An Adaptive Genetic Algorithm for Misalignment Estimation in Spiral, Sequential and Circular Cone-Beam Micro-CT

Stefan Sawall[1], Michael Knaup[1], and Marc Kachelrieß[1,2]
[1]Institute of Medical Physics, University of Erlangen-Nürnberg, Germany
[2]Medical Physics in Radiology, German Cancer Research Center (DKFZ), Heidelberg, Germany

Purpose:

The reconstruction of volumetric datasets based on micro-CT scans is a common task in every small animal imaging lab. The used reconstruction algorithms rely on the actual knowledge of the scanner geometry. If this geometry is misaligned severe artifacts in terms of edge blurring and a loss in spatial resolution appear in the reconstructed images. We propose a novel method to estimate the actual geometry of micro-CT scanners using an adaptive genetic algorithm. The proposed algorithm is able to estimate the actual scanner geometry, the direction vector of table movement and the displacement between different imaging chains of a scanner. The calibration procedure does not rely on dedicated calibration phantoms and a sequence scan of a single metal bead is sufficient to calibrate the whole imaging system for spiral, sequential and circular scan protocols. The algorithm's performance is evaluated using simulations of a micro-CT system with known actual geometry as reference. To assess the quality of the algorithm in a real world scenario the calibration of a micro-CT scanner is performed and several reconstructions with nominal and actual geometry are presented. The results indicate that the algorithm succesfully estimates all geometry parameters as misalignment artifacts in the reconstructed volumes vanish and the spatial resolution is increased as can be shown by the evaluation of MTF measurements.

Materials and Methods:

We assume a micro-CT system with several distinct source-detector chains (threads). For each thread the parameters s, o, u and v have to be estimated (see figure 1 and 2). As the calibration algorithm must not depend on dedicated calibration phantoms only a single metal bead is used as phantom. To acquire the data necessary for the geometry estimation this metal bead is placed at an arbitrary position on the table and a spiral or sequence scan is performed using all threads of the acquisition system resulting in elliptical trajectories on the detector. Thus also the sphere positions with respect to the center of rotation are additional unknown parameters. The geometry estimation task is formulated as optimization problem minimizing the squared distance between the measured sphere trajectories and the current estimate of the geometry, table direction vector and sphere positions. Literature shows that this optimization problem cannot always be reliably solved by standard numerical methods like the Levenberg-Marquardt algorithm. Hence we propose the use of an adaptive genetic algorithm (see figure 3) to find a global optimum of the cost function. The algorithm is tested using simulations and scans of real world objects, e.g. a mouse.

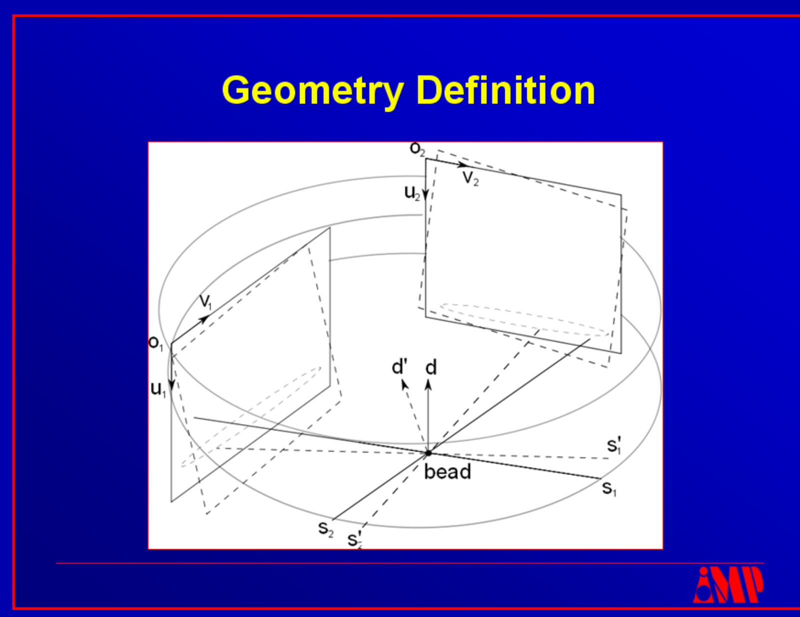

Figure 1: Geometry parameters of a dual-source micro-CT and a spiral scan protocol. Nominal geometry (solid lines) compared to the misaligned geometry (dashed lines).

