Preface

Five years at NTNU have been a rollercoaster ride. Uphills at times, but also a great deal of fun. I'm grateful for the number of marvellous people I have met, the flexibility the student life brings, all the fun with the student society Spanskrøret and not to forget all the things I've learned.

A special thank you go to all the professors who withstand sharing their knownledge every day, even at time when their students seems unmotivated.

The last year I have been warmly included in Magnus Borstad Lilledahl's research group, with Andreas Finnøy, Elisabeth Inge Romijn and Rajesh Kumar. It's been educational to work with them and exciting to get an insight in how they perform their research. Thank you!

I would also like to thank my family, who always have been supportive for the choices I've made.

Lastly, the greatest thanks go to my life companion Yngvild, it wouldn't have been the same without you.

The cheesy quote is..

The future is already here, it's just not very evenly distributed. - William Gibson

Contents

Abstract

What to communicate: goal, overview of experiences made, results

St. Olavs hospital has supplied a dataset of 2703 tissue samples at the tumor peripheral from ≈ 900 patients. NTNU want to examine all tissue samples with image processing to see if second harmonic generation microscope images of tissue can help classify cancer type (I, II, III) or in other words, cancer aggresiveness. This thesis documents a method which automates the microscope imaging of these tissue micro arrays (TMA) and show how images can be structured and correlated to clinical data.

Automated microscope scanning is in principle straight forward, but the implementation is dependent on many aspects of the experimental setup. In general, some of the aspects discussed in this thesis are:

- Create image analysis algorithms that are robust to experimental variations.
- Correction of systematic errors like
    - intensity variations and
    - difference in coordinate systems of scanning raster patterns and stage movement.
- Automatic stitching of regular spaced images with variable degree of signal entropy in seams.
- Adjusting z-plane for large area samples with micrometer precision.

The aspects listed above are not unique to TMA-specimens and the experimental setup, and could be useful for similar projects. But the focus of the thesis will be on TMA and the experimental setup with a Leica SP8 microscope.

The conclusions are:

- Large area scans should adjust speciment plane to be at even distance to the objective to be time effective and avoid out of focus images.

- Using heuristics/constraints improves the reliability to automatic stitching algorithms, failing gracefully on images with little entropy in overlap.
- Leica LAS X version 1.1.0.12420 have limited support for automatic microscopy, but it's possible to work around limitations to leverage fully automatic TMA-scanning.

Chapter 1

Introduction

What to communicate: motivation, brief summary of chapters

With a population just above 5 million[1], three thousand women are diagnosed with breast cancer each year[2] in Norway. This makes breast cancer the most common kind of cancer, affecting one of every eleventh woman. Luckily breast cancer is often treatable, shown by the fatalities which was 649 in 2012[2]. NTNU and St. Olavs hospital have been cooperating on reasearch to find new ways to diagnose patients. The cooperation yielded a study[3] on 37 subjects which showed positive results on difference of collagen structure from different parts of tumor tissue. This thesis seeks to make it possible to expand the study from 37 subjects to the whole dataset available of ≈ 900 subjects.

The means to achieve the expanded dataset is automating the microscope imaging, with main focus on automated scanning of tissue micro arrays. Tissue micro arrays are glass slides with samples arranged in a matrix pattern seen in figure 1.1. As tissue micro arrays is standard procedure, not unique to breast cancer tissue, the work of this master is relevant for other studies too.

The tissue micro array shown in figure 1.1 is $\approx$ 24x15 mm in size. Using a moderate objective of 25x with 400 µm field of view, a single scan of the total dataset will be

$$\frac{24\text{mm}}{400\text{µm}} \cdot \frac{15\text{mm}}{400\text{µm}} = 2250 \text{ images.}$$

Depending on the precission of the microscope stage, images are not necessarry easily put together. Also, keeping microscope in focus for the whole surface can become challenging. Another approach would be not to scan the whole area in one scan, but to scan each of the $14 \cdot 9 = 126$ tissue specimens
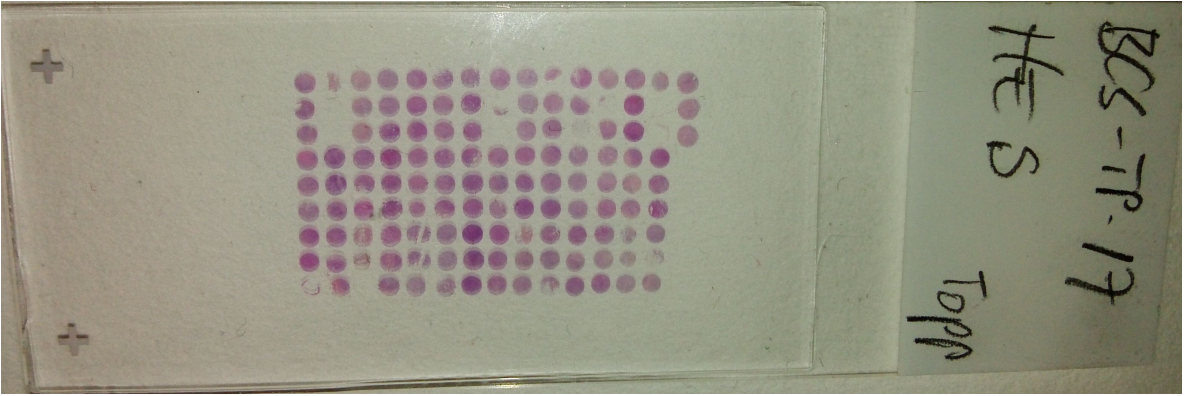
Figure 1.1: Tissue micro array of breast tissue at perifer of tumor. Three test samples are beside the array of 14x9 samples to avoid mix up of patients when rotating the slide.

one by one. The challenge with scanning each region one by one is that the samples are often not equally spaced, and a lot of manual error prone labor is required to define the areas to scan. The method in this thesis tries to simplify the scanning process and prepare the images for further analysis.

The thesis are written with focus on two parts, namely automating the collection of images and correlating samples to clinical data. How this can be used in supervised machine learning will be briefly mentioned in the end. In total the method described should enable researchers to run experiments on large datasets of tissue micro arrays in a structured and determined manner.

A reader of this text should be familiar with general physics. Matters that are specific to scanning microscopy and image processing will be described in the theory section, along with software concepts in use. The method section seeks to make the reader able to replicate the experiment on any kind of microscope, but some software and solutions will be specific to the Leica SP8 microscope. The result section will mark out leverages gained with automated scanning, and the discussion holds details on choices made when developing the method and limitations stumbled upon.

All source code in the thesis will be in the programming language python[4]. The reader does not need to be proficient in python programming, but acquaintance with the syntax is assumed. Code blocks will be used to clarify how problems have been solved or algorithms have been implemented. Details not essential to the problem at hand have been omitted to keep focus on the essential parts. As total amount of source code are above thousand lines it's not included in the appendix, but rather available at github[???] with full history.

As this thesis mainly consists of work on creating automated microscope scanning, the method is also the result of the thesis. Therefore a result chapter is not included, but a brief description of the result

is in the beginning of the method chapter.

ML: En hoveddel i arbeidet har vært automatiseringen av TMA. Skrive noe om TMA og hvorfor automatisert analyse er nødvendig...skal lede opp til en beskrivelse av de tekniske utfordringene som er løst.

