Precision Medicine: Crafting Tailored Therapies in the Modern Age

Panel Discussion, Inspire 2 Live

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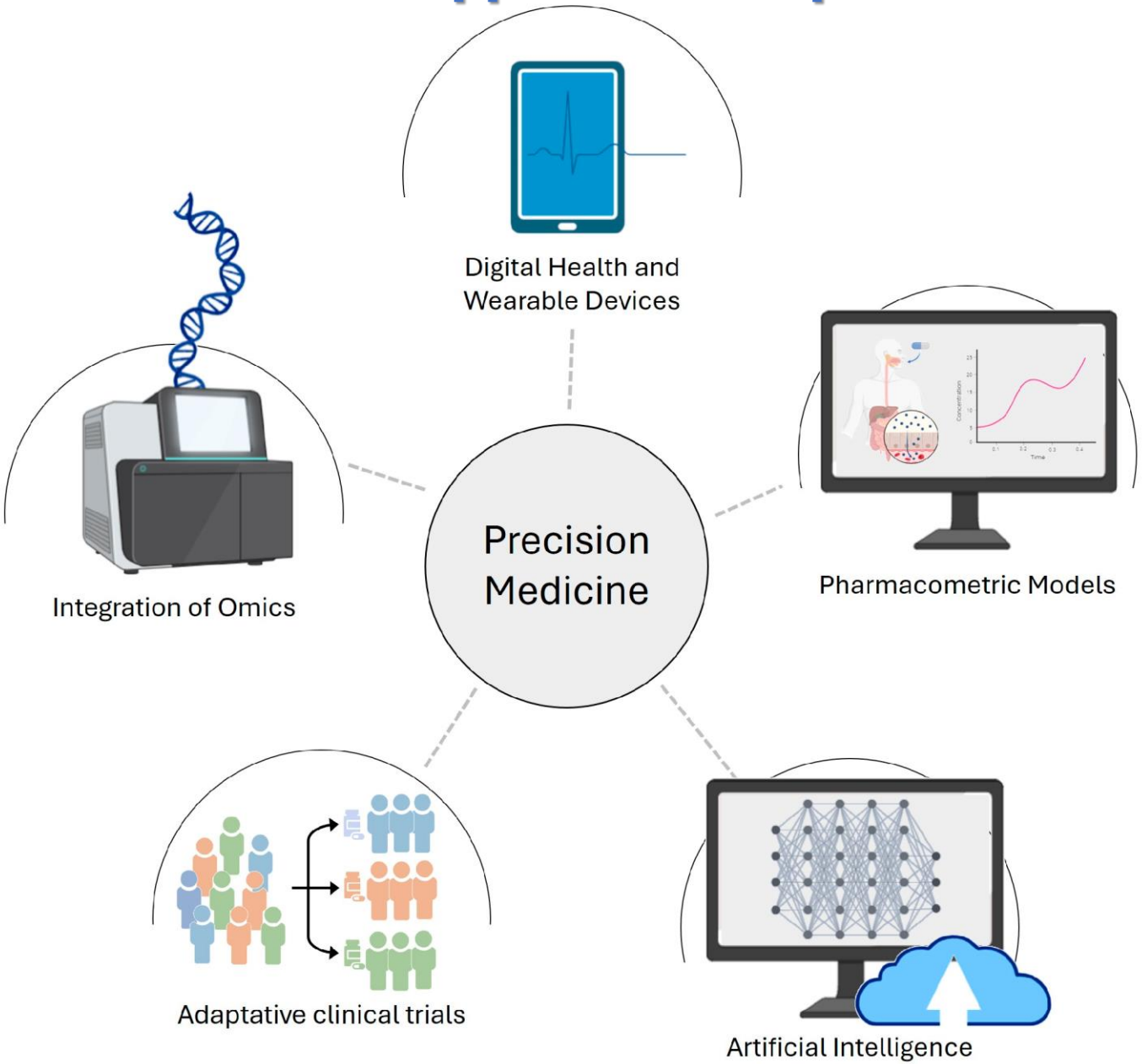
Key elements of in silico approaches in precision medicine

