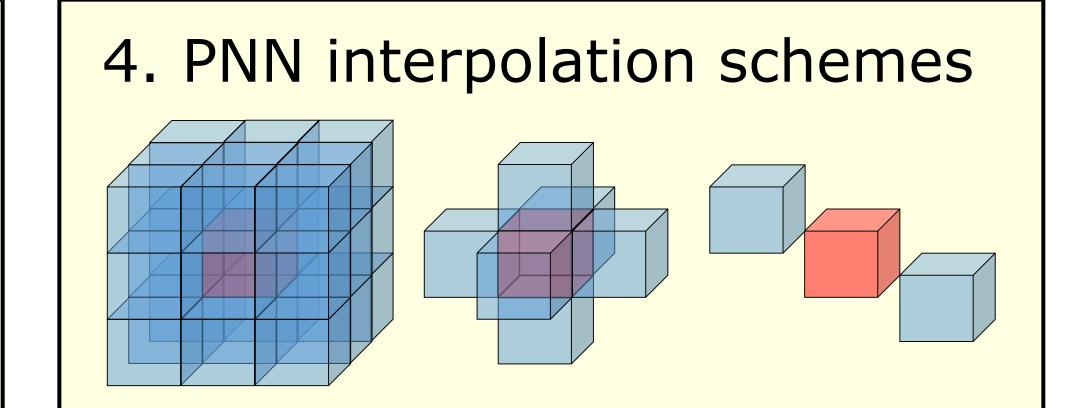
3D Image Reconstruction for Medical Applications

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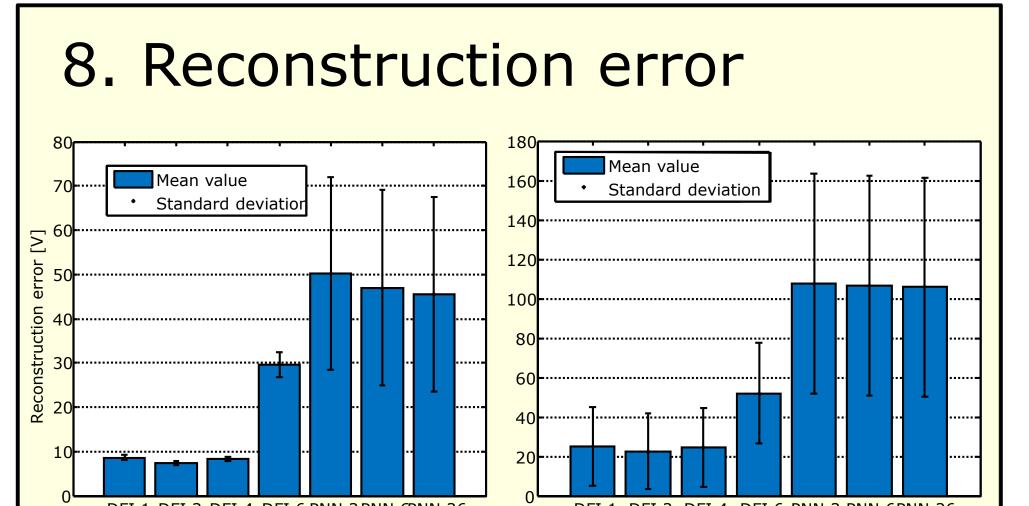
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1. Introduction

- Medical image data is typically <u>acquired line by</u> line, plane by plane, or spiral wise
- The <u>coordinate system of the acquired data is</u> based on physical constrains, i.e. the geometric set up of the acquisition system
- The operator, physician, radiologist, or reader will often require images that are oriented differently



Neighborhoods used in PNN (conventional) experiments: 26 neighbors, 6 neighbors, example of 2 neighbors. The 26-neighborhood and the 6neighborhood are always applied as shown. The 2neighborhood depends on the mean scanning direction, i.e. probe trajectory.



- Furthermore, post processing applications or algorithms might need images that a oriented on predefined fixed grid (e.g. radiation therapy, CAD/CAM)
- A multitude of previously published methods exist that will perform this reconstruction step
- Reconstruction is fast and mathematically simple, if a single spatial transformation exists between acquired image data and the reconstructed image or volume
- In most applications, this is the case: CT, MRI, OCT, CBT, US based on 3D probes, etc.
- However, there are exceptions like free hand <u>ultrasound or "irregular acquisitions"</u> that come with <u>several spatial transformations per volume</u>
- For these exceptions, conventional reconstruction methods easily reach their limits
- Forward reconstruction methods that can deal with <u>unambiguous spatial data</u> are required instead of reverse/backward methods

2. Methods

5. SLERP algorithm

$$=\frac{q_1 \sin((1-u)\Omega) + q_2 \sin(u\Omega)}{\sin\Omega} \qquad \Omega = \arccos(q_1 \cdot q_2)$$

The SLERP algorithm calculates a unit quaternion q' which lies between two known unit quaternions, q_1 and q_2 that represent positions of two adjacent image frames to be interpolated. The angle Ω between these two image frames is calculated by estimating the dot product between q_1 and q_2 , while *u* can take values between 0 and 1 and stands for the distance of the new image frame from the first original image frame

