VENUE

Wissenschaftsetage im Bildungsforum
Am Kanal 47
14467 Potsdam
GERMANY
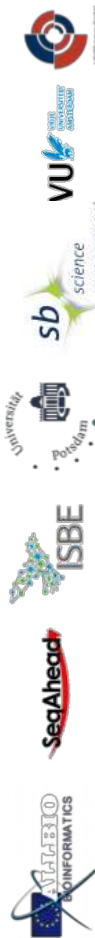
The organising team:
Martijn J. Moné   VU University Amsterdam (NL)
Susanne Hollmann   University of Potsdam (D)
Babette Regierer   LifeGlimmer GmbH (D)

April, 28th - 29th 2014

Managing Big Data

Workshop
Setting the standards for analysing and integrating big data

Add on program: **Tutorial comparative genome annotation methods**

April, 29th - 30st 2014

The life sciences are facing a rapidly increasing amount of data produced worldwide; in particular, when going from fundamental research into applications in, for example, systems medicine, the amounts of data to store, transfer and process are enormous.

The rapid development of modern technologies, especially the Next Generation Sequencing (NGS) technologies, allows the generation of biological data with increasing speed and precision. These new technologies are in place, but the downstream processing, management and the mathematical analysis of the data is still an unsolved problem for the scale needed. For an efficient data management, processing, analysis and integration the datasets must have a high quality, must be accessible, re-usable and connected with sufficient metadata (background information).

Standards and Standard Operation Procedures (SOPs) from data generation to data integration. (or: Standards and SOPs, therefore, become an increasingly critical issue specifically in large scale or applied approaches assuring that data can be accesses, integrated, shared compared.

The development of quality control and standards are key drivers for efficient and successful research pipelines in the life sciences.

This workshop will provide an overview about current standardization initiatives and discuss challenges and needs for a coherent strategy for standardization in the life sciences.

SeqAhead

The next-generation sequencing data analysis network SeqAhead is a COST Action established in 2011 to coordinate efforts in the area of bioinformatics dedicated to data produced by Next Generation Sequencing (NGS) technologies and develop concepts to address the problem of massively increasing amounts of data produced by the new technologies.

seqahead.eu

ISBE

The mission of ISBE is to establish and enable access to an integrated, distributed infrastructure of state-of-the-art facilities and expertise for systems biology across Europe, with a view to transforming our understanding of the life sciences, human health and the environment. To this end ISBE will create a solid pan-European technological, intellectual and training basis and provide services allowing researchers in academia and industry to (i) collect, analyse and process data sets for integration into effective models, and (ii) build predictive models that give insight into the functioning of biological systems. The infrastructure will also serve as a platform from which to launch large-scale integrative projects of great scientific and societal impact

project.isbe.eu

AllBIO

Handling and understanding vast bodies of biological data is only possible with the help of sophisticated mathematical analysis. A broad spectrum of bioinformatics tools has been developed across all areas of the life sciences. AllBIO coordinates the efforts for the generalisation and the broadening of the applicability of the many human-centric bioinformatics facilities to other areas of the life sciences. Via "Test Cases" AllBIO collects information about the existing needs and tries to find solutions together with researchers from the bioinformatics community. One central aim of the AllBIO consortium is to transfer the knowledge of existing bioinformatics tools and webservices among the various life science areas and to identify still unsolved bioinformatics challenges.

allbioinformatics.eu

Program – Setting the standards for analysing and integrating big data

28.04. – data integration

09:30-10:00	Welcome and introductory round
10:00-11:15	Presentations – Session 1
11:15-11:40	Coffee Break
11:40-12:40	Presentations – Session 2
12:40-14:00	Lunch
14:00-15:30	Presentations – Session 3
15:30-16:00	Coffee Break
16:00-17:30	Presentations – Session 4
17:30	get together

29.04 – data generation & analysis

09:30-10:30	Discussion breakout sessions
10:30-11:00	Coffee Break
11:00-12:00	Breakout sessions
12:00-13:00	Lunch
13:00-14:00	Breakout sessions
14:00-14:20	Coffee Break
14:20-15:20	Presentations of the results
15:20-15:40	Coffee Break
15:40-16:40	Discussion/harmonization
16:40-17:00	Coffee Break
17:00-18:00	Structure/contents of a roadmap

tutorial *

comparative genome annotation methods

30 Apr. 2014 tutorial
comparative genome annotation methods

Hands on training in computational methods (fgenesh, augustus, apollo, plaza) in genome annotation (plants).

Please note that the participation is limited

For application and travel grants
please send a short letter of motivation to:
plantsys@uni-potsdam.de

*Venue: University of Potsdam, Campus Golm
Karl-Liebknecht-Str. 24-25 House 25 Room D 002
(computer pool)

http://www.uni-potsdam.de/lageplaene/golmlage.html