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Developement and evaluation of methods for comparison of dose distributions in radiotherapy using calculated, synthetic and simulated measured dose distributions.

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Intensity modulated radiation therapy (IMRT) is becoming a more and more used technique in radiation therapy. The main reason for this is that IMRT treament delivers a more conformal dose to the target together with a better sparing of organs at risk. Quality assurance of the generated IMRT treatment plan is of most importance to ensure that the patient recives the planned dose.

Different methods exist for comparison of dose distributions where the gamma evaluation (Low et al. [19]) is the most commonly used. In this thesis different types of evaluation methods have been implemented in an evaluation software.

Different types of known errors were introduce in an IMRT-plan (synthetic dose distribution). These synthetic dose distributions were then evaluated with a number of evaulation methods to identify what types of criterion needed to discover the introduced errors.

A method for comparison of dose distributions with a statistical approach was also introduced and compared with the gamma evaluation method.

A gamma criteria of 4% of the maximum dose and 4 mm in positioning is needed to discover all introduced errors. For the developed statistical evaluation method (χ^2-test) the standard deviations needed to discover all errors were 1.5% of the maximum dose and 1 mm in positioning.

Keywords:	Dose distribution comparison, gamma evaluation, IMRT quality assurance, synthetic dose distributions, χ^2-test
Language:	English

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Abbreviations and Acronyms

2D	Two-dimensional
3D	Three-dimensional
CT	Computed tomography
DICOM	Digital imaging and communications in medicine - Standard format for digital medical images
DICOM-RT	DICOM extention used in radiotherapy
DTA	Distance to agreement - Evaluation method for dose distributions
IMRT	Intensity modulated radiation therapy
MasterPlan	Oncentra MasterPlan - Treatment planning system from Elekta
MLC	Multileaf collimator
MRI	Magnetic resonance imaging
MU	Monitor units
OAR	Organ at risk
PET	Position emission tomography
SSM	Swedish radiation safety authority (Strålsäkehetsmyndigheten)
TLD	Termoluminescent dosimeter
TPS	Treatment planning system

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Chapter 1

Introduction

1.1 Background

Today cancer is one of the most common diseases and nearly 50 000 new cases of cancer are diagnosed each year in Sweden [25]. According to the International Commission on Radiological Protection (ICRP) and Surveillance, Epidemiology and End Results (SEER) about 40% of all men and women born today will be diagnosed with cancer at some time during their lifetime [6, 23]. In 2004 cancer accounted for around 13% of all deaths according to the World Health Organisation (WHO) [30]. New treatment methods for cancer are continuously developed and introduced in the world of medicine.

For many years radiation therapy in Sweden has been an important modality for the treatment of cancer. It is used as a part of a treatment for almost half of all cancer patients [24]. It can be used as a stand alone treatment or in combination with other treatments e.g hormone-, chemo-, immune therapy and/or surgery. The main purpose of radiation therapy is to accurately deliver an absorbed dose to a specified target (tumor) to either efficiently cure the patient (curative) or to shrink the tumor to relieve the patient from pain (palliative). While doing this one must also minimize the absorbed dose to the normal healthy tissue to avoid unnecessary damage. This means that high requirement on both geometrical and dosimetrical precision are necessary for a successful treatment.

Computed Tomography (CT) is far from the only modality that is used for target delineation. For a more precise delineation of the target and organs at risk (OAR) Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET) or PET/CT are commonly used [28]. A more precise delineation result in more correct margins of the named tissue. However this sets a higher requirement on the precision and dosimetry of the radiotherapy modality.

Conventional external radiation therapy is based on the use of uniform or wedged beams, commonly 2-4 beams. A Multi-Leaf Collimator (MLC) is used to shape the beams and before the MLC individually constructed lead blocks were used. The MLC consist of a large number of leaves that can move independently of each other. In 1988 Brahme [1] suggested a new technique that later would be called Intensity Modulated Radio Therapy (IMRT). This technique requires the intensity to be varied across each beam that is delivered to the patient. The MLC are used to construct these irregular shaped beams that build up an IMRT treatment [20]. Different IMRT-techniques are commercially available: step-and-shoot and sliding-window. In step-and-shoot the MLC-leaves move to position and then the radiation is turned on. In sliding-window the radiation is on while the MLC-leaves moves. The IMRT technique results in a more conformal therapy than the conventional radiation therapy. As always it is of most importance to ensure that the absorbed dose to the patient is correct [13, 14]. Conventionally dosimeters such as ionization chambers, diodes and theromoluminescent dosimeters (TLD) are used for dose verification in one point and diode/ionization chamber arrays or films for dose verification in one plane. In 3D one can use multiple films, several array measurements or gel dosimetry. All fields for an IMRT treatment should be verified before the treatment begins using one of the methods described above. The verification of an IMRT-plan is commonly very time consuming compared to the verification of conventional plans.

1.2   Intensity Modulated Radiation Therapy

Example of an IMRT treatment can be seen in Figure 1.1. Example of diagnosis where IMRT can be of use is in head and neck cancers and for prostate cancers where one can decrease dose to the partiod gland and rectum respectively and still have a sufficient dose to the PTV. Even an increase of the dose to the PTV may be possible [7, 20].

It is of most importance to assure that the linear accelerator accurately delivers the desired dose because of the high precision needed for IMRT treatment, thus high demands needs to be set on quality assurance (QA) of the linear accelerator. Patient position is also very important based on the precision of the treatment delivery [7]. For head and neck cancer patients this is achieved by using a head cast that provide excellent fixation and if needed for prostate patients a body frame. In some cases a cone-beam CT, mounted on the gantry of the linear accelerator, may be available which is very useful with 3D imaging for positioning accuracy.

There exists different techniques to deliver the non-uniform beams that creates the IMRT plan. The two most common techniques uses the MLC to modulate the beams and deliver them from five to nine different gantry

Figure 1.1: Example of an IMRT treatment with seven different gantry angles. Notice the different non-uniform beams.

angles. They are called step-and-shoot and sliding-window and uses different ways to deliver the radiation: segmented and dynamic respectively. A segmented beam consists of small segments, created with the MLC, that together forms the non-uniform beam. The MLC moves to its position for the specific segment and the radiation is turned on. After the set monitor units (MU) have been delivered the radiation is turned off and the MLC-leaves moves to their position for the next segment. When in place the set MU is delivered and so on. The dynamic method is based on MLC movement in a set pattern during continuous radiation [31].

Recently a new technique has been made commercially available: Intensity Modulated Arc-Therapy (IMAT). The vendors have implemented this in somewhat different ways, but the concept is the same: the radiation is delivered during rotation. For example one vendor has implemented this by delivering radiation in a cone-beam-geometry while both the MLC and gantry angle moves in a set pattern. Another vendor has developed an accelerator similar to a CT but with a linear accelerator instead of an x-ray tube with a binary MLC. Radiation is delivered a fan-beam helical pattern much like a spiral CT-scan. Here the binary MLC is used to create the desired dose distribution [31].

1.2.1   IMRT planning

Before the IMRT planning can take place one must first delineate structures, target and OAR, specify the number of gantry angles and dose goals for OAR and target dose objectives. These dose objectives are typically: minimum

and maximum target dose and maximum dose to a sensitive structure (or OAR) or maximum dose to a sensitive structure volume (or volume of OAR). When this is done the IMRT optimization, or inverse planning as it's commonly called, can begin. The whole beam is divided into individual elements (often called beamlets) that together forms the final beam.

Based on the set dose objectives the beam intensity and profiles are calculated via the TPS's IMRT algorithm. The IMRT algorithm uses an iterative weight adjustment of the dose objectives based on single voxels dose values and their dosimetric objectives. If the voxel does not meet the set dose objective (either too high or too low dose) it gets a penalty score and the larger the score the more that voxel influences the change of the beamlet(s). The different objectives can have different penalties, for example: if the dose is too high in the brain stem the penalty is larger than if the dose is to high in the parotis. The total outcome of this will be that some voxels will try to raise the beamlets weight and some will try to decrease the weight of the beamlet. The final influence on the beamlets will be from a weighted average of all voxels. To change the result of the final plan one has to change the set dose objectives or penalty score [7, 15, 20].

1.2.2   IMRT Verification

Guidelines by both the IAEA and the AAPM are available on how to verify IMRT plans [7, 15]. Before any IMRT treatment begins a medical physicist should verify the actual dose being delivered to the patient. This is achieved by using a phantom with a calibrated dosimetry system or films. The direct measurements are done for IMRT fields transfered to a CT-study of a geometric phantom (described in section 3.2.1 on page 16). Today there are many products commercially available for this type of verifications: linear or matrix detector arrays consisting of a large number of either diodes or ionization chambers. One can also use one or multiple radiosensitive films.

It is important to know that this patient specific QA is to check on the dose calculation and delivery system. The patient specific dose accuracy is very much dependent on the accuracy of patient position, internal organ motion and the presence of heterogeneities. To check on the positioning of the patient one uses either 2D beams-eye-view (BEV) images or if available a cone beam CT mounted on the linear accelerator for 3D imaging.

After the measurement is complete different evaluation methods can be used to evaluate the IMRT fields. One has to evaluate both the spatial difference and the dose difference. This can be achieved with different types of evaluation methods where the gamma evaluation is the most accepted. Programs for evaluation are commercially available and are often included with the detector array.

1.3 National Recommendations for Radiation Therapy

All use of ionizing radiation in Sweden is controlled by The Swedish Radiation Safety Authority (SSM). Clinical radiation therapy is controlled by two different constitutions from SSM: Regulations on General Obligations in Medical and Dental Practices using Ionizing Radiation, SSM FS 2008:35, and Regulations on Radiation Therapy, SSM FS 2008:33. These regulations state that every treatment plan in radiation therapy has to be individually optimized for the patient and the dose given to the patient has to be controlled the first time and every other time it seems necessary. In practice this is achieved in conventional radiation therapy by measuring entrance dose for the fields. For IMRT these measurements are often not performed because of complicated measurement sites, but is possible in a cavity using for example a number of TLDs inside a tight flexible plastic tube.

