Diagnostic Medical Image Processing

Summary

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This is a Summary of Diagnostic Medical Image Processing given by Prof. Hornegger. The Theory should be correct in the most cases (read critical) and i never corrected the language, so you will find probably a lot mistakes :). The summary is primarily based on the lecture record, all information is taken out of the record the slides and Larry Zeng's Book.

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1. Math

1.1. Matricies

Nullspace

The nullspace of a matrix is:

$$\mathbf{A}\vec{x} = \vec{0} \tag{1.1}$$

which means all vectors $\vec{x}$ which fullfill the equation are the nullspace of $\mathbf{A}$.
All Matrices have the trivial nullspace: $\vec{0}$.
If a Matrix have a non-trivial nullspace, than this is a clear idicator that this matrix cannot be inverted because the matrix have a rank deficiency.

Rank

The rank of a Matrix is the dimension of the collumn-space. The rank tells you the number of linearly independent Collumn-Vectors.

$$\mathbf{A} = \begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix} = (\vec{a_1}, \vec{a_2}) \tag{1.2}$$

pseudo-inverse

If a Matrix cannot be inverted you can compute the pseudo-inverse, which is as close as possible to the potential inverse.

1.2. SVD

The SVD can compute the pseudo-inverse of a Matrix. You can ignore the rank and all the important stuff you have to know wether a matrix can be inverted or not.

- If the Matrix can be inverted then the SVD will give you the inverse of the Matrix !
- If the Matrix cannot be inverted then the SVD will give you the pseudo-inverse of the Matrix !

SVD is a perfect tool for the:

- computation of singular values
- computation of null space
- computation of (pseudo-)inverse
- solution of overdetermined linear equations
- computation of condition numbers
- enforcing rank criterion (numerical rank)

1.3. Fourier Transform

1.3.1. Symmetry Property of Fourier Transform

There exists a nice property for a real valued discrete signal of length N:

$$F(\xi) = \bar{F}(N - \xi) \tag{1.3}$$

If $F(\xi)$ is real-valued Function the Fourier transformed goes from $[0; N-1]$ elements. The Fourier transform at the point ξ is the conjugate at the Point $\bar{F}(N-\xi)$.

1.3.2. Dirac's δ-function

The δ-function is defined as:

$$\delta(n) = \begin{cases} 1, & \text{if n=0} \\ 0, & \text{otherwise} \end{cases}$$

You can use Dirac's δ-function to select single values in the frequency domain:

$$F(k) = \hat{F}(s) \cdot \delta(k - s)$$

Only when $s = k$ Dirac's δ-function will be not Zero and you get the value at position k.

1.3.3. Hilbert Transform

the Hilberttransform $h(\tau)$ is used for convolution and the spatial/frequency domain pair is:

$$h(\tau) = \frac{1}{\pi\tau}$$
$$H(\omega) = -i\ sgn(\omega)$$

1.4. Statistics

1.4.1. Entropy and Kulback-Leibler Divergence

Entropy

The Entropy measures how close your pdf of the intensity values are to the uniform distribution. The higher the Entropy the closer your pdf of your intensity values look like the pdf of the uniform distribution. The Entropy of a discrete random variable X is defined by:

$$H(X) = -\sum_{i=1}^{n} p(x_i)\log p(x_i)$$

If you measures the KL-Divergence from an pdf to the uniform distribution then you get the Entropy formula above.

KL - Kulback Leibler Divergence

With the Kulback Leiber Divergence you can measure the similarity of two pdfs. You could use:

$$\int \left((p(x) - q(x))^2 \right) dx$$

but with this equation you have the problem that you run into problems if your random variables have different quantisations.
So instead you should use the KL-Divergence:

$$KL(p,q) = \sum_{i=1}^{n} p(x_i)\log\frac{p(x_i)}{q(x_i)} \tag{1.4}$$

Properties of the KL-Divergence:

- $KL(p,q) \neq KL(q,p)$
- $KL(p,q) \geq 0$
- $KL(p,q) = 0 \Leftrightarrow p = q$
- $KL(p,q) \to 0$ if $p \to q$

1.4.2. Independency

When are two random Variables X, Y statistically independent?

- $p(x)$ pdf of X
- $q(y)$ pdf of Y
- $p(x,y)$ joint pdf
- $p(x) \cdot q(y) = p(x,y)$

They are independent when you can factorize the joint pdf.

1.4.3. Regularizer

A closer look to the regularize in the probabilistic context:
where c is the estimated and x the observation:

$$p(c|x) = \frac{p(x,c)}{p(x)} = \frac{p(c) \cdot p(x|c)}{p(x)}$$

for the maximization w.r.t. c $p(x)$ can be ignored, because it does not affect the position of the maximum only the value:

$$\arg\max_c p(c|x) = \arg\max_c p(c)p(x|c) = \arg\max_c \underbrace{\log p(c)}_{\text{regularizer}} + \underbrace{\log p(x|c)}_{\text{data term}}$$

where the data Term $p(x|c)$ contains the information, the observation and $p(c)$ only depends on the class that we considering, which is prior or the regularize.
The regularize only holds information on the classes we want to estimate. So a regularize is just use the objective function (data Term) and adds another term to the objective functions which depends not on the observation only on the parameters ! (is also called prior knowledge because you don't look at the measurements) **take of using prior knowledge in medicine, because patients are usually persons which are not belong to the average**

1.4.4. Marginalization - Hidden Random Variables

If you have a PDF $p(X, Y, Z)$ then the following counts:

$$\int\int\int p(X,Y,Z)dXdYdZ = 1 \tag{1.5}$$

to get the probability of observing X without knowing some thing about Y and Z. You can integrate over Y and Z to get $p(X)$:

$$\int\int p(X,Y,Z)dYdZ = p(X) \tag{1.6}$$

in other words, you can eliminate random Variables by marginalization.

1.5. Homogeneous Coordinates

A two-dimensional point in Cartesian coordinates $p = (x, y)^T \in \mathbb{R}^2$ is represented by $(wx, wy, w)^T \in \mathbb{P}^2$ in homogeneous coordinates, where $w \in \mathbb{R}$ is an arbitrary real valued constant.
A Vector in homogeneous coordinates can be transformed back to Cartesian coordinates by dividing the components with the last component ($\neq 0$).
A 2-D point $(x, y)^T$ in Cartesian coordinates corresponds to a line in 3-D:

$$\begin{pmatrix} x \\ y \end{pmatrix} \to w \cdot \begin{pmatrix} x \\ y \\ 1 \end{pmatrix} \qquad \text{where } w \in \mathbb{R} \tag{1.7}$$

There exists an infinite number of homogeneous points that correspond to one and the same 2-D point!

1.5.1. Rotation and Translation

normally you have to multiply the rotation matrix from the left side and add a 3D translation vector t:

$$\begin{pmatrix} x' \\ y' \\ z' \end{pmatrix} = \mathbf{R} \begin{pmatrix} x \\ y \\ z \end{pmatrix} + t \tag{1.8}$$

if you use homogeneous coordinates you can incorporate the translation:

$$\begin{pmatrix} x' \\ y' \\ z' \\ 1 \end{pmatrix} = \begin{pmatrix} R_{11} & R_{12} & R_{13} & t_x \\ R_{21} & R_{22} & R_{23} & t_y \\ R_{31} & R_{32} & R_{33} & t_z \\ 0 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} \tag{1.9}$$

2. PreProcessing

2.1. Disortion & Interpolation

2.2. Detectors

The Image quality is defined by three major components.

- Noise
- spatial Resolution
- contrast resolution

2.2.1. DQE - Measurement

The detective quantum efficiency (DQE) is a important measurement of a Detector.
$\mathbf{DQE} = \frac{\text{SNR}^2(f)_{out}}{\text{SNR}^2(f)_{in}}$

2.3. Defect Pixel Interpolation

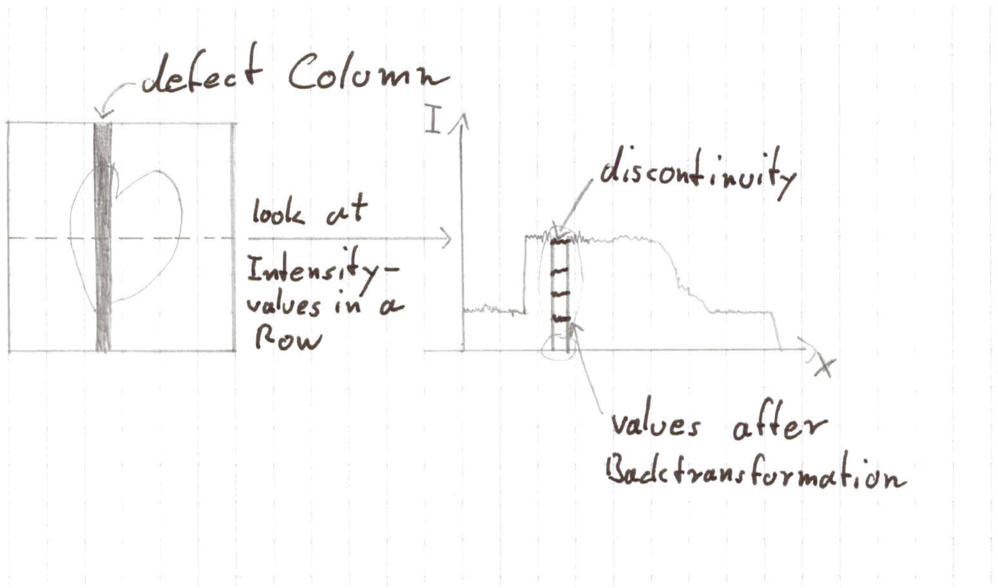
In Interpolation you hit the sampling points exactly, not like regression where you fit a line with the smallest error. Or like extrapolation, where you try to find a sampling point outside your interval of sampling Points.

2.3.1. Defect Pixel

The mathematical model for defect generation is just the multiplication of the original image with a defect mask. Let $f_{i,j}$ denote the intensity value at

$$w_{i,j} = \begin{cases} 1, & \text{if pixel is defect} \\ 0, & \text{otherwise} \end{cases}$$

Defect Pixel Interpolation by band limitation

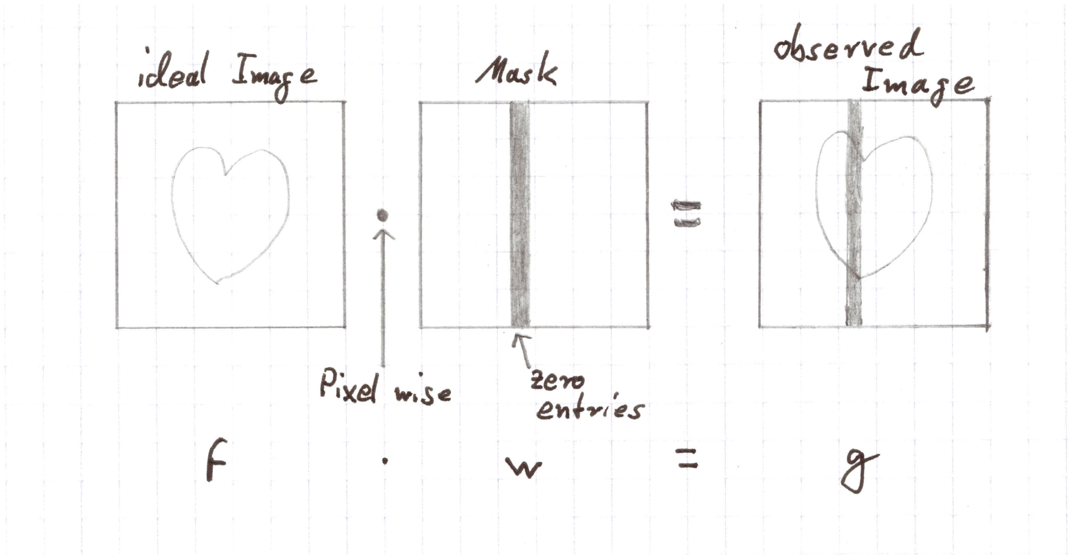


the discontinuity leads to a Signal which have high frequencies and is not band-limited any more ! So the Fourier transform run into the problem that the Fourier transform will not achieve zero values for a certain threshold ξ.
So take the Fourier transform of the signal with the defect and cut off all the frequencies that are larger than the Band-limitation b of the Detector (this is given), back transform the signal and fill in the new values at the defect column.
This Values are not zero but you still have a huge difference. Repeat this proceeder iteratively, at the end you will get a signal which do not violate the band-limitation of the Signal.
Which is nothing else than a low pass filter but it is very important that you do not filter the whole image; only at the defect positions.

```
compute FT of input signal $g(n)$
    set $G(\xi) = 0$ for $\xi > B_u$ or $\xi < B_l$,
    compute inverse FT of corrected $G(\xi)$
    Replace defect samples in $g(n)$ by values of inverse FT
UNTIL  changes are below a threshold
```

- Band limitation must be known
- its computationally expensive, because each iteration requires twice the Fourier transform.
- If the defect is at the border of the observed interval, its a case of extrapolation the results aren't that good.

Frequency Domain Defect Pixel Interpolation



We can interpret our defect Image g as a product of the ideal Image f and a defect mask w. This cant be inverted because the mask contains zero entries (defect Pixels).

$$f(n) \cdot w(n) = g(n)$$
$$F(\xi) * W(\xi) = G(\xi)$$

But we can look in the frequency Domain, where we can compute a deconvolution! All three, the ideal, the mask and the defect Image the Fourier transform satisfies the symmetry property (all three are real valued):

$$F(\xi) = \bar{F}(N-\xi)$$
$$W(\xi) = \bar{W}(N-\xi)$$
$$G(\xi) = \bar{G}(N-\xi)$$

Instead of looking at the whole Fourier transform we only look on the symmetric pairs $G(s)$ and $G(N-s)$ from the corrupted Image and $F(s)$ and $F(N-s)$ from the ideal Image. With these Pairs we can rewrite the Fourier transform using Dirac's δ-function:

$$F(k) = \hat{F}(s)\delta(k-s) + \hat{F}(N-s)\delta(k-N+s)$$

So the Fourier transformation just consists of the too values at s and $N-s$ selected with the δ-function.
You can put that into the convolution; this gets reduced to two elements:

$$G(s) = \underbrace{\frac{1}{N}}_{\text{scaling}} \left(\hat{F}(s)W(0) + \hat{\bar{F}}(s)W(2s)\right)$$

The conjugate complex of this is:

$$G\bar{(}s) = \frac{1}{N}\left(\hat{\bar{F}}(s)\bar{W}(0) + \hat{F}(s)\bar{W}(2s)\right)$$

The $\hat{\bar{F}}(s)$ can be replaced by the original function $F(N-s)$.
Then we have two linear equations($G(s)$ and $\bar{G}(s)$) with two unknowns $F(s)$ and $F(N-s)$ so we can solve it.

$$\hat{F}(s) = N\frac{G(s)\bar{W}(0) - \bar{G}(s)W(2s)}{|W(0)|^2 - |W(2s)|^2}$$

where $|.|$ is the absolute value of the complex number.
This is not for the whole Fourier transform, its only for one pair. We can solve this equations for different Pairs and get estimates for the whole Fourier transform; transform F back and compare it to our measured Image.
So we can iterate over these different pairs and minimize the error between the measured Image and the back transformed Image f multiplied with our mask Image:

$$\Delta_\epsilon = \frac{1}{N}\sum_{n=0}^{N-1}(g(s) - w(n)\cdot f(n))^2 \tag{2.1}$$

```
compute FT of input signal $g(n)$
Initialize $\hat{F}^0(k) = 0$, $G^0(k) = G(k)$, $i = 1$
    Randomly select a line pair $s \neq 0$ $G^{i-1}(s) = G^{i-1}(N-s)$
    Estimate $\hat{F}^i(s)$, $\hat{F}^i(N-s)$ using (6)
    Update spectrum $\hat{F}^i(k)$, compute error $\Delta_\epsilon$ using (8)
    IF      error $\Delta_\epsilon$ above a threshold
    THEN Compute error spectrum $G^i(k)$, increment $i$
UNTIL  error are below a threshold
Compute inverse FT of $\hat{F}^i(k)$
```

2.4. MRT

The magnetic Field in space should be different in each spatial point. The MR-Scanner needs a gradient System which generates this special magnetic field and a RF-System. The RF-System contains a transmission and a receiver coil. The transmitter coil generates a rotating magnetic field for the excitation of a spin system(the nucleus have beside mass and charge their spin as a basic property), and the receiver coil converts magnetic charges in electrical system. So the transmitter causes changes in the System and the receiver coil measures this changes and convert this into intensity values.

Pros:

- patient care, no ionising Rays
- high spatial resolution($50\mu m$)
- excellent contrast resolution (discrimination of soft tissues)
- ...

Cons:

- inhomogeneities caused by radio frequency coil.
- intensity inhomogeneities produce spatial changes in tissue statistics. That means in an MR image the intensity value of water can be 5 but also 5000. Different intensities at different points in the Image may characterize the same molecular structure.
- inhomogeneities can change with different acquisition parameters, from patient to patient and from slice to slice

2.4.1. Intensity Inhomogeneities (IIH) in MRI

Their are different Reasons for inhomogeneities in MRI:

- non-uniform radio-frequency
- inhomogeneity of the static main field
- patient motion

There exists different mathematical models to describe the IIH:

- **Low-Frequency model**: It is assumed that IIH is caused by low-frequency components; the IIH map can be recovered by low-pass filtering

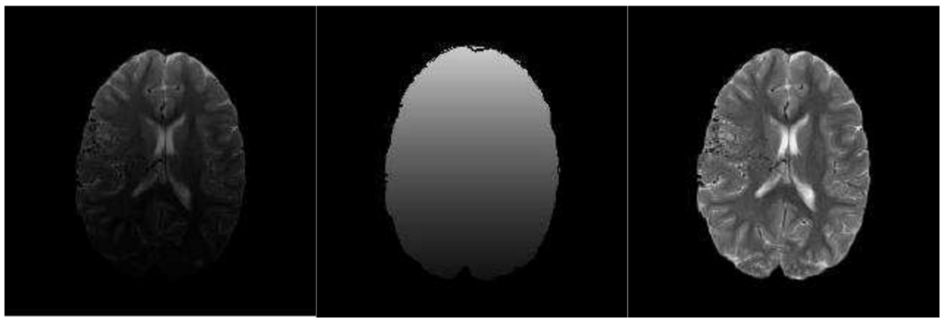


Abbildung 2.1.: Original MR Image(left),gain field (middle), restored image (right)

- **Hypersurface model**:IIH map is represented by a smooth (low-frequency) parametric function; the IIH map can be recovered by least-square-fitting (regression)
- **Statistical model**:IIH map is represented by a stochastic process; the IIH map can be recovered dependent on the selected statistical model by parametric or non-parametric statistical estimation

This multiplicative model is now a days the accepted model, earlier used additive models are not close enough the reality:

$$g_{ij} = f_{ij} \cdot b_{ij} + n_{ij} \tag{2.2}$$

where g_{ij} is the observed Image, f_{ij} the ideal Image and b_{ij} is the gain field and n_{ij} is the noise mostly set as a Gaussian noise. Correction methods mostly will applied to the product of f and b, the noise should be removed before. You can use a homomorphism and apply the logarithm to the equation above to replace the product with a summation.
Hint: if you use the logarithm you have to be aware of that the resulting noise is no Gaussian noise any more !

High pass filtering

The main Idea is to apply a high pass filter on the Image, because the bias field is generated by low frequencies. For a faster filtering transform the measured Image into the frequency domain using the Fourier transform and then multiply it with a high-pass filter Kernel H:

$$H_{k,l} = 1 - \beta \cdot e^{-\frac{k^2+l^2}{2\sigma^2}} \tag{2.3}$$

where β is a scaling factor that ensure that $H_{k,l}$ for all $k, l = 0, .., N-1$ and σ^2 is closely related to the bandwidth of the filter-kernel.
So you get your corrected Image f with:

$$f = \mathrm{FT}^{-1}\Big\{G_{k,l} \cdot H_{k,l}\Big\} \tag{2.4}$$

Homomorphic Filtering

This type of filtering assume IIH is:

- an artefact with low frequencies
- the anatomic structure contribute to the high frequencies in the image

The same assumptions like in the filtering before, but this time we go another way. The main idea is to do a low-pass filtering to get the bias field and subtract this from the measured Image.
Homomorphic filtering is applied to log-transformed images:

- low-pass filterung of the log-transformed image (LFP denotes a low pass filter):

  $$[h_{i,j}] = \mathrm{LPF}([\log g_{i,j}]) \tag{2.5}$$

- IIH corrected log-transformed image results from the difference:

  $$[\log f_{i,j}] = [\log g_{i,j}] - [h_{i,j}] + \mu \tag{2.6}$$

  where μ assures that IIH correction is mean preserving. So you add here a mean-value, to make sure that you have a mean normalisation, you make sure that the final mean intensity value is in a certain range.

Homomorphic Unsharp Masking

Is apply a mean normalization. The idea is, that when you have a Image of the brain, for example, then you should have in patches of the Image the same mean-value, but as shown in Figure 2.1 that not true:

$$f_{i,j} = g_{i,j} \cdot \frac{\mu}{\mu_{i,j}} \tag{2.7}$$

where μ is the global mean of the Image and $\mu_{i,j}$ is the mean of the neighbourhood at pixel i, j.
Hint: take in consideration that this method implies that the local mean is the same

as the gloab mean, which is only true for some cases. A full body scan for example would violate this assumption!

