

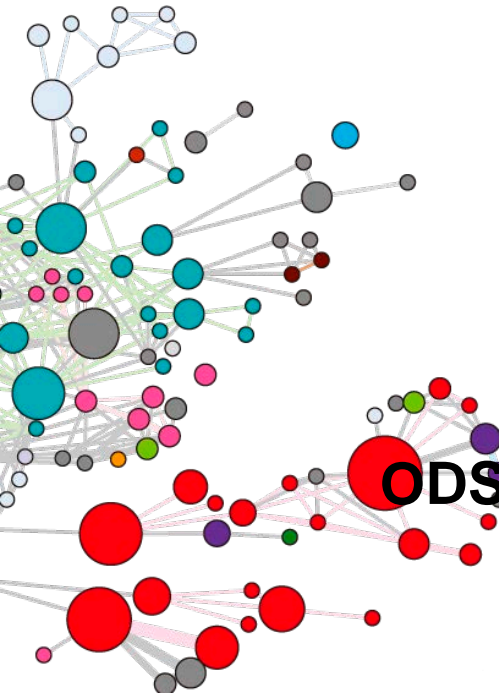


# Using Artificial Intelligence for Alzheimer's Disease Drug Repurposing

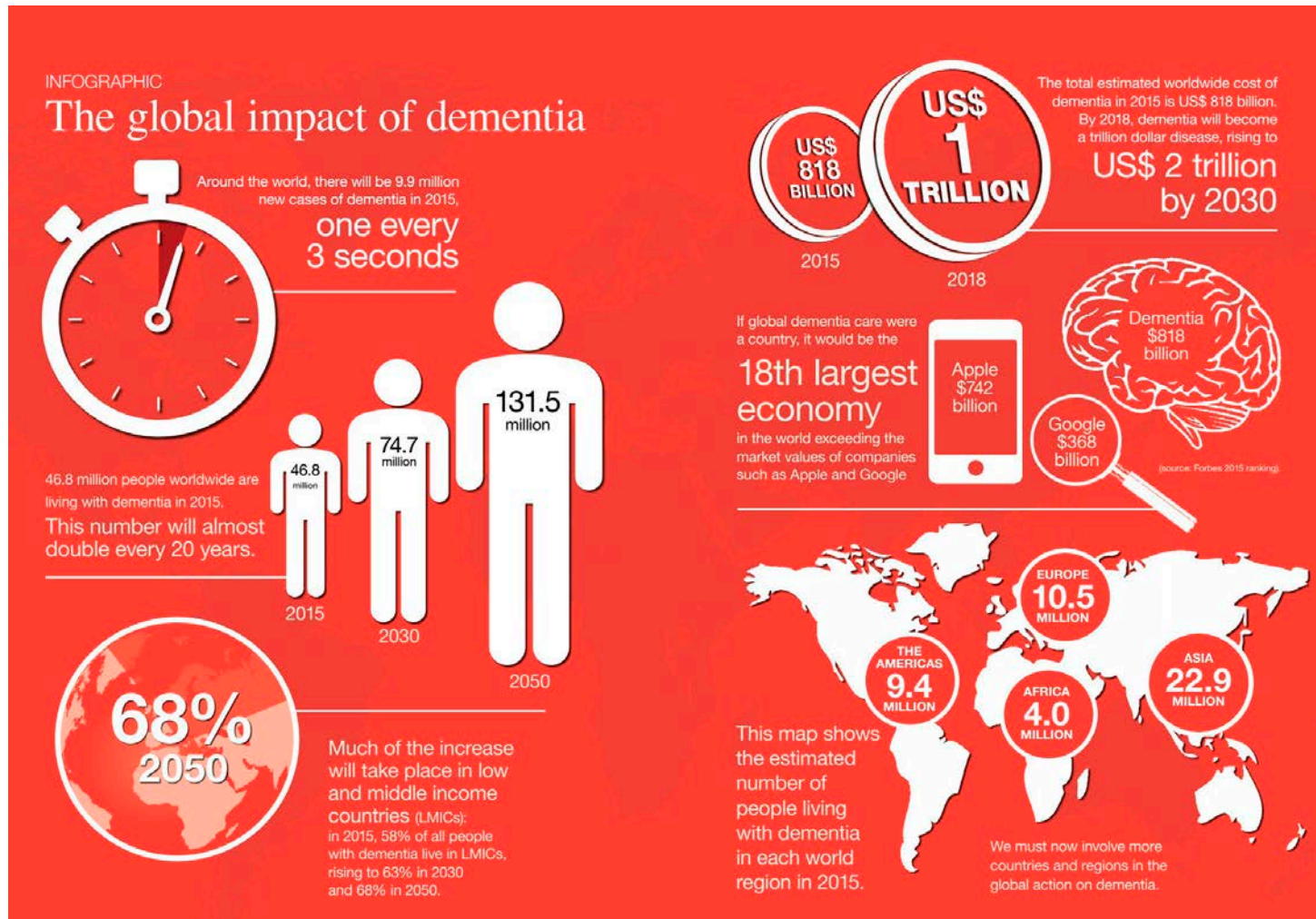
**3 R01 AG066707-02S1**

**Feixiong Cheng, PhD**  
Assistant Professor

**ODSS AI Supplements Closeout Meeting**  
**Room 1, October 31, 2022**

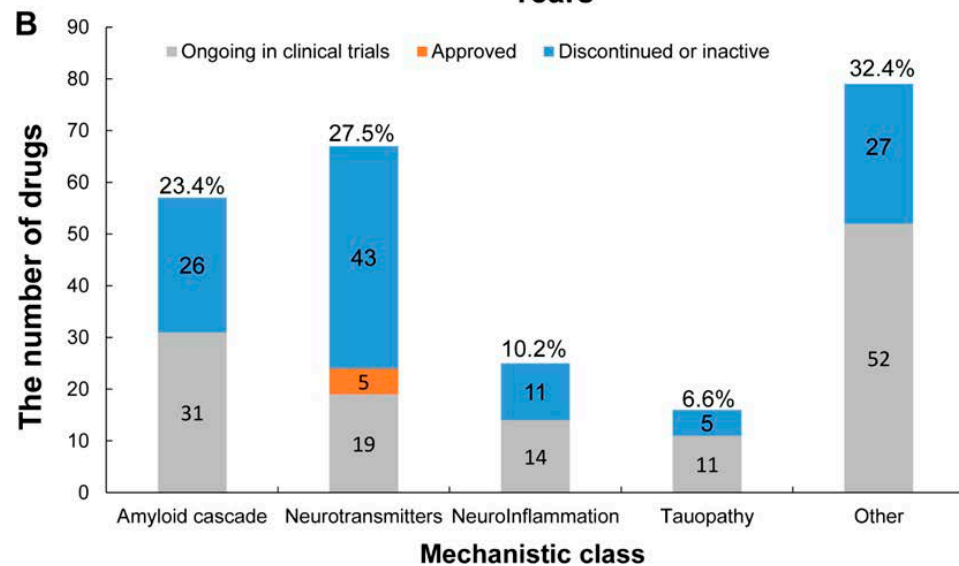
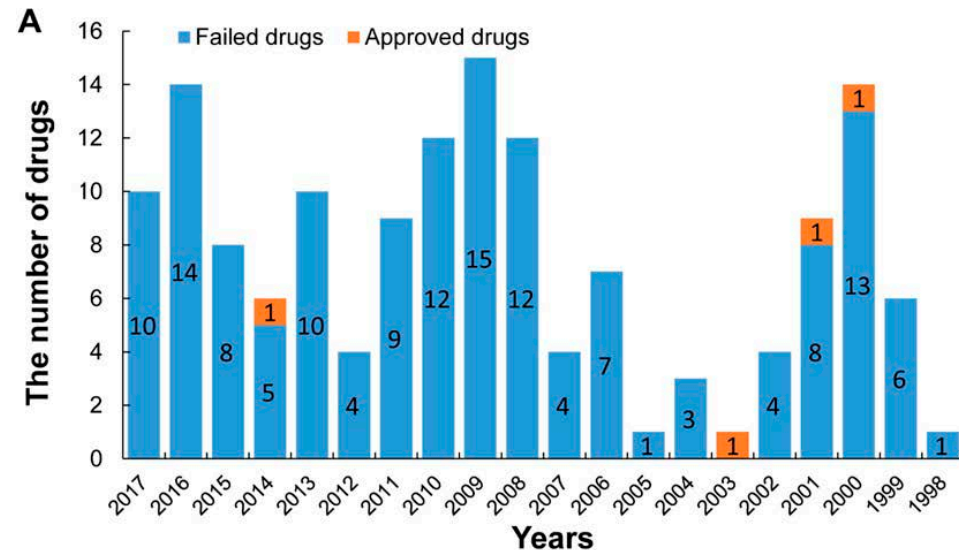


