A review of segmentation methods in short axis cardiac MR images

Volume 15, Issue 2, April 2011, Pages 169-184

Caroline Petitjean | Jean Nicolas Dacher

For the last 15 years, Magnetic Resonance Imaging (MRI) has become a reference examination for cardiac morphology, function and perfusion in humans. Yet, due to the characteristics of cardiac MR images and the great variability of the images among patients, the problem of heart cavities segmentation in MRI is still open. This paper is a review of fully and semi-automated methods performing segmentation in short axis images using a cardiac cine MRI sequence. Medical background and specific segmentation difficulties associated to these images are presented. For this particularly complex segmentation task, prior knowledge is required. We thus propose an
original categorization for cardiac segmentation methods, with a special emphasis on what level of external information is required (weak or strong) and how it is used to constrain segmentation. After reviewing method principles and analyzing segmentation results, we conclude with a discussion and future trends in this field regarding methodological and medical issues. © 2010 Elsevier B.V.

A review of 3D/2D registration methods for image-guided interventions

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Registration of pre- and intra-interventional data is one of the key technologies for image-guided radiation therapy, radiosurgery, minimally invasive surgery, endoscopy, and interventional radiology. In this paper, we survey those 3D/2D data registration methods that utilize 3D computer tomography or magnetic resonance images as the pre-interventional data and 2D X-ray projection images as the intra-interventional data. The 3D/2D registration methods are reviewed with respect to image modality, image dimensionality, registration basis, geometric transformation, user interaction, optimization procedure, subject, and object of registration. © 2010 Elsevier B.V.

Towards robust and effective shape modeling: Sparse shape composition

Volume 16, Issue 1, January 2012, Pages 265-277

Shaoting Zhang | Yiqiang Zhan | Maneesh Dewan | Junzhou Huang | Dimitris N. Metaxas | Xiang Sean Zhou

Organ shape plays an important role in various clinical practices, e.g., diagnosis, surgical planning and treatment evaluation. It is usually derived from low level appearance cues in medical images. However, due to diseases and imaging artifacts, low level appearance cues might be weak or misleading. In this situation, shape priors become critical to infer and refine the shape derived by image appearances. Effective modeling of shape priors is challenging because: (1) shape variation is complex and cannot always be modeled by a parametric probability distribution; (2) a shape instance derived from image appearance cues (input shape) may have gross errors; and (3) local details of the input shape are difficult to preserve if they are not statistically significant in the training data. In this paper we propose a novel Sparse Shape Composition model (SSC) to deal with these three challenges in a unified framework. In our method, a sparse set of shapes in the shape repository is selected and composed together to infer/refine an input shape. The a priori information is thus implicitly incorporated on-the-fly. Our model leverages two sparsity observations of the input shape instance: (1) the input shape can be approximately represented by a sparse linear combination of shapes in the shape repository; (2) parts of the input shape may contain gross errors but such errors are sparse. Our model is formulated as a sparse learning problem. Using L1 norm relaxation, it can be solved by an efficient expectation-maximization (EM) type of framework. Our method is extensively validated on two medical applications, 2D lung localization in X-ray images and 3D liver segmentation in low-dose CT scans. Compared to state-of-the-art methods, our model exhibits better performance in both studies. © 2011 Elsevier B.V.
Efficient MR image reconstruction for compressed MR imaging

Junzhou Huang | Shaoting Zhang | Dimitris Metaxas

In this paper, we propose an efficient algorithm for MR image reconstruction. The algorithm minimizes a linear combination of three terms corresponding to a least square data fitting, total variation (TV) and L1 norm regularization. This has been shown to be very powerful for the MR image reconstruction. First, we decompose the original problem into L1 and TV norm regularization subproblems respectively. Then, these two subproblems are efficiently solved by existing techniques. Finally, the reconstructed image is obtained from the weighted average of solutions from two subproblems in an iterative framework. We compare the proposed algorithm with previous methods in term of the reconstruction accuracy and computation complexity. Numerous experiments demonstrate the superior performance of the proposed algorithm for compressed MR image reconstruction. © 2011 Elsevier B.V.

