



TSINGHUA PBCSF
清华五道口

NIFR
国家金融研究院





TSINGHUA PBCSF
清华五道口

NIFR
国家金融研究院



.....	1
.....	1
.....	3
.....	4
.....	5
.....	5
.....	6
.....	8
.....	9
.....	10
.....	15
.....	16
.....	17
.....	18
.....	19
.....	20
.....	22
.....	22
.....	22
.....	23
.....	25
.....	32
.....	33
.....	34

1-1			2
1-2			4
2-1		!	
2-2		!	
2-3		!	
2-4			8
2-5			9
2-6	AI	ML	10
2-7	AI	ML	14
2-8			16
2-9			17
2-10			18
2-11			19
2-12			20
2-13			21
3-1			23
2-1	AI	ML	11
2-2	AI	ML	14
2-3	AI	ML	21
3-1			26
3-2		AI	29
3-3	AI		31

ADMET

AI +

AI +

AI

Artificial Intelligence AI

“ ”

Machine Learning ML

“AI ”

“AI ” ML

Decision Tree DT

Hidden Markov Model

HMM

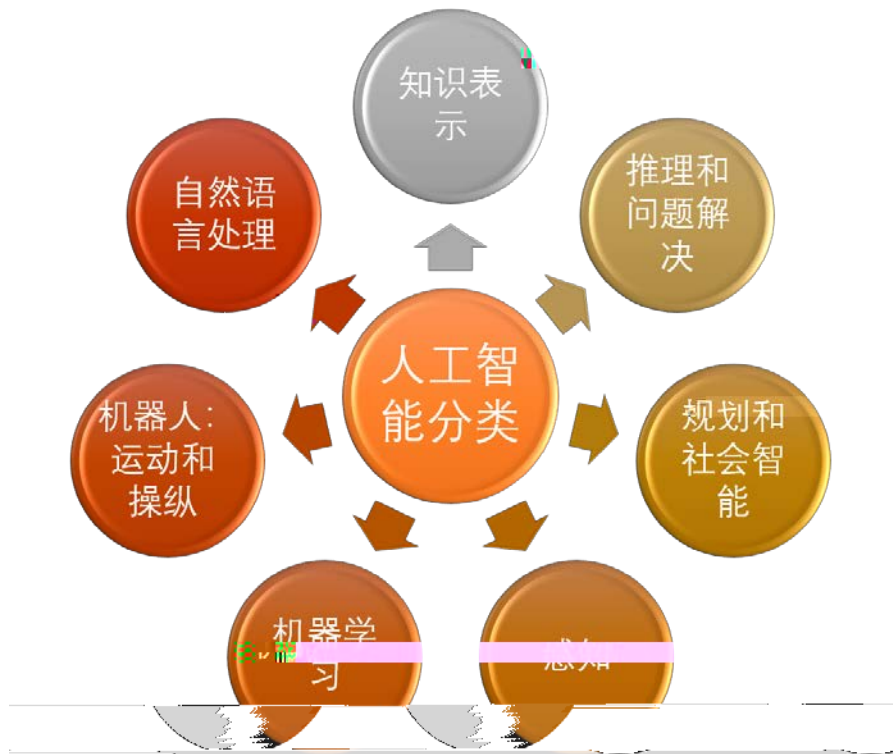
20

Igor Aizenberg

Artificial Neural Network ANN

“

Deep Learning DL ”



1-1

Ribonucleic Acid Sequencing RNA-seq
High-Throughput Sequencing HTS

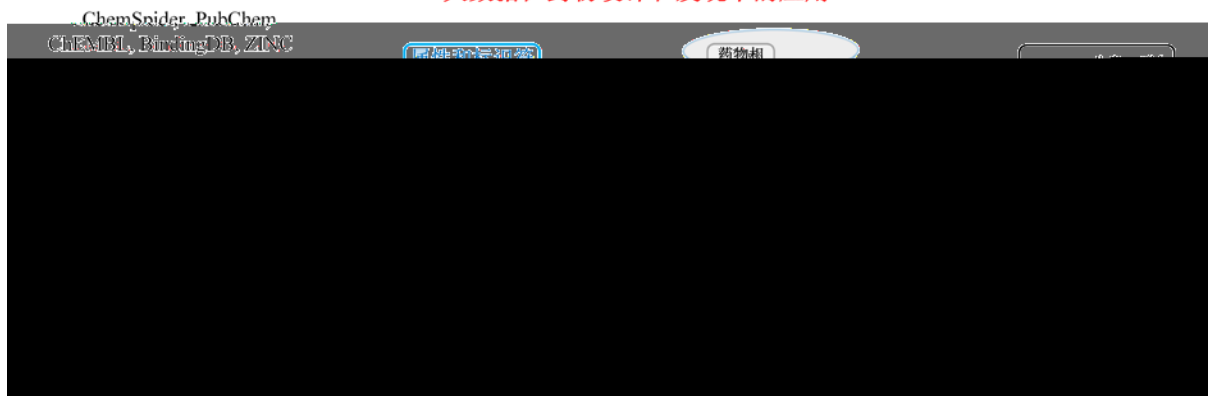
1-2

National Center
for Biotechnology Information NCBI
Gene
Expression Omnibus GEO
The Cancer
Genome Atlas TCGA
Arrayexpress
PubMed

