

The BioPhenics Platform

*High Content Screening for Large Scale Functional Biology,
Drug Discovery & Target Validation*

**Platform's mission is to work with research teams
as **a partner** for both basic and applied research projects**

Basic aim:

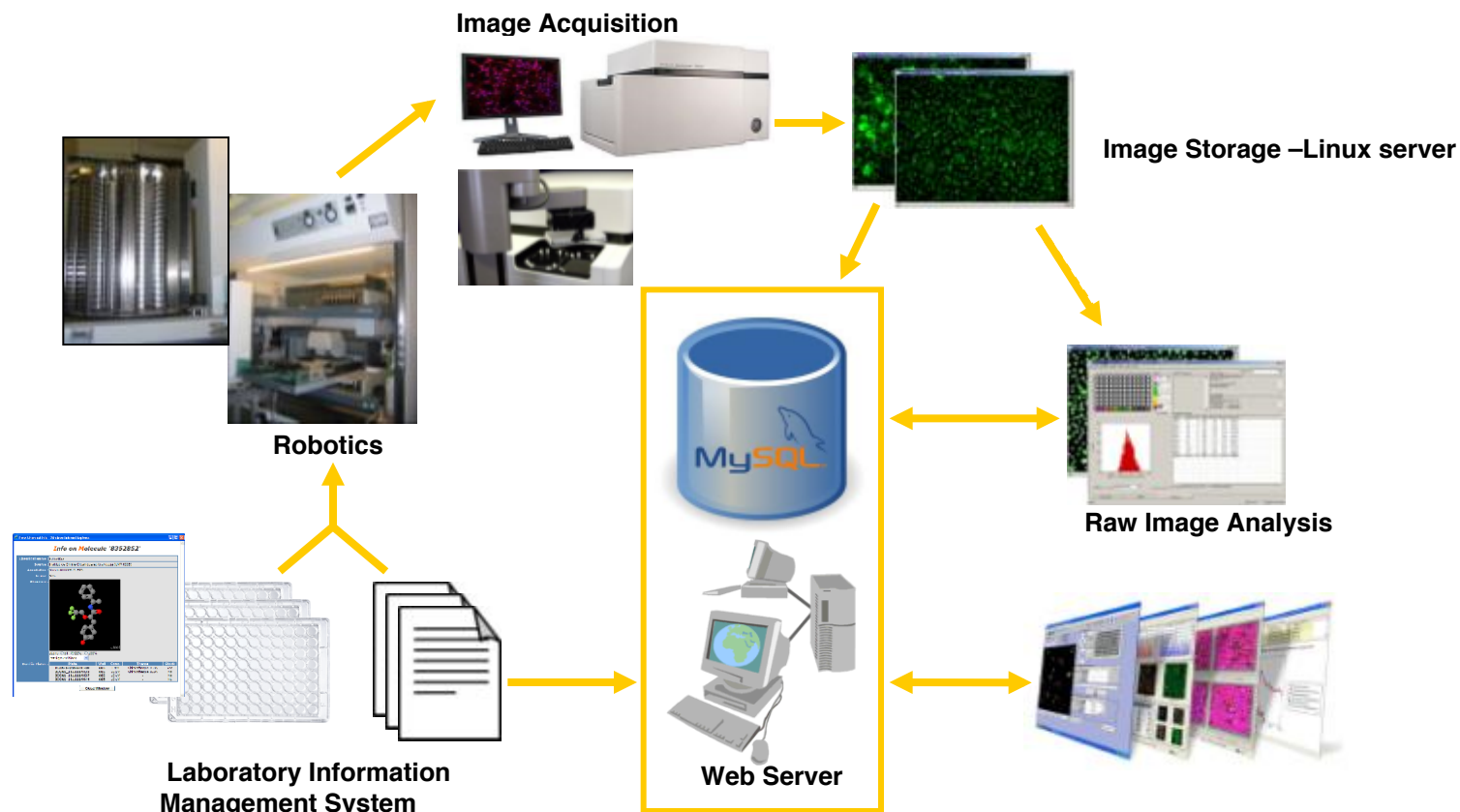
- **as a *validation* approach**
(systematic depletion by siRNA, no *a priori*, just deplete)
- **as a *discovery* tool**
(phenotypic clustering to identify pathways, systematic annotation)

Applied aim:

- **for *target validation***
(toward tailored treatment)
- **for *drug discovery***
(selection of effective drugs, prediction of “downstream” toxicity,
improve effectiveness/toxicity ratio)

Strengths (the facility is 7 years-old)

The platform is equipped to handle all aspects of typical HCS screening workflow (siRNA and Chemical Libraries).



