AI a személyre szabott gyógyításért

XXXIII. NEMZETI MINŐSÉGÜGYI KONFERENCIA 2026

Dr. Peták István

Founder & Chairman

Genomate Health and Oncompass Medicine, Budapest - Boston

Institute of Advanced Studies (iASK), Semmelweis University,

University of Illinois at Chicago (UIC), Széchenyi Istvan University

“Egyszer a rákot is a matematika segítségével fogjuk legyőzni.”

Neumann János (1903 – 1957)



Building the computational precision therapy machine

INPUT

- 200+ cancer types
- 750+ cancer genes
- 29+ million somatic mutations
- 6+ million coding mutations
- 2-12 driver mutations per tumor
- Unknown number of combinations
- + multi-omic variables, epigenomics, proteomics, intratumor heterogeneity



Genomate®

bsi ISO 13485 Quality Management for Medical Devices CERTIFIED

bsi ISO/IEC 27001 Information Security Management CERTIFIED

OUTPUT

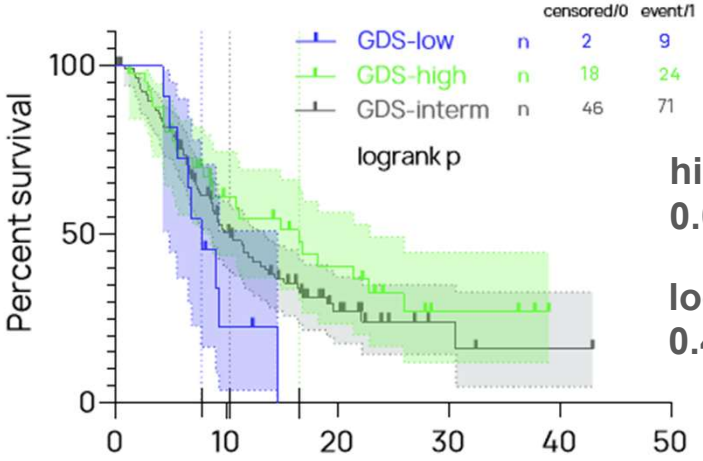
- N-of-1 out of:
- 200+ targeted therapies in clinical use
- 2000+ compounds in clinical development

Clinical efficacy of computational reasoning for personalized treatment planning in a pan-cancer cohort discussed by a French multidisciplinary tumor board: A real-world experience-based analysis. (N=394)

AACR Annual Meeting (Late-Breaking Abstract); Apr 17-22, 2026, San Diego, CA

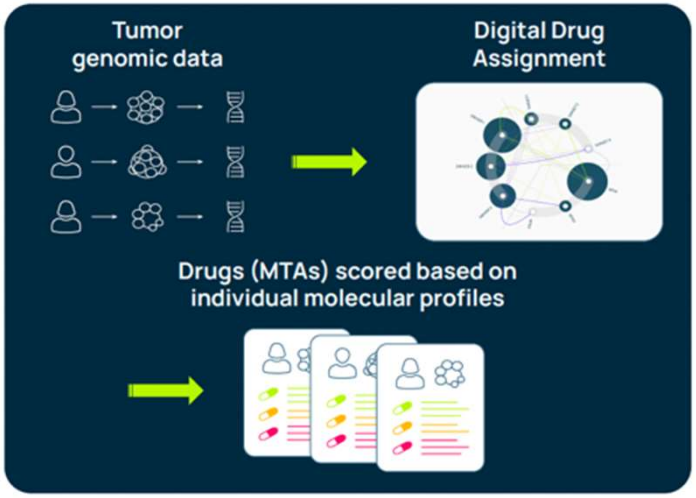
Davos C3 Silicon Valley Healthtech Conference, April 27, 2026, Sunnyvale, CA

AI in Oncology (proffered poster and oral presentation); Jun 22-23, 2026, Paris, France



high vs low: 0.0448

logrank HR: 0.48



OS (months)

+6,7 months, +40%

"AI" low	"AI" IM	"AI" high	chemo
7.8	10.3	16.6	9.9

-2,1months, -20%

58% of patients had G-high therapy options, but only 32% received G-high treatment. Better option in 26%. 45% of those who received ChTX had a G-high option.

+17%, ~ 2X

	Low	IM	High	Sum^{MTA}	Chemo	χ^2 for trend, low-IM-high
ORR	8%	19%	33%	23%	16%	p = 0.0283
DCR	31%	45%	64%	50%	41%	p = 0.0148

-50%

Dawn of the computational age in precision oncology



PRINCIPAL INVESTIGATOR, ONCOLOGIST

”We can only match genes to drugs one by one. We need computers to overcome genomic complexity to warn us about risks and opportunities in precision oncology.”

Prof. Dr. Christophe Le Tourneau

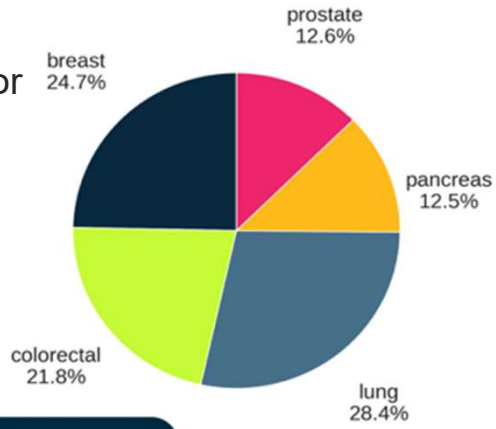
Head of Phase I Unit. Institut Curie, Paris

Clinical utility analysis of a computational reasoning system on large-scale tumor genomic data. *MSK-CHORD real-world clinicogenomic dataset;* **n$^{(all)}$ = 20,923**

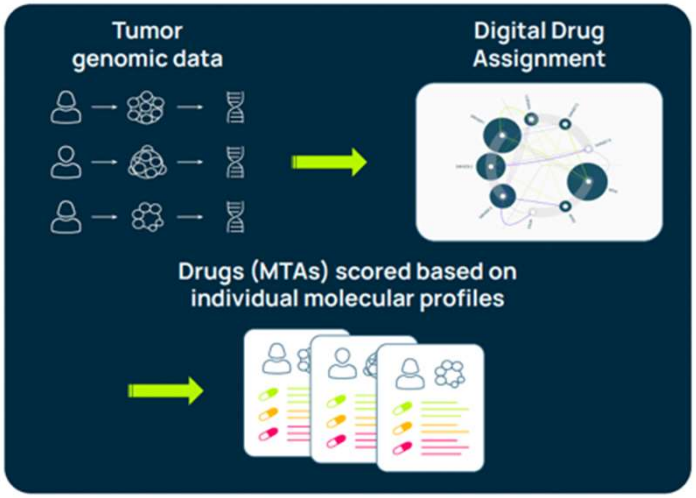
ASCO Annual Meeting, May 29 to June 2, 2026, Chicago, IL