Chapter 2

Theory

What to communicate: theory and details that are not obvious for understanding the rest of the text

ML: I denne delen bør man primært ha med teori som er nødvendig for å forstå det som kommer i metodedelen. Altså ikke skriv for mye her før strukturen og innholdet er mer klart.) ## Tissue micro arrays[5]

Image processing

The term image in this contex a two dimentional array of values, where each position in the array is called a pixel. Resolution is the number of pixels an image holds. E.g. a resolution of 1024x1024 is an image with 1024 pixels in both x- and y-direction, totalling 1×10^6 pixels. Each pixel represent a physical position of the specimen, where the value is the amount of light measured from the detector when scanning the specimen surface with a light source. The physical size of the pixel will depend on sampling rate. All images in this thesis are 8 bit grayscale images, meaning that each pixel can hold $2^8 = 256$ values. In an ideal experiment a pixel value of zero denote zero detected light and 255 is the maximum, but this is an simplification as noise will be measured too.

$f(x, y)$ denotes the intesity of pixel at position (x, y), where $(0, 0)$ is the top left of the image, positive x-direction going left and positive y-direction going down. $m \times n$ will denote the number of pixels in in respectively x- and y-direction. A subscript of the image name is used if several images are discussed, e.g. m_f is the number of x-pixels of image f.

Image registration

Image registration is the process of putting images into the same coordinate system. In this context the sources are images from different microscope stage coordinates. One way of finding how images are displaces is by using correlation. Correlation is defined as the following: If we have an window image w of size $m_w \times n_w$, the correlation of w and f is

$$w(x,y) \star f(x,y) = \sum_{s=-a}^{a} \sum_{t=-b}^{b} w(s,t)f(x+s, y+t). \tag{2.1}$$

Assuming the window size is odd, $a = (m_w - 1)/2$ and $b = (n_w - 1)/2$[6]. As equation 2.1 is sensitive to intensity in w and f, one usually use the normalized correlation

$$\gamma(x,y) = \frac{\sum_s \sum_t [w(s,t) - \bar{w}] \sum_s \sum_t [f(x+s,y+t) - \bar{f}(x+s,y+t)]}{\left\{ \sum_s \sum_t [w(s,t) - \bar{w}]^2 \sum_s \sum_t [f(x+s,y+t) - \bar{f}(x+s,y+t)]^2 \right\}^{\frac{1}{2}}}. \tag{2.2}$$

> Kanskje ta bort dette, jeg bruker stort sett bare phase correlation, likevel om jeg har prøvd template matching.

In the normalized cross correlation, the window is often called a *template* and the process of correlation is called *template matching*. The maximum peak(s) in $\gamma(x,y)$ will be where the template has the best match, which may be in several positions if several matches are made. By padding $f(x,y)$ before correlating one can also match at the border of $f(x,y)$[6].

If f and w are large images, calculation of equation 2.2 is quite computational costly. To reduce the calculation one might use the 2-D discrete Fourier transform (DFT). The DFT $F(u,v)$ of an image $f(x,y)$ is computed by

$$F(u,v) = \mathfrak{F}\{f(x,y)\} = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f(x,y)e^{-i2\pi(ux/m + vy/n)}. \tag{2.3}$$

Here $F(u,v)$ is the frequency domain image and $\mathfrak{F}\{f(x,y)\}$ is the notation for a Fourier transform of $f(x,y)$.

Similar the inverse Fourier is defined as

$$f(x,y) = \mathfrak{F}^{-1}\left\{f(x,y)\right\} = \frac{1}{mn}\sum_{u=0}^{m-1}\sum_{v=0}^{n-1}F(u,v)e^{i2\pi(ux/m+vy/n)}. \tag{2.4}$$

Luckily the sums of equation 2.3 are seperatable, and sums can be done in rows and columns yielding the fast Fourier transform which reduces the $O(mn)$ calculation complexity to $O(m\log m + n\log n)^6$.

DFT has the intresting property that a multiplication in the frequency domain with one of the images complex conjugated is equivalent as a correlation in the real domain. The correlation theorem states

$$f(x,y)\star g(x,y) = \mathfrak{F}^{-1}\left\{F^*(u,v)G(u,v)\right\}. \tag{2.5}$$

Here $F^*(u,v)$ denotes the complex conjugate of $F(u,v)$.

Sliding window filters

Sliding window filters are similar to correlation filters in the sense that they look at neighbouring pixels of a center pixel. The window will be all pixels sourrounding the center pixel defined by the size of the window. A histogram of the values in the window are updated instead of doing computation directly with the values. The histogram is efficient updated by removing the values going out of the window and adding the values comming into the window when moving to the next pixel. Sliding window filters are also called rank filters.

Scanning microscope

Figure 2.1 illustrate the internal workings of a Leica SP8 scanning microscope which have an epi-illumination setup. Epi-illumination is when the detectors (26) and light source (1, 3, 5, 7) are on the same side of the objective (18). But as seen, the epi-setup also allows for external detectors (19). By scanning one means that the light source is focused to a specific part of the specimen and scanned line by line in a raster pattern. While the laser are scanned over the surface, a detector measure light in samples and each measured sample will be saved to an image pixel. The scanning is done by a oscillation mirror (14). The term non descaned detector indicate that the light does not travel by the scanning mirror before reaching the detector. In SP8 (17) and (19) are non descaned detectors, where (17) measure reflected light and (19) measure transmitted light.
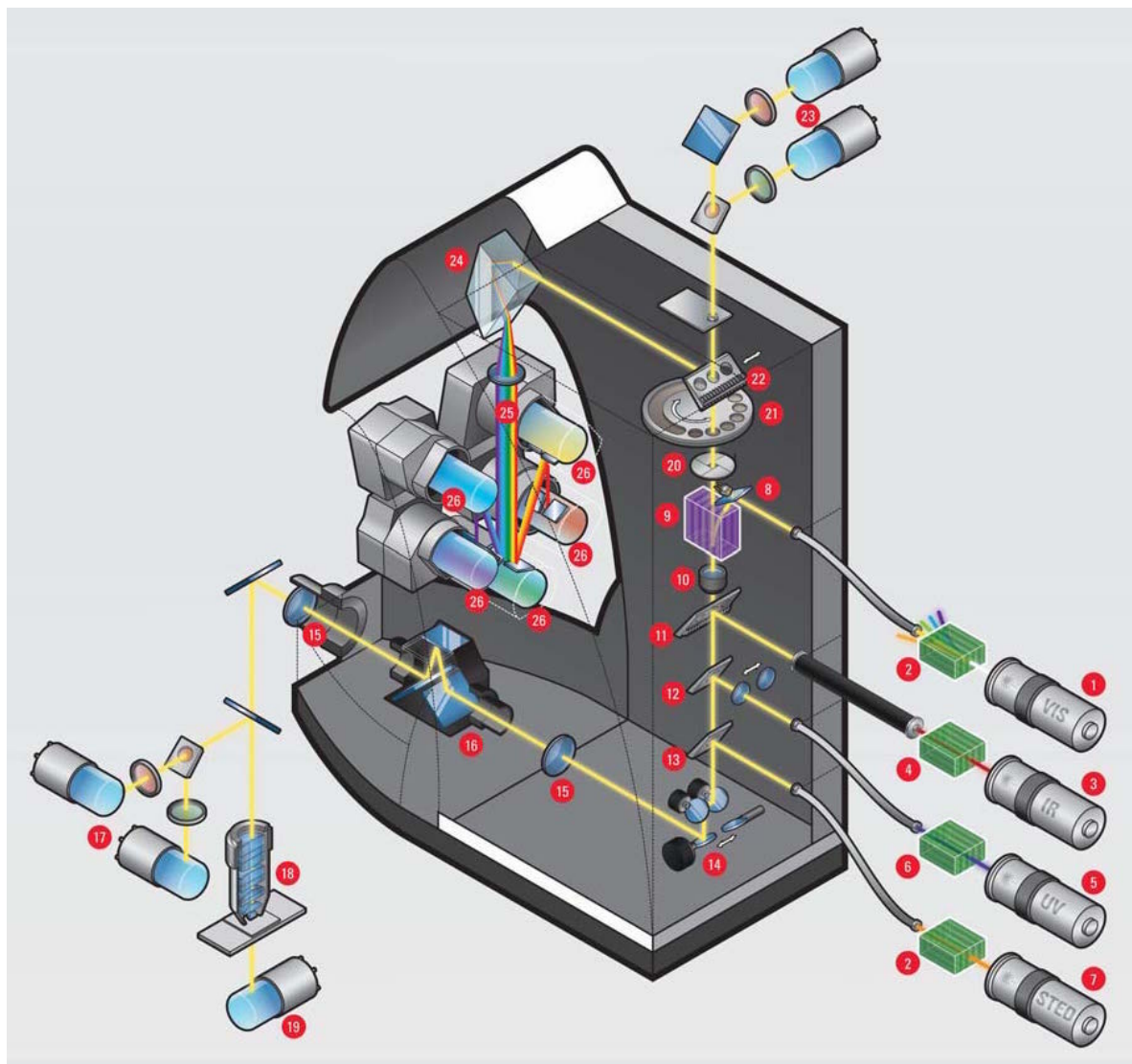
Figure 2.1: Internals of a Leica SP8 microscope. Picture from Leica SP8 brochure[7].