DRAMMS: Deformable registration via attribute matching and mutual-saliency weighting

Yangming Ou | Aristeidis Sotiras | Nikos Paragios | Christos Davatzikos

A general-purpose deformable registration algorithm referred to as "DRAMMS" is presented in this paper. DRAMMS bridges the gap between the traditional voxel-wise methods and landmark/feature-based methods with primarily two contributions. First, DRAMMS renders each voxel relatively distinctively identifiable by a rich set of attributes, therefore largely reducing matching ambiguities. In particular, a set of multi-scale and multi-orientation Gabor attributes are extracted and the optimal components are selected, so that they form a highly distinctive morphological signature reflecting the anatomical and geometric context around each voxel. Moreover, the way in which the optimal Gabor attributes are constructed is independent of the underlying image modalities or contents, which renders DRAMMS generally applicable to diverse registration tasks. A second contribution of DRAMMS is that it modulates the registration by assigning higher weights to those voxels having higher ability to establish unique (hence reliable) correspondences across images, therefore reducing the negative impact of those regions that are less capable of finding correspondences (such as outlier regions). A continuously-valued weighting function named "mutual-saliency" is developed to reflect the matching uniqueness between a pair of voxels implied by the tentative transformation. As a result, voxels do not contribute equally as in most voxel-wise methods, nor in isolation as in landmark/feature-based methods. Instead, they contribute according to the continuously-valued mutual-saliency map, which dynamically evolves during the registration process. Experiments in simulated images, inter-subject images, single-/multi-modality images, from brain, heart, and prostate have demonstrated the general applicability and the accuracy of DRAMMS. © 2010 Elsevier B.V.

MIND: Modality independent neighbourhood descriptor for multi-modal deformable registration

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Deformable registration of images obtained from different modalities remains a challenging task in medical image analysis. This paper addresses this important problem and proposes a modality independent neighbourhood descriptor (MIND) for both linear and deformable multi-modal registration. Based on the similarity of small image patches within one image, it aims to extract the distinctive structure in a local neighbourhood, which is preserved across modalities. The descriptor is based on the concept of image self-similarity, which has been introduced for non-local means filtering for image denoising. It is able to distinguish between different types of features such as corners, edges and homogeneously textured regions. MIND is robust to the most considerable differences between modalities: non-functional intensity relations, image noise and non-uniform bias fields. The multi-dimensional descriptor can be efficiently computed in a dense fashion across the whole image and provides point-wise local similarity across modalities based on the absolute or squared difference between descriptors, making it applicable for a wide range of transformation models and optimisation algorithms. We use the sum of squared differences of the MIND representations of the images as a similarity metric within a symmetric non-parametric Gauss-Newton registration framework. In principle, MIND would be applicable to the registration of arbitrary modalities. In this work, we apply and validate it for the registration of clinical 3D thoracic CT scans between inhale and exhale as well as the alignment of 3D CT and MRI scans. Experimental results show the advantages of MIND over state-of-the-art techniques such as conditional mutual information and entropy images, with respect to clinically annotated landmark locations. © 2012 Elsevier B.V.

Respiratory motion models: A review

J. R. McClelland | D. J. Hawkes | T. Schaeffter | A. P. King

The problem of respiratory motion has proved a serious obstacle in developing techniques to acquire images or guide interventions in abdominal and thoracic organs. Motion models offer a possible solution to these problems, and as a result the field of respiratory motion modelling has become an active one over the past 15 years. A motion model can be defined as a process that takes some surrogate data as input and produces a motion estimate as output. Many techniques have been proposed in the literature, differing in the data used to form the models, the type of model employed, how this model is computed, the type of surrogate data used as input to the model in order to make motion estimates and what form this output should take. In addition, a wide range of different application areas have been proposed. In this paper we summarise the state of the art in this important field and in the process highlight the key papers that have driven its advance. The intention is that this will serve as a timely review and comparison of the different techniques proposed to date and as a basis to inform future research in this area. © 2012.

