



Dr. Sean Ekins, Ph.D., D.Sc. CEO,

Collaborations Pharmaceuticals, Inc.



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### Al is increasingly in the news

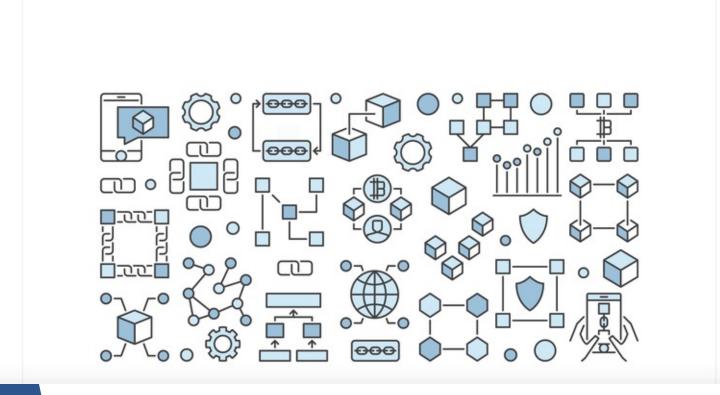
Dec 26, 2020, 04:59pm EST | 2,894 views

## The Increasing Use Of AI In The Pharmaceutical Industry Forbes





#### The FDA and artificial intelligence



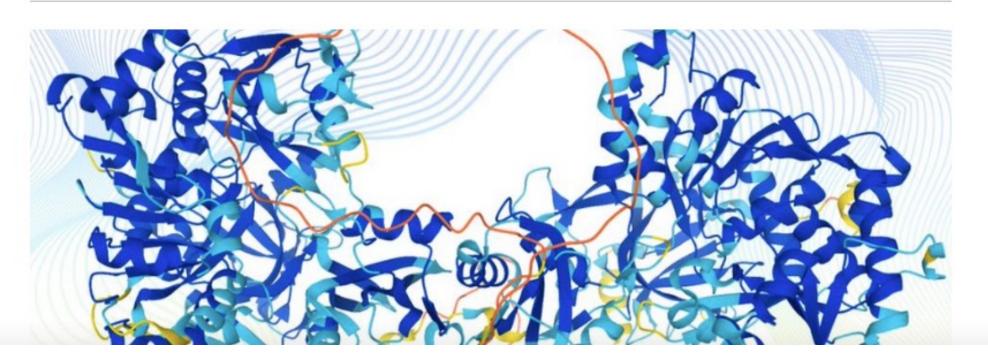


### AI breakthrough could spark medical revolution

By Paul Rincon
Science editor, BBC News website

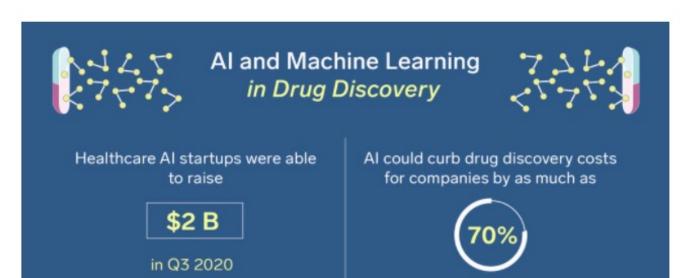
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## Big pharma is using AI and machine learning in drug discovery and development to save lives