The view field of a microscope is the physical size of viewable area. The view field depends on the magnification of the objective and the scanner zoom. Scanner zoom is when the scanner is set to oscillate with less amplitude while still sampling at the same rate. As field of view is at the magnitude of 1×10^{-4} m, specimen must be moved around to image a larger area. The device that moves the specimen is called a stage. The stage position, or specimen position if you like, is denoted with a upper case X to distinguish it from lower case x which denote image pixel position.

Nonlinear light interaction

- focal volume

Software

Leica LAS X

LAS X is the software that contols the Leica SP8 microscope. LAS X comes with an function called *Matrix Screener*, which allows the user to define structured areas to scan. The software uses the concepts fields and wells. A field is essentially an image, and a well is a collection of regular spaced images. The wells may be regular spaced, or an offset between wells can be defined in the graphical user interface. When the scan job is started Leica LAS will store images in a tree of folders in TIFF format.

CAM

In addition to controlling the microscope with the graphical user interface, a function called *Computer Assisted Microscopy* (CAM) can be turned on. CAM is a socket interface, meaning one send bytes over a network interface. This is very similar to how one can write bytes to a file, but in addition the socket interface can respond and send bytes back. The network interface runs on TCP port 8895 and one may communicate locally or over TCP/IP network. A set of 44 commands are available, but only three of them are intresting for the purpose of controlling scans; `load`, `autofocusscan` and `startscan`. More details on the interface can be read in the manual[8] or by studying the source code of the python package 'leicacam"[9]. Code Block 1 show how one can communicate with the microscope in python.

Code block 1 Communicating with the Leica SP8 microscope using the python package leicacam.

```python
from leicacam import CAM

# connect to localhost:8895
cam = CAM()
# load a template named leicaautomator
cam.load_template('leicaautomator')
# start the autofocus scan defined in 'leicaautomator' template
cam.autofocus_scan()
# start the scan job
cam.start_scan()
# read filename in response from microscope when images are scanned
relpath = cam.wait_for('relpath')
```

XML

Extensible Markup Language is a declarative language which most high level programming languages speak, which makes it suitable for computer program communication. A XML-file contain a single root and tree structure with parent and children nodes. Any position in the tree can be specified with an *XPath*. Code Block 2 show a typical structure of a XML-file.

Code block 2 Illustration of a typical XML-tree structure.

```xml
<?xml version="1.0"?>
<root>
    <parent>
        <child attr="val1">text</child>
        <child attr="val2">text2</child>
    </parent>
    <parent>
        <child attr="val3">text</child>
        <child attr="val4">text2</child>
    </parent>
</root>
```

The XML-file might be nested with several childen and parents, but code blocks code block 2 holds for illustration purposes. XPath for the first child in parent will be `./parent/child[@attribute="val1"]`. Here `.` is the root, `/` defines path (or nesting if you like) and `[@attribute="val"]` defines that the attribute named `attr` should be of value `val1`. This XPath will find only the first child of the first parent, but if other childs with same path also had an attribute named `attr` with the value `val1`, the XPath would have found them also. E.g. `./parent/child` will find all children. Code Block 3 show how one would read properties in the XML-file from code block 2.

Code block 3 Accessing XML properties with the python build-in module xml.etree.

```python
import xml.etree.ElementTree as ET

tree = ET.parse('/path/to/file.xml')

first_child = tree.find('./parent/child')
first_child.attrib['attr'] == "val1" # True

all_children = tree.findall('./parent/child')
len(all_children) == 4 # True
```

Scanning Template

A scanning template is a XML-file which defines which regions a scan job exists of. The structure of the file is the following:

- **./ScanningTemplate/Properties** holds experiment settings like start position, displacement between fields and wells, start position, which Z-drive to use, and so on.
- **./ScanFieldArray** holds all fields (images) and their settings as attributes in `./ScanFieldArray/ScanF:`
- **./ScanWellArray** holds all wells (collection of images) and their settings as attributes in `./ScanWellArray/ScanWellData`.

OCR

Optical character recognition (OCR) is recognition of characters in an image. OCR internals are not discussed, but it basically works by looking at patterns in the image to convert it to text.

keep, remove or expand?

Chapter 3

Methods

What to communicate: experimental setup to reproduce results, description of process, brief code block to show usage of software modules

Microscope

The images were collected with a Leica SP8 microscope using LAS X software version 1.1.0.12420 from Leica Microsystems CMS GmbH. Two lasers was in use, a pulsing Coherent laser and a continious LASOS argon laser. Full specifications of lasers are in table 3.1.

Table 3.1: Lasers

Brand	Model	Specifications
Coherent	Chameleon Vision-S	Modelocked Ti:Sapphire, wavelengths 690-1050 nm, 2500 mW, 80 MHz pulsing, $\approx$ 75 ps pulse width
LASOS	LGK 7872 ML05	Argon Continious wave, wavelengths 458, 476, 488, 496 and 514 nm, 65mW

The SP8 microscope has an inverted epi-setup, with four descanned detectors and four non descanned detectors. The descanned detectors use a prism along with adjustable mirrors so that specific wavelengths can be picked out in the signal, ranging from TODO. The descanned detectors was used with band

pass filters of 525/50 nm and 445/20 nm. Two of the descanned detectors are behind the objective and two on opposite side of the objective behind a collector, which makes it possible to measure both backward and forward light.

