuming, PixelFlux has a mode to help you with this task: PixelFlux can calculate the sagittal and frontal angle from the shape of the vessel. Again, this only applies to vessels *in the frontal plane*. Activate this mode by checking the check box `Angle correction according to shape of the vessel`. Then, outline the shape of the single vessel as usual. PixelFlux will determine the ellipse matching most closely the shape of the single vessel. The ellipse will be shown in green:



The ROI you have outlined is shown in white, the perfusion examination is based on this ROI, not on the ellipse. In addition to the ellipse, you see the semi-axes, as well as the angle between the vertical line and the longer semi-axis. This angle corresponds to the frontal angle. The sagittal angle will be calculated by PixelFlux based on the eccentricity of the ellipse, that is, the ratio of the two semi-axes. This is based on the following geometric reason: the elliptic shape of the vessel does not represent the true area of the vessel, but stretches the original circle shape of the

vessel. Therefore, the more eccentric the ellipse, the smaller (in relation) the true size of the ROI and, accordingly, of the perfused area. As before, the total angle between vessel and transducer will be calculated from frontal and sagittal angle. Then, the angle correction will be done in the same manner as explained above.

### Angle correction for ROI in horizontal plane (in 3D mode)

The angle correction for single vessels in the horizontal plane works similarly. Again input the frontal and sagittal angles in the corresponding fields `angle in frontal plane (°)` and `angle in sagittal plane (°)`. PixelFlux computes the total angle and performs the angle correction. Since the way the angle correction is done differs between a ROI in the frontal and a ROI in the horizontal plane, it is important to choose the right option. See also the **Security advices for the use of the software (Section 3.4)**.

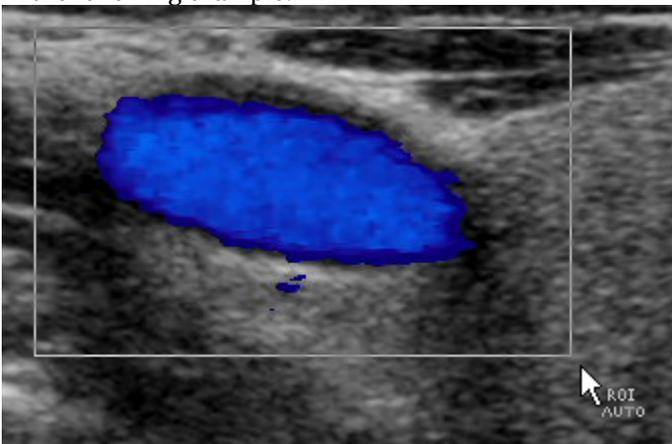
 The velocity and intensity will be corrected by dividing the (uncorrected) velocity by the cosine of the total angle of the vessel with the vertical axis. The area (both the perfused area and the area of the ROI) will be multiplied by the cosine of the total angle. Therefore, the volume is independent of the total angle. Moreover, the correction does not depend on the frontal and sagittal angles, but only on the total angle.

### Automatically determining the single vessel ROI

PixelFlux is able to automatically determine the ROI of a single vessel that is not connected to any other vessel. This mode only applies to perfusion measurements of *single vessels*, as opposed to measurements of more complex vessel structures.

To use this mode, activate the check box `Determine ROI automatically` in the **examination (Section 5)** tool window.

Unlike in the usual set up of the ROI, where you have to precisely encircle your ROI, you now simply define a rectangle that contains the single vessel. To do so, push the left mouse button, hold it and drag the mouse, as shown in the following example:

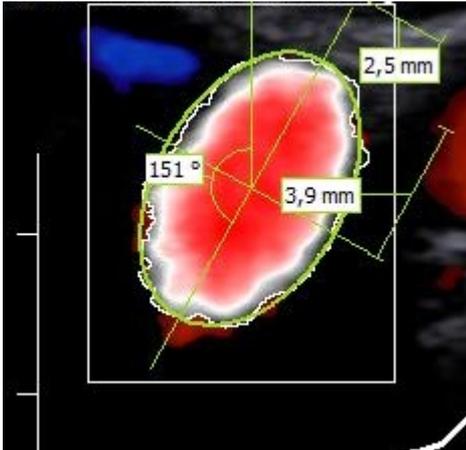


PixelFlux will then first search for the image where the vessel takes its biggest size.

After that, the single vessel, as it is shown in this image, is taken as the ROI for the examination. From this point on, the examination is performed as usual. It is strongly advisable to use this mode only when the single vessel in question is not moving. If it does move, parts of the vessel may, in some images, lie outside the automatically detected ROI.

This mode can be combined with the **angle correction according to the (elliptic) shape** of the vessel.

Then, on the one hand, the vessel will be recognized automatically, and, on the other hand, the angle correction will be performed according to the shape of the vessel, as the following example shows:



Only the largest connected vessel will be used as the ROI for the examination. Smaller vessels in the vicinity (such as the small vessel shown in blue at the upper left) are not counted as the ROI.

## Ignore period

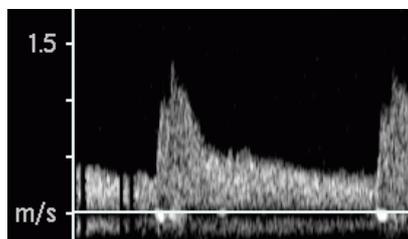
In some situations it can be useful to deactivate PixelFlux' automatic period detection. To do so, activate **Ignore period**. Then, the whole video (as opposed to a single or several complete periods) will be taken for the perfusion examination.

## Cancel normal examination

If you don't want the perfusion examination to start directly after **specifying the ROI (Section 6.5)**, you can discontinue the usual program course. This can be useful if you want to apply a **preset (Section 6.9.1)** upon the ROI. You can do this by activating **Windows | Examination details | Do not start examination yet** (in the examination tool window) before outlining the ROI. Then you specify the ROI and perform further steps. Then, click at **Start examination** and the examination will start as usual. If you want later examinations to start directly after outlining the ROI deactivate **Windows | Examination details | Do not start examination yet**.

## 6.12.5 Spectral envelope analysis

PixelFlux has an integrated module for analyzing spectral curves of the following kind:



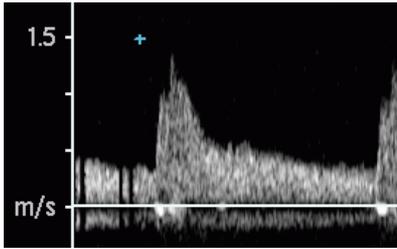
### Content

- **The spectral envelope analysis—Overview**
- **Results of the spectral envelope recognition**
- **Manual editing and correction of the curve**
- **Export the results**

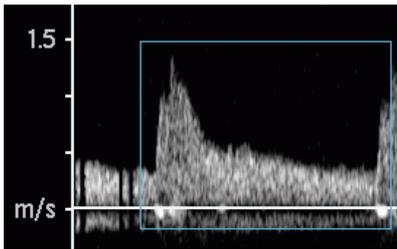
### The spectral envelope analysis—Overview

To analyze these curves, activate the envelope mode by clicking on **A** or **Tools | Envelope (F12)**.

1st step: first, you have to tell PixelFlux the area to be analyzed. Click on the **upper left corner** of a rectangle containing the desired area (x-coordinate: before the beginning of the wave, y-coordinate: above the maximum of the curve). The selected points will be marked with a light blue cross which appears after clicking.

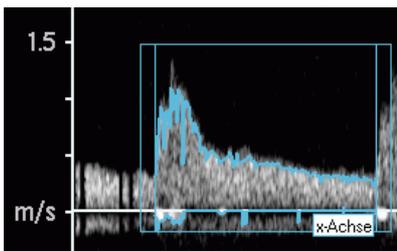


2nd step: click on the **lower right corner** (x-coordinate: *very close* to the beginning of the systole of the next wave, y-coordinate: below the (negative) maximum of the negative velocity). The area corresponding to these two points is marked with a light blue rectangle.



3rd step: click on the **x-axis (time axis)** of the chart. It is of no importance where exactly you click (i.e. the y-coordinate of the point is not important). As already noted PixelFlux shows the point with a small cross and with the caption "x-axis". Now, PixelFlux starts analyzing the envelope of the spectral curve. The spectral curves above and below the x-axis are analyzed (this step uses the contrast threshold, see **below**). PixelFlux shows the curves. They are used to determine which range of x-values (i.e. with respect to time) is really used for the analysis of the curve. First, the beginning is searched for after clicking on the point. Second, the end (i.e. the end of the diastole and the beginning of the new systole) is searched for and will be *very close* to the point you clicked on. Therefore, accuracy is particularly significant when clicking for the second time.

This range is depicted by two vertical lines (in the inner part of the rectangle). All further calculations refer to this range only.



Alternatively, you can specify the range which shall be analyzed manually. To do so, simply hold **Ctrl** pressed when clicking on the two points (of the first two steps).

