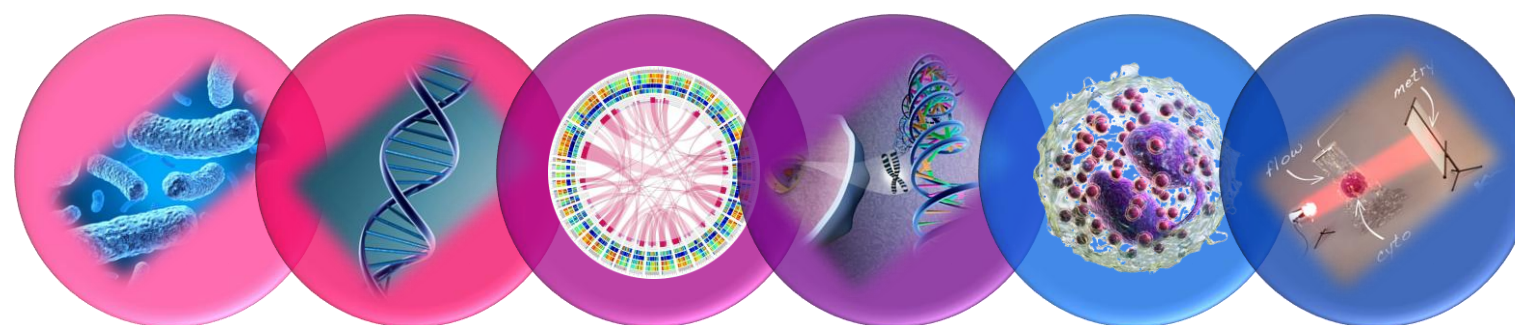


**Daedalus**  
**Interdisciplinary MultiOMIC Project to Advance**  
**Crossanalysis in Translational research**

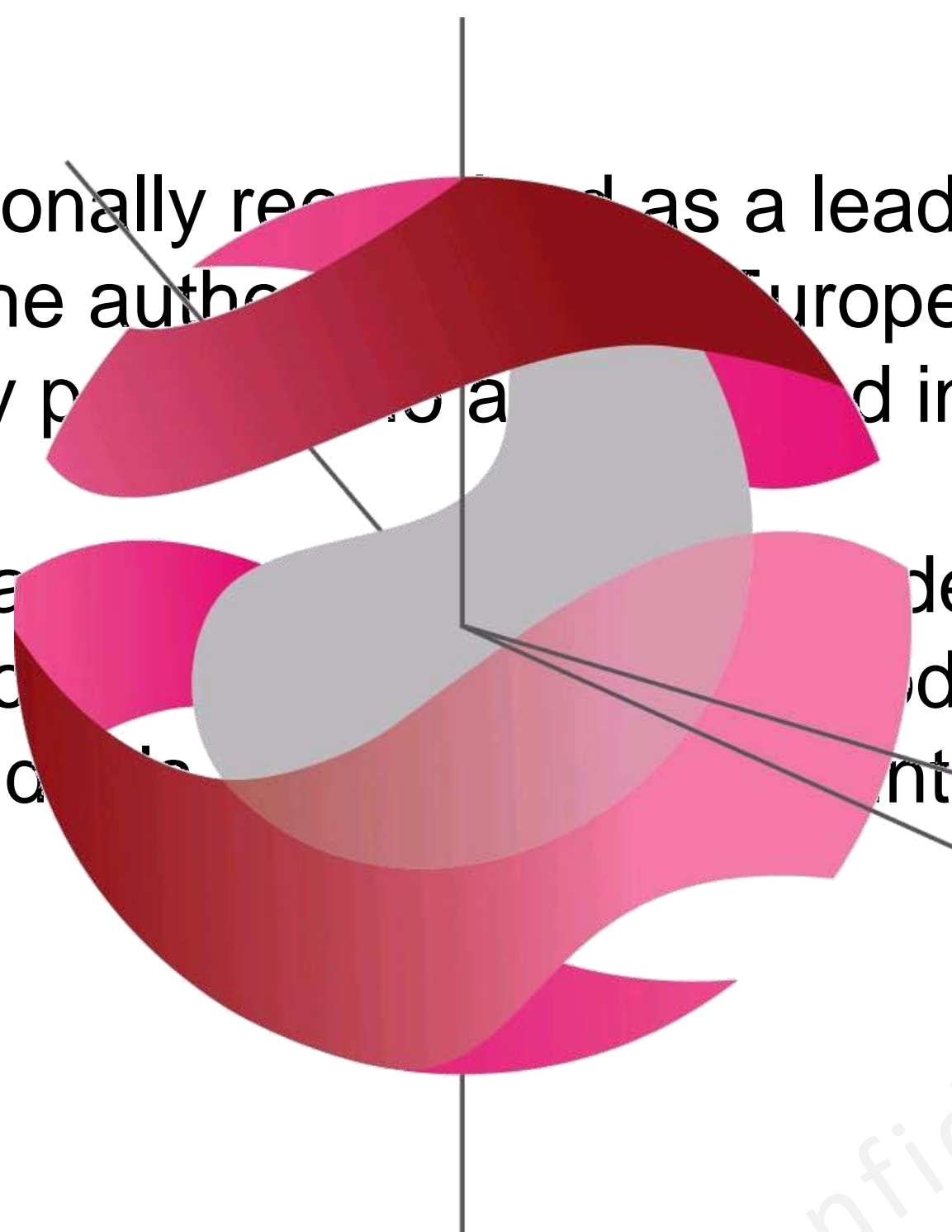
Nicolas Derian, PhD (derian@informatics.bio)  
Iannis Drakos, PhD (drakos@informatics.bio)