SHG images

SHG images was taken with a 25x/0.95 NA water objective. The pulsed infrared laser was set to 890 nm, intensity 20%, gain 40%, offset 80% and electro-optic modulator (EOM) on. Forward light was measured with non descanned PMT sensor behind a 0.9 NA air collector. Band pass filter in front of the detector was 445/20 nm and gain of detector was adjusted so that signal spanned the whole intensity range. Aperture was set to 24 (maximum).

A resolution of 1024x1024 pixels with 8 bit image depth was used. Frequency of scanning mirror was set to 600 lines/second.

Overview images

Overview images was taken with an technique similar to bright-field microscopy except that the light source is a scanning laser. A 10x air objective was used, the lasers in use were the argon laser in table 3.1 with 514 nm emission line, output power set to 2.48% and intensity to 0.10. Forward light was imaged using a 0.55 NA air collector with the non descanned detector having the 525/50 nm bandpass filter. Aperture and detector gain was adjusted so that the histogram of intensities was in the center of the total range without getting peaks at minimum and maximum values.

Zoom 0.75 and 512x512 pixels was chosen, which gives images of ≈ 1500 μm (read more about resolution and image size in the discussion). After images is scanned, they are rotated 270 degrees, as Leica LAS store *.tif*-images with axes swapped in regards to the stage axes.

Automated scanning

Communicate: the procedure of automatic scanning

The automated scanning aims to lift the burden of manually labor and prevent errors in the imaging process by finding regions with the specimens in an overview image. The process consists roughly of the steps:

- Take an overview image with low magnification
- Segment the overview image
- Allow user to confirm or adjust the segmentation
- Scan each region

After overview images was taken, they were equalized and stitched. The equalization step corrects uneven illumination and increases contrast for viewing purposes. To improve robustness of segmentation, a local bilateral population filter was applied to the stitched image before it is thresholded. Each separate region in the segmentation are sorted by their area size, small regions are excluded and the user can exclude or add regions if some of the specimens are not detected. Row and column position of the regions are calculated by sorting them by their position in the image. A more detailed description follows.
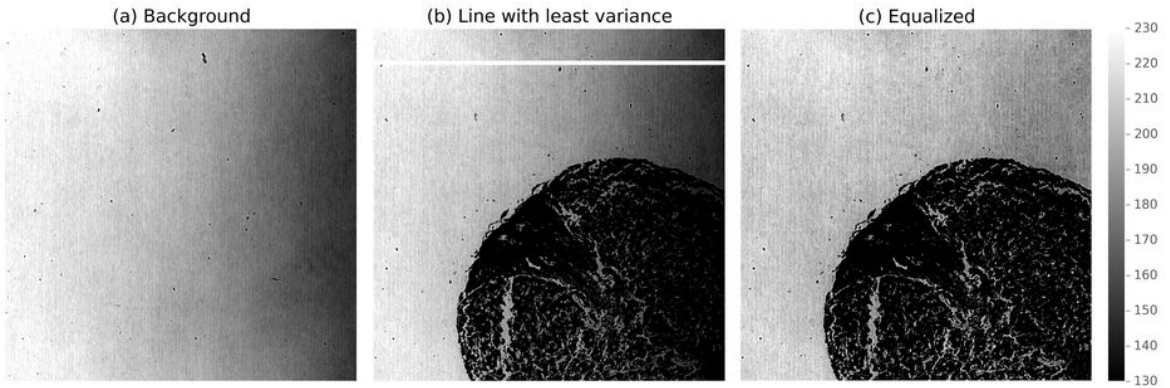
Uneven illumination

Figure 3.1: (a) Image of glass slide only and no tissue for illustrating the uneven illumination. Dots are impurities on the glass slide. **(b)** Original image with part of speciment. The white line is the row with least variance used for equalization. **(c)** Equalized version of (b). Note that (a), (b) and (c) are displaying values from 130 to 230 to highlight the intensity variation, colorbar is shown to the right.

The uneven illumination in the experimental setup is illustrated in figure 3.1(a). By assuming the intensity variation in all pixels are following the slope of the background, equalization was done by dividing each row in the image by the normalized intensity profile of the background.

As seen in code block 4 the image is first normalized. `images_minimum` and `images_maximum` is found by selecting the median of respectively minimum and maximum intensity of all images. By taking

---

Code block 4 Equalizing an image

```python
equalized = img.astype(np.float)         # assure datatype have real division ability
equalized -= images_minimum              # normalize
equalized /= images_maximum - images_minimum
equalized /= intensity_profile           # equalize
equalized[equalized > 1] = 1             # clip values
```

---

the median of all images one avoids outliers and gets the same normalization for all images. Similar technique could be used for normalizing the images after equalization, but clipping gave acceptable results. `intensity_profile` is a curve fit for one of the background rows. The background row was found by selecting the row with least variance (given that the image does have a row with background only). In figure 3.1(b) the row with least variance is indicated with a white line. The same intensity profile is used on all images, and it's fitted to a second degree polynomial to steer clear from noise as illustrated in figure 3.2(a).

The effect on pixel values can be seen in figure 3.2 (b) and (c), where each dot represents a pixel value with increasing image x-position on the x-axis. The intensity variation shown here was directed in one axis only which allowed for the simple divide all rows by the intensity profile. For more complex intensity variations, similiar approach can be done by fitting the two dimentional background to a surface, then divide the image by this intensity surface profile.
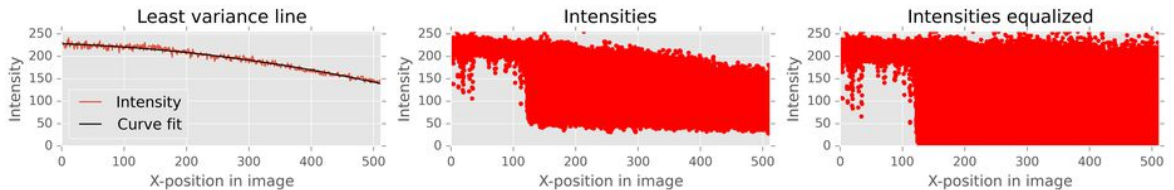

Figure 3.2: **(a)** Intensities for the line with least variance of figure 3.1(b). The curve is fitted to a second degree polynom to supress noise. **(b)** Intensities for image in figure 3.1(b). Each dot represents a pixel. **(c)** Intensities for the equalized image in figure 3.1(c). Each dot represents a pixel. Note that the intensities is both spread across the whole intensity range (0-255) and the skewness is fairly straightened out.

