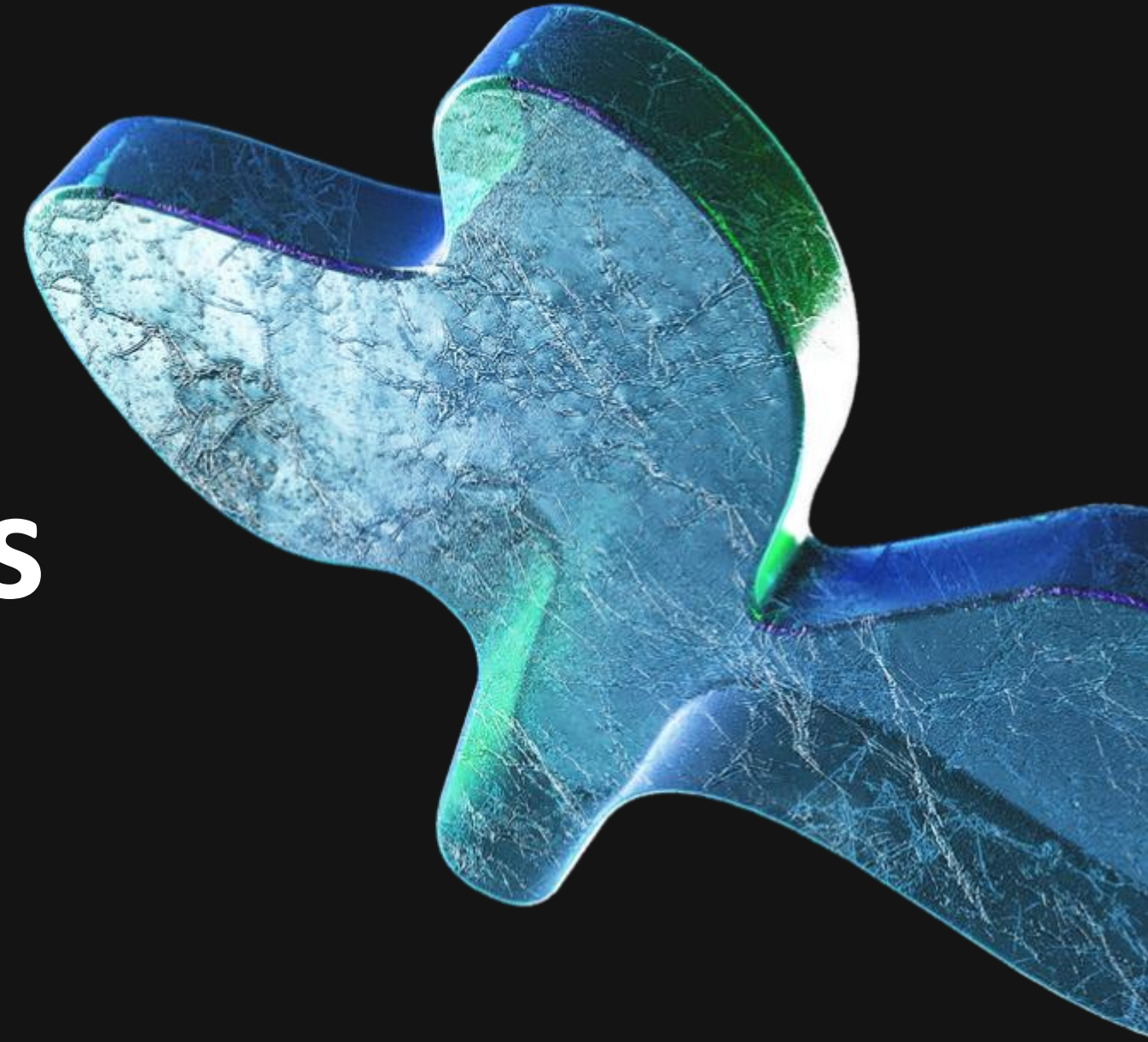




AI-powered modeling approaches to support the development of new therapies for autoimmune diseases



Philippe MOINGEON

Immuno-inflammation, Servier

September 21st, Rosa Webinar series

An independent, global pharmaceutical group governed by a non-profit foundation



31st largest pharmaceutical Group worldwide*
2nd largest pharmaceutical Group in France*



150 countries
in which the Group's medicines
are distributed



22,500 employees



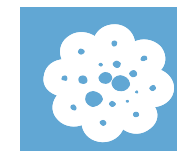
Leader in cardiology

4th leading pharmaceutical group in cardiology worldwide*
3rd leading pharmaceutical group in hypertension worldwide*



€4.7 billion Group revenue in 2019/2020

- Brand-name medicines: €3.3 billion
- Generic medicines: €1.4 billion



Ambition to become

a renowned and innovative player in oncology



€626 million EBITDA in 2019/2020



More than 20% of Group brand-name revenue
invested in R&D each year in average

*Source: IQVIA Analytics Link, MAT Q2-2021



R and D focus:

- Oncology
- Neurology
- Immunoinflammation

Outline

- **AI applications in support to drug development**

- *A pharmaceutical industry perspective*
- *Disease modeling applied to Sjogren syndrome (and Lupus)*
- *Implications for drug design and development*
- *High throughput drug discovery: the Patrimony platform*



- **In silico prediction of drug efficacy**

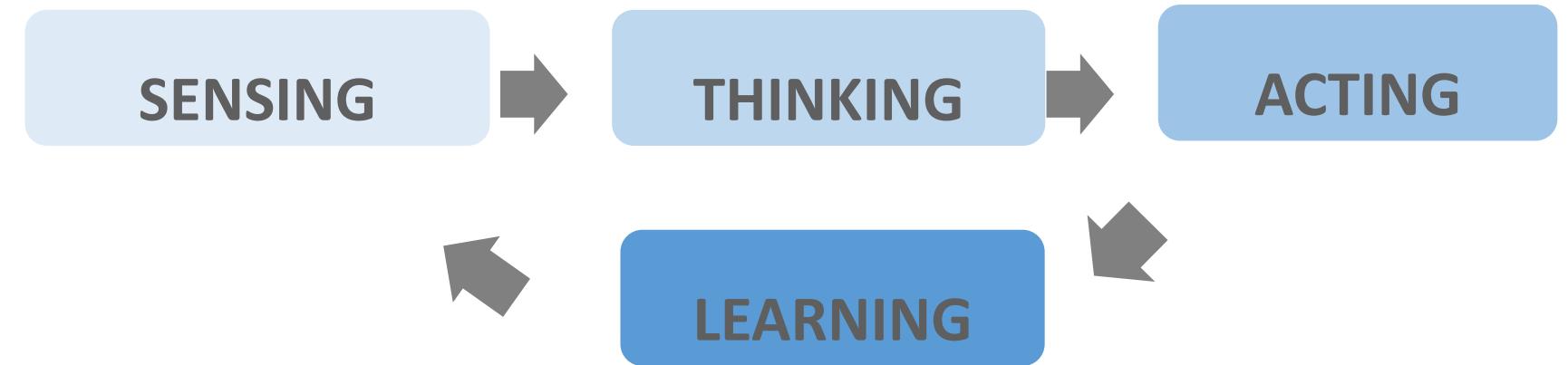
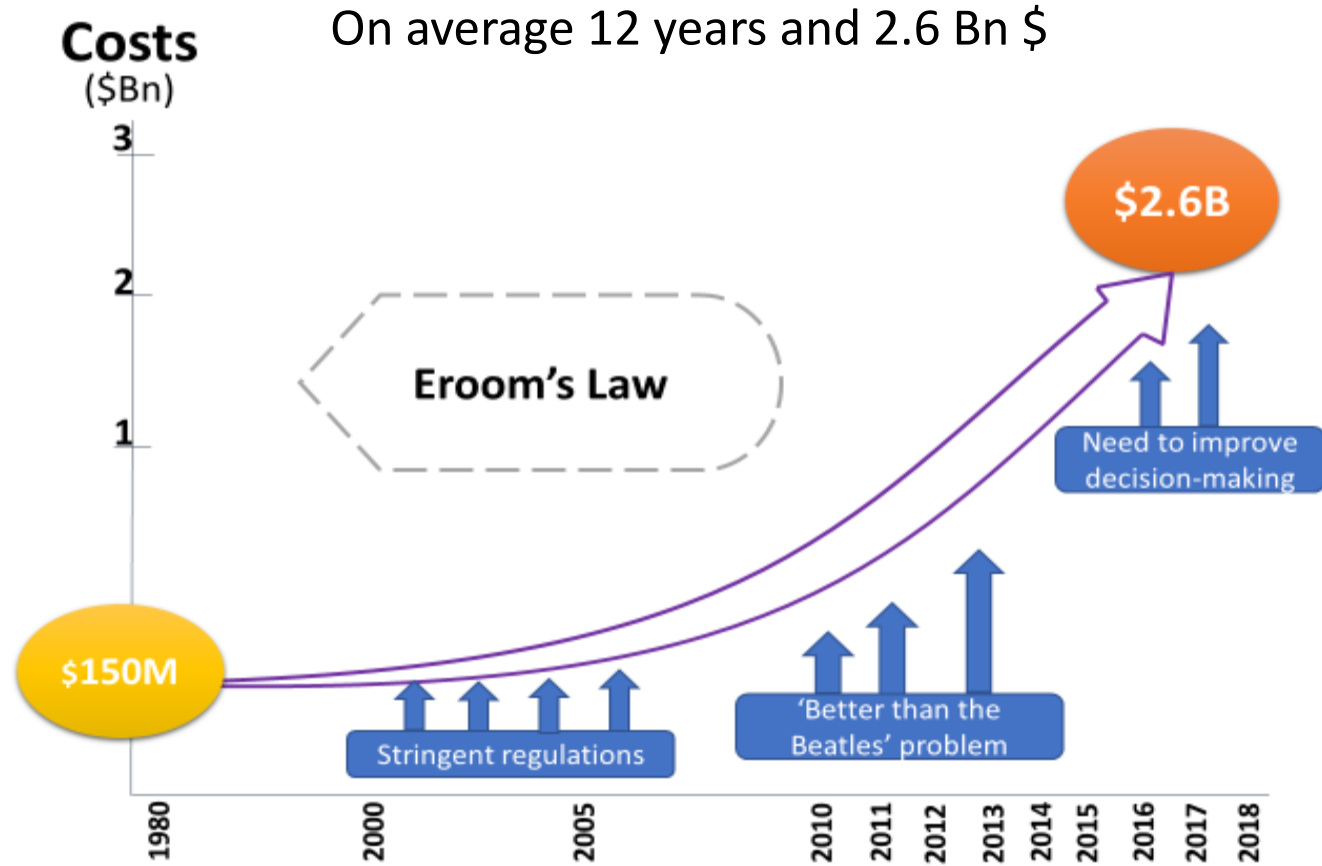
- *QSP model of an anti IFN α Mab in Lupus*
- *Causal disease representation (eg Sjogren)*

- **Conclusions and perspectives**

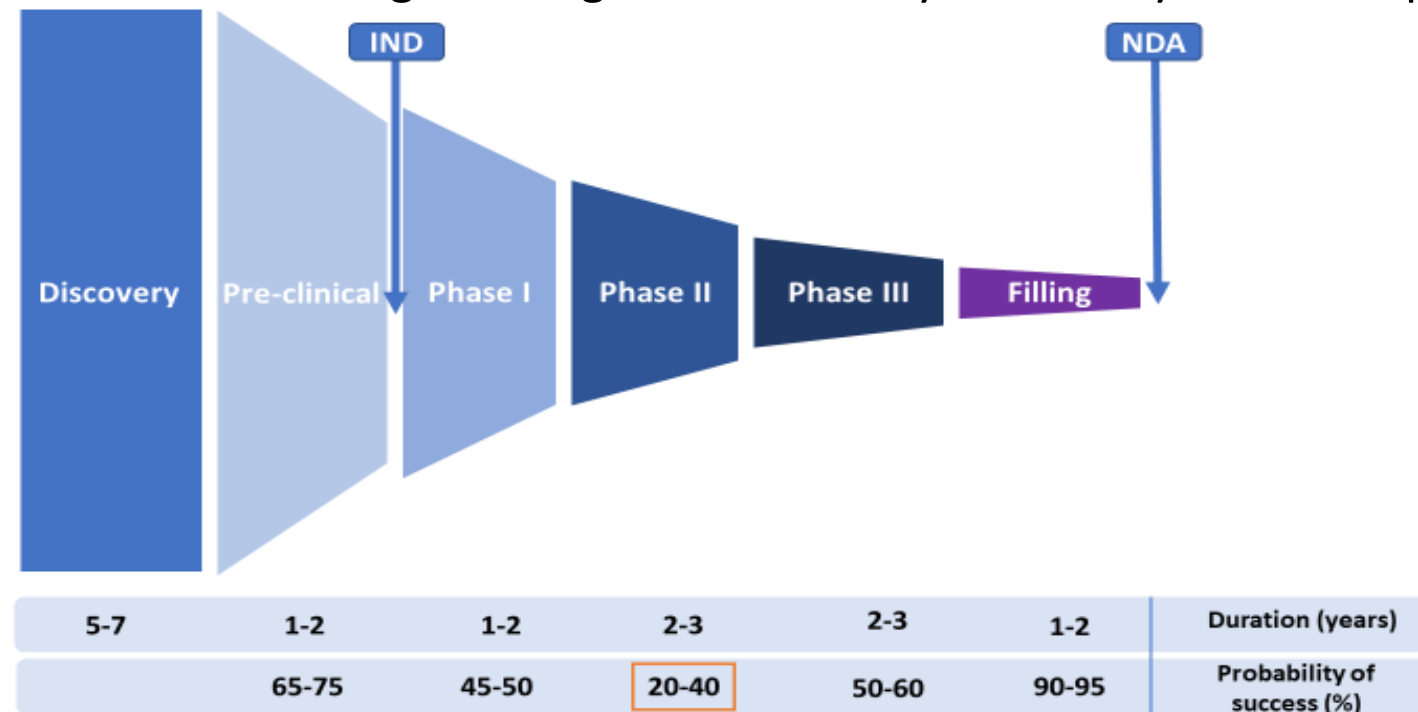


Artificial intelligence applied to challenges associated with new drug development