# ESCCA

## European Society of Clinical Cell Analysis

- ESCCA is internationally recognized as a leading scientific organization and the authority in Europe and European countries to educate and certify people in the cell analysis process.
- Its leader status was achieved through decades of hard work on building a network. Today consists of thousands of individuals from international scientific societies.



# Cytome (flow and mass cytometry)

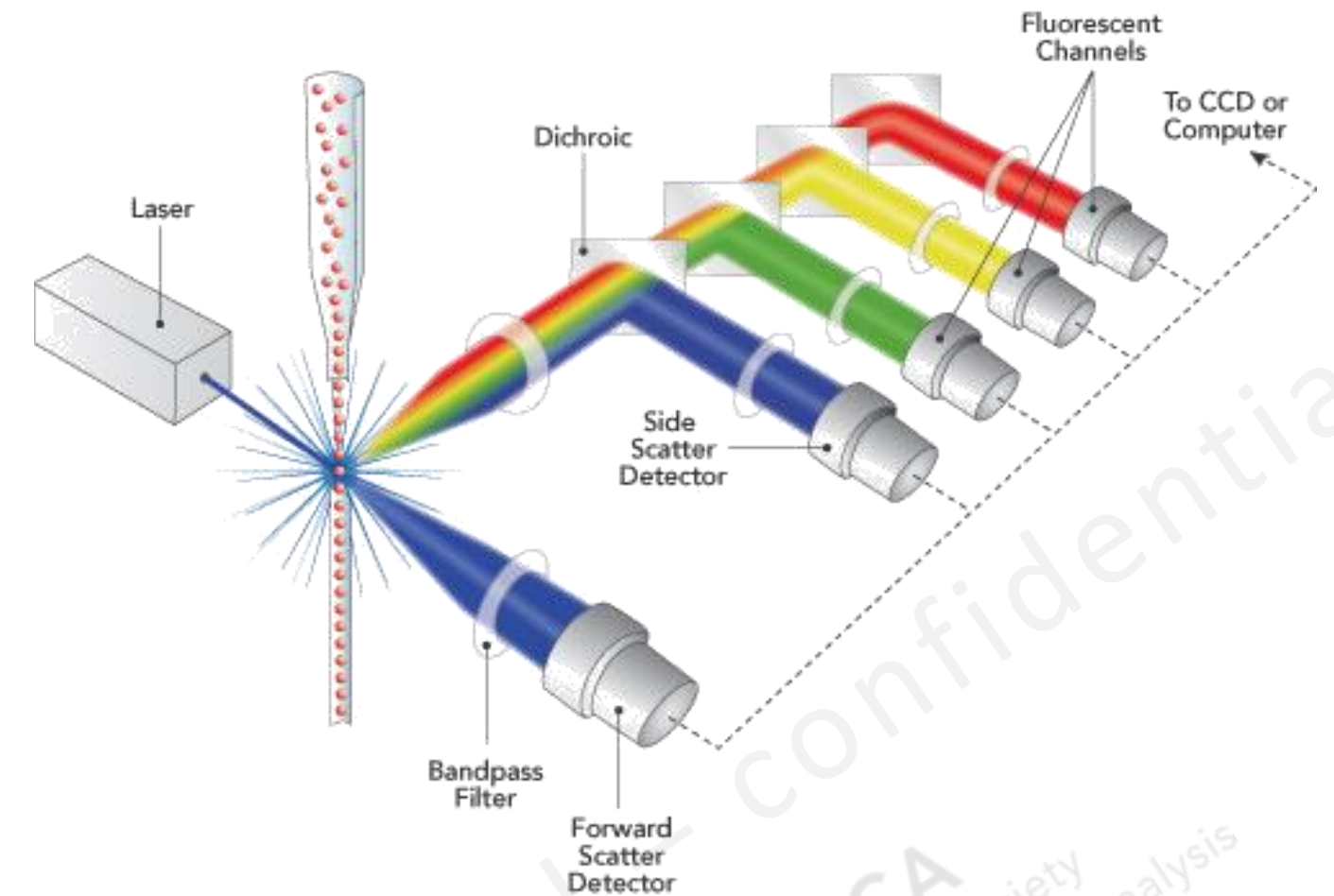
## Why is Cytome absent from NextGen IS

- Extreme multidimensionality
- Higher QC requirements
- Data significantly affected by equipment variations, and calibration of the