1.4 Aim

The aim of this study is to develop, implement and evaluate methods for comparison of dose distributions in 2D and 3D. This was done using calculated, synthetic and simulated measured dose distributions in order to explain experimental results in both commercial and software developed in this study.

Chapter 2

Theory

Comparison of dose distributions can be done using a number of different methods and the theories for the most frequently used evaluation methods will be presented. A statistical evaluation method will also be introduced.

Most evaluation methods can be used in either one, two or three spatial dimensions. The focus will be on the gamma evaluation method, mainly because it is the most accepted evaluation method, but other methods will also be discussed. The nomenclature used in this thesis is the one used by Low and Dempsey [18]. For the ease of the reader the nomenclature is summarized in Table 2.1. All equations in Table 2.1 will be described further in this chapter. Terms for the distributions being compared will be reference, normally the measured distribution and evaluated, normally the calculated distribution.

2.1   Profile Comparison

Profiles in the X, Y or diagonal direction of the dose distributions can be plotted against each other and be visually compared. This tool can be used in one to three dimensions, but becomes more bothersome the more dimensions. This is a method that is very useful when evaluating local deviations between distributions found with other comparison methods, but it is very time consuming by itself.

2.2   Absolute and Relative Dose Difference

The absolute difference is the most straightforward method and is the absolute value of the difference between the two distributions using pixel by pixel subtraction. Note that the dose differences at high dose gradients are

Table 2.1: Nomenclature used in this paper, from Low and Dempsey [18]

Symbol	Equation	Description
$D_e(\vec{r}_e)$	-	Evaluated dose D_e at position $\vec{r}_e$
$D_r(\vec{r}_r)$	-	Evaluated dose D_r at position $\vec{r}_r$
ΔD	-	Dose difference criterion. Can either be local or global. Normally 3% of the maximum dose
Δd	-	Distance-to-agreement (DTA) criterion. Normally 3 mm
$r(\vec{r}_e, \vec{r}_r)$	$r(\vec{r}_e,\vec{r}_r) = \lvert \vec{r}_e - \vec{r}_r \rvert$	Spatial distance between evaluated and reference dose points
$\delta(\vec{r}_e, \vec{r}_r)$	$\delta(\vec{r}_e, \vec{r}_r) = D_e(\vec{r}_e) - D_r(\vec{r}_r)$	Difference between evaluated dose $D_e(\vec{r}_e)$ at position $\vec{r}_e$ and reference dose $D_r(\vec{r}_r)$ at $\vec{r}_r$
$\Gamma(\vec{r}_e, \vec{r}_r)$	$\Gamma(\vec{r}_e, \vec{r}_r)$ $= \sqrt{\frac{r^2(\vec{r}_e,\vec{r}_r)}{\Delta d^2} + \frac{\delta^2(\vec{r}_e,\vec{r}_r)}{\Delta D^2}}$	Generalized Γ function, computed for all evaluated positions $\vec{r}_e$ and reference positions $\vec{r}_r$
$\gamma(\vec{r}_r)$	$\gamma(\vec{r}_r) = \min\{\Gamma(\vec{r}_e, \vec{r}_r)\} \forall \{\vec{r}_e\}$	γ function, the minimum generalized Γ function in the set of evaluated points

of less importance because they can be induced by a small spatial error in the alignment or by interpolation. There is also the possibility to display the difference for the positive and the negative range (relative dose difference). Here it can be discovered how one distribution differs from another. A dose difference criterion, e.g. $\Delta D = 3\%$ of the maximum dose can be set and points passing this criterion receive a value lower than one and points not passing the criterion will get a value higher than one.

2.2.1   Dose Difference Histograms

Histograms of the dose difference can be a useful tool, especially in 3D dose distributions. It reveals large differences even though the spatial information is not evaluated. A histogram can also reveal potential skewness of the dose difference.

2.3   Dose-Gradient Analysis Tool

The dose-gradient analysis tool was developed to evaluate local dose differences based on the dose gradient at each position in the dose distribution [21]. Geometric effects such as small spatial misalignments or a finite size of measurement and calculation grid may dominate in other analysis methods and decrease the quality of the evaluation primary in high gradient regions [21]. These effects can be removed with the dose-gradient analysis tool, resulting in an evaluation that is easier to analyze and more straightforward. The gradient used for this tool is defined as the sum of the squares of all local gradients around each calculated position as defined in equation 2.1. For a calculated 2D or 3D dose distribution the dose difference is calculated between each dose position and the nearest neighbors on the calculation grid (four points in 2D and six points in 3D).

$$G_i = \sqrt{\sum_{j=1}^{n} \left(\frac{\Delta d_{ij}}{\Delta x_{ij}}\right)^2}, \qquad (2.1)$$

where G_i is the generalized gradient at position i, Δd_{ij} is the dose difference between position i and each of its nearest neighbors j and Δx_{ij} is the distance between positions i and each of its nearest neighbors j used in the calculation. After calculating the generalized gradient map for every measured point i, a distance parameter d_{gc} is chosen, which is the size of the geometric uncertainty (typically 1 mm). Dose differences caused by a geometric shift of this distance will be removed from the dose difference distribution by the gradient compensation. The gradient compensation is defined as:

$$DDgc = |DD_i| - G_i \cdot d_{gc}, \qquad (2.2)$$

where DD_{gc} is the gradient compensated dose difference and $|DD_i|$ is the absolute dose difference at the position i in each distribution. The dose difference at each position i is decreased by the product of the generalized gradient and the distance parameter. It is reduced by the difference that could be caused by a geometrical effect with size d_{gc}.

2.4   Distance To Agreement, DTA

The distance-to-agreement (DTA) is the spatial distance between a point in
the reference distribution and the closest point in the evaluated distribution
with the same dose. The definition of DTA at the position $\vec{r}_r$ can be seen in
equation 2.3. A spatial tolerance referred to as a DTA criterion, Δd, must be
set, typically 3 or 5 mm. This is the tolerance for misalignment or rotation
of the phantom at irradiation or the film while scanning. If the DTA at the
comparison position is less than Δd the comparison passes at this point. If
the DTA is greater than Δd then the comparison fails. The comparison is
done for each pixel [9].

$$DTA(\vec{r}_r) = min\left\{|\vec{r}_e - \vec{r}_r|\right\} \forall \left\{\vec{r}_e\right\} \tag{2.3}$$

2.5   Gamma Evaluation

Depending on the situation dose difference or DTA alone may be insufficient
and they are actually complementary to each other. The dose difference gives
suitable results in low dose gradient regions but not in high dose gradient
regions and the DTA is the opposite. The gamma evaluation method is a
combination between the dose difference and the DTA evaluation methods.
This evaluation was first introduced by Low et al. [19]. The gamma evalu-
ation method should not be mistaken for the combined criterion [9], which
only gives binary results.

The gamma evaluation for a 2D case will be presented and explained but
the theory is also applicable in 3D. For a 2D dose distribution the two cri-
teria, dose difference and DTA, incorporates an ellipsoid with the surface
representing the acceptance criterion. The equation for the ellipsoid is

$$1 = \sqrt{\frac{r^2(\vec{r}, \vec{r}_r)}{\Delta d^2} + \frac{\delta^2(\vec{r}, \vec{r}_r)}{\Delta D^2}}, \tag{2.4}$$

where $r(\vec{r}, \vec{r}_r)$ is the spatial distance between the reference position (origin)
and any other position and $\delta(\vec{r}, \vec{r}_r)$ is the dose difference between the refer-
ence position and any other position. In Figure 2.1 the surface of the ellipsoid
represents the acceptance criterion. From Equation 2.4 the right hand side
can be used to define the gamma index,

$$\gamma(\vec{r}_r) = min\left\{\Gamma(\vec{r}_e, \vec{r}_r)\right\} \forall \left\{\vec{r}_e\right\}, \tag{2.5}$$

where

$$\Gamma(\vec{r}_e, \vec{r}_r) = \sqrt{\frac{r^2(\vec{r}_e, \vec{r}_r)}{\Delta d^2} + \frac{\delta^2(\vec{r}_e, \vec{r}_r)}{\Delta D^2}}. \tag{2.6}$$

The expression $r(\vec{r}_e, \vec{r}_r)$ is the spatial distance between the evaluated and the reference positions and $\delta(\vec{r}_e, \vec{r}_r) = D_e(\vec{r}_e) - D_r(\vec{r}_r)$, the dose difference between the two positions. The pass-fail criterion in this method will then be

$$\gamma(\vec{r}_r) \leq 1, \text{calculation passes}, \qquad (2.7)$$
$$\gamma(\vec{r}_r) > 1, \text{calculation fails}. \qquad (2.8)$$

This gamma calculation is done for each pixel in the reference distribution [19]. Commonly used passing criteria are $\Delta D = 3\%$ and $\Delta d = 3$ mm (3%/3 mm) or $\Delta D = 5\%$ and $\Delta d = 5$ mm (5%/5 mm) [18].

Figure 2.1: Geometric representation of combined gamma criterion for dose difference and DTA for a 2D dose distribution [19]. The axes x and y represents the spatial plane and the axis δ represents the difference in dose between the evaluated and the reference position. Definitions for the symbols can be found in Table 2.1.

2.5.1   Global and Local Passing Criteria

Instead of setting a global criteria for the dose difference (e.g. 3% of the maximum dose) one can use a local criteria, 3% of the dose at the reference point. This will result in a harder constraint for the dose difference, especially in parts of the distribution where the doses are close to zero.

2.5.2   Gamma Angle

The gamma angle is the angle between the dose difference axis (δ) and the vector stretching from $D(\vec{r}_r)$ to $D(\vec{r}_e)$, see Figure 2.1. The gamma angle was first presented by Stock et al. [27]. It indicates which parameter influences on the gamma value the most, the dose difference or the DTA. Absolute

values of the dose difference and distance difference are used to calculate the gamma angle, resulting in the angle always being between 0 and $\pi/2$. If the gamma angle is between $\pi/4$ and $\pi/2$ the gamma index is dominated by the DTA criteria and vice versa.