A On average 12 years and 2.6 Bn \$



B Less than 7% of drugs coming from discovery eventually reach the patients

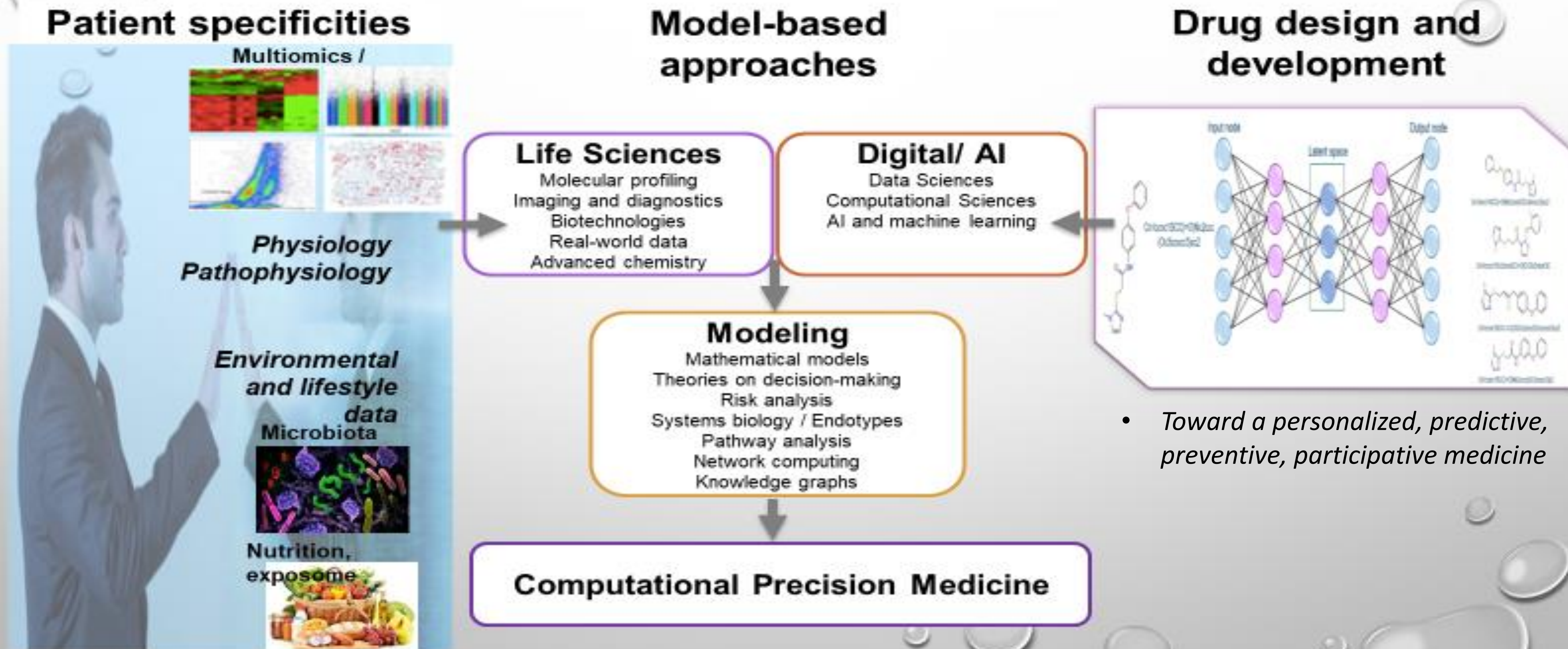


What AI can bring

- Integration of massive, multimodal, structured and unstructured data
- Creation of predictive models
- Support for decision-making

selecting the right therapeutic target, right drug-candidate and right patient

Computational precision medicine to relate patient and drug knowledge spaces



AI applications to new drug development

Disease modeling



Understanding disease complexity and heterogeneity

PATIENT STRATIFICATION

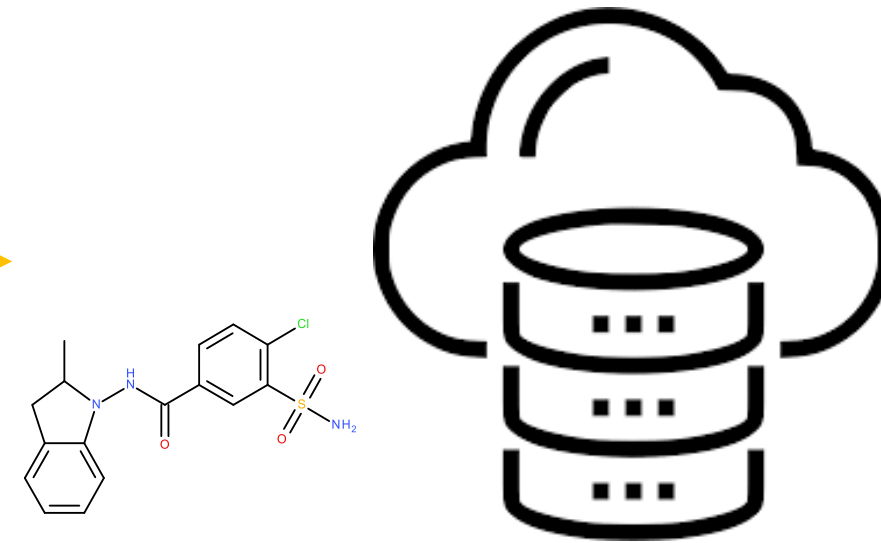
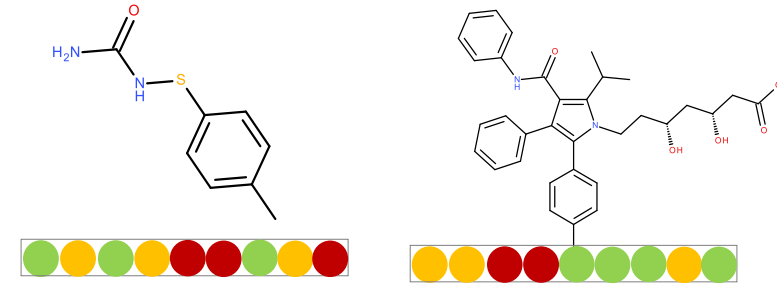
Identification of therapeutic targets



Identification of dysregulated genes/proteins/pathways involved in pathophysiology

SYSTEM BIOLOGY

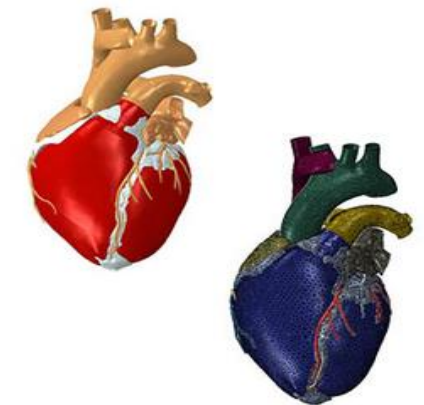
Design/optimization of drug candidates



Identification of molecules interacting with target and with specific properties

MULTITASK PREDICTION OF DRUG PROPERTIES

In silico evaluation of drug efficacy and safety



Digital twins, virtual patients, QSP, causal disease models

IN SILICO TRIAL SIMULATION

Systemic Lupus Erythematosus (SLE) : a complex, heterogeneous auto-immune disease

■ Diverse clinical manifestations:

- Skin, joints, kidney, heart, lungs, central nervous system, blood, etc.

-Fatigue

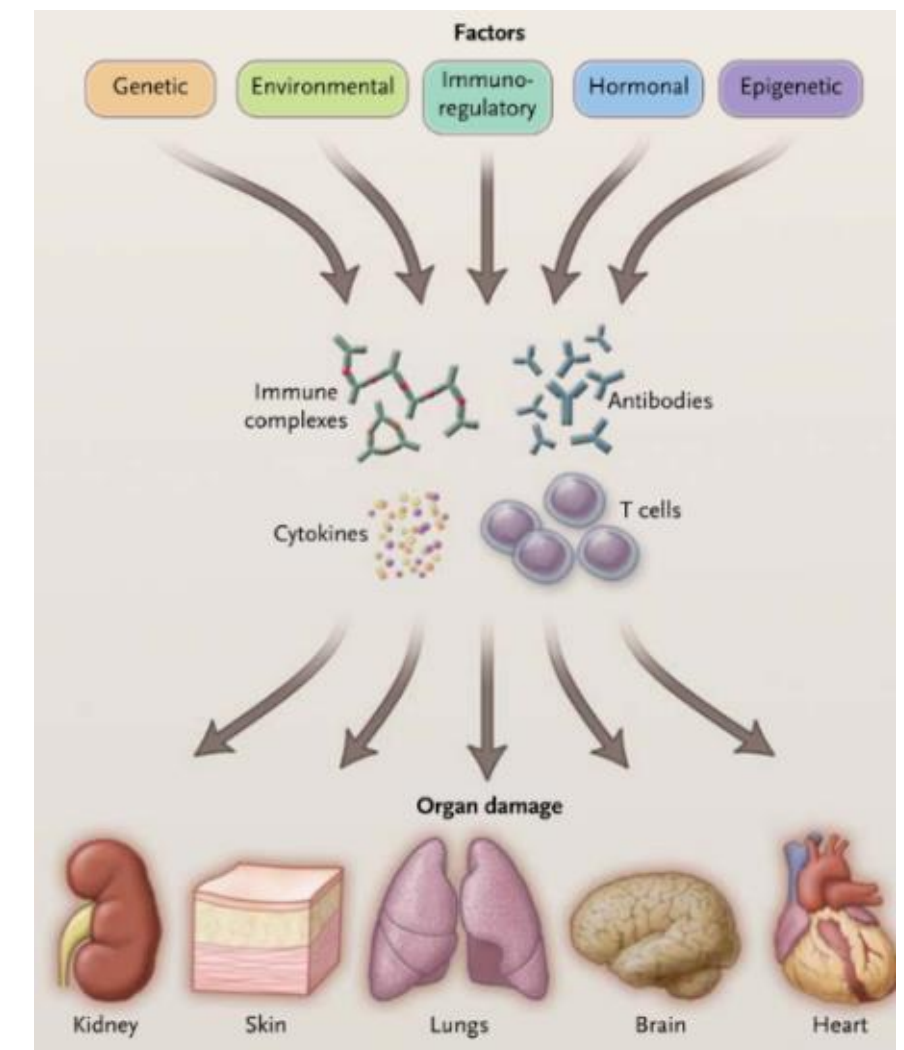
■ Significant morbidity & socio economic burden

Survival after diagnosis ~ 95% (5yrs), 91% (10yrs), 78% (20yrs)

■ Current treatment options:

- Corticosteroids, antimalarials, immunosuppressors (Mycophenolate mofetil, Methothrexate, cyclophosphamide, Azathioprine), anti B cells (Belimumab), anti-IFNR MAb (Anifrolumab)

High residual unmet medical need



Primary Sjögren Syndrome (pSS): a complex, heterogeneous auto-immune disease

- Progressive autoimmune disease characterized by dry eyes, dry mouth
- **Immune infiltrates** leading to destruction of lachrymal and salivary glands
- **Systemic manifestations** involving musculoskeletal and nervous systems, lungs, kidneys, skin and blood vessels
- **Significant quality-of-life impairment (fatigue)**
- **Increased risk** (16- to 44-fold vs general population) of developing **lymphoma**
- Current treatments are symptomatic



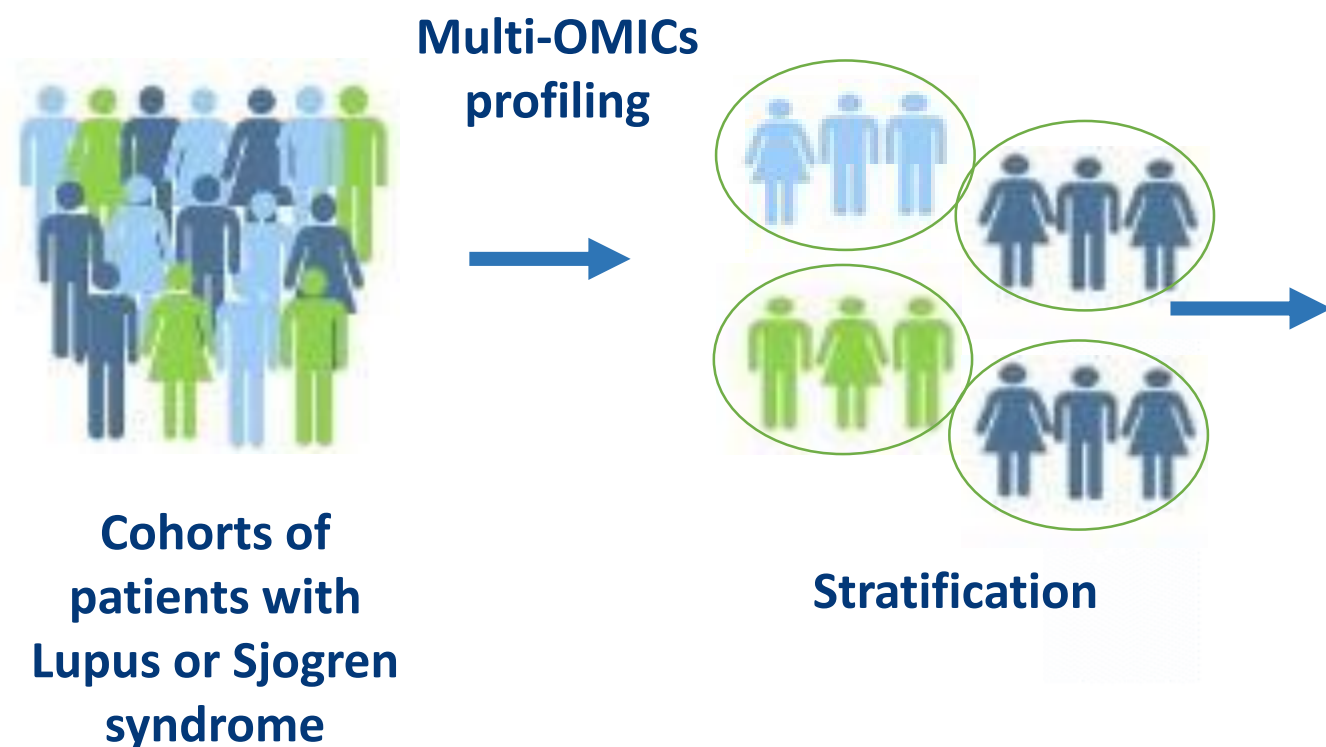
High unmet medical need

Disease modeling to understand patient heterogeneity and identify therapeutic targets: a system biology approach

Stratification of patients into homogeneous subgroups (clusters)

Analysis of dysregulated molecular pathways and target identification

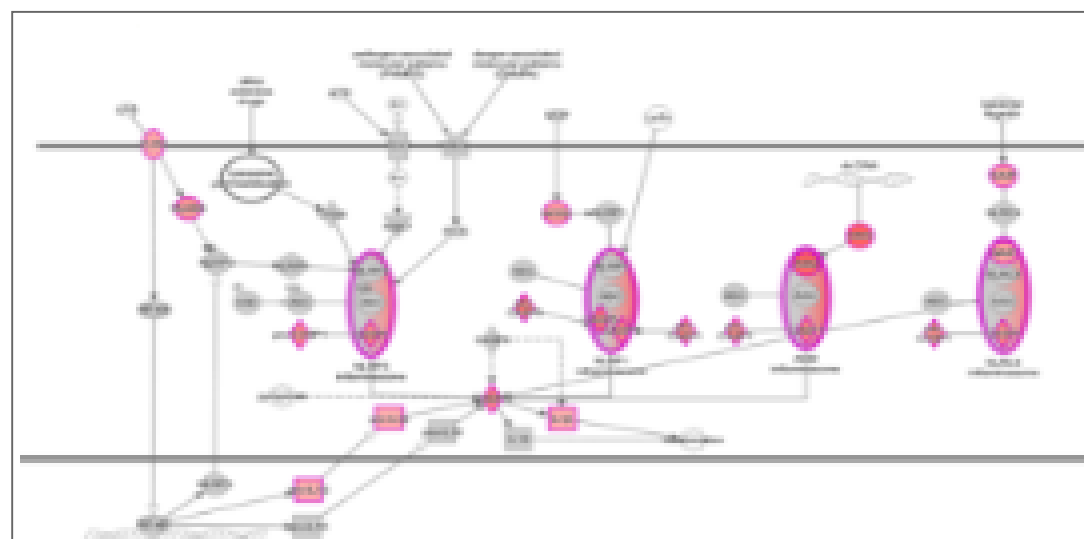
Selection of drug candidates interfering with therapeutic target(s)