Dora Lakatos, Robert Doczi, Maria Kocsis-Steinbach, Gabor Gyorgy Kalmar, Anna Dirner, Eniko Kispeter, Dóra Görög-Tihanyi, Barbara Vodicska, William Beck, and Istvan Petak

J Clin Oncol 44, 1625(2026)



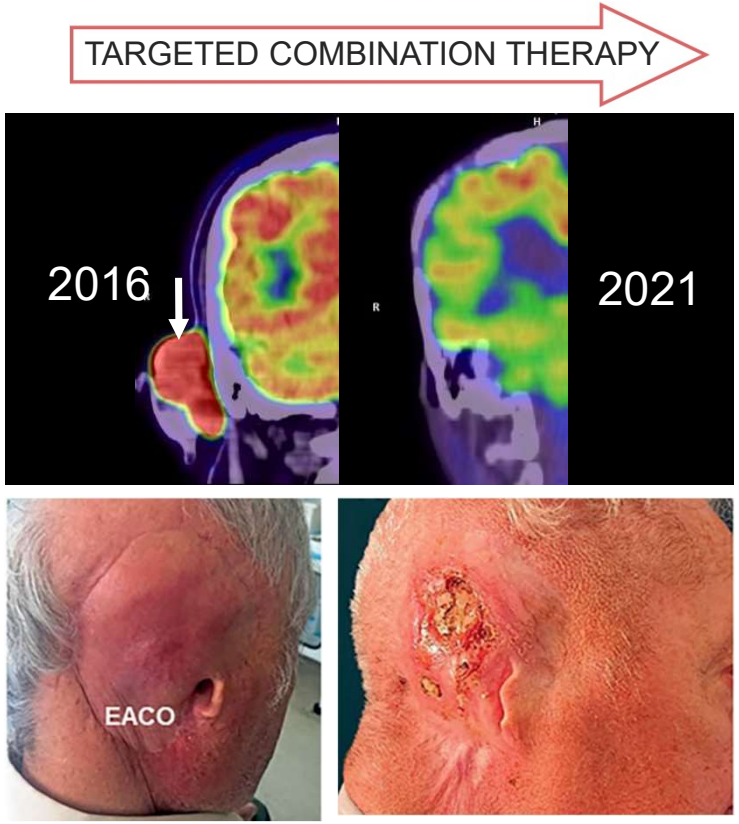
High-score therapies were available:
79.2% (on-label in 55.1%, off-label in 70.9%)
26.5% received in real-life
74% of patients who received chemotherapy, and **21%** of patients who received MTA could have received GDS-high therapy



Tumor site	% of patients (tumor genomes) associated with high-score MTAs				% patients with HS MTA administered*
	developmental MTAs	off-label MTAs	on-label MTAs	all MTAs	
All	74	71	55	75	28
Breast	90	89	86	90	42
Colorectal	68	60	46	69	10
Lung	83	84	79	85	44
Pancreas	86	86	4	86	2
Prostate	21	11	7	24	6

Case study

Lasting Complete Clinical Response of a Recurring Cutaneous Squamous Cell Carcinoma With *MEK* Mutation and *PIK3CA* Amplification Achieved by Dual Trametinib and Metformin Therapy. *Precis Oncol.* 2022 Jan;6:e2100344.



Frequency of cases with similar molecular profiles as identified within MSK CHORD data:

8000 patients in the USA and EU

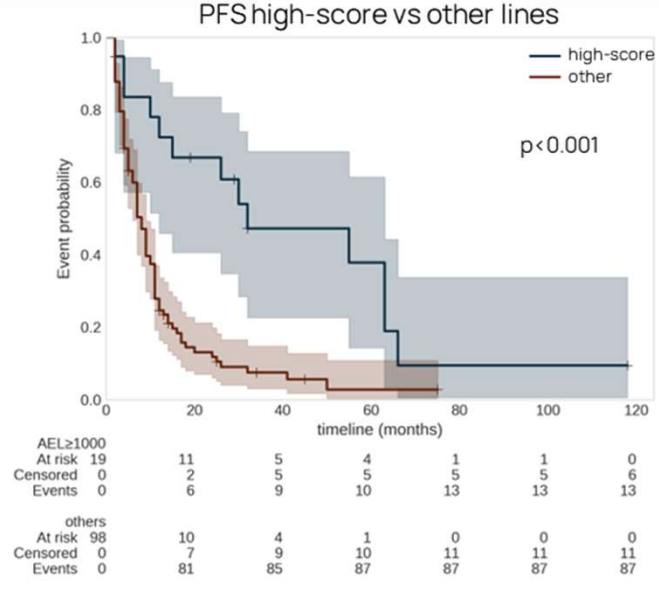
300 patients in Hungary

every year

Real-world performance analysis of a universal computational reasoning model for precision oncology in lung cancer. NPJ Precision Oncology 2025 May 30;9(1):159.