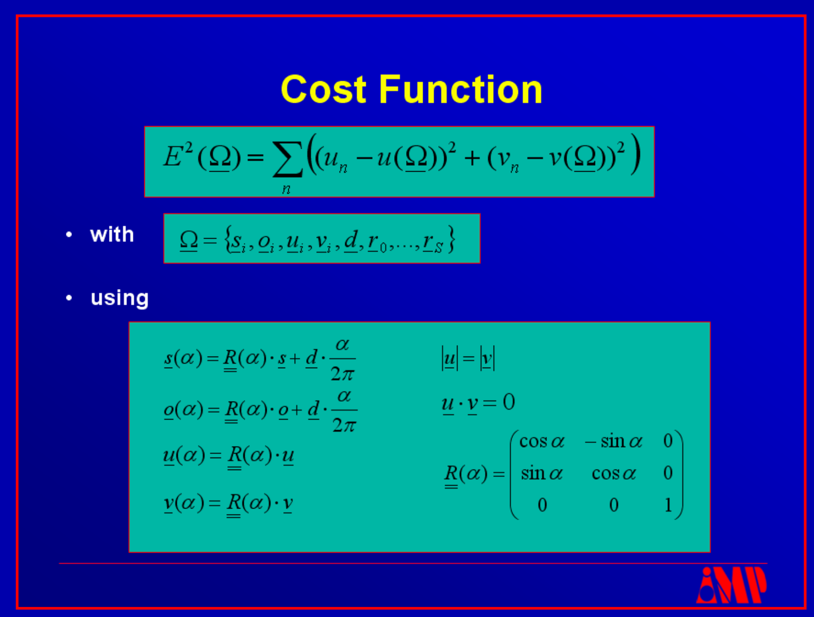

Figure 2: The cost function and the parameter vector Ω including the s, o, u, v, d, vectors for each imaging chain and the sphere positions r_0 to r_S.