- Clusterization of patients into endotypes reflecting pathophysiology



Ingenuity pathway analysis (IPA)



- Positioning of appropriate drug candidates in patient sub-populations (precision medicine)
- Design, selection, optimization of molecules interacting with the target
- Design of combination therapies
- Repurposing of existing molecules

Modeling autoimmune diseases following extensive molecular profiling of patients

STUDY COHORT
SAMPLES & BIOBANKING

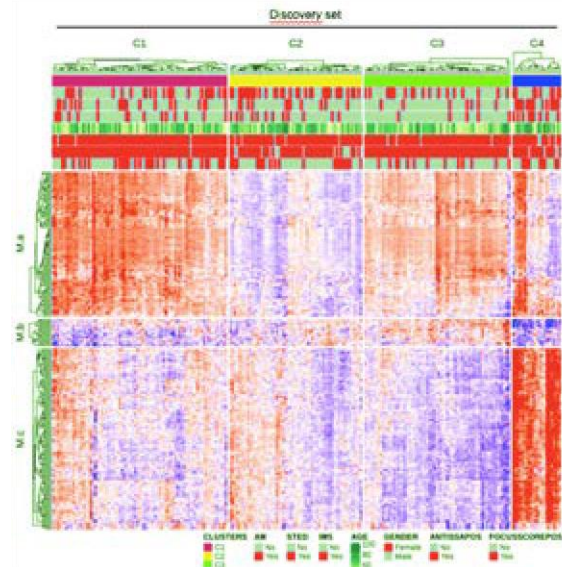
TRANSCRIPTOMIC
DATA

OMICS DATA
INTEGRATION

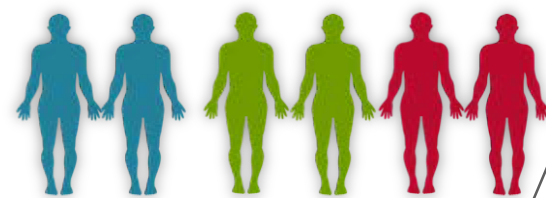
FUNCTIONAL
ANALYSIS



Heatmap based on signature genes in pSS and Lupus PRECISESADS patients

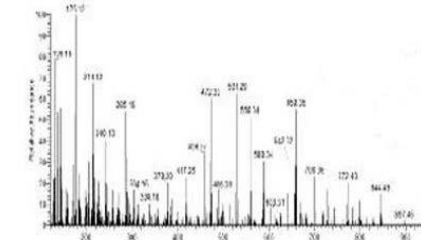


RNASeq data from whole blood

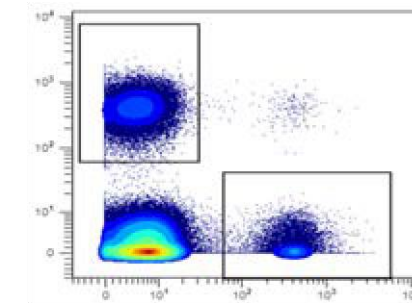


Clusters of patients

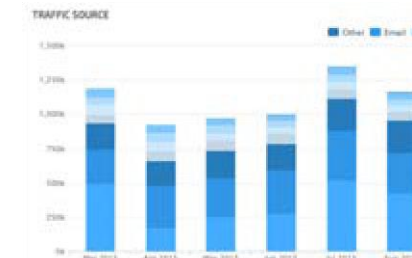
EPIGENETICS



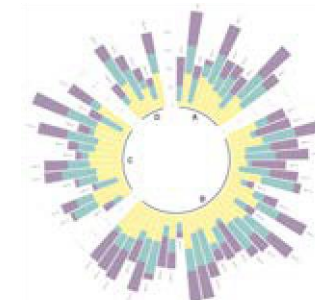
FLOW-CYTOMETRY



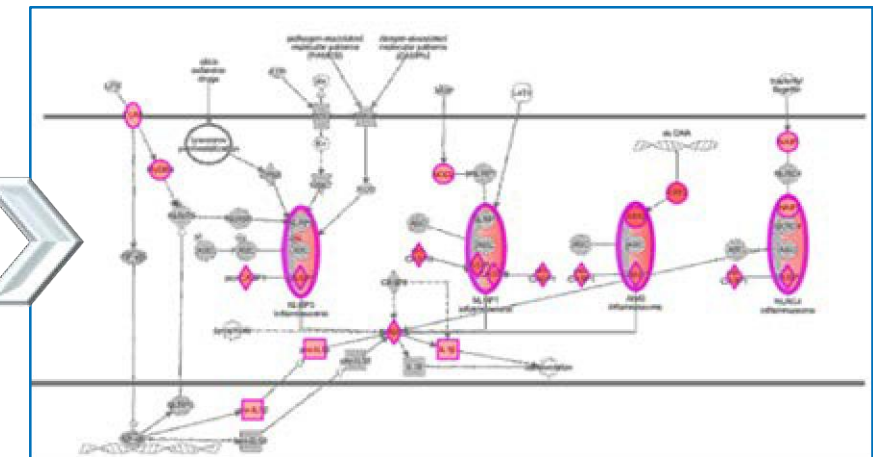
CYTOKINE DOSAGE



CLINICAL DATA



PATHWAYS AND
GENE SET
ENRICHMENT
ANALYSIS



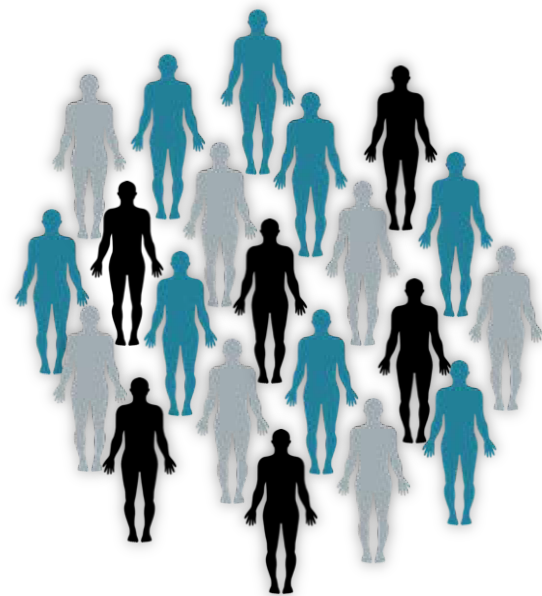
Cohort of 2000 patients with SADs including 382 pSS, 320 Lupus and 330 healthy volunteers

A new molecular classification to drive precision treatment strategies in primary Sjögren's syndrome

Perrine Soret^{1,2,9}, Christelle Le Dantec^{2,2,9}, Emiko Desvaux^{1,2}, Nathan Foulquier², Bastien Chassagnol¹, Sandra Hubert¹, Christophe Jamin^{2,3}, Guillermo Barturen⁴, Guillaume Desachy¹

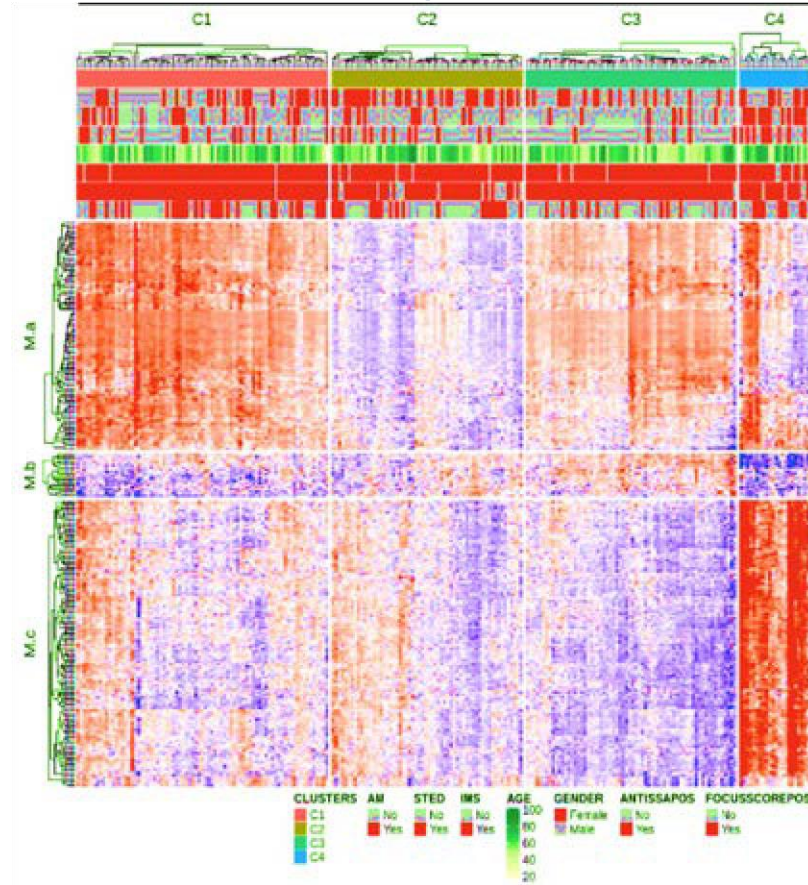
Stratification of pSS patients in 4 homogeneous molecularly defined clusters

304 pSS patients from the PRECISESADS cohort

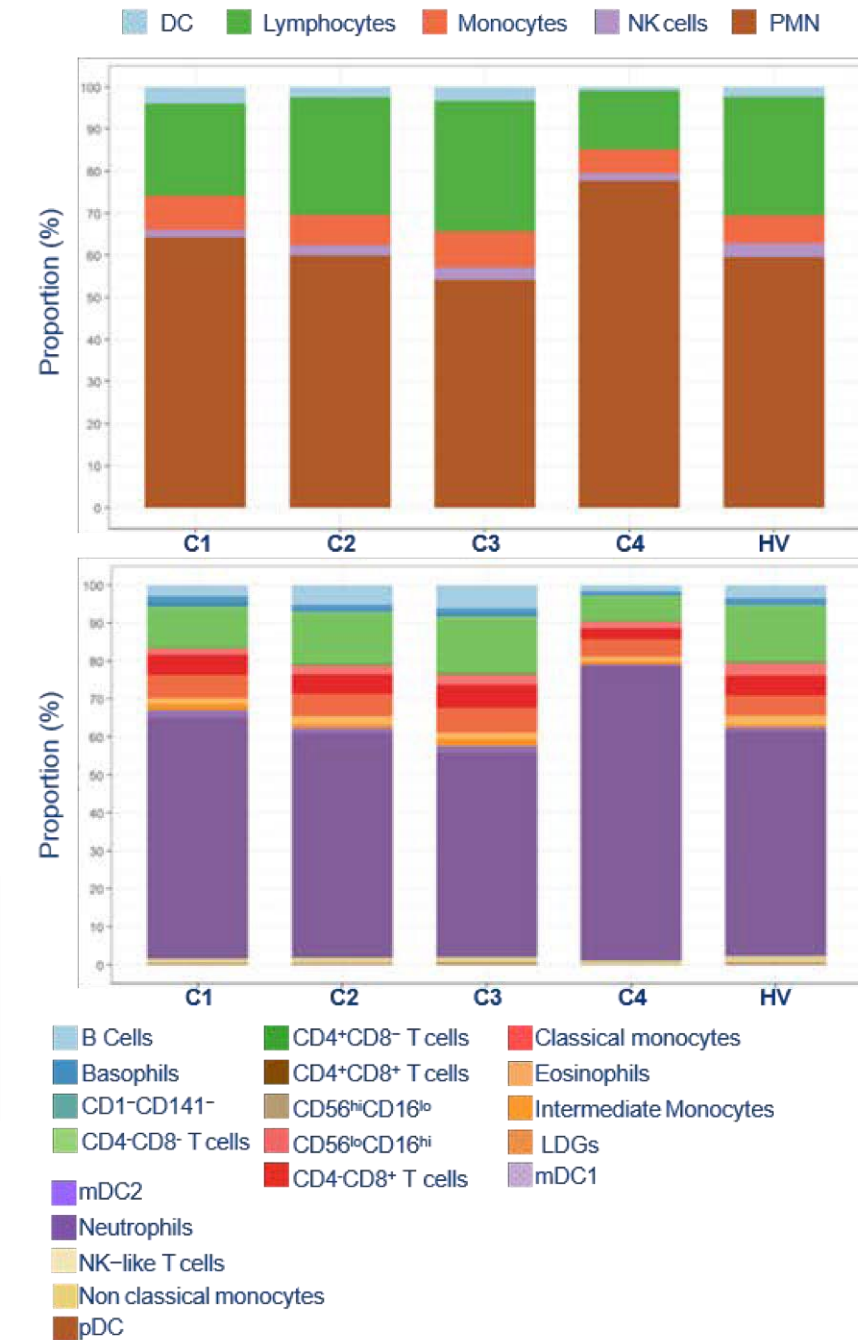
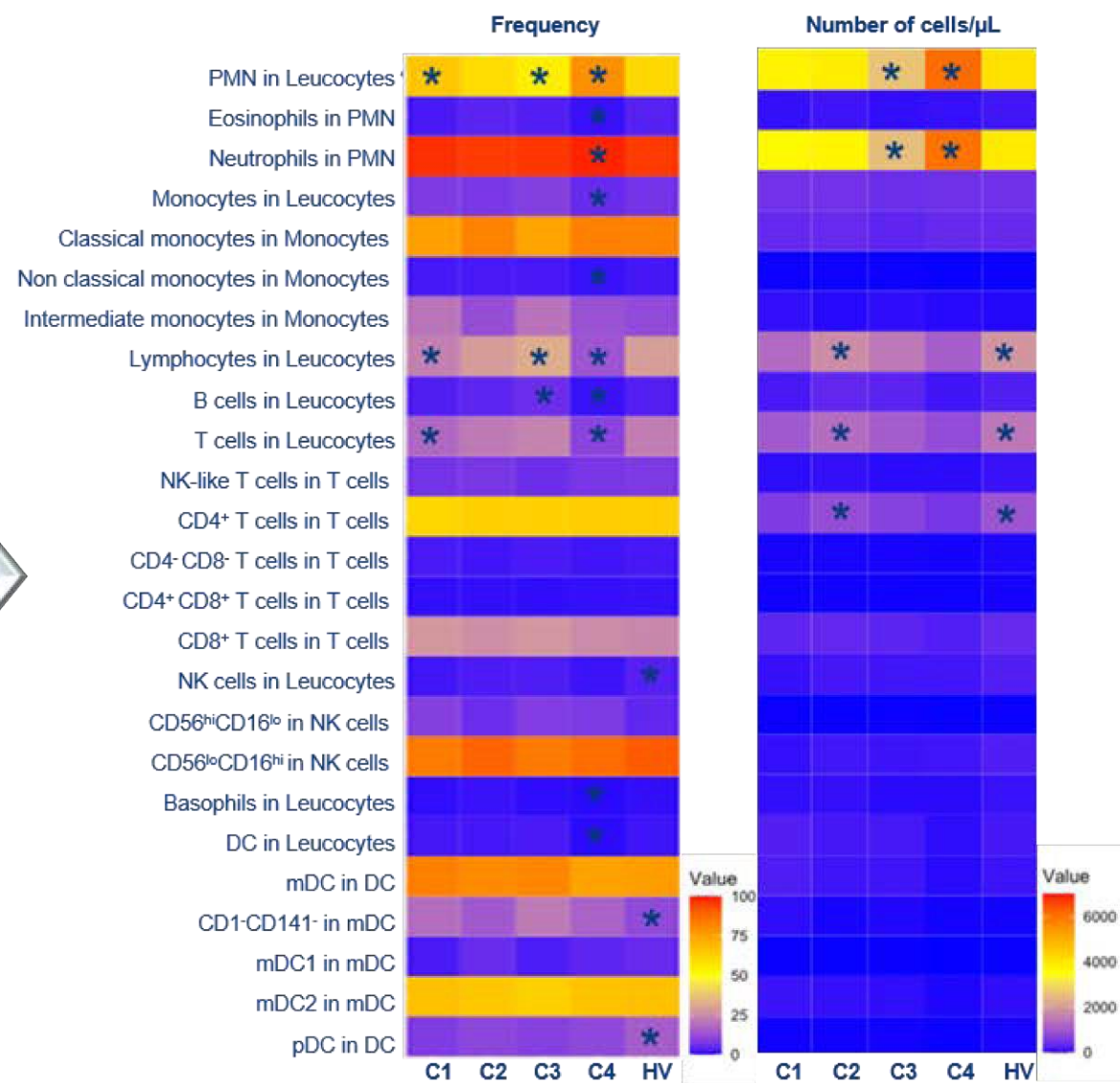


