

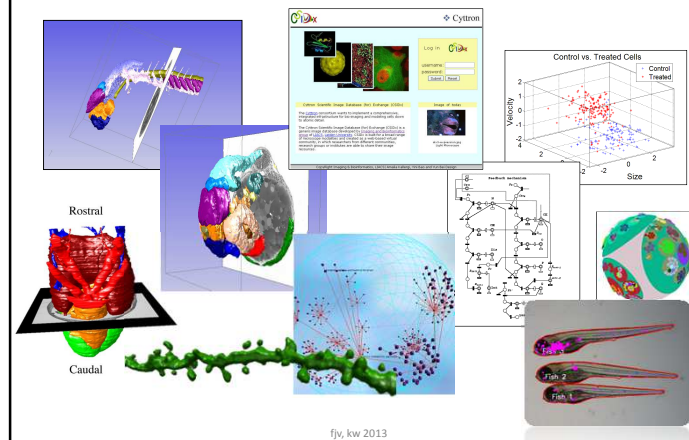
Imaging & Bioinformatics

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Imaging & Bioinformatics @ LIACS



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WEBSERVICES & WORKFLOWS

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Web Services and Workflows for Scientific Reproducibility

- Investigate the use of web services and workflows for improving scientific reproducibility, using case studies from LIACS research.
- Design new interactive user interfaces for a collection of web services and workflows for text mining tools developed at the LUMC

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The Data Deluge

21st C = century of information
 Open access to distributed data
 Open access to analysis tools and algorithms

- World bank/financial
- Climate change data
- Large scale physics
 - Large Hadron collider
 - Astronomy
- Life Sciences
 - 'Omics data
 - Next Gen Sequencing
- Personalised medicine
- eGovernment

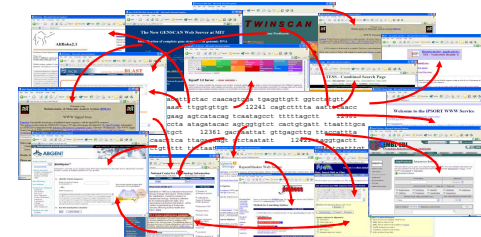


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Exploiting Data Resources and Tools

- Sequential use of distributed tools
- Analysing large data sets and iterating over lots of data
- Repeating the same analyses
- Incompatible input and output formats
- Difficult to record parameter selections



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Web Services

- Machine-to-machine interaction over the network
- Users can access and run analyses and algorithms (services) at distributed locations
- Services are hosted and maintained by their creators – no installation, no maintenance

- WSDL (SOAP) – Web Services Description Language
- REST – REpresentational State Transfer

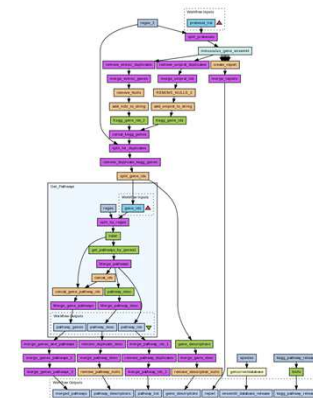


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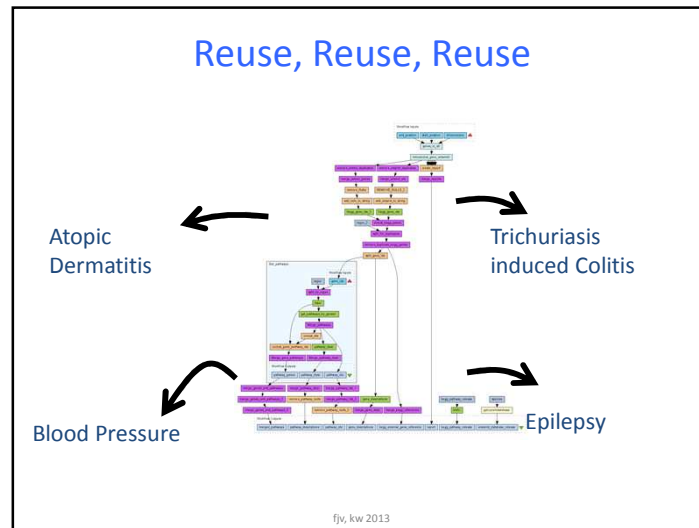
Scientific Workflows (Taverna)