# Alzheimer's Disease



**46.8 million patients in 2015; 16 million patients in U.S. (2050)**

# Emerging Challenges in Alzheimer's Drug Discovery



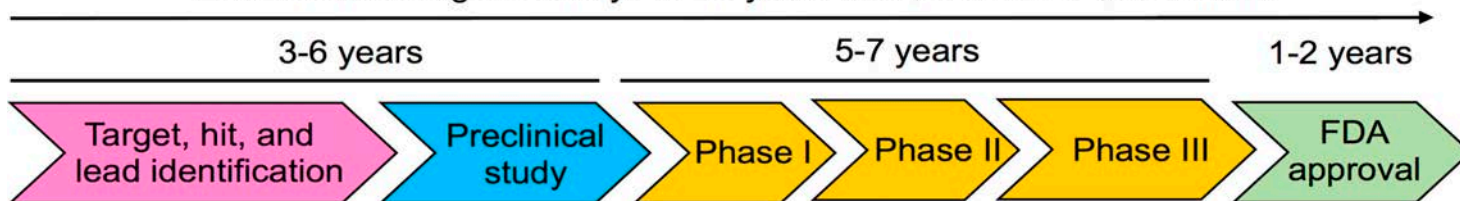
The **attrition rate** for AD clinical trials (2002-2012) is estimated at **99.6%**. Currently **5** available drugs approved by the U.S. Food and Drug Administration (FDA) to alleviate its **symptoms**.

**Aducanumab (June/2021)**  
**Anti-amyloid antibody**  
**(controversial approval)**



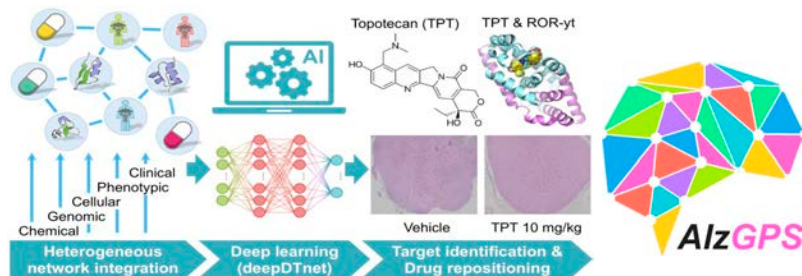
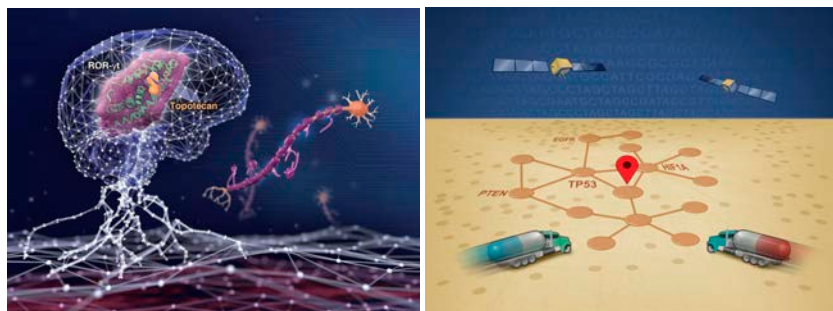
# Drug Repurposing/Repositioning

First-in-class drug discovery: 12-15 years and \$1 billion to \$2.6 billions



Cheng F, *Methods Mol Biol* 2019

Drug repurposing or repositioning:  
3-6 years with ~\$300 million



*Cell Metabolism* 2015; *J Med Chem* 2017; *Oncogene* 2017; *JCI Insights* 2018; *Cancer Res* 2018; *Cell Chemical Biology* 2019; *Chemical Science* 2020 (Cover); *Bioinformatics* 2019 2020 and 2021; *Nature Genetics* 2021; *Cell* 2021; *PLOS Medicine* 2021; *STTT* 2021; *Aging Cell* 2022

*Nature Commun* 2018; 2019a; 2019b, *Pharmacological Reviews* 2020 (Cover); *Cell Discovery* 2020; *JPR* 2020a and 2020b (Cover), *BMC Medicine* 2020; *Lancet Digital Health* 2020 (Cover); *PLOS Biology* 2020; *Genome Biology* 2021; **Genome Research 2021**; **Alzheimer's Research & Therapy 2021a, 2021b, and 2022**; *Nature Aging* 2021; *Nature Biotechnology* 2022, *Cell Reports Medicine* 2022, *Nature Machine Intelligence* 2022

# Challenge to translate genetic (GWAS) and WGS findings for drug target discovery

ARTICLES

<https://doi.org/10.1038/s41588-019-0358-2>

nature  
genetics

Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A $\beta$ , tau, immunity and lipid processing

nature  
genetics

ARTICLES

<https://doi.org/10.1038/s41588-018-0311-9>

Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk

nature  
genetics

ANALYSIS

<https://doi.org/10.1038/s41588-020-00776-w>

Check for updates

Genome-wide meta-analysis, fine-mapping and integrative prioritization implicate new Alzheimer's disease risk genes

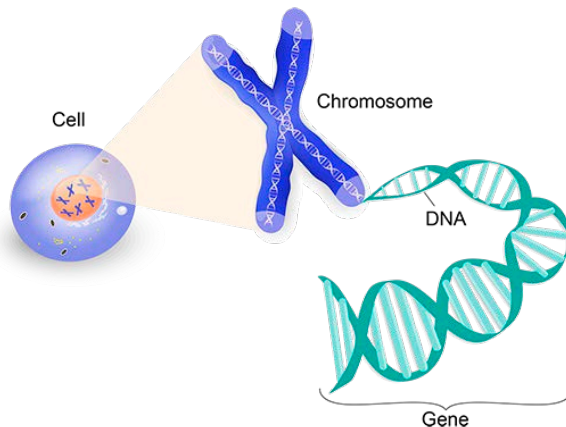
nature  
genetics

LETTERS

<https://doi.org/10.1038/s41588-020-00773-z>

Check for updates

Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimer's disease pathogenesis



95% loci located in non-coding regions?

Likely causal genes for each loci??