6. Evaluated methods

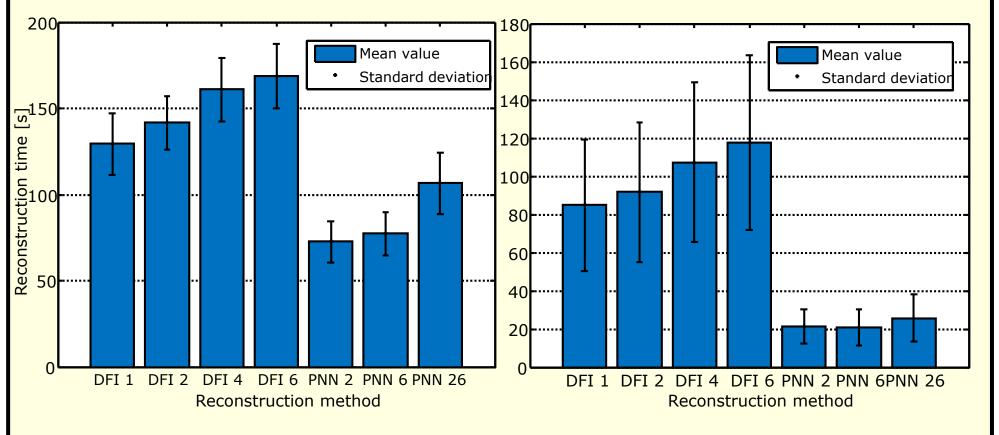
Reconstruction Interpolation method order

Comment

Reconstruction method

Reconstruction errors of laboratory dataset (left) and clinical dataset (right): mean errors or gray value differences together with their standard deviations over datasets between volume reconstructions based on original image series and on reduced image series containing only 50 % of the original images (leave-some-out tests)

9. Reconstruction times

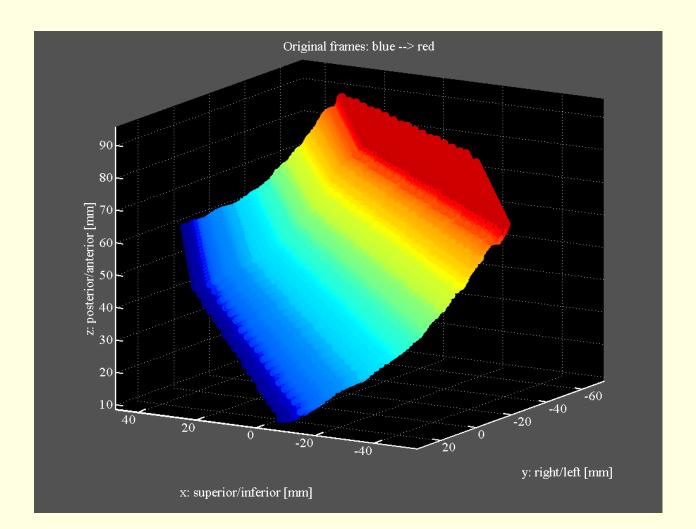


Mean execution times and standard deviations of volume reconstruction for different reconstruction methods of laboratory dataset (left) and clinical dataset (right)

- We present a method that is very fast and robust, also for reconstruction problems that are based on a multitude of spatial transformations
- Because <u>spatial transformations</u> from acquired samples to target samples <u>might be</u> unambiguous, a forward reconstruction method is preferred
- Taking into account the availability of multi threading environments, a new method should allow parallelization of the most time consuming reconstruction steps
- Furthermore, memory nowadays is widely available and no longer a serious bottleneck while fast reconstruction times are still important. So CPU load goes before memory consumption.

| methou | Uluei | |
|--------------------------------|-------|---|
| Direct rame nterpolation | 1 | Nearest neighbor interpolation between image frames. The pixel is filled with the same gray value as the nearest sample, i.e. pixel. |
| | 2 | Linear interpolation between two image frames based on the SLERP method. |
| | 4 | Four point interpolation between four image frames based on the SLERP method. |
| | 6 | Six point interpolation between six image frames based on the SLERP method. |
| NN nterpolation | 2 | Linear interpolation between the two nearest voxels encountered on the scanning path of the transducer. |
| | 6 | Linear interpolation between the six nearest voxels found in all six directions of the cubic grid. |
| | 26 | Linear interpolation between the 26 nearest voxels found in the cube or hull surrounding the voxel to be estimated. |