Nonrigid registration of dynamic medical imaging data using nD+t B-splines and a groupwise optimization approach

C. T. Metz | S. Klein | M. Schaap | T. van Walsum | W. J. Niessen
A registration method for motion estimation in dynamic medical imaging data is proposed. Registration is performed directly on the dynamic image, thus avoiding a bias towards a specifically chosen reference time point. Both spatial and temporal smoothness of the transformations are taken into account. Optionally, cyclic motion can be imposed, which can be useful for visualization (viewing the segmentation sequentially) or model building purposes. The method is based on a 3D (2D + time) or 4D (3D + time) free-form B-spline deformation model, a similarity metric that minimizes the intensity variances over time and constrained optimization using a stochastic gradient descent method with adaptive step size estimation. The method was quantitatively compared with existing registration techniques on synthetic data and 3D + t computed tomography data of the lungs. This showed subvoxel accuracy while delivering smooth transformations, and high consistency of the registration results. Furthermore, the accuracy of semi-automatic derivation of left ventricular volume curves from 3D + t computed tomography angiography data of the heart was evaluated. On average, the deviation from the curves derived from the manual annotations was approximately 3%. The potential of the method for other imaging modalities was shown on 2D + t ultrasound and 2D + t magnetic resonance images. The software is publicly available as an extension to the registration package elastix. © 2010 Elsevier B.V.

Review of automatic segmentation methods of multiple sclerosis white matter lesions on conventional magnetic resonance imaging

Volume 17, Issue 1, January 2013, Pages 1-18

Daniel García-Lorenzo | Simon Francis | Sridar Narayanan | Douglas L. Arnold | D. Louis Collins

Magnetic resonance (MR) imaging is often used to characterize and quantify multiple sclerosis (MS) lesions in the brain and spinal cord. The number and volume of lesions have been used to evaluate MS disease burden, to track the progression of the disease and to evaluate the effect of new pharmaceuticals in clinical trials. Accurate identification of MS lesions in MR images is extremely difficult due to variability in lesion location, size and shape in addition to anatomical variability between subjects. Since manual segmentation requires expert knowledge, is time consuming and is subject to intra- and inter-expert variability, many methods have been proposed to automatically segment lesions. The objective of this study was to carry out a systematic review of the literature to evaluate the state of the art in automated multiple sclerosis lesion segmentation. From 1240. hits found initially with PubMed and Google scholar, our selection criteria identified 80 papers that described an automatic lesion segmentation procedure applied to MS. Only 47 of these included quantitative validation with at least one realistic image. In this paper, we describe the complexity of lesion segmentation, classify the automatic MS lesion segmentation methods found, and review the validation methods applied in each of the papers reviewed. Although many segmentation solutions have been proposed, including some with promising results using MRI data obtained on small groups of patients, no single method is widely employed due to performance issues related to the high variability of MS lesion appearance and differences in image acquisition. The challenge remains to provide segmentation techniques that work in all cases regardless of the type of MS, duration of the disease, or MRI protocol, and this within a comprehensive, standardized validation framework. MS lesion segmentation remains an open problem. © 2012 Elsevier B.V.

New methods for MRI denoising based on sparseness and self-similarity

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This paper proposes two new methods for the three-dimensional denoising of magnetic resonance images that exploit the sparseness and self-similarity properties of the images. The proposed methods are based on a three-dimensional moving-window discrete cosine transform hard thresholding and a three-dimensional rotationally invariant version of the well-known nonlocal means filter. The proposed approaches were compared with related state-of-the-art methods and produced very competitive results. Both methods run in less than a minute, making them usable in most clinical and research settings. © 2011 Elsevier B.V.