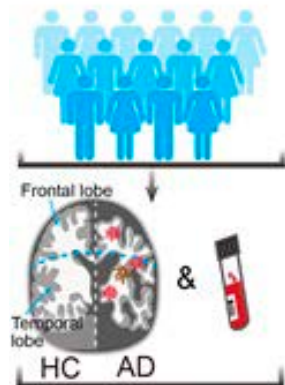
# Opportunities to translate non-coding genome findings to drug discovery



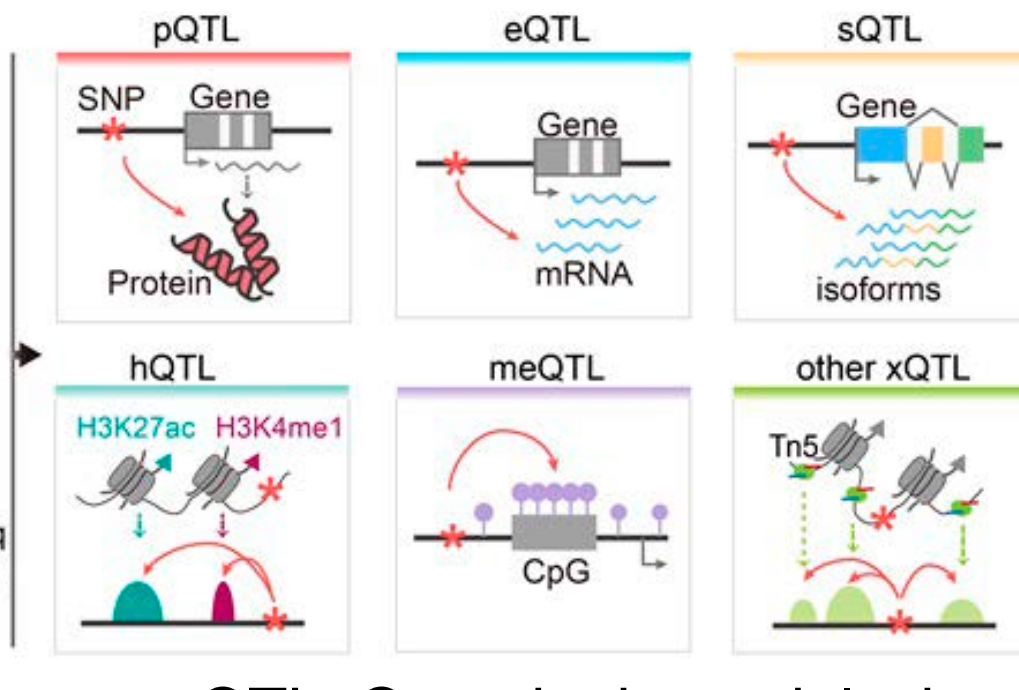
NIAGADS



AD Knowledge Portal  
AMP-AD



- Whole genome-seq
- RNA-seq
- DNA methylation-seq
- ChIP-seq (H3K27ac)
- ATAC-seq
- .....



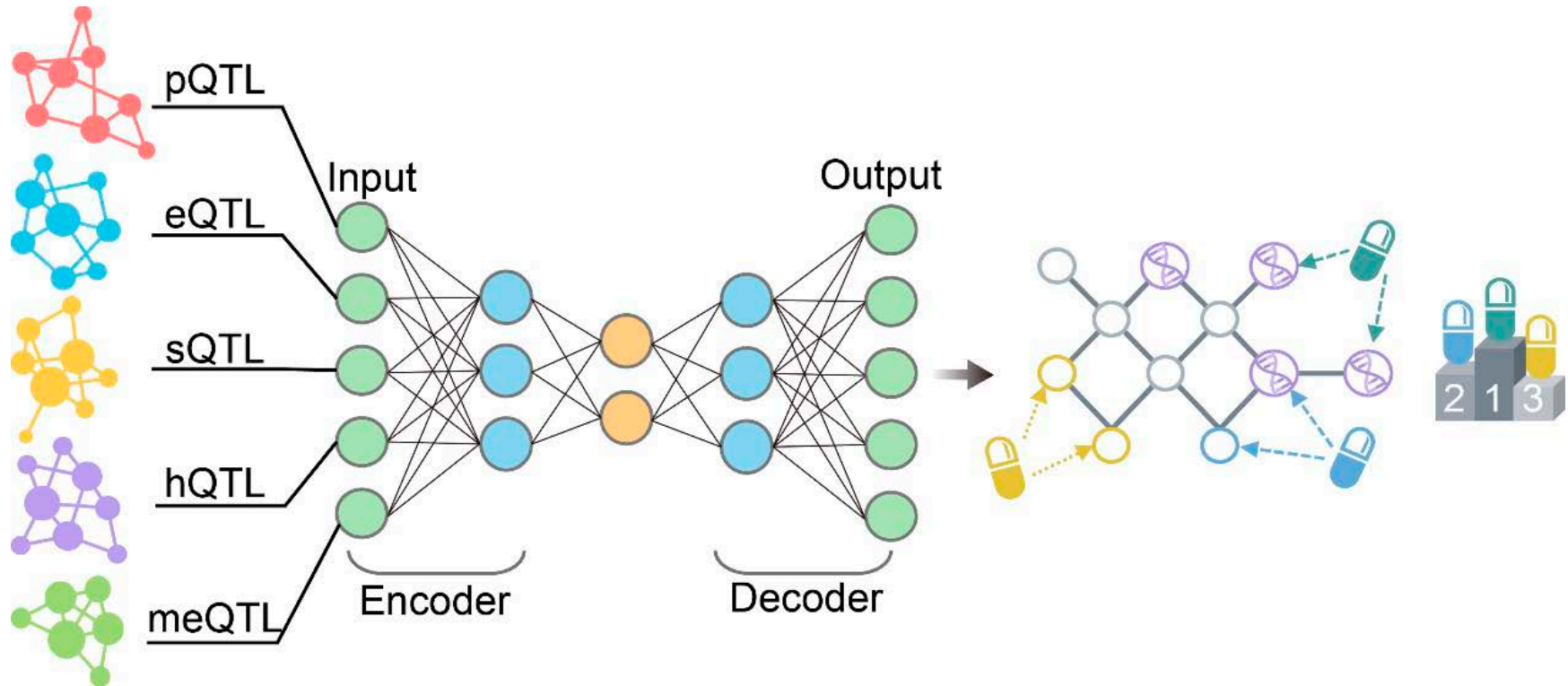
Zhou et al., *Alzheimer Res Ther* 2021;  
*Alzheimer & Dementia* 2022

x-QTL: Quantitative trait loci  
(**e**xpression, **p**rotein, **s**plicing,  
**m**ethylation, **h**istone, others)

