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Project Report

Automatic Detection and Analysis of Tumor Tissue in Prostate Punch Biopsies

Implementation of an Image Processing Pipeline

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Abstract

The prostate cancer is the most common type of cancer we have in Switzerland. Every year about 5300 people develop cancer and around 1300 men die from it. The research for unambiguous indicators for an early detection of the cancer is nowadays an active field in the area of medication. In this context, the aim of a current project at the University Hospital of Zurich is the automatic detection of tumor tissues in prostate punch biopsies. We would like to perform the detection on a cohort from Aarau with samples from about 9900 men to build up a model to describe the cancer's progress.

The current documentation at hand describes the second out of three sub-projects for the automatic detection of the tumor tissues. In the first sub-project we made the acquisition of about 260 images by scanning prostate punch biopsies from the cohort of Aarau. In the current sub-project we implement an image processing pipeline for processing this image data and prepare the pipeline for the upcoming sub-project, which has the aim to find cancerous tissues. The pipeline is based on Microsoft's DirectShow framework and implemented in C++. We offer several base classes which can be used for implementing further steps, so called filters, within the pipeline in a most simple way. As a first example for our pipeline framework we implement a cell nucleus detection algorithm which results can be stored locally or uploaded to a web server. Additionally, we present an evaluation filter which can measure the quality of our detection algorithm.

In the last sub-project we will extend our image processing pipeline with an algorithm for detecting tumor tissues. The algorithm will be optimized using the evaluation filter approach from the current project and the training data from the previous project made by Prof. Dr. Peter Wild.

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Abbreviations

ABI	Application Binary Interface	Interface between program components
AMP	Accelerated Massive Parallelism	C++ library supporting data parallelism
API	Application Prog. Interface	Interface for interacting with a system
BNF	Backus-Naur Form	Notation for context-free-grammars
BPP	Bits Per Pixel	The color depth
C#	C Sharp	Programming language for the CLI
CHM	Microsoft Compiled HTML Help	Help file containing HTML files
CLI	Common Language Infrastruct.	System spec. for platform independency
CLSID	Class Identifier	GUID for COM classes
COM	Component Object Model	Software com. standard by Microsoft
DB	Database	Data collection
DBMS	Database Management Systems	System for managing databases
DLL	Dynamic-Link Library	Shared application library for Windows
FHNW	Fachhochschule Nordwestschweiz	Univ. of Appl. Sc. NW Switzerland
GIT	Global Information Tracker	Revision control system
GUID	Globally Unique Identifier	Unique reference no. within a software
PSR	“Pathology-Study & Research”	Inventory system for study data
TIF	Tagged Image File	Image format for raster graphics
UML	Unified Modeling Language	Modeling language used in software eng.
URL	Uniform Resource Locator	Reference to a resource
USZ	Universitaetsspital Zuerich	University Hospital of Zurich
XML	Extensible Markup Language	Data representation of hierarchical data

1 About the Document

The documentation at hand refers to the implementation of an image processing pipeline for analysis oversized tissue images, by using Microsoft's DirectShow. The documentation starts with the project definition, background and the origin problem to solve in Chapter 2. Before we go into any technical details Chapter 3 refers to a summary of general issues to consider regarding implementing a pipeline system for image data. Following the introduction of the pipeline system, Chapter 4 discusses about its integration in the already existing IT infrastructure and how to evaluate data received from its output. Chapter 5 finally presents the concrete implementation of the pipeline system which was started with a conceptual overview followed by a concrete example of the implementation of an algorithm for cell nucleus detection. To ensure a certain level of quality, the system was tested through several steps as described in Chapter 6 which is important for the current system as well as further evolution mentioned in Chapter 7. The last two chapters 8 and 9 summarize the results of the image processing pipeline and reflect the overall project's achievement.

The documentation excludes UML sequence diagrams as they are hard to read and therefore less beneficial. Instead, we use a simplified version which can be read from the left bottom to the right top. A simple example is shown in Figure 1.1.

```
int main() {
    int a = 0;
    a = inc(a);
    print(a);
};

int inc(int i)    { i++; }
void print(int i) { cout << i << endl; }
```

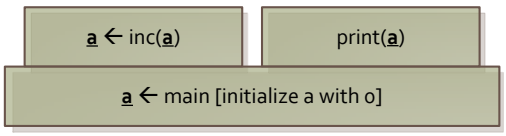


Figure 1.1: Sequence diagram from a short demonstration code.

2 Project Definition

In the previous project called "Implementation of an Inventory System to Acquire Digital Image Data" we built up a process to inventorize patient data and the related punch biopsies from medical studies. Using the system we digitized more than 260 glass slides and annotated around 50 images with cancerous tissue from a cohort of Aarau.

In a next step we would like to analyze this data using a flexible and extendable pipeline system. While the analysis of the image data is mainly part of the upcoming project we focus in the current project on the implementation of the pipeline system. The pipeline supports the ability to analyze image data by using a wide range of algorithms from different domains such as image processing, computer vision and machine learning. Given the new pipeline system we implement a cell detection algorithm as a proof of concept. The algorithm results in several filters which include basic functionalities such as loading and saving an image file or simple transformations such as blur effect or edge detection. Next to the filters required by the analysis task it is also important to measure the performance of the analysis result to benchmark an algorithm. Therefore a precision and recall filter is implemented which can evaluate an extracted feature with the annotations made in the previous project.
The final outcome of the pipeline is again an image file with plotted features, if desired, and an XML file containing analysis information, e.g. about the extracted object features. The XML file structure is based on established applications at the University Hospital of Zurich and therefore can be used in further post processing steps. In this case we also support a point of particular importance: the integration of the pipeline in the already given IT infrastructure.

In the upcoming and last project we will use this pipeline system for detecting tumor tissues and extracting corresponding feature data which represents the final goal of the overall project.

Further details can be found in the attached document "Project definition" which is also enlisted in the appendix 12.9.

2.1 Background

The prostate cancer is the most common type of cancer we have in Switzerland. Every year about 5300 people develop cancer and around 1300 men die from it. A diseased person can be actively medicated, but only with the risk of complications and adverse reactions. The medication is not only restrictively recommended because of the possible risks but also because only 3 out of 40 people die as can be proved by prostate cancer. A major problem presents the early detection of the cancer. All known methods such as the digital rectal examination, the PSA-Test[1] or the biopsy of the prostate do not present unambiguous indicators. It is part of the nowadays ongoing research to find better indicators, e.g. the European Randomized Study of Screening for Prostate Cancer (ERSPC) [1, p.17] [2, p.2]. A current study at the University Hospital of Zurich researches a regression analysis of historical data from patients and extracted features from DNA, RNA and Protein analyses. One sub-project of this regression analysis deals with the extraction of features from prostate images which will be combined with the features from the other areas.
For this purpose an inventory system was implemented where patient data from a cohort of Aarau was put into. Before we can start with the extraction of the feature data we firstly need a robust and flexible data processing pipeline upon which we can base our algorithms. Figure 2.1 shows an overview of the whole project stack.

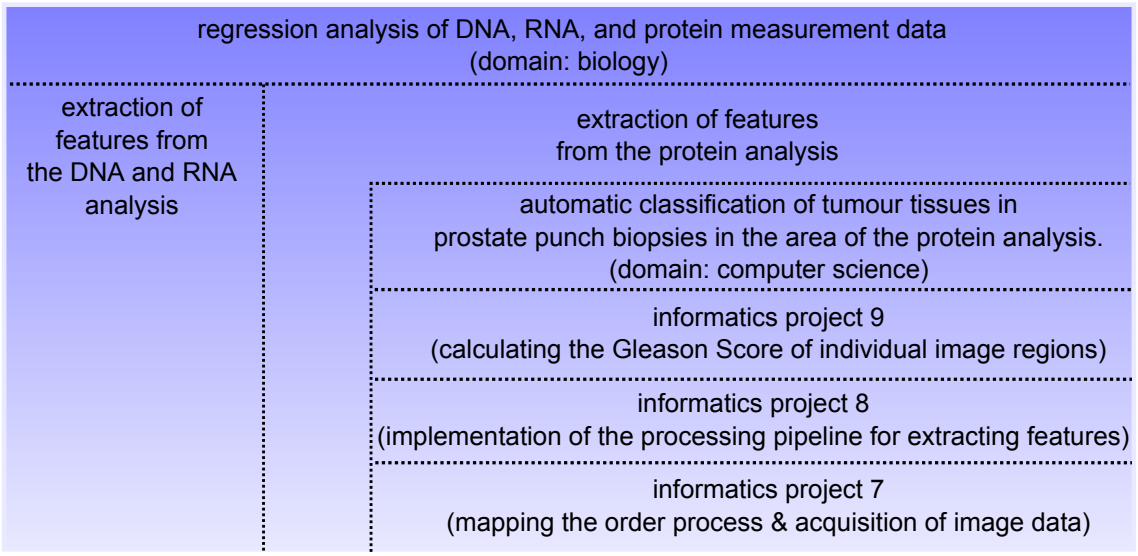


Figure 2.1: Overview of the project stack.

[1] Test method for measure the amount of prostate-specific antigen (PSA) inside the blood.

The main objectives of the roadmap concerning the informatics project (IP) 7 to 9, which are part of the Master education, can be summarized as follows:

Project	**Short description**
IP7	Acquisition of digital image data with the Ventana iScan HT and semi-automation of the inventory process. Additionally, annotation of the image data with areas of healthy and cancerous tissue.
IP8	Implementation of an image processing pipeline. The pipeline's components such as filters or transformations are implemented as plugins which then can be combination in a flexible and extendable way. Based on the new system a cell core segmentation algorithm is developed. To give a qualitative statement about the algorithm we express the performance by its precision and recall.
IP9	Developing an image-based computational score to correlate with the existing Gleason score from the acquired image data for patient stratification and survival analysis. The used algorithms will be evaluated with the annotations from IP7 as a test set and the process from IP8 to measure its performance.

Table 2.1: Overview of the informatics projects.

2.2 Identification of requirements

The University Hospital of Zurich has a developed IT infrastructure which includes an image analysis tool implemented by Norbert Wey. The tool is already in use and connected with other applications. However, the tool was sequentially implemented and is limited in its flexibility and further development. A new system would offer the desired flexibility in an extendable way. Therefore, such a new system was requested, being compatible with the existing infrastructure and following the principal ideas of a modular structure. The current analysis tool is written in C++, which is well established in Norbert Wey's team and runs on a single Windows Server. Based on the given image data from the previous project, the pipeline system has to be able to read BigTIFF files[2] which represent TIFF containers with 64bit offsets.

As a proof of concept a first algorithm should be realized through the new pipeline system to extract cell nucleus. Furthermore, it should be possible to benchmark the algorithm by evaluating the resulting features with the annotations made in the previous project. Based on the given initial situation, the requirements of a processing pipeline are defined as below:

- Implementing a processing pipeline...
  1. allowing the flexible combination of processing steps without restrictions on data types, such as image data
  2. holding an integrated plugin system for further extensibility
  3. being lightweight and supporting performance optimization
  4. being compatible with the existing infrastructure
- Supporting restorable execution plans of pipeline algorithms.
- Enable to evaluate a given algorithm inside the image processing pipeline.
- Implementing a cell nucleus detection algorithm as proof of concept.

[2] `http://www.awaresystems.be/imaging/tiff/bigtiff.html`

3 Image Processing Pipeline

Before we go into technical details about the implementation of the pipeline in the existing IT infrastructure as described in Chapter 4 or how to implement the cell nucleus algorithm as described in Chapter 5 we firstly would like to discuss general issues concerning an image processing pipeline. We discuss advantages and disadvantages for different approaches and give a conclusion which framework fits best for the current project.

3.1 Pipeline System

Talking about a pipeline system in software engineering means a chain of processing steps, so called functions or filters, linked with each other. The pipeline can be filled with data which then traverse through the pipeline being processed by each passing filter. The processed data may or may not result in an output of the pipeline; defined by its behavior.

More specific, the pipeline represents a directed acyclic filter graph as shown in Figure 3.1.

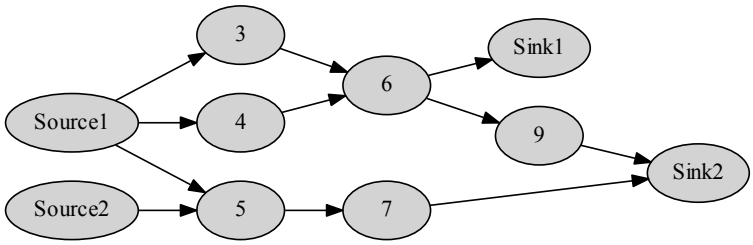


Figure 3.1: Example of a directed acyclic filter graph consisting of ten filters.

We can already find several implementations of such systems so we do not need to start from the beginning. For study purpose a very basic implementation such as Boost's Dataflow and Graph library[1] could be used. However, if we have a more complex system it is helpful if the framework provides not only most basic components of a pipeline system but also provides additional functionalities for managing the underlying graph.

[1] `http://www.boost.org/doc/libs/1_57_0/libs/graph/doc/index.html`
`https://svn.boost.org/trac/boost/wiki/LibrariesUnderConstruction#Boost.Dataflow`

Examples for such functionalities are manipulating the graph's state, e.g. running or pausing the graph, or validating the compatibility while connecting two filters with each other. Such a framework could be the CellProfiler[2] which brings us to a next issue to discuss. The design of the CellProfile prescribes a sequence of consecutively connected steps rather than an acyclic graph which brings strong limitations for the system. We could not implement two execution threads as presented in figure 3.2.

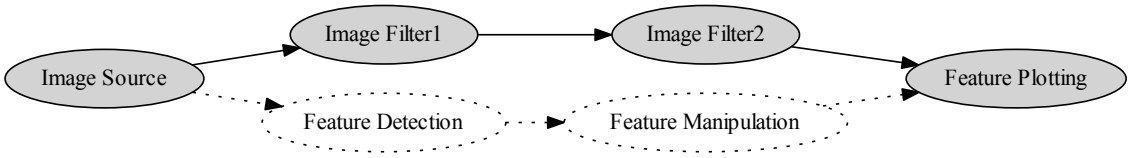


Figure 3.2: Example of two execution threads.

We could simply sequencing the above graph as for example by merging the feature detection, the feature manipulation as well as the two image filter operations into a single filter. However, if we need the first image filter later on in another pipeline combination we could not reuse the merged filter. An example for a more flexible framework fully supporting acyclic filter graphs is Microsoft's DirectShow[3].

3.1.1 Platform Independence

A first and important question to answer before going into any more details is the platform independence. Should our pipeline system run on a single platform or should we support cross-platform compatibility? If we use Java or Python we directly support platform independence where we have to be more careful using programming languages such as C/C++. This especially affects libraries we are able to use for our pipeline system or possible subsystems. Namely the graphical user interface is a key point to mention. Still, we have several options to solve our problem using Qt[4], GTK[5] or Swing[6].

3.2 Plugin Framework

When we talk about a pipeline system we may directly think about a plugin system where each filter represents a single plugin. Indeed, almost all pipeline systems integrate a plugin framework. However, not only the design of a pipeline system which fits perfectly for a plugin integration is the determining factor. If we take an image processing pipeline we could easily think about several dozens base filters, such as a Sobel or Gaussian filter, which one could implement. If such a system supports plugins and

[2] http://www.cellprofiler.org/
[3] https://msdn.microsoft.com/en-us/library/windows/desktop/dd375454(v=vs.85).aspx
[4] https://www.qt.io/
[5] http://www.gtk.org/
[6] http://docs.oracle.com/javase/tutorial/uiswing/

provides a community the software architect only needs to provide the pipeline system whereas the community can implements the corresponding filters. In our case a plugin framework is crucial so later development also from outside the University Hospital of Zurich is possible.

Providing a plugin framework, however, holds some pitfalls we have to discuss in the following sections.

3.2.1 System Calls

Supporting plugins also involves the need of loading them into our system. The plugin, independent it's representation, somehow lays on our file system we need to get access to. If we use Java we have an unified function set for doing so. Under C/C++ and other programming languages we have to care as we can not only use our native functionalities. In C++ for example we could use Apache's Portable Runtime[7] or the libuv[8] library which both supports platform independent system calls.

3.2.2 Binary Compatibility

A more technical problem is the binary compatibility between plugins and the pipeline system. We can distinguish between the application programming interface (API) and the application binary interface (ABI). In a typed programming language the API has to be met during compile time. It specifies e.g. the parameters and abstract methods we have to correctly implement for our plugin. The ABI, however, defines e.g. the order how parameters are pushed onto the stack while initializing a function call. Moreover, it defines the order of virtual functions in an interface or abstract class. This means, as if we use a plugin compiled with an ABI incompatible compiler it might be possible as our pipeline system calls an unexpected method due a wrong virtual function pointer. Again, we do not need to think about this issue using programming languages which do not providing binary compilations such as Java or Python. Nevertheless, if we use e.g. C++ we have to care about it by ourselves, especially if we implement our own plugin framework from the scratch. A corresponding approach using a C communication channel is provided in the appendix 12.1. A great benefit to this subject offer already established pipeline systems or plugin frameworks which provide corresponding functionalities in there base classes.

3.2.3 Plugin Manager

Another issue to discuss is the way we handle our plugins while starting our system and during its runtime. The simplest approach is to load all plugins in binary representation during the system start and do not any further management. More advanced systems provide a plugin manager which can search new plugins also during runtime. If a new

[7] `https://apr.apache.org/`
[8] `https://github.com/libuv/libuv`

object is needed from a plugin we may use a factory which then also can deallocate memory as soon as the object is released. An example implementing a plugin system under C++ using a plugin manager and a corresponding factory can be found in the appendix 12.1.

3.3 Performance Optimization

An important subject concerning image processing is the performance optimization aspect. If we use a pipeline system without any possibilities of performance optimization we may end up with a good overall architecture but insufficient runtime. We only would like to mention a few key aspects when choosing a pipeline system.

3.3.1 Memory Management

When creating new objects or deleting existing ones we need to allocate or deallocate physical memory on our device. Furthermore, if we have function calls with parameters committed by value we face the same effect. Those operations need time especially if we do so excessively. If we consider the internals of a single filter we should care about memory management with an appropriate design. Much more important, however, is the way we pass our data through the pipeline system. Instead of copy a data package each time when passing it over from one filter to another we may think about to use pointers or references. If our programming language do not support such constructs we could use approaches like the factory pattern to manage pipeline-wide data and its memory.

3.3.2 Compilation

If we have a very time sensitive pipeline system we could consider optimization flags while compiling the source code. Depending on the use case one says as applications with repetitive execution sequences may even run faster using a "Just In Time Compiler" (JIT). The substantiation is as follows: Comparing to a generally compiled 32bit code, which is runnable on all 32bit operating systems, an intermediate code could be optimally compiled by a JIT for the architecture the application is used on. If we have repetitive execution sequences we can store the optimized JIT compilation and reuse it later on. If the runtime advantage of the optimized JIT compilation and there reuse is higher than the overhead of the JIT compiling we are faster than native code - in theory[9].

3.3.3 Concurrent & Parallel Computing

An important subject a pipeline system should cover is the ability for concurrent computing. While more programming languages nowadays support concurrent programming

[9] For more details please refer to
`http://stackoverflow.com/questions/5326269/is-c-sharp-really-slower-than-say-c`

we may ask ourselves where to use this technology. Would we use it inside an individual filter or pipeline-wider? A possible approach which is called "Actor Model"[10] could be a single thread handling the whole pipeline system where each filter has its own thread for proceeding incoming data. Alternatively, we could also use a thread pool approach[11] where each idling thread loads data from the source filter and pass them through the pipeline. While in the first approach the largest filter defines the execution time it is the overall longest execution chain in the second approach. We can not give a general statement about which concurrency pattern to use in a pipeline system as it strongly depends on the algorithm used later on. If we discuss about an extendable and flexible pipeline system it is even more uncertain.

Another important aspect to mention is the use of parallelism technologies. Like in concurrency computing we need to choose a programming language with supports appropriate libraries. We then could think about to parallelism filters on other computers or run them on a graphics adapter. However, thinking about parallelism on the level of the whole pipeline also has an enormous impact on the simplicity of our pipeline. We could pass those responsibility to the individual filters and keep the pipeline system lightweight. Each filter then can decide to proceed the incoming data on the graphics card or even outsource the work to another computer. Again, the complexity of such systems grow and we have to weigh up its advantages.

3.4 Reproduceable Execution Plans

Most forgotten is the reproduceability of a pipeline system. Like using an image manipulation program we can process an image in many ways and save them to the hard disk. A year later we still could see the outcome of our work but most probably we could not reproduce the process chain. Depending on the domain the reproduceability could be very important to compare old pipeline results with new ones. Most systems therefore allows to set filter properties and to save the designed filter graph, also called execution plan. In a more advanced system we may even think about to save the filter settings and the corresponding filter graph individually which then can be combined flexible during its initialization.

3.5 Bring It All Together

After having an overview of issues and approaches concerning a pipeline system we can discuss about how to implement our system for the current project. As the old image processing tool at the University Hospital of Zurich is written in C++ and the language is well known by the client it seems likely to use this language for implementing the new pipeline system as well. Using C++ also allows us to migrate the already given

[10] `http://web.fhnw.ch/plattformen/conpr/materialien/scala-actors/11_sl_scala_actors`
[11] `https://msdn.microsoft.com/en-us/library/0ka9477y(v=vs.110).aspx`

algorithms without rewriting the whole code. Furthermore, C++ is a preferred language for high performance applications and also well established in the field of image processing[12]. As the current image analysis tool runs on a Microsoft Server and it is not intended to change the platform we could use a platform-dependent approach which makes the design more simple and understandable.

Based on those pre-definitions we would like to compare three kind of approaches to choose from. The first approach is a self-developed pipeline system starting from the scratch. An intermediate approach is DirectShow which supports us with a pipeline system but is not yet adapted for image data whereas the CellProfiler[13] is an already established image processing pipeline we could use. Table 3.1 compares the three approaches and there advantages.

Issue	**Self-Dev. Pipeline**	**DirectShow**	**CellProfiler**
Filter Graph	(+) At free choice (−) Time consuming	(+) Supports acyclic graphs	(−) Only supports sequential chains
Platform Independence	(+) At free choice (−) Time consuming	(−) Only available under Microsoft Windows	(+) Supported
Plugin Framework	(−) Time consuming (−) ABI issues (−) No default plugin manager	(+) Already included (+) ABI compatibility by base classes (+) Uses system-wide COM-objects	(+) Already included (+) No ABI incompatibility
Performance Optimization	(+) At free choice (+) Supports concurrent programming (+) Supports parallel programming	(+) Is geared toward performance (+) Supports concurrent programming (+) Supports parallel programming	(+) Supports concurrent programming (+) Supports parallel programming
Reproduceable Execution Plans	(+) At free choice	(o) Possible to implement	(o) Possible to implement

Table 3.1: Overview of the informatics projects.

Implementing a new pipeline system would offer a maximum flexibility. Unfortunately, writing all functionalities by ourselves would be very time consuming and exceeding the given budget. Comparing the remaining two approaches we see as DirectShow is platform dependent and the CellProfiler can not proceed acyclic graphs. As platform independency is not a requirement DirectShow is our proffered choice. Another aspect not yet

[12] Some well known tools/libraries written in C++: ITK, OpenCV, Adobe's Photoshop, etc.
[13] The tool was mentioned by the client as possible pipeline solution.

mentioned is the documentation of the frameworks which do not affect the functionality but the development time. Here, DirectShow has an outstanding documentation within the Microsoft Developer Network (MSDN) whereas the CellProfiler has a weak documentation. A last point to mention: the CellProfiler already comes with a ready-to-use set of filters which saves a lot of initial time we have with DirectShow. However, comparing the additional filters of the CellProfiler with DirectShow which supports acyclic graphs and allows its integration into user defined applications (which supports customizable GUIs or security restrictions) do not cover its disadvantages.

