

# [BIO IN DOCKER]

9 - 10 NOVEMBER, WELLCOME BUILDING, LONDON

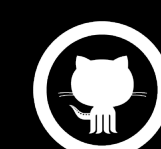
Docker is now establishing itself as the de-facto solution for containerization across a wide range of domains. The advantages are attractive, from reproducible research to simplifying deployment of complex code. Several bioinformatics groups are now utilizing this for various purposes: we would like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

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 project management of **Lucy O'Neill**. Thanks to **Tanya Hardy** from **Mindwave Ventures** for lending us her time. 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** and download the full agenda at: [goo.gl/rQed1k](http://goo.gl/rQed1k)



Join us for the launch of the F1000 channel, 'Container Virtualisation in informatics' at 9:45 on Monday, November 10.  
See it at: [f1000research.com/channels/containers](http://f1000research.com/channels/containers)



At 13:40, there's an afternoon **mini-hackday** 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](https://github.com/KHP-Informatics/bioindocker15)



@bioindocker15  
#bioindocker15

## MONDAY, NOVEMBER 9

9:00	<b>Networking breakfast</b>	Dale Room
9:45	<b>Welcome</b>	
10:00	<b>Peter Belmann</b> Bioboxes	Evaluating and ranking bioinformatics software using docker containers and an overview of the BioBoxes project.
10:40	<b>Nebojsa Tijanic</b> Seven Bridges Genomics	Portable workflow and tool descriptions with Common Workflow Language and Rabix
11:20	<b>Break</b>	Dale Room
11:40	<b>Paolo Di Tommaso</b> Nextflow, CRG	Manage reproducibility in genomics pipelines with Nextflow and Docker containers
12:20	<b>Amos Folarin &amp; Stephen Newhouse</b> NGSeasy, KCL	Next generation sequencing pipelines in Docker
13:00	<b>Lunch</b>	Dale Room
13:40	<b>Tim Hubbard</b> Genomics England, King's College London	Pipelines to analysis data from the 100,000 genomes project as part of the Genomics England Clinical Interpretation Partnership (GeCIP)
14:20	<b>Fabien Campagne</b> Weill Cornell Medicine	MetaR and the Nextflow Workbench: application of Docker and language workbench technology to simplify bio-informatics training and data analysis.
15:00	<b>Break</b>	Dale Room
15:20	<b>Brad Chapman</b> Harvard Chan School	Improving support and distribution of validated analysis tools using Docker
16:00	<b>Elijah Charles</b> Intel	Bioinformatics and the packaging melee
16:25	<b>Kai Davenport</b> ClusterHQ	Data, Volumes and portability with Flocker
17:05	<b>Day ends</b>	Drinks at the nearest bar

## TUESDAY, NOVEMBER 10

9:00	<b>Networking breakfast</b>	Dale Room
9:45	<b>Thomas Ingraham</b> F1000	F1000Research - a publishing platform for the Docker community
10:00	<b>Alfonso Acosta</b> Weaveworks	Weaving Containers in Amazon's ECS
10:40	<b>Aanand Prasad</b> Docker	Orchestrating Containers with Docker Compose
11:05	<b>Matt Banes</b> Jetstack	Manage your infrastructure like Google
11:30	<b>Break</b>	Dale Room
11:50	<b>Clive Stringer &amp; Adam Hatherly</b> King's College London & HSCIC	Docker and real world problems
12:15	<b>Yannick Wurm</b> Queen Mary University of London	OSwitch: One-line access to other operating systems
12:25	<b>Introduction to the mini-hack</b>	Prizes to be announced!
13:00	<b>Lunch</b>	Dale Room
13:40	<b>Mini-hack</b>	Clone our repo and get involved: <a href="https://github.com/KHP-Informatics/bioindocker15">github.com/KHP-Informatics/bioindocker15</a>
16:15	<b>Discussion session and wrap-up</b>	
17:05	<b>Day ends</b>	