4th step: Click on the **y-axis (velocity axis)** of the chart. It is recommended to click on a point of the scale which is refers to a specific velocity (i.e. in the sample

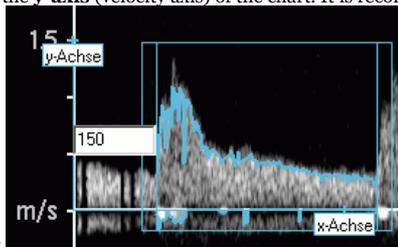


image at 1.5 m/s):

This point as well as the x- and y-axis are depicted. Then, input the velocity corresponding to the scale point of the 4th step. Use the *unit cm/s* in the sample image 150 cm/s (=1.5 m/s).

### Results of the spectral envelope recognition



The results are shown in the envelope window in different categories (labeled in bold letters)

**Velocities (cm/s):** You see the calculated (positive) maximal velocity and the minimal velocity. The latter is usually negative, but if there is no negative curve at all, PixelFlux shows the minimum positive velocity. Finally, you see the end-diastolic velocity.

**Average velocities (cm/s):** PixelFlux calculates the averages of the curves. The positive average refers to the positive curve and similarly for the negative one. The total average is just the sum of both.

**Flow volume (cm<sup>3</sup>/s):** When you input an area of ROI, the flow volume is calculated by multiplying the several average velocities by the area of the ROI. The unit of the volumes is cm<sup>3</sup>/s (=ml/s).

**Flow indices:** Finally, PixelFlux calculates RI (resistance index), PI (pulsatility index) and PPI (peak pulsatility index) according to the following formulae:

$$RI = \frac{v_{max} - v_{min}}{v_{max}}, \quad PI = \frac{v_{max} - v_{min}}{\bar{v}}, \quad PPI = \frac{v_{max} - v_{end-diast.}}{\bar{v}}$$

Here,  $v_{max}$  denotes the maximum velocity,  $v_{min}$  the minimum velocity,  $\bar{v}$  average maximum velocity (average of the maximal velocities at each point within the period) and  $v_{end-diast.}$  end-diastolic velocity. The last is taken from the positive curve, if the corresponding value is not too close to zero, otherwise from the negative curve.

### Further parameters

**Area of ROI (cm<sup>2</sup>):** To calculate flow volumes, input an area of the ROI. PixelFlux offers several possibilities: you can outline a ROI manually. (To stop the perfusion calculation, which normally starts automatically, click on [Windows | Examination details | Do not start examination yet](#) (F11), see [here \(Section 6.12.4\)](#)). When you have outlined a ROI, its area is automatically copied to **ROI (active)**. If you have a circular vessel, you can input its diameter in cm and PixelFlux calculates the area of the vessel.

Additionally, you can input up to three additional values. This is necessary to eliminate deviations of the vessel size (for example because of potential inaccuracies in the image acquisition) by taking the average over several measurements. may be useful, if you have slightly oscillating vessel sizes or other difficulties in image acquisition. See also the **Security advices for the use of the software (Section 3.4)**. All areas which you may specify are used, and PixelFlux calculates the average of these areas. If you do not wish to consider the area of the ROI which was manually outlined, uncheck **ROI (active)**. The average of all areas will be shown. Only this average will be used to calculate flow volumina (see above).

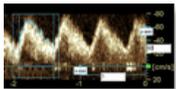
**Angle correction (°):** PixelFlux allows to easily correct the values by an angle correction. This is necessary to obtain the correct values if the vessel which you analyze is not perpendicular to the transducer surface. You can specify the angle between the vessel and the vertical. PixelFlux automatically calculates the

corrected values using the formula  $v = \frac{v_0}{\cos(\alpha)}$ , where v is the corrected velocity,  $v_0$  the uncorrected velocity resulting from the analysis of the spectral envelope and  $\alpha$  is the angle between the vessel and the vertical.

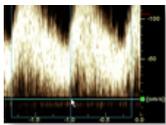
 Some ultrasound devices show the vessel angle. Alternatively, you can measure [angles](#) with PixelFlux.

 If an angle correction was performed with the ultrasound device during or after the image acquisition, the angle correction must not be performed in PixelFlux.

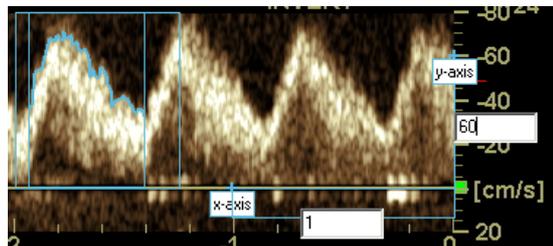
**Pulsation rate:** Optionally you can let PixelFlux calculate the pulsation rate, if the image you are using displays the time scale at the x-axis, such as in the following sample image:



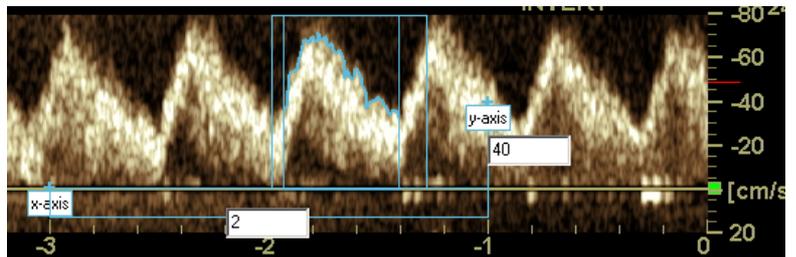
To do so, activate the check box **Calculate pulsation frequency** in the envelope tool window. Then, proceed as follows: do the first to steps as usual (see above). However, be sure to select only *one single cycle* (not multiple ones). In the third step, you will have to consider two requirements: firstly, the point you click at has to lie on the x-axis. Secondly, the point should be located above some point showing a tick mark of the time scale:



The cross-hair moving with the mouse pointer helps you positioning the point: move the mouse such that the horizontal line is at the x-axis while the vertical line hits a tick mark of the time scale (the tick marks are usually depicted under the scale). In the above sample the point was selected at -1 sec. In the fourth step click at a point that is located (with respect to its vertical or y-coordinate) at the height of some tick mark of the y-axis (velocity axis) and, with respect to its horizontal or x-coordinate) above some tick mark of the x-axis. Many manufacturers display the y-axis (usually at the right side of the chart) labelled with 0 seconds (or similarly), so that you can click at the y-axis in that case. The points you have clicked at are labelled with "x-axis" and "y-axis", as described above. Now, you input the velocity value in the input box at the y-axis (as described above). Finally, you input the *difference* of the two x-values (as seen from the two tick marks the points lie over) into the input box beneath the x-axis. The following two examples illustrate the procedure:



At the y-axis the tick mark 40 cm/s was clicked at. At the x-axis it was clicked at the point -1 second. Thus, the input boxes contain the value 60 (y-axis; i.e., 60 cm/s) and 1 (x-axis, i.e., 1 second).



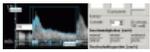
In this sample the third point was put at the x-axis, at the point -3 seconds. The fourth point was (mainly for illustrating purposes here) chosen at the x-value -1 second, the y-value is 40 cm/s. (The point lies at the height of the tick mark 40 cm/s). Thus the input boxes have to be filled with 40 (cm/s) and 2 (x-axis, that is 2 seconds).

After inputting these data the envelope tool window displays the pulsation rate in 1 per minute, that is, "80" signifies a pulsation rate of 80 per minute. The setting, whether you want to let PixelFlux compute the pulsation rate will be saved when you shut down PixelFlux, so that you find the same setting when restarting the program. In order to deactivate the calculation of the pulsation rate, uncheck the checkbox **Calculate pulsation frequency** in the envelope tool window.

### Manual editing and correction of the curve

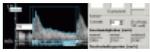
**Contrast threshold** The setting of the contrast threshold allows you to analyze images with different image brightnesses and qualities. The spectral envelope recognition works as follows: points in the image which are brighter than the threshold are considered to belong to the spectral curve, the darker ones are considered not to belong to the curve. Therefore, the threshold affects the result of the analysis. If the threshold is lower, more pixels are considered to belong to the curve.

The default value of the threshold is 50. We recommend not to change the threshold during a scientific study etc., as this may affect your results.



contrast threshold 50.

(100 corresponds to white, 0 corresponds to black)



contrast threshold 30

### Correcting the curve manually

You can correct the automatic recognition of the curve manually. Proceed as follows: Press the Ctrl key, hold it down and outline the part of the curve (with the left mouse button pressed) which you wish to correct. When releasing the mouse button, the positive curve will be corrected. When you use the right mouse button, the negative curve will be corrected. When you additionally press Shift, the curve (positive or negative according to the mouse button) is interpolated linearly, i.e. only start and end point of your mouse movement are taken and between them a linear interpolation is done. In all cases, the corrected curve will be shown and all results are recalculated automatically.

### Export the results

You can export the results of the envelope analysis to the clipboard by clicking on **Export | Export current examination**. By clicking on **Export | Export settings** you may specify which items of the current exam shall be exported. See **Exporting data (Section 9.5)** for further information. The values are separated by tabs, so that you can edit them easily in software such as Microsoft Excel or OpenOffice.