4X longer PFS p<0,001
2,6X+ longer OS p<0,0015

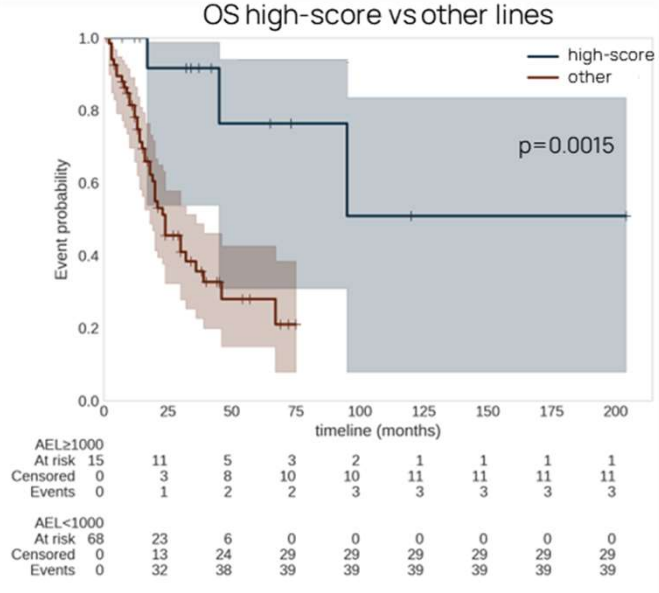
33% versus 6%
5-year OS p<0,01



mPFS

high-score MTA: **32 months**

low-score MTAs and SOC: **8 months**



mOS

1+ line of high-score MTA: **not reached**

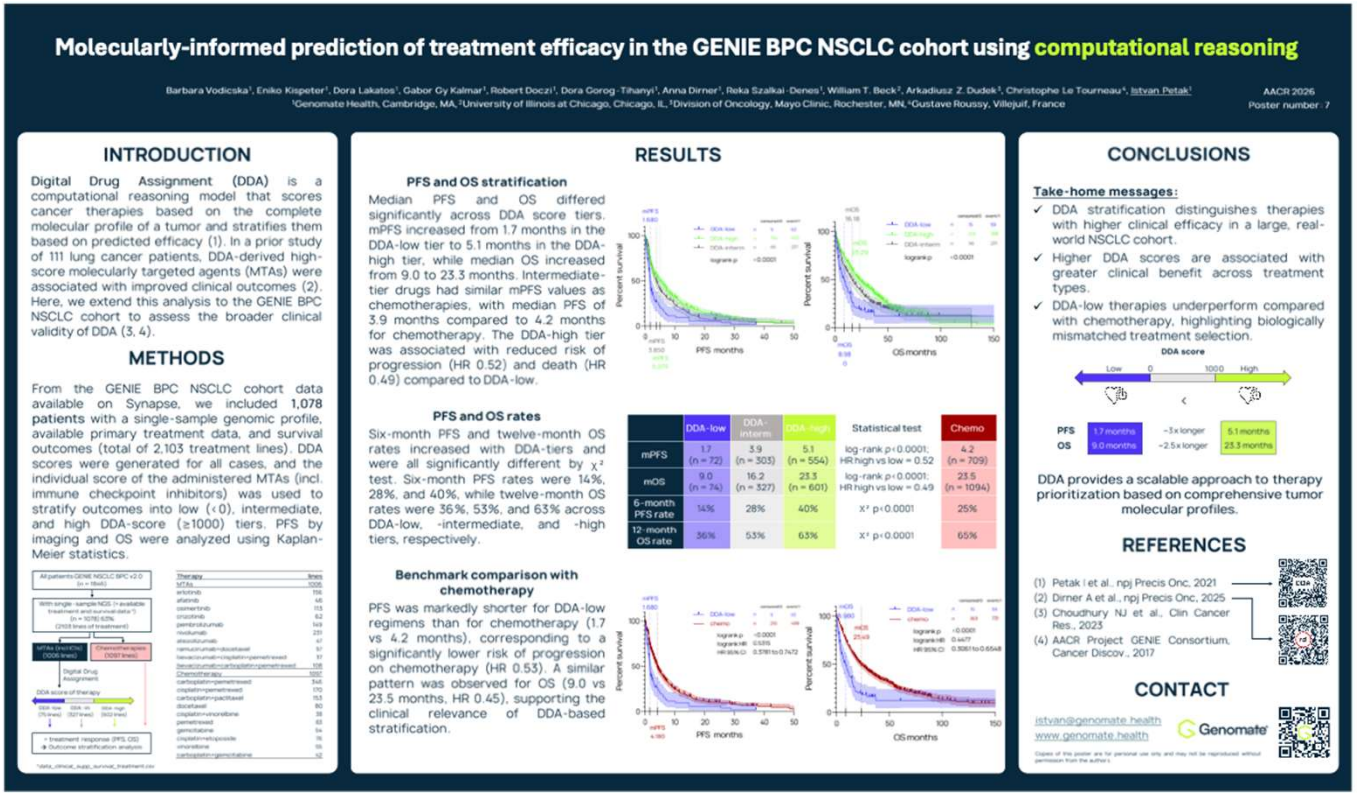
low-score MTAs and/or SOC: **24 months**

Molecularly informed prediction of treatment efficacy in the AACR GENIE BPC NSCLC cohort using computational reasoning

AACR Annual Meeting; Apr 17-22, 2026, San Diego, CA

1 078 patients 2 103 treatment lines Genomate

High versus low: PFS **5,1 vs. 1,7 months** (HR 0,52) , OS **23,3 vs. 9,0 months** (0,49)



Molecularly-informed prediction of treatment efficacy in the GENIE BPC NSCLC cohort using computational reasoning

Barbara Vodicska[1], Eniko Kispeter[1], Dora Lakatos[1], Gabor Gy Kalmar[1], Robert Doczi[1], Dora Gorog-Tihanyi[1], Anna Dirner[1], Reka Szalkai-Denes[1], William T. Beck[2], Arkadiusz Z. Dudek[3], Christophe Le Tourneau[4], Istvan Petak[1]
[1]Genomate Health, Cambridge, MA, [2]University of Illinois at Chicago, Chicago, IL, [3]Division of Oncology, Mayo Clinic, Rochester, MN, [4]Gustave Roussy, Villejuif, France

AACR 2026
Poster number : 7

INTRODUCTION

Digital Drug Assignment (DDA) is a computational reasoning model that scores cancer therapies based on the complete molecular profile of a tumor and stratifies them based on predicted efficacy (1). In a prior study of 111 lung cancer patients, DDA-derived high-score molecularly targeted agents (MTAs) were associated with improved clinical outcomes (2). Here, we extend this analysis to the GENIE BPC NSCLC cohort to assess the broader clinical validity of DDA (3, 4).

METHODS

From the GENIE BPC NSCLC cohort data available on Synapse, we included **1,078 patients** with a single-sample genomic profile, available primary treatment data, and survival outcomes (total of 2,103 treatment lines). DDA scores were generated for all cases, and the individual score of the administered MTAs (incl. immune checkpoint inhibitors) was used to stratify outcomes into low (<0), intermediate, and high DDA-score (≥1000) tiers. PFS by imaging and OS were analyzed using Kaplan-Meier statistics.

RESULTS

PFS and OS stratification

Median PFS and OS differed significantly across DDA score tiers. mPFS increased from 1.7 months in the DDA-low tier to 5.1 months in the DDA-high tier, while median OS increased from 9.0 to 23.3 months. Intermediate-tier drugs had similar mPFS values as chemotherapies, with median PFS of 3.9 months compared to 4.2 months for chemotherapy. The DDA-high tier was associated with reduced risk of progression (HR 0.52) and death (HR 0.49) compared to DDA-low.

PFS and OS rates

Six-month PFS and twelve-month OS rates increased with DDA-tiers and were all significantly different by χ^2 test. Six-month PFS rates were 14%, 28%, and 40%, while twelve-month OS rates were 36%, 53%, and 63% across DDA-low, -intermediate, and -high tiers, respectively.

	DDA-low	DDA-interm	DDA-high	Statistical test	Chemo
mPFS	1.7 (n = 72)	3.9 (n = 303)	5.1 (n = 554)	log-rank p<0.0001; HR high vs low = 0.52	4.2 (n = 709)
mOS	9.0 (n = 74)	16.2 (n = 327)	23.3 (n = 601)	log-rank p<0.0001; HR high vs low = 0.49	23.5 (n = 1094)
6-month PFS rate	14%	28%	40%	X^2 p<0.0001	25%
12-month OS rate	36%	53%	63%	X^2 p<0.0001	65%

Benchmark comparison with chemotherapy

PFS was markedly shorter for DDA-low regimens than for chemotherapy (1.7 vs 4.2 months), corresponding to a significantly lower risk of progression on chemotherapy (HR 0.53). A similar pattern was observed for OS (9.0 vs 23.5 months, HR 0.45), supporting the clinical relevance of DDA-based stratification.

