PROGRAMA WORKSHOP

Lunes 4 Enero

9-9.30am	Acreditación
9.30-9.45am	Palabras de apertura
9.45-10.30am	Steffen Härtel/Mauricio Cerda, título por confirmar
10.30am	Café
11am-12.30pm	Luis Pizarro, Tutorial "Variational Methods in Biomedical Imaging", parte 1 de 3
12.30pm	Almuerzo (no incluido)
2-2.45pm	José Delpiano, Automated detection of fluorescent cells in In-Resin Fluorescence sections for Integrated Light and Electron Microscopy
2.45-3.30pm	Claudio Araya, Analizando las conductas celulares colectivas *in vivo* durante la organogénesis
3.30pm	Café
4-5.30pm	Luis Pizarro, Tutorial "Variational Methods in Biomedical Imaging", parte 2 de 3

Martes 5 Enero

9-9.45am	Pablo Irarrázaval, título por definir (adquisición en resonancia magnética)
9.45-10.30	Sergio Uribe, título por definir (4D flow en resonancia magnética de corazón)
10.30am	Café
11am-12.30pm	Luis Pizarro, Tutorial "Variational Methods in Biomedical Imaging", parte 3 de 3
12.30pm	Almuerzo (no incluido)
2-2.45pm	Daniel Hurtado, Image-based biomechanical analysis of human lung regional deformation
2.45-3.30pm	Cristóbal Bertoglio, 3D-Reconstruction of cardiac diffusion MRI
3.30pm	Café

Más información sobre algunas ponencias

Daniel Hurtado

Short Bio: Daniel Hurtado earned a Ph.D. in Mechanical Engineering from the California Institute of Technology in 2011, and is currently assistant professor of Structural and Geotechnical Engineering at Pontificia Universidad Católica de Chile. His research interests lie in the fields of computational biomechanics and biophysics, particularly on the development of mathematical models that reflect the multiscale and multiphysics behavior of biological media, as well as advanced numerical methods to solve such models. He has been a Fulbright scholar, and is the recipient of the 2011 Robert J. Melosh award and medal.

Título: Image-based biomechanical analysis of human lung regional deformation

Abstract: Under physiological conditions, lung tissue experiences moderate deformation levels necessary to accommodate considerable volumes of air. Overstretch of lung tissue due to high-volume mechanical ventilation may induce damage to the lung parenchyma, triggering inflammation processes that eventually reduce the ventilation capacity. Thus, lung strain plays an important role in both pulmonary physiology and pathophysiology, and the accurate estimation of lung strain in a regional fashion has recently received great attention in the intensive care medical community. In this contribution, we present a finite-element based methodology for the quantification of lung tissue deformation from computed tomography images. By combining non-rigid image registration techniques and strain recovery methods, we construct continuous maps of the deformation-gradient tensor and associated deformation measures. Three-dimensional patient-specific maps of the volumetric strain are obtained for healthy human subjects, displaying a heterogeneous distribution of deformation under physiological conditions. Our method allows for the statistical characterization of volumetric strain in human healthy lungs. We envision that the proposed computational framework will enable a robust and computational efficient way to characterize regional strain in the lung.

Luis Pizarro

Short Bio: Luis Pizarro obtained the Engineering and M.Sc. degrees in informatics from the Technical University Federico Santa Maria, Chile, in 2003. He then spent five months as a research trainee at the INRIA Sophia-Antipolis, France, and a year as a researcher at the Institute for Innovation in Mining and Metallurgy, Chile. In 2005 Luis Pizarro is awarded a DAAD scholarship to pursue doctoral studies in Germany. In 2010 he obtained the Ph.D. degree in computer science from the Saarland University. Dr Pizarro worked as a postdoctoral researcher at Imperial College

London, UK, from 2009 to 2013 and since 2013 he is a research associate in the department of computer science at University College London, UK. Dr. Pizarro's research interests are image processing, computer vision, machine learning, biological and medical imaging.

Tutorial "*Variational Methods in Biomedical Imaging*"

Abstract: Variational methods give rise to some of the best performing approaches to numerous problems in image processing, computer vision, and biomedical imaging. Such energy-based methods allow for the transparent modelling of problem-specific constraints and assumptions, while having a straightforward minimisation/maximisation procedure. These characteristics make the variational framework very attractive both in theory and in practice. This tutorial presents the basic notions of variational methods and it overviews some core formulations in different applications. We distinguish between convex, non-convex, continuous, and discrete approaches; and we discuss different optimisation strategies. The goal of this tutorial is to provide participants with the elementary tools to design and implement variational methods for biomedical imaging applications.

