AI-BASED DRUG DEVELOPMENT AND REPURPOSING THERAPIES

Chances and challenges for breast cancer

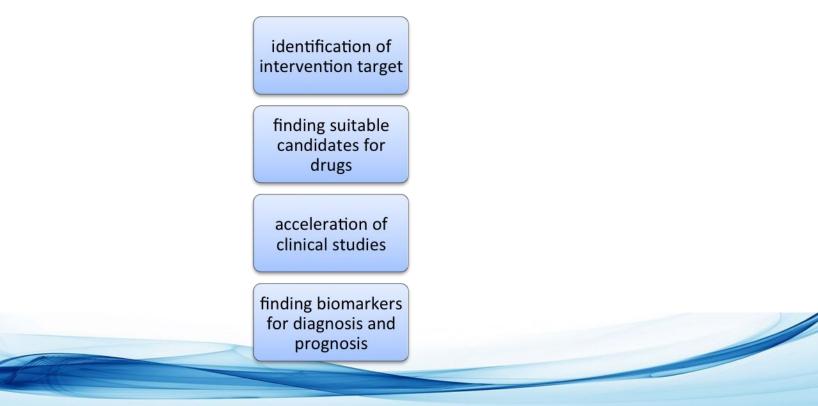
Prof. Evelyne Bischof, MD, MPH, FEFIM



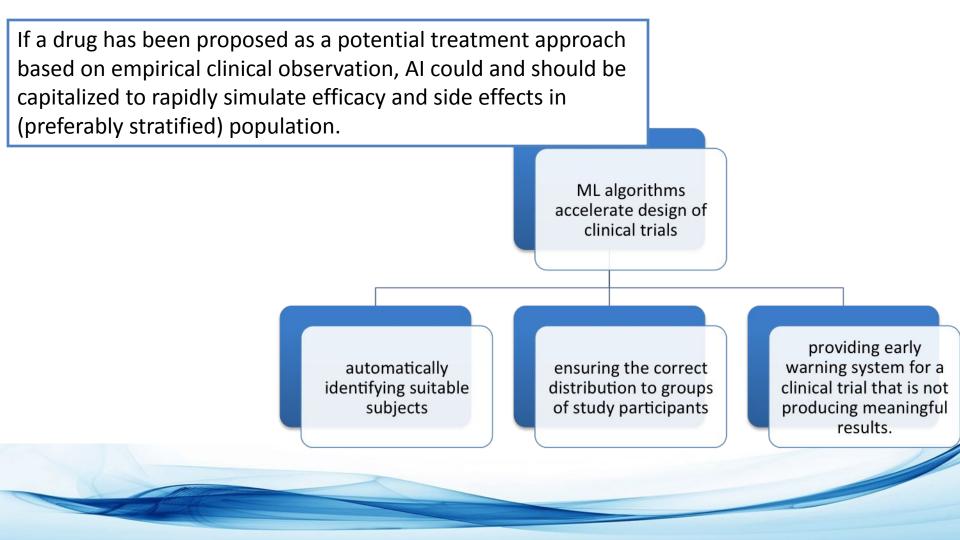


Personalized therapies

- Al-based drug development is an integral element!
- Al can be harnessed towards pharmacostrategies in various steps

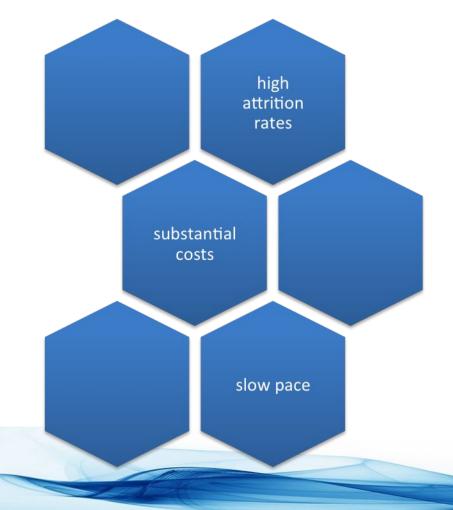


Personalized therapies



Status quo

The drug discovery process today

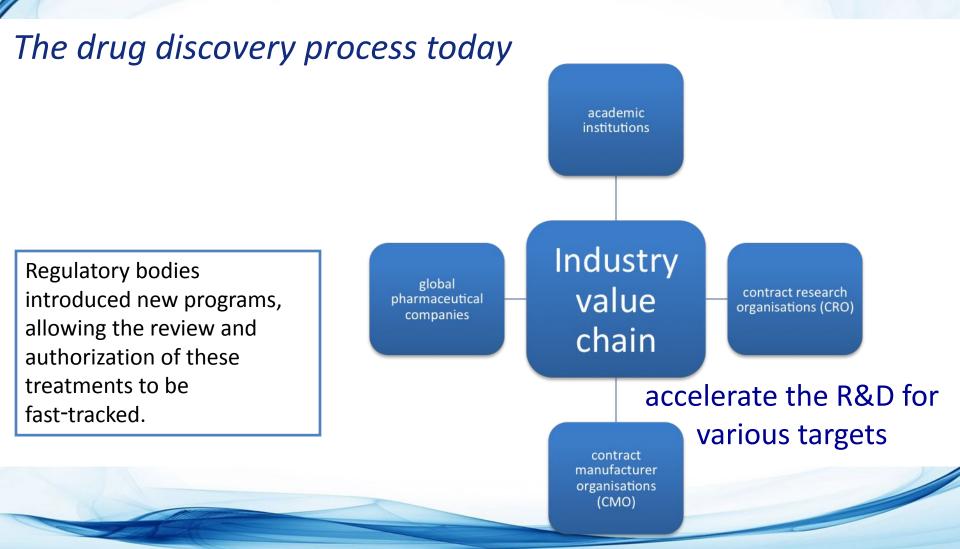


Drug discovery is one of the most complex, risky, and lengthy areas of human development. This process takes decades, billions of dollars, and fails over 90% of the time.