Insider Intelligence Nov 24, 2020, 2:20 PM

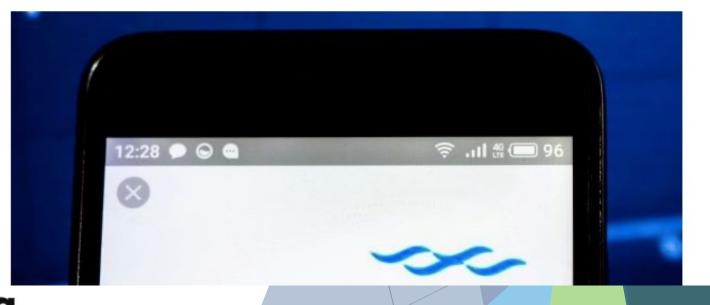




#### AI's infiltration of pharma: How COVID-19 accelerated change

#### Valence Discovery Deal Brings Purpose-Built AI/ML to Charles River Labs' Clients

Published: Apr 06, 2021 By Gail Dutton



ARTIFICIAL INTELLIGENCE, BIOPHARI

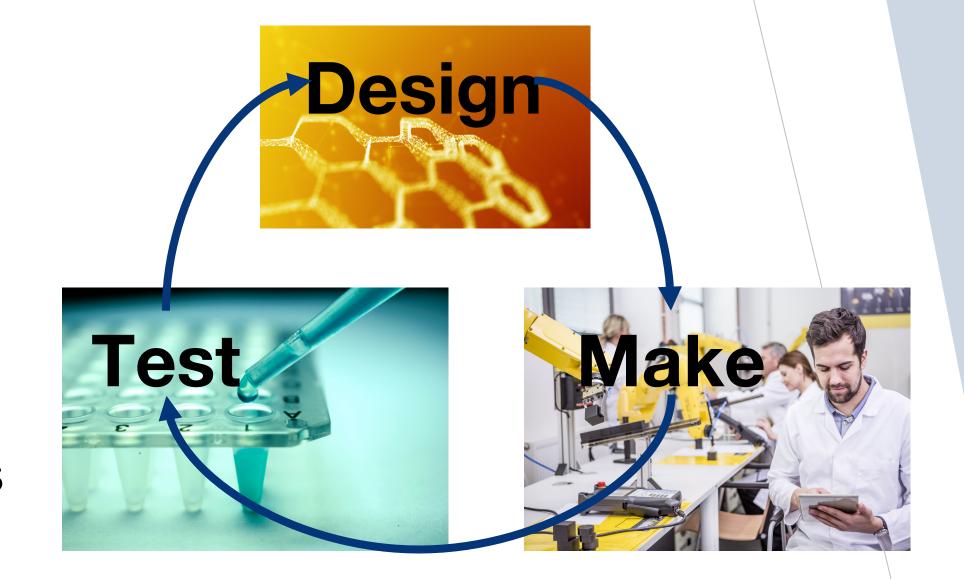
#### AI offers promise but faces barriers in drug development

Inertia is a barrier as is the traditional split between the clinical a the data-driven spheres of drug development. While smaller firm have an edge in bridging the gap, big pharma will eventually get there, said panelists at the INVEST conference session.

■ Post a comment / Dec 10, 2020 at 12:54 PM

#### Al In Industry

- Pharmaceutical
  - Design new molecules
  - Repurpose drugs
  - Predict Toxicity & Drug-drug interactions
- Consumer products
  - Cleaning prioritize endocrine disruption
  - Cosmetics non-animal testing options
  - Environmental impact
- Agrochemical
  - Biodegradation
  - Toxicity to non-target species
- Environmental
  - Predict impact of chemicals
- Animal health
  - Cost-effectively develop new treatments



