

Building a Collaborative Informatics Platform for Translational Research: An IMI Project Experience

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Department of Computing
Imperial College London

Living in the Era of BIG

- Big Data : Massive amounts of information derived from dry /wet lab investigations, feasibility studies and clinical trials.
- Big Science: Research silos are evaporating with the merging of scientific methods. Traditional hypothesis-testing studies will couple with data-driven research.
- Big Collaboration : As evidence accumulates, personalized medicine will become a reality, and patient-specific cancer interventions will become available. Teams of disease specialists, researchers and bioinformaticians working in concert in a virtual frontier.



Collaboration Platform is the Key for Doing Big Science with Big Data



Published online 3 September 2008 | *Nature* **455**, 16-21 (2008) | doi:10.1038/455016a

News Feature

Big data: Welcome to the petacentre

Nature **455**, 30 (4 September 2008) | doi:10.1038/455030a; Published online 3 September 2008

What

trilli Big data: Distilling meaning from data

whic

Nature **455**, 28-29 (4 September 2008) | doi:10.1038/455028a; Published online 3 September 2008

Felice Frar

Big data: How do your data grow?

**Buried in
need to c
Rosalind**

Clifford Lynch¹

1. Clifford Lynch is the executive director of the Coalition for Networked Information, 21 Dupont Circle, Washington DC 20036, USA, and an adjunct professor at the School of Information, University of California, Berkeley, California, 94720-4600, USA. Email: cliff@cni.org

Scientists need to ensure that their results will be managed for the long haul. Maintaining data takes big organization, says Clifford Lynch.

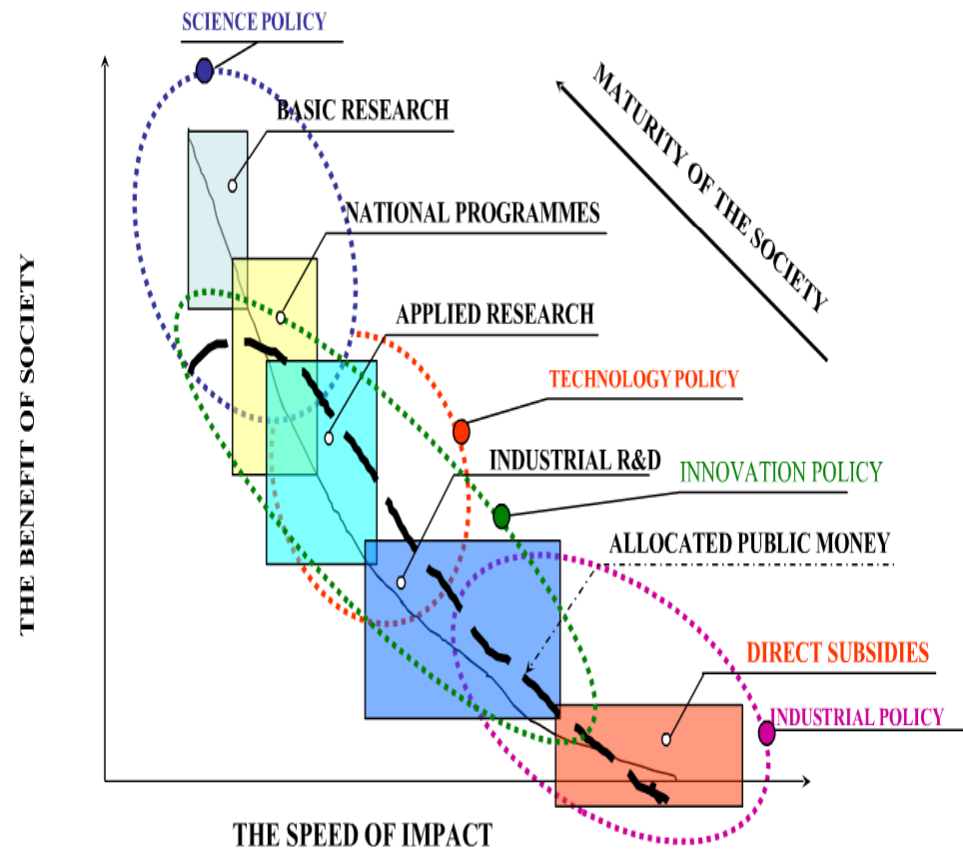
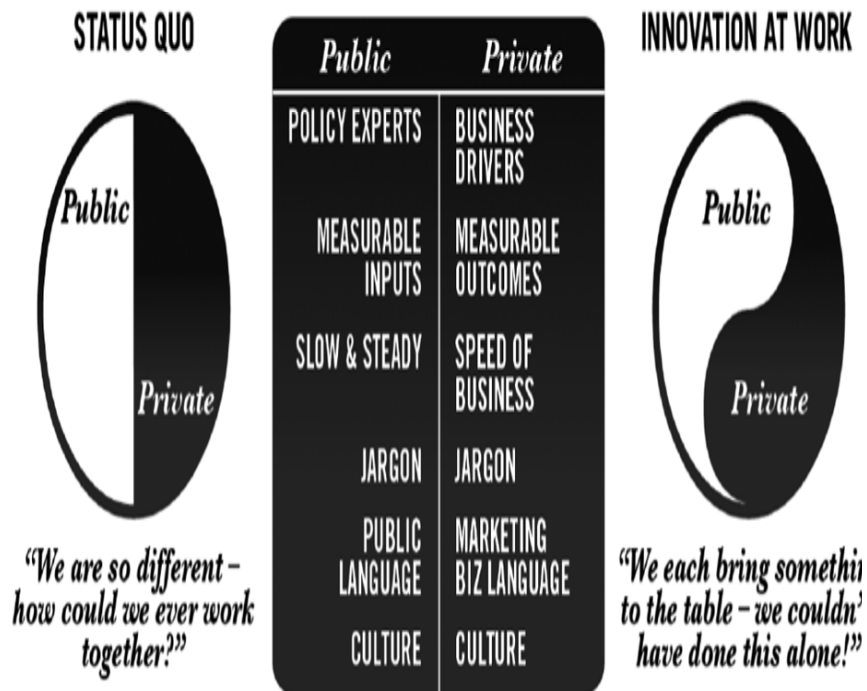
Nature **455**, 1 (4 September 2008) | doi:10.1038/455001a; Published online 3 September 2008

Community cleverness required

Researchers need to adapt their institutions and practices in response to torrents of new data — and need to complement smart science with smart searching.

New Science Economy Model: Public-Private Partnership for Research

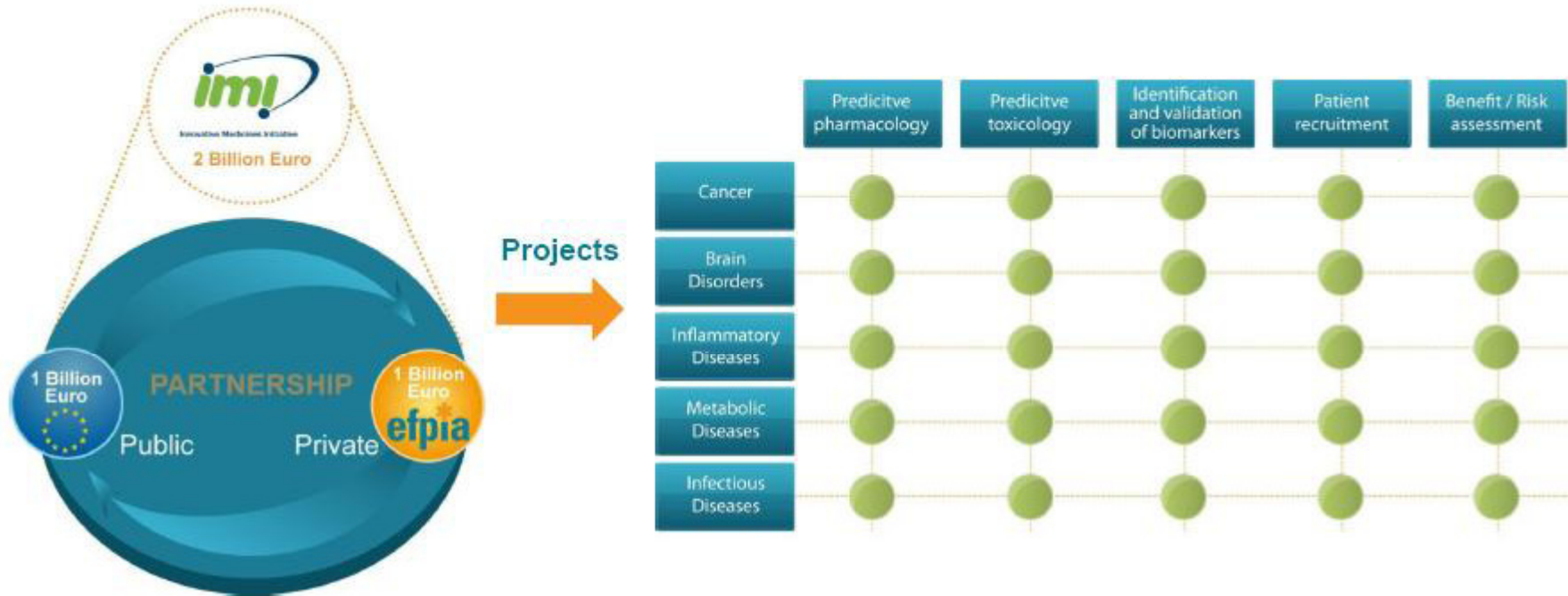
HARNESSING ASSETS AND OVERCOMING BARRIERS



The Requirements for PPP-based Translational Research

- IT Infrastructure : hosted and shared by a community
- Data management: shared with configurable access control by various subgroups of a community
- Software : PaaS for development community
- Analysis : collaborative analysis
- Knowledge management: Dynamic integration of knowledge based on semantics

PPP Example : EU IMI



- New model for Public Private Partnership in Life Science
- Focus on **Efficacy in 5 Disease Areas**, **Safety**, Knowledge Management and Education & Training
- IMI projects address key **pre-competitive bottlenecks** identified by Pharma

U-BIOPRED Project: An IMI Project

Innovative Medicines Initiative (IMI)

- World's largest public private partnership
- 2 Billion Euro: 1 Billion from EU, 1 Billion from EFPIA

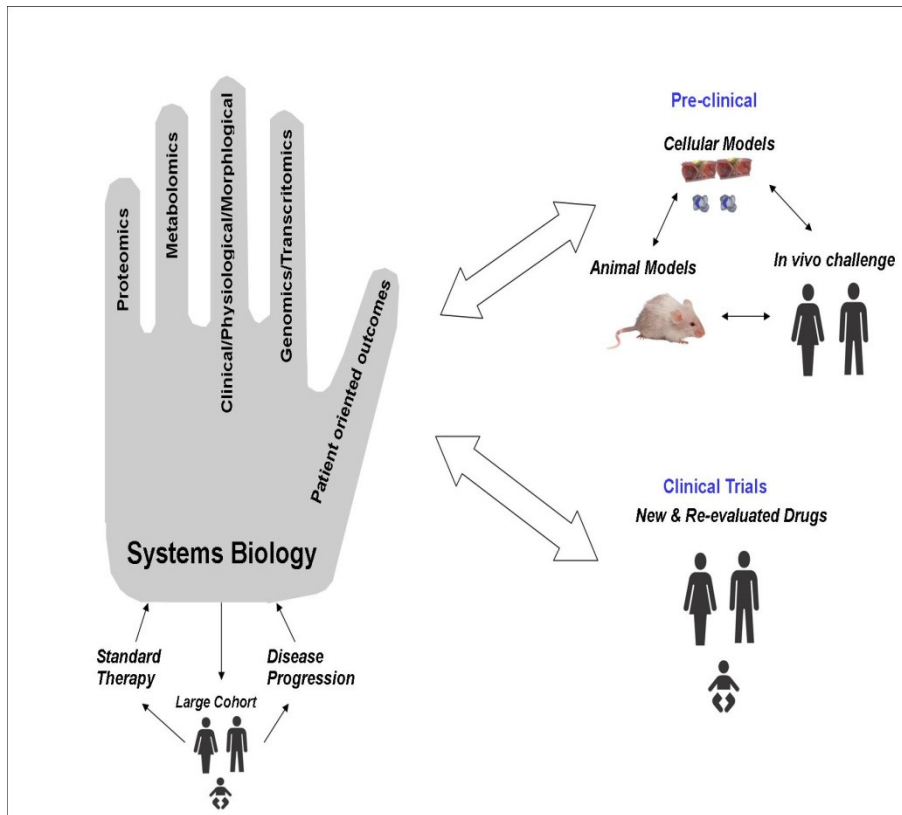
U-BIOPRED: Unbiased Biomarkers for predicting respiratory disease outcomes