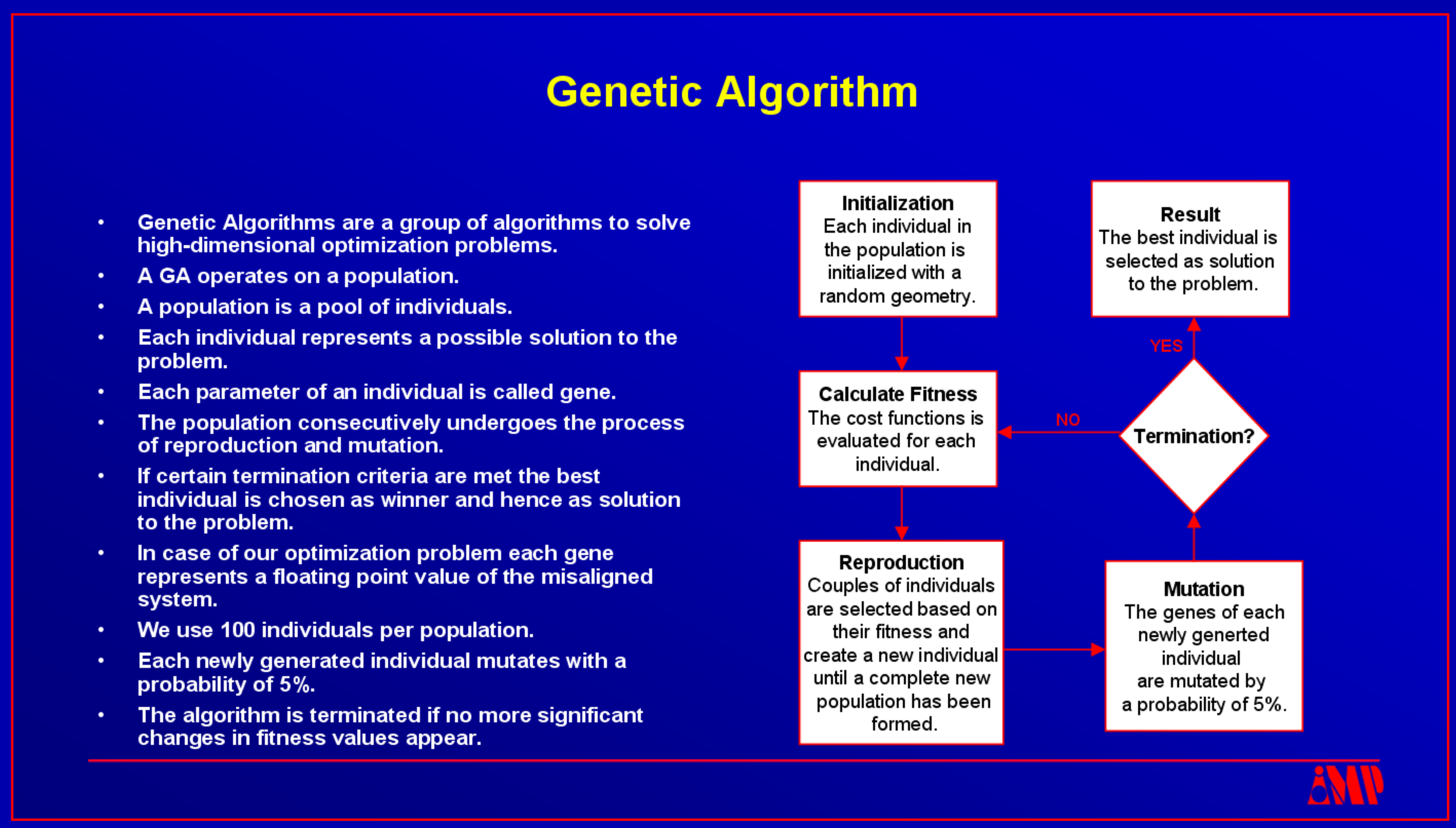

Figure 3: Brief introduction to genetic algorithms. In case of our optimization problem a population of the GA contains 100 individuals. The fitness value is the inverse cost function (see fig. 2), thus an individual that provides a high fidelity to the measurements is assigned a high fitness. This results in an increased probability for reproduction. To ensure convergence of the algorithm the 5 best individuals of each generation are transferred to the next generation without modifications.