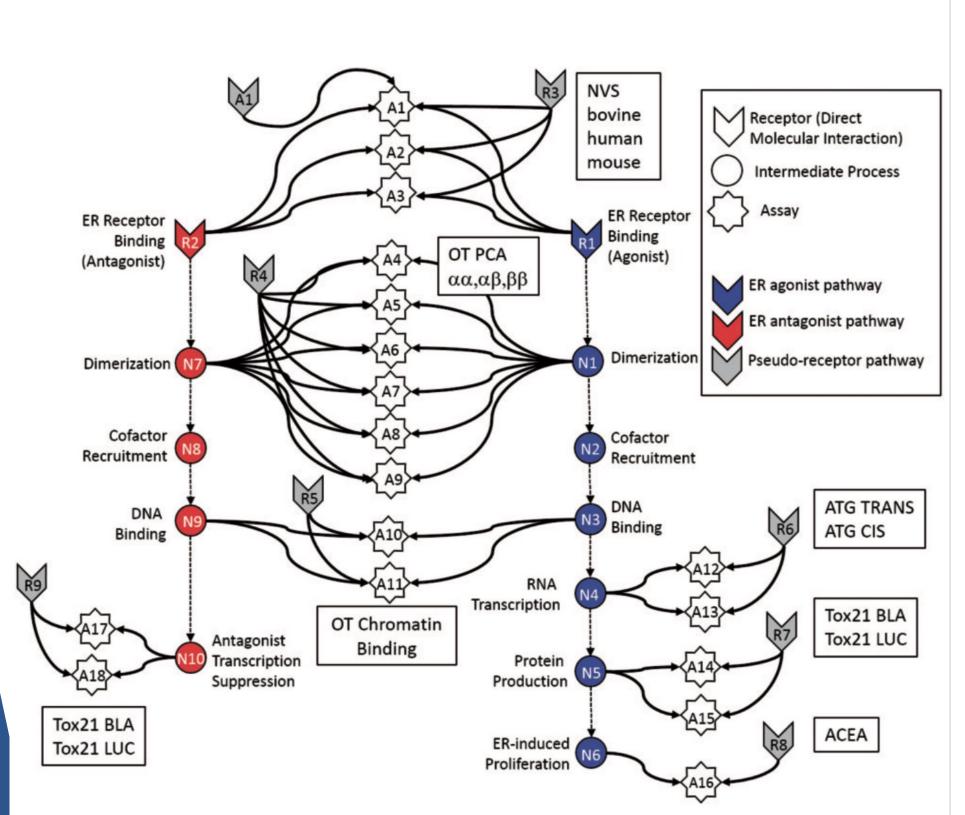


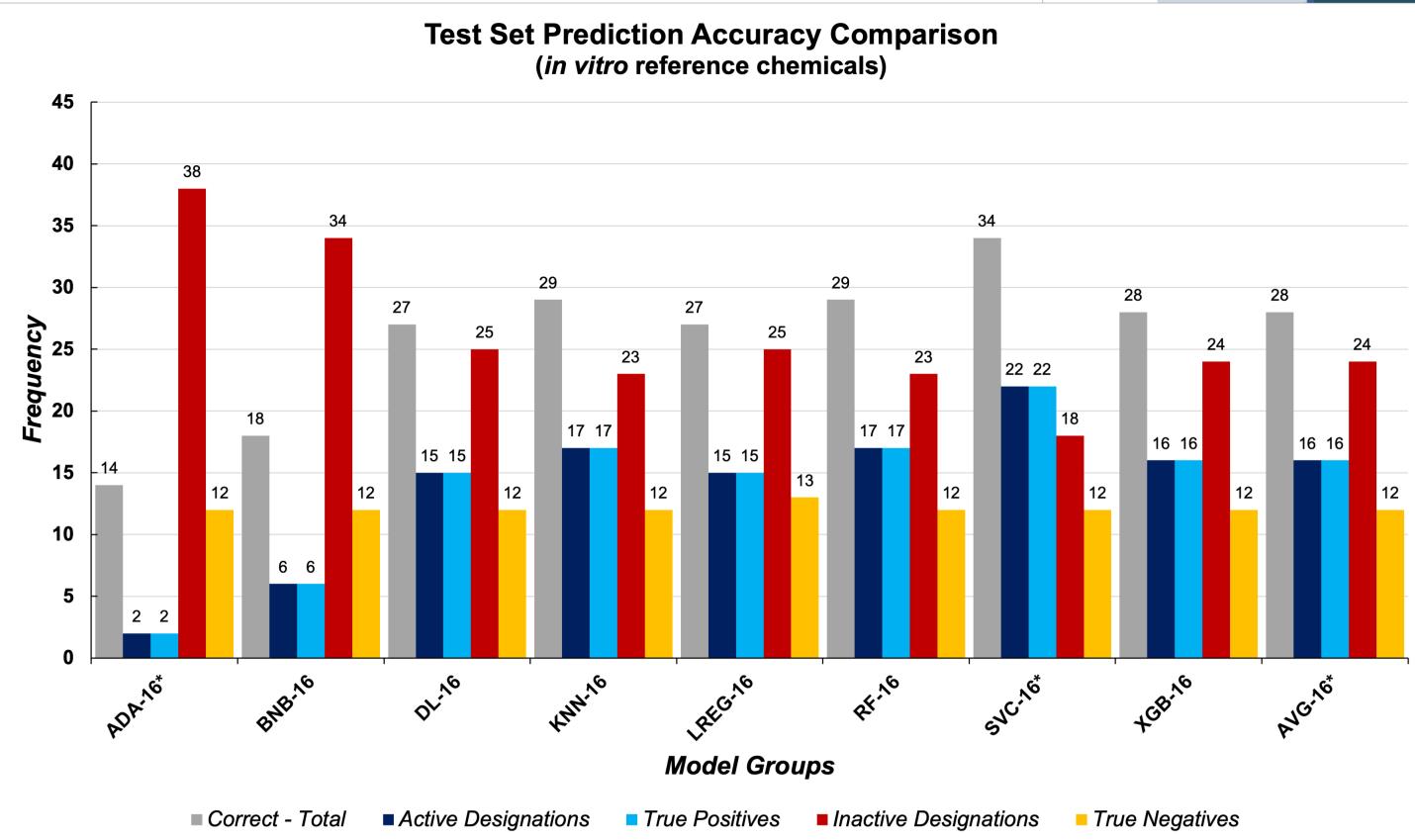


#### Modeling Targets in Pathways

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- 16 assays for ER with 1000s molecules published by the EPA
- Evaluate algorithm performances and identify which is best-suited for predicting ER agonism
- in vitro reference chemicals 40 total, 28 active/12 inactive





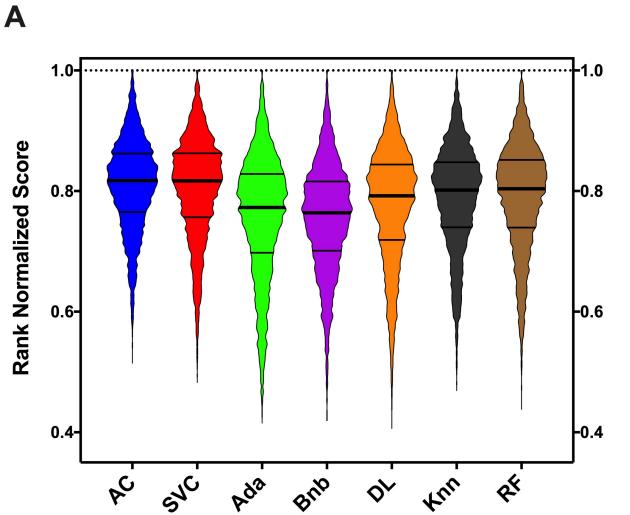
Toxicol Sci. 2015;148(1):137-154. Environ Sci Technol. 2015;49:8804-8814 Mol Pharmaceutics. 2018;15:4361-4370. Environ Sci Technol. 2020;54(19):12202-12213. Environ Sci Technol. 2020;54(21):13690-13700 Environ Sci Technol. 2020;54(23):15546-15555

