Information Memorandum

Next Generation AI for Drug Discovery

Pharma’s problem, AI’s answer

“A selective high-quality molecule will never become a medicine if it is modulating the wrong target. This is why target selection is the most important decision we make in research.”

Mene Pangalos,
former VP, AstraZeneca

“Artificial intelligence is the key to unlocking the vast potential of novel biological targets, transforming the way we discover new drugs. By intelligently mapping the complexity of biology, AI accelerates the identification of promising targets, enhancing the precision and speed of therapeutic breakthroughs."

Demis Hassabis
CEO of Google DeepMind

Executive Summary

Intellomx is a UK-based firm leveraging innovative AI and machine learning to enhance and de-risk drug discovery and develop precision medicine approaches through precise *in silico* technologies:

- **Biology** Our USP lies in our capacity to understand the fundamental biology of disease. This insight allows us to pinpoint the optimum targets and drug candidates, for maximum patient populations.
- **Docking** Post target ID and validation, our docking algorithms can identify lead drug candidates for development.
- **Validation** Our findings have been confirmed in human biology and plant physiology, leading to the creation of in-house assets and intellectual property for both Intellomx and its collaborators.
- **Data** Data is no longer a constraint. We harness both public and proprietary information in genomics, proteomics, metabolomics and transcriptomics to discover new targets that influence disease.
- **Swarm Algorithm** Our algorithms invoke multiple, parallel swarms of analyses rather than compute-resource hungry deep-models. Swarms are 90% more efficient, minimize risk of false discovery and are explainable.
- **Collaboration** Our twin-track business approach features (1) a “fee for service” option, underpinning our internal research discovery initiatives, and (2) shared IP partnerships.
- **The Future** Target ID and docking done, Intellomx is building an integrated model of human disease pathways, captured in the form of the Intellomx Digital Twins - heralding the future in drug discovery.

Intellomx leads the way in this new era of precision drug discovery, utilizing its proprietary AI/ML to identify optimal drug targets and linking those targets to ranked drug candidates – actionable insights for pharmaceutical collaboration.

Solution – Intellomx I^3

I^3-Distiller	***Identification of key genes***
I^3-Driver	***Identification of key disease drivers***
I^3-Miner	***Defining the disease pathway***

I^3-Digital Twin	***Anticipating tox liabilities***

I^3-Pilot	***Identification of novel Small Molecules and Biologics***
I^3-Precise	***Panel optimization for diagnostics***

The Intellomx I^3 toolkits model different aspects of the underlying systems biology of disease, using proprietary Artificial Neural Networks and Machine Learning techniques developed in-house.

The primary tools (Distiller, Driver and Miner) model disease pathways at the molecular level whilst our Digital Twin anticipates toxicity liabilities.