4 System Integration

In the last chapter we discussed about general issues concerning an image processing pipeline and compared different approaches with each other. In the current chapter we would like to discuss how to integrate our chosen pipeline framework, namely Direct Show, into the infrastructure of the University Hospital of Zurich and thereby give an overview of our overall system. The next Chapter 5 then goes into technical details about how we can implement the image processing pipeline into an image analysis tool and how we can realize specialized filters for detecting cell nucleus.

4.1 Overview

As mentioned in Chapter 2.2 an important requirement is the integration of the new image analysis tool inside the existing IT infrastructure. The current tool in use expects a folder with images and corresponding XML files of the same name. The XML file contains information about the image, its origin and how it has to be analyzed within the "ImageFile/Processing" node. A more formal definition is given in Table 4.1.

ImageFile	The file to proceed
Processing	Processing information
Order	[opt] Order information
[System]	[opt] System used for the order
[ID]	[opt] ID of the order
[PatientID]	[opt] Patient ID of the order
[ImageID]	[opt] Image ID of the order
Analysis	Analysis information
[Graph]	Filter graph file containing the analysis pipeline
[ID]	Configuration to choose for the analysis
Source	Source information
[OriginalUri]	Name of the source file
[Width]	Width of the source file
[Height]	Height of the source file
[Zoom]	[opt] Zoom level of the tissue scanned as source file
[Stain]	[opt] Staining of the tissue scanned as source file
[Block]	[opt] Block ID of the tissue scanned as source file
[Schnitt]	[opt] Slice number of the tissue scanned as source file

Target	Target information
[ImageName]	Name of the target file
[X]	X origin on the source file
[Y]	Y origin on the source file
[Width]	Width of the target file
[Height]	Height of the target file
[Xres]	X resolution of the target file (in mm/pixel)
[Yres]	Y resolution of the target file (in mm/pixel)
[Zstack]	[opt] Z position where to take the target file from
[Field]	[opt] Area identifier where to take the target file from
[OverviewName]	[opt] Name for a target thumbnail
Classification	Classification information
ObjectClass	Object's classification definition
[ID]	ID of the object classification
[Color]	Color of the object classification
[Name]	Name of the object classification
Properties	[opt] General property information of the processed file
...	[opt] Specific file property, e.g. <P1>1</P1>
ImageObject	[opt] Extracted object information
[ID]	[opt] ID of the extracted object
[ObjectClass]	[opt] Classification of the extracted object
Properties	[opt] Object's property information
...	[opt] Specific object property, e.g. <P1>1</P1>
Contour	[opt] Object's contour information
[ContourWidth]	[opt] Width of the object's contour
[ContourHeight]	[opt] Height of the object's contour
[ContourArea]	[opt] Area of the object's contour
[ContourCenterX]	[opt] X coordinate of the object's contour center
[ContourCenterY]	[opt] Y coordinate of the object's contour center
Point	[opt] Specific point on the object's contour boundary
[X]	[opt] X coordinate of the object's contour point
[Y]	[opt] Y coordinate of the object's contour point

Table 4.1: XML definition for image metadata.

After proceeding such an image the analysis tool writes its results into the "ImageFile/Properties" and "ImageFile/ImageObject" nodes of the same XML file which later on can be visualized and post processed by a web viewer. If our new image analysis tool would like to be compatible with the old one we have to be able to read a set of images from a specific folder, analyze them and save the result in a new XML file readable by the web viewer. The ability to read a set of images by our processing pipeline is described in Subsection 5.2.1.

Our system is not yet ready to integrate with the given infrastructure. Still, there are several more interfaces to define. Firstly, how does the user interact with the analysis tool? As most of the time we have sets of data to process, the tools at the hospital are intended to be used in batch process. We can easily do so by implementing the analysis tool as a command line application. However, we then face the problems as we need direct access to the tool, we need a Microsoft Windows computer to run an analysis on and most users prefer graphical user interfaces instead of command prompts. We could offer a command line application with a graphical user interface and an intermediate application server which makes our tool accessible also for users at the hospital who do not have direct access. However, this would result in a lot of complexity and additional tools to maintain.

Regarding to the previous project we implemented the tool "Patho Study & Research" (PSR), a web based inventory system with a dedicated Microsoft SQL database. Instead of implementing a complex application server we could easily extend the already given PSR system which then is also available to everybody and independently of its operating system. Furthermore, our analysis tool do not need an additional graphical user interface which reduce complexity and supports maintenance. Figure 4.1 visualize the interaction of both tools.

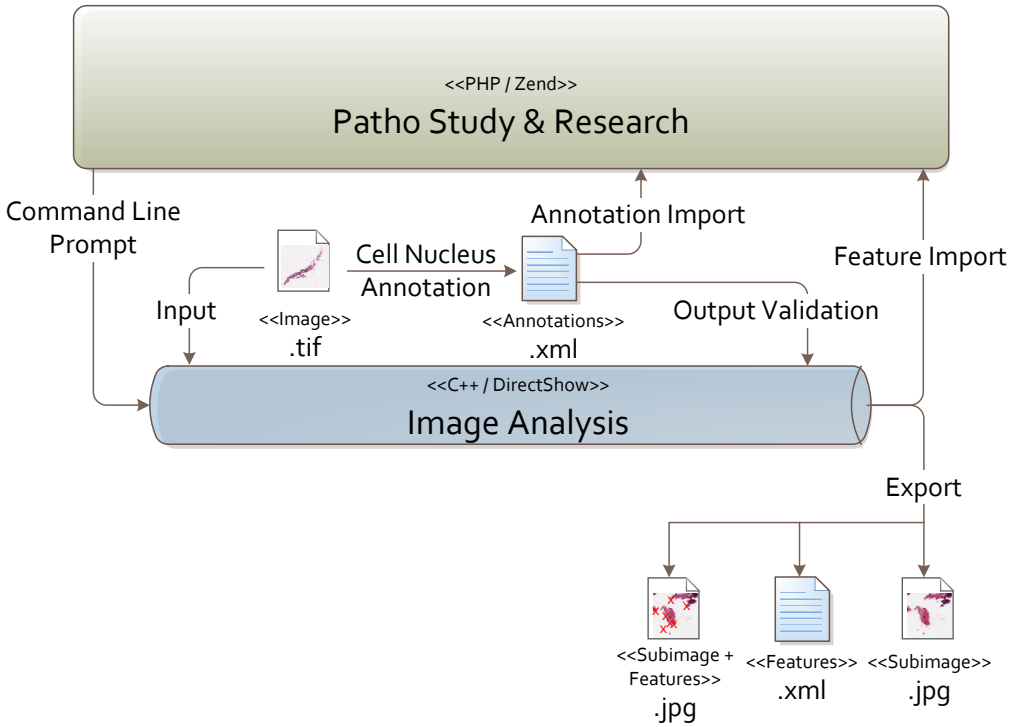


Figure 4.1: Overview of the image analysis pipeline integration.

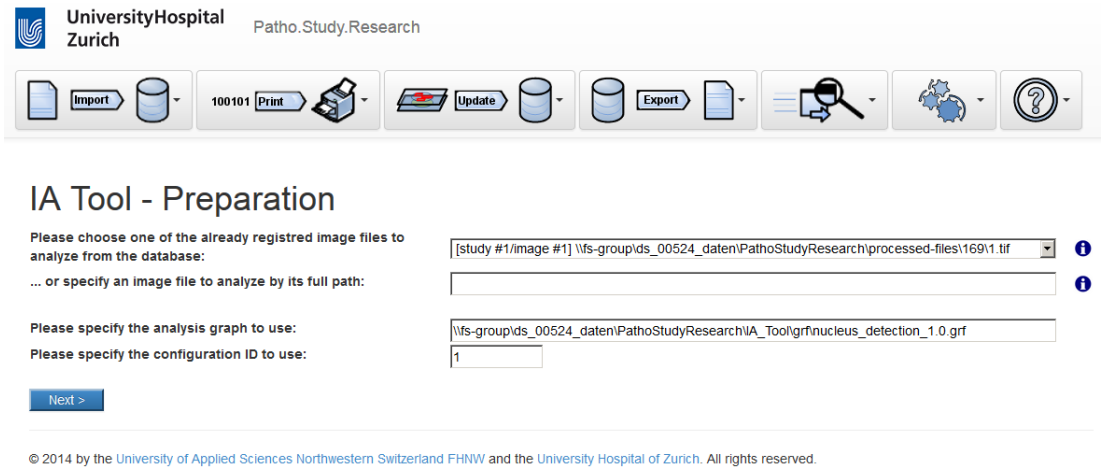
As we can see, the PSR system calls the image analysis tool with parameters which define the path to an image and the properties how to analyze this image. The output, as described, has to be an XML file e.g. with resulting features. Next to the XML file we may provide additional data as e.g. image files. One could be the origin image tile which can be visualized in combination with the XML features by the existing web viewer. Another image tile could directly visualize the features found during the analysis.

A requirement we put aside until now is the ability to evaluate an algorithm from our analysis tool. To do so we firstly need labeled data which we can compare with the outcome of our analysis process. The so obtained evaluation measurements could be saved additionally within the resulting XML file. The labeled data could be load from a simple XML file containing annotations or downloaded from the PSR system which already provides the required functinoalities. The same way we could upload our resulting XML file directly to the PSR tool instead of saving the file locally.

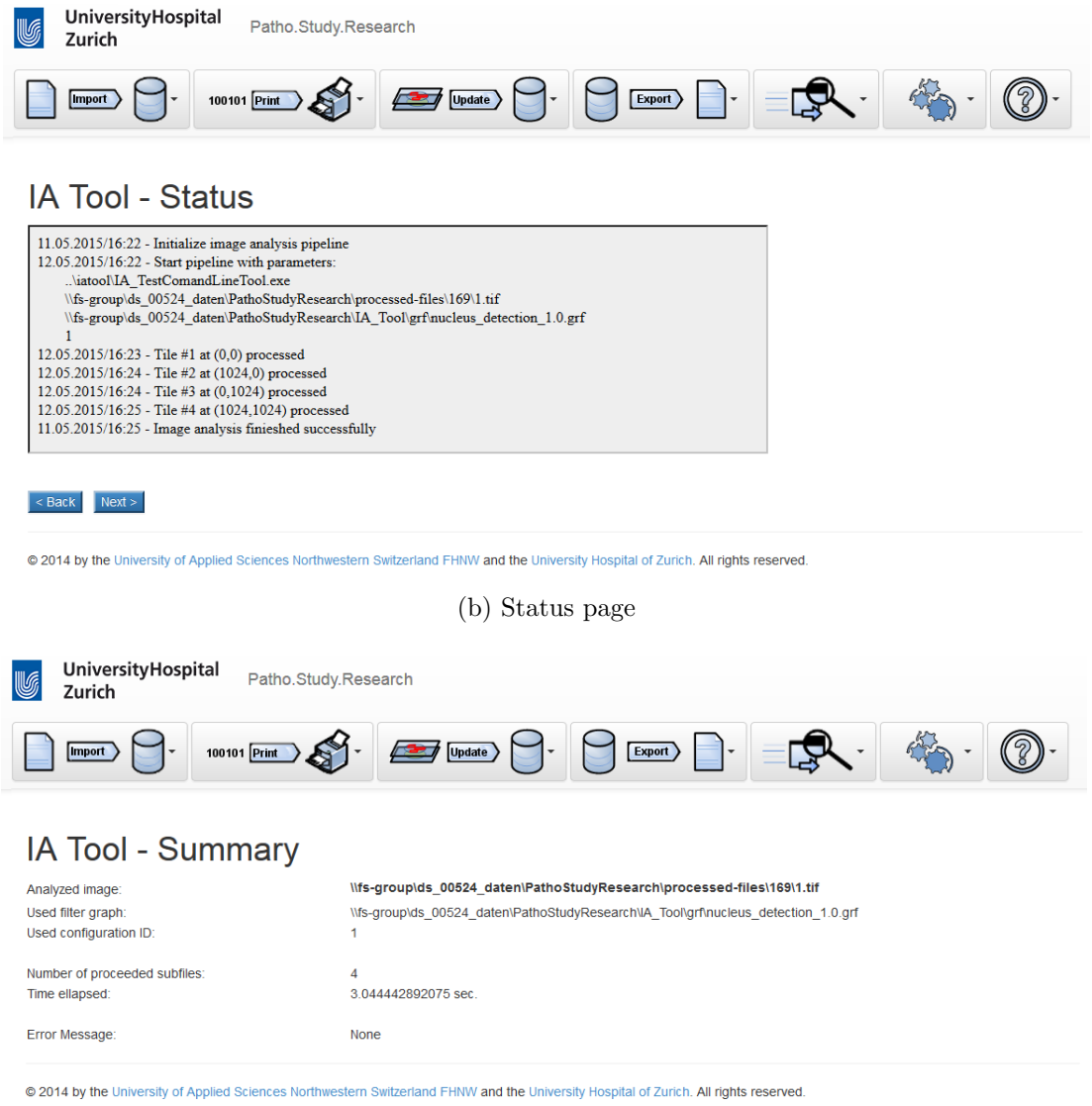
More details about the overall process are provided by the following sections.

4.2 Graphical User Interface

The graphical user interface is implemented in the already given PSR system. Therefore, we extend the system with a new routine as visualized in Figure 4.2 which allows the user to define settings, to run the analysis process and to acquire feedback about the actual results. The settings page is a simple web form which values are used as parameters while calling the image analysis tool by command prompt. The user will see the status of the image analysis tool by an automatically refreshing status page where the underlying web application grab the output of the IA tool, written in the standard output stream (stdout), and prepare it as web content. After the IA tool finished the user is redirected to an overview page containing statistic information and the results from the analysis.



(a) Preparation form



(b) Status page

(c) Process summary

Figure 4.2: Graphical user interfaces of the image analysis process.

When the PSR system calls the IA console tool by command prompt using the function "$\$handle = popen(\$cmdCommand)$" it holds a handle to the executing program. Using this handle with the function "$\$buffer = fgets(\$handle)$" we can access the *stdout* stream and receive all status reports from the IA tool. The PSR system redirect all those information to the status page which is continuously updated for the user.

4.3 Data Transfer

The data transfer between the image analysis tool and the PSR system is web based and described in [3, p.48–50]. To upload a result file from the analysis the PSR tool expects a POST request with XML data. More details about creating and parsing XML files under C++ is given in Chapter 12.5. Depending on the library used the POST header is generated automatically or need to be defined manually. An implementation example is given by the "Contour Sink" filter described in Section 5.3.11. After sending the header information we can start uploading the XML file which structure is given by Table 4.1.

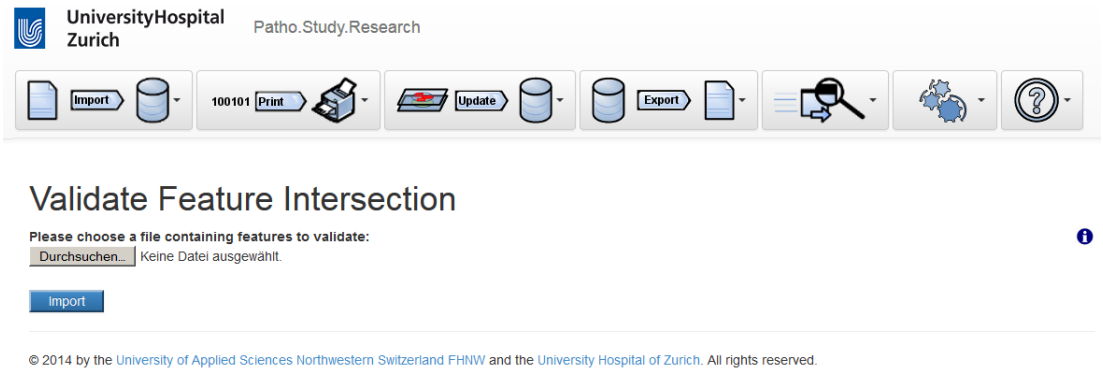
4.4 Training Data Sets

The training data set for the cancerous tissue areas is given by the previous project. However, for our nucleus detection algorithm an additional training set is required containing the annotated cell cores. The annotations were made with the Ventana image viewer and saved as XML files. A detailed description about the XML structure can be found in [3, p.49–50].

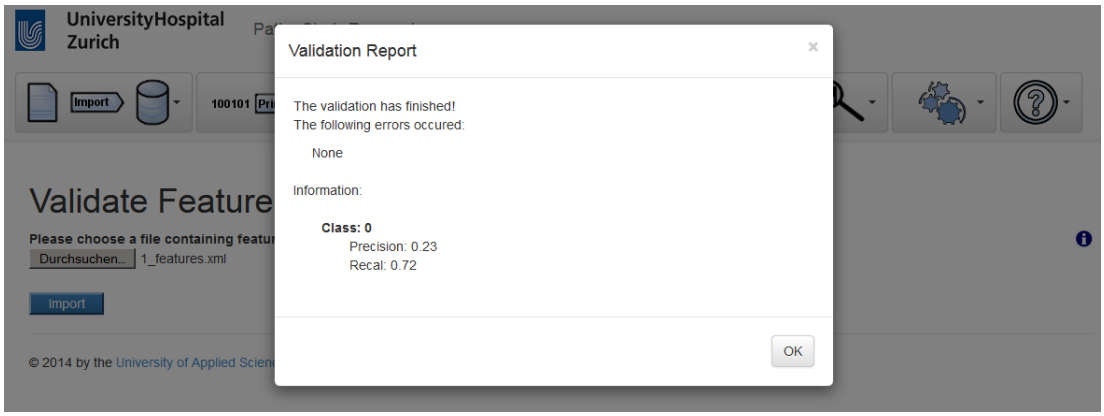
4.5 Data Evaluation

For evaluating an algorithm's result from the image analysis tool we compare its resulting feature objects, the cell nucleus, with the annotations given by the training data. We now can calculate a measurement value like the precision and recall values for expressing the algorithms quality. Like the mean square error (MSE) there are many more statistical approaches for a measurement value. With the precision and recall values we choose a simple and easy to calculate approach which information are already sufficient for tweaking an algorithm as described in Chapter 5.4.

Another functionality to mention in this context is the "feature validation" which allows the manual upload of a resulting XML file from the image analysis tool to the PSR system. Hereby, the system calculates the precision and recall values from the intersections of the given XML data with annotations previously uploaded to the system. The process is visualized in Figure 4.3.



(a) Preparation form



(b) Validation report

Figure 4.3: Graphical user interfaces of the feature validation process.

The intersection itself is calculated on the Microsoft SQL Server which also holds the annotation data. Since SQL Server 2008 spatial data are natively supported which provides useful functions for handling geometry data. For more information we refer to the official documentation at `https://msdn.microsoft.com/en-us/bb933790.aspx`.

5 Image Analysis Tool

The current chapter describes the technical details about the implementation of the Image Analysis tool (IA) using DirectSow as internal image processing pipeline. We start with an overview of DirectShow and discuss specialized filters later on. Software tests and evaluation scenarios can be found in Chapters 6 and 7. The results obtained by the IA tool are described in Chapter 8.

The source code itself is listed in the appendix 12.9 and available as attached material, documented by appropriate comments.

5.1 Overview

The IA tool can be considered as a wrapper for the DirectShow pipeline. The command line tool expects three parameters to initialize and to run the analysis process. The parameters are enlisted in Table 5.1.

Parameter	Description
image file	The image file to analyze.
graph file	A GRF file contains the filter graph to execute. The filter graph defines the filter in use, how they are connected with each other and defines the standard settings. It is also called execution plan.
config id	The configuration ID defines the set of filter configurations to load.

Table 5.1: Parameters of the IA tool.

The internal data flow is visualized in Figure 5.1. We first load the filter graph, set up the participating filters with properties defined by the configuration ID and run the graph with the specified image file. Hereby, the image file parameter is treated like a normal filter property, e.g. the logging level of a filter, and set during the filter configurations.

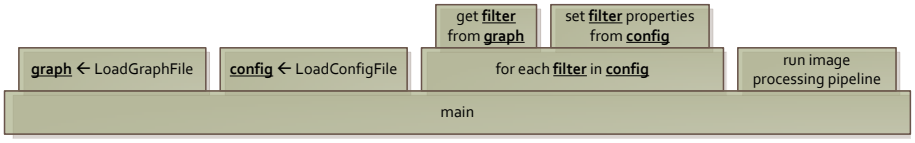


Figure 5.1: Main sequence of the IA tool.

The requirement, enlisted in Chapter 2.2, is the support of a restorable execution plan. Therefore, the tool distinguishes between a graph file and a configuration file for more flexibility. While the graph file containing the graph in a modified Backus-Naur Form (BNF) is specified by Microsoft[1], the configuration file is newly defined in XML notation as given in Table 5.2. All attributes are written in brackets and the XML definition is omitted. XML is the preferable format and widely used in the hospital's environment.

Graph	The root node containing all related configurations
├── [Name]	Name of the graph
├── [Configurations]	Number of available configurations
├── Configuration	A specific configuration
│ ├── [ID]	ID of the configuration
│ ├── Filters	All filters specified by the configuration
│ │ ├── Filter	A specific filter
│ │ │ ├── [Name]	Name of the filter
│ │ │ ├── Settings	All settings of the filter
│ │ │ │ ├── Setting	A specific setting
│ │ │ │ │ ├── Key	Key of the setting
│ │ │ │ │ ├── Value	Value of the setting

Table 5.2: XML definition of a graph configuration.

A possible configuration file may show as follow:

```
<?xml version="1.0" standalone="yes"?>
<Graph Name="Graph001" Configurations="1">
  <Configuration ID="1">
    <Filters>
      <Filter Name="IA (Pre) Simple Transform Filter"/>
        <Settings>
          <Setting Key="LogLevel" value="INFO"/>
          <Setting Key="effect" Value="1005"/>
        </Settings>
      </Filter>
    </Filters>
  </Configuration>
</Segmentation>
```

We now have a configured filter graph which we can run. Regarding how is this filter graph is build up and how we can control it, we start our explanation with a short introduction to DirectShow. However, the concept behind can be found not only in DirectShow but also in many other filter graph pipelines. The graph consists of three filter

[1] The format specification is given at
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd388788(v=vs.85).aspx`

types: a source, a transformation and a sink filter. As the names suggest, the source filter loads a file, the transform filter manipulates them and the sink filter saves them again. The graph can be composed by any number of those filters which then are linked with each other by pins. While the source and sink filter most of the time only provide a single pin and the transformation filter provides two pins there are no hard limitations.

While connecting pins or starting and stopping the graph a single thread is involved: the application thread. This thread validates filter connections for compatibility and, in its very basic form, starts a new thread in each source filter, the so called streaming threads. Such a thread load data from a given source, traverse through the graph and save the data due a sink filter. After handling the data it returns back to the source filter and delete the before allocated memory. Using this approach limits us to a sequential execution of the pipeline without possibility of concurrency. This contradict the requirement of a performance pipeline as described in Chapter 2.2. We could think about to initialize new threads by ourselves and let them run over a defined number of filters or somehow initialize several filter graphs in parallel. A much simpler solution is described in terms of DirectShow filters under Windows Embedded Compact 7[2]. Here, we use the COutputQueue class on each output pin which is managed by a dedicated and individual thread. After loading a data sample in the source filter the first streaming thread hand over his data into a COutputQueue and returns immediately to load a next data sample. The sample is then taken by a second streaming thread which proceed the sample in the down-streaming filter and, again, hand it over to the next COutputQueue. Like before, the second streaming thread returns to his origin queue and take the next sample to proceed. This way, each filter can run concurrently whenever work is available. However, the approach has one pitfall to care about. The more filters we integrate in our graph the more queues we have and the more potential data we could store there. Not to exceed our memory limitations we have to care about this issue by ourselves. Generally we should proceed non-oversized images and reduce there size as the number of filters inside the pipeline increases. Figure 5.2 summarize the described components of a DirectShow filter graph.

