



Data driven insights for improved drug development

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PROPRIETARY, CONFIDENTIAL

Drug development: Lengthy, expensive and risky



Current likelihood of success limited -
based on trial and error:

5.1%

Oncology*

11.1%

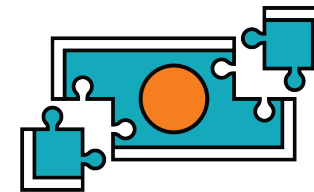
Autoimmune /
inflammation*



Development
costs

\$1.78B

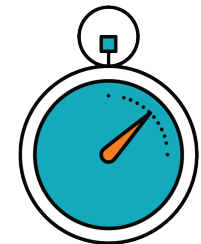
Doubled in the
last 10Y



Development
time

13.5Y

6-7Y in the clinic



Identifying the existing gaps can push these rates much higher

The gaps preventing higher success rates

Machine learning technologies, disease biology and data usage



Technologies cannot differentiate disease signals



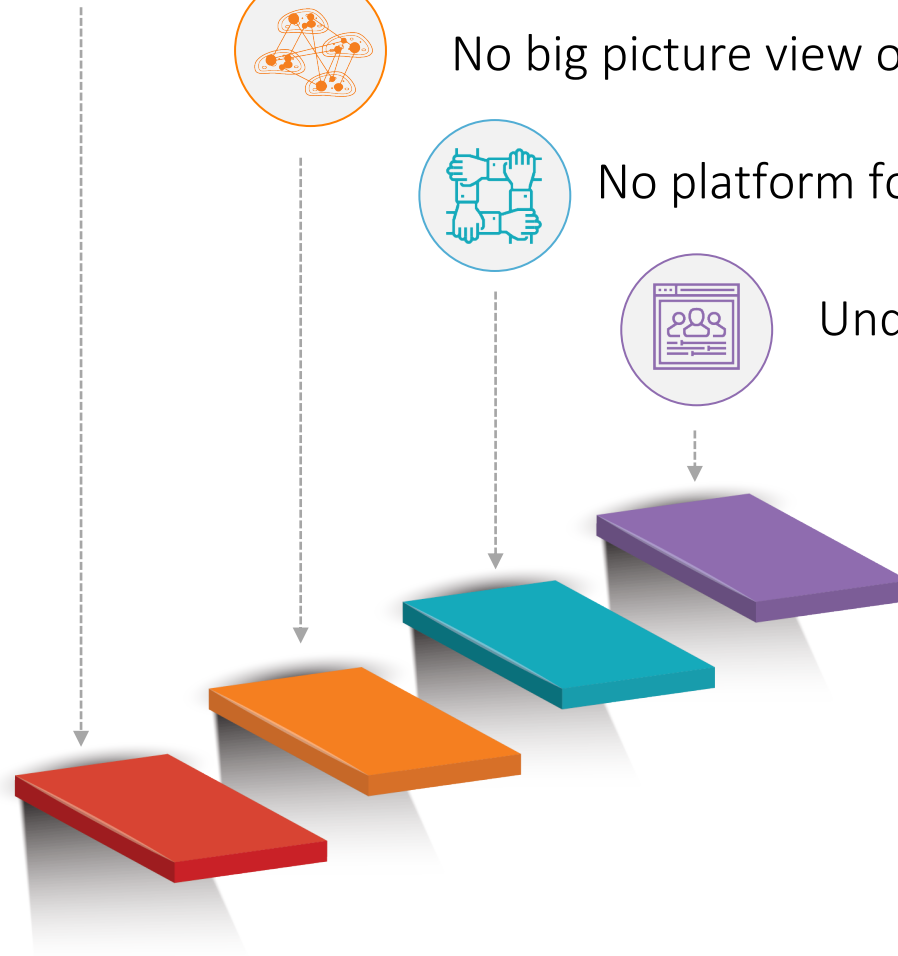
No big picture view of the biology



No platform for leveraging proprietary data



Underutilized public data



CytoReason is using its machine learning **cell-centered-model**,
trained on proprietary and public **data**...