Intellomx I^3 : Intuitive, Informed, Intelligence

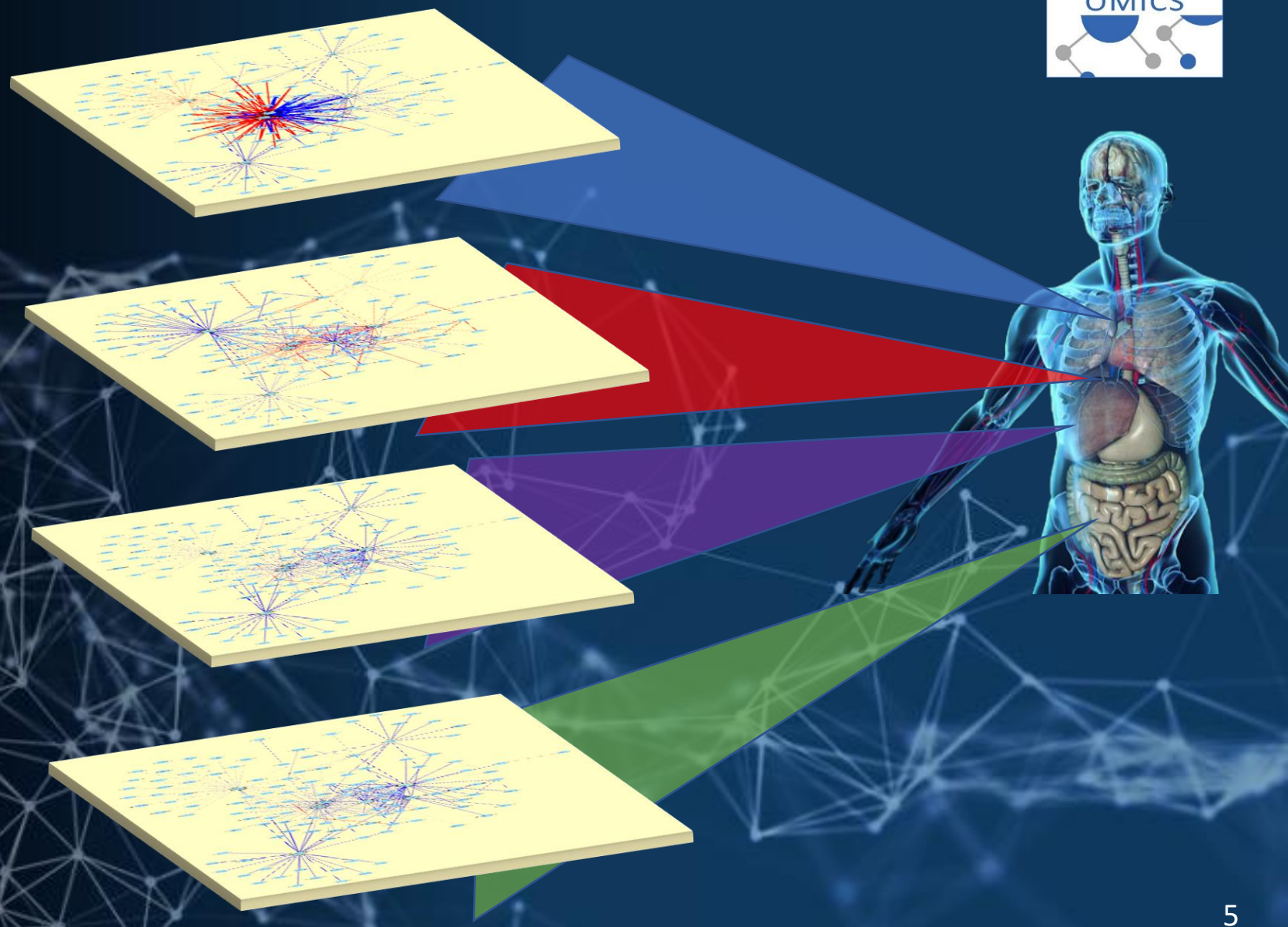
Solution – Intellomx I^3

Digital Twin

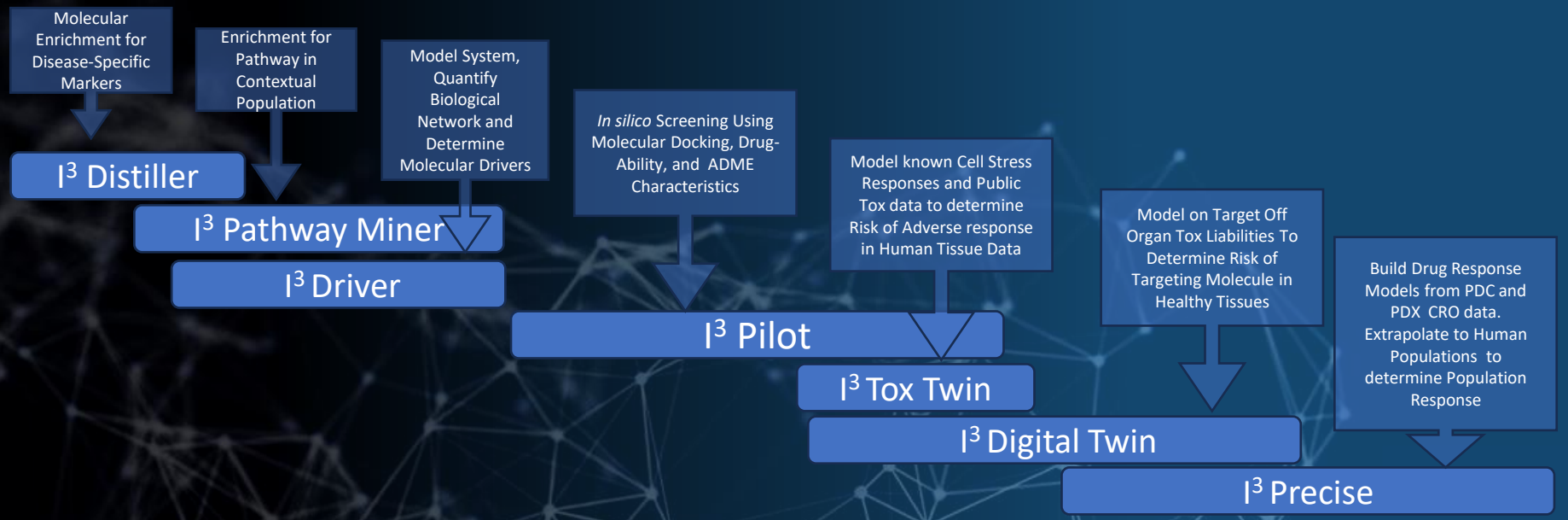
The Intellomx Digital Twin tests drugs in development in an AI-generated human model without risk, giving a clear indication of off-target toxicity.

We can thus prioritise molecules for development, eliminating up to 90% of projects that would fail due to toxicity in later, high-cost stages.

In future, a population of Intellomx Digital Twins will enable *in silico* clinical trials.



Solution: I³ for drug discovery/development



Swarm Based AI Approaches

- Trains large numbers of smaller less deep Neural Network Models
- Each model takes a different view of the data or addresses a different part of the problem
- Data presentation allows the whole problem to be represented with overlaps
- Early stopping and regularisation and Monte Carlo cross-validation built in.
- >1000 models run at the same time on different compute units of a GPU
- All of the transcriptome is considered in parts, starting from a single gene product

Appendix I

Our Swarm-Based AI/ML Approach

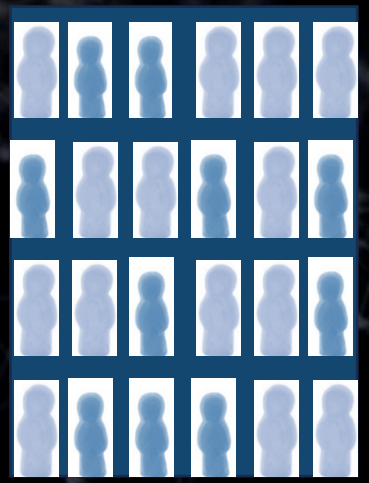
Our Algorithms

- Unique concordance-based approach deploys 5 layers of validation across multiple datasets.
- Unique Swarm ML-based approach increased explainability, reduced false discovery and increased time and energy efficiency
- Unique pathway miner approach fills gaps in pathway knowledge based on evidence from the whole transcriptome
- Unique network inference approach to understand the amount of influence of each molecule in a pathway
- Unique stability-based approach identifies the level of dysregulation of each molecule in the pathway
- Unique digital twin approach builds comparator pathway models for healthy states in tissues of interest and in off-target tissues.
- Unique Tox twin approach models toxicity and cellular stress response across multiple tissues – comparison with pathway models determines the nature of toxicity risk.

Intellomx Pilot – Druggability and Screening

- Incorporates results from I3 to select biological targets of highest relevance.
- Screens biological targets for Druggability based on molecular ontological data.
- Identifies a ranking of small molecules based on ligand-receptor binding; Based on combined ligand, target structural and energetic binding characteristics.
- Screens over 500 million targets.
- Further screening based on ADME characteristics.

Application in Personalized Medicine
I^3 = Profit



Challenge	Solution
My drug failed in clinical trials	I^3 analysis identifies the target patient group and the companion diagnostic delivers the stratification for trials
My drug is efficacious for a small patient population, making development un-economic	I^3 identifies the MAXIMUM stratified patient population and/or identifies additional targets and associated drug molecules to complement the existing drug
We need to maximise the patient population in our discovery process	I^3 calculates the stability of each target across the population, enabling selection of the maximum target group

Note: I^3 application has been proven in re-analysis of failed trials for major pharma, and in identification of maximum populations for diseases with material patient stratification

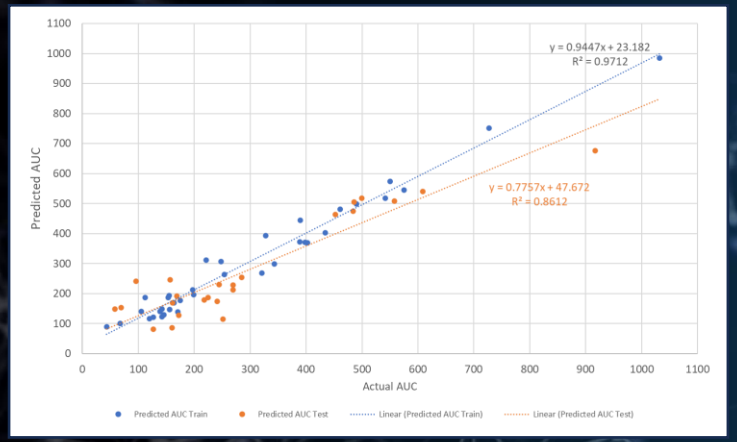
Application in Personalized Medicine:

Prediction of Drug Response from PDC to Patient

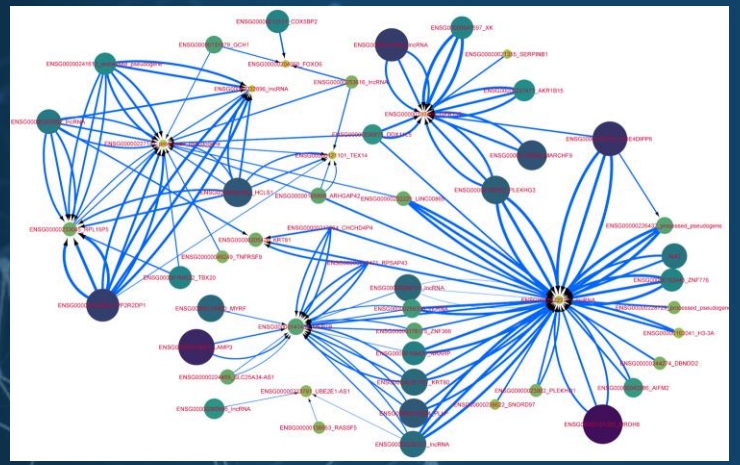
Model Development

Step	Gene	Average Train R
1	ENSG00000101XXX	0.860
2	ENSG00000228XXX	0.917
3	ENSG00000196XXX	0.907
4	ENSG00000266XXX	0.918
5	ENSG00000132XXX	0.922
6	ENSG00000257XXX	0.914
7	ENSG00000245XXX	0.923
8	ENSG00000120XXX	0.909
9	ENSG00000259XXX	0.902
10	ENSG00000254XXX	0.909
11	ENSG00000266XXX	0.905
12	ENSG00000183XXX	0.908

AUC response for Compound X in a PDC tissue model.



Drivers of response

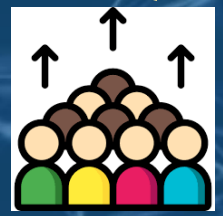


EXTRAPOLATION

In vitro efficacy

In vivo efficacy

Clinical Trial efficacy



Large Scale Population of disease cases

Data Types Utilised by Intellomx

- DNA Sequencing and Genomics
  - Point Mutations
  - Copy Number Variation
- Transcriptomic
  - RNASeq
  - scRNASeq
  - Expression array data (post-2012)
  - Nanostring – nCounter® and GeoMX® data
- Proteomic data
  - Mass spectrometry
  - Protein array
- Methylation
- Clinical, outcome, response and phenotypic data
- Integration of MultiOmics data

Case Study: Obesity

- Pathway: GLP1R molecular system In White adipose Tissue, Normal and Obese
- Data Sets: GSExxxxxx: 68 Obese Cases BMI >30; 142 Non-Obese Cases BMI <25

- Entire transcriptome analyzed for associations with GLP1R
- Separate analysis conducted to determine phenotypic drivers of Obesity
- Overlap explored. Key features available for consideration in ranking analysis:
  - Degree of driver influence of a given gene product in the disease network
  - Degree to which the disease network influences a gene product
  - Degree of pathway connectivity
  - Stability of gene product across the population

GLP1 comparison with phenotypic state:
- GLP1R showed low expression in white adipose tissue
- No overlap with the phenotypic state
- Putative obesity-related targets found in white adipose tissue, independent of GLP1R
- Future exploration of other tissues to identify where GLP1R plays a role and the molecular system surrounding it.

Rank	Gene Function
1	winged helix/forkhead transcription factor
2	synthase via transamidation and mitochondrial translation
3	involved in double-strand break repair
4	Enables estrogen receptor binding activity and histone kinase activity
5	ubiquitin-protein ligase
6	Protein Kinase
7	transferase
8	viral or transposable element protein
9	RNA binding
10	non-receptor serine/thr
11	hydrolase
12	non-motor actin bindin
13	SNARE protein
14	DNA topoisomerase
15	Has epimerase activity.
16	scaffold/adaptor protei
17	Pseudogene
18	RNA splicing factor
19	scaffold/adaptor protei
20	involved in positive reg
21	RNA Binding Protein
22	Pseudogene
23	Mitochondrial Binding F
24	phosphatase
25	transporter
26	RNA metabolism protei
27	RNA processing factor
28	non-receptor serine/thr
29	chromosomal structura
30	secondary carrier transp

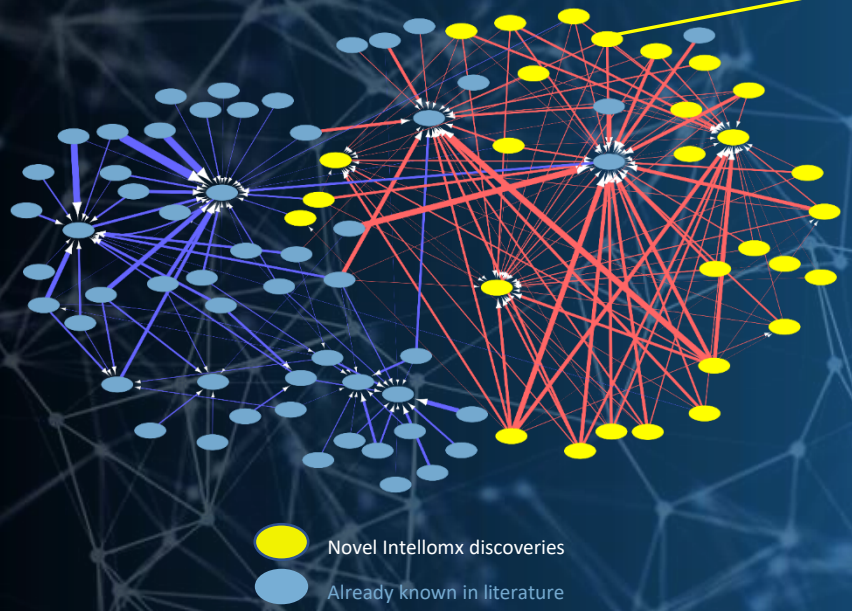
Rank	family
1	actin or actin-binding cytoskeletal protein
2	Zinc Finger protein
3	heterotrimeric G-protein
4	ATP synthase
5	serine protease
6	Pseudo Gene
7	Transmembrane Protein
8	Tumour supressor gene
9	Transmembrane Protein
10	glycosyltransferase
11	G-protein coupled receptor
12	extracellular matrix protein
13	glycosyltransferase
14	suppressor
15	transporter
16	ligase
17	dehydrogenase
18	Long Intergenic Non-Protein Coding RNA
19	scaffold/adaptor protein
20	non-receptor serine/threonine protein kinase
21	scaffold/adaptor protein
22	guanyl-nucleotide exchange factor
23	Protein Phosphotase
24	Vesicular Protein
25	dehydrogenase
26	Aldehyde Dehydrogenase
27	secondary carrier transporter
28	kinase activator
29	galactosidase
30	small GTPase

GLP1R interactors and phenotypic factors sorted by Influence, Connectivity and Stability

Case Study: Lung Cancer

Project led by Intellomx and supported by Innovate Grant. Subcontractors included: Medicines Discovery Catapult and cell-line robotics company Arctoris Ltd.