MR to ultrasound registration for image-guided prostate interventions

Yipeng Hu | Hashim Uddin Ahmed | Zeike Taylor | Clare Allen | Mark Emberton | David Hawkes | Dean Barratt

A deformable registration method is described that enables automatic alignment of magnetic resonance (MR) and 3D transrectal ultrasound (TRUS) images of the prostate gland. The method employs a novel "model-to-image" registration approach in which a deformable model of the gland surface, derived from an MR image, is registered automatically to a TRUS volume by maximising the likelihood of a particular model shape given a voxel-intensity-based feature that represents an estimate of surface normal vectors at the boundary of the gland. The deformation of the surface model is constrained by a patient-specific statistical model of gland deformation, which is trained using data provided by biomechanical simulations. Each simulation predicts the motion of a volumetric finite element mesh due to the random placement of a TRUS probe in the rectum. The use of biomechanical modelling in this way also allows a dense displacement field to be calculated within the prostate, which is then used to non-rigidly warp the MR image to match the TRUS image. Using data acquired from eight patients, and anatomical landmarks to quantify the registration accuracy, the median final RMS target registration error after performing 100 MR-TRUS registrations for each patient was 2.40 mm. © 2010 Elsevier B.V.

A Hough transform global probabilistic approach to multiple-subject diffusion MRI tractography

Iman Aganj | Christophe Lenglet | Neda Jahanshad | Essa Yacoub | Noam Harel | Paul M. Thompson | Guillermo Sapiro

A global probabilistic fiber tracking approach based on the voting process provided by the Hough transform is introduced in this work. The proposed framework tests candidate 3D curves in the volume, assigning to each one a score computed from the diffusion images, and then selects the curves with the highest scores as the potential anatomical connections. The algorithm avoids local minima by performing an exhaustive search at the desired resolution. The technique is easily extended to multiple subjects, considering a single representative volume where the registered high-angular resolution diffusion images (HARDI) from all the subjects are non-linearly combined, thereby obtaining population-representative tracts. The tractography algorithm is run only once for the multiple subjects, and no tract alignment is necessary. We present experimental results on HARDI volumes, ranging from simulated and 1.5T physical phantoms to 7T and 4T human brain and 7T monkey brain datasets. © 2011 Elsevier B.V.
Deformable segmentation via sparse representation and dictionary learning

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Shaoting Zhang | Yiqiang Zhan | Dimitris N. Metaxas

"Shape" and "appearance", the two pillars of a deformable model, complement each other in object segmentation. In many medical imaging applications, while the low-level appearance information is weak or mis-leading, shape priors play a more important role to guide a correct segmentation, thanks to the strong shape characteristics of biological structures. Recently a novel shape prior modeling method has been proposed based on sparse learning theory. Instead of learning a generative shape model, shape priors are incorporated on-the-fly through the sparse shape composition (SSC). SSC is robust to non-Gaussian errors and still preserves individual shape characteristics even when such characteristics is not statistically significant. Although it seems straightforward to incorporate SSC into a deformable segmentation framework as shape priors, the large-scale sparse optimization of SSC has low runtime efficiency, which cannot satisfy clinical requirements. In this paper, we design two strategies to decrease the computational complexity of SSC, making a robust, accurate and efficient deformable segmentation system. (1) When the shape repository contains a large number of instances, which is often the case in 2D problems, K-SVD is used to learn a more compact but still informative shape dictionary. (2) If the derived shape instance has a large number of vertices, which often appears in 3D problems, an affinity propagation method is used to partition the surface into small sub-regions, on which the sparse shape composition is performed locally. Both strategies dramatically decrease the scale of the sparse optimization problem and hence speed up the algorithm. Our method is applied on a diverse set of biomedical image analysis problems. Compared to the original SSC, these two newly-proposed modules not only significant reduce the computational complexity, but also improve the overall accuracy. © 2012 Elsevier B.V.

Exudate-based diabetic macular edema detection in fundus images using publicly available datasets

Volume 16, Issue 1, January 2012, Pages 216-226

Luca Giancardo | Fabrice Meriaudeau | Thomas P. Karnowski | Yaqin Li | Seema Garg | Kenneth W. Tobin | Edward Chaum