...to support discovery, pipeline and portfolio
decision-making

CytoReason in a nutshell



Founded Oct '16

located in Tel Aviv



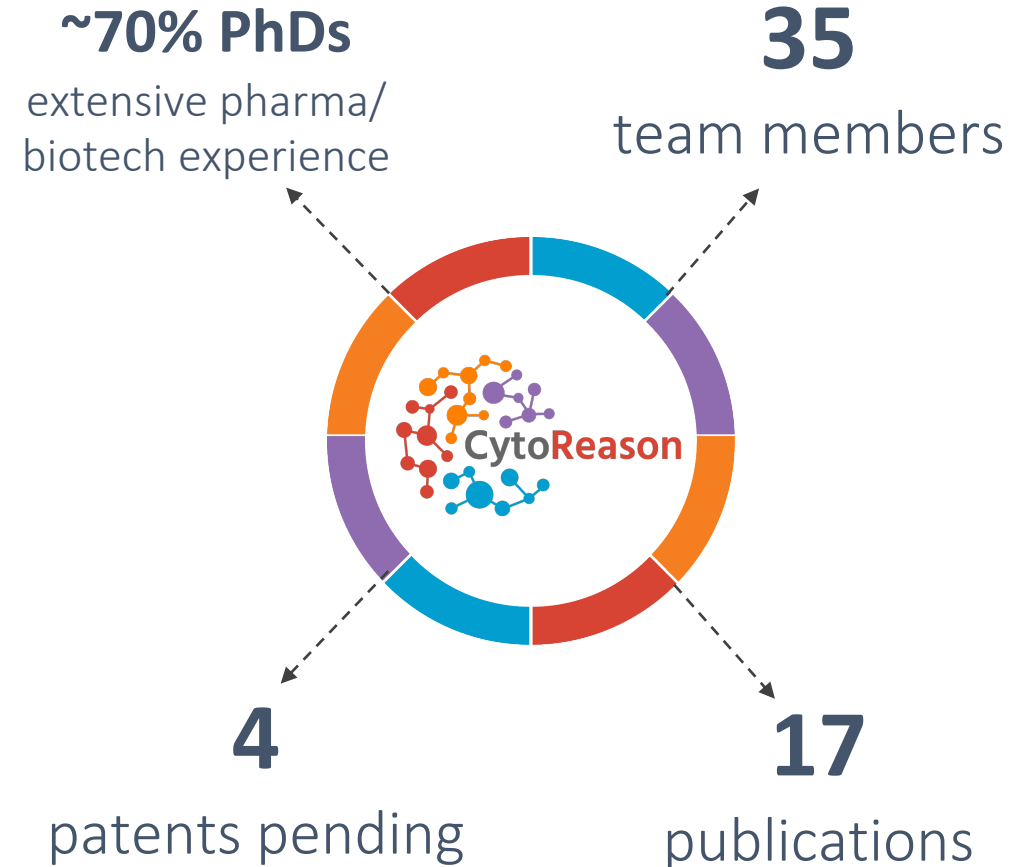
Based on 10 years' research from
Stanford and Technion



Revenue funded
from inception



8 collaborations
with the likes of **Pfizer, Janssen,**
GSK and **Parker Institute for**
Cancer Immunotherapy