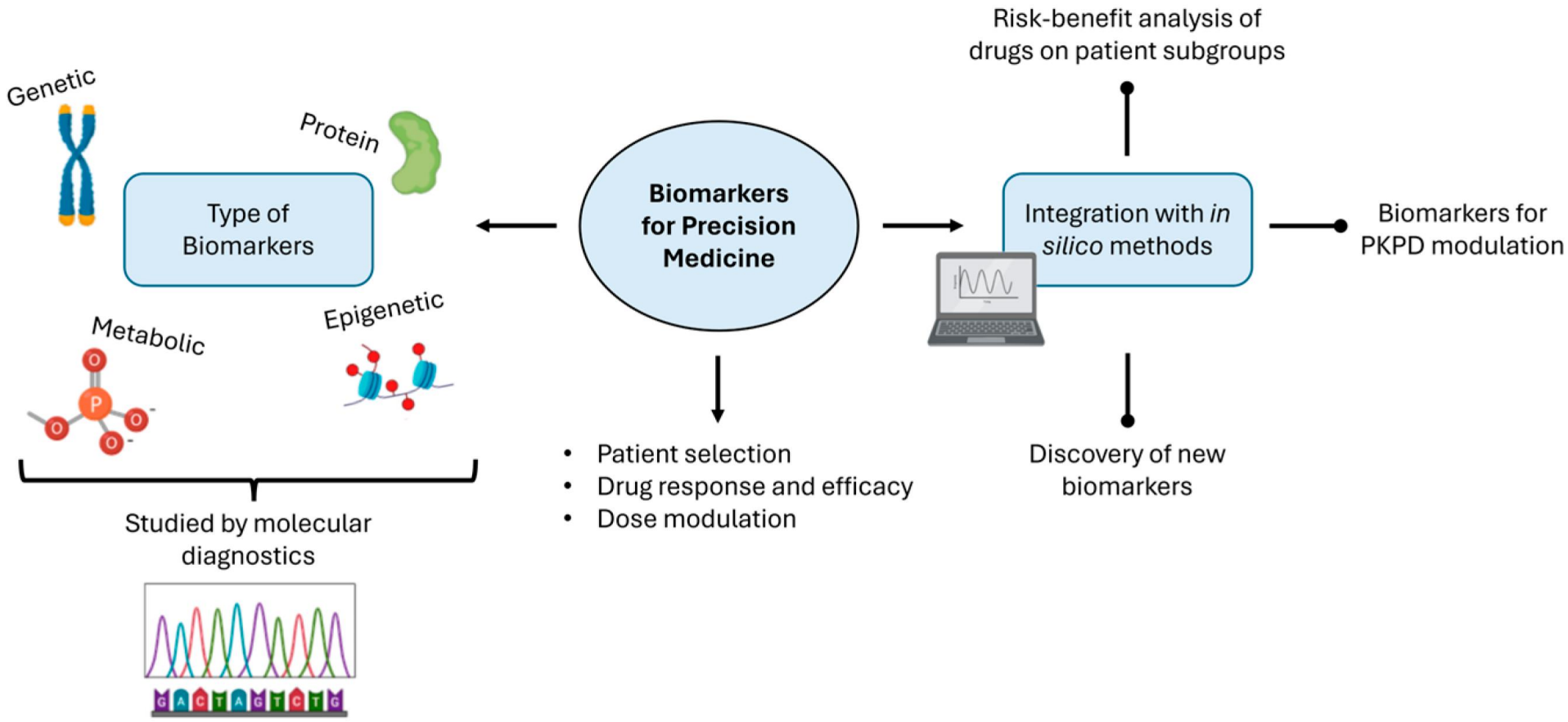


https://www.mdpi.com/2694272

Some new therapeutic molecular personalized medicines approved by the FDA

	Therapeutic Indication
	Cancer
Products	Abecma (multiple myeloma)
	Exkivity (lung cancer)
	Lumakras (lung cancer)
	Jemperli (endometrial cancer)
	Rybrevant (lung cancer)
	Scemblix (myeloid leukaemia)
	Tepmetko (lung cancer)
	Truseltiq (cholangiocarcinoma)
	Rare Diseases
	Amondys (muscular dystrophy)
	Evkeeza (homozygous familial hypercholesterolaemia)
	Nexviazyme (Pompe disease)
	Nulibry (molybdenum cofactor deficiency)
	Vyvgart (Myasthenia Gravis)
	Welireg (von Hippel–Lindau)
	Other Diseases
	Bylvay (progressive familial intrahepatic cholestasis)
	Cabenuva (HIV-1)
	Leqvio (hypercholesterolaemia)