- Sophisticated analysis pipelines
- A set of services to analyse or manage data (either local or remote)
- Automation of data flow
- Iteration over data sets
- Control of service invocation
- Provenance collection
- Experimental protocol



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Web Services and Workflows for Scientific Reproducibility

- Develop web service interfaces for tools and algorithms produced @ LIACS
- Integrate these tools into workflows with existing tools and resources
- Investigate the implications of providing a web service interfaces on:
 - Scientific reproducibility
 - Providing and maintaining the service
- Requirements: Java, XML

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Alternative Interfaces for the Anni Text Mining Suite

- Anni <http://biosemantics.org/index.php?page=anni-2-0>
- Anni already has web services and a series of workflows (developed @ LUMC)
 - Create new user interfaces that use the web services and workflows
 - Transform user requirements into technical specifications
 - Explore new ways of interacting with the services
 - E.g. Plugins to other environments, Android apps etc
- Requirements: Java, XML

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VISUALIZATION

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LIACS BigEye VideoWall

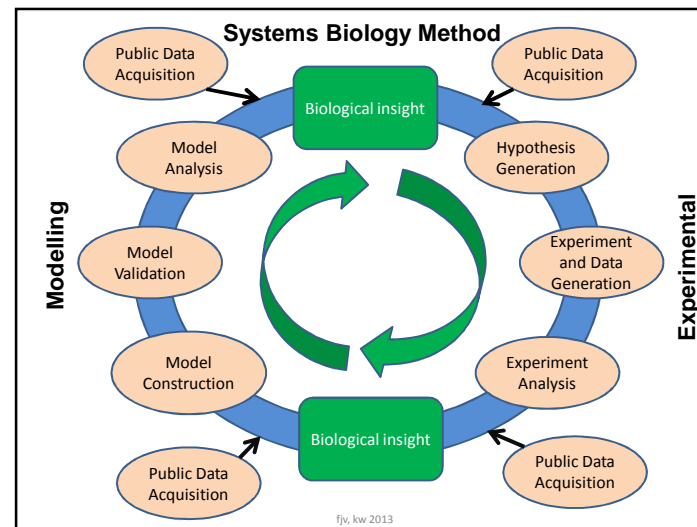
With Kinect or Wii-Mote

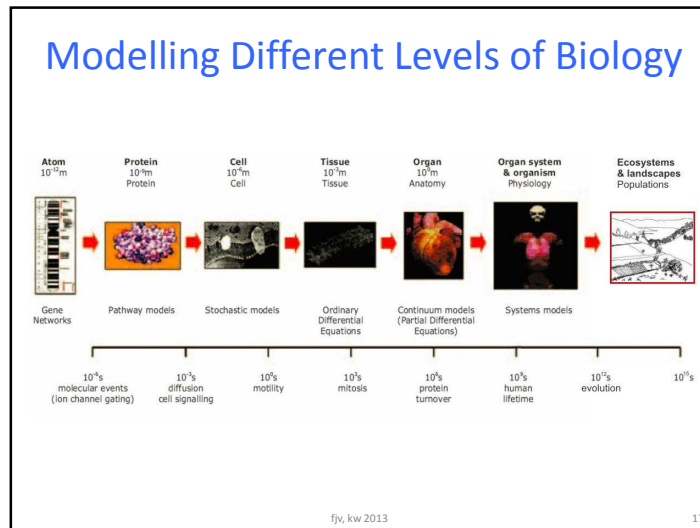
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Visualising and Exploring Systems Biology Models