7. Reconstructed volume



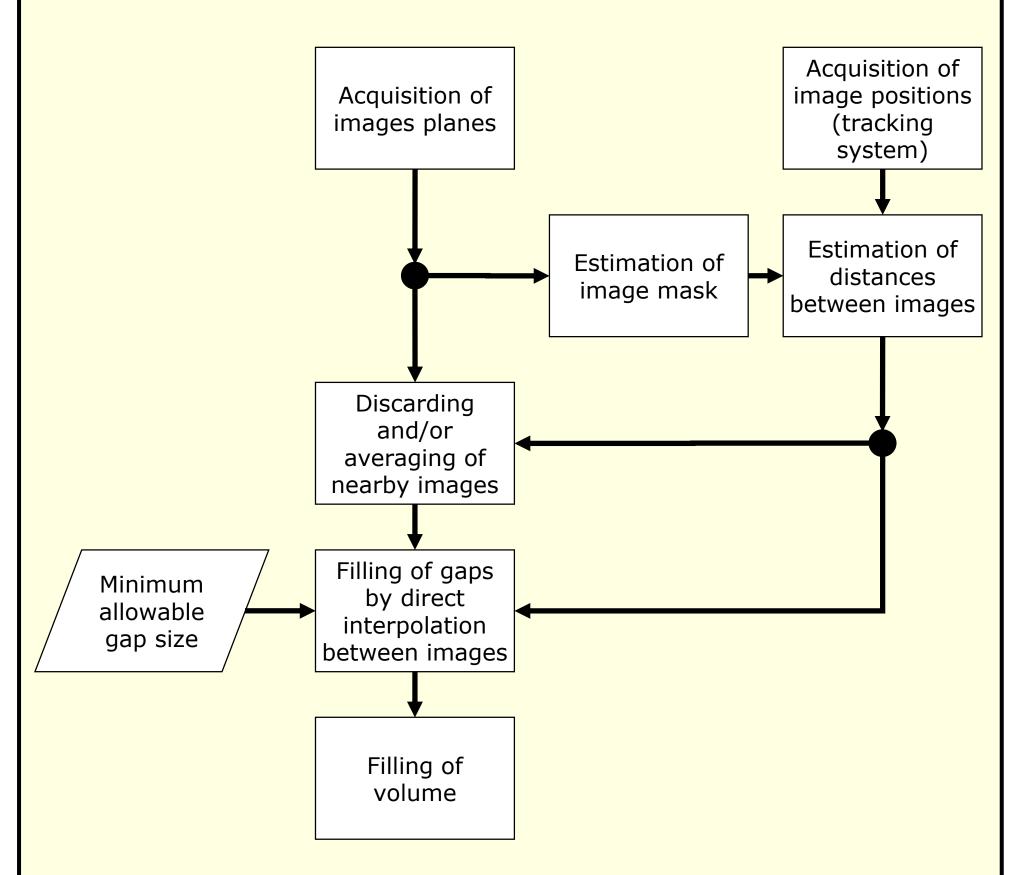
10. Dataset sizes

| Environment | Number of acquired | Average size of volume / voxels | | |
|-------------|-----------------------|---------------------------------|-----|-----|
| | image series | Х | У | Z |
| Laboratory | 8 | 507 | 551 | 503 |
| Clinic | 73 | 422 | 379 | 402 |
| | | | | |

11. Conclusion

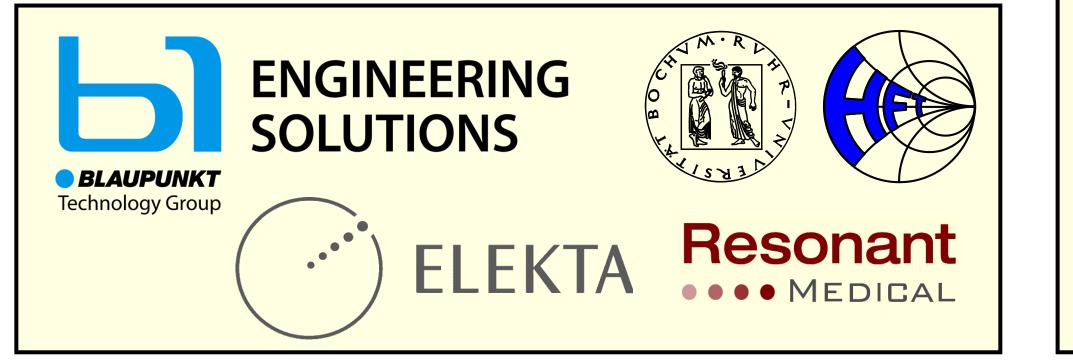
- What is shown is that the direct frame interpolation method yields a very low reconstruction error, that is lower than the error of the compared conventional methods (making <u>up for missing data</u>)
- Furthermore, the required <u>reconstruction time</u> of the proposed method is within the ranges of the conventional method used for comparison
- Further execution time improvements were achieved when porting the algorithms from MATLABTM to C++
- The proposed method replaced conventional reconstruction methods in the Resonant Medical/Elekta Clarity[™] system

3. Block diagram: DFI method



Block diagram of direct frame interpolation method (DFI). The method consists of three main steps: averaging and/or discarding of close images, interpolation and insertion of new intermediate images, conversion of images to volume.

Example frame series of 156 frames taken from the laboratory image series. Relatively slow and constant scanning speeds were used for the laboratory datasets while faster and irregular scans were typically found in the clinical datasets.



12. References

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