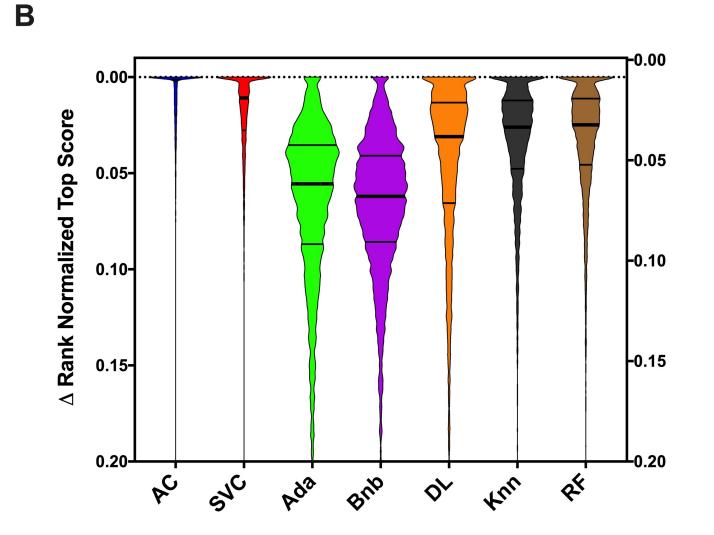
#### Model Human Diseases and Biology / Targets









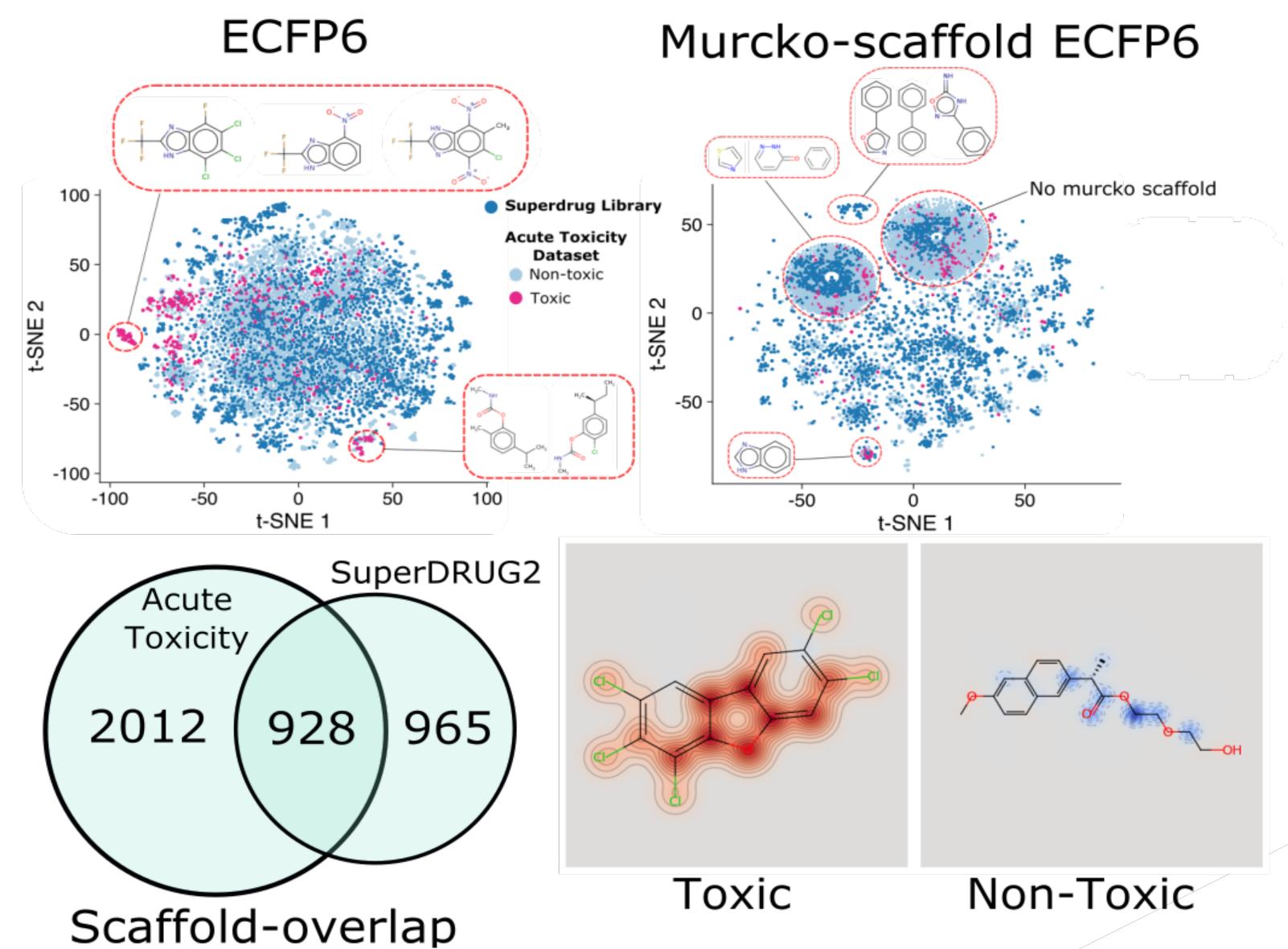


Lane et al., Mol Pharm. 2021;18(1)403-415.