ML

Han [1]

2019 DriverML ML



1-2

PubChem

ChEMBL

Absorption,

Distribution, Metabolism and Excretion ADME

DrugBank

LINCS L1000 PDB

Computer Aided Drug Design CADD

ML DL

Quantitative Structure Activity

Relationship QSAR

ML

2-1



2-1

2 50

2-2

Yan [2] 2020 DL Antimicrobial peptides AMPs Deep-AmPEP30 AmPEP30

Convolutional Neural Network, CNN

DeoxyriboNucleic Acid DNA

AMP

—

AMPs

Zhavoronkov [3]

GENTRL

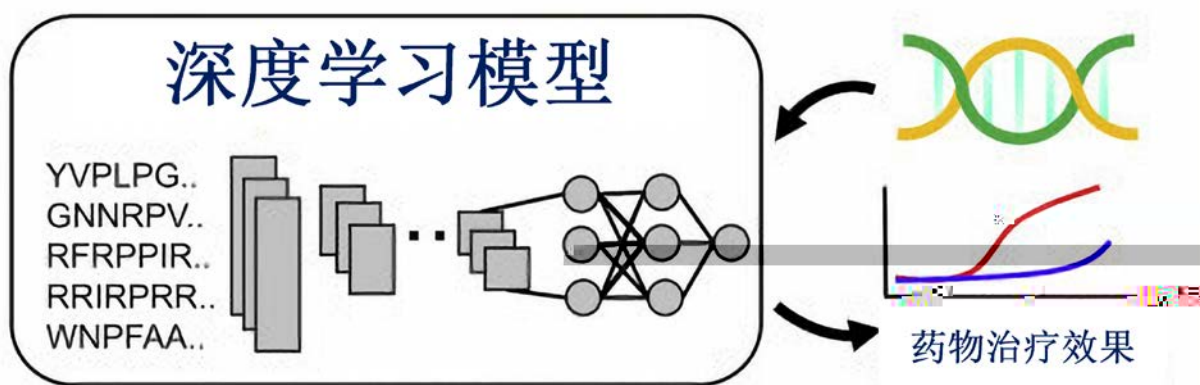
<https://github.com/insilicomedicine/GENTRL>

DDR1 McCloskey [4] DNA

DNA-Encoded small molecule Libraries DEL

ML

Xing [5] XGBoost



2-3

DisGeNET

STRTCH

STRING

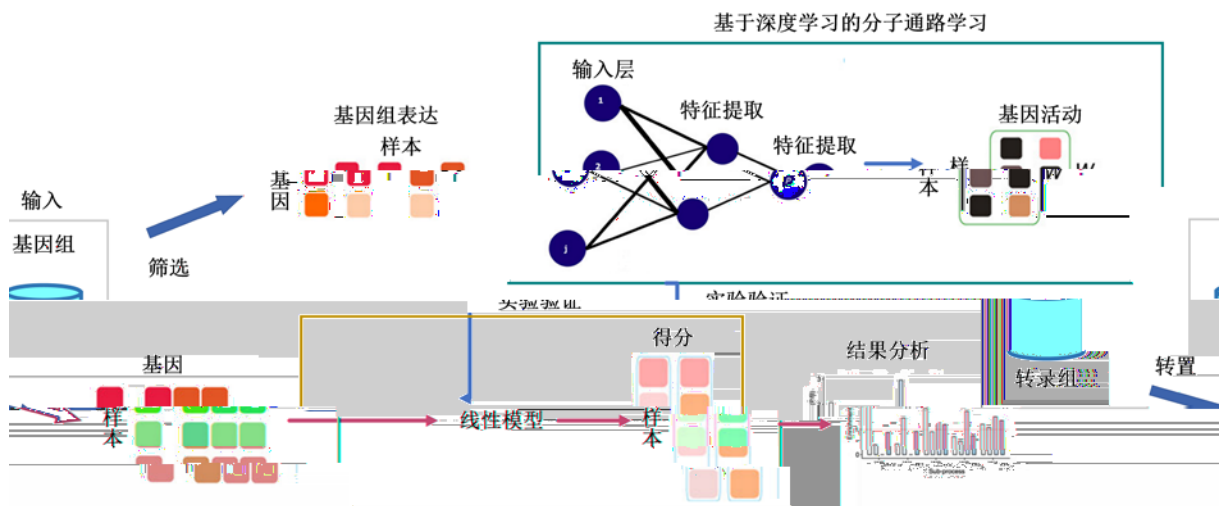
Gu

[6]