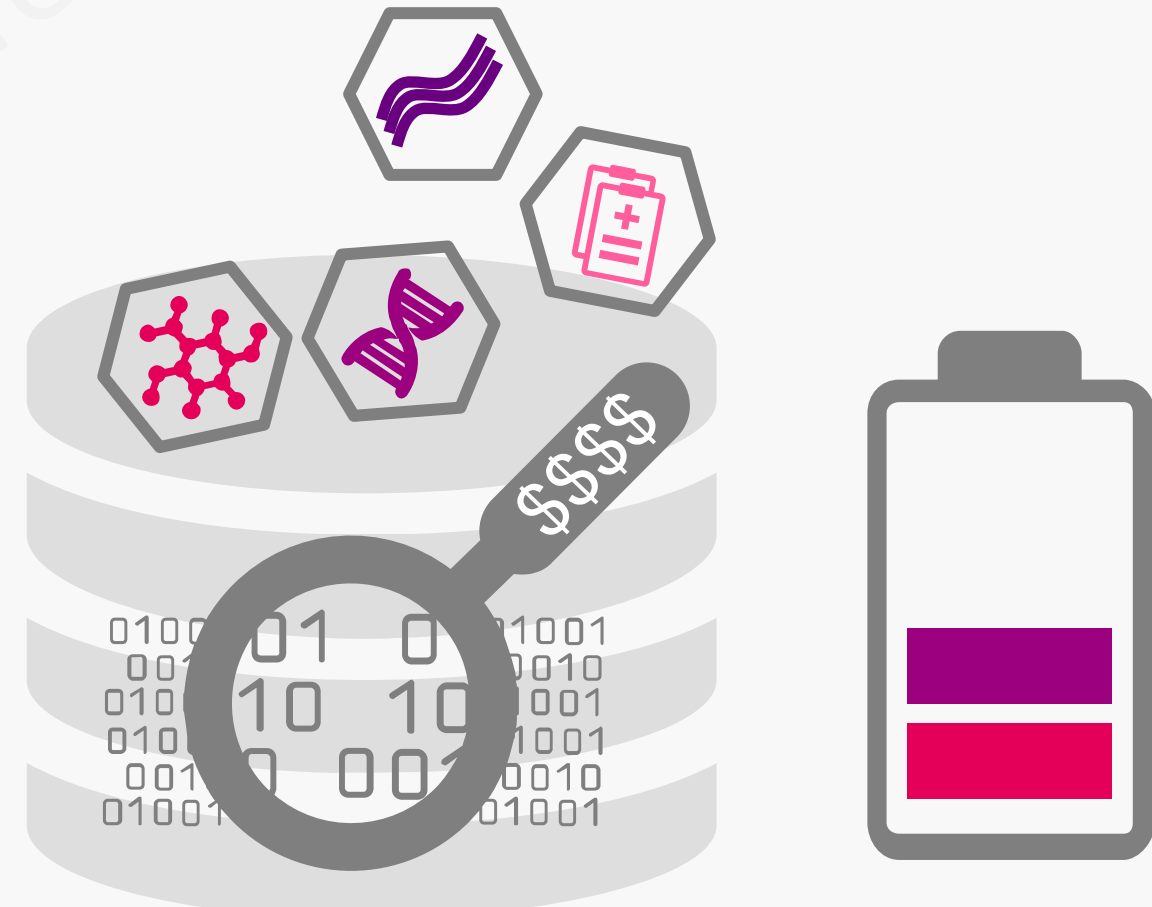
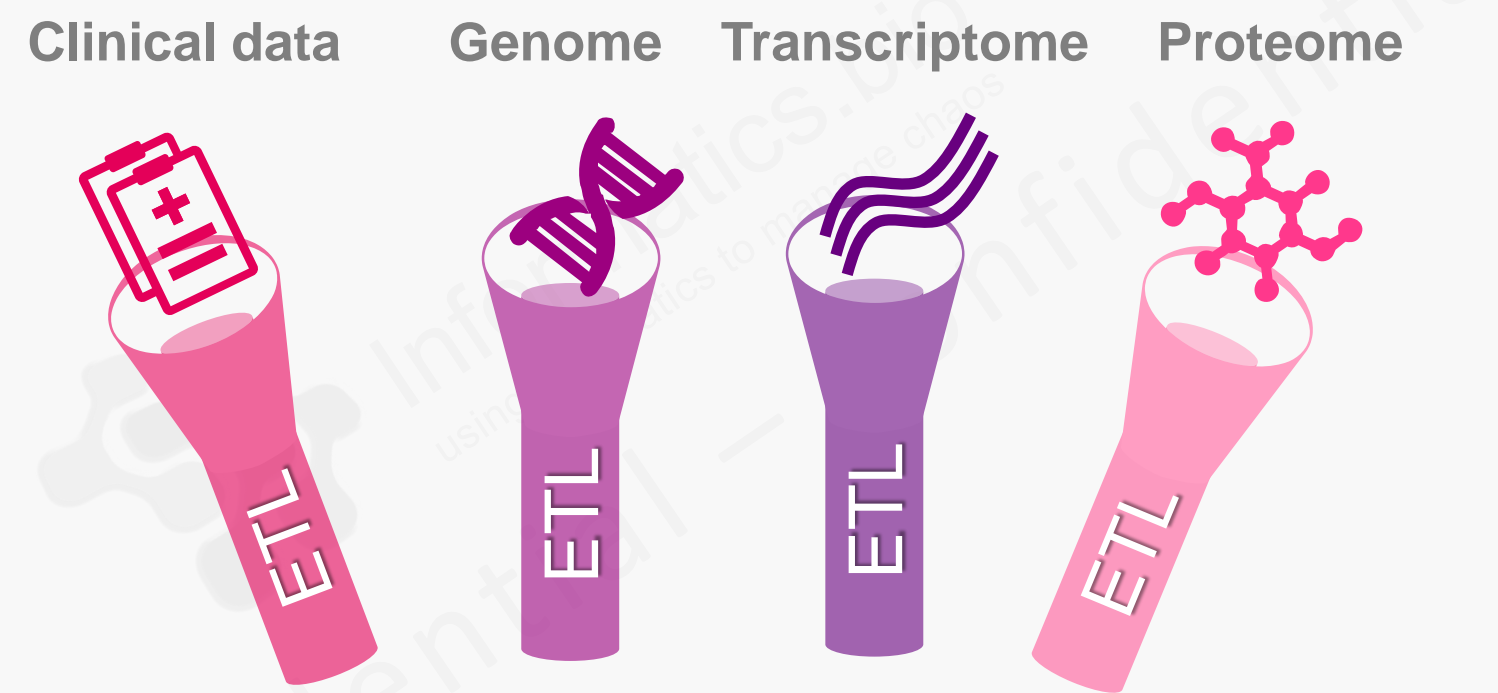
G

For each single nucleotide read (A or C) analysts processes corresponding is a multidimensional matrix