2.5.3 Gamma Histograms

The gamma histogram was first introduced by Spezi and Lewis [26] and is essentially the same as a dose difference histogram but a histogram over the gamma values. This can be a useful tool when evaluating plans in 3D, because the only useful way to visually view the 3D gamma picture is in 2D slices. Gamma histograms (GH) are presented either as a frequency gamma histograms (fGH) or cumulative gamma histograms (cGH). Gamma histograms can also be presented over a specified volume (in 3D), e.g. OAR or target or e.g. over the 90% dose region.

2.6 Statistical Evaluation Method

A statistical evaluation method (χ^2-test) has been developed in this study. It evaluates the dose distributions in both the spatial and dose domain but it is viewed from a statistical point of view, unlike the gamma evaluation methods mathematical approach.

One assumes that the positioning of a detector is normally distributed and the spatial directions are independent of each other. The detected dose is also considered to be normally distributed and independent from the positioning of the detector. The standard deviation in positioning can be estimated with a good approximation and the standard deviation in dose can be determined by a repeated number of measurements by using the formula for estimating standard deviation from a sample [22]:

$$\sigma = \sqrt{\frac{\sum_{i=1}^{n} (x_i - \overline{x})^2}{n-1}}, \tag{2.9}$$

where $\overline{x}$ is the mean value of the detected dose and x_i is the detected dose for each measurement.

The value calculated for each position in the TPS is considered to be the mean value in dose. If one measures the dose at this position the result should be found in the normal distribution around the mean dose. For the positioning the same assumption is made. The positioning of the device is considered normally distributed and the dose indicated by the dose distribution from the TPS should be detect with a 99% probability within three standard deviations in positioning. With this in mind all of the variables

(one for each direction and one for dose) will be combined into one χ^2-test statistics according to ([22]):

$$\chi_k^2 = \sum_{i=1}^{k} \left(\frac{O_i - E_i}{\sigma_i} \right)^2,$$
(2.10)

where O_i is either the observed distance or dose for a specific position and E_i is the expected dose or distance for the same position. This is done for each reference position and the comparison positions are all the positions in the evaluated distribution within three standard deviations. This results in a χ^2-distribution where the p-value for χ_k^2 can be obtained from a χ^2-table using k degrees of freedom. If the resulting p-value is lower than a set p-value the result is that this position deviates with at least this set statistical significance level (e.g. 95% if a p-value of 0.05 is used). For a 2D dose distribution comparison (three degrees of freedom) the formula in Equation 2.10 will be:

$$\chi_3^2 = \left(\frac{O_{dose} - E_{dose}}{\sigma_{dose}} \right)^2 + \left(\frac{O_{pos_x} - E_{pos_x}}{\sigma_{pos_x}} \right)^2 + \left(\frac{O_{pos_y} - E_{pos_y}}{\sigma_{pos_y}} \right)^2.$$
(2.11)

In this thesis an evaluation of the χ^2-test method was performed to evaluate what standard deviations are needed to give the introduced errors in the synthetic dose distributions (see section 3.2.2 on page 17) a p-value lower than 5%, which is regarded as statistically significant.

Chapter 3

Materials and Methods

3.1 The Developed Gamma Evaluation

Implementation of the gamma evaluation was performed in the MATLAB® software environment (The MathWorks Inc.) based on the theory by Low *et al*, see section 2.5 on page 9. See Appendix A.1 for details (Matlab code).

3.1.1 Software for comparison

The developed gamma evaluation was compared with other softwares gamma evaluation methods to ensure accuracy of the developed gamma evaluation method.

Software useful in radiation therapy research are available for free online: CERR [2], Doselabs [5]. A commercial product was also used, the OmniPro-I'mRT [12], normally used together with the I'mRT MatriXX phantom (IBA Dosimetry). All of the named software has implemented methods for gamma evaluation. Comparison between the resulting gamma matrices was done with the relative difference method. Nine IMRT fields were used for validation. Calculated dose distributions were used as reference distributions. For evaluated distributions the same dose distributions were used but bilinearly interpolated down to a 32x32 matrix and then bilinearly interpolated back to the reference size of 300x300 matrix (1 mm resolution) to introduce errors. Both the reference and evaluated dose distributions were normalized to a maximum value of one respectively, for a relative comparison. Criteria was the same in all gamma evaluation methods and set to $\Delta D = 3\%$ and $\Delta d = 3$ mm (3%/3 mm).

3.1.1.1   CERR

CERR stands for *Computational Environment for Radiotherapy Research*
and is written in the Matlab language. It can be used to import and display
treatment plans from a wide variety of commercial or academic treatment
planning systems and may only be used for non-commercial and non-clinical
use. CERR itself is a very useful tool in radiation therapy research with
its wide variety of possibilities. With the CERR software a 2D gamma
evaluation is available implemented as a .dll MEX-file (C/ C++ or For-
tran source code). This does not only make the source code unavailable
but also because it has been compiled on a 32-bit Windows Operating
System (OS) it cannot be used on a 64-bit OS or a non-Windows OS.
However the gamma evaluation is relatively quick, depending on the pro-
cessor speed the time varies between 2 to 5 seconds (using the function:
meshgamma2d(slice1,slice2,dosecriterion,DTA)) for a 300x300 pixel distri-
bution. Another problem with the meshgamma2d in CERR is that the
largest value in the gamma matrix is never larger than the value 1. Essen-
tially this means that all calculation positions passes all the time, see Eq.
2.7. These problems lead to the dismissing of the CERR gamma evaluation
for validation.

3.1.1.2   Doselab

Doselab is an open source software for quantitative comparison of dose dis-
tributions written in the Matlab language. Doselab's gamma evaluation is
available from the Doselab-package as a Matlab m-file and can be used as a
standalone Matlab function. Irrelevant values in these gamma results exists
along the edges and the reason for this is that the method does not calcu-
late the gamma value along the edges. This area is seven pixels from the
edges and can be explained as a frame around the gamma result with values
of zero. A solution to this problem is to make sure that the IMRT field is
inside the frame.

3.1.1.3   OmniPro-I'mRT

OmniPro-I'mRT is the software used clinically for validation of IMRT-fields,
together with the I'mRT MatriXX, at the Department of Medical Radiation
Physics, Malmö University Hospital. Many different comparison methods are
available and the gamma evaluation was used in this study. While using the
software a maximum value of two in the gamma evaluation was noted. Re-
sults from the OmniPro-I'mRT gamma evaluation was exported as inverted
16-bit TIFF-images, imported into Matlab and rescaled to a maximum value
of two for the validation. The rescaling was done because the TIFF-images

uses all 16-bits to define the values (the maximum gamma value will receive the value 40 000 when exported as a 16-bit TIFF-image).

3.1.2 Improvement of the Gamma Evaluation

The in-house-developed gamma evaluation was improved with a defined search range that was noted in the open source software Doselab's. The gamma angle [27] was also implemented. See Appendix A.2 for details (Matlab code). The main difference from the first gamma evaluation is the speed. Instead of searching all the pixels in the evaluated distribution for each reference pixel the new code only searches in a defined search range surrounding the reference pixel (see Figure 3.1). Search range in the gamma evaluation method is set to three times the DTA-criterion as recommended by Wendling et al. [29]. Additionally a border around the input matrices is added with the width of the search range so that the gamma evaluation was done for all positions. A lower limit was also implemented so the improved gamma evaluation skipped points with a value lower than a set lower limit.

Figure 3.1: Search range for the gamma evaluation. The red indicates the reference point and the gray area the search range in the evaluated dose distribution.

3.1.3 Implementation of 3D Gamma Evaluation

The code for the improved gamma 2D evaluation was extended to search in three dimensions. See Appendix A.3 for details (Matlab code). When going from two to three dimensions one increases the number of comparison points, even when using a limited search range, resulting in a very large number of comparison points. For example if one uses a search range of 20x20 pixel the total number of comparison points for each reference point in 2D will be approximately $20^2 = 400$. In 3D the number of points will be $20^3 = 8000$ (using two dose distributions with 1 mm resolution). For 2D evaluation this number is acceptable but when evaluating 3D dose distribution the gamma calculation can take up to a few hours.

A number of articles have been presented on ways of decreasing the time for 3D evaluation [3, 9, 16, 17, 27, 29] both for the gamma evaluation and new developed comparison methods. However it is beyond the scope of this thesis to implement any of these methods and a 3D evaluation based on theory by Low et al. [19] have been implemented. The 3D gamma evaluation uses a relatively small search area (9x9x9 pixels for a $\Delta d = 3$mm) to decrease the evaluation time, but it can easily be changed if needed.

3.2   Dose Distributions

A dose distribution can be either calculated, synthetic or measured. They can be calculated using a treatment planning system (TPS) or Monte-Carlo (MC). Measurements can be done in many different ways. For the main part of this thesis synthetic dose distributions were used, see section 3.2.2. In step-and-shoot and sliding window-IMRT the TPS creates dose distributions from a preset number of different angles, five to nine, which results in a more conformal radiation therapy not achievable with conventional radiation therapy.

3.2.1   Calculated Dose Distributions

The distributions were first optimized using an IMRT module in the TPS on a CT scan of the patient. After the optimization the IMRT fields were transferred, one by one, to a homogeneous reference phantom using a SSD of 95 cm. The reference phantom was created in the TPS with a size of 40x40x11 cm^3 and with a density of one. For each of the field the TPS calculated a 300x300x23 pixel 3D dose distribution with 1 mm resolution in a plane through the isocenter and 5 mm resolution in the field axis. At 5 cm depth and perpendicular to the field axis the dose distributions were extracted, resulting in a 300x300 pixel 2D calculated dose distribution with 1 mm resolution at a plane through the isocenter. Distributions were calculated with the pencil beam algorithm in MasterPlan without inhomogeneity correction. The dose distributions calculated with MasterPlan and used as a 2D reference are presented in Appendix B.

A calculated 3D dose distribution on the CT scan of the patient was also used with the 3D gamma evaluation. The distributions were calculated with 3 mm resolution in the x and y direction and with a 5 mm resolution in the z direction. The pencil beam algorithm was used with inhomogeneity correction in MasterPlan. In 3D the dose distributions were interpolated down to 1 mm resolution in all directions before evaluation.