- Assessment of KRAS/MEKK inhibition in Lung Cancer
- Top 200 drivers evaluated via analysis of 9 lung cancer datasets, generating 30 novel targets in KRAS (22 in MEKK)



IO:03 KRAS inhibitor

IO:0301 Small molecule	wild type
IO:0302 Small molecule	wild type
IO:0303 Small molecule	wild type+G12C
IO:0304 Monoclonal	wild type+G12C

IO:04 KRAS/MEKK inhibitor

IO:0404 Small molecule	G12C
IO:0405 Small molecule	G12C

IO:02 MEKK inhibitor

IO:0202 Small molecule	wild type+G12C

- 3 biological targets and 7 molecules prioritized for development and partnering

Case Study: IPF

- Question: are we able to identify causal factors/drivers of Idiopathic Pulmonary Fibrosis

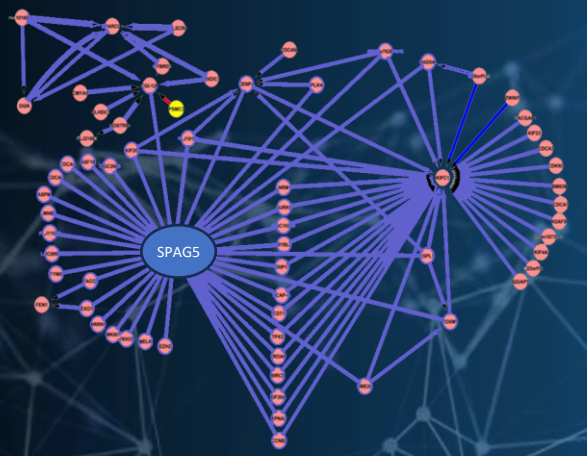
- Publicly available transcriptomic data set analyzed GSE150910 - 103 IPF cases, 104 Non-IPF case
- Key pathway used as interrogation framework Pathway: Cellular Senescence – 127 gene products
- Entire transcriptome analyzed for associations with selected pathway components

- Key features available for consideration in ranking:
  - Influence of a given gene product in the network
  - Influence of disease network on gene product
  - Degree of pathway connectivity
  - Stability of gene product across the population
  - Gene influence in healthy lung, liver and blood

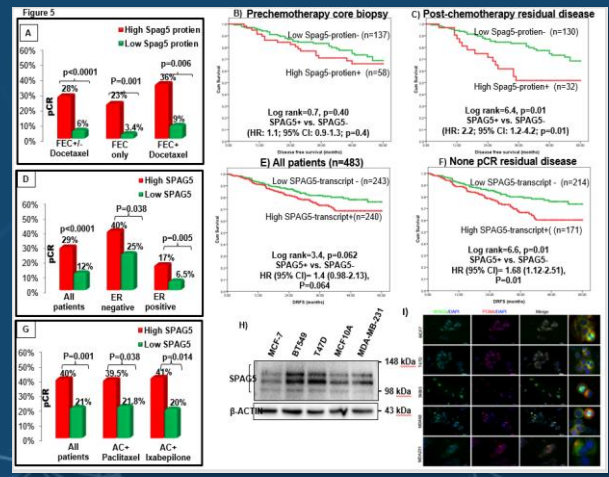
- Work-in-progress …

Gene Identifier	In Cellular Senescence list	Pathway Miner Connectivity	Connectivity Rank	Influence Rank IPF	Stability Score	OVERALL RANK	Protein Class
31	NO	20	114	49	44	1	apoptosis inhibitory protein
826	NO	18	190	32	81	2	metalloprotease
161	NO	21	76	158	85	3	oxidoreductase
139	NO	18	190	98	47	4	Golgi-localized complex
643	NO	21	76	177	99	5	Solute Carrier Protein
672	NO	17	228	116	12	6	C2H2 zinc finger transcription factor
666	NO	14	342	18	20	7	regulator of G protein signaling
376	NO	16	266	27	101	8	membrane traffic protein
293	NO	15	304	24	88	9	GTP-binding elongation factor
683	NO	18	190	131	102	10	RNA Binding Protein
279	NO	14	342	44	46	11	membrane traffic protein
601	NO	16	266	62	107	12	RING Finger Protein
599	NO	18	190	208	48	13	ubiquitin-protein ligase
470	NO	14	342	104	4	14	regulatory protein
201	NO	19	152	288	17	15	mannosyltransferase activator
4	NO	14	342	101	29	16	scaffold/adaptor protein
46	NO	20	114	341	23	17	transmembrane protein dislocase
412	NO	11	456	15	14	18	phosphatase
339	NO	11	456	26	5	19	scaffold/adaptor protein
734	NO	14	342	51	95	20	Kelch Like Family Member

Case Study: Breast Cancer



- Question: can we identify markers that predict proliferation in breast cancer?



- Datasets: Nottingham, Uppsala, Metabric and TCGA breast cancer tissue expression array data. (3554 cases). 34 genes found consistently in the top 100 PANN ranked genes out of 50,000 genes across 5 questions across 3 data sets

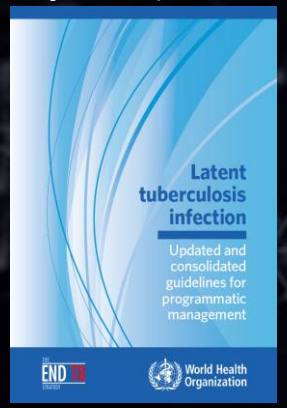
- SPAG5 (Hub) validated as new driver of breast cancer

Case Study: TB Diagnostic Discovery

"We believe this work will herald a new beginning for TB treatment and prevention."

Chairman Chen, Wuhan Pulmonary Hospital

"There is no gold standard test for LTBI (Latent TB Infection)."



WHO 2024

- **Question**: Can we create a diagnostic to differentiate between latent and active Tuberculosis?

Category	Test	Active TB	Latent TB[1]	BCG[2]
Host response	**TB-PRECISE**	✓	✓	✓
Host response	MTB-HR	✓	✗	✓
Skin test	TST	✓	✗	✗
IGRA	QFT-Plus	✓	✗	✗
Live bacteria	Actiphage	✓	✗	✓

1 test provides sensitivity and specificity >85%
2 test results unaffected by patient BCG status

Intellomx receives coveted approval in China

20 Dec 2022

The Ministry of Science & Technology (MOST) in Beijing announced this week that UK drug-discovery AI company Intelligent OMICS has been granted approval for its Tuberculosis study in Wuhan, China.

The study aims to validate both a panel of diagnostic biomarkers that predicts the presence of latent Tuberculosis and to validate potential biological drug targets that provide new treatment options.