There are very few truly novel drugs on the market. In 2020, the FDA approved 53 novel drugs, and that was the record year.

Many of these drugs were small molecules that modulated the function of well-known molecular targets. Discovering a novel molecule for a novel target for a broad disease indication is extremely rare.

Status quo



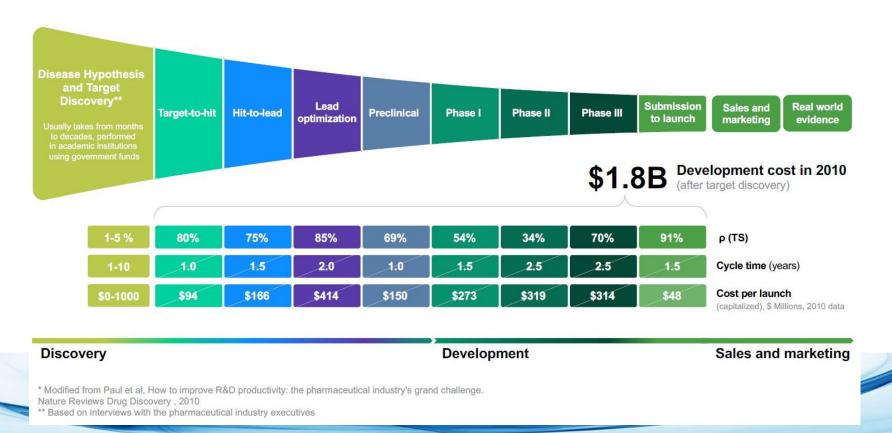
Status quo

Insilico Medicine

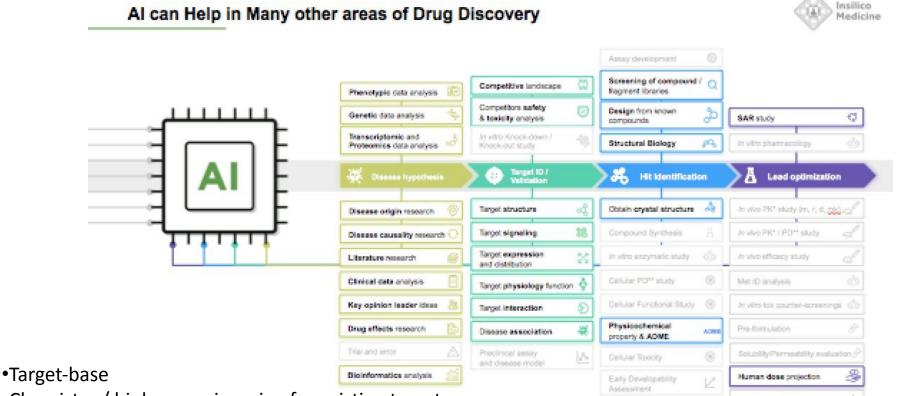
The drug discovery process today and yesterday

Traditional drug R&D takes >10 years and >\$2.6B

for a novel drug from discovery to launch (in 2010 and constantly increasing)



The drug discovery process today



Chemistry / biology engineering for existing targets

Development of personalized medicine solutions

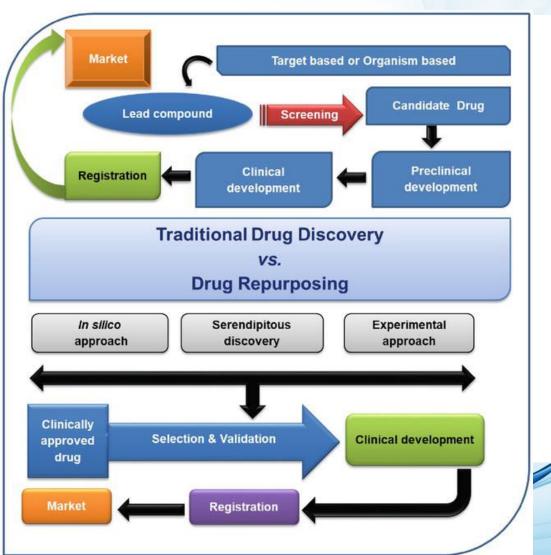
Large amounts of data coming from robotics experiments or clinical data, or a combination used.

Some targets already entered human clinical trials (by in-licensing compounds).

But...

Can AI identify

Novel Targets and Novel Molecules?



Translationstudy

D Safer

Hore Molecule

O Potenico ctivito

synthesis

14

O STALINE O BOODEL O STALES O HORES

HovelTarget

2021:

invitio assays

Invivo

First AI-generated novel molecule for a novel target discovered with AI demonstrated efficacy in a broad therapeutic area and reached preclinical candidate stage.

Yann LeCun liked this.