Diabetic macular edema (DME) is a common vision threatening complication of diabetic retinopathy. In a large scale screening environment DME can be assessed by detecting exudates (a type of bright lesions) in fundus images. In this work, we introduce a new methodology for diagnosis of DME using a novel set of features based on colour, wavelet decomposition and automatic lesion segmentation. These features are employed to train a classifier able to automatically diagnose DME through the presence of exudation. We present a new publicly available dataset with ground-truth data containing 169 patients from various ethnic groups and levels of DME. This and other two publicly available datasets are employed to evaluate our algorithm. We are able to achieve diagnosis performance comparable to retina experts on the MESSIDOR (an independently labelled dataset with 1200 images) with cross-dataset testing (e.g., the classifier was trained on an independent dataset and tested on MESSIDOR). Our algorithm obtained an AUC between 0.88 and 0.94 depending on the dataset/features used. Additionally, it does not need ground truth at lesion level to reject false positives and is computationally efficient, as it generates a diagnosis on an average of 4.4. s (9.3. s, considering the optic nerve localisation) per image on an 2.6. GHz
Medical image processing on the GPU - Past, present and future

Volume 17, Issue 8, December 2013, Pages 1073-1094

Anders Eklund | Paul Dufort | Daniel Forsberg | Stephen M. LaConte

Graphics processing units (GPUs) are used today in a wide range of applications, mainly because they can dramatically accelerate parallel computing, are affordable and energy efficient. In the field of medical imaging, GPUs are in some cases crucial for enabling practical use of computationally demanding algorithms. This review presents the past and present work on GPU accelerated medical image processing, and is meant to serve as an overview and introduction to existing GPU implementations. The review covers GPU acceleration of basic image processing operations (filtering, interpolation, histogram estimation and distance transforms), the most commonly used algorithms in medical imaging (image registration, image segmentation and image denoising) and algorithms that are specific to individual modalities (CT, PET, SPECT, MRI, fMRI, DTI, ultrasound, optical imaging and microscopy). The review ends by highlighting some future possibilities and challenges. © 2013 Elsevier B.V.

STEPS: Similarity and Truth Estimation for Propagated Segmentations and its application to hippocampal segmentation and brain parcelation

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M. Jorge Cardoso | Kelvin Leung | Marc Modat | Shiva Keihaninejad | David Cash | Josephine Barnes | Nick C. Fox | Sebastien Ourselin

Anatomical segmentation of structures of interest is critical to quantitative analysis in medical imaging. Several automated multi-atlas based segmentation propagation methods that utilise manual delineations from multiple templates appear promising. However, high levels of accuracy and reliability are needed for use in diagnosis or in clinical trials. We propose a new local ranking strategy for template selection based on the locally normalised cross correlation (LNCC) and an extension to the classical STAPLE algorithm by Warfield et al. (2004), which we refer to as STEPS for Similarity and Truth Estimation for Propagated Segmentations. It addresses the well-known problems of local vs. global image matching and the bias introduced in the performance estimation due to structure size. We assessed the method on hippocampal segmentation using a leave-one-out cross validation with optimised model parameters; STEPS achieved a mean Dice score of 0.925 when compared with manual segmentation. This was significantly better in terms of segmentation accuracy when compared to other state-of-the-art fusion techniques. Furthermore, due to the finer anatomical scale, STEPS also obtains more accurate segmentations even when using only a third of the templates, reducing the dependence on large template databases. Using a subset of Alzheimer's Disease Neuroimaging Initiative (ADNI) scans from different MRI imaging systems and protocols, STEPS yielded similarly accurate segmentations (Dice=0.903). A cross-sectional and longitudinal hippocampal volumetric study was performed on the ADNI database. Mean±SD hippocampal volume (mm3) was 5195±656 for controls; 4786±781 for MCI; and 4427±903 for Alzheimer's disease patients and hippocampal atrophy rates (%/year) of 1.09±3.0, 2.74±3.5 and 4.04±3.6 respectively. Statistically significant (p < 10 - 3) differences were found between disease groups for both hippocampal volume and volume change rates. Finally, STEPS was also applied in a multi-label segmentation propagation scenario using a leave-one-out cross validation, in order to parcellate 83 separate structures of the brain. Comparisons of STEPS with state-of-the-art multi-label fusion algorithms showed
Regression forests for efficient anatomy detection and localization in computed tomography scans

