

# Large Scale Biological Data Handling and Analysis Using Open Source Alternatives

*Dr Karol Kozak*

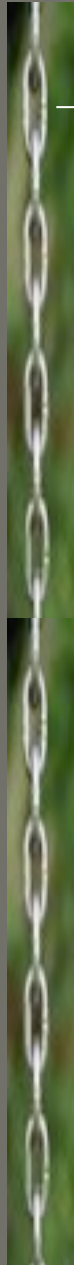
ETH Zurich

**May 2009, Paris OME**

# Large Scale Experiments and Informatics



# Large Scale Experiments and Informatics



Instrument management

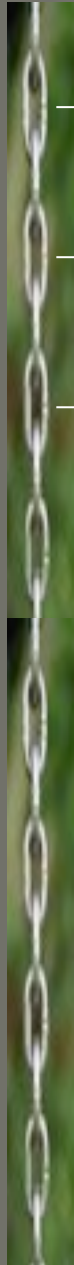
# Large Scale Experiments and Informatics



Instrument management

Data acquisition

# Large Scale Experiments and Informatics

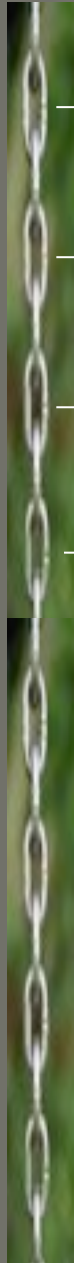


Instrument management

Data acquisition

Image processing

# Large Scale Experiments and Informatics



Instrument management

Data acquisition

Image processing

Normalization, QC

# Large Scale Experiments and Informatics



Instrument management

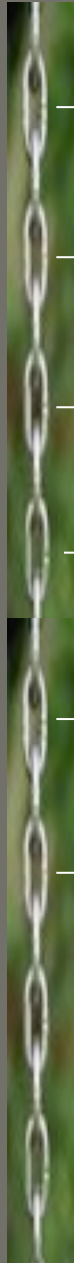
Data acquisition

Image processing

Normalization, QC

Data storage

# Large Scale Experiments and Informatics



Instrument management

Data acquisition

Image processing

Normalization, QC

Data storage

Archiving



# Large Scale Experiments and Informatics



Instrument management

Data acquisition

Image processing

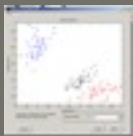
Normalization, QC

Data storage

Archiving

Data mining

# Large Scale Experiments and Informatics



Instrument management

Data acquisition

Image processing

Normalization, QC

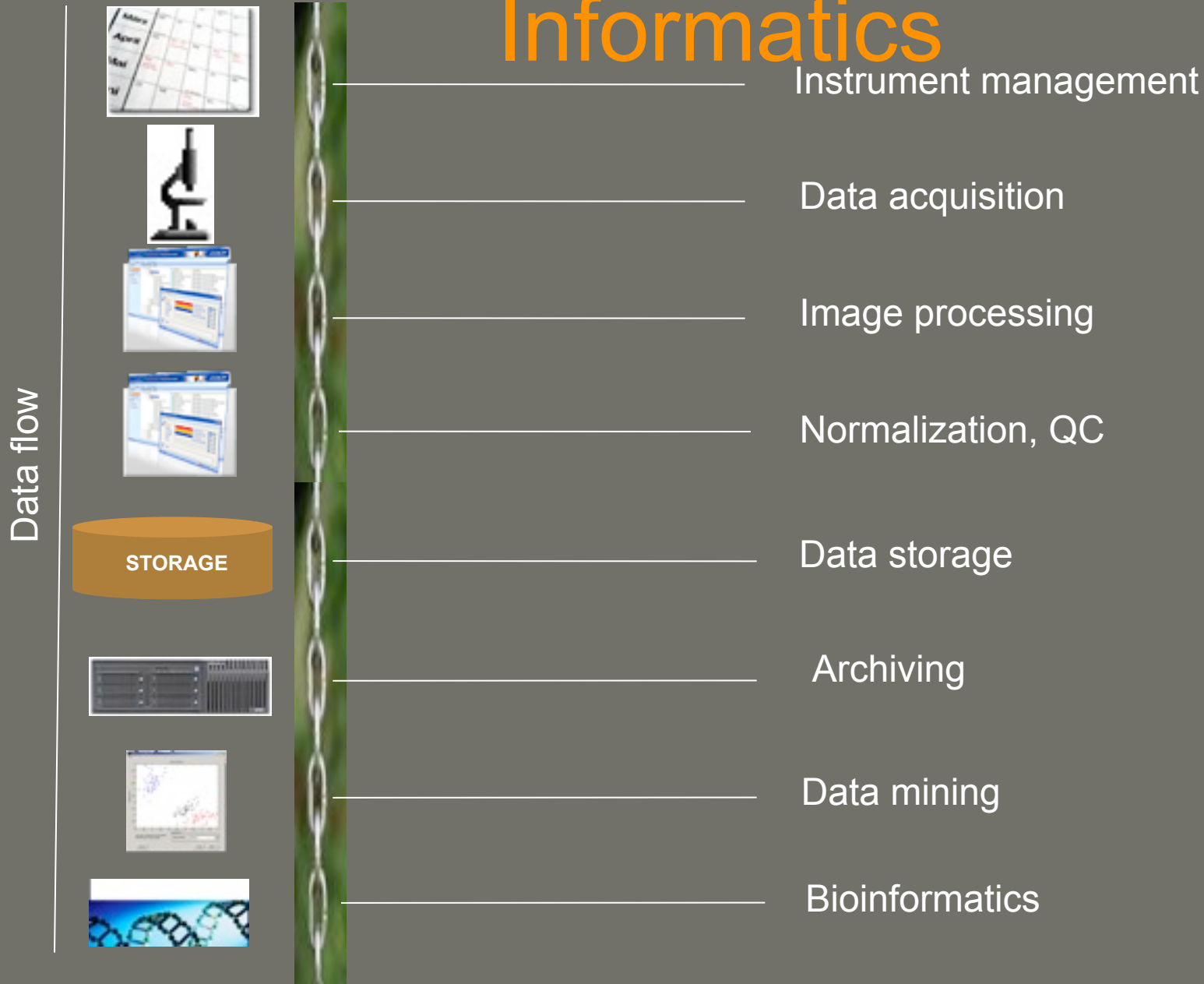
Data storage

Archiving

Data mining

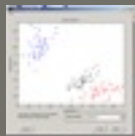
Bioinformatics

# Large Scale Experiments and Informatics



# Large Scale Experiments and Informatics

Data flow



Instrument management

Data acquisition

Image processing

Normalization, QC

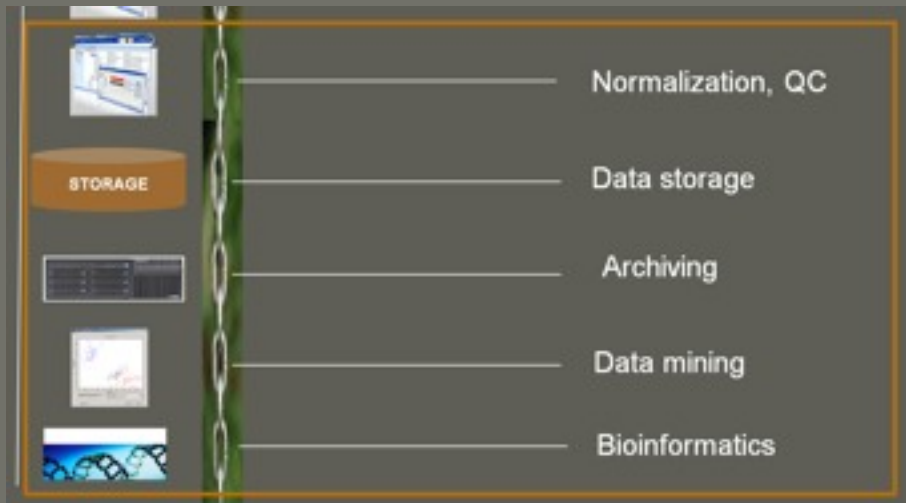
Data storage

Archiving

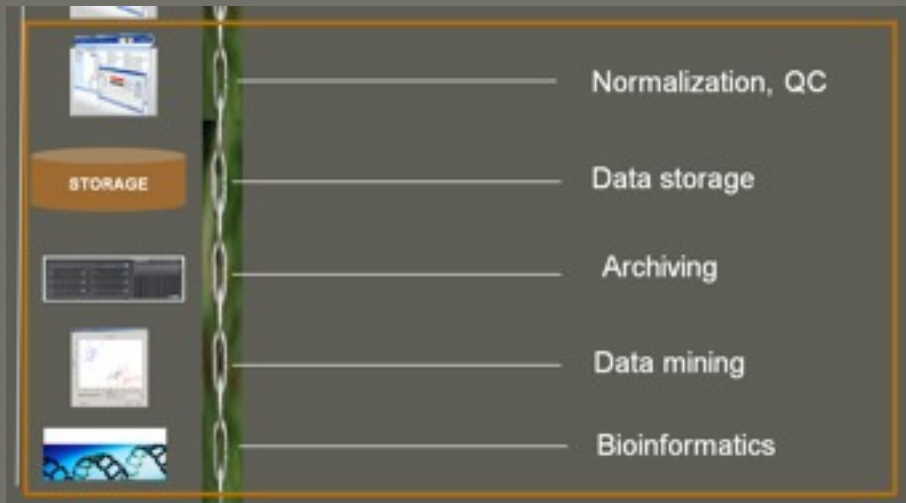
Data mining

Bioinformatics

# Detection points



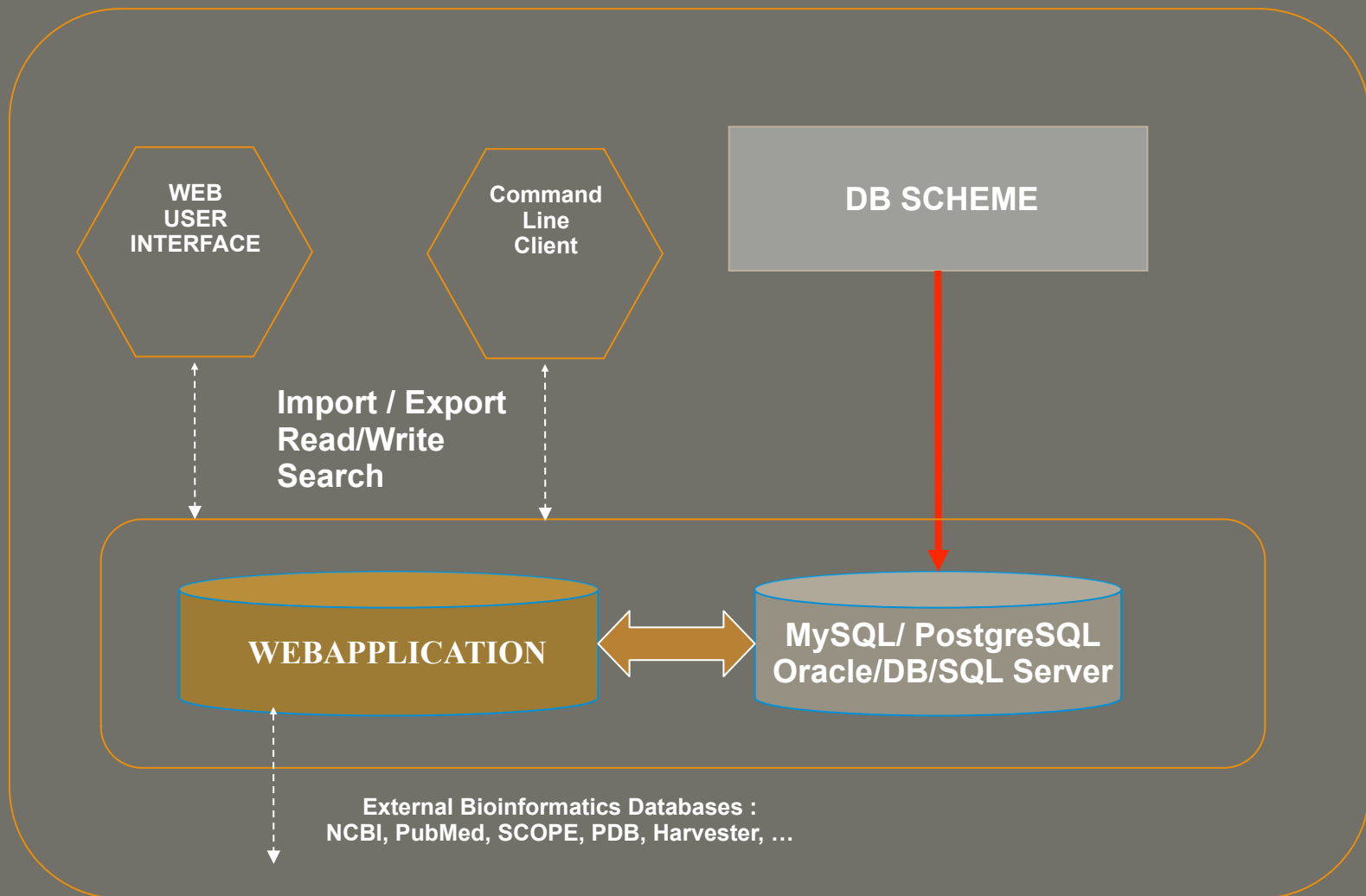
# Detection points



## Data Automation:

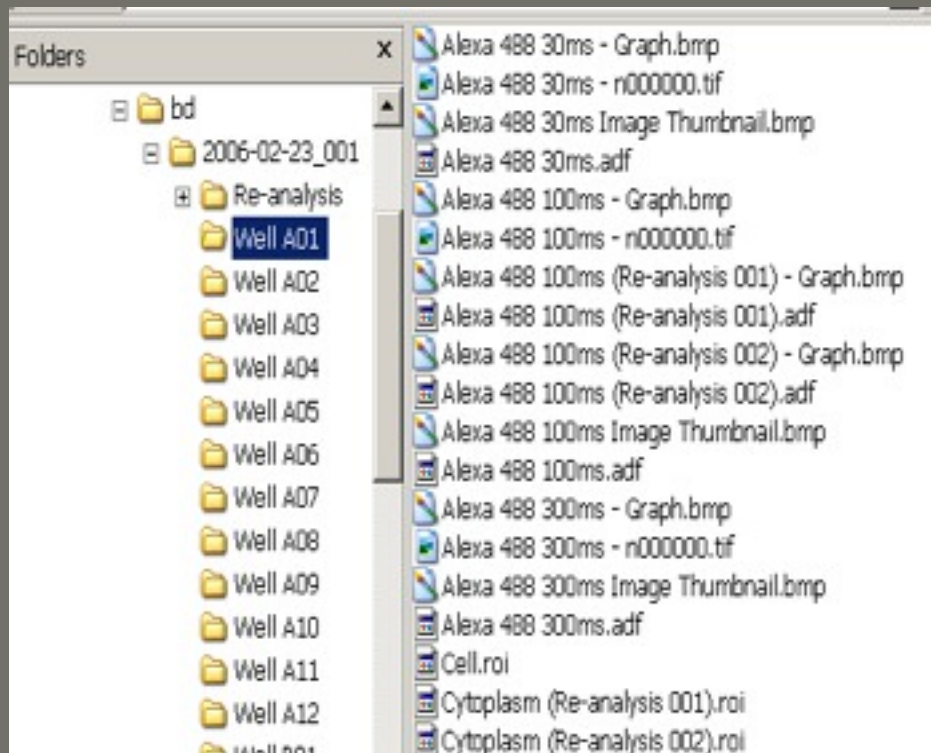
- Library Handling
- Robotics
- Microscopy
- Image processing
- Cell reliability
- Hit Definition

# Database architecture



STORAGE

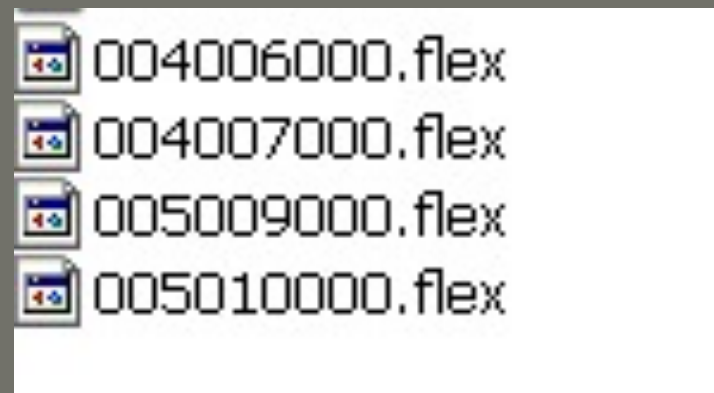
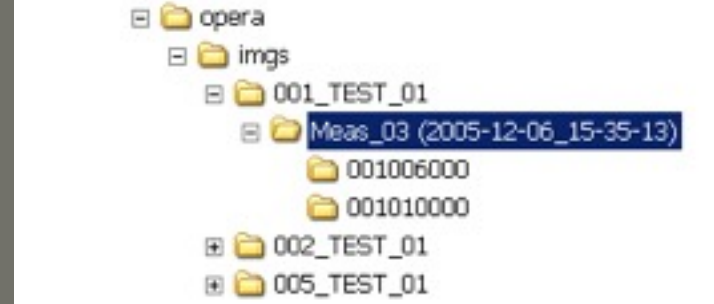
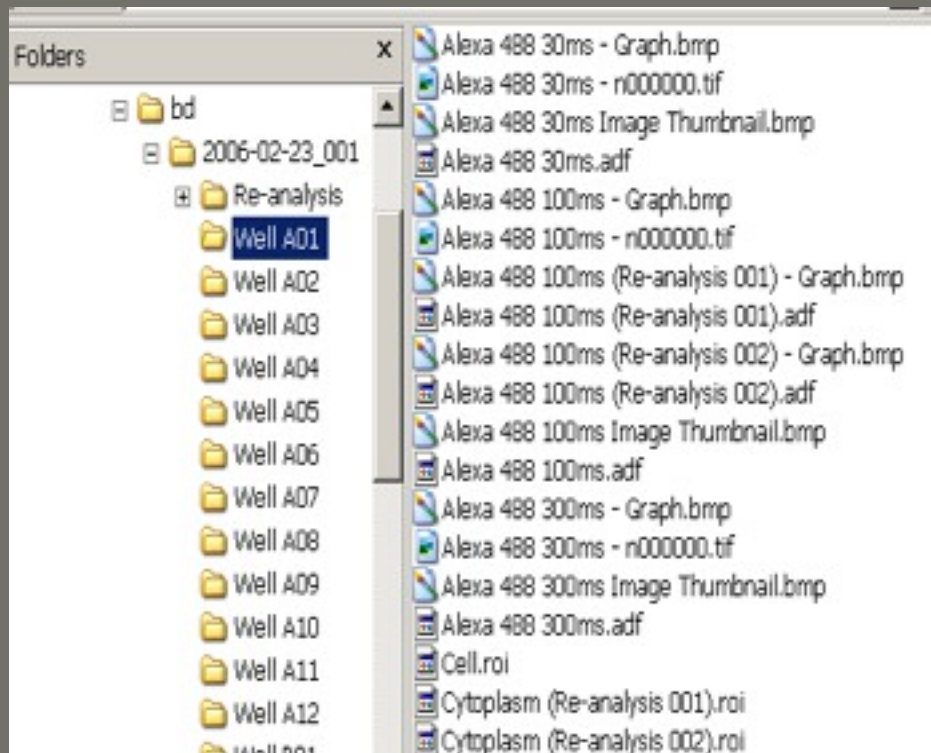
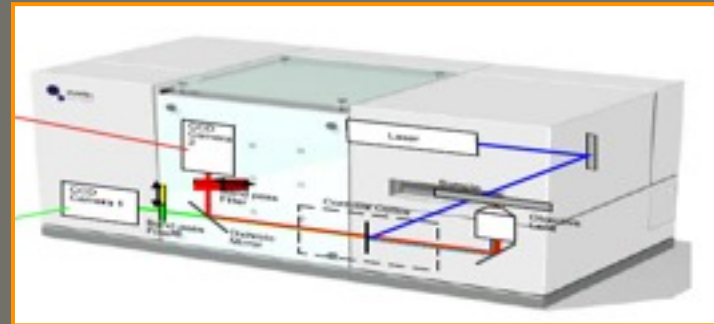
# Link to microscope





STORAGE

# Link to microscope



STORAGE

# Link to microscope



thermo  
experiment1  
platebarcode

CELLOMICS\_051115160001\_B06f02d0.TIF  
CELLOMICS\_051115160001\_B06f03d1.TIF  
CELLOMICS\_051115160001\_B06f03d2.TIF  
CELLOMICS\_051115160001\_C04f00d3.TIF  
CELLOMICS\_051115160001\_C04f01d2.TIF  
CELLOMICS\_051115160001\_C04f02d0.TIF  
CELLOMICS\_051115160001\_D05f01d0.TIF  
CELLOMICS\_051115160001\_D05f01d2.TIF

# Link to microscope



```

└─ thermo
  └─ experiment1
     └─ platebarcode
  
```

```

└─ MD_MICRO
  └─ experiment1
     └─ 2008-06-28_001barcode
  
```

```

└─ CELLOMICS_051115160001_B06f02d0.TIF
└─ CELLOMICS_051115160001_B06f03d1.TIF
└─ CELLOMICS_051115160001_B06f03d2.TIF
└─ CELLOMICS_051115160001_C04f00d3.TIF
└─ CELLOMICS_051115160001_C04f01d2.TIF
└─ CELLOMICS_051115160001_C04f02d0.TIF
└─ CELLOMICS_051115160001_D05f01d0.TIF
└─ CELLOMICS_051115160001_D05f01d2.TIF
  