Alternatively, you can click on to save the examination in the database.

## 6.12.6 Calibration toolwindow

The calibration tool window allows for monitoring and adjusting a variety of settings related to the color scale and, more generally, the recognition of colors in the PixelFlux perfusion examination algorithms. It can also affect the distance (cm) calibration.

As other **tool windows (Section 6.11.1)**, this window can be docked and hidden.



### Content

- **Color scale settings**
- **Use external color scale profiles**
- **Load the color scale from another file**
- **Consider only the upper part of the color scale for examination purposes**
- **Colors and velocities**
- **Distance (cm) calibration**

### Color scale settings

In the upper part of the calibration toolwindow you see settings and information pertaining to the color scale. As the correct recognition and use of the color scale may influence the perfusion parameters of the perfusion examination, you should always take the appropriate settings here. See also the **Security advices for the use of the software (Section 3.4)**. The color scale, as it is currently recognized is shown at the top of the window. PixelFlux saves a list of color scales that you already have marked as correctly recognized (see also **options (Section 6.10.8)**). PixelFlux therefore tries to match the current color scale with the already saved ones. The result of this search is shown at the left of the color scale: if the scale was recognized, you see a check . If the color scale is not recognized, you see . Should the checking of color scales be disabled, you see a question mark , which reminds you of double-checking the color scale yourself once again. These icons are also shown in the image next to the color scale as well as in the status bar of the main window.

### Use external color scale profiles

An option for videos and images without color scale is the use of predefined, external color scale profiles. This means that the color information corresponding to a scale are already stored in PixelFlux, so that you can use this information instead of the (non-existent) color scale of the image.

To use such a profile, click at **Use external color scale profiles** in the color scale toolwindow. Then, choose the profile corresponding to the video or image, i.e. which color information matches the colors of the image. Then you do the examination as usual. The name of the external color scale profile is shown in the image and will also be stored in the database. This way you know the profile which gave rise to the examination.

The setting, whether you use external color scale profiles, will be stored when PixelFlux shuts down, so that you find your working environment at the program's next start. Please use this option only after consulting Chameleon Software.

### Load the color scale from another file

If you use videos/images/DICOM files without a color scale, you can still quantify perfusion using these videos, if you have another video which displays a colour scale corresponding to the current video.

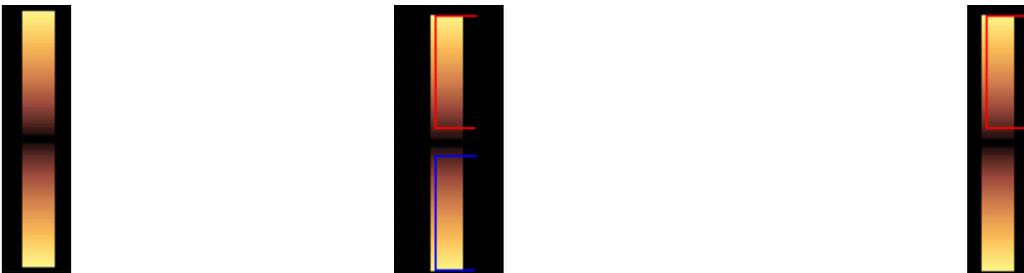
This situation may occur, when your source are videos using 4D techniques. These videos often fail to display a colour scale, but the colour scale is common, as the 4D video is developed on the basis of non-4D videos which possess a color scale.

To do this, simply proceed this way: First, open the video which possesses a color scale. The color scale will be shown, as it was detected automatically by PixelFlux. Then, uncheck the checkbox **Load color scale when opening file** in the color scale tool window, which is usually in the lower tool window container on the right side of the main form. Then, open the file which lacks the color scale, but whose color information corresponds to the former color scale. The color scale is saved (which is different from the normal procedure, during which the color scale is reloaded every time you open a video file). If you perform a perfusion examination now, this color scale will be used for computing the perfusion of the video.

If you use a color scale from another file, this is shown in the image and will also be stored in the **database (Section 8.1)**.

### Consider only the upper part of the color scale for examination purposes

In power Doppler mode (also known as PW Doppler mode), which as a rule does not allow a distinction between different blood flow directions, some ultrasound devices nonetheless display two identical parts of the color scale. For example in the left image below:



Since PixelFlux takes a priori both parts of the scale for the examination (middle image, the two recognized parts of the scale are depicted by blue and red lines), you can tell the program in such cases to discard the lower part of the scale and take only the upper part into account for examinations (rightmost image). To do so, click at **Consider upper part of the color scale, only**.

### Colors and velocities

The color scale tool window also examines the point where you currently move the mouse over. It displays the color

of the current pixel. PixelFlux seeks the color of the color scale(s) which is the closest to the current pixel is displayed (closest color of color scale), and PixelFlux calculates the distance between these two colors (Distance). Moreover, the distance to closest gray color (i.e., a color whose red, blue and green components are all equal) is displayed (Distance to gray line (R=G=B)). Finally, the velocity (in % of the maximum velocity) is displayed, if the current pixel corresponds to a perfusion velocity. A number of **options (Section 6.10.7)** is available for fine tuning of the internal PixelFlux algorithm.

## Distance (cm) calibration

Usually, the distance (cm) calibration information is reset when you open a new video or image file. That is, the length of a cm in the image has to be reset. If you have many image or video files having the *same* scale you can check **Reset cm calibration when opening files**. In that case the scale will not be reset when you open a file, but will be kept from the previous file. This mode is shown in the image as follows:



## 6.12.7 Magnifier

When you need to make a very precise click, e.g. to perform an angle measurement precisely according to the position of a vessel, the magnifier will help you to view the image. The available zoom options are 2x, 4x or 6x.

You can choose whether you wish to see the add-ons, i.e. calibration markings, additional tools such as the ruler, in the magnifier, too. If not, check the checkbox **image only**.

The magnifier is one of the tool windows of the main form. By default, it is located at the right bottom docking container of the mainform. You can move and dock it elsewhere. For this, please see general description of the **tool windows (Section 6.11.1)**.

The magnifier will be shown automatically if you do a manual **calibration (Section 6.3)** of the image. However, you can change this behavior in the **options (calibration) (Section 6.10.7)**.

## 6.12.8 Shape analysis

The shape analysis was created in order to allow an objective assessment of shapes of anatomical objects, such as vessels, (parts of) organs or follicles.

### Content

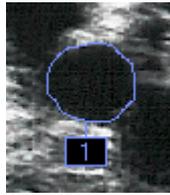
- **How to**
- **Parameters**
- **Examples**
- **Export**

### How to

To use shape analysis, activate the corresponding **mode (Section 6.11.3)** by clicking **Tools | Shape analysis** or . The currently active mode is also shown in the status bar at the bottom of the main module.

To analyse a shape, outline it with the mouse: press the left mouse button, outline the region and release the mouse

button. The shape will be marked with a light blue line:



To evaluate multiple forms, simply repeat the above steps. You can edit and delete shapes. First, click on the appropriate button in the **shape tool window (Section 6.11.1)**:  for editing and  for deleting a shape. To edit, click on the shape which you wish to correct. Simply outline the part of the shape which you want to edit. To delete a shape, simply click on it.

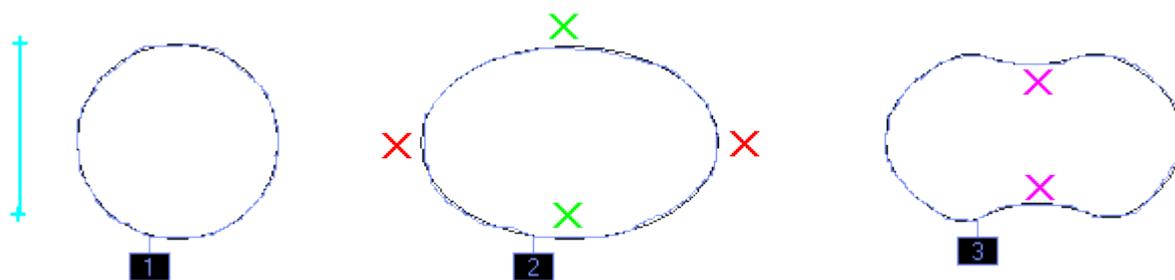
### Parameters

The following parameters are evaluated and shown in the shape toolbox:

1. The *areas* of the shapes in cm<sup>2</sup> (or in pixel, if the **scale (Section 6.3)** is not yet specified).
2. The mean curvature of the shapes. Here *curvature* is the inverse of the radius of an approximating circle (see [curvature, Wikipedia](#) for further details). If the scale is not yet specified, the curvature is the inverse of the radius in pixels.
3. Variance of the curvature is calculated. More precisely, the variance of a normed curvature, i.e. before calculating the variance the curvature distribution is divided by the mean curvature. The anatomic-medical interpretation of the curvature variance is assumed to be a stiffness or firmness of the corresponding object (e.g. a vessel or a follicle). The firmer the respective object is, the more it will resemble a circle shape (in a cross-section). The variance measures the deviation from this circle shape.