The Platform Team

(coll. with Bioinfo team)



Elaine DEL NERY
Platform Manager



Aurianne LESCURE
Automation Specialist

Sarah TESSIER

Elodie ANTHONY

Cellular Assays
Development



Nabil AMIROUCHEN, MD
PhD Student
Oncologist



Grégory DUVAL
Web Developer

The scientific staff

(use the platform to their research)



Jacques CAMONIS
Research Director U830
Analysis of transduction pathways



Franck PEREZ
Research Director UMR 144
*Microtubule Dynamics and
Intracellular Trafficking*

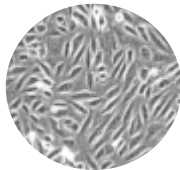


Philippe BENAROCH
Research Director U932
*Intracellular Transport &
Immunity*

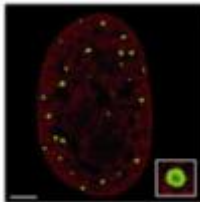
How the researcher arrives to us ?



Scientific question

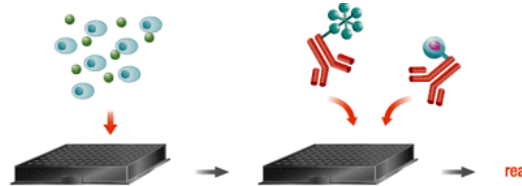


Cell model

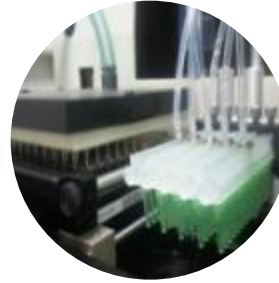


**Tools to detect
the target of
interest/or cell
structure**

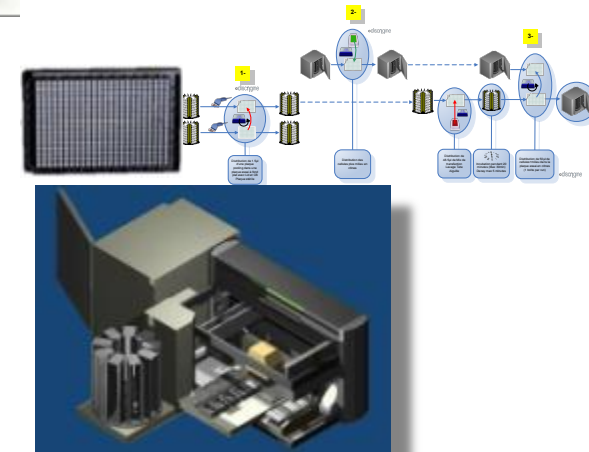
**Minituarization steps
in 96-well plates**



- Optimal cell density
- siRNA transfection efficiency
- DMSO sensibility
- Others: biotin, IL-1, arsenic addition
- Immunofluorescence protocol
- Check assay controls