```

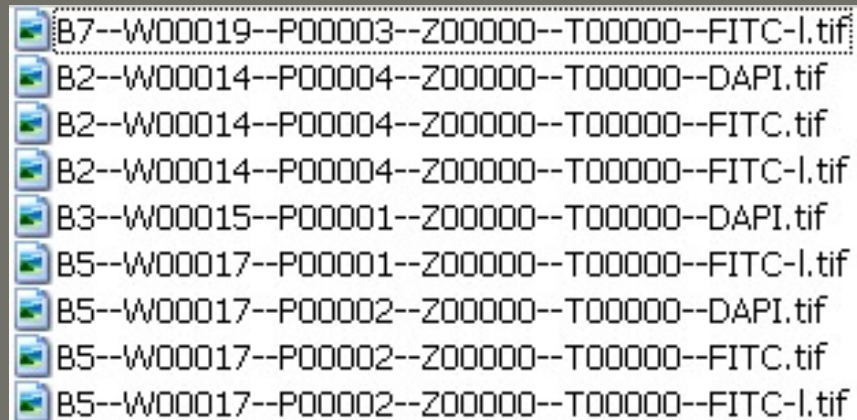
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└─ 2008-06-28_000_A01_00_dapi.tif
└─ 2008-06-28_000_A01_00_yfp.tif
└─ 2008-06-28_000_A02_00_dapi.tif
└─ 2008-06-28_000_A02_00_yfp.tif
└─ 2008-06-28_000_A03_00_dapi.tif
└─ 2008-06-28_000_A03_00_yfp.tif
└─ 2008-06-28_000_A04_00_dapi.tif
└─ 2008-06-28_000_A04_00_yfp.tif
└─ 2008-06-28_000_A05_00_dapi.tif
└─ 2008-06-28_000_A05_00_yfp.tif
└─ 2008-06-28_000_B02_02_yfp.tif
└─ 2008-06-28_000_B02_03_dapi.tif
└─ 2008-06-28_000_B02_03_yfp.tif
  
```

# Link to microscope



Olympus **SCAN R**





# Data archiving

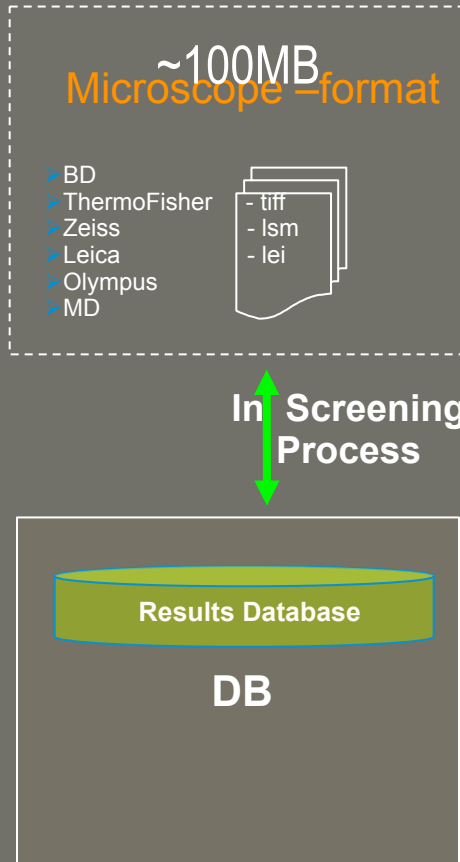
~100MB  
Microscope-format

- BD
- ThermoFisher
- Zeiss
- Leica
- Olympus
- MD



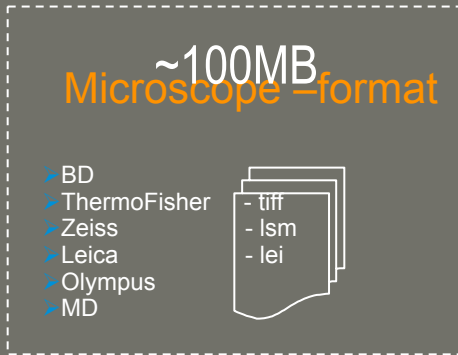


# Data archiving

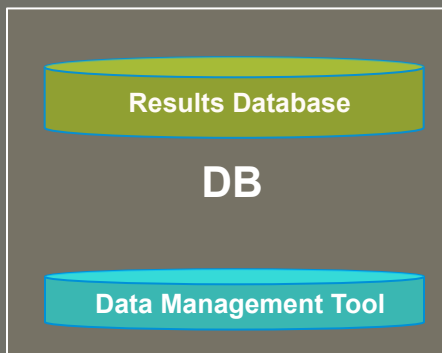




# Data archiving

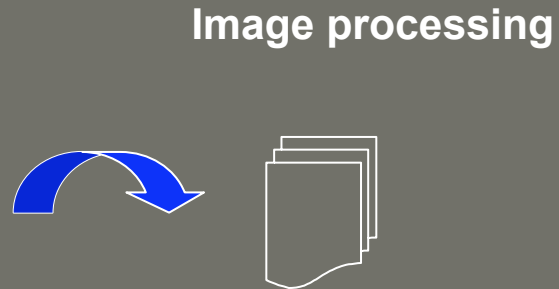
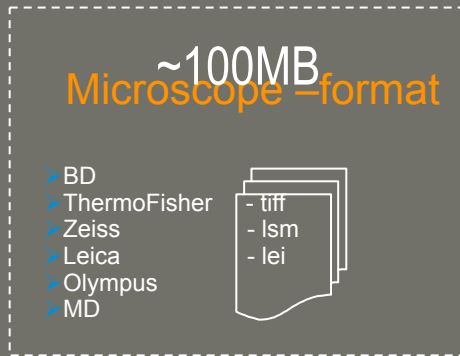


In Screening  
Process

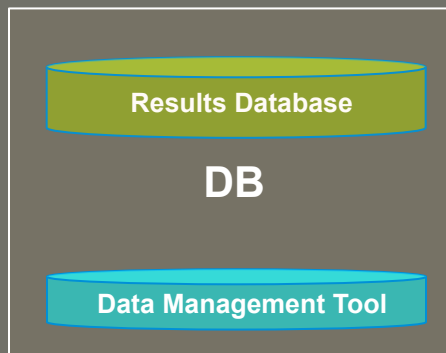




# Data archiving



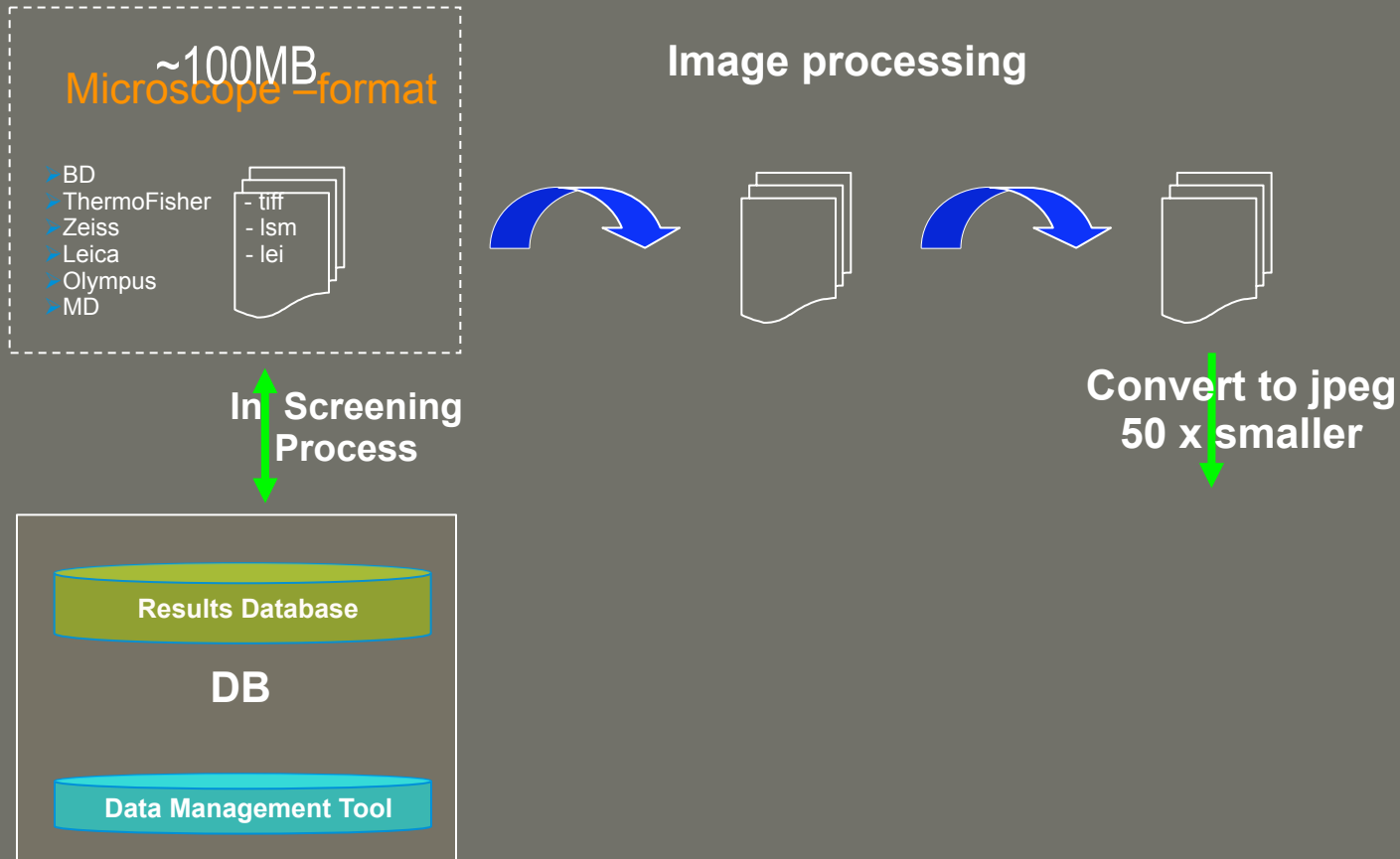
In Screening Process





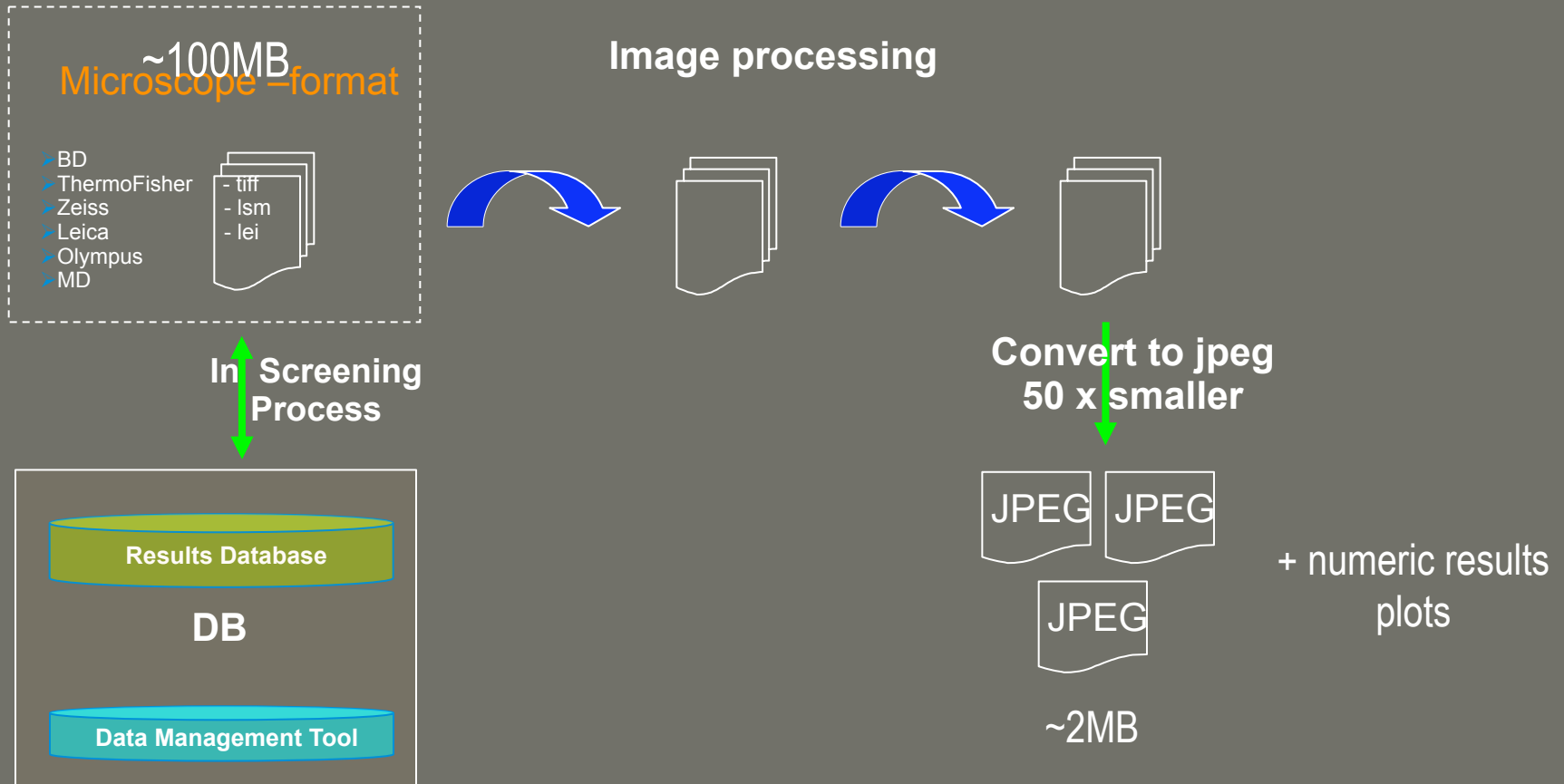


# Data archiving



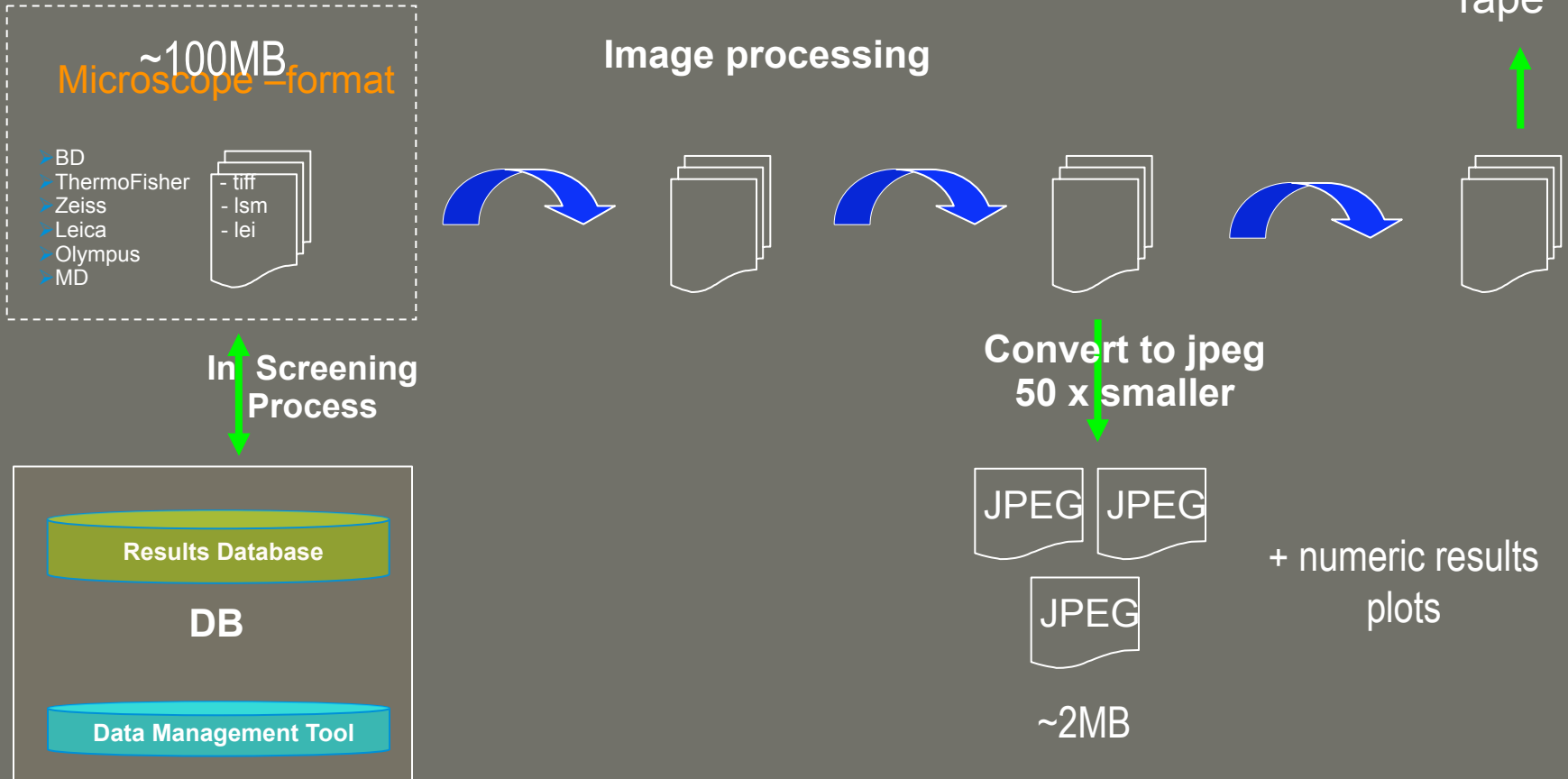


# Data archiving



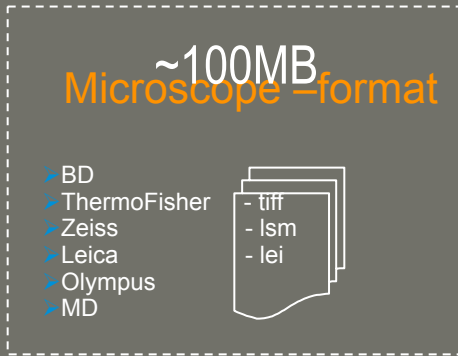


# Data archiving

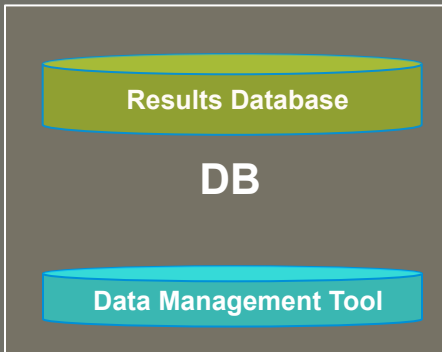




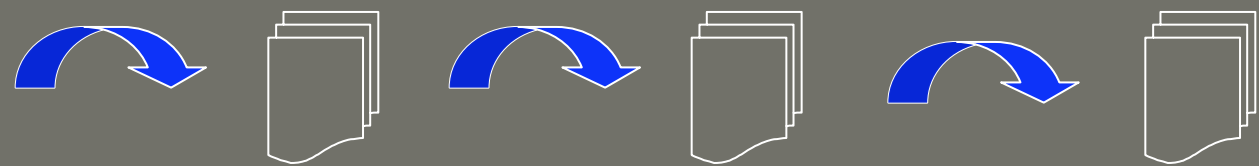
# Data archiving



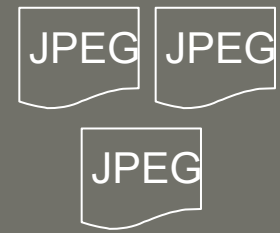
~~In Screening Process~~



## Image processing



**Convert to jpeg  
50 x smaller**



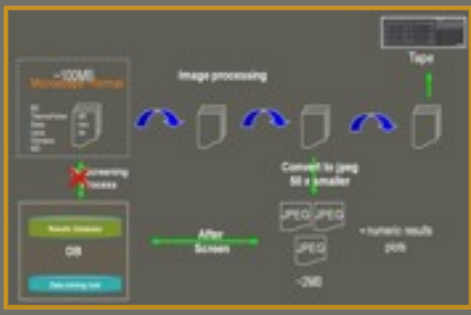
+ numeric results plots

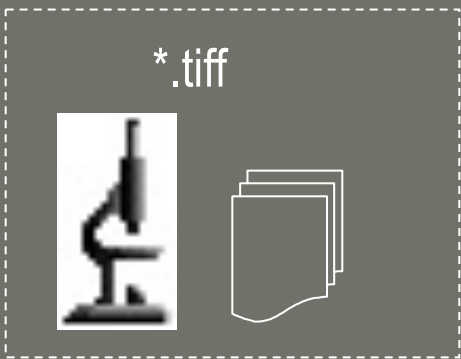
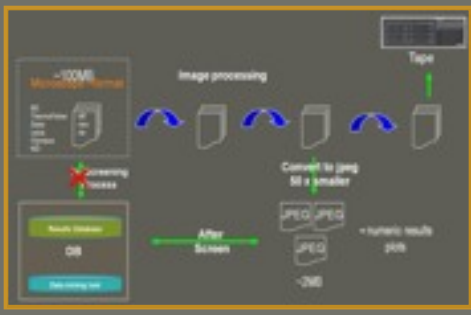
~2MB

**After Screen**

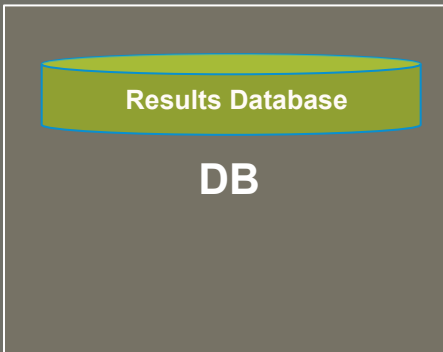
**Tape**

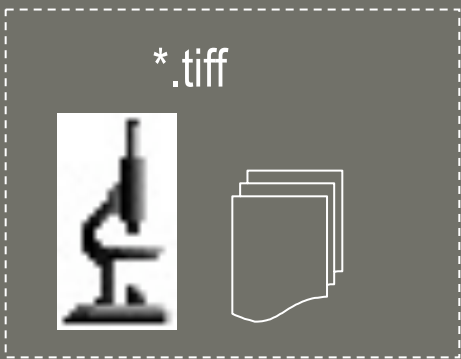
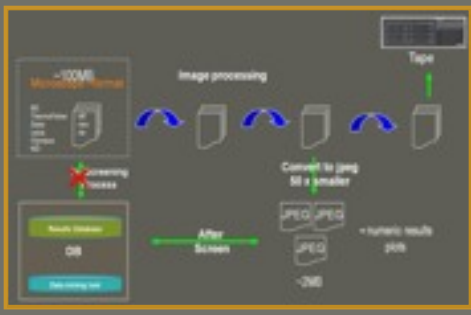






~~In Screening Process~~

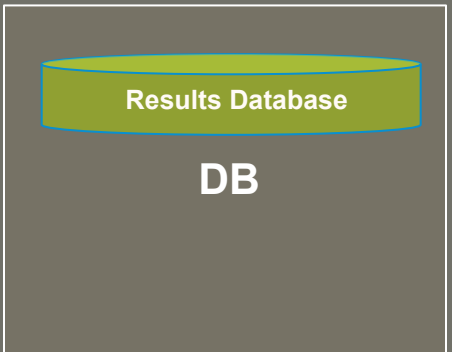


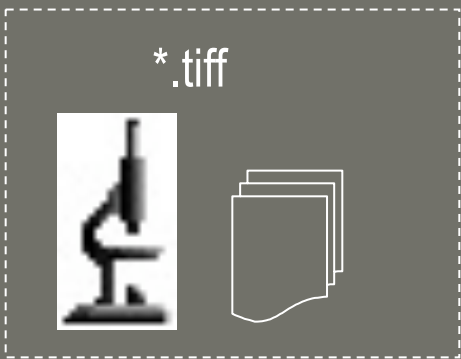
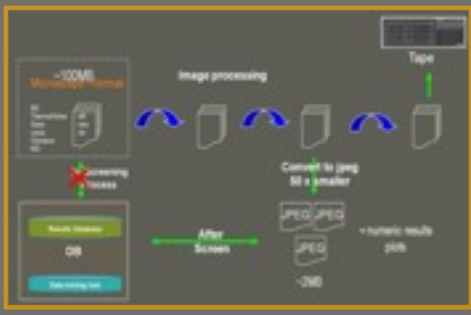


~~In Screening Process~~

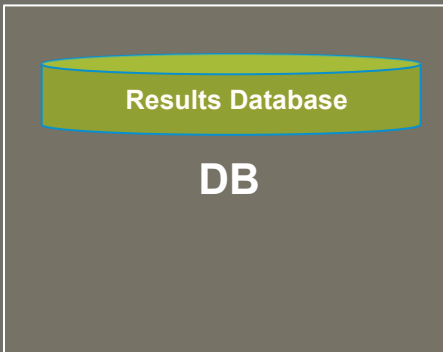


Buffer server





~~In Screening Process~~



Buffer server



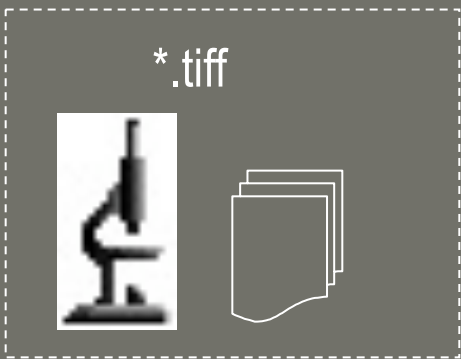
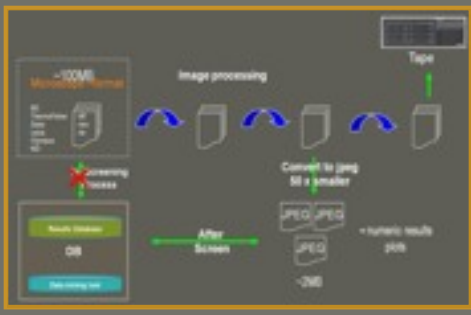
2x25TB  
LMC (6 weeks)



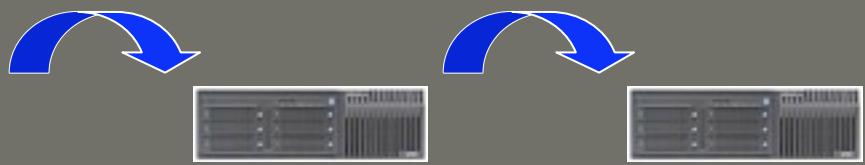
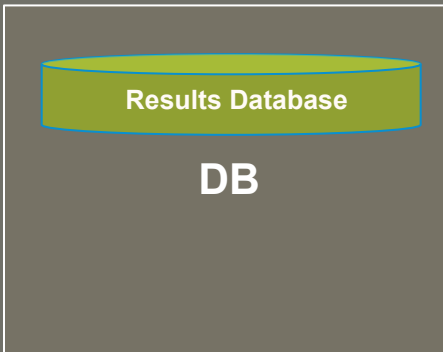
+ numeric results plots

~0.5MB



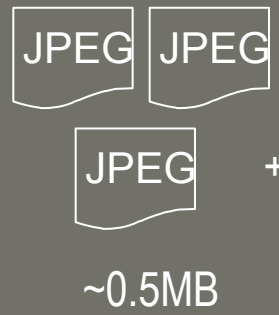


~~In Screening Process~~



Buffer server

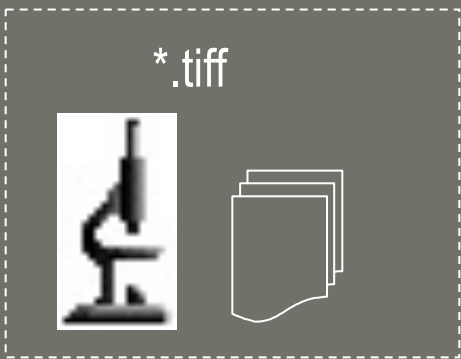
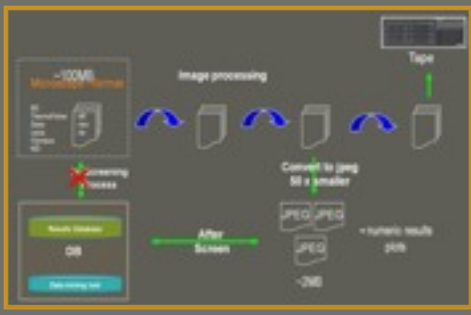
2x25TB LMC (6 weeks)



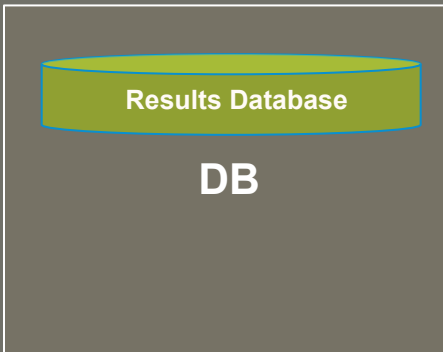
After Screen

+ numeric results plots

~0.5MB



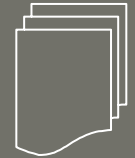
~~In Screening Process~~



Buffer server



2x25TB  