- >5000 ChEMBL datasets, >100 compounds in each
- Compared support vector classification, AdaBoosted decision trees, multiple Bayesian methods, deep learning, K nearest-neighbors, and random forests
- Assessed five-fold cross-validation statistics
- External testing on various ADME/Tox datasets
- www.assaycentral.org

## Exploring Toxicity Property Space

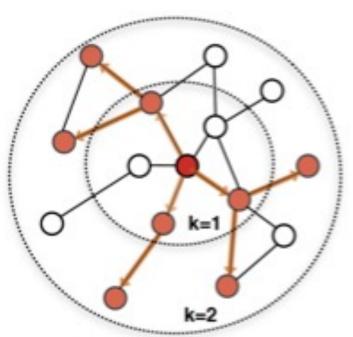




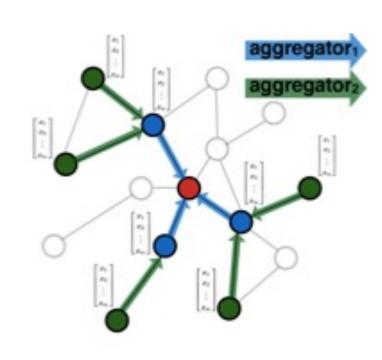
Environ Health Perspect. 2021 Apr;129(4):47013 ACS Sustainable Chem. Eng. 2020, 8, 42, 16020–16027

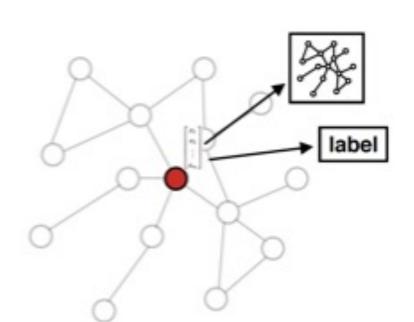
#### Model Protein Networks With Graphs





Sample neighborhood



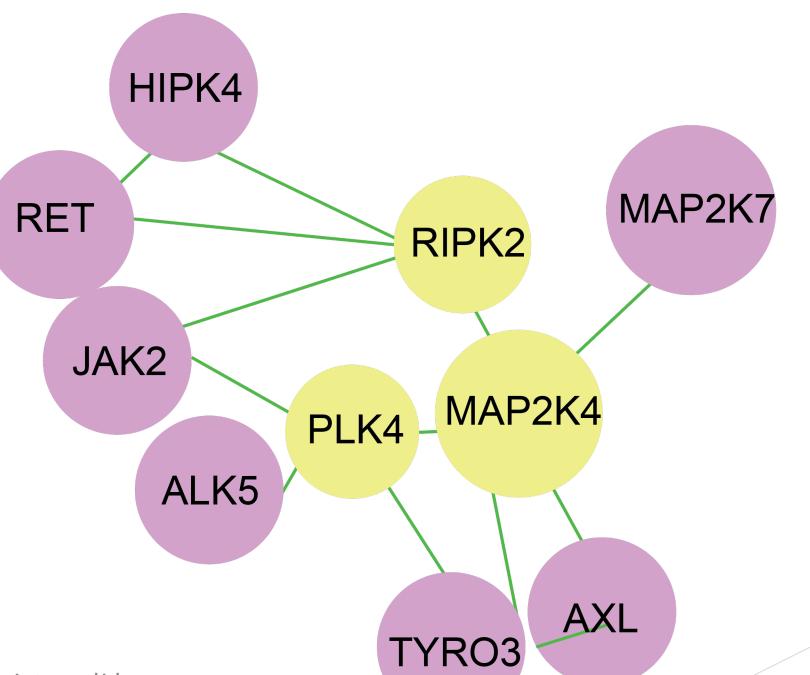


Inductive Representation Learning on Large Graphs. W.L. Hamilton, R. Ying, and J. Leskovec *arXiv:1706.02216 [cs.SI]*, 2017.

Aggregate feature information from neighbors

Predict graph context and label using aggregated information

 By including drug-target interactions along with target kinase features in a graphbased model, we can use "transfer learning" to make better drug-target predictions, including kinases with little data.



robust drug-target interaction datasets

sparse drug-target interaction datasets

#### Graph-based Kinase Model: EGFR



#### EGFR ROC = 0.83 with examples in training data

graphSAGE can scale to hundreds or thousands of targets

MegaKinase: 475 human kinase targets (all ChEMBL human kinase data to date). Activity threshold: 100nM for any target.

