

# **Computing the Future of Medicine**

Is Drug Discovery a Data Science Problem?

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#### **Forward looking statement**

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## GalOmic – ETX RNA Drug Platform



Computational Biology Platform Target nomination



· Gene silencing · Hepatocyte targeting · Proprietary chemistry · GalNAc-siRNA candidate generation Therapeutic pipeline

### **ETX RNA Drug Platform: Information Molecules**

RNA drugs are a form of computation



![](_page_3_Figure_3.jpeg)

![](_page_3_Picture_4.jpeg)

We know the DNA sequence of hepatocytes, and the corresponding **mRNA code** for all genes

![](_page_3_Picture_6.jpeg)

Design complementary **'anti-code' siRNA sequences**, opposite to a region of the mRNA code

![](_page_3_Picture_8.jpeg)

We **deliver** siRNAs to **hepatocytes** using **GalNAc** to trigger the natural intracellular interference process

![](_page_3_Picture_10.jpeg)

The cell **silences the expression** of the target disease-associated gene (no protein made)

### **GalOmic: ETX RNAi Platform**

Novel target prosecution at pace and with a patient-friendly profile

Management team has >10-year track record and scientific experience in RNAi therapeutics

- We can inhibit any gene in hepatocytes
- Commercial stage modality, with 5 approved drugs
- **Powerful, validated technology:** highly specific, well tolerated, long duration of action, subcutaneous administration
- Generated data demonstrating at least equivalent
   performance to market lead across multiple genes
- 17 patent applications filed to protect novel GalOmic platform and target inventions

#### Typical performance profile of our RNA platform

![](_page_4_Figure_9.jpeg)

## We go from gene target selection to *in vivo* dose response experiments in 6 months, costing only ~£500,000

### mAbs History as Precedent of new Therapeutic Modality

Monoclonal antibodies are now established as a drug class

H

**100<sup>th</sup> mAb** product approved by the FDA in May 2021

mAb market estimated to reach **\$300B** in 2025

**Limitations:** extracellular targets only, duration of action

![](_page_5_Figure_6.jpeg)

Development of therapeutic antibodies for the treatment of diseases. J Biomed Sci Jan 2020

## HepNet: Our Computational Biology Platform

Which gene, in which disease?

![](_page_6_Picture_2.jpeg)

Gal**Omic** 

Target

nomination

RNAi platform

Therapeutic pipeline

### Hepatocyte Biology – A Central Trafficking System

![](_page_7_Figure_1.jpeg)

Please note numbers are derived from ETX proprietary curation and analysis of public 'omics data, proprietary data derived from NLP processing of literature and network-aware ML-driven analysis of curated pathway data

### High Degree of Overlap in Competitive Landscape

Multiple players are targeting obvious liver-expressed genes

Hepatocyte Genes	HBV	LP(a)	AAT	PCSK9	TTR	HSD	XDH	C3
	×		×	×	×	×	×	
on arrowhead	X	×	X			×	×	×
Dicema pharmaceuticals (acquired by Novo Nordisk for \$3.3bn)	X	×	X					×
<b>SILENCE</b> THERAPEUTICS		×						×
IONIS*	×	×		×	×			

\*antisense oligonucleotides

### Modelling Biology In A Computer: Clotting Cascade

![](_page_9_Figure_1.jpeg)

#### Directed biological process network model

Directed network containing 100 nodes constructed using ETX proprietary interactome which includes directed interactions from NLP and curated pathway data.

Target identification using KPA on the network model

Top ranked proteins using the KPA approach. Triage of the top decile led to the identification of two RNAi targets and selection for evaluation (magenta arrows)

### HepNet: a Centralised 'Google for Hepatocytes'

A discovery resource and engine for target ID, under a user-friendly GUI (in progress)

![](_page_10_Figure_2.jpeg)

### **A Highly Differentiated Pipeline of RNAi Candidates**

We are prosecuting several preclinical candidates drugging our novel targets

![](_page_11_Figure_2.jpeg)

### ETX Powered by Generative Al

![](_page_12_Picture_1.jpeg)

### How do Generative AI Models work?

## In simple terms, they predict the next word...

![](_page_13_Figure_2.jpeg)

#### How do emergent properties arise?

"Emergent properties are a necessary result of the task of <u>predicting</u> the next word as in order to perform that prediction task more perfectly, a machine must derive an <u>understanding</u> of the reality described in the various materials used in training."

lya Sutskever, Chief Scientist at OpenAl

### **Integration of Generative AI**

Further evolving HepNet with creation of ETX specialist agents

![](_page_14_Figure_2.jpeg)