[2] `https://msdn.microsoft.com/en-us/library/jj659790(v=winembedded.70).aspx`

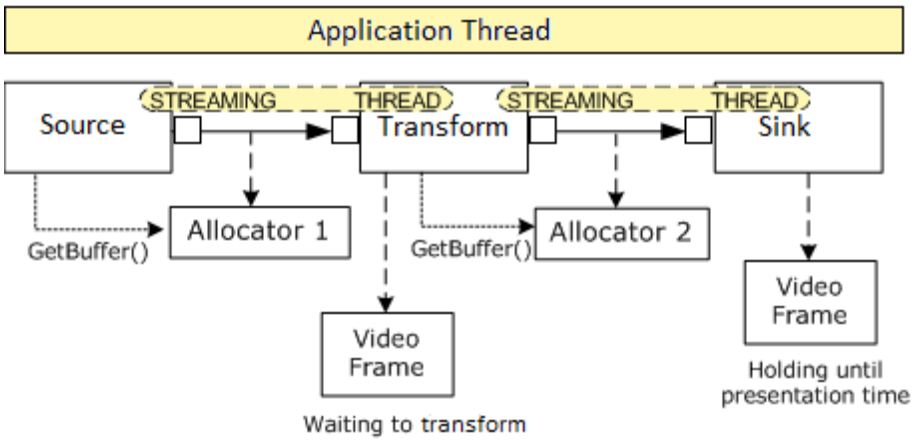


Figure 5.2: Components of a DirectShow filter graph[1].

The following sections describe the base filters which are provided by Microsoft more in detail. The source code is provided with the Windows SDK and located under "[SDK Root]/Samples/Multimedia/DirectShow/BaseClasses". Compiling the base classes results in the library "strmbase.lib" which is used later on for the image analysis filters described in Section 5.2.1.

5.1.1 Build Up A Filter Graph

Before we go into any details about how a filter looks like we would like to start more generally by building up a first filter graph. We can do so either using a graph editor with a graphical user interface such as GraphEdit from Microsoft or programmatically within our own application. We starting with a simple example using GraphEdit. We would like to proceed our before acquired images by an edge detection algorithm. Therefor, we simply start GraphEdit and insert the "IA TIFF Ventana Source Filter" over the menu "Graph/Insert Filters..." as visualized in Figure 5.3. The filter is then located in the category "Image Analysis". We do the same for the filter "IA (Rep) Sobel Filter".

[1] Adapted from
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd390948(v=vs.85).aspx`

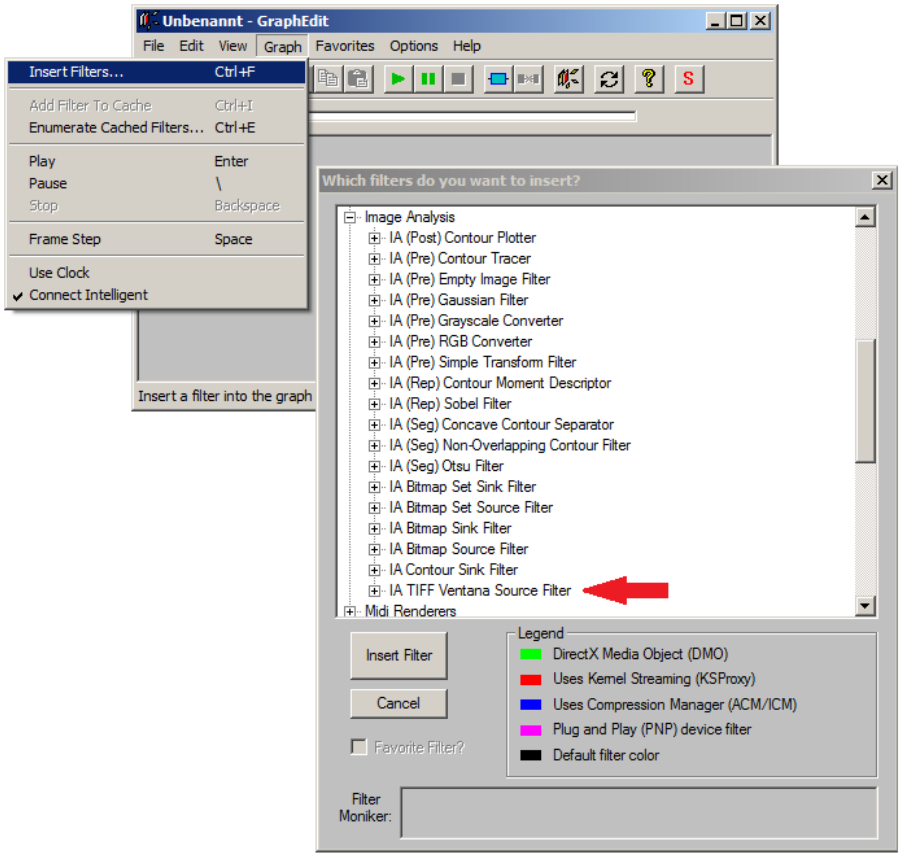


Figure 5.3: Inserting a filter in GraphEdit.

By clicking and holding the mouse button on a filter's input pin an arrow occur which than can be dragged to a desired output pin to connect. By releasing the mouse button on the output pin the connection is tried to be establish. If the connection fails an error message appears, otherwise the arrow remains. Doing so from the source filter to the Sobel filter automatically implies an RGB converter which is necessarily as the format of the Ventana images is RGB24 while the Sobel filter expects RGB32 images. Finally, we perform a right click on the Sobel filter's output pin and choose "Render Pin" for including Microsoft's standard "Video Renderer" as visualized in Figure 5.4.

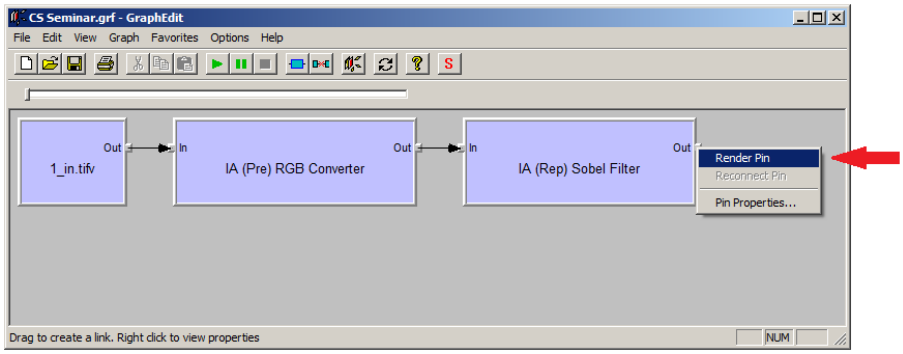


Figure 5.4: Rendering a pin in GraphEdit.

We now have an executable pipeline which can be applied for all tiles of the source image using the run button ( ) or can process each tile separately using the seek function ( ). Moreover, we can also save the current filter graph by "File/Save Graph (.GRF)" which later on can be restored by the FilterGraph or imported in our own application. For more information about the FilterGraph we refer to the official MSDN page at `https://msdn.microsoft.com/en-us/library/dd377601(VS.85).aspx`.

The graph editor is is not only useful for creating and saving filter graphs but is also practical for debugging, testing and prototyping. However, we may would like to implement a filter by ourselves without using any filter graph. Therefore we present the programmatically way of our above example in Listing 5.1.

```
void main(int argc, char* argv[]) {
    IGraphBuilder *pGraph = NULL;
    IMediaControl *pControl = NULL;
    IMediaEvent   *pEvent = NULL;

    // Initialize the COM library.
    HRESULT hr = CoInitialize(NULL);

    // Create filter graph manager & query for interfaces.
    hr = CoCreateInstance(CLSID_FilterGraph, NULL, CLSCTX_INPROC_SERVER,
        ↪IID_IGraphBuilder, (void **)&pGraph);

    hr = pGraph->QueryInterface(IID_IMediaControl, (void **)&pControl);
    hr = pGraph->QueryInterface(IID_IMediaEvent, (void **)&pEvent);

    // Load the Ventana TIFF source filter
    IBaseFilter *pTiffSource = nullptr;
    const GUID CLSID_IATIFFSOURCE{0x30f6349d,0xb832 0x4f09,
        ↪{0xa9,0x16,0xb7,0xd5,0xcf,0xcf,0xeb,0x6c}};
    hr = CoCreateInstance(CLSID_IATIFFSOURCE, NULL, CLSCTX_INPROC_SERVER,
        ↪IID_PPV_ARGS(&pTiffSource));
```

```
    // Set the image to proceed
    IFileSourceFilter* fileSourceFilter = nullptr;
    pTiffSource->QueryInterface(IID_IFileSourceFilter,
        ↪(void**)&fileSourceFilter);
    fileSourceFilter->Load(L"C:\\tmp\\myImage.tif", NULL);

    hr = pGraph->AddFilter(pTiffSource, L"IATIFFSource");

    // Load the Sobel filter
    IBaseFilter *pSobelFilter = nullptr;
    const GUID CLSID_IASOBELFILTER{0x71ac9203,0x4afc,0x42a9,
        ↪{0xae,0x17,0x12,0x69,0x9f,0x55,0xaa,0x3}};
    hr = CoCreateInstance(CLSID_IASOBELFILTER, NULL,
        ↪CLSCTX_INPROC_SERVER, IID_PPV_ARGS(&pSobelFilter));
    hr = pGraph->AddFilter(pSobelFilter, L"IASobelFilter");

    // Establish connections
    IPin *pOut = NULL;
    hr = FindUnconnectedPin(pTiffSource, PINDIR_OUTPUT, &pOut);
    hr = ConnectFilters(pGraph, pOut, pSobelFilter);
    pOut->Release();

    hr = FindUnconnectedPin(pSobelFilter, PINDIR_OUTPUT, &pOut);
    pGraph->Render(pOut);
    pOut->Release();

    // Optionally save filter graph
    // SaveGraphFile(pGraph, L"C:\\tmp\\myGraph.grf");

    if (SUCCEEDED(hr)) {
        // Run the graph.
        hr = pControl->Run();
        if (SUCCEEDED(hr)) {
            long evCode;
            pEvent->WaitForCompletion(20000/*ms*/,&evCode);
        }
    }

    SafeRelease(&pTiffSource);
    SafeRelease(&pSobelFilter);

    pControl->Release();
    pEvent->Release();
    pGraph->Release();
    CoUninitialize();
}
```

Listing 5.1: Programmatically implementation of a filter graph.

The programmatically implementation is quite similar to the filter graph buildup with GraphEdit. We create the filter graph itself and the participating filters, connect the pins with each other, add the video renderer and run the graph. As before, the RGB

converter is automatically involved due image format incompatibility as described before. The implementation of all additional functions given in Listing 5.1 can be found at MSDN as follow:

General Graph-Building Techniques - Connect Two Filters
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd387915(v=vs.85).aspx`
General Graph-Building Techniques - Find an Unconnected Pin on a Filter
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd375792(v=vs.85).aspx`

5.1.2 Source Filter

The most interesting part on the source filter is not the filter itself but its related pin "CSourceStream". Whenever the filter graph changes from a stopped state into a running or paused state its application thread calls the "Active" method on all pins inside the graph. Thereby, "CSourceStream" pins react in a special way and create a new streaming thread each. Such a thread has his own, never ending, "ThreadProc" routine and reacts on commands sent by the application thread. If the filter graph is running or paused the streaming thread enters the "DoBufferProcessingLoop" and creates an empty sample, fills it with data, delivers it to the output queue and releases it afterward. During all this steps we only call once the underlying source filter "CSource". This is, when we call the method "FillBuffer". Inherit from a source filter means we have only to implement the "FillBuffer" method to compile a valid source filter. Figure 5.5 visualizes the sequence diagram of the "CSourceStream".

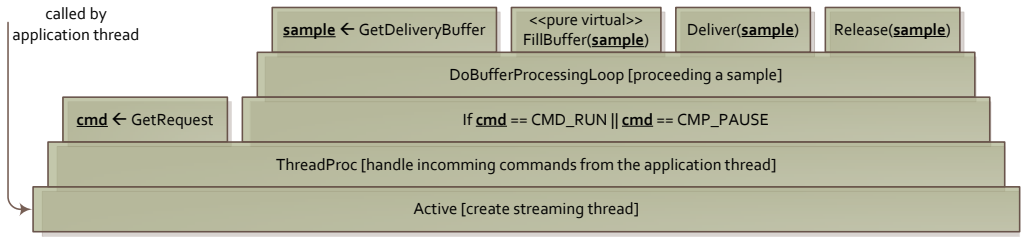


Figure 5.5: Sequence diagram of the "CSourceStream" pin.

5.1.3 Transform Filter

The transform filter "CTransformFilter" is prepared for holding two pins. One input pin "CTransformInputPin" and one output pin input pin "CTransformOutputPin". When receiving a sample from an up-stream filter the "Receive" method of the input pin is called. The pin calls the same method on "CTransformFilter" which then process the sample. It firstly initializes a new output sample and copies the header information

from the input to the output sample. It then transform the input sample into the output sample and delivers the output sample to the down-stream's input pin. At the end it releases the output sample again (the input sample will be released by the caller of "CTransformInputPin::Receive"). Inherit from the transform filter means we have only to implement the "Transform" method to compile a valid transformation filter. Figure 5.6 visualizes the sequence diagram of the "CTransformFilter".

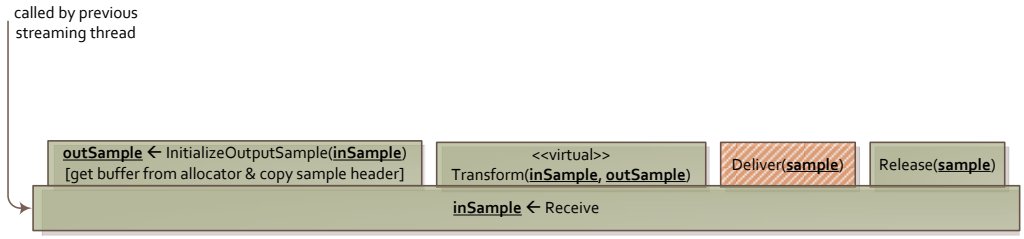


Figure 5.6: Sequence diagram of the "CTransformFilter".

An inconsistency is highlighted in Figure 5.6. When delivering a sample to the input pin of the down-stream filter the base implementation directly calls the "Receive" method of this pin. In this situation the "CTransformOutputPin" has no functionality but only links the transform filter with the input pin from a down-stream filter. Instead, we should call the "Deliver" method of the output pin so we could invoke additional functionality before sending the sample. This behavior is corrected in the "CIABaseTransform" filter as described later on.

5.1.4 Sink Filter

The simplest of all base filters is the sink filter. When receiving a sample from an up-stream filter the "Receive" method of the "CRenderInputPin" is called which only validates the sample. For a meaningful action we should call a method like "SaveSample" on the underlying sink filter. As there is no explicit base sink filter available we have to implement one by ourselves; inheriting from "CBaseFilter.

5.1.5 Filter Connection

DirectShow has an intelligent system for validating pin connections. Generally, each output pin has to proved one or more so called media types. The media type defines the content of a sample by its type (e.g. Video), subtype (e.g. RGB24) and format (providing additional information like bits per pixel). When connecting an output pin with an input pin all provided media types by the output pin are tried until either the input pin accepts or the connection is rejected. The base transform filters provide an additional check when connecting the output pin with a down-stream input pin. We still

enumerate through all media types provided by the output pin and try to find a compatible one. However, as soon as we found one we do not yet connect the two pins. An additional method "CheckTransform" is invoked to verify as we can transform the input type into the output type. This method is essential for converters. Figure 5.7 visualizes the validation sequence (also called "Media Type Negotiation") when trying to connect an output pin with an input pin. The validation is performed by the application thread.

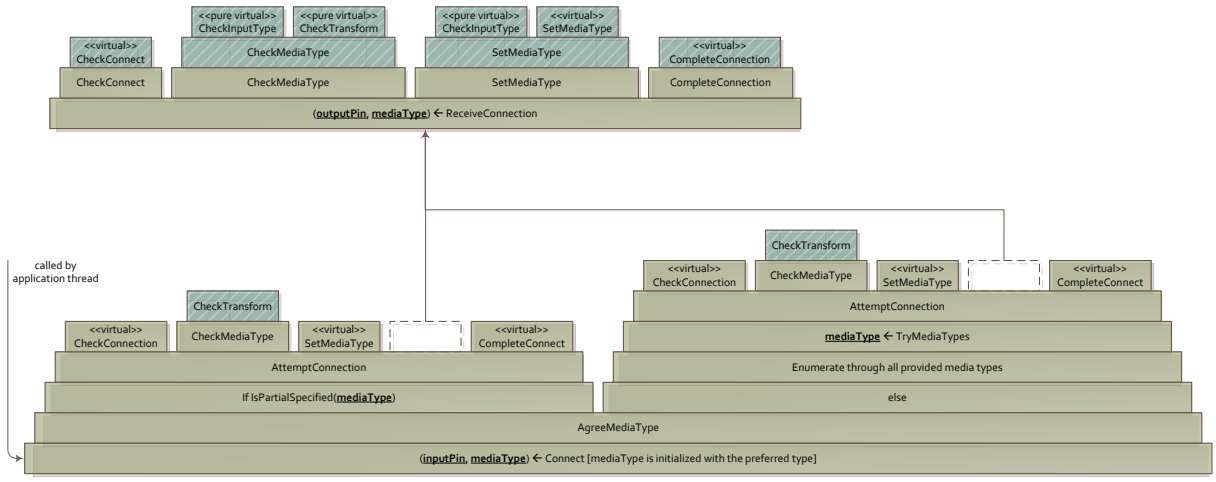


Figure 5.7: Sequence diagram from the connection process of two pins. The solid green boxes represents input respective output pins while the shaded blue boxes represents filter methods.

Moreover, DirectShow provides a mechanisms called "Intelligent Connection" which makes connection possible even two media types are not compatible with each other. Therefore, additional filters are systematically tried between the two incompatible pins, hoping to find a valid conversion filter. An example for such a conversion filter is described in Section 5.2.3. We do not go into more details which can be found at the following website: `https://msdn.microsoft.com/en-us/library/windows/desktop/dd390342(v=vs.85).aspx`

5.1.6 Passing Data Between Filters

As described in Chapter 5.1 DirectShow uses so called sample packages as data containers which then are passed from one filter to another. A sample contains a header and an arbitrary data body whereas the header describes the data representation more in detail. The header mainly contains the media type of the data, its size and time, if the sample is part of a time ordered sequence, e.g. an image from a video. The media type itself can be split up again in smaller attributes as presented in Figure 5.8.

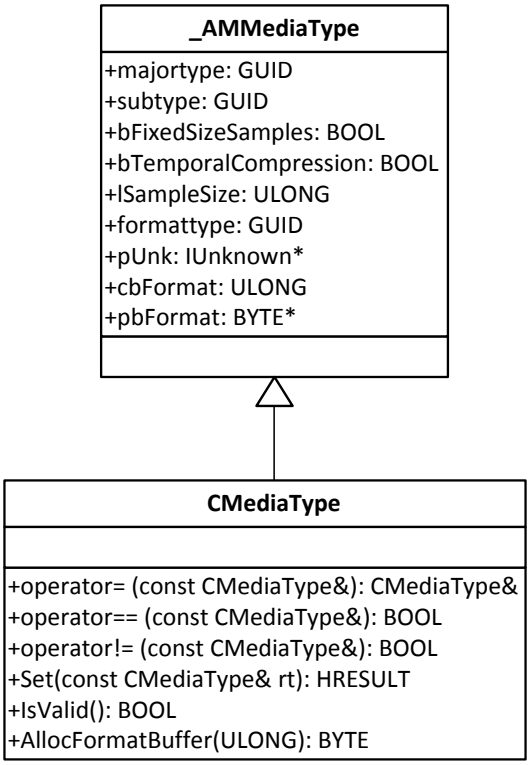


Figure 5.8: Class diagram of "CMediaType".

The major, sub and format types define together the representation of the data body. Each type is related with a globally unique identifier (GUID) specified by Microsoft[3]. Nevertheless, as described in Chapter 5.2 we can also define our own media types for user defined data types. Whereas the major and sub types only consists of a single GUID the format type can be split up again in smaller attributes. As we see in Figure 5.8 the attribute "pbFormat" is only a pointer and can hold any kind of data, specified by the format type. We first can allocate memory using the method "AllocFormatBuffer" and then assign format information like a "VIDEOINFOHEADER"[4]. For a better understanding we give a code snipped in Listing 5.2 as well as the "VIDEOINFOHEADER" and its internal "BITMAPINFOHEADER" structure in Figure 5.9.

[3] The type descriptions are given at
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd390670(v=vs.85).aspx`
[4] `https://msdn.microsoft.com/en-us/library/windows/desktop/dd407325(v=vs.85).aspx`

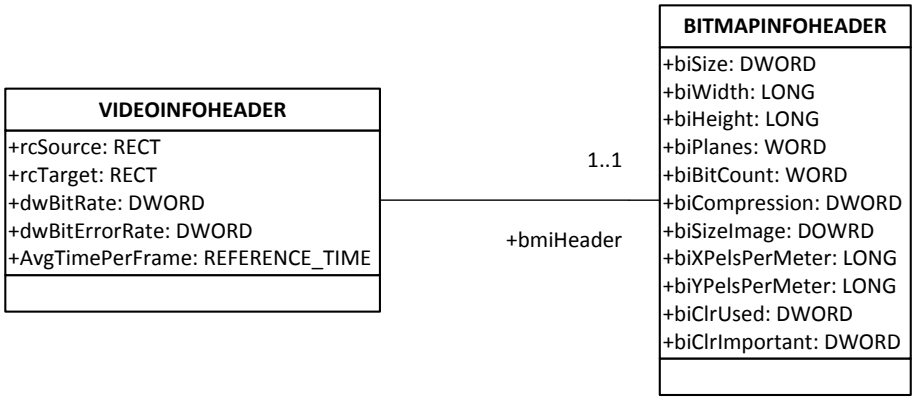


Figure 5.9: Class diagram of the "VIDEOINFOHEADER" and "BITMAPINFOHEADER".

```
VIDEOINFOHEADER *pvi =
    ↪(VIDEOINFOHEADER*)pMediaType->AllocFormatBuffer(
    ↪sizeof(VIDEOINFOHEADER));
ZeroMemory(pvi, sizeof(VIDEOINFOHEADER));

pvi->bmiHeader.biWidth = 1024;
pvi->bmiHeader.biHeight = 1024;
pvi->bmiHeader.biBitCount = 24;
pvi->bmiHeader.biCompression = BI_RGB;

...
```

Listing 5.2: Initialization of a "VIDEOINFOHEADER".

For a detailed description about the attributes in "VIDEOINFOHEADER" and "BITMAPINFOHEADER" we refer to the corresponding MSDN documentation as given above.

Until now we put back the question how we create or destroy a sample and how we manage its life-cycle. As addressed in Figure 5.2 we can find a memory allocator between each two filters which is initialized by the application thread due the creation of the filter graph. The thread calls the "DecideBufferSize" method on each output pin which then asks its up-stream allocator's buffer size or manually calculates the buffer size depending on the media type and the number of requested buffers to reserve. The so obtained buffer specification is then set for the next down-stream allocator. Figure 5.10 visualizes the sequence more in detail.