3.2.2 Synthetic Dose Distributions

A synthetic dose distribution is essentially the same as a calculated dose distribution but known errors or modifications has been introduced before (in the DICOM-RT plan) or after the dose calculation (in the dose distribution). This was done by either importing the DICOM-RT-file in MATLAB ® (The Mathworks Inc) or converting the file to an xml-file, introducing modification in the plan and then converting the IMRT-plan back to a DICOM-RT file. The free software DCMTK [4] was used to convert the DICOM-RT file to xml and back. A summary of the errors introduced can be seen in Table 3.1. The types of errors introduced were:

- Change of energy (From 6 MV to 10 and 18 MV)

- One stuck MLC-leaf

- Slight change of one MLC-leaf position

- Removed segments

In some cases noise was added to the calculated distributions (multiplicative noise with a standard deviation of the set criteria for the gamma evaluation and two times the set standard deviation in dose for the χ^2-test). Simulated measurements and bicubic interpolation (when needed) was done to evaluate if one could still locate the introduced errors.

To evaluate the error in 3D one field with an introduced error was transfered back to the 3D data of the patient according to the original IMRT treatment plan to replace the original field. This was only done for the smallest error introduced: one missing segment with 3 MU. This resulted in two plans with only one difference being one missing segment. Before the evaluation an interpolation (bicubic) up to 1 mm resolution in all directions of the 3D dose distributions was done.

3.3 Simulating Measurements

A measured dose distribution is a distribution measured in 2D or 3D for example with a diode- or ion chamber array, EPID, radiographic film or gel. When measuring with a 2D array (either diode or ion chamber) or a film one will receive a 2D slice of the 3D distribution.

One can simulate single points detection by extracting single pixels from the calculated or synthetic dose distribution. This way it is possible to evaluate if the introduced errors are detectable with for example a diode detector array with a specific spatial separation specified by the user (assuming perfect dose detection and dose delivery).

Table 3.1: Summary of induced errors.

Field No	Energy 10 MV	Energy 18 MV	Stuck MLC leaf	Slight move of one MLC	Removed segment
1	X	X	MLC 22 stuck at -200 mm	-	Seg. 3 6 MU
2	X	X	MLC 22 stuck at -200 mm	-	Seg. 5 6 MU
3	X	X	MLC 22 stuck at -200 mm	-	Seg. 7 7 MU
4	X	X	MLC 22 stuck at -200 mm	MLC 62, seg 6, (15 MU) moved 1.7 cm	Seg. 12 3 MU
5	X	X	-	-	Seg. 9 15 MU
6	X	X	-	-	Seg. 3 4 MU
7	X	X	-	-	Seg. 6 5 MU
8	X	X	-	-	Seg. 3 10 MU
9	X	X	-	-	Seg. 5 3 MU

When using a detector array with ionization chambers the detector has a finite size ($\varnothing = 4$ mm [11]). Here the dose distributions can be convolved with the spatial response function of a single ionization chamber to account for the finite size of the ion chambers. Single pixels with distance equal to the distance between the center of the ionization chambers can be extracted. In this case the specifications for the I'mRT MatriXX [11] (7.62 mm between the center of the 1020 ionization chambers, which are equally spaced on an area of 24.4x24.4 cm^2 and result in a 32x32 detector array) were used because this detector array is the one used for verification of IMRT plans in the department of radiotherapy at Malmö University Hospital. The spatial response function was taken from Herzen et al. [10] who measured it in 1D. The 1D data was converted to a 2D rotation symmetric spatial response function, see Figure 3.2, with the assumption that the response of the chambers can be regarded as isotropic. The spatial response function taken from Herzen et al. [10] resulting in a total summation of the spatial response function was equal to one.

A measurement of any dose distribution could be simulated by convolving it

with the spatial response function. The improved gamma evaluation method was used to detect the errors introduced in the simulated measured synthetic dose distributions. Only the pixels representing the detectors in the detector array are true positions and thus the gamma evaluation will be done for each of these pixels.

The spatial response function of one ionization chamber can also be used to remove the gradient errors that arise from the spatial spread of the ionization chamber. When evaluating a measurement performed with the I'mRT MatriXX one can reduce the influence of the spatial spread of the detector by convolving the calculated dose distribution with the spatial response function of the detector.

Figure 3.2: 2D spatial response function for one ion chamber in I'mRT MatriXX. The response function is normalized so that the summation of all values are equal to one.

3.4 Development of an Evaluation Program

A graphical interface is preferred when evaluating dose distributions with different methods. A program including all the evaluation methods named above together with the possibility to translate and interpolate the dose distributions is of great value to ease the process of evaluation. During this thesis an evaluation program (Progg) was developed in the MATLAB® software environment (The MathWorks Inc.). MATLAB® has many tools for manipulating and performing calculations on large matrices. MATLAB® also has a powerful graphical user interface (GUI) development tool called GUIDE, which speeds up the development of the user interface window. All functions and the GUI for Progg were written in MATLAB® version 7.6.0, and tested in versions 7.4.0, 7.6.0 and 7.8.0.

Chapter 4

Results and Discussion

4.1 Validation

The results from validation of the in-house-developed (this study) gamma evaluation with other methods are presented. Dose distributions (reference and evaluated) and results for relative difference between the different gamma evaluations for two of the nine IMRT fields (fields 5 and 7) are presented visually (Figure 4.1 and 4.2), and a summation is presented for each validation (Table 4.1 and 4.2). In this case the reference distribution is the calculated dose distribution and the evaluated dose distribution is the same dose distribution but it has been interpolated down to a 32x32 matrix and then interpolated back to the original size of 300x300 as described in section 3.1.1. These results validates the correctness of the in-house-developed gamma evaluation.

4.1.1 Doselabs

There was good agreement between the in-house-developed gamma evaluation and Doselab's gamma evaluation (Table 4.1). The reason that the maximum values are not zero is that Doselabs has a defined search range of seven pixels and there is a pixel that gives a lower gamma value outside this search range with the in-house-developed gamma evaluation method. This can be avoided by increasing the search range.

4.1.2 OmniPro-I'mRT

The comparison with OmniPro-I'mRT also gave mean values and standard deviations close to zero (Table 4.2). Differences between the OmniPro-I'mRT's and the in-house-developed gamma evaluation methods are very

small (Figure 4.1d and 4.2d), note the diffrent scales. The difference in values also arise because of the rescaling of imported gamma images (the exported images had 40 000 possible values). It was noticed that the maximum gamma value allowed by OmniPro-I'mRT was two. The reason for this is not clear from the vendor's documentation.

4.1.3 Improvement of the Gamma Evaluation

The gamma evaluation (this study) was further improved in speed by using a defined search range. The improvement in speed for a 300x300 pixel distribution comparison was from about 500 seconds to 2 seconds on an Intel® Core^{TM}2 Duo Mobile Processor T7300 using $\Delta D = 3\%$ and $\Delta d = 3$ mm. The time for evaluation increased with increased Δd because of the greater size of the search range.

The validation was performed before the completion of the improved gamma evaluation method. No difference was noted between the two methods for any tested dose distribution thus validating the new improved gamma evaluation method.

(a) Reference, rescaled to a maximum of 1.

(b) Evaluated, rescaled to a maximum of 1.

(c) Relative difference between the developed and Doselab's gamma evaluation

(d) Relative difference between the developed and OmniPro-I'mRT's gamma evaluation

Figure 4.1: Dose distributions and results for field 5.

Table 4.1: Results summation for validation against Doselabs after using relative difference.

Field No	Mean	Max	Min	Stdev
1	0.0000	0.2075	0.0000	0.0009
2	0.0000	0.0314	0.0000	0.0001
3	0.0001	0.5395	0.0000	0.0065
4	0.0000	0.0000	0.0000	0.0000
5	0.0000	0.1015	0.0000	0.0005
6	0.0012	0.5065	0.0000	0.0155
7	0.0000	0.0645	0.0000	0.0003
8	0.0000	0.0000	0.0000	0.0000
9	0.0000	0.0253	0.0000	0.0001

(a) Reference, rescaled to a maximum of 1.

(b) Evaluated, rescaled to a maximum of 1.

(c) Relative difference between the developed and Doselab's gamma evaluation

(d) Relative difference between the developed and OmniPro-I'mRT's gamma evaluation

Figure 4.2: Dose distributions and results for field 7.

Table 4.2: Results summation for validation against OmniPro-I'MRT after using relative difference.

Field No	Mean	Max	Min	Stdev
1	0.0000	0.0010	-0.0010	0.0002
2	0.0000	0.0006	-0.0007	0.0001
3	0.0000	0.0007	-0.0006	0.0002
4	0.0000	0.0006	-0.0007	0.0001
5	0.0000	0.0008	-0.0008	0.0002
6	0.0000	0.0007	-0.0008	0.0001
7	0.0000	0.0009	-0.0009	0.0002
8	0.0000	0.0009	-0.0009	0.0002
9	0.0000	0.0009	-0.0010	0.0002

4.2   Comparison of 2D Synthetic Dose Distributions

Comparison between the calculated and synthetic dose distribution represents the ideal case where 1 mm resolution is possible and no interpolation errors or limitations of detectability exists. This is not the case when using a 2D detector array, as will be demonstrated.

All introduced errors were visible with all evaluation methods when the calculated dose distributions were compared to the synthetic dose distributions. However depending on the criteria some errors were too small to e.g. give a failed gamma value. The usefulness of these results demonstrates how the error would be presented in the ideal case and which criterion is needed to detect a specific error. Some evaluation methods were shown to be more sensitive than others. In Figure 4.3 samples of results from the various evaluation methods are presented with different criteria. Introduced errors with large differences, faulty energy (18MV) and a stuck MLC-leaf, were detected with all methods. Very loose criteria (5%/5 mm) for both the gamma evaluation method and high standard deviations in dose and positioning (3%/3 mm) for the χ^2-test could be set and still resulting in a gamma value over one or $p < 0.05$, respectively. The field with a slight change in one MLC-leaf position was also easily detected because of the large amount of monitor units (MU) in this segment (15 MU).

The gradient-analysis tool (Figure 4.3d) was found to be less useful when comparing calculated dose distributions with synthetic dose distributions because there are no errors introduced by the gradients and rather the gradient-analysis tool introduces unnecessary information. Also when comparing fields with different energies it can give a devious result.