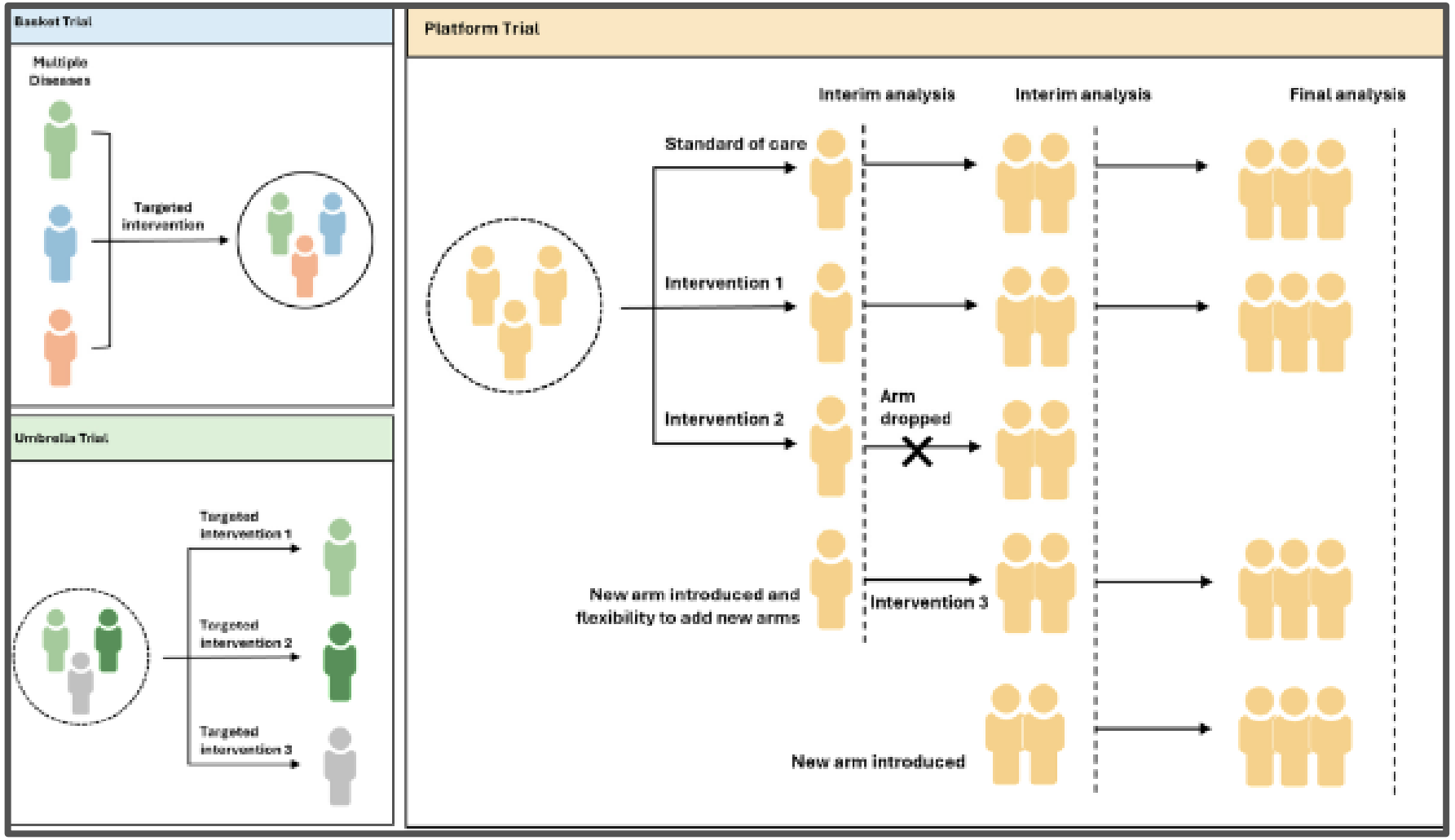
Biomarker integration in precision medicine



The uses and benefits of EHRs

EHR Benefits	Integration of EHR in Healthcare
Information access and sharing	EHRs facilitate quick and secure access to patients' medical information, allowing healthcare professionals to make informed decisions and order care.
Better care management	EHRs help you better manage the care of chronic patients by enabling continuous monitoring and adjustment of treatment plans based on real-time data.
Integration and coordination	The integration of RSE (remote sensing and earth observation) into healthcare systems allows for more efficient coordination between different healthcare providers, improving continuity of care.
Clinical research	RSE data can be used in clinical research to identify health trends, evaluate the effectiveness of treatments, and improve evidence-based medicine. Furthermore, omics data, which encompasses genomic, transcriptomic, proteomic, and metabolomic information, plays a crucial role in precision medicine. This data enables the personalization of treatments based on the genetics and individual characteristics of each patient, improving the effectiveness of care. Omics data analysis also helps identify genetic markers of diseases, enabling early prevention and diagnosis.