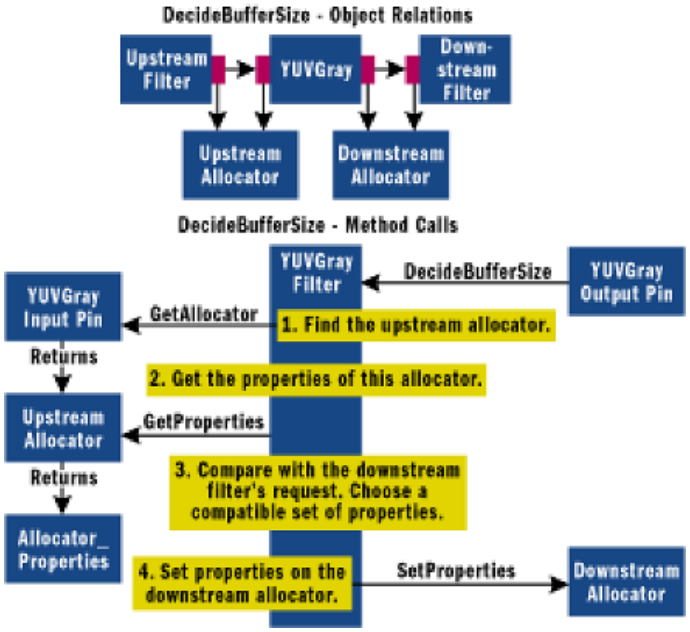


Figure 5.10: Sequence diagram of the "DecideBufferSize" method[1].

Depending on the above reserved memory a streaming thread can now ask an allocator for an empty sample and proceed it. If no memory is available the thread is paused until a currently existing sample becomes obsolete. Making a sample obsolete is straight forward. Whenever a streaming thread receives or creates a sample it has to release it after its proceeding. When calling the method "sample->Release()" the internal reference count is decreased. If this counter reaches 0 the sample get automatically deleted and the free memory is announced to the allocator originally allocating the memory.

For completing our excursion we have to talk about how to pass a sample from one filter to another one. If no other functionality is implemented a filter calls the "Deliver" method of its output pin which then calls "m_pInputPin->Receive(pSample)" to pass the sample to the connected input pin of the down-stream filter. Not to forget: the sample has to be released after returning from the down-stream filter.

[1] Adapted from `https://msdn.microsoft.com/en-us/magazine/cc301631.aspx`

5.1.7 Filter Registration

Before we can finally use our DirectShow filters we have to register them to the system. Therefore, we have to compile them as a dynamic link library (DLL) offering three C functions: "DllMain", "DllRegisterServer" and "DllUnregisterServer". Where the first function is the entry point of our dynamic library the following two functions implement the registration and unregistration routines. Listing 5.3 gives an example of those routines.

```
STDAPI DllRegisterServer()
{
    HRESULT hr;
    IFilterMapper2 *pFM2 = NULL;

    hr = AMovieDllRegisterServer2(TRUE);
    if (FAILED(hr)) return hr;

    hr = CoCreateInstance(CLSID_FilterMapper2,NULL,
        ↪CLSCTX_INPROC_SERVER, IID_IFilterMapper2,(void **)&pFM2);
    if (FAILED(hr)) return hr;

    hr = pFM2->CreateCategory( CLSID_ImageAnalysisCategory,
        ↪MERIT_NORMAL, L"Image Analysis");
    if (FAILED(hr)) return hr;

    hr = pFM2->RegisterFilter(
          CLSID_MYFILTER,         // Filter CLSID.
          L"MyFilter",            // Filter name.
          NULL,                   // Device moniker.
          &CLSID_IACategory,      // Filter category.
          L"MyFilter01",          // Instance data.
          &rf2FilterReg           // Filter information.
    );

    pFM2->Release();
    return hr;
}

STDAPI DllUnregisterServer()
{
    HRESULT hr;
    IFilterMapper2 *pFM2 = NULL;

    hr = AMovieDllRegisterServer2(FALSE);
    if (FAILED(hr)) return hr;

    hr = CoCreateInstance(CLSID_FilterMapper2, NULL,
        ↪CLSCTX_INPROC_SERVER, IID_IFilterMapper2,(void **)&pFM2);
    if (FAILED(hr)) return hr;

    hr = pFM2->UnregisterFilter( &CLSID_ImageAnalysisCategory,
        ↪L"MyFilter", CLSID_MYFILTER);
```

```
    pFM2->Release();
    return hr;
}

//
// DllEntryPoint
//
extern "C" BOOL WINAPI DllEntryPoint(HINSTANCE,ULONG,LPVOID);

BOOL APIENTRY DllMain(HANDLE hModule, DWORD  dwReason, LPVOID
    ↪lpReserved)
{
    return DllEntryPoint((HINSTANCE)(hModule), dwReason,
        ↪lpReserved);
}
```

Listing 5.3: Methods for register and unregister a DirectShow filter.

"DllRegisterServer" firstly creates a filter mapper object witch then can be used to register the new filter category "Image Analysis", if not yet existing, and then to register the filter itself. The function "DllUnregisterServer" do the same but unregister the filter again. Each filter is defined by an unique class identifier (CLSID), which represents a global unique identifier (GUID). This means as the class to register is only identified by its GUID "CLSID_MYFILTER".

A last important fragment of the registration process is the "CFactoryTemplate". When registering a DirectShow filter the template gives all necessarily information such as the function pointer to a method which can instantiate a filter object or the pointer to setup information. If last one is set the filter is automatically registered within the "DirectShow Filters" category. As we would like to use our own category we set the parameter to "NULL". Listing 5.4 gives an example of the "CFactoryTemplate".

```
CFactoryTemplate g_Templates[1] =
{
    {
        L"MyFilter",                // Filter name
        &CLSID_MYFILTER,            // Filter CLSID
        MyFilter::CreateInstance,   // Instantiation func.
        NULL,                       // Init. function
        NULL                        // Set-up information
    },
};
```

Listing 5.4: Example of a template factory.

Additional information about registering a DirectShow filter can be found at `https://msdn.microsoft.com/en-us/library/windows/desktop/dd389099(v=vs.85).aspx` or in the Doxygen documentation of the source code as listed in 12.9.

5.2 Image Analysis Filters

After we get a deeper understanding on how DirectShow works we can start implementing our own image filters and integrate them into a filter graph. However, there are still mechanisms missing or the above described sequences are not yet fully implemented. Therefore, we implement a set of base filters specially for the Image Analysis tool which are described in the next section. Afterward, we go into more details about how to create used defined media types and how to convert them. Finally, we give an overview of the implemented image analysis filter, there specifications and specialties.

5.2.1 IA Base Filters

As DirectShow we offer three base filters for image analysis: "CIABaseSource", "CIABaseTransform" and "CIABaseSink". While inheriting from one of the DirectShow base classes implicates the implementation of at least one pin class and its underlying filter class we would like to simplify this circumstance by offering a single filter class without the need of an additional pin class. We therefor implementing the origin DirectShow base classes and redirect abstract pin methods to its underlying filter class. This makes it possible to inherit from a single filter class and combine all implementation details together. Following we give a more detailed insight about the three image analysis base classes.

IA Base Source The "CIABaseSource" class, which is inherited from "CSource", can be used to load full images or tiles of images to proceed. At first place, the "Load" method is called when including the filter into the filter graph due inheritance from "IFileSourceFilter". Hereby, the chosen file name is stored and the two abstract methods "OpenFile" and "CloseFile" are called. In the first method we can open a handle to the file and load all relevant information like width, height, bits per pixel (BPP) and number of tiles. The first three values are important so the buffer allocator can be initialized when connecting the output pin of our source filter with a down-streaming input pin. Hereby, we can calculate the required buffer size by $Width * Height * BPP$. The number of tiles is important to know when we proceed the last image from a file so we can stop the graph afterward. We do so by incrementing a counter variable "m_iFrameNumber" each time we deliver a sample. If this counter reaches the maximum number of tiles available we return the HRESULT "S_FALSE" from the "FillBuffer" method and set the counter back to 0; same happens when we stop the filter graph to indicate a reset. Under DirectShow this means an "EndOfStream" message is delivered down-stream. After calling "OpenFile" the method "CloseFile" releases the file handle again so we can get access to the file as long as our graph is stopped. As soon as we change the state from stopped to run or paused the application thread will call the method "Activate" which again calls "OpenFile". If we load the whole image into the buffer we can just ignore the call. However, if we need additional information from the file we can reopen it here. Vice versa, if the graph changes to the stop state the application thread calls "Inactive" and with it the method "CloseFile".

Now as we know how the file is accessed we need to read its data and pack it into a sample to deliver. We do so by extending the data flow from 5.5. Within the method "FillBuffer" we call the abstract method "GetImageDataPointer" with the actual frame number as parameter. Depending on this parameter we can now either giving back a pointer to the corresponding tile or a pointer to the whole image if we do not support tiles.

As mentioned in Chapter 5.1 we would like to use a "COutputQueue" within our "CIABaseSourcePin" for the parallel execution of filter procedures. Hereby, we adapt the same mechanism as we do for opening and closing the image handle. When calling the "Active" method we initialize the "COutputQueue" and when calling the "Inactive" method we destroy it again. Destroying the queues including all so far proceeded samples is possible as a stop command means we reset the whole filter graph. So our frame counter is also reset to 0 and we have to start all over again with our analysis.

This is a base implementation and the behavior can freely be adapter. One example is the "CIABaseSetSource" class which inherits directly from "CIABaseSource". The above described approach to read data works just fine for a single file. If we have a set of images e.g. in a specify directory we have to call the "OpenFile" method not only when we run the filter graph but each time we increment the frame counter. This is exactly what happens in the "FillBuffer" method of the "CIABaseSetSource" class. We first call "OpenFile" with the current frame number as parameter, get the pointer to the image data by "GetImageDataPointer" amd close the file handle again by "CloseFile".

A class diagram of the relation between "CIABaseSource" and "CIABaseSourcePin" can be found in the appendix 12.4. Additional information can also be found in the Doxygen documentation of the source code as listed in 12.9.

IA Base Transform The "CIABaseTransform" class, which is inherited from "CTransform", can be used to manipulate our image data, packed inside a sample, while heading down the filter stream. When receiving a sample through the "CTransformInputPin" it is forwarded to our "Transform(inSample, outSample)" method inside "CIABaseTransform". We expect most of the time as we only manipulate the input data. This means we do not need the input as well as the output sample separately. Because of that, we simply copy the input data into the new output sample and forward it the abstract method "Transform(pMediaSample)". In this way a programmer do not even need to think about how to handle input and output samples but can directly work on the output sample which is then directly forwarded to the next filter. This behavior however may not be intended all the time. If we think about a media type converter we need both, the input as well as the output sample. Because there is not guarantee as both samples have the same size we can not simply copy data from the input to the output sample. For this reason the "Transform(inSample, outSample)" method is declared as *virtual* so we can override it if needed.

As mentioned in Figure 5.6 there is an inconsistency in delivering a sample by the "CTransform" filter. Because of that the method "Receive" was slightly adapted so the "Deliver" method of the output pin is called.

Like the "CIABaseSourcePin" also the transform output pin is extended by a "COutputQueue". The mechanisms and behaviors are thereby the same as described for the "CIABaseSource" class.

A class diagram of the relation between "CIABaseTransform" and "CTransformInputPin" can be found in the appendix 12.4. Additional information can also be found in the Doxygen documentation of the source code as listed in 12.9.

IA Base Sink The "CIABaseSink" class, which is inherited from "CBaseFilter", can be used to save image data traversed the processing pipeline. When a sink filter receives data its input pin "CIABaseSinkInputPin" is called by the method "Receive". Hereby, we call the methods "OpenFile", "SaveFrame" and "CloseFile" from the underlying "CIABaseSink".

As we only save data when we receive it we do not need to care if we read from a single source of from a set of images. We only save sequentially our data and release the handle as soon as work is done. For that, we do not need a class like "CIABaseSetSink".

A class diagram of the relation between "CIABaseSink" and "CIABaseSinkInputPin" can be found in the appendix 12.4. Additional information can also be found in the Doxygen documentation of the source code as listed in 12.9.

5.2.2 User Defined Media Types

As previously described, based on the "VIDEOINFOHEADER", we can change the format type of the media type with a user defined one of our choice. With our image processing pipeline we would like to establish an own information header to store additional meta data. If e.g. we send an input image through the pipeline we would like to save the resulting images at the same directory into a new results folder. However, until now we can not pass this information through the pipeline so we have to extend the given "VIDEOINFOHEADER". The following Listing 5.5 shows the relevant code fragments.

```
typedef struct tagIAVIDEOINFOHEADER : public tagVIDEOINFOHEADER
{
    wchar_t* sourceName;
    wchar_t* sourcePath;
    ...
} IAVIDEOINFOHEADER;
```

```
HRESULT MySource::GetMediaType(CMediaType *pMediaType)
{
    IAVIDEOINFOHEADER *pvi =
        ↪(IAVIDEOINFOHEADER*)pMediaType->AllocFormatBuffer(
        ↪sizeof(IAVIDEOINFOHEADER));
    ZeroMemory(pvi, sizeof(IAVIDEOINFOHEADER));

    pvi->bmiHeader.biWidth = 1024;
    pvi->bmiHeader.biHeight = 1024;
    pvi->bmiHeader.biBitCount = 24;
    pvi->bmiHeader.biCompression = BI_RGB;

    // Additional meta information
    pvi->sourceName = L"MySource.png";

    ...
}
```

Listing 5.5: Initialization of an "IAVIDEOINFOHEADER".

The above example only extends the format type but do not yet represents a new media type. If we think about our cell nucleus detection algorithm, described in Chapter 5.3, we could imagine as we only send found geometries of cell nucleus within sample packages and not the whole image as such. We therefore need a new media type describing the data structure we use for saving the geometry. In our case, we would like to send a collection of centroids. However, before we go into details about the data structure we firstly need a new major, sub and format type to define as given in Listing 5.6.

```
// new media type
// {05797C20-D86F-44D7-82A3-FAC3991048AC}
DEFINE_GUID(MEDIATYPE_Metadata,
0x5797c20,0xd86f,0x44d7,0x82,0xa3,0xfa,0xc3,0x99,0x10,0x48,0xac);

// new media sub-type
// {B836F1E4-BDB4-4D3A-87CB-28073BC72AB6}
DEFINE_GUID(MEDIASUBTYPE_CONTOURCOLLECTION,
0xb836f1e4,0xbdb4,0x4d3a,0x87,0xcb,0x28,0x7,0x3b,0xc7,0x2a,0xb6);

// new media format type
// {96ABD28C-C961-4AB1-A281-3997B8FDFC3C}
DEFINE_GUID(FORMAT_IAMetaInfo,
0x96abd28c,0xc961,0x4ab1,0xa2,0x81,0x39,0x97,0xb8,0xfd,0xfc,0x3c);
```

Listing 5.6: GUID definitions of a new media type.

In a next step we can define the new media type format the same way like we did for "IAVIDEOINFOHEADER" as given in Listing 5.7.

```
typedef struct tagIAMETAINFOHEADER {
    ...
    int surfaceWidth;
    int surfaceHeight;

    IACONTOURINFOHEADER ciHeader;
} IAMETAINFOHEADER;

typedef struct tagIACONTOURINFOHEADER {
    IADataStruct  dataStruct;
    IAElementType elementTypes;
    int containerSize;
} IACONTOURINFOHEADER;

enum IADataStruct  { dARRAY, dVECTOR, dLIST, dSTACK };
enum IAElementType { eBYTE, eINT, eFLOAT, eDOUBLE,
                     eBYTE_PTR, eINT_PTR,
                     eFLOAT_PTR, eDOUBLE_PTR,
                     eCOORDINATE,
                     eCOORDINATE_PTR};
```

Listing 5.7: Definition of the new media type format "IAMETAINFO".

With the above structures we can now chose which data structure and which data types we would like to implement. For our above centroid example we may use an integer array. We then set the $IACONTOURINFOHEADER :: dataStruct = dARRAY$ and $IACONTOURINFOHEADER :: elementTypes = eINT$. The sample we would like to fulfill with our data only expects a byte array so we can assign any arbitrary data we like.

5.2.3 Media Type Conversion

A more complex example of a transform filter is a conversion filter. Again, we would like to give an example from the given implementation. As described in Chapter 2.2 we work with a BigTIFF file format containing BGR24 images. This means as each pixel consists of 24 bits which are equally used for the blue, green and red channel. This format should not be confused with RGB24 which stores the channels in inverted order. The BGR24 format however can not be visualized by the given renderer from Microsoft. We therefore need a converter. Again, the new BGR24 format can easily be established by defining a new media sub-type as described in the previous chapter. Firstly, we need to define the supported media types which includes two methods, the "CheckInputType" and "GetMediaType". The first method is called when a down-streaming input filter tries a connection with our filter. Within "CheckInputType" we can decide to accept or refuse the proposed media type. Listing 5.8 gives an example.

```
HRESULT MyConv::CheckInputType(const CMediaType *mtIn)
{
    if (IsEqualGUID(*mtIn->Type(), MEDIATYPE_Video))
    {
        if (IsEqualGUID(*mtIn->Subtype(), MEDIASUBTYPE_BGR24))
        {
            VIDEOINFOHEADER *pvi =
                (VIDEOINFOHEADER *) mtIn->Format();
            if (pvi->bmiHeader.biBitCount == 24)
                return NOERROR;
        }
    }
    return E_FAIL;
}
```

Listing 5.8: Example of the "CheckInputType" method.

In a next step our converter will try to connect to a down-stream filter's input pin. We therefore can offer supported media types by the "GetMediaType" method. When we try to open a connection the application thread will ask this method for our supported media types, each time with another position pointer. This process stops as soon as an accepted media type is found or we return the value "VFW_S_NO_MORE_ITEMS". Listing 5.9 gives an example.

```
HRESULT MyConv::GetMediaType(int iPos, CMediaType *mtOut)
{
    // Read input media type
    HRESULT hr = m_pInput->ConnectionMediaType(mtOut);
    VIDEOINFOHEADER *pvi = (VIDEOINFOHEADER*)mtOut->pbFormat;
    if (FAILED(hr)) { return hr; }

    switch (iPos) {
        case 0:
            // Convert header information
            mtOut->SetSubtype(&MEDIASUBTYPE_RGB32);
            pvi->bmiHeader.biBitCount = 32;
            mtOut->SetSampleSize(
                ↪pvi->bmiHeader.biWidth*pvi->bmiHeader.biHeight*4);
            pvi->bmiHeader.biSizeImage =
                ↪pvi->bmiHeader.biWidth*pvi->bmiHeader.biHeight*4;
            break;
        case 1:
            ...
        default:
            return VFW_S_NO_MORE_ITEMS;
    }

    return S_OK;
}
```

Listing 5.9: Example of the "GetMediaType" method.

As mentioned in paragraph 5.2.1 after we found a valid media type we can still refuse the connection due the "CheckTransform" method. Here, we can finally decide if a conversion is possible or not.

The transformation takes place in the method "Transform(inSample, outSample)" where we get an input sample with the before set input media type and the output sample with enough allocated memory to store the converted data in. In a first step we copy the media header from the input to the output sample and adapt its header information for the converted output media type. We then start converting the data. Listing 5.10 gives a simplified example.

```
HRESULT MyConv::Transform(IMediaSample *pIn, IMediaSample *pOut)
{
    // Copy the header information
    HRESULT hr = Copy(pIn, pOut);
    if (FAILED(hr)) { return hr; }
    // Adapt output media type
    CMediaType pmtOut;
    m_pOutput->ConnectionMediaType(&pmtOut);
    pOut->SetMediaType(&pmtOut);
    FreeMediaType(pmtOut);

    // Start convertion
    CMediaType mtIn = m_pInput->CurrentMediaType();
    VIDEOINFOHEADER *pviIn =
        (VIDEOINFOHEADER *) mtIn.pbFormat;
    CMediaType mtOut = m_pOutput->CurrentMediaType();
    VIDEOINFOHEADER *pviOut =
        (VIDEOINFOHEADER *) mtOut.pbFormat;

    PBYTE pbInData, pbOutData;
    hr = pIn->GetPointer(&pbInData);
    if (FAILED(hr)) { return S_FALSE; }
    hr = pOut->GetPointer(&pbOutData);
    if (FAILED(hr)) { return S_FALSE; }

    if (IsEqualGUID(mtIn.subtype, MEDIASUBTYPE_BGR24) &&
        IsEqualGUID(mtOut.subtype,MEDIASUBTYPE_RGB32) )
    {
        RGB24* pxlIn  = (RGB24*) &pbInData[0];
        RGB32* pxlOut = (RGB32*) &pbOutData[0];

        for(int y=0; y<pviIn->bmiHeader.biHeight; y++) {
            for(int x=0; x<pviIn->bmiHeader.biWidth; x++) {
                pxlOut->byte0 = pxlIn->byte0;
                pxlOut->byte1 = pxlIn->byte1;
                pxlOut->byte2 = pxlIn->byte2;
                pxlOut->byte3 = 0;
```

```
                pxlIn++; pxlOut++;
            }
        }
    }

    ...

    return Transform(pOut);
}
```

Listing 5.10: Example of the "Transform" method.

We now have an operational converter which however is lake in one thing. If we would like to connect two incompatible filters together the "Intelligent Connection" mechanism will not try our converter yet. We therefore need to to set the merit during to a higher level than "MERIT_DO_NOT_USE" as done in section 5.1.7, e.g. "MERIT_UNLIKELY". Not to overstrain the mechanism we should rarely use merits higher than "MERIT_DO_NOT_USE". Otherwise, the mechanism need to check more and more filters while connecting invalid filters with each other which then needs more and more time.

5.2.4 Sample's Memory Management

A subject not yet discussed in details is the memory management of samples. As mentioned in section 5.1.6 we can increase and decrease a sample's reference counter to indicate if we need its data for further proceeding or if we release its resources. Figure 5.11 shows the life cycle of a sample and the method calls in which the reference counter increases (<<AddRef>>) and decreases (<<Release>>).

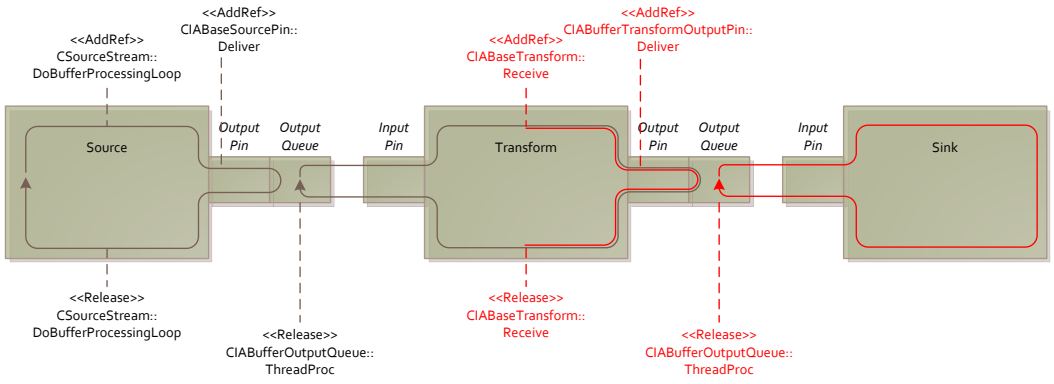


Figure 5.11: Life cycle of a sample and its reference counter.

A sample is either created in the method "CSourceStream::DoBufferProcessingLoop" or "CIABaseTransform::Receive" which both set the reference counter to *1*. To release the

sample again we call the corresponding method at the end of the same method after we finished proceeding the sample. A problem occurs as the streaming thread hand over the sample into an output queue and return right after to release the sample again, proceeding the next incoming sample. In this case the sample in the output queue will not be valid anymore for further proceeding. Because of that we increase the reference counter whenever delivering the sample to the output queue and decrease the reference count whenever a queue thread returns from a down-stream filter. This approach works with with both an output queue with and without running an independent streaming thread. Furthermore, the behavior is implemented already into the image analysis base classes which do not need any more consideration. For filters which do not follow the standard approach we have to handle a sample's reference count ourselves. An example is given by the "IA - Contour Tracer" filter.