ROC of the full 475 human kinase model on a 15% test set is 0.86 (predicting a heterogenous mix of activities on each of the targets)

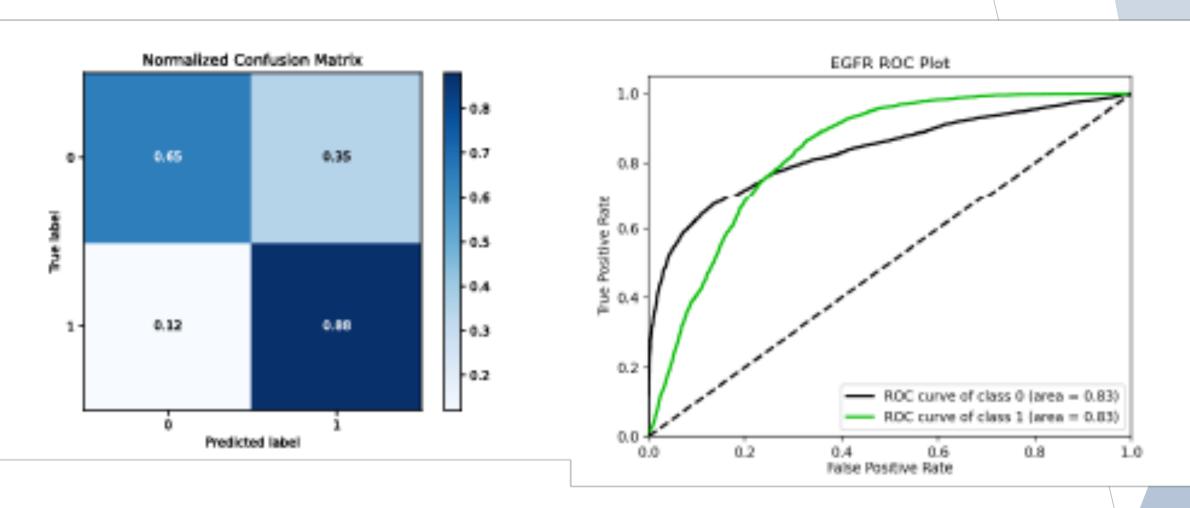
ROC on EGFR validation: 0.83

ROC on EGFR, when the model has not seen any examples on EGFR itself: 0.67

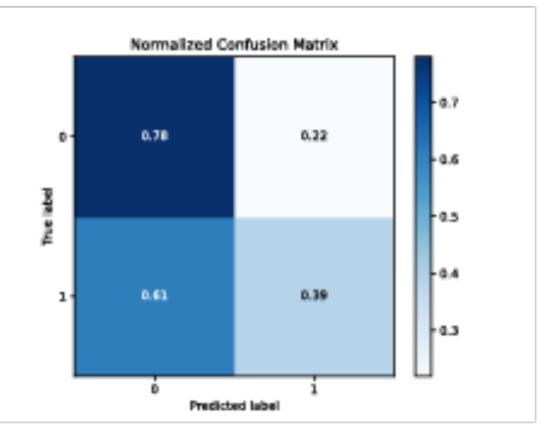
Useful for dark kinases

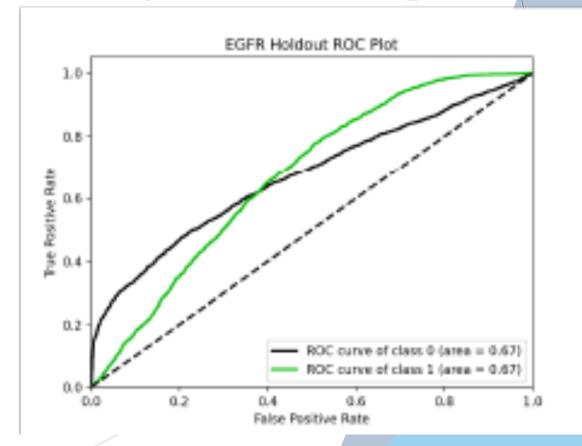
Other proteins with limited data

Apply in toxicology modeling



#### EGFR ROC = 0.67 with no examples in training data

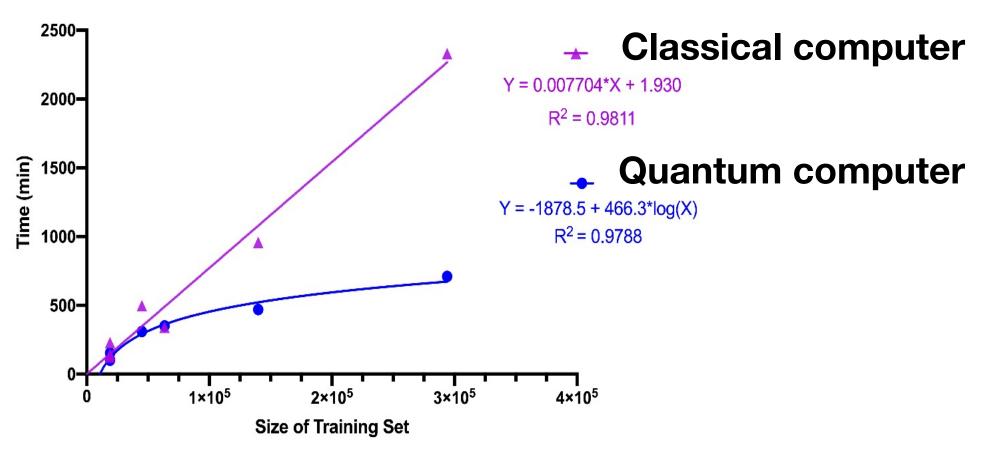




#### Quantum Machine Learning (QML)

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- As the dataset size increases, we need faster methods to build complex models (SVM etc)
- QC simulation outperforms classical computers with increased data set size
- Comparing accuracy and run time results for *M. tuberculosis* inhibition datasets (18,886 compounds) using data re-uploading classifier on classical vs quantum computer with 5-fold cross validation. On 54Qubit IBM machine QML Faster with trade off in accuracy



Dataset threshold	Time on CC	CC Accuracy	Time on	QC Accuracy		
(number of actives)	(min)	(%)	QC (min)	(%)		
100 nM (645)	125	97.1	104	90.5		
1 μM (2351)	144	90.4	101	81.4		
10 μΜ (7762)	229	75.6	153	54.9		