Clustering of pSS patients

Based on RNASeq data from whole blood

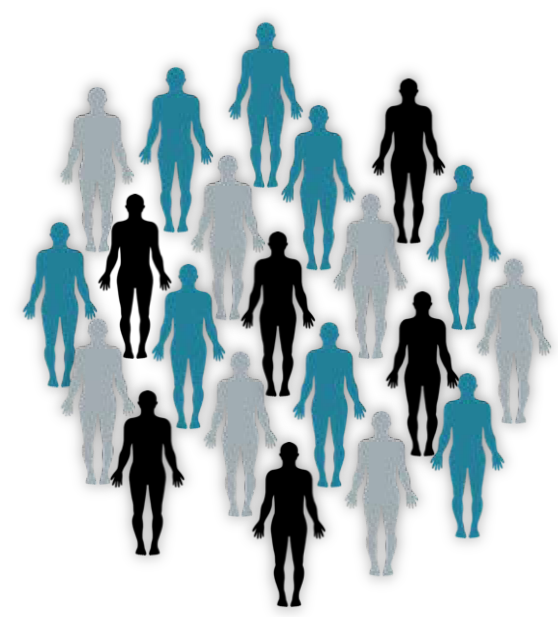


→ 4 distinct clusters of pSS patients defined by 3 gene modules (hierarchical and k-means clustering)

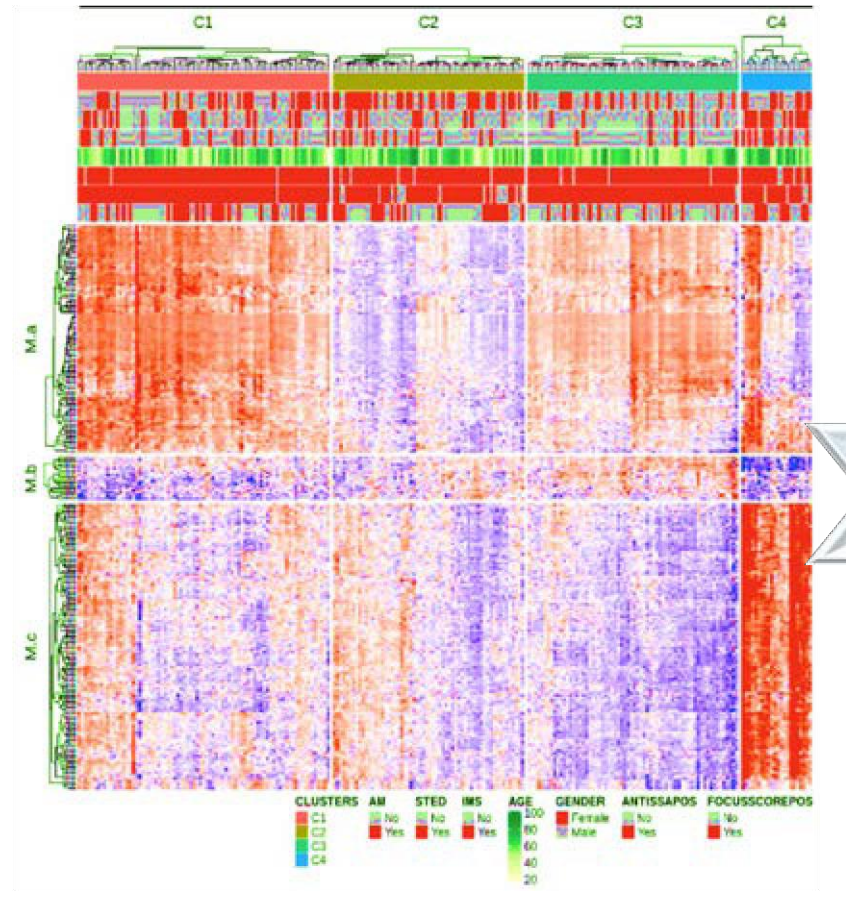


Identification of dysregulated molecular pathways in individual pSS patient clusters

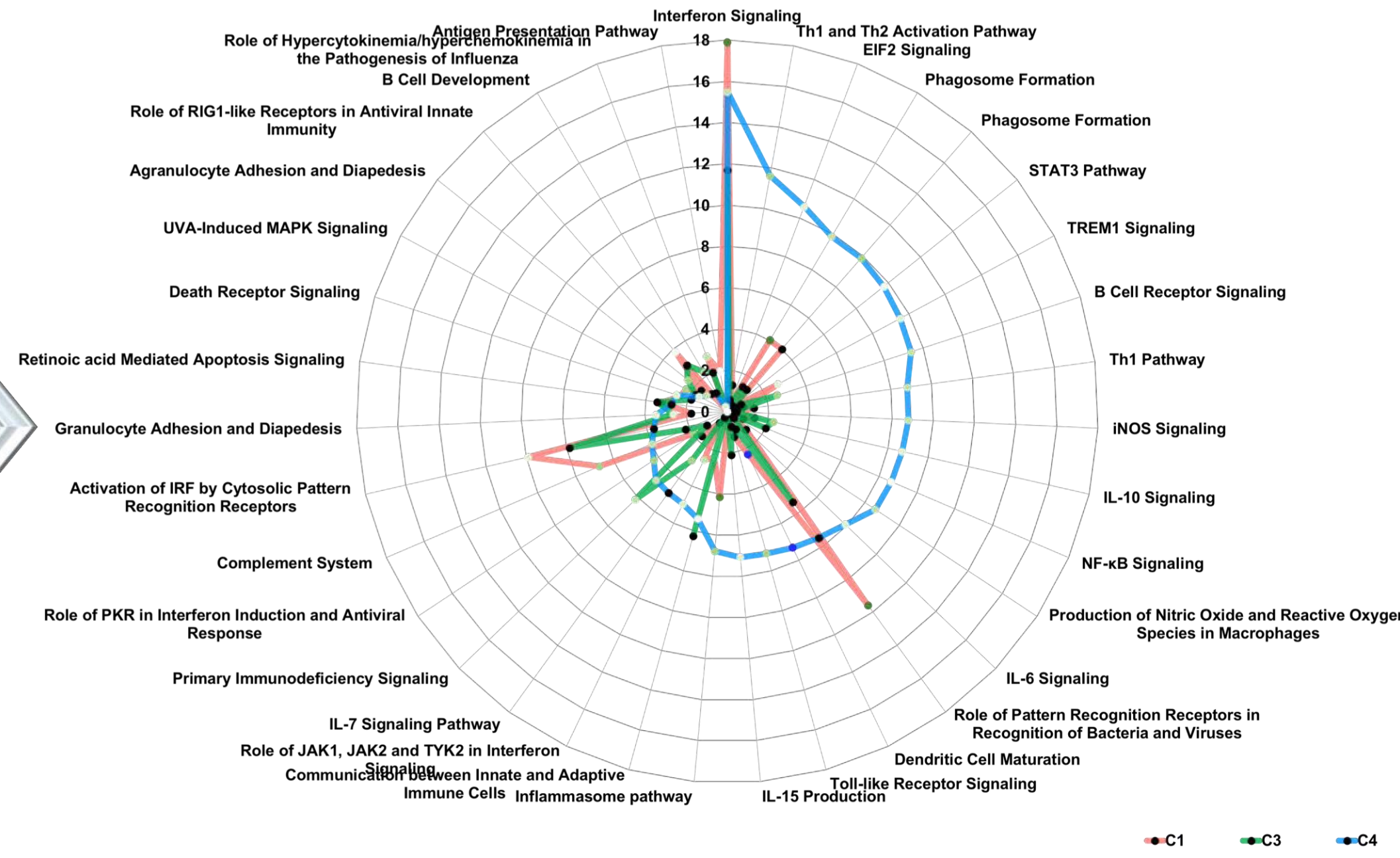
304 pSS patients from the PRECISESADS cohort



Clustering of pSS patients
Based on RNASeq data from whole blood



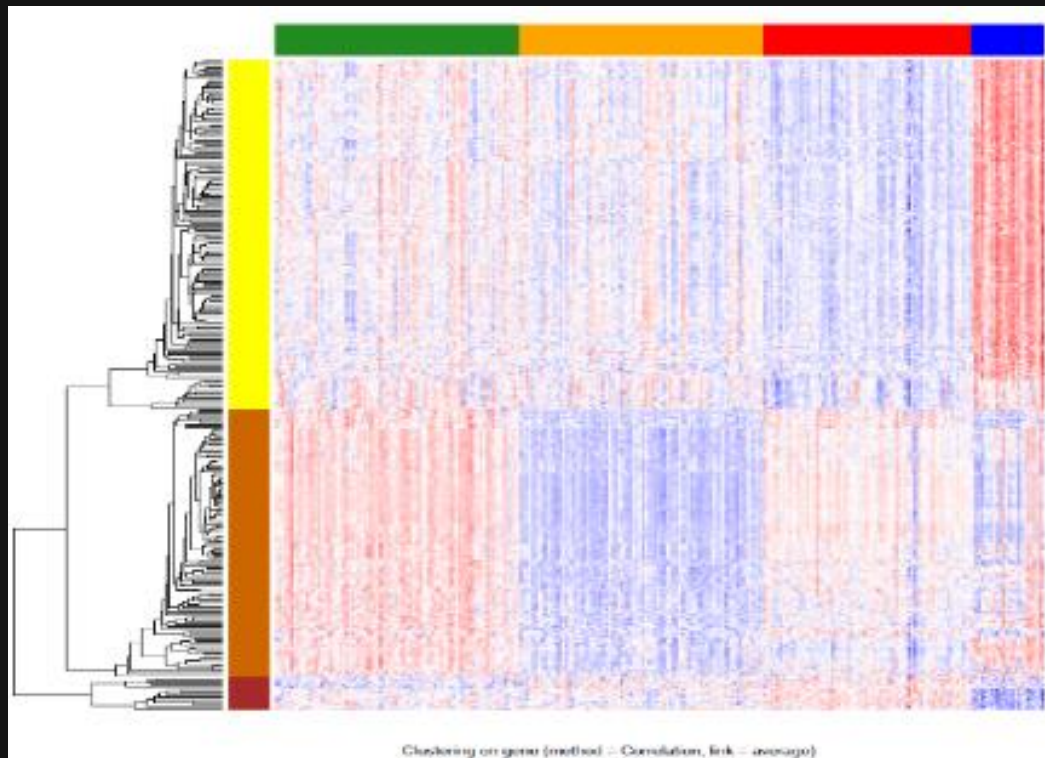
→4 distinct clusters of pSS patients defined by 3 gene modules