For the in-house-developed gamma evaluation, the criteria needed to give all the introduced errors a gamma value larger than one was 4%/4 mm. With 5%/5 mm criteria one of the removed segments were noticed but still resulting in a gamma value lower than one (Table 4.3). A few of the 10 MV fields also passed for all points with these criteria (Table 4.4). The 18 MV fields failed in almost all points even with 5%/5 mm criteria. The fields with stuck MLC were also easily detected with 5%/5 mm gamma criteria.

With the χ^2-test standard deviations were varied to find out which standard deviations needed to detect all errors ($p < 0.05$, Table 4.3 and 4.4). This was only done for the 10 MV fields and the fields with removed segments. The large errors, faulty energy (18MV) and a stuck MLC-leaf, where easily detected with generous standard deviations (3%/3 mm.). The missing field (Figure 4.3e) was detected but not below a p-value of 0.05 because the standard deviations was set too high.

(a) Relative dose difference of stuck MLC in Field 3. Scale is in Gy.

(b) DTA evaluation of missing segment (7 of 69 MU) in Field 2. Points over one fail the criterion, $\Delta d = 3$ mm.

(c) Gamma evaluation result of changed energy (10 MV) in Field 4. Criteria 3%/3 mm.

(d) Gradient-analysis tool with absolute dose difference for Field 4 with moved MLC-leaf, $d_{gc} = 1$mm. Scale is in Gy.

(e) Results from the χ^2-test (P-value map) of Field 6 with missing segment (4 of 100 MU). Standard deviations: 3 mm in positioning and 3% of the maximum dose. The error is detected but the p-value is greater than 0.05.

Figure 4.3: Sample of results from different evaluation methods used for different introduced errors. Calculated dose distributions were used as reference and synthetic dose distributions were evaluated.

Table 4.3: Results from evaluation of criteria for the gamma evaluation method and the χ^2-test for fields with missing segments. "Yes" indicates that the outcome has pixels above one (gamma) or below 0.05 (χ^2-test) and "No" indicates the opposite. See Table 3.1 for information about each field.

Method	Gamma	Gamma	Gamma	χ^2-test	χ^2-test	χ^2-test	χ^2-test	Dose Difference
Criteria	5%/5mm	4%/4mm	3%/3mm	3%/3mm	2%/2mm	2%/1mm	1.5%/1mm	-
Error	Rem. Seg.	Rem. Seg.	Rem. Seg.	Rem. Seg.	Rem. Seg.	Rem. Seg.	Rem. Seg.	Rem. Seg.
Outcome	$\gamma > 1$	$\gamma > 1$	$\gamma > 1$	$p < 0.05$	$p < 0.05$	$p < 0.05$	$p < 0.05$	Mean dose diff / Max dose [Gy]
Field								
1	Yes	Yes	Yes	Yes	Yes	Yes	Yes	0.050 / 0.47
2	Yes	Yes	Yes	Yes	Yes	Yes	Yes	0.050 / 0.28
3	Yes	Yes	Yes	Yes	Yes	Yes	Yes	0.062 / 0.35
4	No	Yes	Yes	No	No	No	Yes	0.026 / 0.55
5	Yes	Yes	Yes	Yes	Yes	Yes	Yes	0.13 / 0.44
6	Yes	Yes	Yes	No	Yes	Yes	Yes	0.033 / 0.46
7	Yes	Yes	Yes	Yes	Yes	Yes	Yes	0.040 / 0.44
8	Yes	Yes	Yes	Yes	Yes	Yes	Yes	0.080 / 0.38
9	Yes	Yes	Yes	No	Yes	Yes	Yes	0.022 / 0.35

Table 4.4: Results from evaluation of criteria for the gamma evaluation method and the χ^2-test for fields with 10 MV. "Yes" indicates that the outcome has pixels above one (gamma) or below 0.05 (χ^2-test) and "No" indicates the opposite. The energy for each field was changed from 6 MV to 10 MV.

Method	Gamma	Gamma	Gamma	χ^2-test	χ^2-test	χ^2-test	Dose Difference
Criteria	5%/5mm	4%/4mm	3%/3mm	3%/3mm	2%/2mm	2%/1mm	-
Error	10 MV	10 MV	10 MV	10 MV	10 MV	10 MV	10 MV
Outcome	$\gamma > 1$	$\gamma > 1$	$\gamma > 1$	$p < 0.05$	$p < 0.05$	$p < 0.05$	Max difference / Max dose [Gy]
Field							
1	Yes	Yes	Yes	No	Yes	Yes	0.033 / 0.47
2	Yes	Yes	Yes	No	Yes	Yes	0.018 /0.28
3	Yes	Yes	Yes	No	Yes	Yes	0.021 / 0.35
4	No	Yes	Yes	No	Yes	Yes	0.034 / 0.55
5	Yes	Yes	Yes	No	Yes	Yes	0.031 / 0.44
6	Yes	Yes	Yes	No	Yes	Yes	0.026 / 0.46
7	Yes	Yes	Yes	No	Yes	Yes	0.031 / 0.44
8	Yes	Yes	Yes	No	Yes	Yes	0.027 / 0.38
9	Yes	Yes	Yes	No	Yes	Yes	0.022 / 0.35

4.3   Evaluation of Simulated Measured 2D Dose Distributions

The simulated measurements was performed on calculated and synthetic 2D dose distributions. If nothing else is mentioned all simulated measurements have been performed using convolution data from the I'mRT MatriXX (see section 3.3 on page 17 for information on simulated measurements). For evaluation, most attention will be directed towards the gamma evaluation method and the χ^2-test.

4.3.1   Calculated Dose Distributions

The simulated measurements were produced from on the calculated dose distributions, i.e. the dose distributions with no errors. The resulting simulated measured dose distributions will then contain deviations caused by the spatial spread of the ionization chambers. During the evaluation process the simulated measured dose distributions were used as reference distributions and the calculated dose distributions were used as evaluated distributions.

The results for the gamma evaluation are shown in Figure 4.4 and results for χ^2-test are shown in Figure 4.5. These results reveal how evaluation of simulated measurements of calculated dose distributions would look like without any errors introduced. The two methods indicate similar differences. It also reveals that the finite size of the ionization chambers will result in some deviations as one single point of the calculated distribution cannot be detected (a detected dose from an ionization chamber ($\varnothing = 4mm$) is compared with a 1 mm^2 pixel in the calculated dose distribution).

Figure 4.4: Gamma evaluation for simulated MatriXX measurement of calculated dose distributions with criteria $\Delta D = 4\%$ of the maximum dose and $\Delta d = 4$ mm.

Figure 4.5: P-value map from the χ^2-test for simulated MatriXX measurement of calculated dose distributions with set standard deviations: in position 1 mm and in dose 1.5% of the maximum dose.

4.3.2   Synthetic Dose Distributions

From the results of the simulated measurements of the synthetic dose distributions we can deduce that the limited spatial resolution in the measurement will result in problems when trying to detect errors that are geometrically limited (Figure 4.6a). The results can be misinterpreted as a gradient error and not as a missing segment. If the calculated dose distribution is convolved with the spatial response function of one ionization chamber and followed by the evaluation, the error becomes more evident (Figure 4.6b).

The smallest error introduced, a removed segment of 3 MU from a field with 143 MU, was detected with the criteria 4%/4 mm in the gamma evaluation and with 1 mm positioning and 1.5% of maximum dose standard deviations (Figure 4.7). The simulated measurements did not change the outcome of results regarding pass or fail criteria for the two evaluation methods, i.e. the results in Table 4.3 and 4.4 are valid also for simulated measured synthetic dose distributions.

(a) Gamma result when no convolution of the evaluated distribution has been done.

(b) Gamma result when convolution of the evaluated distribution has been done.

Figure 4.6: Gamma result from simulated measurements for field 8 with a missing segment. The missing segment was very small (6 cm^2) and the error can be misinterpreted as a gradient error. Criteria: 4%/4 mm.

(a) Gamma result for comparison with the synthetic dose distribution.

(d) Results from χ^2-test for comparison with the synthetic dose distribution.

(b) Gamma result for simulated measurement of the synthetic dose distribution.

(e) Results from χ^2-test for simulated measurement of the synthetic dose distribution.

(c) Gamma result for simulated measurement of the synthetic dose distribution with added multiplicative random noise with standard deviation 4%.

(f) Results from χ^2-test for simulated measurements of the synthetic dose distribution with added multiplicative random noise with standard deviation 3%.

Figure 4.7: Results for comparison of field with missing segment in field 4 (gamma map and p-value map). The segment that was removed had 3 MU of 143 total MU. The gamma criteria was 4%/4 mm and standard deviations for the χ^2-test was set to 1 mm in positioning and 1.5% of the maximum dose.

4.4   Evaluation of 3D Dose Distributions

The results from the 3D gamma evaluation of the 3D calculated dose distri-
bution and the 3D synthetic dose distribution with one error (Figure 4.8a
and Figure 4.8b respectively) indicate that this error would not be detected
using the set criteria (3%/3 mm, Figure 4.8d). The reason for this is that
the segment contributes with such a small dose, maximum contribution of
about 1.3 Gy out of the total prescribed dose of 70 Gy (Figure 4.8a). The
total time for the 3D evaluations was approximately two seconds for the 3D
dose difference and approximately two minutes for the 3D gamma evalua-
tion. The fastest way to compare synthetic dose distributions was using the
relative dose difference, which could be used since no spatial misalignment
between the distributions existed.

(a) A 2D slice from the 3D calculated dose
distribution with no error. Scale is in Gy.

(b) A 2D slice from the 3D synthetic dose
distribution with a removed segment. Scale
is in Gy.

(c) A 2D slice of the 3D relative dose differ-
ence evaluation between the two dose dis-
tributions. Scale is in Gy and is positive
because the evaluated dose distribution is
missing this absorbed dose.

(d) A 2D slice of the 3D gamma evaluation
between the two dose distributions, criteria
3%/3 mm.

Figure 4.8: Input dose distributions (a and b) and results (c and d) from the 3D
evaluation. A slice of the dose distributions and the same slice is shown for the
results.