Polynomial filtering

KL Divergence Minimization

It allows the incorporation of prior knowledge

Fuzzy C-means Clustering

The main idea is to use a probabilistic k-means algorithm. So you calculate the distance to the Clusters but incorporate the probability that the feature belongs to a Cluster.
The fuzzy C-means objective function for partitioning the observation into N_c clusters and allows one data point belong to more than one class:

$$J(x_1, x_2, ..., x_n) = \sum_{i=1}^{N_c} \sum_{k=1}^{n} a_{i,k}^d ||x_k - c_i||^2 \tag{2.8}$$

- Prior: number of tissue classes
- $c_1, c_2, ..., c_{N_c}$ are the prototypes of the clusters
- $x_1, x_2, ..., x_n$ are the data points, in ours case the logarithms of ideal intensities

The objective function has to be minimized with respect to $c_i, a_{i,k}$. The optimization needs the constraint that the probability that a feature belongs to a cluster sum up to one:

$$\text{minimize} \sum_{i=1}^{N_c} \sum_{k=1}^{n} a_{i,k}^d ||x_k - c_i||^2 \tag{2.9}$$

$$\text{subject to} \sum_{i=1}^{N_c} a_{i,k} = 1 \tag{2.10}$$

This can be solved with the Lagrange multiplier method.
There are few drawbacks we have to consider and incorporate into the Method, so we can apply it on the bias field correction:

- the current objective function with the probabilistic assignment of data points to classes does not consider dependencies of neighboring data points (intuition: neighboring data points most probably belong to the same class)

- probabilistic approach required mutually independent intensities The question now is, how can we incorporate dependencies of neighboring data points?

A solution for the first drawback is to incorporate a regularize (more Information about regularizer: 1.4.3):

$$J(x_1, x_2, ..., x_n) = \underbrace{\sum_{i=1}^{N_c}\sum_{k=1}^{n} a_{i,k}^d ||x_k - c_i||^2}_{\text{data Term}} + \underbrace{\sum_{i=1}^{N_c}\sum_{k=1}^{n} \frac{\lambda}{\#\mathcal{N}_k} a_{i,k}^d \sum_{x_r \in \mathcal{N}_k} ||x_r - c_i||^2}_{\substack{\text{data term whith prior;} \\ \text{incorporates neighbourhood}}} \quad (2.11)$$

The neighbourhood is considered in the following way: we can say, we sum over all the pixels(x_r) in a local neighbourhood ($\mathcal{N}_k$) and we compute the distance between the assigned class c_r to the currently considered class/cluster c_i, then we weight them also by probabilities ($a_{i,k}^d$) and scale them by the size of the neighbourhood ($\frac{\lambda}{\#\mathcal{N}_k}$).
Next step is to incorporate the bias field:
We replace the logarithm of ideal intensity value x_k using $x_k = y_k - \beta_k$ and minimize the optimization problem with respect to the probability a, the cluster c_i and the bias β:

$$\{\hat{\mathbf{A}}, \hat{c}_i, \hat{\beta}_i\} = \underset{\mathbf{A}, c_i, \beta_i}{\arg\min} \sum_{i=1}^{N_c}\sum_{k=1}^{n} a_{i,k}^d ||x_k - c_i||^2 + \sum_{i=1}^{N_c}\sum_{k=1}^{n} \frac{\lambda}{\#\mathcal{N}_k} a_{i,k}^d \sum_{x_r \in \mathcal{N}_k} ||x_r - c_i||^2$$

$$\text{subject to: } \sum_{i=1}^{N_c} a_{i,k} = 1 \text{ for all } k = 1, 2, ..., n$$

with this we try to compute the bias field β_k of pixel x_k.
This can be done with setting up the optimization with a Lagrange multiplier and at the end of the day we get close form solutions for all three parameters:

$$J_R = \sum_{i=1}^{N_c}\sum_{k=1}^{n}\left(a_{i,k}^d D_{i,k} + \frac{\lambda}{\#\mathcal{N}_k} a_{i,k}^d E_{i,k}\right) + \sum_{k=1}^{n} \eta_k (1 - \sum_{j=1}^{N_c} a_{j,k}) \quad (2.12)$$

$$\text{where } D_{i,k} = \|y_k - \beta_k - c_i\|^2 \quad (2.13)$$

$$E_{i,k} = \sum_{(y_r - \beta_r) \in (N)_k} \|y_r - \beta_r - c_i\|^2 \quad (2.14)$$

the computation of the zero crossings of the gradient results in the following estimator for the partition matrix:

$$\hat{a}_{i,k} = \frac{1}{\sum_{j=1}^{N_c} \left(\frac{\#\mathcal{N}_k D_{i,k} + \lambda E_{i,k}}{\#\mathcal{N}_k D_{j,k} + \lambda E_{j,k}} \right)^{\frac{1}{d-1}}} \tag{2.15}$$

..leads to Cluster Prototype Update:

$$\hat{c}_i = \frac{\sum_{k=1}^{n} a_{i,k}^d \left((y_k - \beta_k) + \frac{\lambda}{\#\mathcal{N}_k} \sum_{y_r \in \mathcal{N}_k} (y_r - \beta_r) \right)}{(1+\lambda) \sum_{k=1}^{n} a_{i,k}^d} \tag{2.16}$$

and to the Bias Field Estimator:

$$\hat{\beta}_k = y_k - \frac{\sum_{i=1}^{N_c} a_{i,k}^d \cdot c_i}{\sum_{i=1}^{N_c} a_{i,k}^d} \tag{2.17}$$

Probabilistic Correction of Bias Fields

Like in the fuzzy C-means-clustering this idea combines the bias field correction with an simultaneously image segmentation step.
But in this approach we want to compute the unbiased image where tissue classes of pixels (i.e. segmentation) and the bias field itself are unknown! So we don't know which pixel belongs to which class and at the same time we do not know which bias is present in this particular pixel.
The core Idea of this approach is to use the trick of Marginalization 1.4.4: We will characterize our Image by assuming the tissue classes are known, the bias field is known and we have an given observation and at the end we compute a probability for the given Image by integrate out the bias and integrating out the tissue classes with this marginalisation trick.
To use the **E**xpectation and **M**aximization Algorithm have to fit this idea into the following framework:

- observable random measurement: bias logarithmic intensity value
- hidden random measurement: tissue class for each pixel
- parameter estimation problem: computation of the bias field

Instead of saying the bias field is an unknown parameter, we can also say the bias field is an hidden random variable, depends on how we want to Setup the estimation

problem. This is an incomplete data estimation problem.
The used probabilistic model consists of the following components:

- logarithmic intensity Values $x_{i,j} = \log g_{i,j}$ belonging to tissue classes Γ are normally distributed:

$$p(x_{i,j}|\Gamma;\beta_{i,j}) = \mathcal{N}(x_{i,j};\mu_\Gamma + \beta_{i,j}, \Sigma_\Gamma) \tag{2.18}$$
$$= \frac{1}{\sqrt{|2\pi\Sigma_\Gamma|}} e^{-\frac{1}{2}(x_{i,j}-\mu_\Gamma-\beta_{i,j})^T \Sigma_\Gamma^{-1}(x_{i,j}-\mu_\Gamma-\beta_{i,j})} \tag{2.19}$$

  where

  - $x_{i,j}$: observed log intensity
  - Σ_Γ: covariance matrix of tissue class Γ
  - $\beta_{i,j}$: bias at point (i,j)
  - μ_Σ mean log intensity of tissue class Σ

- prior probability of tissue class,i.e. without considering any observation (you get this from an anatomic Atlas):

$$p(\Gamma), \text{for} \qquad \Gamma = 1, 2, ..., N \tag{2.20}$$

- prior density of bias field:

$$p(\beta_{i,j} = \mathcal{N}(\beta_{i,j}; 0, \Sigma_\beta)) \tag{2.21}$$

  that means the parameters we want to estimate, they also underlay a certain PDF. For example if you look at the low frequencies changes in MR Images and if you see its brighter on one side and darker on the other side and fit in a PDF that characterizes this behaviour.
  We Assume the bias field is Normally-Distributed (it works !)

- elimination of unknown tissues class Γ by marginalization:

$$p(x_{i,j};\beta_{i,j}) = \sum_{\Gamma=1}^{N} p(\Gamma)p(x_{i,j}|\Gamma;\beta_{i,j}) \tag{2.22}$$

  which means we built up a probabilistic model where we assume we know the class assignment $p(\Gamma)p(x_{i,j}|\Gamma;\beta_{i,j})$. But we don't know the class assignment, so we use marginalization to get rid of the class assignment. For this we multiply our model with the prior knowledge that a certain tissue class occurs and sum up over all tissue classes.

Due to the fact that $p(\beta_{i,j})$ is assumed to be Gaussian, the bias field is now considered as a random variable. We do estimate the bias field $\beta = [\beta_{i,j}]$ by the maximization of posteriors given the logarithmic image $\mathbf{x} = [x_{i,j}]$:

$$\hat{\beta} = \arg\max_{\beta} p(\beta|\mathbf{x}) = \arg\max_{\beta}(\log p(\beta) + \log p(\mathbf{x}|\beta)) \tag{2.23}$$

with the Assumption that the Intensities are **mutually independent** we can compute the joint density for the whole Image by multiply over all pixels the probability that we observe this intensity $x_{i,j}$ given the bias $\beta_{i,j}$ (commonly used simplification !):

$$p(\mathbf{x}|\beta) = \prod_{i,j} p(x_{i,j}|\beta_{i,j}) = \prod_{i,j} \sum_{\Gamma=1}^{N} p(\Gamma)p(x_{i,j}|\Gamma, \beta_{i,j}) \tag{2.24}$$

The estimation of the bias field can be done iteratively, but the current model includes hidden variables. In total, we have to estimate the following parameters using the EM-Algorithm:

- bias field β
- covariance Σ_Γ
- priors $p(\Gamma)$
- means μ_Γ and covariances σ_Γ

Once all the parameters are estimated, the segmentation result is required. The final tissue class of each pixel can be estimated by the maximization of the posteriors:

$$\hat{\Gamma} = \arg\max_{\Gamma} p(\Gamma|\vec{x}_{i,j}; \beta_{i,j}) \tag{2.25}$$

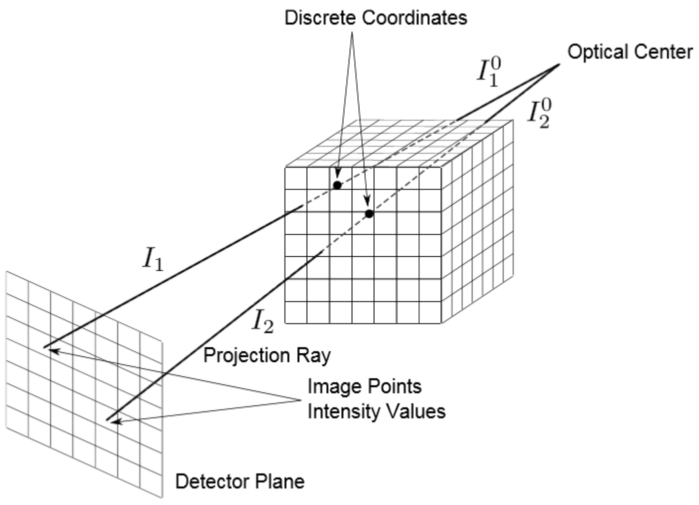
$$= \arg\max_{\Gamma}(\log p(\Gamma) + \log p(x_{i,j}|\Gamma; \beta_{i,j})) \tag{2.26}$$

Remark: in practice the bias field is not estimated for all components $\beta_{i,j}$. but usually approximated by a parametric function:

$$\beta_{i,j} = \sum_{k=0}^{M} \theta_k \phi_k(i, j) \tag{2.27}$$

where we have $\theta_k \in \mathbb{R}$ and ϕ_k are proper base functions. The bias field estimation thus reduces to the computation of the θ_k's. The Parameters can be estimated with the EM-Algorithm

3. Projection and Homogeneous Coordinates



We have to find a representation of the Projection Ray's to handle the reconstruction Problem.

3.0.2. Projections

There existing different Projection Models:

- Orthographic projection

$$\begin{pmatrix} x \\ y \\ z \end{pmatrix} \rightarrow \begin{pmatrix} x \\ y \end{pmatrix} \tag{3.1}$$

  which is a linear mapping and can be written in homogeneous coordinates.

- Weak perspective projection

$$\begin{pmatrix} x \\ y \\ z \end{pmatrix} \rightarrow \begin{pmatrix} k \cdot x \\ k \cdot y \end{pmatrix} \tag{3.2}$$

  which is a linear mapping and can be written in homogeneous coordinates.

- Perspective projection

$$\begin{pmatrix} x \\ y \\ z \end{pmatrix} \rightarrow \begin{pmatrix} f \cdot x/z \\ f \cdot y/f \end{pmatrix} \tag{3.3}$$

  where f is the distance to the image plane to origin.
  This is a **non-linear mapping** of the points !

The projection model of X-Ray systems can be approximated by perspective projection. A downside is that this model is not a linear one. But we can fix this with Homogeneous Coordinates.
We will now formulate projections from 3D to 2D using Homogeneous coordinates:

- Orthographic Projection in homogeneous coordinates id defined by:

$$\tilde{\mathbf{P}} = \begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} \rightarrow \begin{pmatrix} x \\ y \\ 1 \end{pmatrix} \qquad \tilde{\mathbf{P}}' = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \tilde{\mathbf{P}} \tag{3.4}$$

  this mapping from $\mathbb{P}^3 \rightarrow \mathbb{P}^2$ can be simply written in matrix form as:

$$\begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} \rightarrow \begin{pmatrix} x \\ y \\ y \end{pmatrix} \Rightarrow \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} = \begin{pmatrix} x \\ y \\ 1 \end{pmatrix} \tag{3.5}$$

- Perspective Projection in homogeneous coordinates is defined by:

$$\tilde{\mathbf{P}} = \begin{pmatrix} x \\ y \\ 1 \end{pmatrix} \to \begin{pmatrix} f \cdot \frac{x}{z} \\ f \cdot \frac{y}{z} \end{pmatrix} \to \begin{pmatrix} fx \\ fy \\ z \end{pmatrix} \qquad \tilde{\mathbf{P}}' = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix} \tilde{\mathbf{P}} \tag{3.6}$$

  where f is the focal length!
  this mapping from $\mathbb{P}^3 \to \mathbb{P}^2$ can be simply written in matrix form as:

$$\begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} \to \begin{pmatrix} x \\ y \\ z \end{pmatrix} \Rightarrow \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & \boxed{1} & \boxed{0} \end{pmatrix} \begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} = \begin{pmatrix} x \\ y \\ z \end{pmatrix} \tag{3.7}$$

Both orthographic Projection and Perspective Projection can be written in terms of a linear Mapping, both matrices differ only in the red marked elements.

3.1. Extrinsic Camera Parameters

Extrinsic Parameters are the translation and rotation which are applied to the Camera in the 3D-World. There existing 6 extrinsic Parameters: 3 Translation $(x, y, z)^T$ and 3 rotations.
To get an affine linear mapping we can use homogeneous coordinates (1.5.1). Then it is just a matrix multiplication from the left side:

$$\begin{pmatrix} x' \\ y' \\ z' \\ 1 \end{pmatrix} = \mathbf{D} \begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix} \tag{3.8}$$

where $\mathbf{D}$ include the rotation and the translation and is a 4×4 Matrix for the extrinsic Parameters.

3.2. Intrinsic Camera Parameters

The intrinsic Camera parameters have 5 degrees of Freedom:

- the angle of the CCD-Chip (1 degrees of Freedom)
- the scaling in X-Y Direction, because we have non-rectangular Pixels (in this scaling the focal length included) (2 degrees of Freedom)
- the ideal coordinate System, which is used for the discussion, has an offset $(u,v)^T$ regarding to the coordinate System of the CCD-Chip(2 degrees of Freedom). The origin of the ideal coordinate system is defined by the optical axes (the X-Ray which hits the image plane orthogonal), this is the offset.

The intrinsic parameters do not change if the camera moves. the mapping for the

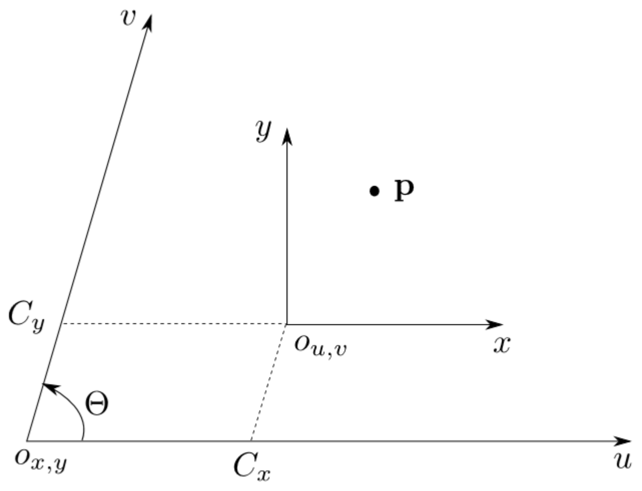


Abbildung 3.1.: $(u;v)$ detector and $(x;y)$ image coordinate system

figure above we get by looking at the base-vectors and their difference:

$$\vec{x} = \begin{pmatrix} 1 \\ 0 \end{pmatrix} \curvearrowright \begin{pmatrix} \frac{1}{k_x} \\ 0 \end{pmatrix} \qquad \vec{y} = \begin{pmatrix} 0 \\ 1 \end{pmatrix} \curvearrowright \begin{pmatrix} \frac{1}{k_y}\cos\theta \\ \frac{1}{k_y}\sin\theta \end{pmatrix} \tag{3.9}$$

the required transform from (x,y) to the (u,v) coordinate system is given by the inverse of the matrix:

$$\mathbf{T} = \begin{pmatrix} \frac{1}{k_x} & \frac{1}{k_y}\cos\theta \\ 0 & \frac{1}{k_y}\sin\theta \end{pmatrix}^{-1} = \begin{pmatrix} k_x & -k_x\frac{\cos\theta}{\sin\theta} \\ 0 & \frac{k_y}{\sin\theta} \end{pmatrix} \tag{3.10}$$

We can combine $\mathbf{T}$ and the displacement Vector $(c_x, c_y)^T$ using homogeneous coordinates to get the intrinsic camera parameter matrix $\mathbf{K}$:

$$\mathbf{K} = \begin{pmatrix} T_{11} & T_{12} & -c_x \\ T_{21} & T_{22} & -c_y \\ 0 & 0 & 1 \end{pmatrix} \tag{3.11}$$

3.3. Complete Projection

Now we can put all Matrices we have thought about in one step and get the Projection matrix $\mathbf{P}$:

$$\rho\tilde{q} = \mathbf{P} \cdot \tilde{p} = \mathbf{K} \cdot \mathbf{P}_{\text{proj}} \cdot \mathbf{D} \cdot \tilde{p} \tag{3.12}$$

3.4. Calibration

We use a Calibration Pattern with Points where we know the coordinates:

$$x_i = \begin{pmatrix} x_1 \\ y_1 \\ z_1 \end{pmatrix}, \begin{pmatrix} x_2 \\ y_2 \\ z_2 \end{pmatrix}, \ldots, \begin{pmatrix} x_n \\ y_n \\ z_n \end{pmatrix} \in \mathbb{R}^3 \tag{3.13}$$

we observe with our X-ray system a set of 2D-Points:

$$\begin{pmatrix} u_1 \\ v_1 \end{pmatrix}, \begin{pmatrix} u_2 \\ v_2 \end{pmatrix}, \ldots, \begin{pmatrix} u_n \\ v_n \end{pmatrix} \in \mathbb{R}^2 \tag{3.14}$$

the Projection Matrix we want to estimate have 12 entries, whereby we are in homogeneous coordinate so our solution is unique up to a scaling (we lose here one degree freedom). So we have eleven unknowns to estimate. In other words we need eleven equations to solve this, and each Point on the Calibration Pattern gives us two equations, which means we need at least 5.5 Points to solve this estimation Problem.

with our Projection Matrix $\mathbf{P}$ we know the mapping between these points, up to scaling w_i:

$$\forall i : \begin{pmatrix} w_i \cdot u_i \\ w_i \cdot v_i \\ w_i \end{pmatrix} \hat{=} \mathbf{P} \begin{pmatrix} x_i \\ y_i \\ z_i \\ 1 \end{pmatrix} \Leftrightarrow \begin{pmatrix} r_1^T \\ r_2^T \\ r_3^T \end{pmatrix} \begin{pmatrix} x_i \\ y_i \\ z_i \\ 1 \end{pmatrix} = \begin{pmatrix} \vec{r}_1^T \vec{x}_i \\ \vec{r}_2^T \vec{x}_i \\ \vec{r}_3^T \vec{x}_i \end{pmatrix} \hat{=} \begin{pmatrix} u_i \\ v_i \\ 1 \end{pmatrix} \tag{3.15}$$

Hint: there is a change from the x component to the complete vector $\vec{x}_i$, take care of this !
This formulation, where we split up our Projection matrix into the rows $\vec{r}_1^T, \vec{r}_2^T$ and $\vec{r}_3^T$, leads to:

$$u_i = \frac{\vec{r}_1^T \vec{x}_i}{\vec{r}_3^T \vec{x}_i} \qquad v_i = \frac{\vec{r}_2^T \vec{x}_i}{\vec{r}_3^T \vec{x}_i} \tag{3.16}$$

to get the estimation of the rows, we can set up a least square estimator:

$$u_i - \frac{\vec{r}_1^T \vec{x}_i}{\vec{r}_3^T \vec{x}_i} \overset{!}{=} 0 \qquad v_i - \frac{\vec{r}_2^T \vec{x}_i}{\vec{r}_3^T \vec{x}_i} \overset{!}{=} 0 \tag{3.17}$$

because of the ratio, this is non-linear, but we can fix this by multiplying with the denominator:

$$u_i \cdot \vec{r}_3^T \vec{x}_i - \vec{r}_1^T \vec{x}_i = 0 \tag{3.18}$$

$$v_i \cdot \vec{r}_3^T \vec{x}_i - \vec{r}_2^T \vec{x}_i = 0 \tag{3.19}$$

and this is now linear in the components of the projection matrix and we can finally set up our least square estimator:

$$\hat{\mathbf{P}} = \arg\min_{\mathbf{P}} \sum_{i=1}^{N} \left[u_i \cdot \vec{r}_3^T \vec{x}_i - \vec{r}_1^T \vec{x}_i \right]^2 + \left[v_i \cdot \vec{r}_3^T \vec{x}_i - \vec{r}_2^T \vec{x}_i \right]^2 \tag{3.20}$$

$$\text{subject to: } \|\mathbf{P}\|_F = 1 \tag{3.21}$$

because $\mathbf{P}$ is unique up to scaling we incorporate the constraint that the Frobenius-norm[1] of $\mathbf{P}$ have to be equal to 1.
Rule of thumb: Always optimize differences in the image space resp. in space of observation.
This rule gets violated when we multiply with the denominator. But after multiplying with he denominator we have a linear optimization problem and get a closed form solution. Without multiplying with the denominator we have a non-linear opti-