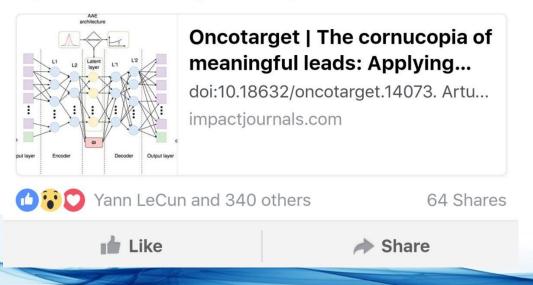
Yoshua Bengio

2 hrs · 🚷



January 2017

Auto-encoders with a GAN objective in the latent layer for cancer drug discovery:



nature biotechnology

BRIEF COMMUNICATION https://doi.org/10.1038/s41587-019-0224-x

Deep learning enables rapid identification of potent DDR1 kinase inhibitors

Alex Zhavoronkov^{©1*}, Yan A. Ivanenkov¹, Alex Aliper¹, Mark S. Veselov¹, Vladimir A. Aladinskiy¹, Anastasiya V. Aladinskaya¹, Victor A. Terentiev¹, Daniil A. Polykovskiy¹, Maksim D. Kuznetsov¹, Arip Asadulaev¹, Yury Volkov¹, Artem Zholus¹, Rim R. Shayakhmetov¹, Alexander Zhebrak¹, Lidiya I. Minaeva¹, Bogdan A. Zagribelnyv¹, Lennart H. Lee^{®2}, Richard Soll², David Madge², Li Xing², Tao Guo^{®2} and Alán Aspuru-Guzik^{3,5,6}

We have developed a deep generative model, generative tensorial evinforcement learning (GENTRL), for de novo small-molecule design. GENTRL optimizes synthetic feasibility, novelty, and biological activity. We used GENTRL to discover potent inhibitors of discolid nomain receptor 1 (DDR), a kinase target implicated in fibrosis and other diseases, in 21 days. Four compounds were active in biochemical assays, and two were validated in cell-based assays. One lead candidate was tested and demonstrated favorable pharmacokinetics in mice.

Drug discovery is resource intensive, and involves typical timelines of 10–20 years and costs that range from US80.5 billion to US82.6 billion¹⁴. Artificial intelligence promises to accelerate this process and reduce costs by facilitating the rapid identification of induces that use neural networks to produce new data objects. These techniques can generate objects with certain properties, such as activity against a given target, that make them well suited for the discovery of drug candidates. However, few camples of generative drug design have achieved experimental validation involving synthesis of novel compounds for in vitro and in vivo investigation¹².

Discoidin domain receptor 1 (DDR1) is a collagen-activated proinflammatory receptor tyrosins kinase that is expressed in epithelial cells and involved in fibrosis". However, it is not clear whether DDR1 directly regulates fibrotic processes, such as myolibroblat activation and collagen deposition, or earlier inflammatory events that are associated with reduced macrophage infiltration. Since 2013, at least eight chemotypes have been published as selective DDR1 (or DDR1 and DDR2) small-molecule inhibitors (Supplementary Table 1). Recently, a series of highly selective, spiro-indoline-based DDR1 inhibitors were shown to have potential therapeutic efficacy against renal fibrosis in a *Col4a3*⁺ mice model of Alport syndrome". A wider diversity of DDR1 inhibitors sword therefore enable further basic understanding and therapeutic intervention.

We developed generative tensorial reinforcement learning (GENTRL), an anchine learning approach for de novo drug design. GENTRL prioritizes the synthetic feasibility of a compound, its effectiveness against a given biological target, and how distinct it is from other molecules in the literature and patent space. In this work, GENTRL, was used to rapidly design novel compounds that are active against DDR1 kinase. Six of these compounds, each complying with Lipinski's rules', were designed, synthesized, and

experimentally tested in 66 days, which demonstrates the potential of this approach to provide rapid and effective molecular design (Fig. 1). To create GENTRL, we combined reinforcement learning, variational inference, and tensor decompositions into a generative twostep machine learning algorithm (Supplementary Fig. 1)¹⁷. First, we learned a mapping of chemical space, a set of discrete molecular graphs, to a continuous space of 50 dimensions. We parameterized the structure of the learned manifold in the tensor train format to use partially known properties. Our auto-encoder-based model compresses, the space of structures onto a distribution that parameterizes the latent space in a high-dimensional lattice with an exponentially large number of multidimensional classius in its nodes. This parameter, without their explicit input. In the second step, we explored this space, with peinforcement learning to allo forcement ensormed.

with reinforcement learning to discover new compounds. GENTRL use three distint est-forganizing maps (SOMs) as reward functions: the trending SOM, the general kinase SOM, and the specific kinase SOM. The trending SOM is a Kohonen-based reward function that scores compound novely using the application priority date of structures that have been disclosed in patents. Neurons that are abundantly populated with novel chemical entities reward the generative model. The general kinase SOM is a Kohonen map that distinguishes kinase inhibitors from other classes of molcuelus. The specific kinase SOM biotacle DDR1 inhibitors from the total pool of kinase-target molecules. GENTRL prioritizes the structures it generates by using these three SOMs in sequence.