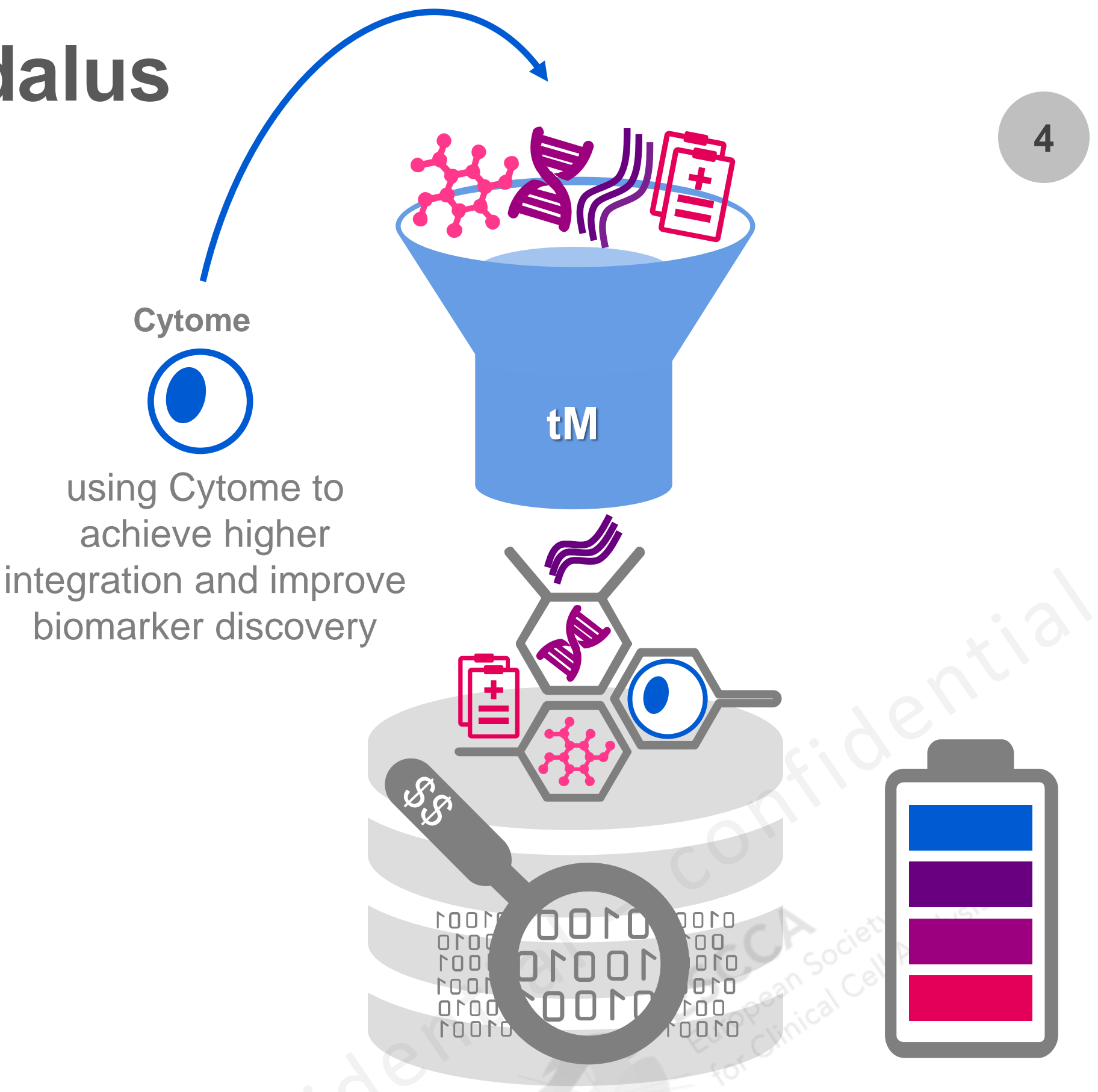
	1	1111
	2	1111
	3	1111
	4	0001
Byte Order	Bit Mask	
P01		
P02		
P03		
P04		
P05		
P06		
P07		
P08		
P09		
P10		
P11		
P12		
P13		
P14		



# Daedalus



Cross-analysis empowers discovery rate at an increased data management cost



NextGen IS are dramatically increasing options for cross-analyses without extra costs

