









9 - 10 NOVEMBER, WELLCOME BUILDING, LONDON

Docker is now establishing itself as the de-facto solution for containerization across a wide range of domains. The advantages are attractive, from reproducible research to simplifying deployment of complex code. Several bioinformatics groups are now utilizing this for various purposes: we would like to bring together some notable cases to discuss how adavantage of this new technology can best be acheived.

This event has been organised by Dr. Stephen J. Newhouse and Dr. Amos Folarin, both senior members of the NIHR Maudsley Biomedical Research Centre (BRC), Bioinformatics Core and made possible by the expert organisation and project management of Lucy O'Neill. Thanks to Tanya Hardy from Mindwave Ventures for lending us her time and project management skills. The agenda and poster have been designed by Jessica Morgan.

The symposium is generously supported by Genomics England and the Medical Research Council.

All events will take place in the Franks/Steel room.



Join us for the launch of the F1000 channel, 'Container Virtualisation in informatics' at 9:45 on the second day of the conference on November 10. See it at: f1000research.com/channels/ containers



At 13:40, we'll conduct an afternoon minihackday to introduce, demonstrate, and invite participation using Docker on some interesting and well-scoped problems. Sign up, clone our repo and get involved with our github: github.com/KHP-Informatics/ bioindocker15



Follow the action throughout the day at @bioindocker15 on Twitter and using the hashtag #bioindocker15.

Download the full agenda at: goo.gl/rQed1k

MONDAY, NOVEMBER 9

TUESDAY, NOVEMBER 10

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9:00	Networking breakfast	Dale Room	9:00	Networking breakfast	Dale Room
9:45	Welcome		9:45	Thomas Ingraham & Michael Markie	F1000Research – a publishing platform for the Docker community
10:00	Peter Belmann Bioboxes	Evaluating and ranking bioinformatics software using docker containers and an overview of the BioBoxes project.	10:00	Alfonso Acosta Weaveworks	Weaving Containers in Amazon's ECS
10:40	Nebojsa Tijanic Seven Bridges Genomics	Portable workflow and tool descriptions with Common Workflow Language and Rabix	10:40	Aanand Prasad Docker	Orchestrating Containers with Docker Compose
11:20	Break	Dale Room	11:05	Matt Banes	Manage your infrastructure like Google
11:40	Paolo Di Tommaso Nextflow, CRG	Manage reproducibility in genomics pipelines with Nextflow and Docker containers		Jetstack 	
			11:30	Break	Dale Room
12:20	Amos Folarin & Stephen Newhouse NGSeasy, King's College London	Next generation sequencing pipeines in Docker	11:50	Clive Stringer & Adam Hatherly King's College London	Docker and real world problems
13:00	Lunch	Dale Room		& Enterprise Architect HSCIC	
13:40	Tim Hubbard Genomics England, KCL	Pipelines to analysis data from the 100,000 genomes project as part of the Genomics England Clinical Interpretation Partnership (GeCIP)	12:15	Yannick Wurm Queen Mary University of London	OSwitch: One-line access to other operating systems
			12:25	Introduction to the mini-hack	Prizes to be announced!
14:20	Fabien Campagne Weill Cornell Medicine	MetaR and the Nextflow Workbench: application of Docker and language workbench technology to simplify bioinformatics training and data analysis.	13:00	Lunch	Dale Room
15:00	Break	Dale Room	13:40	Mini-hack	Sign up, clone our repo and get involved with our github: github.com/KHP-Informatics/bioindocker15
15:20	Brad Chapman Harvard Chan School	Improving support and distribution of validated analysis tools using Docker	16:15	Discussion session and wrap-up	
			17:05	Day ends	
16:00	Elijah Charles Intel	Bioinformatics and the packaging melee			
16:25	Kai Davenport ClusterHQ	Data, Volumes and portability with Flocker			
17:05	Day ends	Drinks at the nearest bar			