Approval enables data to be shared for the first time between Wuhan Pulmonary Hospital and the company's research team. Transfer of genetic material and data is strictly controlled within China and has proved a significant challenge for western pharmaceutical and biotech companies. It has taken Intelligent OMICS two years to achieve this valuable milestone under China's Human Genetic Resources Administrative Licensing regulations.

Dr Simon Haworth, Director of Intellomx

"Our team in China, led by Ms Nicole Song, has worked tirelessly to address the complexities of Chinese regulation," comments the Intellomx Director Dr Simon Haworth. "Few international companies have achieved this Approval, making cross-border genetics-related research impossible for most. But TB is a critical global issue and our ability to diagnose TB in its latent, hidden state is going to make a very significant impact in disease prevention and in understanding of the underlying disease pathways. This is clearly valued in China - as well as in India and other geographies with a high TB burden. Ultimately, we expect to apply this research to identify new therapies for TB that take effect prior to the acquisition of drug resistance so that we can address the twin issues of **latent TB** and **multi-drug resistance infection**. But first, we are absolutely delighted to be able to progress this important study in China and look forward to reporting results in Q2 2023."

Nicole Song, team leader Intellomx, Wuhan PRC

- Note: Generalisation
  Markers refined in the Intellomx Han Chinese population trial were originally identified in Caucasian and South African datasets using alternative data collection methods. This provides a high degree of confidence in the applicability of TB-PRECISE in the wider global population.

Validation

Intellomx output has been validated in multiple disease areas and clinical contexts. Examples:

Lung cancer

Validation:

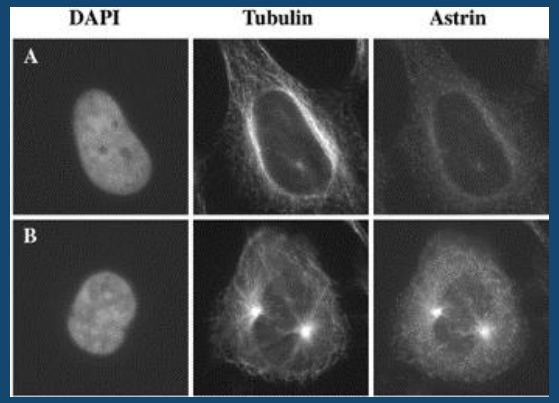
WP 1.1 siRNA Screen: phenotypic outcome 24, 48, 72 and 96h
WP 1.2 Pathway Analysis screen: siRNA transfection. Target depletion confirmed
WP 2 Compound Screen: siRNA transfection. Target depletion results validated in Wild Type and Mutated cell lines

"Our system validated the targets and then tested drugs against those targets. Results were clear – the targets identified by Intelligent OMICS are indeed important, previously unknown targets in lung cancer and the novel drugs identified by the team modulate those targets, all as predicted by the AI."

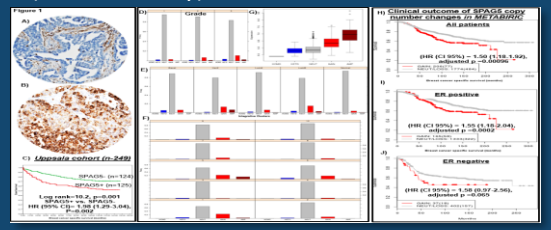
Martin Bittner
CEO

ARCTORIS

Breast cancer



SPAG5 (Hub) validated in >15000 cases – Chemotherapy response.
Cell line studies show functionality.
P(false discovery) $<1x10^{-78}$



SPAG5: new driver of proliferation validated in over 15,000 cases. Patent Ref: US10775381B2

Tuberculosis

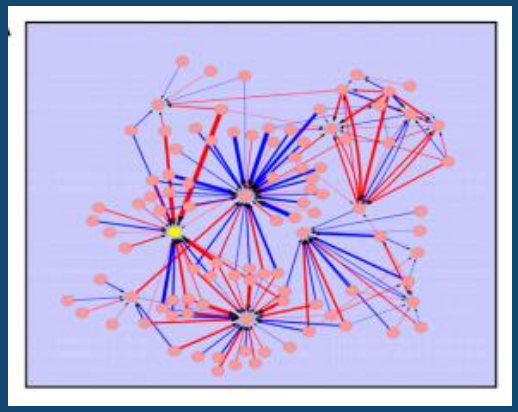
TB diagnostic tested in the Han population, showing high sensitivity and specificity. Work ongoing for a multi-site clinical trial in China.

Trial results	Sensitivity	Specificity	AUC	Markers
Latent v Control	100%	87.9%	0.82	4
Active v Control	100%	100%	1.00	4
Active v Latent	100%	93.0%	0.91	5

Celebrating successful validation of our TB Diagnostic with the UK Dep Consul General in Wuhan, the the hospital Chairman and team

Plant biology

Two transcription factors were discovered using data mining and Network Inference. Development of transgenic fruit demonstrated on/off switching of ripening.



syngenta

Intellomx I^3 recap

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I^3-Miner	***Defining the disease pathway***
I^3-Digital Twin	***Anticipating tox liabilities***
I^3-Pilot	***Identification of novel Small Molecules and Biologics***
I^3-Precise	***Panel optimization for diagnostics***

The Intellomx I^3 technology platform delivers validated targets, linked to *in silico* drug candidates.

Our algorithms deploy 5 layers of validation across multiple datasets, addressing data issues and dramatically reducing the probability of false discovery whilst our digital twins build comparator pathway models for healthy state in tissue of interest and in off-target tissues.

Results fill knowledge gaps based on evidence (whole transcriptome), quantifying the influence of each molecule in a pathway, identifying levels of dysregulation of each molecule and linking drug candidates with targets, ranked on multiple criteria.

The Intellomx I^3 technology swarm-based approach is not constrained by the availability of compute resource. Our swarms undertake multiple analyses, ranking results by concordance, with the option to drill into any single result or group of analyses to facilitate understanding and derive optimal drug targets.