LMC (6 weeks)



ETH NAS  
User storage

After Screen



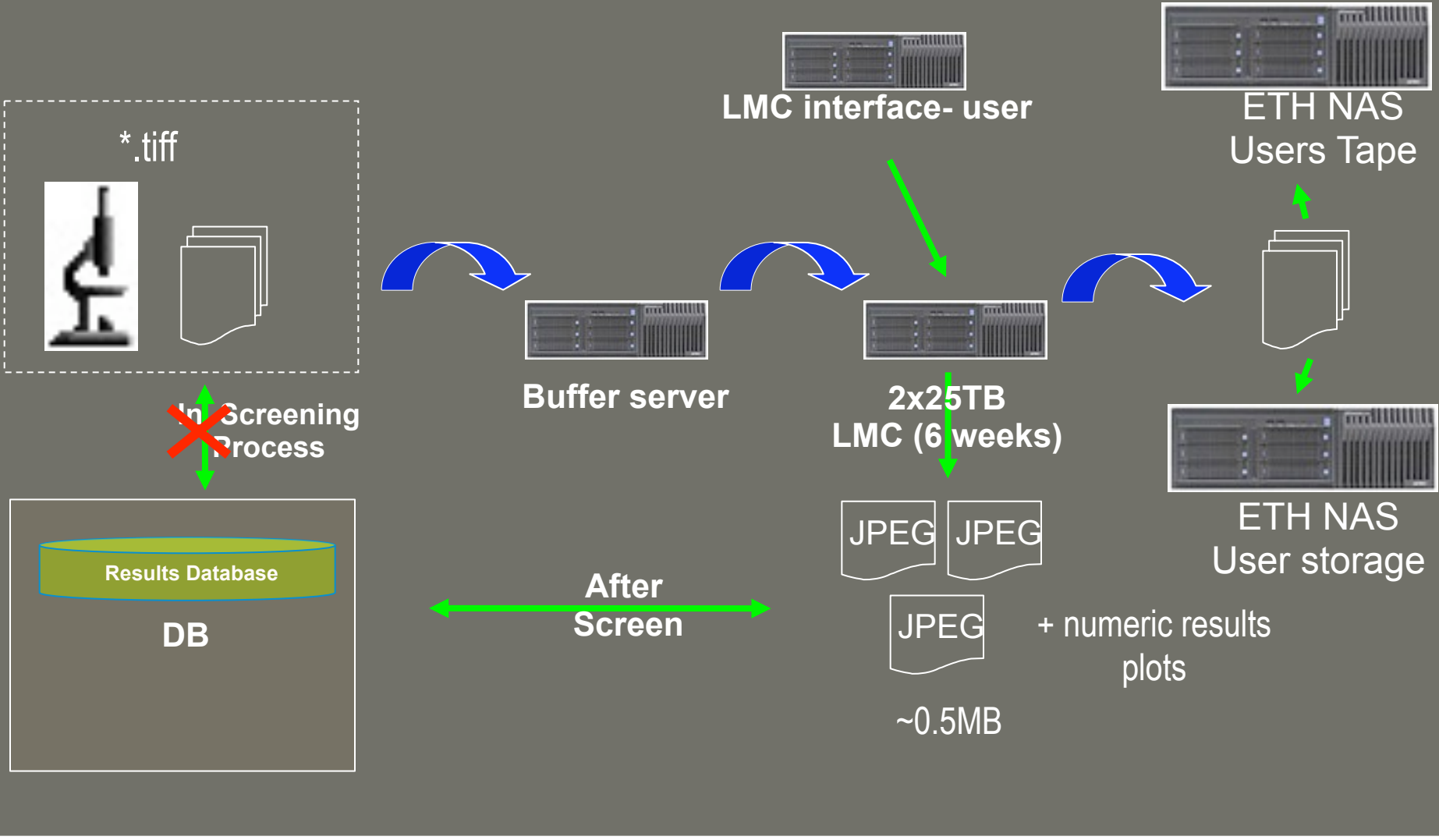
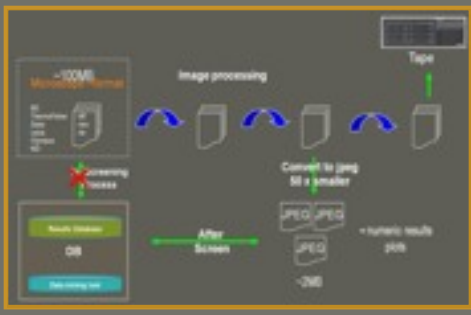
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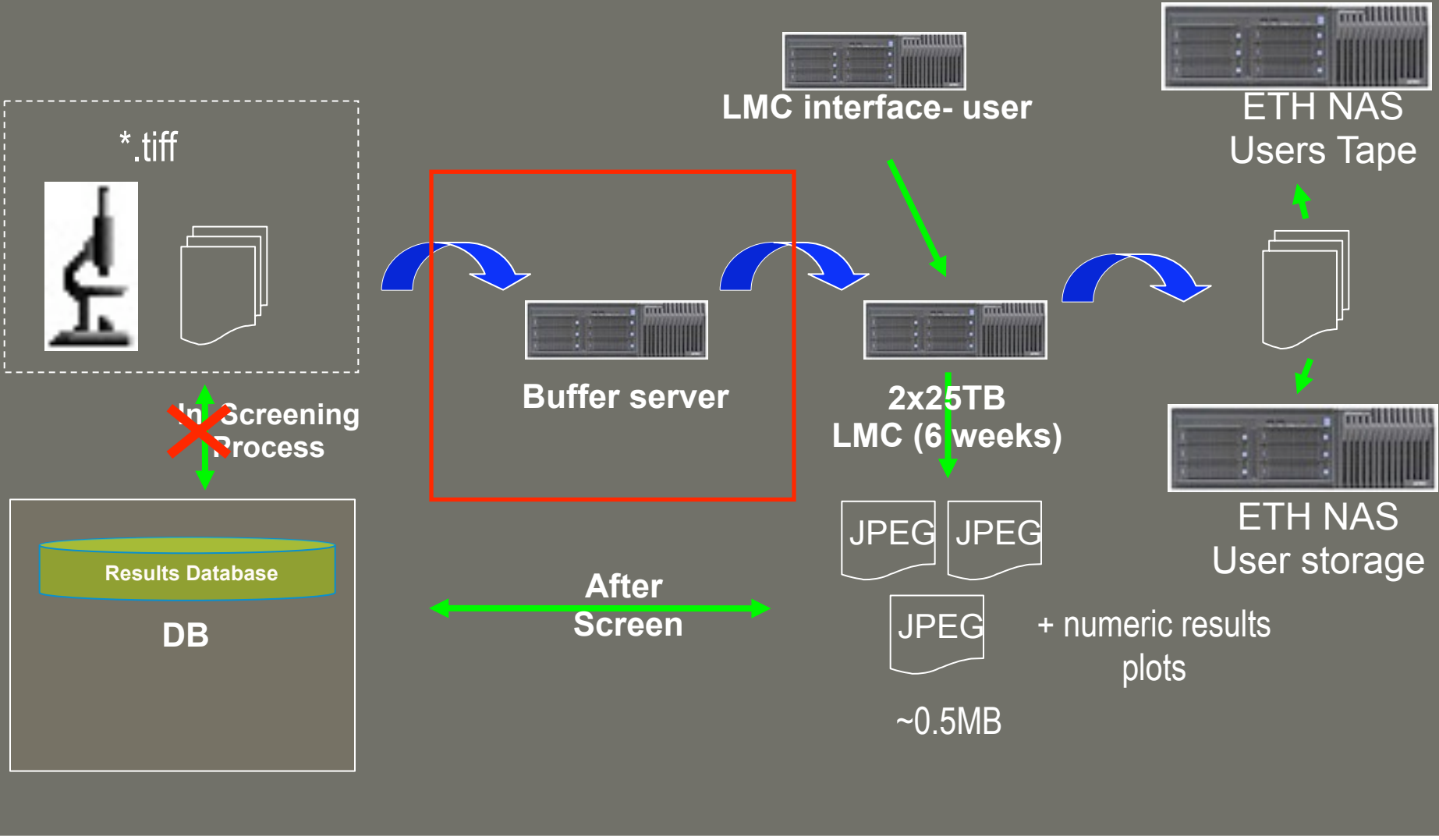
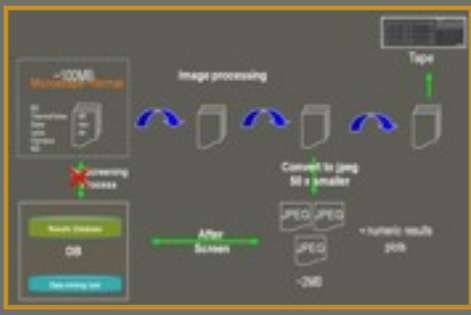
+ numeric results plots

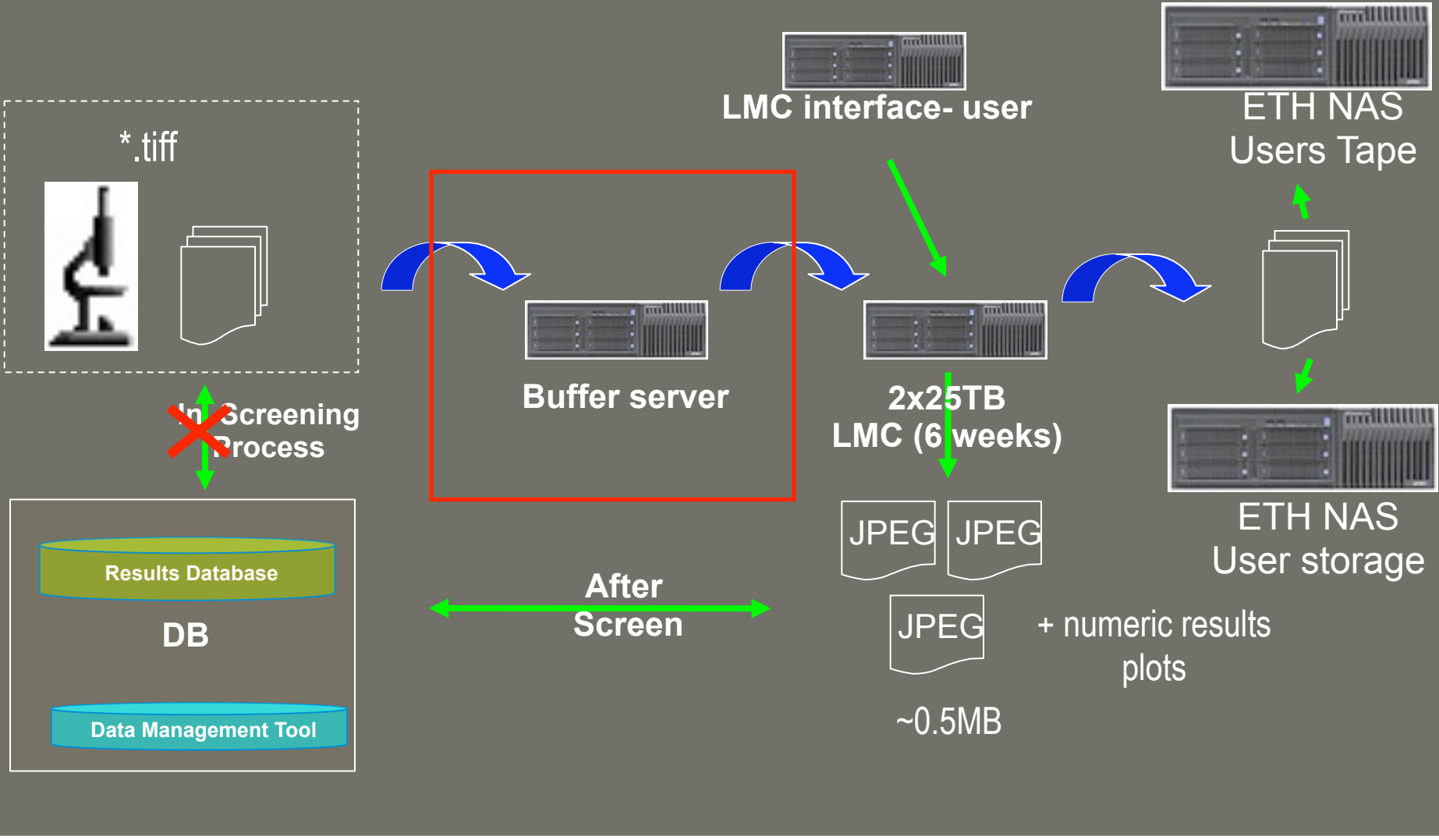
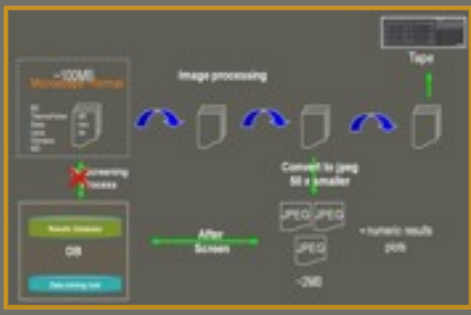


ETH NAS  
Users Tape

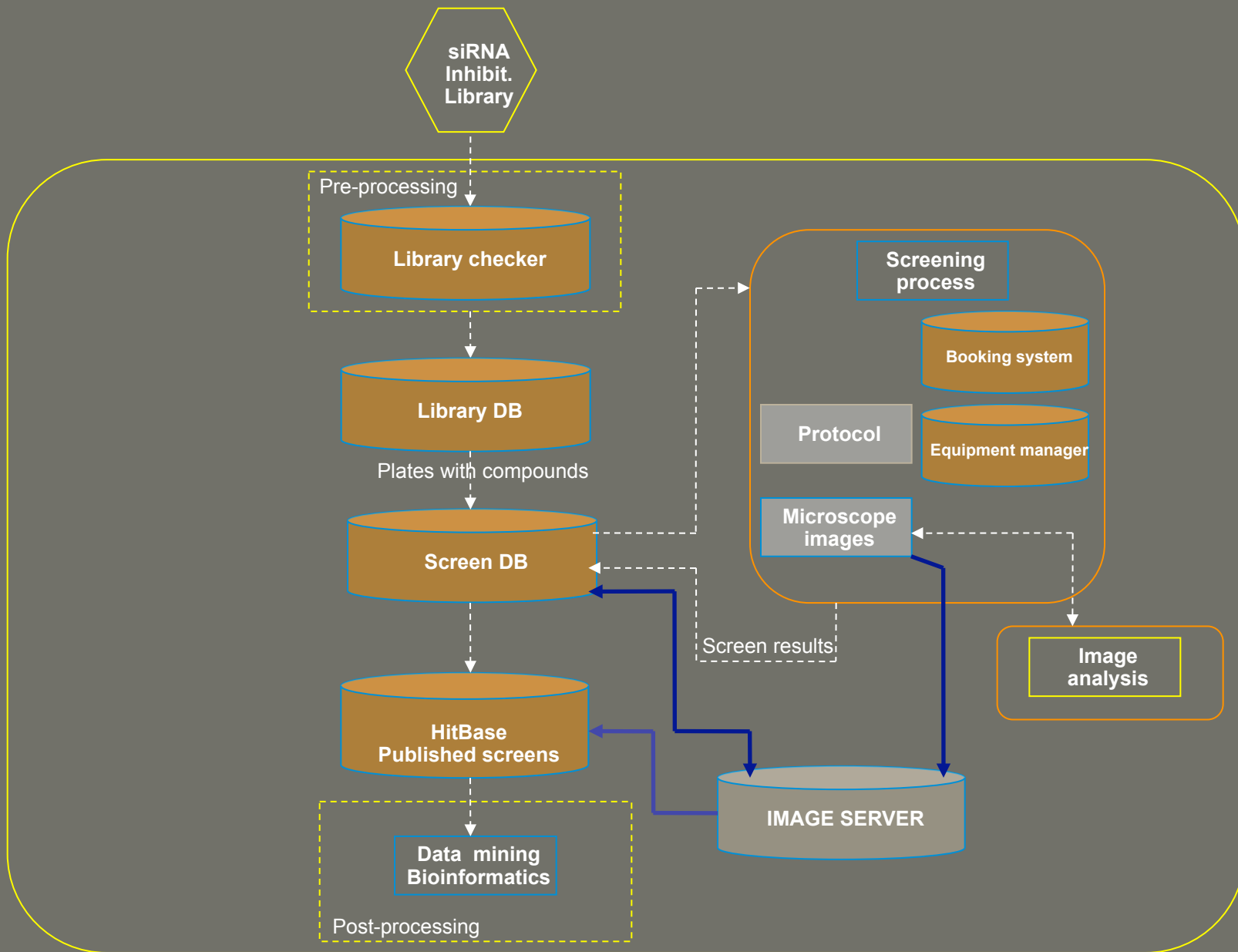




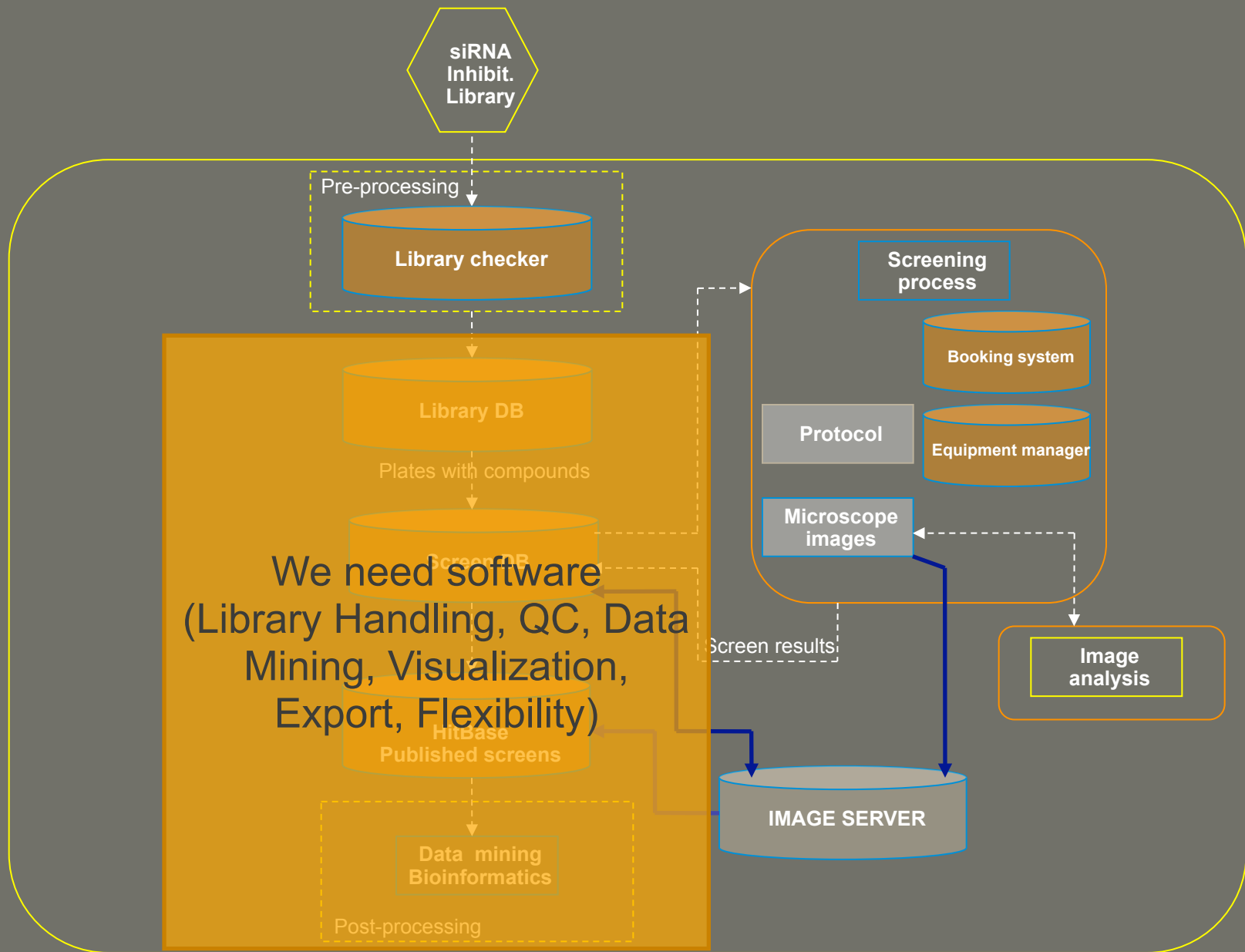




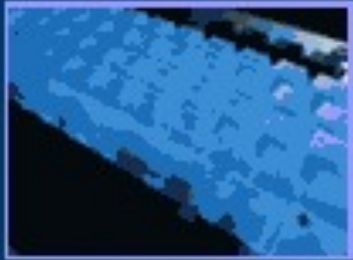
# Dataflow architecture



# Dataflow architecture



# HC/DC



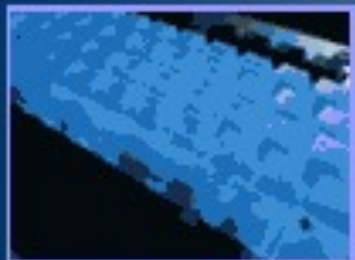
H<sub>igh</sub> C<sub>ontent</sub> analysis D<sub>ata</sub> C<sub>hain</sub>  
Data Handling Unit



based on Eclipse / R / Weka / KNIME



# HC/DC



H<sub>igh</sub> C<sub>ontent</sub> analysis D<sub>ata</sub> C<sub>hain</sub>  
Data Handling Unit



based on Eclipse / R / Weka / KNIME



# Read data from database

The screenshot displays the HC/DC software interface. The top menu bar includes File, Edit, View, Search, Node, and Help. The toolbar contains various icons for file operations and workflow management, along with a zoom level of 100%. The main workspace shows a workflow project named "step\_by" with a single node labeled "Database Reader". Below the main workspace, the Node Repository is visible, showing a tree structure of nodes under categories like HTS/HCS, IO, Write, Artificial Data, Cache, and Data Manipulation. The "IO" category is expanded, showing "Read" and "File Reader" nodes. The "Database Reader" node is highlighted in the Node Repository.

Workflow Projects:

- HC\_DC\_project
- QC\_demo
- step\_by

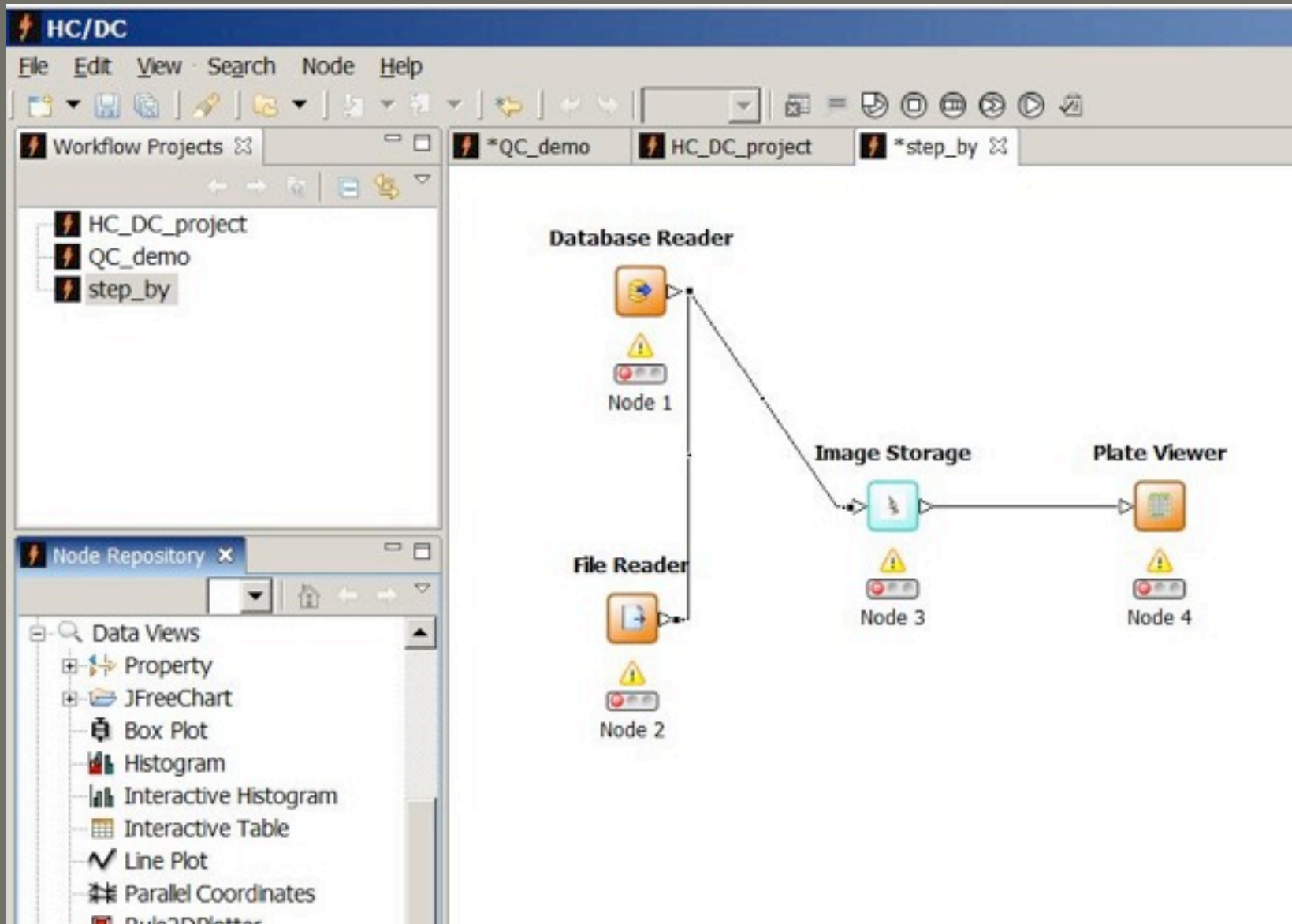
Node Repository:

- HTS/HCS
  - Create Layout
  - Image Storage
  - Plate Viewer
- IO
  - Read
    - ARFF Reader
    - Database Reader
    - File Reader
    - Model Reader
    - Table Reader
- Write
- Artificial Data
- Cache
- Data Manipulation

Main Workspace:

- Database Reader
  - Node 1
- File Reader
  - Node 2

# Link with image storage



# Link with image storage

The screenshot displays the HC/DC software interface. The top menu bar includes File, Edit, View, Search, Node, and Help. Below the menu is a toolbar with various icons. The main workspace shows a workflow diagram with four nodes: Node 1 (Database Reader), Node 2 (File Reader), Node 3 (Image Storage), and Node 4 (Plate Viewer). Node 1 is connected to Node 3, and Node 2 is also connected to Node 3. Node 3 is connected to Node 4. The Node Repository panel on the left lists various data views, with a red circle highlighting the 'Property' node.

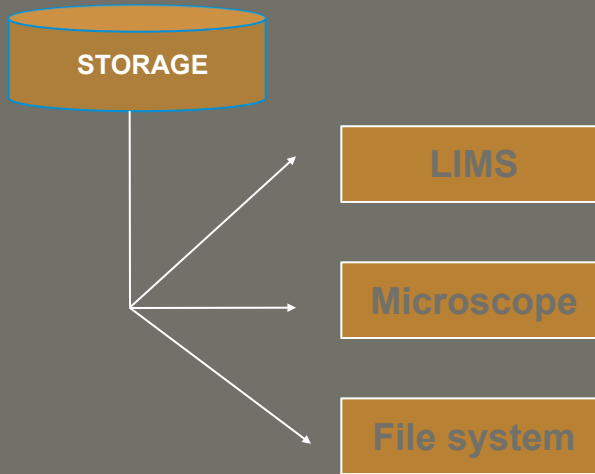
**Workflow Diagram:**

