Drug Discovery 2016

ACC, LIVERPOOL
13th - 14th October 2016

ELRIG

Genedata Workshop

THURSDAY 13TH OCTOBER: ROOM 11A

Today, screening, imaging and genomics are the main sources of experimental data in drug discovery, boosted by standardization, laboratory automation and falling cost per data point. Analyzing and interpreting screening data in discovery projects remains challenging, however, for three reasons:

New in-vitro assay systems tuned for physiological relevance tend to be more complex and yield more complex data as well
New detection technologies and modalities provide richer information, sometimes down to the single cell / molecular level
Drug discovery projects require tighter-knit collaboration on screening data and results, in short cycles.

This is becoming an even greater challenge with the collaborative R&D outsourcing. Thus, screening scientists need to handle daily the biological, technical and collaborative complexity of experimental data. We will discuss in this workshop how this can be done efficiently: Adopting a harmonized best-practice approach to analysis for generating interpretable results; extending it with assay- and technology-specific procedures as needed; managing data and results on a collaborative platform for secure sharing, access, and full use of that information in discovery projects.

The workshop will consist of a series of presentations and discussions outlining modern standard approaches to analysis and management of screening data, e.g.:

A collaborative platform for managing experimental results from all in-vitro assays
Integrating complementary information from multiple screening technologies for hit qualification, lead optimization, profiling and safety.
From biophysical screens to molecular binding parameters
Phenotypic high content assays and their analysis
Combination screens for oncology: simplifying synergy

This workshop is for screening scientists who want to advance their knowledge of analysis procedures, find ways to more efficiently analyze their data and understand approaches to data and result sharing.

TIME	PRESENTER	TRACK
9:30 - 9:40	**Stephan Heyse,** Genedata	**Welcome and Introduction**
9:40 - 10:00	**Margarita Shatalina,** Genedata	**A foundation in the murky waters of Discovery: Laying a platform across piles of in-vitro screens**
10:00 - 10:30	**Dave Murray,** AstraZeneca	**Integrating screening data across a large multisite pharma organization**
10:30 - 11:00	**Emilie Bureau,** MRCT	**Phenotypic high-content screen measuring aggregate clearance in neurodegenerative diseases**
11:00 - 11:30	**COFFEE BREAK**	
11:30 - 12:00	**Lope Florez,** Genedata	**High-content screening: How to easily select meaningful feature combinations**
12:00 - 12:30	**Michelle Newman,** MRCT	**Drug combinations as potential oncology therapeutics: Data analysis with Genedata Screener**
12:30 - 13:00	**John Vincent,** AstraZeneca	**Simplifying synergy: Combination screens**