2020

197

DisGeNET



2-3

Neurodegenerative Diseases

NDDS

ML

ML

Protein-

Virtual Screening VS

CADD

ML VS

ML

VS

VS

基于配体的虚拟筛选

基于结构的虚拟筛选



2-5

VS

2-5

VS

Structural Based Virtual Screening SBVS

VS

Ligand Based Virtual Screening LBVS

AI ML

COVID-19

2 SARS-CoV-2

COVID-19

COVID-19

AI ML COVID-19

2-6 2-

1

2-1		AI	ML
AI	ML	SARS-CoV-2	
[13]		https://github.com/Murali-group/SARS-CoV-2-network-analysis	

[14]5 Yi ”QC04x0X’ÒØ ’9ÓQ À†



[22]

https://github.com/uhrerlab/covid19_repurposing

FDA

SARS-CoV-2

[29] Zhu [21]

AI

InfinityPhenotype

FDA

Liquiritin I

COVID-19

[30]

AI ML

Nguyen

[24] MathPose

MathDL

SARS-CoV-2 3CL

MathPose

MathDL

COVID-19 15

AI ML [31–33]

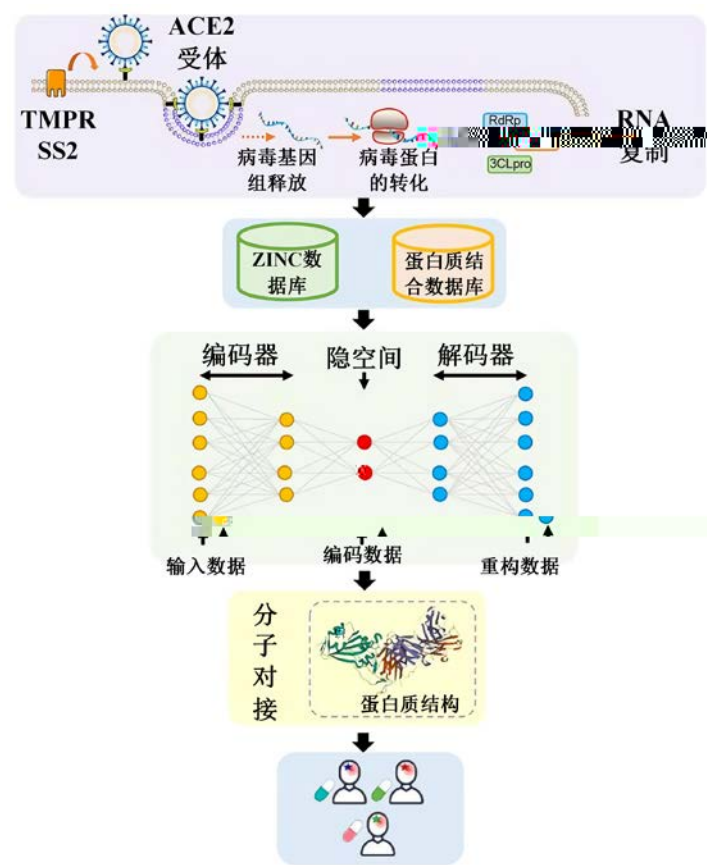
2-7

2-2

[34] Zhavoronkov [35]

COVID-19

COVID-19



2-7 AI ML

2-2 AI ML

AI ML		
[35]		
Q [37]		https://github.com/tbwxmu/2019-nCov

[38]		
[39]	SMILES	
[40]		
[41]		https://github.com/pkuwangsw/COVIDVS
[36]		

Quantitative Structure-
Activity Relationship QSAR

QSAR

Gaussian Process GPs

Vega

(<https://www.vega-qsar.eu/>) QSAR-Co^[42] Transformer-CNN^[43]

Chemception (<https://github.com/Abdulk084/Chemception>) QSAR

C

L qsw. Á >-i£ \$ %ođaE4A3Dj <0431BE6>-8 4 Td/M

Hooshmand [45]

16 HCoV

12



2-8

2-9

Web LimTox pkCSM admetSAR

Toxtree DeepTox^[46] PrOCTOR^[47]