- 40 Party Collaboration between 10 Pharma & 30 Academic Medical Centres

Knowledge Management Work Package

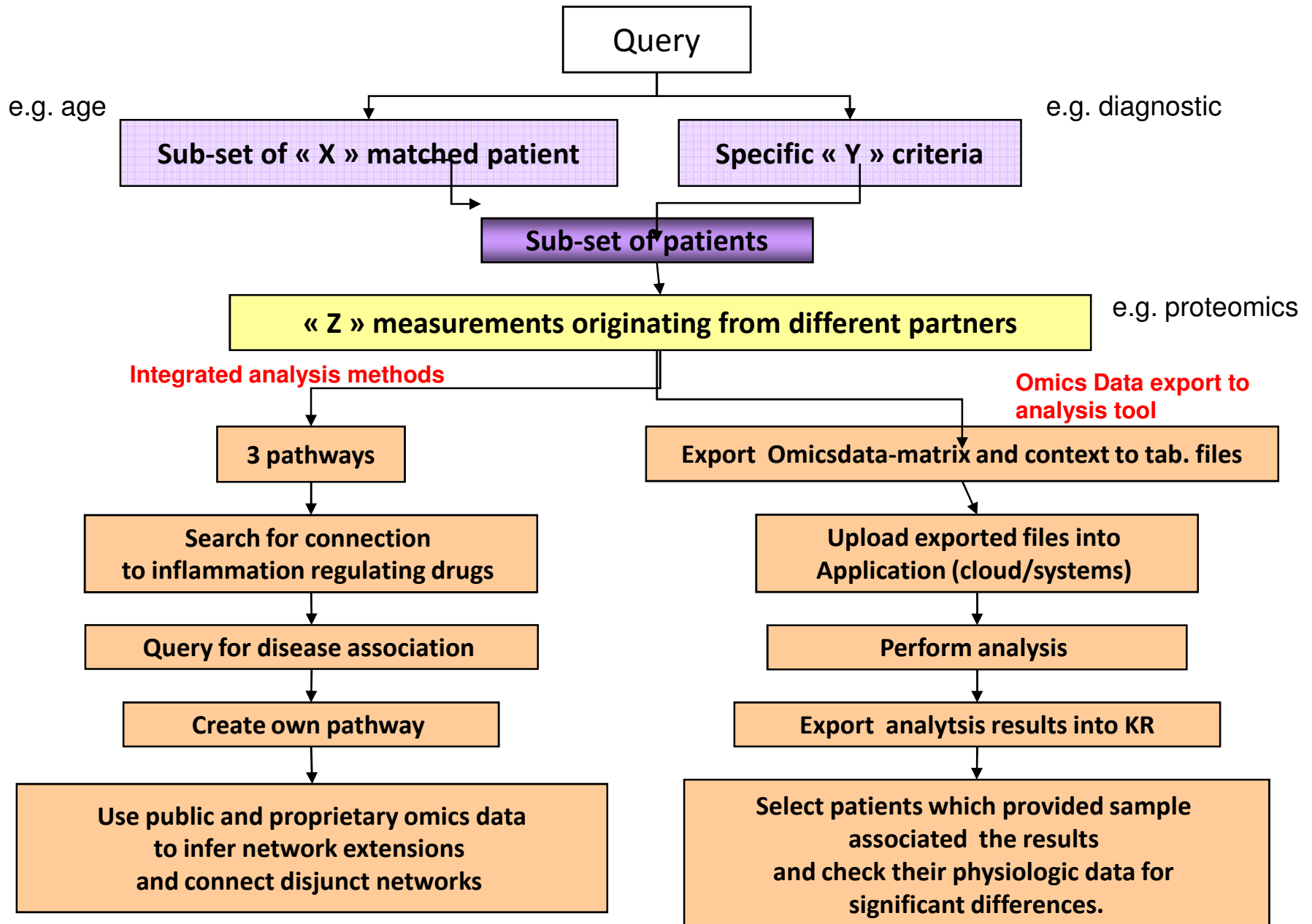
- Imperial Data Co-ordinator, JnJ TranSMART
- AZ, Roche, UCB, CNRS

UBIOPRED Knowledge Product : Handprints



1. Reaching international consensus on diagnostic criteria
2. Creating adult/pediatric cohorts and biobanks
3. Creating novel biology 'handprints' by combining molecular, histological, clinical and patient-reported data
4. Validating such 'handprints' in relation to exacerbations and disease progression
5. Refining the 'handprints' by using preclinical and human exacerbation models
6. Predicting efficacy of gold-standard and novel interventions
7. Refining the diagnostic criteria and phenotypes
8. Establishing a platform for exchange, education and dissemination

A Typical Querying Process



The Challenge in Building the KM for UBIOPRED

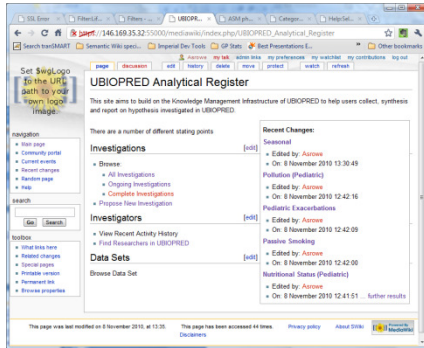
- The consortium formed as a loosely coupled virtual organisation
- Such a VO conducts highly collaborative and multidisciplinary scientific activities
- Data is generated by many people in the VO with a wide range
- of connected modalities
- Knowledge is build through an iterative knowledge production process where data need to be incrementally collected, flexibly integrated, systematically analysed and interactively reported
- Project has a period but knowledge need to be managed forever
- Very big task with very little money

U-BIOPRED KM System Design Goal and KM Key Features

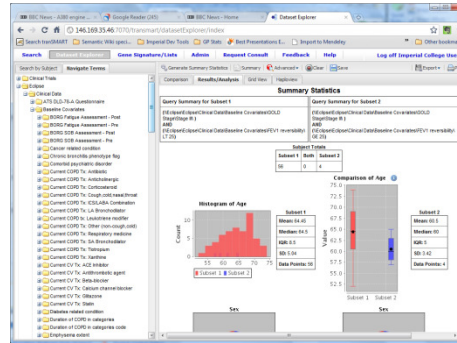
- Cohort-based information integration to support clinical driven integrative biomarker study
- Cloud based infrastructure to facilitate collaborative translational research
- An integrated framework supports the management of a collaborative knowledge production process (curation, analysis, content enhancement, reporting, modeling and simulation)
- A sustainable environment with longevity and total ownership : workflow-based PaaS for integrative analytics:
 - Curation ETL workbenches
 - Analytics workbenches
- A scalable platform adaptable for future science/technology development (such as NGS technology; medical image et.al)

UBIOPRED Collaborative TR Platform

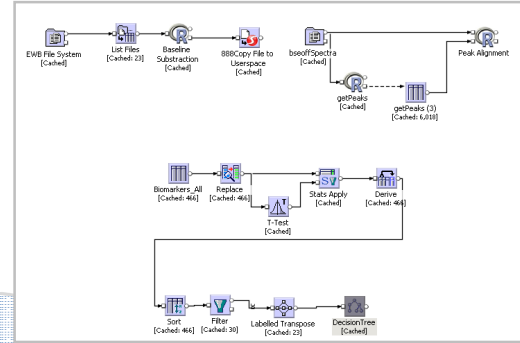
Analytical Register :
Research Collaboration
Management



TranSMART:
Cohort-based Omics
Data Management



IDBS InforSense Workflow:
Analytical Engine +
Development PaaS



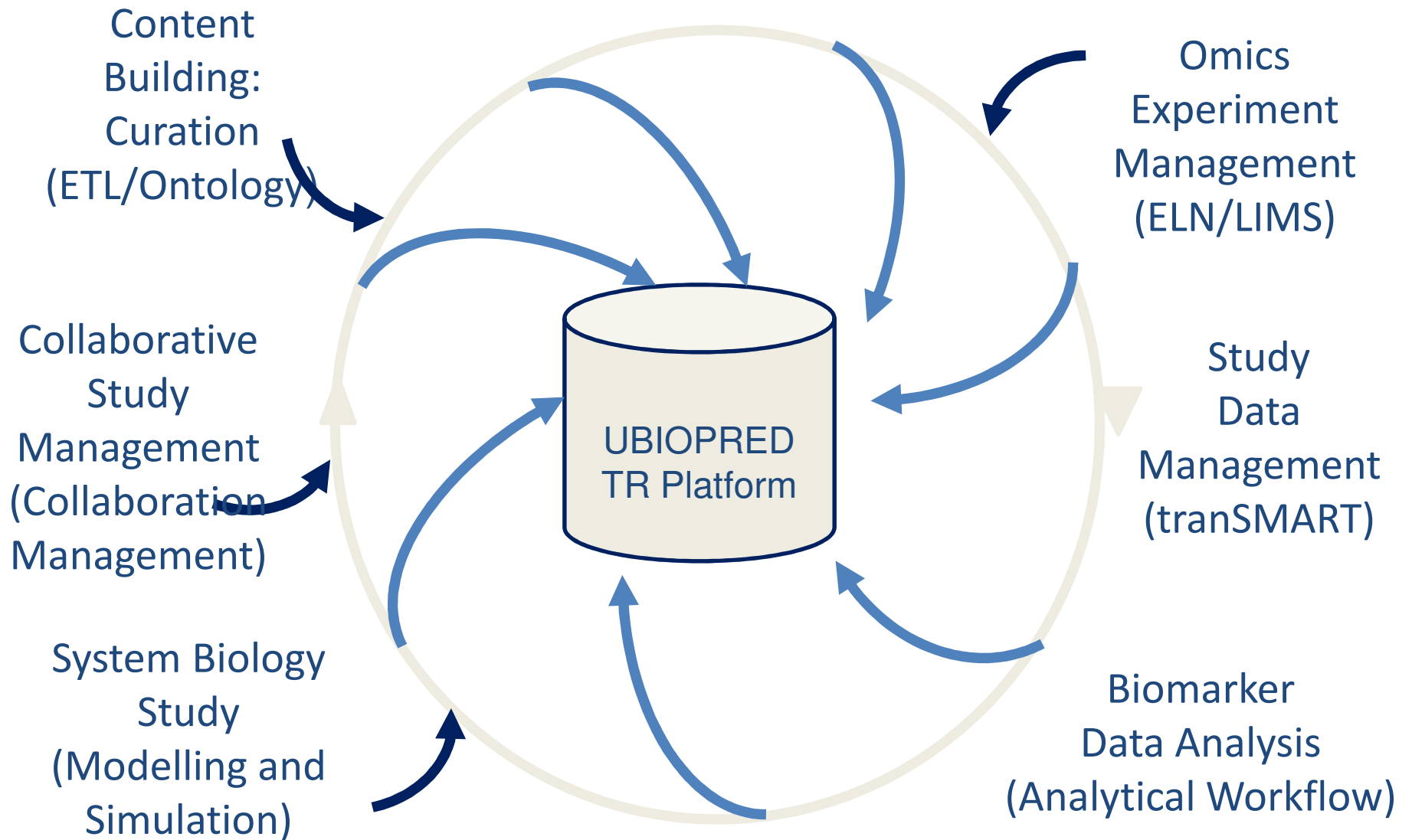
TSmart DB Sample Tracking Gene Pattern&R Analytical Registry EWB for Assay Data Management InforSense KDE Workflow