We used as it data sets to build the model (1) a large set of mocules derived from a ZIRC data set, (2) known DDRI kinase inhibitors, (3) common kinase inhibitors (sositive set), (4) molecules that act on non-kinase targets (negative set), (5) patent data for biologicully active molecules that have been claimed by pharmaceutical companies, and (6) three-dimensional (3D) structures for DDRI inhibitors (Supplementary Table 1). Data sets were preprocessed to exclude gross outliers and to reduce the number of compounds that contained similar structures (see Methods).

We started to train GENTRL (pretraining) on a filtered ZINC database (data set 1, described earlier), and then continued training using the DDRI and common kinase inhibitors (data set 2 and data set 3). We then launched the reinforcement learning stage with the reward described earlier. We obtained an initial output of 30,000 structures (Supplementary Data Set), which were then

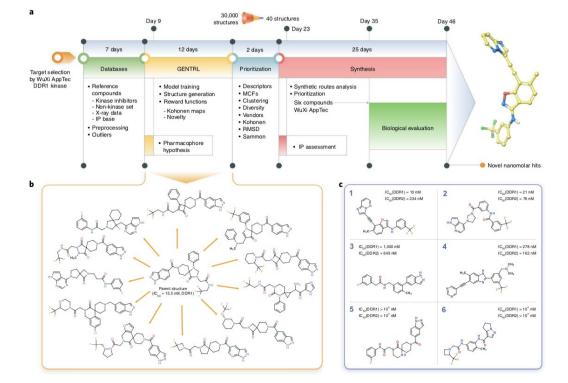


Fig. 1 | GENTRL model design, workflow, and nanomolar hits. a, The general workflow and timeline for the design of lead candidates using GENTRL. IP, intellectual property. b, Representative examples of generated structures compared to the parent DDR1 kinase inhibitor. c, Generated compounds with the highest inhibition activity against human DDR1 kinase.



Drug Discovery Today Volume 20, Issue 8, August 2015, Pages 1027-1034



Definitions

Review

Post-screen

Drug repositioning and repurposing: terminology and definitions in literature

Joris Langedijk ^{1, 2}, Aukje K. Mantel-Teeuwisse ¹ ♀ ⊠, Diederick S. Slijkerman ², Marie-Hélène D.B. Schutjens ^{1, 3}

Trending terms in represent novel drug development strategies.



definition range from brief and general to extensive and specific

nature reviews drug discovery

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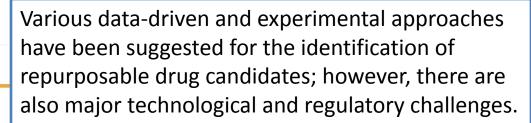
Published: 12 October 2018

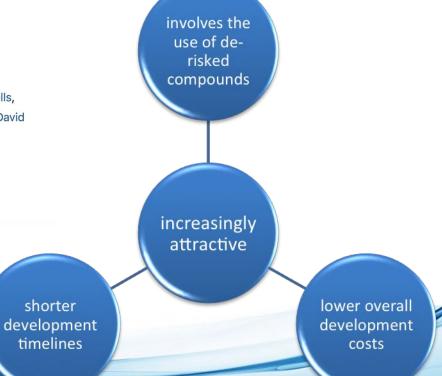
Drug repurposing: progress, challenges and recommendations

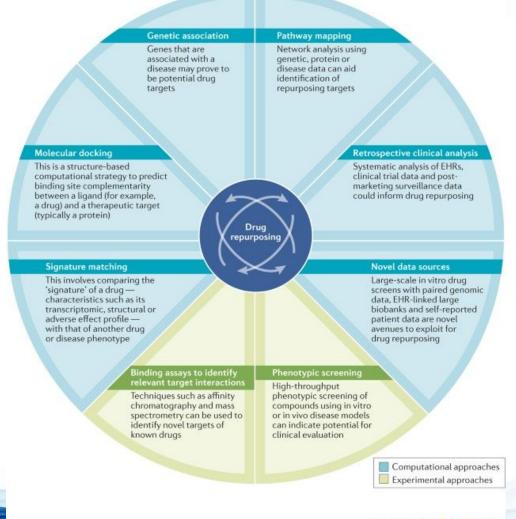
Sudeep Pushpakom, Francesco Iorio, Patrick A. Eyers, K. Jane Escott, Shirley Hopper, Andrew Wells, Andrew Doig, Tim Guilliams, Joanna Latimer, Christine McNamee, Alan Norris, Philippe Sanseau, David Cavalla & Munir Pirmohamed 🖂

Nature Reviews Drug Discovery 18, 41–58 (2019) Cite this article

39k Accesses | 778 Citations | 341 Altmetric | Metrics







Oncology appropriate for DRR: a single mechanism or biomarker is frequently linked to a broad range of tumor types.

Merck's Keytruda[®] (pembrolizumab) which was first approved for advanced melanoma, now it is approved for 14 cancer types, including lung cancer and lymphoma. The company is constantly evaluating Keytruda for more cancers, such as triple-negative breast cancer.

Due to its similar PD-1-based mechanism of action (MOA), Bristol-Myers Squibb's (BMS) Opdivo[®] (nivolumab) is currently approved for 10 cancer types and the company is continuing to investigate the drug's efficacy for other indications.

Novartis' drug Arzerra (ofatumumab), a monoclonal antibody that targets the CD20 protein, was initially developed to treat chronic lymphocytic leukemia (CLL). However, clinical studies are currently underway to determine its effectiveness as a treatment for adult patients with relapsing forms of multiple sclerosis (MS).