# Predicting Billions of Molecules Bottleneck: DNA Encoded Libraries



Scaling up: DNA encoded libraries often require

scoring >billion compounds

Problem- ECFP6 algorithms represent a costly

bottleneck: too slow

Solution: SMILES based end-to-end

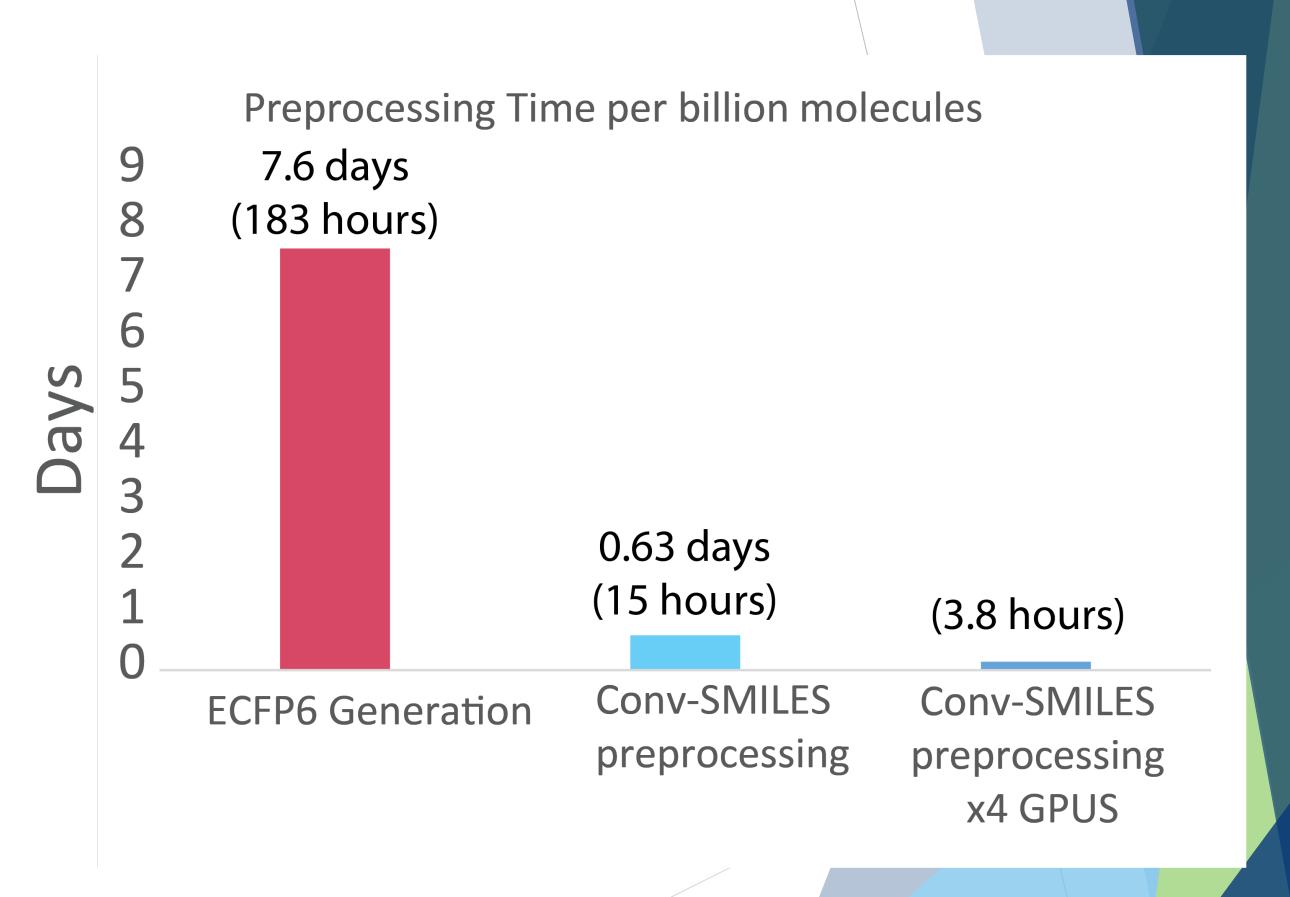
Convolution-LSTM model

The model uses encoded SMILES as input to perform classification

~12-15x increase in processing speed on a 1080ti: from a week of preprocessing to hours

GPU enabled: All calculations take place on the GPU, allowing parallel model prediction/preprocessing: 4x GPUs = ~50x speedup on predictions:

No secondary preprocessing storage necessary: SMILES only input



### The Need For Speed: Faster End to End Models

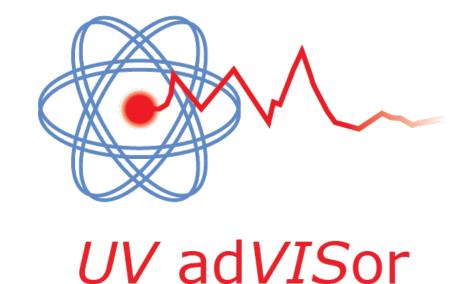