- Systems Biologists use mathematical models to represent complicated dynamic relationships in living systems
- Models need to be visualised and integrated to interpret biological functions
- Exploring new ways of interactively visualising and navigating Systems Biology models by creating mash-ups of existing tools and resources

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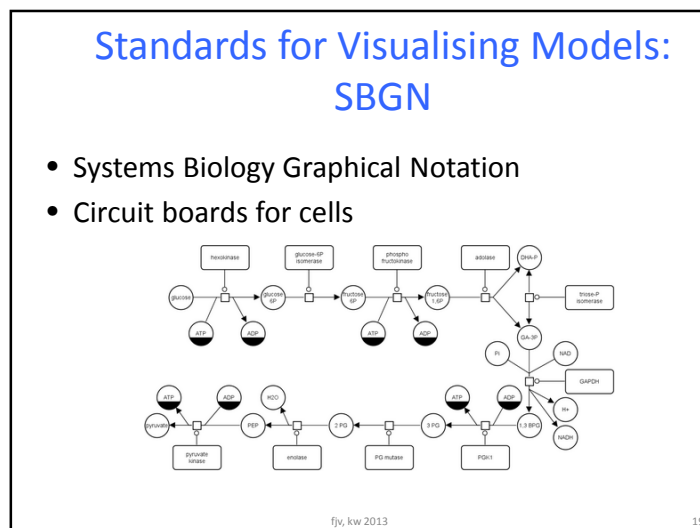


Tools for Visualising Biological Networks: Cytoscape

(<http://www.cytoscape.org>)

The screenshot displays the Cytoscape interface with a network graph on the left and a 3D molecular structure on the right. The network graph shows nodes connected by edges, with various colors and shapes representing different components. The 3D structure shows a complex protein or molecular assembly.

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- ## Project Summary
- Develop new approaches to visualising and navigating through and between Systems Biology models using Cytoscape (or other visualisation tools) and SBGN.
 - Mash-ups of existing tools
 - Visualisation techniques
 - Integration of distributed data
 - Requirements: Java and XML
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COMPUTATION

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Cluster



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Scientific Cluster

- 48 Dell 2u 8x cores
- Cluster
 - Head Node
 - Main Node
 - Worker Nodes
- Map computational intensive programs to Cluster
 - image processing/analysis
 - pattern recognition
 - bioinformatics jobs from workflows
- RESEARCH
 - Develop strategy/template for web-services
 - Develop strategy for Parallelization

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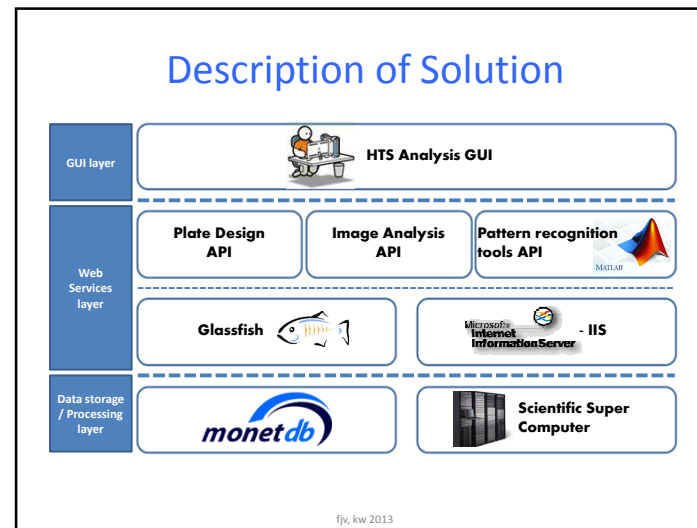
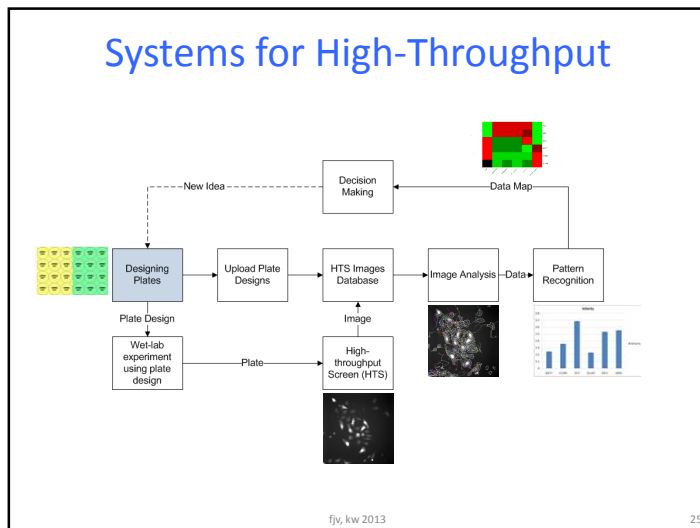
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Cluster Computation