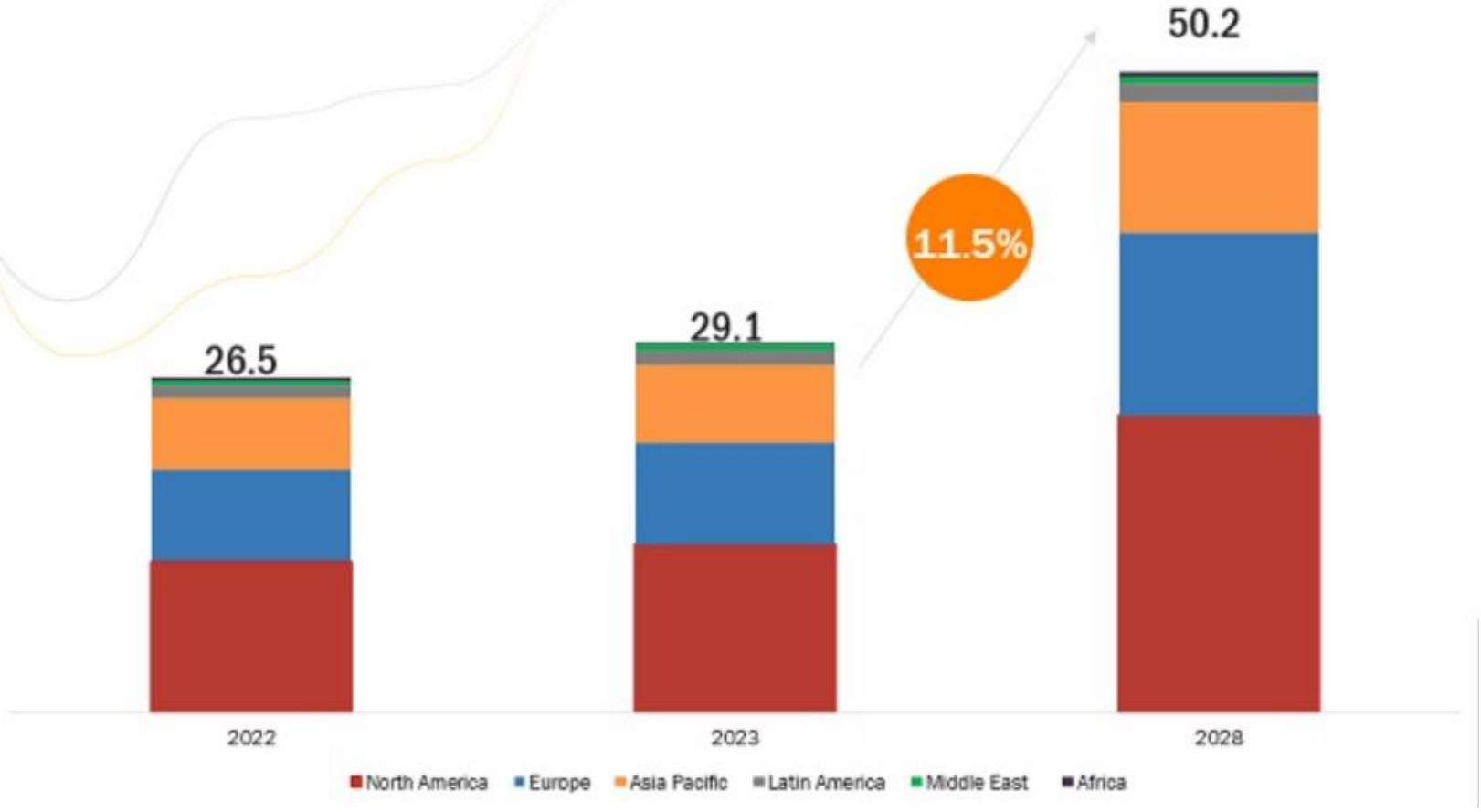
Representation of basket trials, umbrella trials, and platform trials



CAGR

11.5%

The global precision medicine market is projected to reach USD 50.2 billion in 2028 from USD 29.1 billion in 2023, growing at a CAGR of 11.5%.



An Open-Science Framework

- **Generate and Share Data:**
  - Use a portal system to access global coherent datasets
  - Build an inter-operable infrastructure for collation, curation and hosting of datasets for the R&D community
  - Common standards and methods for the collection of the world's largest biomarker repositories for respiratory disorder
- **Generate and Share Tools:**
  - Collectively develop next-generation animal models, imaging tools, stem cell lines, biosensors, and more…
- **Generate and Share Models:**
  - Apply advanced clinical informatics, computational biology and visualization tools to create dynamic interactive Disease Maps and inform Clinical Decisions Support and Practice Guidelines
- **Create Insights:**
  - Tap Global Expertise (multi-disciplinary & global) – crowd-sourced solutions

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Courtesy Mag[illegible]

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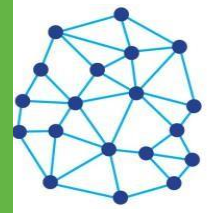
TB Data Commons



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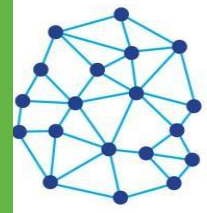
Open Tuberculosis Data Commons

The Patient-Centric TB Information Commons seeks enable Tuberculosis drug discovery and development through clinical and translational research.

Our Aims:

1. To pilot the development of global patient-centric data commons for Tb.
2. To load multi and high dimensional datasets to enable TB clinical and translational research.
3. To encourage data sharing in the global TB community by providing a sharable resource.