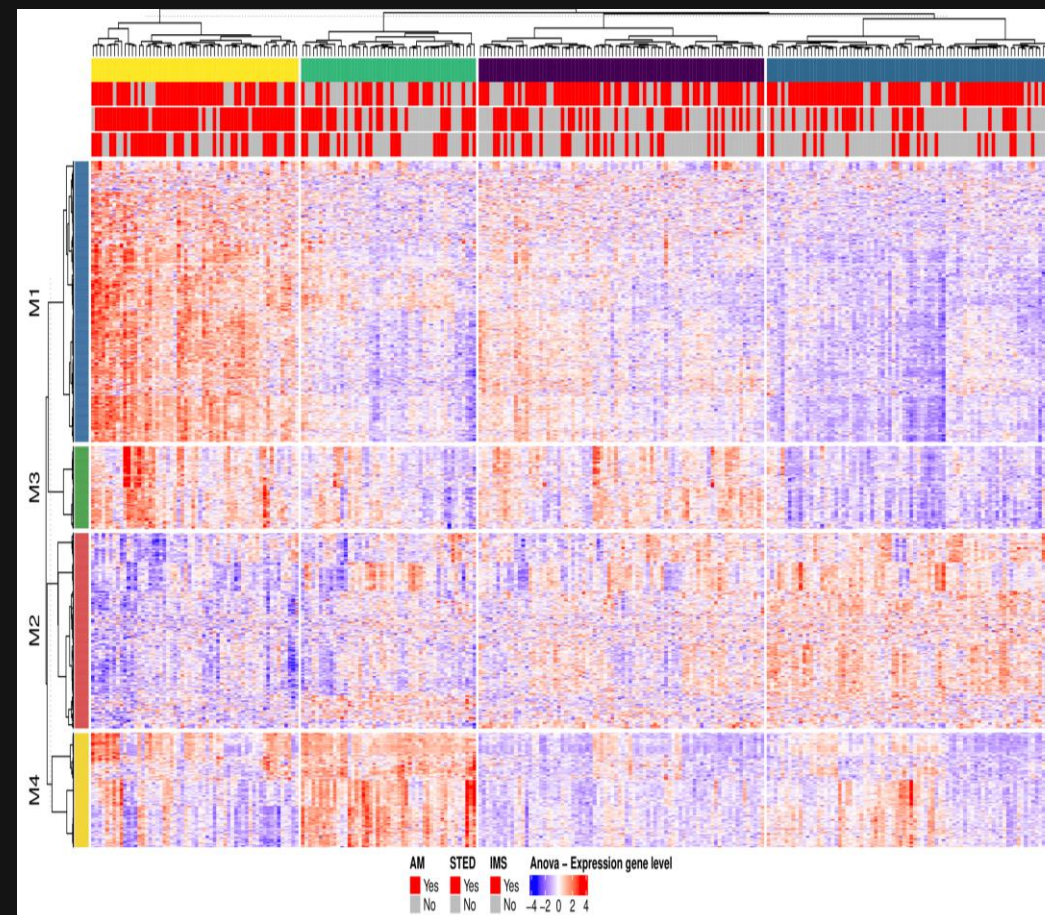
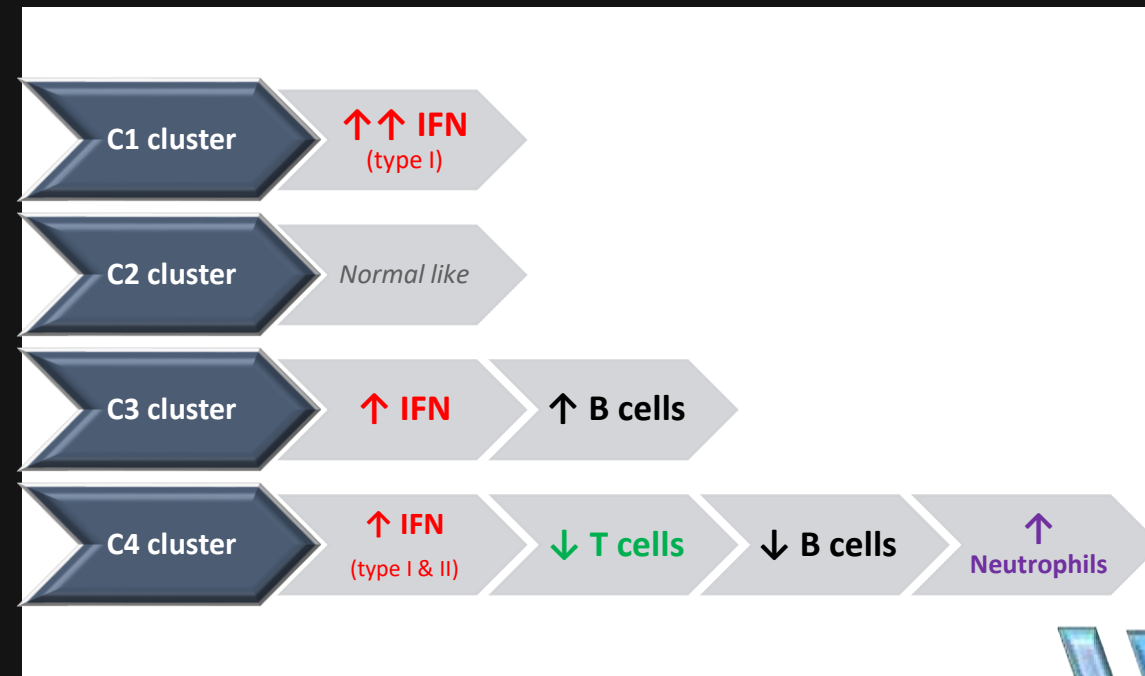
Functional annotation of each of 4 clusters of Lupus or Sjögren patients leads to working hypotheses regarding candidate therapeutic targets

Heat maps from transcriptomics data in the blood

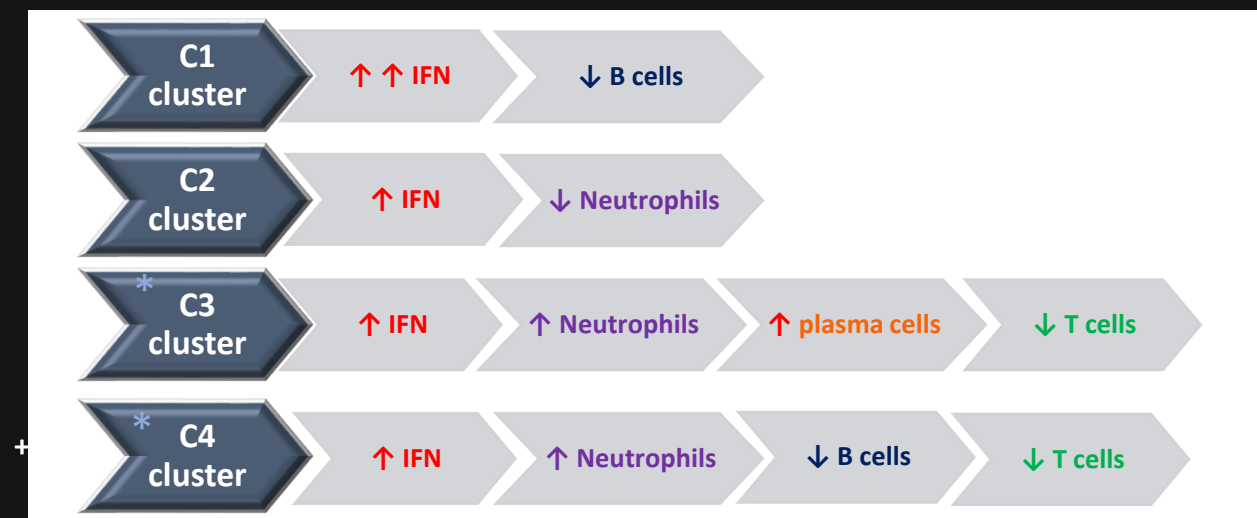
Schematic representations of patient clusters



Sjogren



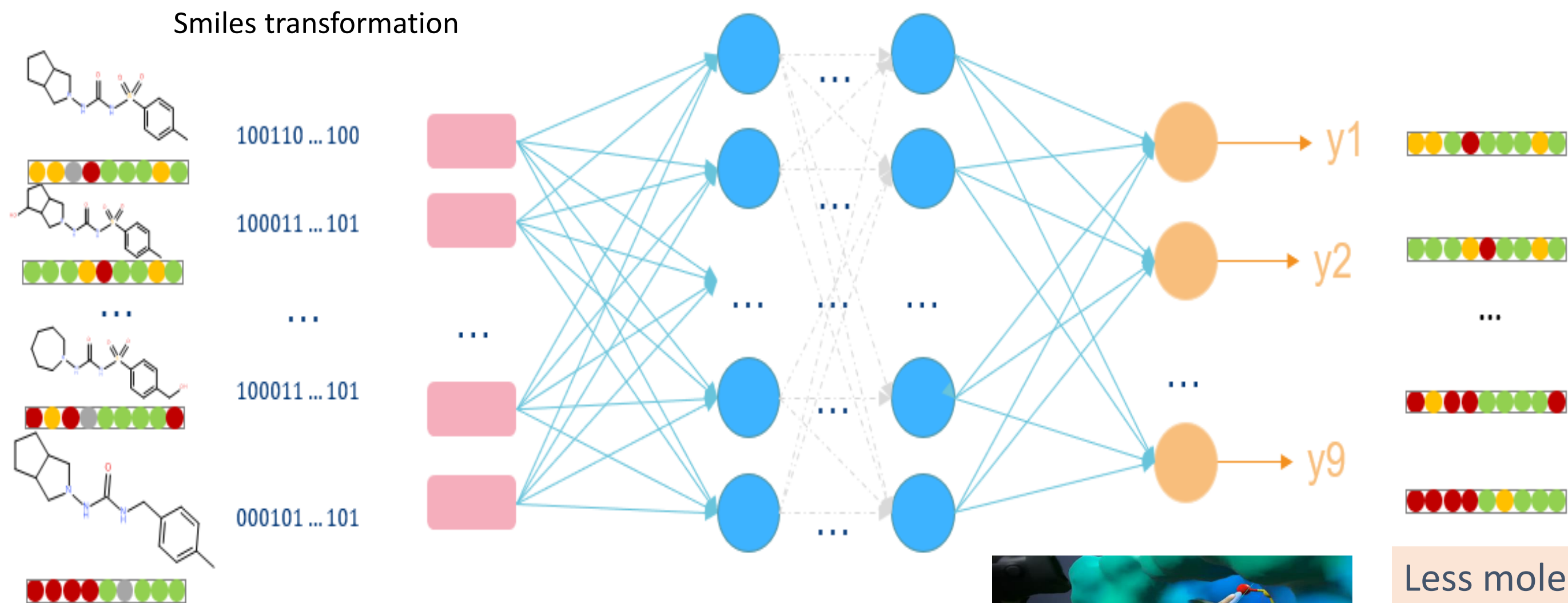
Lupus



- IFN α pathway
- Combination therapies
- Pleiotropic targets

From target to drug design and optimization

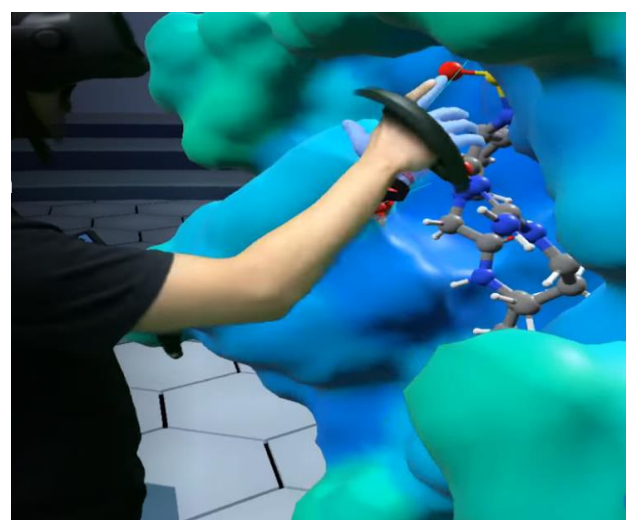
- Machine learning to train neural networks for predicting properties of small chemical molecules



- Multitask parallel prediction of:
 - ✓ binding to the target (quantitative structure activity relationship, free energy prediction)
 - ✓ absorption, metabolism, distribution, excretion toxicity
 - ✓ stability...

- Generative AI to enhance the chemical space

- *Generation of new molecules*
- *Retrosynthesis*



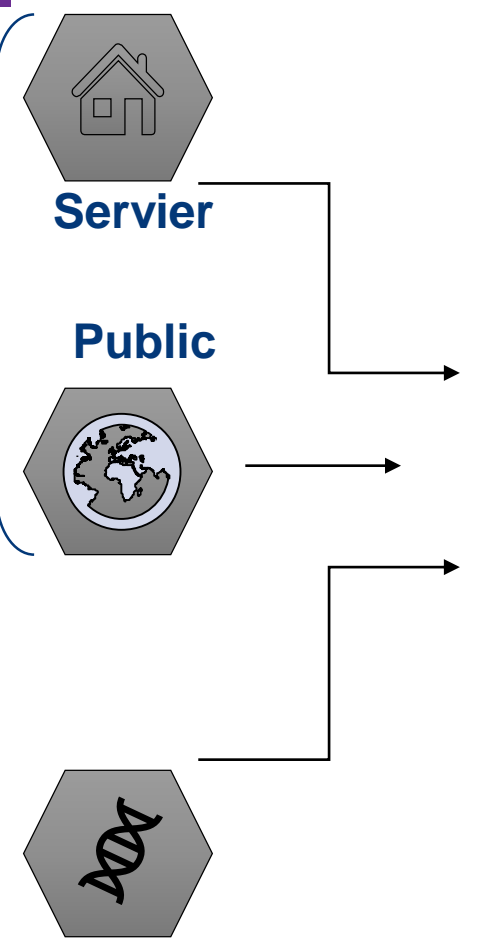
Less molecules to synthesize and test in wet labs

Nanome

Industrializing AI-powered drug discovery: lessons learned from the *Patrimony* computing platform

Mickaël Guedj et al, 2022

- Identify disease relevant targets**
- New disease targets
 - Repurposing
 - Combinations
 - Life cycle management



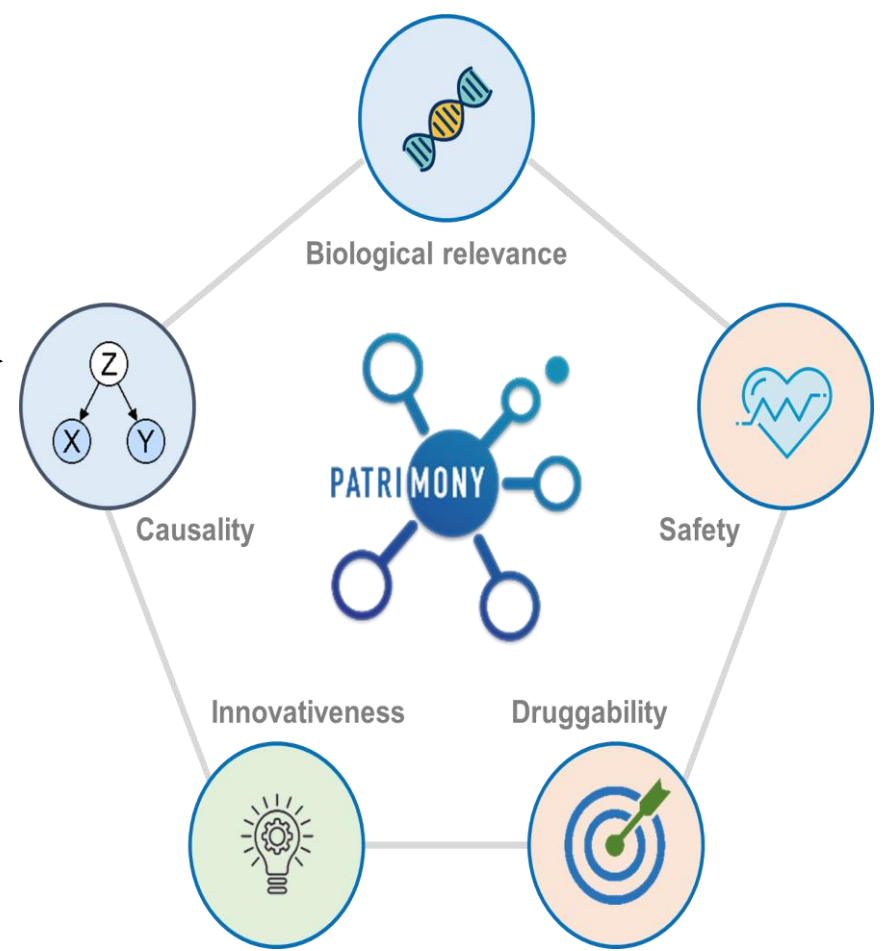
- TTD
- GWASCatalog
- Uniprot
- NCBI Gene
- Cmap
- SIDER
- STRING
- MEDDRA
- GO
- EFO
- Drugbank
- LINCS
- GTEX
- OpenTarget
- KEGG
- RWE
- sources...