A. Criminisi | D. Robertson | E. Konukoglu | J. Shotton | S. Pathak | S. White | K. Siddiqui

This paper proposes a new algorithm for the efficient, automatic detection and localization of multiple anatomical structures within three-dimensional computed tomography (CT) scans. Applications include selective retrieval of patients images from PACS systems, semantic visual navigation and tracking radiation dose over time. The main contribution of this work is a new, continuous parametrization of the anatomy localization problem, which allows it to be addressed effectively by multi-class random regression forests. Regression forests are similar to the more popular classification forests, but trained to predict continuous, multi-variate outputs, where the training focuses on maximizing the confidence of output predictions. A single pass of our probabilistic algorithm enables the direct mapping from voxels to organ location and size. Quantitative validation is performed on a database of 400 highly variable CT scans. We show that the proposed method is more accurate and robust than techniques based on efficient multi-atlas registration and template-based nearest-neighbor detection. Due to the simplicity of the regressor’s context-rich visual features and the algorithm’s parallelism, these results are achieved in typical run-times of only ~4 s on a conventional single-core machine. © 2013 Elsevier B.V.

Patient-specific electromechanical models of the heart for the prediction of pacing acute effects in CRT: A preliminary clinical validation


Cardiac resynchronisation therapy (CRT) is an effective treatment for patients with congestive heart failure and a wide QRS complex. However, up to 30% of patients are non-responders to therapy in terms of exercise capacity or left ventricular reverse remodelling. A number of controversies still remain surrounding patient selection, targeted lead implantation and optimisation of this important treatment. The development of biophysical models to predict the response to CRT represents a potential strategy to address these issues. In this article, we present how the personalisation of an electromechanical model of the myocardium can predict the acute haemodynamic changes associated with CRT. In order to introduce such an approach as a clinical application, we needed to design models that can be individualised from images and electrophysiological mapping of the left ventricle. In this paper the personalisation of the anatomy, the electrophysiology, the kinematics and the mechanics are described. The acute effects of pacing on pressure development were predicted with the in silico model for several pacing conditions on two patients, achieving good agreement with invasive haemodynamic measurements: the mean error on dP/dt max is 47.5±35mmHg/s, less than 5% error. These promising results demonstrate the potential of physiological models personalised from images and electrophysiology signals to improve patient selection and plan CRT. © 2011 Elsevier B.V.
Multiple q-shell diffusion propagator imaging

Maxime Descoteaux | Rachid Deriche | Denis Le Bihan | Jean François Mangin | Cyril Poupon

Many recent high angular resolution diffusion imaging (HARDI) reconstruction techniques have been introduced to infer an orientation distribution function (ODF) of the underlying tissue structure. These methods are more often based on a single-shell (one b-value) acquisition and can only recover angular structure information contained in the ensemble average propagator (EAP) describing the three-dimensional (3D) average diffusion process of water molecules. The EAP can thus provide richer information about complex tissue microstructure properties than the ODF by also considering the radial part of the diffusion signal. In this paper, we present a novel technique for analytical EAP reconstruction from multiple q-shell acquisitions. The solution is based on a Laplace equation by part estimation between the diffusion signal for each shell acquisition. This simplifies greatly the Fourier integral relating diffusion signal and EAP, which leads to an analytical, linear and compact EAP reconstruction. An important part of the paper is dedicated to validate the diffusion signal estimation and EAP reconstruction on real datasets from ex vivo phantoms. We also illustrate multiple q-shell diffusion propagator imaging (mq-DPI) on a real in vivo human brain and perform a qualitative comparison against state-of-the-art diffusion spectrum imaging (DSI) on the same subject. mq-DPI is shown to reconstruct robust EAP from only several different b-value shells and less diffusion measurements than DSI. This opens interesting perspectives for new q-space sampling schemes and tissue microstructure investigation. © 2010 Elsevier B.V.