Virtual Machines

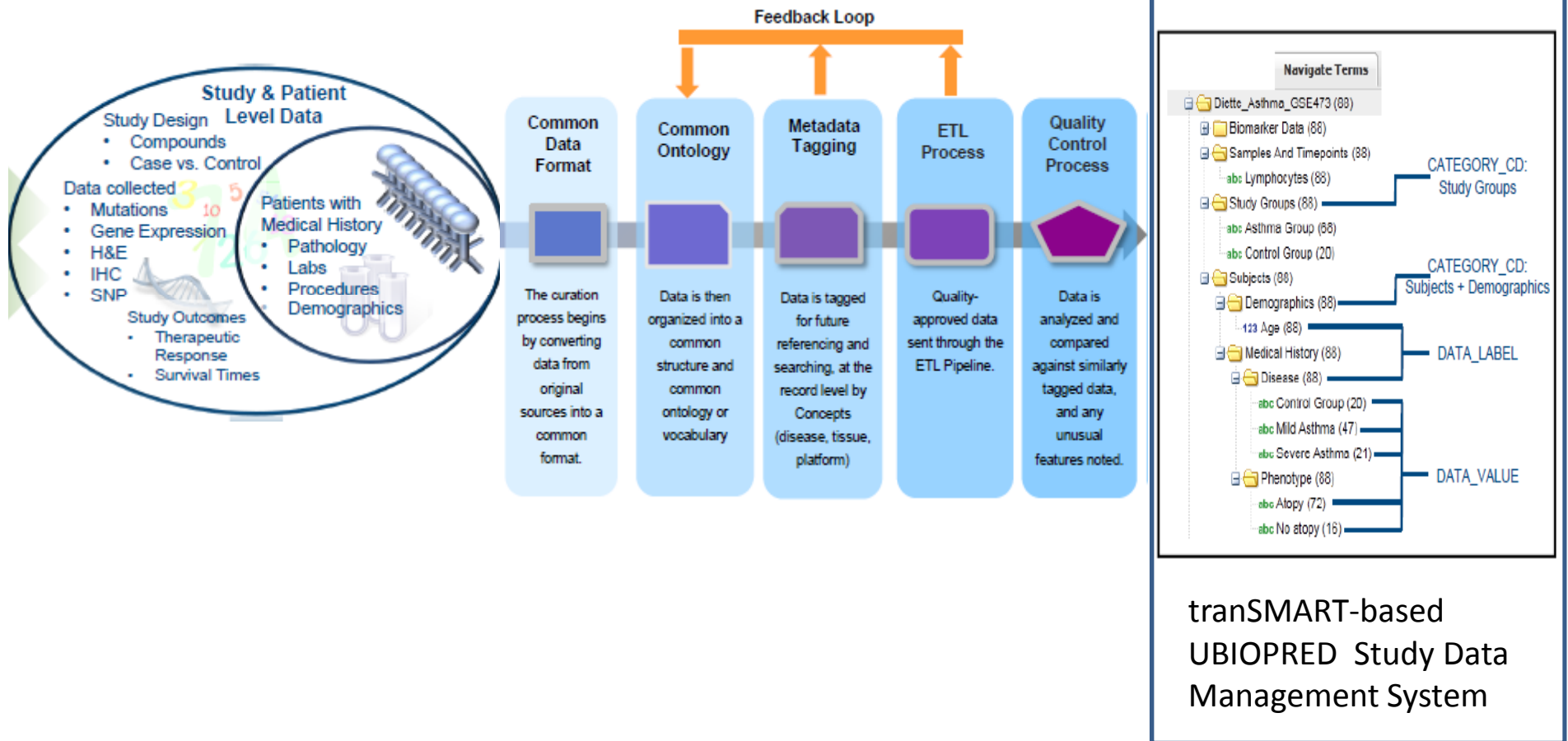
IC Cloud (Virtualisation Layer)

Physical Layer (Imperial Based Data Centre)

UBIOPRED TR Platform Components

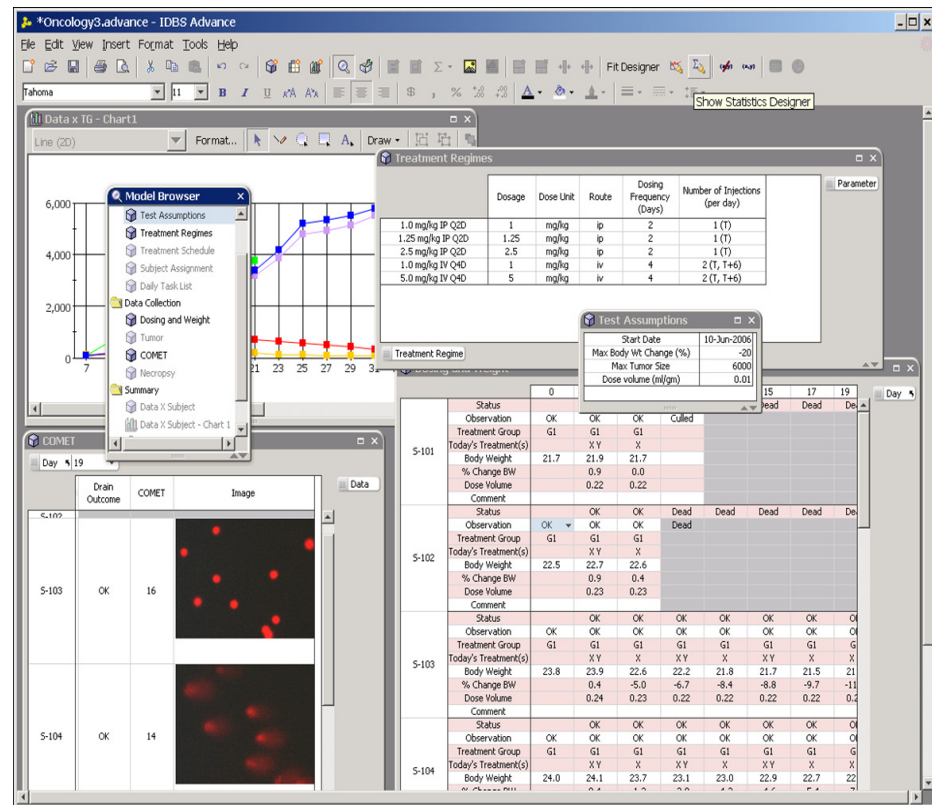
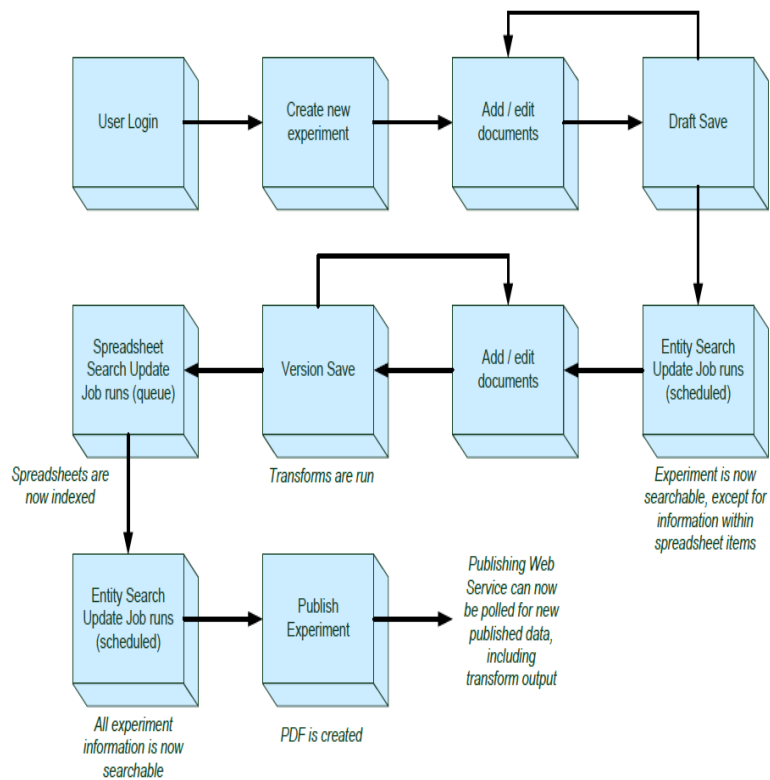


Curation: Building Study Contents and Background Knowledge



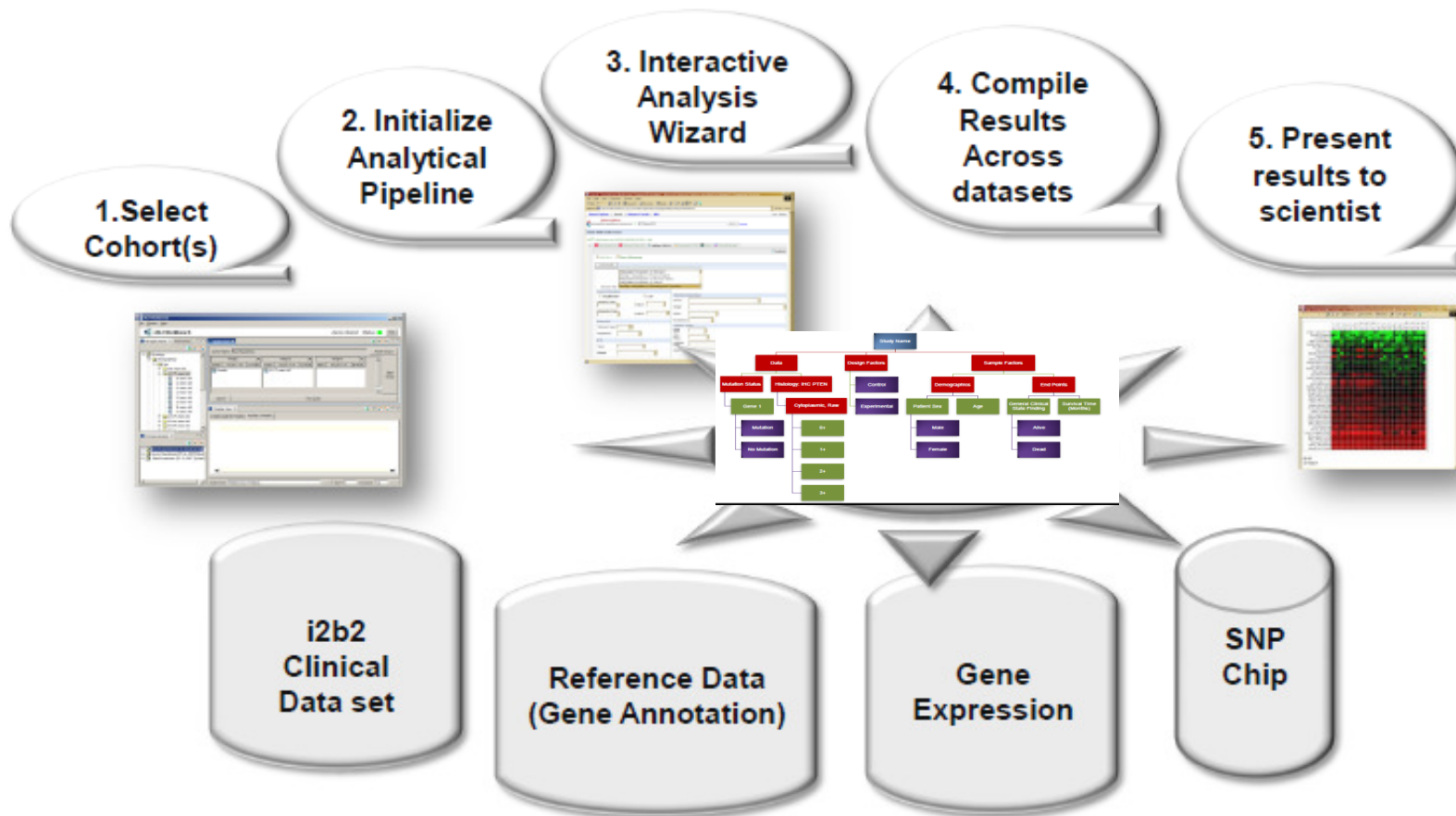
Omic Experiment Management

Omic experiments (Proteomics, lipidomics experiments (WP7) and pre-clinical study (WP6) are managed with EWB of IDBS