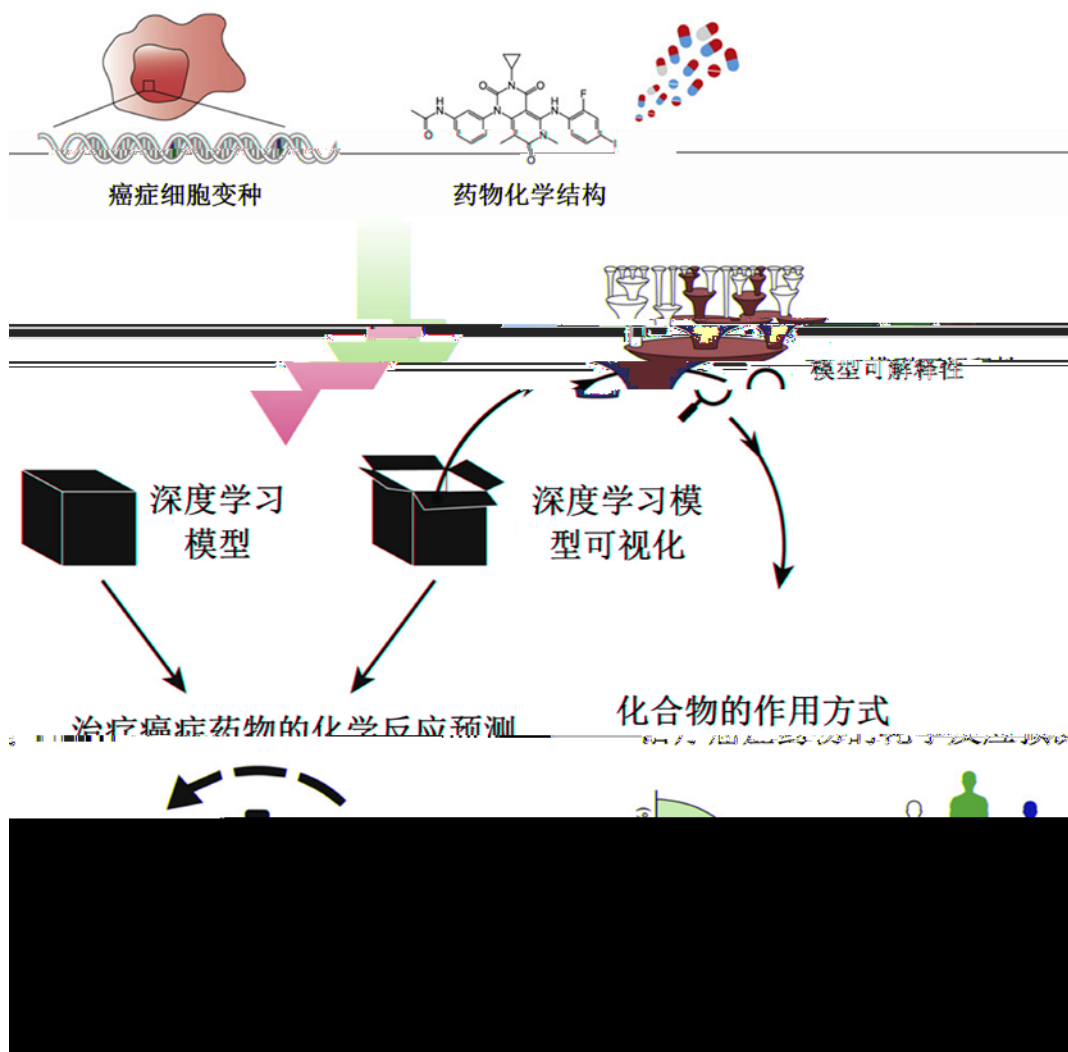
Robledo-Cadena [48]