[1]whichs means the sum of squares of the components of $\mathbf{P}$ have to be one

mization problem which is hard to solve, but we can optimize this with a numerical approach like Newton-Raphson Method and use the closed-form Solution as an Initialization, which leads to better results and due to the Initialization the method converges fast.
To make life easier, we can rewrite the linear part in matrix form, where the measurement matrix **M** will include the information on the 3-D calibration points and the measured 2-D points according the equations in 3.18. The equations in 3.18 looks then like:

$$\mathbf{M}\begin{pmatrix} p_{1,1} \\ p_{1,2} \\ \vdots \\ p_{3,3} \\ p_{3,4} \end{pmatrix} = 0 \tag{3.22}$$

with this, the calibration problem is reduced to the computation of the nullspace of measurement matrix **M**, which can be done using SVD. And due to our knowledge about the calibration parameters and the constraint we know that the rank of matrix **M** is 11 and thereby **M** have a non-trivial nullspace !
The objective function for this looks like:

$$\|\mathbf{Mp}\|^2 \rightarrow \min, \qquad \text{subject to } \|\mathbf{p}\|^2 = 1 \tag{3.23}$$

which can be done with the Lagrange multiplier method:

$$\mathbf{p}^T\mathbf{M}^T\mathbf{Mp} - \lambda(\mathbf{p}^T\mathbf{p} - 1) \rightarrow \min \tag{3.24}$$

compute the derivative and the zero crossings:

$$2\mathbf{M}^T\mathbf{Mp} - 2\lambda\mathbf{p} = 0 \tag{3.25}$$

which is nothing else then:

$$\mathbf{M}^T\mathbf{Mp} = \lambda\mathbf{p} \tag{3.26}$$

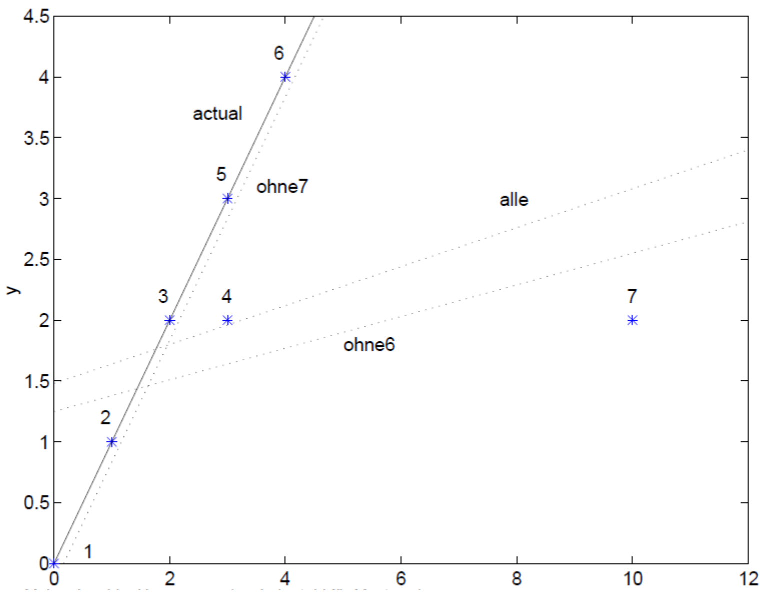
So the components of the projection matrix **P** result from the eigenvector belonging to the smallest eigenvalue. As mentioned above this linear estimate of **P** is an excellent initialization for the non-linear least square estimation of the projection matrix!

3.5. RANSAC

Problem in calibration are inaccuracies in observations and outliers, there are 2 types of outliers:

- badly localized points
- wrong correspondence

in figure 3.5 we can see the impact of those points.The dotted line „alle “ shows very good that a outlier like Point 7 can mess up the whole calibration progress. The **RAN**dom **SA**mple **C**onsensus, short RANSAC, algorithm try to handle this



problems:

- draw samples uniformly and at random from the input data set
- cardinality of sample set: smallest size sufficient to estimate the model parameters compute the model parameters for each element the sample data
- evaluate the quality of the hypothetical models on the full data set
- cost function for the evaluation of the quality of the model
- inliers: data points which agree with the model within an error tolerance
- The hypothesis which gets the most support from the data set: best estimate.

In the case of our calibration this means, draw randomly the minimal amount of Points (6) we need to estimate **P** from the data set, do the estimation and then use the estimated Projection matrix to compute the difference between the projected

Points and the measured Points. With this we can identify outliers and at the end we can use all good Points to estimate **P** without Points which affects the estimate badly.

4. Reconstruction

4.1. Thomography

the basic idea of Thomography is to solve the Puzzel in figure 4.1

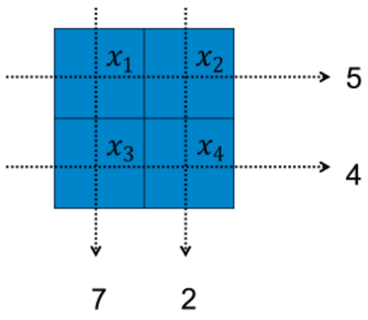


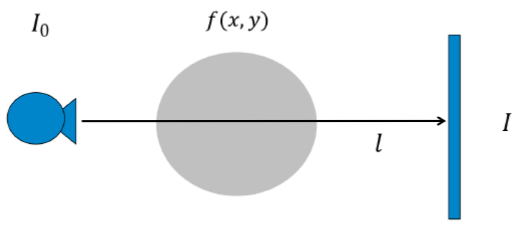
Abbildung 4.1.: basic Tomography Idea

$$\begin{aligned} x_1 &+ x_3 &= 7 \qquad x_1 &= 3 \\ x_2 &+ x_4 &= 2 \qquad x_2 &= 2 \\ x_1 &+ x_2 &= 5 \qquad x_3 &= 4 \\ x_3 &+ x_4 &= 4 \qquad x_4 &= 0 \end{aligned} \tag{4.1}$$

for real data this kind of method gets very fast very large, imagine a size of $512 \times 512 \times 512$ leads to 134 217 728 unknowns !

4.2. X-Ray attenuation Law - Beer's Law

The physical observation about X-Ray projection is that you start with an Intensity at the X-Ray source I_0 and the Object have a density function $f(x, y)$, which gives you a attenuation value in the space, and then the X-Ray hits the detector where we measure the Intensity I. The attenuation is characterized by the line Integral along



the line l, where you integrate the function of the object along the line l, which gives you the measured Intensity I: **Beer's Law** describes that in the way that we

$$\begin{aligned} I =& I_0 e^{-(\int f(x,y)dl)} \\ ln\frac{I}{I_0} =& -\int f(x,y)dl \qquad \overset{!}{=} p \end{aligned}$$

Abbildung 4.2.: Beer's Law

have an exponential decay along the line l from the original Value I_0 down to I. computing the function f of the object out of many line Integrals is more or less the problem of solving a system of integral equations, which is the reconstruction process. Radon has shown that if we have a infinite number of X-Ray projections you can reconstruct it properly, in practice a finite number of Projections is enough for meaningful reconstructions.
If we consider only those points that sit on the line going through the origin (see fig: 4.3), we can describe these lines with this equation:

$$\vec{n}^T\vec{x} - d = 0 \tag{4.2}$$

where $\vec{n}$ is the normal vector of the line. This equation is fulfilled if a point lies on the line and returns the signed distance to the line if not. We can rewrite the line integral to a double integral over all x- and y-values and preserve the line integral using Dirac's delta function 1.3.2. If the points lie on the Line Dirac's delta function

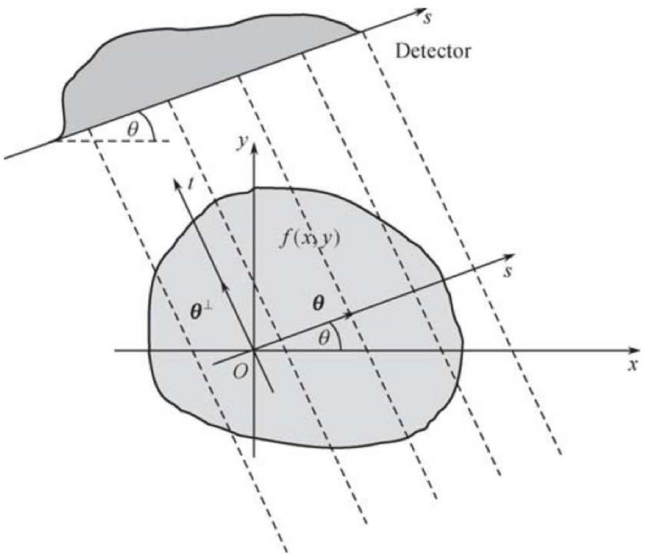


Abbildung 4.3.: parallel projection rays

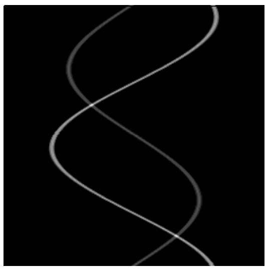


Abbildung 4.4.: The x-axis represents s and the y-axis represents the rotation-angle θ

give use 1 and otherwise 0, which means the double integral collapses down to the line integral. We get this reformulated formula:

$$p(s,\theta) = \int f(x,y)dl = \int\int f(x,y)\delta(x\cdot\cos\theta + y\cdot\sin\theta - s)dxdy \tag{4.3}$$

the parameter s is the offset if we move our straight line from the origin to another point (such that the line is still parallel to the line though the origin, like in figure 4.3) We can now follow a Detector-element over the acquisition process and build up a so called Sinogram, where on the x-axis we plot s and on the y-axis the rotation-angle. A point in the Rotationcenter will be a straight line, a point which is not in the Rotationcenter will shows a sinusoid-curve (simple Example with 2 Points 4.4). As a simple Example we reconstruct the Problem of 4.1, where **P** are the measurements and Matrix **A** represents the linear equations we set up 4.1:

$$\mathbf{P} = \mathbf{A}\mathbf{X} \tag{4.4}$$

$$\mathbf{P} = \begin{pmatrix} 7 \\ 2 \\ 5 \\ 4 \end{pmatrix}, \quad \mathbf{A} = \begin{pmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 \end{pmatrix}, \quad \mathbf{X} = \begin{pmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \end{pmatrix} \tag{4.5}$$

To solve the reconstruction Problem we have to Inverse **A** (which does not work, but pseudo-inverse works):

$$\mathbf{A}^{-1}\mathbf{P} = \mathbf{X}$$

But a Problem in practise is the size of the Matrix. Imagine we have a Object with $512 \times 512 \times 512$ we want to measure and our detector captures Images of size 512×512 and we do 512 projections from different Angles, this leads to the following Size of the Matrix:

$$\mathbf{A} \in \mathbb{R}^{512^3 \times 512^2 \times 512}, \qquad 512^6 \cdot 4\text{Byte} = 65536\text{TB}$$

so measuring a small object with a low resolution still needs a 65536 Terabyte for Matrix **A**!

4.3. Back-projection

A Idea of reconstruction is the Back-projection. Which means we smear back additive the measured values along the projection line: So we need a mathematical description

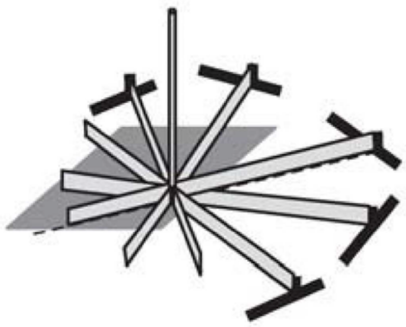


Abbildung 4.5.: smear back additive the measured Values

for Backprojection. Backprojection is the adjoint of projections, which is explicitly not the inverse of Projection. We described the Projection with the Matrix **A**, so the adjoint of a Matrix is its transposed. So the Backprojection is a Matrix multiplication with the transposed projection matrix:

$$\text{Projection: } \mathbf{A}\vec{x} = \vec{p}, \qquad \Rightarrow \qquad \mathbf{A}^T\mathbf{A}\vec{x} = \underbrace{\mathbf{A}^T\vec{p}}_{\text{Backprojection}} \tag{4.6}$$

Applying Backprojection on our introduction Example 4.1 we get: where $\vec{p}$ is the

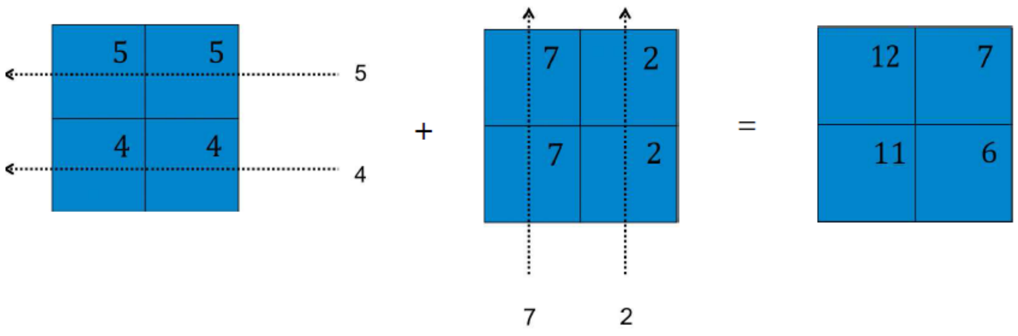


Abbildung 4.6.: smear back additive the measured Values

observed part (projections), $\vec{x}$ is function to be reconstructed and **A** is the system matrix which carries the Geometry (the Matrix is fixed by the Geometry-Setup) this are obviously not the correct Result, but the structure comes back up to scaling, if we look at the Values from the beginning we see that we have on the left side two higher values and on the right side to lower values and these value pairs are similar. This structure we can also see in 4.6.
The mathematical expression of this example is:

$$\mathbf{B} = \mathbf{A}^T\mathbf{P} \tag{4.7}$$

$$\mathbf{P} = \begin{pmatrix} 7 \\ 2 \\ 5 \\ 4 \end{pmatrix}, \qquad \mathbf{A}^T = \begin{pmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 \end{pmatrix}, \qquad \mathbf{B} = \begin{pmatrix} 12 \\ 7 \\ 11 \\ 6 \end{pmatrix} \tag{4.8}$$

which is only a intermediate-Step to get the result $\vec{x}$.
For the continuous case in Integral notation we get:

$$b(x,y) = \int_0^\pi p(s,\theta) \qquad \underbrace{|_{s=x\cos\theta+y\sin\theta}}_{\text{normal vector of the given line}} \qquad d\theta \tag{4.9}$$

so you sum up - integrate - over all considered rotation angles for a given line.
If you smear back all the Projections we get something like this: For a good Re-

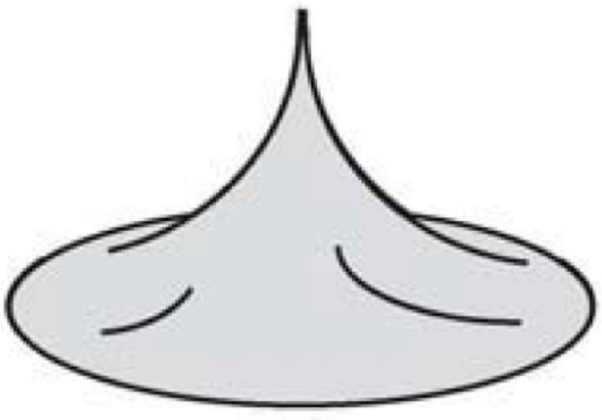


Abbildung 4.7.: smear back additive the measured Values

construction of the Point we need some „negative Wings“at the smearing back step such that only the Points gets reconstructed. This can be done with a filter step, but before introduce this filter which allows a good reconstruction we should look in the mathematical steps.

4.4. Central Slice Theorem

Beside beer's Law the Central Slice Theorem is the second core component for the function of CT and Reconstruction.
Basically the Central Slice Theorem says:

> The Fouriertransform of the Projection is equal to the 1-D Fouriertransform of the 2D-Object trough the Origin, parallel to the Projectionline (in our case the Detector)

This can be described in the (for the oral exam very important) Picture: **Picture Explanation:**
If you fouriertransform the Projection of the 2D-Object with the density Function

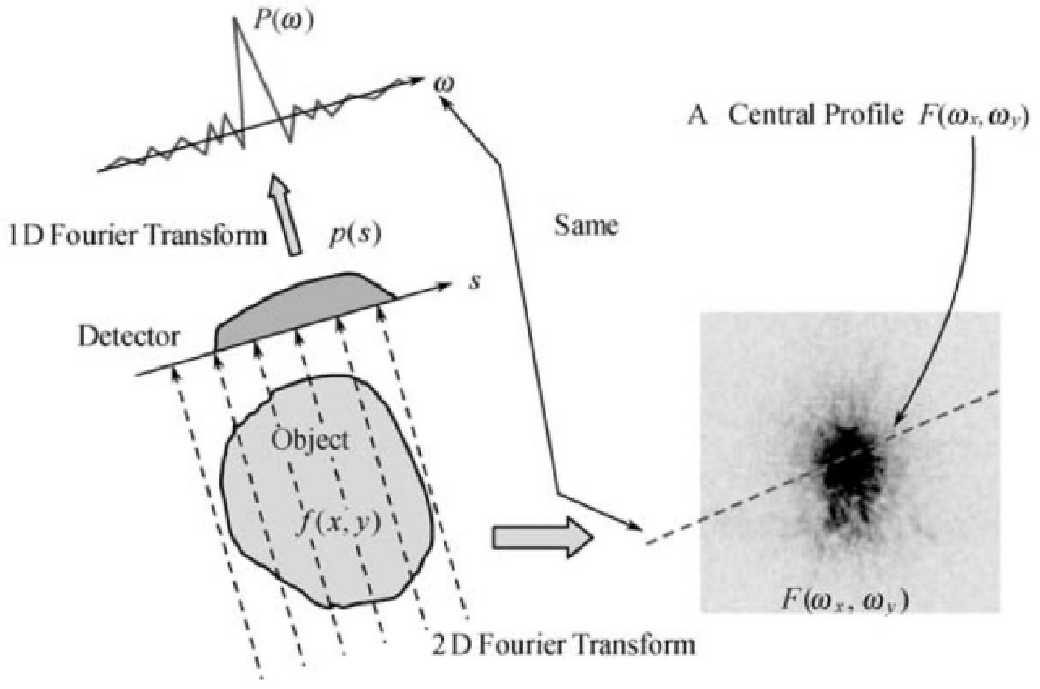


Abbildung 4.8.: Central Slice Theorem

$f(x, y)$, then you can find exactly that function on a line in the 2D-Frouriertransform of the Object which goes trough the Origin and is parallel to the Projection line. Of course the central slice theorem is a mathematical approach: Lets Fouriertransform the projection with the angle $\theta = 0$:

$$FT((s, 0)) = \int_{-\infty}^{\infty} p(s, 0) e^{2\pi i \omega s} ds$$

know look at how we get $p(s, 0)$: We project our object function $f(x, y)$ according to beer's law on the projectionline with the angle $\theta = 0$. So we just use the definition of the Projection: $p(s, 0) \int_{-\infty}^{\infty} f(x = s, y) dy$:

$$\int_{-\infty}^{\infty} \int_{-\infty}^{\infty} \underbrace{f(s, y) dy}_{p(s,0)} \quad e^{-2\pi i \omega s} \quad ds$$

rename s back to x (for easier reading) and bring $e^{-2\pi i\omega s}$ into the inner Integral (this is allowed because it does not depend on y):

$$\int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x,y)e^{-2\pi i\omega x}dx\ dy$$

and now add to the e-function in the exponent the value $(+0\cdot y)$:

$$\int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x,y)e^{-2\pi i\omega x+0\cdot y}dx\ dy$$

and this is the just the 2D-Fouriertransform at the point $\omega = 0$ in frequency Space! This can be generalized and shown that its true for all Angle θ.

