Matching Lung Volume Data Sets – A Novel Approach

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A B S T R A C T

There is a significant demand in matching CT datasets of the lung. The increasing number of CT slices per examination due to the higher resolution of modern CT scanners and the need for quantification of the progress of disease and healing processes in follow-up studies. A volunteer's lung was scanned by the means of multidetector CT in two different states of ventilation. The necessary lung structures for the matching procedure like lung surface and branching points were segmented. A thin-plate spline method was used to calculate the matched lung volume. The preliminary results show an average error of 2 voxel, i.e. 2mm. The calculation of the transformation matrix takes about one second on a conventional PC, which is considerably faster than other methods described in literature. The method described may be apt to be introduced in radiological practice when it comes to compare high resolution CT scans in follow-up studies quantitatively.

Key words: *computed tomography, lung volume data set matching, non-rigid transformation*

Introduction

Due to the finding of the Tyrolean Iceman in 1991[1] new imaging, postprocessing and visualization techniques were introduced into medicine and anthropology. In the early nineties major developments and improvements were made like the invention of high resolution and spiral CT as well as the feasibility of 3-dimensional reconstructions and rapid prototyping techniques.

Horst Seidler has been becoming a main contributor in the fast growing research field of »Anthropology-Radiology« since then. He set up a strong and very fruitful collaboration with the Depart-

ment of Radiology II, University Hospital Innsbruck and showed how modern imaging techniques can be successfully applied in anthropology. Throughout the collaboration a number of unique results and findings have been discovered.

The Iceman's skull was the first in the world to be built with stereolithography even before this technique was used in preoperative planning[2,3]. With the advent of high-end graphics workstations and biomedical image-processing software-packages 3-dimensional reconstructions were established as a routine tool for analyzing volume data sets[4]. These techniques opened totally new insights in the field of physical anthropology[5]. Computed tomography appeared to be an ideal research tool to get access to internal structures of various precious fossils without touching or even destroying them. Many of the most precious specimens from the species Autralopithecus africanus and Australopithecus boisei, Homo heidelbergensis, Homo ergaster or Homo sapiens neanderthalensis were scanned during the last years.

Often the fossils are filled with stone matrix or other materials. During the postprocessing routines highly advanced algorithms – originally developed or modified for bio-medical image analysis and related fields – were used to remove these incrustations. Thus it was possible to get access to morphological structures that lie beneath the matrix[6]. On the other hand unfortunately some specimens are partly destroyed. The missing parts were reconstructed on computer screen in order to get good estimations of the brain volume, a field of major interest in anthropology[7]. Moreover the computerized form of the data allows new descriptions of morphologic structures by the means of statistical shape analysis and geometric morphometrics. Some of the results may change aspects and interpretations in human evolution[8]. Thus the introduction of

new imaging and postprocessing techniques created a new field of research and Horst Seidlers team invented the term as well as it plays a leading part in the scientific community: Virtual Anthropology[9].

Many of the imaging and postprocessing techniques used and evaluated in anthropology can be successfully applied in medicine – and vice versa. The success of the interdisciplinary work group »Anthropology-Radiology« convinced Horst Seidler to establish an international team focusing on some of the major questions in human evolution in applying new – mathematical – methods to describe morphology and its development. This resulted finally in enthusing Fred Bookstein among other prominent researchers in the field to join the group. Although the main focus was on statistical shape description in anthropology there has been considerable interest in introducing these techniques into radiological research and practice. For the first time these techniques validated in anthropology are transferred to a challenging topic in medical imaging: the matching of CT data sets of the largely deformable organ lung.

Computed tomography has been developing to the method of lung examination of choice. Recent developments both in CT technology and image analysis allow quantitative lung image analysis. There is a considerable interest for these techniques in order to identify lung diseases early and to follow the progression of disease and/or healing processes.

Although the radiologist's interpretation and report is definitely of great importance, there is increasing recognition that the human observance is lacking of reproducibility when unaided by computer methods. This is essentially of importance when it comes to quantification of disease. The only reasonably working and recognized methods seem to be the automatic detection and quantification of

lung disease. On the other hand there is an increasing demand to make CT datasets easier accessible for the radiologists during routine examinations because the new technologies acquire about 10 times more images for the same examination compared to the techniques available just 5–7 years ago. Computed aided diagnosis (CAD) is in fact a very vivid field of image analysis and image processing research.