### Examples

To understand these entities, look at the following examples (for clarity, they are abstracted from the medical context):



There are three shapes. The first is (approximately) a circle, the second an ellipse, the third an ellipse with "dents". The light blue crosses with the joining line show the scale (1cm). PixelFlux computes the following values:

Shape	Area (cm <sup>2</sup> )	Curvature	Variance
1	1.047	1.74	0.125
2	1.51	1.412	0.321
3	1.356	1.439	1.019
<b>Average</b>	<b>1.305</b>	<b>1.53</b>	<b>0.488</b>

The variance of the curvature of the circle-like shape is the smallest. When perfectly outlining the circle (note the small deviations of the light-blue shape from the black circle), it would be 0, as the curvature of a circle is constant at every point. Compared to this, the variance of the ellipse is higher, as the curvature varies: on the left and right side (marked with red) the curvature is higher than at the green points. The third shape, the dented ellipse, has the highest variance of curvature: in the dents (violet marks), the curvature is negative, since the shape is concave at

these points (the dent points towards the interior). This increases the variance substantially.

## Export

To copy the shape examination to the **database (Section 8.1)** without a perfusion examination, click on or . You can export the results of the shape analysis to the clipboard by clicking on [Export | Export current examination](#). By clicking on [Export | Export settings](#) you can specify which items of the current examination are exported. See **exporting data (Section 9.5)** for further information. The values are separated by tabs so that you can easily paste them into other programs such as Microsoft Excel or OpenOffice.

### 6.12.9 Quick view

The quick view **tool window (Section 6.11.1)** summarizes the last few examinations and shows them in a bar chart.

You can select which perfusion parameter is being displayed: average velocity, area, intensity, dominant volume (this only applies to single vessel measurements), the area of the ROI, or, the intensity of **black-and-white measurements (Section 6.12.4)**. For the first three parameters, the average of red and blue value is shown, respectively. These values are the same as shown in the **analysis (Section 7.1)** and **database (Section 8.1)** modules. (See **here (Section 7.2)** for their explanation.)

Moreover, the average is calculated.

Whenever an examination is done, a bar with the corresponding value will be added. You may empty the list, if you wish so.

### 6.12.10 Direct help

The direct help in the **main window (Section 6.1)** shows you a short introduction to the currently active mode. Click at [Detailed help](#) to obtain more detailed information.

The direct help is located in a **tool window (Section 6.11.1)**.

## 7 Analysis module

### 7.1 Overview of the analysis module

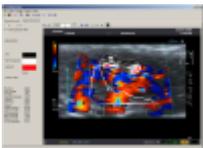
The analysis module is opened after the perfusion examination or when you click on  in the **main module (Section 6.1)**. It contains all perfusion parameters, the charts and numeric results. In addition you can see the video with the **perfusion relief (Section 7.4)**, as well as (if applicable) **notifications and warnings (Section 6.7)** pertaining to the current examination.

#### (Section 6.1)

You can do the following tasks:

- **view (Section 7.2)** analysis data from the video file
- **open and save (Section 7.6)** analysis files
- **save (Section 9.3)** analysis results in the database
- **print (Section 7.7)** findings of one examination
- **export (Section 7.5)** analysis results (charts, image, raw data, results)
- adjust the **period (Section 7.3)**.

For doing these tasks use the menu or the tool bar of the analysis form. Click on an icon to learn more about its purpose.



### 7.2 Visualization of analysis data

The main task of the analysis module is the visualization of analysis data. PixelFlux uses a table containing numeric results and charts depicting the dependence of velocity, area, intensity, and flow volume on time.

#### Content

- **Fundamental remarks**
- **Periods and charts**
- **Average, RI, PI**
- **Output**

#### Fundamental remarks

Every calculation of any perfusion parameter is divided into two parts: one concerns the **red** "part" of the parameter, the other one the **blue** "part". This division corresponds to the division of the color scale which has been calibrated in the **main module (Section 6.1)**. Every color represents a direction of the blood flow. (This division only applies to examinations using a color duplex sonographical video or image, unlike power mode examinations in which case

the color scale is not divided into two parts).

On the basis of this differentiation, four parameters are calculated:

- **Flow velocity v.** The unit of the velocity is cm/s. The velocity corresponds to the color values in the video combined with the maximum velocity, which stems from the color scale (see **Image calibration (Section 6.3)**.)
- **Area A.** Its unit is cm<sup>2</sup>. The area specifies the amount of colored pixels in the video images. The area is influenced by the **cm-distance (Section 6.3)**.
- **Intensity I [cm/s].** The definition of the intensity is based on the following equation:

$$I = \frac{v \cdot A}{A_{ROI}}$$

where **A<sub>ROI</sub>** is the area of the outlined **region of interest (Section 6.5)**. The intensity is intended to increase the objectivity and comparability of perfusion data. It corresponds to the average velocity, provided that the whole region of interest is perfused homogeneously.

- **flow volume V.** It is defined as the product of flow velocity v and perfused area A. Its unit is cm<sup>3</sup>/s. The dominant volume is either the red or the blue volume, depending on which one of the two is bigger.

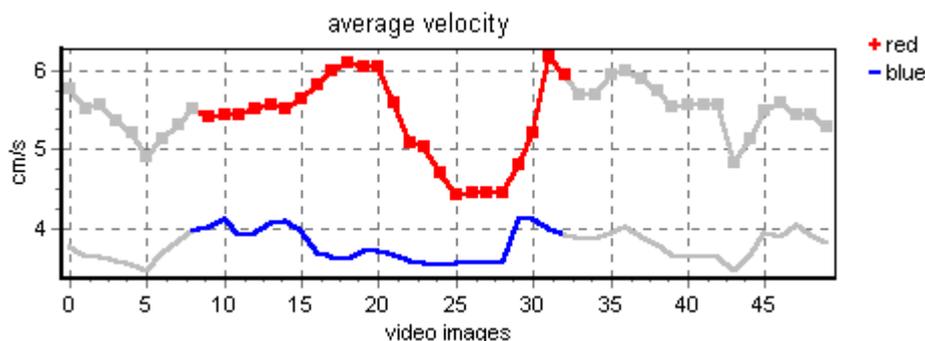
 Please do not use the flow volume unless you do a perfusion examination of a single vessel. The flow volume is not applicable for multiple vessels or for chaotic vessel structures. See also **Security advices for the use of the software (Section 3.4)**.

Each video contains a number of images. PixelFlux calculates the perfusion data (red and blue velocity, intensity, area) for each of the images.

All parameters (v, A, I, and V) are calculated for **red** and **blue** values, separately. The average of a **red** and the corresponding **blue** value is called the mixed value. Example: v mix RI means the average of the RI of the red velocity (v red RI) and RI of the blue velocity (v blue RI).

## Periods and charts

These data are the basis for four diagrams (velocity, area, intensity and flow volume). The x-axis (horizontal axis) is the time-axis. The unit of the x-axis is images, i.e. every data point represents one image. The y-axis (vertical) gives the particular parameters with its unit.



Usually, all parameters have a temporal fluctuation caused by the periodic heart action. A precise calculation of averages must consider these fluctuations. PixelFlux automatically calculates the periodicity and chooses one or multiple whole periods (if there are any) as basis of all further calculations. PixelFlux computes the period automatically, but you can **modify (Section 7.3)** it manually.

You can see the period in the charts as the coloured (with **red** or **blue**) zone. The outside zone is drawn in gray. You can zoom and scroll in the charts, for which see the explanation in **Visualization of the database (Section 8.2)**.

You can adjust the period manually in the charts directly. See **here (Section 7.3)**.

## Average, RI, PI

For all parameters PixelFlux computes the average, the RI and PI. These results **refer to the period** as shown in the charts.

RI (resistance index) and PI (pulsatility index) are defined for each parameter (e.g. x=velocity rec):

$$RI = \frac{x_{\max} - x_{\min}}{\overline{x}}$$

$$PI = \frac{x_{\max} - x_{\min}}{\overline{x}}$$

$\overline{x}$  is the average of the parameter during the period. Therefore,  $\overline{x}$  is a real average. Minimum and maximum concern the period, too.

## Output

In addition to the charts and the table with averages, RI, PI you can see further important perfusion results:

- The **clipping area** [cm<sup>2</sup>] gives the size of the outlined **region of interest (Section 6.5)** (ROI).
- The **total intensity** [cm/s] is the sum of the red and blue intensities ( $I_{\text{red}} + I_{\text{blue}}$ ), the **average intensity** is the mean of red and blue intensity.
- The **total volume**. This is the sum of the red and blue volume.
- The **dominant volume**. This is either the red or the blue volume, depending on which one is larger.

Moreover, you see whether an **angle correction (Section 6.12.4)** has been performed as well as the corresponding angles (total angle, and (if applicable) frontal and sagittal angle).



Another very useful feature for understanding the local perfusion distribution is the **Perfusion relief (Section 7.4)**.