```
graph TD; Node1[Database Reader] --> Node3[Image Storage]; Node2[File Reader] --> Node3; Node3 --> Node4[Plate Viewer];
```

**Node Repository:**

- Data Views
- Property
- JFreeChart
- Box Plot
- Histogram
- Interactive Histogram
- Interactive Table
- Line Plot
- Parallel Coordinates
- Rule2DPlotter

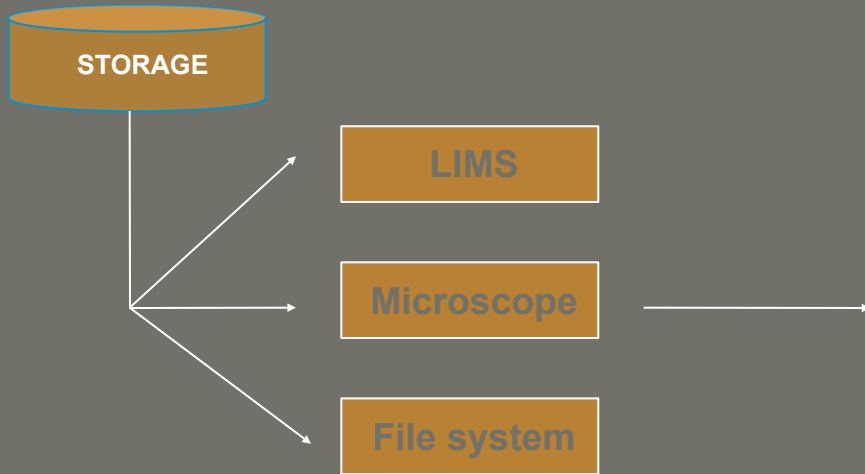
# Data mining



# Data mining

## Statistics

- One/two parameters
- Normalization
- Correlation
- Compare distribution
- Ex. Statistical tests, Z-score, Z', etc



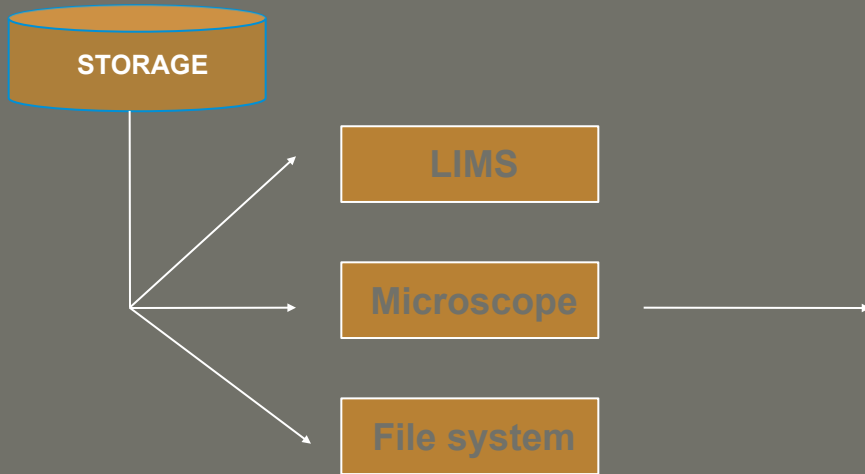
# Data mining

## Statistics

- One/two parameters
- Normalization
- Correlation
- Compare distribution
- Ex. Statistical tests, Z-score, Z', etc

## Pattern recognition – Machine Learning

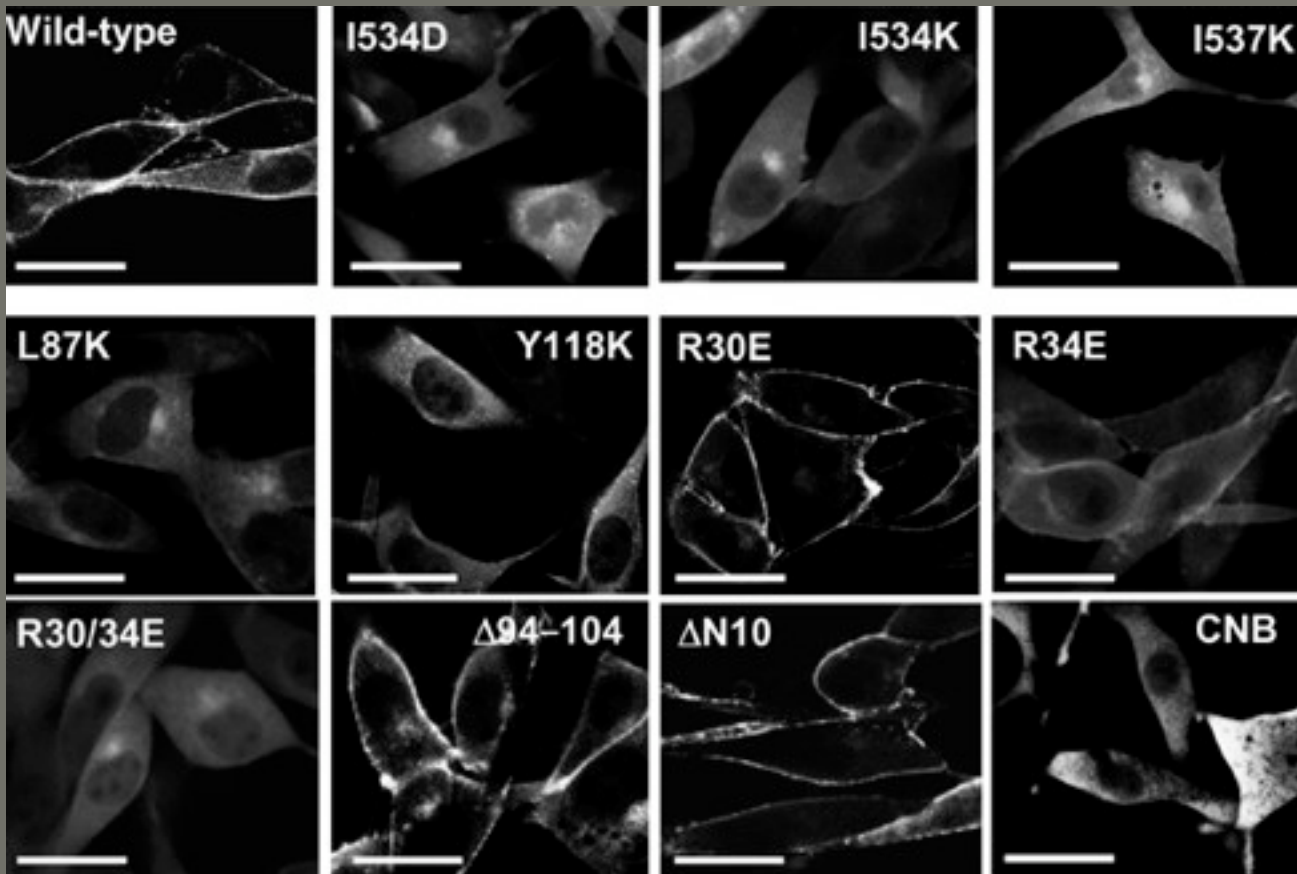
- Multi-parameters
- Clustering
- Dimensionality reduction
- Check parameter importance





# Classification

- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes

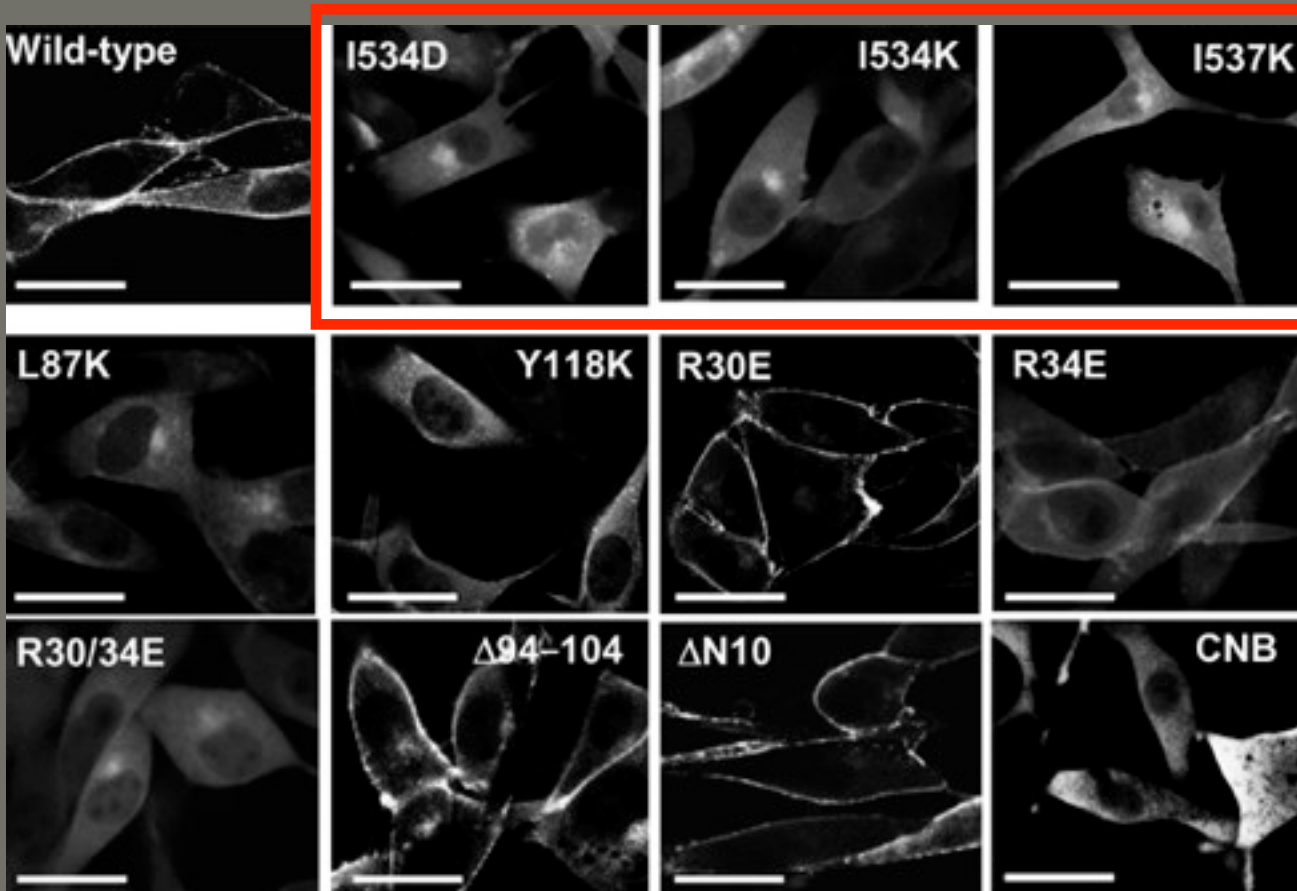






# Classification

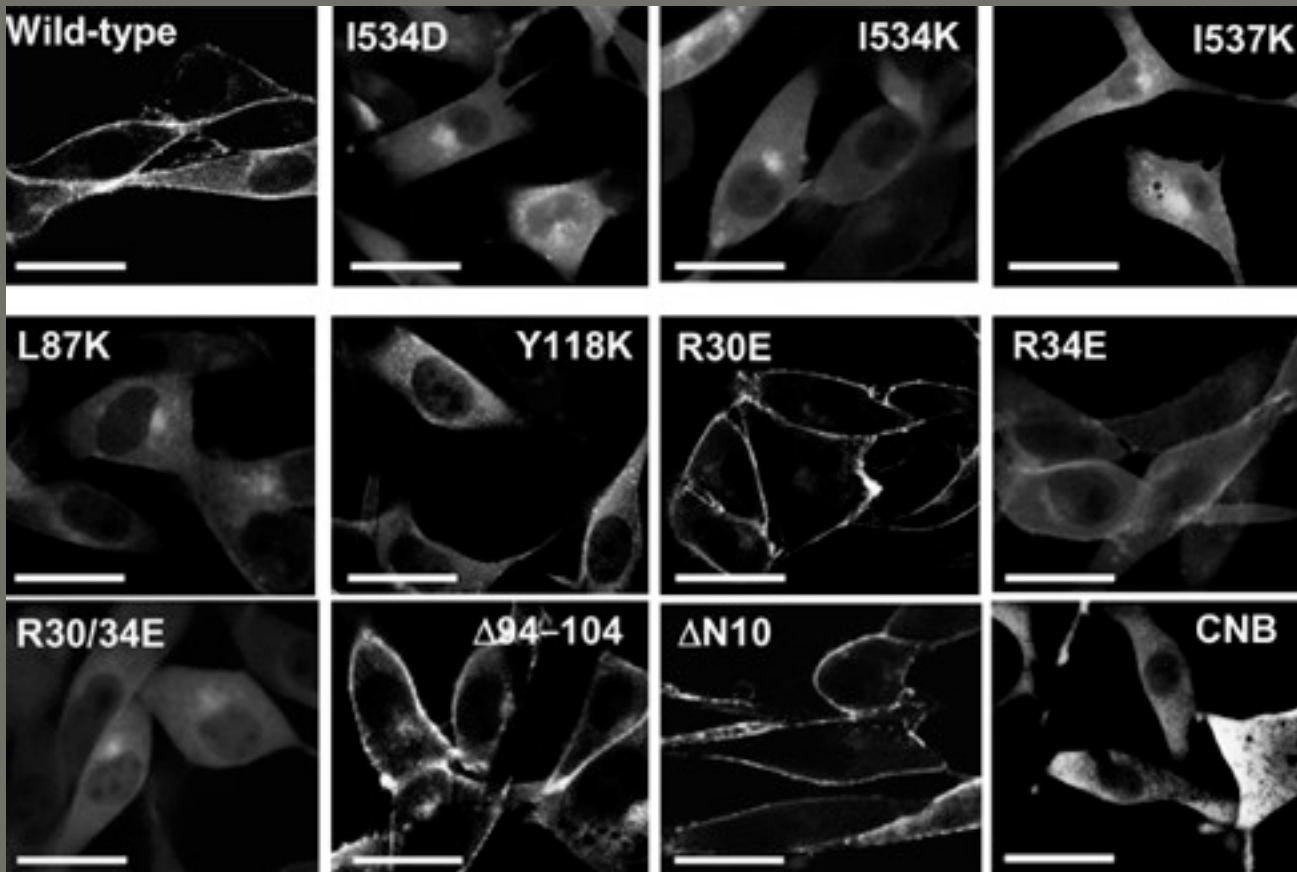
- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





# Classification

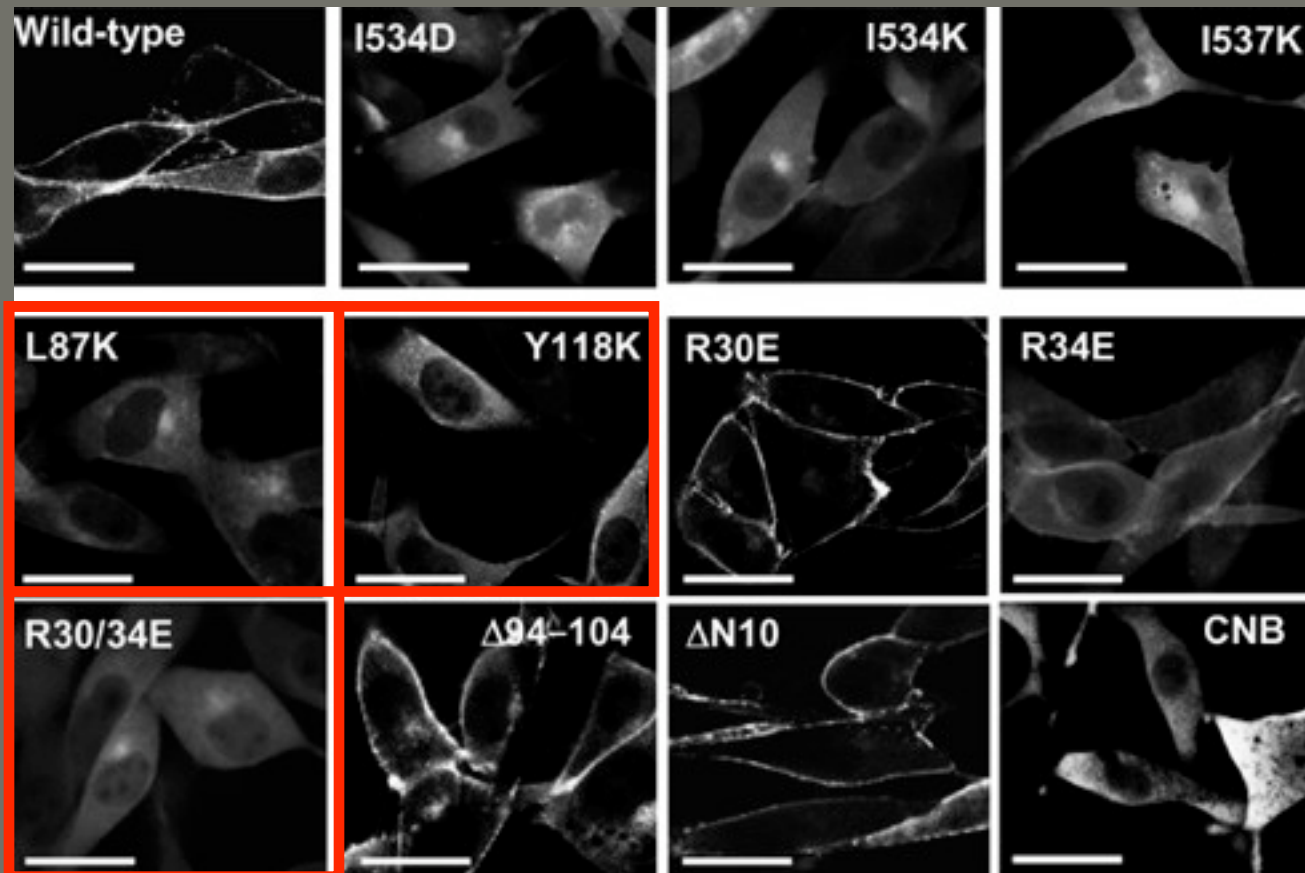
- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





# Classification

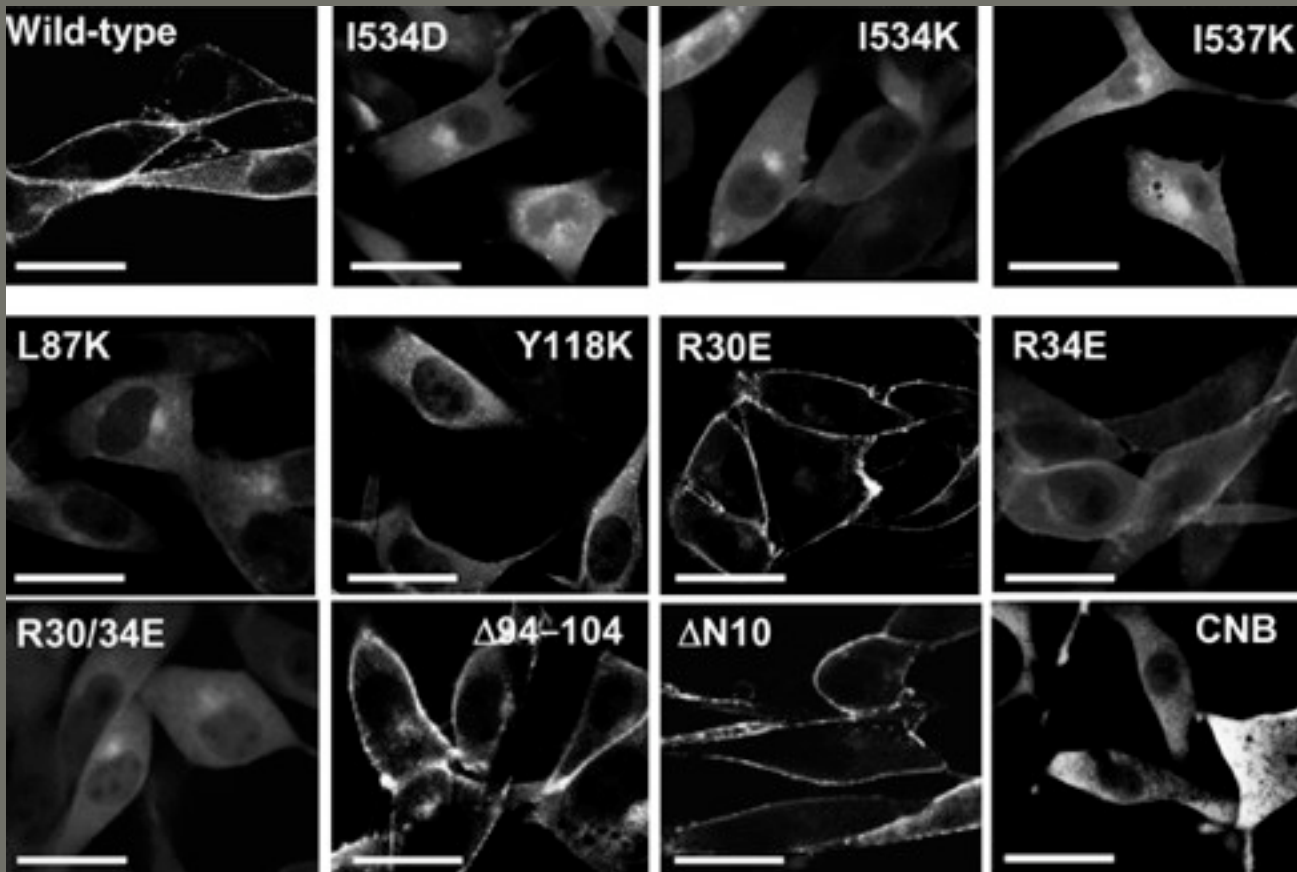
- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





# Classification

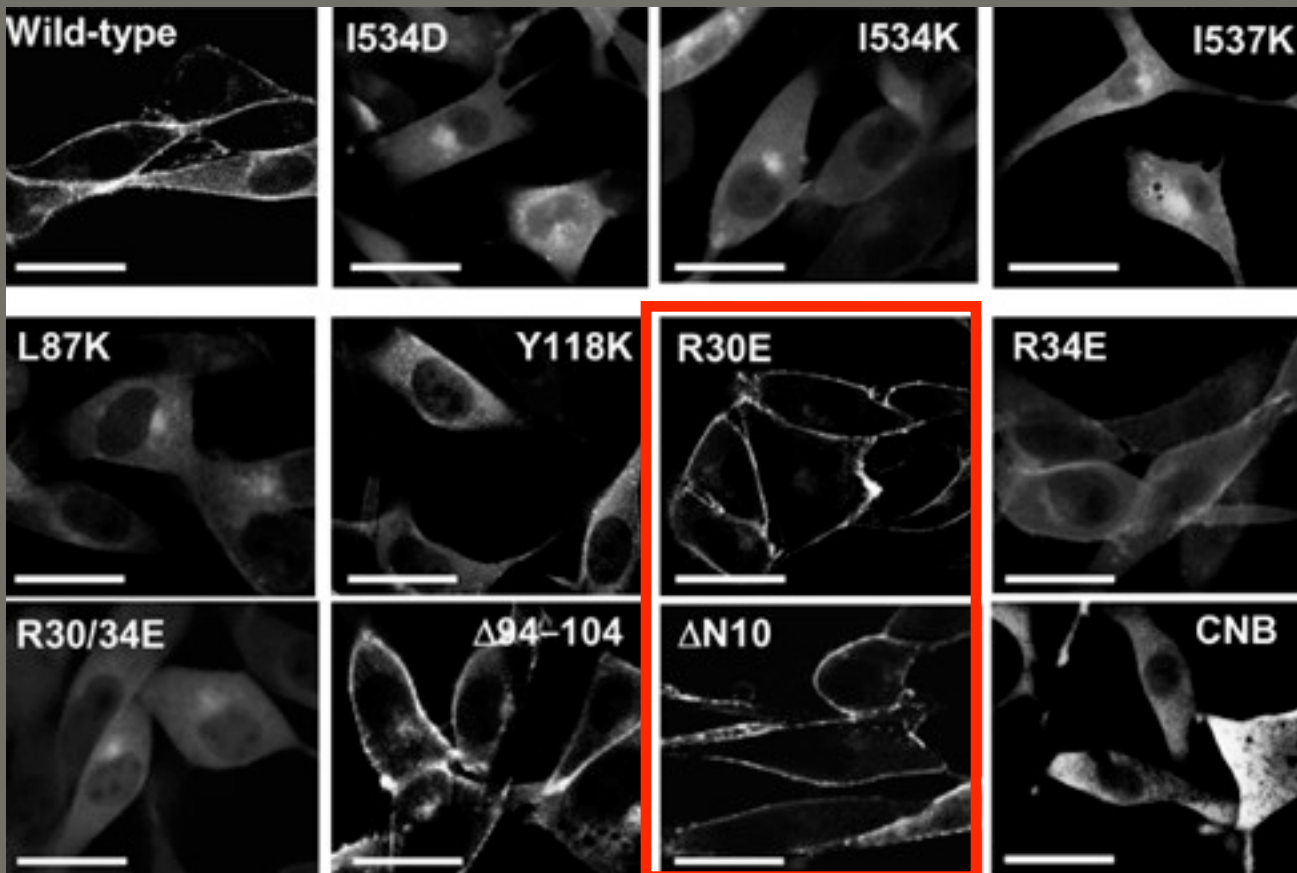
- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





# Classification

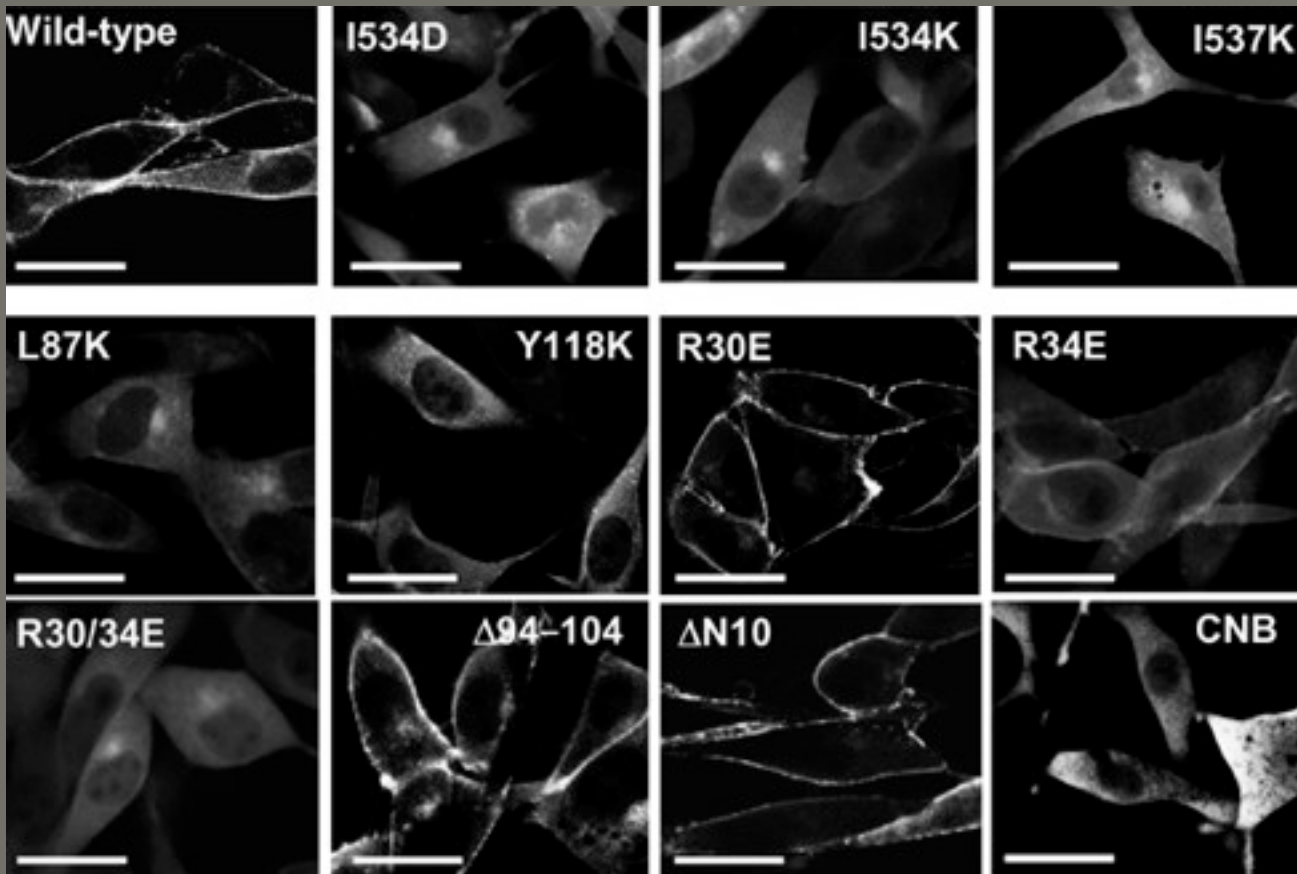
- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





# Classification

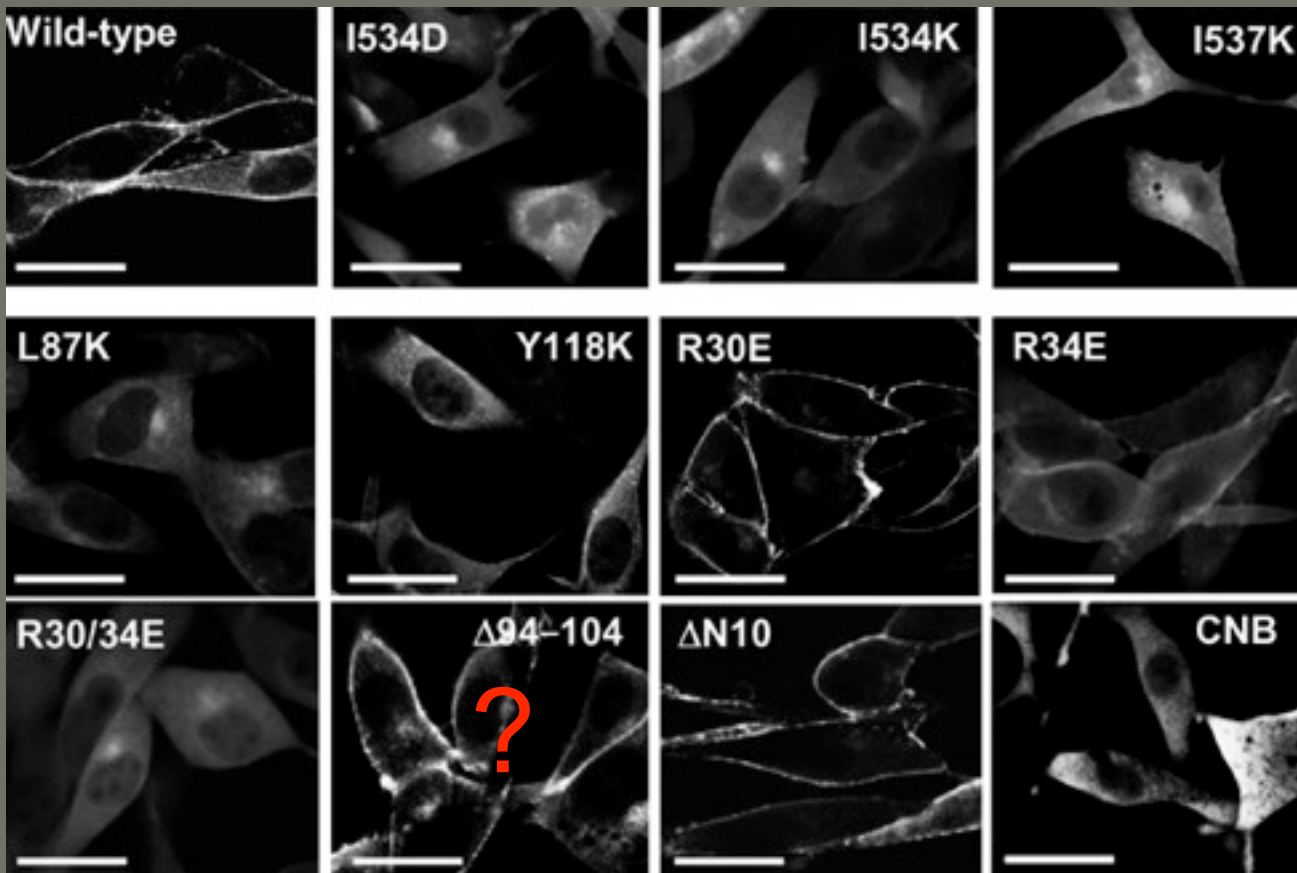
- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





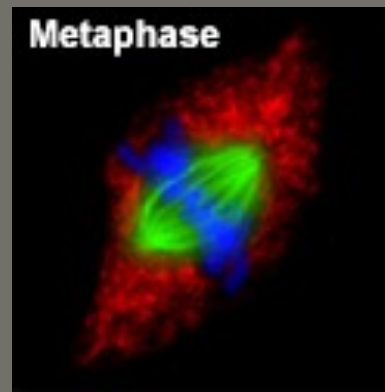
# Classification

- Unsupervised learning (Cluster analysis, Clustering) seeks to discover the classes





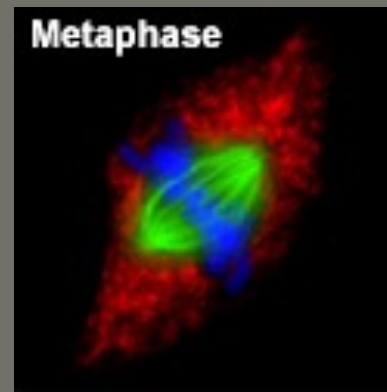
# Classification problem



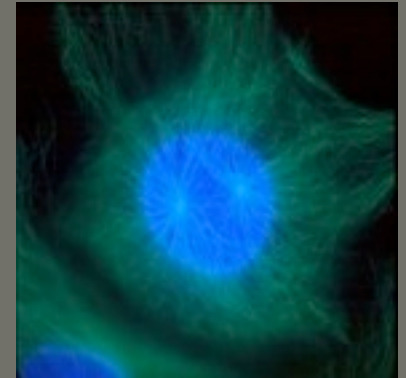




# Classification problem

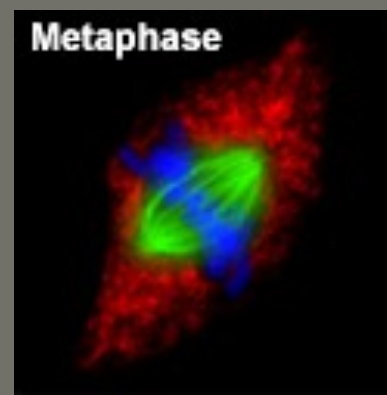


?

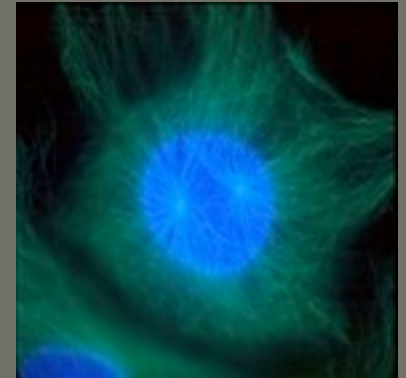




# Classification problem



?

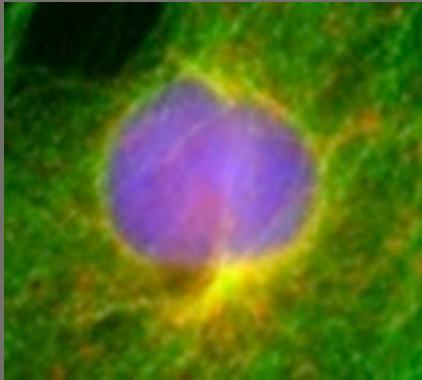


- Supervised learning (Classification)  
assumes classes are known

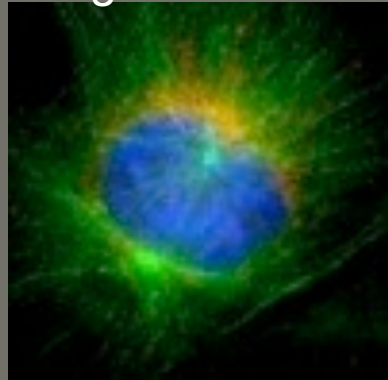


# 2 class problem

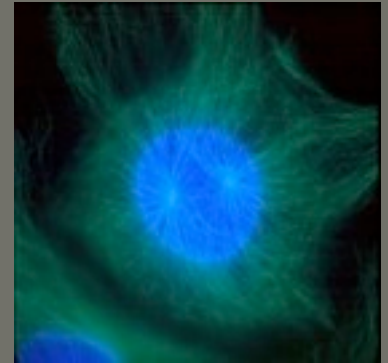
Positive control



Negative control

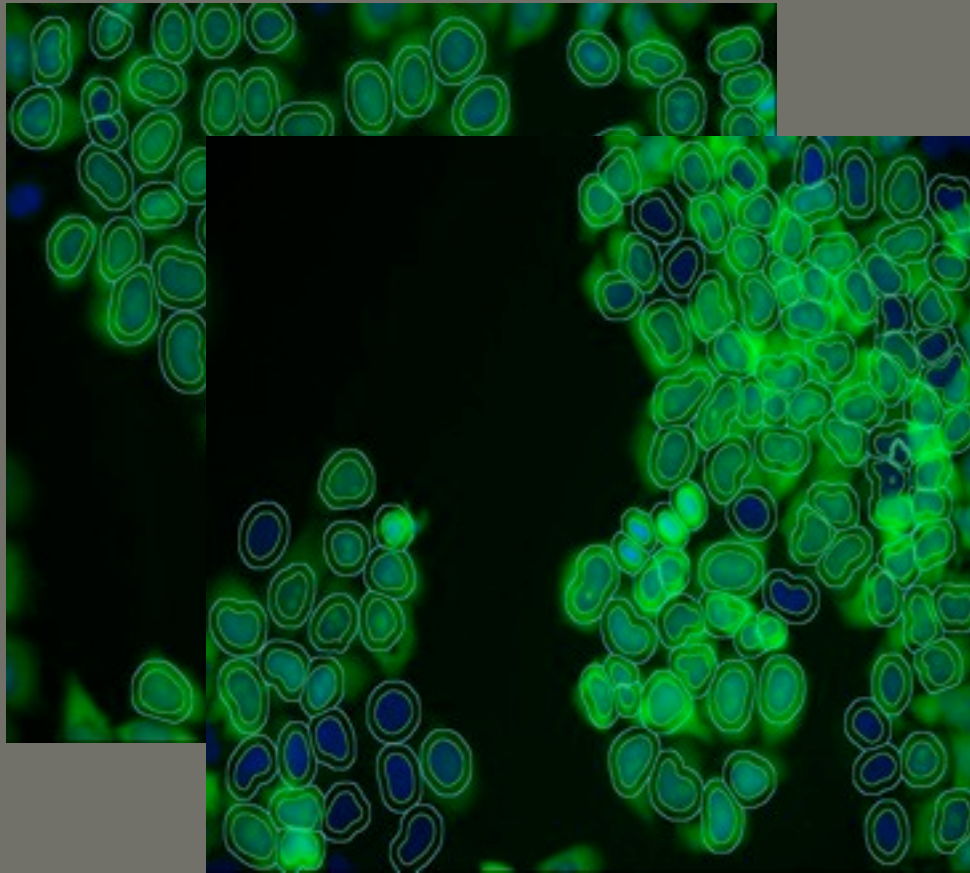


?



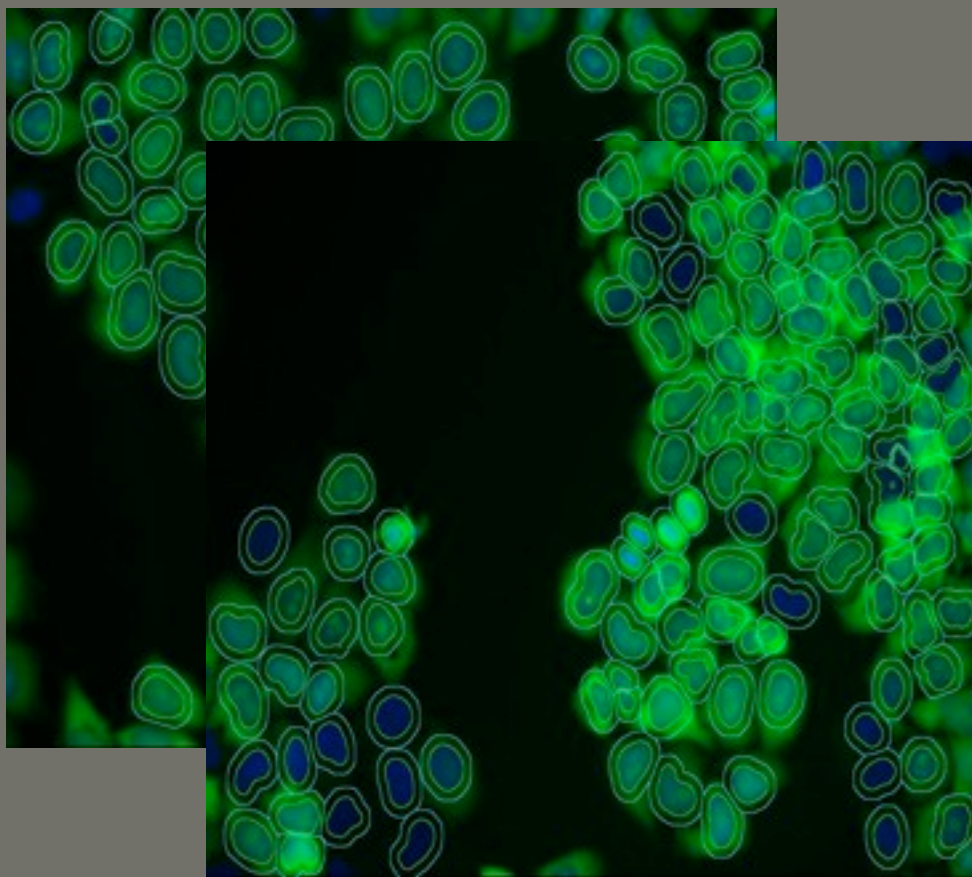


# Train data for supervised learning





# Train data for supervised learning

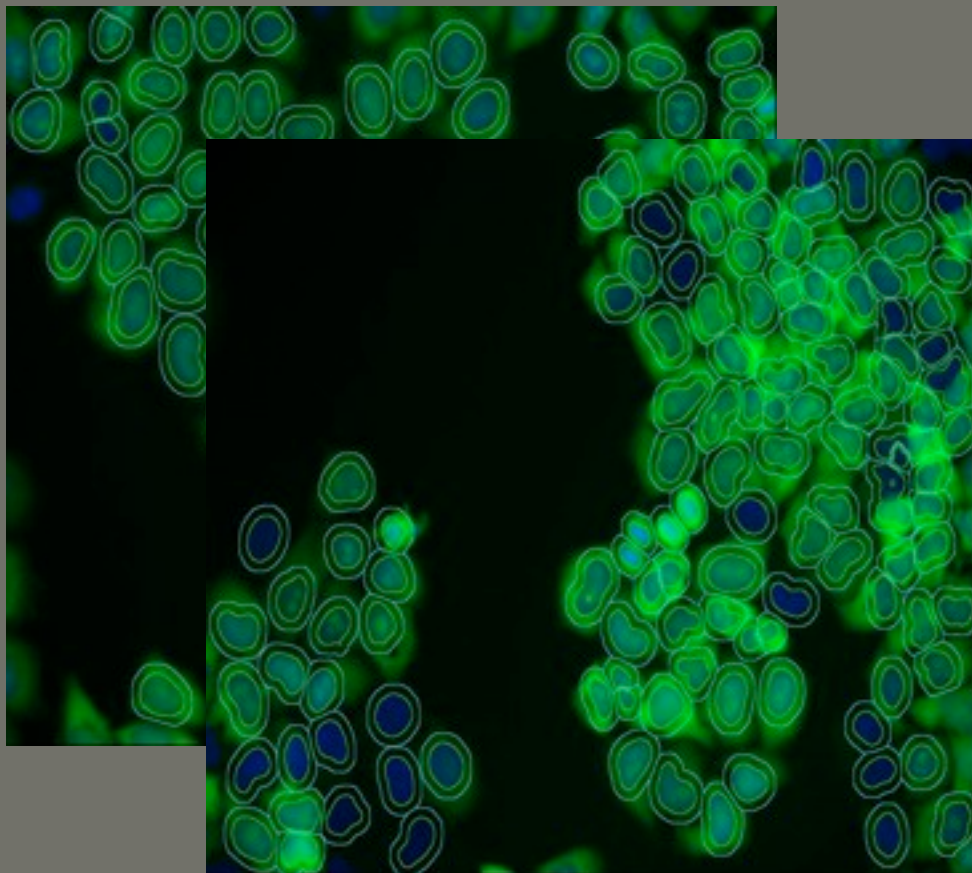


5 people

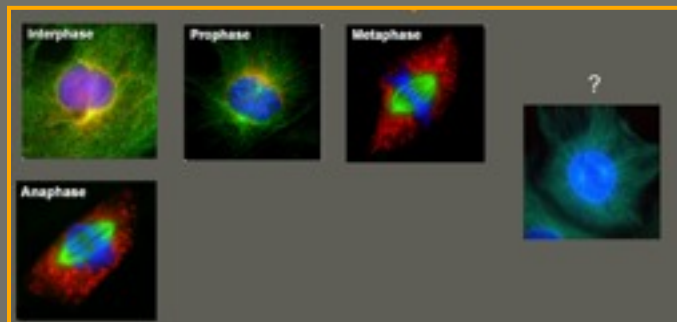




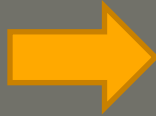
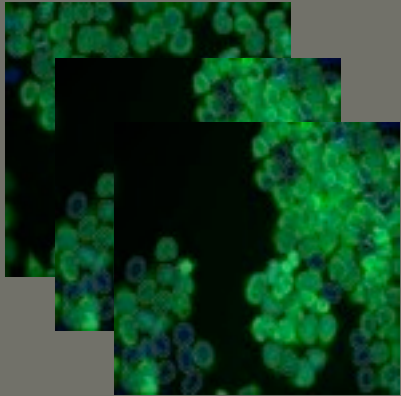
# Train data for supervised learning



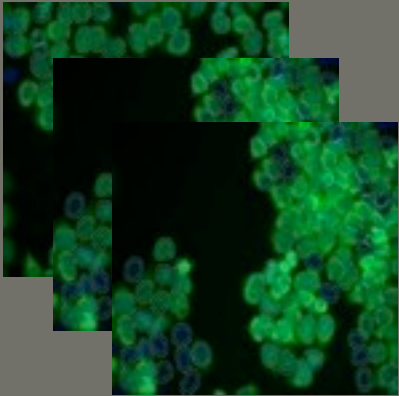
5 people



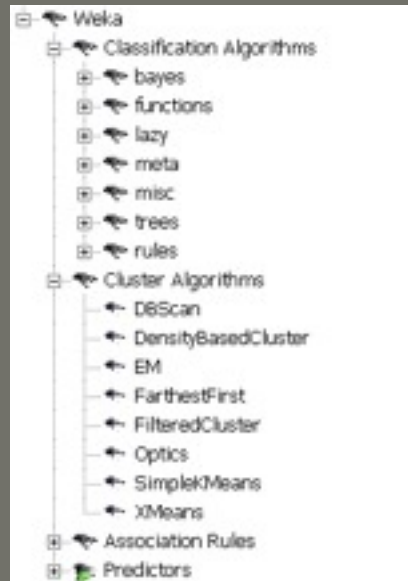
# Train data for supervised learning



# Train data for supervised learning

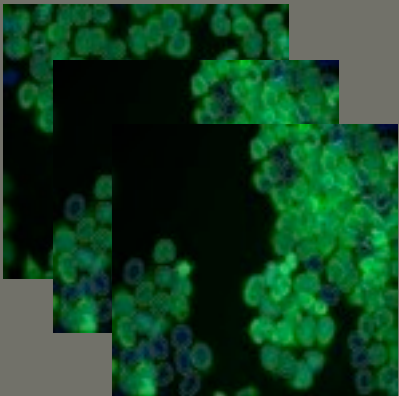


## WEKA/R-Project nodes (KNIME)

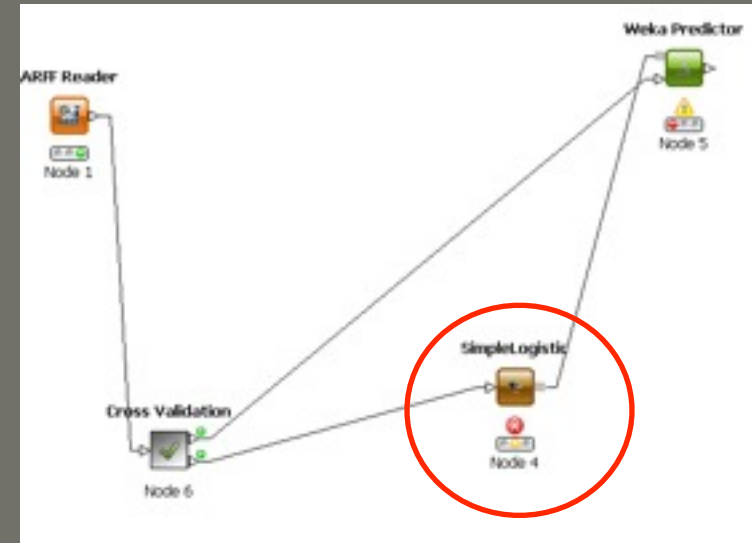
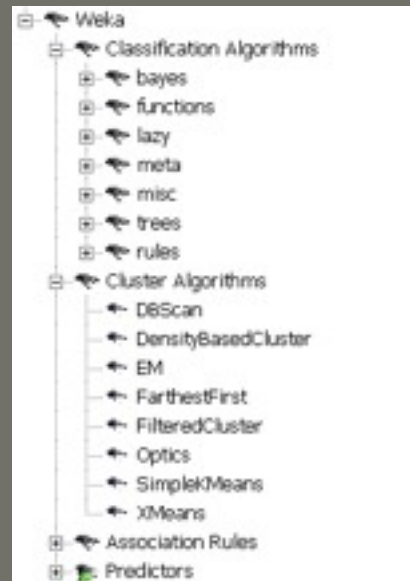




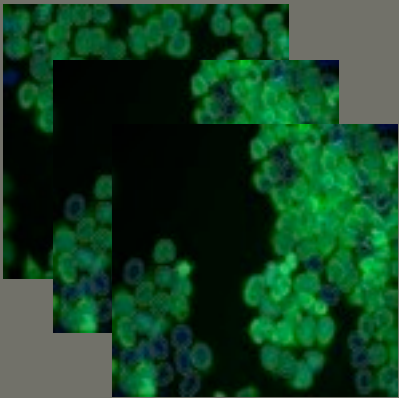
# Train data for supervised learning



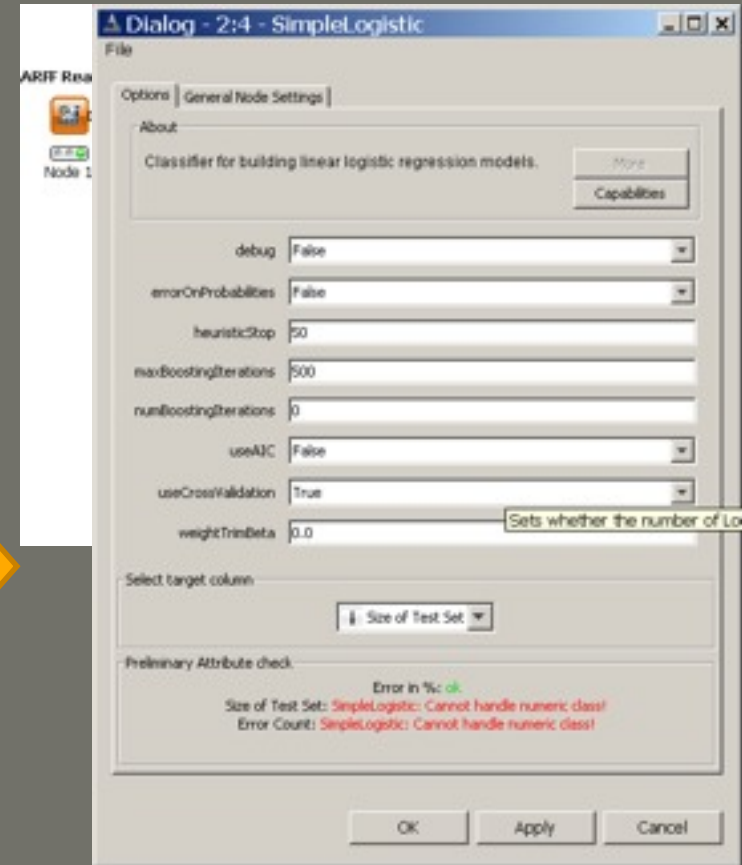
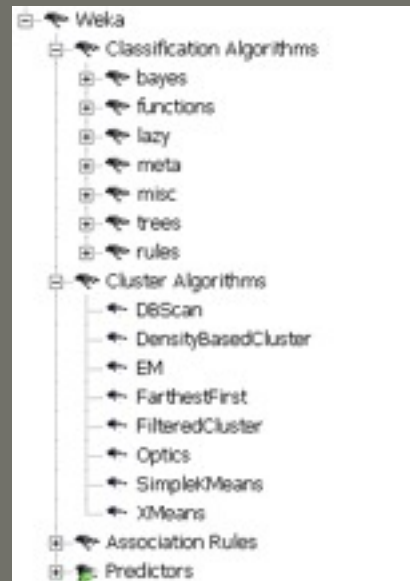
WEKA/R-Project  
nodes (KNIME)



# Train data for supervised learning



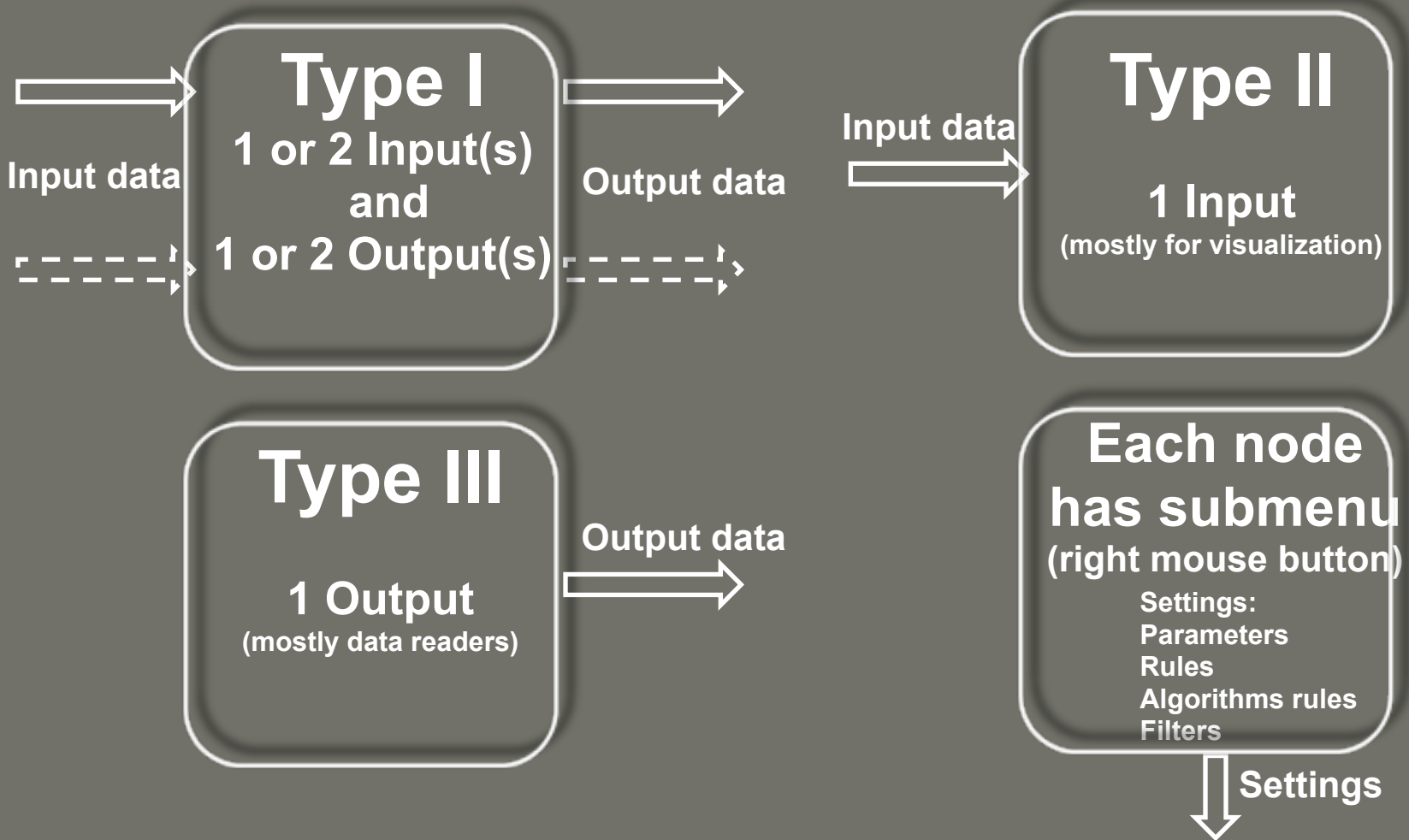
WEKA/R-Project  
nodes (KNIME)



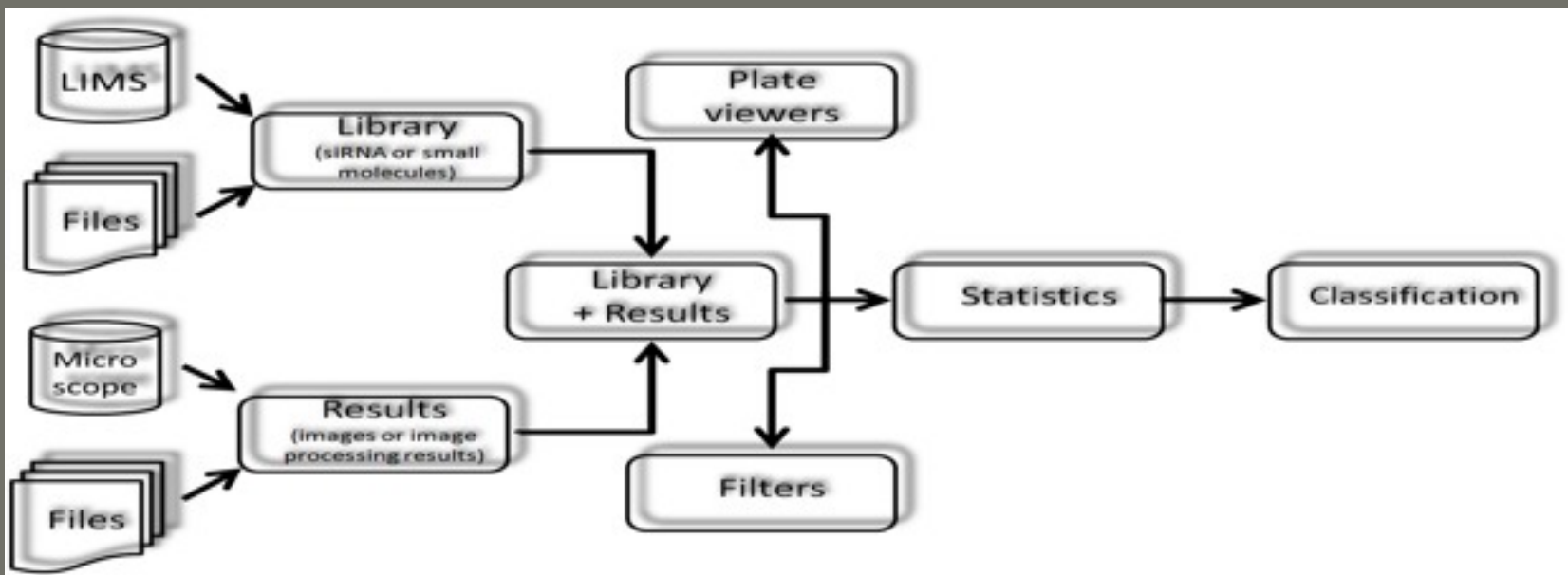
Niels Landwehr, Mark Hall, Eibe Frank  
(2005). Logistic Model Trees.

**92% Accuracy**

# HC/DC

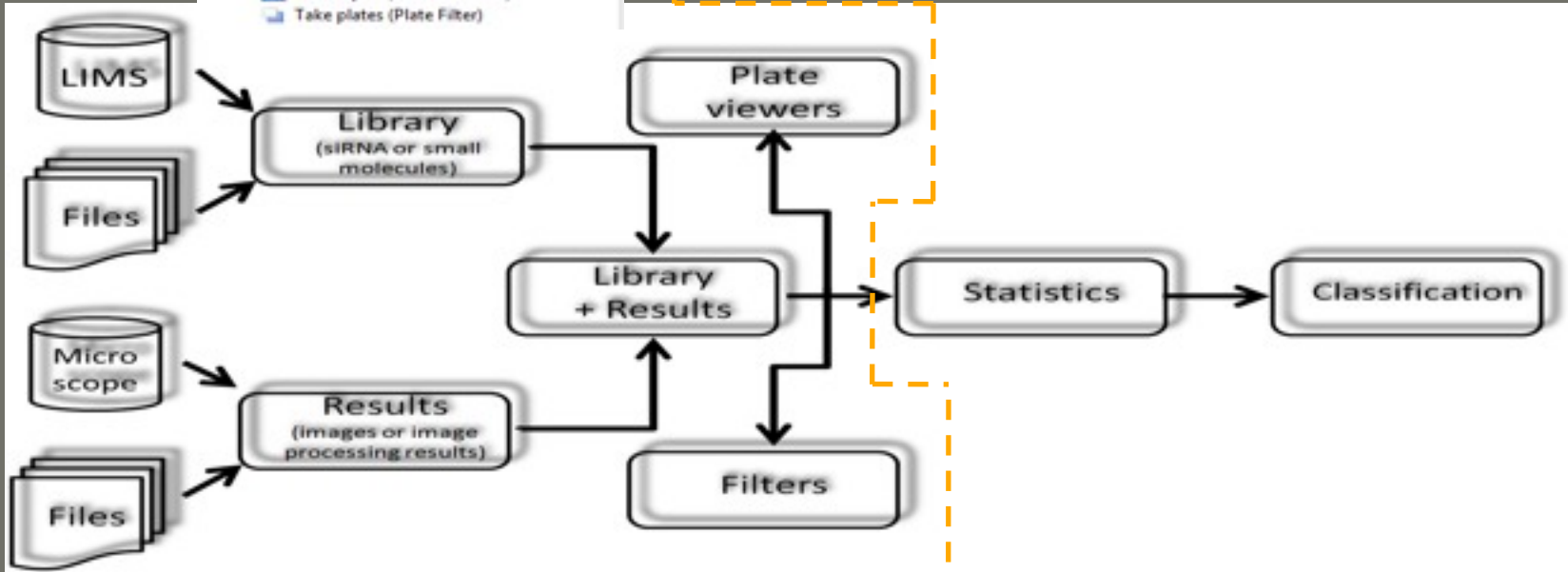
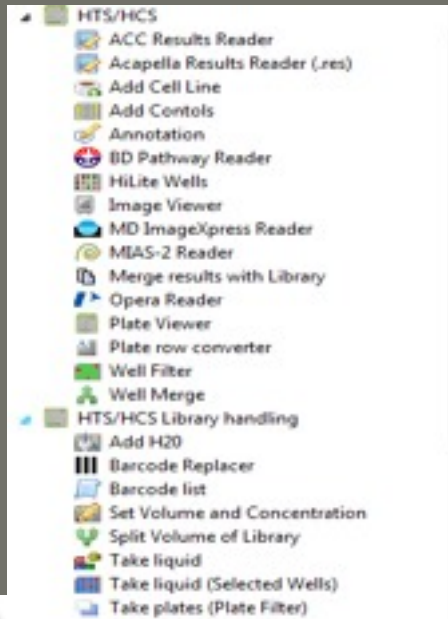


# HC/DC



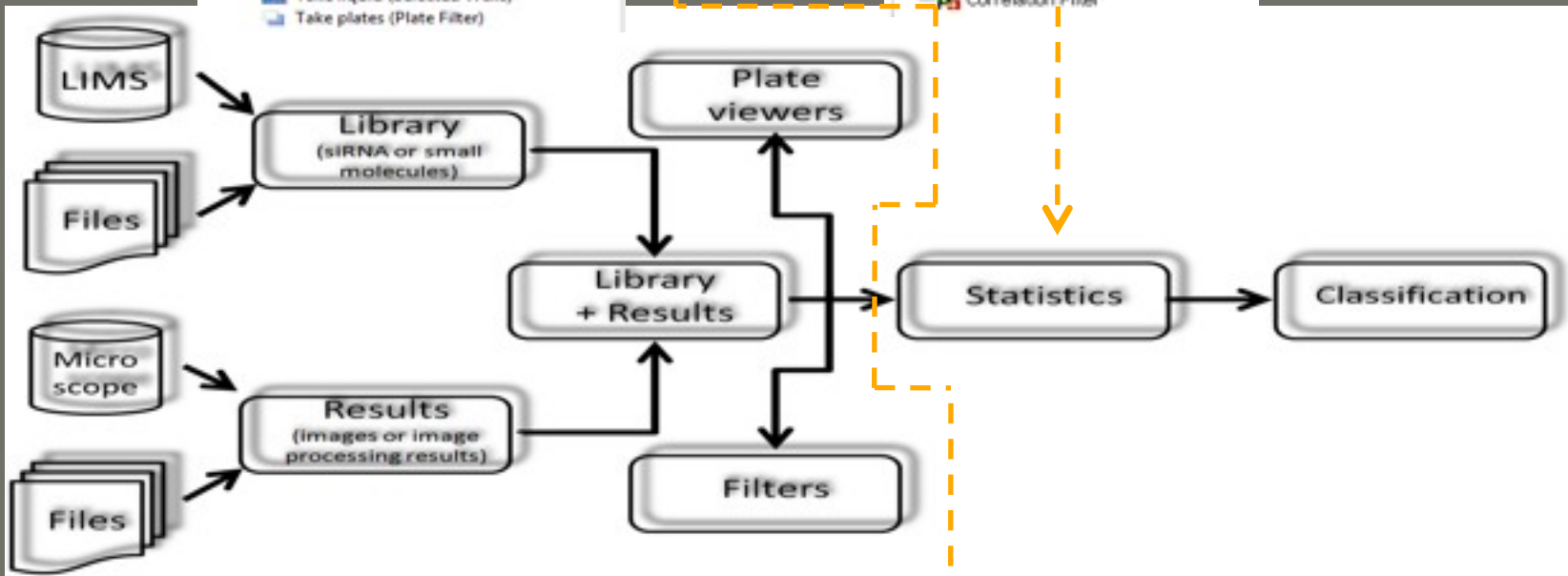
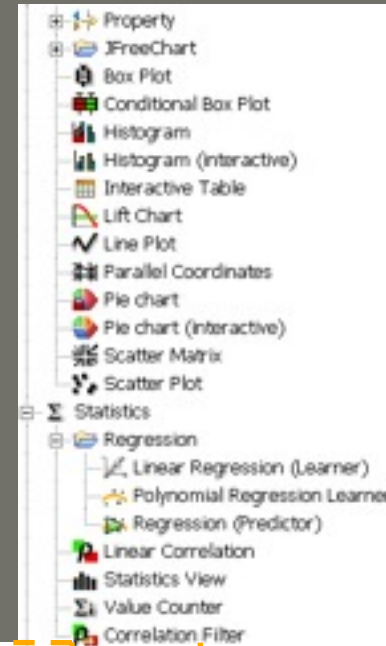
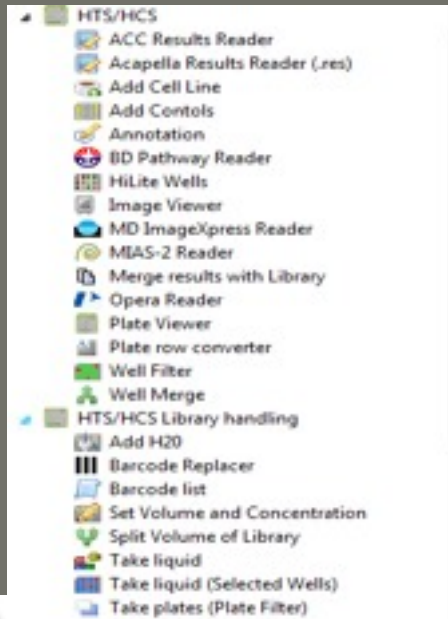
# HC/DC

## HC/DC nodes



# HC/DC KNIME nodes

## HC/DC nodes



# HC/DC

KNIME nodes

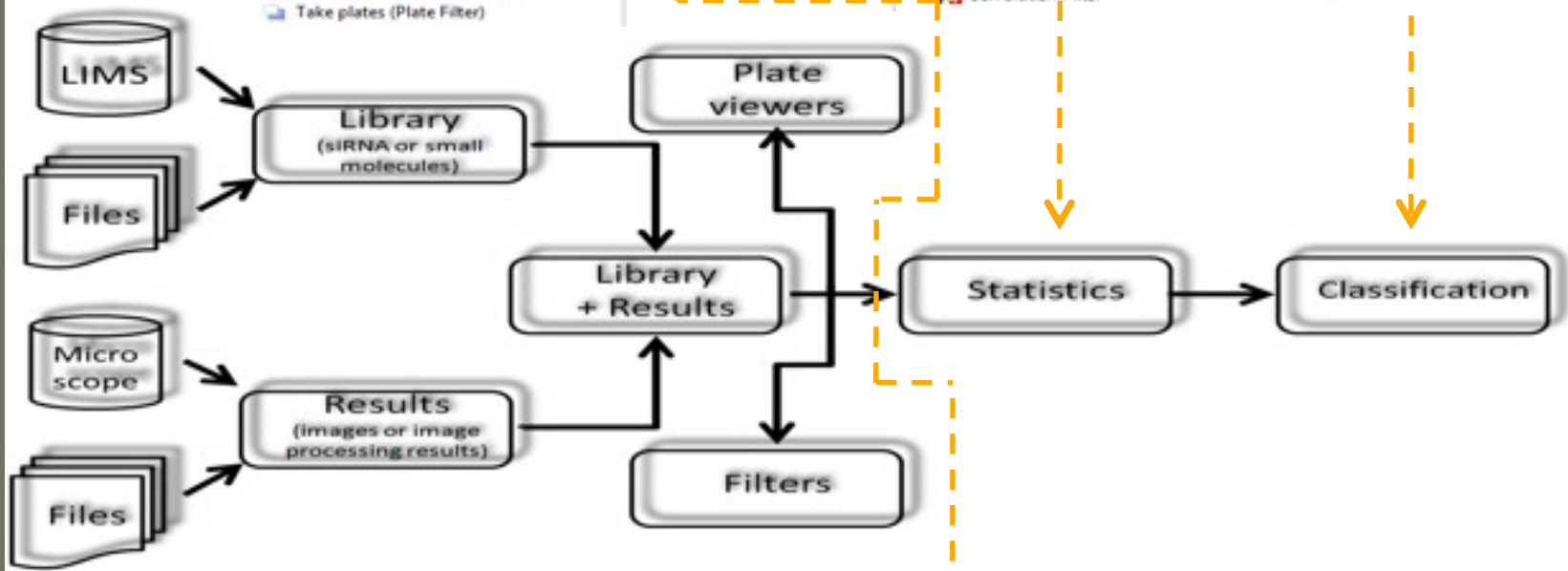
WEKA/R-Project nodes (KNIME)

HC/DC nodes

- HTS/HCS
  - ACC Results Reader
  - Acapella Results Reader (.res)
  - Add Cell Line
  - Add Controls
  - Annotation
  - BD Pathway Reader
  - HiLite Wells
  - Image Viewer
  - MD ImageXpress Reader
  - MIAS-2 Reader
  - Merge results with Library
  - Opera Reader
  - Plate Viewer
  - Plate row converter
  - Well Filter
  - Well Merge
- HTS/HCS Library handling
  - Add H2O
  - Barcode Replacer
  - Barcode list
  - Set Volume and Concentration
  - Split Volume of Library
  - Take liquid
  - Take liquid (Selected Wells)
  - Take plates (Plate Filter)

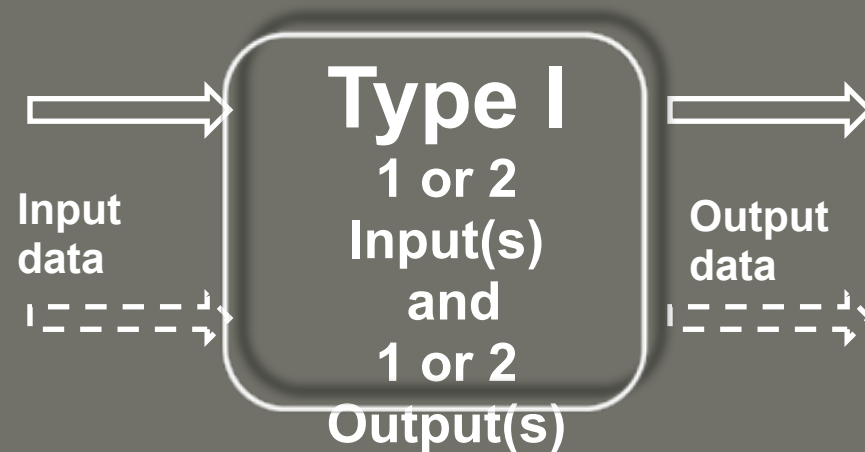
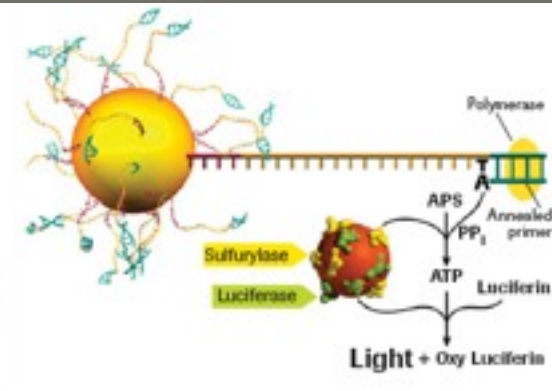
- Property
- JFreeChart
  - Box Plot
  - Conditional Box Plot
  - Histogram
  - Histogram (interactive)
  - Interactive Table
  - Lift Chart
  - Line Plot
  - Parallel Coordinates
  - Pie chart
  - Pie chart (interactive)
  - Scatter Matrix
  - Scatter Plot
- Statistics
  - Regression
    - Linear Regression (Learner)
    - Polynomial Regression Learner
    - Regression (Predictor)
  - Linear Correlation
  - Statistics View
  - Value Counter
  - Correlation Filter

- Weka
  - Classification Algorithms
    - bayes
    - functions
    - lazy
    - meta
    - misc
    - trees
    - rules
  - Cluster Algorithms
    - D8Scan
    - DensityBasedCluster
    - EM
    - FarthestFirst
    - FilteredCluster
    - Optics
    - SimplekMeans
    - XMeans
  - Association Rules
  - Predictors



# Next-Generation sequencing nodes

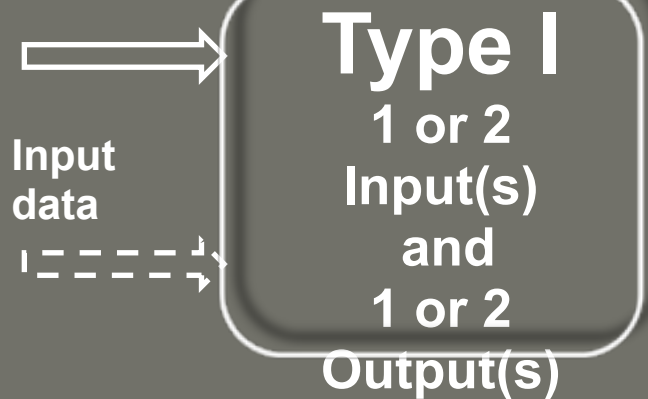
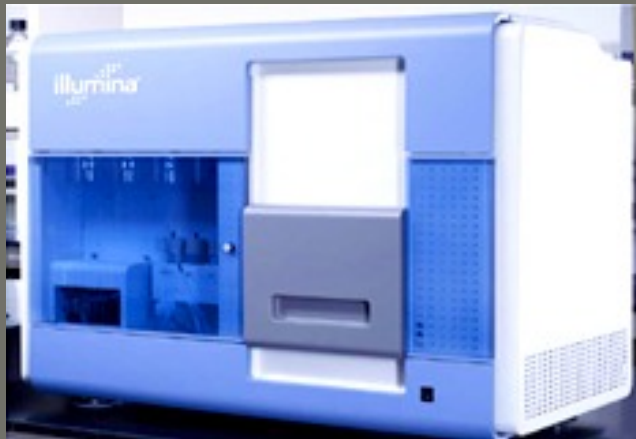
Roche 454



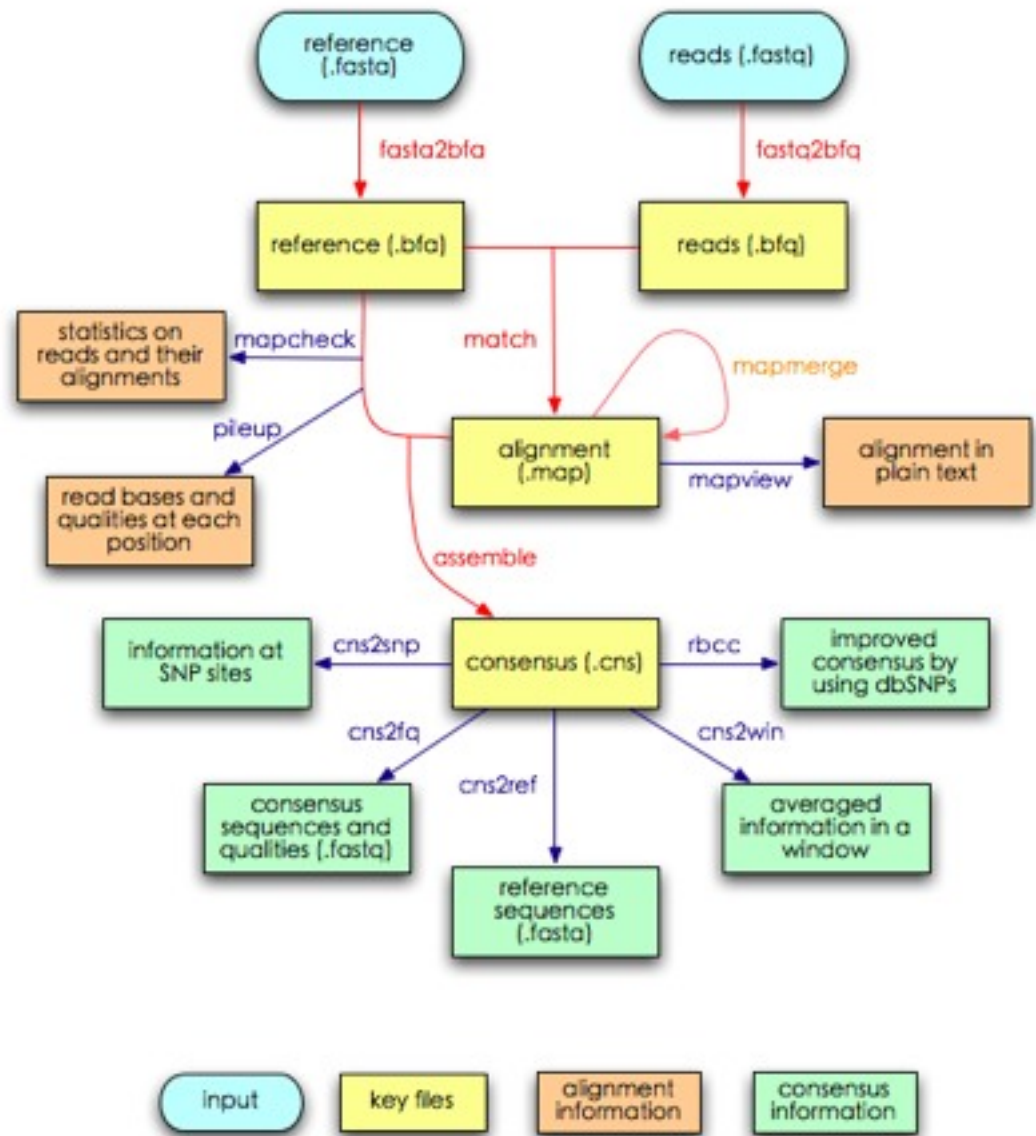


# Next-Generation sequencing nodes

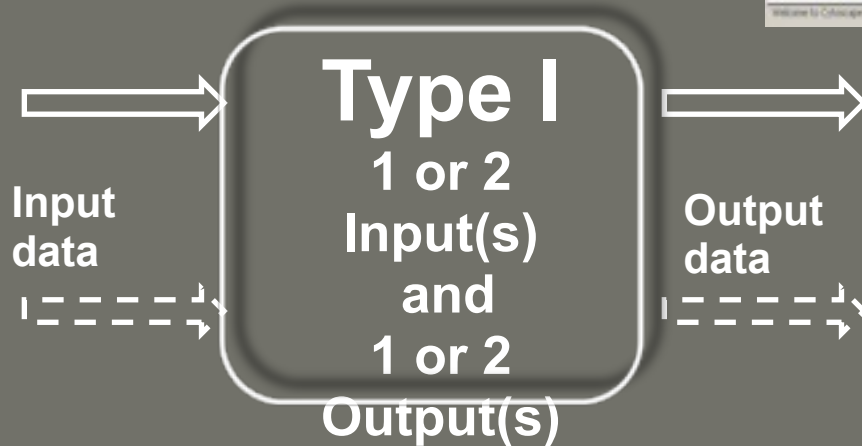
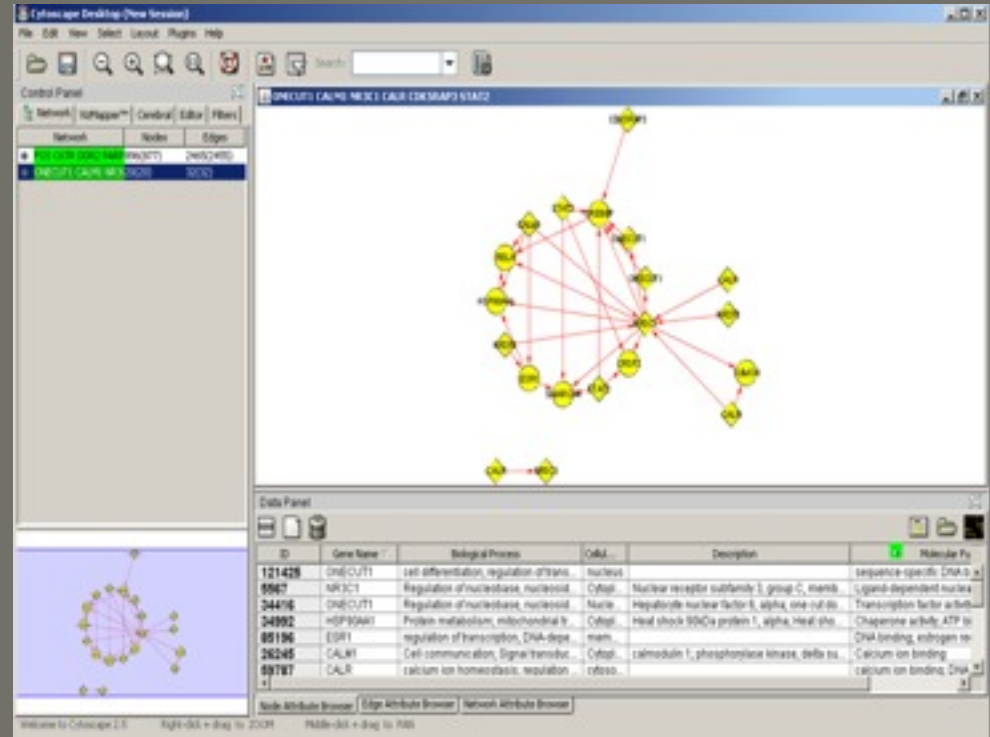
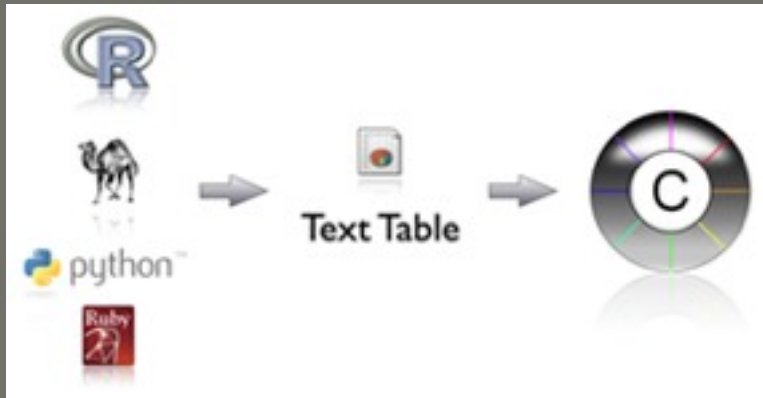
SOLEXA  
Illumina



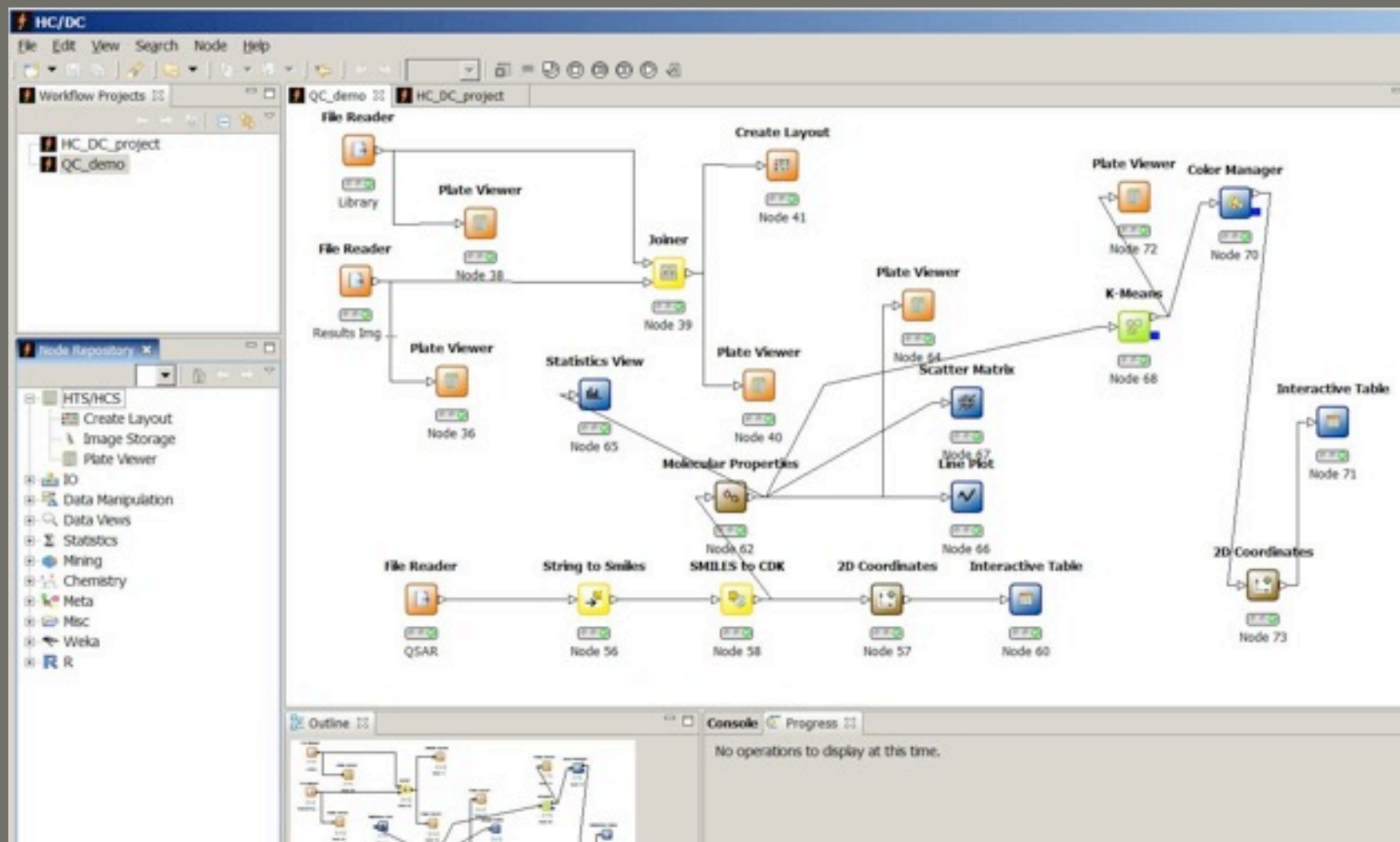
## Mapass2 Work Flow



# Proteomics



# Drag-and-drop



# Pioneering study

The screenshot displays the Orange data mining software interface. The main workspace contains a workflow with the following nodes and connections:

- File Reader** (top left) connects to **Plate Viewer** (Node 38).
- Library** (bottom left) connects to the top **Plate Viewer**.
- File Reader** (middle left) connects to **Plate Viewer** (Node 38) and **Results Img ...**.
- Results Img ...** connects to **Plate Viewer** (Node 38).
- Plate Viewer** (Node 38) connects to **Joiner** (Node 39).
- Joiner** (Node 39) connects to **Create Layout** (Node 41).
- Joiner** (Node 39) also connects to a **Plate Viewer** (bottom right).
- Statistics View** (bottom center) is also connected to the **Joiner**.

The **Node Description** panel on the right provides details for the **File Reader** node:

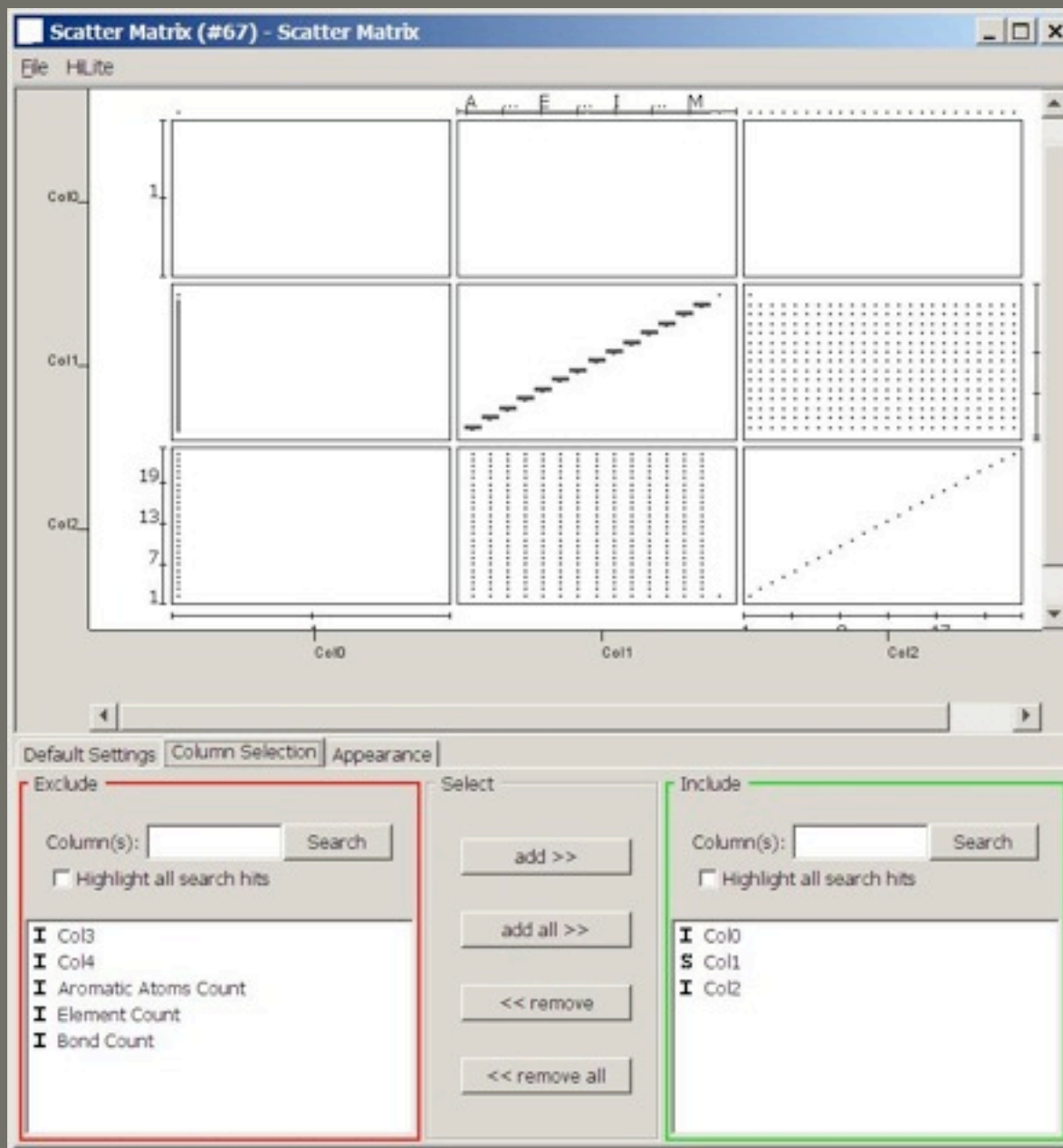
**File Reader**

This node can be used to read data from an ASCII file or URL location. It can be configured to read in various formats.

When you open the node's configuration dialog and provide a filename, it will try to guess the reader's settings by analyzing the beginning of the file. Check the results of these settings in the preview table. If the data shown is not correct or an error is reported, you can adjust the settings manually (see below).

When the node is executed it reads in the entire file and caches it in a temporary file for faster access by the connected successor nodes. It also stores all possible values it came across for each column.

# Plot image parameters/descriptors



# Compound screening

Key	Molecules	CAS RN	Available Renderers
742	<chem>CN(C)C(=O)OCC(=O)N=[N+]</chem>	115-02-6	Default Standard Double Percentage Gray Scale Bars
757	<chem>CCOC1=CC=C2C(=C1)C(=O)N(C)C2=O</chem>	64-86-8	
1026	<chem>C1CCN(C1)C(=O)O</chem>	52-52-8	
3024	<chem>O=C1=CC=C(C=C1)N</chem>	104-91-6	
4599	<chem>OS(=O)(=O)c1ccc(O)cc1</chem>	999-99-9	

**Molecular Properties**

Create new columns holding molecular properties, computed for each structure. The computations are based on the CDK (<http://cdk.sf.net>) toolkit and include logP, molecular weight, number of aromatic bonds, and many others.

**Dialog Options**

**Column Selection**  
Select the column containing the molecular structure.

**Properties**  
Move the available properties into the INCLUDE (left) list.

**Ports**

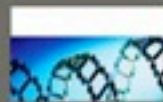
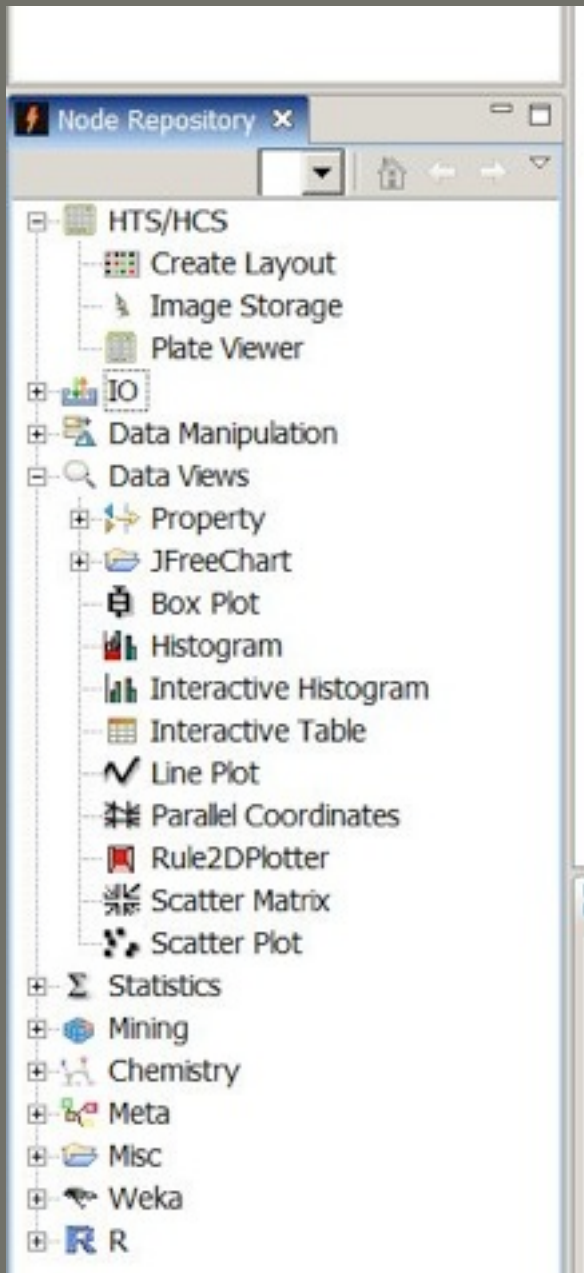
**Data Input**  
Table containing molecular structure based on which the properties should be calculated.

**Data Output**  
As input but with additional columns (one for each calculated property).

# Menu HC/DC

The screenshot displays a software interface with two main panels. On the left is the 'Node Repository' window, which contains a hierarchical tree of nodes. The tree is organized into several categories, each with a small icon: 'HTS/HCS' (grid icon), 'Data Manipulation' (person icon), 'Data Views' (magnifying glass icon), 'Statistics' (sum symbol icon), 'Mining' (globe icon), 'Chemistry' (molecule icon), 'Meta' (document icon), 'Misc' (folder icon), 'Weka' (umbrella icon), and 'R' (R logo icon). Under 'HTS/HCS', there are three sub-nodes: 'Create Layout' (grid icon), 'Image Storage' (image icon), and 'Plate Viewer' (grid icon). Under 'Data Views', there are ten sub-nodes: 'Property' (double-headed arrow icon), 'JFreeChart' (chart icon), 'Box Plot' (box plot icon), 'Histogram' (bar chart icon), 'Interactive Histogram' (bar chart icon), 'Interactive Table' (table icon), 'Line Plot' (line graph icon), 'Parallel Coordinates' (parallel lines icon), 'Rule2DPlotter' (rule icon), 'Scatter Matrix' (matrix icon), and 'Scatter Plot' (scatter plot icon). On the right is the 'File Reader' panel, which contains an orange 'File Reader' icon with a document and arrow, a yellow warning triangle icon, and a red stop icon. Below these icons is the text 'Node 2'. At the bottom of the interface is an 'Outline' panel, which shows a vertical list of icons corresponding to the nodes in the repository.

# Menu HC/DC



Instrument management

Data acquisition

Image processing

QC

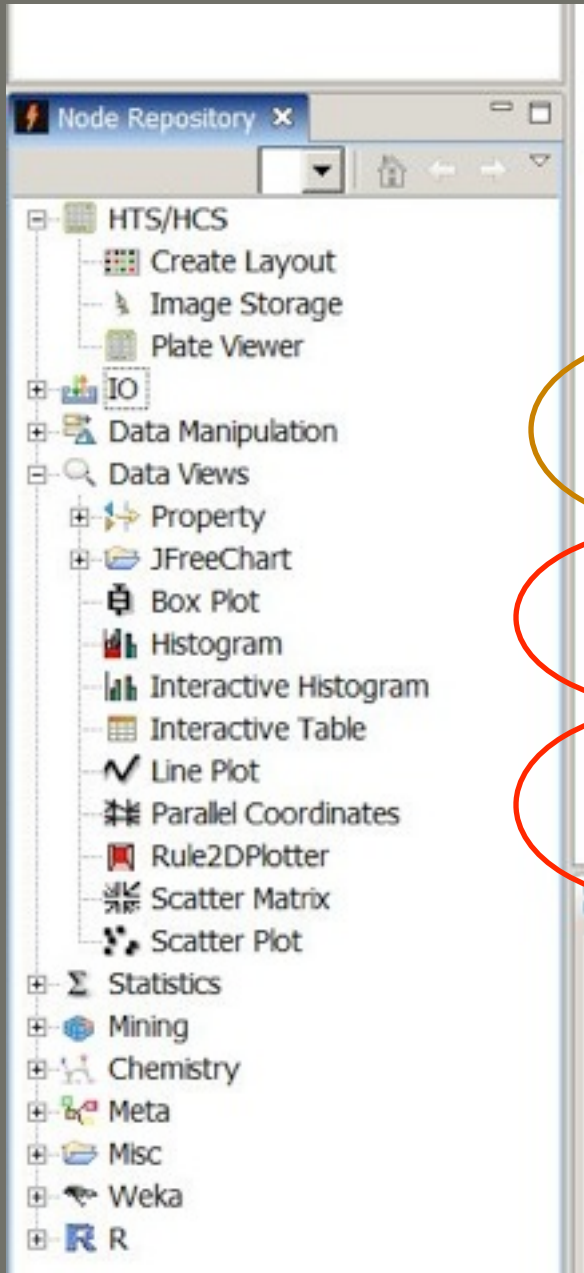
Data storage

Archiving

Data analysis,  
Bioinformatics



# Menu HC/DC



Instrument management

Data acquisition

Image processing

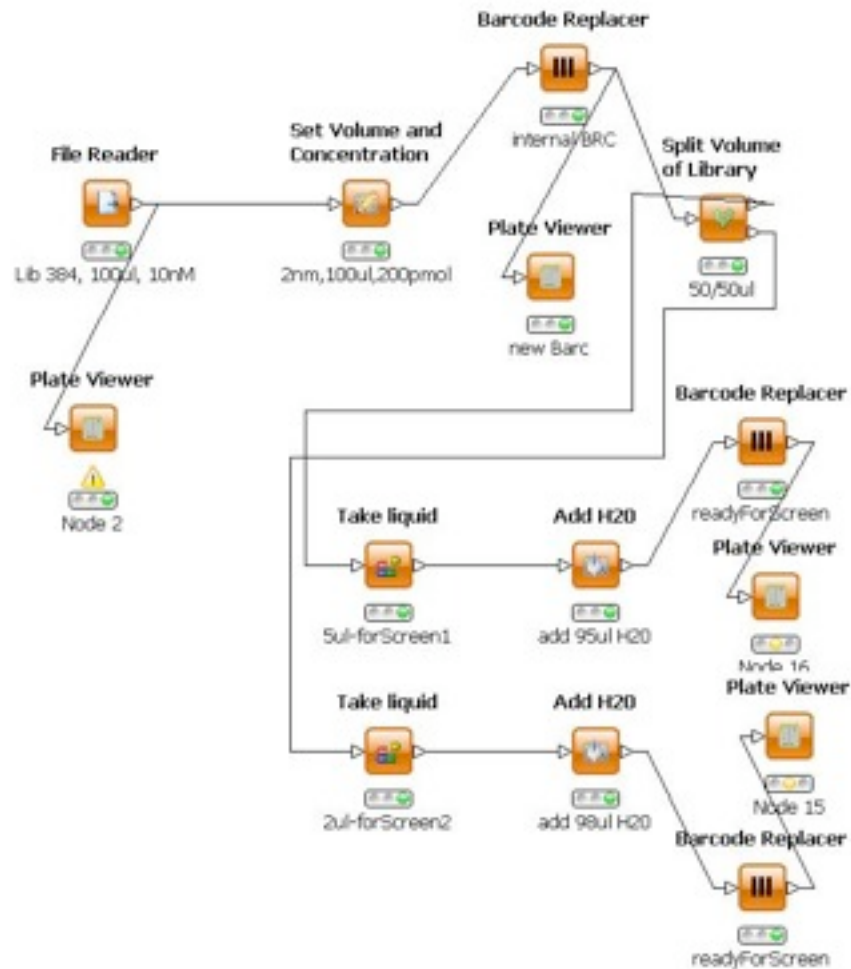
QC

Data storage

Archiving

Data analysis,  
Bioinformatics

# Library Handling

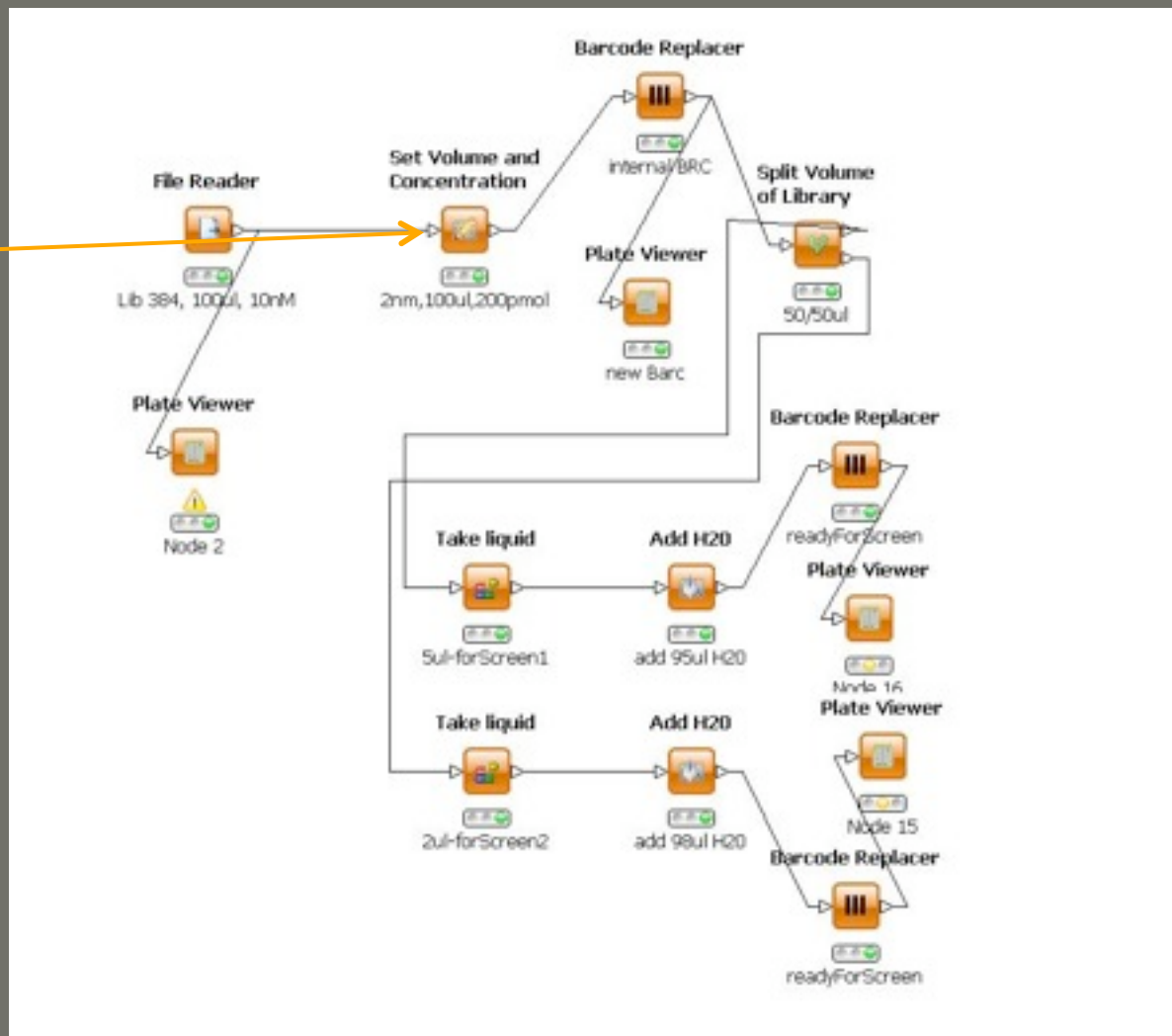


- HTS/HCS Library handling
  - Add H2O
  - Barcode Replacer
  - Barcode list
  - Set Volume and Concentration
  - Split Volume of Library
  - Take liquid
  - Take plates (Plate Filter)

# Library Handling

Data Automation:

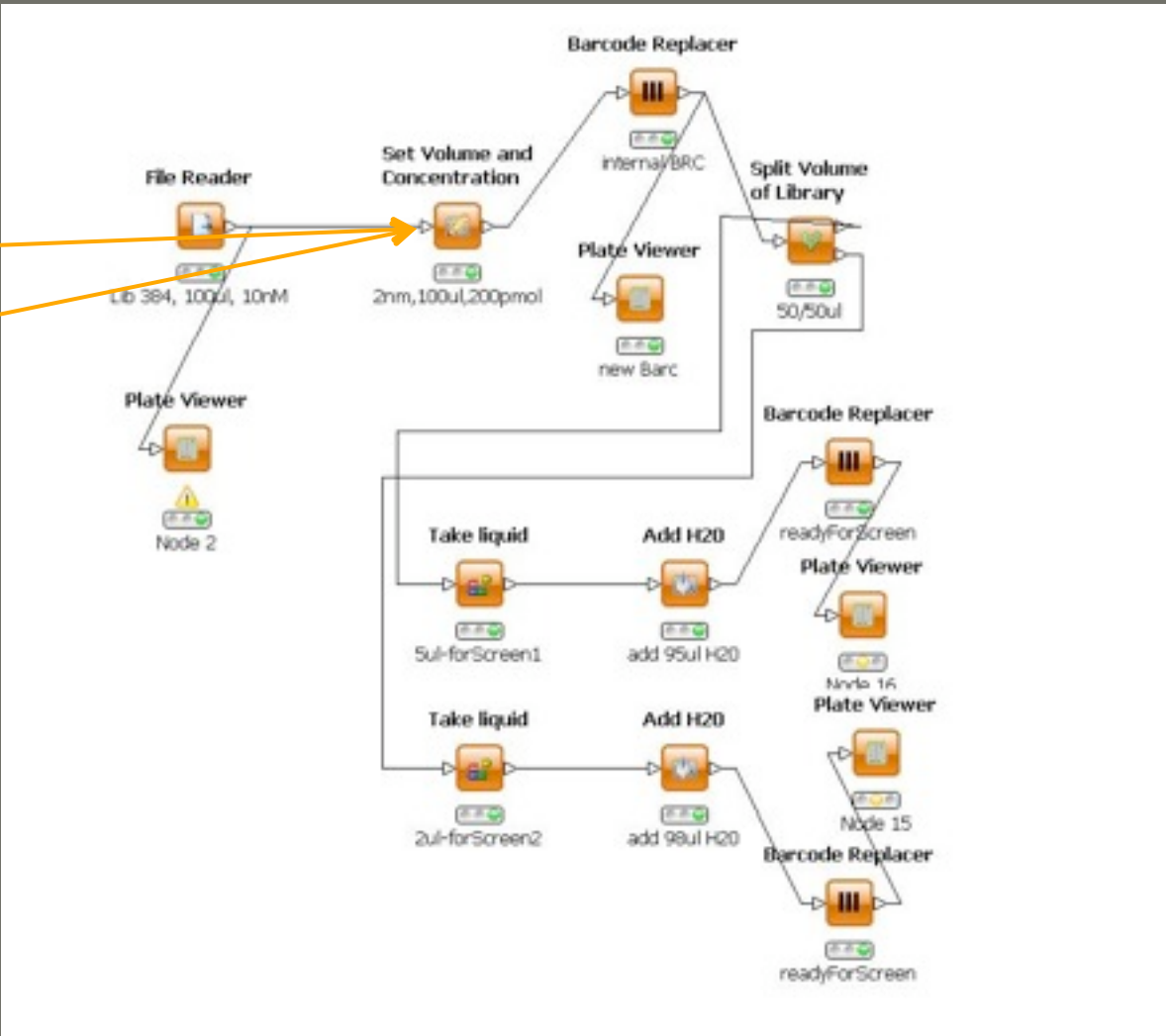
- HTS/HCS Library handling
  - Add H2O
  - Barcode Replacer
  - Barcode list
  - Set Volume and Concentration
  - Split Volume of Library
  - Take liquid
  - Take plates (Plate Filter)



# Library Handling

Data Automation:  
- Volume

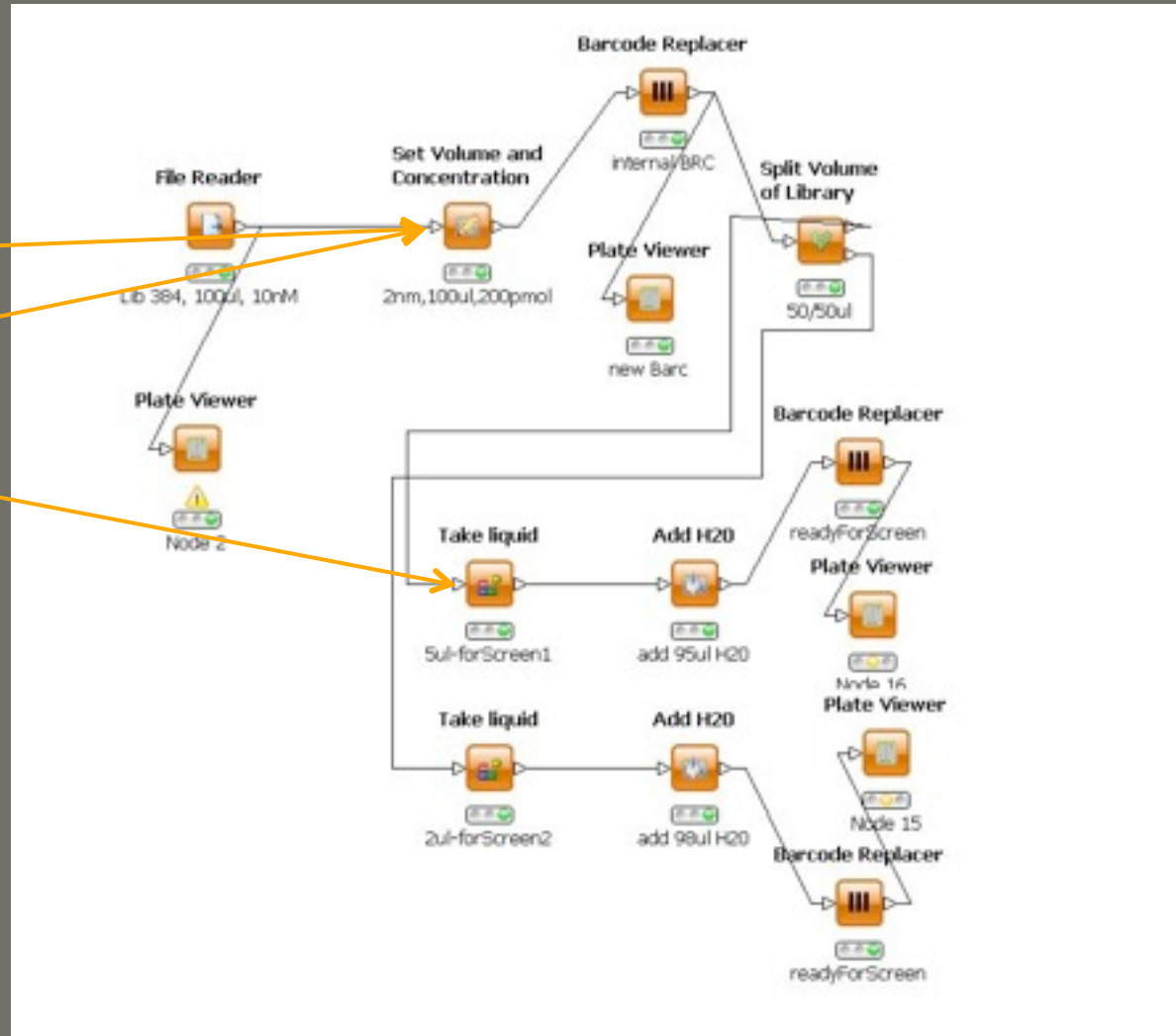
- HTS/HCS Library handling
  - Add H2O
  - Barcode Replacer
  - Barcode list
  - Set Volume and Concentration
  - Split Volume of Library
  - Take liquid
  - Take plates (Plate Filter)



# Library Handling

## Data Automation:

- Volume
- Concentration

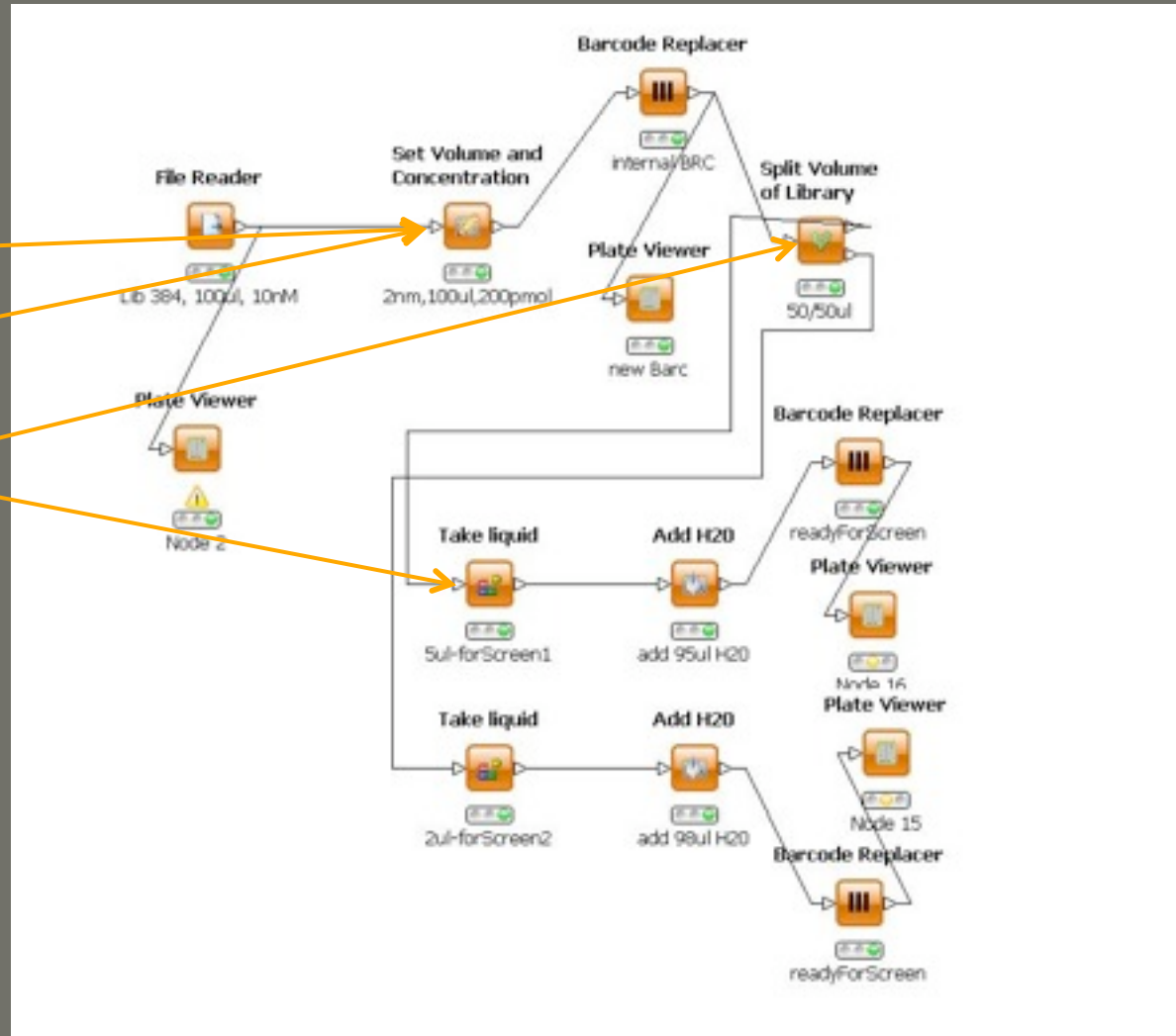


- HTS/HCS Library handling
  - Add H2O
  - Barcode Replacer
  - Barcode list
  - Set Volume and Concentration
  - Split Volume of Library
  - Take liquid
  - Take plates (Plate Filter)

# Library Handling

## Data Automation:

- Volume
- Concentration
- Dilutio

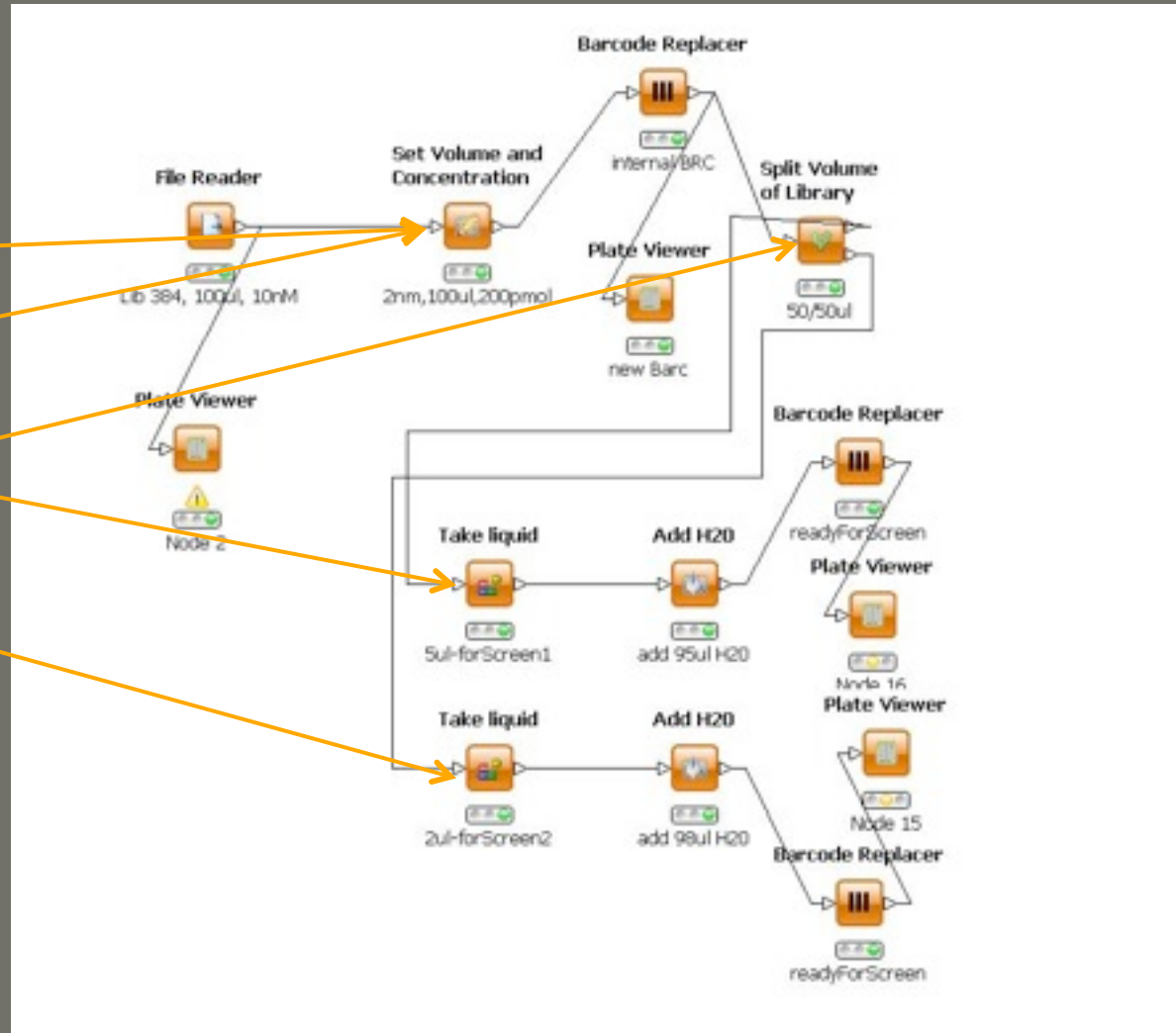


- HTS/HCS Library handling
  - Add H2O
  - Barcode Replacer
  - Barcode list
  - Set Volume and Concentration
  - Split Volume of Library
  - Take liquid
  - Take plates (Plate Filter)

# Library Handling

## Data Automation:

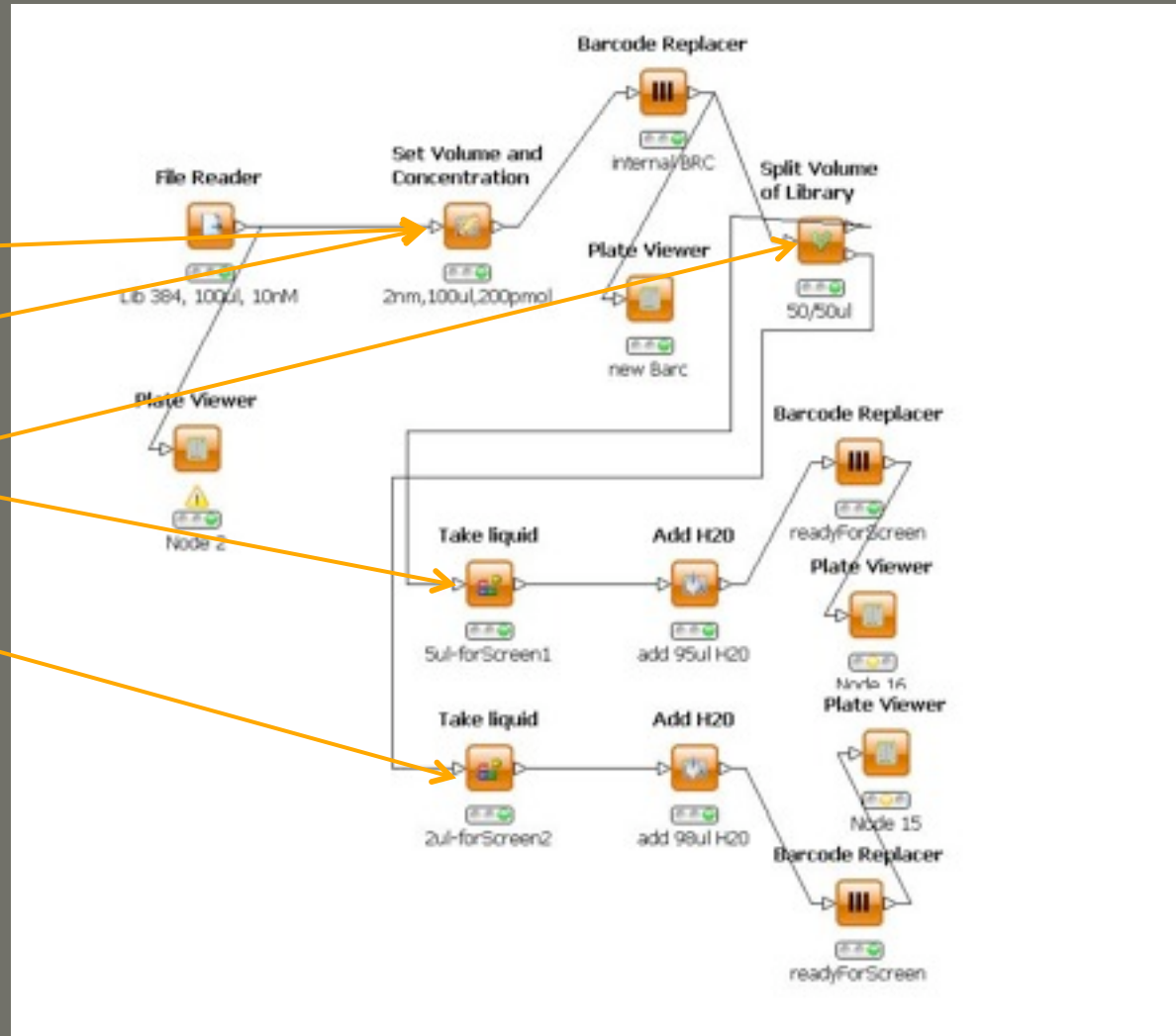
- Volume
- Concentration
- Dilutio
- Splitting



# Library Handling

## Data Automation:

- Volume
- Concentration
- Dilutio
- Splitting
- Take liquid

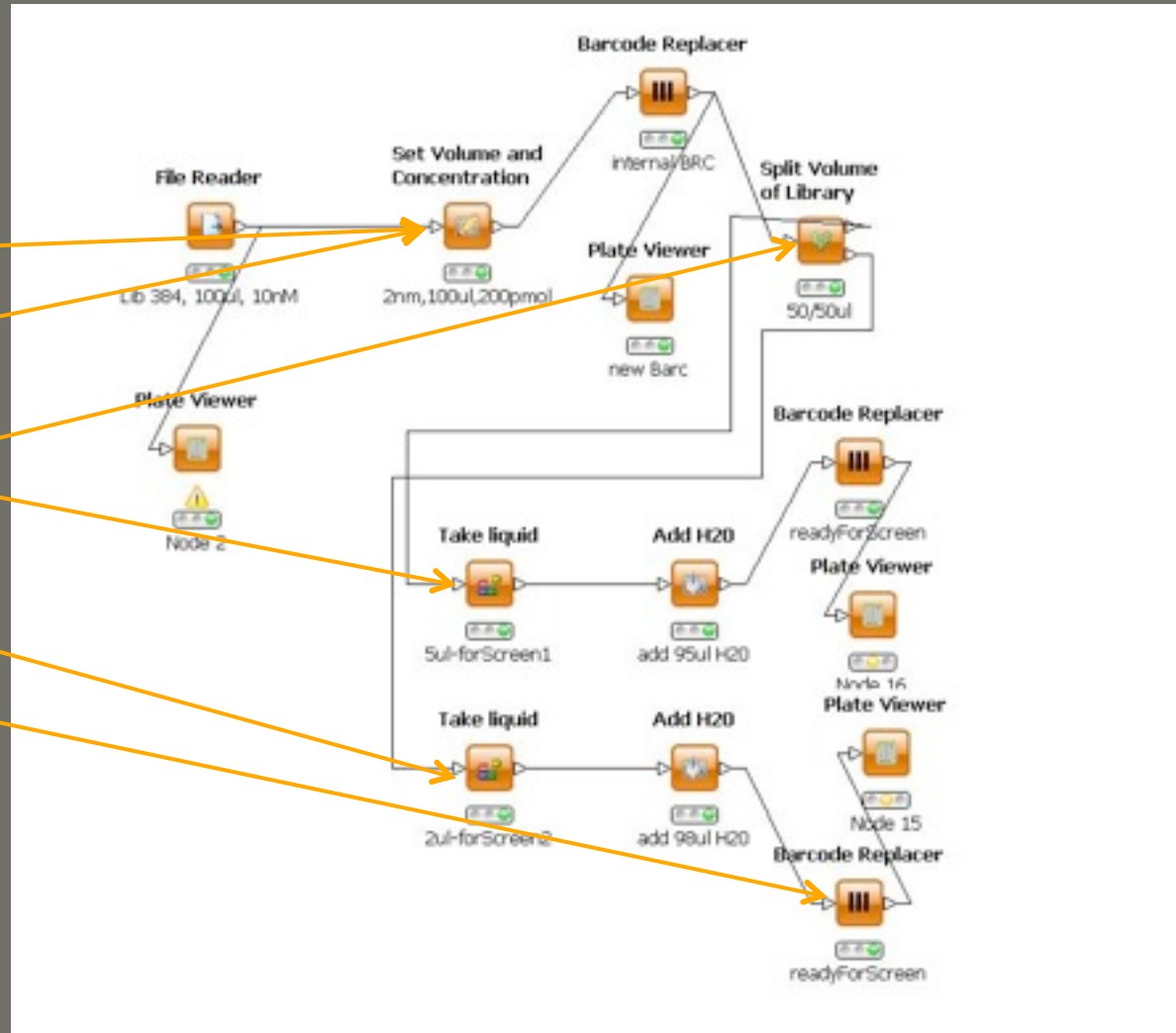




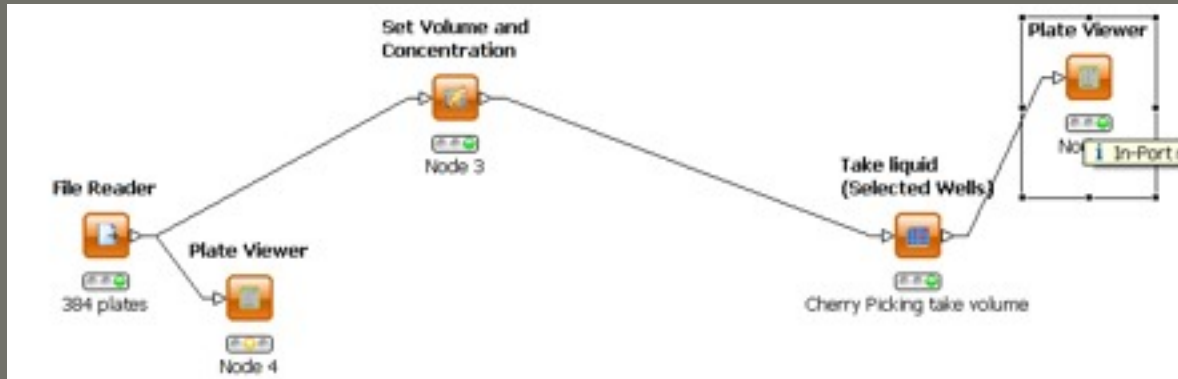