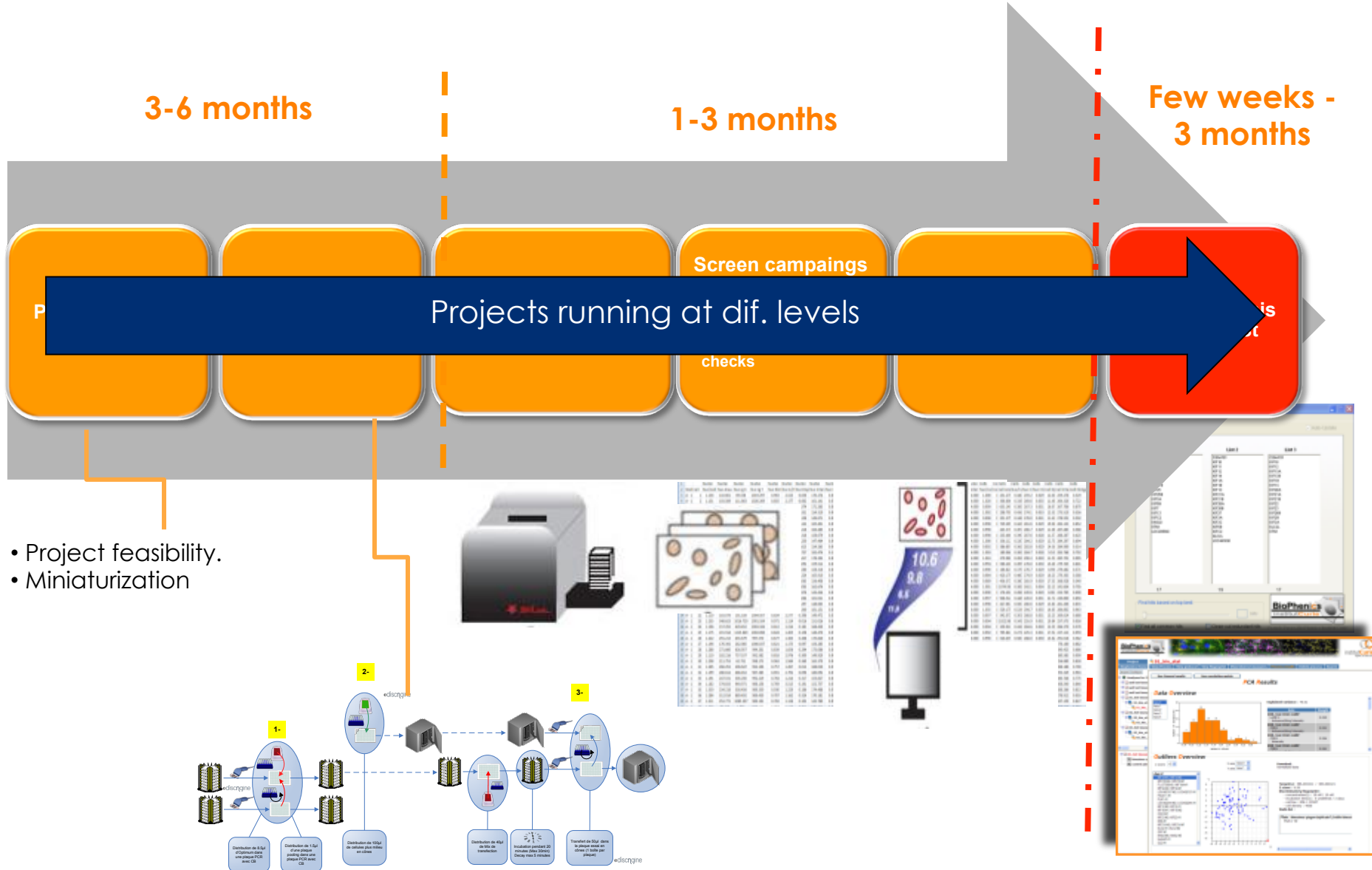


**Minituarization steps
in 384-well plates**