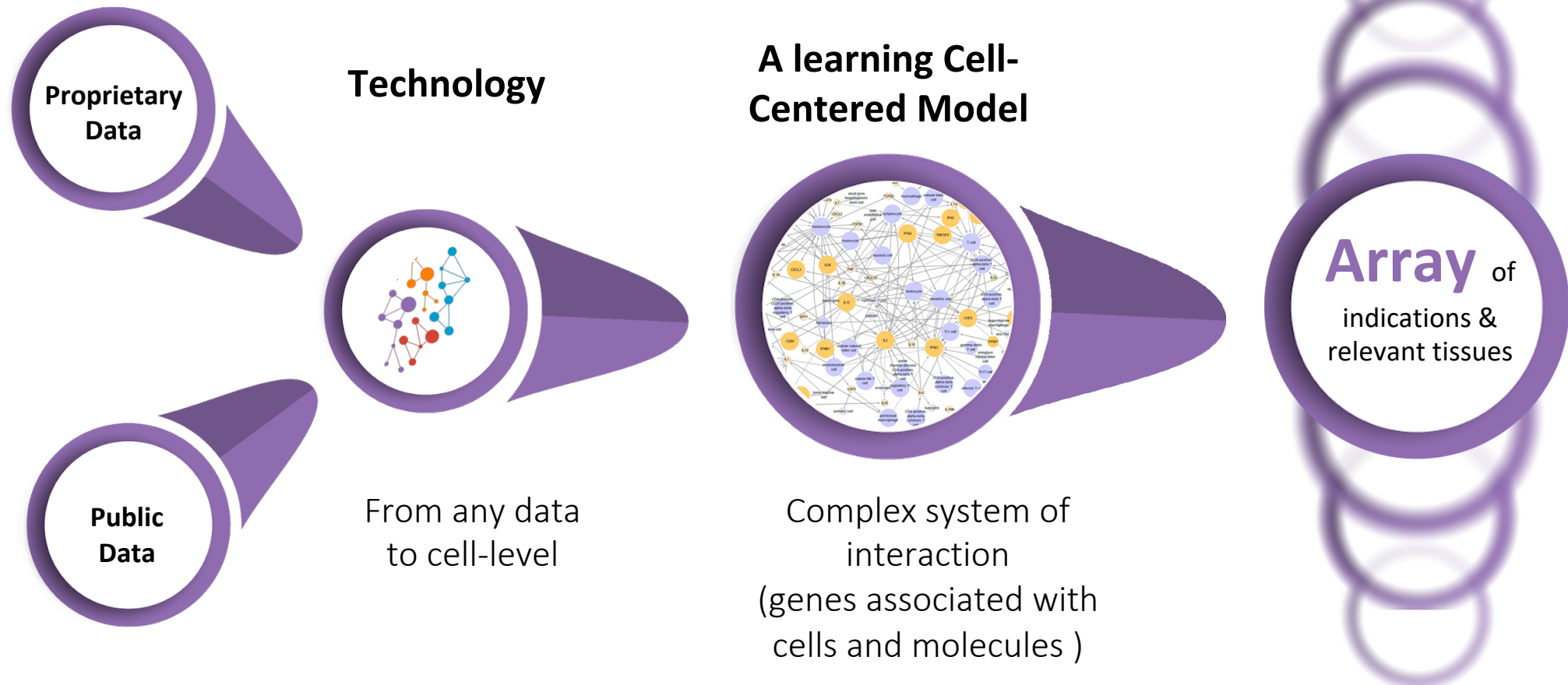


At the heart of it all: The CytoReason Cell-Centered Model



Built on a cellular level:

Replicating biology to crack key biological challenges – growing and learning from every data set