CONCLUSIONS

Take-home messages:

- ✓ DDA stratification distinguishes therapies with higher clinical efficacy in a large, real-world NSCLC cohort.
- ✓ Higher DDA scores are associated with greater clinical benefit across treatment types.
- ✓ DDA-low therapies underperform compared with chemotherapy, highlighting biologically mismatched treatment selection.

DDA score: Low — 0 — 1000 — High

PFS	1.7 months	~3x longer	5.1 months
OS	9.0 months	~2.5x longer	23.3 months

DDA provides a scalable approach to therapy prioritization based on comprehensive tumor molecular profiles.

REFERENCES

(1) Petak I et al., npj Precis Onc, 2021
(2) Dirner A et al., npj Precis Onc, 2025
(3) Choudhury NJ et al., Clin Cancer Res., 2023
(4) AACR Project GENIE Consortium, Cancer Discov., 2017

CONTACT

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Genomate

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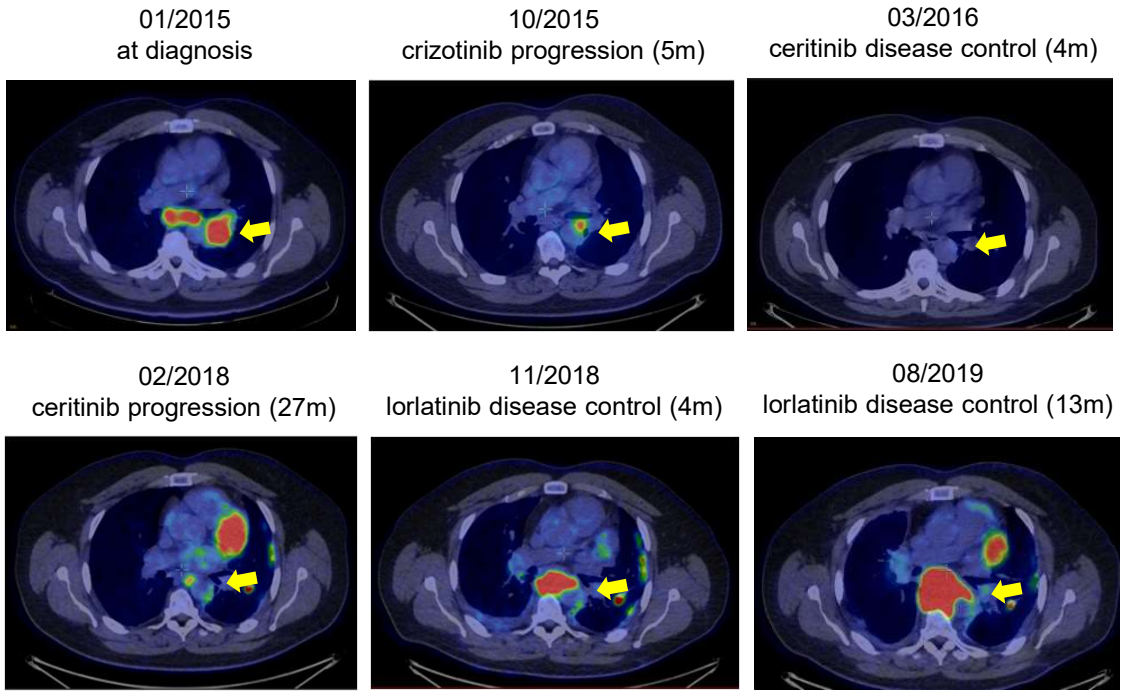
DDA score

Low — 0 — 1000 — High

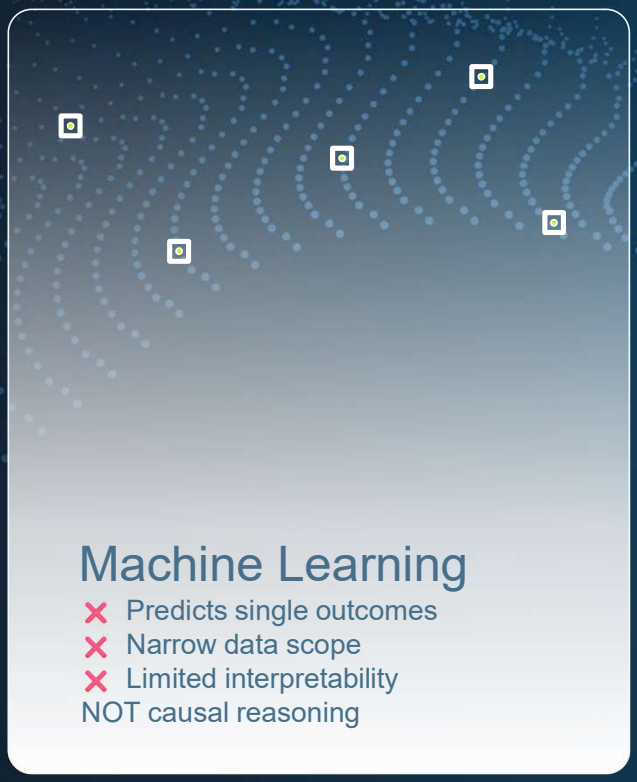
PFS	1.7 months	~3x longer	5.1 months
OS	9.0 months	~2.5x longer	23.3 months

Case study

Efficacy of Incremental Next-Generation ALK Inhibitor Treatment in Oncogene-Addicted, *ALK*-Positive, *TP53*-Mutant NSCLC.
J Personalized Medicine. 2020 Aug 28;10(3):107.