## 7.3 Manual modification of the period

While computing the perfusion data, PixelFlux also calculates the perfusion period (the period refers to the intensity). The period is shown in the charts as **colored area (Section 7.2)**. PixelFlux is able to take two periods into consideration, if the video contains two full periods.

### Influencing the period manually

In some cases, the period being automatically calculated might be inaccurate (e.g. if the video contains artifacts because of movement of the patient and such, see also the **Security advices for the use of the software (Section 3.4)**).

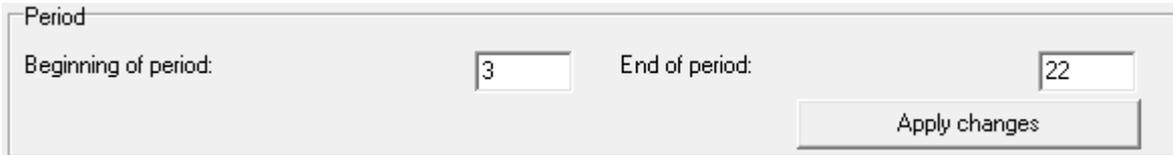
To avoid these errors, which have an effect on the averages of all data, you can modify the period manually. You can move beginning or end of the period using the following commands:

	Period   <u>B</u> eginning forward	 + 1	moves the beginning of one image forward (towards the beginning of video)
	Period   <u>B</u> eginning backwards	 + 2	moves the beginning backward (to the video's end)
	Period   <u>E</u> nd backwards	 + 3	moves the end backward (beginning)

 **Period | End forward**  **Ctrl** + 4 moves the end forward (end)

To undo your manual changes of the period, click  or **Period | Reset** ( **Ctrl + Z**).

You can also change the beginning or the end of the period using the edit boxes in the right part of the analysis module:



In addition, you can change the period manually in the charts directly. To change the beginning of the period, move the mouse at or near the beginning of the period, i.e., the region where the red and blue part of the chart begins. Then, hold the keys  **Ctrl+Shift** and move the mouse where you want the period to begin. While you are moving the mouse, the adjusted period is shown. Analogously, you can change the end of the period by placing the mouse near the end of the period.

### Notification for significant changes of perfusion parameters

If a manual change of the period leads to a significant change of the perfusion parameters, a corresponding **notification (Section 6.7)** will be shown.

## 7.4 Perfusion relief

One of the most useful and impressive features of PixelFlux is the perfusion relief.

It serves to give you a quick visual impression of the perfusion parameters. PixelFlux takes each pixel in the ROI separately and calculates the perfusion parameters of this tiny ROI consisting of this pixel.

You can show the perfusion relief for the area and the intensity, respectively. The area value is simply the count of images which are perfused (red or blue) at the given pixel divided by the number of images in the video. The intensity value is the average intensity of this pixel.

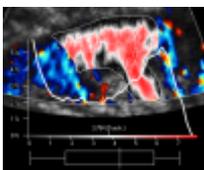
The perfusion relief is calculated with reference to all images of the video, i.e. there is no correlation with the **period (Section 7.3)**.

### (Section 7.3)

#### Content

- **What is the perfusion relief?**
- **Quantitative information concerning the perfusion relief**

### What is the perfusion relief?



This is an example of the perfusion relief in the analysis module. You can view the ROI (thin white line) and in the ROI the perfusion relief. The parts displayed in red have a high intensity. The maximum intensity is 7.945 cm/s (the precise value can be read off the quantitative table, see below). White regions have an intensity of about 4 cm/s and black ones have little intensity. You can change these colors in the **options form (Section 6.10.5)**.

Below the ROI, you see the numerical evaluation of the perfusion relief. First, the average intensity of the ROI is 3.784 cm/s. The chart shows you how many pixels of the ROI have an intensity of the respective value. In the above chart, relatively many pixels have low intensity, middle intensity occurs less often, and high intensity occurs again more often. This information may help to estimate perfusion features. For precise quantitative information, please see below.

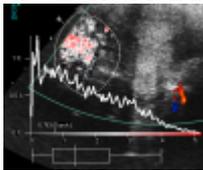
The perfusion reliefs are automatically saved and linked to the examination, so that you can see them in the database, too.

## Quantitative information concerning the perfusion relief

PixelFlux analyzes the perfusion relief. To be more precise, it calculates significant values characterizing shape of the distribution of the area and intensity with the methods of descriptive statistics. The following parameters are calculated (all of them either refer to the intensity or to the area distribution):

- maximum of the distribution
- true average of the distribution: this is the average of all pixels.
- average of the distribution: this is the average of all pixels possessing intensity (or area, dependent on what you are currently viewing) different from zero.
- standard deviation, variance, skewness, kurtosis, sample kurtosis: these are the usual statistical descriptions of the data set. Please note that these data refer to the distribution, where the pixels *possessing intensity* (or area) *zero, are not considered* (similarly to the average of the distribution, in contrast to the true average). This is, since usually the percentage of pixels possessing intensity zero is relatively high and if these pixels were considered for the calculations as well, the standard deviation etc. would be distorted. If you wish to learn more about the meaning and formulae of these items, please consult Wikipedia (visit the following sites: [standard deviation](#), [variance](#), [skewness](#), [kurtosis and sample kurtosis](#)).

As an indication for the usefulness of the quantitative analysis of the perfusion relief, compare the above example, which has a skewness of -0.299 (which means slightly right-skewed, i.e. higher intensities are dominating over lower ones), and the following one, which has a skewness of 0.801 (which indicates that the distribution is slanted towards lower intensities):



- percentiles: 2.5%, 25%, 50% (median), 75% and 97.5%-percentiles are available. These percentiles are also shown below the diagram in the box-plot. The whisker shows the 2.5% and 97.5% percentiles, respectively, the box in the middle corresponds to 25% and 75% percentiles and the 50% percentile is indicated by the vertical line in the box. Outliers are not depicted. Please see [box plot](#) and [percentile](#) for further information).

These items can be viewed in the **analysis module (Section 7.1)** (on the [image information](#) page) and in the **database (Section 8.1)** (on the [Single examination](#) page) and can be **exported (Section 9.5)** from the database.

## 7.5 Export analysis data

You can copy *raw data*, *results*, *charts* as well as the *image* to the clipboard or save them into individual files. You can use these functions for patient files, to create presentations or scientific material.

### Content &nbsp;

- **Raw data**
- **Results**
- **Charts**
- **Image**

### Raw data

Use [Export | Copy raw data](#) (  **Ctrl + A** ) to copy the raw data (the red and blue velocity, area, intensity).

The format of the copied raw data is adjusted to applications such as Microsoft Excel. The columns are separated by tabulators.

	A	B	C	D	E	F
1	Velocity red	Velocity blue	Area red	Area blue	Flow red	Flow blue
2	1,028	1,230	3,731	5,267	0,256	0,432
3	1,022	1,208	3,677	5,331	0,250	0,429
4	1,032	1,199	3,447	5,289	0,237	0,423
5	1,024	1,194	3,145	5,232	0,215	0,416
6	0,997	1,175	3,179	5,137	0,211	0,402
7	1,009	1,174	3,629	5,122	0,244	0,401

## Results

Above the raw data, you can copy all results (**averages, RI, PI (Section 7.2), clipping area, total and average intensity (Section 7.2)**). Click on **Export | Copy results** (  Ctrl + C ). The format of the exported results is similar to the format of the raw data.

## Charts

You can either copy each chart which you see in the analysis form into the clipboard of Windows or save them as graphic files.

For this, use the commands **Export | Save chart ...** and **Export | Copy chart**. Choose the desired chart in the following submenu.

## Image

Above the chart you can also copy and save the ultrasound image (this image shows the first frame of the analyzed video file). Use **Export | Save video image ...** and **Export | Copy video image** (  Ctrl + B ) to copy and save the image. See **Save and copy (parts of) the image (Section 9.1)**.

## 7.6 Opening and saving analysis data

It is recommended to use the **database form (Section 8.1)** to manage your perfusion data. The database offers more comfortable storing modes than the analysis.

The routines **open** and **save** are sufficient, when you only wish to save the perfusion data of one examination.

### Open

To open an existing measurement file (with the extension .pxm), click on , **File | Open ...** (  Ctrl + O ).

The pxm-files contain all raw data (which are displayed in the charts), the results (total and average intensity ...) as well as the **period (Section 7.3)** information. However, they do not contain the ultrasound image.

### Save

After you have performed a perfusion calculation, you can save the perfusion parameters in a separate file. Click on  or **File | Save ...** (  Ctrl + S ) and save the file in the appearing dialog.

## 7.7 Print single findings



A single finding in the sense of this function is a table-like list of perfusion parameters of a single perfusion examination. However, it does not contain a medical diagnosis since the software does not suggest or formulate any diagnosis. See also the **General information about the software (Section 3.2)**.

If you wish to print the diagnosis finding of one examination, click on  or File | Print finding ... ( Ctrl + P) in the **analysis form (Section 7.1)**.