Stitching

Due to little signal in areas between samples, automatic stitching with correlation methods are prone to fail. To remedy this, the same overlap was chosen when stitching the overview image. Using the same overlap in this context gives reliable stitching with negligible errors. The overlap is chosen by
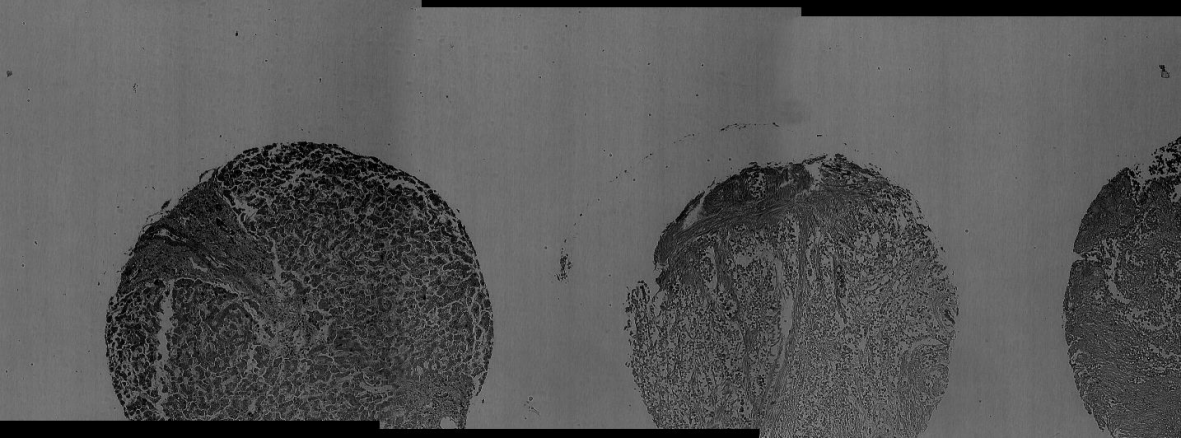
Figure 3.3: Stitch of three images with scanning pattern rotated compared to stage movement. Calculating stage position by y-equivalent to equation 3.3 will fail, giving a systematic error in the y-position.
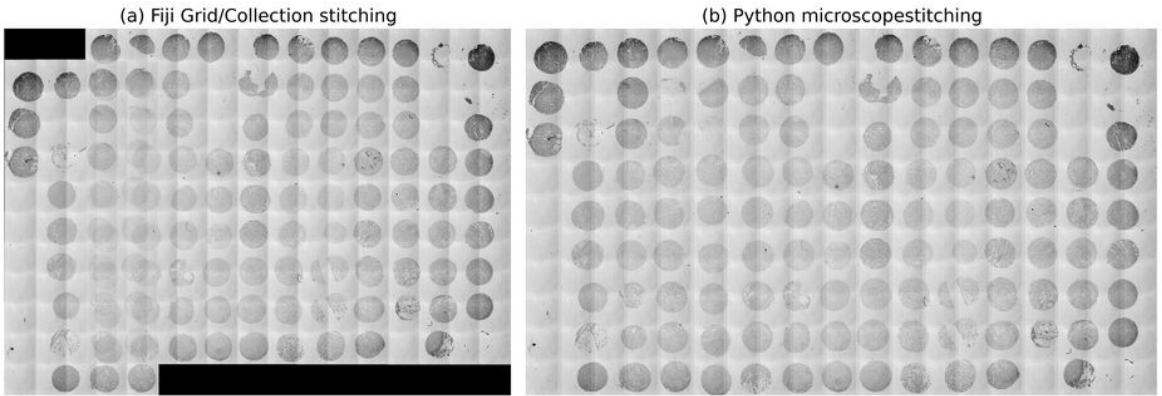

Figure 3.4: (a) Unreliable automatic stitching with Fiji, the image translation calculated by phase correlation is chosen without adhering to displacement constraints. **(b)** Using same overlap for all images gives negliable errors, here using the python package *microscopestitching*.

calculating all overlaps with phase correlation and taking the median. The stitching was put in a python package and can be used as shown in code block 5.

Code block 5 Stitching images with the python package *microscopestitching.*

```python
from microscopestitching import stitch
from glob import glob

files = glob('path/to/images/*')
images = []
for i, file in enumerate(files):
    # rectangle of 4 rows and len(files)//4 columns
    row = i % 4
    column = i // 4
    images.append((file, row, column))

stitched_image = stitch(images)
```
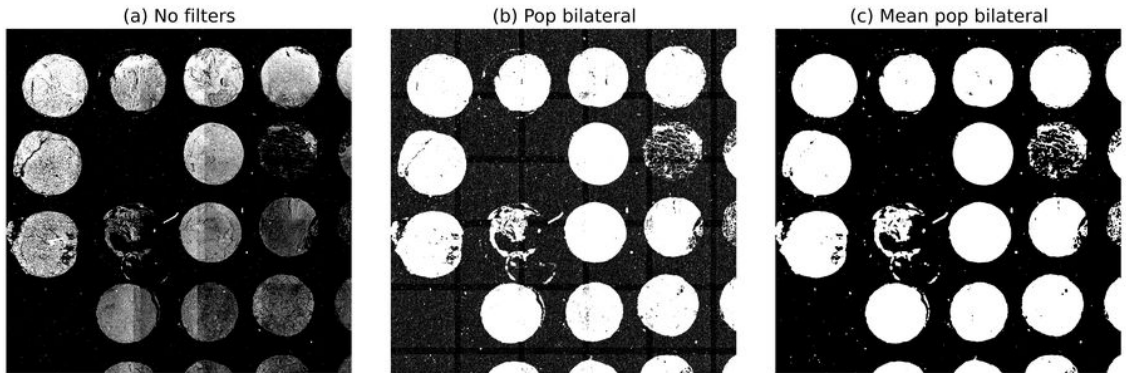

Segmentation

Figure 3.5: Otsu thresholding of figure 3.4(b). **(a)** Otsu thresholding applied without any filters. Picks out dark areas, but disjointed, especially for brighter sample spots in bottom left. **(b)** Thresholding after a local bilateral population filter. Quite noisy in the background. **(c)** Thresholding after local bilateral population and local mean filter. Background noise is gone and sample spots are coherent.

As seen in figure 3.4(b), the samples at the edge are darker than the samples in the center. To improve this intensity variation, the overview image is filtered with a local (reverse) bilateral population filter. Reverse in this sense means that the filter counts number of neighbouring pixels that are outside a specified range. The effect of the filter is a less computational demanding and somewhat similar to an entropy filter. Areas with low signal variation (the background) give low values and areas with high

signal variation (the samples) give high values.

To reduce noise after the bilateral population filter, a mean filter was applied. The size of structure elements was 9x9 pixels for both filters. Figure 3.5(a), (b) and (c) show how the segmentation is affected by the filters. Code for reproducing the steps are in code block 6.

Code block 6 Filter and segment an image with local bilateral population and Otsu thresholding.

```python
from skimage.morphology import square
from skimage.filters import threshold_otsu
from leicaautomator.filters import mean, pop_bilateral

selem = square(9)
filtered = pop_bilateral(image, selem)
filtered = mean(filtered, selem)

threshold = threshold_otsu(filtered)
segmented = filtered >= threshold # high values indicate signal
```

After segmentation, regions was sorted by their area size and only the largest regions are kept. Row and column was calculated by sorting regions by position, measuring the distance between them and increment row or column number when there is a peak in the distance to previous region. The code can be seen in code block 3 and figure 3.6 illustrate typical area size (a), position (b) and position derivative (c).
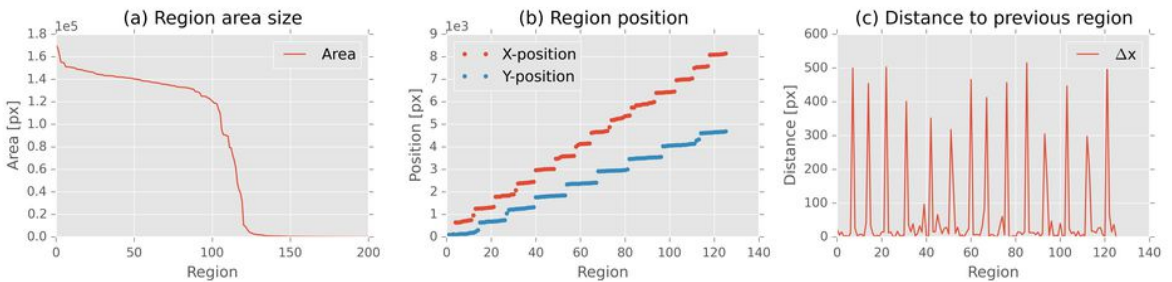