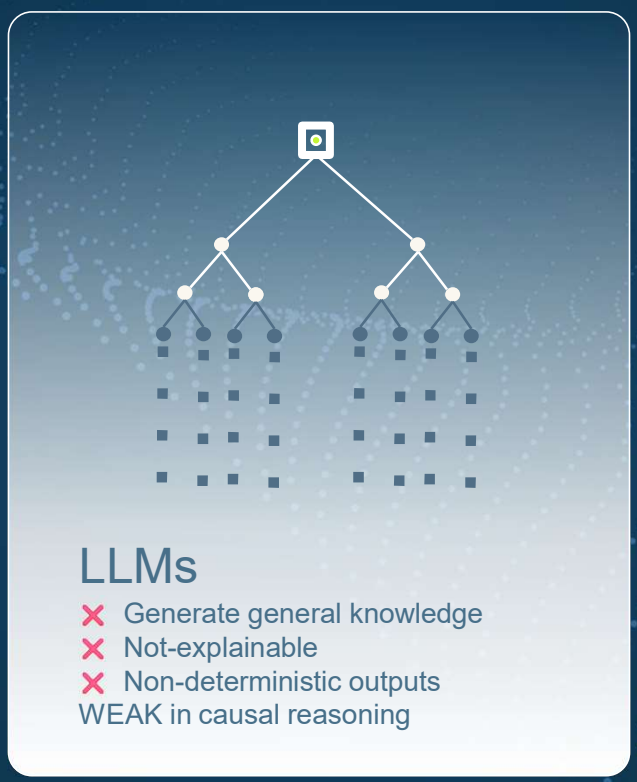
Genomate®: special purpose-built medical AI for causal therapeutic reasoning



Machine Learning

- ✕ Predicts single outcomes
- ✕ Narrow data scope
- ✕ Limited interpretability

NOT causal reasoning



LLMs

- ✕ Generate general knowledge
- ✕ Not-explainable
- ✕ Non-deterministic outputs

WEAK in causal reasoning

PATENTED SCIENTIFIC BREAKTHROUGH TECHNOLOGY PUBLISHED IN **NATURE'S PRECISION ONCOLOGY JOURNAL.**



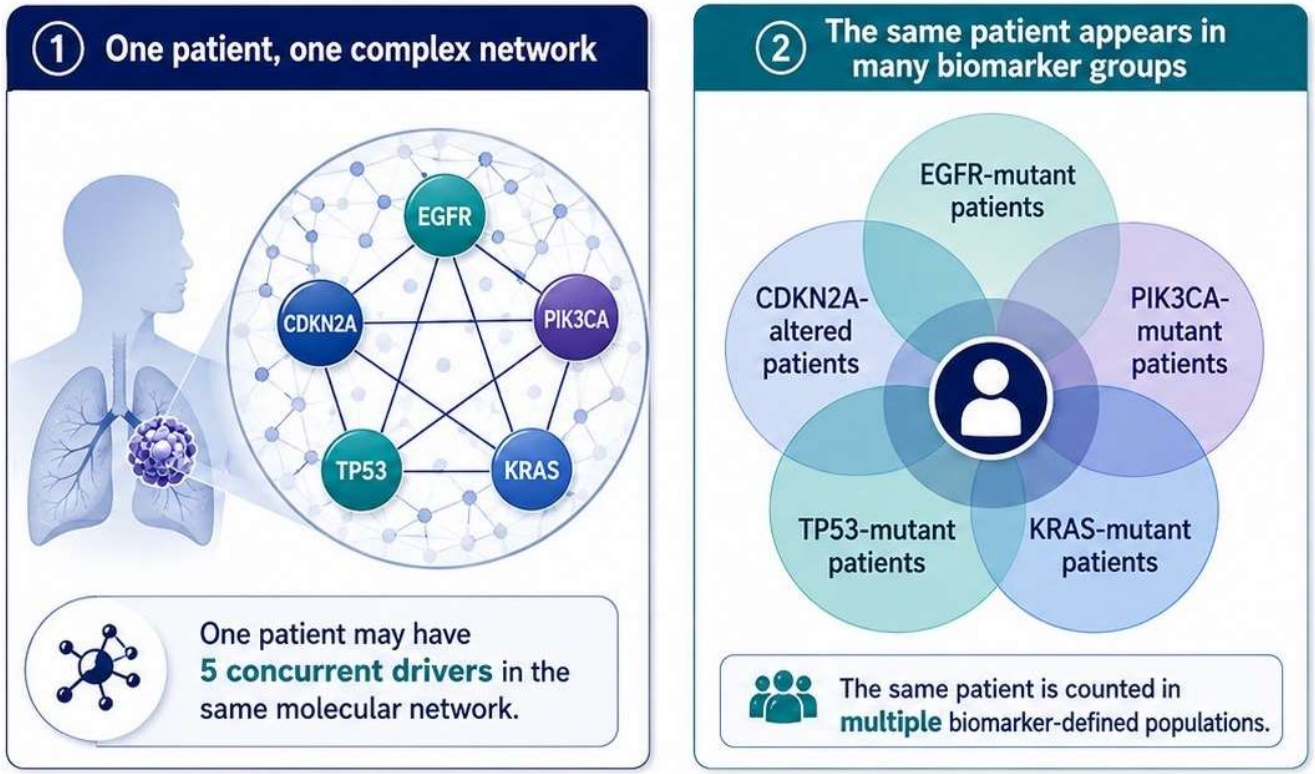
Genomate®

- ✓ Models the full cancer profile
- ✓ Evaluates hundreds of treatment options for each patient
- ✓ Transparent, evidence-based

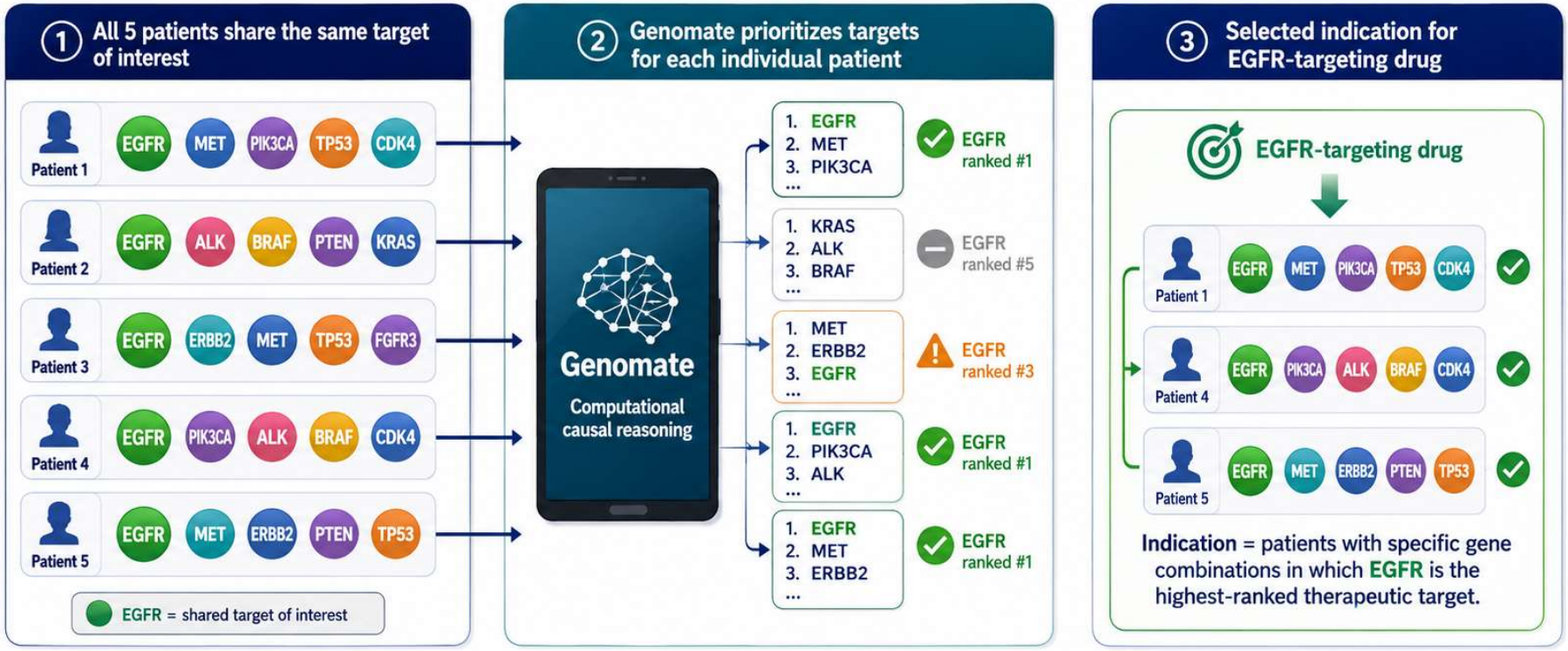
NEITHER APPROACH IS DESIGNED TO COMPUTE THE MOST OPTIMAL THERAPY ACROSS THE FULL BIOLOGICAL SYSTEM.