### Adding AI Language Capability Not a ChatBot

![](_page_15_Picture_1.jpeg)

Impact of LLM addition Allows ETX Al Agents To:

"Understand" "Reason" "Infer" Code/Self Code Access the Internet

Computing the Future of Medicine<sup>™</sup>

### **ETX Specialist 'Al Agents'**

![](_page_15_Picture_6.jpeg)

Fine-tuned to our business, projects and processes

![](_page_15_Picture_8.jpeg)

Trained with hepatocyte-specific data

![](_page_15_Picture_10.jpeg)

Trained with siRNA sequences/constructs

![](_page_15_Picture_12.jpeg)

Trained on all relevant scientific papers

### **ETX Powered by Generative AI – Use Cases**

![](_page_16_Picture_1.jpeg)

### **Use Case: HepNet Powered by Generative Al**

An 'intelligent' System

![](_page_17_Figure_2.jpeg)

#### Inputs:

#### Limitations:

- Data
- Network • analytics
- Search heavy ٠ Limited NLP •

![](_page_17_Picture_8.jpeg)

**Expert review and Competitive Intelligence** 

![](_page_17_Picture_10.jpeg)

![](_page_17_Picture_11.jpeg)

#### Inputs:

## **Generative Al**

- Any data ٠
- Any format •
- **Added Generative Al** capability:
- Understanding •
- Reasoning •
- Inference ٠
- Ability to invent
- Automation .

![](_page_17_Picture_23.jpeg)

![](_page_17_Picture_24.jpeg)

![](_page_17_Picture_25.jpeg)

### **Use Case: Unstructured Data Patent Mining**

To extract, analyse and formulate a patent strategy that accounts for all 400,000 RNAi-related patents from 2001

(13) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT) (19) World Intellectual Property Organization International Publication Date 26 MN 2016 (20.65.2016) WIPO PCT WO 2016/081444 A1		Old Approach	ETX AI Patent Agent
Bit Interventional Peters Casadification: (201)     Bit Interventional Peters Casadification: (201)     Bit Interventional Application Number:     Casadification Number:     Casa	Extract and store all relevant patents	+++	$\checkmark$
<ul> <li>Las Pontentinue</li> <li>Thi, TT, TZ, UK, OO, UK, UZ, VC, YV, ZK, ZM, ZM, ZW, WY, WY, SK, SK, SK, SK, WY, WY, SK, SK, SK, SK, WY, WY, SK, SK, SK, SK, SK, SK, SK, SK, SK, SK</li></ul>	Summarise and categorise patents	+	$\checkmark$
<ul> <li>Mor That Streek, July How, Cambridge, MA (2124) (2015).</li> <li>Mor That Streek, July That Streek, July How, Cambridge, MA (2124) (2015).</li> <li>Mor That Streek, July T</li></ul>	Extract all sequences, constructs and performance	++	✓
Agents Astronomics, Standard Lettering et al., No. — with sequence finding part of description (Back 3.2(n))     Option (Ds.)	Cross-talk with HepNet	+	$\checkmark$
	Understand the syntax of patent documents	Manual	$\checkmark$
CAPCD give, and methods of using such thXA spaces is tability expression of APCD and methods of reading subjects having an APCD anschild durinker, e.g. hyperhyphycelosia.	Find gaps for FTO and new IP	Manual	$\checkmark$
AD, or The double stranded RNAI agent of chaim 1 or 12, wherein the ligand is	Find new learnings to infer new information	Manual	$\checkmark$
<ul> <li>31. The double strandsci RNA i agent of claim 1 or 12, wherein the ligand is attached to the 3' end of the same strand.</li> <li>32. The double strandsci RNA i agent of claim 31, wherein the RNA i agent is conjugated to the ligand as shown in the following schematic</li> </ul>	Find patents in other drug modalities relevant to our targets	Manual	$\checkmark$
<ul> <li>"Same Sum of the organization of claim 1 or 12, wherein said RNAI agent further compress at least one phosphorothioate or methylphosphonate internucleotide linkage.</li> <li>34. The double stranded RNAI agent of claim 33, wherein the phosphorothioate or</li> </ul>	Write new patent applications	Manual	$\checkmark$

![](_page_18_Picture_5.jpeg)