4.5. Filtered Backprojection

Just start with the definition for the Projection:

$$P(\omega,\theta) = \int_{-\infty}^{\infty} p(s,\theta)e^{-2\pi i\omega s}ds$$

now take the definition for arbritrary Angle use the dirac's delta notation:

$$= \int_{-\infty}^{\infty}\int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x,y)\delta(x\cos\theta + y\sin\theta - s)dx\ dy e^{-2\pi i\omega s}\ ds$$

now we can reorganize the terms:

$$= \int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x,y)\int_{-\infty}^{\infty} \delta(x\cos\theta + y\sin\theta - s)e^{-2\pi i\omega s}\ ds\ dx\ dy$$

we can drop now the inner Integral because only for $x\cos\theta + y\sin\theta = s$ the dirac's delta function is not Zero:

$$= \int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x,y)e^{-2\pi i\omega(\underbrace{x\cos\theta + y\sin\theta}_{s})}\ dx\ dy$$

this looks like the 2D-Fouriertransform of the function $f(x, y)$, to make this more obvious we can write this more clear:

$$F(\omega\cos\theta, \omega\sin\theta) = \int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x,y)e^{-2\pi i((\underbrace{\omega\cos\theta}_{\zeta})\cdot x+(\underbrace{\omega\sin\theta}_{\eta})\cdot y)}\ dx\ dy$$

This is the 2D-Fouriertransform of $f(x, y)$ in **Polarcoordinates** ! IMAGE : EXPLAIN
The coordinate Transform needs to incorporate into the Integral:

$$f(x,y) = \int_{-\infty}^{\infty}\int_{-\infty}^{\infty} F(\zeta,\eta)e^{2\pi i(\zeta x+\eta y)}\ d\zeta\ d\eta$$

So we need here to apply a coordinate transform:

$$\zeta = \omega\cos\theta$$
$$\eta = \omega\sin\theta$$

to do this we need to multiply with the determinant of the Jacobian: the first column is the derivative with respect to ω and the second column with respect to θ:

$$\text{Jacobian} = \begin{pmatrix} \cos\theta & -\omega\sin\theta \\ \sin\theta & \omega\cos\theta \end{pmatrix} \Rightarrow \det \text{J} = \omega(\underbrace{\cos^2\theta + \sin^2\theta}_{=1}) = \omega$$

now we can write our integral with $\omega\cos\theta$ and $\omega\sin\theta$ and multiply it with the Determinant of th Jacobian as it is required for the coordinate transform:

$$\int_{0}^{2\pi}\int_{-\infty}^{\infty} |\omega|\underbrace{F(\omega\cos\theta,\omega\sin\theta)}_{2D-\text{Ft in Polar}}e^{2\pi i\omega(x\cos\theta+y\sin\theta)}\ d\omega d\theta$$

outer Integral (θ): the θ goes from 0 to 2π because we rotate around the whole object
inner Integral (Omega): the omega is just the scaling factor of our unit vector in terms of Polar coordinates, if you go from $-\infty$ to ∞ we count twice. We make the ω absolute because you always read only positive values: e.g. for the angle 15ř you just read the positive values of the vector, if you want the negative you just rotate to 195ř and read again only the positive values.

We know that the Fouriertransform of the function we look for in polarcoordinates is the same as the fouriertransform of all the projections. So we can replace $F(\omega\cos\theta, \omega\sin\theta)$ with the Fouriertransform of the Projections:

$$\int\limits_{0}^{2\pi}\int\limits_{-\infty}^{\infty} |\omega| \cdot P(\omega\cos\theta, \omega\sin\theta) \cdot e^{2\pi i\omega(x\cos\theta + y\sin\theta)} \quad d\omega d\theta$$

know we see a product of the Fouriertransform with the absolute Value $|\omega|$ which is in the spatial domain a Convolution ! So the determinant of the Jacobian is a Filter !

meaning of the Filter: because we sample the Fouriertransform of the function we look for in polar coordinates we have a lot of samples around the origin and less samples farer away from the origin. So we have to weight the view outer samples higher than the inner samples (where we have a lot from). And if you look the function of the absolute Value it does exactly this.

> So our Filter weights the inner Samples with lower weights and the outer Samples with higher weights !

The outer Integral (from 0 to 2π) is the Backprojection (smear it back) and the multiplication with $|\omega|$ is the Filter step. In practice the Filter needs some modifications. The absolute value function weights the sample in the origin with 0 because there we have theoretically an infinite number of Samples but in practice we have not. Also we cant integrate to ∞ so we need some point where we cut the absolute Value.

4.5.1. Reconstruction with Hilbert Backprojection

An alternative way for reconstruction is to use the Hilbert-transform. For this we have to rewrite the $|\omega|$ in the following way:

$$|\omega| = (2\pi i\omega) \cdot \left\{ \frac{1}{2\pi}[-i \; sign(\omega)] \right\}$$

the multiplication with $- \; sign(\omega)$ in frequency Domain is the Hilbert transform. Now we can describe the reconstruction as follows:

- Compute first derivative of the detector row (derivative w.r.t. s):

$$q_1(s, \theta) = \frac{\partial p(s, \theta)}{\partial s}$$

- Apply Hilbert Transform:

$$q_2(s,\theta) = \frac{1}{2\pi^2 s} * q_1(s,\theta)$$

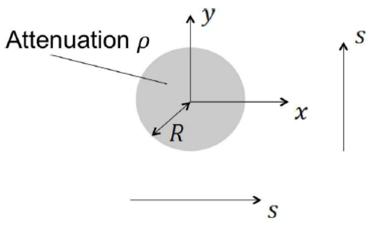
- Backproject $q_2(s,\theta)$:

$$f(x,y) = \int_0^{\pi} q_2(s,\theta)|_{s=x\cos\theta+y\sin\theta}\ d\theta$$

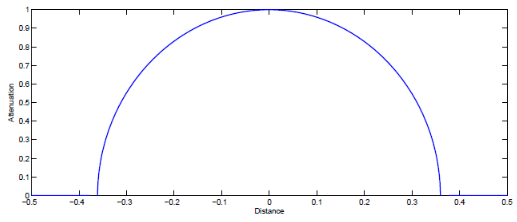
but take into consideration that we compute the first derivative. And the computation of derivatives from measured, and so noisy data, could be cause problems because the derivation can double the error in the worst case !

4.6. Practical aspects of FBP

Lets look at a very simple case, our object is a disk with Attenuation ρ The Back-



(a) Object



(b) Projection of the Object

projection could look like:

$$q(s,\theta) = h(s) * p(s,\theta) \qquad h(s) = \int_{-\infty}^{\infty} |\omega| e^{2\pi i\omega s} d\omega$$

$$f(x,y) = \int_0^{\pi} q(s,\theta)|_{s=x\cos\theta+y\sin\theta}\ d\theta$$

So the projections will be convolved with the Filterkernel $h(s)$. Here we get the problems shortly remarked in the FPB-section. A usable representation of the Filterkernel is to cut at $-\frac{1}{2}$ and $\frac{1}{2}$ and compute the spatial domain representation of this kernel:

$$h(s) = \int_{-\frac{1}{2}}^{\frac{1}{2}} |\omega| e^{2\pi i\omega s}\ d\omega \Rightarrow h(s) = \frac{1}{2}\frac{\sin \pi s}{\pi s} - \frac{1}{4}\left[\frac{\sin\frac{\pi s}{2}}{\frac{\pi s}{2}}\right]^2$$

and the discretisation of this is called the **Ram-Lack** convolver:

$$h(n) = \begin{cases} \frac{1}{4}, & n = 0 \\ 0, & n \text{ even} \\ -\frac{1}{n^2\pi^2}, & n \text{ off} \end{cases}$$

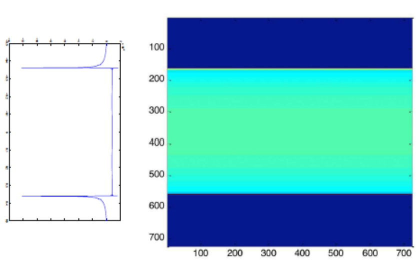
the discrete spatial form of the Kernel-filtering return a weight not 0 at the Origin, so it take into account that we have not an infinite number of Samples there(this number is only theoretical).
If we look at the computational complexity of the reconstruction:

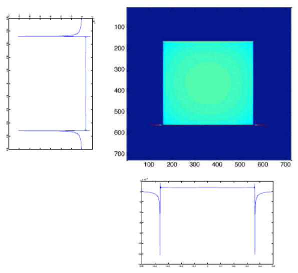
- Precompute filter $h(s)$ in spatial domain: $\mathcal{O}(N)$
- Transform filter to frequency domain $H(\omega)$ via FFT: $\mathcal{O}(N \log N)$
- For each of $\#P$ projections:
  - Compute FFT of $p(s, \theta)$: $\mathcal{O}(N \log N)$
  - Apply filter $P(\omega, \theta) \cdot H(\omega)$: $\mathcal{O}(N)$
  - Compute filtered projection $q(s)$ via FFT: $\mathcal{O}(N \log N)$

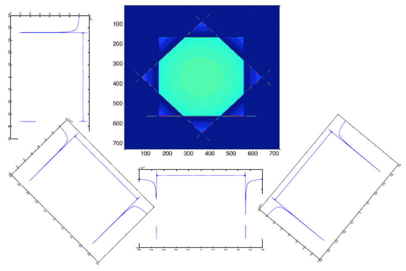
⇒ so we get a total complexity of:

$$\mathcal{O}(N + N \log N + \#P(N + 2N \log N)) = \mathcal{O}(\#PN \log N)$$

so the important aspect is here,**the complexitity** of the reconstruction **is linearly in the number of Projections** ($\#P$)


(c) Backprojection with one Projection


(d) Backprojection with two Projection


(e) Backprojection with four Projection

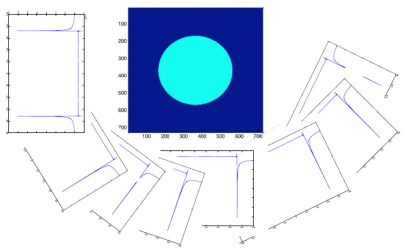
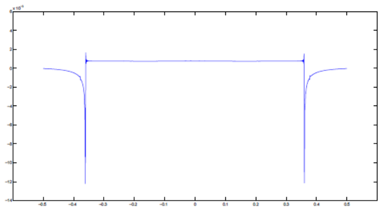

(f) Backprojection with all Projection

Abbildung 4.9.: Example Backprojection of one Slice from the disk-Object

Practical Problems with Noise

In the real world we use sensors and so we have to handle with Noise. Beside the analytical point of view the reconstruction Algorithm differ in the numerical handling of the noise data.
in this figure we can see, that the noisy Data are very dirty after Filtering. This


(a) Non-Noisy Projection convolved with the Ramp-Filter

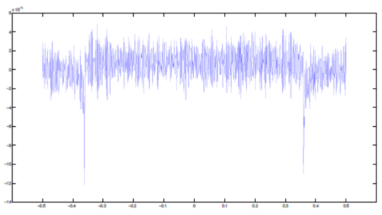
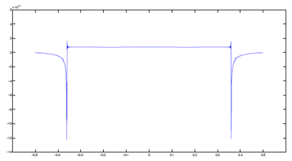

(b) Noise Projection convolved with the Ramp-Filter

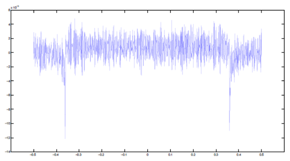
Abbildung 4.10.: Projection convolved with the Ramp-Filter

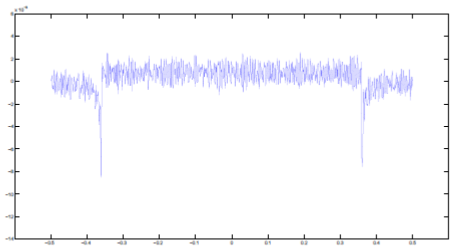
will definitively result into very bad reconstruction !
We can incorporate into the Filtering process a Windowing Function to smooth the Noise and reduce the bad impact. For this we can use the associative properties from Filters, so we multiply the Ramp-Filter with a Windowing-Filter and this combined

Filter we multiply with the Projection.
Possible Windowing-Filter:

- Rectangular Window (rectangular in frequency domain)
- Cosine Window: $cos(\pi x)$
- Shepp-Logan Window: $\frac{\sin(\pi x)}{\pi x}$


(a) Non-Noisy


(b) Noise Projection convolved with the Ramp-Filter


(c) Noise Projection convolved with the Shepp-Logan-Filter

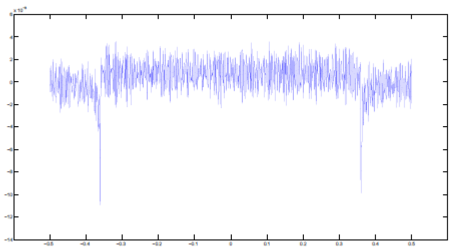

(d) Noise Projection convolved with the Cosin-Filter

Abbildung 4.11.: Example Backprojection of one Slice from the disk-Object

Obvious the Windowing gives us better results but they are different. The Shepp-Logan-Filter reduces the Noise-Impact very good, but we can see that the two spikes into the negative direction are not that „long“(badly for sharp edges). The cosine-Filter does not reduce the noise as good as shepp-logan but the negative spikes are longer. From this example we can summarize that the Filter we use for reconstruction depends to the result we want to have.
Summarize about Noise:

- Is amplified by ramp Filter
- Has to be taken care of an appropriate manner
- is indirectly proportional to the applied dose (we have low-dose Images because of the patient health)
- Affects different reconstruction methods differently (for example hits hilbert-approach due to the differentiation)

4.7. Fan Beam Geometry

All considerations above are done on the parallel beam Geometry, so the X-Rays are parallel. And now we want to look at geometries where the x-rays are not parallel. The Parallel beam algorithm cannot be applied directly anymore. We **do not** have

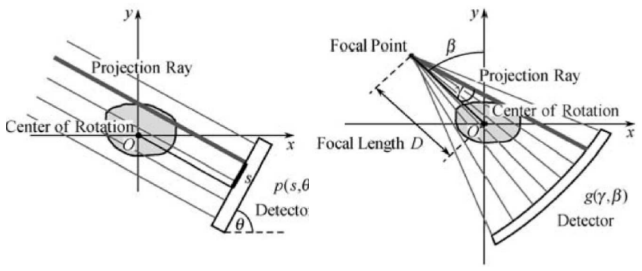


Abbildung 4.12.: left the considered parallel Beam geometry. Right the Fan Beam geometry we consider in this chapter

a central slice theorem anymore !

Basic Idea: is to use all acquired Images and reorganize the measured Values such that we get back the parallel beam geometry and with that the central slice theorem so we can reconstruct as we consider before.

in the Following some Examples how the Projection of the Object could change in Fan-Beam geometry setup: Before we come to the sketched Idea, we take a short

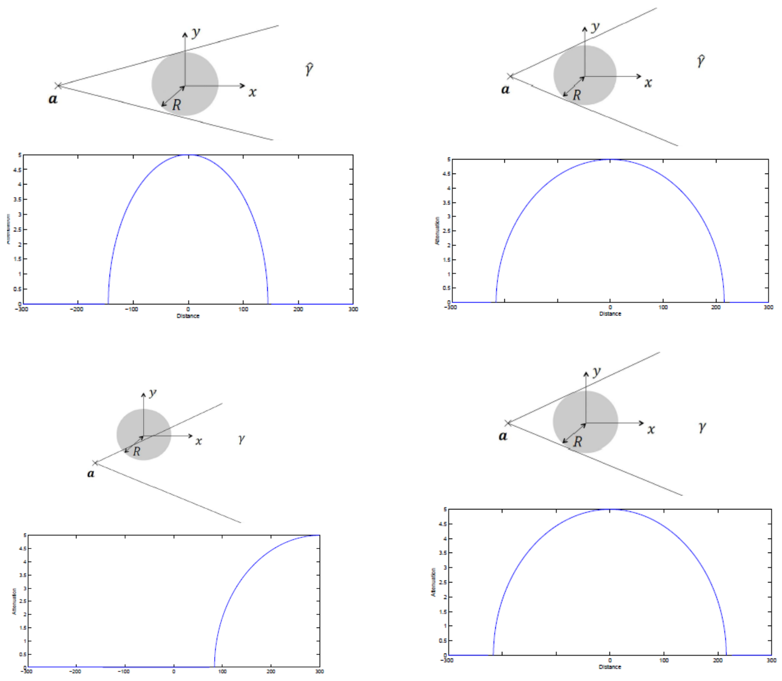
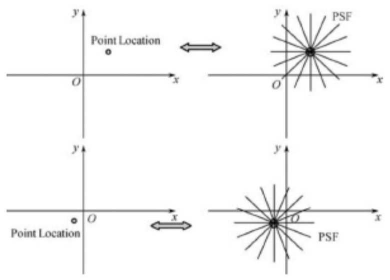


Abbildung 4.13.: Example Fan-Beam Projections of the Object

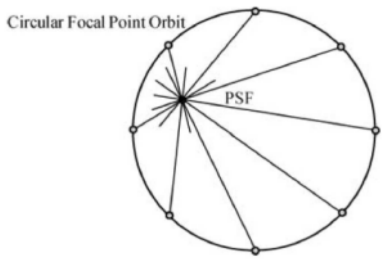
look on the Point Spread Function:

Point-Spread-Function

Do a normal Backprojection (without Filter) of a Single point out of all Projections we have acquired. The Point-Spread-Function tells us how a single Point is „smeared“by the System in the Backprojection step. It tells us how is a single Point blurred by the acquisition Device.



(a) PSF - Parallel Beam



(b) PSF - Fan Beam

Abbildung 4.14.: PSF for parallel and fan Beam geometry

- For Parallel Beam Geometry: Draw a line through the reconstructed point that is perpendicular to the detector and repeat for every detector position.

⇒ In this case, the point spread function is shift-invariant, i.e. every reconstfucted point shows the same pattern

- For Fan Beam Geometry: Draw a line trough the reconstructed point and the source position and repeat for every source position.

⇒ For a complete circle, the pattern is also shift-invariant

It can be shown that the full circle PSF is equivalent to the parallel beam PSF.

> This observation tells us that if you project and backproject an image, you will get the **same blurred** version of that image, **regardless** of the use of parallel-beam or fan-beam geometry !

If the original image is $f(x,y)$ and tghe backprojection of the projection data is $b(x,y)$, then the PSF can be shown to be $\frac{1}{r}$ where r is the distance of the currently considered point to the rotation axis: $r = \sqrt{x^2+y^2}$. b and f are related by:

$$\begin{aligned} b(x,y) &= f(x,y) ** \frac{1}{r} \\ B(\omega_x,\omega_y) &= F(\omega_x,\omega_y) \cdot \frac{1}{\sqrt{\omega_x^2+\omega_y^2}} \\ F(\omega_x,\omega_y) &= B(\omega_x,\omega_y) \cdot \sqrt{\omega_x^2+\omega_y^2} \end{aligned}$$

The relation ship of b and f after the Fourier transform is shown in line 2, the Fourier transform of $r = \frac{1}{\sqrt{x^2+y^2}}$ is $\frac{1}{\sqrt{\omega_x^2+\omega_y^2}}$.

We know that we need to apply a 2D ramp filter to the backprojected Image b to get the original Image f. We can use the same approach for the fan-beam geometry. So apply the 2D ramp filter $|\omega| = \sqrt{\omega_x^2+\omega_y^2}$ on both sides leads to the third Line. Know we just have to apply the inverse Fourier transform on $F(\omega_x,\omega_y)$ to get the original Image $f(x,y)$.
This is the **backproject-then-filter** algorithm !

Parallel-Beam to Fan-Beam Algorithm Conversion

We want to have a filter-then-backproject (FBP) algorithm, so we need another approach than the above with the PSF.
Now we come back to the sketched basic Idea from the beginning of the Fan-Beam chapter.
We need to find equal rays in both geometries. For that we need a description for the rays.

- Parallel-Beam: we used the rotation Angle of the detector θ and the pixel index s to describe the Ray.
- Fan-Beam: we can use β which is the angle between the central ray which is perpendicular to the detector and the y-axis and then the angle γ between the central Ray and the Ray we want to consider.