To print a finding from the **database (Section 8.1)**, select one or more examinations from the list and click on Database | Print single findings.

The finding contains:

- patient data (surname, first name, date of birth)
- examination data (colour frequency, organ, part of organ, further text field)
- all perfusion charts (velocity, area, intensity)
- region of interest and ultrasound image
- numeric results (averages of the velocity, area, intensity, RI, PI, whole & average intensity)

When you print the findings in the analysis form, all patient data and examination data are filled with blanks (\_\_\_\_\_).



## Single examinations

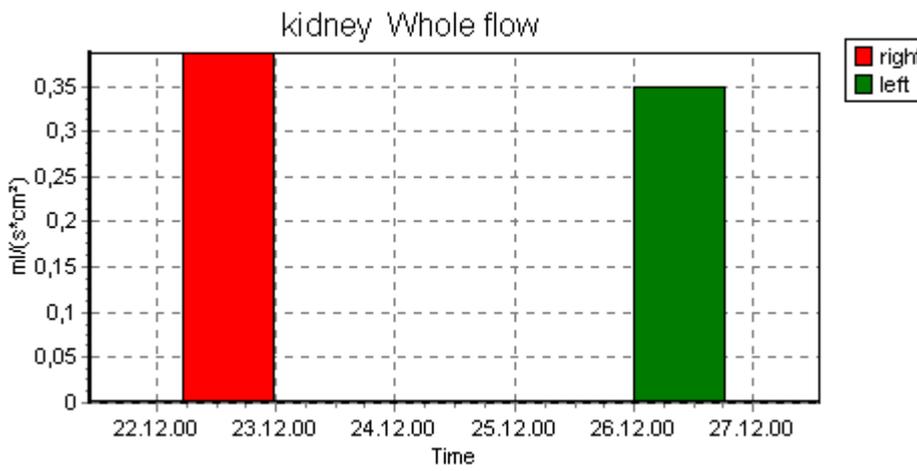
Displaying single examinations is the same as in the **analysis form (Section 7.1)**. Choose a parameter by clicking on an item in the menu Current parameter, for example Current parameter | v - A - I | v velocity (  Ctrl + G).

## Series

A series simultaneously displays various examinations in one chart.

PixelFlux displays all examinations with the same organ from a patient file. Click on an entry of the organ drop-down-menu and choose the organ from the list of available organs.

PixelFlux summarizes these examinations to groups according to the part of organ. All examinations (bars) with the same part of organ possess the same color which is shown in the legend on the right side of the chart.



 In every chart of PixelFlux, you can zoom every region. Click with the left mouse button on the upper left corner, keep the button pressed and move the mouse. Release it on the lower right corner. To restore the image simply proceed it reversely (click, hold, move from lower right to upper left corner). In the single examination charts (both in **analysis view (Section 7.1)** and database view) If you hold the key  Ctrl pressed when starting the zoom, the zoom will be done in the direction of the time axis only, i.e., the y-axis representing velocity, area or intensity will be unchanged.

 To scroll the chart region, click on the chart with the right mouse button, hold it and move the mouse.

## 8.3 Open patient files

You can open patient files directly from the database module. Click on  or Database | Open ... (  Ctrl + O).

Choose the desired file from the list of files to open it. For this, double-click on an item or click on an item and click **OK**.

 If the list of files is very long, you may insert the first letters of the name of the patient in the edit field below the patient list. The list of patients with the selected initials will be displayed.

 By default the patient files are located in the folder  $[ProgDir]\Patienten\$ , of which  $[ProgDir]$  is the directory containing the file *PixelFlux.exe*. The extension of the patient files is *.ppp*. The header of the file (surname, first name, date of birth) is saved in the file name. The examinations in the file may contain other patient data than the header. You can change the patient file directory by using the **user profiles window (Section 6.11.2)**.

## 8.4 Create patient files

To create a new, empty patient file, click on  in the tool bar of the database form or **D**atabase | **N**ew ...  Ctrl + N. In the next dialog, you have to input surname, first name and the patient's date of birth. Click on **O**K to confirm your input. The new file is created and the list of examinations in the database form is emptied.

 If the list of files is very long, you may insert the first letters of the name of the patient in the edit field below the patient list. The list of patients with the selected initials will be displayed.

 By default the patient files are located in the folder *[ProgDir]\Patienten\*, of which *[ProgDir]* is the directory containing the file *PixelFlux.exe*. The extension of the patient files is *.ppp*. The header of the file (surname, first name, date of birth) is saved in the file name. The examinations in the file may contain other patient data than the header. You can change the patient file directory by using the **user profiles window (Section 6.11.2)**.

## 8.5 Editing data

### 8.5.1 Edit examination data

You can change the additional information of an examination (date of examination, organ, part of organ, colour frequency and additional text).

To do this, you have to

- mark one or more examinations in the list of existing examinations
- click on  or **D**atabase | **E**xamination data ( Ctrl + E).

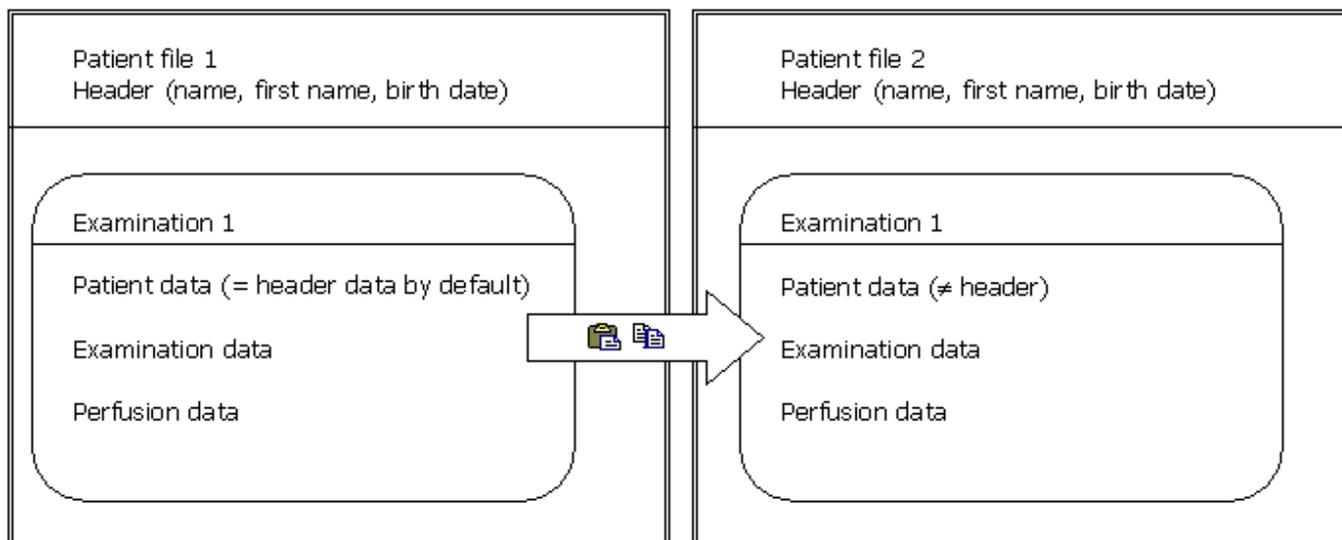
Now, you can change the content of each selected examination. The appearing dialog is similar to the one which appears, when you **save (Section 9.3)** perfusion examinations into the database.

### 8.5.2 Edit patient data

Similarly to examination data, you can edit patient data of each examination.

By default, the file name of a patient file determines the "header" of the file, i.e. the patient's surname, first name and date of birth. When you **add (Section 9.3)** perfusion data from the analysis form to a patient file, these examinations are combined with the "header patient".

To build scientific series, it can be useful to compare different patients in one patient file. For example, you can use **copy (Section 8.5.3)** to collect perfusion and examination data from different patient files. When you copy or paste examinations, the patient data of these examinations are copied as well.



You can view the header data of the current patient file on the top border of the database window. The patient data of the current examination (which can be selected from the list of examinations) is displayed in the part of the database window between the tool bar and the list of examinations.

To edit the patient data of separate examinations, mark one or more examinations and click on  or **Database | Patient information** ( Ctrl + D).

The following dialog shows the existing patient data of the examination. Edit them, if necessary, and click on **OK** to confirm your input. Then the patient file is updated as well as the database module.

### 8.5.3 Edit patient files

PixelFlux allows you to use standard clipboard operations to handle your perfusion data: *cut*, *copy*, *paste* and *delete*.

 Please do not mix up editing of patient **files** and editing of **patient data (Section 8.5.2)**. The former means moving etc. of **whole** examinations (including date, organ, part of organ, etc. as well as the perfusion data), while the latter refers to the modification of "header" contents of **single** examinations.

#### Content

- **Cut**
- **Copy**
- **Paste**
- **Delete**

#### Cut

To cut examinations, select them from the list of examinations in the database form and click on  or **Edit | Cut** ( Ctrl + X). The selected examinations will be deleted and copied in the internal clipboard. The previous content of the clipboard will be overwritten.