The central mathematical challenge of precision oncology

One Drug = One Molecular Target ≠ Tumor/Patient
One or a combination of drugs = Molecular Network = Tumor/Patient



Finding the right patients for the right drug based on the whole individual molecular context of each tumor



Increasing the value of precision oncology: health economics of Genomate/Oncompass powered workflow. ASCO Breakthrough Innovations in Oncology Award, NEAK OENO 28981 (2019)

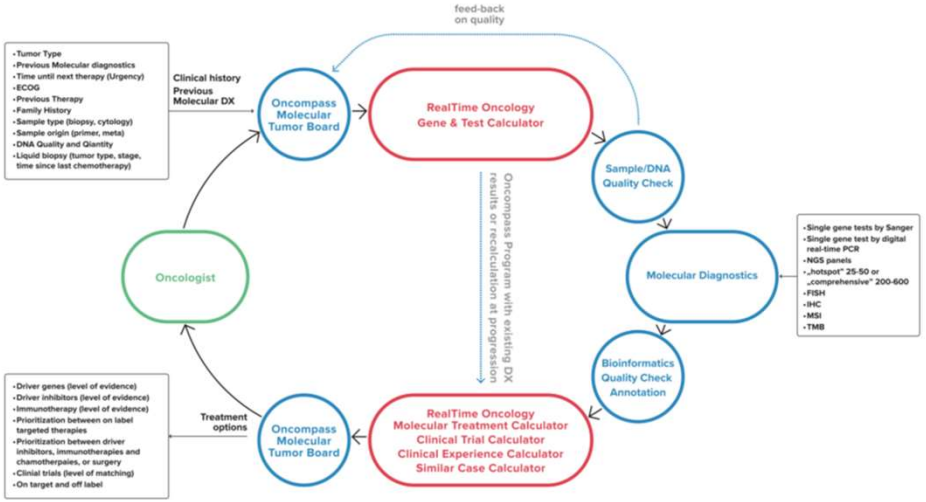
CONQUER CANCER® THE ASCO FOUNDATION | MISSION ENDOWMENT

AI oncology algorithm and dynamic real-world learning health care system for precision oncology.

I. Petak[1], Cs. Hegedüs[1], D. Tihanyi[1], R. Dóczi[1], P. Filotas[1], A. Mate[2], M. Bacskai[3], R. Schwab[1], I. Valyi-Nagy[4]
[1]Oncompass Medicine Hungary Ltd, Budapest, Hungary [2]eHealth Software Solutions Kft., Budapest, Hungary [3]Healthware Tanacsado Kft., Budapest, Hungary [4]Centrum Hospital of Southern Pest, National Hematology and Infectology Institute

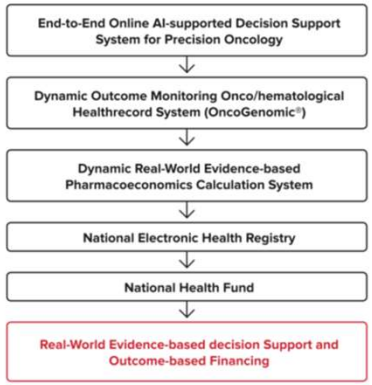
BACKGROUND

Most tumours harbor multiple driver genetic alterations and many driver alterations are linked to multiple targeted therapies with various level of evidence. In addition, a specific treatment can be linked to multiple genetic alterations in the same tumor. Several public and private databases and software solutions are available to link driver alterations to treatments options, but in clinical practice of precision oncology we need a solution to select the right treatment for our patients based on the highest level of evidence also in case of complex molecular profiles.



METHODS

We have developed an AI oncology algorithm and rule-engine to prioritise treatment options for every cancer patient based on the individual molecular of their tumor. This IT solution can now prioritise 1200 compounds in clinical use or clinical development based on the computing of 24,000 evidence-based associations ("rules") between drivers, targets and compounds. The software calculates a numeric score, the "aggregated evidence level" for each driver alterations and compounds. We have linked this decision support software to a dynamic patient case management system, which records responds to therapy to create learning system to provide dynamic decision support through several lines of therapies of each patient and to use real-life evidence to further improve the algorithm.



A model to Integrate Precision Oncology into the Healthcare System (Hungary, population of 10 million) developped within the framework of the National Oncogenomic and Precision Oncotherapy Program with the support of the Hungarian National Research, Development and Innovation Office.



Precision Oncology Centers supported with the same central decision support system

RESULTS

Our first results indicate that system allows individualised decision of diagnostic option between single gene tests to comprehensive 600 gene NGS panels and identification of actionable alterations in 83% of cancer cases.