With the advent of so-called low dose protocols which comprise of a total radiation exposure of only 1 to 2 conventional thorax x-ray examinations but delivering volume data sets with 1mm slice thickness, preventive care examination of the lung seems feasible in terms of ethic considerations and patient care. Certainly the signal to noise ratio is limited with these protocols, but an overall analysis as part of preventive care medicine is still possible. Sophisticated image analysis software packages allow deriving most out of these data with the goal of early detection of lung disease like interstitial lung defects[10].

Advanced histogram analysis allows the detection of air and blood content in the lung as well as the lung tissue part on a regional basis. There is a number of sophisticated image analysis techniques described[11,12] to get access to the parenchymal tissue characterization like diffuse lung diseases, e.g. emphysema processes or lung fibrosis at an early stage. Many of these techniques were developed and/or validated at the University of Iowa and are partly implemented in a software package called PASS (Pulmonary Analysis Software Suite).

One of the prerequisits in some cases is the matching of whole CT lung volume datasets in all three spatial dimensions to compare quantitatively on a regional basis two lungs (»what happens where and when to what extent«) in follow-up studies. Warping (or matching) the lung volumes allows also to get access to biomechanical properties, disease development and therapeutic effects on the lung.

Currently there are a few methods published because of the complexity of the method. Lungs are extremely deformable objects and many of the classical methods won't work sufficiently. Each of them is based on different approaches and algorithms and has their advantages and disadvantages. Some methods use kinds of rigid transformation[13] which may be accurate enough to find and measure lung nodules in a follow up study, others are using non-rigid techniques and they are accurate enough for functional studies on a regional basis. But rigid methods cannot be used for functional analysis and the non-rigid approaches described may be too computer power intensive and therefore too slow for practicable clinical use. One may think of the quantification of aeration in specified volumes of interest in the lung which can be of great interest in respiratory therapy.

In a hospital environment a quick and accurate approach is necessary. Recent developments in landmark based non-affine transformation methods seem to make it possible to apply these technologies in matching largely deformable organs like the lung.

The results presented here should be considered as »preliminary«, it is the first »prove of concept« of our approach.

Methods

Computed tomography

Multidetector CT of the newest generation comprise of at least 16 detectors and a rotation speed of 0.5 sec and below. In fact for our test data set a Siemens Sensation 16 with 375 ms rotation time and 16 detectors was used. The volume data sets with a spatial resolution of 0.6x0.6x0.6 mm consisted of about 600

images. The scans were performed with 40 mAs and 120 kV. A volunteer's lung was scanned at two different states of inspiratory level: at the functional redual capacity and at the tidal volume of the lung representing a lung volume change of about 35%.

Image processing and analysis

Computed tomography is an accurate method to determine volume and regional gray value distribution, i.e.: lung density. The primary steps in evaluating the lung may include:

- Lung segmentation (includes identifying structures like bronchial tree, extracting the lung surfaces);
- Identifying bronchial branches and its centerline (i.e. finding true landmarks for the following matching process);
- Lung volume matching.

In a further analysis these steps can be performed:

- Regional histogram evaluation;
- Texture analysis;
- Categorize lung regions according to functional parameters like respiratory protocols, perfusion and ventilation.

As mentioned above, our team focuses on development of methods, which allow the comparison of different lung volume CT scans. In the clinical practice the success of a therapy is usually controlled by follow up CT scans. Our methods shall lead to a software package, which will help the radiologists in a faster analysis and quantification of those follow up scans by automatically displaying the equivalent regions within different lung volumes.

Methods for data comparison and matching in lung CT images

CT scans are steadily gaining better resolution and therefore delivering significantly more images. Several attempts have been made to provide computer aided analysis for more efficiency. The majority of these tools scan one dataset for suspect structures and display the region of those structures for further examination by the radiologists.

Challenge

Given an arbitrary position xyz of a voxel in lung volume A, the position x'y'z' of the equivalent voxel in lung volume B has to be determined. To be able to calculate the position x'y'z' a transfer function F: x'y'z' = F (xyz) has to be found.

