Short description of the project

Integration and provision of pipelines for automated analysis and visualization of large-scale high-content phenotype screening data of human cells

One aim is to set up, run, and maintain a web-based workflow unit for high-content screening and image processing in close collaboration with other partners in HD-HuB. Users will be supported by a web-based software repository providing workflows for high-content data analysis, or by customized solutions. We will further develop the GenomeRNAi database to integrate phenotypic data, and extend the analysis workflows to provide a comprehensive and user-friendly pipeline from data acquisition to visualization and data mining. Major objectives include (i) web-based solutions providing access to workflows and pipelines for large-scale phenotype analysis, (ii) development of workflows for high-content screening (HCS) (e.g. bioimage data analysis, visualization and interfacing to GenomeRNAi), and (iii) development of novel tools to visualize multi-phenotype data in GenomeRNAi.

Screening data analysis flow

- Targeted Imaging
- Image and metadata management
- Automatic upload of phenotypes

Publications


de.NBI services

- Solutions providing access to workflows and pipelines for large-scale phenotype analysis
- Workflows for High-Content Screening (HCS) data addressing bioimage data analysis
- Support in the planning phase and during projects on systematic cellular phenotyping
- Integration and data mining of RNAi gene-phenotype associations on the GenomeRNAi website

Progress report

- Identification of user needs addressing bioimage analysis
- Evaluation of web-based software solutions for the analysis of large-scale image data and extraction of cellular phenotypes
- Development of software tools and web-based solutions for automated analysis of microscopy images
- Development of pre-configured bioimage data analysis workflows based on Galaxy (http://galaxyproject.org) and KNIME (http://www.knime.org)
- Implementation of analysis pipelines into a common accessible web-based workflow repository.
- Extension of the GenomeRNAi website by a graphical functionality to display complex gene-phenotype associations
- Provision of documentation and training materials