So we have our known Function $p(s,\theta)$ for parallel beam geometry and for fan-beam geometry we got $g(\gamma,\beta)$. For each fan-beam ray-sum $g(\gamma,\beta)$, we can find a parallel-beam ray-sum $p(s,\theta)$ that has the same orientation as the fan-beam ray with the relations seen in following figure: **Figure description:** They Rays are fan-beam

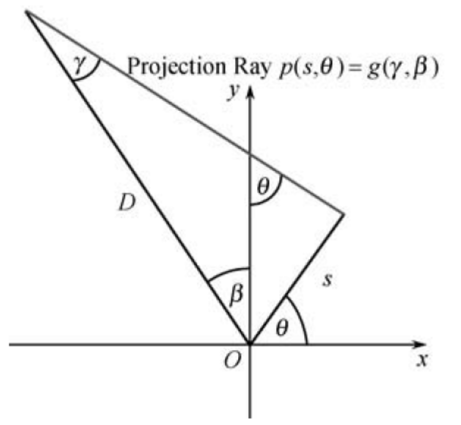


Abbildung 4.15.: A fan-beam ray can be represented using the parallel-beam, geometry parameters (called: Rebinning)

geometry Rays but the detector-line (where θ and s are written) is used from the parallel-beam geometry. So we mixed both geometry to find the relation-ship !
With basic knowledge about the interior Angle in a triangle (180°) and basic trigonometry we can find the following representations:

$$\theta = \gamma + \beta$$
$$s = D \cdot \sin\gamma$$

where D is the focal length. Describe the big triangle with γ, β:

$$180 = \gamma + \beta + 180 - \theta \Rightarrow \theta = \gamma + \beta$$

Now we can assign $p(s, \theta) = g(\gamma, \beta)$. After rebinning the fan-beam data into the parallel-beam format we then use a parallel-beam image reconstruction algorithm to reconstruct the Image. A big disadvantage of this approach is that we need to interpolate in the rebinning step, and interpolation introduce errors because we don't know the real function and can only approximate it.
We can use the Idea from above and incorporate it directly into the parallel-beam integral notation. So we start with the FPB:

$$f(x,y) = c \cdot \int_0^{2\pi} \int_{-\infty}^{infty} p(s,\theta) \cdot h(x\cos\theta + y\sin\theta - s)\ ds\ d\theta$$

change this to polar coordinates with $x = r \cdot \cos\varphi$ and $y = r \cdot \sin\varphi$:

$$f(r,\varphi) = c \cdot \int\limits_{0}^{2\pi} \int\limits_{-\infty}^{infty} p(s,\theta) \cdot h(r \cdot \cos\varphi \cos\theta + r \cdot \sin\varphi \sin\theta - s)\ ds\ d\theta$$

simplify:

$$f(r,\varphi) = c \cdot \int\limits_{0}^{2\pi} \int\limits_{-\infty}^{\infty} p(s,\theta) \cdot h(r \cdot \cos(\theta - \varphi) - s)\ ds\ d\theta$$

we know from the consideration above that $p(s,\theta) = g(\beta,\gamma)$ only for the case:

$$\theta = \beta + \gamma \qquad \text{and} \qquad s = D \sin\gamma$$

so we can replace p with g, but we have to make sure that the mentioned case is fulfilled. That is guaranteed if we replace θ and s with the formulas. If we do that, we change the variables over we integrate so we need again the determinant of the Jacobian:

$$f(r,\varphi) = c \cdot \int\limits_{0}^{2\pi} \int\limits_{-\frac{\pi}{2}}^{\frac{\pi}{2}} g(\gamma,\beta) \cdot h(r \cos(\underbrace{\gamma + \beta}_{\theta} - \varphi) - \underbrace{D \sin\gamma}_{s}) \underbrace{D \cdot \cos\gamma}_{det(J)} d\gamma\ d\beta$$

The bad thing about this it is no convolution. And a convolution is much easier to compute than an numerical integration. To get a convolution we have to consider the point we want to reconstruct in another coordinate System. We can describe

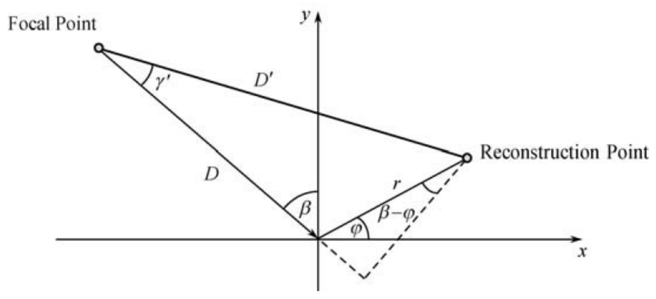


Abbildung 4.16.: The reconstruction point (r,φ) defines the angle γ' and distance D'

the point we want to reconstruct instead of r, φ with γ', D'. Because we change the inner integral, the β is arbitrary but fixed: so rewrite $r \cdot \cos(\beta + \gamma - \varphi) - D \sin \gamma$ with the other coordinate system as shown in figure:

$$r \cdot \cos(\beta + \gamma - \varphi) - D \sin \gamma = D' \sin(\gamma' - \gamma)$$

$$\implies \qquad f(r, \varphi) = c \cdot \int_0^{2\pi} \int_{-\frac{\pi}{2}}^{\frac{\pi}{2}} g(\gamma, \beta) \cdot h(D' \sin(\gamma' - \gamma)) D \cdot \cos \gamma \; d\gamma \; d\beta$$

and this almost looks like a convolution, now we take a property of the ramp-filter:

$$h(s) = \int_{-\infty}^{\infty} |\omega| e^{2\pi i \omega s} d\omega \Rightarrow h(D' \sin(\gamma' - \gamma)) = \int_{-\infty}^{\infty} |\omega| e^{2\pi i \omega D' \sin(\gamma' - \gamma)} d\omega$$

this formula can be massaged and end the end we get the ramp-filter for fan-beam:

$$h_{fan} = \frac{D}{2} (\frac{\gamma}{\sin \gamma})^2 \cdot h(\gamma)$$

this we can put into our reconstruction algorithm:

$$f(r, \varphi) = \int_0^{2\pi} \frac{1}{D'^2} \int_{-\frac{\pi}{2}}^{\frac{\pi}{2}} \cos \gamma \; g(\gamma, \beta) h(\gamma' - \gamma) \; d\gamma \; d\beta$$

and this is the Filtered-Backprojection-Algorithm for the Fan-Beam geometry (for curved Detector, so for equiangular Detectors)!
The $\cos \gamma$ is called **cosine weighting**, and we can see, the more the ray diverge from the central ray the smaller the weight gets.
Because at this point its very confusing with all the coordinate systems we consider and we use to get these formula here are all used coordinate systems:

- (θ, s)-coordinate system
- (β, γ)-coordinate system
- (x, y)-coordinate system
- (r, φ)-coordinate system
- (D', γ')-coordinate system

Another important point is, that the backprojection formula is different for the different detectors. The Filtered-Backprojection-Formular we dirved above is valid for the right Detector-type! In Summary here again the Algorithm:

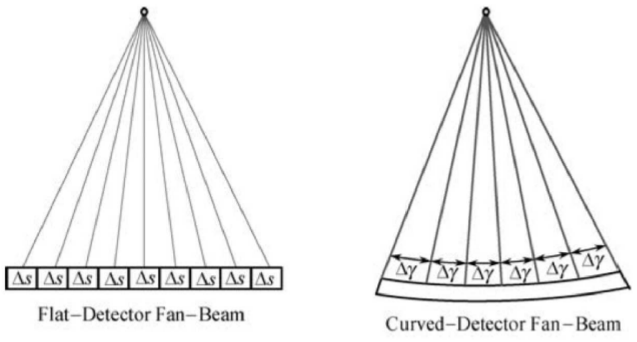


Abbildung 4.17.: Left is an Equally-spaced and right an Equiangular Detector

- Perform cosine weighting:

$$g_1(\gamma,\beta) = g(\gamma,\beta)\cos\gamma$$

- Apply fan beam filter:

$$g_2(\gamma,\beta) = g_1(\gamma,\beta) * h_{fan}(\gamma)$$
$$h_{fan}(\gamma) = \frac{D}{2}\Big(\frac{\gamma}{\sin\gamma}\Big)h(\gamma)$$

- Backproject with distance weight:

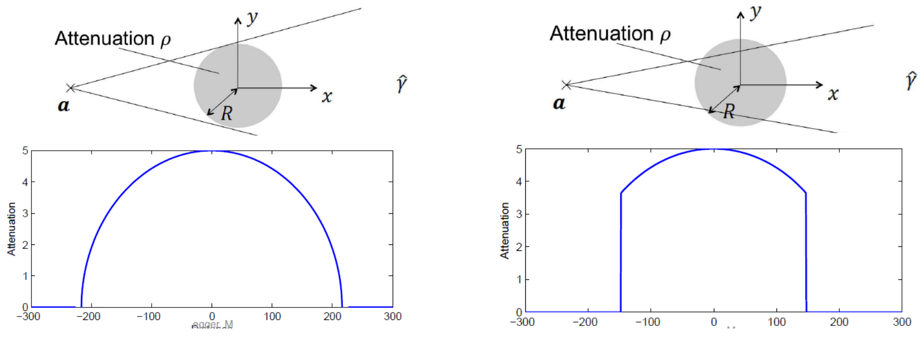
$$f(r,\varphi) = \int_0^{2\pi} \frac{1}{D'^2} g_2(\gamma',\beta)\ d\beta$$

Short Scan - Redundancy of Rays

In the case of parallel beam geometry it is obvious that after an 180° degree rotation the rays gets the same, just the direction is switched. So with a full 360° degree measurement we measure twice.
In the case of Fan-Beam geometry this is different. There are cases where you have the ray two times and and some not, so you have to be aware that some measurement are measured twice and some not. There exists a standard weighting scheme called Parker weight.

4.8. Truncation

Truncation leads to reconstruction artefacts so we have to handle it.
On the left we see that the object is in the full fan, and we can measure the com-

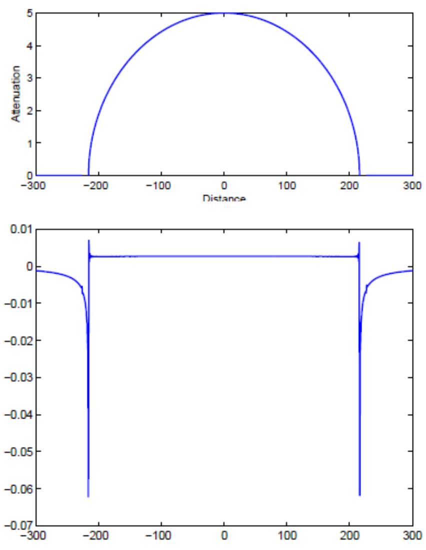


(a) No Truncation (b) with Truncation

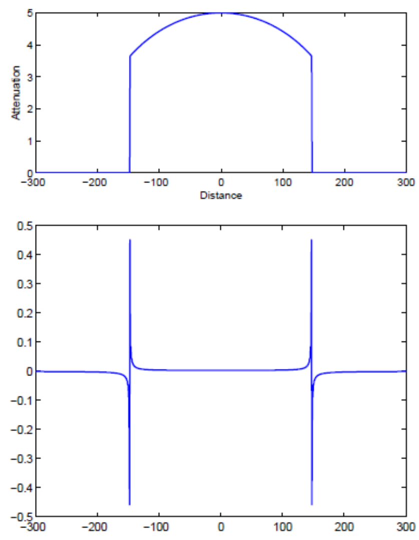
Abbildung 4.18.: Truncation and the results in the Projection

plete projection of the object. On the right side we can see that the object is not completely in the fan and due to this we get an incomplete projection of the object. So this problem is a missing Data problem.
We can model the truncation as the complete projection multiplied with an rectangular window function, the result would look like the projection on the right side.
The main Problem is, that the ramp-filter is in fact a high-pass filtering and as you can imagine a high pass filtering on these huge steps (which are actually not real) will lead to problems. Lets take a look on the filtered Projections: As expected the huge steps which comes from the truncation leads to high filter response. If you compare the filter result with the left one (non Truncation) you can easily see that the filtered projections are completely different. After the filter step, the backprojection step is applied, so imagine you smear back the right filter response instead of the left: On the left side we can the a Water Cylinder reconstructed without truncation. On the Right side we see the same Water Cylinder but this time it was the truncation case. We can directly map the results to the filter response we have looked at. The very high valued edges on the right image are correlated to the high filter response due to the truncation, and afterwards like in the filter response the values drop fast to a low level, as we can observe in the right image.
This Intensity drop from outside to inside is called **„cupping“artifact**.
Truncation is not an academical Problem, there are reasons why we have truncation in real systems:

- Small Field of View: Detector too small to fit the whole anatomy
  - Typical for abdomen and thorax scans

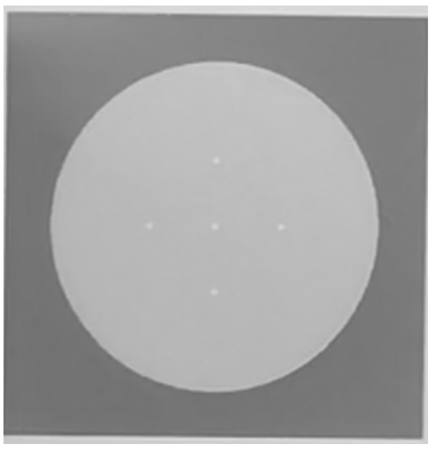


(a) filtered Projection without Truncation

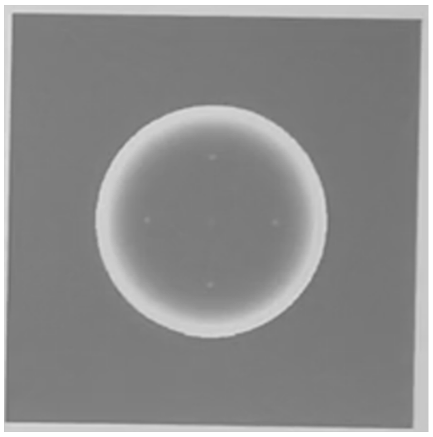


(b) filtered Projection with truncation

Abbildung 4.19.: Comparison of the filter result between projection with and without truncation



(a) No Truncation



(b) with Truncation (croped outside of FoV)

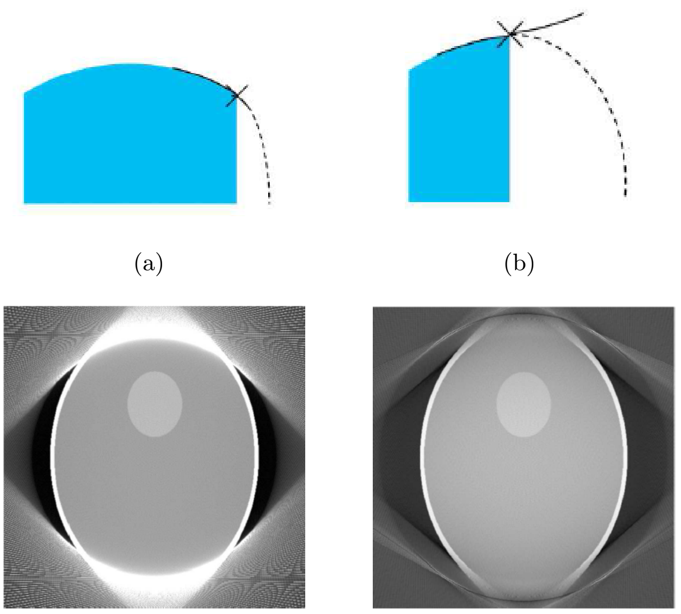
Abbildung 4.20.: Water Cylinder With Beads - Reconstruction

  - Medical instruments that extend the Field of View

- Collimation: Intentional truncation to reduce radiation dose
  - lead plates in x-ray source can be adjusted to focus on an ROI
  - lead absorbs most x-ray photons $\longrightarrow$ No information in projection

There are different ideas to solve the truncation problem, basically all solutions try to compensate the missing Data (all extrapolation methods make he assumption that the object is not infinite and will go to Zero at some point):

- Solution 1: Defect Pixel extrapolation
  - Model extrapolation as deconvolution: Use defect pixel interpolation algorithm from the beginning of the lecture
  - Unfortunately, the algorithm works not as well as expected
- Solution 2: Heuristic extrapolation
  - Use mirroring for extrapolation. In order to enforce a limited size of the object, a cosine-like weighting is added:


(a) (b)

(c) truncated without correction

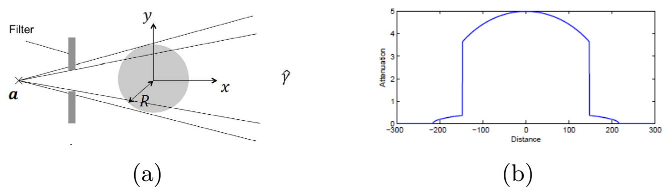
(d) heuristic extrapolation

Abbildung 4.21.: Efficient correction for CT image artefacts caused by object extending

- Solution 3: Water Cylinder Assumption: Assume that the imaged object consists of water: Fit water cylinder model to observed data and use model to extrapolate
  - will work perfectly, if a water cylinder is imaged
  - yields good results for most objects (head, abdomen, etc..)

  - will yield suboptimal results if water cylinder assumption is violated. There exists other methods which makes other object assumptions out of water

- Solution 4: Use of Prior Knowledge: Do a full-scan with low-dose and a ROI scan (with truncation) with high dose
  - Use data from low-dose scan to complete the data from the second scan
  - Correction will be perfect, if the object did not change !
- Solution 5: Semi-transparent Filter



(a) (b)

Abbildung 4.22.: Semi-transparent Filter

  - use the low signal for extrapolation
  - Filter boundary must be located correctly (which may be influenced by the object)
  - Method has to be applied carefully in order not to introduce artificial high frequencies
  - yields perfect truncation correction

Phatoms

Phantoms are used to evaluate reconstruction algorithms. Phantoms are used because x-rays are ionizing (so badly for patients) and we don't know the geometry of the patient but we know the geometry from the phantom exactly. So we know how the phantoms should look like and we can compare our reconstruction results with this.
We distinguish two kinds of phantoms:

Numerical / simulated phantoms: Originate from computer simulations, they are know exactly but have only limited realism

  - Shepp-Logan phantom (specified for 2D)
  - Forbild phantom (more complicated thatn shepp-logan)

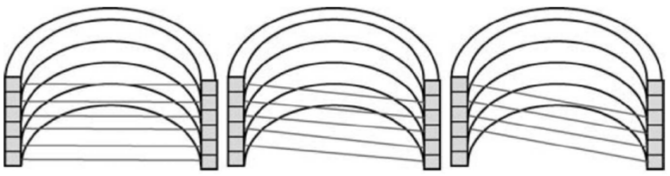
– X-Cat phantom (targeting the realism part)

Real phantoms: are designed with desired properties and are manufactured with a high accuracy.

4.9. 3D - Reconstruction

We have considered the 2D-Case of reconstruction.In reality detectors have multiple lines and instead of a fan-beam the x-ray source propagate the x-rays in a cone-beam. So we have to adjust our reconstruction approaches to the 3D-cases.
One Idea for the 3D-case is to do a slice-by-slice 2D reconstruction, and this is what we first discuss in the following. After that we discuss a another approach with the radon-transform. The assumption behind this idea is that the Projection-Rays are perpendicular to the rotation angle. Before we look what happens if this is not true we look at the sampling of the fourierspace

4.9.1. Parallel-Line Integral Data



In the left case the projection lines are perpendicular to the rotation axis and we will get complete Data and can do our slice-by-slice 2D reconstruction. The middle and the right case will lead to missing data, so we cannot reconstruct the function properly with the slice-by-slice 2D reconstruction approach.

4.9.1.1. Central Slice Theorem for 3D

First of all we have to check if the central slice theorem for the 1D/2D-case can be generalized or be lifted up to the 2D/3D case, so we can still reconstruct.
and of course we can generalize the the central slice Theorem to higher dimensions (just look at the proof for 1D/2D and lift it up to higher dimensions). So in this case we want to sample the 3D-Fourier transform. For each measurement we get a plane, and at the end we get the sampled fourier transform of the object in cylindric-coordinates (like the Polar-coordinates for the 1D/2D-case): Like in the 1D/2D-case this holds for parallel beams and not for the cone-beam geometry.

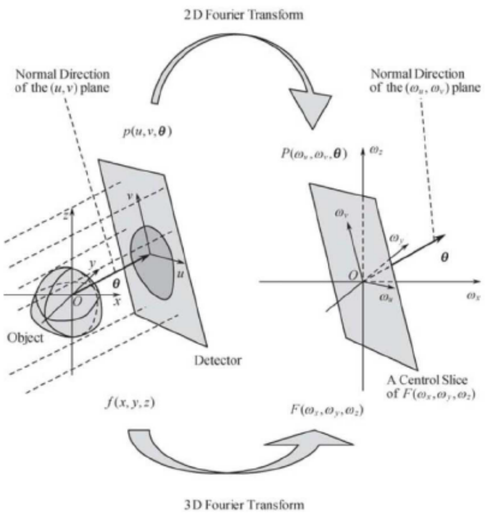
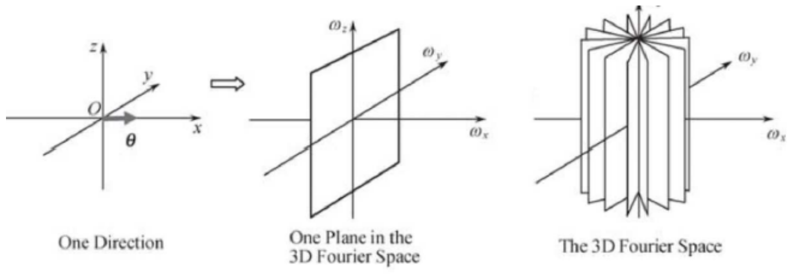
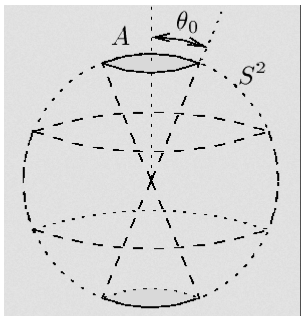

2D Fourier Transform
Normal Direction of the (u, v) plane
Normal Direction of the (ω_u, ω_v) plane
$p(u, v, \theta)$
$P(\omega_u, \omega_v, \theta)$
Object
Detector
A Central Slice of $F(\omega_x, \omega_y, \omega_z)$
$f(x, y, z)$
$F(\omega_x, \omega_y, \omega_z)$
3D Fourier Transform

Abbildung 4.23.: Central-Slice-Theorem for the 3D-Case



4.9.1.2. Orlov's condition

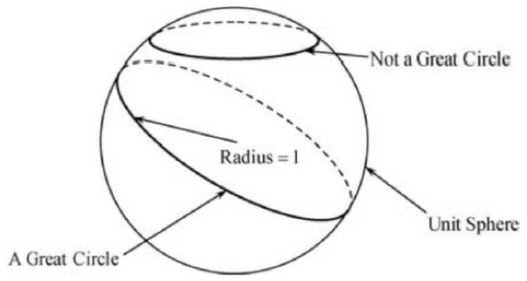
As we sketched above, what happens if the projection rays are not perpendicular to the rotation axis, how does the sampling of the Fourier space looks like? Lets consider that we have an angle which is not 90° between the projection lines and the rotation axis, then we will get missing Data (see figure 4.9.1 middle and left). We will miss two Cones (like shown in the figure) in the Fourier space: this will lead



to artefacts in the reconstruction.

Orlovs condition makes sure that we sample the whole Fourierspace and don't miss data:

> A Complete data set can be obtained, if every great circle intersects the trajectory



If we move our X-Ray source on a great circle on a sphere (the shown unit sphere) we can sample the Fourierspace complete. A few Examples: The first three examples

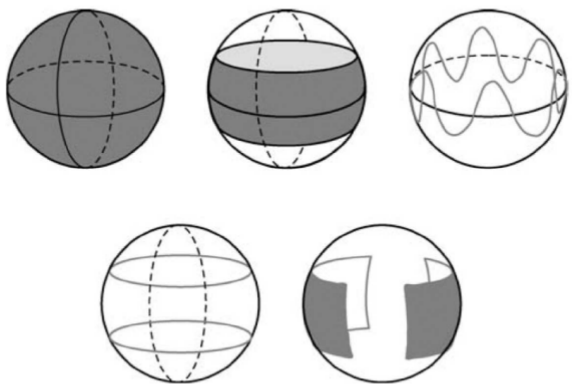


Abbildung 4.24.: Examples for trajectories

fulfil orlovs condition, all great circle you can draw on this sphere will intersects your trajectory. The two example below violate orlovs condition, we can draw great circles which will not intersect. So in the two examples below we cannot have a proper sampling of the Fourierspace !