This transfer function has to respect two major issues:

First the position and orientation of a patient in the CT gantry is different each time.

Second the lung is a non–rigid organ (on the contrary to the brain where image fusion is successfully used since years), which leads to different volumes according to the amount of the breath the patient has taken.

Approach

The theory of morphometrics, which can be seen as the art of shape description, provides us with the mathematical background for the determination of the function F. Geometric morphometrics can be seen as a collection of approaches for the multivariate statistical analysis of Cartesian coordinate data.

The data base of a morphometric inquiry consists of samples of discrete points, which correspond among all the forms of a data set. According to Bookstein these points are called landmarks[14].

Within the lung volume the branching points of the bronchial tree serve as landmarks. Hence as the first step of the determination of the transfer function from lung volume A to lung volume B, the corresponding branching points have to be determined and as the result of this step

for later use arranged in pairs of coordinates xyz and x'y'z'.

In a second step the landmarks are used to calculate the thin plate spline function which describes the shape deformation between the volume A and volume B.

The name »thin plate spline« refers to a physical analogy involving the bending of a thin sheet of metal. In the physical setting, the deflection is in the z direction, orthogonal to the plane. In order to apply this idea to the problem of coordinate transformation, one interprets the lifting of the plate as a displacement of the x or y coordinates within the plane. Thus, in general, two thin plate splines are needed to specify a two-dimensional coordinate transformation, and three thin plate splines are used for the three dimensional transformation of the lung volumes.

A thin-plate spline $f(x,y)$ is a smooth function which interpolates a surface that is fixed at the landmark points P_i at a specific height h_i. If one imagines this surface as a thin metal plate, then this plate will take a shape in which it is least bent, i. e. it minimizes the quantity:

$$\oiint \left[\left(\frac{\partial^2 f}{\partial x^2} \right)^2 + 2 \left(\frac{\partial^2 f}{\partial x \partial y} \right)^2 + \left(\frac{\partial^2 f}{\partial y^2} \right)^2 \right] \quad (1)$$

This quantity is called the bending energy of the thin-plate spline function. Instead of assuming that f corresponds to a displacement orthogonal to the image plane at the landmarks, one can assume a displacement in the image plane. By using two separate thin-plate spline functions f_x and f_y which model the displacement of the landmarks in the x and y direction we arrive at a vector – valued function F which maps each point of the image into a new point in the image plane:

$$F: (x,y) \rightarrow (f_x(x,y), f_y(x,y))$$

A thin-plate spline interpolation function can be written as:

$$f(x,y) = a_0 + a_x x + a_y y + \sum_{i=1}^{n} w_i U\left(\left| (x,y) - P_i \right| \right)$$

where:

$$U(r) = r^2 \log(r^2)$$

is a so-called fundamental solution of the biharmonic equation that satisfies the condition of bending energy minimization. By appropriately choosing a n x 2 matrix W of the coefficients w_i, the function F maps F (P_i) = P'_I for all. i = 1...n.

It can be shown that the transformation F minimizes the bending energy in eq. (1) and that the value of the bending energy is proportional to tr $(W^T Y)$ where Y is a n x 2 matrix of the evolved landmarks P'. The bending energy of a thin-plate spline is zero only if the coefficients w_i of f are all zero. Moreover, the bending energy is invariant under affine transformations like scaling, rotation and translation.

The function F can be extended from 2D to 3D by using the function:

$$U(r) = |r|$$

Once the function F has been calculated it can be used to find for each voxel xyz of lung volume A the corresponding voxel F (xyz) in lung volume B[15,16].

In our »prove of concept« study the lung surfaces were extracted by the means of the AnalyzeAVW[17] software package. The bronchial tree segmentation including the definition of the corresponding branching points was performed with a software package developed by Jürg Tschirren[18]. The corresponding branching points of the bronchial tree were proved and validated by three independently working students.

Results

Within a CT image viewer, which is able to display two different datasets si-

multaneously, the implemented transfer function will let the radiologist quickly check matching regions between two different data sets. The crucial point, the calculation of the transformation matrix, takes about one second on a conventional PC. The unmatched datasets differed to about 8mm from each other, the matched lung volumes showed an error of about 2mm in all spatial direction when compared to the »ideal match« which would be the identical volume with zero matching error. In practice this means an error plus minus one to two CT slices.