Industrialization
Web interface

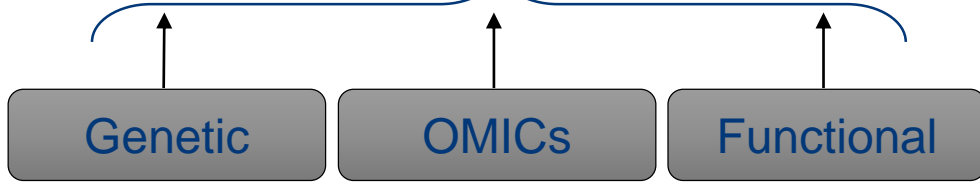
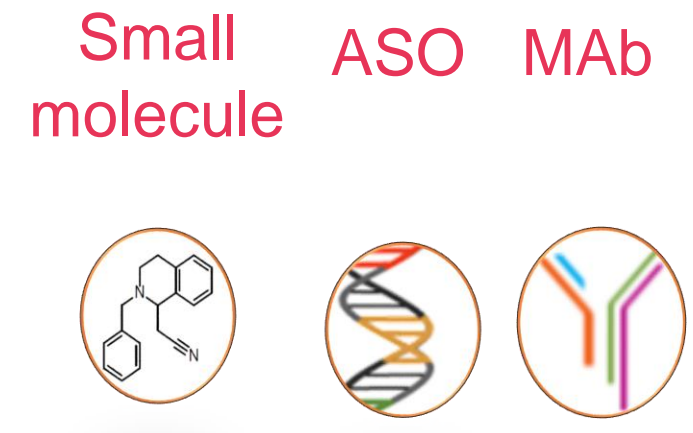
Proprietary Network



Target prioritization



Selection of therapeutic modality and drug candidate(s)



- Key achievements since 2018**
- **3 diseases modeled** Sjögren & Lupus, 1 neurodegenerative disease
 - **1 therapeutic project** launched for Sjögren
 - **Proposal for existing drugs** to be repurposed in severe COVID-19

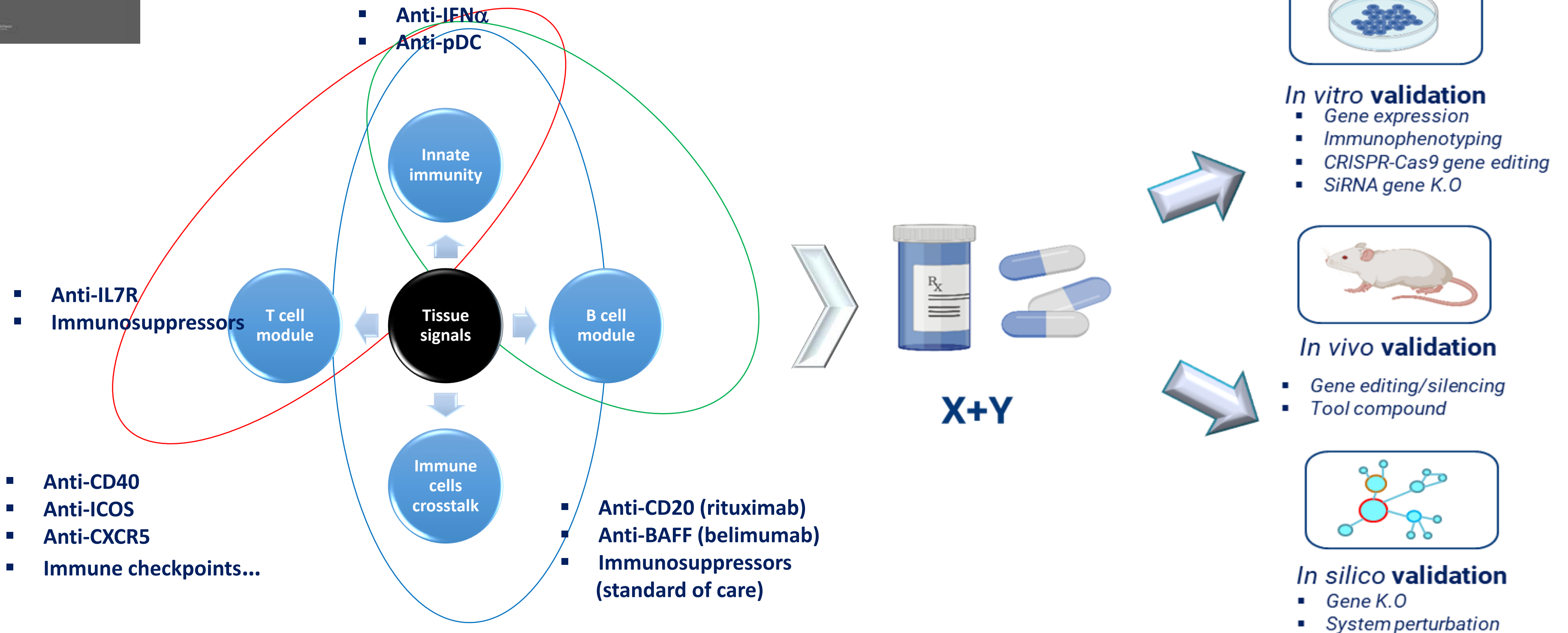


Model-based computational medicine to design combination therapies for autoimmune diseases

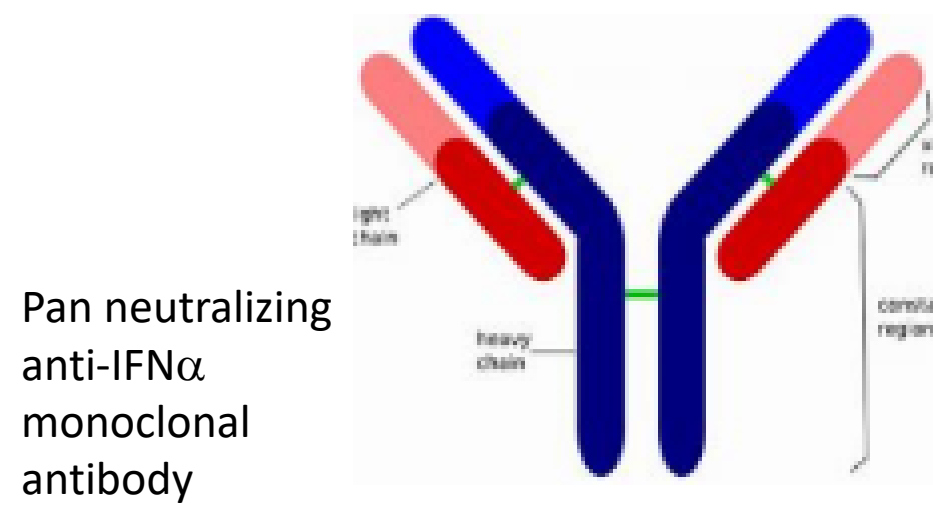
Desvaux E et al, 2021

EXPERT
REVIEW

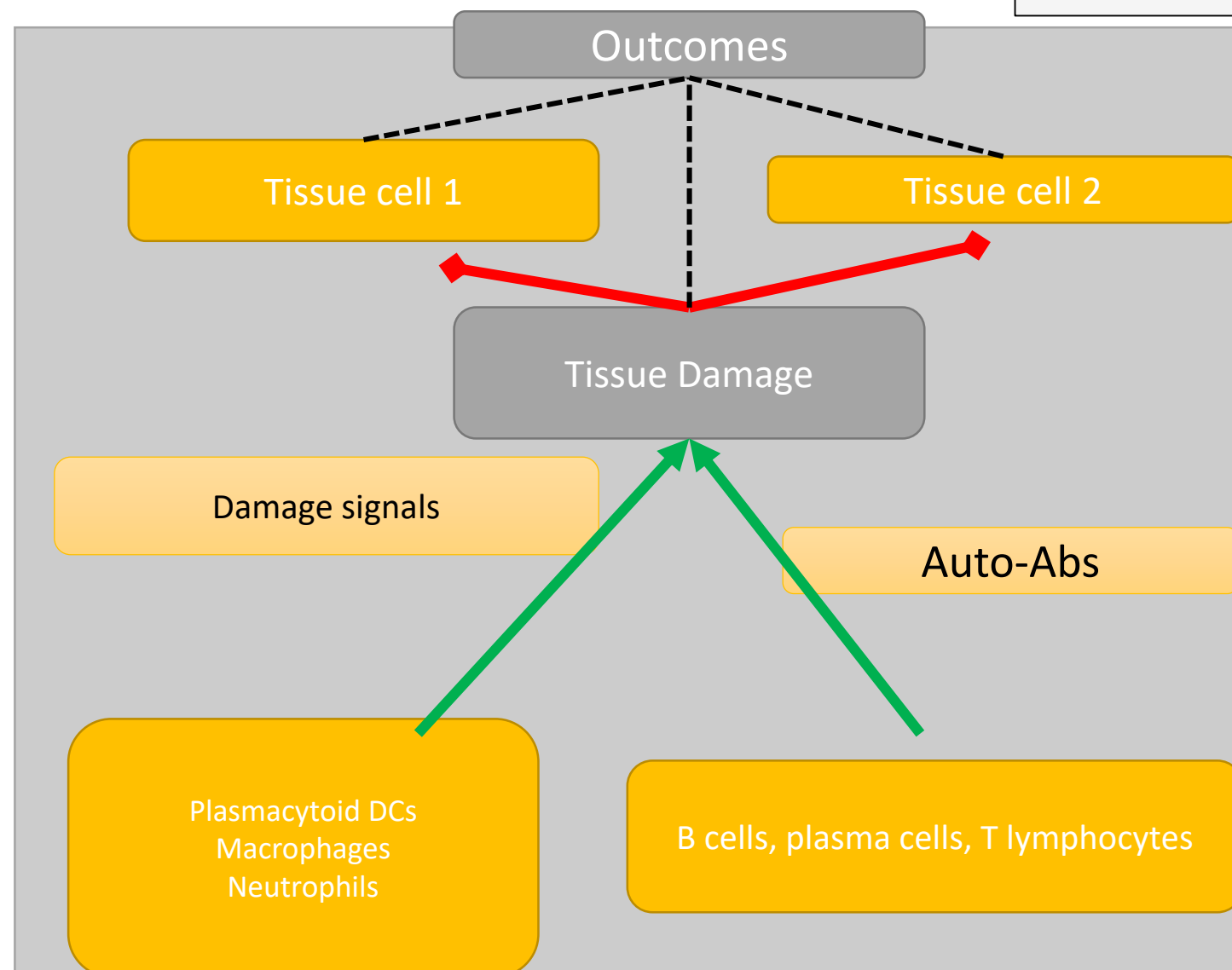
OF CLINICAL IMMUNOLOGY



Quantitative system pharmacology modeling to predict the efficacy of an anti-IFN α Mab (S95021) in cutaneous Lupus



- Mechanistic, quantitative and dynamic model integrating data on biological processes, clinical symptoms, drug characteristics (PK/PD modeling)
- Model based on a thorough analysis of the scientific literature + proprietary data
- Representation as differential mathematical equations of **dynamic interactions between components**
- Prediction of drug efficacy, identification of candidate BMKs, dose selection, virtual patients, combination therapies



Molecular mediators

- IFN α and IFNAR
- Pro and anti inflammatory mediators
- Auto Abs, cytokines, chemokines

Cells

- Immune cells
- Keratinocytes

Physiological compartments

- Blood
- Lymph Nodes
- Target tissue

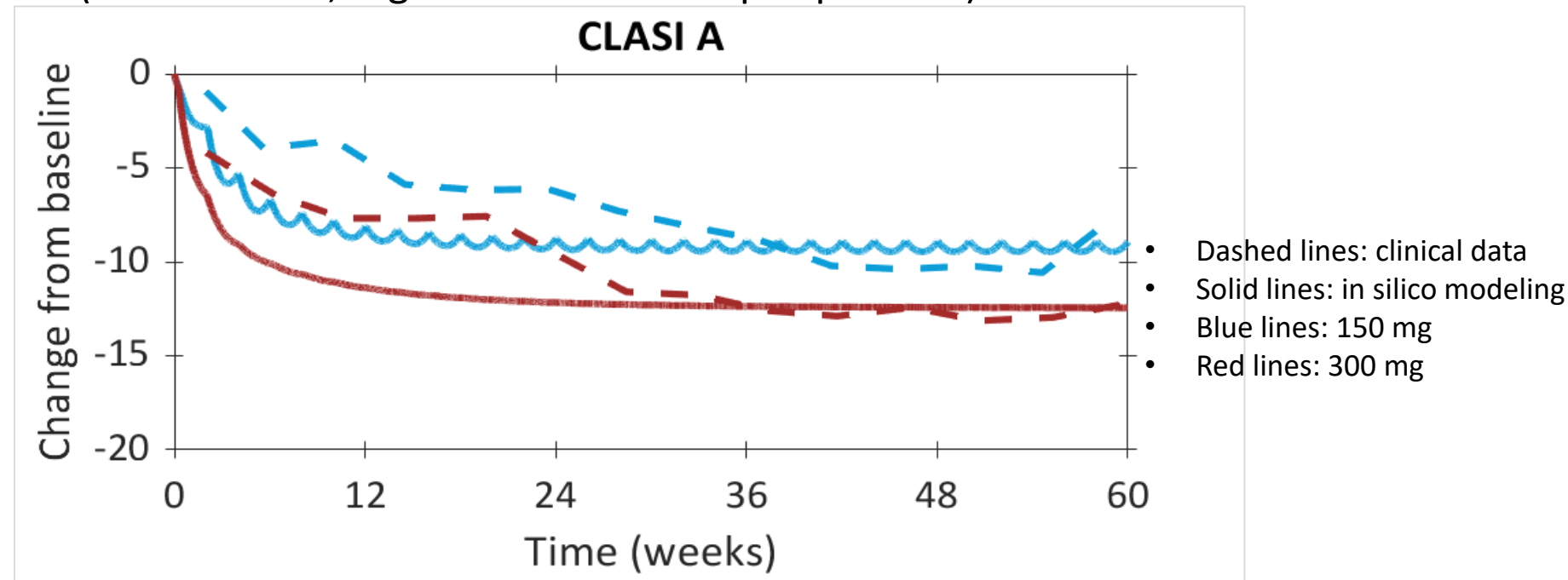
Clinical outcomes

- Erythema, scaling, depigmentation...
(components of the CLASI A cutaneous scoring)