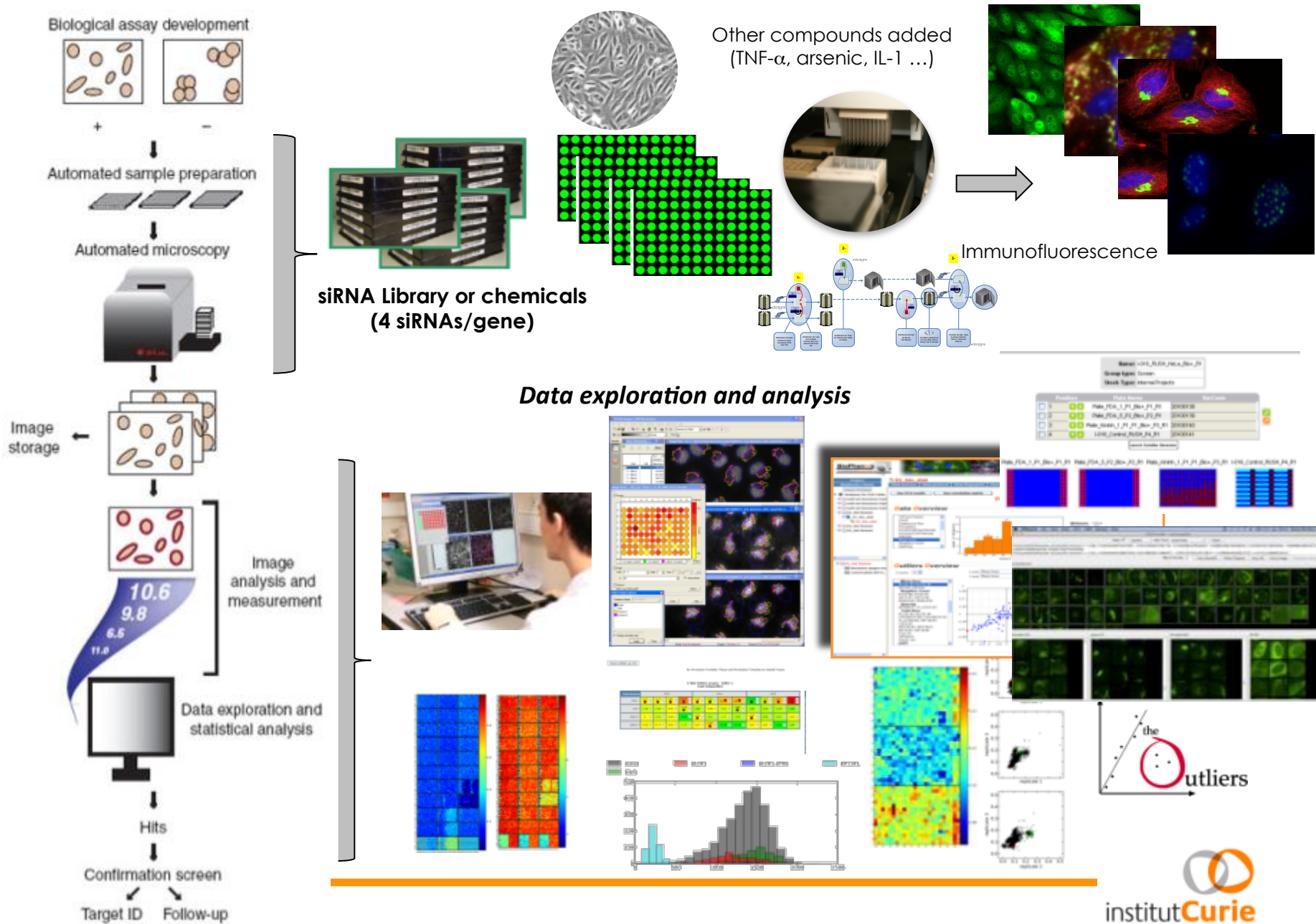


From bench to robotics

How long does it take to run a screening project ?