NSCLC	KRAS/EGFR/ALK/ROS1 WT	
	Oncompass	Control
Cost	42460	43659
LYG	1,46	1,4
ICER	-20623	

NSCLC	EGFR/ALK/ROS1 inhibitor resistant	
	Oncompass	Control
Cost	34049	23909
LYG	1,39	1,02
ICER	26894	

NSCLC	BOTH INDICATION	
	Oncompass	Control
Cost	40836	39846
LYG	1,39	1,02
ICER	26894	

COLON CC	RAS WT LIVER MET ONLY	
	Oncompass	Control
Cost	18207	9879
LYG	0,79	0,64
ICER	58379	

BREAST TN		
	Oncompass	Control
Cost	25366	3804
LYG	1,3705	0,934
ICER	55979	

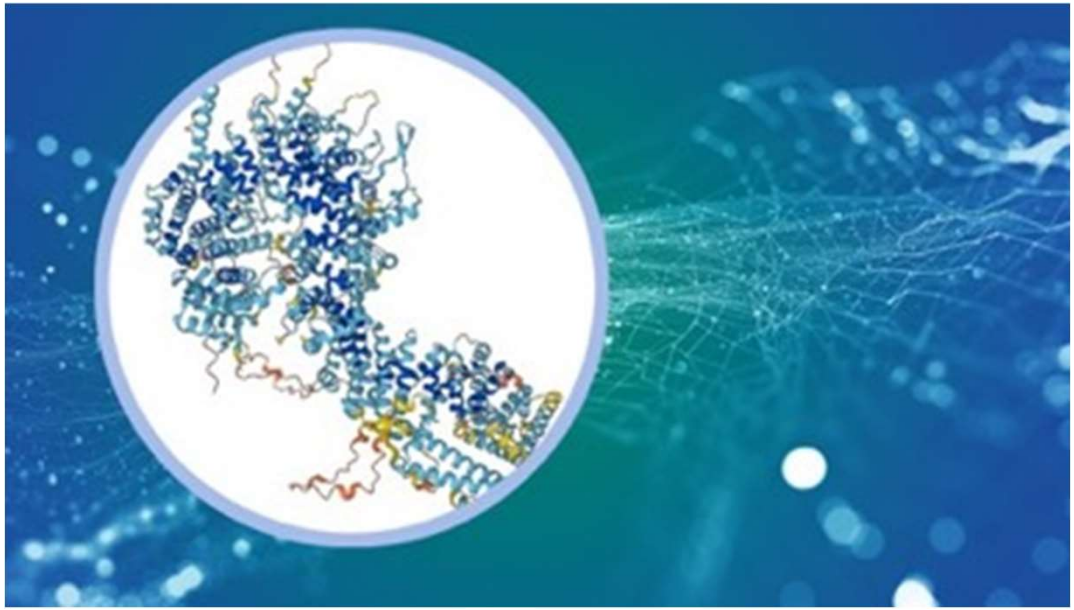
Technological assessment results the precision oncology programs based on 58 gene NGS panel and additional 3 FISH, MSI, PDL-1 IHC tests.

CONCLUSION

This system can be a first working solution to standardise clinical decisions precision oncology, which also helps the real-life evaluation of novel multigene molecular diagnostic tests and therapies to find their best indications and accelerate their reimbursement by insurance companies and national health funds. It is crucial to have an established protocol in the community of practice to indicate effective and eliminate ineffective genomics-driven treatments based on molecular profiling. The technology assessment provided evidence that standardized decision support of the molecular tumor board (MTB) to select diagnostic tests and treatments can assure clinical utility and cost effectiveness of multigene testing (NGS). This medical procedure (protocol) received a positive evaluation as effective and cost effective by the Hungarian National Health Insurance Fund based on QUALY gain calculation and value-based technology assessment.

Sponsored by Oncompass Medicine and grants (NVKP_16-1-2016-0005, KFI_16-1-2016-0048, GINOP-2.1.1-15-2015-00509)

Are we there yet? We need more drugs to tackle the 750 cancer genes and 6 million mutations





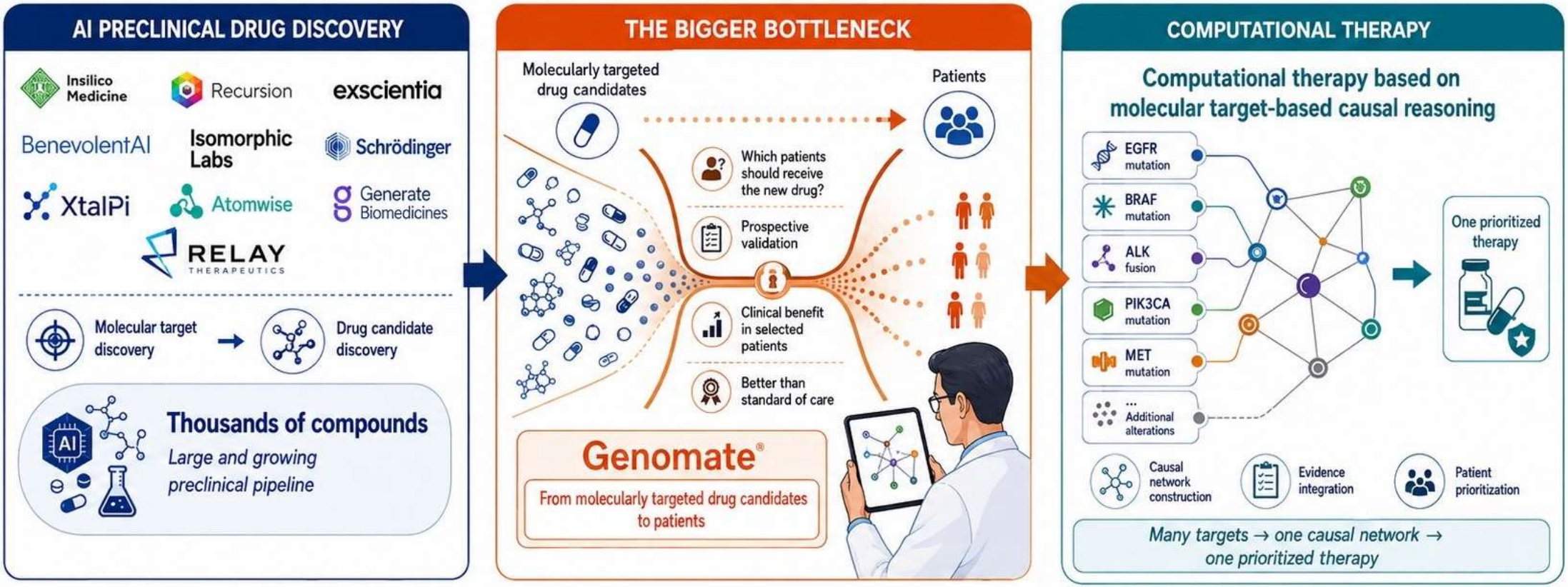
AlphaFold AI, Google DeepMind, Nobel Prize in 2024

AI in drug discovery: AI has accelerated the preclinical phase, target discovery and drug design, but not the clinical development

$20B invested ⇨ 10 years passed ⇨ 0 FDA approved drug

Bender, A., Thomas, M.C., Scannell, J.W. et al. Artificial intelligence in drug discovery — what it is, where we stand and the path forward. Nat Rev Drug Discov (August 7, 2026).