Bykova et al., *Human Molecular Genetics* 2022



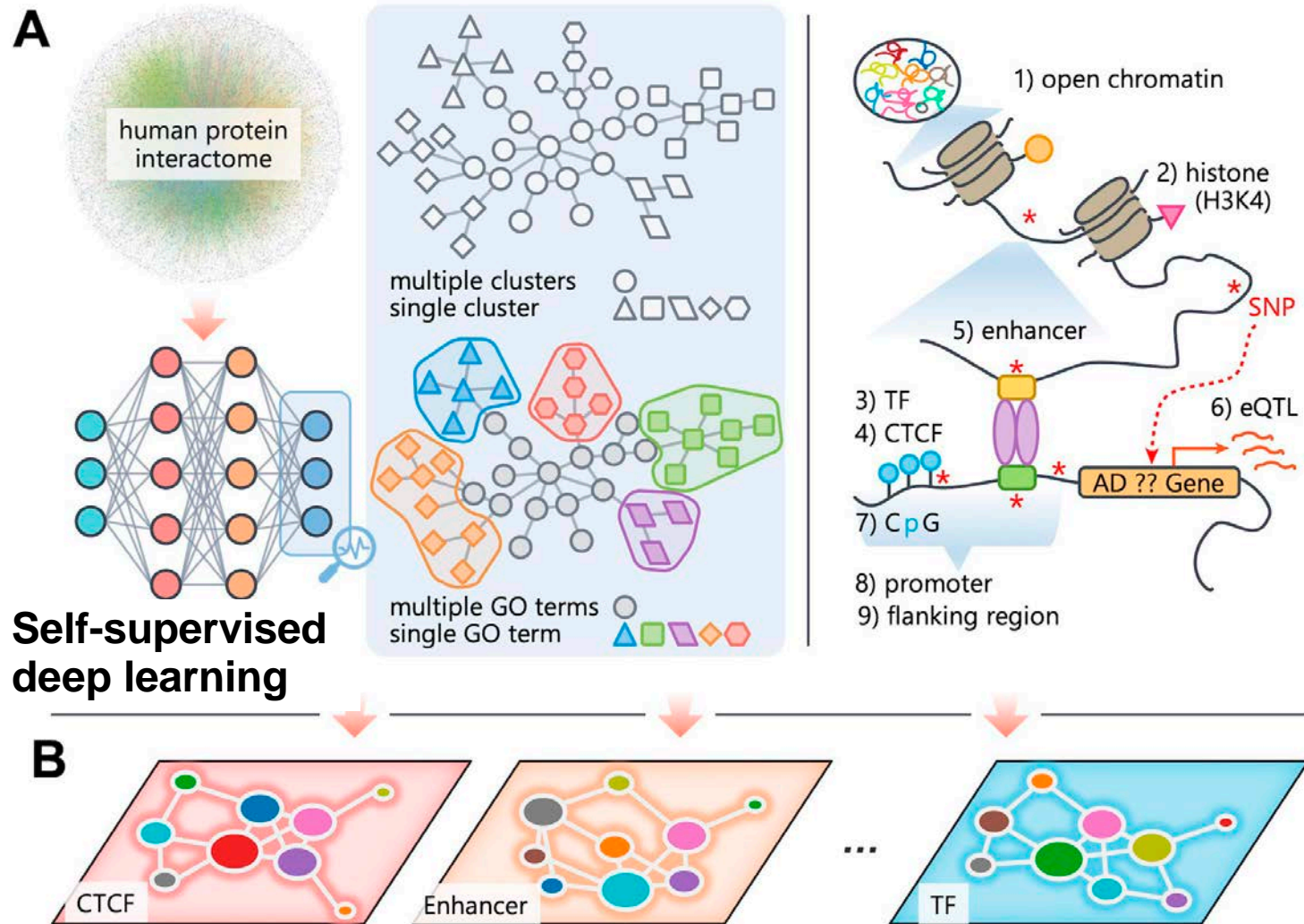
# Hypothesis: Translate multi-omics findings to rapid therapeutic development using AI\ML approaches



**Hypothesis:** AI\ML approaches enable utilize multi-omics data for identifying likely risk genes for better understanding of disease mechanisms and drug targets in Alzheimer's disease (AD).

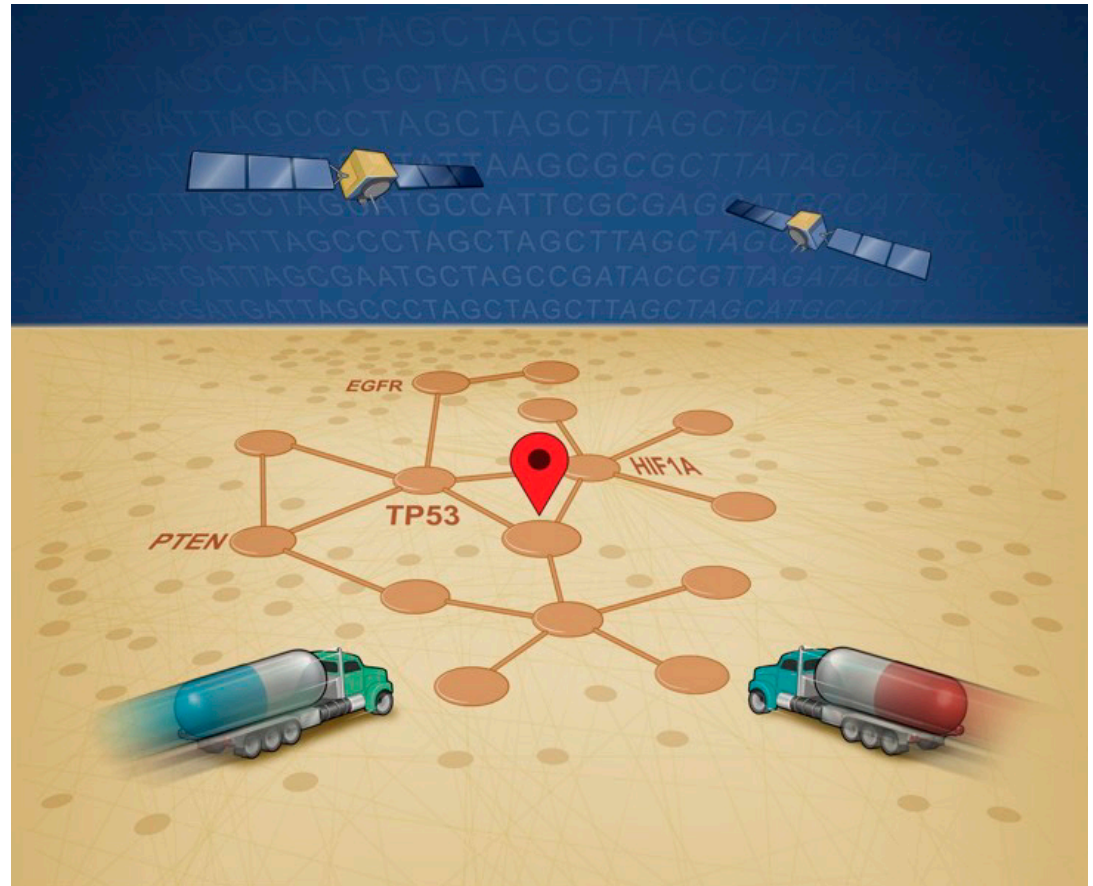
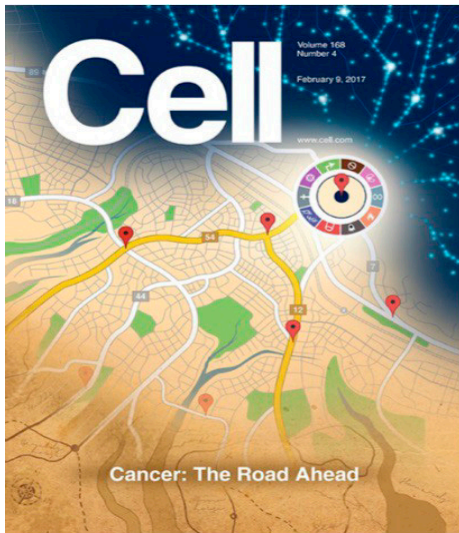
# Multi-omics informed target identification