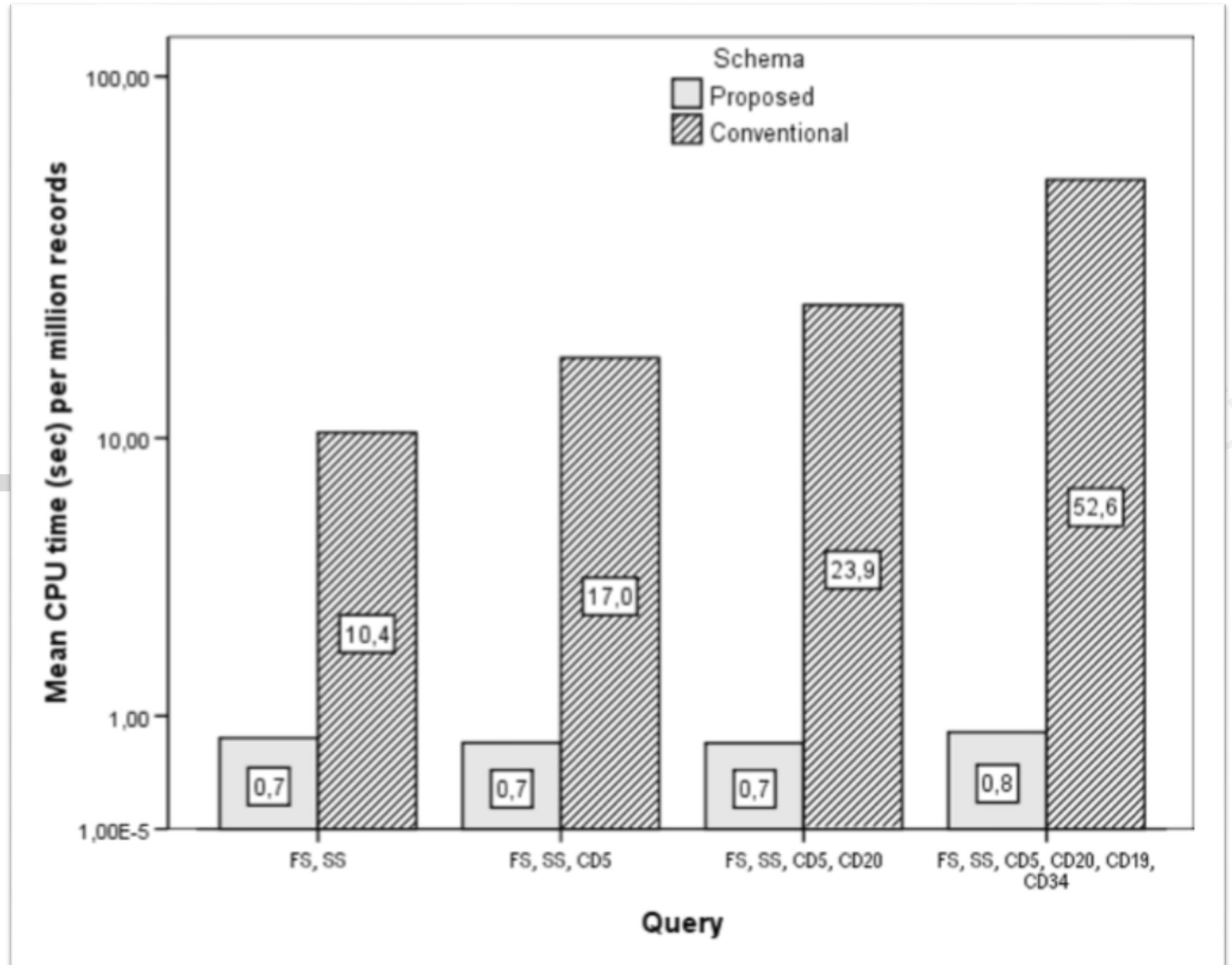
# What we have

## Published Database schema

**A perspective for biomedical data integration:  
Design of databases for flow cytometry**  
BMC bioinformatics, 2008

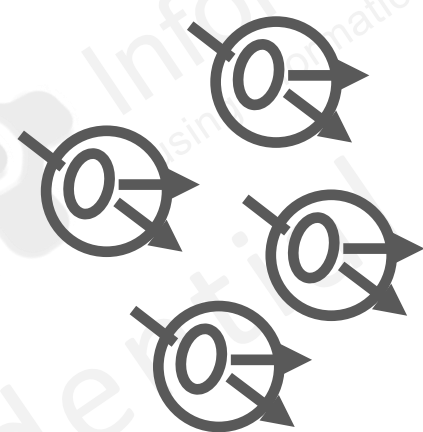
**An environment for efficient flow cytometry data management**  
ESCCA 2009