PrOCTOR

2,576

16

2



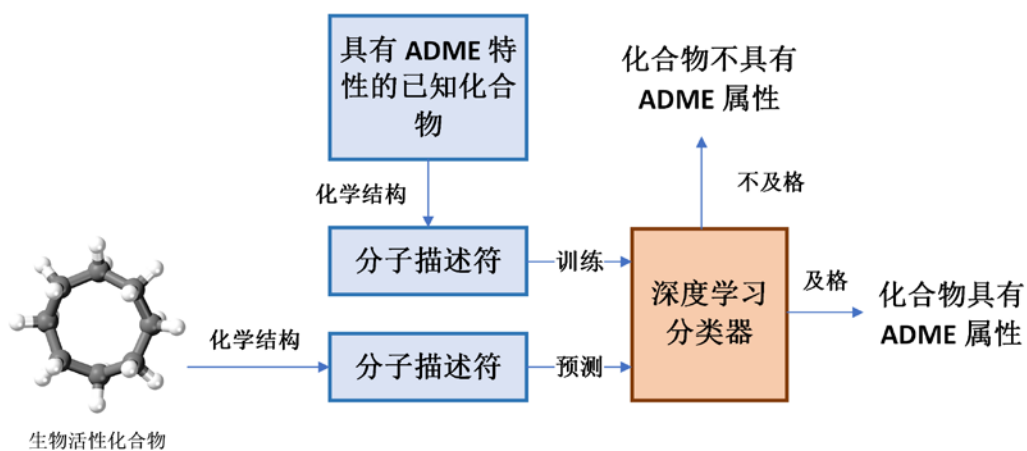
2-9

2-10

SMILES

Coulomb matrices

Deep Neural Networks DNN



2-10

ChemMapper

ML DL

[49]

KronRLS SimBoost DeepDTA Padme

ML

DL

2-11

Shen

[50]

AI-PRS

AI-PRS

Parabolic

Response Curve PRC

10 HIV

AI-PRS 33%

Tang [51]

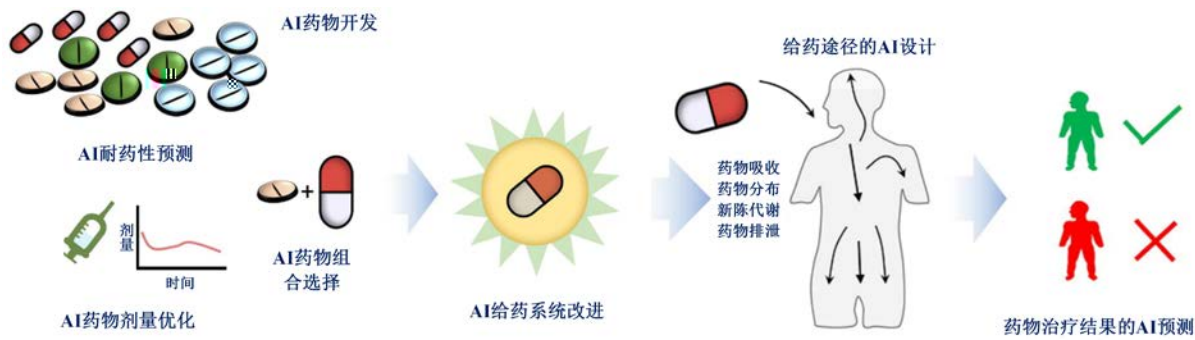
ML

Hu [52]

K ML

Digoxin Imai [53]

Vancomycin



2-11

2-12

CATALYST

Wu

DL

RF

WDL-RF

<https://zhanglab.ccmb.med.umich.edu/WDL-RF/>

G

G Protein-Coupled Receptors

GPCRs

Cichonska

[54]

pairwiseMKL

<https://github.com/aalto-ics-kepaco>

[55]



2-12

2-13

2-3

COVID-19

[56]

Fast

[57]

MARIA

NetMHCpan4

SARS-CoV-2

T

B

405

T

MHC-I

MHC-II

S B

COVID-19

2-3 AI ML

AI ML		
[57]	SARS-CoV-2 T	
XGBoost[58]	B	
[59]	SARS-CoV-2 HLA	
[60]		https://github.com/zikunyang/DCVST

2-13

Prachar [59] 174

SARS-CoV-2 11 HLA

SARS-

CoV-2 HLA

SARS-CoV-2

COVID-19 Yang [60]

DeepVacPred

DeepVacPred		694aa		16	B
82	CTL	89	HTL	SARS-CoV-2	RNA



3

Graphic Processing Unit GPU

Tensor Processing Unit TPU

Central

Processing Unit CPU GPU

Field Programmable Gate Array FPGA

AI/ML

2014

Generative Adversarial Networks GANs

2014

2015

AI

AI

Exscientia

Insilico Medicine

AI

AI

Benevolent AI				Baricitinib
Exscientia				Exscientia AI

Atomwise				
Recursion				NME 2019 Recursion Takeda 60 6
Insilico Medicine				7 IND-enabling COVID-19 3CL MAT2A USP1 “ ” 0 1
				rCARD GPU NVIDIA Clara Discovery Pipeline GROMACS Autodock-GPU
				AI AI

				PandaOmics Chemistry42
				“ ”
				AI
				AI

AI

2019

AI

Benevolent AI

Atomwise Recursion

3-2AI

3-2		AI			
Benevolent AI	2019	9	17	- BenevolentAI 9000	
	2018	4	19	- BenevolentAI 1.15	
	2015	8	26	- BenevolentAI 8700	
Exscientia	Exscientia	9		4.744	
		2022	1 10	IPO	
	2022	1	10	IPO - 1.534bD\ >8700	
		2022	1	s 10 -	