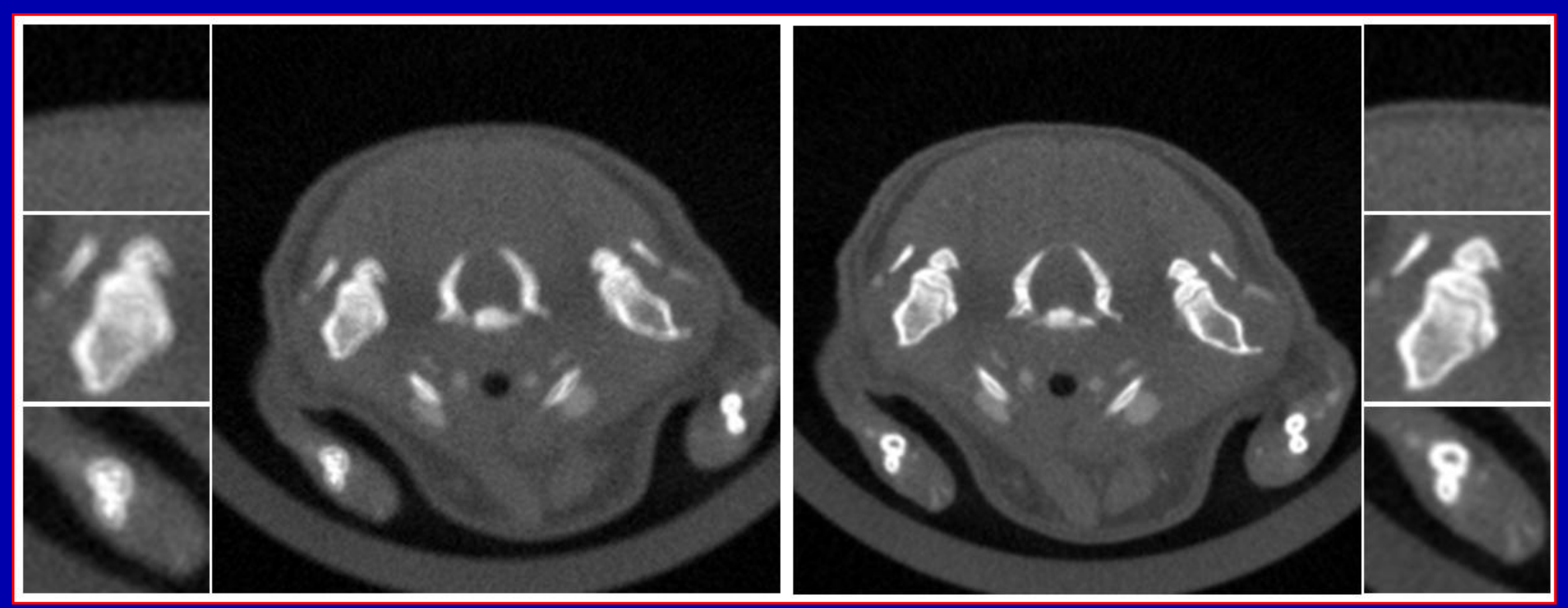

Figure 4: Scan of a contrast enhanced mouse and selected regions of interest reconstructed without proper misalignment estimation (left) compared to a reconstruction using the misalignment parameters estimated by the proposed method (right).