Nonlinear registration of longitudinal images and measurement of change in regions of interest

Dominic Holland | Anders M. Dale

We describe here a method, Quarc, for accurately quantifying structural changes in organs, based on serial MRI scans. The procedure can be used to measure deformations globally or in regions of interest (ROIs), including large-scale changes in the whole organ, and subtle changes in small-scale structures. We validate the method with model studies, and provide an illustrative analysis using the brain. We apply the method to the large, publicly available ADNI database of serial brain scans, and calculate Cohen's d effect sizes for several ROIs. Using publicly available derived-data, we directly compare effect sizes from Quarc with those from four existing methods that quantify cerebral structural change. Quarc produced a slightly improved, though not significantly different, whole brain effect size compared with the standard KN-BSI method, but in all other cases it produced significantly larger effect sizes. © 2011 Elsevier B.V.
Thoracic respiratory motion estimation from MRI using a statistical model and a 2-D image navigator

A. P. King | C. Buerger | C. Tsoumpas | P. K. Marsden | T. Schaeffter

Respiratory motion models have potential application for estimating and correcting the effects of motion in a wide range of applications, for example in PET-MR imaging. Given that motion cycles caused by breathing are only approximately repeatable, an important quality of such models is their ability to capture and estimate the intra- and inter-cycle variability of the motion. In this paper we propose and describe a technique for free-form nonrigid respiratory motion correction in the thorax. Our model is based on a principal component analysis of the motion states encountered during different breathing patterns, and is formed from motion estimates made from dynamic 3-D MRI data. We apply our model using a data-driven technique based on a 2-D MRI image navigator. Unlike most previously reported work in the literature, our approach is able to capture both intra- and inter-cycle motion variability. In addition, the 2-D image navigator can be used to estimate how applicable the current motion model is, and hence report when more imaging data is required to update the model. We also use the motion model to decide on the best positioning for the image navigator. We validate our approach using MRI data acquired from 10 volunteers and demonstrate improvements of up to 40.5% over other reported motion modelling approaches, which corresponds to 61% of the overall respiratory motion present. Finally we demonstrate one potential application of our technique: MRI-based motion correction of real-time PET data for simultaneous PET-MRI acquisition. © 2011 Elsevier B.V.

Non-local statistical label fusion for multi-atlas segmentation

Andrew J. Asman | Bennett A. Landman

Multi-atlas segmentation provides a general purpose, fully-automated approach for transferring spatial information from an existing dataset ("atlases") to a previously unseen context ("target") through image registration. The method to resolve voxelwise label conflicts between the registered atlases ("label fusion") has a substantial impact on segmentation quality. Ideally, statistical fusion algorithms (e.g., STAPLE) would result in accurate segmentations as they provide a framework to elegantly integrate models of rater performance. The accuracy of statistical fusion hinges upon accurately modeling the underlying process of how raters err. Despite success on human raters, current approaches inaccurately model multi-atlas behavior as they fail to seamlessly incorporate exogenous intensity information into the estimation process. As a result, locally weighted voting algorithms represent the de facto standard fusion approach in clinical applications. Moreover, regardless of the approach, fusion algorithms are generally dependent upon large atlas sets and highly accurate registration as they implicitly assume that the registered atlases form a collectively unbiased representation of the target. Herein, we propose a novel statistical fusion algorithm, Non-Local STAPLE (NLS). NLS reformulates the STAPLE framework from a non-local means perspective in order to learn what label an atlas would have observed, given perfect correspondence. Through this reformulation, NLS (1) seamlessly integrates intensity into the estimation process, (2) provides a theoretically consistent model of multi-atlas observation error, and (3) largely diminishes the need for large atlas sets and very high-quality registrations. We assess the sensitivity and optimality of the approach and demonstrate significant improvement in two empirical multi-atlas experiments. © 2012 Elsevier B.V.
Temporal diffeomorphic free-form deformation: Application to motion and strain estimation from 3D echocardiography

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Mathieu De Craene | Gemma Piella | Oscar Camara | Nicolas Duchateau | Etelvino Silva | Adelina Doltra | Jan D’hooge | Josep Brugada | Marta Sitges | Alejandro F. Frangi