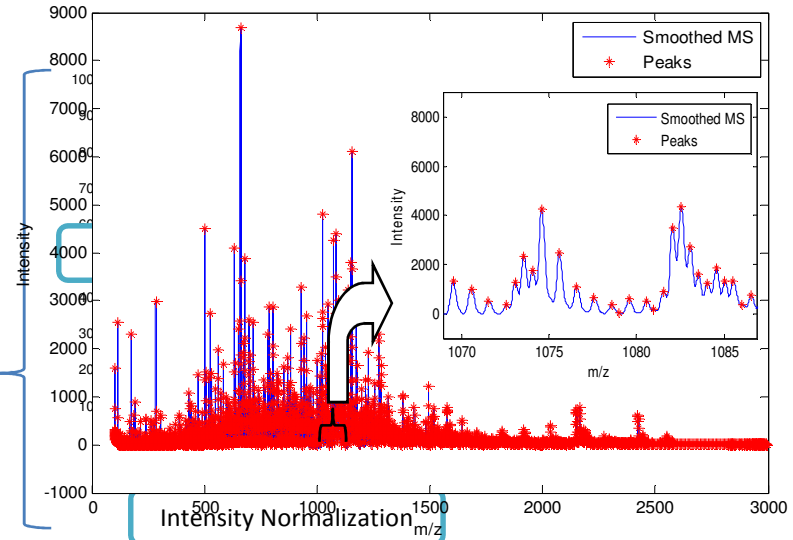
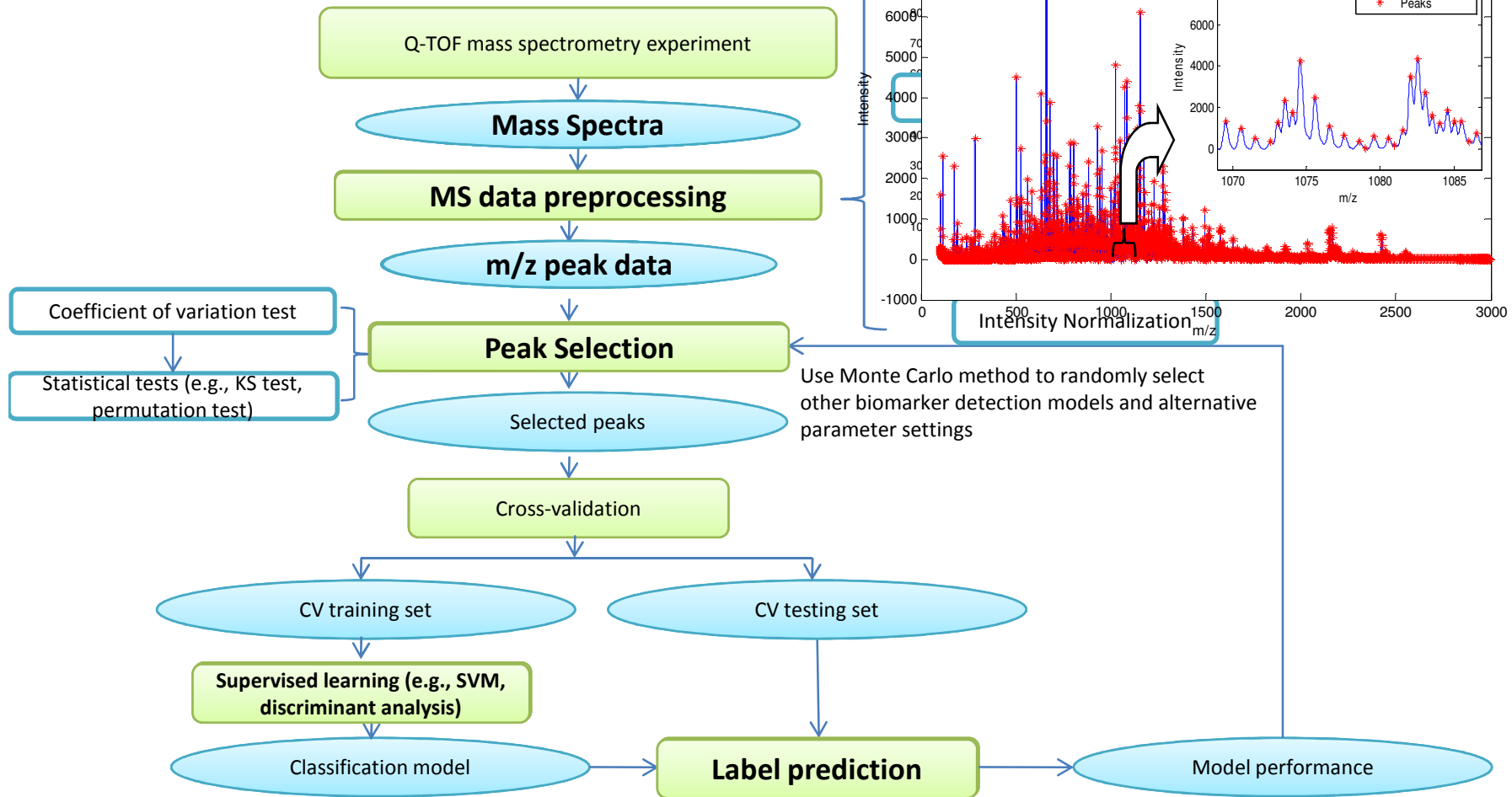
Study Data Management

Study oriented curated data together with patient information are integrated and warehoused in tranSMART for analysis (WP8)



From John Shon et.al tranSMART , AMIA TBI 2012

Workflow-based Analytics: A Proteomics Example



Workflows in InforSense

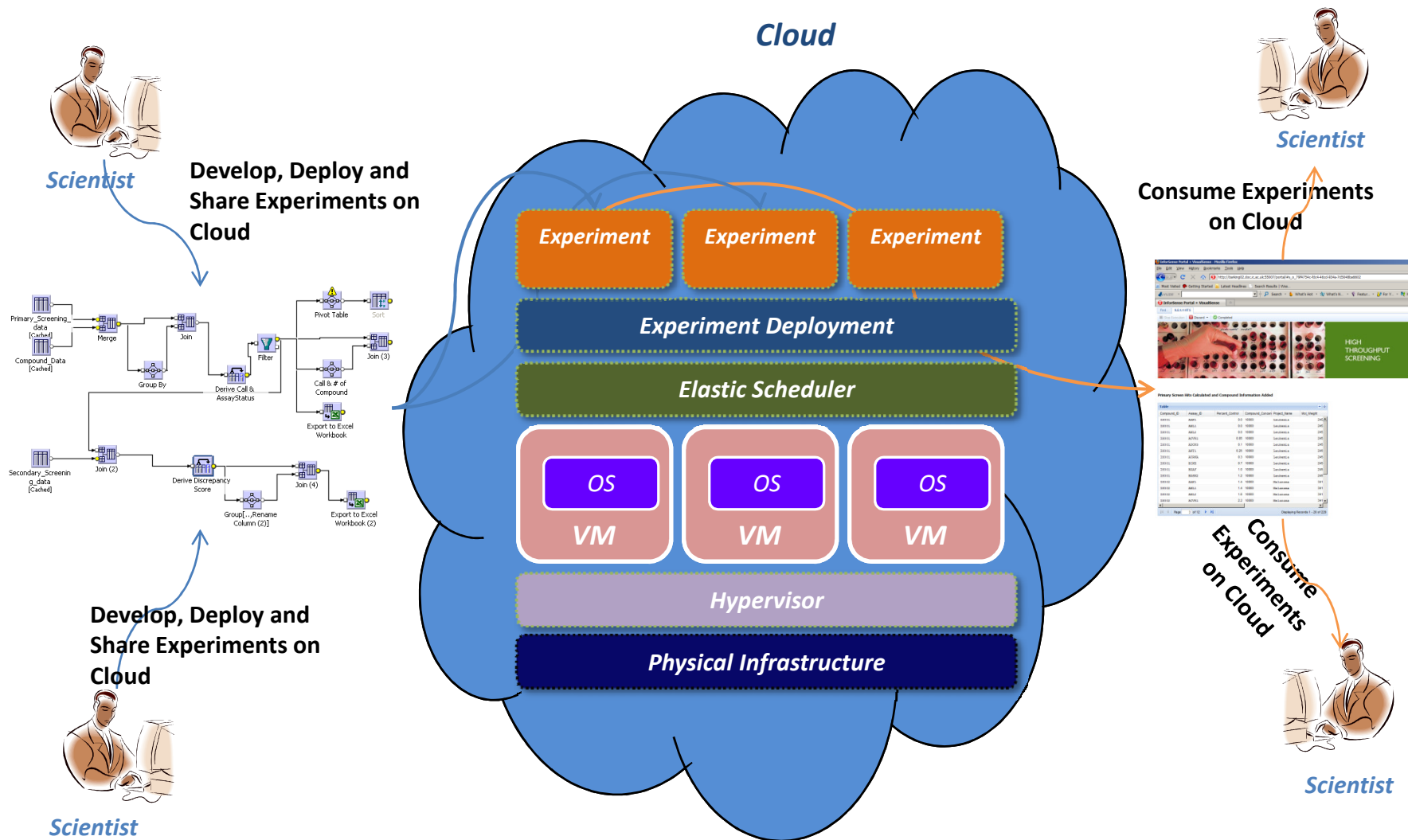
The screenshot displays the InforSense software interface, which is used for data analysis workflows. The interface is divided into several sections:

- XML Wrapper:** The top window title is "XML Wrapper". It contains a "File" menu and a "Tools" menu.
- Project Tree:** On the left, a tree view shows the project structure under "Matlab Integration Projects". Key folders include "MMSample (MMS)", "Prometics (Prometics)", "DataPersist", "Preprocess", "Model_selection", "image (image test)", "maanova (maanova)", "matlab (prototype)", "matlabdemo (matlab demo)", "microarray (test of microarray)", and "simpleMicroarray (simpleMicroarray)".
- Code Editor:** The central window, titled "Edit File - baseli", shows a MATLAB script for a function named "baselineRemove". The code is as follows:

```
function [ data ] = baselineRemove(data)
numSample = length(data);

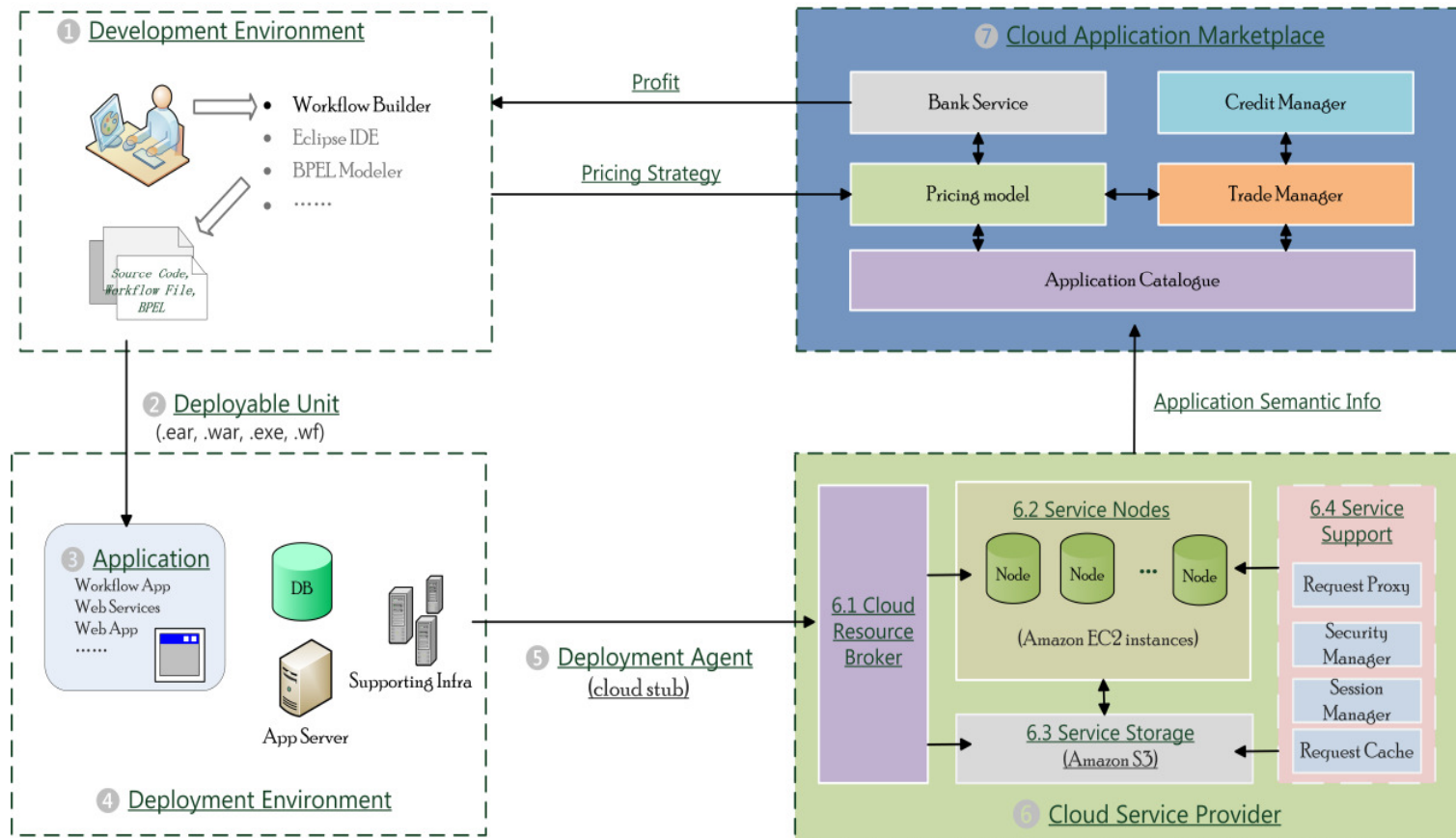
for j = 1:numSample
    intensity = data{j}(:,2);
    mz = data{j}(:,1);
    % data{j}(:,2) = msbackad
    % data{j}(:,2) = msbackad
    data{j}(:,2) = msbackadj(mz,intensity);
end
end
```
- Workflow Diagram:** The main workspace, titled "demo (已更改) Proteomics", shows a data flow process. It starts with a "MAT-file" input, followed by a "Calibration" step. The data then flows through "Baseline Remove" and "smooth" steps. From "smooth", the flow splits into two parallel paths: one through "Peak detection" and "peak alignment", and another through "peak alignment" and "normalization". Both paths converge into a "Save Data" step, which then leads to "Automatic Biomarker detection" and finally a "Result Viewer".
- Preprocess Summary:** A yellow box in the bottom right corner, titled "Preprocess", lists the steps in the workflow:
 - 1 calibration
 - 2 baseline remove
 - 3 smooth
 - 4 peak detection
 - 5 peak alignment

Workflow Deployed as Cloud Applications



A Development Cycle of Cloud Application Building via Workflow

Current development/deployment paradigm + Elasticity + Economic Model



Analytical Register: Enables Collaborative Knowledge Management

The screenshot shows the U-BIOPRED Analytical Register web interface. At the top left is the U-BIOPRED logo, a blue square with a white hand icon and the text 'U-BIOPRED'. To its right is the title 'U-BIOPRED Analytical Register' and the breadcrumb 'Foswiki > UBIOPRED Web > WebHome'. In the top right corner, there are 'Edit' and 'Attach' buttons. Below the header, the user is greeted with 'Hello Michelle Osmond' and a 'Log Out' link. A 'Home' link is also present. A horizontal dotted line separates the header from the main content. On the left side, there is a navigation menu with icons for Home, Studies, Work Packages, Cohorts, Investigations, Procedures, Researchers, and Organisations. Below this is a 'Toolbox' section with links for Recent Updates, TranSMART, Feedback/Bugs, Create New Topic, and Admin Tools. The main content area features a 'Recent Updates' section with a list of document updates, each with a document icon and a timestamp. The updates include: 'Knowledge Management User Manual' (6 hours and 58 minutes ago), 'Validate ECLIPSE microarray data loaded into tranSMART' (1 week, 4 days ago), 'Immunopathology phenotype as part of handprint' (1 week, 4 days ago), 'Transmart Smoke Test' (1 week, 6 days ago), 'Pre-processing raw Affymetrix microarray data for Analysis' (1 week, 6 days ago), 'Debreceen RMA' (1 week, 6 days ago), 'Influence of gender' (2 weeks, 1 day ago), 'Influence of pollution (postal code)' (2 weeks, 1 day ago), 'Adult onset versus childhood onset' (2 weeks, 1 day ago), and 'Upper vs lower airways phenotypes' (2 weeks, 1 day ago). A 'more...' link is provided below the list. Below the updates, there is a 'Pages for you' section, followed by a 'Procedures:' section with a bulleted list of 'Knowledge Management User Manual' and 'Transmart Smoke Test'. Finally, there is a 'Cohorts:' section.

U-BIOPRED Analytical Register
Foswiki > UBIOPRED Web > WebHome

Hello Michelle Osmond
[Log Out](#)

[Home](#)

Welcome to the Analytical Register.

Recent Updates

- [Knowledge Management User Manual](#) (Michelle Osmond, 6 hours and 58 minutes ago)
- [Validate ECLIPSE microarray data loaded into tranSMART](#) (Michelle Osmond, 1 week, 4 days ago)
- [Immunopathology phenotype as part of handprint](#) (Michelle Osmond, 1 week, 4 days ago)
- [Transmart Smoke Test](#) (Michelle Osmond, 1 week, 6 days ago)
- [Pre-processing raw Affymetrix microarray data for Analysis](#) (Michelle Osmond, 1 week, 6 days ago)
- [Debreceen RMA](#) (Michelle Osmond, 1 week, 6 days ago)
- [Influence of gender](#) (Michelle Osmond, 2 weeks, 1 day ago)
- [Influence of pollution \(postal code\)](#) (Michelle Osmond, 2 weeks, 1 day ago)
- [Adult onset versus childhood onset](#) (Michelle Osmond, 2 weeks, 1 day ago)
- [Upper vs lower airways phenotypes](#) (Michelle Osmond, 2 weeks, 1 day ago)

[more...](#)

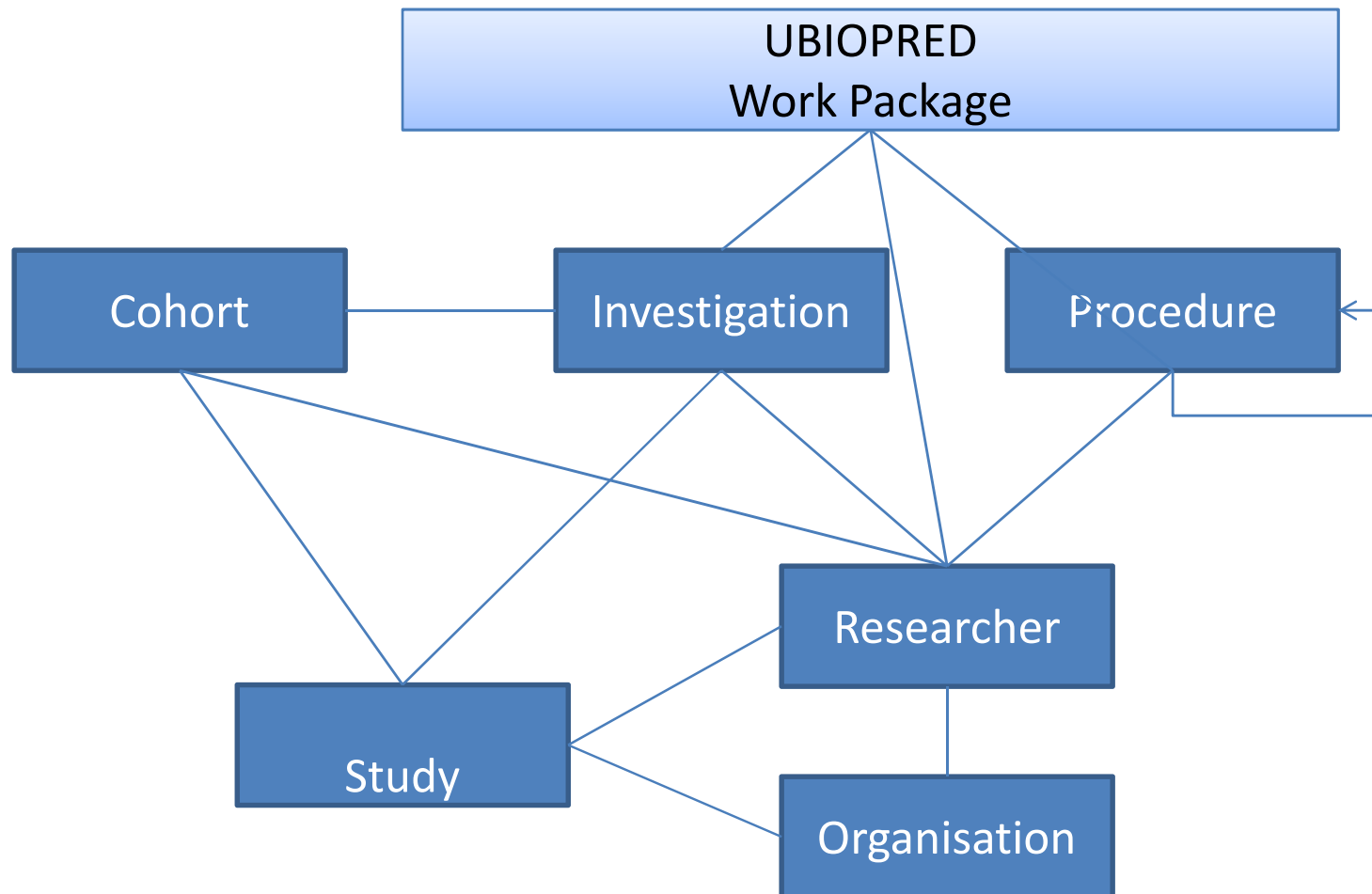
Pages for you

Procedures:

- [Knowledge Management User Manual](#)
- [Transmart Smoke Test](#)

Cohorts:

Mapping Research Collaboration in UBIOPRED



Analytical Register: A Study View

Browser address bar: <https://ubiopred.doc.ic.ac.uk/ar/bin/view/UBIOPRED/UBIOPREDStudy>

U-BIOPRED Analytical Register
UBiopred > UBIOPRED Web > AllStudies > UBIOPREDStudy

Hello Li Guo
Log Out

Study: U-BIOPRED [Edit](#) [Attach](#)

About

The U-BIOPRED study will collect various data types to support the generation of the Handprint. Each data set is used to generate an individual fingerprint that in turn will be combined into a specific handprint.