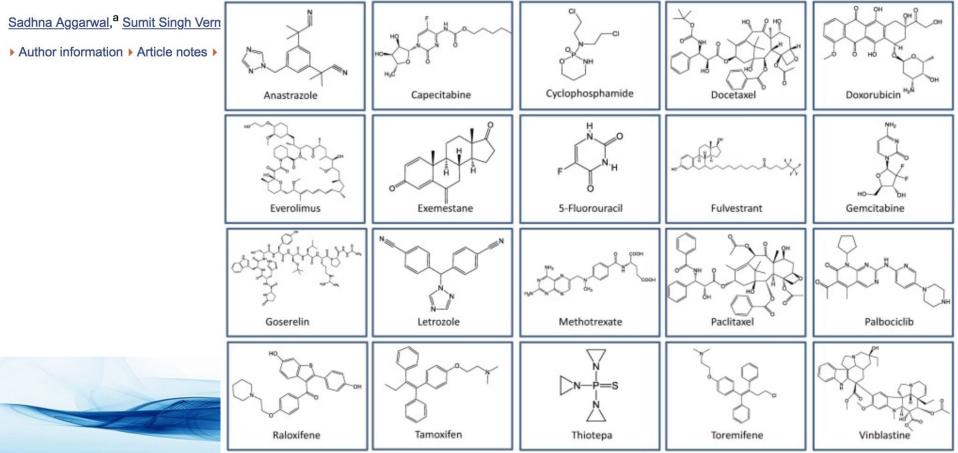


Semin Cancer Biol. 2021 Jan; 68: 8-20.

Published online 2019 Sep 21. doi: 10.1016/j.semcancer.2019.09.012

PMCID: PMC7128772 PMID: <u>31550502</u>

Drug repurposing for breast cancer therapy: Old weapon for new battle



Drug			Breast cancer	N		
Category	Chemical name	Commercial name	stage	Mechanism	Original indication	
Alkylating agent	Cyclophosphamide	Cytoxan, Clafen, Neosar	Early and advanced	Inhibits DNA replication by damaging genetic material of the cell	As immuno-modulator in autoimmune diseases	
	Thiotepa	Thioplex, Tespa, Thiophosphoamide, TSPA, Tepadina	Early and advanced		Immunosuppressant	
Anthracyclins	Doxorubicin	Adriamycin, Caelyx, Rubex	Advanced	DNA intercalation	Antibiotic from <i>Streptomyces</i> peucetius bacterium	
	Capecitabine	Xeloda	Metastatic and advanced	False building block incorporation during cell growth	Colon cancer	
Antimetabolite	Fluorouracil	Adrucil, Carac	Early, advanced and metastatic		Keratoacanthomas, actinic keratosis, and skin warts	
Antimetabolite	Gemcitabine	Gemzar	Metastatic and advanced		Anti-viral drug	
	Methotrexate	Mexate, Folex, Rheumatrex	Early and advanced		Leukemia	

	CDK 4/6 inhibitor	Palbociclib, Palbonix	Ibrance	ER+, PR+, HER2-, advanced	Interferes with cell cycle	CDK 4/6 inhibitor
н	HT-SERM	Tamoxifen	Nolvadex, Apo-Tamox, Tamifen, Soltamox	ER+, PR+, advanced	Binds to ER	Albright syndrome, ovulation induction
		Toremifene	Fareston	ER+, PR+		Infertility with an ovulatory disorders
		Raloxifene	Evista	ER+, PR+		Osteoporosis in postmenopausal women
		Exemestane	Aromasin	ER+, PR+		Ovulation induction
HT-Ar inhibit	HT-Aromatase	Letrozole	Femara	ER+, PR+, early and advanced	Lowers estrogen amount	Ovulation induction
	minoror	Anastrazole	Arimidex	ER+, PR+, advanced		Ovulation induction
	HT-SERD	Fulvestrant	Faslodex	ER+, PR+, HER2-, advanced	ER degradation	Antiestrogen
	HT-LHRH agent	Goserelin	Zoladex	ER+, PR+, early	Reduces amount of estrogen	Prostate cancer, uterine fibroids, assisted reproduction
	mTOR inhibitor	Everolimus, Votubia, Evertor	Afinitor	HER2+, HER2-	Interferes with mTOR kinase	Immunosuppressant during organ transplants, wound healing
		Docetaxel	Taxotere	Early and		Hormone-refractory prostate cancer
	Mitotic inhibitor			advanced	Interferes with cell division	
		Paclitaxel	Taxol, Onxol	Early and advanced	interferes with cen division	Ovarian cancer, atrial restenosis
		Vinblastine	Velban, Velsar, Adria, Velbe	Advanced	Interferes with genes	Hodgkin lymphoma, non-Hodgkin's

ournal List > Oncoscience > v.2(6); 2015 > PMC4506360

Oncoscience

<u>Oncoscience.</u> 2015; 2(6): 576–580. Published online 2015 Jun 30. doi: <u>10.18632/oncoscience.173</u> PMCID: PMC4506360 PMID: <u>26244164</u>

Challenges and perspective of drug repurposing strategies in early phase clinical trials

Shumei Kato,¹ Stacy L. Moulder,² Naoto T. Ueno,² Jennifer J. Wheler,¹ Funda Meric-Bernstam,¹ Razelle Kurzrock,³ and Filip Janku¹