Figure 3.6: (a) Sorted region areas. Area size drops dramatically around region 125 according to number of samples on slide. Plot does not have corresponding x-axis with (b) and (c), as regions are sorted by size. **(b)** Regions sorted by position. The two plots do no share the same x-axis. There is a gap between the positions when row and columns are increasing. **(c)** X distance to previous region when regions are sorted by x-position. Same x-axis as in (b) for the x-position plot. 14 peaks indicate that the image contain 15 columns.

```python
from skimage.measure import label, regionprops

labels = label(segmented, background=0) # background=0: exclude background
regions = regionprops(labels)           # measure region properties
regions.sort(key=lambda r: -r.area)     # sort by area size, largest first

max_regions = 126
if len(regions) > max_regions:
    regions = regions[:max_regions]     # only keep max_regions

for r in regions:
    r.y, r.x, r.y_end, r.x_end = r.bbox # for convenience

for direction in 'yx':                  # same algorithm for row and columns
    regions.sort(key=lambda r: getattr(r, direction))

    previous = regions[0]
    for region in regions:              # calc distance to previous region
        dx = getattr(region, direction) - getattr(previous, direction)
        setattr(region, 'd' + direction, dx)
        previous = region
```

The whole process of segmentation was done interactive as part of the python package *leicaautomator*, where settings can be adjusted to improve segmentation and regions can be moved, deleted or added with mouse clicks. The interface is shown in figure 3.7.
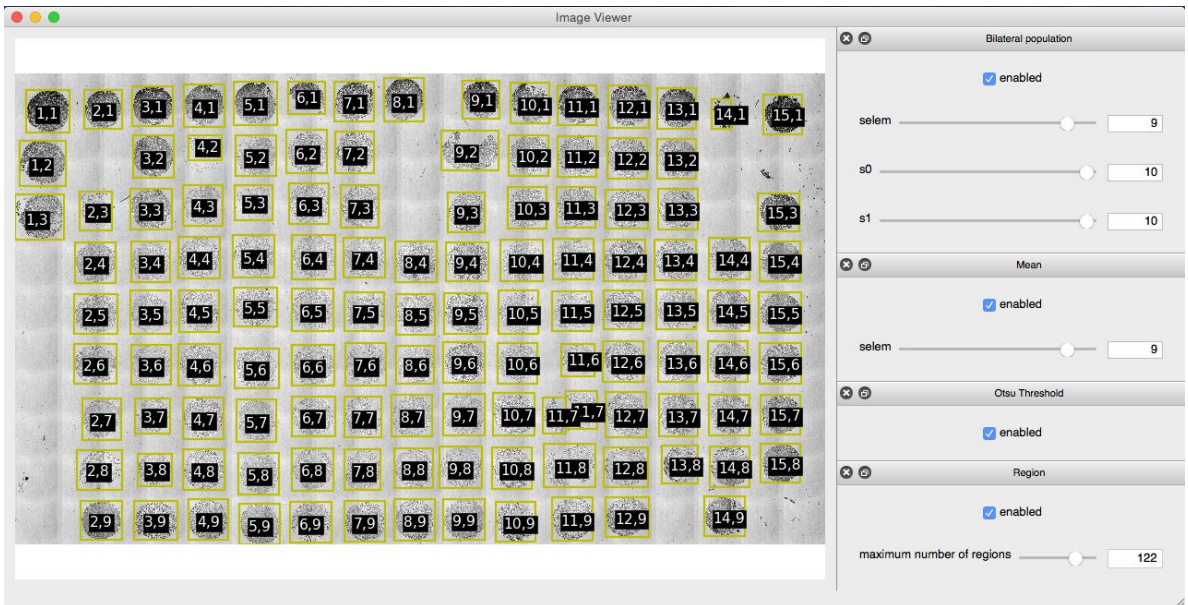

Figure 3.7: The process of segmentation in a graphical user interface. Regions 4,2, 11,7 and 14,1 might be adjusted by the user, all other regions are detected fairly well.

Calculate stage position from pixel position

After regions was localized, pixel-size in meters was calculated by

$$x_{resolution} = \frac{\Delta x}{\Delta X}.$$

(3.1)

Here Δx is displacement in pixels and ΔX is stage displacement in meters read from the overview scanning template in the experiment `AdditionalData/{ScanningTemplate}overview.xml` at XPath `./ScanningTemplate/Properties/ScanFieldStageDistanceX`. Left most left pixel was calculated by

$$X_{start} = X_{center} - \frac{m}{2} \cdot x_{resolution}.$$

(3.2)

In equation 3.2 X_{center} is the stage position and m is number of pixels in the image from the overview scan. X_{center} was read from the overview scanning template at XPath `./ScanFieldArray/ScanFieldData[@WellX="1"][@WellY="1"][@FieldX="1"][@FieldY="1"]` `/FieldXCoordinate`. The stage x-coordinate for any pixel was then calculated by

$$X = X_{start} + x \cdot x_{resolution}.$$

(3.3)

To be able to scan regions of different shape and size, a bounding box for the region was used to calculate the scanning area. Moving the stage to the boundary position will center the boundary in the image, and therefor start position of first image is calculated by

$$X_{start} = X + \frac{\Delta X_{job}}{2}.$$

(3.4)

Here, ΔX_{job} is stage displacement between images in the job scanning template. X_{start} will have an error of

$$\epsilon = \frac{1}{2}(\Delta X_{job} - \Delta X_{img}),$$

(3.5)

where ΔX_{img} is the total size of the scanned image. This was considered neglectible as $\Delta X_{job} \approx \Delta X_{img}$ and number of columns scanned was calculated by

$$f_x = \lceil \frac{\Delta X}{\Delta X_{field}} \rceil.$$

(3.6)

Scanning each region

To avoid unnecessary long stage movements between rows or columns, regions was looped through in
a zick-zack pattern, given by their row and column position. For each region the scanning template
was edited, the template was loaded and the scan was started through CAM. Single templates was
used due to a Leica LAS software limitation; scanning templates with irregular spaced wells can not be
loaded. Code Block 7 illustrates the process.