4.9.1.3. Parallel Line Backprojection-then-Filtering Algorithm

If we perform the Backprojection first then the following steps describe the algorithm:

- If the original image is $f(x, y, z)$ and the Backprojected image is $b(x, y, z)$, then:
$$b = f *** h$$

where h is the Point-Spread-Function and $***$ denotes the 3D convolution.

- if we have the trajectory like in Figure 4.24 in the left upper case is shown then the PSF is:
$$h(x,y,z) = \frac{1}{x^2+y^2+z^2} = \frac{1}{r^2}$$

- the Fourier transform looks then like:

$$B(\omega_x,\omega_y,\omega_z) = F(\omega_x,\omega_y,\omega_z)H(\omega_x,\omega_y,\omega_z)$$
$$H(\omega_x,\omega_y,\omega_z) = \frac{\pi}{\sqrt{\omega_x^2+\omega_y^2+\omega_z^2}}$$

- to get the original Function just devide through the PSF and then apply the inverse Fourier transform

$$F(\omega_x,\omega_y,\omega_z) = B(\omega_x,\omega_y,\omega_z)\frac{\sqrt{\omega_x^2+\omega_y^2+\omega_z^2}}{\pi}$$

- In general, 3D line-integral data are measured with heavy redundancy. therefore, the image reconstruction algorithm is not unique because you can always weight redundant data differently.

4.9.1.4. Filtered-Backprojection

For the filtered Backprojection we can use the idea from the 1D/2D-case. The filtering with the filter-Kernel is described by:

$$g(\boldsymbol{\theta},u,v) = p(\boldsymbol{\theta},u,v) ** h(\boldsymbol{\theta},u,v)$$
$$G(\boldsymbol{\theta},\omega_u,\omega_v) = P(\boldsymbol{\theta},\omega_u,\omega_v)\cdot H(\boldsymbol{\theta},\omega_u,\omega_v)$$

$\boldsymbol{\theta}$ is a 3D-Angle and describes the plan and u, v are the coordinates on this Plane, you can look up the situation in Figure 4.23. The Filter $H_{\boldsymbol{\theta}}(\omega_u,\omega_v)$ is often view-dependent, for the unit-sphere the filter is view-independent.

4.9.2. Parallel Plane-Integral Data

Above we described the approach of the slice-by-slice 2D reconstruction to reconstruct 3D Objects.
Let us consider know the reconstruction for 3D-objects completely new without fall back to the 2D-case.
In 3D, the parallel plane-integreal $p(s,\boldsymbol{\theta})$ of an object $f(x,y,z)$ is referred to as the

Radon transform (see Figure 4.25). The Radon transform in 3D is worthwhile to investigate because is has a simple and nice inversion and can be used to solve other related imaging problems. For this study we imagine a 1D detector that is able to

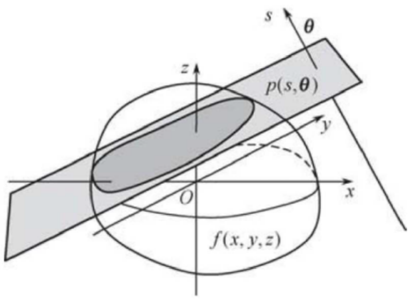
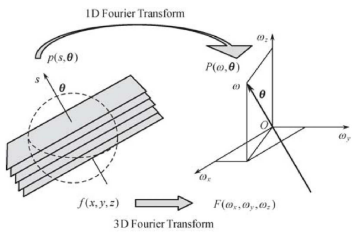
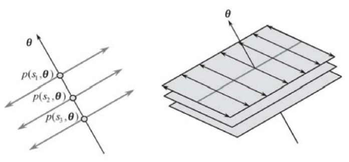


Abbildung 4.25.: In 3D, the plane integral of an object is the Radon transform

measure plane-integrals $p(s, \boldsymbol{\theta})$ [2] with the planes orthogonal to the detector. The detector is aling the direction $\boldsymbol{\theta}$ which is a 2D angle (inner plane rotation + outer plan rotation).
The **central slice theorem** for the radon transform in 3D states that the 1D Fourier trasnfor $P(\omega, \boldsymbol{\theta})$ of the projection $p(s, \boldsymbol{\theta})$ of a 3D function $f(x, y, z)$ is equal to a 1D profile through the origin of the 3D Fourier transform $F(\omega_x, \omega_y, \omega_z)$ of that function which is parallel to the detector (see figure 4.26) So nice, we have a central



(a) In 3D, the plane integral of an object is the Radon transform

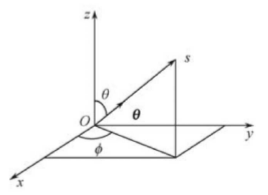

$\boldsymbol{\theta}$
$\boldsymbol{\theta}$
$p(s_1,\boldsymbol{\theta})$
$p(s_2,\boldsymbol{\theta})$
$p(s_3,\boldsymbol{\theta})$

(b) $p(s, \boldsymbol{\theta})$

Abbildung 4.26.: In 3D, the plane integral of an object is the Radon transform

slice theorem for the 3D case ! But we do not have a 1D detector which can measure plane-integrals. But we can handle this problem by using a 2D-detector which can measures the line Integrals in the plane, and then integrate over these line-integrals to get the plane-integral.
take care: that the intersection line of the plane (we want to integrate) and the detector must not correspond with a pixel-row on the detector ! So we have to compute the intersection-line of the plane and the detector to know which measured line-integrals we have to integrate over.

[2] in the real case, the detector is 2D and we integrate the line Integrals such that we get the plan integral



The Backprojection is different, eachs point on the 1D $p(s, \boldsymbol{\theta})$ correspond to a plane, so a point has to be backprojected as a plane in 3D.
The inversion Formular of the Radon transform is given by the second order derivative of $p(s, \boldsymbol{\theta})$ with respect to s (this step is called filtering !) and then backproject the filtered data to the 3D image array:

$$f(x,y,z) = \frac{1}{8\pi^2} \int\int_{4\pi} \frac{\partial p(s,\boldsymbol{\theta})}{\partial s^2}\Big|_{s=\boldsymbol{x}\cdot\boldsymbol{\theta}} \ \sin\theta \ d\theta \ d\phi \qquad \text{with} \quad \boldsymbol{\theta} = \begin{pmatrix} \sin\theta\cos\phi \\ \sin\theta\sin\phi \\ \cos\theta \end{pmatrix}$$

the second order derivative is from numerical perspectives on noisy data not a good idea!
which gives us the **Backprojection-Then-Filterin Algorithm:**

- The backprojection of the image is obtained as

$$b(x,y,z) = \int\int_{2\pi} p(s,\boldsymbol{\theta})|_{s=\boldsymbol{x}\cdot\boldsymbol{\theta}} \ \sin\theta \ d\theta \ d\phi$$

- For the 3d Radon case, the PSF is given as:

$$H(\omega_x,\omega_y,\omega_z) = \frac{1}{\omega_x^2+\omega_y^2+\omega_z^2}$$

- Hence the image can be obtained by:

$$F(\omega_x,\omega_y,\omega_z) = B(\omega_x,\omega_y,\omega_z)\cdot(\omega_x^2+\omega_y^2+\omega_z^2)$$

- in spatial domain this can be written as:

$$f(x,y,z) = \Delta b(x,y,z) = \frac{\partial^2 b(x,y,z)}{\partial x^2} + \frac{\partial^2 b(x,y,z)}{\partial y^2} + \frac{\partial^2 b(x,y,z)}{\partial z^2}$$

4.9.3. Cone Beam Geometry

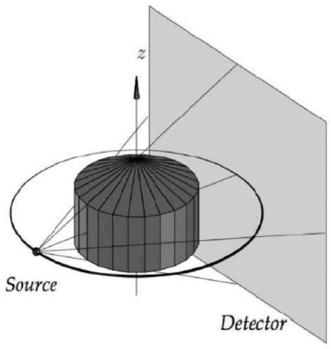


Abbildung 4.27.: Cone Beam Geometry

This is a very popular geometry. A flat pane oder multi-row detector can detect considerably more data at a time.
As in the 2D/1D case there is not directly a central slice theorem for cone beam geometry, we can think of the type of resampling like in fan-beam geometry with the plane-integrals. The Projection and backprojection can be described using projection matrices.

4.9.3.1. Tuy's condition - complete Data

first lets look at Tuy's condition which describe how we have to capture images with the cone beam geometry to sample the fourierspace complete:

> Tuy's condition say: Every plane that intersects the object of interest must contain a cone beam focal point !

We can see, only a rotation with fan beam geometry around the object does **not** full fill tuy's condition, so we don't sample the Fourierspace properly. Only the slice in the plan with the focal point will reconstruct properly. A solution would be a

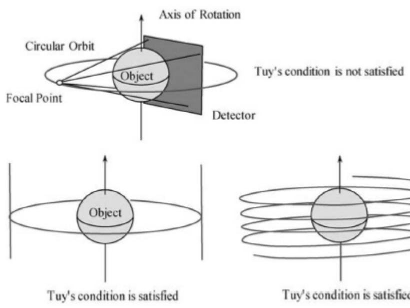

Axis of Rotation
Circular Orbit
Object
Tuy's condition is not satisfied
Focal Point
Detector
Object
Tuy's condition is satisfied
Tuy's condition is satisfied

Abbildung 4.28.: Tuy's condition

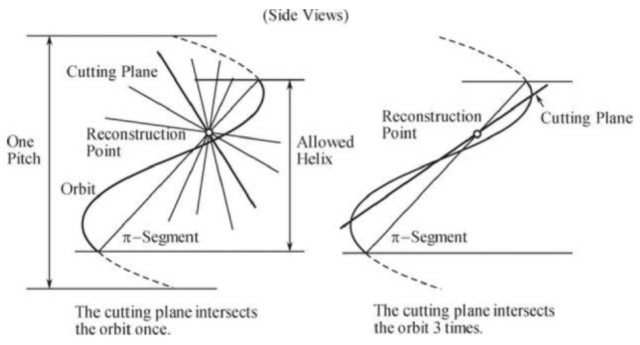


Abbildung 4.29.: The π-segment defines a section of helix. A cutting plane is a plane passing through the reconstruction point. The cutting plane either intersect the section helix once or three times

complete rotation and afterwards include a line shift (lower left picture) or use a helical trajectory.
Nevertheless also the cone-beam geometry have redundant data which we have to take in consideration in the reconstruction process with the proper weighting of the measurements. In the helix case there exsists point which are measured two or some times even three times:

4.9.3.2. Feldkamps Algorithm

This is the algorithm which is very often used in standard CT-setup with 2D-Detectors. It is basically a filtered-backprojection with a proper weighting of the projection rays. The algorithm is based on a circular trajectory (which means we have incomplete data !). The algorithm it is based on the fan beam algorithm with appropriate cosine weights. For the central Ray is just the pure fan-beam reconstruction algorithm and for all others we have to extrapolate the idea of fan beam to another angle. The geometry for Feldkamps algorithm s shown: The short words the algorithm works like: We take the measurements and do the weighting. Convolve the signal with a filter (ramp-filter) and at the end we just integrate up over all the volume.

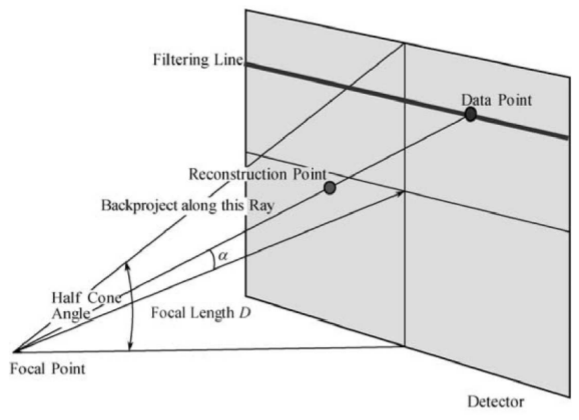


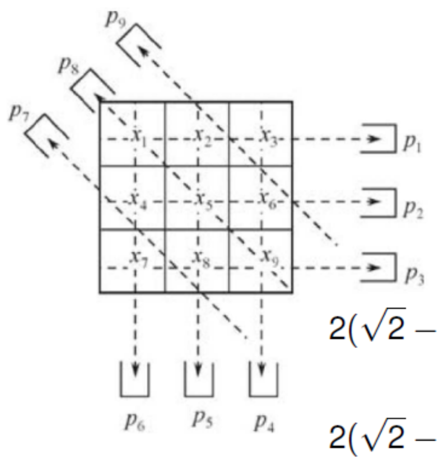
Abbildung 4.30.: Geometry for Feldkamps Algorithm

4.10. ART - Algebraic Reconstruction Technique

Since the computational power especially due to GPU's rises extremely there is a renaissance of the algebraic approach. First CT-scanner used this, but then the number of linear equations which need to be solved explode and the computational power was not enough to deal with this (short rethinking: for a Volume with $512 \times 512 \times 512$ we have 2^{27} unknowns). That's why the Backprojection was and is still the „working horse"of CT-Reconstruction.

4.10.1. Linear Equations

In the Figure we see, how the linear equations generally can build up, we use the length of the ray trough the Voxel as a weighting factor how much this ray contributes to the value we end up with: this system can be rewritten in Vector-Matrix-



$$\begin{aligned}
x_1 + x_2 + x_3 &= p_1 \\
x_4 + x_5 + x_6 &= p_2 \\
x_7 + x_8 + x_9 &= p_3 \\
x_3 + x_6 + x_9 &= p_4 \\
x_2 + x_5 + x_8 &= p_5 \\
x_1 + x_4 + x_7 &= p_6 \\
2(\sqrt{2}-1)x_4 + (2-\sqrt{2})x_4 + 2(\sqrt{2}-1)x_8 &= p_7 \\
(\sqrt{2})x_1 + (\sqrt{2})x_5 + (\sqrt{2})x_9 &= p_8 \\
2(\sqrt{2}-1)x_2 + (2-\sqrt{2})x_3 + 2(\sqrt{2}-1)x_6 &= p_9
\end{aligned}$$

Abbildung 4.31.: An example with 9 unknowns and 9 measurements

Notation:

$$\mathbf{A}\vec{x} = \vec{p} \qquad \Leftrightarrow \qquad \vec{x} = \mathbf{A}^{-1}\vec{p} \qquad \Leftrightarrow \qquad \vec{x} = (\mathbf{A}^T\mathbf{A})^{-1}\mathbf{A}^T\vec{p}$$
$$\vec{x} = (x_1, x_2, ..., x_p)^T \qquad \vec{p} = (p_1, p_2, ..., p_9)^T$$

where **A** is the system matrix with elements $a_[ij]$, each $a_[ij]$ describes the contribution of each voxel to each ray.
We can solve with the inverse of **A**, but the problem is most of the time we have more unknowns than equations. And then the Matrix can't inverted, this could be solved if we compute the pseudo-inverse (which is the close form solution of the least square estimator of: $|\mathbf{A}\vec{x} - \vec{p}|_2^2 \rightarrow min$).
We look for a Solution that does not require the inversion of **A** or a product of **A** (obviously because of the high dimension of the Matrix).
Simple Example: there can be used a simple example to sketch the idea:
think about a non-trivial but very easy object we want to reconstruct: An object with 2 Voxels, we have two unknowns x_1, x_2 and two measurements p_1, p_2. Then we have to solve these two linear equations:

$$a_{11}\vec{x}_1 + a_{12}\vec{x}_2 = \vec{p}_1$$
$$a_{21}\vec{x}_1 + a_{22}\vec{x}_2 = \vec{p}_1$$

we can write this in the matrix notation:

$$\mathbf{A}\vec{x} = \vec{p}$$

$$\text{Systemmatrix: } \mathbf{A} = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} \qquad \text{measurement: } \vec{p} = \begin{pmatrix} p_1 \\ p_2 \end{pmatrix} \qquad \text{Volume: } \vec{x} = \begin{pmatrix} x_1 \\ x_2 \end{pmatrix}$$

we can rewrite the Matrix **A** in terms of row-vectors (a_1^T, a_2^T):

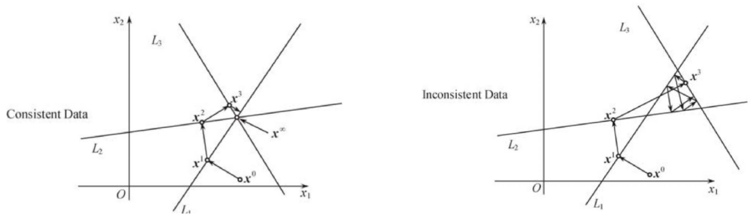
$$\begin{pmatrix} a_1^T \\ a_2^T \end{pmatrix} \vec{x} = \vec{p}$$

then we can rewrite our initial equations:

$$a_{11}\vec{x}_1 + a_{12}\vec{x}_2 = \vec{p}_1 \Longleftrightarrow a_1^T\vec{x} = \vec{p}_1$$
$$a_{21}\vec{x}_1 + a_{22}\vec{x}_2 = \vec{p}_1 \Longleftrightarrow a_2^T\vec{x} = \vec{p}_2$$

and this is interesting, because we can read the right hand side as the Hesse-normal form of a linear manifold where a_1^T is the normal vector of the line and p_1 is the

distance of this line to the origin !
We know looking for a $\vec{x}$ that fulfil both equation, and this is the intersection point of both lines!
We can find the intersection of both lines with an simple iterative scheme: Start with a point x^0 (e.g. we get this from a backprojection) and then compute the orthogonal projection of this point to one of the lines (this is then called x^1). Then project the point x^1 orthogonally to the other line (x^2). Repeat this till you find the intersection point(see left Figure 4.32). The more Orthogonal the lines are the faster the scheme



(a) Example with two Voxels

(b) Example with two Voxels and incosistent Data

Abbildung 4.32.: Example of the iterative scheme to find the intersection

converge !
Lets take a look at the iteration scheme in mathematical notation. We have a point $\vec{p}$ and want to compute $\vec{p}\,'$ which is the orthogonally projection on the straight line $\vec{n}^T\vec{x} = d$:

$$
\begin{aligned}
&(I) \quad \vec{p}\,' - \vec{p} = \lambda\vec{n} && \text{(orthogonality criterion)}\\
&(II) \quad \vec{n}^T\vec{p}\,' = d && (\vec{p}\,' \text{ is the projection so it fulfil the line equation})\\
&\vec{n}^T(\lambda\vec{n} + \vec{p}) = d && \text{(put I into II and solve to } \lambda)\\
&\qquad = \lambda\vec{n}^T\vec{n} + \vec{n}^T\vec{p} && \\
&\qquad = \lambda\,\|\vec{n}\|_2^2 + \vec{n}^T\vec{p} && (\vec{n}^T\vec{n} = \|\vec{n}\|_2^2)\\
&\lambda = \frac{d - \vec{n}^T\vec{p}}{\|\vec{n}\|_2^2} && \\
& && \text{(now put } \lambda \text{ into (I) and solve to } \vec{p}\,')\\
&\vec{p}\,' - \vec{p} = \frac{d - \vec{n}^T\vec{p}}{\|\vec{n}\|_2^2}\vec{n} && \\
&\vec{p}\,' = \vec{p} + \frac{d - \vec{n}^T\vec{p}}{\|\vec{n}\|_2^2}\vec{n} &&
\end{aligned}
$$

and this is the iterative scheme, we can lift it up to our Matrix notation, which is then the originally method published by Kaczmarz. For each pixel p_i and each row $\mathbf{A}_i$ of $\mathbf{A}$ perform the following update:

$$\vec{x}^{k+1} = \vec{x}^{k} + \frac{p_i - \mathbf{A}_i \vec{x}^{k}}{\mathbf{A}_i \mathbf{A}_i^T} \mathbf{A}_i^T$$

there are some nice facts:

- is has been shown that the iterative scheme converges to the solution, if there exists a unique solution
- the angle between hyper planes influences the rate of convergence to the solution
- if hyper planes are orthogonal to each other, it is obvious that the method converges rapidly
- Orthogonalization methods applied in advance to iterations will improve convergence. Or alternative: careful selection of sequence of projections !
- Overdetermined systems and noise: no unique solution and oscillation
- a main drawback of ART is the slow convergence !

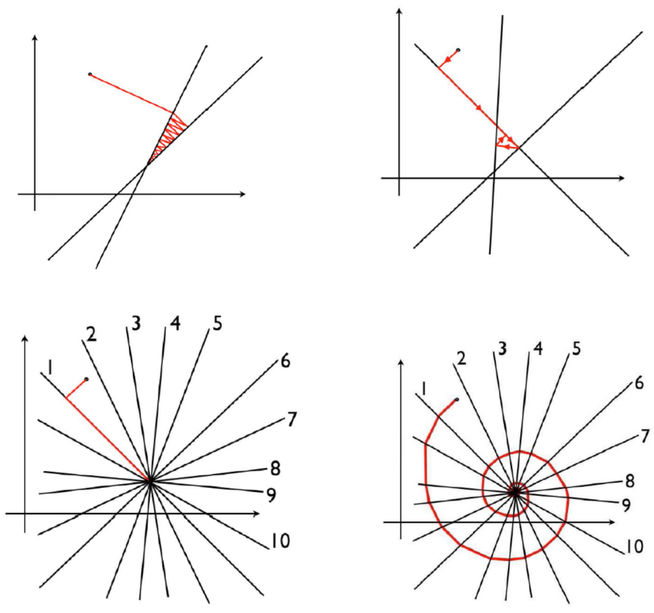


Abbildung 4.33.: Example convergence of the iterative scheme

there exist different method which improve the convergence speed:

SART: The idea is to compute parallel all different Projections of the point to the different lines and then compute the mean between all projected points and start with again. This convergence also, but faster.