# Library Handling

## Data Automation:

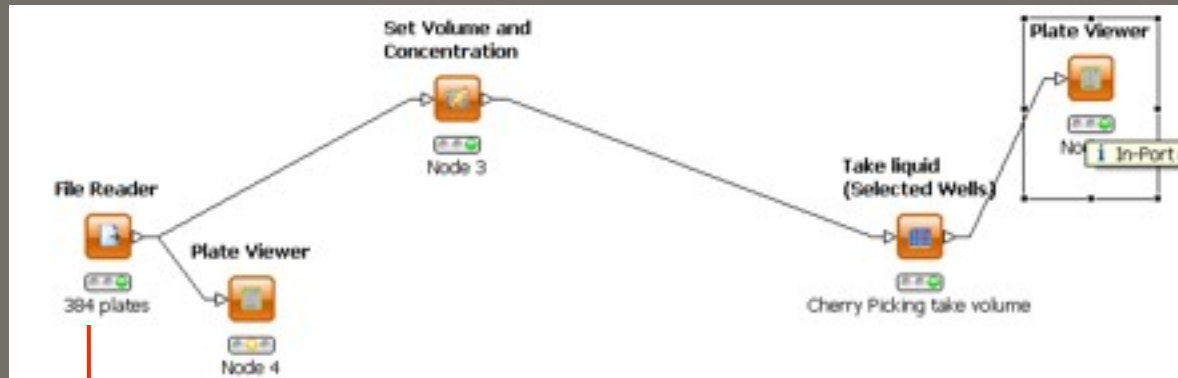
- Volume
- Concentration
- Dilutio
- Splitting
- Take liquid
- Barcode



# Workflows for HCS



# Workflows for HCS

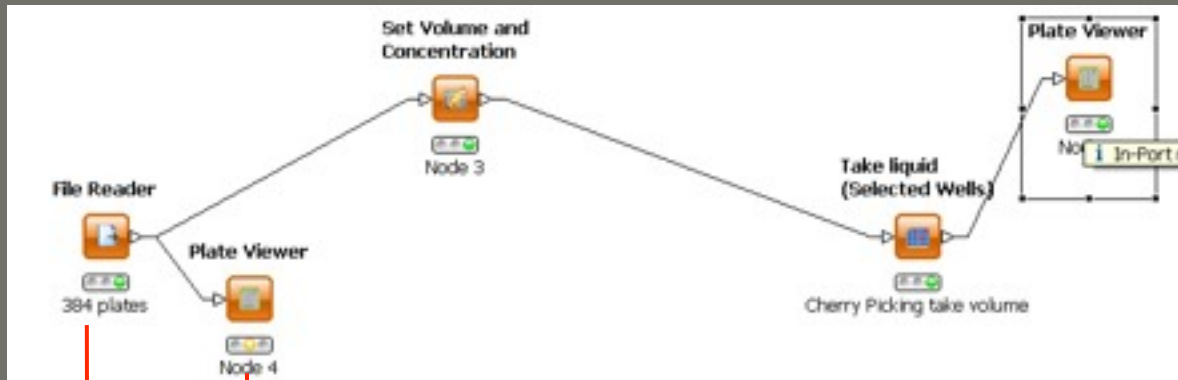


File Table - 6:1 - File Reader (384 plates)

Table "geneLibrary.txt" - Rows: 1152 | Spec - Columns: 13 | Properties

Row ID	Barcode	Row	Col	geneID	Symbol
Row0	2006-02-23_001	A	1	gene1	geneID_1
Row1	2006-02-23_001	A	2	gene2	geneID_2
Row2	2006-02-23_001	A	3	gene3	geneID_3
Row3	2006-02-23_001	A	4	gene4	geneID_4
Row4	2006-02-23_001	A	5	gene5	geneID_5
Row5	2006-02-23_001	A	6	gene6	geneID_6
Row6	2006-02-23_001	A	7	gene7	geneID_7
Row7	2006-02-23_001	A	8	gene8	geneID_8
Row8	2006-02-23_001	A	9	gene9	geneID_9
Row9	2006-02-23_001	A	10	gene10	geneID_10
Row10	2006-02-23_001	A	11	gene11	geneID_11
Row11	2006-02-23_001	A	12	gene12	geneID_12
Row12	2006-02-23_001	A	13	gene13	geneID_13
Row13	2006-02-23_001	A	14	gene14	geneID_14
Row14	2006-02-23_001	A	15	gene15	geneID_15
Row15	2006-02-23_001	A	16	gene16	geneID_16
Row16	2006-02-23_001	A	17	gene17	geneID_17
Row17	2006-02-23_001	A	18	gene18	geneID_18
Row18	2006-02-23_001	A	19	gene19	geneID_19
Row19	2006-02-23_001	A	20	gene20	geneID_20
Row20	2006-02-23_001	A	21	gene21	geneID_21
Row21	2006-02-23_001	A	22	gene22	geneID_22

# Workflows for HCS



File Table - 6:1 - File Reader (384 plates)

Table "genelibrary.txt" - Rows: 1152 | Spec - Columns: 13 | Properties

Row ID	Barcode	Row	Col	geneID	Symbol
Row0	2006-02-23_001	A	1	gene1	geneID_1
Row1	2006-02-23_001	A	2	gene2	geneID_2
Row2	2006-02-23_001	A	3	gene3	geneID_3
Row3	2006-02-23_001	A	4	gene4	geneID_4
Row4	2006-02-23_001	A	5	gene5	geneID_5
Row5	2006-02-23_001	A	6	gene6	geneID_6
Row6	2006-02-23_001	A	7	gene7	geneID_7
Row7	2006-02-23_001	A	8	gene8	geneID_8
Row8	2006-02-23_001	A	9	gene9	geneID_9
Row9	2006-02-23_001	A	10	gene10	geneID_10
Row10	2006-02-23_001	A	11	gene11	geneID_11
Row11	2006-02-23_001	A	12	gene12	geneID_12
Row12	2006-02-23_001	A	13	gene13	geneID_13
Row13	2006-02-23_001	A	14	gene14	geneID_14

3 rows of first view - 6:1 - Plate Viewer

File: genel

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
B	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
C	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

PlateView: 6 4 Barcode: 2004-02-23\_001  
 Row: 8  
 Col: 8  
 geneID: gene4  
 #plate: geneID\_6  
 productName: M1\_C0158\_11  
 #row: 004158 #R\_004158 #R\_001870 #R\_001870 #R\_001874 #R\_001874  
 productID: 830069079

# Workflows for HCS



File Table - 6:1 - File Reader (384 plates)

Table "geneLibrary.txt" - Rows: 1152 | Spec - Columns: 13 | Properties |

Row ID	Barcode	Row	Col	geneID	Symbol
Row0	2006-02-23_001	A	1	gene1	geneID_1
Row1	2006-02-23_001	A	2	gene2	geneID_2
Row2	2006-02-23_001	A	3	gene3	geneID_3
Row3	2006-02-23_001	A	4	gene4	geneID_4
Row4	2006-02-23_001	A	5	gene5	geneID_5
Row5	2006-02-23_001	A	6	gene6	geneID_6
Row6	2006-02-23_001	A	7	gene7	geneID_7
Row7	2006-02-23_001	A	8	gene8	geneID_8
Row8	2006-02-23_001	A	9	gene9	geneID_9
Row9	2006-02-23_001	A	10	gene10	geneID_10
Row10	2006-02-23_001	A	11	gene11	geneID_11
Row11	2006-02-23_001	A	12	gene12	geneID_12
Row12	2006-02-23_001	A	13	gene13	geneID_13
Row13	2006-02-23_001	A	14	gene14	geneID_14

Dialog - 6:3 - Set Volume and Co...

File

Settings | Flow Variables | General Node Settings

Initial concentration [nM]  Calculate this

Initial volume [µl]  Calculate this

Initial amount [pmol]  Calculate this

Name of concentration column

Name of volume column

Name of amount column

OK Apply Cancel

3 rows of first view - 6:4 - Plate Viewer

File: gene

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
B	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
C	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
D	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
E	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
F	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
G	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
H	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
I	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
J	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
K	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
L	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
M	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
N	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
O	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
P	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
Q	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
R	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
S	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
T	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
U	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
V	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
W	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
X	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
Y	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
Z	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

PlateView: 8 x 8 Barcode: 2004-02-23\_001

Row: 8

Col: 8

geneID: gene4

#plate: geneID\_6

productName: M\_C0158\_11

workstationID: NR\_004150 NR\_001870 NR\_001870 NR\_001870 NR\_001870

productID: 830069079

# Workflows for HCS



File Table - 6:1 - File Reader (384 plates)

Table "genelibrary.txt" - Rows: 1152 | Spec - Columns: 13 | Properties |

Row ID	Barcode	Row	Col	geneID	Symbol
Row0	2006-02-23_001	A	1	gene1	geneID_1
Row1	2006-02-23_001	A	2	gene2	geneID_2
Row2	2006-02-23_001	A	3	gene3	geneID_3
Row3	2006-02-23_001	A	4	gene4	geneID_4
Row4	2006-02-23_001	A	5	gene5	geneID_5
Row5	2006-02-23_001	A	6	gene6	geneID_6
Row6	2006-02-23_001	A	7	gene7	geneID_7
Row7	2006-02-23_001	A	8	gene8	geneID_8
Row8	2006-02-23_001	A	9	gene9	geneID_9
Row9	2006-02-23_001	A	10	gene10	geneID_10
Row10	2006-02-23_001	A	11	gene11	geneID_11
Row11	2006-02-23_001	A	12	gene12	geneID_12
Row12	2006-02-23_001	A	13	gene13	geneID_13