This paper presents a new registration algorithm, called Temporal Diffeomorphic Free Form Deformation (TDFFD), and its application to motion and strain quantification from a sequence of 3D ultrasound (US) images. The originality of our approach resides in enforcing time consistency by representing the 4D velocity field as the sum of continuous spatiotemporal B-Spline kernels. The spatiotemporal displacement field is then recovered through forward Eulerian integration of the non-stationary velocity field. The strain tensor is computed locally using the spatial derivatives of the reconstructed displacement field. The energy functional considered in this paper weighs two terms: the image similarity and a regularization term. The image similarity metric is the sum of squared differences between the intensities of each frame and a reference one. Any frame in the sequence can be chosen as reference. The regularization term is based on the incompressibility of myocardial tissue. TDFFD was compared to pairwise 3D FFD and 3D+t FFD, both on displacement and velocity fields, on a set of synthetic 3D US images with different noise levels. TDFFD showed increased robustness to noise compared to these two state-of-the-art algorithms. TDFFD also proved to be more resistant to a reduced temporal resolution when decimating this synthetic sequence. Finally, this synthetic dataset was used to determine optimal settings of the TDFFD algorithm. Subsequently, TDFFD was applied to a database of cardiac 3D US images of the left ventricle acquired from 9 healthy volunteers and 13 patients treated by Cardiac Resynchronization Therapy (CRT). On healthy cases, uniform strain patterns were observed over all myocardial segments, as physiologically expected. On all CRT patients, the improvement in synchrony of regional longitudinal strain correlated with CRT clinical outcome as quantified by the reduction of end-systolic left ventricular volume at follow-up (6 and 12. months), showing the potential of the proposed algorithm for the assessment of CRT. © 2011 Elsevier B.V.

Hierarchical adaptive local affine registration for fast and robust respiratory motion estimation

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Christian Buerger | Tobias Schaeffler | Andrew P. King

Non-rigid image registration techniques are commonly used to estimate complex tissue deformations in medical imaging. A range of non-rigid registration algorithms have been proposed, but they typically have high computational complexity. To reduce this complexity, combinations of multiple less complex deformations have been proposed such as hierarchical techniques which successively split the non-rigid registration problem into multiple locally rigid or affine components. However, to date the splitting has been regular and the underlying image content has not been considered in the splitting process. This can lead to errors and artefacts in the resulting motion fields. In this paper, we propose three novel adaptive splitting techniques, an image-based, a similarity-based, and a motion-based technique within a hierarchical framework which attempt to process regions of similar motion and/or image structure in single registration components. We evaluate our technique on free-breathing whole-chest 3D MRI data from 10 volunteers and two publicly available CT datasets. We demonstrate a reduction in registration error of up to 49.1% over a non-adaptive technique and compare our results with a commonly used free-form registration algorithm. © 2011 Elsevier B.V.
Coupled minimum-cost flow cell tracking for high-throughput quantitative analysis

Volume 15, Issue 4, August 2011, Pages 650-668

Dirk Padfield | Jens Rittscher | Badrinath Roysam

A growing number of screening applications require the automated monitoring of cell populations in a high-throughput, high-content environment. These applications depend on accurate cell tracking of individual cells that display various behaviors including mitosis, merging, rapid movement, and entering and leaving the field of view. Many approaches to cell tracking have been developed in the past, but most are quite complex, require extensive post-processing, and are parameter intensive. To overcome such issues, we present a general, consistent, and extensible tracking approach that explicitly models cell behaviors in a graph-theoretic framework. We introduce a way of extending the standard minimum-cost flow algorithm to account for mitosis and merging events through a coupling operation on particular edges. We then show how the resulting graph can be efficiently solved using algorithms such as linear programming to choose the edges of the graph that observe the constraints while leading to the lowest overall cost. This tracking algorithm relies on accurate denoising and segmentation steps for which we use a wavelet-based approach that is able to accurately segment cells even in images with very low contrast-to-noise. In addition, the framework is able to measure and correct for microscope defocusing and stage shift. We applied the algorithms on nearly 6000 images of 400,000 cells representing 32,000 tracks taken from five separate datasets, each composed of multiple wells. Our algorithm was able to segment and track cells and detect different cell behaviors with an accuracy of over 99%. This overall framework enables accurate quantitative analysis of cell events and provides a valuable tool for high-throughput biological studies. © 2010 Elsevier B.V.