Code block 7 Automated scanning of regions with CAM.

```python
from leicascanningtemplate import ScanningTemplate
from leicaautomator import zick_zack_sort
from leicacam import CAM

cam = CAM() # instantiate connection to microscope

# regions sorted as [r(1,1), r(1,2), r(2,2), r(2,1), r(3,1), r(3,2), ...]
# here r(2,1) is region(col=2, row=1)
regions = zick_zack_sort(regions, ('well_x', 'well_y'))

tmpl_path = r"C:\Users\TCS-User\AppData\Roaming\Leica Microsystems\LAS X" + \
            r"\MatrixScreener\ScanningTemplates" + "\\"
tmpl_name = tmpl_path + '{ScanningTemplate}leicaautomator'
for n, region in enumerate(regions):
    # alternate between tmpl_name0/1.xml, due to a
    # bug LAS cannot load the same name twice
    tmpl = ScanningTemplate(tmpl_name + str(n%2) + '.xml')

    tmpl.move_well(1, 1, region.real_x, region.real_y)
    tmpl.write()

    cam.load_template(tmpl.filename)

    # do an autofocus
    cam.autofocus_scan()
    cam.wait_for('inf', 'scanfinished')

    # run the scan job
    cam.start_scan()
    # record output filename
    region.experiment_name = cam.wait_for('relpath')['relpath']

    # continue with next region when scan is done
    cam.wait_for('inf', 'scanfinished')
```

Alignment of z-plane

The samples in figure 1.1 are 5 µm thick and keeping the sample plane at same distance from .
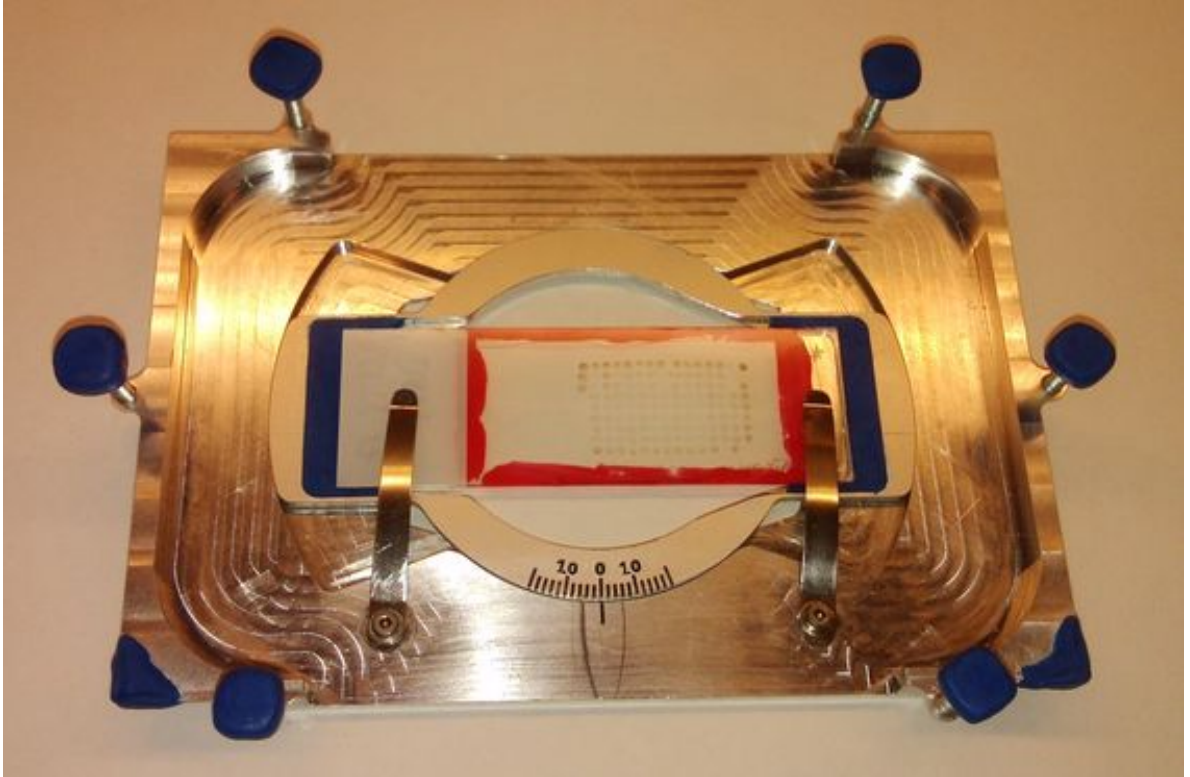

Figure 3.8: Sample holder with adjustment of z-plane.

Correlating images with patient data

Slide maps, seen in figure 3.9, and patient database was given by St. Olavs. As the slide maps contained circles, slide maps were filtered to remove all but text before it was read with OCR. The OCR text output was checked for errors programatically (id should be of correct format, id should increment, patients should be registered with correct slide in database column TP_nr, each patient should have three samples). OCR errors was fixed manually and other errors was recorded (see section Slide map errors in the appendix).

Every pasient id from the slide map was then saved to a stata database along with its slide number,
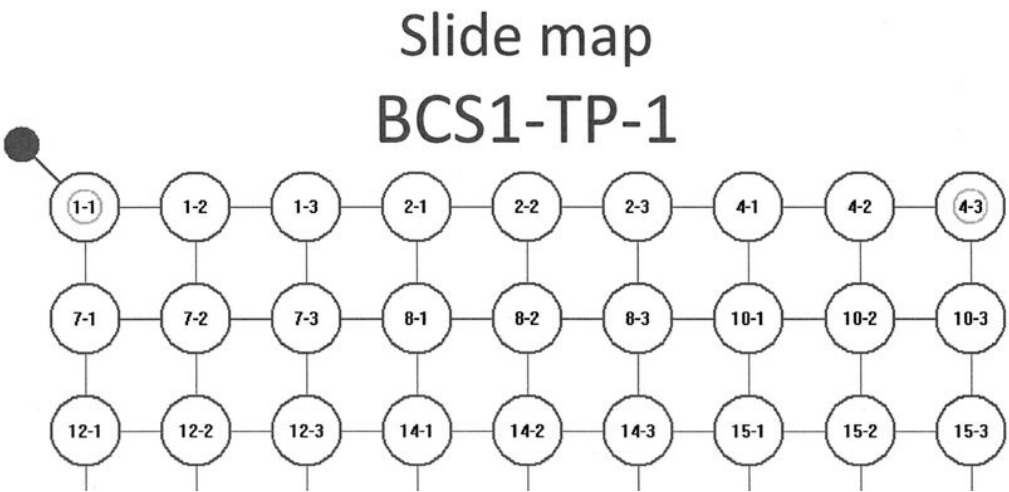
Figure 3.9: Top of slide map TP-1. Ids are not incrementing systematically and need to be registered to correlate samples to respective patients. Ids are inside circles and hard to read with OCR. First part of id is same as `ID_deltaker` in patient database, second number is sample number. There should be three samples for each patient.

row and column. Code Block 8 show how the clinical data was correlated with samples.

Code block 8 Get patient outcome of sample on TP-1 row 3 column 5.

```python
import pandas as pd

# read databases
locations = pd.read_stata('data/ids/locations.dta')
clinical_data = pd.read_stata('data/clinic_data.dta')

# position query
condition = (locations.TP_nr == 1) & \
            (locations.TP_rad == 3) & \
            (locations.TP_kolonne == 5)

# get patient id
patient_id = locations[condition]['ID_deltaker']

# check exactly 1 patient registered at given row/col
assert len(patient_id) == 1

# clinical data query
condition = clinical_data.ID_deltaker == patient_id.iloc[0]

# get outcome
outcome = clinical_data[condition]['GRAD']
```

Chapter 4

Discussion

What to communicate: discuss results, limitations, possibilities for improvement

ML: Hvilke valg har blitt tatt, hva er viktig for neste bruker, hva er begrensninger, utviklingsmuligheter, pros/cons, hvor bra fungerer det. . . .)

