

Asclepios : a Research Project at INRIA for the Analysis and Simulation of Biomedical Images

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Abstract. Asclepios¹ is the name of a research project officially launched on November 1st, 2005 at INRIA Sophia-Antipolis, to study the Analysis and Simulation of Biological and Medical Images. This research project is following a previous one, called Epidaure, initially dedicated to Medical Imaging and Robotics research. These two project teams were strongly supported by Gilles Kahn, who used to have regular scientific interactions with their members. More generally, Gilles Kahn had a unique vision of the growing importance of the interaction of the Information Technologies and Sciences with the Biological and Medical world. He was at the origin of the creation of a specific *BIO* theme among the main INRIA research directions, which now regroups 16 different research teams including the Asclepios one, whose research objectives are described and illustrated in this article.

1 Introduction

1.1 The revolution of biomedical images and quantitative medicine

There is an irreversible evolution of medical practice toward more quantitative and personalized decision processes for prevention, diagnosis and therapy. This evolution is supported by a constantly increasing number of biomedical devices providing *in vivo* measurements of structures and processes inside the human body, at scales varying from the organ to the cellular and even molecular level. Among all these measurements, *biomedical images* of various forms play a more central role everyday.

Facing the need of a more quantitative and personalized medicine based on larger and more complex sets of measurements, there is a crucial need for developing 1) advanced image analysis tools capable to extract the pertinent information from biomedical images and signals, 2) advanced models of the human body to correctly interpret this information and 3) large distributed databases to calibrate and validate these models.

¹ Asclepios was a Greek hero who later became the Greek god of medicine and healing. His most famous sanctuary was located in Epidaurus which is situated in the northeastern Peloponnese (from Ron Leadbetter)

1.2 Advanced Biomedical Image Analysis

Tremendous progress has been made in the automated analysis of biomedical images during the past 2 decades [16, 3]². For instance, for rigid parts of the body like the head, it is now possible to fuse in a completely automated manner images of the same patient taken from different imaging modalities (e.g. anatomical and functional), or to track the evolution of a pathology through the automated registration and comparison of a series of images taken at distant time instants [20, 41] (cf. Figure 1). It is also possible to obtain from a Magnetic Resonance image of the head a reasonable segmentation into skull tissues, white matter, grey matter, and cerebro-spinal fluid [42], or to measure some functional properties of the heart from dynamic sequences of Magnetic Resonance [2], Ultrasound or Nuclear Medicine images [22].

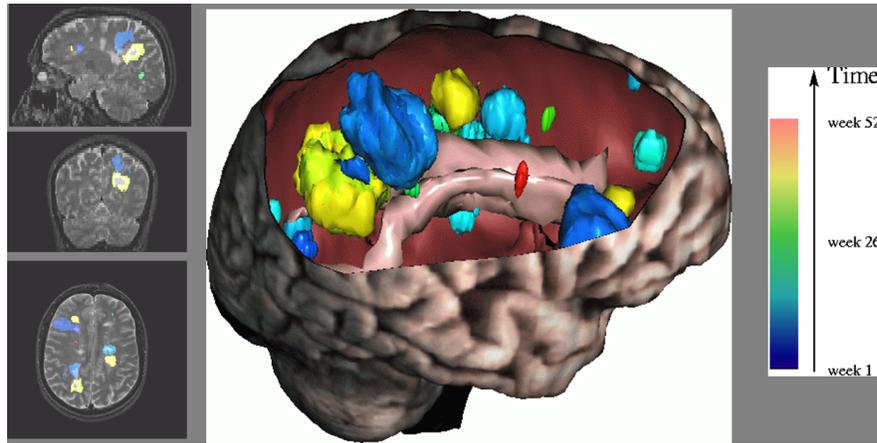


Fig. 1. Automatic detection of the evolution of multiple sclerosis lesions from a time sequence of 3-D magnetic resonance images of the head of a patient (from D. Rey et al. [33]).

Despite these advances and successes, one can notice that statistical models of the anatomy are still very crude, resulting in poor registration results in deformable regions of the body, or between different subjects. If some algorithms exploit the physical modeling of the image acquisition process, only a few actually model the physical or even physiological properties of the human body itself. Coupling biomedical image analysis with anatomical and physiological models of

² One can have a good vision of the state of the art with the proceedings of the most recent conferences MICCAI'2006 (Medical Image Computing and Computer Assisted Intervention) or ISBI'2006 (Int. Symp. on Biomedical Imaging) as well as from the most recent issues of journals like IEEE Trans. on Medical Imaging or Medical Image Analysis (Elsevier)

the human body could not only provide a better comprehension of the observed images and signals, but also more efficient tools to detect anomalies, predict evolutions, simulate and assess therapies.

1.3 Computational Models of Anatomy and Physiology

Computational Models of the Human Body constitute an emerging and rapidly progressing area of research whose objective is to provide a better understanding of the anatomical variability (Computational Anatomy) and of the major functions of the human body (Computational Physiology), as well as to provide effective algorithmic tools for their realistic numerical simulations [4, 14, 5].

Quite advanced models have already been proposed to study at the molecular, cellular and organ level a number of physiological systems (e.g. cardiac, respiratory, digestive, nervous (central and peripheric), reproductive, etc. [23]). For instance, computational models of the heart have been proposed to interpret the cardiac electromechanical activity from medical images and electrophysiological measurements [6, 9], or to study the properties of physiological flows in blood vessels [32], in order to predict the apparition of cardiovascular diseases. Computational Models have also been proposed to explore the structures and the activity of the brain from anatomical and functional images and signals in order to better understand a number of brain diseases (e.g. Alzheimer's disease, Multiple Sclerosis, Creutzfeldt-Jakob disease, Epilepsy or Schizophrenia) [13]. Advanced models of abdominal organs including the liver [14] and the intestine [21] have been developed in the context of image-guided surgery cf. Figure 2 and surgery simulation (cf. Figure 3). Other models have been developed to predict the evolution of cancerous lesions in various organs [38, 37, 24].