**A functional framework for total MDS (digital) management**  
ESCCA 2010



# What we have

From A to Z, fully automatically and standardized Cytome pipeline



## Data processing

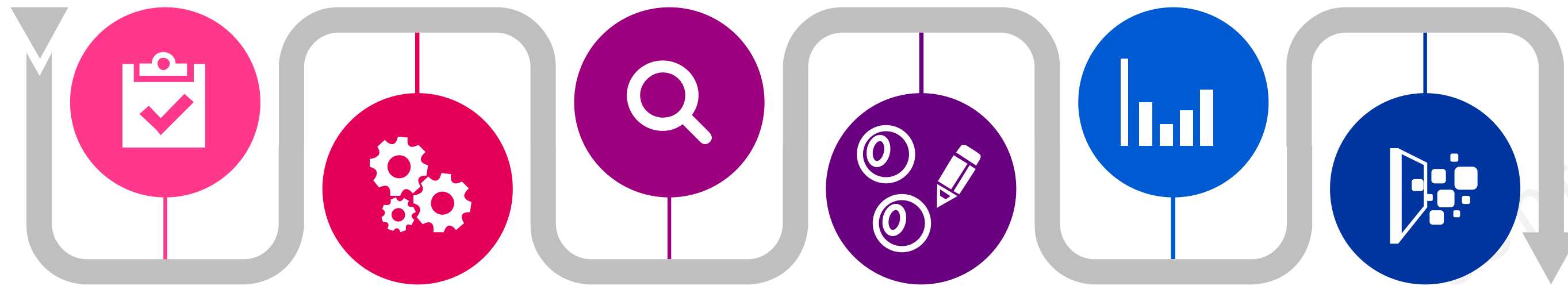
Including compensation, cleaning and data transformation steps

## Automatic cell populations annotation

Based on user knowledge and automatic analyses

## The power of tranSMART

Cytome integration further improves biomarker discovery in the most advanced NextGen IS



## Data curation

Automated method that can take advantage of the domain expert

## Automatic cell populations discovery

Using our tailor-made methodology

## Data analysis

Including state of the art statistical and cytometry-dedicated analyses



confidential - Informatics to manage change - confidential - EccCA Society Cell Analysis

# Benefits for the community

## Improved biomarker discovery while expanding the reach of tranSMART

### Be part of a strong network

Daedalus is running with the support of ESCCA, a network of thousands of cytometry specialists in Europe

### Fulfill an anticipated community request

Integrating cytometry data into tranSMART

### Solve an open problem

Providing a quantitative and standardized method to handle (raw) Cytome data

### Improved access to a growing market

Cytome is heavily involved in both clinical and research practices

### Cross-OMICs benefits

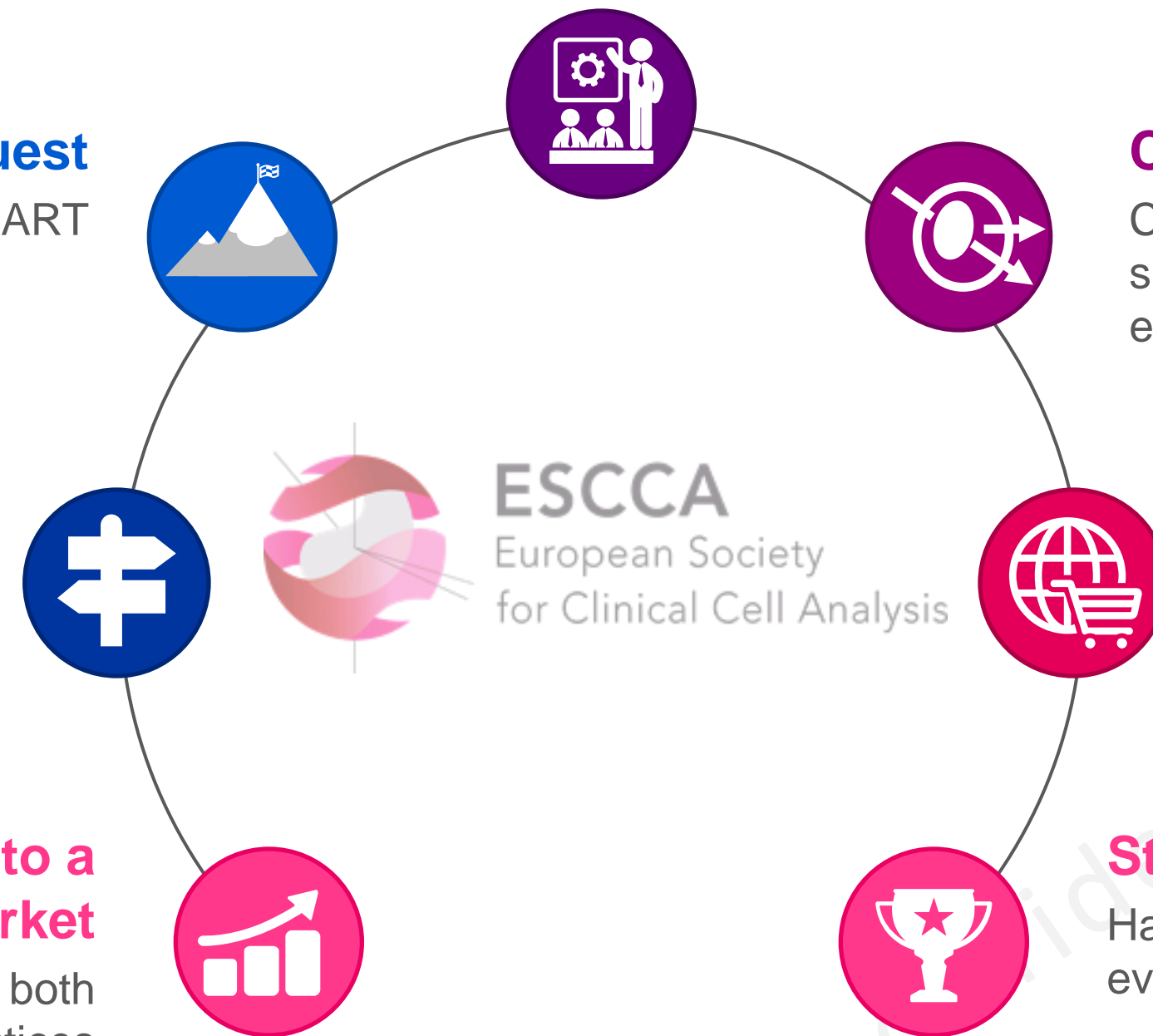
Cross-analyzing OMIC data with Cytome significantly improved biomarker discovery on each OMIC field