Automated scanning

The reason for automating the scanning is to steer clear from error prone work. Glass slides with TMA samples can contain up to 1000 samples for each glass slide[5], and helping the microscope operator and researcher organize the work is vital. The glass slides in discussion here holds 14 columns of specimen, which is 60 non-overlapping images with a 25x objective. The operator of the microscope will have to always be aware of his position in the array. A movement of 1.7 mm will shift columns by one, which describes the accuruancy required.

Though the complexity can become much for a human to handle, the situation is not terrible. The tissue is somewhat aranged, tools in microscope software exists for scanning large structures, specimen are rounded making them easy to spot. In addition, the specimen have quite equal properties like shape and size, making automated detection with image processing a low hanging fruit.

Using the matrix screener of Leica LAS, a normal TMA scan would roughly contain the steps:

1. Count number of rows and columns.

2. Align TMA in microscope.

3. Measure average inter sample displacement.

4. Measure maximum specimen size.

5. Define an experiment holding the correct number of rows, columns, displacement between samples and sample size.

6. Identify inter sample offsets.

7. Potetially disable fields with smaller size than the largest.

8. Identify and rule out missing samples.

9. Create predictive focus map or make sure positions for autofocus are in regions with signal (e.g. specimen should be included in the autofocus image).

10. Scan.

An error in some of the steps above can potentially disrupt steps further down the line. In example, with inaccuriancy in average displacement between samples one might have to adjust the offset of many if not all wells, accidentally bumping the sample holder could impose restart of the procedure, and so on. The procedure was tested out and step 6 was the most labor intensive, browsing through 126 samples aligning them. An alignment of one sample took about 40 seconds, giving 1.5 hours of intensive

A simple means to avoid some of the steps in the intricate procedure above is using a single scan containing the whole matrix area. The procedure then simplifies to:

1. Align TMA in microscope.

2. Find outer boundaries.

3. Create predictive focus map or select more or less regular spaced intervals with specimens to do autofocus.

4. Scan.

5. Separate specimen and assign row and column to them.

Compared to the first procedure listed, this procedure have the advantage of being less labor intensive. But manually browsing through $24\,\text{mm} \cdot 15\,\text{mm} / (400\,\mu\text{m})^2 = 2250$ images may be a daunting task without a specialized tool. Several hundred images will also be empty images.

The main concern with this method was focus. A few scans which yielded out of focus parts confirmed the concern. To overcome this one can define an autofocus more often or even at every specimen. This implies manual labor browsing around the TMA selecting the places to autofocus or finding them in an automatic way.

As the goal was to reduce manual labor, selecting

find the specimen areas manually or with an overview image. As

scan is also vulnerable to errors in autofocus causing parts of scan to come out of focus. Additionally the scan will consist of several hundred empty images.

The

The developed approach described in the method chapter remedies the draw backs of scanning the whole slide in one scan and doesn't add any considerable amount of work. The procedure is reduced to:

1. Align TMA in microscope.
2. Take overview image.
3. Let software find specimen up front.
4. Scan.

The result is images easily separated by their row and column. The advanteages to

Chapter 5

Conclusion

What to communicate: brief summary of the result and discussion, advice for further work

ML: Automatic imaging and segmentation of TMA has been demonstrated)...and....

Chapter 6

Appendix

Python packages

Any python package mentioned in the code blocks is install-able through pip. In example `leicacam` can be installed by typing `pip install leicacam` in a terminal on a computer that have `pip`[10] and the required compilers if the package contain compiled languages.

A lot of scientific python packages have algorithms implemented in compiled languages as Fortran and C. By using a Python distribution like Anaconda one avoids installing compilers and can install pre built packages directly.

Leica LAS design:

- user should be mainly in LAS
- automating on the side as a supplement
- load before CAM can be used
- does not load all settings from XML

Slide map errors

```
TP2, row  3, col  6 - pasient id missing in db: 66
TP6, row  1, col  9 - pasient id missing in db: 222
TP3, row  1, col  3 - id 68, wrong TP_nr in db: 3.0 != 2.0
```

```
 TP6, row  1, col  3 - id 209, wrong TP_nr in db: 6.0 != 4.0
 TP6, row  1, col  6 - id 221, wrong TP_nr in db: 6.0 != 5.0
TP22, row  2, col  6 - id 130, wrong TP_nr in db: 22.0 != 3.0
TP22, row  2, col  9 - id 244, wrong TP_nr in db: 22.0 != 5.0
TP22, row  3, col  3 - id 281, wrong TP_nr in db: 22.0 != 6.0
TP22, row  3, col  6 - id 296, wrong TP_nr in db: 22.0 != 6.0
TP22, row  3, col  9 - id 309, wrong TP_nr in db: 22.0 != 6.0
TP22, row  4, col  3 - id 318, wrong TP_nr in db: 22.0 != 6.0
TP22, row  4, col  6 - id 376, wrong TP_nr in db: 22.0 != 7.0
TP22, row  4, col  9 - id 396, wrong TP_nr in db: 22.0 != 8.0
TP22, row  5, col  3 - id 413, wrong TP_nr in db: 22.0 != 8.0
TP22, row  5, col  6 - id 449, wrong TP_nr in db: 22.0 != 9.0
TP22, row  5, col  9 - id 453, wrong TP_nr in db: 22.0 != 9.0
TP22, row  6, col  3 - id 487, wrong TP_nr in db: 22.0 != 10.0
TP22, row  6, col  6 - id 493, wrong TP_nr in db: 22.0 != 10.0
TP22, row  6, col  9 - id 525, wrong TP_nr in db: 22.0 != 10.0
TP22, row  7, col  3 - id 728, wrong TP_nr in db: 22.0 != 15.0
 TP3, row  9, col  6 - TP_nr not registered in db for ID_deltaker 140
 TP5, row  9, col  9 - TP_nr not registered in db for ID_deltaker 251
 TP9, row 10, col  9 - there should be 3 samples: ['467a-1']
 TP9, row 11, col  3 - there should be 3 samples: ['467b-1', '467b-2']
 TP9, row 12, col  6 - there should be 3 samples: ['471a-1', '471a-2']
 TP9, row 12, col  9 - there should be 3 samples: ['471b-1']
TP10, row  8, col  6 - there should be 3 samples: ['507-1', '507-2']
TP10, row 12, col  6 - there should be 3 samples: ['525-2', '525-3']
TP11, row 11, col  6 - there should be 3 samples: ['566-1', '566-2']
 TP3, row  1, col  3 - pasient id did not increment: ['68-1', '68-2', '68-3'] <
                                                ['102b-1', '102b-2', '102b-3']
 TP4, row  1, col  3 - pasient id did not increment: ['162a-1', '162a-2', '162a-3'] <
                                                ['163-1', '163-2', '163-3']
 TP6, row  1, col  3 - pasient id did not increment: ['209-1', '209-2', '209-3'] <
                                                ['268-1', '268-2', '268-3']
TP11, row  6, col  3 - pasient id did not increment: ['549-1', '549-2', '549-3'] <
                                                ['552-1', '552-2', '552-3']
TP22, row  2, col  6 - pasient id did not increment: ['130-1', '130-2', '130-3'] <
```

['3067-1', '3067-2', '3067-3']

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