**NETTAG**: network topology-based deep learning framework to identify AD-associated genes



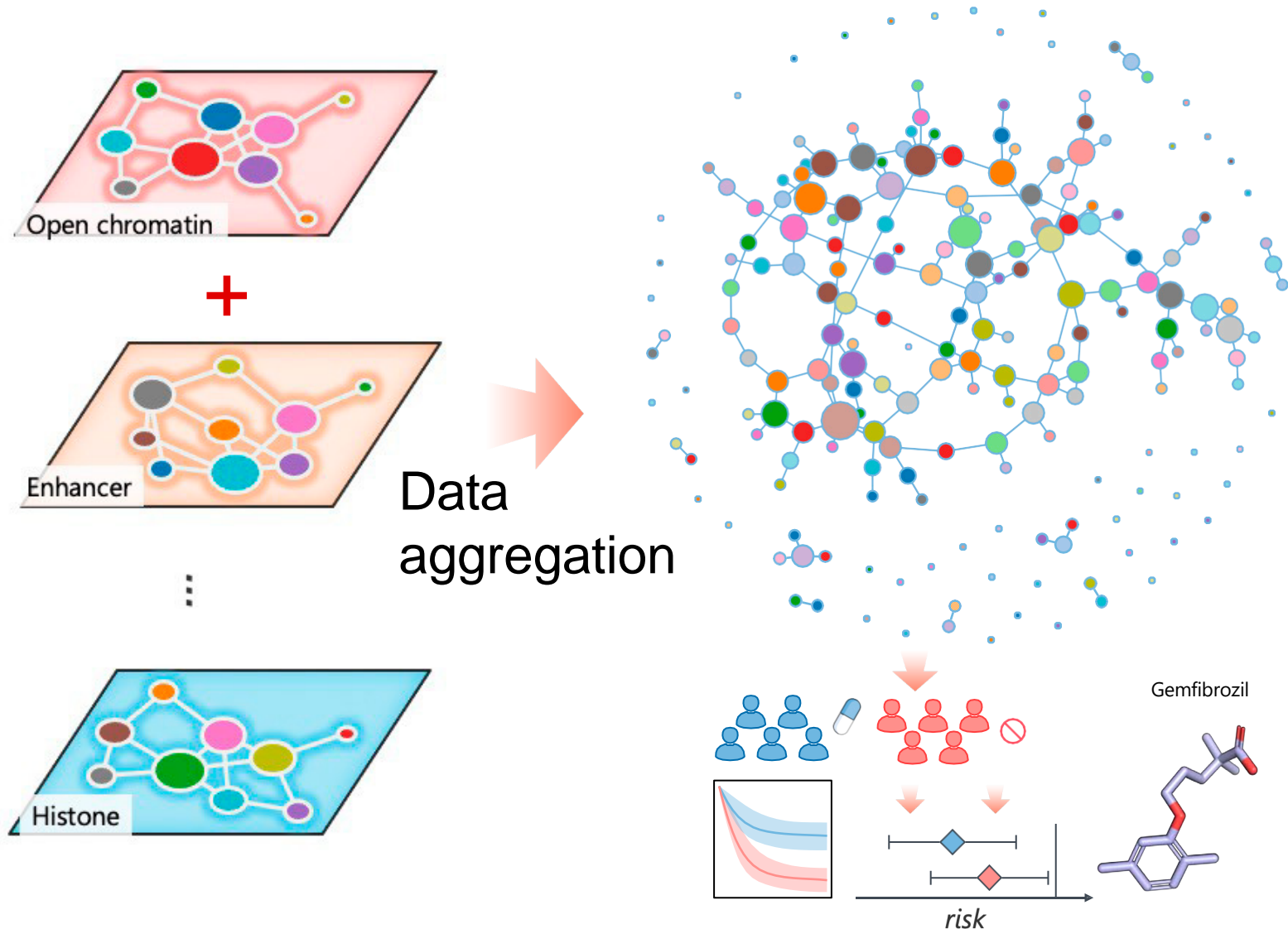


# Interpretability of PPI network impacted by disease mutations



**GPSnet:** Cheng et al., *Nature Commun* 2019  
Xu et al., *Genome Research* 2021

# Interpretability of NETTAG



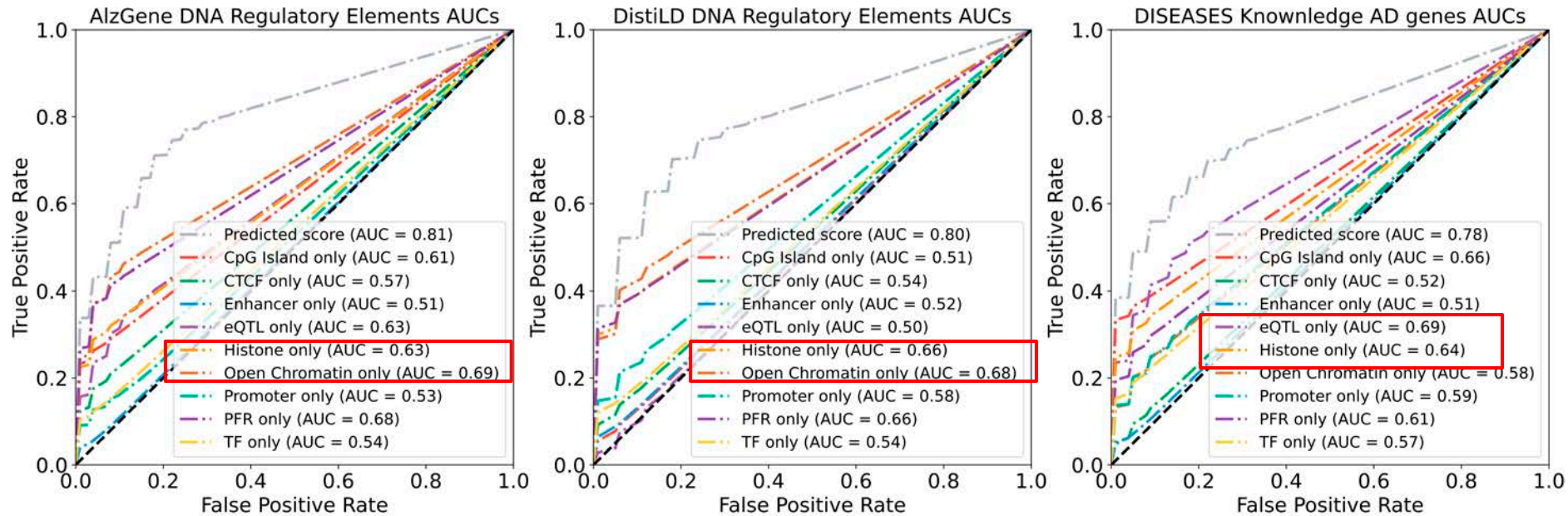
# AD GWAS from NIAGADS

ID	Ethnic	# of SNPs	# of Sample size (case/control)	# of SNPs ( $P < 10^{-5}$ )	Reference
1	USA ,UK	17,343	1,808/2,062	2	PMID:17317784
2	USA	313,504	2,391/2,464	11	PMID:19136949
3	USA, Europe	529,205	5,964/10,188	44	PMID:19734902
4	Europe	537,029	6,010/8,625	53	PMID: 19734903
5	USA, Europe	2,540,000	5,038/19,970	10	PMID: 20460622
6	USA	483,399	2,269/3,107	11	PMID: 20885792
7		565,336	2,465/2,564	11	PMID: 21379329
8	USA, Europe	496,763	19,870/39,846	61	PMID: 21460840
9	USA	2,324,889	11,840/10,931	169	PMID: 21460841
10	USA	1,016,423	4,167/4,336	12	PMID: 22005931
11	African American		1,968/3,928	4	PMID: 23571587
12	Europe	191,777	3,129/119,777	1	PMID: 23150908
13	Europe	7055881;11632	25,580/48,466	20	PMID: 24162737
14	European ancestry	180,882	143,706/766,756	50	PMID: 30617256
15	Non-Hispanic Whites	36,648,992	35,274/59,163	56	PMID: 30820047

eQTLs, pQTL, histone-QTLs, and TF-QTLs from GTEx, NIH RoadMap, FANTOM5, and NIH 4D Nucleome. **Brain-specific and AD-specific functional genomics: MetaBrain, ROSMAP, MSBB, Mayo (NIA-funded AD Knowledge portal)**