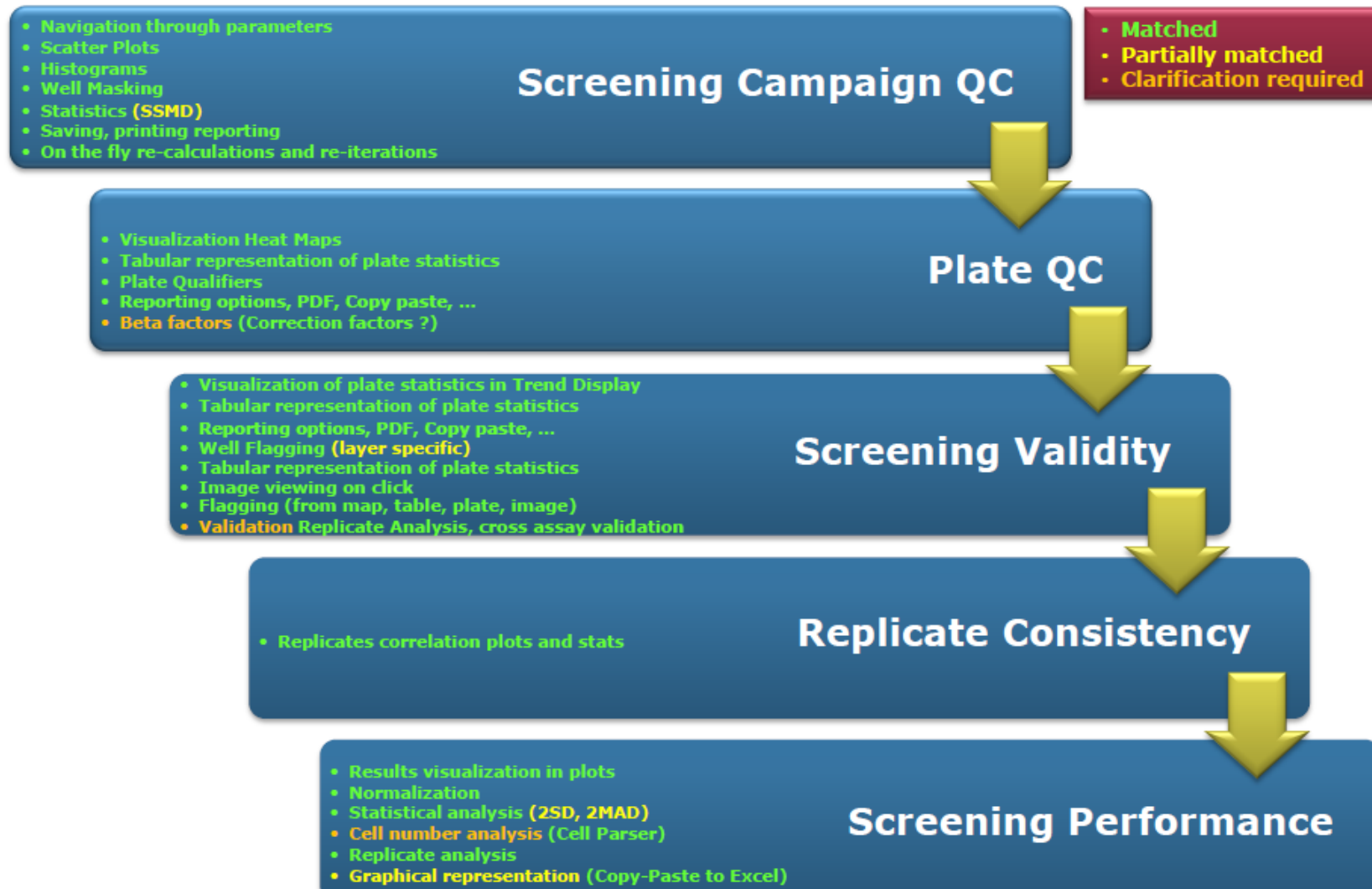


High-Content Screening Platform



Work in progress – by levels

Level 1 : Data organization and processing steps (a central challenge)



Work in progress

Level 2 : High-level exploration of phenotypic data

Population analysis

Validate results, weed out noise and redundant data, increase internal consistency

Descriptive statistics

Correlation analysis

1v1 distributions

Outlier detection

Highlight possible targets in global space or subspace of interest, perform preliminary clustering

PCA, ICA

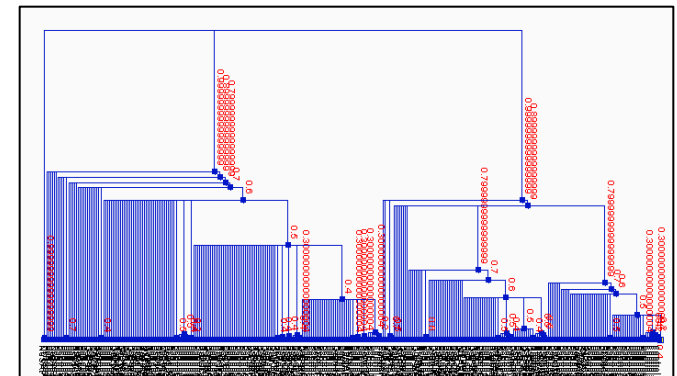
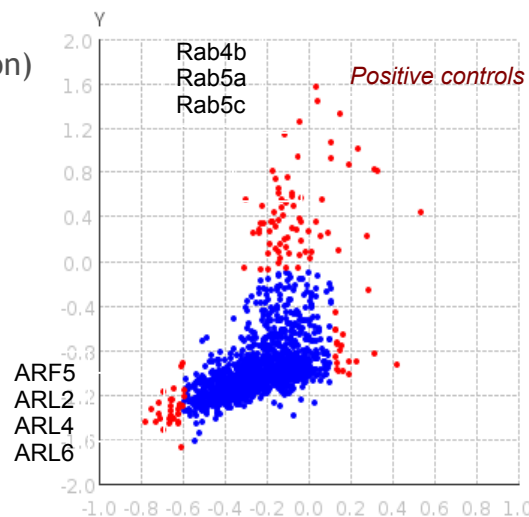
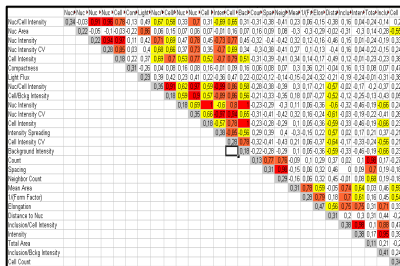
Multiparametric Clustering

Detect fingerprinting profiles, local and global similarities in a unified environment