Cristóbal Bertoglio

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M.Sc. in Structural Eng., PUC, 2007
Ph.D. in Applied Mathematics, INRIA, 2012
Postdoc in Cardiac Modeling, TU Munich, 2012-2014
Researcher in Numerical Biomedicine, CMM U. Chile, 2015-

Título: 3D-Reconstruction of cardiac diffusion MRI

Abstract: Biophysical (multiphysical and multiscale) cardiac models have the potential to perform predictive computational simulations and hence help to improve therapies like radio-frequency ablation, or cardiac resynchronization therapy.

Models of the cardiac input, however, require the knowledge (or the estimation using measured data) of constitutive tissue properties, like electrical conductivity, passive and active mechanical constants. It is however known that cardiac tissue is anisotropic, hence having different properties in the main fiber and cross fiber directions (i.e along and across the myocytes, respectively). Therefore, determining the fiber direction a priori is crucial.

It is widely accepted that fiber arrangement in tissue can be estimated using diffusion MRI (DMRI). The reconstruction of the fibers rely in spatially co-existant diffusion information, what is however not possible to be achieved in moving organs like the heart.

In this talk we will propose to estimate the local fiber direction in ventricles directly from greyvalues of sparse and arbitrarily spaced DMRI. The approach is based on the solution of a non-linear inverse problem using a continuous parametric and space-dependent mathematical representation of the diffusion tensor and histological knowledge of the cardiac fibers architecture. We also show the potential of the method for improving the efficiency of the data acquisition by relaxing the requirements of the acceptance window for respiratory navigation during acquisition. We will also discuss the extension of this technique to tissue perfusion.

José Delpiano

Short Bio: José Delpiano received his diploma in Electrical Engineering from Pontificia Universidad Católica de Chile in 2004 and his PhD in Electrical Engineering (Computer Vision) from Universidad de Chile in 2013. He is a lecturer at Universidad de los Andes. He has served as reviewer in the IEEE International Conference on Neural Networks since 2007. During part of 2015, he was a Visiting Lecturer at University College London. His research interests are biomedical image analysis and computer vision.

Título: Automated detection of fluorescent cells in In-Resin Fluorescence sections for Integrated Light and Electron Microscopy

Abstract: The recent introduction of integrated or correlated light and electron microscopy (CLEM) allows for the extraction of both functional and structural information from a single specimen. The process for acquisition of CLEM data is highly laborious for expert microscopists. Current tools for automated acquisition of EM data (https://youtu.be/h-mT5rxdEZo) do not consider the fact that electron microscopy flattens the fluorescence signal in biological samples. A crucial step for an automated process of CLEM is the localisation of cells of interest in fluorescence images, in order to direct further EM imaging of the sample. We propose a simple method that accurately segments and localises most cells in a 2k x 2k image in about 5 seconds, with a user providing just minimum and maximum cell diameter of typical cells and a background-foreground threshold parameter. Our experimental results with images of HeLa cells verify the effectiveness of this method, when compared to the segmentations of expert microscopists. Future work should concern the characterisation of detected cells in order to select the most interesting ones to interrogate them about specific biological questions.

Claudio Araya

Short Bio: El Dr Claudio Araya estudia la morfogénesis tisular en vivo en embriones vertebrados, utilizando al pez cebra como modelo animal. Tras licenciarse en Biología en la Universidad Austral (2004), realizo sus estudios doctorales en el University College London y luego en el King's College London (Reino Unido, 2010). Actualmente, el Dr Araya es docente e investigador de la Universidad Austral de Chile y aplica herrameintas de imagenología (segmentación, 3D y flujo óptico) a fin de extraer parámetros cuantitativos que permiten entender las bases celulares y tisulares implicados en el desarrollo normal de órganos y la contribución genética a la malformación de estos.

Título: Analizando las conductas celulares colectivas *in vivo* durante la organogénesis

Abstract: El movimiento colectivo de grandes grupos se manifiesta a varios niveles de la Biología, ya sea en un hormiguero, en un cardumen de peces o en el establecimiento de sociedades humanas. De forma similar, durante la formación inicial de nuestros tejidos y órganos en la embriogénesis, nuestras células exhiben un comportamiento altamente colectivo. Pero, de qué forma se coordinan estos movimientos celulares a fin de generar estructuras tan complejas como un corazón y un cerebro?, y qué papel juegan los genes en esto? En esta charla mostraré cómo es posible estudiar el movimiento colectivo en vivo durante la embriogénesis animal bajo herramientas de análisis de imágenes y flujo óptico a fin de reconstruir la escala espacial y temporal de las conductas celulares colectivas y como este conocimiento nos ayuda a entender otras fenomenologías como el cáncer.