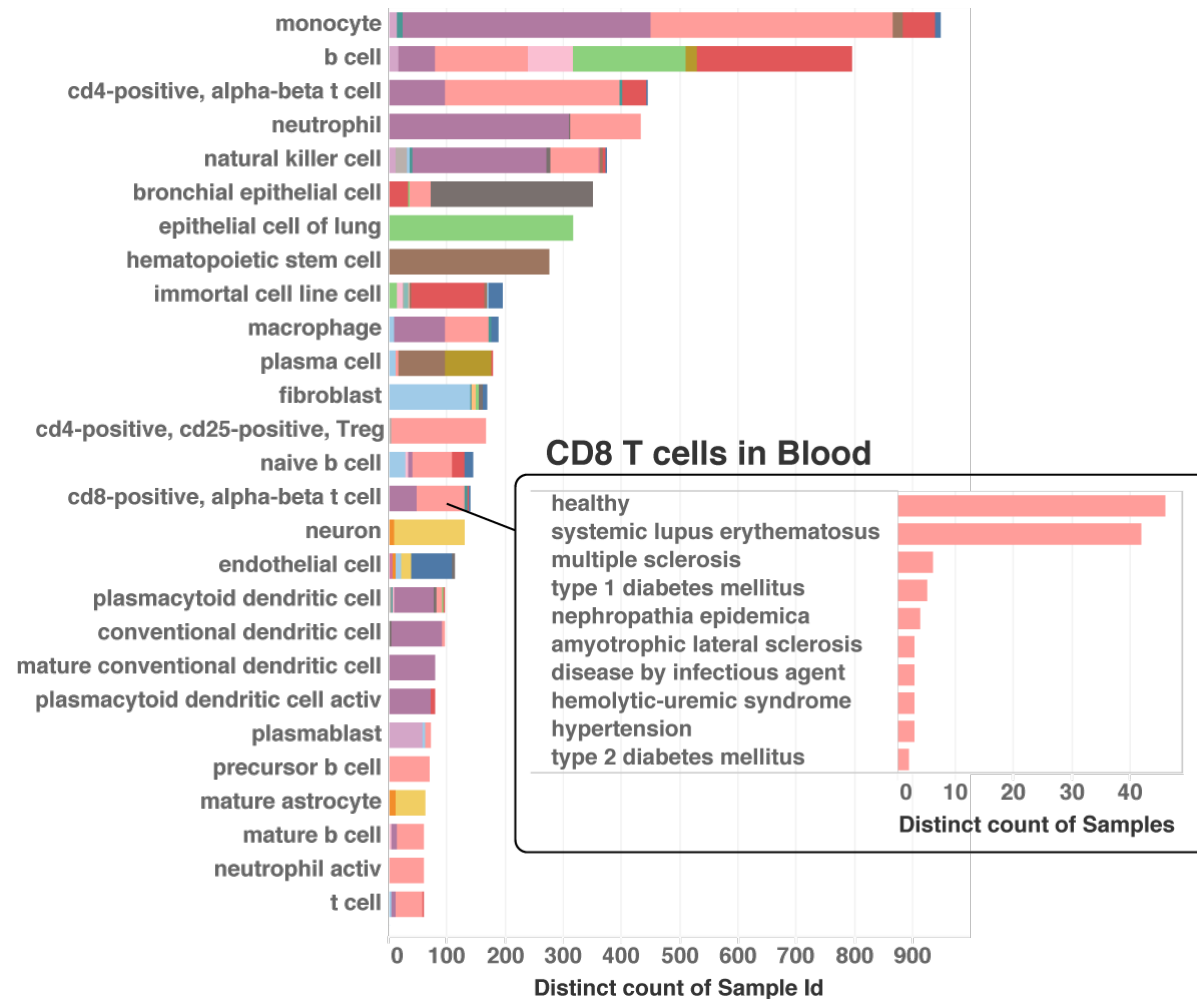
CytoReason's data assets

Cell signatures and disease / treatment references



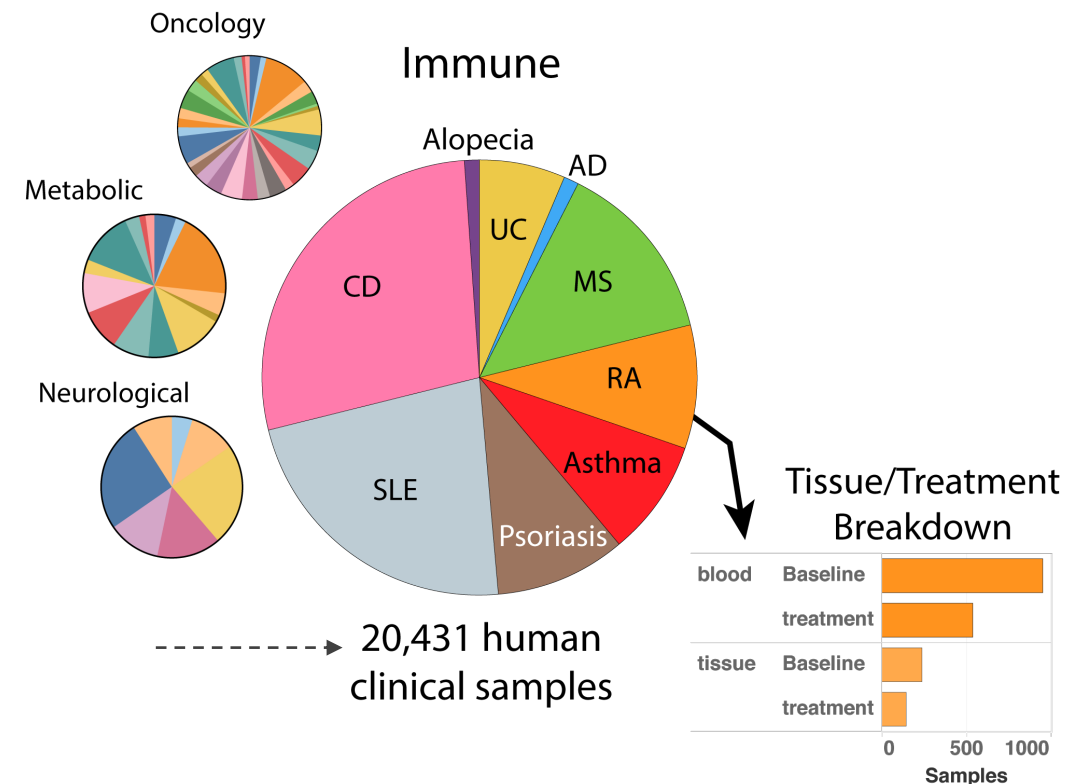
Cell Signature Database

9000 samples (colored by tissue)



Disease Reference Database

Human clinical samples (colored by disease)



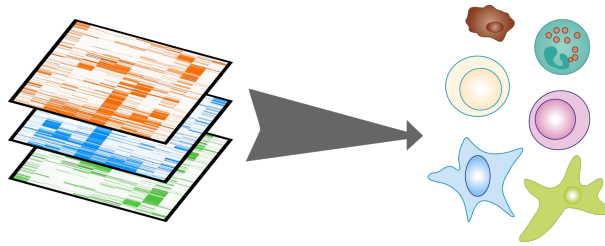
CytoReason's technology assets

The six building blocks



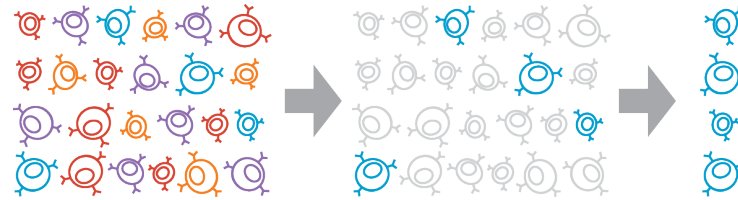
Deconvolution

Rebuilding cellular proportion and information from bulk measurement data



Cell Specificity