Not only these models and others need to be developed, refined and validated, but new methods must be designed to automatically adjust the model parameters to a given person from the available biomedical signals (in particular medical images) and also from prior genetic information. Building such patient-specific models is a challenging goal which requires in particular the development of new data assimilation methods coping with massive numbers of measurements and unknowns.

1.4 Large Distributed Databases

Another important milestone to make progress in these directions is the development of large databases of subjects and patients including biomedical signals and images as well as genetic information, and the development of specific tools to correlate for instance the shape and evolution of anatomical structures (phenotype) with the genetic information (genotype) and/or with a certain number of pathologies. The construction and exploitation of these databases require the development of specific measurement platforms regrouping cutting edge imaging facilities with easy access provided to internal and external research teams (e.g. the Neurospin³ platform of CEA).

³ URL of Neurospin: <http://www.meteoreservice.com/neurospin/>

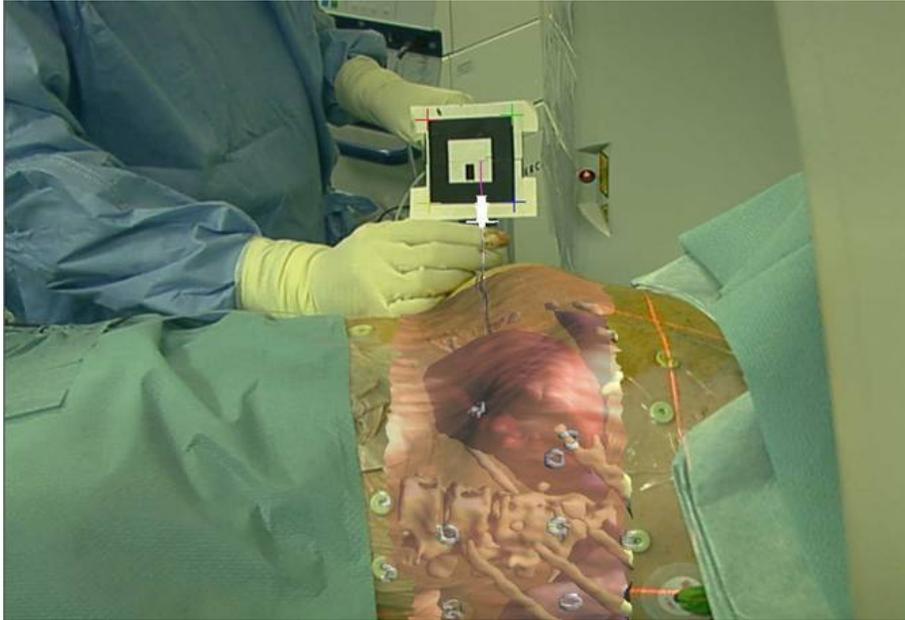


Fig. 2. Augmented reality for image-guided radio-frequency ablation of a liver tumor (from S. Nicolau, L. Soler et al. [27])

Huge computing power is already required to run advanced computational models in their direct mode (for prediction) or inverse mode (to adjust to a specific patient from biomedical measurements). The amount of required computing power to process large databases will require the development of grid-enabled algorithms capable to exploit distributed computing power and data in large international networks.

2 From Epidaure to Asclepios

To address the above issues, the Asclepios research project was launched on November 1st, 2005 at INRIA Sophia Antipolis after a final approval by INRIA CEO Gilles Kahn. It was built on the results of the previous research project Epidaure, initially launched at INRIA Rocquencourt in 1989 and later installed in Sophia-Antipolis in October 1992 thanks to the strong support of Gilles Kahn and Pierre Bernhard (at this time respectively VP for Science and Director of INRIA Sophia-Antipolis). The original scientific objectives were the quantitative analysis of medical images and the coupling of medical imaging with medical robotics and surgery simulation.

Some important contributions of the Epidaure project were published in an invited article of the IEEE Transactions on Medical Imaging in November 2003

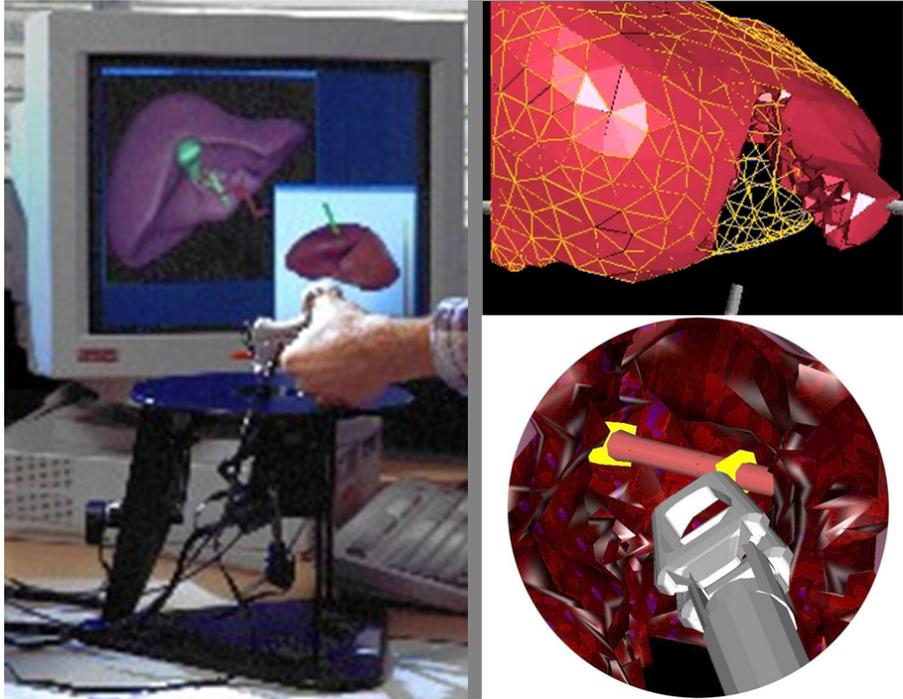


Fig. 3. Surgery simulation with visual and force feedback. (cf. S. Cotin, G. Picinbono, C. Forest et al. [12, 31, 18])