Intellomx I^3 : Intuitive, Informed, Intelligence

Our Clients

Intelligent OMICS

Johnson&Johnson

UNIVERSITY OF OXFORD

SERVIER

Examples of corporate contracts:

Public Health England
LGC
AstraZeneca
RANDOX
Nxera
MOLOGIC
Oxford Biomedica
Takeda
InFocus Therapeutics
onyvax vaccine therapies
syngenta
Exonate
biose
apitope
PharmaEngine 智 擎 生 技 製 藥
武汉市肺科医院/武汉市结核病防治所 Wuhan Pulmonary Hospital/Wuhan Institute for Tuberculosis Control
ALMAC
[dstl]

Examples of Academic collaborations:

The Open University
UNIVERSITY OF LEICESTER
NOTTINGHAM TRENT UNIVERSITY
LONDON SCHOOL of HYGIENE &TROPICAL MEDICINE
CARDIFF UNIVERSITY
PRIFYSGOL CAERDYDD
The University of Nottingham
UNIVERSITY OF Southampton
UCL
UNIVERSITY OF LEEDS
University of Dundee

Key papers + illustrations:

Articles

Lancet oncology

Supplementary data available on request

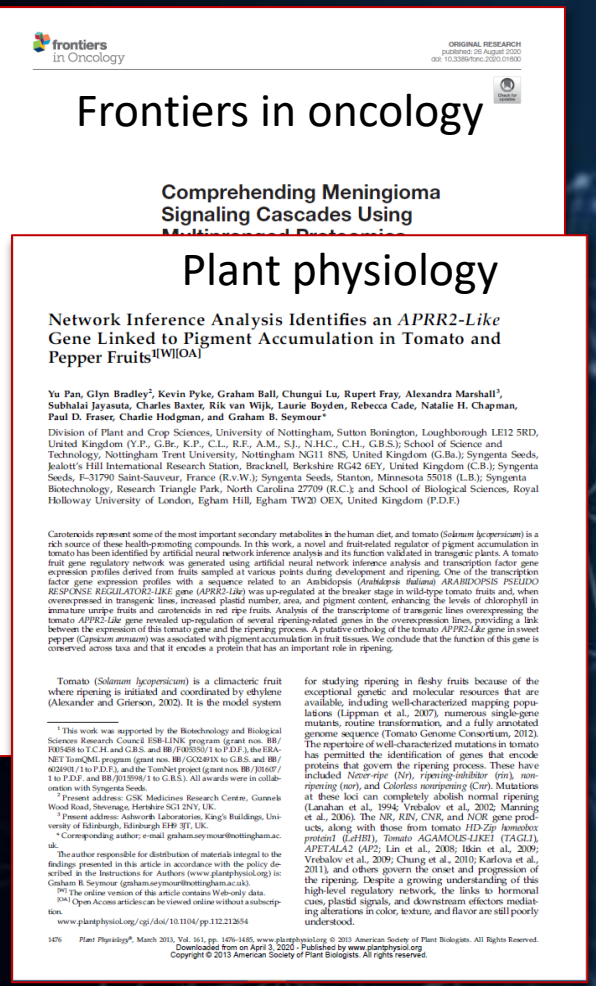
SPAG5 as a prognostic biomarker and chemotherapy sensitivity predictor in breast cancer: a retrospective, integrated genomic, transcriptomic, and protein analysis

REGULAR ARTICLE

blood advances

Blood advances

A parsimonious 3-gene signature predicts clinical outcomes in an acute myeloid leukemia multicohort study



frontiers in Oncology

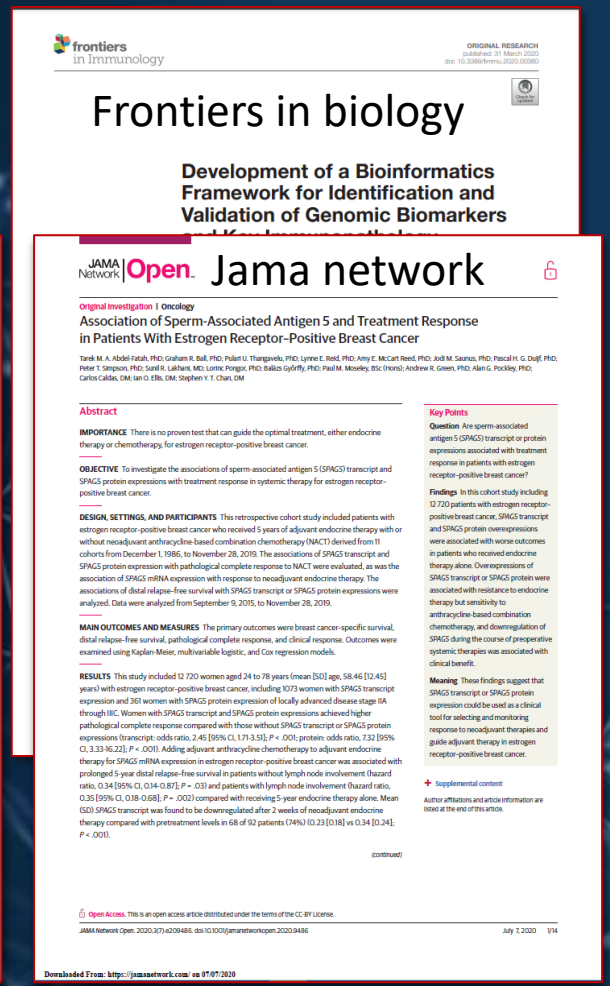
ORIGINAL RESEARCH

Frontiers in oncology

Comprehending Meningioma Signaling Cascades Using

Plant physiology

Network Inference Analysis Identifies an *APRR2-Like* Gene Linked to Pigment Accumulation in Tomato and Pepper Fruits[1][W][OA]



frontiers in Immunology

ORIGINAL RESEARCH

Frontiers in biology

Development of a Bioinformatics Framework for Identification and Validation of Genomic Biomarkers

JAMA Network Open

Jama network

Original Investigation | Oncology

Association of Sperm-Associated Antigen 5 and Treatment Response in Patients With Estrogen Receptor–Positive Breast Cancer

obn Issue 5 Autumn 2021

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MEMBERSHIP DIRECTORY

OBN supporting and bringing together the UK's life sciences companies, corporate partners and investors

CONNECT

DDI & drug

Intelligent OMICS

Innovate UK

CATAPULT Medicines Discovery

ARCTORIS

Conquering KRAS!

The AI drug discovery revolution that is here to stay

Intelligent OMICS is delighted to announce successful completion of its recent Innovate UK grant program, in collaboration with the Medicines Discovery Catapult (MDC) and Arctoris Limited.

5 key conclusions:

- Application in oncology identifies novel KRAS-inhibiting drugs for lung cancer, one of which is even effective regardless of KRAS mutation;
- AI-driven drug discovery is at last proven, and ready for application across multiple diseases;
- The AI approach discovers new drugs because it focusses on the drivers or causes of the disease state, rather than focussing on the symptoms or effects of a disease state;
- The evidence-based analysis produces original results, without reliance on prior hypotheses or literature, allowing creation and control of new Intellectual Property.
- AI discovery methods can achieve greater than 90% reduction in carbon footprint compared to traditional high-throughput screening

The project, led by Intelligent OMICS and funded by Innovate UK, sought to demonstrate the carbon efficiency of an AI-based drug discovery program compared to traditional pharma methods. The case study used in the project was assessment of Non-Small Cell Lung Cancer – thought to account for over 80% of all lung cancer cases.