Hierachical Clustering

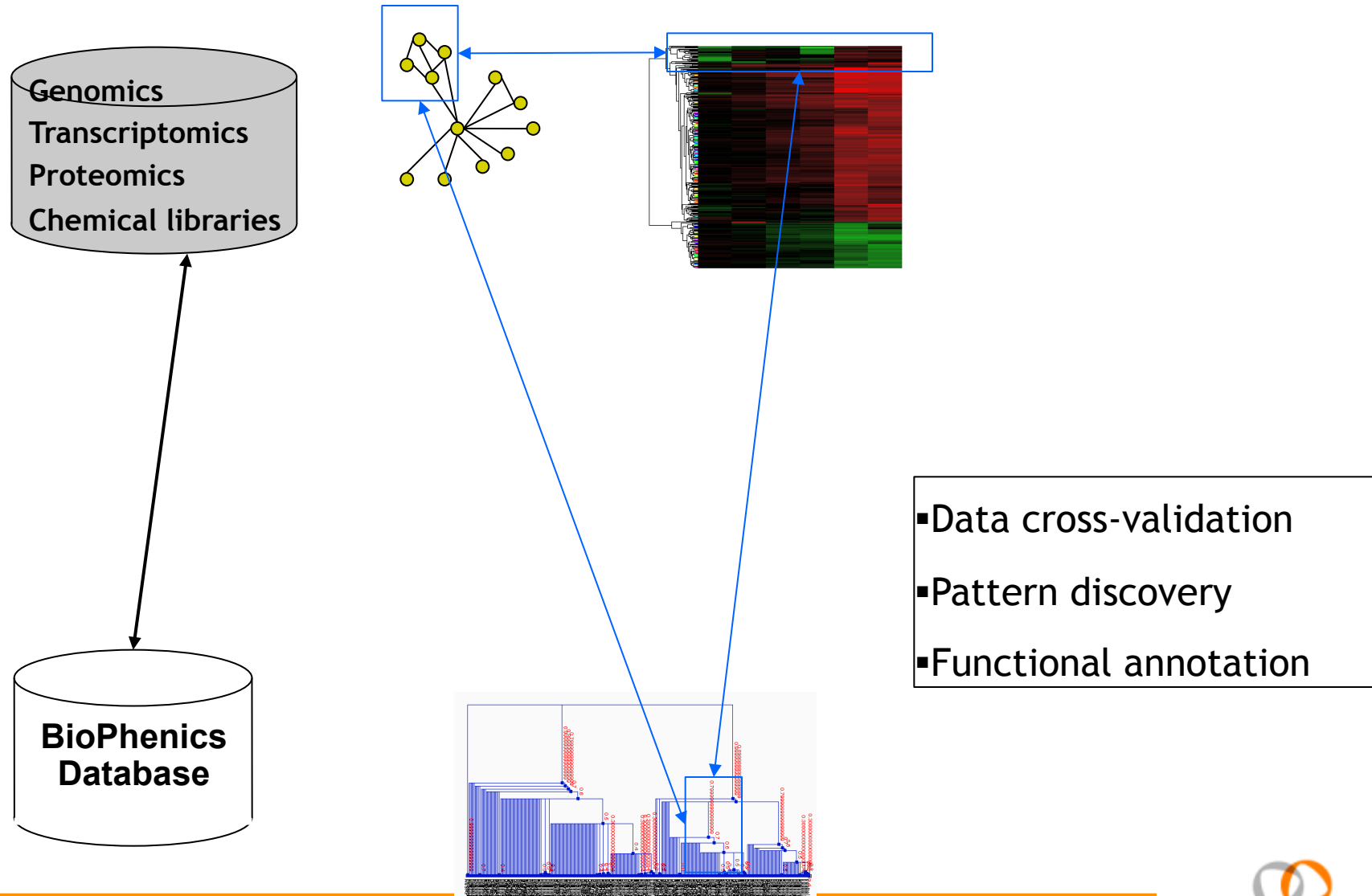
DBSCAN (density-based)

CLIQUE (subspace exploration)