Removal of non-specific cell signals to reveal pure disease-related cell / gene maps



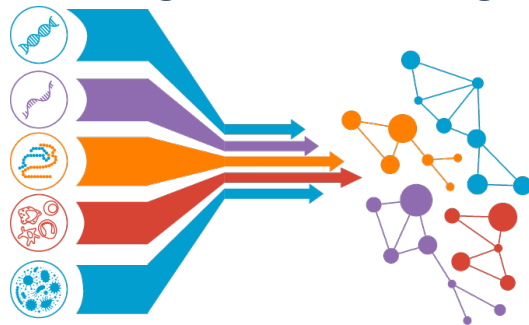
Natural Language Processing

Generating biological correlations from the literature



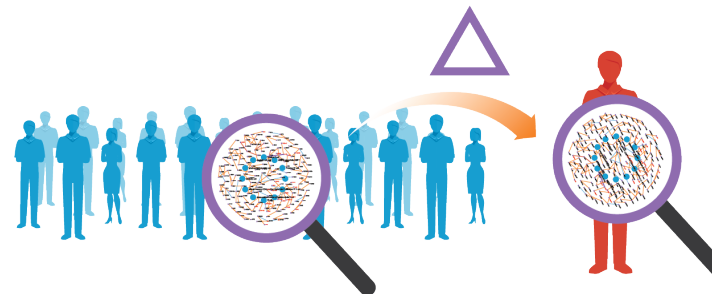
Multi omics

Integrating data types to improve our biological understanding



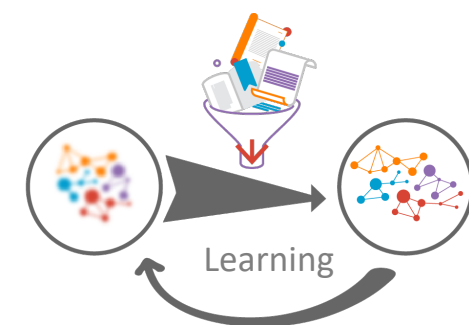
Disruption networks

Generating insights from small data sets



Statistical learning

Incorporating prior knowledge to improve prediction power and accuracy



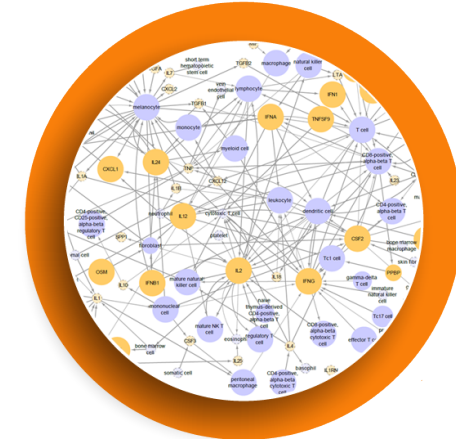
A cell-centered-model for each disease-related tissue