			2			2021	2
	19		SciClone Pharmaceuticals		1.34		
	2021	2	19		- SciClone Pharmaceuticals		1.34
	2016	12	21		-Healenvoy		300
			1		2000		
	2020	7	9				
	2020	7	9		2000		
	2018	7	3				
	SIG						
	2020	3	16		1000		A
	2021	08			4		D
					IMO Ventures		
					Neumann Capital		Artisan Partners
					Artisan Partners		
						2020	9
			3.188		C		
	2						
	Mirae Asset						
					IMO Ventures		Parkway
							SIG
	2021	10	20				
	2022	06	22		A		5

2000

3-3

3-3 AI

	AI DrugSpaceX ModelArts		
	80%		
	CPCR CPCR		
	DNA 2021 10 MindSpore		

	AlphaFold2		
	2 3		
	1.5		
	2019		
	11 FDA		

Artificial Intelligence AI

Artificial Neural Network ANN

Computer Aided Drug Design CADD

,

Convolutional Neural Network CNN

Deep Learning DL

Machine Learning ML

Protein-Protein Interaction, PPI

Quantitative Structure-Activity Relationship

QSAR

- [1] Han Y , Yang J , Qian X , et al. DriverML: a machine learning algorithm for identifying driver genes in cancer sequencing studies[J]. Nuclc Acids Research, 2019(8):e45-e45.
- [2] Yan J , Bhadra P , Li A , et al. Deep-AmPEP30: Improve Short Antimicrobial Peptides Prediction with Deep Learning[J]. Molecular Therapy - Nucleic Acids, 2020.
- [3] Zagribeln Yy B A , Zhavoronkov A , Aliper A , et al. Deep learning enables rapid identification of potent DDR1 kinase inhibitors[J]. Nature Biotechnology, 2019, 37(9):1038-1040.

- [4] Mccloskey K , Sigel E A , Kearnes S , et al. Machine learning on DNA-encoded libraries: A new paradigm for hit-finding[J]. arXiv, 2020.
- [5] Xing G , Liang L , Deng C , et al. Activity Prediction of Small Molecule Inhibitors for Antirheumatoid Arthritis Targets Based on Artificial Intelligence[J]. ACS Combinatorial Science, 2020, 22(12): 873–886.
- [6] Gu S , Lai L H . Associating 197 Chinese herbal medicine with drug targets and diseases using the similarity ensemble approach[J]. Acta Pharmacologica Sinica, 2019, 41(3): 7.
- [7] Zhu-Hong, You, Ying-Ke, et al. Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis[J]. BMC Bioinformatics, 2013, 14(10): S10.
- [8] Serafim, Mateus Sa Magalhaes, et al. The application of machine learning techniques to innovative antibacterial discovery and development. [J]. Expert opinion on drug discovery, England: 2020, 15(10): 1165 – 1180.
- [9] Zoete V , Daina A , Bovigny C , et al. SwissSimilarity: A Web Tool for Low to Ultra High Throughput Ligand-Based Virtual Screening[J]. Journal of Chemical Information & Modeling, 2016:1399 – 1404.
- [10] Imbernon B , JM Cecilia, Perez-Sanchez H , et al. METADOCK: A parallel metaheuristic schema for virtual screening methods[J]. Experimental Mechanics, 2018, 32(6):789-803.
- [11] Hongjian L , Kwong-S. L , Man-H. W , et al. USR-VS: a web server for large-scale prospective virtual screening using ultrafast shape recognition techniques[J]. Nucleic Acids Research, 2016(W1):W436-W441.
- [12] Pablo A J , Modenutti C P , Demian A , et al. AutoDock Bias: improving binding mode prediction and virtual screening using known protein-ligand interactions[J]. Bioinformatics, 2019, 35(19): 3836 – 3838.

- [13] Law J N , N Tasnina, Kshirsagar M , et al. Identifying human interactors of SARS-CoV-2 proteins and drug targets for COVID-19 using network-based label propagation[J]. arXiv preprint arXiv:2006.01968, 2020.
- [14] Zhang, Haiping, et al. Deep Learning Based Drug Screening for Novel Coronavirus 2019-nCov.[J]. Interdisciplinary sciences, computational life sciences, 2020, 12(3): 368 – 376.
- [15] Bo R B , Shin B , Choi Y , et al. Predicting commercially available antiviral drugs that may act on the novel coronavirus (2019-nCoV), Wuhan, China through a drug-target interaction deep learning model[J]. Computational and Structural Biotechnology Journal, 2020, 18:784-790.
- [16] Majumdar S , Nandi S K , Ghosal S , et al. Deep Learning-Based Potential Ligand Prediction Framework for COVID-19 with Drug–Target Interaction Model[J]. Cognitive Computation, 2021(4): 1 – 13.
- [17] Zeng X , Song X , Ma T , et al. Repurpose Open Data to Discover Therapeutics for COVID-19 using Deep Learning[J]. Journal of Proteome Research, 2020, 19(11): 4624 – 4636.
- [18] Hsieh K L , Wang Y , Chen L , et al. Drug Repurposing for COVID-19