[3]. One can note that the Epidaure team also contributed with a few other teams to the establishment of Medical Image Analysis and Simulation as a well identified discipline in the field of computer science with its own scientific community, its scientific peer-reviewed journals and conferences; in particular we contributed to the founding of the Medical Image Analysis journal (MedIA) and the MICCAI conference (Medical Image Computing and Computer Assisted Intervention), again with the encouragements of Gilles Kahn who attended the precursor conference CVRMed'95 (Computer Vision, Virtual Reality and Robotics in Medicine) organized by INRIA in Nice in April 1995, and the MICCAI'04 conference organized by INRIA in Saint-Malo in September 2004.

2.1 Personalized models for diagnosis and therapy

If several of the problems listed in the 1989 Epidaure research proposal were solved, some important ones remain unsolved while new challenging problems have appeared. The research objectives of the Asclepios proposal take into account this situation and are organized around 5 research directions, namely 1) Medical Image Analysis, 2) Biological Image Analysis, 3) Computational

Anatomy, 4) Computational Physiology, 5) Clinical and Biological Validation. Only directions 1 and (part of) 5 correspond to a smooth continuation of the former research objectives of the Epidaure project, whereas directions 2, 3 and 4 correspond to novel objectives related to emerging problems.

Figure 4 somehow summarizes the overall objectives of the Asclepios project. The computational models of the human body that we consider often have 4 different main components including geometry, statistics, physics and physiology. In order to personalize a generic model, it is necessary to identify its parameters by confronting it to a set of patient-specific biomedical images and other biomedical signals. The personalized model can then in turn be projected back on the images and signals to better interpret them, and to provide an help for the diagnosis of diseases. The personalized model can also be used to predict an evolution, or to plan and simulate an intervention. This provides an help for the prevention and therapy of diseases.

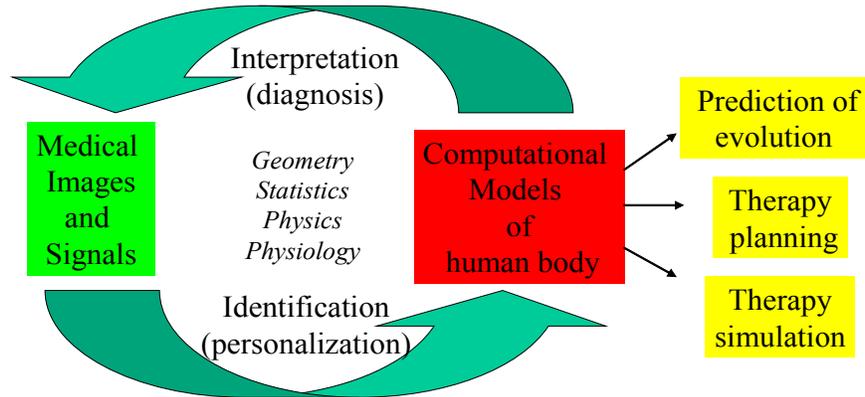


Fig. 4. Objectives of the Asclepios project

In the sequel of this article we provide four illustrations of several aspects of this current research respectively on a) the automatic measurement of the variability of the geometry of some brain structures, b) the simulation of the growth of personalized brain tumors, c) the simulation of personalized electromechanical activity of cardiac ventricles, and d) the construction of large mosaics of microscopic molecular images acquired *in vivo* and *in situ*, before we conclude.

3 Measuring Brain Variability from Sulcal lines

The objective of Computational Anatomy is the modeling and analysis of biological variability of the human anatomy⁴. Typical applications cover the simulation of average anatomies and normal variations, the discovery of structural differences between healthy and diseased populations, and the detection and classification of pathologies from structural anomalies.

Studying the variability of biological shapes is an old problem (cf. the remarkable book "On Shape and Growth" by D'Arcy Thompson [39]). Significant efforts have been made since that time to develop a theory for statistical shape analysis, one can refer to [15] for a good synthesis, to a specific special issue of Neuroimage [40] or more recently to the first international workshop on the *Mathematical Foundations of Computational Anatomy* organized by Xavier Pennec and Sarang Joshi at MICCAI'2006 [29].

Computational Anatomy lies at the intersection of geometry, statistics and medical image analysis. A 3 stage approach to compute statistics on anatomical shapes is proposed by M. Miller in [26]: 1) construction from medical images of anatomically representative manifolds based on feature points, curves, surfaces and volumes); 2) assignment of a point to point correspondence between these manifolds (possibly through a restricted class of geometric transformations, e.g. rigid, affine, diffeomorphism); 3) generation of probability laws of anatomical variation from these correspondences.

We provide below an illustration of a similar approach applied to the study of the variability of some brain cortical structures. Through a longstanding collaboration⁵ with the LONI research group of UCLA (Pr. Paul Thompson), we developed a method to study the variability of the so called sulcal lines which are defined by neuroanatomists at the bottom of brain cortical foldings. These lines can be extracted and labeled manually by experts (this is the case here on a database of 700 subjects), or automatically by expert systems like the one developed at CEA by the group of J.F. Mangin [34].

Figure 5 shows a typical set of sulcal lines extracted on the cortical surface of a brain of the LONI database. With V. Arsigny and P. Fillard we developed an original approach to register all the images of the database in a common reference frame after an affine normalization, followed by an individual registration of all homologous sulcal lines together. This allowed us to compute for each sulcal line an average sulcal line, and along each of these lines a local measure of variability under the form of covariance matrix computed at regularly sampled points.

Thanks to new metrics defined in the space of Symmetric Positive Definite Matrices (also called "tensors" in our community), we were able to propose a method to extrapolate this local measures of variability to the whole cortex in a plausible manner [28, 1]. We see in Figures 6 a color representation of the

⁴ cf. the summer school organized at UCLA in July 2004 by P. Thompson (UCLA) and M. Miller (Johns Hopkins) cf. www.ipam.ucla.edu/programs/mbi2004/

⁵ cf. Associated Teams BRAIN-ATLAS <http://www-sop.inria.fr/epidaure/Collaborations/UCLA/>

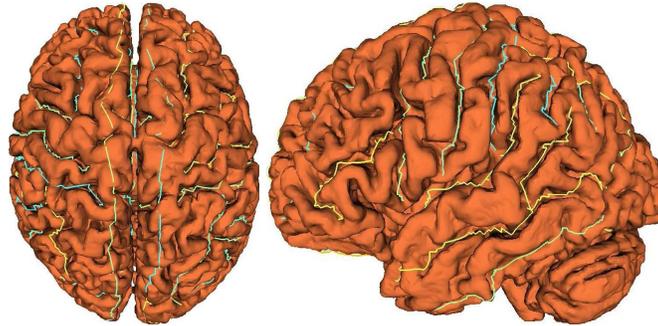


Fig. 5. Example of sulcal lines drawn on the cortical surface of one of the brains of the UCLA database (courtesy of P. Thompson).

variability measured in various regions of the brain which quantitatively confirms previous observations made on a more qualitative basis by neuroanatomists. These results are published in [17].

Statistical information about variability can be used to help guiding the superposition of a brain atlas on the brain images of a specific patient. This was shown with a different statistical database and in an image-guided radiotherapy context by O. Commowick et al. in [11].

Another study, conducted during the PhD work of Jonathan Boisvert [8], concerned the statistical analysis of the variability of the scoliotic spine. By using an articulated model based on the relative position and orientation of successive vertebrae (through rigid body transformations), we were able to estimate the variability of the spine shape over a database of more than 300 patients. This was used to assess the evolution of the deformation during orthopedic treatments; moreover, the first four modes of variation appeared to be closely correlated to the usual clinical classification of scolioses, which reinforces the clinical interest of the chosen approach. Figure 7 illustrates a typical result.

4 Simulation of Tumor Growth

Combining anatomical, physical and physiological models of the human body is part of the Computational Physiology research field. The next two examples belong to this field. The first one concerns the simulation of diffusive tumor growth based on medical images. The objective is to identify the parameters of a generic dynamic model from a sufficient number of observations on a specific patient, in order to better characterize the nature of the observed tumor. This image-based characterization of the tumor aims at better predicting its plausible evolution, and anticipating the effects of possible therapies (e.g. radiotherapy, surgery, chemotherapy).

The work described in [10] includes three main levels of modeling: the first level is geometrical and includes the extraction of the main structures of the head

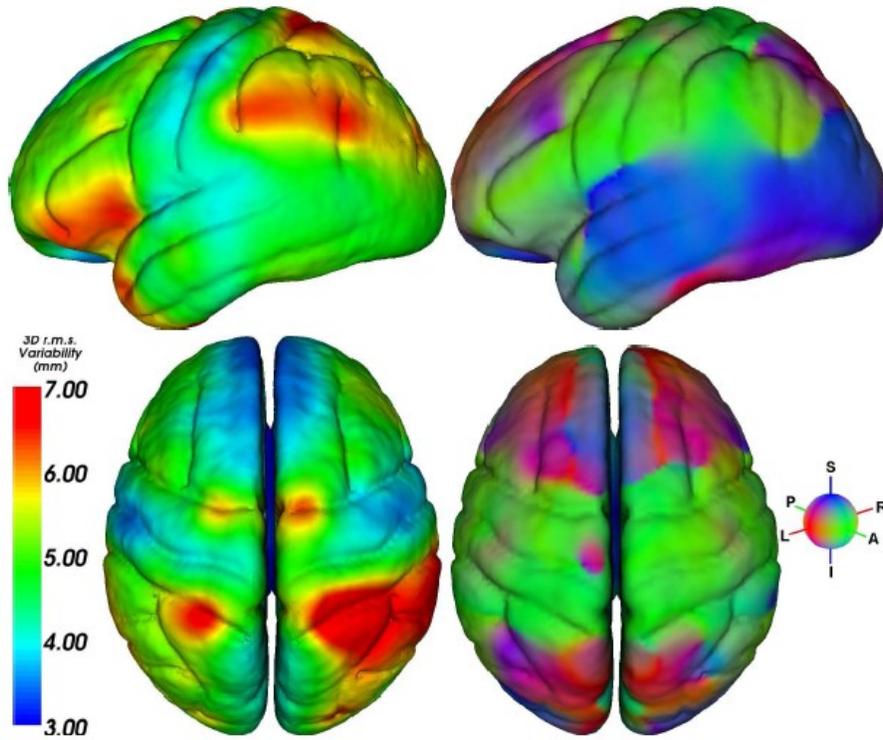


Fig. 6. Color maps showing the geometrical variability of the cortical structures extrapolated from the sulcal variability and a mathematical Riemannian framework. Left column shows the amplitude of the variability (hot colors mean high variations among subjects). Right column shows the main direction of variability. (color code: Red: left-right oriented tensor, Green: posterior-anterior oriented, Blue: inferior-superior oriented. Cf. P. Fillard, V. Arsigny et al. [17])

from a set of multisequence magnetic resonance images (MRIs). Among these structures are 1) the skull, 2) the gray and 3) the white matter of the brain, 4) the cerebrospinal fluid and 5) the falx cerebri. Figure 8 shows a typical representation of these structures. The accurate geometric description of these structures plays an important role as the proliferation and migration of glial tumor cells strongly depend on the nature of the tissues and also on the orientation of the white matter fibers.

The second level of modeling refers to biomechanics. The aim is to simulate the deformation of the brain induced by the tumor growth, also called "mass effect". We build a finite element model of the previously extracted head structures under the hypothesis of an inhomogeneous isotropic linear elastic behavior of the biological tissues. Linearity is a reasonable assumption because the amplitude of the deformations is small. Inhomogeneity takes into account the mechanical variability of the tissues.

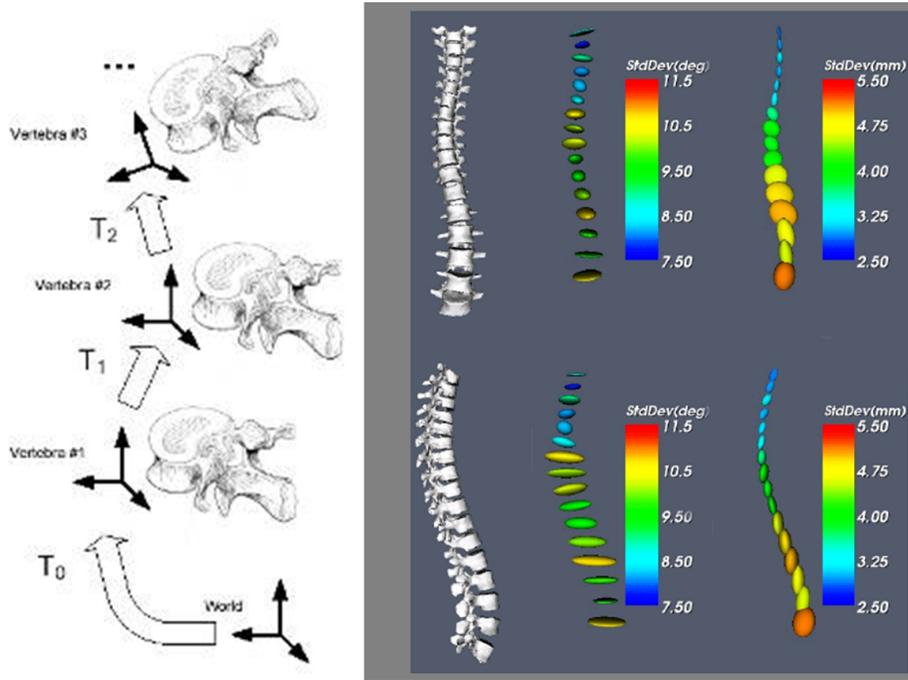


Fig. 7. Statistical spine model. From left to right: mean spine model reconstructed from a database of 300 patients with scoliosis, rotation and translation covariance measuring the local variability of each vertebra (color encodes the determinant of the covariance matrices). Top: Postero-anterior view. Bottom: lateral view. (cf. J. Boisvert [8])

The third level of modeling concerns the physiopathology of the tumor itself. We consider a macroscopic description of the tumor cell density through a Fisher-Kolmogorov reaction diffusion equation. The reaction component is a second order polynomial which corresponds to a logistic proliferation law: exponential increase of number of cells followed by a reduced proliferation rate until an asymptotic value is reached. The diffusion component models the migration of tumor cells in their neighborhood. Because glioma cell migration is preferential along the white matter fibers, the main bundles of white matter fibers are included in the model, through diffusion tensor MRI. The biomechanical coupling with the reaction-diffusion equation is introduced in the constitutive equation through a local pressure proportional to the tumor cell density.

Figure 9 shows an example of the simulation of the progression of a glioblastoma during a 6 month period, with a good correspondence between observations and simulations. The identification of the parameters of the model followed an interactive and semi-automatic procedure. It is the current PhD work of E. Konukoglu [25] to identify automatically these parameters from the observations

at two time points, and to measure the predictive power of the model against a third time point.

Once validated, we believe that such models could be used to better delineate for instance the dosimetry planning in radiotherapy, by proposing a margin outside of the visible contours of the tumor which would take into account the actual proliferation and diffusion parameters of the model, as well as the privileged directions of the main white matter fibers.

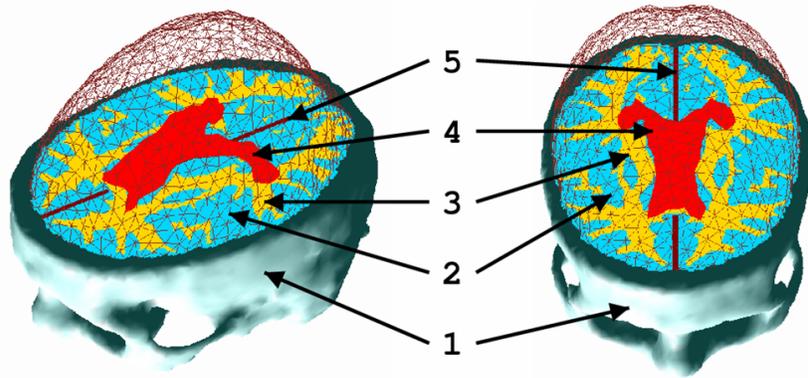


Fig. 8. The different tissues included in the biomechanical model of the head. 1 Skull. 2 Grey matter. 3 White matter. 4 Ventricles. 5 Falx cerebri

5 Personalized Electro-Mechanical Model of the Heart

Building a personalized electro-mechanical model of the heart ventricles is an important task to simulate and analyze the electrical or mechanical activity of the heart of a specific patient.

We started the research on this topic at INRIA about 6 years ago through a collaborative action ICEMA⁶ funded by the scientific direction of INRIA. This collaborative action was closely followed and supported by Gilles Kahn. It involved several research project teams at INRIA including Sosso, Caiman, Epidaure, Opale and Macs, and external research groups at NIH (E. Mc Veigh), Guy's Hospital (R. Razavi), and Philips (O. Gérard). This collaboration was even reinforced more recently through a specific INRIA consortium called CardioSense3D⁷, currently involving the INRIA teams Asclepios, Macs, Reo and Sosso2, as well as the previous NIH, Guy's Hospital and Philips research groups.

⁶ www-rocq.inria.fr/sosso/icema2/icema2.html

⁷ <http://www-sop.inria.fr/CardioSense3D>

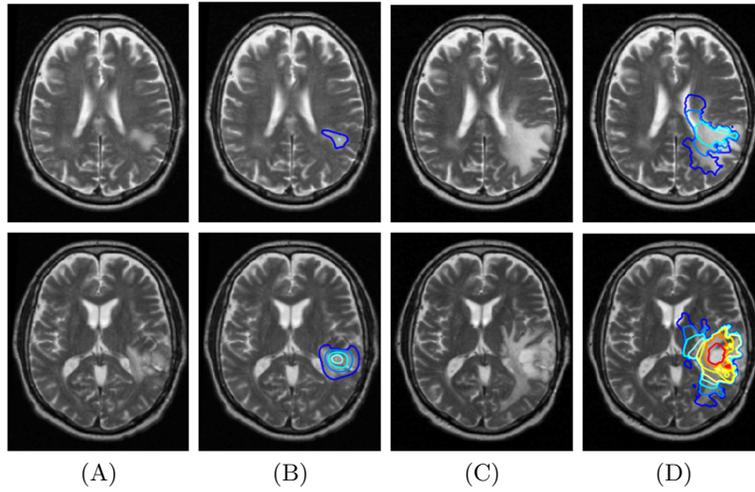


Fig. 9. Six months simulation of a glioblastoma growth. (A) T2 MRI of the patient, March 2002. (B) Previous MRI with superimposed tumor cell isodensity contours used for initialization. (C) T2 MRI of the same patient in September 2002 (6 months later). (D) Previous MRI with superimposed tumor cell isodensity contours simulated with the model.

The current models include again 3 levels of description [35]. The first level is a geometrical description of the anatomy of the cardiac ventricles which is adapted to the specific geometry of a given patient through image processing methods. The direction of the cardiac fibers is projected onto this geometric model by automatically mapping an average description which comes from a previous statistical analysis [30].

The second level of modeling is a macroscopic description of the evolution of the action potential of cardiac cells, which measures the difference between the extra-cellular and the intra-cellular electrical potentials. This evolution is modeled through a set of reaction diffusion equations (initially proposed by Fitzugh and Nagumo, and later refined by Aliev and Panfilov). These equations take into account a higher conductivity in the direction of the fibers at each point of the previous geometrical description, and allow a realistic simulation of the depolarization and repolarization waves within the cardiac tissues.

The third level of modeling is the electro-mechanical coupling which describes how the action potential variations actually controls the contraction and the relaxation of the cardiac fibers. We chose a macroscopic model of Bestel, Clément and Sorine [7]: a set of partial differential equations combines locally the behavior of an active elastic contractile element controlled by the previous action potential, with in addition two passive elastic elements respectively in parallel and in series. This model, initially inspired by the model of Hill-Maxwell is based on a multiscale analysis from the nanoscopic to the macroscopic scale. We see in

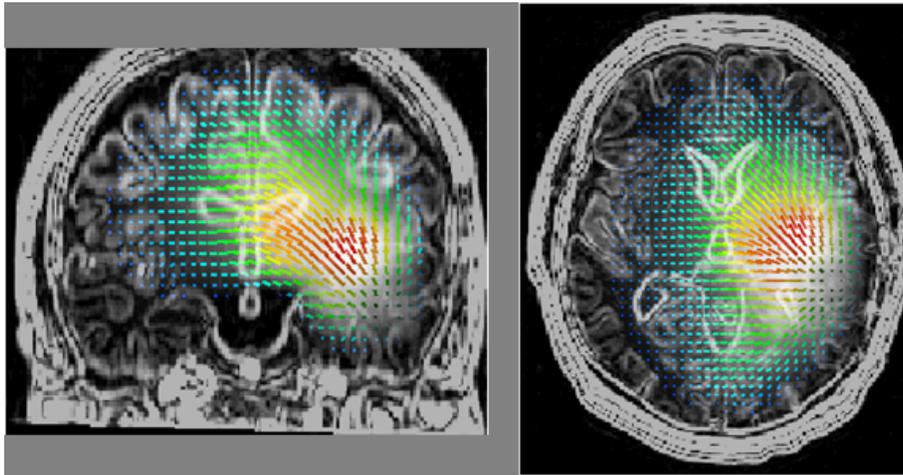


Fig. 10. The simulated displacement of the brain parenchyma due to the development of the previous tumor model in (left) coronal and (right) transverse views.

Figure 11 an illustration of the realistic simulation of the contraction of a generic instance of this model.

The personalization of such a generic model must then be done through a set of specific measurements obtained through cardiac imaging (e.g. Ultrasounds, Magnetic Resonance, Computed Tomography or Nuclear Medicine Imaging) and electrophysiology (typically the electrocardiogram or ECG). This is a difficult inverse problem which can be attacked through several strategies (cf. for instance [36]). Figure 12 shows the personalization of the model obtained through tagged MRI and specific electrophysiological measurements obtained with an endovascular procedure.

The future objectives of this research include the simulation of various therapies, like for instance Cardiac Resynchronization Therapy (CRT), or radiofrequency ablation procedures, or the effect of stem cells therapy.

6 Building Large Mosaics of Microscopic Images

The last example concerns microscopic imagery. During the past few years, we have conducted a research activity on the digital processing of microscopic images acquired *in vivo* and *in situ*. This was made possible through the development of new imaging devices enabling the acquisition of confocal microscopic images at the end of a very thin optical probe. The probe can be introduced in the operator canal of an endoscope in order to provide images of the cellular architecture of suspicious tissues on line. This operation can also be seen as an "optical biopsy".

One of the issues with this type of imaging is the limited field of view of the microscopic images: because these images have a resolution of the order of the

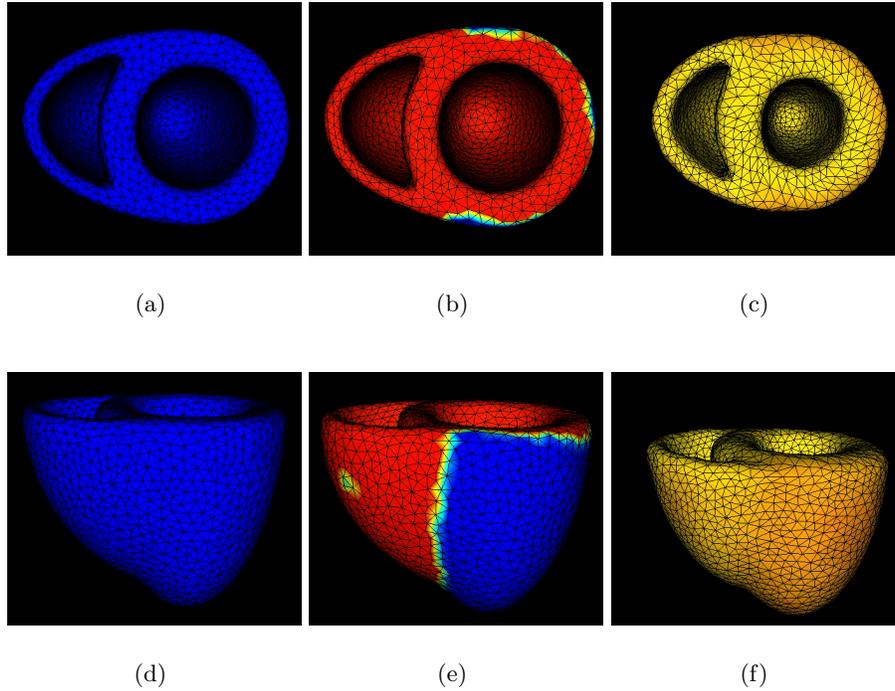
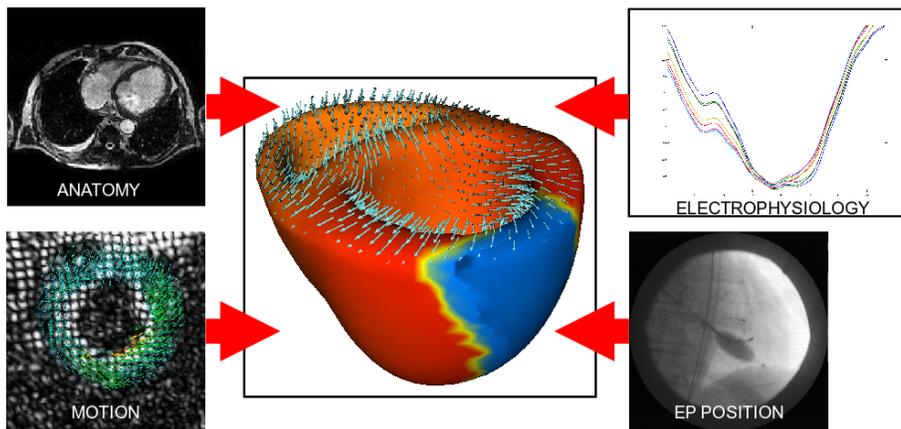


Fig. 11. Short axis (top row) and long axis (bottom row) views of an electromechanical heart model during end diastole (left column), ventricular depolarization (middle column) and end systole (right column).

micron, the covered field of view is usually limited to a few hundreds of microns. This is a problem when the analysis of the cellular architecture requires a larger field of view (this can be the case for instance when observing human colonic crypts), or when some statistical measurements would require a larger number of cells or vessels, or simply when it is necessary to reposition the probe exactly in a given location (when doing a temporal series of images at distant time points to study a slow dynamic phenomenon for instance). Through a collaboration with the Mauna Kea Technology company, T. Vercauteren [43] proposed during his PhD research an original method to build a larger scene from the video sequence of microscopic images acquired during a smooth motion of the acquisition probe. The mosaic of images is obtained by replacing all of them in a common reference frame. This is a difficult problem because of the possible deformations induced by the motion of the probe and the non-rigid nature of the observed tissues. Figure 13 shows a typical example of the reconstruction of such a mosaic. Other work on the construction of large mosaics of 3-D confocal images acquired from in vitro samples can be found in [19]



(a)



(b)

Fig. 12. (a) Intervention in the XMR room at Guy's Hospital (Pr. Reza Razavi) that allows to combine MRI and Xray acquisition (b)Integration of XMR data providing anatomy, motion and electrophysiology measurements of a specific patient into the previous generic electromechanical model to get a personalized electro-mechanical cardiac model. (cf. [36])

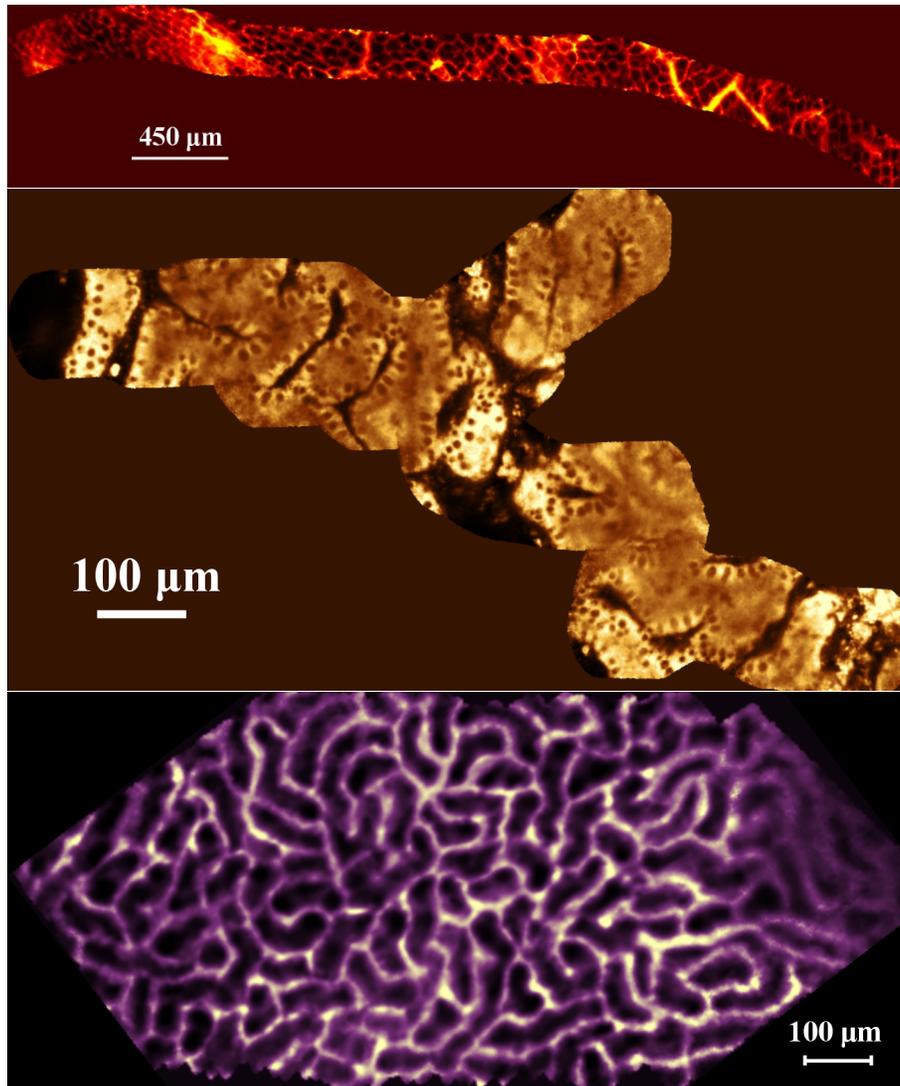


Fig. 13. Top : *in vivo* mouse colon vascularization after injection of FITC-Dextran high MW (300 input frames, Courtesy of M. Booth, MGH, Boston, MA); Middle : Ex vivo reflectance imaging of the human colon (mosaic includes 1500 input frames); Bottom : Microcirculation of the peritubular capillaries of a live mouse kidney with FITC-Dextran high MW (31 input frames). (cf. T. Vercauteren et al. [43])

7 Conclusion

We described and illustrated in this article the current research objectives of the Asclepios project at INRIA whose main application areas are in medicine and biology. The pharmaceutical domain is also an application area, as computational models of the human body can be exploited to better predict and quantify the effect of new drugs.

We strongly believe that the development of advanced biomedical image analysis methods combined with specific computational models of living systems will allow a more profound understanding of the anatomy and physiology of the human body, and of the correlation between anatomical or physiological anomalies with the development of certain pathologies. We also believe that this research effort will be helpful to better exploit the huge amount of available biomedical signals (from *in vivo* molecular and cellular imaging to macroscopic organ imaging) as well as the genetic information potentially available on each patient.

An important clinical objective will be to increase significantly the potential for pre-symptomatic diagnosis and early treatment for a maximum medical efficiency. This research could also help the simulation and evaluation of various therapies, in particular traditional or minimally invasive surgery, radiotherapy, chemotherapy, and also some currently experimental therapies like genetic or cellular therapy. It should also contribute to the promotion of image guided therapies.

Gilles Kahn strongly encouraged this research while he was the scientific director of INRIA Sophia-Antipolis and later the Vice-President for Science and finally the CEO of INRIA. Through his numerous scientific interactions with the involved researchers, through his exceptional vision of the future, he stimulated this activity and gave the involved scientists the necessary confidence to explore new directions sometimes far away from their traditional background. For all these reasons we are proud to dedicate this article to the memory of Gilles Kahn.

8 Acknowledgements

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