Method

The team analysed nine lung cancer datasets from the Intellomx Curated Data Library, using the Intelligent OMICS I³ platform. The datasets include human transcriptomic data plus confirmation of a disease v healthy diagnosis for lung cancer for approximately 2,000 patients. Proprietary AI was used to model the underlying systems biology - first creating a list of the most important genes defining the disease v healthy diagnosis, then modelling the interaction of those genes in a disease pathway map based on the evidence in the data.

"The real benefit of our technology is evident when we compare our results with what is known in the literature," says Intellomx CEO Dr Simon Haworth. **"We can immediately spot errors and omissions in pathway maps documented in KEGG, for example, and because our analysis only focusses on the most influential drivers in each pathway we know that any such differences are genuinely important. For our lung cancer work, focussing on EGFR and KRAS, the comparison led us to 8 really exciting new lung cancer targets."**

The next step of the process was to validate *in silico* targets in the wet lab, to link validated targets to possible drugs and then to test the impact of those novel drugs on cancer cells.

Subcontractor Arctoris, with its world leading fully automated drug discovery platform and robotic cell line system, provided rapid validation of the targets using knock down analysis on KRAS G12C mutant and KRAS wild type cell lines. Data from Arctoris proved the validity of the targets by

Press service

Differentiation vs Large Language Models and other AI approaches

Traditional Pharma Model	AstraZeneca, gsk, NOVARTIS	Slow and expensive Lab-based Constrained by hypotheses
1st Generation AI	Benevolent AI, Insilico Medicine, RECURSION pharmaceuticals, Exscientia, Atomwise	Based on LLMs, Deep Learning or Binary Classifiers High computational requirement - inefficient Prone to false discovery and interpretation. Difficult to explain Over-reliant on known biology
2nd Generation AI	Intelligent OMICS	Swarm-Based Neural Networks – Optimised parallel computing Extensive cross-validation through concordance Explainable – Knowledge Graph easily interpretable Evidence-based on mathematics, not language Reveals the hidden biology of disease Multi-parameter probability ranking – optimised drug targets

Differentiation vs Large Language Models and other AI approaches

	Benefit	Intellomx	InSilico	Exscientia	Owkin	In Sitro	Precision Life
Evidence based, data driven approach to biomarker discovery	• Avoids bias of LLMs • Reveals novel biology • Eliminates false discovery	✓	✗	✗	✓	✓	✓
Network Inference modelling determines molecular causality	• Quantifies pathway • Reveals drivers • Determines dysregulation • Facilitates digital twin	✓	✗	✗	✗	✗	✗
Reliant on human disease tissue	• Clinically relevant • Eliminates bias/downstream failure of cell/animal models	✓	✗	✗	✓	✗	✓
Target biomarker discovery matrix	• Systematically evaluates whole transcriptome • Rapidly determines actionable targets (10 parameters)	✓	✗	✗	✗	✗	✗

Differentiation vs Large Language Models and other AI approaches

Discovered and in the literature

Discoverable by LLMs from the literature

de novo discoveries from Molecular data

We DON'T rely on flawed reductionist knowledge graphs or literature mining to identify the key drivers of each disease.

Instead, we use de novo, evidence-based modelling that discovers the underlying systems biology of each disease by direct analysis and then exploits that knowledge to create a stream of new drugs.

What happens next?

From first contact to project initiation typically takes 6 weeks. At first meeting the Intellomx team explains the utility and validation of the I^3 tool box, reveals prior work in the disease area of interest and reviews what progress has already been made by the partner company. The team then helps clarify the clinical questions that need to be answered (see common queries at each research stage below).

Following the meeting, the Intellomx team reviews possible data sources and provides a formal proposal for review.

Disease
Pathway
Target
Drug
Trials

At the disease level, can we develop a new Diagnostic?
Discern disease progression – systems biology v clinical standard?
Factors controlling exacerbation?

Which are the most important targets, ranked?
Can we identify the underlying disease pathway from scratch?
Do the known pathways omit critical biology?
What are the causal factors driving the pathway?
Personalised meds: is the pathway consistent for all patients?

Have we selected the right target?
Rank targets according to 7 criteria (eg tox, druggability, stability)
How does target A compare to target B in terms of tox elsewhere?
Is there a better target than the one held by our competitor?

Companion diagnostic? Complementary target/drug?
For investors: does the asset holder understand the underlying systems biology?

Data check → Proposal

Contact

"To complete a long journey, it really helps if one sets off in the right direction. In our sector that basically means **selecting the right target**.

Our AI reveals the underlying biology of disease in order to identify optimum drug targets. *In silico* docking identifies drug candidates, and engagement with the full power of downstream AI enables us to de-risk drug development.

This is the decade in which the IP for a stream of new drugs will be secured, reversing the troubling trend in drug discovery globally. **Our technologies write the papers that LLMs will eventually read**."

Professor Graham Ball, Founder, Intellomx

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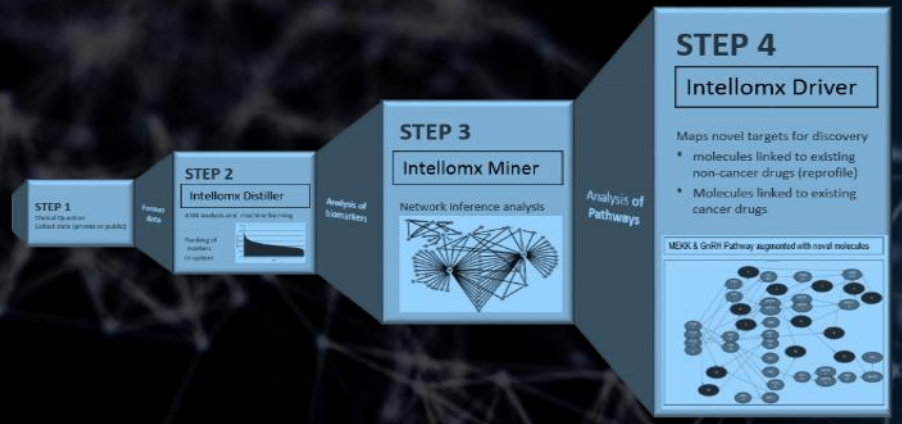
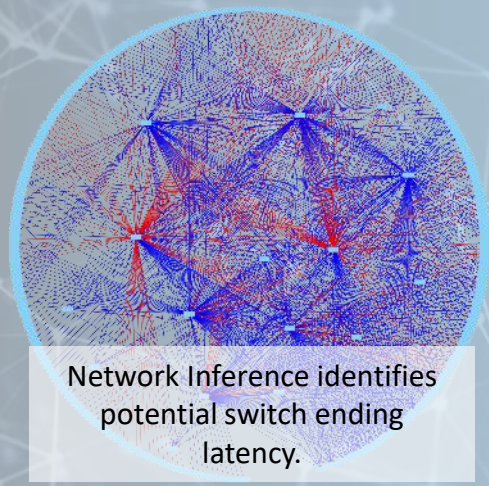
drug discovery AI

