

Day 1 – Wednesday 23rd June 2021

<https://ucl.zoom.us/j/99134795495>

All times are in BST (+1 hour for CEST)

09:00	Peter Coveney	Welcome and introduction to AHM agenda
09:10	Hector Martinez-Navarro, The Institute for Experimental Medical Research and Simula	Assessment of left ventricular function in pulmonary arterial hypertension using in silico rat models of cardiac function
09:30	Ritabrata Dutta, University of Warwick	Designing optimal lockdown for COVID-19
09:50	Ana Teresa Maia, University of Algarve	Integrative use of allelic expression imbalance data to characterise cancer risk and development
10:20		
10:50	Sarah Harris, University of Leeds	CCPBioSim: Community building for biomolecular simulations
11:10	Andrea Townsend- Nicholson, UCL	Medical student training in CompBioMed
11:30	LEXIS Team	LEXIS: Orchestration & Data Platform with HPC/Cloud/Big Data Convergence and Collaboration with CompBioMed
11:50	Debora Testi, DICE project	DICE, Data Infrastructure Capacity for EOSC
12:10		
13:10	Pattern #3 meeting	Short introductory presentations from related projects

		<ul style="list-style-type: none"> • QCG-PilotJob for flexible and efficient execution of many computing tasks (Tomasz Piontek and Bartosz Bosak, PSNC) • Derek Groen, Hidalgo • Daniele Lezzi, BioExcel
13:40		<p>Consideration of some of the applications and how they can be expanded and use this pattern</p> <ul style="list-style-type: none"> • Architecture and scaling of BoneStrength simulation (Antonino Amedeo la Mattina, UNIBO) • GPAS: a global pathogen analysis service for SARS-CoV-2 and other pathogen diagnostics. (Philip Fowler, UOXF) • Ensemble protein-ligand Monte-Carlo molecular simulations and featurization for machine-learning binding affinity prediction (Jose Carlos Gómez-Tamayo, Jannsen)
14:10		Discussion with all members
15:00	<i>Break/Tea and Coffee</i>	
15:20	Machine Learning	<ul style="list-style-type: none"> • Heng Ma, Argonne National Lab • Ivan Benemerito, USFD • Vicente Grau, UOXF • Agastya Bhati, UCL
		Discussion with all members
17:00	End of meeting for all but General Assembly members	
17:00	General Assembly	
17:30	<i>End of day</i>	

Day 2 – Thursday 24th June 2021
<https://ucl.zoom.us/j/99134795495>

Parallel Sessions		
09:00	WP1: Emily Lumley	Management, Dissemination and Innovation
09:20	WP2: Gabor Zavodszky	Research and Applications

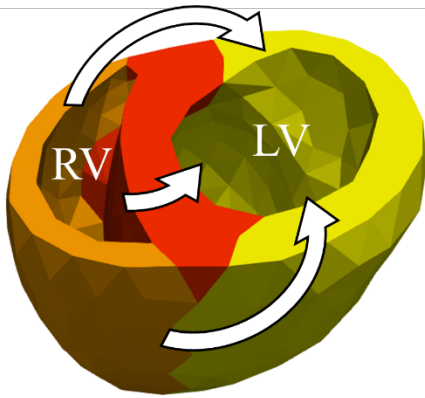
10:20	Break	
10:40	WP3: David Wifling	Data and Analytics
11:00	WP4: Marco Verdicchio	Operations and Services
11:20	WP5: Mariano Vazquez	Incubator Activities
11:50	WP6: Alberto Marzo	Training, Engagement and Sustainability
12:20	Lunch	
13:20	External Expert Advisory Board - TBC	
15:00	Break	
15:30	Break-out sessions for WP2/3/4/5 – technical insight on the internal project work (services and tools available)	
16:15	Break-out sessions for WP2/3/4/5 – Containers	
17:00	Break-out sessions for WP2/3/4/5 – Scaling & Performance	

Hector Martinez-Navarro

To preserve cardiac function in increased afterload conditions, the right ventricle (RV) adapts by developing muscular hypertrophy through progressive tissue remodelling. This process may lead to a vicious cycle with detrimental effects on RV function, as seen in pulmonary arterial hypertension (PAH) patients. However, how RV overload affects left-ventricular (LV) function and remodelling remains an open question. Computational models of cardiac physiology offer an opportunity for investigating mechanisms difficult or impossible to analyse otherwise due to the existence of overlapping factors and technical limitations. We aim to assess how PAH may alter LV regional mechanical properties in an anatomically-based computational model of healthy rat heart.

A computational simulation pipeline of cardiac mechanics has been implemented using the anatomy and strain measurements from a healthy rat using MR imaging. Whereas LV function was modelled realistically using catheter data obtained from the same subject than the MR imaging, RV function was based on representative literature values for healthy and PAH rats with diverse severities of PAH. The cardiac cycle was simulated for all cases whilst keeping LV anatomy, pressure and volumes constant, which allowed quantifying the effects of RV overload on LV function.

This approach is able to provide mechanistic evidence on how RV overload and increased passive myocardial stiffness causes a redistribution of strain and fibre stress in the LV, which may play a significant role in LV remodelling and function.



Ana-Teresa Maia

Allelic expression imbalance (AEI) is a recognised feature of healthy and cancer genomes. At its basis is cis-regulatory variation, polymorphic DNA variants located at cis-regulatory elements of gene expression. As everyone has a unique combination of alleles at these variants, we all express our genes at varying levels, which manifests as phenotypic variability between humans. In tumours, mutations at non-coding regulatory sequences can have the same effect. We integrate AEI data in the study of the role of cis-regulatory variation in cancer susceptibility and tumour clinical heterogeneity. We developed a method to identify and characterise causal variants and target genes in known risk loci for breast cancer. More recently, we gathered striking evidence that AEI of somatic mutations in the key cancer gene *PIK3CA* has a prognostic impact on breast cancer. We are now extending our studies to all somatically mutated genes in breast cancer.

Sarah Harris

CCPBioSim is an EPSRC funded UK network that brings together biomolecular simulators through conferences and training workshops. Here I will present our current and future focus for 1) developing core skills and capabilities in our community, and 2) pushing scientific boundaries.

Key questions for discussion will be: How can we work together to integrate experiment and simulation into a multiscale modelling framework? How can our community develop biomolecular simulation into a mature and quantitative computational tool?