4.5 χ^2-test

The χ^2-test was shown to be useful as a new method for comparison of dose distributions. Most of the introduced errors were detected with a standard deviation of 2% of the maximum dose and 2 mm in positioning. However the result from evaluation of the smallest error (3 of 143 MU) indicates that standard deviations needed to detect the errors are relatively tight (see Table 4.3 and 4.4). If this is the standard deviations needed for the χ^2-test then it might not be applicable for some clinical cases.

The χ^2-test has the possibility to include additional uncertainties, for example linear accelerator output uncertainty or the uncertainty regarding light- and radiation field positioning.

In principle, the χ^2-test requires that dose and position can be considered independent. These two variables might be correlated for an individual field, but in general it is not possible to predict the correlation. For example, consider measuring a large number of different IMRT fields and setting up the detector array for each new field. From this one can assume that the correlation between positioning and measured dose is negligible because the expected dose in each position will vary from field to field.

4.6   The Developed Evaluation Program, Progg

Progg was developed in the MATLAB® software environment (The Math-Works Inc.). The program can handle both 2D and 3D dose distributions. Possible input distributions are: calculated, synthetic (DICOM) and measured (MatriXX measured) dose distributions. The program can simulate measurements with MatriXX chamber array (IBA Dosimetry). The program can translate the distributions in the X and Y direction, interpolate them and add noise if wanted. Evaluation methods that have been implemented are the gamma evaluation (2D and 3D), gamma angle (2D), dose difference (2D and 3D), DTA (2D), χ^2-test (2D) and the gradient analysis tool (2D and 3D). It is possible to view histograms of the results. Progg also comes with the possibility to save and load evaluation data. A screen shot of the program can be seen in Figure 4.9.

Figure 4.9: Screen shot of the developed program Progg.

Chapter 5

Conclusions

In this thesis different types of evaluation methods have been implemented in an evaluation software. Implementation of the gamma evaluation method has been done in both 2D and 3D according to theory. A method for comparison of dose distributions with a statistical approach was also introduced and compared with the gamma evaluation method.

The in-house developed (this study) 2D gamma evaluation software was validated against available dose evaluation programs (Doselabs and Omnipro-I'mRT, IBA Dosimetry). The cacluation time for the comparison in both 2D and 3D was decreased greatly by using a defined search range, but no other methods for decrease in calcualtion time were implemented.

A statistical evaluation method (χ^2-test) was developed, but further evaluation is needed to conclude the value of this statistical method in a clinical setting. The advantage of the χ^2-test is that it is directly related to the significance of the observed deviations and the actual uncertainties present during measurements. It should be noted that the proposed standard deviations needed to detect certain errors could be small, however one can of course turn this question around and ask if it is acceptable to have such large criteria in positioning (3-5 mm) with the gamma evaluation. Further developments of the χ^2-test would be interesting, both in a clinical setting based on true measurement uncertainties and for evaluation of 3D dose distributions.

With the use of synthetic dose distributions one can implement known errors. Together with the simulated measurements this tells us how the errors will be present in a clinical setting. This indicates what experimental data would look like, and if errors existed within a dose distribution if they would be detected. It was also shown that the spatial resolution of the detector introduces additional uncertainties in the evaluation results (Figure 4.4 and 4.5). One way to avoid these uncertainties is to convolve the evaluated

(calculated) distribution with the spatial response function of an ionization chamber before the evaluation. The simulated measurements of any detector array could be implemented as long as the spatial response function and position of the detectors are known.

The developed software (Progg) is still under development but can at present be use for example when validating other comparison software to ensure that the software calculations are correctly. The program is also adjustable and can be programmed for certain needs for example in research.

Bibliography

[1] A. Brahme. Optimization of stationary and moving beam radiation therapy techniques. *Radiotherapy and Oncology*, 12(2):129–140, 1988.

[2] CERR. Web page: http://radium.wustl.edu/cerr/.

[3] M. Chen, W. Lu, Q. Chen, K. Ruchala, and G. Olivera. Efficient gamma index calculation using fast Euclidean distance transform. *Physics in Medicine and Biology*, 54(7):2037–2047, 2009.

[4] DCMTK. Web page: http://dicom.offis.de/dcmtk.php.en/.

[5] Doselabs. Web page: http://doselab.sourceforge.net/.

[6] Surveillance Epidemiology and End Results (SEER). Web page: http://seer.cancer.gov/.

[7] G.A. Ezzell, J.M. Galvin, D. Low, J.R. Palta, I. Rosen, M.B. Sharpe, P. Xia, Y. Xiao, L. Xing, and C.X. Yu. Guidance document on delivery, treatment planning, and clinical implementation of IMRT: Report of the IMRT subcommittee of the AAPM radiation therapy committee. *Medical Physics*, 30(8):2089–2115, 2003.

[8] V. Gates, E. Kangaroo, M. Roachcock, and WC Gall. Stuperspace. *Physica D: Nonlinear Phenomena*, 15(1-2), 1985.

[9] W.B. Harms Sr, D.A. Low, J.W. Wong, and J.A. Purdy. A software tool for the quantitative evaluation of 3D dose calculation algorithms. *Medical Physics*, 25(10):1830–1836, 1998.

[10] J. Herzen, M. Todorovic, F. Cremers, V. Platz, D. Albers, A. Bartels, and R. Schmidt. Dosimetric evaluation of a 2D pixel ionization chamber for implementation in clinical routine. *Physics in Medicine and Biology*, 52(4):1197–1208, 2007.

[11] IBA Dosimetry I'mRT-MatriXX. Brochure: http://www.iba-dosimetry.com/Home.957.0.html.

[12] IBA Dosimetry OmniPro-I'mRT. Web page: http://scanditronix-wellhofer.com/ OmniPro-I-m-i-RT-i.453.0.html.

[13] ICRU, International Commission on Radiation Units and Measurements. *ICRU 50: Prescribing, Recording, and Reporting Photon Beam Therapy*. ICRU Publications, Bethesda, MD, USA, 1993.

[14] ICRU, International Commission on Radiation Units and Measurements. *ICRU 62: Prescribing, Recording, and Reporting Photon Beam Therapy (Supplement to ICRU Report 50)*. ICRU Publications, Bethesda, MD, USA, 1998.

[15] International Atomic Energy Agency. Transition from 2-D Radiotherapy to 3-D Conformal and Intensity Modulated Radiotherapy. IAEA-TECDOC-1588, 2008.

[16] S.B. Jiang, G.C. Sharp, T. Neicu, R.I. Berbeco, S. Flampouri, and T. Bortfeld. On dose distribution comparison. *Physics in Medicine and Biology*, 51(4):759–776, 2006.

[17] T. Ju, T. Simpson, J.O. Deasy, and D.A. Low. Geometric interpretation of the γ dose distribution comparison technique: Interpolation-free calculation. *Medical Physics*, 35(3):879–887, 2008.

[18] D.A. Low and J.F. Dempsey. Evaluation of the gamma dose distribution comparison method. *Medical Physics*, 30(5):2455–2464, 2003.

[19] D.A. Low, W.B. Harms, S. Mutic, and J.A. Purdy. A technique for the quantitative evaluation of dose distributions. *Medical Physics*, 25(5): 656–661, 1998.

[20] P. Metcalfe, T. Kron, and P. Hoban. *The Physics of Radiotherapy X-Rays and Electrons*. Medical Physics Publishing, Madison, 2007. ISBN 978-1-930524-36-1.

[21] J.M. Moran, J. Radawski, and B.A. Fraass. A dose gradient analysis tool for IMRT QA. *Journal of Applied Clinical Medical Physics*, 6(2): 62–73, 2005.

[22] R.F. Mould. *Introductory Medical Statistics, Third Edition*. Medical Physics Publishing, London, 1998. ISBN 0-7503-513-4.

[23] International Commission on Radiological Protection (ICRP). Web page: http://www.icrp.org/.

[24] U. Ringborg, D. Bergqvist, B. Brorsson, E. Cavallin-ståhl, J. Ceberg, N. Einhorn, J. Frödin, J. Järhult, G. Lamnevik, C. Lindholm, et al. The Swedish Council on Technology Assessment in Health Care (SBU)

Systematic Overview of Radiotherapy for Cancer including a Prospective Survey of Radiotherapy Practice in Sweden 2001–Summary and Conclusions. *Acta Oncologica*, 42(5-6):357–365, 2003.

[25] Socialstyrelsen (SOS). Web page: http://www.socialstyrelsen.se/.

[26] E. Spezi and D.G. Lewis. Gamma histograms for radiotherapy plan evaluation. *Radiotherapy and Oncology*, 79(2):224–230, 2006.

[27] M. Stock, B. Kroupa, and D. Georg. Interpretation and evaluation of the γ index and the γ index angle for the verification of IMRT hybrid plans. *Physics in Medicine and Biology*, 50(3):399–411, 2005.

[28] H. Svensson and T.R. Möller. Developments in Radiotherapy. *Acta Oncologica*, 42(5-6):430–442, 2003.

[29] M. Wendling, L.J. Zijp, L.N. McDermott, E.J. Smit, J.J. Sonke, B.J. Mijnheer, and M. Herk. A fast algorithm for gamma evaluation in 3D. *Medical Physics*, 34(5):1647–1654, 2007.

[30] World Health Organisation (WHO). Web page: http://www.who.int/.

[31] P.C. Williams. IMRT: delivery techniques and quality assurance. *British Journal of Radiology*, 76(911):766–776, 2003.