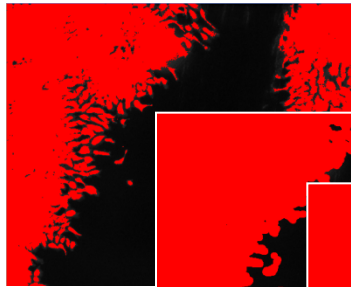
Future work

Level 3: Towards data integration

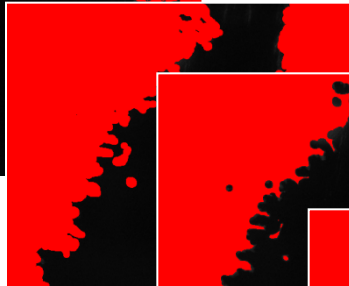


Develop Image segmentation is a permanent need

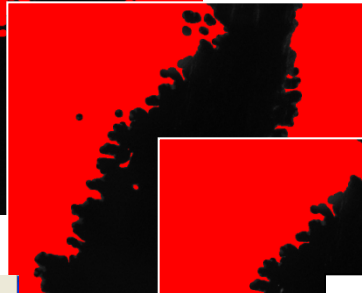
Intensity segmentation



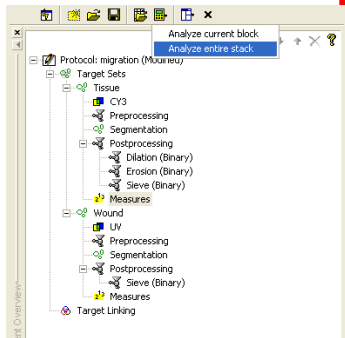
Binary dilation



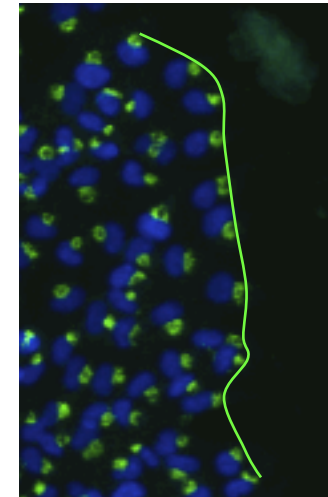
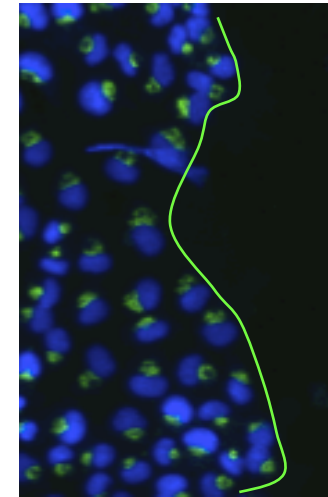
erosion



sieving of 'orphaned' spots.



Define 'wound' area
Multi-color edge detection
Migration and polarization
quantification



Cell Migration

Cell Polarization


Education

• Meeting organization

Two-day meeting - 170 people for all over Europe, no fee

November 28-29th, 2012

***High Throughput Cell Biology:
From screening to applications***



INVITED SPEAKERS:

Sandrine Baghdoyan, I-STEM
Yolanda Chong, Janssen Pharmaceutica
Ana Dinarina, Thermo Scientific
Benny Geiger, Weizmann Institute
Xavier Gidrol, CEA Grenoble
Nir Hacohen, Broad Institute of Harvard and MIT
Peter Horvath, ETH Zurich
Thouis Jones, Harvard University
Philippe Masson, IVENTIVA
Victor Racine, Fluotarma
Rafael E. Carazo Salas, University of Cambridge UK
Luc Selig, Collectis bioresearch
Emmanuelle Soleilhac, CEA Grenoble
Sharon Toozé, Cancer Research UK
Marino Zerial, Max Planck Institute

Institut Curie - Amphithéâtre
Constant Burg
12, rue Lhomond 75005 PARIS

More information :
hcs.meeting2012@curie.fr

ORGANIZERS :
Philippe Benaroch, Jacques Camonis
Elaine Del Nery & Franck Perez

Inscriptions :

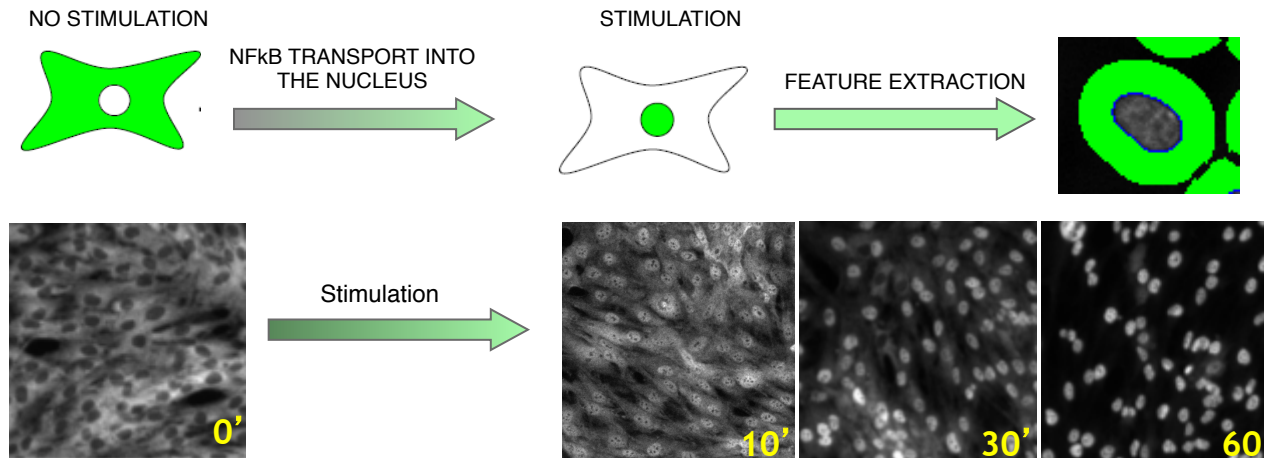
<http://curie.fr/fondation/high-throughput-cell-biology-screening-applications>