Ordered Subsets: Employs knowledge on the acquisition sequence, select subsets of equations that are most likely orthogonal to each other

Towards more Realism: instead of taking the length from the ray through the Voxel as a weight try to find more realistic approximations to build up the system matrix. Include scattering, noise, etc.

4.10.2. Gradient Descent Algorithm

Formulate the reconstruction problem as an optimization Problem, find an optimum via peak condition. This enables the use of various methods that are common in optimization.
We can write the objective function as:

$$\chi(\vec{x}) = \|\mathbf{A}\vec{x} - \vec{p}\|_2^2 = (\mathbf{A}\vec{x} - \vec{p})^T(\mathbf{A}\vec{x} - \vec{p})$$

for this we can compute either the close form solution with the pseudo inverse:

$$\vec{x} = (\mathbf{A}^T\mathbf{A})^{-1}\mathbf{A}^T\vec{p}$$

or we reformulate the optimization problem as an iterative procedure:

$$\vec{x}^{k+1} = \vec{x}^k - \lambda\Delta$$

so in each step we want to go one step towards the minimum, i.e. opposite gradient direction $-\lambda\Delta$. At the end this looks like:

$$\vec{x}^{k+1} = \vec{x}^k - \lambda(\underbrace{2\mathbf{A}^T(\mathbf{A}\vec{x} - \vec{p})}_{\text{gradient}}) \iff \vec{x}^{k+1} = \vec{x}^k + \lambda(\mathbf{A}^T(\vec{p} - \mathbf{A}\vec{x}))$$

4.10.3. Maximum-Likelihood Expectation-Maximization Methods

Formulate the objective function as likelihood function. Find the optimum of the likelihood function, i.e. the most likely solution. This can be solved with the Expectation Maximization Algorithm.
A very basic example to show how you can reformulate a optimization problem into the language of statistics:

- if we want to compute $ax - b = 0$ we can setup the minimization problem: $\sum_i \|ax_i - b\|^2 \rightarrow \min$ for various x and minimize this with respect to a and b.
- if you look at the term: $(ax_i - b)(ax_i - b)$ you can see that you can put the inverse of a covariance matrix between these two and then we have the exponent of a Gaussian:

  $$e^{-(ax_i - b)\Sigma^{-1}(ax_i - b)}$$

  and know we can maximize the value of the Gaussian PDF with respect to a and b:

  $$\prod_i e^{-(ax_i - b)\Sigma^{-1}(ax_i - b)} \rightarrow \max$$

and this is the idea we want to apply to the reconstruction Problem.
Lets consider for the following an emission tomography problem. The probability density function for a random variable r to emit a certain amount of energy follows the Poisson distribution:

$$P(r|\lambda) = e^{-\lambda}\frac{\lambda^r}{r!}$$

the expected value of this random variable is λ the observed value at each detector bin is:

$$p_i = \sum_j c_{ij}$$

where $\lambda_{ij} = E(c_{ij}) = a_{ij}x_j$
parenthesis the Expectation definition is: $E[x] = \int x \cdot p(x)dx$
So a detector pixel p is a sum of random variables.
To summarize we can say we maximize the function for the given observations !

4.10.4. Regularized Reconstruction

Again the problem what we consider is $\mathbf{A}\vec{x} = \vec{p} \Rightarrow \|\mathbf{A}\vec{x} - \vec{p}\|_n^2 \rightarrow \min$, where n is some norm.
But we can say that we want to introduce a regularizer into the optimization problem:

$$\|\mathbf{A}\vec{x} - \vec{p}\|_d + \lambda \cdot R(\vec{x}) \rightarrow \min$$

for example $R(\vec{x})$ could be smoothness $\|\nabla\vec{x}\| \rightarrow$ small, so we optimize our problem with respect the smoothness which means the difference between the neighbours should be small.

> We introduce additional information into the reconstruction precess to enforce a certain solution

with this we can incorporate prior knowledge about the Volume we want to reconstruct.
TV-Norm The Total Variation Norm is popular combination of a sparsifying transform with L_1 norm, the sparsifying transform is the gradient image. But it can be shown that reconstruction with TV-regularization is identical to FBP reconstruction with subsequent non-linear edge preserving filtering !

4.11. Bilateral Filter

We need filter in reconstruction. But if you use simple a mean-Filter to reduce noise you will destroy sharp edges, so we image gets blurred. We look for a filter which is edge preserving.
To get the idea we start with a simple Filter which weights the neighbouring ($\mathcal{N}(x, y)$ describes the Neighbourhood of Pixel (x, y)) values by their distance to the Pixel we want to compute the new value for:

$$g(x, y) = \sum_{(x',y')\in\mathcal{N}(x,y)} c(x', y') \cdot f(x', y')$$

to get an intuition: for a mean filter with a 3-by-3 Neighbourhood the c(closeness) would look like:

$$c(x', y') = \begin{cases} \frac{1}{9}, & \text{if}(x', y') \in \mathcal{N}(x, y) \\ 0, & \text{otherwise} \end{cases}$$

So after we have introduce the basic idea of filter we have to define what does edge preserving means:

> if you have high differences in between the grey values / intensity values then you want to slow down your filter-operation in a sense that you do not filter too much. If your differences are just on the noise level, you want to have the full effect of your filter

the idea of bilateral Filtering is that we introduce beside the weights for the geometric structure a new weights which measure the distance between the intensity values! this leads to:

$$g(x,y) = \sum_{(x',y')\in\mathcal{N}(x,y)} c(x',y')\cdot s(f(x',y'),f(x,y))\cdot f(x',y')$$

the disadvantage is that with the new weight s we lose the shift-invariant property of the filter.
Now lets define all term mathematically:

Low-Pass Domain Filter Let us consider spatial domain filtering of continuous 2D image functions defined via convoltion:

$$h(x,y) = k_d(x,y)\int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x-\mu,y-\nu)c(x,y,\mu,\nu)\ d\mu\ d\nu$$

where the convolution kernel is usually restricted to a local neighbourhood and $f(x,y)$ denotes the observed image and $c(x,y,\mu,\nu)$ measures the geometric closeness between the neighbourhood center (x,y) and the point (μ,ν).

Low-Pass range Filter apply similar idea to the intensity values:

$$h(x,y) = \frac{\int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f(x-\mu,y-\nu)s(f(x,y),f(x-\mu,y-\mu))\ d\mu\ d\nu}{k_r(x,y)}$$

where again the convolution kernel is usually restricted to a local neighbourhood and $f(x,y)$ denotes the observed image and $s(f(x,y),f(x-\mu,y-\mu))$ measures the photometric similarity between the neighbourhood center (x,y) and points in its neighbourhood $(x-\mu,y-\nu)$

Bilateral Fiter now combine both considered filters:

$$h(x,y) = \frac{\int_{-\infty}^{\infty}\int_{-\infty}^{\infty} f\cdot c\cdot s\ d\mu\ d\nu}{k(x,y)}$$

where f is the observed image, c measures the geometric closeness (Low-Pass Domain Filter) and s measures the photometric similarity (Low-Pass Range Filter)

Example Closeness function:

$$c(x, y, \mu, \nu) = e^{-\frac{1}{2}\left(\frac{\left\|\binom{x}{y} - \binom{\mu}{\nu}\right\|}{\sigma_d}\right)^2}$$

Example Similarity function:

$$s(f_1, f_2) = e^{-\frac{1}{2}\left(\frac{\|f_1 - f_2\|}{\sigma_r}\right)^2}$$

For a good imagination, here is a plottet example:

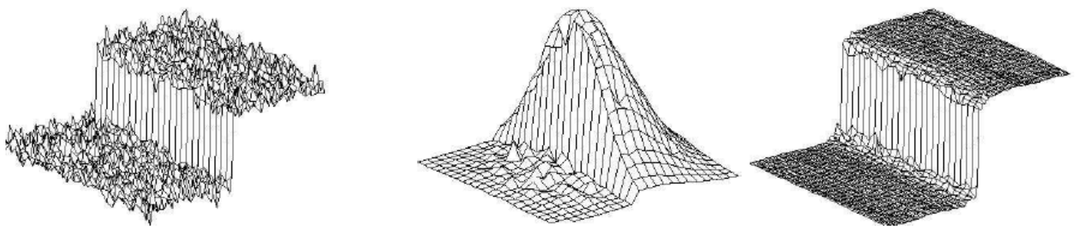


Abbildung 4.34.: Filter the Image (left side) with the Bilateral-Filter(middle) and we get the edge preservred filtered image (right)

5. Image Registration

In Basic image registration is:

> the process of transforming the different images into one common coordinate system. The registration of volumes is also subsumed by the term image registration

We distinguish between two major classes:

rigid registration: subsumes the process of computing a rigid transform for registration. In this case we have only 6 degrees of Freedom: 3 for translation and 3 for rotation.

non-rigid registration: includes all the methods of deforming the different images such that they can be represented in one common coordinate system.

For Image Registration in the medical context, the patient gets often fixed markers on their body(mostly used for the head).
nice to know: You need exactly three of these markers to compute the 3-translation and 3-rotation unknowns !

5.1. 2D/2D Point based rigid Registration

The problem can described:
Assume a set of corresponding 2-D points in two images:

$$C = \{(\boldsymbol{p}_k, \boldsymbol{q}_k); k = 1, 2, ..., N\}$$

where $\boldsymbol{p}_k, \boldsymbol{q}_k \in \mathbb{R}^2$ is the k-th pair of corresponding image points.
Problem: Compute the transform that maps the $\boldsymbol{q}_k$'s to the $\boldsymbol{p}_k$'s
To map these Points we need a Rotation $\boldsymbol{R}$ with $\varphi \in [0, 2\pi]$ and a translation $\vec{t}$:

$$\boldsymbol{R} = \begin{pmatrix} \cos\varphi & -\sin\varphi \\ \sin\varphi & \cos\varphi \end{pmatrix} \qquad \vec{t} = (t_1, t_2)^T$$

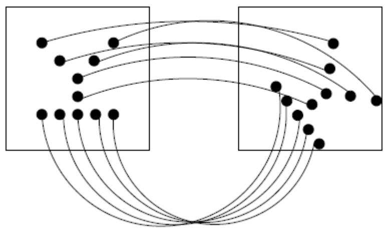


Abbildung 5.1.: Corresponding 2-D point features

this gives us:

$$\vec{p}_k = \boldsymbol{R}\vec{q}_k + \vec{t}$$

due to our noisy data, we need to build up an optimization problem instead of solving the equations:

$$\arg\min_{\varphi,t_1,t_2} \sum_{k=1}^{N} \left\| \vec{p}_k - \boldsymbol{R}\vec{q}_k - \vec{t} \right\|_2^2$$

sadly this is a **non-quadratic** function and so we have a **non-linear** optimization problem, because the unknown ϕ is a argument for some sin and cos-functions and is somehow combined within in the norm.
And of course we don't like this, we would like a linear-optimization such that we can solve it with SVD or the second best approach would be if the optimization problem is at least quadratic so we have a unique solution. **1. Approach:** we analyse the Rotation matrix: the columns of the rotation matrix are images of the base vectors of the original coordinate system (valid for all linear mappings !), the matrix is orthogonal and the determinant of the rotation matrix is one.
We can look at the Matrix and see that there are just two unknowns : $\cos\varphi$ and $\sin\varphi$:

$$\boldsymbol{R} = \begin{pmatrix} \cos\varphi & -\sin\varphi \\ \sin\varphi & \cos\varphi \end{pmatrix} \Longrightarrow \begin{matrix} r_1 = \cos\varphi \\ r_2 = \sin\varphi \end{matrix} \quad ; \quad r_1^2 + r_2^2 = 1$$

with this we can setup a new optimization problem:

$$\arg\min \sum_{k=1}^{N} \left\| \vec{p}_k - \left(\begin{smallmatrix} r_1 & r_2 \\ r_2 & r_1 \end{smallmatrix}\right)\vec{q}_k - \vec{t} \right\|_2^2$$
$$\text{subject to:} r_1^2 + r_2^2 = 1$$

this is know a quadratic function with a unique solution and you can set this up with a Lagrangian multiplier

2. Approach The second Approach uses complex numbers to deal with the Problem:

Lets take a look how complex numbers appear in a coordinate system so if somebody

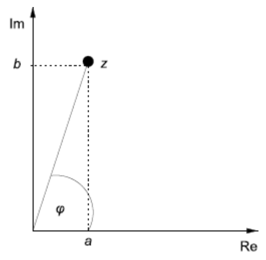


Abbildung 5.2.: Geometric representation of complex numbers

gives you an real-part a and an imaginary-part b you can draw the point $z = a + ib$ in the coordinate system. This is exaclte the way how you would draw a point in the Cartesian coordinate system of somebody gives you a vector with $\vec{z} = \binom{a}{b}$. We can see that as a one-to-one-relationship between a point in the 2D-plane and complex numbers (and we trust Hornegger :D).
That means it does not matter whether we get the points p_1 and q_1 in terms of 2D-dimensional coordinates or as complex numbers.
We also can adapt the idea that we can write a 2D-point in cartesian coordinates with polar coordinates, so with an angle and the absolute value of this:

$$z = a + ib = |x|e^{i\varphi} \qquad \text{(called euler-representation)}$$

if we look how this representation behaves if we multiply two such numbers:

$$x_1 \cdot x_2 = |x_1|e^{i\varphi_1}|x_2|e^{i\varphi_2} = |x_1||x_2|e^{i(\varphi_1+\varphi_2)}$$

or geometrically: so the multiplication of two complex numbers can be interpreted

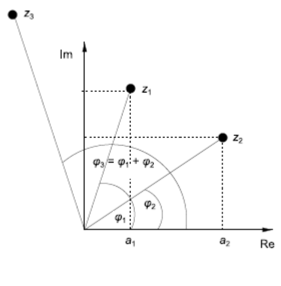


Abbildung 5.3.: multiplication of two complex numbers in euler-representation

as a rotation and scaling. So if we have a unit number it's just a rotation. Now we can describe our problem as:

> find the complex number that we have to multiply to all other such that the mapping has a minimal error

and know the get rid of the rotation matrix and sin and cos and we end up with a system of linear equations:
new Problem representation:
So if we consider the points $p_i, q_i \in \mathbb{C}$, the rotation $r \in \mathbb{C}$ and the translation $t \in \mathbb{C}$ all as Complex numbers then we can write our Problem as follows:

$$\begin{aligned} p_k &= r \cdot q_k + t \\ p_{k,1} + ip_{k,2} &= (r_1 + ir_2)(q_{k,1} + iq_{k,2}) + t_1 + it_2 \\ \text{where} \quad |r| &= 1 \end{aligned}$$

we can now multiply out the brackets:

$$\begin{aligned} \forall k: \quad p_{k,1} + ip_{k,2} &= r_1 \cdot q_{k,1} - r_2 \cdot q_{k,2} + t_1 + i(r_1 \cdot q_{k,2} + r_2 \cdot q_{k,1} + t_2) \\ (I) \quad p_{k,1} &= r_1 \cdot q_{k,1} - r_2 \cdot q_{k,2} + t_1 && \text{(for all k)} \\ (II) \quad p_{k,2} &= r_1 \cdot q_{k,2} + r_2 \cdot q_{k,1} + t_2 && \text{(for all k)} \end{aligned}$$

now we can forget about the complex world, for each pair p_k, q_k we get two equations and if we take all correspondencies we get two times the correspondencies linear equation we have to solve. They are linear in r_1, r_2, t_1, t_2
conclusion:

For N-point correspondencies, we get $2N$ linear equations.

we can write these equations in Matrix notation and can solve it with SVD! :D.
Example:

$$\boldsymbol{A}\vec{x} = \begin{pmatrix} q_{1,1} & -q_{1,2} & 1 & 0 \\ q_{1,2} & p_{1,1} & 0 & 1 \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \end{pmatrix} \begin{pmatrix} r_1 \\ p_2 \\ t_1 \\ t_2 \end{pmatrix} = \begin{pmatrix} p_{1,1} \\ p_{1,2} \\ \vdots \\ \vdots \end{pmatrix}$$

remarks:

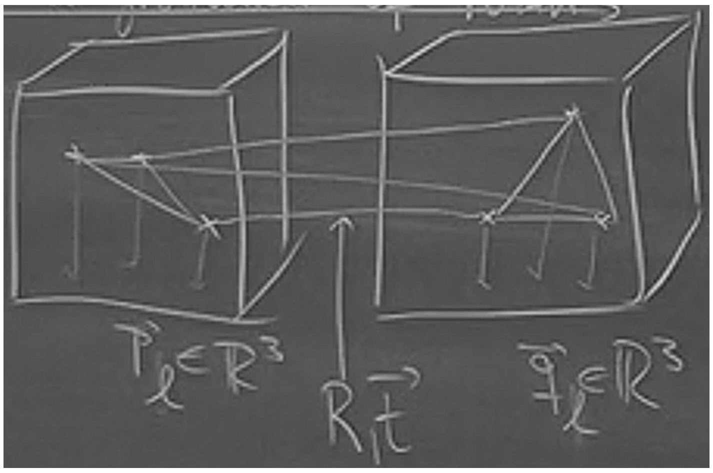
- in this algorithm we compute rotation as well as translation simultaneously
- Using SVD we compute the pseudo inverse of **A** and thus get both rotation and translation
- 2-D/2-D image registration using point correspondences results in a linear problem

- Rotation matrices imply the constraint that $r_1^2 + r_2^2 = 1$. This can be enforced by a proper scaling of the solution of the example above

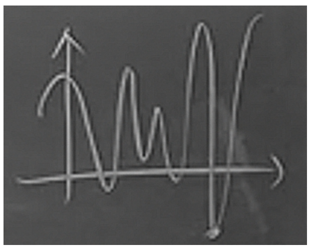
Now we have to lift the complex numbers idea up to characterize 3-D rotations

5.2. 3D/3D Point rigid registration

Of course we could set up the optimization problem for this with a Rotation matrix, which describes the 3D rotation, and the translation, but this function will oscillate because of the sin- and cos-functions and to find in such a function the minimum is very difficult.



(a) 3D/3D Point rigid registration



(b) Optimization Problem with Rotation Matrix

Abbildung 5.4.: 3D/3D Point rigid registration

$$\forall l \vec{p}_l = \boldsymbol{R}\vec{q}_l + \vec{t} \Rightarrow \min \sum_l \left\| \vec{q}_l - \boldsymbol{R}\vec{p}_l - \vec{t} \right\|_2^2$$

To solve this efficiently we have to look for other representations of the rotation matrix. We will look into three different types:

1. Representation: Euler Angles

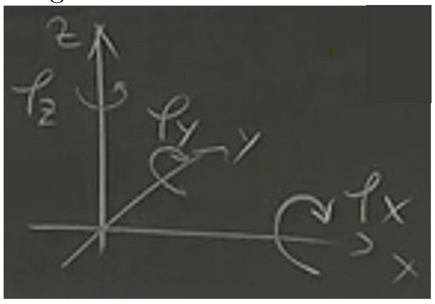


Abbildung 5.5.: Euler-representation of Rotation

$$\boldsymbol{R} = \boldsymbol{R}_{\varphi_z}\boldsymbol{R}_{\varphi_y}\boldsymbol{R}_{\varphi_x}$$

Matrix multiplication is not commutative, which is a huge disadvantage ! To compute the single rotation matrices take the base-vector and look how they behave.

Conclusion: we won't work with this representation, because there are too many disadvantages !

2. Representation: Axis / angle - Representation

This representation states: every rotation can be represented by an arbitrary rotation-Axis in 3D and a rotation around this axis.

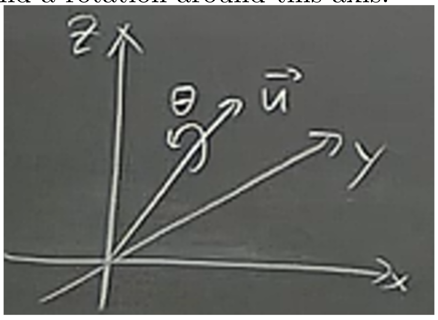


Abbildung 5.6.: Axis-Angle representation of Rotation

A nice effect of this representation is that you can represent this rotation on a computer with one 3D-Vector, the vector represents the axis and the rotation around these axis is the magnitude of the vector.