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dosage required for the treatment of a novel disease usually differs from that of its original target disease - > discovery begins from Phase I

finding of new formulation and distribution mechanisms of existing drugs to the noveldisease-affected areas

patent right issues leverage and critically evaluate existing evidence and to investigate the efficacy/ effectiveness and safety of drug for potential repurposing

pre-clinical, clinical and observational research need to generate complementary information

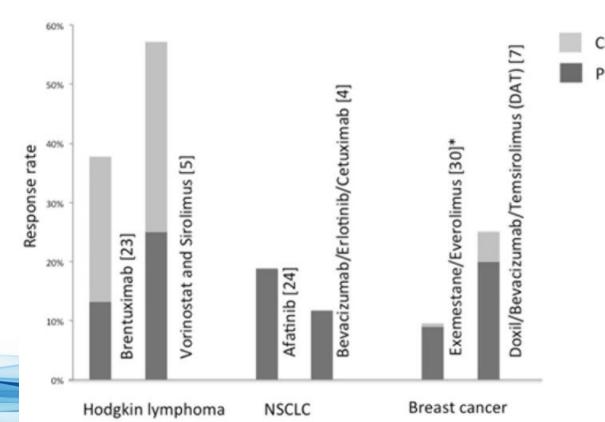
DD/DRR in oncology



Historically, the expected response rate in Phase I trials with unselected populations of patients has ranged from 4% to 11%.

However, with recent advances in targeted therapies and molecular matching, the response rates in Phase I trials have ranged from 19% to 77%, and some agents that demonstrated high response rates are now FDA approved.

Even in heavily pretreated patients, drug repurposing combination regimens have yielded response rates ranging 12% to 57%. Selected FDA approved targeted therapies and Phase I repurposing strategies from MDACC



Journal List > Oncoscience > v.2(6); 2015 > PMC4506360



<u>Oncoscience.</u> 2015; 2(6): 576–580. Published online 2015 Jun 30. doi: <u>10.18632/oncoscience.173</u> PMCID: PMC4506360 PMID: 26244164

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A Phase I clinical trial combining liposomal doxorubicin, bevacizumab, and temsirolimus (DAT) for patients with advanced cancers was designed to test the preclinical rationale that resistance to anthracyclines is driven through upregulation of hypoxia-inducible factor alpha (HIF-1 α), which promotes angiogenesis and tumor survival. Thus inhibiting angiogenesis, such as with the VEGF inhibitor bevacizumab, may overcome anthracycline resistance. However, resistance to bevacizumab is also driven by upregulation of HIF-1 α . Addition of temsirolimus, a potent inhibitor of mTOR and consequently HIF-1 α , can overcome this resistance.



Journal List > Oncoscience > v.2(6); 2015 > PMC4506360



PMCID: PMC4506360 PMID: <u>26244164</u>

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During the dose-escalation phase MD Anderson team noticed remarkable activity in several distinct tumor types, including **metaplastic breast cancer (MpBC)**.

Despite the aggressive nature of this cancer:

2 responses (1 complete [CR],1 partial response [PR]) in 5 patients with treatment-refractory MpBC.

In extended observation, objective responses in 5 of the 12 patients with MpBC (42%, 2 CR and 3 PR) and stable disease (SD) > 6 months in another 6 [50%].



Drug repurposing against breast cancer by integrating drug-exposure expression profiles and drug-drug links based on graph neural network

Chen Cui, Xiaoyu Ding, Dingyan Wang, Lifan Chen, Fu Xiao, Tingyang Xu, Mingyue Zheng ☎, Xiaomin Luo ☎, Hualiang Jiang, Kaixian Chen

Bioinformatics, btab191, https://doi.org/10.1093/bioinformatics/btab191

predict new drugs for breast cancer, outperforming previous state-of-the-art approaches and some classic machine learning methods

- graph neural network model GraphRepur based on GraphSAGE for drug repurposing against breast cancer
- integrated two major classes of computational methods, drug network-based and drug signature-based
- differentially expressed genes of disease, drug-exposure gene expression data and the drug–drug links information were collected -> extracting the drug signatures and topological structure information contained in the drug relationships

Review

Drug Repurposing for Triple-Negative Breast Cancer

Marta Ávalos-Moreno ^{1,†}, Araceli López-Tejada ^{1,2,†}, Jose L. Blaya-Cánovas ^{1,2}, Francisca E. Cara-Lupiañez ^{1,2}, Adrián González-González ^{1,2}, Jose A. Lorente ^{1,3}, Pedro Sánchez-Rovira ² and Sergio Granados-Principal ^{1,2,*}

novel and inclusive classification of DRR approaches whereby drug repurposing can be achieved in silico: structure-based, transcriptional signaturesbased, biological networksbased, and data-mining-based the most relevant research, both at preclinical and clinical settings, aimed at repurposing pre-existing drugs to treat TNBC on the basis of molecular mechanisms and signaling pathways such as androgen receptor, adrenergic receptor, STAT3, nitric oxide synthase, or AXL ability and relevance of cancer stem cells (CSCs) to drive tumor aggressiveness and

poor clinical outcome -> focus on those molecules repurposed to specifically target this cell population to tackle recurrence and metastases associated with the progression of TNBC