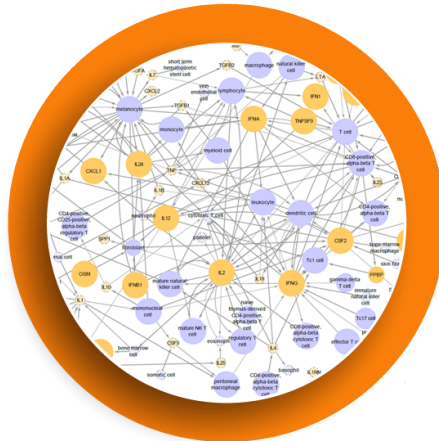
Psoriasis (lesion)



CRC (tumor tissue)

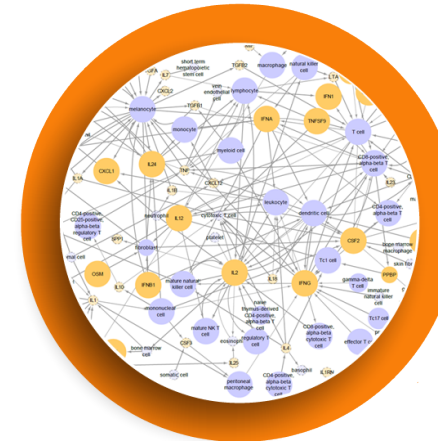


Melanoma (blood)



Array
of indications &
relevant tissues

UC (inflamed tissue)