 You can mark more than one examination this way: click on one examination and press  Ctrl, hold it and mark each further examination. If you wish to select several examinations in a row, click on the first, press and hold  Shift and click on the last examination which you want to select.

#### Copy

To copy examinations, mark them and click on  or **Edit | Copy** (). The examinations will be copied in the internal clipboard.

## Paste

You can paste examinations by clicking on  or on **Edit | Paste** (). The content of the clipboard (if there is any content) will be pasted. The list of examinations will be updated.

## Delete

When you click on **Edit | Delete** ( or , the marked examinations will be deleted. Then they cannot be pasted again.

## 8.6 Views of the database

You can use the following commands:

 **View | New exam**

 **F4** Closes database and (if necessary) analysis module and shows the dialog to open a video file for a new perfusion examination. This way, you can accelerate the building of large examination series by clicking only once.

 **View | Maximize** (or Minimize)

 **F5** Hides the list of examinations, the series values as well as the patient information concerning the current examination. This way the series chart or the video frame can be displayed in a larger size. Minimize undoes the changes of Maximize.

**View | Next sheet**

 **F6** Shows the next sheet (e.g., if **Single examination** is active, **Series** will be shown)

**View | Previous sheet**

 **F7** Show the previous sheet (e.g., from **Video** to **Series**)

 To switch between the different views, you can also double-click on a series item (bar). The video corresponding to the examination will be shown. Then double-click on the video, to show the single examination sheet. When you double-click on the single examination chart, PixelFlux switches to the series sheet.

## 8.7 Printing findings

### 8.7.1 Print single findings

 A single finding in the sense of this function is a table-like list of perfusion parameters of a single perfusion examination. However, it does not contain a medical diagnosis since the software does not suggest or formulate any diagnosis. See also the **General information about the software (Section 3.2)**.

If you wish to print the diagnosis finding of one examination, click on  or **File | Print finding ...** () in the **analysis form (Section 7.1)**.

To print a finding from the **database (Section 8.1)**, select one or more examinations from the list and click on **Database | Print single findings**.

The finding contains:

- patient data (surname, first name, date of birth)
- examination data (colour frequency, organ, part of organ, further text field)
- all perfusion charts (velocity, area, intensity)
- region of interest and ultrasound image
- numeric results (averages of the velocity, area, intensity, RI, PI, whole & average intensity)

When you print the findings in the analysis form, all patient data and examination data are filled with blanks (\_\_\_\_\_).

## 8.7.2 Print series findings



A series finding in the sense of this function is a table-like list of perfusion parameters of a number of perfusion examination. However, it does not contain a medical diagnosis since the software does not suggest or formulate any diagnosis. See also the **General information about the software (Section 3.2)**.

To print a finding, which contains perfusion parameters and examination data of a series of perfusion examinations, click on  or [Database | Print series finding](#) (  Ctrl + P).

The printed finding contains the following elements:

- patient data (surname, first name, date of birth)
- series information (organ, part of organ, selected parameter)
- the chart of the series
- the table of values of the chart

## 9 Functions available in several modules

### 9.1 Save and copy (parts of) the image

In all three modules (**main module (Section 6.1)**, **analysis module (Section 7.1)** und **database module (Section 8.1)**) you can *copy* parts of the image (including additional markings such as calibration markers, ruler etc.) or the whole image to the clipboard or you can *save* the image.

#### (Section 6.1)

##### Content

&nbsp;

- **Save image**
- **Copy (part of) the image**

#### Save image

To save the image, click on  or

- **Export | Save video image** ( Ctrl + S, main module),
- **Export | Save video image ...** (analysis module) or
- **Export | Save video image** (database module).

Then input the file name.

#### Copy (part of) the image

To copy the whole image or a rectangular part:

In the main module you first have to activate the corresponding mode by clicking on **Export | Copy (part of) image** ( Ctrl + C) or .

If you wish to copy the whole image, simply click on an arbitrary point in the image. If you wish to copy a rectangular part instead, press and hold the left mouse button at the upper left corner and move it to the lower right corner and release the mouse button. The selected area will automatically be copied to the clipboard, so that you can paste it in any other third party application.

### 9.2 Playing video files

All three modules (**Overview of the main module (Section 6.1)**, **Overview of the analysis module (Section 7.1)** and **Overview of the database module (Section 8.1)**) of PixelFlux allow you to browse the currently opened video.

#### Play functions

The following functions are available. You can either use the tool bar above the video screen or the main menu of the main module, analysis module or database module (the menu items are located under **Video**).

-  first image
-  previous image
-  next image
-  last image
-  play video (starts with the current image and plays until the end of the video)
-  pause
-  stop (and jump to the first image of the video)

The icons are located in the appropriate register card ( **Video** in the database module and **image information** in the analysis module).

Additionally, you can input an image number in the input box on the toolbar to jump to this image.

## Options

In the database, PixelFlux searches for videos, when they are not (no longer) in their original place. This way, you can handle the common situation of your files being on your hard disk when you performed the measurements, but are at another location (including network drives or mass storage).

PixelFlux searches for the video files in the following way: if the video file exists with its "old" file name and position, this file is played. Otherwise, PixelFlux looks in the specified search directories (in their given order) to find a file with the given file name.

You can adjust these directories with **Video | Video directories** or . In the next dialog you can add, delete or change the sequence of the search directories.

Click on **OK** to confirm your inputs. Now all video files in all patient data will be searched in the new search directories according to their sequence.

## 9.3 Save perfusion examination in the database

To copy the perfusion examination in a database file, click on **File | Save in database** ( **Ctrl + D**) or , both in the **main module (Section 6.1)** and the **analysis module (Section 7.1)**. Alternatively you can use the **automode (Section 6.8)**. When using it, specify examination and patient data directly after specifying the ROI.

Please note that perfusion parameters are available in the analysis module only. From the main module, the function therefore mainly serves to save results of the **spectral curve analysis (Section 6.9.7)** and the **shape analysis (Section 6.12.8)**.

To complete the information on the exam, PixelFlux needs additional information:

1. **examination data**
2. **patient data**

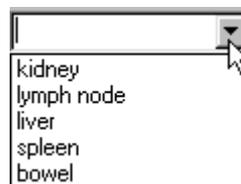
### Examination data

The examination data contains date, organ, part of organ, colour frequency and optional further information.



When you use DICOM files, the examination date is extracted from the DICOM header. Otherwise the default value of the examination date is the current date. To change it, click on the drop-down-button  and choose a date by clicking on it or use your keyboard.

All fields except the **further text** save the last ten inputs typed in. PixelFlux does not distinguish between capitals and non-capitals, i.e. "heart", "Heart" and "HEART" are considered identical. Also here, use the drop-down-button to choose among recent inputs.



Click on **OK** to confirm the examination data.

When the **automode (Section 6.8)** is active, you can use the option **immediately open next file afterwards**. This means, that after you have specified the examination data and the patient data (see below), PixelFlux will automatically open the next file in the directory where your current DICOM/video file was (similar to **Open next file (Section 6.2.1)**).

Depending on the organ, PixelFlux checks whether an organ specific upper bound is exceeded and will warn you in that case (see **here (Section 6.7)** for more detailed information).

Click on **Reset** in order to delete all inputs. Click on **OK** to proceed with saving the

examination (including the just added information on organ, part of organ etc.) Click on **Cancel** to cancel the action.

### Saving examinations to patient files

You can save the examination data, i.e. the perfusion parameters as well as additional information on organ etc. in a patient file. To do so, you can choose between either saving the examination to an existing patient file or creating a new patient file.

If you want to add a perfusion examination to an existing file, select it from the list of patient files by double-clicking on it or clicking on **OK**.

**💡** If the list of files is very long, you may insert the first letters of the name of the patient in the edit field below the patient list. The list of patients with the selected initials will be displayed.

**💡** By default the patient files are located in the folder `[ProgDir]\Patienten\`, of which `[ProgDir]` is the directory containing the file `PixelFlux.exe`. The extension of the patient files is `.ppp`. The header of the file (surname, first name, date of birth) is saved in the file name. The examinations in the file may contain other patient data than the header. You can change the patient file directory by using the **user profiles window (Section 6.11.2)**.

### Creating a new patient file



To create a new patient file and to save the examination into this newly created file, click on **New ...**. The dialog on the left appears:

Input name, first name and date of birth of the new patient. Click on **OK** to create the new file specified by the patient data. To cancel the input, click on **Cancel**. Click on **Reset** to delete all inputs.

You can review the list of previously used patient's profiles in the drop-down-box below.

**💡** When you use DICOM files as video input, name, first name and date of birth of the patient are extracted from the DICOM header, so that you do not have to specify it. Additionally, when you use the automode, PixelFlux will skip this step for DICOM files and will automatically extract the patient information from the DICOM header and save the measurement in the appropriate file (or create it, if it does not exist). Therefore, the usage of DICOM files is strongly recommended. Also see **Security advices for the use of the software (Section 3.4)**.