### Increase revenue

Wider audience, stronger demand for services

### Stay on top

Having a NextGen IS which supports even more datatypes



# Special Thanks

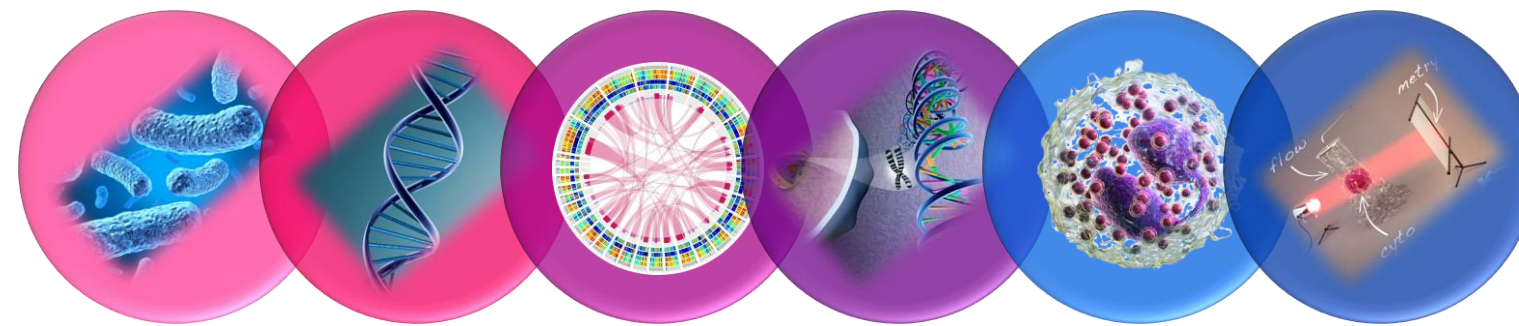
to Daedalus project team

- **Katherina Psarra, PhD.**  
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- **Silvia Della Bella, MD, Prof.**  
*University of Milan.*
- **Frank Preijers, PhD.**  
*Head of the Cytometry and Immunophenotyping lab, Radboud University Medical Center.*
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- **Stefano Papa, MD, Prof.**  
*University of Urbino.*
- **Jose-Enrique, Prof.**  
*University of Valencia.*
- **Andy Rawstron, PhD.**  
*Leeds Teaching Hospitals NHS Trust.*
- **Jordi Petriz, PhD**  
*University of Barcelona.*
- **Claudio Ortolani, MD, Prof.**  
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*Bone Marrow Laboratory Director, Karaiskakio Foundation.*



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**Thank you !**