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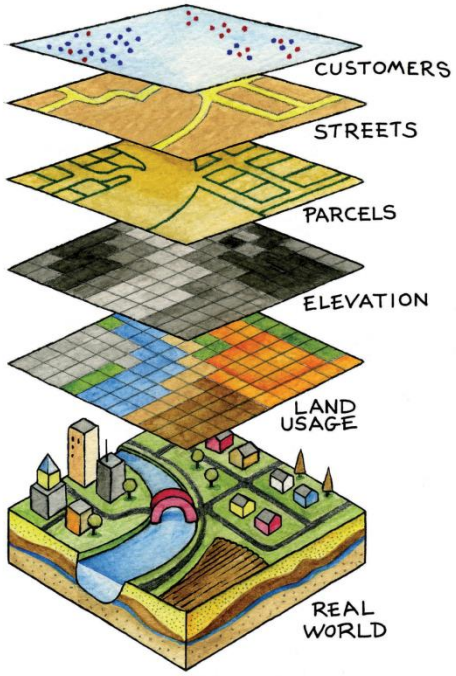
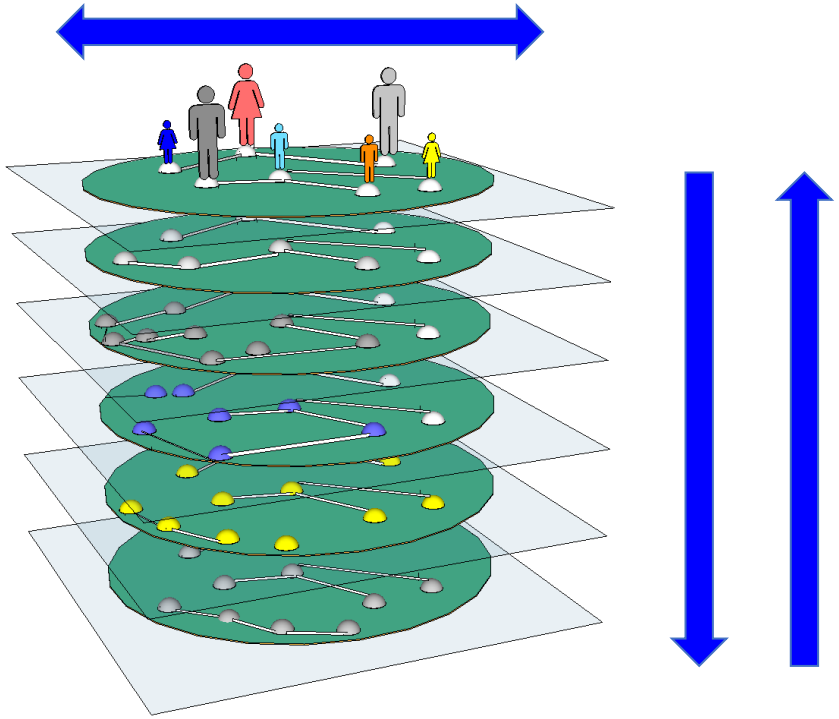
A Patient-Centric Data Commons for TB



GIS Data Layers



Patient Data Layers

" It's like Google Maps for Healthcare" – Paul Avillach

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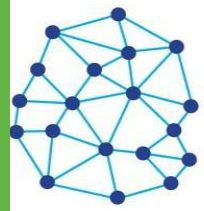
Goals for the TB Patient-Centric Data Commons

- Enabling new approaches to translational science and systems biology
  - E.g., Precision Medicine
- Building, managing and deploying an integrative Patient-centered Data Commons
  - Genetics / Genomics
  - Cells and Tissues
  - Biochemical assays
  - Circulating metabolites
  - Phenotypic information and EHR Data
- Providing accessibility to state-of-the-art infrastructure
  - Efficiencies of cloud-based platforms
  - Effectiveness of open-source / open-data collaboration



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Clinical Data Sets for Patient-Centric Data Commons for TB