Analytical drug discovery tools

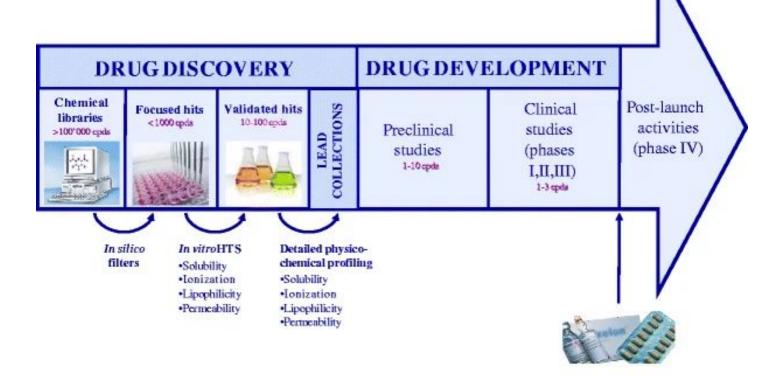
Based on deep learned transcriptomics-, proteomics-, blood biochemistry-based biomarkers of multiple diseases, predictors of alternative therapeutic uses of multiple drugs and analytical tools for high-throughput screening.

> The measurement of physicochemical properties at an early phase of drug discovery and development is crucial to reduce attrition rates due to poor biopharmaceutical properties., •lipophilicity •solubility •lonization •permeability mandatory to predict the pharmacokinetic behavior of NCEs.

> Due to the high number of NCEs, the analytical tools used to measure these properties are automated and progressively adapted to high-throughput technologies.

Henchoz, Y., Bard, B., Guillarme, D. et al. Analytical tools for the physicochemical profiling of drug candidates to predict absorption/distribution. Anal Bioanal Chem

Analytical drug discovery tools



Henchoz, Y., Bard, B., Guillarme, D. et al. Analytical tools for the physicochemical profiling of drug candidates to predict absorption/distribution. Anal Bioanal Chem LAUNCH

In silico + in vitro and in vivo

Trends in Pharmacological Sciences

Volume 40, Issue 8, August 2019, Pages 577-591



Review

Special Issue: Rise of Machines in Medicine

Artificial Intelligence for Clinical Trial Design

Stefan Harrer ¹ [∧] [⊠], Pratik Shah ², Bhavna Antony ¹, Jianying Hu ³

Suboptimal patient selection and recruiting techniques, paired with the inability to monitor and coach patients effectively during clinical trials, are two of the main causes for high trial failure rates.

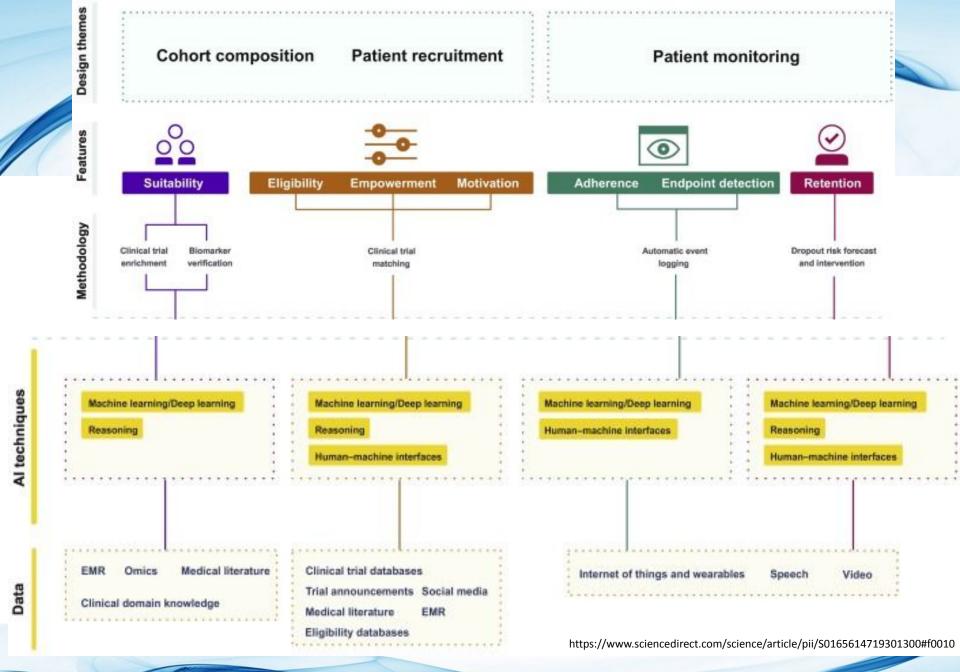
High failure rates of clinical trials contribute substantially to the inefficiency of the drug development cycle: that fewer new drugs reach the market despite increasing R&D investment.

Al techniques have advanced to a level of maturity that allows them to be employed under real-life conditions to assist human decisionmakers. Al has the potential to transform key steps of clinical trial design from study preparation to execution towards improving trial success rates, thus lowering the R&D burden.



Trends in Pharmacological Sciences







Therapies Volume 59, Issue 3, May–June 2004, Pages 297-304



PHARMACOLOGIE CLINIQUE Clinical Trial Simulation in Drug Development

Pascal Girard ¹ 은 쩓, Michel Cucherat ², David Guez ³ Participants in Round Table No. 2, Giens XIX

Utilizes massive amounts of data about the targets, diseases, clinical trials, and even scientists involved with the study at the preclinical and clinical stages.

Prospective validation is the best way to predict the outcomes of clinical trials.