Data available

Data Class	Assay/Data Source	Cell Types	Number of Samples	Contact
Clinical	ECRF			Kerry Dyson
Clinical	Patient Reported Outcomes			Kerry Dyson
Clinical	Patient Diaries			Florian Singer
Transcriptomics	Human Genome U133 Plus 2.0 Array			WP7- LOIC
Proteomics	Unselective ESI			Paul Skipp
Proteomics	MSe			Paul Skipp
Lipidomics				Tony Postle
Lipidomics	Ecosinoids			Craig Wheelock
Lipidomics				WP7-Krakow
Breathomics	eNose			Peter Brinkman
Breathomics				Philips
Metagenomics				Peter Howarth
CT	AirProm			Sumit Gupta
Histology	Waiting for Agreement	Broncoscopy		Susan Wilson

Work Packages in this study:

- [UBIO-WP10](#)
- [UBIO-WP2](#)
- [UBIO-WP3](#)
- [UBIO-WP4](#)
- [UBIO-WP5](#)
- [UBIO-WP6](#)
- [UBIO-WP7](#)
- [UBIO-WP8](#)
- [UBIO-WP9](#)

Metadata Panel:


- Provider: U-BIOPRED Consortium (UBIOPRED)
- Owner: [Manohara Batuwitage \(LOIC\)](#)
- Contacts: [Anthony Rowe \(JNJ\)](#)
- Relevant Disease Areas: Asthma
- Types of Data collected: Clinical Transcriptomics, Proteomics Lipidomics, Breathomics Metagenomics CT, Histology
- Number of Patients: [blank]
- Date imported to Transmart: [blank]

[edit](#)

Analytical Register: Work Package View

← → C <https://ubiopred.doc.ic.ac.uk/ar/bin/view/UBIOPRED/UBIOWP5> ☆ ↻ 🌐 📄

Search 🔍 | [f](#) [a](#) [YouTube](#) [CNN](#) [📺](#) [📧](#) [👁](#)

 **U-BIOPRED Analytical Register**
U-BIOPRED > UBIOPRED Web > AllWorkPackages > UBIOWP5

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[Admin Tools](#)

[Edit](#) [Attach](#)

Work Package: UBIO-WP5

Name: UBIO-WP5
Study: U-BIOPRED
[edit](#)

Investigations

- [Viral-induced changes handprints](#)
- [The IL33/IL1RL1 axis in asthma](#)
- [Exome re-sequencing in asthma](#)
- [Investigation of Genes from GWAS of lung function in asthma](#)
- [Genome Wide Association study of Airway Remodelling Measures in asthma](#)
- [GWAS - Quantitative Trait Loci approaches in asthma](#)
- [The role of urokinase receptor in asthma](#)
- [Epithelial genetics in asthma](#)

Researchers


- [Norbert Krug](#)
- [Peter Sterk](#)
- [Scott Wagers](#)

WorkPackageForm [edit](#)

[Edit](#) | [Attach](#) | [Print version](#) | [History](#) | [Backlinks](#) | [View wiki text](#) | [Edit wiki text](#) | [More topic actions](#)

Topic revision: r1 - 08 Jun 2011 - 11:46:25 - MichelleOsmond

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Analytical Register: A Cohort View

U-BIOPRED Analytical Register

U-BIOPRED > UBIOPRED Web > AllCohorts

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Cohorts

[Add new cohort](#)

Filter by Study: **All** · AirProm · Debrecen RMA · ECLIPSE · Fan Macrophage · U-BIOPRED

Showing all cohorts.

Name	Study	Researcher	Size (1)	Size (2)	Transmart
Sputum Microarray for Gold II and Gold III patients	ECLIPSE	Shu Lin Yan (LOIC)	69	58	1787986 ↗
Severe asthmatics with irreversible airflow limitation (as defined by ten Brinke et al)	U-BIOPRED	Ariane Wagener (AMST)			1788005 ↗
Severe asthmatics with irreversible airflow limitation (as defined by TENOR)	U-BIOPRED	Ariane Wagener (AMST)			1788007 ↗
Severe asthmatics with irreversible airflow limitation (as defined by ERS guidelines)	U-BIOPRED	Ariane Wagener (AMST)			1788011 ↗
Identifying severe asthmatics with irreversible airflow limitation (as defined by ten Brinke et al)	ECLIPSE	Michelle Osmond (LOIC)	132		1787916 ↗
Identifying severe asthmatics with irreversible airflow limitation (as defined by TENOR)	ECLIPSE	Michelle Osmond (LOIC)	191		1787922 ↗
FEV1 vs Exacerbation Rate	ECLIPSE	Anthony Rowe (JNJ)	148		1787925 ↗
COPD Patients for Clustering Analysis	ECLIPSE	Manohara Batuwitage (LOIC)	148		1787928 ↗
Normal BMI	U-BIOPRED	David Gibbon (LOIC)			
Virus Cohort 1		Anthony Rowe (JNJ)			
Cluster probesets based on the similarity of variation of expression patterns across samples		Yang Li (LOIC)			


11 found.

[Add new cohort](#)

[Edit](#) | [Attach](#) | [Print version](#) | [History](#) | [Backlinks](#) | [View wiki text](#) | [Edit wiki text](#) | [More topic actions](#)

Topic revision: r9 - 04 Apr 2011 - 15:59:09 - MichelleOsmond

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Analytical Register: Interfacing to Cohort Selection

The screenshot displays the Analytical Register web interface. At the top, there is a navigation bar with links for Search, Dataset Explorer, Gene Signature/Lists, Admin, Request Consult, Feedback, Help, and Log off Imperial College User. Below this, a secondary navigation bar includes Search by Subject, Navigate Terms, Generate Summary Statistics, Summary, Advanced, Clear, Save, Export, and Print. The main interface is divided into two columns: Search and Comparison. The Search column contains a search box, a dropdown for Type (set to ALL), and buttons for SEARCH and CLEAR. The Comparison column is split into two panels, Subset 1 and Subset 2. Each panel contains a list of criteria with associated AND, Exclude, and X buttons. The criteria in Subset 1 include: ...Baseline Day 1\, ...Baseline Day 1\, ...F\, ...M\, ...Age at Consent\, and ...A: Severe non-smoking asthma\, ...B: Severe smoking asthma\.

Search | Dataset Explorer | Gene Signature/Lists | Admin | Request Consult | Feedback | Help | Log off Imperial College User

Search by Subject | Navigate Terms

Generate Summary Statistics | Summary | Advanced | Clear | Save | Export | Print

Comparison | Results/Analysis | Grid View | Haploview

Subset 1 | Exclude | X

...Baseline Day 1\

AND | Exclude | X

...Baseline Day 1\

AND | Exclude | X

...F\
...M\
AND | Exclude | X

...Age at Consent\
AND | Exclude | X

...A: Severe non-smoking asthma\
...B: Severe smoking asthma\
AND | Exclude | X

Subset 2 | Exclude | X

AND | Exclude | X

AND | Exclude | X

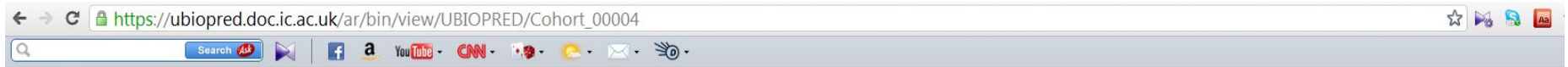
AND | Exclude | X

AND | Exclude | X

AND | Exclude | X

Fiddler Disabled

Analytical Register – Cohort View



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- Toolbox**
- [Recent Updates](#)
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Cohort: Sputum Microarray for Gold II and Gold III patients

[Edit](#) [Attach](#)

Sputum Microarray for Gold II and Gold III patients

Subset 1

Size: 69

Query:

Affymetrix Gene Chip HG-U133 Plus 2: **Sputum**
 and
 GOLD: **Gold II**

Subset 2

Size: 58

Query:

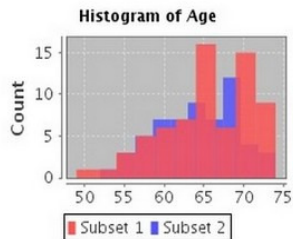
Affymetrix Gene Chip HG-U133 Plus 2: **Sputum**
 and
 GOLD: **Gold III**

Cohort ID:	Cohort_00004
TransSMART:	1787986 edit
Study:	ECLIPSE
Researcher:	Shu Lin Yan (LOIC) edit

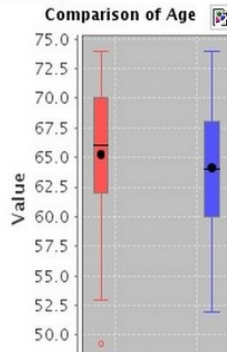
Used in the following:

- Investigation : [Validate ECLIPSE microarray data loaded into tranSMART](#)

Subject Totals		
Subset 1	Both	Subset 2
69	0	58



Subset 1	
Mean:	65.29
Median:	66
IQR:	8
SD:	5.62
Data Points:	69




Subset 2	
Mean:	64.14
Median:	64
IQR:	8
SD:	5.03
Data Points:	58

Analytical Register: An Investigation View

← → ↻ https://ubiopred.doc.ic.ac.uk/ar/bin/view/UBIOPRED/AllInvestigations?q_study=UBIOPREDStudy ☆

Search Ask

f a YouTube CNN

 **U-BIOPRED Analytical Register**
UBIOPRED > UBIOPRED Web > AllInvestigations

Hello Li Guo [Log Out](#)

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Filter by:

- Status
- Study
 - Any
 - AirProm
 - Debreccen RMA
 - ECLIPSE
 - Fan Macrophage
 - U-BIOPRED**
- Work Package
- Category

Showing all investigations from U-BIOPRED, all work packages, in any categories.

[The role of urokinase receptor in asthma](#)
Proposed; Initiator: Dominick Shaw Contributors: Dominick Shaw
16 Apr 2012 - 10:38 ... Background: We have identified that polymorphisms spanning urokinase plasminogen activator receptor (uPAR) are susceptibility markers for the development of bronchial hyper-responsiveness and predictors of lung function decline in asthma (1). In asthma we have identified an elevated uPAR protein level in the epithelium in asthma patient biopsies and elevated uPAR in bronchial epithelial cells cultured in vitro had a defective repair phenotype (2). Therefore accumulating data suggests uPAR is a functionally relevant receptor in asthma and the genetic data suggest that uPAR polymorphisms may contribute to a predisposition to airway remodelling.
Aims: i) To extensively genotype and/or sequence the uPAR in all subjects and associate the presence and absence of polymorphisms with a) clinical relevant outcomes, b) cellular outcomes, c) molecular outcomes and d) biopsy remodelling outcomes. ii) To investigate the relative expression of uPAR in all biological fluids and biopsies and relate to the presence of SNPs and clinical outcomes and airway remodelling.
preclinical, inflammation/remodelling, biomarkers ECLIPSE, U-BIOPRED UBIO-WP3,
UBIO-WP4,
UBIO-WP5,
UBIO-WP6,
UBIO-WP7

[Epithelial genetics in asthma](#)
Proposed; Initiator: Dominick Shaw Contributors: Dominick Shaw
16 Apr 2012 - 10:38 ... Background: GWAS data in asthma suggests that multiple genes of relevance to airway epithelial function are potentially altered. These findings require the characterisation of cellular responses in carriers and non-carriers of relevant risk alleles.
Aims: To identify carriers and non carriers of relevant risk alleles and characterise primary bronchial epithelial cell functions relevant to these targets e.g. SMAD3 SNPs and TGF-1 signalling.
genotypes U-BIOPRED UBIO-WP3,
UBIO-WP4,
UBIO-WP5,
UBIO-WP6,
UBIO-WP7

[GWAS - Quantitative Trait Loci approaches in asthma](#)
Proposed; Initiator: Dominick Shaw Contributors: Dominick Shaw
16 Apr 2012 - 10:35 ... Background: Data relating genetic polymorphism with mRNA expression in asthma subjects is sparse. With advances in genomics approaches it is now possible to generate a GWAS SNP dataset and global mRNA expression profile from any tissue or cell. These data will potentially aid the translation of recent findings from asthma GWAS and potentially take our understanding of asthma in new directions.
Aims: To complete a GWAS and quantify gene expression in all subjects e.g. Affymetrix array from a) lung tissue, b) bronchial epithelial cells, c) airway fibroblasts, d) airway smooth muscle cells and e) peripheral blood mononuclear cells and generate eQTL datasets.
ECLIPSE, U-BIOPRED UBIO-WP3,
UBIO-WP4,
UBIO-WP5,
UBIO-WP6

[Genome Wide Association study of Airway Remodelling Measures in asthma](#)
Proposed; Initiator: Dominick Shaw Contributors: Dominick Shaw
16 Apr 2012 - 10:34 ... Background: Structural alterations termed "airway remodelling" occur in asthma and the extent of remodelling is variable. Airway remodelling is characterised by; smooth muscle hypertrophy/hyperplasia, sub-epithelial fibrosis, basement membrane thickening, increased extracellular matrix deposition, angiogenesis and more recently alterations in epithelial functions have been identified including metaplasia and goblet cell hyperplasia. The mechanisms underlying airway remodelling remain to be determined.