- [21] Zhu J , Deng Y Q , Wang X , et al. An artificial intelligence system reveals liquiritin inhibits SARS-CoV-2 by mimicking type I interferon. 2020.
- [22] Belyaeva A , Cammarata L , Radhakrishnan A , et al. Causal network models of SARS-CoV-2 expression and aging to identify candidates for drug repurposing[J]. Nature Communications, 2021, 12(1): 1024.
- [23] Pham, Thai-Hoang, et al. A deep learning framework for high-throughput mechanism-driven phenotype compound screening and its application to COVID-19 drug repurposing[J]. Nature machine intelligence, 2021, 3(3): 247 – 257.
- [24] Nguyen D D , Gao K , Chen J , et al. Potentially highly potent drugs for 2019-nCoV[J]. bioRxiv, Cold Spring Harbor Laboratory, 2020.
- [25] Karki N K , Verma N , Trozzi F , et al. Predicting Potential SARS-COV-2 Drugs - In Depth Drug Database Screening Using Deep Neural Network Framework SSnet, Classical Virtual Screening and Docking. 2020, 22(4).
- [26] Mohapatra S , Nath P , Chatterjee M , et al. Repurposing therapeutics for COVID-19: Rapid prediction of commercially available drugs through machine learning and docking[J]. PLoS ONE, 2020, 15(11):e0241543.
- [27] Liu L , Zhang L R , Dao F Y , et al. A computational framework for identifying the transcription factors involved in enhancer-promoter loop formation.[J]. Molecular therapy. Nucleic acids, 2021, 23: 347 – 354.
- [28] Liu L , Li Q Z , Jin W , et al. Revealing Gene Function and Transcription Relationship by Reconstructing Gene-Level Chromatin Interaction.[J]. Computational and structural biotechnology journal, 2019, 17: 195 – 205.
- [29] Killick R, Ballard C, Doherty P, et al. Transcription-based drug repurposing for COVID-19.[J]. Virus research, 2020, 290: 198176.
- [30] Zulfiqar H , Masoud M S , Yang H , et al. Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through

Molecular Docking Approach[J]. Computational and Mathematical Methods in Medicine, 2021, 2021(1):1-9.

[31] Hasan, Md Mehedi, et al. NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning.[J]. Briefings in bioinformatics, England: 2021, 22(6).

[32] Charoenkwan P , Nantasenamat C , Hasan M M , et al. BERT4Bitter: a bidirectional encoder representations from transformers (BERT)-based model for improving the prediction of bitter peptides[J]. Bioinformatics, 2021.

[33] Phasit C , Wararat C , Chanin N , et al. StackIL6: a stacking ensemble model for improving the prediction of IL-6 inducing peptides[J]. Briefings in Bioinformatics, 2021(6):6.

[34] Xu B , Liu D , Wang Z , et al. Multi-substrate selectivity based on key loops and non-homologous domains: new insight into ALKBH family[J]. Cellular and molecular life sciences : CMLS, 78(1):129-141.

[35] Zhavoronkov A , Aladinskiy V A , Zhebrak A , et al. Potential 2019-nCoV 3C-like protease inhibitors designed using generative deep learning approaches[J]. 2020.

[36] Srinivasan S , Batra R , Chan H , et al. Artificial Intelligence-Guided De Novo Molecular Design Targeting COVID-19[J]. ACS Omega, 2021, 6(19):12557-12566.

[37] Tang B , He F , Liu D , et al. AI-aided design of novel targeted covalent inhibitors against SARS-CoV-2[J]. BioRxiv, Cold Spring Harbor Laboratory, 2020.

[38] Ton A T , Gentile F , Hsing M , et al. Rapid Identification of Potential Inhibitors of SARS-CoV-2 Main Protease by Deep Docking of 1.3 Billion Compounds.[J]. Molecular informatics, 2020, 39(8): e2000028.