- NeCEN
 - Netherlands Centre for Electron Nanoscopy
- Cell Observatory
 - Collaboration within Faculty of Science
 - IBL, LIC, LION, LIACS
- High-Throughput imaging
 - 3D zebrafish imaging

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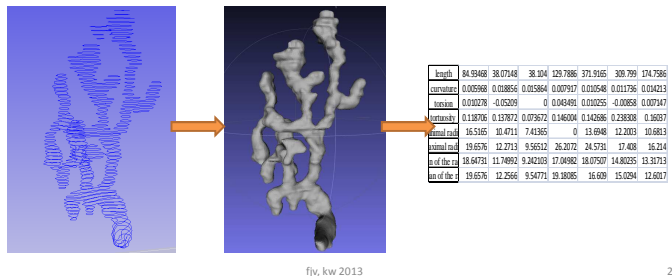
- ### Project Summary
- Analyze software to be ported to the Cluster
 - Develop mapping to the cluster architecture
 - Apply the results to a dataset
 - Generalize
 - NeCEN: C, Python, Java
 - Cell Observatory: Java
 - High Troughput: Java
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ANALYSIS & VISUALIZATION

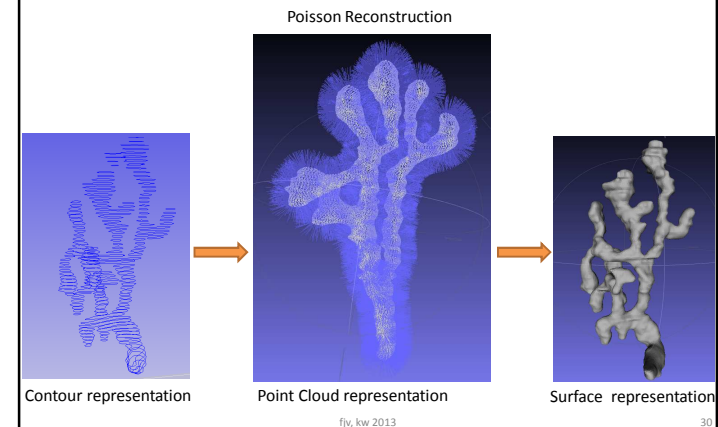
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3D Model optimization

- We start from 3D models obtained from various sources
- Measurement



Surface Reconstruction



Connecting Components

- Read files
- Reconstruction & Optimization
 - Poisson reconstruction
 - Fourier based reconstruction
 - (L.Cao & FJ Verbeek, Electronic Imaging 2013)
- Visualization
 - VTK (visualization toolkit)
 - Geometrical data-structures
- GUI components

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Project Summary

- Analyze components
- Develop infrastructure that fits workflow for 3D modelling
- Develop interface
- Connect components
- C, C++, QT, VTK

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URL

<http://bio-imaging.liacs.nl/projects>