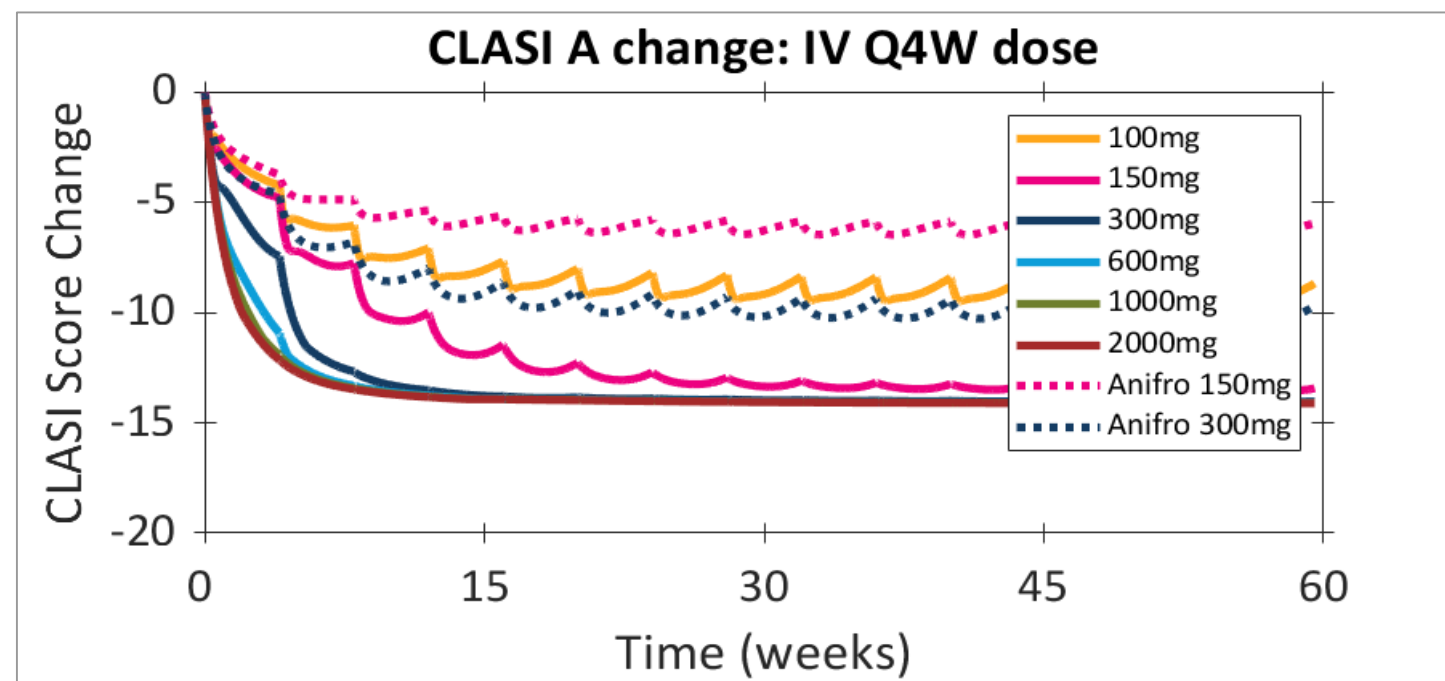


Quantitative System Pharmacology predicts the efficacy of the S95021 drug candidate to treat cutaneous Lupus

QSP confirms the efficacy of the anti IFNR MAb Anifrolumab (Astra Zeneca, registered to treat Lupus patients)

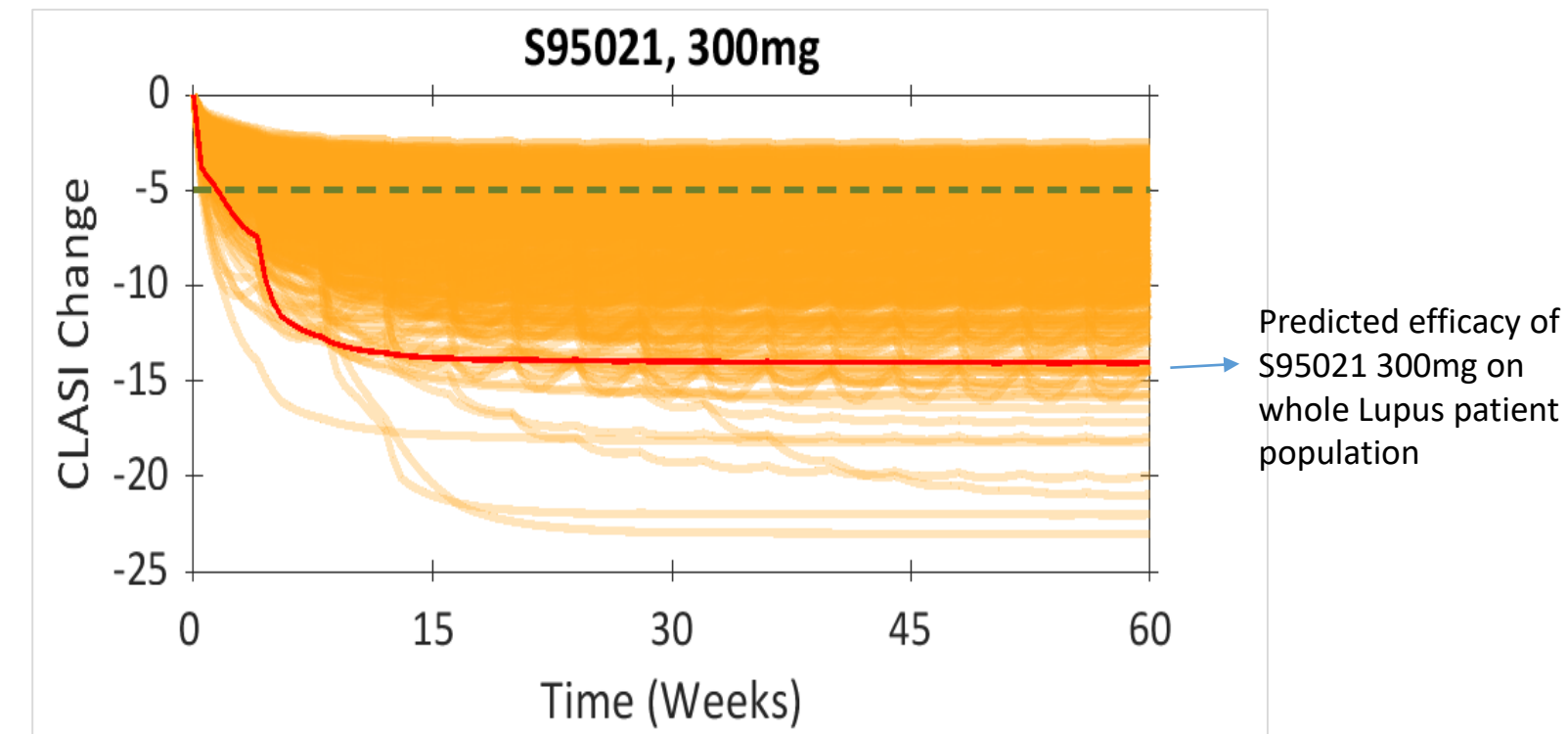


QSP predicts the efficacy of the S95021 Mab in cutaneous lupus, while suggesting the interest of high dosing regimens



Creation of virtual patients by varying parameters related to the targeted biological pathway

- *eg levels of IFN and its receptor, immune cells producing or responding to IFN*

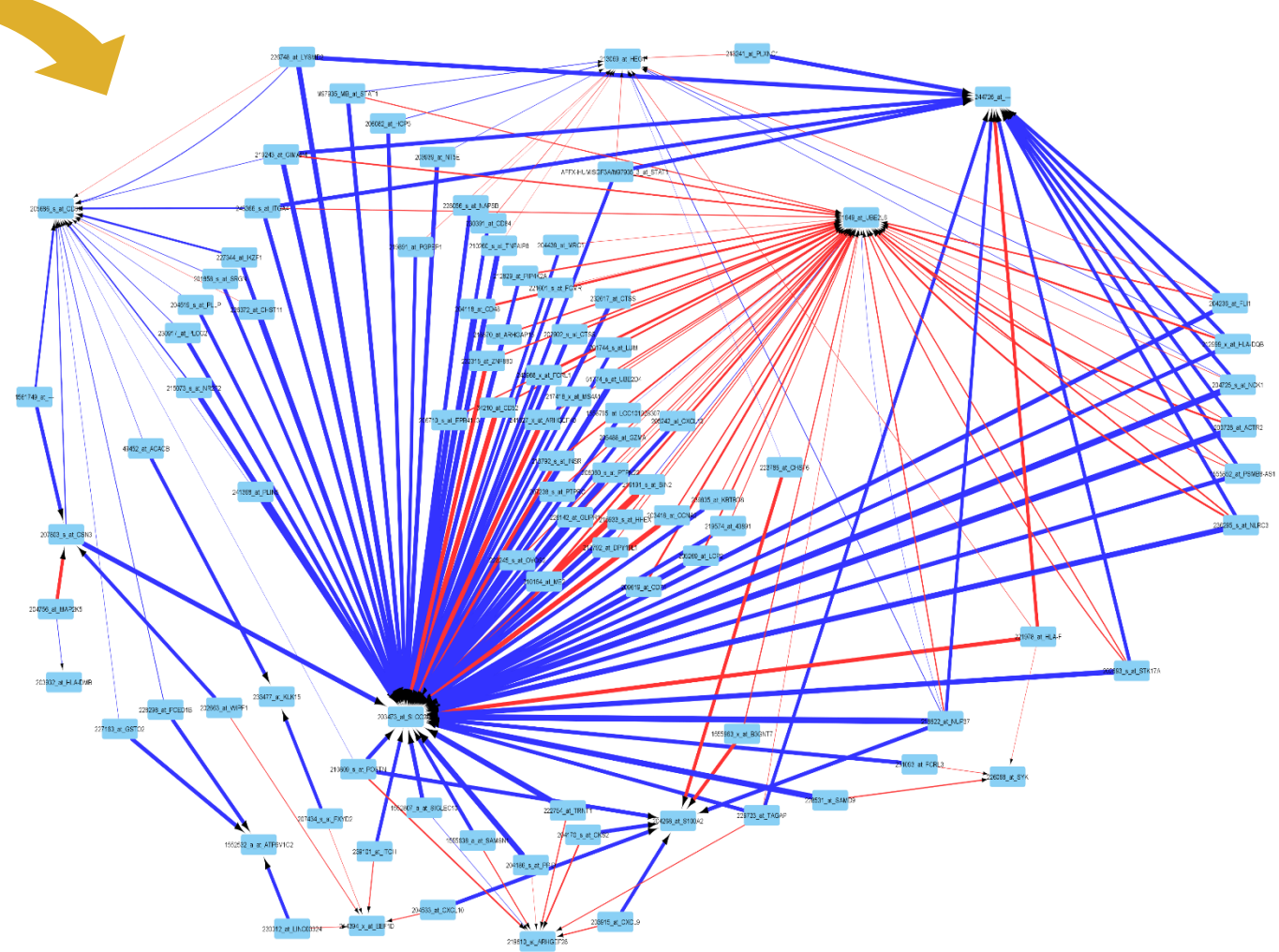
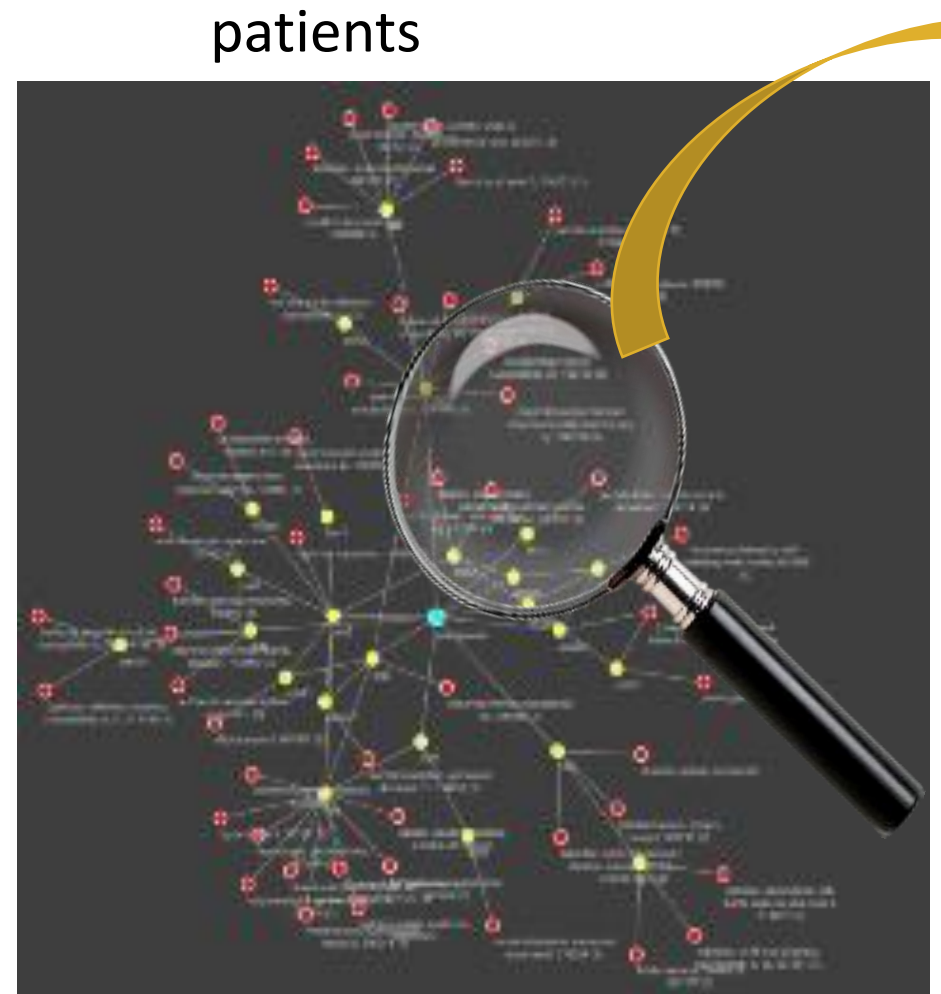
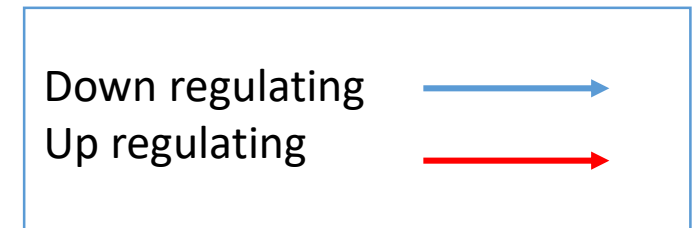




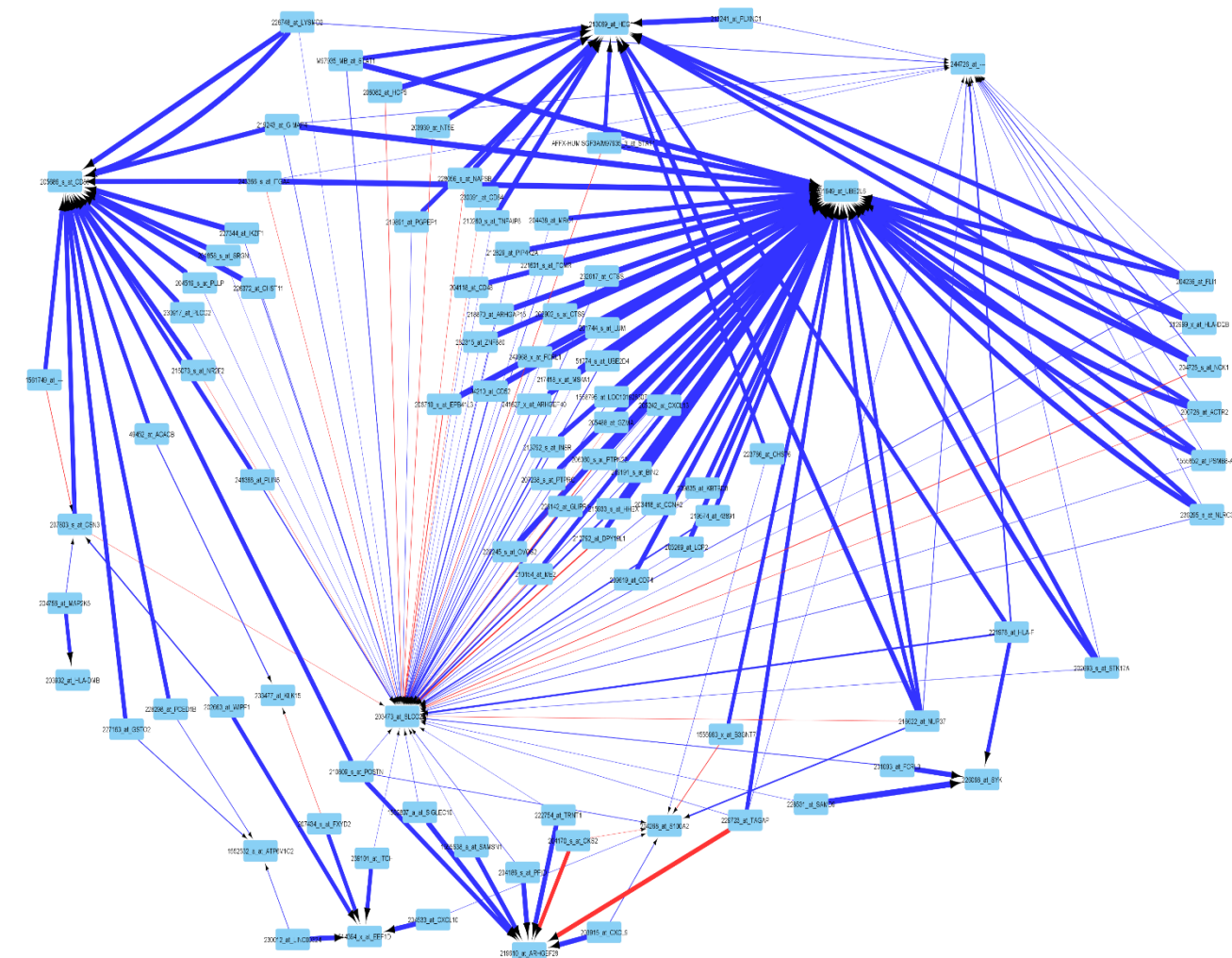
Causal disease modeling of Sjogren in salivary glands by using network computing