Title	Description	Samples	Notes
GSE107995: A modular transcriptional signature identifies phenotypic heterogeneity of human tuberculosis infection	This SuperSeries is composed of the SubSeries listed above: GSE107991, GSE107992, GSE107993 and GSE107994	414 samples 262 patients some at multiple timepoints	latent vs. active TB RNAseq expression
GSE19491: Blood Transcriptional Profiles in Human Active and Latent Tuberculosis	This series regroups different datasets (training set, test set, validation set, longitudinal set, separated cell set) to identify and characterise a ... (Superseries of 6 studies above: GSE19435 GSE19439 GSE19442 GSE19443 GSE19444 GSE22098)	498 samples 498 patients	Array expression GPL6947
GSE83456: The transcriptional signature of active tuberculosis reflects symptom status in extra-pulmonary and pulmonary tuberculosis	Background: Mycobacterium tuberculosis infection is a leading cause of infectious death worldwide. Gene-expression microarray studies profiling the ...	202 samples 202 patients	Array expression GPL10558
GSE42834: Human whole blood microarray study to compare patients with tuberculosis, sarcoidosis, pneumonia, and lung cancer	This SuperSeries is composed of the SubSeries listed above: (GSE42825 GSE42926 GSE42827 GSE42830 GSE42831 GSE42832)	356 samples 356 patients	Array expression GPL10558 Human whole blood microarray study to compare patients with tuberculosis, sarcoidosis, pneumonia, and lung cancer
GSE31368: Profiling proteome-scale antibody responses to M. tuberculosis	SuperSeries of the studies listed above: (GSE30721 and GSE30722)	567	Proteome microarray GPL9790
GSE19433: Profiling antibody responses to M. tuberculosis proteins in TB suspects' sera using full-proteome microarrays.	Understanding the immune response to tuberculosis requires greater knowledge of humoral responses. To characterize antibody targets and the effect of...	625	Proteome microarray GPL9790 proteomic profiling
GSE28623: Pathway and functional association analysis of whole blood gene expression profiles reveal functional networks underlying TB pathogenesis. [Agilent-01...	Tuberculosis (TB) is an ancient infectious disease that remains one of the major health threats in humans worldwide. Biosignatures can play a signific...	108	Array expression GPL4133
GSE31348: Tuberculosis Patients Blood Gene Expression Through Treatment	Background Accurate assessment of treatment efficacy would facilitate clinical trials of new anti-tuberculosis drugs. TB patients exhibit altered per...	135	Array expression GPL570
GSE58411: Blood Transcriptional Signature of hyperinflammation in HIV-associated Tuberculosis	Patients with HIV-associated TB are known to experience systemic hyperinflammation, clinically known as immune reconstitution inflammatory syndrome (I...	107	Array expression GPL10558 Hiv Hyperinflammation
GSE67589: Excessive Cytolytic Responses Predict Tuberculosis Relapse After Apparently Successful Treatment	Background Identification of patients at risk of tuberculosis relapse following treatment would revolutionize clinical trials of new drugs and regimen...	57	Array expression GPL570 relapse marker study

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Summary Statistics

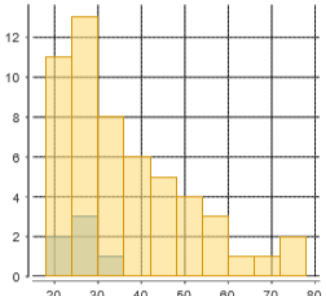
Query Summary for Subset 1
(\\Tuberculosis\Tuberculosis\Chaussabel(2009) GSE19491\Disease Ontology\Disease State\Active Pulmonary TB\)

Query Summary for Subset 2
(\\Tuberculosis\Tuberculosis\Chaussabel(2009) GSE19491\Disease Ontology\Disease State\Control BCG\)

Subject Totals

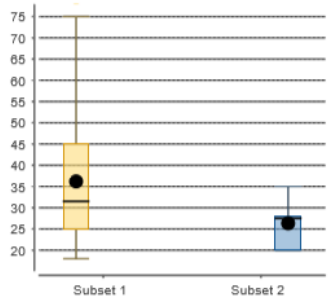
Subset 1	Both	Subset 2
54	0	6

Age



Subset 1	Subset 2
Mean: 36.2	Mean: 26.33
Median: 31.5	Median: 27.5
IQR: 20.0	IQR: 8.0
SD: 14.39	SD: 5.68
Data Points: 54	Data Points: 6

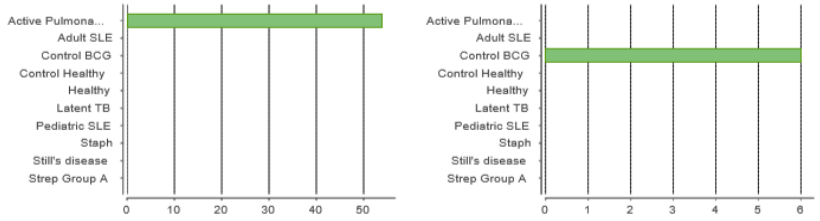
Age



Analysis of Disease State

\\Tuberculosis\Tuberculosis\Chaussabel(2009) GSE19491\Disease Ontology\Disease State

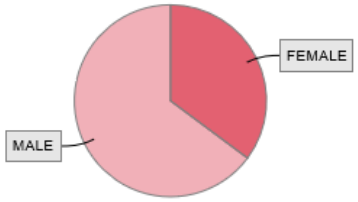
No χ^2 test calculated: subsets are disjointed



Category	Subset 1 (n)	Subset 1 (%n)
Active Pulmonary TB	54	100.0 %
Adult SLE	0	0.0 %
Control BCG	0	0.0 %
Control Healthy	0	0.0 %
Healthy	0	0.0 %
Latent TB	0	0.0 %
Pediatric SLE	0	0.0 %