Analytical Register: Investigation Drill Down



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Investigation: Is there a relationship between Exacerbation Rate and FEV-1 in COPD subjects?

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Owner:	Manohara Batuwitige (LOIC)
Contributors:	Anthony Rowe (LOIC), Manohara Batuwitige (LOIC)
Status:	Ongoing
Categories:	Methodology
Studies used:	ECLIPSE

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Research Hypothesis

A core dogma of COPD research is that as FEV-1 decreases the number of exacerbations a COPD sufferer experiences will increase. Or to put simply it is expected that exacerbations will increase as lung function deteriorates.

This study investigates whether this correlation exists in the Eclipse study data.

Cohorts Used

- [FEV1 vs Exacerbation Rate \(TranSMART: 1787925\)](#)

[+ Add link to cohort...](#)

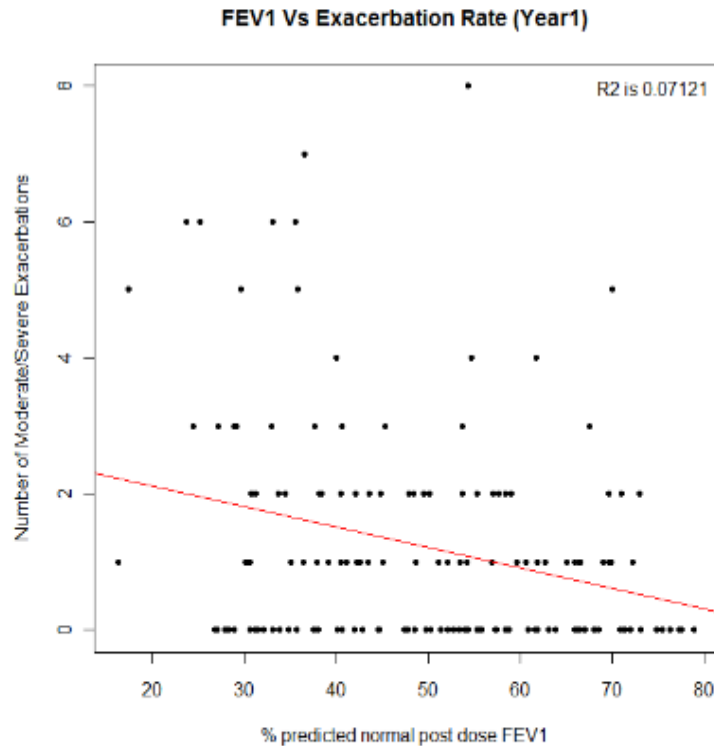
Method and Results

Analytical Register Further Drill Down: Method

Method and Results

Based on the [ECLIPSE](#) cohort of patients we fitted linear models between the % predicted normal post-dose FEV1 score and the exacerbation rate that patients had in Years 1,2 & 3 of the [ECLIPSE](#) study. Selection of the patient data was conducted through [TranSMART](#) and the patient data extracted and analysed using the R platform. (The R Code for this analysis is attached [here](#))

- Year 1 - FEV1 VS Exacerbation Rate (R2 = 0.07121):



- Year 2 - FEV1 VS Exacerbation Rate (R2 = 0.06442):

Analytical Register: Interfacing to Sample Tracking

U-BIOPRED

U-BIOPRED Analytical Register

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Investigations

Medical Research
SampleTracker

Sam Oper Help [Data Management](#)

Home Samples Locations **Patients** Projects Shipments Receive Search +

Patient **Alan** Customize Page | Printable View | Help for this Page

< Back to List: Patients Samples:0

Patient Detail Edit Delete Clone Sharing

Patient Name	Alan	Owner	Sam Oper [Change]
Date Of Birthday	05/08/2010		
Gender	Male		
Created By	Sam Oper, 31/08/2011 19:50	Last Modified By	Sam Oper, 31/08/2011 19:50

Edit Delete Clone Sharing

Samples New Sample Samples Help

No records to display

Medical Research
SampleTracker

Sam Oper Help [Data Management](#)

Home Samples **Locations** Patients Projects Shipments Receive Search +

Location **Fridge2** Customize Page | Printable View | Help for this Page

< Back to List: Patients SubLocations To Location:1 | Samples:0

Location Detail Edit Delete Clone Sharing New SubLocation

Location Name	Fridge2	Owner	Sam Oper [Change]
Created By	Sam Oper, 31/08/2011 19:46	Last Modified By	Sam Oper, 31/08/2011 19:46

Edit Delete Clone Sharing New SubLocation

SubLocations To Location New SubLocation To Location SubLocations To Location Help

Action	Sub Location	Created By	Created Date	Last Modified By	Last Modified Date
Edit Del	Box023	Sam Oper	31/08/2011 19:56	Sam Oper	31/08/2011 19:56

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Analytical Register: Fully Integrated with TranSMART

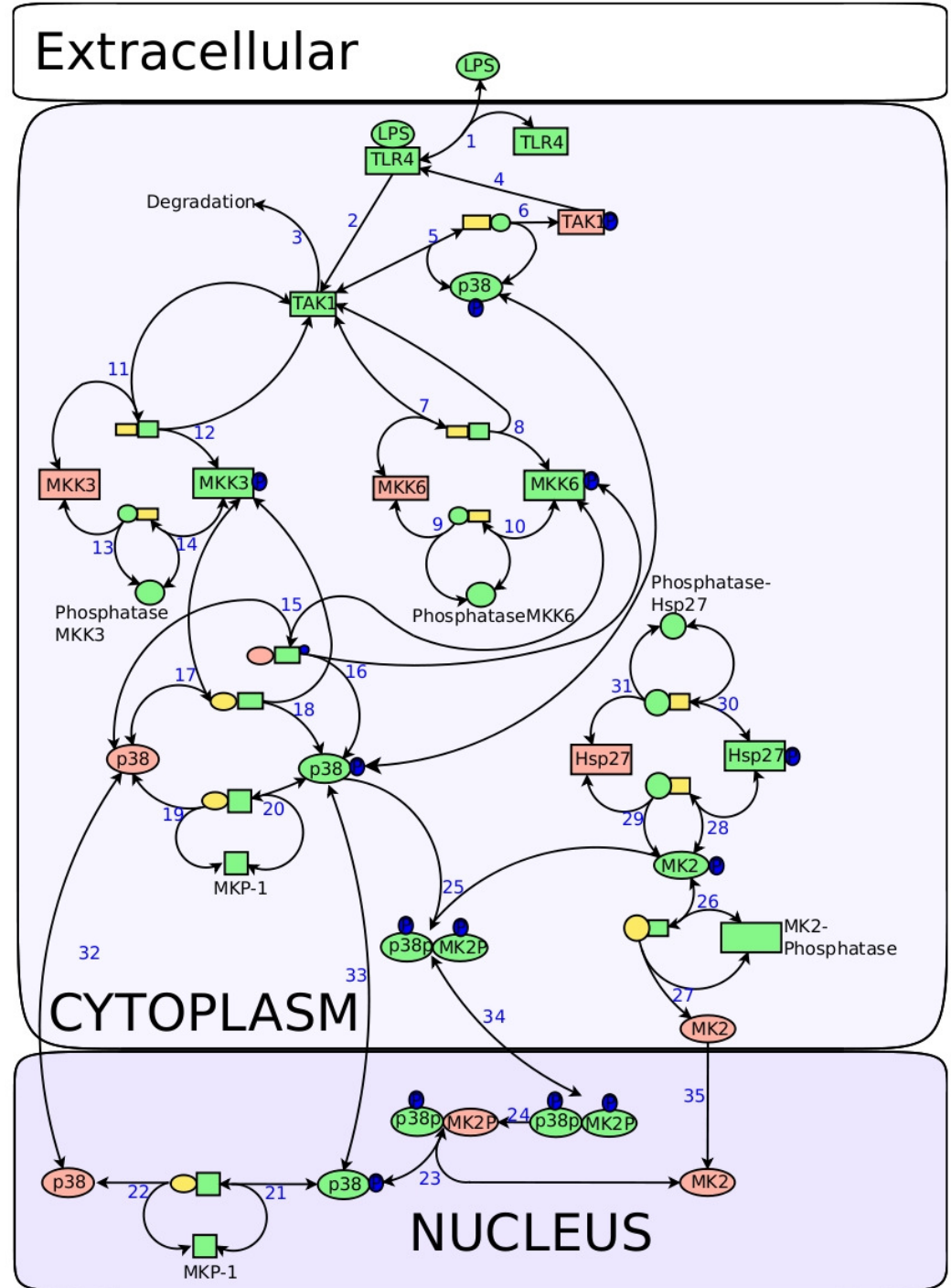
The screenshot displays the Analytical Register interface, which is fully integrated with TranSMART. The interface is divided into several sections:

- Navigation Bar:** Includes links for Search, Dataset Explorer, Gene Signature/Lists, Admin, Request Consult, Feedback, Help, and Log off Imperial College User.
- Search Section:** Features a search box, a dropdown menu for "Type" (set to "ALL"), and buttons for "SEARCH" and "CLEAR".
- Summary Statistics Section:** Contains a "Query Summary for Subset 1" with a complex query string: `(\WMI Studies\WMI Studies\UBIOPRED\Clinical Data\Lung function tests\Reversibility\FEV1 post salbutamol (L) \Baseline Day 1\) AND (\WMI Studies\WMI Studies\UBIOPRED\Clinical Data\Lung function tests\Reversibility\FVC post salbutamol (L) \Baseline Day 1\) AND (\WMI Studies\WMI Studies\UBIOPRED\Subjects\Demographic Data\Gender\F\ OR \WMI Studies\WMI Studies\UBIOPRED\Subjects\Demographic Data\Gender\M\) AND (\WMI Studies\WMI Studies\UBIOPRED\Subjects\Demographic Data\Age at Consent\) AND (\WMI Studies\WMI Studies\UBIOPRED\Study Group\Cohort\A: Severe non-smoking asthma\ OR \WMI Studies\WMI Studies\UBIOPRED\Study Group\Cohort\B: Severe smoking asthma\)`
- Subject Totals Table:** A table with three columns: "Subset 1", "Both", and "Subset 2". All values are currently 0.
- Comparison of Age:** A section with a placeholder for a comparison chart.
- Histogram of Age:** A section with a placeholder for an age histogram.