A reduction in the number of failed clinical development projects, the number of negative phase II and III clinical trials, or in just their cost and duration, are among the expected benefits of modelling and simulation in clinical drug development.

https://www.sciencedirect.com/science/article/pii/S0165614719301300#f0010

nature > scientific reports > articles > article

Article Open Access Published: 10 December 2019

Virtual clinical trials identify effective combination therapies in ovarian cancer

Emilia Kozłowska, Tuulia Vallius, Johanna Hynninen, Sakari Hietanen, Anniina Färkkilä 🗠 & Sampsa Hautaniemi 🖂

Scientific Reports 9, Article number: 18678 (2019) Cite this article

https://www.sciencedirect.com/science/article/pii/S0165614719301300#f0010



European Journal of Cancer Volume 85, November 2017, Pages 78-85



Original Research

Clinical trial simulations in paediatric oncology: A feasibility study from the Innovative Therapies for Children with Cancer Consortium

Optimizing drug development in oncology by clinical trial simulation: Why and how? 🚥

Jocelyn Gal ➡, Gérard Milano, Jean-Marc Ferrero, Esma Saâda-Bouzid, Julien Viotti, Sylvie Chabaud, Paul Gougis, Christophe Le Tourneau, Renaud Schiappa, Agnes Paquet ... Show more

This in silico medicine opens the way to the P4 medicine: predictive, preventive, personalized and participatory.

Drug activity modeling coupled with disease modeling, optimal use of medical data and increased computing speed should allow leap forward.

The realization of CTS requires not only bioinformatics tools to allow interconnection and global integration of all clinical data but also a universal legal framework to protect the privacy of every patient.

Simulation Modeling of Cancer Clinical Trials: Application to Omitting Radiotherapy in Lowrisk Breast Cancer @

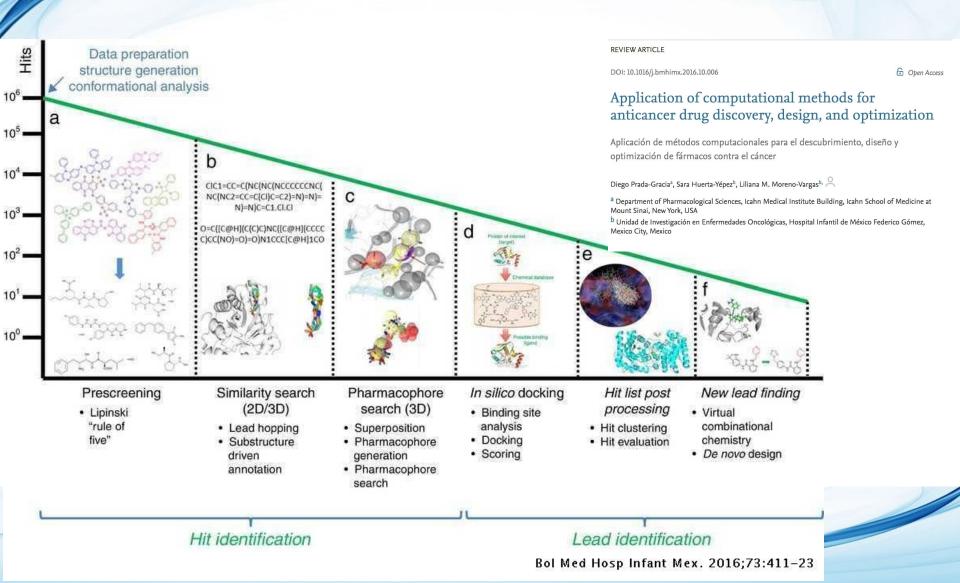
Jinani Jayasekera ⊠, Yisheng Li, Clyde B Schechter, Reshma Jagsi, Juhee Song, Julia White, George Luta, Judith-Anne W Chapman, Eric J Feuer, Richard C Zellars ... Show more

Author Notes

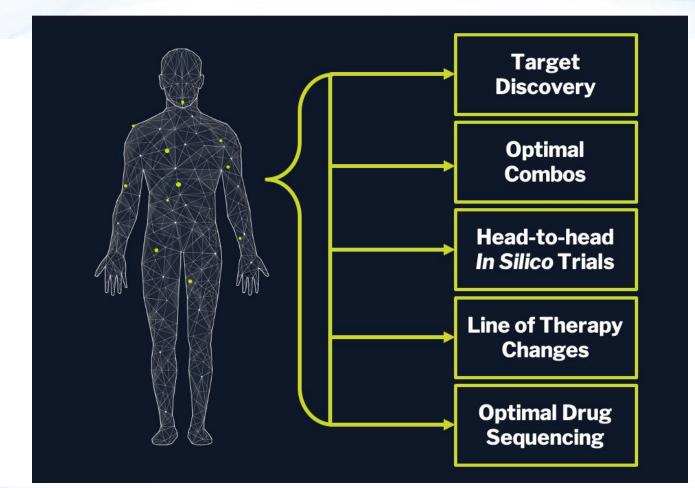
JNCI: Journal of the National Cancer Institute, Volume 110, Issue 12, December

A paradigm shift is necessary to bring the benefits of CTS-based drug development to cancer patients, in which biomarkers and prognostic markers of OS are assessed to predict treatment outcome and disease progression.

Future?



Future?



https://www.gnshealthcare.com/gemini-in-silico-patient/



Thank you

Never tire to study and to teach others.



学而不厌 诲人不倦