In our test data sets an average misalignment of characteristic structures was as presented on Figures 1–3.
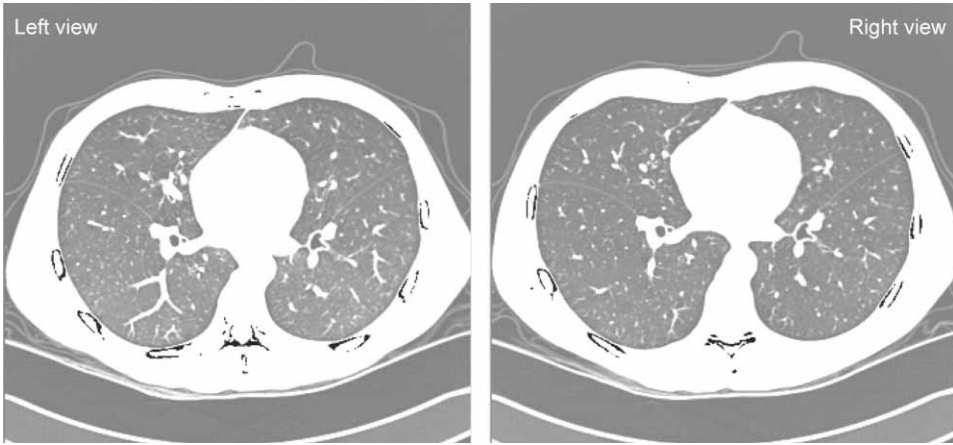

Fig. 1. This figure represents the »ideal match«: One can find the exact structure equal in different lung volumes. But different of status aeration show a different pattern on radiological images.
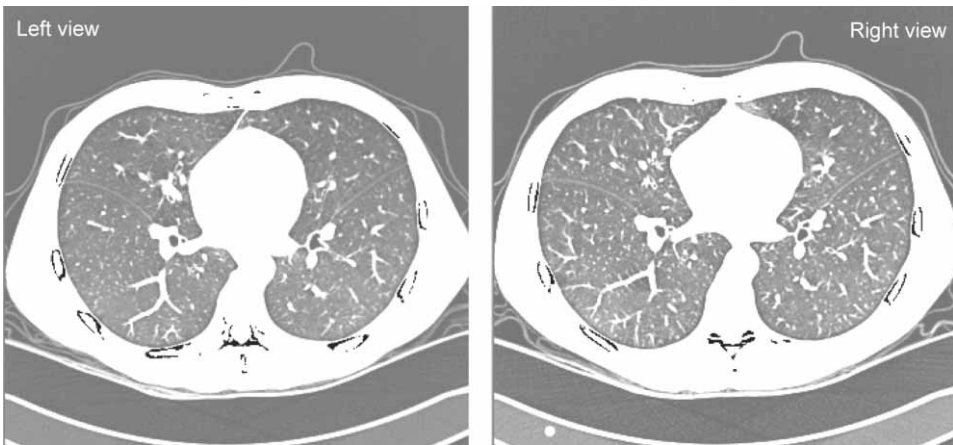

Fig. 2. The same slice number of two lung datasets before matching, it is obvious that the pictures represent different regions of the lung.
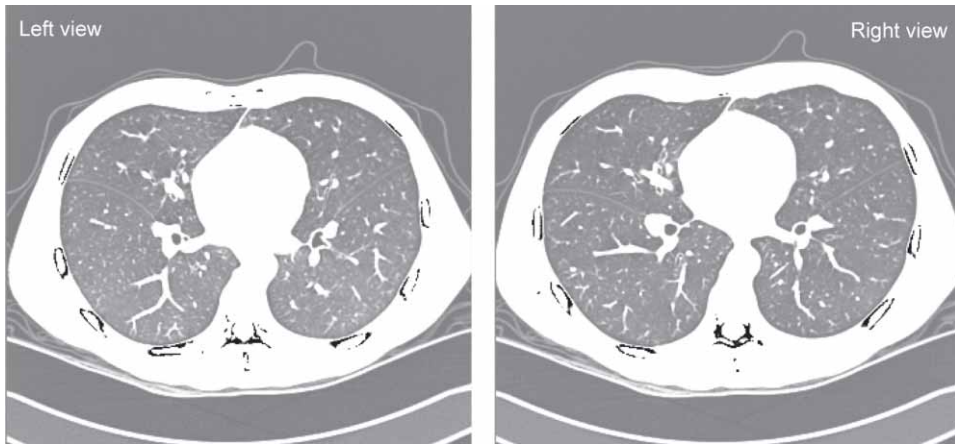
Fig. 3. This figure shows a slice of the matched volumes: The images look quite similar though one can find significant changes: Most of them are caused by movements of vessels. Nevertheless the same anatomical position in two different datasets could be found with a precision of approximately 2 mm along each axis. The accuracy of finding the correlated part of the tissue in the follow up scan is dependent on the location within the lung volume. Further studies and improvements of the algorithms have the goal of gaining a better exactness special in regions where landmarks are rare.