# Performance (AUC) Evaluation of NETTAG

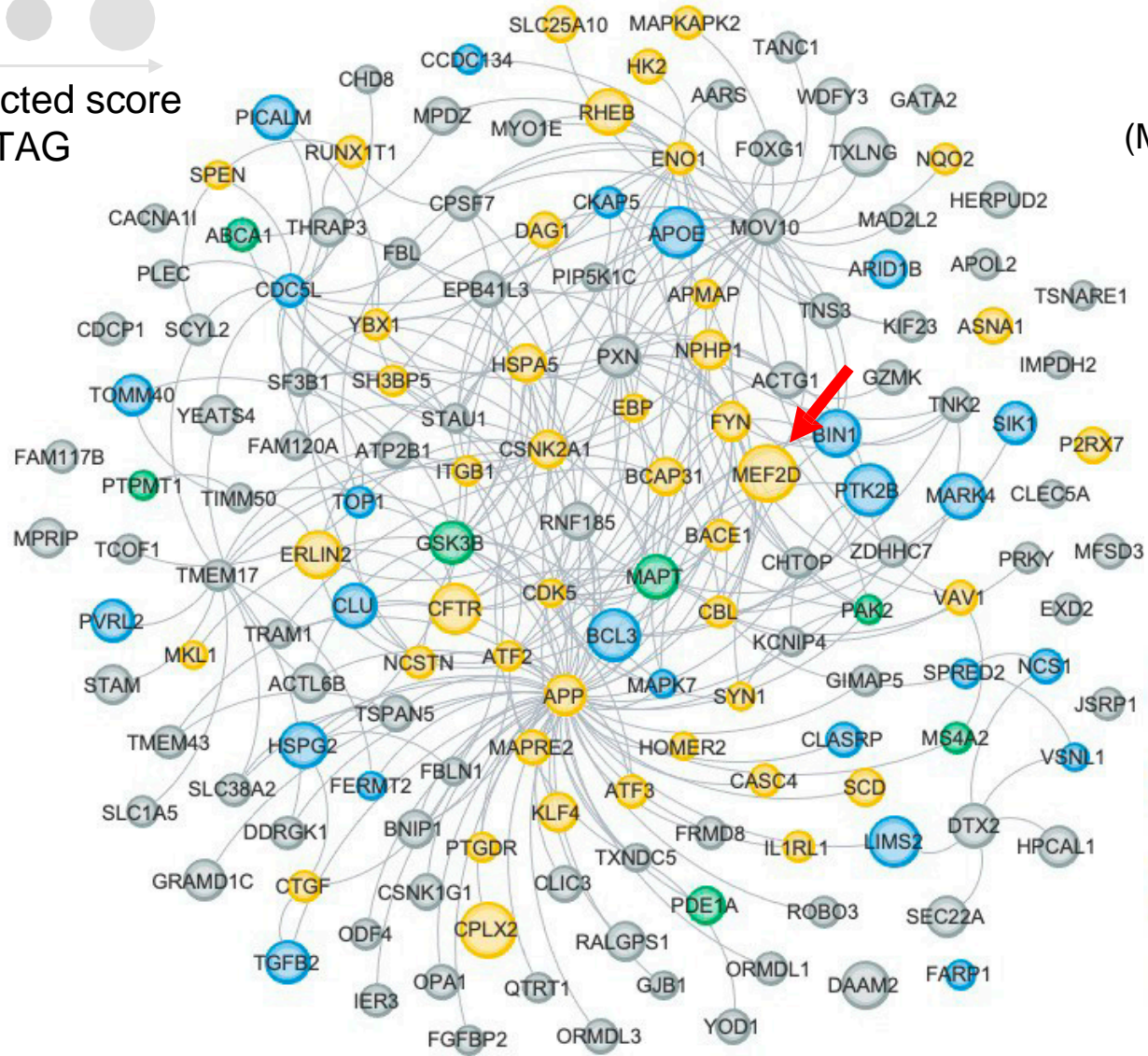


Test/Validation Sets of AD-associated genes collected from four public databases: Alzgene, DistilD, DISEASES, TIGA

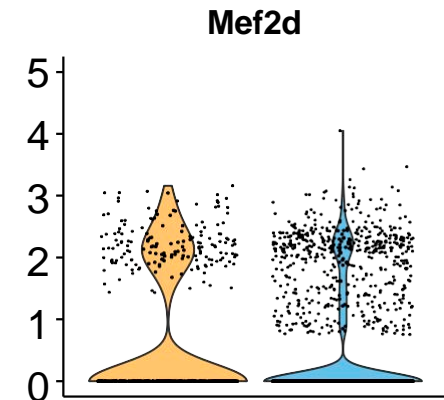
**Integration of functional genomic (multi-omics) data improve accuracy (AUC) by 10%-25%**





# PPI network module of 156 predicted AD genes


  
 predicted score  
 NETTAG



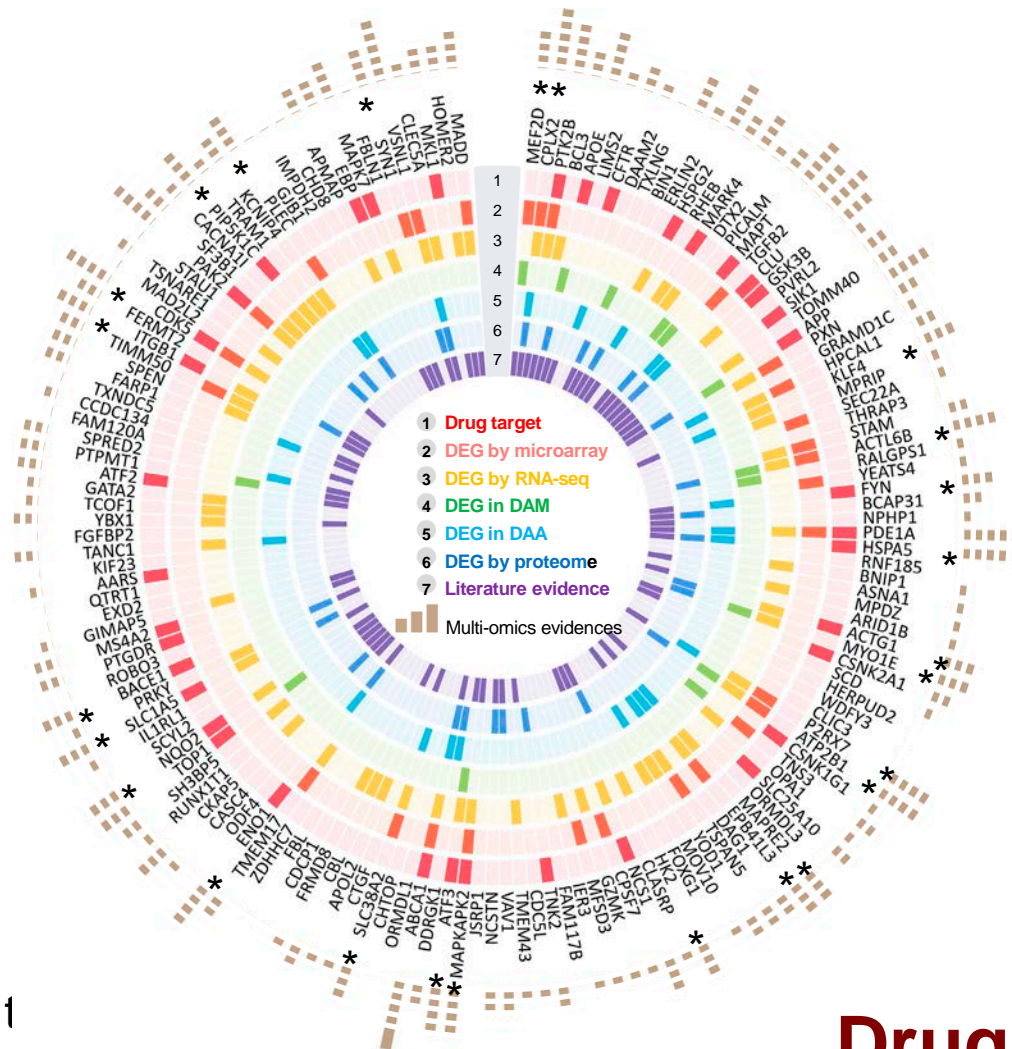
**MEF2D**  
 (Myocyte Enhancer Factor 2D)