Row13	2006-02-23_001	A	14	gene14	geneID_14

Dialog - 6:3 - Set Volume and Co...

Settings | Flow Variables | General Node Settings |

Initial concentration [nM]  Calculate this

Initial volume [µl]  Calculate this

Initial amount [pmol]  Calculate this

Name of concentration column

Name of volume column

Name of amount column

OK Apply Cancel

Dialog - 6:2 - Take liquid (Selected Wells) (Cherry Picking take v...

Settings | Flow Variables | General Node Settings |

Selected wells: A1,A2,B1,B2,C1,C2,M1,M2,O1,O2,

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
B	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
C	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
D	<input type="checkbox"/>	<input type="checkbox"/>																						
E	<input type="checkbox"/>	<input type="checkbox"/>																						
F	<input type="checkbox"/>	<input type="checkbox"/>																						
G	<input type="checkbox"/>	<input type="checkbox"/>																						
H	<input type="checkbox"/>	<input type="checkbox"/>																						
I	<input type="checkbox"/>	<input type="checkbox"/>																						
J	<input type="checkbox"/>	<input type="checkbox"/>																						
K	<input type="checkbox"/>	<input type="checkbox"/>																						
L	<input type="checkbox"/>	<input type="checkbox"/>																						
M	<input type="checkbox"/>	<input type="checkbox"/>																						
N	<input type="checkbox"/>	<input type="checkbox"/>																						
O	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
P	<input type="checkbox"/>	<input type="checkbox"/>																						

Take amount [pmol]  Max to take: 210.0

Take volume [µl]  Max to take: 100.0

New concentration [nM]

Calculate next

Review of first view - 6:4 - Plate Viewer

File: genel

gene	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
B	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
C	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
D	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
E	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
F	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
G	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
H	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
I	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
J	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
K	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
L	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
M	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
N	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
O	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
P	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK

Position: B 4 Barcode: 2004-02-23\_001

Row: B

Col: 4

geneID: gene4

Symbol: geneID\_4

Product Name: M4\_C00158\_13

Product Barcode: NR\_004159 NR\_004160 NR\_004161 NR\_004162 NR\_004163 NR\_004164 NR\_004165

Product ID: 830045979

# Workflows for HCS



File Table - 6:1 - File Reader (384 plates)

Row ID	Barcode	Row	Col	geneID	Symbol
Row0	2006-02-23_001	A	1	gene1	geneID_1
Row1	2006-02-23_001	A	2	gene2	geneID_2
Row2	2006-02-23_001	A	3	gene3	geneID_3
Row3	2006-02-23_001	A	4	gene4	geneID_4
Row4	2006-02-23_001	A	5	gene5	geneID_5
Row5	2006-02-23_001	A	6	gene6	geneID_6
Row6	2006-02-23_001	A	7	gene7	geneID_7
Row7	2006-02-23_001	A	8	gene8	geneID_8
Row8	2006-02-23_001	A	9	gene9	geneID_9
Row9	2006-02-23_001	A	10	gene10	geneID_10
Row10	2006-02-23_001	A	11	gene11	geneID_11
Row11	2006-02-23_001	A	12	gene12	geneID_12
Row12	2006-02-23_001	A	13	gene13	geneID_13
Row13	2006-02-23_001	A	14	gene14	geneID_14

Dialog - 6:3 - Set Volume and Co...

Settings | Flow Variables | General Node Settings

Initial concentration [nM]  Calculate this

Initial volume [µl]  Calculate this

Initial amount [pmol]  Calculate this

Name of concentration column

Name of volume column

Name of amount column

OK Apply Cancel

row view of first view - 6:4 - Plate Viewer

gene	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
B	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
C	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
D	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
E	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
F	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
G	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
H	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
I	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
J	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
K	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
L	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
M	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
N	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
O	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
P	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK

Plate View: 8 x 4 Barcode: 2004-02-23\_001  
 Row: 8  
 Col: 8  
 geneID: gene4  
 #plate: geneID\_6  
 productName: NS\_C0158\_11  
 #rowBarcode: NR\_004159 NR\_004160 NR\_004161 NR\_004162 NR\_004163 NR\_004164 NR\_004165  
 productID: 830463979

Out-Port name - 6:2 - Take liquid (Selected Wells) (Cherry Pick)

Row ID	Barcode	Row	Col	geneID	Symbol	prod
Row0	2006-02-23_001	A	1	gene1	geneID_1	NS_A01
Row1	2006-02-23_001	A	2	gene2	geneID_2	NS_A02
Row24	2006-02-23_001	B	1	gene1	geneID_1	NS_A03
Row25	2006-02-23_001	B	2	gene2	geneID_2	NS_A04
Row48	2006-02-23_001	C	1	gene1	geneID_1	NS_A05
Row49	2006-02-23_001	C	2	gene2	geneID_2	NS_A06
Row112	2006-02-23_001	N	1	gene1	geneID_1	?
Row113	2006-02-23_001	N	2	gene2	geneID_2	NS_P006
Row106	2006-02-23_001	O	1	gene1	geneID_1	NS_P007
Row107	2006-02-23_001	O	2	gene2	geneID_2	NS_P008
Row94	2006-02-23_001	A	1	gene1	geneID_1	NS_O01
Row95	2006-02-23_001	A	2	gene2	geneID_2	NS_O02
Row408	2006-02-23_001	B	1	gene1	geneID_1	NS_P011
Row409	2006-02-23_001	B	2	gene2	geneID_2	NS_P012
...	...	...	...	...	...	...

Dialog - 6:2 - Take liquid (Selected Wells)

Settings | Flow Variables | General Node Settings