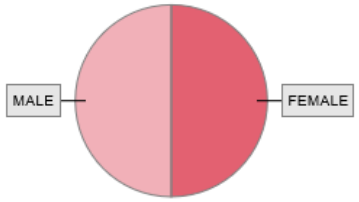
Category	Subset 2 (n)	Subset 2 (%n)
Active Pulmonary TB	0	0.0 %
Adult SLE	0	0.0 %
Control BCG	6	100.0 %
Control Healthy	0	0.0 %
Healthy	0	0.0 %
Latent TB	0	0.0 %
Pediatric SLE	0	0.0 %
Staph	0	0.0 %
Still's disease	0	0.0 %
Strep Group A	0	0.0 %

Sex



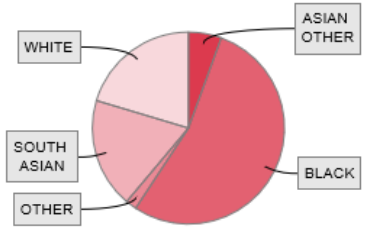
Category	Subset 1 (n)	Subset 1 (%n)
FEMALE	19	35.19 %
MALE	35	64.81 %

Sex



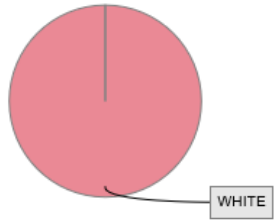
Category	Subset 2 (n)	Subset 2 (%n)
FEMALE	3	50.0 %
MALE	3	50.0 %

Race



Category	Subset 1 (n)	Subset 1 (%n)
ASIAN OTHER	3	5.56 %
BLACK	29	53.7 %
OTHER	1	1.85 %
SOUTH ASIAN	10	18.52 %
WHITE	11	20.37 %

Race



Category	Subset 2 (n)	Subset 2 (%n)
WHITE	6	100.0 %

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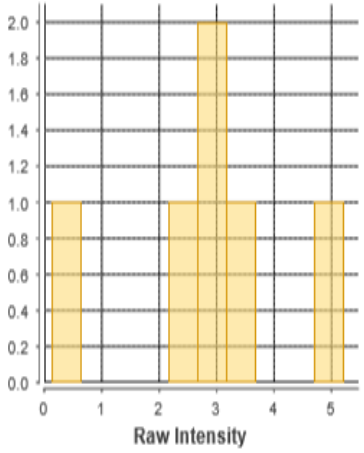
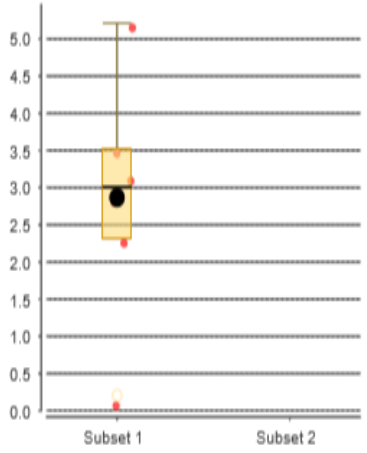
Analysis of IL22 in CD4 cells

...\Chaussabel(2009) GSE19491\Biomarker Data\Gene Expression\Illumina HumanHT-12 V3.0 expression beadchip\Baseline\CD4 cells

No T-test calculated: not enough data



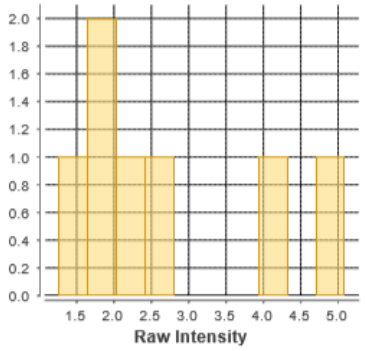
	Subset 1	Subset 2
Mean	2.87	-
Median	3.01	-
IQR	1.21	-
SD	1.66	-
Data Points	6	0



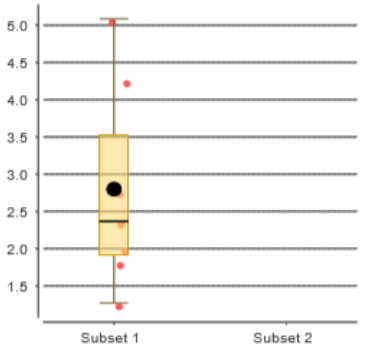
Analysis of IL22 in Monocytes

...\Chaussabel(2009) GSE19491\Biomarker Data\Gene Expression\Illumina HumanHT-12 V3.0 expression beadchip\Baseline\Monocytes

No T-test calculated: not enough data



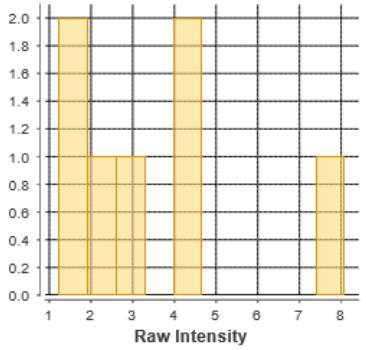
	Subset 1	Subset 2
Mean	2.8	-
Median	2.37	-
IQR	1.6	-
SD	1.38	-
Data Points	7	0