- [39] Chenthamarakshan V , Das P , Hoffman S C , et al. Cogmol: target-specific and selective drug design for COVID-19 using deep generative models[J]. arXiv preprint arXiv:2004.01215, 2020.
- [40] Bung N , Krishnan S R , Bulusu G , et al. De novo design of new chemical entities for SARS-CoV-2 using artificial intelligence[J]. Future Medicinal Chemistry, 2021(2): 575 – 585.
- [41] Wang S , Sun Q , Xu Y , et al. A transferable deep learning approach to fast screen potential antiviral drugs against SARS-CoV-2[J]. Briefings in bioinformatics, Oxford University Press, 2021.
- [42] Ambure P , Halder A K , H González-Díaz, et al. QSAR-Co: An Open Source Software for Developing Robust Multi-tasking or Multi-target Classification-Based QSAR Models[J]. Journal of Chemical Information and Modeling, 2019, 59(6): 2538 – 2544.
- [43] Karpov P , Godin G , Tetko I V . Transformer-CNN: Swiss knife for QSAR modeling and interpretation[J]. Journal of Cheminformatics, 2020, 12(1): 17.
- [44] Luo H , Li M , Wang S , et al. Computational Drug Repositioning using Low-Rank Matrix Approximation and Randomized Algorithms[J]. Bioinformatics(11): 1904 – 1912.
- [45] Hooshmand S A , · Mohadeseh, Ghobadi Z , et al. A multimodal deep learning-based drug repurposing approach for treatment of COVID-19[J]. Molecular Diversity, 2020:3: 1717 – 1730.
- [46] Mayr, Andreas, et al. DeepTox: toxicity prediction using deep learning[J]. Frontiers in Environmental Science, Frontiers, 2016, 3: 80.
- [47] Kaitlyn M, Gayvert, Neel S, et al. A Data-Driven Approach to Predicting Successes and Failures of Clinical Trials[J]. Cell Chemical Biology, 2016, 23(10): 1294–1301.

- [48] Gilvary C , Elkhader J , Madhukar N , et al. A machine learning and network framework to discover new indications for small molecules[J]. PLoS Computational Biology, 2020, 16(8):e1008098.
- [49] Zelik R , H Ztürk, A Zgür, et al. ChemBoost: A Chemical Language Based Approach for Protein – Ligand Binding Affinity Prediction[J]. Molecular Informatics, 2020, 40(5): 2000212.
- [50] Harnessing Artificial Intelligence to Optimize Long - Term Maintenance Dosing for Antiretroviral - Naive Adults with HIV - 1 Infection[J]. Advanced Therapeutics, 2020, 3(4): 1900114.
- [51] Tang J , Liu R , Zhang Y L , et al. Application of Machine-Learning Models to Predict Tacrolimus Stable Dose in Renal Transplant Recipients[J]. Scientific Reports, 2017, 7:42192.
- [52] Hu YH, Tai CT, Tsai CF, Huang MW. Improvement of Adequate Digoxin Dosage: An Application of Machine Learning Approach.[J]. Journal of healthcare engineering, 2018, 2018: 3948245.
- [53] Imai S , Takekuma Y , Miyai T , et al. A New Algorithm Optimized for Initial Dose Settings of Vancomycin Using Machine Learning[J]. Biological & Pharmaceutical Bulletin, 2020, 43(1):188-193.
- [54] Jiansheng W, Qiuming Z , Weijian W , et al. WDL-RF: predicting bioactivities of ligand molecules acting with G protein-coupled receptors by combining weighted deep learning and random forest[J]. Bioinformatics, 2018, 2(13):13.
- [55] Cichonska, Anna, et al. Learning with multiple pairwise kernels for drug bioactivity prediction. [J]. Bioinformatics, 2018, 34(13): i509 – i518.
- [56] Wang J , Wang H , Wang X , et al. Predicting Drug-target Interactions via FM-DNN Learning[J]. Current Bioinformatics, 2020, 15(1): 68 – 76.

[57] Fast E, Chen B. Potential T-cell and B-cell epitopes of 2019-nCoV[J]. BioRxiv, Cold Spring Harbor Laboratory, 2020.

[58] Ong E , Mei U W , Huffman A , et al. COVID-19 coronavirus vaccine design using reverse vaccinology and machine learning. 2020, 11: 1581.

[59] Prachar M , Justesen S , Steen-Jensen D B , et al. Identification and validation of 174 COVID-19 vaccine candidate epitopes reveals low performance of common epitope prediction tools[J]. Scientific Reports, 2020, 10(1): 20465.

[60] Yang Z , Bogdan P , Nazarian S . An in silico deep learning approach to multi-epitope vaccine design: a SARS-CoV-2 case study[J]. Scientific Reports, 2021, 11(1): 3238.



TSINGHUA PBCSF
清华五道口

NIFR
国家金融研究院

zhuysh@pbcfs.tsinghua.edu.cn

0 1

“ ”

/

“ ”

1

2

/

3

/

4

/

Exscientia

Atomwise Recursion Insilico Medicine

“ ”