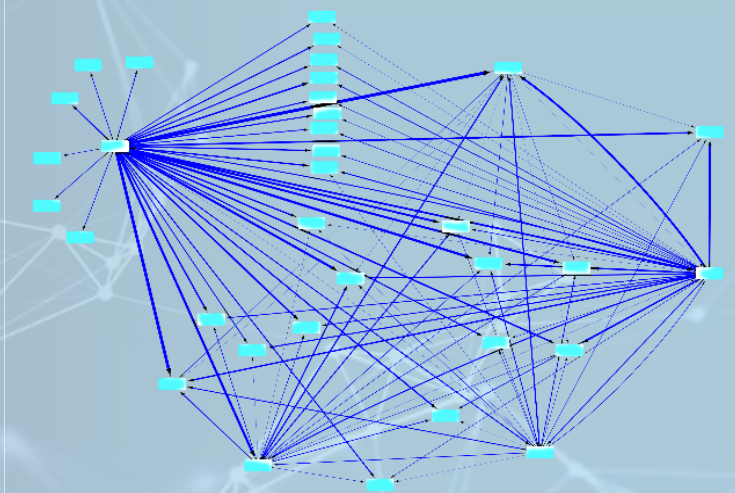
Case study: Schizophrenia



- Question: can we identify novel, key markers for schizophrenia and link these to potential drug compounds?



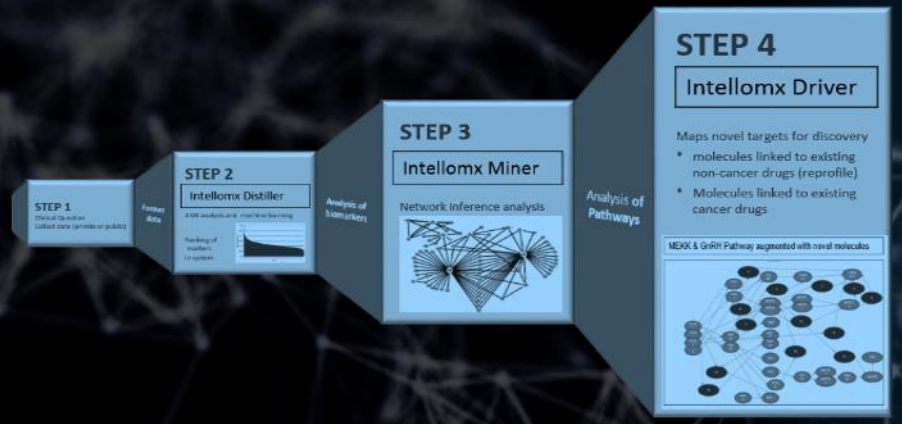
Network Inference identifies potential switch ending latency.



Primary analysis identified a small number of critical hubs that drive disease state, representing drug targets. NCEs and drugs for reprofiling have been identified that are linked to these targets.

Appendix II

Case study: COPD



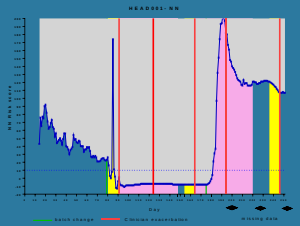
Question: can we improve the Mologic COPD panel for application on hand-held device in a clinical trial?

Intellomx POSitive service:

Mologic's COPD panel was highly effective but impractical to use due to high numbers of biomarkers. The Intellomx POSitive service enabled the panel to be reduced to 12 biomarkers.

Intellomx built a decision support model and code enabling the customer to deploy the companion diagnostic on mobile phone apps.

Original panel: 500 biomarkers



Refined panel:

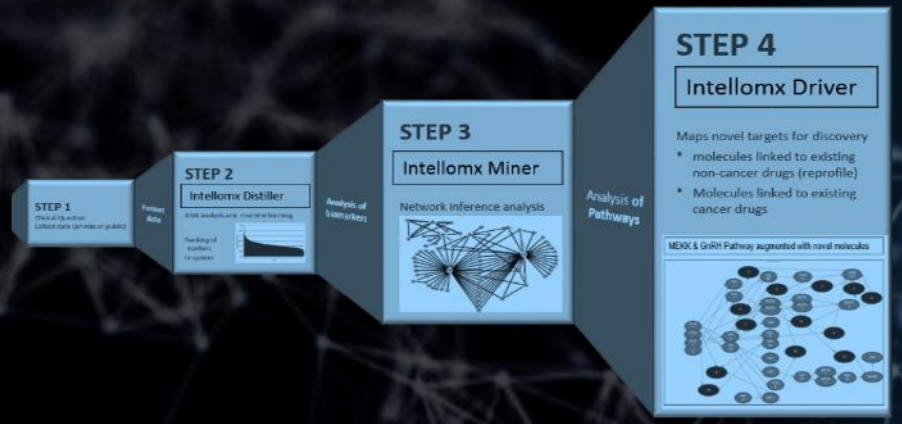
12

12 features of 5 biomarkers

Conclusion: Existing panel optimised and software provided for application on hand-held devices/mobile phone application

Appendix II

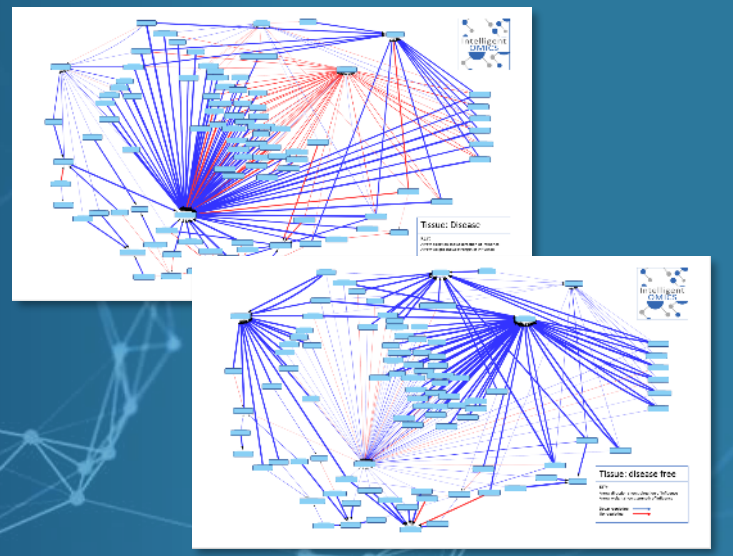
Case study: Auto-immune Disease



Question: Can we develop new drugs for autoimmune disease?

Intellomx completed Primary Analysis for Autoimmune disease based on both client data and publicly available data, identifying 156 key genes mapped in the disease pathway.

The pharma co provided details of two targets:
Target 1 was validated and linked to the disease pathway
Target 2 was shown to be of negligible relevance in the disease



Analysis of a complex system to explain phenotype and stratification

Appendix II