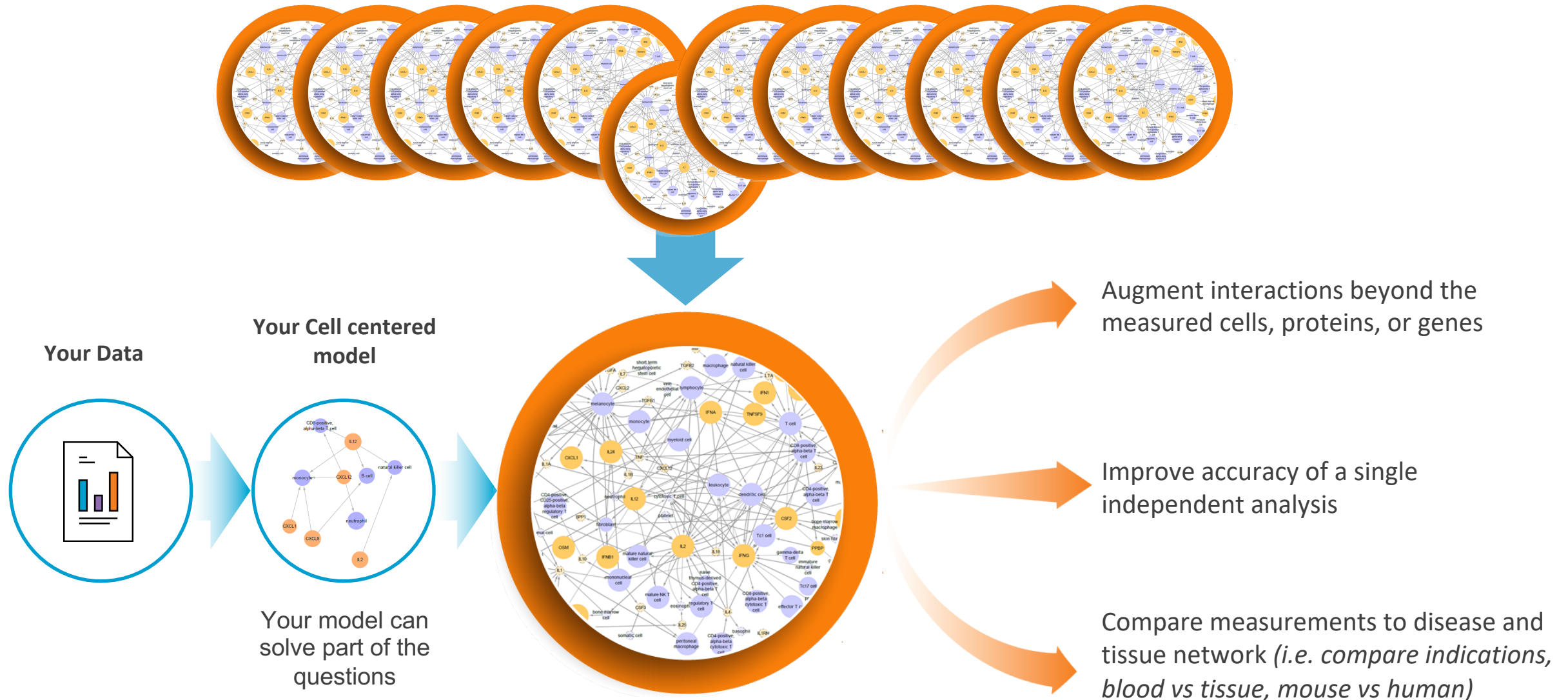
- ## BIOMARKERS

- ## INDICATION

- Prioritization
- Expansion

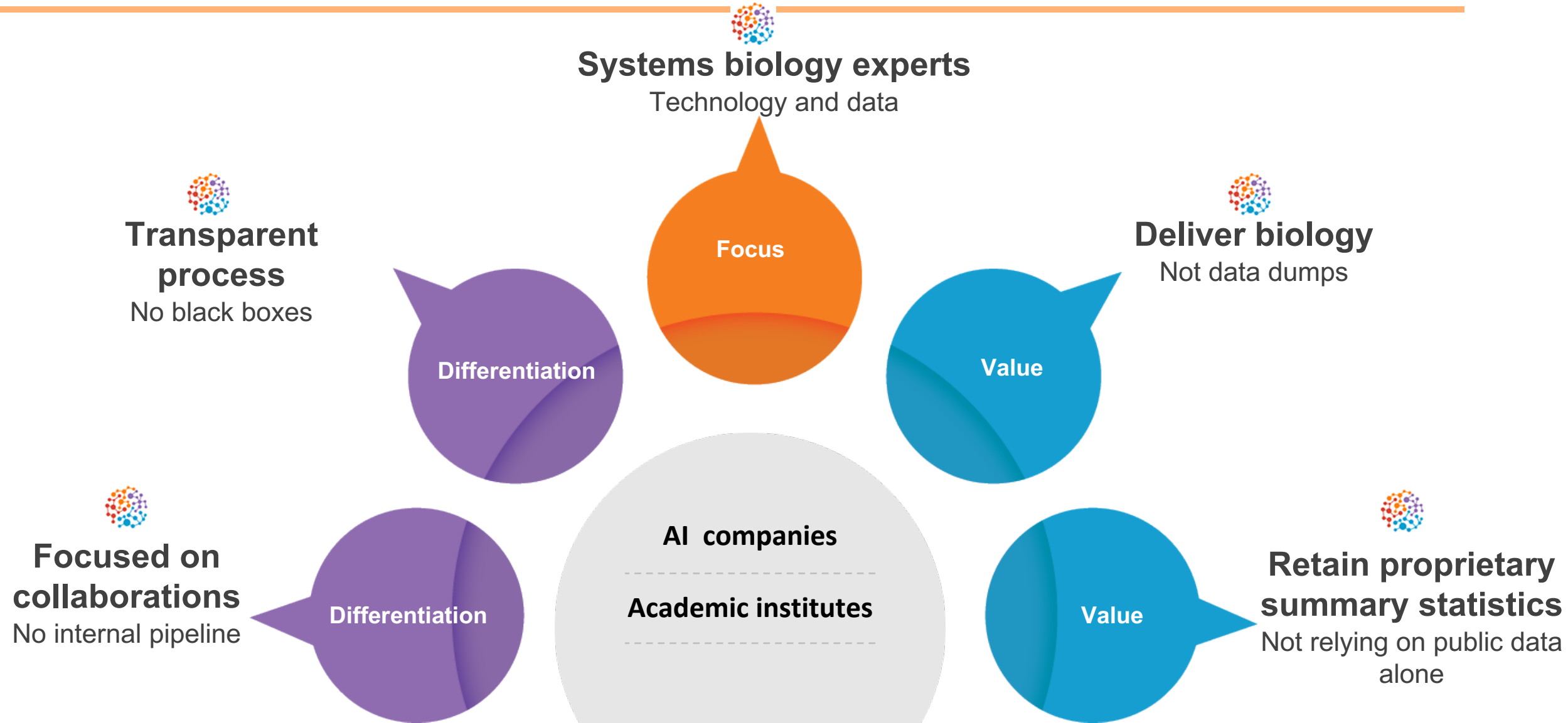
CytoReason's two steps process

Leveraging our cell centered model to improve your own cell-centered model's output



Competitive edge

Clear value, differentiation and focus





CytoReason as a partner

CytoReason collaboration plan



Technology PoC project
*MoA, targets, indications
and biomarkers*

Long term collaboration
*MoA, targets, indications
and biomarkers*

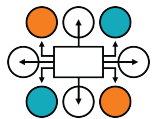
GOAL	Evaluate the model/technologies capabilities	Leverage CytoReason's model and know-how to support drug discovery and development
SCOPE	3-6 months, two projects	2-3 years, one or more parallel workstreams each with consecutive projects
OUTPUT PROVIDED PER PROJECT	Project report, presentation and interactive data visualization reports (which can be updated periodically)	Project report, presentation and interactive data visualization reports (which can be updated periodically)

Collaboration outline



Data retention – machine learning

- By the nature of the machine learning system, a summary statistics of the data will remain in the model
- No raw data or project-based questions and answers retained
- Strict data retention policy



Use of retained data

- Data cannot be backtracked
- No disclosure of the data source (company name)
- No disclosure of the drug tested
- No collaborator has access to CytoReason cell centered model



Intellectual property

- All IP arising from the collaboration will be assigned to the Collaborator upon IP option exercise
- Exclusions: Any improvements to CytoReason's model and/or technologies



Scientific Publications of Methods and Results



Scientific Publications of Methods and Results (continued)



application	Tofacitinib for polyarteritis nodosa: a tailored therapy. <i>Annals of the Rheumatic Diseases, 2016</i>	➤	Repositioning case study of tofacitinib for vasculitis with potential for companion diagnostic based on JAK-STAT baseline and response levels.	2016