Appendix A

Matlab Code

A.1 First 2D Gamma Evaluation Function

```matlab
function G = gamma2d(A1,A2,DTA,dosed)
%This functions does a gamma evaluation out of the two 2D
    input matrices
%DTA should be specified in mm, ex 3mm, and dose should be
    specified in %,
%ex 3% is 0.03
size1=size(A1);
size2=size(A2);
%dosed = dosed*max(A1(:));
% maxDoseA1 = max(A1(:));
% maxDoseA2 = max(A2(:));
% A1 = A1 / maxDoseA1;
% A2 = A2 / maxDoseA2;

G=zeros(size1);
Ga=zeros(size1);
if size1 == size2
    tic
    for i = 1:size1(1)
        for j = 1:size1(2)
            for k = 1:size1(1)
                for l = 1:size1(2)
                    r2 = (i-k)^2+(j-l)^2;
                    d2 = (A1(i,j)-A2(k,l))^2; %Reference -
                        Evaluated.
                    Ga(k,l) = r2/(DTA^2) + d2/dosed^2;
                end
            end
            G(i,j)=min(min(Ga));
        end
    end
```

```matlab
29        G = sqrt(G);
30        toc %prints the total time for the gamma evaluations.
31   else
32        fprintf=('Matrix size does not agree\n');
33   end
```

A.2 Improved 2D Gamma Evaluation Function with Gamma Angle

```matlab
1   function [G, gammaAngle] = gamma2dnewandgammaangle(Reference
        ,Evaluated,DTA,dosed,minLim,localorglobal)
2   %This functions does a gamma evaluation out of the two 2D
        input matrices
3   %The resolution of the 2D input matrices should be in mm.
        They should be
4   %spatially matched before running this function and have the
        same size.
5   %DTA should be specified in mm, ex 3mm, and dose specified
        in %, ex 3% is 0.03
6   %minLim is the minimum tolerance and can be set to zero it
        should also be
7   %specifield in %, ex 5% is is 0.05.
8   size1 = size(Reference)
9   size2 = size(Evaluated)
10  %dosed = dosed*max(Reference(:));%Defines the global gamma
11  minLim = minLim*max(Reference(:));
12  %G = zeros(size1);
13  %gammaAngle = zeros(size1);
14  searchRange = round(3*DTA+1);
15
16  if size1 == size2
17      tic
18      %This parts adds a "border" around both input matrices
            so that the gamma
19      %evaluation can be done for all pixels
20      tempReference = zeros(size1+searchRange*2);
21      tempReference(searchRange+1:size1(1)+searchRange,
            searchRange+1:size1(2)+searchRange) = Reference;
22      tempEvaluated = zeros(size2+searchRange*2);
23      tempEvaluated(searchRange+1:size1(1)+searchRange,
            searchRange+1:size1(2)+searchRange) = Evaluated;
24      Reference = tempReference;
25      Evaluated = tempEvaluated;
26      G = zeros(size(Reference));
27      gammaAngle = zeros(size(Reference));
28
29      %defines the global or local criteria
30      if strcmpi(localorglobal,'global')
```

```matlab
31            dosed = zeros(size(Reference)) +  dosed*max(
                 Reference(:));
32        elseif strcmpi(localorglobal,'local')
33            dosed = Reference .*dosed;
34        end
35        %Create the DTAsearch range and the DTAMatrix
36        %The DTAMatrix is the same for each evaluated pixel
37        DTAMatrix = zeros(2*searchRange+1,2*searchRange+1);
38        %Sets the center position to 1
39        DTAMatrix(searchRange+1,searchRange+1) = 1;
40        %DTAMatrixSave = bwdist(DTAMatrix);
41        %Calulates the euclidean distance to all points from the
                 center point,
42        %divides with DTA-criterion and quadrates this matrice.
43        DTAMatrix = (bwdist(DTAMatrix)/DTA).^2;
44
45        positionAngle = zeros(size(Reference));
46        X = zeros(size(positionAngle));
47        Y = zeros(size(positionAngle));
48        Size = (2*searchRange+1);
49
50        X(1:Size,round(Size/2)) = 1;
51        Y(round(Size/2),1:Size) = 1;
52        X = bwdist(X);
53        Y = bwdist(Y);
54        X(:,1:round(Size/2)) = X(:,1:round(Size/2))*-1;
55        Y(round(Size/2):Size,:) = Y(round(Size/2):Size,:)*-1;
56        Angle = (atan2(Y,X)/pi*180);
57
58        %Defines the vectors for dose difference calculation
59        x = -(searchRange):1:(searchRange);
60        y = -(searchRange):1:(searchRange);
61
62
63        for i = searchRange+1:size1(1) + searchRange
64            for j = searchRange+1:size1(2) + searchRange
65
66                if Reference(i,j) < minLim %This part skips "
                     unessecary" pixels
67                    G(i,j) = 0;
68                    continue
69                end
70
71                doseDiffSave = ((Reference(i,j)-Evaluated(i+x,j+
                     y)));%/dosed).^2;
72                doseDiff = (doseDiffSave./dosed(i,j)).^2;
73
74                %The Gamma matrice
75                Ga = DTAMatrix + doseDiff;
```

```
76                    %minimum of Gamma
77                    G(i,j)=min(Ga(:));
78                    MinGa = min(Ga(:));
79                    [r c] = find(Ga == MinGa);
80                    [mr nr] = size(r);
81                    [mc nc] = size(c);
82                    if numel(r) ~= 0
83
84                        if mr == 1 && mc == 1 && nr == 1 && nc == 1
85                            %if G(i,j) == 0 || (doseDiffSave(r(1),c
                                 (1)) > -0.005 && doseDiffSave(r(1),c
                                 (1)) < 0.005)
86                            %   gammaAngle(i,j) = 0;
87                            %else
88                            gammaAngle(i,j) = atan(DTAMatrix(r(1),c
                                 (1))/abs(doseDiff(r(1),c(1))));
89                            positionAngle(i,j) = Angle(r(1),c(1));
90                            %end
91                            %If more than one point in Gamma has the
                                 minimum value this part
92                            %selects the point closest to the
                                 reference point
93                        elseif (r(1)-(searchRange+1))^2 + (c(1)-(
                             searchRange+1))^2 == (r(2)-(searchRange
                             +1))^2 + (c(2)-(searchRange+1))^2
94                            gammaAngle(i,j) = atan(DTAMatrix(r(1),c
                                 (1))/abs(doseDiff(r(1),c(1))));
95                            positionAngle(i,j) = Angle(r(1),c(1));
96                        elseif (r(1)-(searchRange+1))^2 + (c(1)-(
                             searchRange+1))^2 > (r(2)-(searchRange
                             +1))^2 + (c(2)-(searchRange+1))^2
97                            gammaAngle(i,j) = atan(DTAMatrix(r(2),c
                                 (2))/abs(doseDiff(r(2),c(2))));
98                            positionAngle(i,j) = Angle(r(2),c(2));
99                        elseif (r(1)-(searchRange+1))^2 + (c(1)-(
                             searchRange+1))^2 < (r(2)-(searchRange
                             +1))^2 + (c(2)-(searchRange+1))^2
100                           gammaAngle(i,j) = atan(DTAMatrix(r(1),c
                                 (1))/abs(doseDiff(r(1),c(1))));
101                           positionAngle(i,j) = Angle(r(1),c(1));
102                       end
103                   end
104               end
105       end
106       %calculates the gamma
107       G = sqrt(G);
108       fprintf('Elapsed time for gamma evaluation: %6.4f
              seconds\n',toc);
109 elseif sum(size1 == [32 32]) == 2 && sum(size2 == [244 244])
```

```
               == 2
110         tic ;
111         matrixxpos = 122 + 10*[−11.810  −11.048  −10.286  −9.524
                 −8.762  −8.000  −7.239  −6.477  −5.715  −4.953  −4.191
                 −3.429  −2.667  −1.905  −1.143  −0.381  0.380  1.142  1.904
                  2.666  3.428  4.190  4.952  5.714  6.476  7.237  7.999
                 8.761  9.523  10.285  11.047  11.809];
112         matrixxpos = round( matrixxpos ) ;
113         G = zeros (32 ,32) ;
114         gammaAngle = zeros (32 ,32) ;
115
116         tempEvaluated = zeros ( size2+searchRange *2) ;
117         tempEvaluated ( searchRange +1: size2 (1)+searchRange ,
                 searchRange +1: size2 (2)+searchRange ) = Evaluated ;
118
119         Evaluated = tempEvaluated ;
120
121         if strcmpi ( localorglobal , ’ global ’ )
122             dosed = zeros ( size ( Reference ) ) +  dosed *max(
                    Reference ( : ) ) ;
123         elseif strcmpi ( localorglobal , ’ local ’ )
124             dosed = Reference *dosed ;
125         end
126
127         positionAngle = zeros ( size ( Reference ) ) ;
128         X = zeros ( size ( positionAngle ) ) ;
129         Y = zeros ( size ( positionAngle ) ) ;
130         Size = (2*searchRange +1) ;
131
132         X( 1 : Size ,round ( Size /2) ) = 1;
133         Y( round ( Size /2) ,1 : Size ) = 1;
134         X = bwdist (X) ;
135         Y = bwdist (Y) ;
136         X( : ,1 : round ( Size /2) ) = X( : ,1 : round ( Size /2) ) *−1;
137         Y( round ( Size /2) : Size , : ) = Y( round ( Size /2) : Size , : ) *−1;
138         Angle = ( atan2 (Y,X) / pi *180) ;
139
140
141         %Create the DTAsearch range and the DTAMatrix
142         %The DTAMatrix is the same for each evaluated pixel
143         DTAMatrix = zeros (2*searchRange +1,2*searchRange +1) ;
144         %Sets the center position to 1
145         DTAMatrix ( searchRange +1,searchRange +1) = 1;
146         %DTAMatrixSave = bwdist (DTAMatrix) ;
147         %Calulates the euclidean distance to all points from the
                    center point
148         %and divides with DTA and quadrates this matrice .
149         DTAMatrix = ( bwdist (DTAMatrix) /DTA) . ^2;
150
```

```
151        %Defines the vectors for dose difference calculation
152        x = −(searchRange):1:(searchRange);
153        y = −(searchRange):1:(searchRange);
154        for i = 1:32
155            for j = 1:32
156                if Reference(i,j) < minLim %This part skips "
                       unessecary" pixels
157                    G(i,j) = 0;
158                     continue
159                end
160
161                doseDiffSave = ((Reference(i,j)−Evaluated(
                       matrixxpos(i)+searchRange+x,matrixxpos(j)+
                       searchRange+y)));%/dosed).^2;
162                doseDiff = (doseDiffSave./dosed(i,j)).^2;
163
164                Ga = DTAMatrix + doseDiff;
165                %minimum of Gamma
166                G(i,j)=min(Ga(:));
167                MinGa = min(Ga(:));
168                [r c] = find(Ga == MinGa);
169                [mr nr] = size(r);
170                [mc nc] = size(c);
171                if numel(r) ~= 0
172                    if mr == 1 && mc == 1 && nr == 1 && nc == 1
173                        %if G(i,j) == 0 || (doseDiffSave(r(1),c
                             (1)) > −0.005 && doseDiffSave(r(1),c
                             (1)) < 0.005)
174                        %    gammaAngle(i,j) = 0;
175                        %else
176                        gammaAngle(i,j) = atan(DTAMatrix(r(1),c
                             (1))/abs(doseDiff(r(1),c(1))));
177                        positionAngle(i,j) = Angle(r(1),c(1));
178                        %end
179                        %If more than one point in Gamma has the
                             minimum value this part
180                        %selects the point closest to the
                             reference point
181                    elseif (r(1)−(searchRange+1))^2 + (c(1)−(
                           searchRange+1))^2 == (r(2)−(searchRange
                           +1))^2 + (c(2)−(searchRange+1))^2
182                        gammaAngle(i,j) = atan(DTAMatrix(r(1),c
                             (1))/abs(doseDiff(r(1),c(1))));
183                        positionAngle(i,j) = Angle(r(1),c(1));
184
185                    elseif (r(1)−(searchRange+1))^2 + (c(1)−(
                           searchRange+1))^2 > (r(2)−(searchRange
                           +1))^2 + (c(2)−(searchRange+1))^2
186                        gammaAngle(i,j) = atan(DTAMatrix(r(2),c
```

```
                                      (2))/abs(doseDiff(r(2),c(2))));
187                    positionAngle(i,j) = Angle(r(1),c(1));

188
189              elseif (r(1)-(searchRange+1))^2 + (c(1)-(
                      searchRange+1))^2 < (r(2)-(searchRange
                      +1))^2 + (c(2)-(searchRange+1))^2
190                    gammaAngle(i,j) = atan(DTAMatrix(r(1),c
                          (1))/abs(doseDiff(r(1),c(1))));
191                    positionAngle(i,j) = Angle(r(1),c(1));

192
193                end
194            end
195        end
196    end
197    G = sqrt(G);
198    fprintf('Elapsed time for gamma evaluation: %6.4f
           seconds\n',toc);
199 else
200    fprintf('Matrix sizes does not agree\n')
201 end
202 %Removes the added border
203 if size1 == size2
204    G(1:searchRange,:) = [];
205    G(:,1:searchRange) = [];
206    G(size1(1)+1:size1(1)+searchRange,:) = [];
207    G(:,size1(2)+1:size1(2)+searchRange) = [];
208    gammaAngle(1:searchRange,:) = [];
209    gammaAngle(:,1:searchRange) = [];
210    gammaAngle(size1(1)+1:size1(1)+searchRange,:) = [];
211    gammaAngle(:,size1(2)+1:size1(2)+searchRange) = [];
212    positionAngle(1:searchRange,:) = [];
213    positionAngle(:,1:searchRange) = [];
214    positionAngle(size1(1)+1:size1(1)+searchRange,:) = [];
215    positionAngle(:,size1(2)+1:size1(2)+searchRange) = [];
216 end
217 %figure
218 %imagesc(positionAngle)
219 %colormap('jet')
220 %colorbar
```