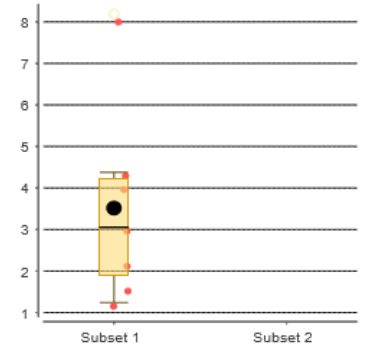
Analysis of IL22 in Neutrophils

...\Chaussabel(2009) GSE19491\Biomarker Data\Gene Expression\Illumina HumanHT-12 V3.0 expression beadchip\Baseline\Neutrophils

No T-test calculated: not enough data



	Subset 1	Subset 2
Mean	3.52	-
Median	3.05	-
IQR	2.31	-
SD	2.33	-
Data Points	7	0



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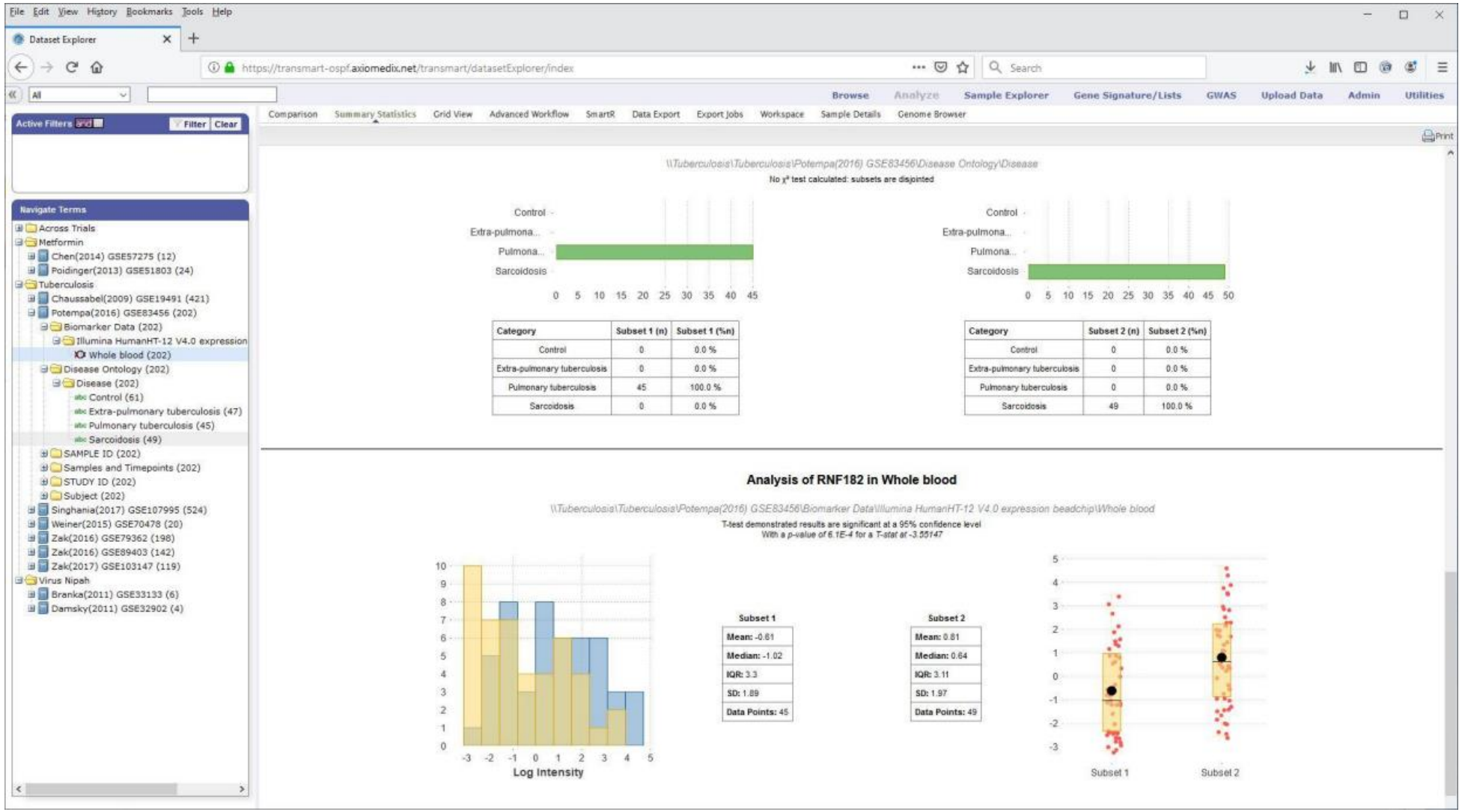

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Acknowledgements

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THANK YOU