## 9.4 Versions

Features	Standard	Professional	Scientific
<b>Automatic perfusion examination of an arbitrary ROI (Section 6.5)</b>	x	x	x
Context sensitive help system and <b>direct help (Section 6.12.10)</b>	x	x	x
Automatic video recognition	x	x	x
<b>Anaylsis of perfusion parameters (Section 7.1)</b>	x	x	x
Create and print <b>single findings (Section 7.7)</b>	x	x	x
Automatic <b>period calculation (Section 7.3)</b>	x	x	x
Calculate further parameters relevant for the perfusion (averages, RI, PI, total intensity etc.)	x	x	x

Various <b>checks (Section 6.10.8)</b> ensuring valid perfusion examinations	x	x	x
<b>Export (Section 9.5)</b> all perfusion parameters	x	x	x
<b>Handle examinations in the database (Section 8.1)</b>		x	x
<b>Create (Section 8.4) and edit patient files (Section 8.5.3)</b>		x	x
Compare examinations via <b>series (Section 8.2)</b>		x	x
Print <b>series findings (Section 8.7.2)</b>		x	x
Geometric <b>tools (Section 6.9.1)</b> and presets			x
<b>Interactive charts (Section 8.2)</b> (zoom, scrolling)			x
<b>Watch video files (Section 9.2)</b> together with the ROI and perfusion relief			x
<b>Export perfusion data (Section 9.5)</b>			x
<b>Options (Section 6.10.1)</b> (especially automatic maximum velocity recognition)			x
<b>Perfusion relief (Section 7.4)</b>			x
<b>Automatic ROI recognition (Section 6.6) and angle correction according to the shape of the ROI (Section 6.12.4)</b> (single vessels)			x

## 9.5 Export examinations

There are various ways to export all data and images pertaining to your perfusion examinations to third party applications.

### Content &nbsp;

- **Overview**
- **Commands**
- **Options**

### Overview

In the **database module (Section 8.1)** and in the **main module (Section 6.1)** you can export the perfusion data of the current examination(s) to the clipboard. Click on  $\Sigma$  or **Export | Export examinations** ( Ctrl + K) in the database or **Export | Export current examination** (main module).

In the database module, all examinations of the currently opened patient file are exported. In the main module, the current examination is exported. Please note that the results of the perfusion examination are available in the main module only after the perfusion examination has been completed. The export in the main module is intended mainly for the **spectral envelope analysis (Section 6.9.7)** and **shape analysis (Section 6.12.8)**.

The exported items are separated by tabs. You can easily use the exported content in third party software such as Microsoft Excel or OpenOffice. Click on **Edit|Paste** or  Ctrl+V to paste it into the spreadsheet in the respective program.



In case of doubt, always export all items of the database. This way you ensure that all diagnostic questions can be addressed using the exported data.

### Commands

The following contents of the database can be exported.

Content type	Command	Icon	Comment
Single examination chart	Export   Copy single exam, Export   Save single exam		Copies the current single examination chart to the clipboard or saves it to a graphic file. You can <b>select (Section 8.2)</b> the current chart via the main menu <b>Current parameter</b> .
Series chart	Export   Copy series, Export   Save series		Copies the series chart to the clipboard or saves it. Click <b>here (Section 8.2)</b> for further information about selecting the current type of series chart.
perfusion parameters	Export   Export examinations (  Ctrl + K)	$\Sigma$	Copies the perfusion parameters (averages, RI, PI of velocity, area, intensity, patient and video information) of all examinations of the open patient file to the clipboard. The examinations are separated by lines, the fields of the export are separated by tabulators. Hence, when you paste them in common applications such as Microsoft Excel, the information will be properly pasted in the cells. Click <b>here</b> to receive further information.
perfusion parameters of <b>all</b> examinations	Export   Export all patients		Copies the perfusion parameters of <b>all</b> former patient files of the current user, i.e. all patient files in the user's patient directory (this directory is set in the <b>user (Section 6.11.2)</b> form). To carry out this command may take a while, if you have many large patient files. The format and options of this function are the same as when exporting a single examination.

## Options

To determine, which of the fields shall be copied, click on **Export | Export settings**.

Activate the hooks of the fields which shall be exported. Set **Paste title** to receive a brief description of the columns in the first line of the exported data. You can change the order of the items via drag&drop (press the left mouse button, move the mouse, and release the mouse button).

The items refer to:

- **[v / A / I][mix / red / blue][average / RI / PI]** means: first, view the specified parameter v (velocity), A (area) or I (intensity); second, take the mix value (average of red and blue one), the red or the blue value, respectively. Third, take the average, RI or PI. This number will be exported.
- **whole intensity** and **average intensity** is the sum and the average (= (red + blue)/2) of the average (during the period) of the intensity (average intensity is the same as *I mix average*, is only there for backward compatibility).
- **color frequency** refers to the color frequency of the transducer (as input by the user).
- **maximum velocity** refers to the automatically recognized or manually input Doppler maximum velocity.
- **scale** refers to how many pixels are 1 cm (recognized either by manual calibration or by automatic recognition).
- **ruler, parallelogram (1st edge)** and **parallelogram (2nd edge)** gives the corresponding lengths (or 0, if not used)
- **scaling factor (ring or inner part)** gives the factor which was used to stretch the ROI (if the mode "ring" or "inner part" (see **presets (Section 6.9.1)**) was used).
- **area of ROI** refers to the area of the ROI in cm<sup>2</sup>.
- **area of ROI (area-only measurement)** refers to the area of the ROI, when the mode was "area-only-measurement" (see **examination modes (Section 6.12.4)**).
- **artifact warning** exports, when PixelFlux raised an artifact warning for the examination (using auto mode, only) (see **artifact warning (Section 6.10.8)**)
- **special algorithm** exports, whether PixelFlux used the special algorithm during the examination (see **special scale detection (Section 6.10.7)**).
- **relief information (intensity)** and **further relief information (intensity)**: quantitative results obtained by analyzing the perfusion relief (see **perfusion relief (Section 7.4)**). You can choose whether you want to

export these data with reference to intensity or area distribution.

- The **editing time** informs you when the PixelFlux measurement was performed. (This is not identical with the examination date, which is the date of performance of the ultrasound examination).
- The **avg. shape area**, **avg. shape curvature** and **avg. curvature variance** are the average values of the **shape analysis (Section 6.12.8)**.
- The item **angle (angle correction, in °)** is the angle used for the **angle correction (Section 6.12.4)** (both for usual and for 3D examinations). If no angle correction is done, this field will be void.
- **additional information (strings)** exports a some additional information concerning the examination: the **label (Section 6.9.1)** you (might) have placed somewhere in the image, **a few selected items of the DICOM header (Section 6.12.2)**, the program version of PixelFlux and the user name you have used when creating the examination.
- **volume (single vessels only)** exports the flow volume. Use the volume for examinations of single vessels only.

## 10 Glossary

### C

#### **Calibration**

Calibration is the gauging process of the image with respect to the scale and the Doppler maximum velocity. See **image calibration (Section 6.3)**.

#### **Click mode**

The click mode is the status the main form is currently in. Depending on the currently active mode, a click on the image will be interpreted differently. For example, if the ruler mode is active, a click will set a point of the **ruler (Section 6.9.1)**, in ROI mode, the **ROI (Section 6.5)** will be outlined etc. See **Click mode (Section 6.11.3)**.

#### **Clipboard**

The clipboard can be used for transporting information between several programs. Data, such as graphic files, exported by PixelFlux to the clipboard can be pasted in third-party applications (usually with *Ctrl+V*).

### M

#### **Menu**

The main menu is at the upper border of a window. It allows for the selection of the commands which are available in this window.

### P

#### **Perfusion examination**

A perfusion examination is the analysis of an ultrasound image or video with respect to the colored depiction of perfused areas by the ultrasound machine.

#### **Perfusion parameters**

The perfusion parameters are the data calculated during a perfusion examination. These are flow velocity, area, intensity, and (only for examinations of single vessels) flow volume. Siehe **Visualization of analysis data (Section 7.2)** for further information.

### S

#### **Status bar**

The area at the lower border of a window. It usually shows information about the program status.

### T

#### **Toolbar**

The tool bar contains the icons, which allow you access the program's functions in a graphical way. Usually a tool bar icon corresponds to a main menu item and vice versa. The tool bar is located at the top of every window.

## 11 Activating PixelFlux

Downloading PixelFlux trial versions is free. We kindly ask for your understanding, that the trial versions have to be activated with Chameleon Software. The activation process is quick and easy: after you have installed PixelFlux, start the program. It shows a window with your personal computer code:



In this sample screenshot the computer code would be 144293001438. Please **send (Section 3.1)** us the code which is displayed at your computer. We will send back the activation code, which is necessary to use PixelFlux without functional restrictions, immediately. When you have received the activation code, restart PixelFlux and input the activation code in the lower input box. Now, you have access to all functions of PixelFlux. The activation process is finished.

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