Lets take a deeper look in the rotation matrix which is generated by this representation:

All points on the Axis are not affected by the rotation. The implication of this is that the eigenvector which belongs to the Eigenvalue 1 of these matrix have to be $\vec{u}$:

$$\vec{x} = \boldsymbol{R}\vec{x} \Longrightarrow \vec{x} = \vec{u}$$

Given $(\vec{u}, \theta)$ and we want to Compute $\mathbf{R}$ we need the **Rodrigues formular**.
Parenthesis: Skew matrix: before we can look at the details, we need a short rethinking of the linearity of the cross-product:
For 3-D vectors we have:

$$\vec{u} \times \vec{v} = [\vec{u}]_\times \vec{v}$$

the skew matrix is defined by:

$$[\vec{u}]_\times = \begin{pmatrix} 0 & -u_3 & u_2 \\ u_3 & 0 & -u_1 \\ -u_2 & u_1 & 0 \end{pmatrix}$$

The matrix $[\vec{u}]_\times$ is called the skew matrix of $\vec{u}$ and it is basically produce the crossproduct between $\vec{u}$ and the vector which is multiplied by this matrix.
with this we can read the **rodrigues formular** which gives us the matrix we want:

$$R(\vec{u}, \theta) = \vec{u}\vec{u}^T + (1 - \vec{u}\vec{u}^T)\cos\theta + [\vec{u}]_\times \sin\theta$$

we can get this formula by looking at the geometric process:

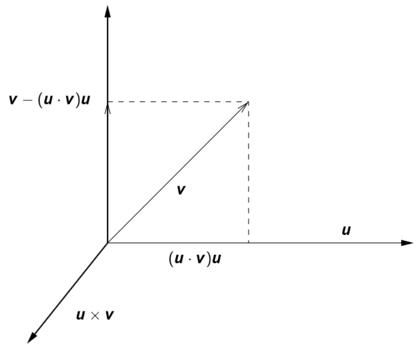

$\boldsymbol{v} - (\boldsymbol{u} \cdot \boldsymbol{v})\boldsymbol{u}$
$\boldsymbol{v}$
$\boldsymbol{u}$
$(\boldsymbol{u} \cdot \boldsymbol{v})\boldsymbol{u}$
$\boldsymbol{u} \times \boldsymbol{v}$

Abbildung 5.7.: Othogonal base vectors of the coordinate system

We have our $\vec{u}$ and want to rotation in the 3D the point $\vec{v}$. These two span an plane, if you compute the orthogonal vector of these plane we have a 3D-coordinate system. We can compute this vector with the cross-product: $\boxed{\vec{u} \times \vec{v} = [\vec{u}]_\times \vec{v}}$.
Additional we want a vector which is orthogonal to $\vec{u}$ but is in the plane which is span by $\vec{u}, \vec{v}$. We get this vector with $\vec{v} - (\vec{u}\vec{v})\vec{u}$[3] which we can rewrite to: $\boxed{(1 - \vec{u}\vec{u}^T)\vec{v}}$.

[3]for this compute the projection of $\vec{v}$ on $\vec{u}$

The projection of $\vec{v}$ on $\vec{u}$ is: $(\vec{v}^T\vec{u})\vec{u}$ we can reorganize this such that we find the definition of the outer product and so we come up with this rewritten form of the projection: $\boxed{(\vec{u}\vec{u}^T)\vec{v}}$.
And know we have nearly all components which are in the rodrigues formula. Summarized in other words, we have build up a artifical coordinate system in 3D based on $\vec{u}$ and $\vec{v}$. Now we can compute the components of $\vec{v}$ with respect to this coordinate system:

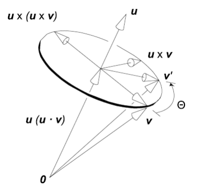


Abbildung 5.8.: artificial coordinate system

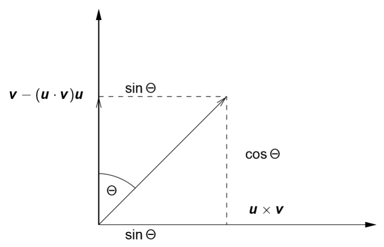


Abbildung 5.9.: Coordinate transform implied by rotation around the $\vec{u}$-axis

which leads us exactly to the rodrigues formular. If we multiply this with $\vec{v}$: $R(\vec{u}, \theta) \cdot \vec{v}$ we get exactly our base vectors of the artificial coordinate system as hey a written in the boxes.

3. Representation: Quaternion - Representation

the inspiration for quaternions comes from the registration idea with the complex numbers.

Quaternion representation:

Quaternions can be understood as an extension of complex numbers:
Three different numbers that are all square roots of -1:

$$i \cdot i = -1 \qquad j \cdot j = -1 \qquad k \cdot k = -1$$
$$i \cdot j = -j \cdot i = k \qquad j \cdot k = -k \cdot j = i \qquad k \cdot i = -i \cdot k = j$$

So a quaternion is a linear combination:

$$\boldsymbol{r} = w + xi + yj + zk$$

where

$$w, x, y, z \in \mathbb{R}$$

the conjugate and magnitude are defined as:

$$\bar{r} = w - xi - yi - zk$$
$$|r| = \sqrt{r \cdot \bar{r}} = \sqrt{w^2 + x^2 + y^2 + z^2}$$

The multiplication and summation are associative but the multiplication is **not** commutative: $r_1 r_2 \neq r_2 r_1$. The inverse quaternion of a unit quaternion is its conjugate.

We represent quaternions by a row vector $(w, x, y, z) = (w, \vec{v})$ where $\vec{v}^T = (x, y, z)$. With this notation the product of two quaternions $\boldsymbol{r}_1 = (w_1, \vec{v}_1)$ and $\boldsymbol{r}_2 = (w_2, \vec{v}_2)$:

$$\begin{aligned}
\boldsymbol{r}_1 &= w_1 + x_1 i + y_1 j + z_1 k \\
\boldsymbol{r}_2 &= w_2 + x_2 i + y_2 j + z_2 k \\
\boldsymbol{r}_1 \cdot \boldsymbol{r}_2 &= (w_1 w_2 - x_1 x_2 - y_1 y_2 - z_1 z_2) \\
&\quad + (w_1 x_2 + x_1 w_2 + y_1 z_2 - z_1 y_2) i \\
&\quad + (w_1 y_2 - x_1 z_2 + y_1 w_2 + z_1 x_2) j \\
&\quad + (w_1 z_2 + x_1 y_1 - y_1 x_2 + z_1 w_2) k
\end{aligned}$$

this product rewritten in matrix notation:

$$_*[\boldsymbol{r}_2] = \begin{pmatrix} w_2 & x_2 & y_2 & z_2 \\ -x_2 & w_2 & -z_2 & y_2 \\ -y_2 & z_2 & w_2 & -x_2 \\ -z_2 & -y_2 & x_2 & w_2 \end{pmatrix}$$

such that:

$$\boldsymbol{r}_1 \quad _*[\boldsymbol{r}_2] = \boldsymbol{r}_1 * \boldsymbol{r}_2$$

this is the same idea like in the skew matrix.

Now we take a look how we can express rotations with quaternions:

Let

$\vec{p} \in \mathbb{R}^3$ a 3-D point to be rotated,

$\vec{u} \in \mathbb{R}^3$ the axis of rotation, $\vec{u} = 1$,

$\theta \in \mathbb{R}$ the angle of rotation.
The rotation quaternion according to a rotation given in axis/angle representation is defined by:

$$\boldsymbol{r} = \left(\cos\frac{\theta}{2}, \sin\frac{\theta}{2} \cdot \vec{u}^T\right)$$

and now we interpret all 3-D points $\vec{p}$ we have as quaternions $\boldsymbol{p}' = (0, \vec{p})$.
Then te **rotation** can be computed by:

$$\boldsymbol{p}'_{\text{rot}} = \boldsymbol{r} \cdot \boldsymbol{p}' \cdot \bar{\boldsymbol{r}}$$

Note: there should be 0 but we can also put any value into the scalar part of the quaternion representation of our point. Also we should use a **unit quaternion**, since that will allow us to use the fact that the inverse of a quaternion is its conjugated of it (this hold only for unit quaternions !)
If we remember our problem with quaternions: we want to compute the rotation from $\vec{p}$ to get $\vec{q}$, and we interpret our 3D-Points as quaternions:

$$\begin{aligned} \boldsymbol{p}' &= (0, \vec{p}_i^T) \\ \boldsymbol{q}' &= (0, \vec{q}_i^T) \\ \forall i \qquad \boldsymbol{q}'_i &= \boldsymbol{r}\boldsymbol{p}'_i\bar{\boldsymbol{r}} \end{aligned}$$

the corresponding optimization problem:

$$\sum_i \|\boldsymbol{q}'_i - \boldsymbol{r}\boldsymbol{p}'_i\bar{\boldsymbol{r}}\| \longrightarrow \min$$

but the Problem is that this optimization Problem is **not linear**!
to come up with a linear solution we multiply the rotation equation 5.2 with $\boldsymbol{r}$ from the right:

$$\begin{aligned} \forall i \qquad \boldsymbol{q}'_i &= \boldsymbol{r}\boldsymbol{p}'_i\bar{\boldsymbol{r}} && (| \cdot \boldsymbol{r}) \\ \boldsymbol{q}'_i \cdot \boldsymbol{r} &= \boldsymbol{r}\boldsymbol{p}'_i\bar{\boldsymbol{r}} \cdot \boldsymbol{r} \\ \boldsymbol{q}'_i \cdot \boldsymbol{r} &= \boldsymbol{r}\boldsymbol{p}'_i && (\text{this is linear in } \boldsymbol{r}) \end{aligned}$$

out of the last line we can set up our linear optimization problem:

$$\hat{\boldsymbol{r}} = \arg\min_{\boldsymbol{r}} \|\boldsymbol{q}'_i\boldsymbol{r} - \boldsymbol{r}\boldsymbol{p}'_i\|^2$$

both terms $\boldsymbol{q}_i'\boldsymbol{r}$ and $\boldsymbol{r}\boldsymbol{p}_i'$ are products of quaternions they are linear in the component of $\boldsymbol{r}$ and we can rewrite this in matrix notation and do SVD to compute the quaternions !
the disadvantage of this representation is that we can't incorporate the translation into this optimization problem. So we have to do the translation into advance. A usable way is to compute the centre of gravity (then we have a estimation of t) compute then the rotation and repeat this in an iterative scheme until we are find with the results.
Hint: if you want to compute the mean of different rotation matrices you can use quaternions. Simple sum up and divide by the number does not work because we won't end up with an orthonormal matrix, so we have no rotation matrix any more. But if we use quaternions we can simple compute the mean !

Conclusion: We have the optimization Problem:

$$\min \sum_l \left\| \vec{q}_l - \boldsymbol{R}\vec{p}_l - \vec{t} \right\|_2^2$$

and we can represent the rotation matrix either in:

Euler-representation:

$$\mathbf{R} = \boldsymbol{R}_{\varphi_z}\boldsymbol{R}_{\varphi_y}\boldsymbol{R}_{\varphi_x}$$

Axis/Angle representation:

$$R(\vec{u},\theta) = \vec{u}\vec{u}^T + (1 - \vec{u}\vec{u}^T)\cos\theta + [\vec{u}]_\times \sin\theta$$

quaternions:

$$\begin{aligned} \mathbf{R}\vec{p}_l &\curvearrowright \boldsymbol{r}, \boldsymbol{p}_l' \\ \vec{p} \in \mathbb{R}^3 &\curvearrowright \boldsymbol{p}' = (0, x, y, z) \\ \hat{\boldsymbol{r}} &= \arg\min_{\boldsymbol{r}} \left\| \boldsymbol{q}_i'\boldsymbol{r} - \boldsymbol{r}\boldsymbol{p}_i' \right\|^2 \end{aligned}$$

Euler-representation and **Axis/Angle representation** gives us a **non-linear** optimization problem while the **quaternions** give us a linear optimization problem we can solve with SVD.

5.3. 3D/2D registration

Another case that appears is that we have a 3D-Volume and a 2D image and we want to register these two. So we need to compute the rotation and the translation and afterwards the projection.
This we have already solved, its basically the solution we considered in the chapter of calibrating perspective cameras. There we have a calibration pattern and compute a rotation, translation and a projection from 3D to 2D.
Hint: For all the introduced algorithms for registration used point correspondences the point correspondence has to be known, and normally that is not the case !

5.4. registration without makers

we also can apply our registration methods to datasets without marker which gets applied to the patient. We need a pre-computing step where we compute so called **anatomic landmarks**. A good example is the bronchial tree where you can compute the points where the vessels split up and use these point at the ramifications for point correspondence.

5.5. Similarity measures - registration without point-correspondences

How can we register Images using intensities only, so we have no point correspondences ?
So we have only a intensity based image registration.
The notation for the following:

- $[f_{i,j}]$: reference image
- $[g_{i,j}]$: image to be registered
- T: transform
- $\bar{f}$ mean intensity value of reference Image
- $\bar{g}$ mean intensity value of second image

5.5.1. Single mododal Registration

In the first case we look at images which are acquired by the same modality:
Basic Idea:

> What we are looking for is a similarity measurement, a function that gives us a number, where this number is a hint whether they two images are well registered or not.

The first similarity Measures we consider is the sum of squared differences (SSD). If you take two pictures with the same modality and the object has moved then the SSD values raise up, if both images show exactly the same situation then the SSD-value is a very small value (due to Noisy it is not Zero):

$$\sum_{i,j}(f_{i,j} - g_{i,j})^2 = SSD(f, g)$$

If the two images are taken from a different perspective than the SSD also goes up. With this we can build up a system which can compute a rigid transform based on intensity values: by doing the transform on the incidences of the second image and minimize that difference, if two images differ only by rotation and translation (so rigid transform) this will work:

$$\hat{T} = \arg\min_T \sum_{i,j} \|f_{i,j} - T\{g_{i,j}\}\|^2$$

these similarity measures are not independent on scaling from the intensity values, so if we have two images showing the same scene but with scales intensity values (due to illumination or changing X-Ray dose etc.) our SSD will be not as low as it could be and our transform approach above can't solve it properly.
This gives us the second similarity measure the Cross-correlation coefficient: normalize the intensities with respect to the mean value, the dominator does the proper scaling of the intensity values

$$\hat{T} = \arg\max_T \frac{\sum_{i,j}(f_{i,j} - \bar{f})(T\{g_{i,j}\} - \bar{g})}{\sqrt{\sum_{i,j}(f_{i,j} - \bar{f})^2 \sum_{i,j}(T\{g_{i,j}\} - \bar{g})^2}}$$

with this you can register two images which shows the same structure but differ in the intensity level.
Hint: if the structure in the two images differ (e.g. a shrinking Tumor due to the therapy) and you use the approach above then the registration will not work properly because it tries to reduce the avager error. A solution to this would be: extract non-changing structure (e.g. bones) compute the transform for this and apply it to

the whole image. Then you have a good registration and can compute for example the difference in the volume of the two tumors.
To check how good the registration is, you can split both images into small patches and build a new image out of the patches from the two images, then if we have a perfect registration we should not see the checkerboard (th patches). If re registration is not good we can identify the patches because the structure does not match.

5.5.2. Multi-modal Registration

To register two images captured by different modalities we need another approach. The quest is how can we perform intensity based image registration using images acquired by different modalities?
This problem can be solved with statistic. If we have for example an CT and an PET dataset. If they show somehow the same scene then we can they this are two random variables which a not independent, and we look for the mutual information. We can measure this with the Kulback-Leiber divergence:

$$KL(p||q) = \int\int p(x,y) \log \frac{p(x,y)}{q(x,y)} dxdy$$

if p and q are the same, the logarithm is one, so the KL is Zero. The more p, q differ the higher the KL gets.
We core thought is:

> If we have a transformation T to register an CT image f with an PET image g, then the pixel should be statistically dependent as much as possible

in lecture this was explained based on communication channels. I would they think link is due to the fact that we measure the same object but with different methods but the measurement is totally linked because we get from the object with each modality a subset of the whole object information.
In statistically notation the statistically dependent can be written as:

$$p(f,g) \neq p(f)p(g)$$

if they are statistically dependent, then we cant split $p(f,g)$ in that way. So if we want to maximize the mutual information, the statistical dependent then we can they $p(f,g)$ should be different to $p(f), p(g)$:

$$KL(p||q) = \int_f \int_g p(f,g) \log \frac{p(f,g)}{p(f)p(g)} dfdg$$

the higher the KL is the more $p(f,g)$ and $p(f)p(g)$ differ and that mean the more statistically dependent f and g are. This KL-divergence is a very powerful similarity measure !
We go with an „Example:“
registration of CT) and MR data set:

1.Step:

$$\sum_{i,j} p(S(i,j),R(i,j)) \log \frac{p(S(i,j),R(i,j))}{P(S(i,j))P(R(i,j))}$$

we can compute the joint density and with marginalization we can compute the single pdf's. Or we take the relative frequencies out of the histogram.

2.Step: parametrization: Rigid transform: rotation, translation $\rightarrow$ 6 degrees of Freedom

3.Step:

$$\text{maximize} \quad \sum_{i,j} p(S(i,j),R(i,j)) \log \frac{p(S(i,j),R(i,j))}{P(S(i,j))P(R(i,j))}$$

5.5.3. General Meta-Registration Algorithm intensity based

We can think about an abstract algorithm where we can put in our similarity measurement.
An intensity based registration:

1. Define a similarity measure
2. Define the „parametrization“of the transform
3. Optimization algorithm

Example Registration of two CT-data sets with source S and reference R.

1. Step: = Similarity measure SSD:

$$\sum_{i,j} (S(i,j - R(i,j)))^2$$

2. Parametrization: Rigid transform: rotation, translation $\rightarrow$ 6 degrees of Freedom

3. Optimization:

$$\text{minimize} \quad \sum_{i,j} (S(i,j) - R(i,j))^2$$

5.6. Iterative Closest Point (ICP)

In the real world the ICP is a often used algorithm to do registration with point correspondence. And as in the real world its normal, the point correspondences are not known. The ICP computes the registration by iterating the following steps:

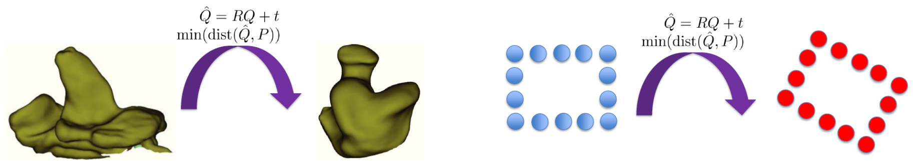

$\hat{Q} = RQ + t$
$\min(\text{dist}(\hat{Q}, P))$
$\hat{Q} = RQ + t$
$\min(\text{dist}(\hat{Q}, P))$

Abbildung 5.10.: Problem description: find the transformation such that both meshes fit to each other

1. Computation of correspondences between to point clouds
2. Computation of a transformation which minimize the distance between the corresponding points

The Algorithm in Words:
start with an initial point correspondence (very simple correspondence) and then repeat the following until convergence:

- transform the Point with the estimated transformation and calculate the closest point to $T(p)$ in q
- Compute the difference between the transformed point and the closest point: If this difference is below a threshold encode in binary that this is a good assignment (weight by 1) or its not a good assignment if its over the threshold (weighted by zero)
- Compute a new estimate of the transformation with the minimization of the similarity measurement which takes only well assign points

Algorithm 1: Iterative closest point [6]

Input : Two point clouds: P, Q

Output: Transformation $\boldsymbol{T}$, which aligns P and Q

```
$\boldsymbol{T} \leftarrow \boldsymbol{T}_0$;
while not converged do
    for $i \leftarrow 1$ to $N$ do
        $\boldsymbol{c}_i \leftarrow$ GetClosestPointInQ($\boldsymbol{T} \cdot \boldsymbol{p}_i$);
        if $\| \boldsymbol{T} \cdot \boldsymbol{p}_i - \boldsymbol{c}_i \| \leq \theta_{max}$ then
            $\omega_i \leftarrow 1$;
        else
            $\omega_i \leftarrow 0$;
        end
    end
    $\boldsymbol{T} \leftarrow \underset{\boldsymbol{T}}{\arg\min} \sum_i^N \omega_i \| \boldsymbol{T} \cdot \boldsymbol{p}_i - \boldsymbol{c}_i \|^2$;
end
```

Abbildung 5.11.: ICP in Pseudo-code

6. Exercise1

1 SVD

1a

Create a Matrix: $\mathbf{A} = \begin{bmatrix} 11 & 10 & 14 \\ 12 & 11 & -13 \\ 14 & 13 & -66 \end{bmatrix}$ Check the determinant of this matrix. Compute the inverse matrix of **A** without using MATLAB command **inv**:

```
A = [11 10 14 ;
    12 11 -13;
    14 13 -66];

 [U S V] = svd(A);%make the SVDecomposition

 Ainverse = V * S^(-1) * U' %compute the pseudo-inverse . If the matrix is invertible
                            %then the pseudo-invers will be the inverse
```

Compare the result to $\mathbf{inv(A)}$ → it's the same
How do we get the condition number and what does the condition number express?
The condition Number can be computed with SVD: divide the largest number of **S** by the smallest. (Hint: the first divided by the last element on the diagonal of**S**).

```
 kappaA = S(1,1) / S(length(S),length(S))
```

- a condition number near to 1 means the matrix is well-conditioned.
- a condition number which far away from 1 means the matrix is.

1b

With the command **eigshow** you can see how the Matrix affect the unit-ball (for 2D). Because you use the uni-vectors for this you can see in a way the geometrical representation of the Matrix.

1c

If you set the threshold $\epsilon = 10^{-3}$, you get a rank deficiency. How can you get the null space and the rank of the Matrix **A**? The null space determine all vectors which fulfil the following equation (the zero-vector is the trivial case): $\mathbf{A}\vec{x} = 0$ You can use SVD to determine the null space. Take the collumn-vector of **V** which is related to the zero-entries on the diagonal of **S**. In our example case, the last diagonal entry will be zero after you applied the Threshold. Which means the last collumn of **V** is the null space for Matrix **A**.

```
kernelA = V(:,3)
```

The rank of a Matrix can also be determine with SVD. Just count the non-zero entries in the diagonal of **S**:

```
%The rank of the matrix are all non-zero entries on the diagonal of S
rankA = nnz(S)
%The range are the related collumns in U to the non-zero entries in S
rangeA = U(:,1:2)
```

The range of the Matrix **A** is then the collumn-vectors of **U** which are related to the non-zero entries of **S**.

1.1

Show that a variation of elements of $\vec{b}$ by 0.1% implies a change in $\vec{x}$ by 241%.

```
b = [1.001;0.999;1.001];
x = Ainverse * b
%Console:
x =
   -0.6830
    0.8430
    0.0060

%changing b by 0.1%
b = [1.002001;0.999;1.001];
x = Ainverse * b
%Console:
x =
   -1.2406
    1.4536
    0.0080
```

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