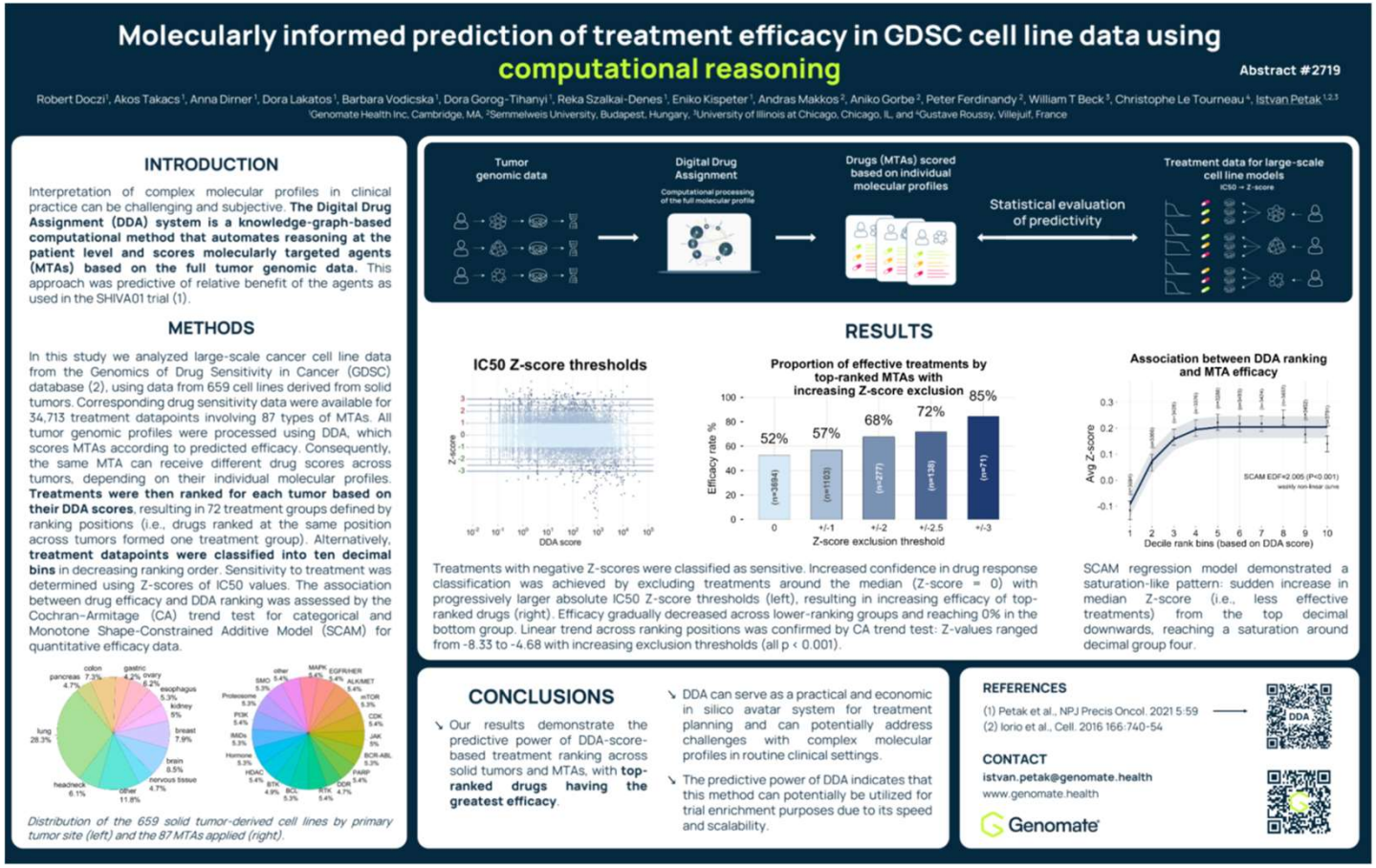
We need to solve the bottleneck in the clinical development



Molecularly informed prediction of treatment efficacy in GDSC cell line data using computational reasoning

659 cell lines, 87 targeted therapies, 34,713 data points

AACR Annual Meeting; Apr 17-22, 2026, San Diego, CA



Global impact opportunity (estimated) from Genomate-powered **repurposing, clinical trial enrichment, and drug rescue** of existing drugs in clinical use (200+) or in clinical development (2000+)

- ✓ **+40%, +6 months OS benefit potential**
- ✓ **For 50% of advanced solid tumor patients**
- ✓ **2,5-5 million life-year impact ($90B+ new global market)**

+The same impact potential for new drugs in pre-clinical development

With the current version of the platform

Lehetőségek Magyarország számára a Genomate technológiai támogatásával:

A vízió: ***Magyarország mint a precíziós onkológia bölcsője***

„Nem lehetünk a legnagyobbak, de lehetünk a legokosabbak.”

- ✓ **A klinikai vizsgálatok páneurópai digitális platformjának létrehozása Magyarországon működő központtal.** *A DIGITALEUROPE - Executive Council támogatásával*

Cél: a klinikai vizsgálatok számának növelése Európában, valamint a betegek országok közötti bevonásának elősegítése. Hozzáférés a jövő gyógyszereihez. Bevétel az egészségügyi rendszereknek. A hazai healtech, medtech, biotech bekapcsolása a platformba.

- ✓ **CANCERX-EU köz- és magánszféra összefogásának EU-szintű platformjának létrehozása rákkutatás és az onkológiai ellátás támogatására Magyarországon lévő központtal.** *A CANCERX-USA, MIT-REAP támogatásával.*

Cél: a külföldi közvetlen tőkebefektetések ösztönzése hazai K+F-központú cégekbe, startupokba, valamint a K+F-intenzív export növelése az egészségipari szektorban az EU-ban és Magyarországon. Az innovációs potenciál kihasználása az egészségügy számára, valamint a piac növelése a startupoknak. „Reverse pitch” és állami közbeszerzés az innovációra.

- ✓ **Mesterséges intelligenciával támogatott precíziós onkológiai ellátás bevezetése Magyarországon.** *Hazai és nemzetközi innovatív egészségügyi startupok támogatásával.*

Cél: a daganatos halálozás csökkentése. („három beteg per nap”). Minőségbiztosítás növelése: minden beteg megkapja a számára elérhető célzott kezelést. A nagy értékű célzott daganatellenes gyógyszerek költséghatékonyságának növelése molekuláris evidencia segítségével. Az új gyógyszerek befogadásának felgyorsítása. Az egyedi méltányossági döntések felgyorsítása.


Minden beteg egyedi.
A kezelési stratégia is legyen az.





Dr. Vodicska Barbara



Dr. Dóczi Robert



Dr. Lakatos Dóra

Thank you!

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