Subset 1	Both	Subset 2
0	0	0

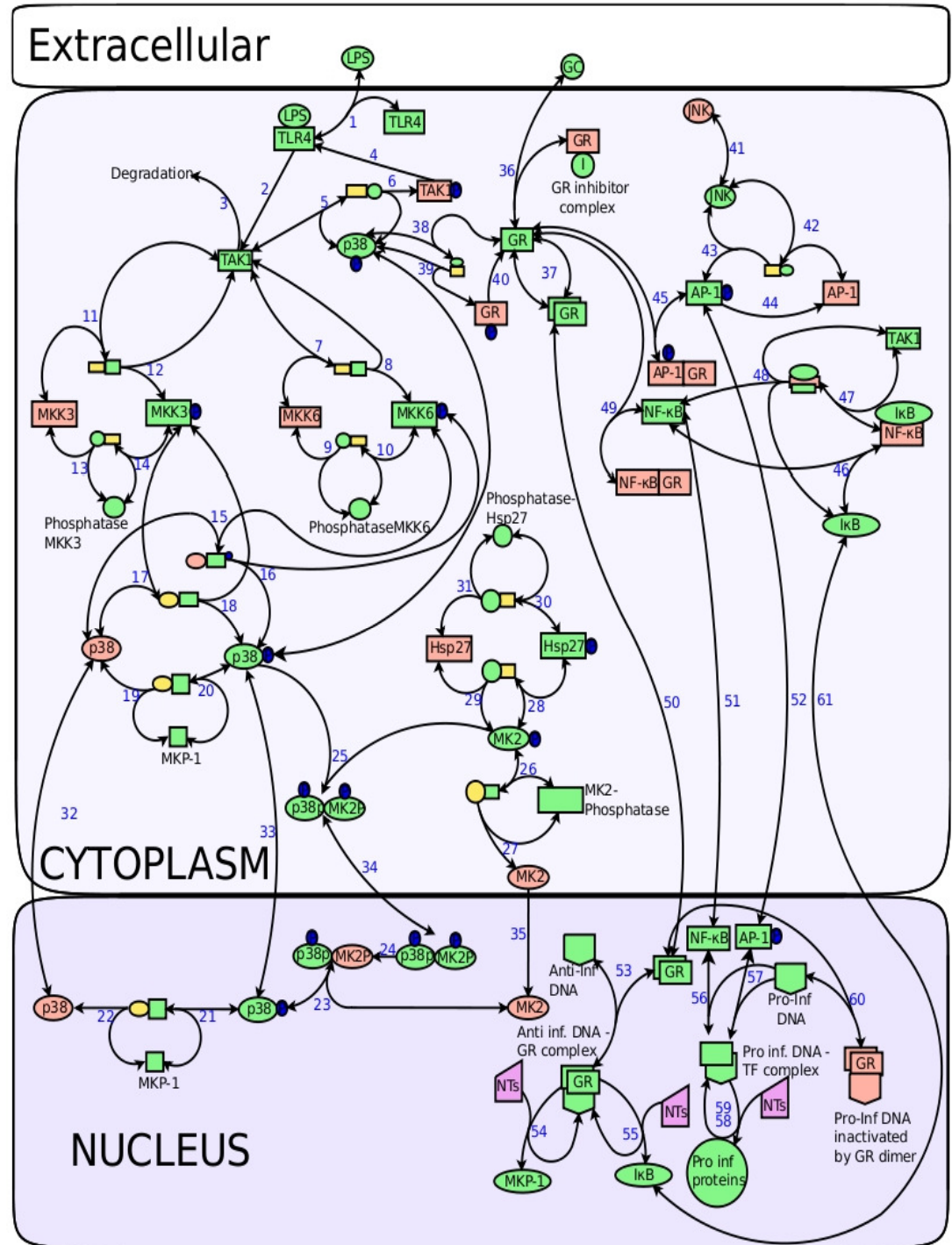
UBIOPRED System Biology Study

1. We have developed p38 pathway model in SBML and perform simulation through MATLAB.

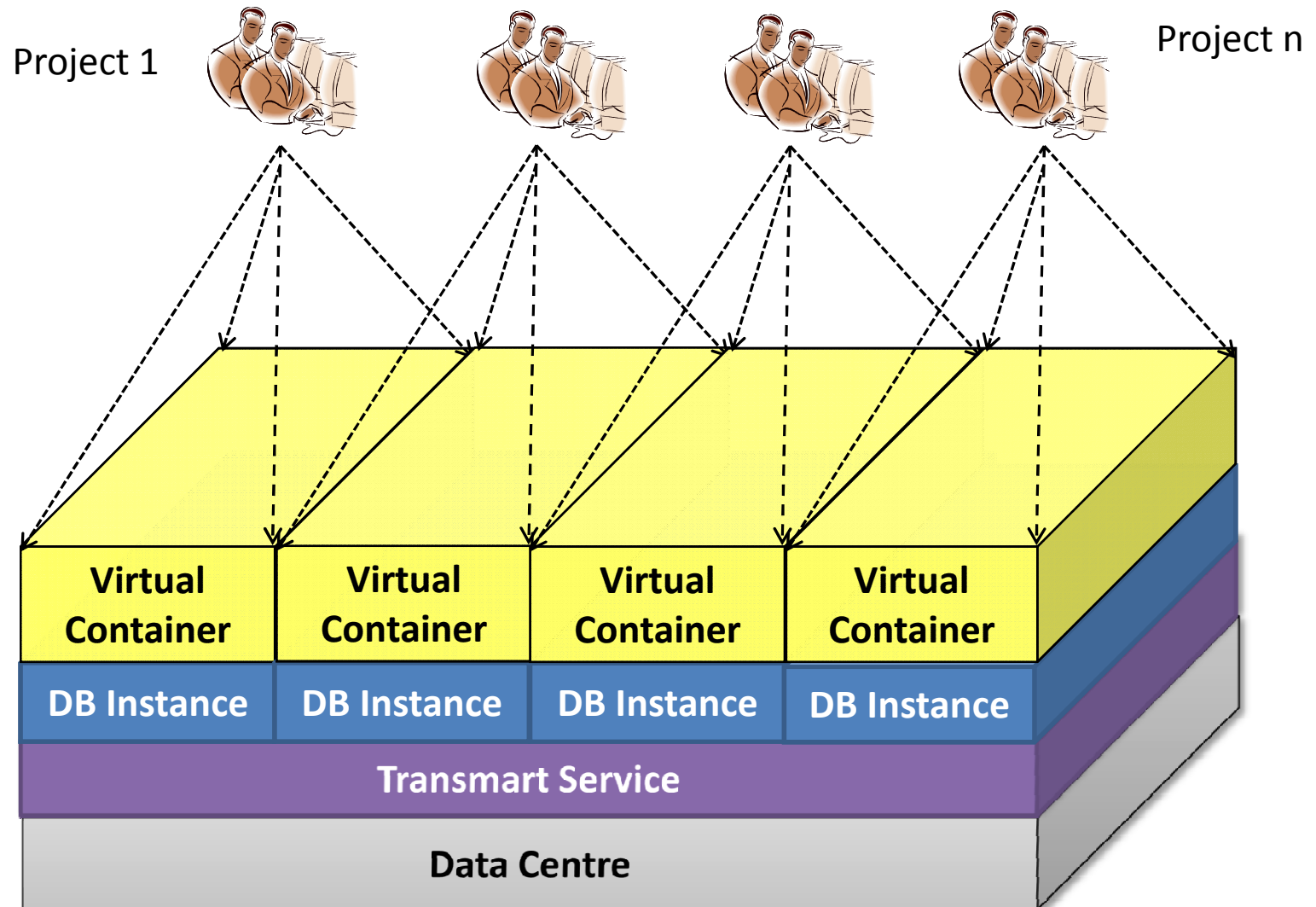


UBIOPRED System Biology Study

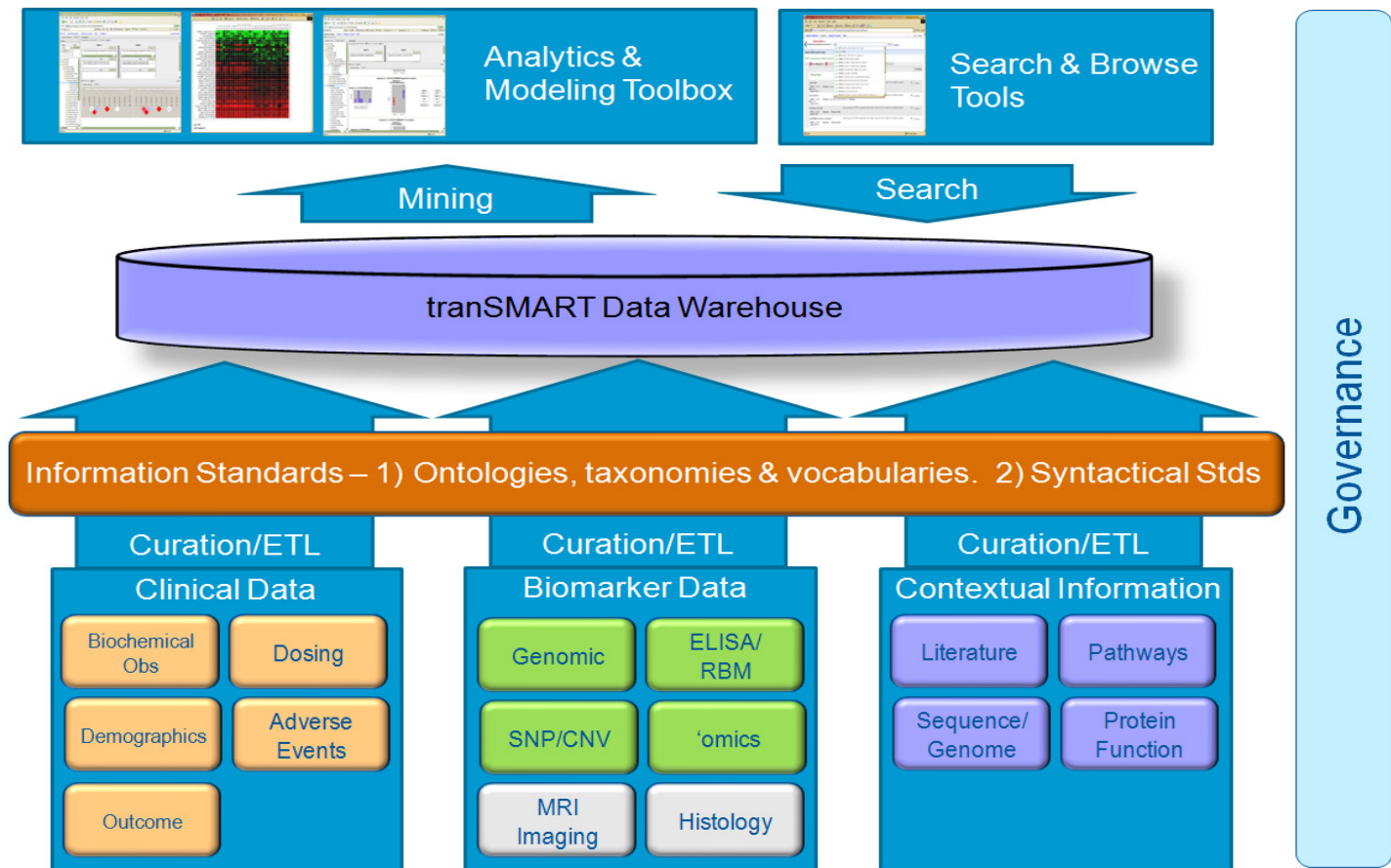
3. We have proposed some hypotheses to suggest possible crosstalk between GC and p38 pathways.
4. We then construct the integrated pathway model in SBML.
5. Test the stability of this integrated model.



Extending UBIOPRED to Support Multiple Projects



eTRIKS : European translational research and knowledge management services



Conclusion: the end of the beginning

- UBIOPRED knowledge management system supports cross-institutional large scale translational research
- UBIOPRED knowledge management system support the entire knowledge production process
- For PPP-based TR projects, collaborative research support in a VO environment is circuital
- Modern technology such as cloud and workflow provide the technical foundation for its implementation
- The development is moving forward to support IMI translational projects in general by eTRIKS project