-  GWAS Catalog, no regulatory evidence
-  GWAS Catalog, with single/multiple regulatory elements
-  alzRGs with other evidence
-  other predicted alzRGs



# Multi-omics validation of 156 predicted AD genes



DEG: differentially expressed genes/prot

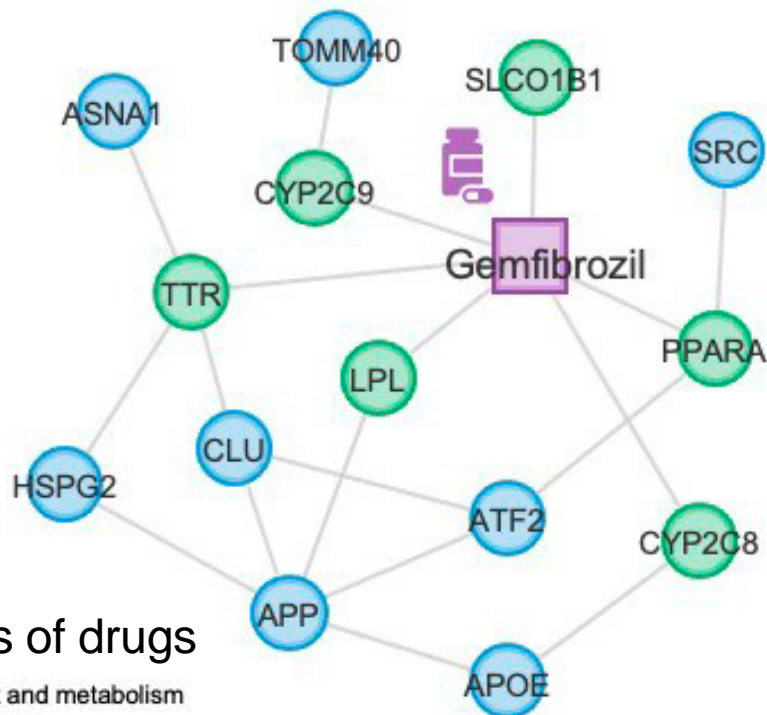
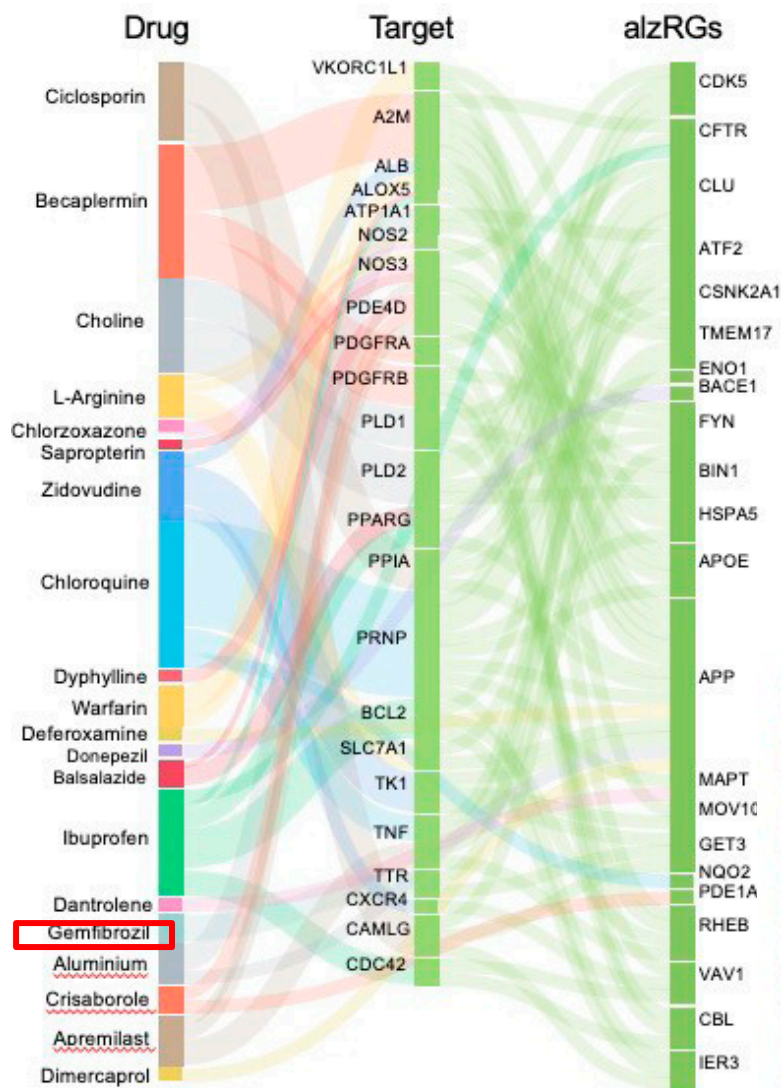
DAM: disease-associated microglia

DAA: Disease-associated astrocyte

**Drug targets**



# Identifying Repurposing Drugs via Targeting AD Risk Genes

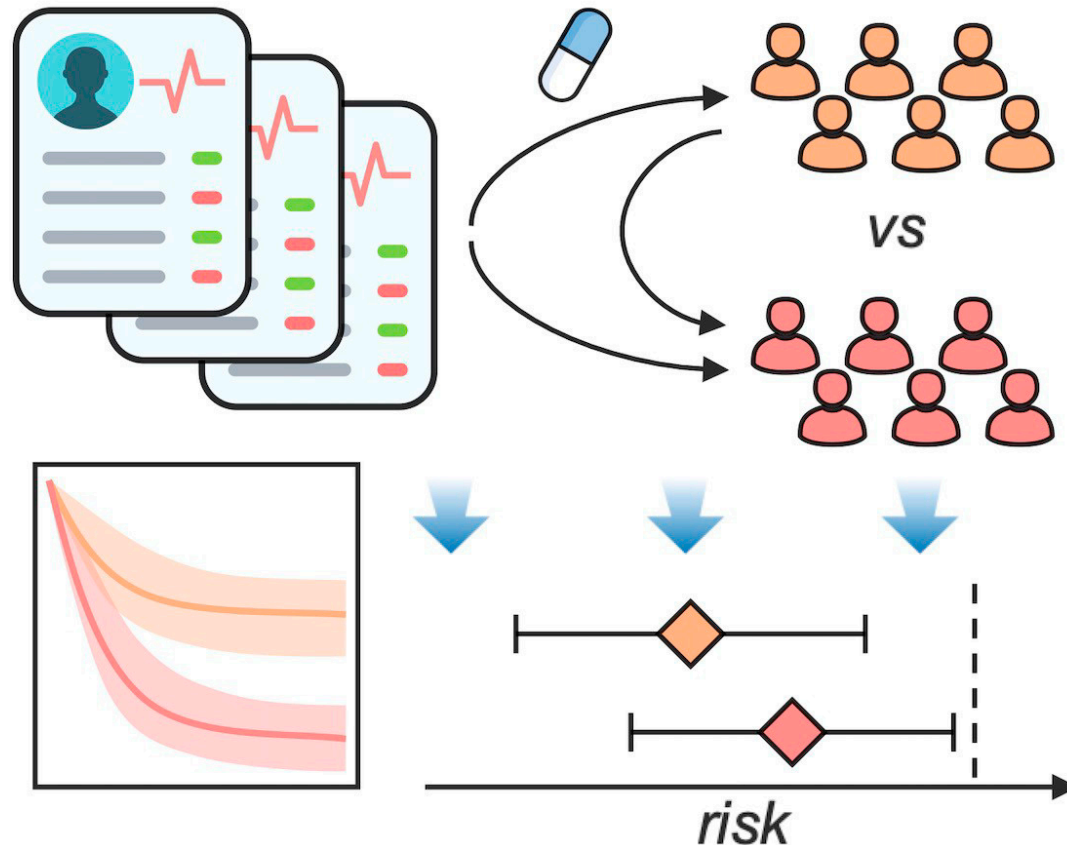


## ATC codes of drugs

- Alimentary tract and metabolism
- Respiratory system
- Dermatologicals
- Blood and blood forming organs
- Various
- Genito-urinary system & sex hormones
- Sensory organs
- Cardiovascular system
- Antiparasitic products
- Antiinfectives for systemic use
- Nervous system
- Systemic hormonal preparations
- Musculo-skeletal system
- Antineoplastic and immunomodulating
- Not available