Collaboration: basically french research groups and small pharma

Role of cysteine proteases in TLR3 signalling

Philippe Benaroch's group



PNAS

Cleavage of Toll-like receptor 3 by cathepsins B and H is essential for signaling

Alejandra Garcia-Cattaneo^{a,b}, François-Xavier Gobert^{a,b}, Mélanie Müller^{a,c}, Florent Toscano^d, Marcella Flores^{a,b}, Aurianne Lescure^{a,c}, Elaine Del Nery^{a,c}, and Philippe Benaroch^{a,b,1}

^aInstitut Curie, Centre de Recherche, 75005 Paris, France; ^bInstitut National de la Santé et de la Recherche Médicale, Unité 932, 75005 Paris, France; ^cInstitut Curie, Translational Department, BioPhenics Platform, Hôpital Saint Louis, 75010 Paris, France; and ^dCentre de Recherche en Cancérologie de Lyon, Institut National de la Santé et de la Recherche Médicale, Unité Mixte de Recherche 5286/Centre National de la Recherche Scientifique, 69008 Lyon, France

Edited by Ira Mellman, Genentech, Inc., South San Francisco, CA, and approved April 18, 2012 (received for review September 15, 2011)

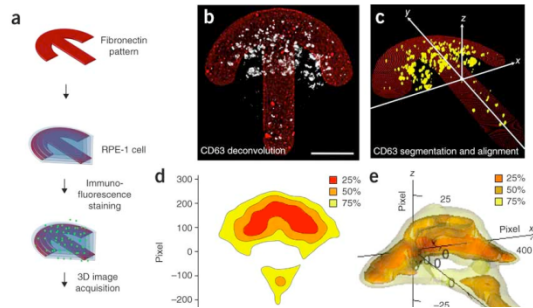
Some Projects from Lab Bench to BioPhenics

Towards the understanding of cell organisation

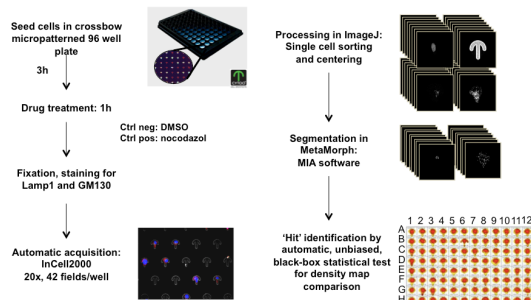
560 | VOL.7 NO.7 | JULY 2010 | **NATURE METHODS**

Probabilistic density maps to study global endomembrane organization

Kristine Schauer & Bruno Goud

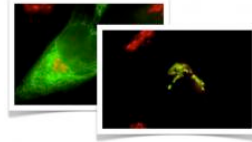


Density-based approach in micropatterned cells towards quantitative analysis of cellular organization in high-content approaches.



Regulated secretion

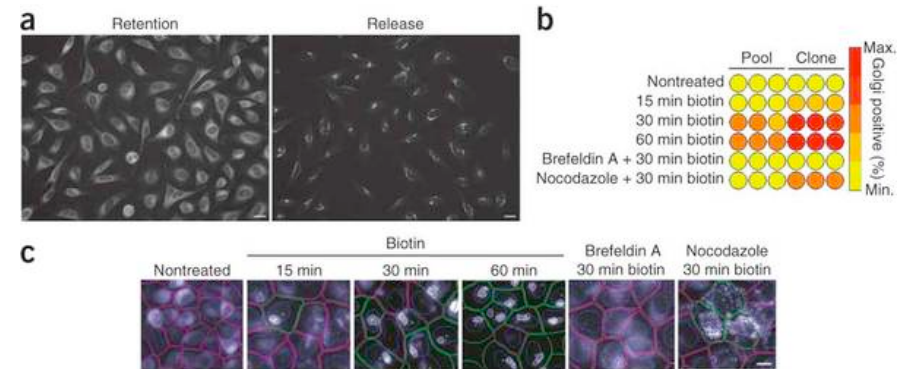
RUSH (Retention Using selective Hook)



ADVANCE ONLINE PUBLICATION | **NATURE METHODS**

Synchronization of secretory protein traffic in populations of cells

Franck Perez's group



The RUSH SYSTEM to understand the mechanisms of trafficking and enable screens for molecules that perturb pathological protein transport