Conclusion

With the advent of the multislice technology in CT imaging, the strategy of accessing the huge amount of data for the radiologists has changed or will be changing significantly. It is definitely a challenge to examine chest CT scans – especially in follow-up studies – in a conventional manner, i.e. looking at axial slices which can sometimes be as much as 1000 images. The amount of CT images acquired by one examination increased about 10 times during the last 5 to 7 years. This is one argument to introduce computer aided diagnosis in routine radiological examination: the capability to manage the data in sufficient way. The second argument is directly connected to the imaging procedure itself of the lung: the lack of the human eye to resolve certain patterns which can predict lung diseases at an early stage. Further on, the quantification of healing or disease processes as a function of time is definitely improved using advanced algorithms in lung diagnosis. Much of this work has been accomplished at the University of Iowa.

Our approach in lung volume matching, which is necessary to get quantitative information of healing/disease processes in the lung or therapy outcomes seems to be a feasible and fast way compared to other techniques described in literature. Betke et al. used a rigid transformation in order to get access to the location of lung noduls in follow up studies. Similar techniques are in use in commercial lung nodule detection packages like the Siemens Pulmo software. In this special case the technique seems to work with sufficient accuracy and sufficient speed. But when it comes to the intrasubject and intersubject comparison (the intersubject method is already in use to develop a normative lung atlas[19]) of lung function and lung structures this approach is not feasible. Therefore the nonrigid transformation with thin-plate spline interpolation was introduced. Chis-

tensen and colleagues describe a rather accurate method but it seems to lack of the necessary speed in clinical environment.

One major benefit of the described method in comparison with other methods is the respectively fast execution of the algorithms, which is crucial for utilization in clinical praxis. The study limits are obvious: Only one data set was examined but still the prove of concept of our matching method worked out sufficiently and encourages us to perform further studies and optimization.

One of the next steps in this project will be the combination of the processing steps into a single software package in order to make it more accessible for clinical studies. A number of evaluation studies still have to be performed to get a sense of the »ground truth«.

Our – very prelimiray and experimental – results though suggest the usefulness of this approach in a clinical environment.

In the meanwhile some research papers argue that with the advent of these technologies and their introduction in radiological practice may make methods in nuclear medicine like SPECT (Secondary Positron Emission Computed Tomography) of lung function diagnosis obsolete: an advantage for the patient preventing her/him from unnecessary dose exposure and help the hospital owner on behalf of patient management and cost effectiveness.