Selected wells: A1,A2,B1,B2,C1,C2,N1,N2,O1,O2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
B	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
C	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
D																								
E																								
F																								
G																								
H																								
I																								
J																								
K																								
L																								
M																								
N	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
O	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>																						
P																								

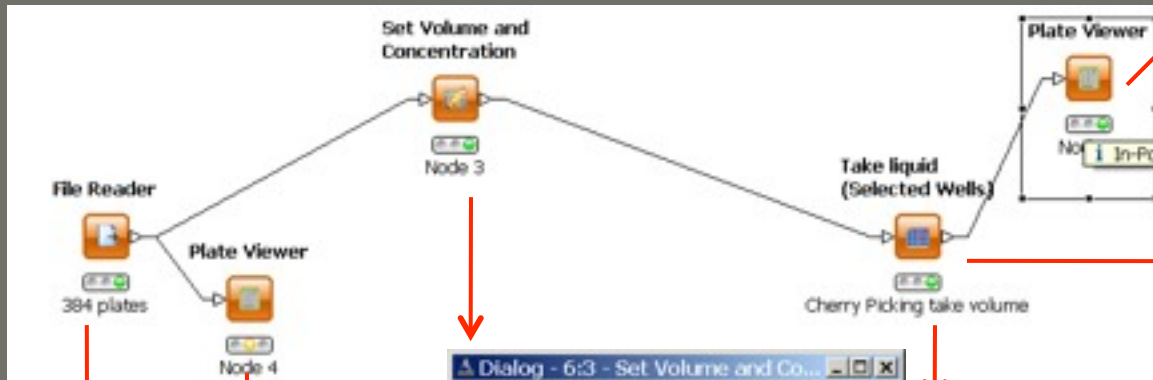
Take amount [pmol]  Max to take: 210.0

Take volume [µl]  Max to take: 100.0

New concentration [nM]

Calculate next

# Workflows for HCS



File Table - 6:1 - File Reader (384 plates)

Row ID	Barcode	Row	Col	geneID	Symbol
Row0	2006-02-23_001	A	1	gene1	geneID_1
Row1	2006-02-23_001	A	2	gene2	geneID_2
Row2	2006-02-23_001	A	3	gene3	geneID_3
Row3	2006-02-23_001	A	4	gene4	geneID_4
Row4	2006-02-23_001	A	5	gene5	geneID_5
Row5	2006-02-23_001	A	6	gene6	geneID_6
Row6	2006-02-23_001	A	7	gene7	geneID_7
Row7	2006-02-23_001	A	8	gene8	geneID_8
Row8	2006-02-23_001	A	9	gene9	geneID_9
Row9	2006-02-23_001	A	10	gene10	geneID_10
Row10	2006-02-23_001	A	11	gene11	geneID_11
Row11	2006-02-23_001	A	12	gene12	geneID_12
Row12	2006-02-23_001	A	13	gene13	geneID_13
Row13	2006-02-23_001	A	14	gene14	geneID_14

Dialog - 6:3 - Set Volume and Co...

Settings | Flow Variables | General Node Settings

Initial concentration [nM]  Calculate this

Initial volume [µl]  Calculate this

Initial amount [pmol]  Calculate this

Name of concentration column

Name of volume column

Name of amount column

OK Apply Cancel

row(s) of first view - 6:4 - Plate Viewer

Row	Col	geneID	Symbol
Row 8	Col 1	gene1	geneID_1
Row 8	Col 2	gene2	geneID_2
Row 8	Col 3	gene3	geneID_3
Row 8	Col 4	gene4	geneID_4
Row 8	Col 5	gene5	geneID_5
Row 8	Col 6	gene6	geneID_6
Row 8	Col 7	gene7	geneID_7
Row 8	Col 8	gene8	geneID_8
Row 8	Col 9	gene9	geneID_9
Row 8	Col 10	gene10	geneID_10
Row 8	Col 11	gene11	geneID_11
Row 8	Col 12	gene12	geneID_12
Row 8	Col 13	gene13	geneID_13
Row 8	Col 14	gene14	geneID_14

row(s) of first view - 6:5 - Plate Viewer

Row ID	Barcode	Row	Col	geneID	Symbol	product
Row0	2006-02-23_001	A	1	gene1	geneID_1	hs_ACP1
Row1	2006-02-23_001	A	2	gene2	geneID_2	hs_APL1
Row2	2006-02-23_001	A	3	gene3	geneID_3	hs_CDC1
Row3	2006-02-23_001	A	4	gene4	geneID_4	hs_DUSP
Row4	2006-02-23_001	A	5	gene5	geneID_5	hs_JUPB
Row5	2006-02-23_001	A	6	gene6	geneID_6	?
Row6	2006-02-23_001	A	7	gene7	geneID_7	hs_P396
Row7	2006-02-23_001	A	8	gene8	geneID_8	hs_P396
Row8	2006-02-23_001	A	9	gene9	geneID_9	hs_P396
Row9	2006-02-23_001	A	10	gene10	geneID_10	hs_P396
Row10	2006-02-23_001	A	11	gene11	geneID_11	hs_P396
Row11	2006-02-23_001	A	12	gene12	geneID_12	hs_P396
Row12	2006-02-23_001	A	13	gene13	geneID_13	hs_P396
Row13	2006-02-23_001	A	14	gene14	geneID_14	hs_P396

Dialog - 6:2 - Take liquid (

Settings | Flow Variables | General Node Settings

Selected wells: A1,A2,B1,B2,C1,C2,N1,N2,O1,O2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
B	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
C	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
D	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
E	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
F	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
G	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
H	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
I	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
J	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
K	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
L	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
M	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
N	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
O	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
P	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

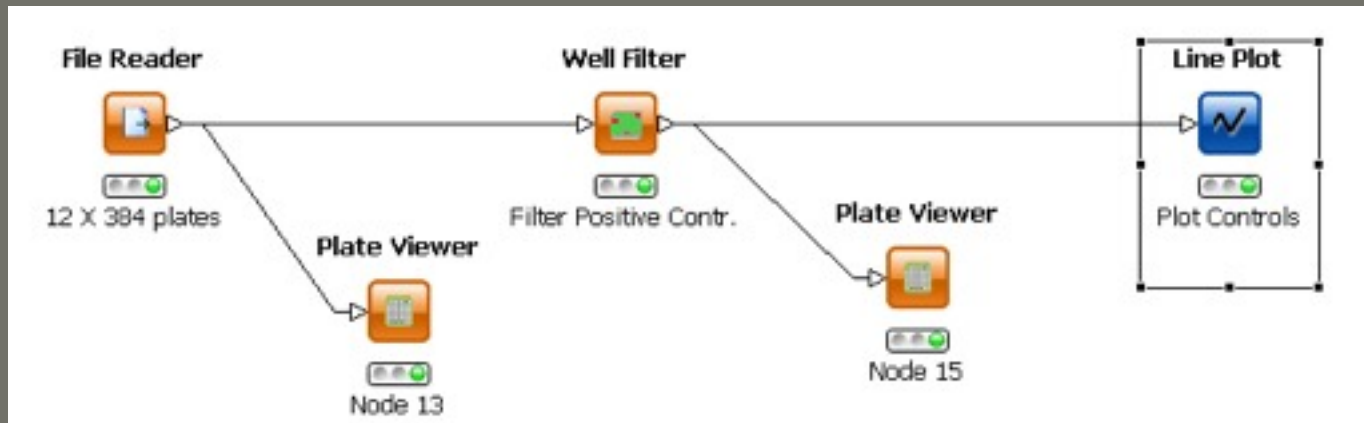
Take amount [pmol]  Max to take: 210.0

Take volume [µl]  Max to take: 100.0

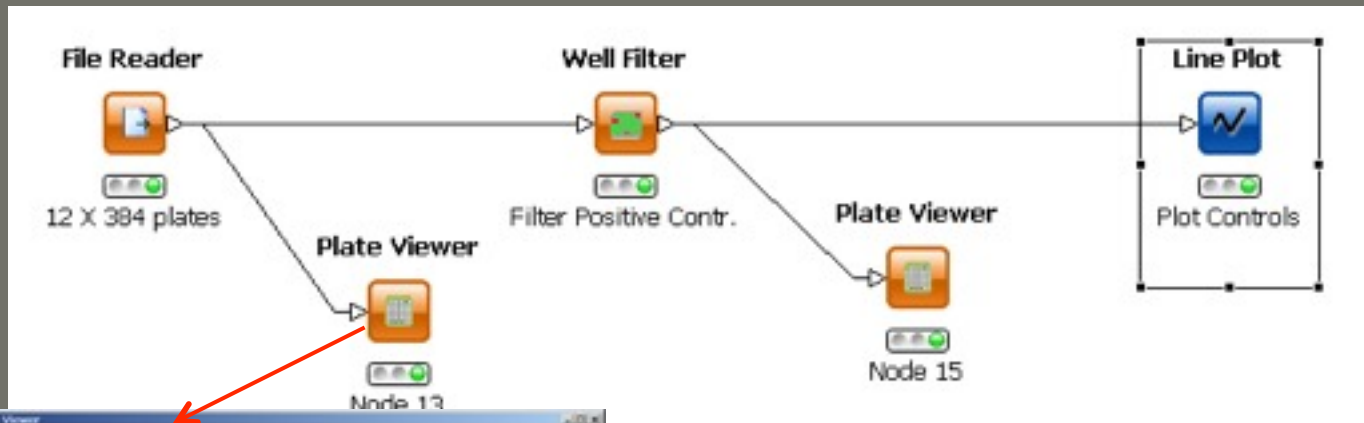
New concentration [nM]  Calculate next



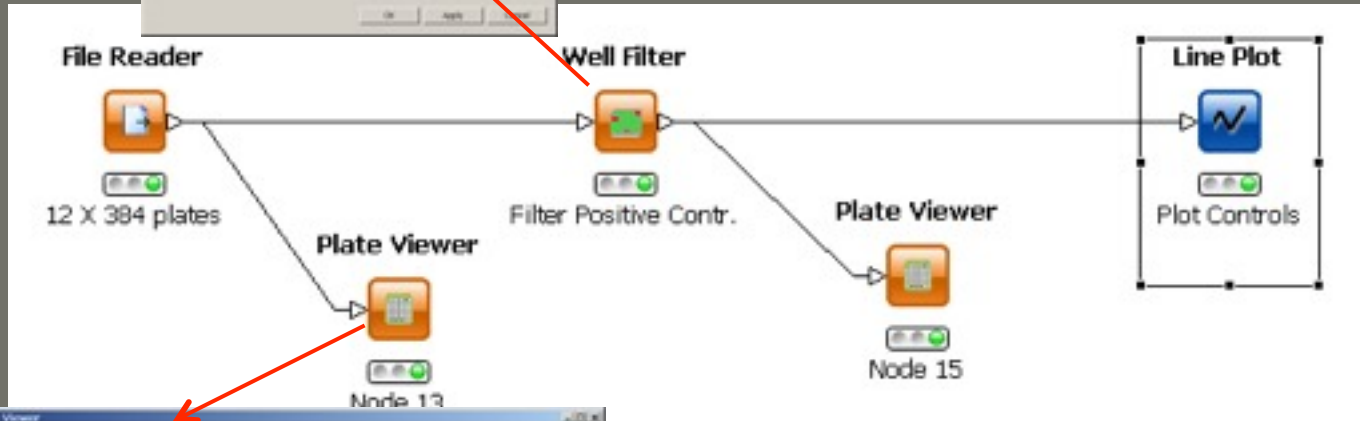
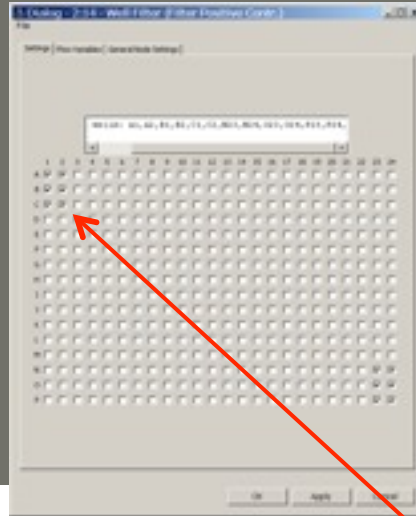
# Workflows for HCS



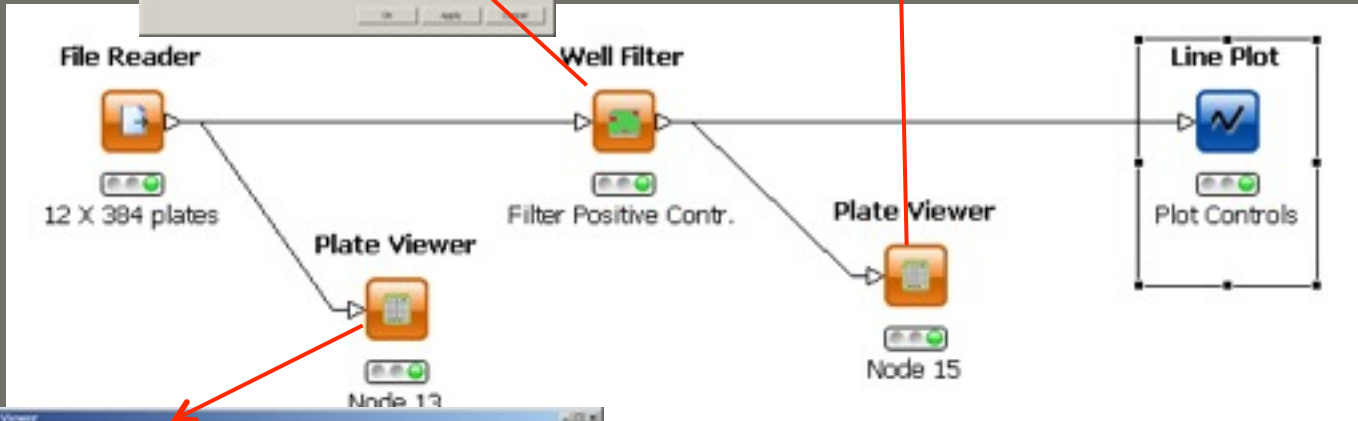
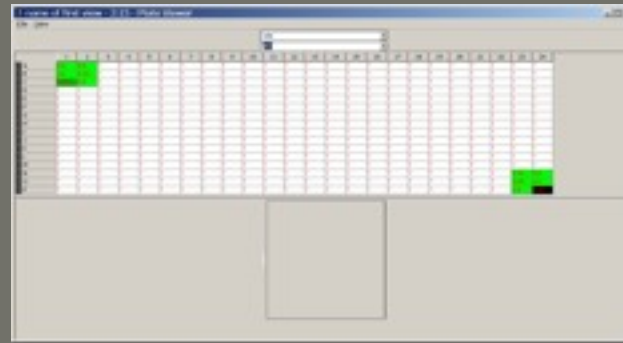
# Workflows for HCS



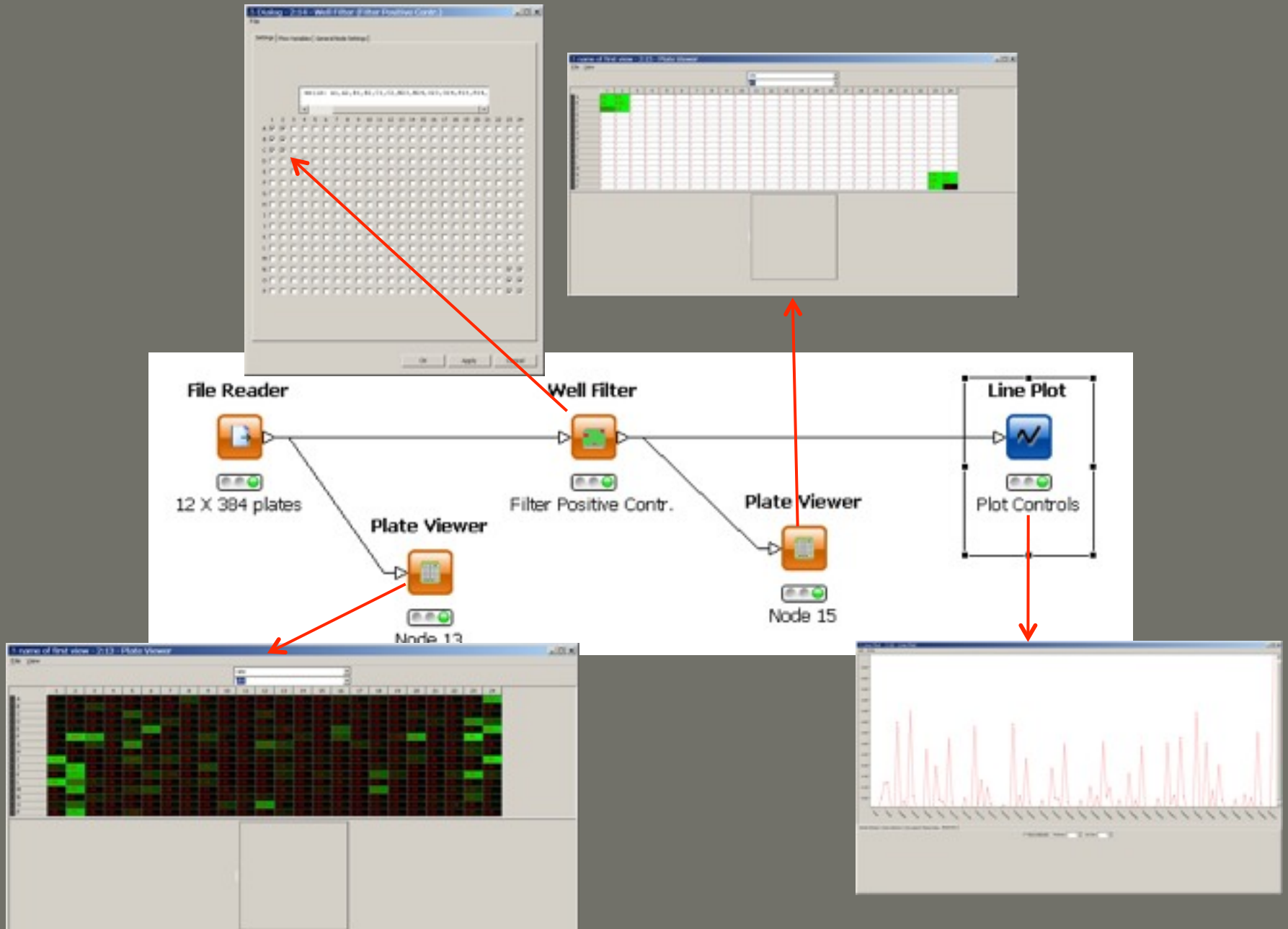
# Workflows for HCS



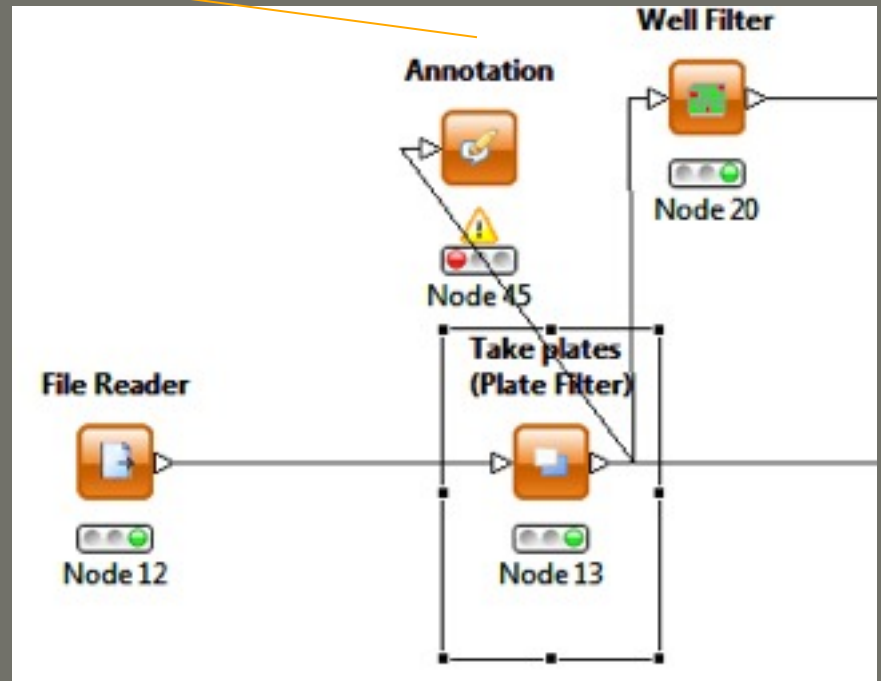
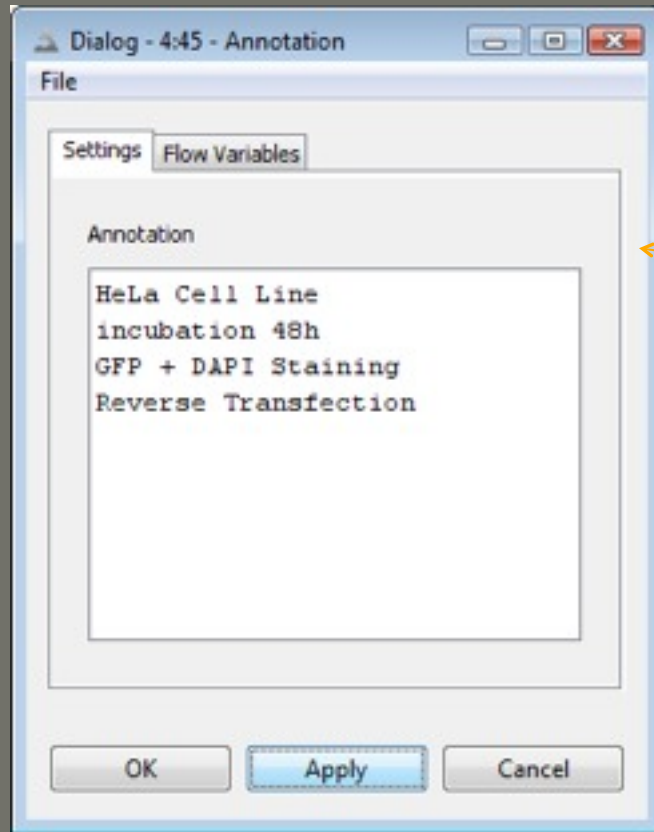
# Workflows for HCS



# Workflows for HCS



# Workflows for HCS



# Workflows for HCS

## BD Pathway Reader



Node 40

## MD ImageXpress Reader



Node 41

## MIAS-2 Reader



Node 42

## Opera Reader

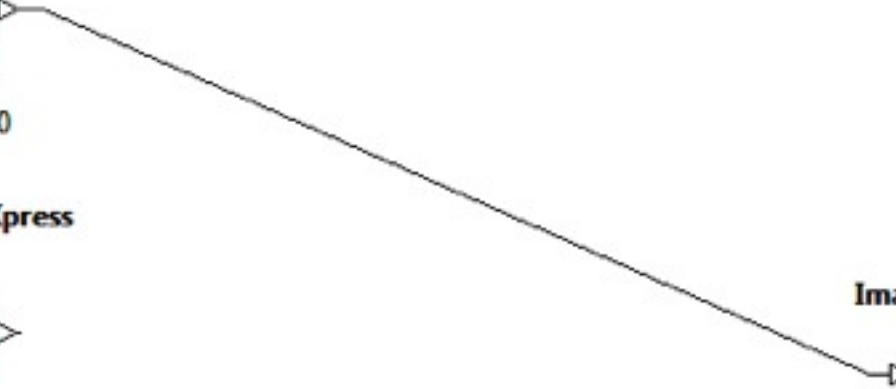


Node 43

## Image Viewer



Node 44



# Workflows for HCS

## BD Pathway Reader



Node 40

## MD ImageXpress Reader



Node 41

## MIAS-2 Reader



Node 42

## Opera Reader

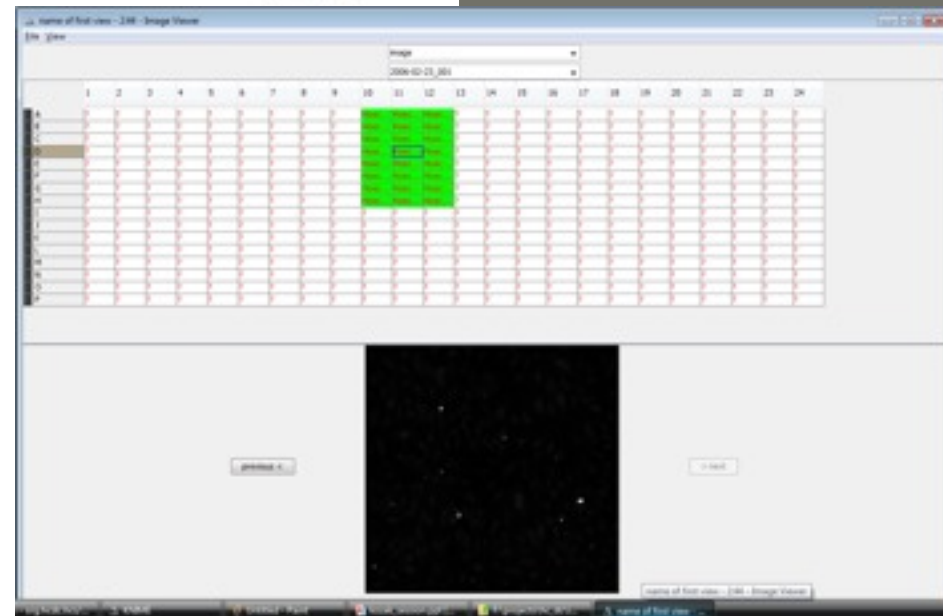


Node 43

## Image Viewer



Node 44





# Workflows for HCS



## BD Pathway Reader



Node 40

## MD ImageXpress Reader



Node 41

## MIAS-2 Reader



Node 42

## Opera Reader

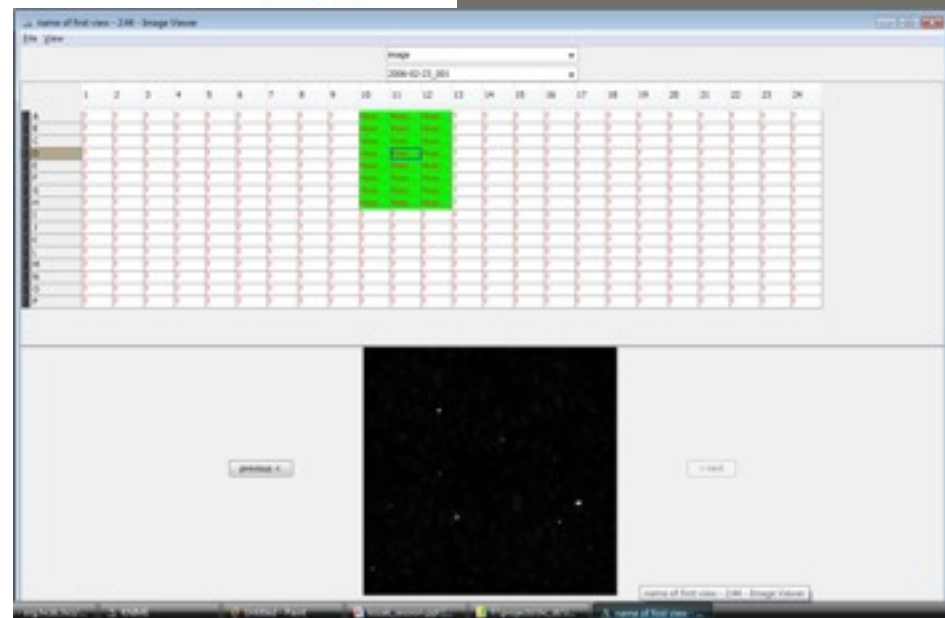
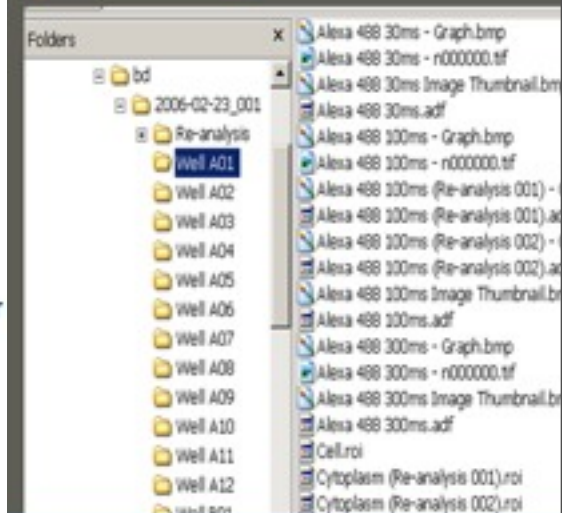


Node 43

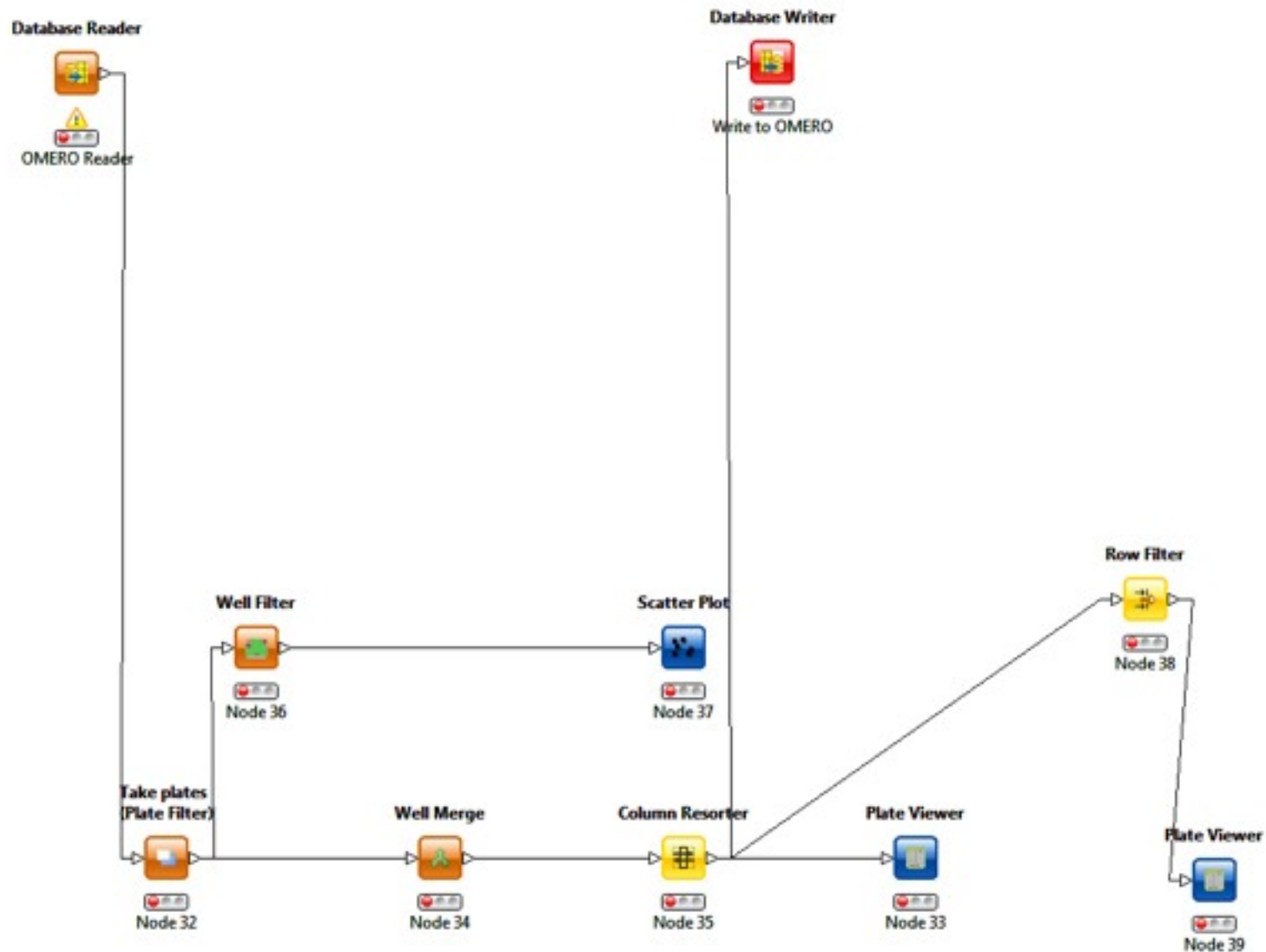
## Image Viewer



Node 44



# Link to OME/OMERO



# Acknowledgements & Partners:

**ETH**

Eidgenössische Technische Hochschule Zürich  
Swiss Federal Institute of Technology Zurich



**KNIME**

Konstanz Information Miner

# Acknowledgements & Partners:



Contribution in development:



**MPI-CBG, Dresden**

Eberhard Krausz (former) & team  
Eugenio Fava & team  
Marc Bickle & team



**ETH Zurich**

**LMC-RISC**: Gabor Csucs & team  
**SystemX** Adrian Honegger & team



**MPI-IB, Berlin**

Nikolaus Machuy & team



# WebPage

HCDC: <http://hcdc.ethz.ch>

Workshops HCDC+ KNIME:

16-17.10.2009

2 days ETH Zurich