Modeling based on transcriptomics data in salivary glands of Sjogren vs Sicca patients

Interactomes of genes with inferences of influence



Sjogren in parotid glands



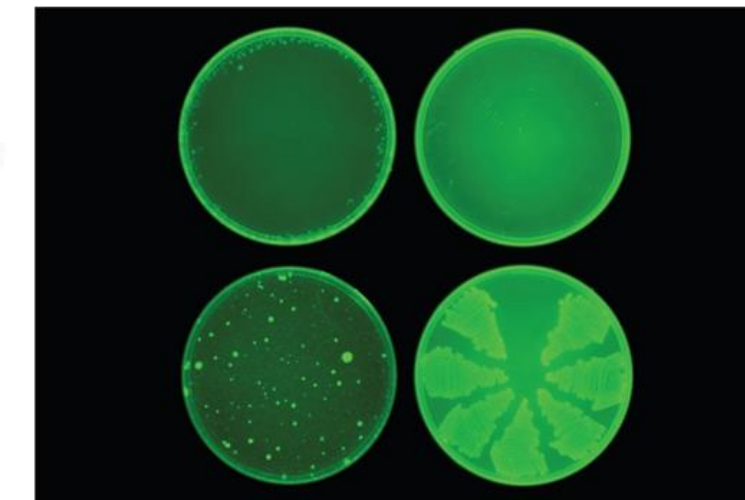
Control parotid

- Identification of master regulators (potential therapeutic targets)
- Computational perturbations to mimic the impact of single drug or combo therapies

Conclusions: A revolution in new drug development





Artificial intelligence yields new antibiotic
A deep-learning model identifies a powerful new drug that can kill many species of antibiotic-resistant bacteria.
Anne Trafton | MIT News Office
February 20, 2020



- Supporting decision-making all along drug discovery and development
- Shortening the timelines for the discovery phase
- De-risking the choice of therapeutic targets and drug candidates
- Decreasing the need for wet-lab experiments and clinical studies
- Increasing probabilities of success while reducing costs

From design to preparation of phase 1 in one to two years

 **Exscientia** 
Announces First AI-Designed Immuno-Oncology Drug to Enter Clinical Trials

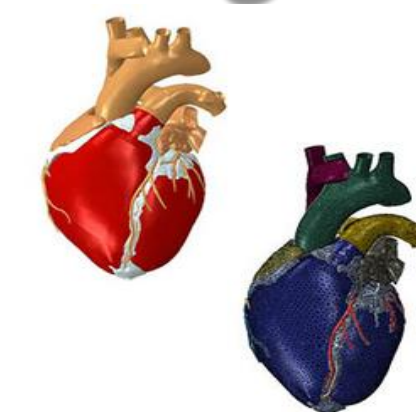


- Regulatory acceptance of evidence generated by predictive modeling

- Interest of major agencies (eg FDA and EMA) in Model-Informed Drug development to Refine, Reduce and Replace (3 R's)

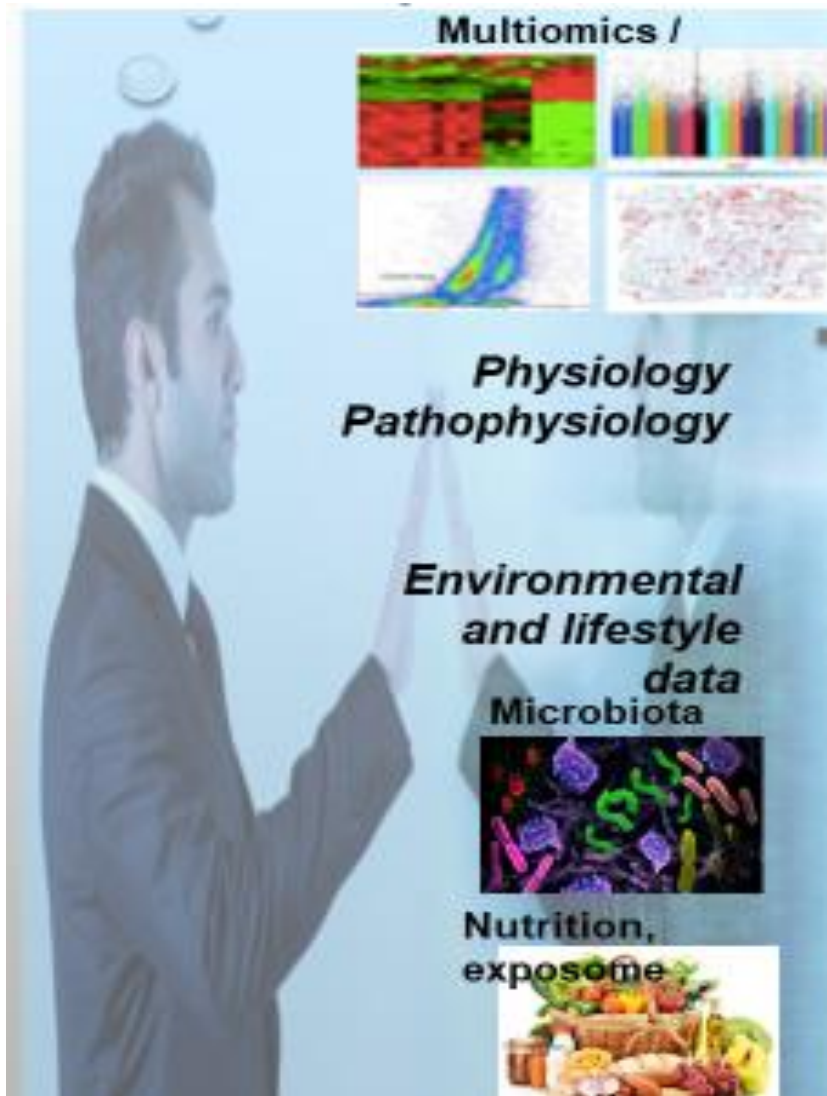
- Statement from US authorities (Committee on Appropriations, 2018):

« In silico trials protect public health, advance personalized treatment, can be executed quickly and for a fraction of the cost of a full scale live trial »

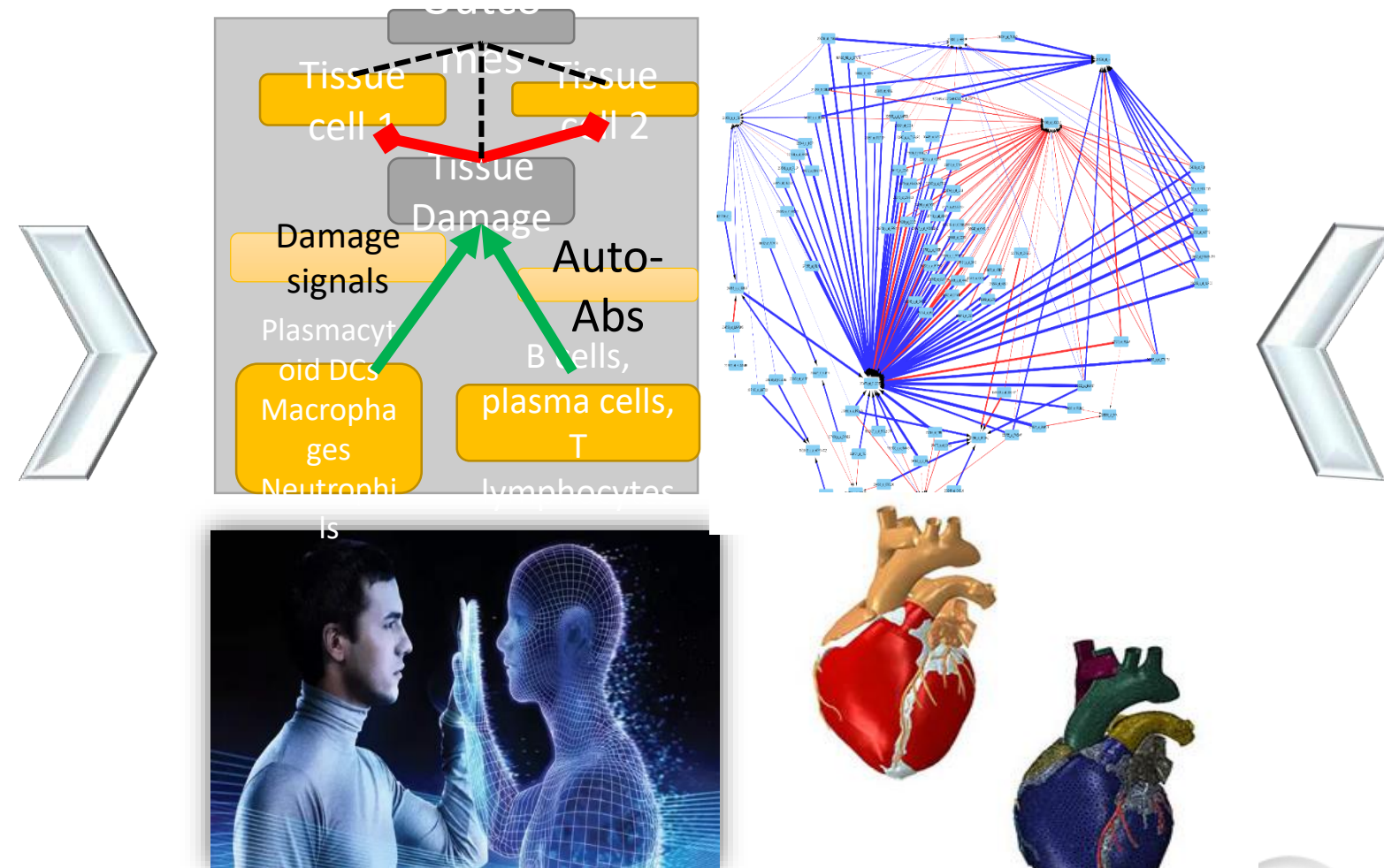


Perspectives: *in silico* prediction of drug efficacy as an important dimension of computational precision medicine

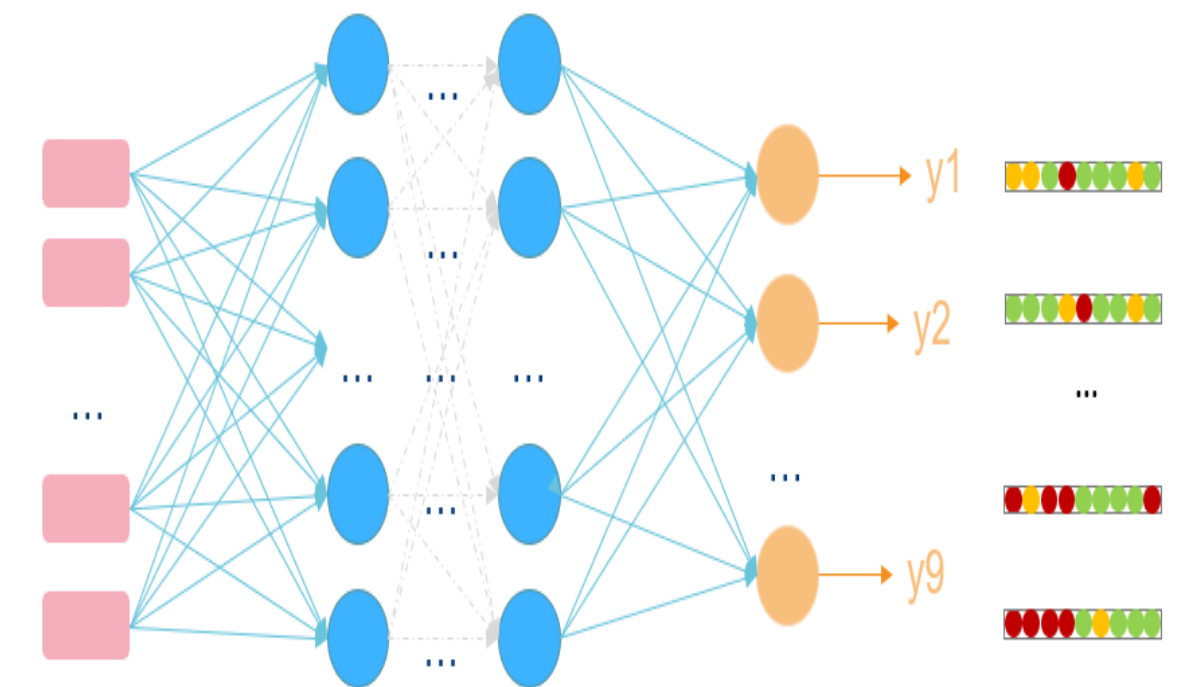
Patient specificities understood



Drug efficacy and safety predicted across patient heterogeneity



Drug candidate properties predicted



Acknowledgements

- **Servier**

Audrey Aussy

Emiko Desvaux

Sylvain Fouliard

Sandra Hubert

Glenn Gauderat

Mickaël Guedj

Laurence Laigle

Perrine Soret

- **Brest University**

Jacques-Olivier Pers

- **Intellomx**

Graham Ball

Simon Hayworth

Dimitrios Zafeiris

- **Rosa**

Krishnakant Dasika

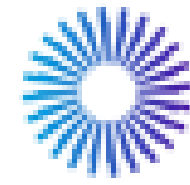
Christina Friedrich

Vincent Hurez

Katherine Kudrycki

Robert Sheehan

Mike Reed



PRECISESADS

Molecular Reclassification to Find
Clinically Useful Biomarkers for
Systemic Autoimmune Diseases

necessity



ROSA