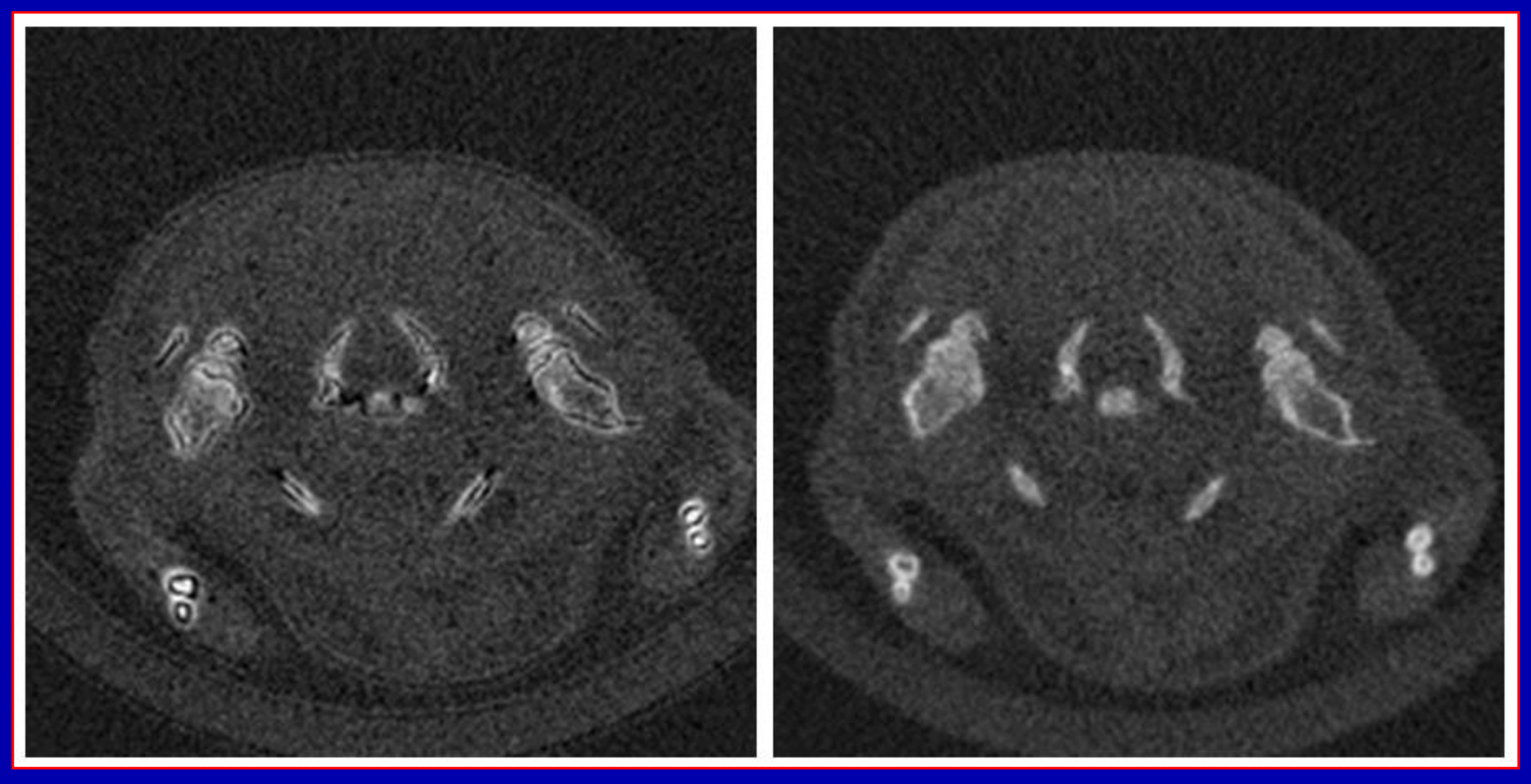

Figure 5: Difference images between thread 1 and thread 2 of a dual–energy scan. Reconstructions obtained using the nominal geometry (left) and reconstructions obtained using the estimated parameters (right). (C=0 HU, W=50 HU)

Results:

The simulations show that the estimated parameters differ by less than 2 % from the simulated parameters thus indicating that the proposed algorithm is able to accurately estimate the misalignment. Reconstructions originating from our scanner (TomoScope Synergy Twin, CT Imaging GmbH, Erlangen, Germany) obtained by using the nominal and estimated geometry can be found in figures 4 and 5. For comparison reasons the left parts of the figures show reconstructions using the nominal geometry. Due to the misalignment the inserts in case of the mouse phantom and the bones in case of the real mouse scan appear blurry and distorted. The right hand sides of figure 4 and 5 show similar slices of the same objects reconstructed with the parameters estimated by the method presented here. The blur is removed and object borders appear sharper than in the reconstructions using the nominal geometry.

Conclusion:

The proposed algorithm is a new method to estimate the actual geometry of a micro-CT systems. It was proven by simulation that the algorithm is capable of accurately estimating all geometric parameters as well as the table direction vector. The algorithm was further assessed to calibrate a real micro-CT system. The comparison of reconstructions obtained with nominal parameters and estimated parameters shows that the proposed algorithm can significantly improve image quality.

Acknowledgements:

This work was supported in parts by the Deutsche Forschungsgemeinschaft (DFG) under grant FOR 661 and in parts by the AiF under grant KF2336201FO9. The reconstruction software RayConStruct–IR was provided by RayConStruct®, Nürnberg, Germany.

Send correspondence requests to:

Stefan Sawall
Institute of Medical Physics (IMP), University of Erlangen-Nürnberg
Henkestr. 91, 91052 Erlangen, Germany
stefan.sawall@imp.uni-erlangen.de

GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION