

Visualising the future of medicine

Modelling a physiology is no mean feat, but doing so has the potential to change the way we look at healthcare. We explore the advances being made

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I direct the Scientific Computing and Imaging Institute at the University of Utah. We're an inter-disciplinary research institute of around 200 faculty staff and students, and we specialise in visualisation research, image analysis and scientific computing. I also direct the NIH/NCRR Center for Integrative Biomedical Computing, which is in its 14th year and focuses on image-based modelling, simulation and visualisation.

The work we do is essentially a piece of the personalised medicine pie – creating biological-subject-specific-based models from images, such as from MRIs, X-Rays and CT scans. Those images are then segmented in order to obtain the geometry of the patient or parts we're focusing on and used to create patient-specific computer-generated models. From the models, we perform functional simulations such as simulating the electrical activity in the heart,

localising epileptic seizures within the brain and calculating stresses or strain on artificial joint transplants. The results of the simulations and models are then visualised and ultimately taken to clinics to be used for diagnosis and treatment.

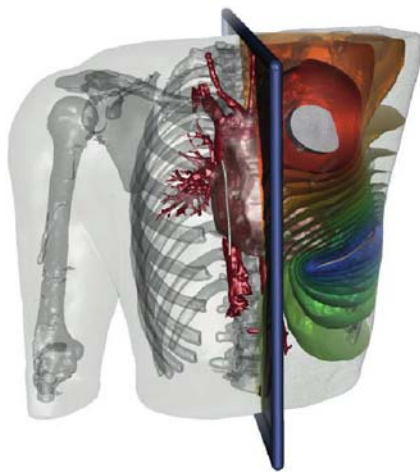
Behind the scenes we write all the software involved in this process and it's taken us at least 10 years of hard work to get to the point where we're actually able to do the whole process of image-based modelling, simulation and visualisation for real-world clinical application. Currently, we're working with a cardiac surgeon on the simulation and visualisation of atrial fibrillation for surgical planning, working with neuro-scientists and neurologists for localising the source of epileptic seizures, and designing internal, implantable defibrillation electrodes and optimising their efficacy.

The software we've created is a set of tools that take you through that entire process. Each

one is open source, available to download from the website and runs on multiple platforms. The first piece of software we use to do the segmentation of the images is called Seg3D. To do a simulation of an epileptic seizure, for example, we would first take an MRI of the head. The Seg3D software has automatic algorithms that locate the boundaries of the skull and cortex of brain and the pulls that information out from each slice of the image, which provides us with sets of surfaces. This can also be done in three dimensions if 3D images are used. To run the simulation we need volumes and so the next piece of software we use is BioMesh3D, which takes those images and creates full 3D geometric meshes – the digital geometry necessary for the simulation. Our next set of software, SCIRun, does the finite element or boundary element simulation required in electric source modelling. Our final piece of software, ImageVis3D, provides visualisation of the simulation.

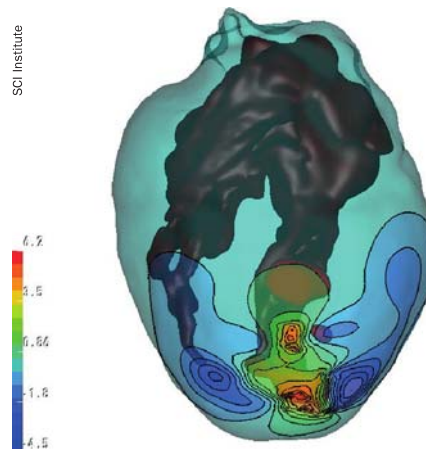
To create software that's useable is a multi-year process. I think a lot of people underestimate how difficult and challenging it is to do, and we have a number of gifted and talented software engineers who work incredibly hard on achieving just that. The challenges along the way are many, especially because when doing biomedical modelling and simulation we need to recognise that our biology is incredibly complicated. We can never truly address all that complexity and so need to simplify things in some ways and decide on the level of complexity we do want to address.

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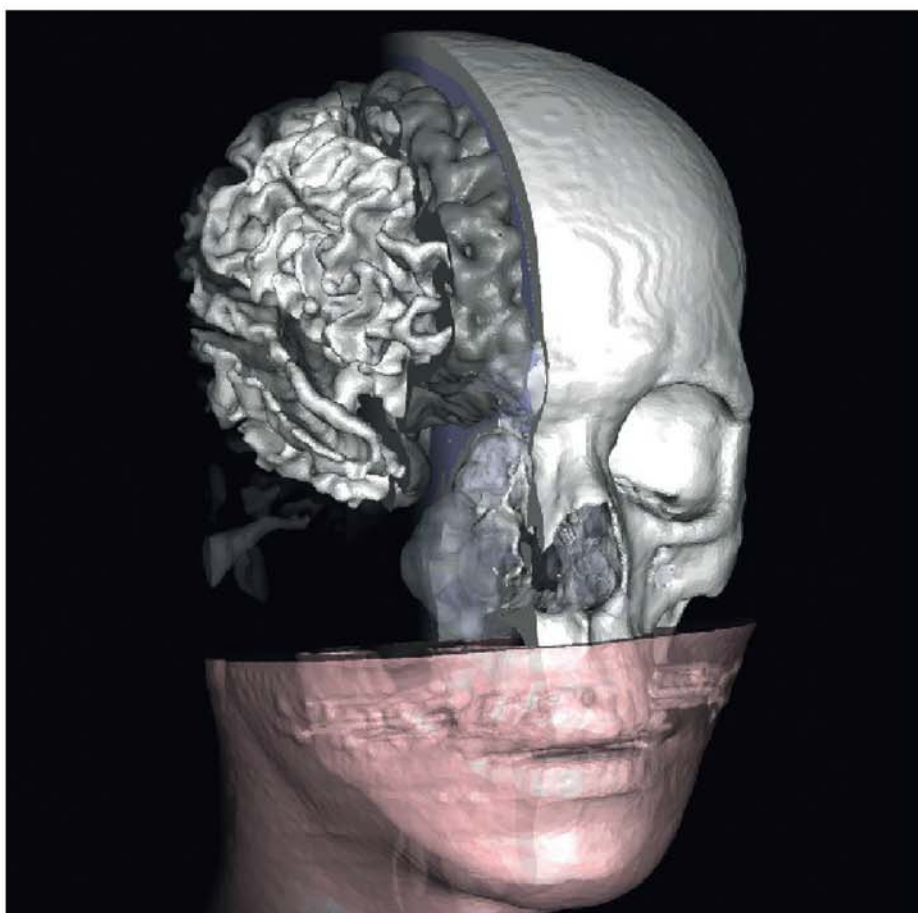


Simulation of the electric field generated by an implanted cardiac defibrillator in a patient-specific computer model

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The mesh near the apex of the heart showing solved bidomain simulation of epicardial potentials during acute ischemia

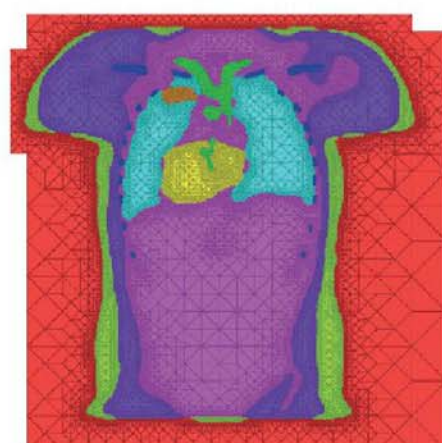


BioMesh3D being utilised for tetrahedral mesh generation of multi-material quality meshes from segmented biomedical image data

Over the past few years we've been continually addressing more complexity, which means larger scale models and larger amounts of data that need to be dealt with in order to compute and run simulations and visualisations.

We work with a lot of clinical and biomedical collaborators and the one important fact is that they're not computer scientists; they don't want to write programs, they want a software package that's easy to use. Because of this, there's a good deal of effort

made in the design of the user interface and there are a lot of iterations between us and our collaborators trying to make everything as intuitive as possible. We then put everything through testing phases; however, no matter how much time or effort you put into making the software work, users will find ways to break it! We receive emails from people saying that it's not working for them and in many cases we would never have dreamed of the software being used in those particular ways!



Tetrahedral meshing of image data for biomedical simulation

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But we work to try to correct the issue and enable them to use the software.

The ultimate goal is to create this system of visualisation and simulation modelling techniques and corresponding software. I think there is a tremendous movement towards personalised medicine. People are recognising that one size doesn't fit all and that we can give a better level of diagnosis and treatment if we tailor things to an individual. That's really what we're working towards and while it's taking longer than we thought, we're making significant progress. I do believe that in the near future it will be possible to create treatments like implantable defibrillators and optimise their placement, and that we'll create custom-fit joint replacements. And I think that's going to be a very exciting time.

The ScalaLife Project

Scalable Software Services for Life Science (ScalaLife) is a European initiative launched in 2010 with the ambitious mission of implementing new techniques for efficient parallelisation combined with throughput and ensemble computing for the life science community. ScalaLife seeks to establish a new approach for targeting the entire pipeline from problem formulation through algorithms, simulations and analysis by focusing heavily on actual application issues. In particular, the project will provide long-term support for major European software

by establishing a pilot Competence Centre for scalable software services for the life science community to foster Europe's role as a major software provider.

The Barcelona Supercomputing Center is participating as main partner of ScalaLife and holds the responsibility of connecting the latest research on scalability and hardware design with application software work, and to properly document algorithms and optimisation techniques so that they can also be applied to other life science simulations. Professor Modesto Orozco,

BSC director of Life Science, and Databases Work Package leader of the ScalaLife project, explained that the future of structure-based drug discovery, for example, relies on software tools capable of scaling on multi-core supercomputers.

'ScalaLife will provide the life science community with fast and flexible access to high-performance computing resources,' he said. Additionally, Professor Orozco is coordinating the development of standards for handling both the storage and exchange of the ever-increasing amount of life science simulation data.