- drug
- drug target only
- module node only

# Drug-Cohort Design using Real-world Patient Data

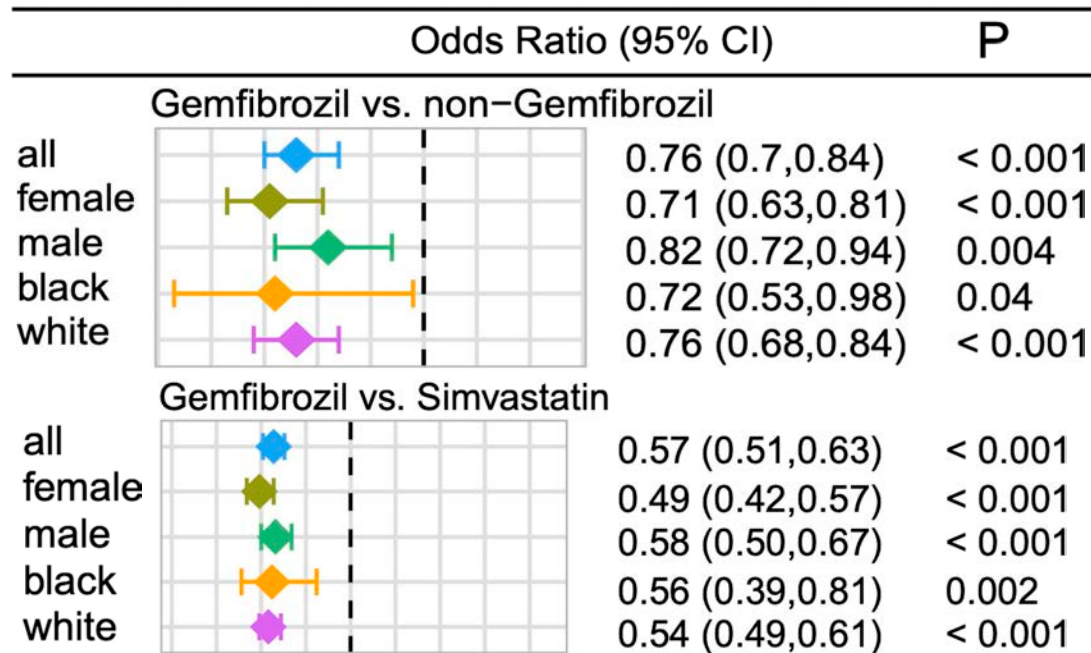


## Gemfibrozil users vs. non-Gemfibrozil users

Active comparator design

Propensity score matching cohort studies adjust various confounding factors (age, sex, race, disease comorbidities, etc).

# Gemfibrozil is associated with 40% reduced risk of Alzheimer's Disease in Real-World EHR data (10 million patients)



Propensity score matching cohort studies reveals that **gemfibrozil** (anti-lipid medicine) is significantly associated with 43% reduced risk of AD compared to **Simvastatin** (an anti-lipid drug in a Phase II AD clinical trial [NCT00486044 and NCT00939822]) (10 million patients from Northwestern University EHR systems)



# Preliminary Summary

- We demonstrated that AL\ML approaches offer powerful tools to identify risk genes and drug targets in Alzheimer's disease
- Unique integration of brain-specific functional genomics (xQTL) data synergistically improve performance in prediction of risk genes in AD.
- We identified **gemfibrozil** as a candidate drug for AD.
- More functional and clinical validation of **gemfibrozil** using Alzheimer's disease models and patients are highly warranted.

# Open Science and Data Sharing (AI\ML Supplement)

AlzGPS Network-based multi-omics analysis informs Alzheimer's patient care and Therapeutic development



A Genome-wide Positioning Systems platform for Alzheimer's disease



Drug name or DrugBank ID

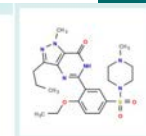
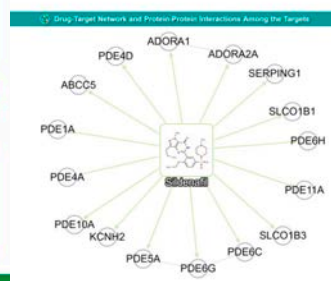


MISSION

To enable searching, sharing, visualizing, querying, and analyzing multi-omics (genomics, transcriptomics, proteomics, metabolomics, and interactomics) datasets types of heterogeneous bio-networks, and clinical databases for effective prevention and treatment of Alzheimer's disease.

Developed at and supported by  
 Cleveland Clinic  
Lerner Research Institute

OVERVIEW  
DRUGS: Bilirubin  
TYPE: small molecule  
GROUPS: approved, investigational  
ATC: G01AE15, G04BE03  
SMILES: COC1=NC(=C2C=NC(=C1)OC2)OC3=CC=CC=C3O



Drug Target Network and Protein-Protein Interactions Among the Targets  
PLOT CONTROLS  
X Network  
Network legend  
Show network on map  
Remove network  
Reset network  
LEGEND  
Drug  
Drug target  
Drug reagent interaction  
Protein-protein interaction

TACA The Alzheimer's Cell Atlas

A Single-Cell Type Transcriptomics And Network Pathobiology Map For Target Identification And Drug Repurposing

21 Datasets (151,170 Cells/Nuclei)  
1,193 DE Comparisons (353 Cell-Cell Interaction Analyses)  
Protein-Protein Interaction Drug-Target, Drug-Perturbation Ligand-Receptor  
Virtual Drug Screens Enrichment Analyses

**1.1+ million single-cell/nuclei transcriptomes**

SEARCH FOR GENES  
Gene Entrez ID or symbol  
Gene information, QTL data, protein-protein interactions, summaries of genes in the datasets  
Examples: APOE 4137

SEARCH FOR DRUGS  
Drug name or DrugBank ID  
Drug target networks, virtual screenings, mechanism-of-actions  
Examples: DB00203 Pioglitazone

EXPLORE DATASETS

Human Mouse

Developed at and supported by  
 Cleveland Clinic  
Lerner Research Institute

TACA: <https://taca.lerner.ccf.org>

Codes: <https://github.com/ChengF-Lab>

To enable utilize multi-omics data to identify/validate drug targets and disease mechanisms for AD via AI\ML tools.

# Acknowledgements

## Cheng Lab

- Jielin Xu
- Yuan Hou
- Yadi Zhou
- William Martin
- Jessica Castrillon
- Yunguang Qiu
- Yayan Feng
- Dhruv Gohel
- Marina Bukova
- Lijun Dou
- Yichen Li
  
- Lab Alumni
- Jiansong Fang
- Yin Huang

## Cleveland Clinic

- Jeffrey Cummings
- James Leverenz

## CWRU

- Andrew Pieper
- Jonathan Haines

## Indiana University

- Pengyue Zhang

## Northwestern ADRC

- Margaret Flanagan
- Yuan Luo
- Chengsheng Mao



**3 R01 AG066707-02S1**