### **Use Case: Is There A Secret Language in Genetic Sequences?**

CCCCGCAGCGCCGGAGTCAAAGCCGGTTCCCGGCCCAGTCCCGTCCTGCAGCAGTCTGCCTCCTCTTTCAACATGACAGA TGCCGCTGTGTCCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCCGCAGCCATCTCCAAGACGGCGGTAGCGCCCATCG TGCGTGGTCCGTATTCCCAAGGAGCAGGGAGTTCTGTCCTTCTGGCGCGGTAACCTGGCCAATGTCATCAGATACTTCCC CACCCAGGCTCTTAACTTCGCCTTCAAAGATAAATACAAGCAGATCTTCCTGGGTGGTGGGACAAGAGAACCCAGTTTT GGCTCTACTTTGCAGGGAATCTGGCATCGGGTGGTGCCGCAGGGGCCACATCCCTGTGTTTTGTGTACCCTCTTGATTTT GCCCGTACCCGTCTAGCAGCTGATGTGGGTAAAGCTGGAGCTGAAAGGGAATTCCGAGGCCTCGGTGACTGCCTGGTTAA GATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCTGTGCAGGGTATTATCATCTACCGAGCCG CCTACTTCGGTATCTATGACACTGCAAAGGGAATGCTTCCGGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATC GCACAGACTGTCACTGCTGTTGCCGGGTTGACTTCCTATCCATTTGACACTGTTCGCCGCCGCATGATGATGCAGTCAGG GCGCAAAGGAACTGACATCATGTACACAGGCACGCTTGACTGCTGGCGGAAGATTGCTCGTGATGAAGGAGGCAAAGCTT TTTTCAAGGGTGCATGGTCCAATGTTCTCAGAGGCATGGGTGGTGCTTTTGTGCTTGTCTTGTATGATGAAATCAAGAAG TACA CATAAGTTATTTCCTAGGATTTTTCCCCCCTGTGAACAGGCATGTTGTATTATATAACATATCTTGAGCATTCTTGA CAGACTCCTGGCTGTCAGTTTCTCAGTGGCAACTATTTACTGGTTGAAAATGGGAAGCAATAATATTCATCTGACCAGTT ATTTGGAGAAATAAAAATATCTAAAATAAATTTTGTCTGCAGTATATTTTCATATAAAAATGCATATTTGAGTGCTACAT TCGAATAAATACTACCTTTTTAGTGAA

Gene 'string'

![](_page_19_Figure_3.jpeg)

3D view of gene

### Can we design & predict the activity of our drug computationally?

### **Use Case: ETX RNA AI Agent**

Is there a secret language in genetic sequences?

Aim: To treat mRNA sequences as a language and predict siRNA efficacy in downstream tasks

![](_page_20_Picture_3.jpeg)

Pre-Training Model to understand mRNA structure

#### AGGCUAGUC<MASK>UCAG<MASK>UCCA

![](_page_20_Picture_6.jpeg)

![](_page_20_Picture_7.jpeg)

Downstream task to make siRNA efficacy predictions using mRNA structure knowledge

#### mRNA: AGGCUAGUCUUCAGCUCCA siRNA: UCCGAUCAGA

![](_page_20_Picture_10.jpeg)

### **Fully Computational siRNA Drug Design**

#### ETX siRNA designR

- Proprietary deep learning algorithm for predicting siRNA efficacy
- Ranks siRNAs to minimise, and potentially eliminate, *in vitro* screening
- Can currently accurately <u>predict</u>
   <u>6 of the top 10 siRNAs per gene</u> (ranked by knockdown efficacy)
- Working on enhancing predictive performance using large language (transformer) models to represent information of RNA sequences

#### Validated using ETX designs

![](_page_21_Figure_7.jpeg)

#### **Classification Performance Metrics**

Strong performance classifying siRNAs as active vs inactive (AUC : 0.952)

	Current Approach	ETX RNAi Agent
Number of siRNA screened	Up to 400	<10
Time to lead identification (potential clinical candidate)	6 months	1 month
Cost of screening	£500,000	£50,000

### A Unique Generalisable Model for Drug Discovery

Significant reduction in wet lab work & even clinical trials

![](_page_22_Picture_2.jpeg)

![](_page_22_Picture_3.jpeg)

Unparalleled ability to **model complex** human biology

![](_page_22_Picture_5.jpeg)

Identification of **novel gene targets** 

![](_page_22_Picture_7.jpeg)

Rapid design of safe and potent RNAi medicines that silence those genes

Computing the Future of Medicine<sup>™</sup>

**Drug Discovery Is A Data Science Problem** 

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Accelerated progress of in-house pipeline across multiple diseases

### e therapeutics

www.etherapeutics.co.uk