A.3   3D Gamma Evaluation Function

```
1 function G = gamma3d(Reference, Evaluated,DTA,dosed,minLim,
      localorglobal)
2 %This functions does a gamma evaluation out of the two 3D
      input matrices
3 %The resolution of the 3D input matrices should be in mm.
4 %DTA should be specified in mm, ex 3mm, and dose specified
      in %, ex 3% is 0.03
```

```matlab
5    %minLim is the minimum tolerance and can be set to zero.
6    size1 = size(Reference);
7    size2 = size(Evaluated);
8    %dosed = dosed*max(Reference(:));%Defines the global gamma
9    G = zeros(size1);
10   minLim = minLim*max(Reference(:));
11   %DTAdist = zeros(size1);
12   %gammaAngle = zeros(size1);
13   searchRange = round(DTA+1);
14   wBar = waitbar(0,'Calculating_gamma_evaluation ... ');
15   total = size1(1);
16   iter = 0;
17   %Create the DTAsearch range and the DTAMatrix
18   %The DTAMatrix is the same for each evaluated pixel
19   DTAMatrix = zeros(2*searchRange+1,2*searchRange+1,2*
         searchRange+1);
20   %Sets the center position to 1
21   DTAMatrix(searchRange+1,searchRange+1,searchRange+1) = 1;
22   %DTAMatrixSave = bwdist(DTAMatrix);
23   %Calulates the euclidean distance to all points from the
         center point
24   %and divides with DTA and quadrates this matrice.
25   DTAMatrix = (bwdist(DTAMatrix)/DTA).^2;
26   if size1 == size2
27
28       tempReference = zeros(size1+searchRange*2);
29       tempReference(searchRange+1:size1(1)+searchRange,
             searchRange+1:size1(2)+searchRange,searchRange+1:
             size1(3)+searchRange) = Reference;
30       tempEvaluated = zeros(size2+searchRange*2);
31       tempEvaluated(searchRange+1:size1(1)+searchRange,
             searchRange+1:size1(2)+searchRange,searchRange+1:
             size1(3)+searchRange) = Evaluated;
32       Reference = tempReference;
33       Evaluated = tempEvaluated;
34       G = zeros(size(Reference));
35
36       if strcmpi(localorglobal,'global')
37           dosed = zeros(size(Reference)) + dosed*max(
                 Reference(:));
38       elseif strcmpi(localorglobal,'local')
39           dosed = Reference *dosed;
40       end
41       %Defines the vectors for dose difference calculation
42   end
43   x = -(searchRange):1:(searchRange);
44   y = -(searchRange):1:(searchRange);
45   z = -(searchRange):1:(searchRange);
46
```

```
47  if size1 == size2
48      tic
49      for i = searchRange+1:size1(1) + searchRange
50          for j = searchRange+1:size1(2) + searchRange
51              for k = searchRange+1:size1(3) + searchRange
52              %dosed = max(max(Reference(:,:,k)))*dosed;
53              if Reference(i,j,k) < minLim %This part skips "
                    unessecary" pixels
54                  G(i,j,k) = 0;
55                   continue
56              end
57
58              doseDiffSave = ((Reference(i,j,k)-Evaluated(i+x,
                    j+y,k+z)));%/dosed).^2;
59              doseDiff = (doseDiffSave./dosed(i,j,k)).^2;
60
61              %The Gamma matrice
62              Ga = DTAMatrix + doseDiff;
63              %minimum of Gamma
64              G(i,j,k)=min(Ga(:));
65              end
66              %disp('a')
67          end
68          iter = iter + 1;
69          waitbar(iter/total,wBar)
70      end
71      %calculates the gamma
72
73  else
74      disp('A')
75      tic
76      resolutionDiff = size2./size1;
77      G = zeros(size1);
78      RefposX = round((1:size1(1))*resolutionDiff(1));
79      RefposY = round((1:size1(1))*resolutionDiff(2));
80      RefposZ = round((1:size1(1))*resolutionDiff(3));
81
82      tempReference = zeros(size1+4);
83      tempReference(1+2:size1(1)+2,1+2:size1(2)+2,1+2:size1(3)
                +2) = Reference;
84      Reference = tempReference;
85
86      tempEvaluated = zeros(size2+searchRange*2);
87      tempEvaluated(searchRange+1:size2(1)+searchRange,
                searchRange+1:size2(2)+searchRange,searchRange+1:
                size2(3)+searchRange) = Evaluated;
88      Evaluated = tempEvaluated;
89      if strcmpi(localorglobal,'global')
90          dosed = zeros(size(Reference)) +  dosed*max(
```

```matlab
                     Reference(:));
 91        elseif strcmpi(localorglobal,'local')
 92            dosed = Reference *dosed;
 93        end
 94        for i = 1:size1(1)
 95            for j = 1:size1(2)
 96                for k = 1:size1(3)
 97                    if Reference(i,j,k) < minLim || i<3 ||i>
                           size1(1)-3 || j<3 ||j>size1(2)-3 || k<3
                           ||k>size1(3)-3 %This part skips "
                           unessecary" pixels
 98                        G(i,j,k) = 0;
 99                         continue
100                    end
101                %fprintf('i=%d, j=%d, k=%d \n',i,j,k)
102                %fprintf('i=%d, j=%d, k=%d \n',RefposX(i),
                       RefposY(j),RefposZ(k))
103                doseDiffSave = ((Reference(i+2,j+2,k+2)-
                       Evaluated(RefposX(i)+searchRange+x,RefposY(j
                       )+searchRange+y,RefposZ(k)+searchRange+z)));
                       %/dosed).^2;
104                doseDiff = (doseDiffSave./dosed(i,j,k)).^2;
105
106                Ga = DTAMatrix + doseDiff;
107                %minimum of Gamma
108                G(i,j,k)=min(Ga(:));
109                end
110            end
111            iter = iter + 1;
112            waitbar(iter/total,wBar)
113        end
114
115  end
116  G = sqrt(G);
117        waitbar(total/total,wBar)
118        fprintf('Elapsed time for gamma evaluation: %6.4f
            seconds\n',toc);
119  close(wBar)
120  %Removes the added border.
121  if size1 == size2
122      G(1:searchRange,:,:) = [];
123      G(:,1:searchRange,:) = [];
124      G(:,:,1:searchRange) = [];
125      G(size1(1)+1:size1(1)+searchRange,:,:) = [];
126      G(:,size1(2)+1:size1(2)+searchRange,:) = [];
127      G(:,:,size1(3)+1:size1(3)+searchRange) = [];
128  end
```

Appendix B

Calculated Dose Distributions

All calculated dose distributions are presented visually here with 1 mm resolution. Scale is in Gy.

(a) Field 1

(b) Field 2

(c) Field 3

(d) Field 4

(e) Field 5

(f) Field 6

(g) Field 7

(h) Field 8

(i) Field 9

Figure B.1: Calculated fields from OMP, 1 mm resolution, scale in Gy.