method	Activation of the reward system boosts immunity. <i>Nature Medicine, 2016</i>	➤	A new method of high dimensional cellular immune profiling coupled with novel algorithm for increased signal to noise detection.	
method	Systems immunology reveals markers of susceptibility to West-Nile Virus infection. <i>Clinical and Vaccine Immunology, 2015</i>	➤	A new method for identifying cell type specific gene expression differences, undetectable otherwise, via flow cytometry and NanoString data integration.	2015
application	Systems analysis of immunity to Influenza vaccination across multiple years and in diverse populations reveals shared molecular signatures. <i>Immunity, 2015</i>	➤	Application of our gene expression deconvolution techniques to estimate cell type proportions where flow data was missing, validating the observed cell differences post-vaccination.	
method	Reconstructing the genomic content of microbiome taxa through shotgun metagenomic deconvolution. <i>Computational Biology, 2013</i>	➤	A new method for increased resolution of meta-genomic data	2013
method	Sensitivity analysis for inference with partially identifiable covariance matrices. <i>Computational Statistics, 2013</i>	➤	A new method for an ultra-high dimensional single cell cytometry measurement by estimation from overlapping marker panels.	
method	Extracting cell-type-specific gene expression differences from complex tissues <i>Nature Methods, 2010</i>	➤	A new method for estimating cell-type specific expression differences from whole blood. Applied to identify a signature of graft rejection in specific cell-type, undetectable otherwise.	2010
method	Towards a cytokine-cell interaction knowledgebase of the adaptive immune system. <i>Pacific Symposium on Biocomputing, 2009</i>	➤	A novel method for generating an immune inter-cellular interactions from the literature using text-mining.	2009

Thank you!



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