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R E F E R E N C E S

1. SEIDLER, H., W. BERNHARD, M. TESCHLER-NICOLA, W. PLATZER, D. ZUR NEDDEN, R. HENN, A. OBERHAUSER, T. SJØVOLD, Science, 258 (1992) 455. – 2. ZUR NEDDEN, D., R. KNAPP, K. WICKE, W. JUDMAIER, W. A. MURPHY JR, H. SEIDLER, W. PLATZER, Radiology, 193 (1994) 269. – 3. ANDERL, H., D. ZUR NEDDEN, W. MUHLBAUER, K. TWERDY, E. ZANON, K. WICKE, R. KNAPP, Br. J. Plast. Surg., 47 (1994) 60. – 4. RECHEIS, W., G. W. WEBER, K. SCHAFER, H. PROSSINGER, R. KNAPP, H. SEIDLER, D. ZUR NEDDEN, Coll Antropol., 23 (1999) 495. – 5. SEIDLER, H., D. FALK, C. STRINGER, H. WILFING, G. B. MULLER, D. ZUR NEDDEN, G. W. WEBER, W. RECHEIS, J. L. ARSUAGA, J. Hum. Evol., 33 (1997) 691. – 6. PROSSINGER, H., H. SEIDLER, L. WICKE, D. WEAVER, W. RECHEIS, C. STRINGER, G. B. MULLER, Anat. Rec., 273B (2003) 132. – 7. RECHEIS, W., R. MACCHIARELLI, H. SEIDLER, D. S. WEAVER, K. SCHAFER, L. BONDIOLI, G. W. WEBER, D. ZUR NEDDEN, Coll. Antropol., 23 (1999) 397. – 8. BOOKSTEIN, F., K. SCHAFER, H. PROSSINGER, H. SEIDLER, M. FIEDER, C. STRINGER, G. W. WEBER, J. L. ARSUAGA, D. E. SLICE, F. J. ROHLF, W. RECHEIS, A. J. MARIAM, L. F. MARCUS, Anat. Rec., 257 (1999) 217. – 9. WEBER, G. W., K. SCHAFER, H. PROSSINGER, P. GUNZ, P. MITTEROCKER, H. SEIDLER, J. Physiol. Anthropol. Appl. Human Sci., 20 (2001) 69. – 10. HOFFMAN, E. A., J. M. REINHARDT, M. SONKA, B. A. SIMON, J. GUO, O. SABA, D. CHON, S. SAMRAH, H. SHIKATA, J. TSCHIRREN, K. PALAGYI, K. C. BECK, G. MCLENNAN, Acad. Radiol., 10 (2003) 1104. – 11. SLUIMER, I. C., P. F. VAN WAES, M. A. VIERGEVER, B. VAN GINNEKEN, Med. Phys., 30 (2003) 3081. – 12. UPPALURI, R., E. A. HOFFMAN, M. SONKA, G. W. HUNNINGHAKE, G. MCLENNAN, Am. J. Respir. Crit. Care Med., 159 (1999) 519. – 13. KO, J. P. M. BETKE, Radiology, 218 (2001) 267. – 14. BOOKSTEIN, F.: Morphometric tools for landmark data: Geometry and biology. (Cambridge University Press, Cambridge, 1991). – 15. BOOKSTEIN, F., Med. Image Anal., 1 (1997) 225. – 16. DRYDEN, I. L., K. V. MARDIA: Statistical shape analysis. (Wiley and Sons, New York, 1998). – 17. MAYO CLINIC AND FOUNDATION: Analyze AVW. (http:// www.analyzedirect.com). – 18. TSCHIRREN, J., K. PALÁGYI, J. M. REINHARDT, E. A. HOFFMAN, M. SONKA, MICCAI, 2 (2002) 12. – 19. LI, B., G. E. CRISTENSEN, E. A. HOFFMAN, G. MCLENNAN, J. M. REINHARDT, Acad. Radiol., 10 (2003) 255.

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USPOREDBA PODATAKA O VOLUMENU PLUĆA – NOVI PRISTUP

S A Ž E T A K

Postoji znatna potreba da podaci dobiveni CT-pretragom pluća budu usporedivi. Danas se povećao broj CT rezova u svakom ispitivanju zahvaljujući većoj rezoluciji modernih CT uređaja, te potrebi za kvantifikacijom napredovanja bolesti i procesa ozdravljenja u longitudinalnim studijama. Pluća dobrovoljaca pregledana su pomoću višedetektorskog CT uređaja u dva različita stanja ventilacije. Segmentirane su one strukture pluća koje su nužne za proceduru usporedbe kao što je to površina pluća i točke grananja. Kako bi se izračunao usporedni volumen pluća korištena je metoda tanke ploče. Preliminarni rezultati pokazali su prosječnu pogrešku od 2 voxela, tj. 2 mm. Korištenjem osobnog računala, za izračunavanje transformacijske matrice potrebna je 1 sekunda što je znatno brže od drugih metoda opisanih u literaturi. Opisana metoda prikladna je za uvođenje u radiološku praksu kada je u longitudinalnoj studiji potrebno kvantitativno usporediti rezultate pretrage napravljene CT uređajem visoke rezolucije.