A more challenging problem are samples containing dynamic data such as a contour vector. The standard samples which hold image data provide a fix memory block which size can be previously defined by the images width, its height and the bits per pixel (BPP). A contour vector, however, could contains zero or several hundreds or contours each with a different number of contour points. Because of that we can not take the same approach as used for the RGB or grayscale converters which takes the down-stream filter's media type, again containing the image's dimensions and the BPP, to distinguish the actual require memory to allocate. Another solution would be to calculate the contour array and its size while running the filter and establish a new media type to the down-stream filter[5]. This process however has a lot of disadvantages. Firstly, the data stream has to be blocked while reconnecting the pin to the down-stream filter with a new media type. The approach needs a lot of additional resources as all the down-stream filters might need a reconnection due the media type change. Moreover, the new media type might not be accepted by a down-stream filter which will interrupt the whole graph's execution. In this situation we will lose all proceeding samples currently inside the pipeline. A more robust solution is therefore preferred. As mentioned, if we could keep the sample size constant, we do not need a reconnection during the filter graph's execution. We can do so by saving only a pointer to a contour structure inside the sample which then has always the same size. We now face a new problem: who cleans the contour structure's memory when a sample is released? The simplest solution would be to do so in a down-stream filter. But, this is not a valid solution as we can not assure a secure cleaning. A third party filter might not even know as it needs to clean the sample. Another problem comes when we split up the filter graph into two branches. Which branch has to clean the contour structure and how can we manage the circumstance as a filter from one branch could clean up the contour structure while another filter from the other branch still needs the data? There is only one proper solution left: we have to implement a customized memory allocator. As described in section 5.1.3 each sample has it's own reference counter. As soon as this counter falls to zero it calls its allocator for releasing the memory. With a customized allocator we could invoke this process and

[5] For more details please refer to
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd388731(v=vs.85).aspx`

release the memory by ourselves. The main advantage is as the down-stream filters do not need to know about how to clean up the sample but only decrease the sample's reference counter whenever they finished proceeding the sample. The code of such a customized allocator is given in Listing 5.11.

```
class MyAllocator : public CMemAllocator
{
public:
    MyAllocator(HRESULT *phr) :
        ↪CMemAllocator(TEXT("MyAlloc\0"),NULL,phr) {};
    ~CIAContourMemAllocator() {};

    HRESULT Alloc() {
        // allocate requested memory & prepare samples
        // see also implementation of "CMemAllocator"
        // user defined samples can be initialized here
    };
    STDMETHODIMP ReleaseBuffer(IMediaSample *pSample) {
        /* Release the COM object before reusing its address pointer */
        IUnknown* comObject;
        pSample->GetPointer((BYTE**)&comObject);
        comObject->Release();

        // put sample back on free list for recycling
        // see also implementation of "CMemAllocator"
    };
};
```

Listing 5.11: Implementation of a memory allocator.

In a next step we need to integrate the new allocator into one of our filters. Talking about the contour structure initialized in a transformation filter we have to set the output pin's allocator to our customized one. An important fact to know is as the output pin by default tries to assign to the down-stream's input pin's allocator by calling the method "CIATransformInputPin::GetAllocator" before initializing an own one[6]. Because of that we have to overwrite two methods. Firstly, the "CIABufferTransformOutputPin::DecideAllocator" method: here, we need to skip the trial of assigning the input pin's allocator which would be successful if no unexpected error occurred while building up the filter graph. In a next step the output pin tries its own allocator by calling the "CIABufferTransformOutputPin::InitCustomOutPinAllocator" method. An example implementation of this method is given in Listing 5.12.

[6] For more details please refer to
https://msdn.microsoft.com/en-us/library/windows/desktop/dd377477(v=vs.85).aspx

```
HRESULT MyFilter::InitCustomOutPinAllocator(IMemAllocator **ppAlloc) {
    HRESULT hr = S_OK;
    MyAllocator *pAlloc = new MyAllocator(&hr);
    if (!pAlloc) return E_OUTOFMEMORY;
    if (FAILED(hr))
    { delete pAlloc;
      return hr;
    }
    return pAlloc->QueryInterface(IID_IMemAllocator, (void**)ppAlloc);
}
```

Listing 5.12: Example of the "InitCustomOutPinAllocator" method.

For more details we refer to the implementation of the "IA - Contour Tracer" filter.

5.3 Cell Nucleus Detection

After the discussion about the basics of DirectShow and our image analysis filter, we would like to provide a concrete example of a filter graph, as shown in Figure 5.12. for detecting cell nucleus. We will use this pipeline later to analysis our given images from the previous project as described in Chapter 2.2.

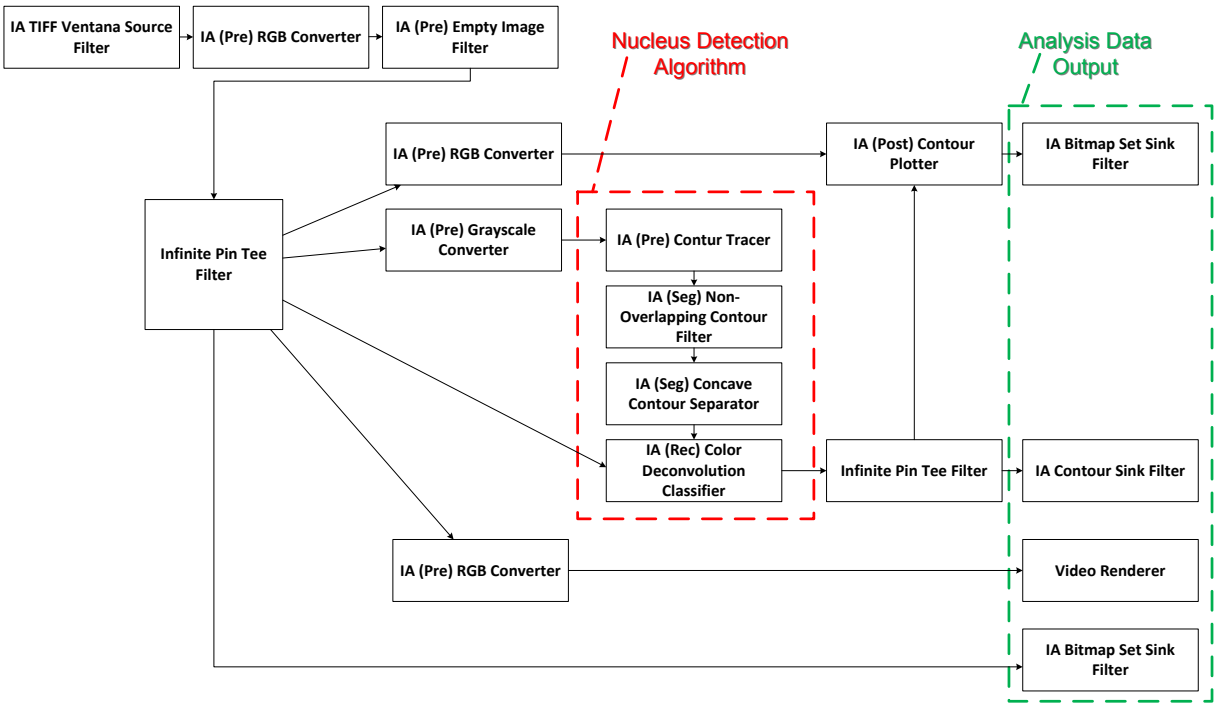


Figure 5.12: Filter graph of the cell nucleus detection algorithm.

We start with a source filter which is able to read a BigTIFF image created by Ventana's slide scanner, iScan HT. The resulting tiles are BGR24 images which we then convert

into RGB32 images. The "Empty Image Filter" search for homogeneous images without edges and drop them from the pipeline. As our images contain up to 80% background we can save a lot of computation power by dropping those tiles in an early pre-processing step. Those sample which are not dropped are then duplicate by a standard "Infinite Pin Tree Filter". On the first copy we draw all found nucleus contours obtained by the nucleus detection algorithm which needs a second copy to work on. The last two copies are once rendered in a separate window as visual feedback for the proceeding tile and once saved as original tile image. The "Contour Sink Filter" finally evaluates the contour information with the trainee data and calculates its precision and recall values. Those values and the related contour information are then locally saved as XML file and uploaded to the PSR system and saved in its database. More information about the evaluation process is given in section 5.4.

Research Of An Appropriate Algorithm The heart of our pipeline is the nucleus detection which consists of several filters. It should be a more complex example which proves the flexibility and potential of our pipeline system for further use. We therefore make a research on the paper [4, p.97–114] which gives an actual overview of nucleus detection methods. Our filter criteria are based on the given prostate tissue images we have.

- The tissue has to be H&E stained.
- The objects to detect are nucleus of prostate; no lymphocyte nucleus.
- The objects to detect are healthy nucleus; neither mitotic nor cancerous nucleus.

We compose three presented approaches: [5], [6] and [7]. Comparing the metrics that we find [7] gets the best result. It discovers 91% of all existing nucleus (TPR) which represents 86% of all nucleus, detected by the algorithm (PPV). In addition to the metrics, the approach of using image processing algorithms fits to our purpose of an IA pipeline. Furthermore, the theory behind the algorithms is known by the student, which reduce the risk of failing while implementing one of the other approaches. Namely the active contour model and the multiphase level set segmentation are not well known. Unfortunately, this also holds for another article [8] introduced by Qing Zhong which is based on superpixels.

We may over-simplify our research and could get better results by relaxing the criteria. Still, we did the trade off between quality insurance and risk reduction which affects the time available for improving our pipeline system. Also, the pipeline system is important for further studies and can be used productively at the University Hospital of Zurich while the algorithm has currently no major purpose.

The Processing Steps Paper [7] describes six major processing steps we have to discuss and implement later on.

(a) Detection of all possible closed contours

(b) Contour evaluation

(c) Generation of a non-overlapping segmentation

(d) Contour optimization

(e) Concave object separation

(f) Classification into cell nuclei and other objects

The detection of all possible contours (a), as described in the paper, uses a scan line algorithm. We iterate over each pixel in an image row and search for a local minimum, a local maximum as well as the pixel in-between with a maximum local gradient P. Starting from this point P we use the simple contour tracing algorithm "8M" as described by the paper in method S6 for tracing an objects contour. The object's foreground pixels are thereby given by the range [local minimum value, local maximum value]. The so found contours are then evaluated (b) by there so called contour value which measures the sharpness of the contour against the background. In case of overlapping contours we only keep the contour with the highest contour value (c). We now have a set of contours which may have ripped edges we would like to smooth (d). We do so by using a distance transformation and remove pixels with a large distance to the object's centroid which results in a compact object shape. In a last transformation step we separate multiple cell nucleus which are detected as one single object by clustering the contour points into groups. The last step uses color deconvolution for classifying objects as nucleus or other objects by there nucleus-specific color information. We do not go into more details which are well described in the paper but give a simple example for a better understanding as visualized in Figure 5.13.

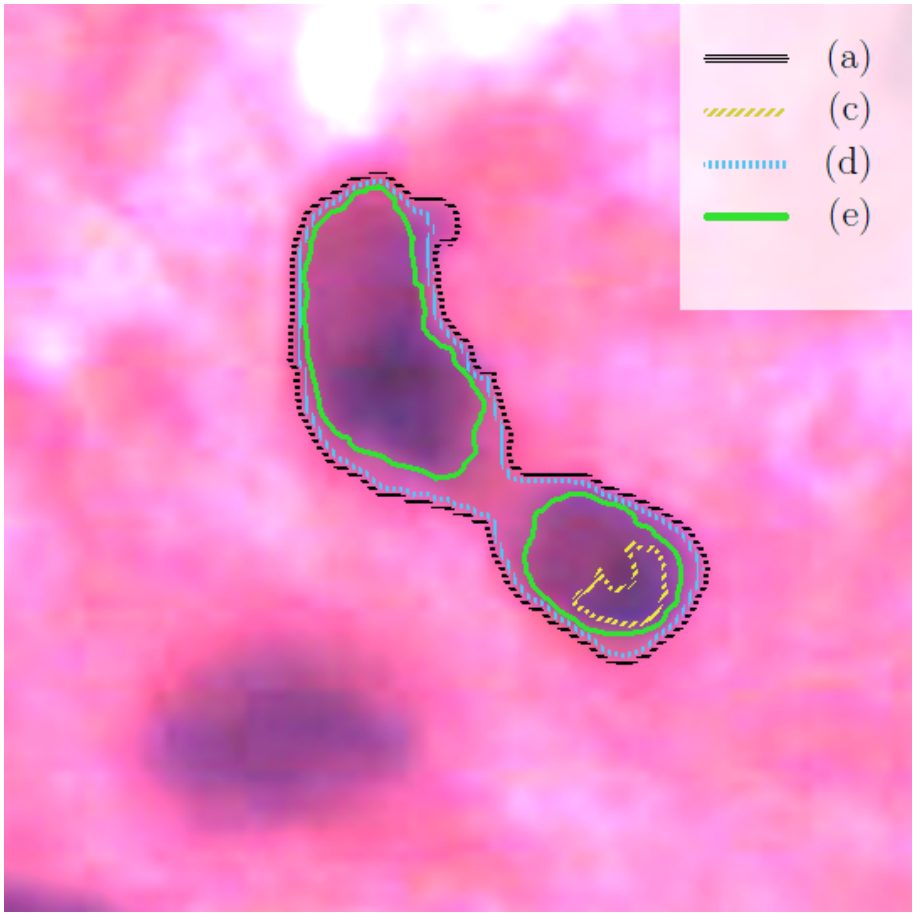


Figure 5.13: Contour extraction steps on an example. Steps (b) and (f) are not listed. (a) Contour detection; (c) To be removed overlapping contour; (d) Optimized contour; (e) Separated objects.

If we implement the algorithm as described we can think about six filters, each proceeding one of the above steps. However, this will be inefficient as we could combine several steps in order to prevent us from looping over the entire image in each step. While detecting the contour we can easily calculate its contour value which combines steps (a) and (b); see filter "Contour Tracer". Steps (c) and (d) both works with a label or distance map which again could be combined; see filter "Non-Overlapping Contour Filter". While implementing each filter separately we need around $0.55 seconds$ for a 1024 x 1024 tile on a nowadays standard laptop[7] which means around $2.5 hours$ for an entire image. By combining the filters we still need $0.35 seconds$ which means $1.5 hours$ for an entire image. While analyzing the pipeline, it appears that the contour detection and the later remove of overlapping contours need most of the time. If we could omit already invalid contours we should be able to improve our performance significantly. We could do so by setting an empirically determined threshold while following the contour and

[7] Intel Core i7 (2.4 GHz); 16GB RAM; Windows 7

calculating its contour value. If the contour do not satisfy an expected contour value, after a few contour points are proceeded we declare the whole contour as invalid and stop the tracing algorithm. We may lose some nucleus using this approach but expect a dramatically improvement in the performance.

The following sections describe the image analysis filters more in detail and give possible alternative implementations. For more details about Microsoft's "Infinite Pin Tee Filter" and "Video Renderer Filter" please refer to the corresponding documentation:
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd390336(v=vs.85).aspx`
`https://msdn.microsoft.com/en-us/library/windows/desktop/dd407349(v=vs.85).aspx`

5.3.1 TIFF Ventana Source Filter

Properties	**Description**
Filter	Source filter for loading Ventana TIFF files and pass its subfiles through the pipeline.
Input	TIFF files with a 64bit offsets, also called BigTIFF. The difference to a normal 32bit offset TIFF file is also pointed out by the version number which is *0x2B* and not *0x2A* as defined by the TIFF 6.0 specification[6]. By agreement a normal TIFF reader will refuse such a file due the wrong version number.
Output	A BGR24 subfile of the TIFF container. This means, a 24 byte array storing the red channel in byte 0, the green channel in byte 1 and the blue channel in byte 2. Therefore, each channel can hold a value from 0 to 255[7].

As mentioned in the previous section we deal with BigTIFF files which contains images up to 60 gigabyte in an uncompressed form. As most computers nowadays do not have enough sufficient memory for handling the image at once we need to find an alternative strategy. One would be to split up the image in a pre-processing step. This is possible e.g. using the tool "TiffMakeMosaic" from the Large TIFF Tools collection[8]. This strategy would also be compatible with the existing IA tool which expects a directory with JPEG files as input. Using the tool, however, will result in a large set of images which represents only duplicates but do not contain any additional information than the original source. Therefore, we have to create and delete the images each time we analyze them. A more elegant solution would be to read the subfiles directly from the BigTiff file instead of saving them onto the harddisk in a first place. We can do so adapting the original source already given by the "TiffMakeMosaic" which represents an open source

[6] `https://partners.adobe.com/public/developer/en/tiff/TIFF6.pdf`
[7] `https://msdn.microsoft.com/en-us/library/windows/desktop/dd407253(v=vs.85).aspx`
[8] `http://www.imnc.in2p3.fr/pagesperso/deroulers/software/largetifftools/`

tool. This code simply jump to a specific image file directory and read its data. As we know, our BigTIFF files contains 13 subfiles where the first contains a thumbnail of the overall image, the second contains the region of interests and the follow-up files store the actual image in different resolutions, starting from the largest to the smallest one. In this case, reading from the pointer of the third image, or with a zero-based index the second one, gives us access to the largest image which is given in tiles of the size 1024 x 1024 pixel. Figure 5.14 visualize the data representation.

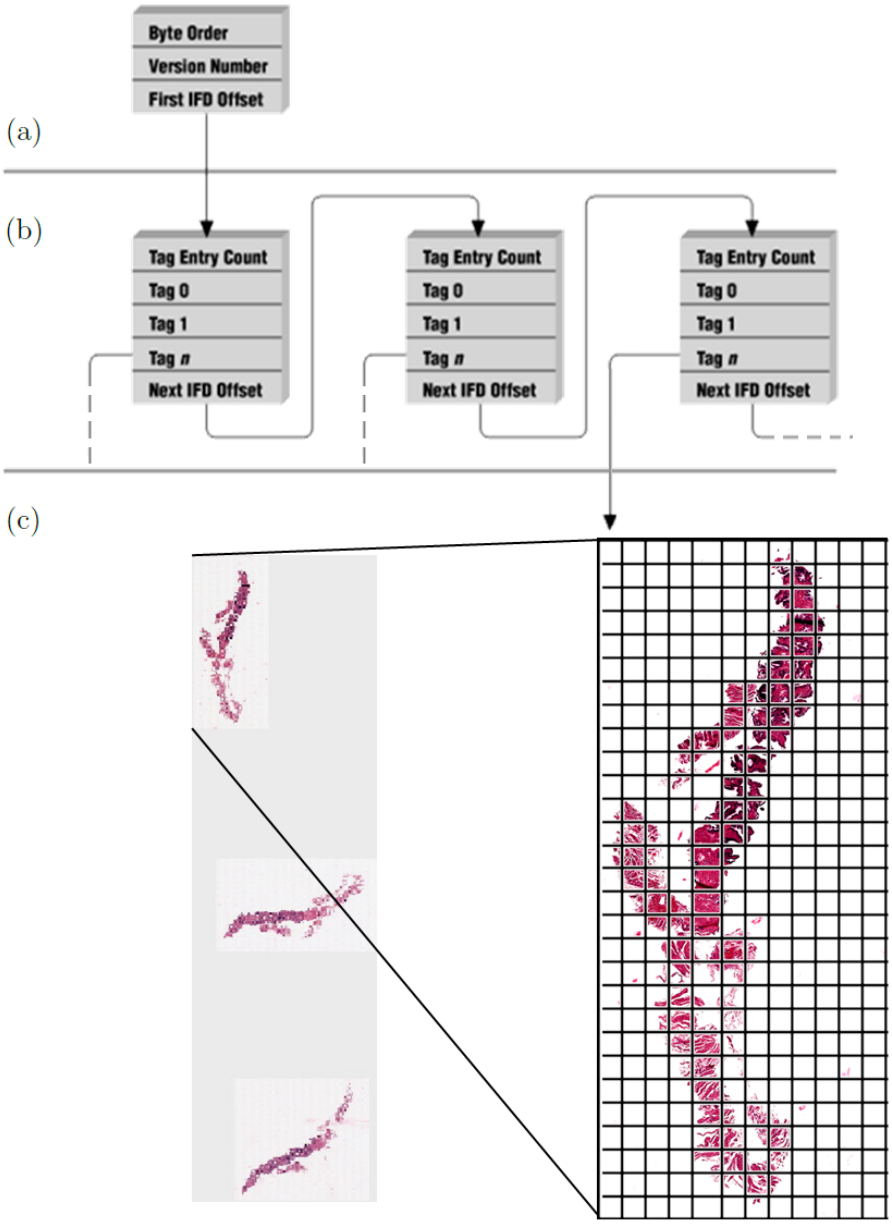


Figure 5.14: Ventana's TIFF structure[9]. (a) The image file header, (b) the image file directory and (c) the tiled image data.

A more detailed description of the TIFF structure can be found at
`http://www.fileformat.info/format/tiff/egff.htm`.

For the sake of completeness we offer an additional source filter called "IABitmapSetSource". Like the original IA tool it can read a directory of images and send each of them through the pipeline system.

5.3.2 RGB Converter

Properties	**Description**
Filter	Pre-processing transformation filter for converting an RGB/BGR image.
Input	RGB24/BGR24/RGB32/BGR32 image.
Output	RGB24/BGR24/RGB32/BGR32 image.

The filter is implemented based on the description of section 5.2.3. We therefore need to offer all four supported media types in the "GetMediaType" method and accept all media types in the methods "CheckInputType" and "CheckTransform". In the "Transform" we then firstly copy the input sample into the output sample which may expand or compress our image file by the alpha channel. In a next step we check if we have to flip the red and blue channel, depending on the conversion of an RGB/BGR into a BGR/RGB image.

5.3.3 Empty Image Filter

Properties	**Description**
Filter	Pre-processing transformation filter for dropping images without *content* such as tissues.
Input	RGB32 image.
Output	An RGB32 image if the image has content, nothing otherwise.

The filter calculates the contrast and entropy of the image using a co-occurrence matrix as described in [9, p.849–859]. We empirically identified the following classifier as a good threshold for images with content: $contrast > 1.5f\ OR\ entropy > 3.0$. If an image do not hold this classifier we return the value "S_FALSE" from the "Transform" method which, as defined by DirectShow, prevents the sample for being passed down-stream.

[9] Adapted from `http://www.fileformat.info/format/tiff/egff.htm`.

5.3.4 Grayscale Converter

Properties	Description
Filter	Pre-processing transformation filter for converting an RGB image into a grayscale image.
Input	RGB24/BGR24/RGB32/BGR32/GRAYSCALE32 image. Where GRAYSCALE32 represents a 32bit integer array storing a single value for the grayscale value.
Output	RGB32/GRAYSCALE32 image. Where the RGB32 image stores the grayscale value in each 8bit channel (expecting the alpha channel which remains to 0) and the GRAYSCALE32 image only stores the grayscale value as a single 32bit integer.

The filter is implemented the same way as the previously described "RGB Converter". See sections 5.2.3 and 5.3.2 for more details.

5.3.5 Contour Tracer

Properties	Description
Filter	Pre-processing transformation filter for extracting contour signatures of cell nucleus.
Input	GRAYSCALE32 image. Where GRAYSCALE32 represents a 32bit integer array storing a single value for the grayscale value.
Output	Collection of contour signatures. The collection is implemented as $vector<IAContour*>$where the "IAContour" represents an extended vector of points.

The contour tracer extracts a set of contours by scanning each line of a given image. For each two found extreme values in a row we calculate the maximum local gradient in-between and define the foreground of the so found object by the range [*local minimum value*, *local maximum value*]. Figure 5.15 gives a visual example of this step.

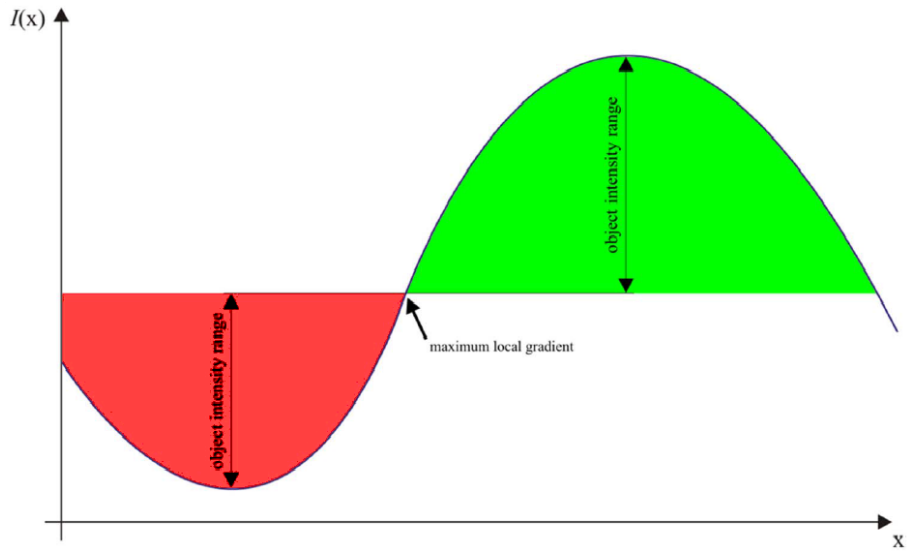


Figure 5.15: Derivation of an objects intensity range while proceeding a row of the image's function $I(x)$[8].

Using a simple tracing algorithm[9] we can extract the contour's signature. While following the contour we also calculate a so called contour value for evaluating a contours quality. The contour value is the product of the "mean gradient" and the "gradient fit". Whereas the "mean gradient" describes the sharpness of the contour against the background the "gradient fit" describes the number of contour pixels which represents a local maximum within a $3x3$ neighborhood, which center is given by the coordinate (x_i, y_i). The formulas are given as follow where S represents the Sobel operator, C_i the ith contour and p_{ij} its jth contour pixel. Applying the Sobel operator on the point p_{ij} returns the corresponding intensity value on the Sobel image:

$$|S| = \sqrt{(I * G_x)^2 + (I * G_y)^2} \qquad G_x = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix} \quad G_y = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 1 \end{bmatrix}$$

$$GradientFit_i = \frac{\sum_j p_{ij}^{max}}{|C_i|},$$

$$p_{ij}^{max} := \begin{cases} 1 & \text{if } max|S(p_{nm})| = |S(p_{ij})| \quad \forall\, n, m \quad \begin{matrix} x_i - 1 \leq n \leq x_i + 1 \\ y_i - 1 \leq m \leq y_i + 1 \end{matrix} \quad \cap \\ 0 & \text{otherwise} \end{cases}$$

$$MeanGradient_i = \frac{\sum_j |S(p_{ij})|}{|C_i|}$$

[8] Adapted from [7].
[9] We used the "8M" algorithm as described by [7] in method S6

$ContourValue_i = MeanGradient_i \cdot GradientFit_i$

For performance reason we only keep contours which contains between 70 and 1000 contour points and which contour values are greater or equal the value 2.5.

5.3.6 Non-Overlapping Contour Filter

Properties	Description
Filter	Segmentation filter for discard overlapping contours and optimizing remaining ones.
Input	Collection of contour signatures. The collection is implemented as $vector<IAContour*>$where the "IAContour" represents an extended vector of points.
Output	Collection of contour signatures. The collection is implemented as $vector<IAContour*>$where the "IAContour" represents an extended vector of points.

The current filter searches for overlapping contours and only keep the one with the highest contour value. Additionally, it optimizes the remaining contours by removing filaments. As both steps require a label or intensity map we combine them together. We first draw all contours on a map. If we draw on a pixel already containing a contour we compare both contour values with each other and discard the one with a smaller value. Afterward, we have a label map where we can perform a distance transformation as described in [10, p.444]. On this map we remove non-compact pixels as described in [7] by method S7. Because the process on how to obtain such a map is not mentioned by the paper we give a more detailed description here. Firstly, we introduce a new data structure, the contour map. The "contour map" consists of two internal maps, a "label map" which is a static 2D integer array with the size of the image currently analyzing and a dynamic "region map". The "region map" is defined as follow:

```
map<int ,map<int ,Region*>*> regionMap;
```

It represents a 2D map containing "Region" structures. Each of those regions can store additional information such as its x and y coordinate, the pixel's value and an assigned contour as well as its contour point. While the "label map" contains a value for each pixel in the image the "region map" only holds assigned contour points. This reduce the memory overhead of our structure. Figure 5.16 visualizes the new "contour map".

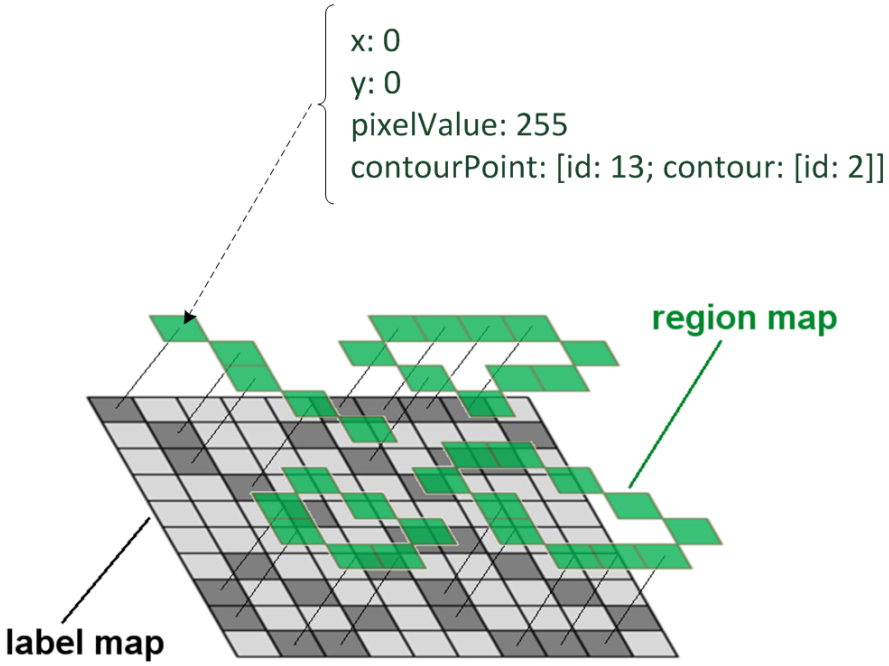


Figure 5.16: Schematic representation of the "contour map". It contains a normal label map with a virtual region map on its top containing additional information such as the assigned contour point.

The "contour map" can be used such as a normal array structure as visualized in Listing 5.13.

```
ContourMap contourMap(image->width, image->width);
for (int i=0; i < contour->size(); i++) {
    IAContourPoint* cPoint = contour->at(i);
    *contourMap[cPoint->x][cPoint->y] = cPoint;
}

int x=5, y=7;
ContourMap::Region* region = contourMap->at(x,y);
if (region)
  if (region->relatedContCoord->isConvexPoint())
      ...
```

Listing 5.13: Code example of the "contour map".

The simplicity is given by an internal "ContourMapRow" proxy which is returned when accessing the first dimension of the "contour map". Using again the index operator on the proxy for accessing the second dimension dereferencing the actual region.

The advantage of this structure is as we can assign all given contours to the "contour map" which then mark overlapping contours for deleting and the same way build

up the label map. After removing the marked contours we can directly apply the distance transformation on the label map for optimizing the remaining contours. We can so combine two steps instead of using two separate map structures.

5.3.7 Concave Contour Separator

Properties	Description
Filter	Segmentation filter which splits contours containing more than one nucleus.
Input	Collection of contour signatures. The collection is implemented as $vector<IAContour*>$where the "IAContour" represents an extended vector of points.
Output	Collection of contour signatures. The collection is implemented as $vector<IAContour*>$where the "IAContour" represents an extended vector of points.

The concave contour separation filter iterates through each pair of concave points (C_1, C_2) on a contour and calculates a "separation score" for them. The score consists of two terms. Firstly, the "length score" which settles the distance of both concave points from the convex hull ($depth_1$, $depth_2$) of the contour and the there distance (r). Secondly, the "angle score" take account of the angle between the new cutting line ($\overline{C_1C_2}$) and the convex hull. Therefore, we follow each concave point forward and backward ,searching for there next convex neighbor points and form a line between those two convex points ($\overline{A_1B_1}$, $\overline{A_2B_2}$). We then settles the angle (α_1) between the lines $\overline{A_1B_1}$ and $\overline{C_1C_2}$ and the angle (α_2) between the lines $\overline{A_2B_2}$ and $\overline{C_1C_2}$. The best pair of concave points is given by a minimum "separation score" which decrease the closer both points are to each other, the farther both points lay from the convex hull and the perpendicular α_1 and α_2 stands on the cutting line $\overline{C_1C_2}$. The formulas are given as follow:

$$LengthScore = \frac{r}{r + depth_1 + depth_2}$$

$$AngleScore = \frac{\alpha_1 + \alpha_2}{2\pi}$$

$$SeparationScore = \frac{LengthScore + AngleScore}{2}$$

The algorithm is partly described in [7] by method S8.

5.3.8 Color Deconvolution Classifier

Properties	Description
Filter	Recognition filter for classifying extracted contours as nucleus by color deconvolution.
Input	Collection of contour signatures. The collection is implemented as *vector<IAContour*>*where the "IAContour" represents an extended vector of points.
Output	Collection of contour signatures. The collection is implemented as *vector<IAContour*>*where the "IAContour" represents an extended vector of points.

The color deconvolution filter is not yet implemented. Due the limited amount of time we decided to spend more effort into the overall image analysis pipeline and do not implement the current filter. For a future implementation we refer to the website `http://web.hku.hk/~ccsigma/color-deconv/color-deconv.html` which gives a good and understandable introduction including a Matlab code for cell extraction.

5.3.9 Contour Plotter

Properties	Description
Filter	Post-processing filter for plotting contour signatures on an image.
Input	Pin 1: RGB32 image. Pin 2: Collection of contour signatures. The collection is expected as *vector<IAContour*>*where the "IAContour" represents an extended vector of points.
Output	RGB32 image.

The filter is not necessarily for the nucleus detection but very helpful in debugging the given algorithm. As it is not easy to evaluate the extracted contours only by there points nor the precision and recall values an easy way to get a first impression is to draw the found contours on the original image. We then can easily evaluate the results and see faults made by the algorithm. An output example of the filter is given in Chapter 8.

5.3.10 Bitmap Set Sink Filter

Properties	Description
Filter	Sink filter for saving a set of images into a file directory.
Input	RGB24/RGB32 image.
Output	Each image is saved as JPG image with an individual filename containing its position on the source image.

The filter uses the ATL component "CImage" which gives provides an easy interface for loading and saving JPEG, GIF, BMP and PNG images. Further details can be found at MSDN under `https://msdn.microsoft.com/en-us/library/bwea7by5.aspx`. The "Bitmap Set Sink Filter" and the "Bitmap Sink Filter" are identically. The only difference is, as the "Bitmap Set Sink Filter" reads the additional meta data, if available, from the sample's header and concatenate its position on the source image within the filename. If no meta data are available the filter uses its own internal counter within the filename.

5.3.11 Contour Sink Filter

Properties	**Description**
Filter	Sink filter for evaluating cell nucleus detection algorithm.
Input	Collection of contour signatures. The collection is expected as $vector<IAContour*>$where the "IAContour" represents an extended vector of points.
Output	An XML file on the file system which follows the definition of Table 4.1. Optionally, this file can also be send to the PSR system for storing its information inside the patient database.

The contour sink filter contains the actual algorithm evaluation which is described more in detail in Chapter 5.4. The given contour vector is compared with the source image's annotation file generated by Ventana's image viewer. The XML structure of the annotation file, which has to be named like its source file, can be found in [3, p.49]. The algorithm takes all annotations from the XML file contained within the tile's dimensions and compare them with the extracted contour information. The so obtained precision and recall values are then saved as property attributes into the resulting XML file which structure is given in Table 4.1. The file is also filled with all extracted contours and additional meta information about the source file and the proceeded tile image for further traceability and post-processing. Optionally, this XML file can also be send to the PSR system which parse the file and save its content into its Microsoft SQL database.

For more information about how to write an XML structure or sending data to a web server we refer to the source code documentation and the appendix 12.5.

5.4 Algorithm Evaluation

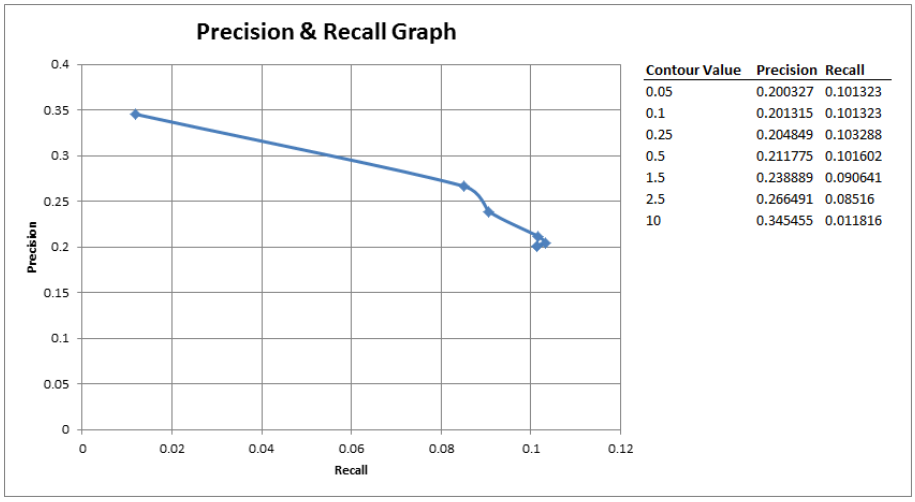
An important feature of our pipeline system has to be the ability of evaluating a given algorithm as enlisted in Chapter 2.2. With the flexibility of DirectShow we have many ways to achieve such an evaluation. We could implement it fundamentally into our base filters or somehow in the framework's process. This, however, would limit our flexibility. We have to define the place where our evaluation takes place in the process flow and

define interfaces. Another approach would be to expect a result file from the pipeline system which then is post-processed and evaluated outside the DirectShow environment. It might not be intuitive to find the evaluation algorithm outside the DirectShow graph or inside the IA console tool which previously executes the filter graph. Also, we have to define specific interfaces so our evaluation algorithms can read the outputs of the filter graph and, most disadvantageous, the evaluation algorithm is not easily exchangeable or extendable if we do not offer another plugin system there. However, an advantage would be as we can independently execute the evaluation whenever needed without starting the whole processing pipeline.

We finally followed the approach of DirectShow and do not give any restriction for evaluation algorithms. We expect them to be implemented such as every other DirectShow filter. We then can integrate the new filter wherever we like inside our filter graph. The evaluation filter most probably is a sink filter which stores its evaluation information into a file on the file system or send it to a web server. However, we can also combine a separate filter graph which source filter reads the output of the image analysis pipeline and evaluate it by another evaluation filter. We than can also execute the evaluation independently from the image analysis pipeline.

Following, we give a concrete example of our "Contour Sink Filter" which represents such an evaluation filter. It reads the contour data given, our features to evaluate, and compare them with the annotations within a test data set. The test data set in our case is the XML file generated by Ventana's image viewer which contains manually delineated annotations. In our case, for each tile we set a window, with the dimensions and source of our tile, on the annotation data and evaluate only the annotations within this window with the extracted contours from the nucleus algorithm. We then calculate the precision and recall values which then are saved as XML file on the file system or send to the PSR system.

The results, evaluating our before presented nucleus algorithm on the image *169S1.tif* ($image_{ID} = 1$, $patient_{ID} = 169$) are given in Figure 5.17. Hereby, we changed the contour value threshold defining a valid contour and calculate the precision and recall for each run. As visualized the algorithm in its current state only discovers around 10% of all cell nucleus where only 20% are true positives (contour value = 2.5). The approach is adapted from [11] and will be very useful for the follow-up project when tuning the tumor detection algorithm.



Contour Value	Precision	Recall
0.05	0.200327	0.101323
0.1	0.201315	0.101323
0.25	0.204849	0.103288
0.5	0.211775	0.101602
1.5	0.238889	0.090641
2.5	0.266491	0.08516
10	0.345455	0.011816

Figure 5.17: Precision and Recall graph of the implemented nucleus detection algorithm with variable contour value thresholds.

The given graph states a poor performance for our nucleus algorithm. This, however, is not surprisingly as we did not yet implement the "Color Deconvolution Classifier" nor extensively tweak the detection algorithm. As mentioned, we therefore put more effort in the pipeline system itself. However, as the graph shows we are able to evaluate an algorithm within the filter graph which is the actual requirement we have to met. Nevertheless, with the given evaluation algorithm and the nucleus detection filters it will be easy to finish the implementation in one or two weeks including testing and deploying.

6 Software Testing

To ensure as the PSR system as well as the IA tool work correctly the software were tested continuously by function and system tests. During the function tests the individual workflows of the PSR system as well as the one of the IA tool were evaluated while the system test combines all workflows together.

6.1 Function Tests

During the implementation phase the individual workflows of the PSR system were tested as done in the previous project. We therefore used the following test cases:

Use Case	**[UC001] Import image feature data**
Description	The user uploads an XML file, containing feature data, to the PSR system.
Precondition	- The user already face the start page of the PSR system - The user has an XML file containing feature data to upload - Image data related to the uploading features are already imported [given by previous project]
Postcondition	All feature data are stored inside the PSR database.
Process	- Go to: Update/Update features of scanned images - Choose the XML file to upload and process - Verify the import report
Pass	- All data are imported correctly into the database
Fail	- An error occur during the importing process - Not all data are imported correctly into the database

Use Case	**[UC002] Export image feature data**
Description	The user exports feature data from a specific image entry for further analysis.
Precondition	- The user already face the start page of the PSR system - Image features are already imported [UC001]
Postcondition	The feature data are exported into an XML representation readable by the Ventana image viewer.
Process	- Go to: Export/Export features from database - Choose a study containing the image which features to export - Choose an image which features to export - Start the export procedure - Verify the export report and the created XML file
Pass	- The exported XML file contains all data chosen - The exported XML file is readable by the Ventana image viewer
Fail	- The exported XML file do not contains all data chosen - The exported XML file is not readable by the Ventana image viewer

Use Case	**[UC003] Intersect image features with annotations**
Description	The user uploads a file with image features and intersects them with the given annotations.
Precondition	- The user already face the start page of the PSR system - Image annotations are already imported [given by previous project]
Postcondition	The user get the precision and recall values of the intersection.
Process	- Go to: Analysis/Validate image feature intersection - Choose the XML file to upload and process - Verify the analysis report
Pass	- The analysis report do not provide any errors
Fail	- The analysis report do provide errors

Use Case	**[UC004] Analyze an image using the IA tool**
Description	The user configure the image processing pipeline and run an analysis.
Precondition	- The user already face the start page of the PSR system - Data of the image to analyze are already imported [given by previous project] - The filter graph file to use is available - The configurations for the graph are defined
Postcondition	The user get feedback about the analysis results.
Process	- Go to: Analysis/Analysis image with the IA tool - Choose the image file to process - Choose the filter graph to use - Choose the graph configurations to use - Start the analysis process - Verify the status output - Proceed when analysis is finished - Verify the analysis summary - Verify the analysis results
Pass	- The analysis ends without any error - The analysis results are as expected; depending on the pipeline chosen
Fail	- The analysis ends with an error - The analysis results are not as expected (invalid or missing data).

In the same way as for the PSR system we can also define a use case concerning the IA tool.

Use Case	**[UC005] Analyze an image from the command prompt**
Description	The user analysis an image by manually using the IA tool.
Precondition	- The image to analyze is available - The filter graph file to use is available - The configurations of the graph are defined
Postcondition	The user get feedback about the analysis results.
Process	- Start the IA tool from the command prompt with all necessarily parameters - Verify the status output - Verify the analysis results
Pass	- The analysis ends without any error - The analysis results are as expected; depending on the pipeline chosen
Fail	- The analysis ends with an error - The analysis results are not as expected (invalid or missing data).

Beside the use cases, visible by the end user, we also tested the internal filters of the IA tool separately. We do so by defining specific test data and validated the expected outcome. Some filters still contains test blocks with test data to validate single functions or workflows within a filter. The test data mainly has there origin in examples from the corresponding scripts. There, we also have the expected results to validate with.

Furthermore, also Norbert Wey was working with the IA tool and tested the filters using different filter graphs and test data. His valuable feedback was continuously integrated into the internally published GIT repository.

6.2 System Test

The system test is a combination of all function tests. As in the previous project the Selenium tests were extended by the new use cases given in the previous section. The Selenium tests can be found in the appendix 12.7. As the IA tool only has a single purpose we do currently not offer any system tests.

7 Evolution

Before we discuss the obtained results from the IA tool in Chapter 8 and reflect about the overall project in Chapter 9 we would like to have a look into the future. The IA tool is meant to be extended in the future so we have to discuss about potential evolution scenarios in the following sections.

7.1 IA Filter Extension

An important requirement as described in Chapter 2.2 says as the pipeline system has to be extendable in the future. This circumstance is already met by the DirectShow framework which supports any new filters with a COM interface. This however is not enough to ensure a robust life cycle of further filter pipelines. We support this circumstance by implementing a default life cycle into our base IA filters. When inherit from such a filter we do not need to care about memory allocation and cleaning, initializing and assigning filter pins or proceeding samples with individual streaming threads for supporting parallelization. This makes the implementation of an image processing filter very easy as long as we do not extend the given workflow. If we do so we need to understand the given approach as described in Chapter 5.2 which gives several examples extending the default behavior. Without respecting the architecture we will struggle with memory leaks and unwanted behaviors. We now have a maximized flexibility in extending and adapting the given image analysis pipeline in the future. An important recommendation is to implement each filter independently from any other. We strongly advice e.g. not to allocating memory in one filter and release it in another one. Other users than the creator of this two filters might not combine them and run into memory problems. To solve this problem we can use a customized allocator as described in Section 5.2.4.

7.2 GPGPU

Another important aspect is the migration of existing or new code onto the graphics adapter - also called "general-purpose computing on graphics processing units". An easy example would be the "Gaussian" or "Sobel" convolution filters. As already contemplate we implemented those filters using the AMP programming model[1] from Microsoft which makes the migration easily possible by changing the restriction specifier to "restrict(amp)". However, we are not depended on those technology but could use

[1] For more details please refer to
`https://msdn.microsoft.com/en-us/library/hh265137.aspx`

any parallelization technique provided for C++. Please keep in mind the following recommendations which cased problems while implementing AMP code into IA filters:

- Only parallelize code with less conditional statements.
- A parallelized code should not run longer than 2 seconds. Otherwise, the TDR (Timeout Detection and Recovery) takes place and stops the execution of the GPU code.
- The required memory on the GPU has to be known a priori. An example for such a problem is to trace a contour on the GPU as we do not know how long this contour is and how much memory we need to reserve for the contour points to store. While allocating a large memory block results in a performance issue when copying memory blocks between CPU and GPU, proceeding only a small set of contours implies a lot of content switches between GPU and CPU which again prevents the GPU from using its potential.

7.3 Distributed Pipeline Systems

A requirement which could appear in the future is to distribute work packages onto other computers. This is theoretically possible e.g. by implementing a filter for dividing a problem into smaller problems and a second filter for retrieving and merging the results. A possible approach could be "Map Reduced" as described in [12, p.107–113] using MPICH[2]. While waiting for the distributed work packages we could include additional filters into the filter graph. This approach however contradict the idea as each filter should be independent as described in section 7.1.

7.4 Windows Media Foundation

The current implementation is based on DirectShow which should be replaced by the Windows Media Foundation in the future. Several functions are already ported from DirectShow to the Media Foundation. However, yet not all functionalities are available and especially the provided samples are very limited. Examples for the Media Foundation currently only covers video or audio pipelines which makes the adaption more difficult - especially without previous knowledge of the technology. We therefore decided to use DirectShow which already gives insights of extending the pipeline system for non-video pipelines. However, with the hereby given approaches and the further development of the Media Foundation and its demo samples we would recommend to adapt the DirectShow code onto the new standard. Also Microsoft announced not to continue with DirectShow it is unlikely as the support of DirectShow will be suspend in the next years. DirectShow, previously ActiveMovie, already exists since about 20 years and is

[2] For more details please refer to
`http://www.mpich.org/`

widely-used in video and audio processing which will not change in the near future. A comment on stackoverflow says: "Whatever marketers from MS say, DirectShow is here to stay. Too many applications use it, so MS will support it forever, just as all other COM-based technologies. And since DirectShow has much more features and is native for C++ programming, I suggest sticking with it."[3].

[3] http://stackoverflow.com/questions/4407446/directshow-vs-media-foundation-for-video-capture

8 Results

After the implementation of our image processing pipeline and the nucleus detection algorithm we would like to summarize and reflect about its most important results which also include the given requirements in Chapter 2.2.

Benefits The image processing pipeline itself offers many advantages when implementing a new filter or creating a filter graph. The key points are given as follow:

1. Very good performance due the design of DirectShow and the implementation of C++.
2. The plugin system of DirectShow allows third party contribution for new filters.
3. Offers a set of base classes already implementing the process workflow.
4. The base classes hide most of the COM interfaces for a better usability.
5. The memory management for samples is already done by the memory allocators of the base classes.
6. All base classes support a buffered output pin which allows the parallel execution of all filters within a filter graph.
7. The base classes inherits from the "CPersistStream" which allows to set filter properties from outside the pipeline and to set a logging level.
8. A minimum IA filter, inheriting from an IA base filter, can be realized by only implementing two methods.
9. A filter can take advantage of an arbitrary C/C++ library such as OpenCV[1], e.g. for computer vision.
10. Due to new media types common media samples can now be extended by additional meta data.
11. Due to the new COM memory allocator it is possible to deliver samples between two filters without copying its media data.
12. The IA filters are compatible with the standard filters of Microsoft.

[1] `http://opencv.org/`

13. All IA converters support the "Intelligent Connection" mechanism which allows the connection of two incompatible filters using a converter filter in-between.

14. Solutions for a wide range of problems are already given due a set of example filters, e.g. the "Contour Plotter" filter which implements more than one input pin.

Furthermore, the IA console tool which internally holds the image processing pipeline is fully integrable into the existing IT infrastructure at the hospital and offers the following advantages:

1. Loading of configuration files for reproduceable execution plans.

2. Support of batch jobs.

3. Dynamically composition of filter graphs.

4. Dynamically setting filter properties.

In this project a lot of effort was made in the extendability and user-friendliness of the IA base filters. It should be easy to extend the set of filters and also support complex filters using e.g. machine learning algorithms. Next to our work, DirectShow comes along with many more conveniences such as a graph editor and the system wide registration of our filters which could be very useful for further projects. Especially the Graph Editor invites for playing with new filter combinations and the respective results.

Disadvantages During the implementation we faced certain trade-offs which yield the following disadvantages:

1. As we use the DirectShow framework we only support Microsoft operating systems.

2. Future filters have to be implemented in C++, C# or Visual Basic.

3. As DirectShow mainly is an audio and video framework few image filters are available[2].

4. The memory management is not trivial and needs a better understanding of DirectShow if one would like to extend the IA base filters (otherwise the memory handling is already given).

5. No support for Microsoft's Media Foundation, which is the successor of DirectShow.

[2] An example is the MontiVision Workbench at `www.montivision.com`.

Cell Nucleus Detection The cell nucleus detection algorithm could not be totally implemented. The "Color Deconvolution Classifier" is missing for classifying the found contour signatures. Furthermore, the parameters of the already given filters are not yet optimized and offer space for improvements. However, the implementation represents a complex algorithm which answers many important questions relevant for future filters:

1. Passing dynamic data structures down the filter graph.
2. Reading Ventana's TIFF image files.
3. Offering filter properties changeable from outside the filter graph.
4. Offering the ability of logging events.
5. Sending data to a web server.
6. Parsing XML data and writing XML files.
7. Evaluating the implemented algorithm by calculating its measurement values.

The obtained knowledge can now be transferred into the IP9 where we will implement an algorithm for detecting cancerous tissues.

9 Reflection

After the detailed discussion about the image processing pipeline, we would like to take a step back and reflect the overall process. Compared with the previous project, the documentation process has been improved significantly. The writing plan evolved easily as the report did. The close cooperation with the stakeholders was established during the whole project which supported the better understanding of their requirements and resulted in a fast reaction time on requests. In additions, the extension and migration of the PSR tool was not an issue anymore which is explained by the better understanding of the client's environment. Apart of time schedule, the project management was very successful.

The extendability of the PSR tool was a great help to implement new image feature functions. Unfortunately, we did not have enough time for re-factoring the data access layer of the tool. As mentioned by Prof. Stamm, we should not access data from the database by specific query statements within the access layer but query database views which provide the already prepared data. Nevertheless, the implementation was prompt and we did not need to modify any core functionalities.

One of the best decisions was the use of DirectShow as our basic framework to process image data. It provided a great insight in DirectShow and improved the knowledge in C++ significantly. Especially the introduction to C++/CX, the fundamentals of implementing a plugin system under C++, the use of Doxygen and the implementation of the decoding filter for Ventana's TIFF images resulted in a deeper understanding on the issue. Thanks to the flexible design of DirectShow and the image analysis components we strongly recommend the use of the pipeline in further projects. If compatibility is an issue with DirectShow, a migration of the current image analysis filters to Microsoft's Media Foundation or the open source multimedia framework "GStreamer"[1] is possible.

In [3, p.63] we gave general recommendations which we expand here in terms of C++ and the image processing pipeline as listed below:

[1] Official website at `http://gstreamer.freedesktop.org/`

- A key point in C++ is a good designed memory management. During processing several gigabytes of data, an unresolved memory leak will not be unnoticed. In our case, memory of media samples should always be managed by its allocator while local allocated memory should be released whenever possible within the same method. Memory should never be allocated in one filter and released in another as we can not define any restrictions in filter combinations. In this situation, one may not know or forget the second filter and end up with a memory leak.

- Methods should be implemented in a general way for a better re-usability in later applications or filters. In terms of DirectShow filters, it makes it possible to combine them in various ways with other filters. However, if an algorithm lakes on performance, it might be necessary to implement specific methods or combine two filters so that internal structures do not need to be initialized twice. The decision of such a trade-off depends on the situation and should be discussed with the stakeholders.

- A simple and understandable class responsibility significantly reduce the overall complexity. In terms of DirectShow, there are many functions involving the data flow from a source to a sink filter. It is recommended to handle functinalities to deliver and receive samples within the corresponding input or output pins. The transformation of a sample, however, should be implemented into the filter class itself which provides a clear division of responsibilities. Furthermore, the data flow becomes more understandable as no filter code is involved while passing samples from one filter to another.

- C++ has evolved during the last years and offers new keywords and operators. Using such extensions can both improve productivity and avoid errors. In our case, C++/CX for example offers the same reference counter mechanism as provided by COM without the need of implementing the query method for supported interfaces. A total restructuring within DirectShow using C++/CX is, however, not easily possible because the basic interfaces expect COM structures to handle which requires to adapt all the DirectShow base classes.

10 Bibliography

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11 Declaration of Originality

I hereby confirm that I am the sole author of the written work here enclosed and that I have compiled it in my own words. Parts excepted are corrections of form and content by the supervisor.

Date	Signature
_____	_____

12 Appendix

12.1 A Cross-Platform Plugin Framework For C/C++

As we used a DirectShow we did not need to take care about the underlying plugin framework ourselves. However, this is an interesting subject we would like to pick up here in a few words.

The following section is based on the article "Building Your Own Plugin Framework" at `http://www.drdobbs.com/cpp/building-your-own-plugin-framework-part/204202899` and discuss about the implementation of a plugin framework under C++. As mentioned in section 3.2 a main issue is the binary compatibility between the plugin system and its plugins which might be violated using C++ interfaces. This is due the virtual table (vtable) representation which can vary between different compilers such as GCC or Microsoft's C++ compiler. To solve this problem we could restrict the plugin development for only vtable compatible compilers or, a more elegant solution, we use C interfaces instead of C++ ones. As C only supports a subset of the C++ features, holds a cumbersome API and is much more difficult to debug we put aside the idea of implementing the whole application in C. However, if we only use C for the interfaces but program the plugin system as well as its plugins in C++ we can combine the advantages of both languages; and we are ABI compatible and do not need to worry about name mangling[1]. Figure 12.1 visualize this C/C++ approach.

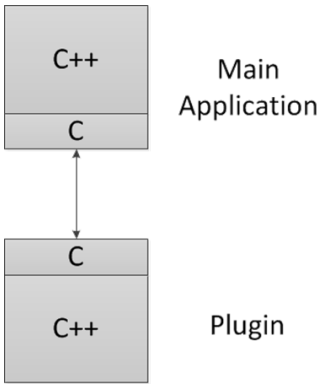

Figure 12.1: Approach of implementing a C++ plugin system with C interfaces.

[1] An overview of calling conventions can be found at `https://msdn.microsoft.com/en-us/library/deaxefa7.aspx`

An even more flexible and interesting approach is described in the above given article; using so called "dual classes". It describes the implementation of the C interfaces using wrapper classes which then hides the C fragments and allows the developer programming only against decorated C++ interfaces. Moreover, the approach even makes it possible to switch the communication channel of the plugin system and a plugin between C and C++. As expected it also holds disadvantages which are listen in Table 12.1.

	Dual class model
Advantages	Plugin development possible in C or C++ Simple interface definition for communication between plugin system and plugin Developer do not see underlying C interfaces The plugin system can use C++ member functions due wrapper classes
Disadvantages	Wrapper and adapter mechanisms impacts the performance Using pure C implementation is not possible by using the described approach due the plugin manager

Table 12.1: Advantages and disadvantages of a dual class model.

While DirectShow also uses C interfaces for the communication it disclaim the usage of a dual model which omits the performance disadvantage. The implementation of such an C interface under DirectShow is given in the following Listing 12.1 where we build our own virtual tables to avoid incompatibility between compilers. The code was simplified and most macros resolved for better readability. The implementation of the function "IBaseFilter::FindPin" is done in standard C++ and not enlisted below.

```
struct IBaseFilter : public IMediaFilter {
public:
    virtual HRESULT FindPin(LPCWSTR Id, IPin **ppPin) = 0;
    ...
};

#ifdef __cplusplus extern "C"{ #endif
interface IBaseFilter {
    const struct IBaseFilterVtbl *lpVtbl;
};
typedef struct IBaseFilterVtbl {
    BEGIN_INTERFACE
    HRESULT ( STDMETHODCALLTYPE *FindPin )(
        IBaseFilter * This,
        /* [string][in] */              LPCWSTR Id,
        /* [annotation][out] */ __out   IPin **ppPin);
    ...
};
#ifdef __cplusplus } #endif
```

Listing 12.1: C-interface snippets

```
#ifdef __cplusplus extern "C"{ #endif
HRESULT BaseFilter_FindPin(IBaseFilter *iface,
                           LPCWSTR Id, IPin **ppPin)
{
    return iface->FindPin(Id, ppPin);
}
#ifdef __cplusplus } #endif
```

Listing 12.2: C-wrapper code snippets

Another important part of a plugin system is the plugin manager which searches and manages plugins. As described in the above article it could initialize a plugins object,e.g. a DirectShow filter, and offers services, e.g. stopping the filter graph, for the plugins due function pointers. A functionality not given in DirectShow is the plugin factory for the dual class model. Whenever needed, it creates new objects from the plugins using the plugin manager. The resulting objects offer C interfaces which then optionally are decorated by a C++ adapter. Again, we obtain the possibility of switching between C/C++ interfaces whereas we lose performance.

As can be read in the above given article there is much more to consider while implementing a plugin system. Additional information can easily be found as e.g. at MSDN `https://msdn.microsoft.com/en-us/library/ms972962.aspx`.

12.2 Doxygen Documentation

The documentation enlisted in section 12.9 was generated using Doxygen. Doxygen can easily be run by the following command:

```
doxygen Doxyfile > last_build.log
```

Hereby, the the “Doxyfile” contains all configurations used while generating the documentation whereas logging information are written into the “last_build.log” file. The interesting fragments of the Doxyfile are given in Listing 12.3.

```
#---------------------------------------------------------------------------
# Configuration options related to the input files
#---------------------------------------------------------------------------
INPUT                  = "<filter_src_paths>"

#---------------------------------------------------------------------------
# Configuration options related to the HTML output
#---------------------------------------------------------------------------
GENERATE_HTML          = YES
HTML_OUTPUT            = html
HTML_FILE_EXTENSION    = .html
GENERATE_HTMLHELP      = YES
CHM_FILE               = ../chm/documentation.chm
HHC_LOCATION           = "<hhc_path>"

#---------------------------------------------------------------------------
# Configuration options related to the preprocessor
#---------------------------------------------------------------------------
ENABLE_PREPROCESSING   = YES
MACRO_EXPANSION        = YES
EXPAND_ONLY_PREDEF     = YES
PREDEFINED             = \
  "DECLARE_INTERFACE(name)=class name" \
  "DECLARE_INTERFACE_(name,base)=class name:public base" \
  "STDMETHOD_(result,name)=virtual result name" \
  THIS= \
  "STDMETHOD(name)=virtual HRESULT name" \
  THIS_= \
  "PURE= = 0" \
  __cplusplus

...
```

Listing 12.3: Excerpt of the Doxygen configuration file.

In the first part we define all paths to the source folder of each IA filter. In the second part we define the output as HTML files which then are combined into a single HTML help file (so called CHM file). The third part contains the most interesting part. As we implement interfaces under C++ we use macros like "DECLARE_INTERFACE". This macros can only be evaluated by Doxygen if all header files are included containing the relevant definitions. As we only have a few macros neccesarily for Doxygen for generating a correct documentation we give its definition manually here. This also omit the circumstance as the path to necessarily header files may change depending on the users installation paths which needs a modification in the script each time. By enabling the Doxygen's pre-processor we tell Doxygen to use a simple substitution process right before we generate the documentation. The substitution rules are set by the parameter "PREDEFINED" which looks as follow: term=substitution. More information can be found at `http://www.stack.nl/~dimitri/doxygen/manual/preprocessing.html`.

12.3 Using DirectShow Filters Inside Microsoft's MediaPlayer

DirectShow filters are COM objects, registered on the operating system and therefore accessible from everywhere. The following chapter gives such an example by using the "TIFF Ventana Source Filter"[2] within Microsoft's MediaPlayer. We already know as the filter can process Ventana's image files and provides its tiles as RGB24 images. Also the RGB24 images are not directly supported by the MediaPlayer it can use the "Intelligent Connection" mechanism for searching conversion filters. Doing so he will find the image analysis' "RGB Converter" which can convert an RGB24 image into an RGB32 image, readable by the MediaPlayer. The "RGB Converter" therefore needs a merit higher than "MERIT_DO_NOT_USE", in our case "MERIT_UNLIKELY". When trying to render the output pin of our "TIFF Ventana Source Filter" e.g. by the Filter Graph Editor of Microsoft we can see as the standard "Video Render" is used which will not fail but use the "RGB Converter" due intelligent connection. Before we can use this mechanism with the MediaPlayer we need two more steps to perform. Firstly, we need to link Ventana's TIFF file format with our DirectShow filter. Doing so makes it possible to open the image file format with all DirectShow based applications. We do so by adding the following registry entry:

```
[HKEY_CLASSES_ROOT\Media Type\Extensions\.tifv]
"Source Filter"="{30F6349D-B832-4F09-A916-B7D5CFCFEB6C}"
"Description"="Format of Ventana's TIFF files"
```

We now can drag and drop our Ventana images (with the file extension "TIFV") e.g. into the Filter Graph Editor of Microsoft which then automatically build up the render pipeline for the image file. In a last step we only need to tell the Microsoft MediaPlayer to use DirectShow with our "TIFV" files for rendering them. Again, we do so by a registry entry:

```
[HKEY_LOCAL_MACHINE\SOFTWARE\Microsoft\Multimedia\WMPlayer
    ↪\Extensions\.tifv]
"Permissions"=dword:00000001
"ReplaceApps"="*.*"
"Runtime"=dword:00000007
```

Hereby, the "Runtime" defines to use DirectShow for the render process.

If we use a 64bit Windows operating system we may have to set up the registry entries also for the following entries, depending if we use the 32bit or 64bit version of the MediaPlayer:

[2] see also Section 5.3.1

```
[HKEY_CLASSES_ROOT\Wow6432Node\Media Type\Extensions \.tifv]
...
[HKEY_LOCAL_MACHINE\SOFTWARE\Wow6432Node\Microsoft
    ↪\Multimedia\WMPlayer\Extensions\.tifv]
```

Moreover, if we do not want to link a file directly by its extension but its binary representation with a DirectShow filter we can also doing so by corresponding registry entries. A detailed description is given at the MSDN `https://msdn.microsoft.com/en-us/library/windows/desktop/dd377513(v=vs.85).aspx`.

12.4 IA Base Class Diagrams

This sections visualizes the class diagrams of the three base image analysis base classes and there related pins.

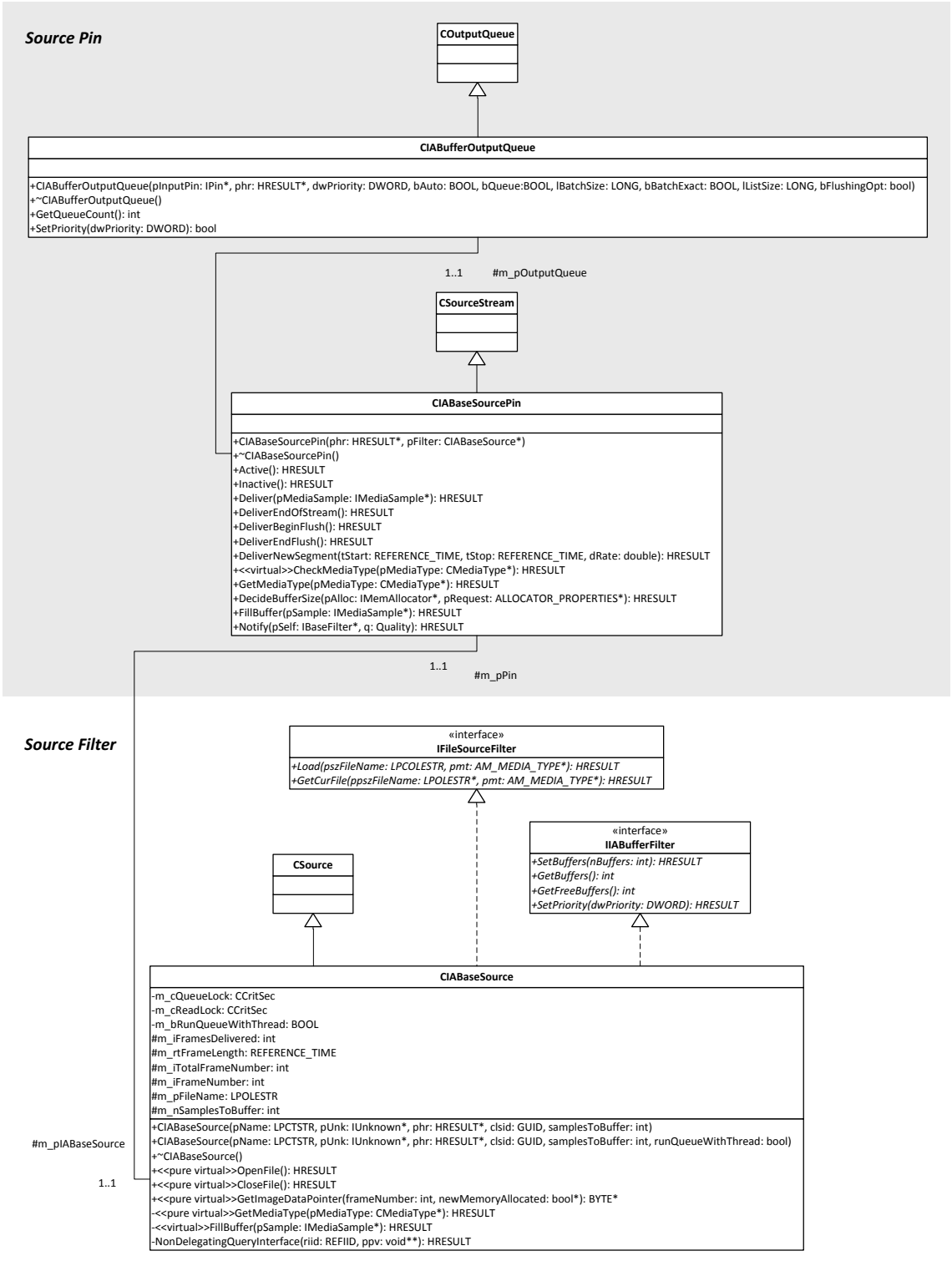

Figure 12.2: Class diagram of the “CIABaseSource” class.

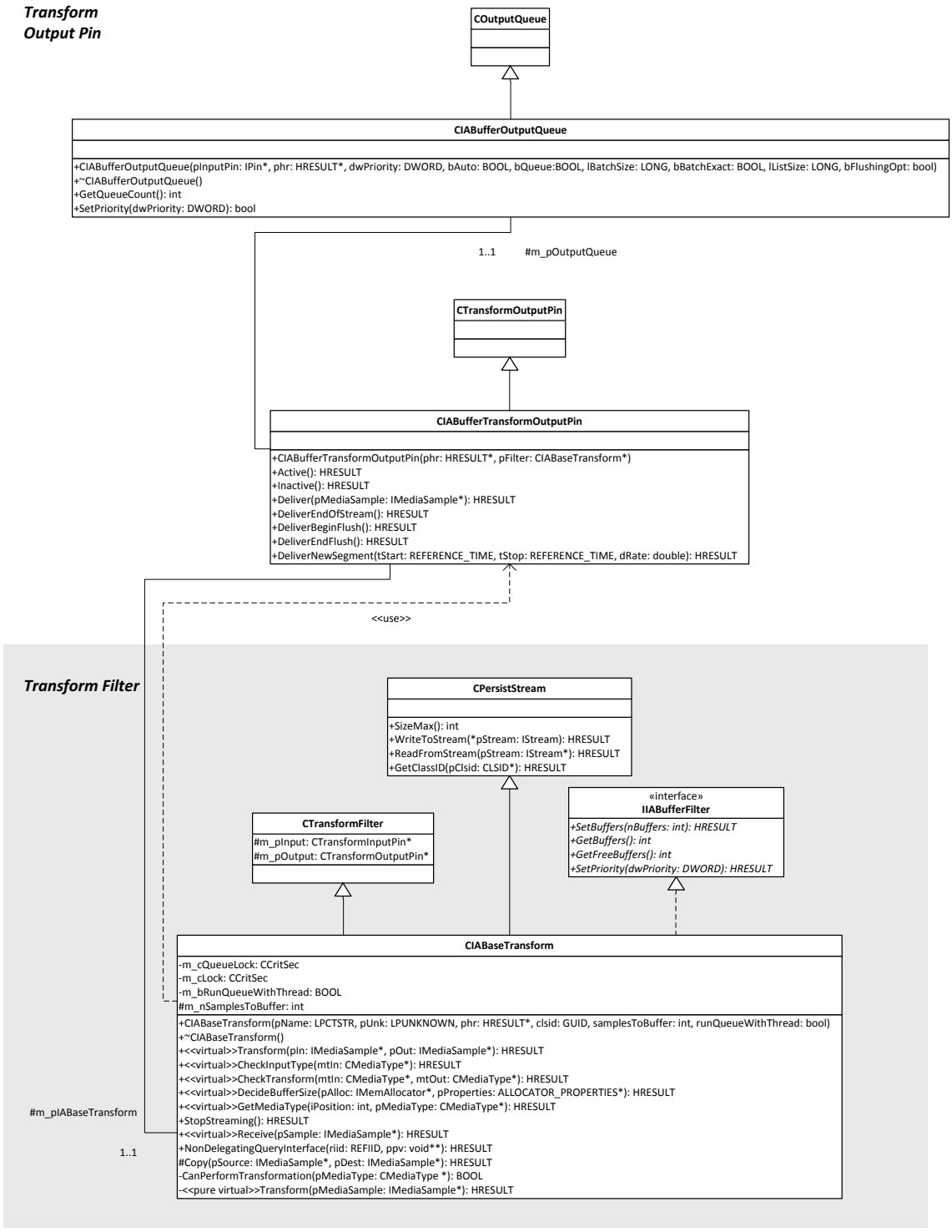

Figure 12.3: Class diagram of the “CIABaseTransform” class.

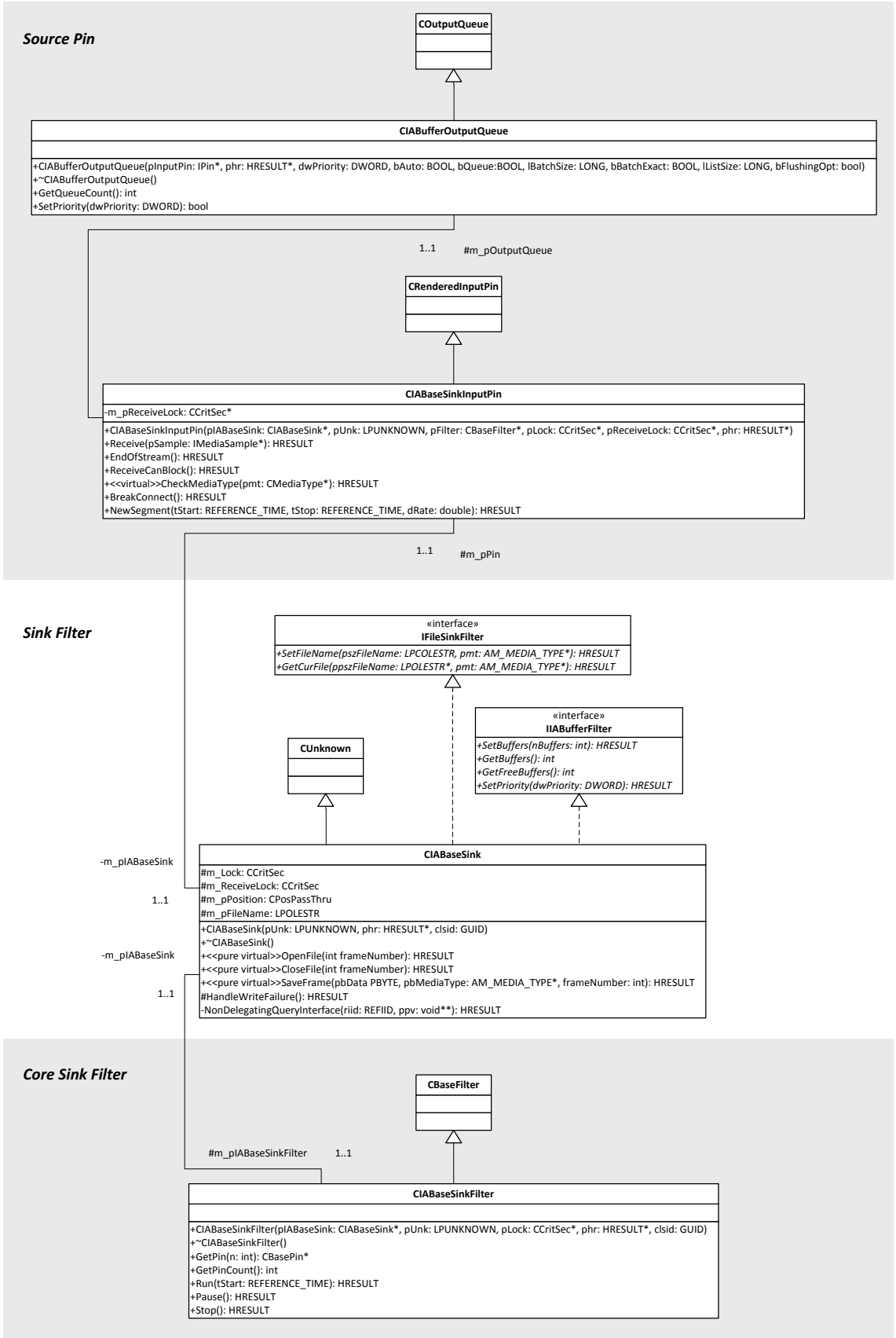

Figure 12.4: Class diagram of the “CIABaseSink” class.

12.5 XMLLite

The following section introduce XMLLite, an easy to use, performance and standard compliance XML parser from Microsoft for C++. Before using XMLLite the only required header file is $< xmllite.h >$. Following, we present three simple example on how to use the library. Listing 12.4 shows how to read an XML file while Listings 12.5 and 12.6 show how to write data into an XML file or temporarily into a memory stream. The code samples and detailed information can be found at MSDN and the MSDN magazine:
`https://msdn.microsoft.com/en-us/library/windows/desktop/ms752872(v=vs.85).aspx`
`https://msdn.microsoft.com/en-us/magazine/cc163436.aspx`

```
IStream *pFileStream = NULL;
IXmlReader *pReader = NULL;
XmlNodeType nodeType;

//Open read-only input stream
SHCreateStreamOnFile(L"C:\\tmp\\test.xml", STGM_READ, &pFileStream);
CreateXmlReader(__uuidof(IXmlReader), (void**)&pReader, NULL);
pReader->SetProperty(XmlReaderProperty_DtdProcessing,
    ↪DtdProcessing_Prohibit);
pReader->SetInput(pFileStream);

// Reading XML file
vector<vector<cv::Point>*> annotations;
vector<cv::Point>* currAnnotation = NULL;

const WCHAR* pwszPrefix;
const WCHAR* pwszLocalName;
const WCHAR* pwszValue;
while (S_OK == (hr = pReader->Read(&nodeType))) {
    if (nodeType == XmlNodeType_Element) {
        pReader->GetLocalName(&pwszLocalName, NULL);

        // we found an element node, e.g. <Element>
        if (wcscmp(pwszLocalName, L"ElementName") == 0) {
            // Read element attributes
            pReader->MoveToFirstAttribute();
            pReader->GetValue(&pwszValue, NULL);
            int val = _wtoi(pwszValue);
            pReader->MoveToNextAttribute();
            pReader->GetValue(&pwszValue, NULL);
            // ...
        }
    }

    // we found an element end-node, e.g. </Element>
    if (nodeType == XmlNodeType_EndElement) {
        // ...
    }
}
```

```
if (pFileStream){ pFileStream->Release(); } pFileStream = NULL;
if (pReader)    { pReader->Release();     } pReader = NULL;
```

Listing 12.4: Code example of the XML reader.

```
HRESULT hr = S_OK;
IStream *pFileStream = NULL;
IXmlWriter *pWriter = NULL;

//Open write-only output stream
SHCreateStreamOnFile(xmlFilename, STGM_WRITE, &pFileStream);
CreateXmlWriter(__uuidof(IXmlWriter), (void**)&pWriter, NULL);
pWriter->SetProperty(XmlWriterProperty_Indent, 4);
pWriter->SetOutput(pFileStream);

// Create XML structure
// <?xml version="1.0" encoding="UTF-8"?>
pWriter->WriteStartDocument(XmlStandalone_Yes);

// <order>
//   <item date="2/19/01" orderID="136A5"></item>
//   <note>text</note>
// </order>
pWriter->WriteStartElement(NULL, L"order", NULL);
pWriter->WriteStartElement(NULL, L"item", NULL);
pWriter->WriteAttributeString(NULL, L"date", NULL, L"2/19/01");
pWriter->WriteAttributeString(NULL, L"orderID", NULL, L"136A5");
pWriter->WriteFullEndElement();
pWriter->WriteElementString(NULL, L"note", NULL, L"text");
    pWriter->WriteEndElement();

    // Write the XML to file
pWriter->WriteEndDocument();
pWriter->Flush();

if (pFileStream){ pFileStream->Release(); } pFileStream = NULL;
if (pWriter)    { pWriter->Release();     } pWriter = NULL;
```

Listing 12.5: Code example of the XML file writer.

```
HRESULT hr = S_OK;
IStream *pMemStream = NULL;
IXmlWriter *pWriter = NULL;

//Open write-only output stream
pMemStream = ::SHCreateMemStream(NULL, 0);
CreateXmlWriter(__uuidof(IXmlWriter), (void**)&pWriter, NULL);
pWriter->SetProperty(XmlWriterProperty_Indent, 4);
pWriter->SetOutput(pMemStream);
```

```
// Create XML structure
// <?xml version="1.0" encoding="UTF-8"?>
pWriter->WriteStartDocument(XmlStandalone_Yes);
IStream_WriteStr(pMemStream,
    ↪L"<order><item ...></item><note/></order>");

    // Write the string
PWSTR pwStr = NULL;
    IStream_ReadStr(pMemStream, &pwStr);
    wstring xmlString(pwStr);

if (pMemStream){ pMemStream->Release(); } pMemStream = NULL;
if (pWriter)   { pWriter->Release();    } pWriter = NULL;
```

Listing 12.6: Code example of the XML memory writer.

12.6 C++/CX Analogies

DirectShow is based on COM objects which is also visible in the implementation of all IA base classes described in section 5.2.1. In a more detailed investigation we can see as there are mainly two common features in use:

1. A counter which holds the number of references to an object. If the counter reaches zero the object is deleted automatically.

2. A method for queuing an interface from a COM object by a given GUID.

Especially the implementation and use of an interface involves a lot of COM specific mechanisms. The same mechanisms are now available by the new component extensions of C++, so called C++/CX. It provides a new handle declarator ^(also "hat" declarator) and a new keyword "interface". Using the handle declarator increments the internal reference counter whenever a new object is created or copied and decremented whenever the existing object is set to null or goes out of scope. Also the new interfaces become easier as we can avoid macros such as "STDMETHOD" and do not need to generate a related GUID anymore. Generally, C++/CX handles and hides several COM mechanisms we had to implement by ourselves before. For a better understanding we give a short example in the Listings 12.7 and 12.8 which use the "IIABufferFilter" interface.

```
/* 1) Interface declaration */
DEFINE_GUID(IID_IIABufferFilter,
0x63EF0035,0x3FFE,0x4C41, 0x92,0x30,0x43,0x46,0xE0,0x28,0xBE,0x20);

DECLARE_INTERFACE_(IIABufferFilter, IUnknown)
{
    STDMETHOD_(int,GetBuffers) (THIS) PURE;
    STDMETHOD(SetBuffers) (THIS_ int nBuffers) PURE;
    STDMETHOD_(int,GetFreeBuffers) (THIS) PURE;
    STDMETHOD(SetPriority) (THIS_ DWORD dwPriority) PURE;
};

/* 2) Method implementation for queuing an interface */
class MyFilter : public IIABufferFilter
{
    ...

    STDMETHODIMP MyFilter::NonDelegatingQueryInterface(REFIID
        ↪riid,void **ppv)
    {
        if (riid == IID_IIABufferFilter) {
            return GetInterface(
                ↪static_cast<IIABufferFilter*>(this),ppv);
        }
        return CBaseFilter::NonDelegatingQueryInterface(riid,ppv);
    }
}

/* 3) Using the interface */
void main(int argc, char* argv[]) {
    MyFilter* myFilter = new MyFilter();
    IIABufferFilter* bufferFilter = nullptr;
    myFilter->QueryInterface(IID_IIABufferFilter,
        ↪(void**)&bufferFilter);
    bufferFilter->SetBuffers(2);
    ...
    bufferFilter->Release();
    myFilter->Release();
}
```

Listing 12.7: Implementation and use of a COM interface.

```
/* 1) Interface declaration */
public interface struct IIABufferFilter
    {
            int GetBuffers() = 0;
            void SetBuffers(int nBuffers) = 0;
            int GetFreeBuffers() = 0;
            void SetPriority(DWORD dwPriority) = 0;
    };

/* 2) Method implementation for queuing an interface */
ref class MyFilter sealed : public IIABufferFilter {
    ...
}

/* 3) Using the interface */
void main(int argc, char* argv[]) {
    MyFilter^ myFilter = ref new MyFilter();
    IIABufferFilter^ bufferFilter = myFilter;
    bufferFilter->SetBuffers(2);
    ...
    // We do not need to release any object.
    // Both are going out of scope when
    // reaching the function body's end.
    // Alternative: We can also set the objects to null
    myFilter = nullptr;
    bufferFilter = nullptr;
}
```

Listing 12.8: Implementation and use of a CX interface.

We may ask if we could not replace the COM mechanism with purely CX interfaces. As the DirectShow framework expects our filters to implement the "IUnknown" interface which then is used to queue interfaces by the "NonDelegatingQueryInterface(REFIID riid,void **ppv)" method we have to provide a COM compatible interface anyway. We may provide ref objects within the "NonDelegatingQueryInterface" method but this would bring compatibility problems between COM and CX. As CX do not support native types such as "GUID" or "void**" (see parameter of the "NonDelegatingQuery-Interface" method) we have to provide a wrapper class. We do not provide such wrappers at the current moment.

More information about C++/CX can be found at MSDN under the following links:

Overview of CX	https://msdn.microsoft.com/en-us/library/xey702bw.aspx
Handle declarator	https://msdn.microsoft.com/en-us/library/yk97tc08.aspx
Ref classes	https://msdn.microsoft.com/en-us/library/hh699870.aspx
Ref new & gcnew	https://msdn.microsoft.com/en-us/library/te3ecsc8.aspx
Castings	https://msdn.microsoft.com/en-us/library/hh755802.aspx

For starting with C++/CX we strongly recommend the following two websites. On the MSDN blog of the Visual C++ Team you can find a great introduction on CX and the relation to COM objects: http://blogs.msdn.com/b/vcblog/archive/2012/08/29/cxxcxpart00anintroduction.aspx. The second link on Pavel's blog explains how to set up Visual Studio to use the new component extensions (CX): http://blogs.microsoft.co.il/pavely/2012/09/29/using-ccx-in-desktop-apps/.

12.7 Selenium Test Cases

The following tables describe the new Selenium test cases relevant for the IP8 which were successfully performed. The old test cases can be found in [3, p.68–71]. For further information about the syntax please visit http://docs.seleniumhq.org/docs/02_selenium_ide.jsp#script-syntax.

Update_Test (2)		
open	dbimport/main	
click	xpath=(//button[@type='button'])[4]	
clickAndWait	link=Update features of scanned images	
type	name=input_file	C:\tmp\Features_169.xml
click	id=submitbutton	
waitForText	class=information	2 feature(s) updated.
verifyText	class=information	2 feature(s) updated.
click	css=div.modal-footer > button.btn.btn-default	

Table 12.2: Update test case.

Analysis_Test		
open	analysis/main	
click	xpath=(//button[@type='button'])[6]	
clickAndWait	link=Analysis image with the IA tool	
select	name=db_file	label=[study #1/image #1] C:\PSR\169\1.tif
type	name=graph_file	C:\IA_Tool\grf\nucleus_detection_1.0.grf
type	name=configuration_id	1
click	id=submitbutton	
pause	1000	
selectFrame	id=cmd	
waitForNotText	body	*The IA pipeline terminated with an unexpected error*
waitForNotText	body	*Unexpected error*
selectWindow		
click	//input[@value='Next >' and @name='submit']	
waitForText	//tr[8]/td[2]	None
verifyText	//tr[8]/td[2]	None

Table 12.3: Analysis test case.

Export_Test		
open	dbexport/main	
click	xpath=(//button[@type='button'])[5]	
clickAndWait	link=Export image features from database	
select	name=study	label=1
select	name=image	label=[1] 169S1.tif
click	id=submitbutton	
waitForText	css=span.progress-value	regexp:^Export complete!$
waitForText	css=h1	Export completed without errors.
assertText	css=h1	Export completed without errors.

Table 12.4: Export test case.

12.8 Image Results

In the following section we present selective extracted tiles resulting form the nucleus detection algorithm.

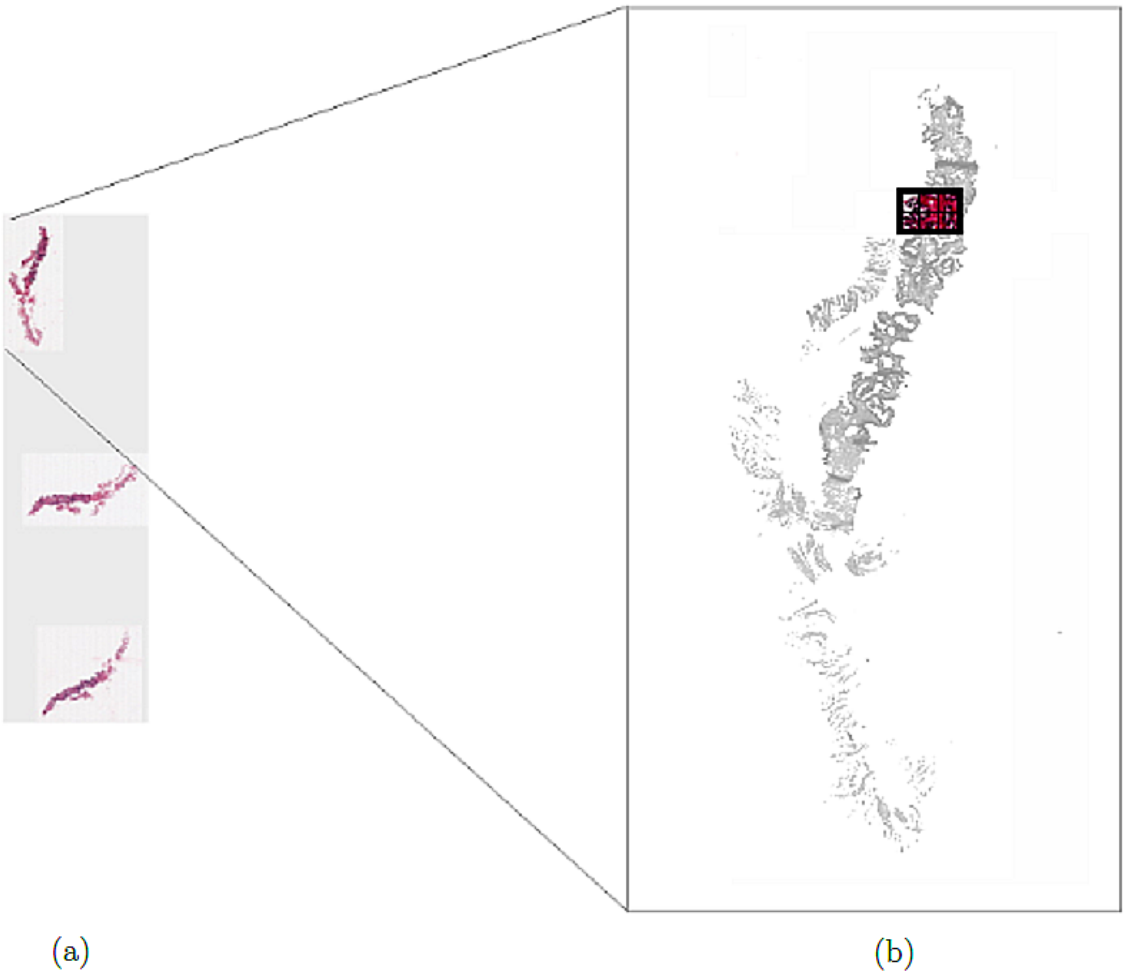

Figure 12.5: (a) Overview of the processed source image. (b) Selective extracted tiles.

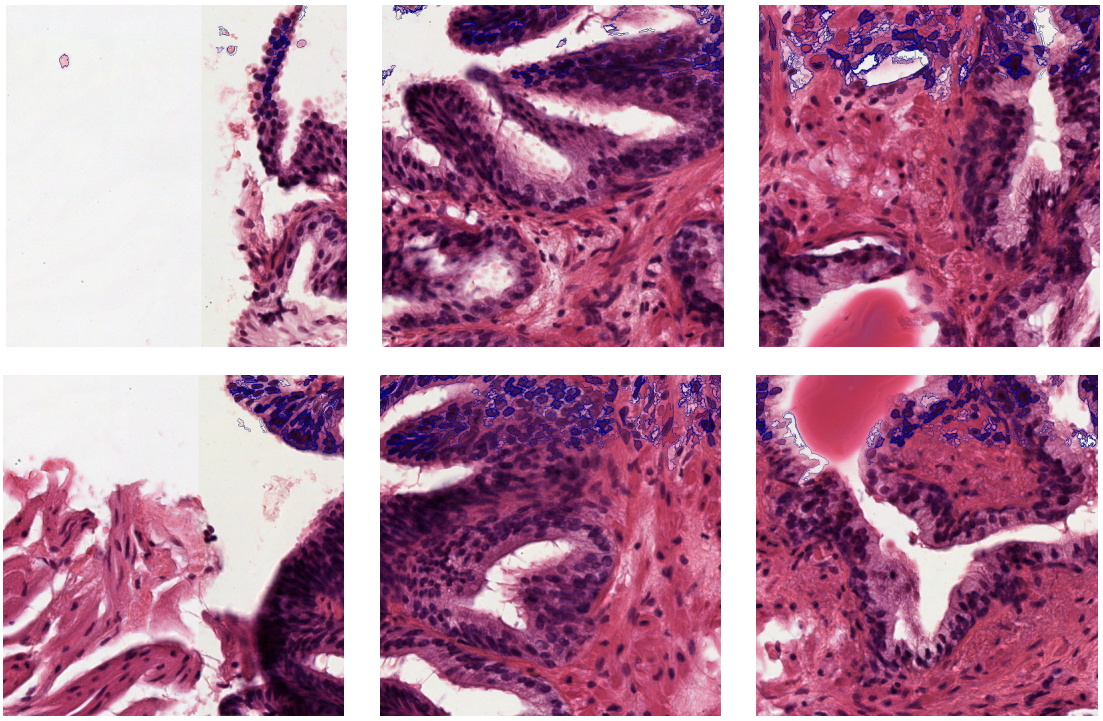

Figure 12.6: Selective extracted tiles from the nucleus detection algorithm.

12.9 Attached Materials

This report is related to the following materials which are deployed together:

- Project definition
- User-manual for the PSR system
- Source code of the PSR system
- Source code of the File Organizer
- Source code of all DirectShow IA filters
- Source code of the Image Analysis console tool
- Source code documentation of the PSR system
- Source code documentation of the File Organizer
- Source code documentation of the DirectShow IA filters
- DirectShow IA filters & dependencies
- Batch file for installing/uninstalling the DirectShow filters
- SQL script for creating the inventory database
  (includes data of all currently scanned images)
- Tools: GraphStudio, GraphStudioNext, DSFMgr
- Selenium test cases
- Excel report about the scanned tissue slides
- Excel sheet containing the precision & recall graph