SMILES based end-to-end Convolution-LSTM model have similar or better predictive power compared to ECFP6-based classification models

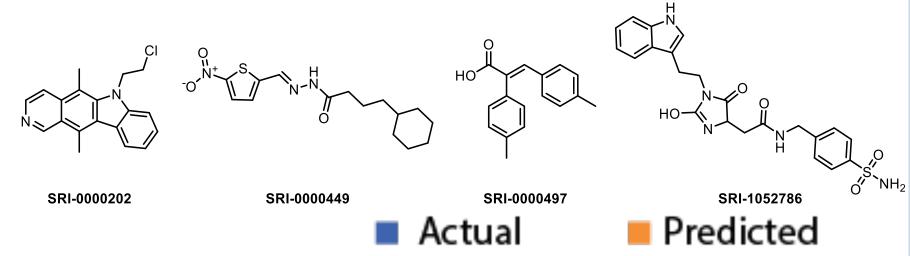
$$tp = \frac{tp}{tp + \frac{1}{2}(fp + fn)}$$

#### 5x cross-validation F1 Score of multiple models and datasets vs. Conv-LSTM

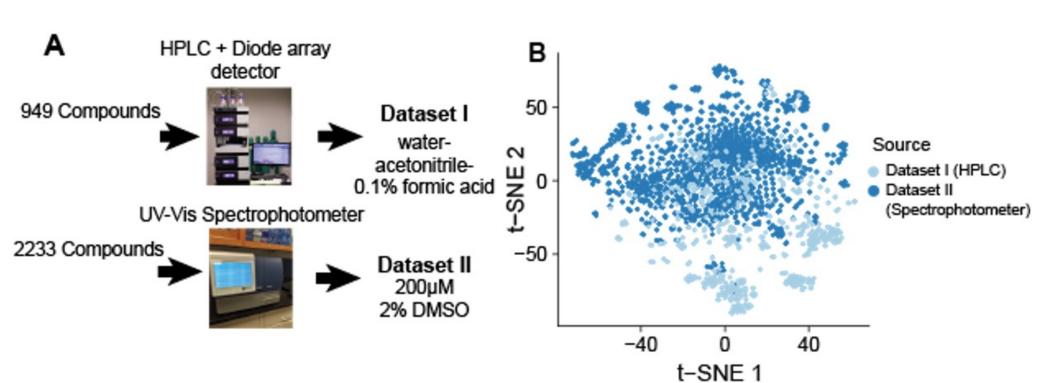
Model Datasets	Adaboost	Bayes	Xgboost	K-NN	Linear Regression	Random Forest	SVC	Conv- LSTM
Water Solubility	0.24	0.38	0.48	0.48	0.25	0.27	0.30	0.49
Ames Mutagenesis	NA	0.70	NA	NA	0.75	NA	NA	0.78
Blood-Brain Barrier	0.93	0.93	0.95	0.91	0.91	0.95	0.96	0.93
CHO Cytotoxicity Assay	0.68	0.71	0.70	0.70	0.66	0.72	0.69	0.74
CYP3A4 Inhibition	0.84	0.83	0.85	0.82	0.80	0.83	0.85	0.80
hERG Ki	0.85	0.87	0.86	0.81	0.84	0.86		0.85
Plasma Protein Binding	0.85	0.84	0.87	0.86	0.85	0.87	0.88	0.82



# Predicting UV-Vis Spectra For Molecules Without Physical Samples

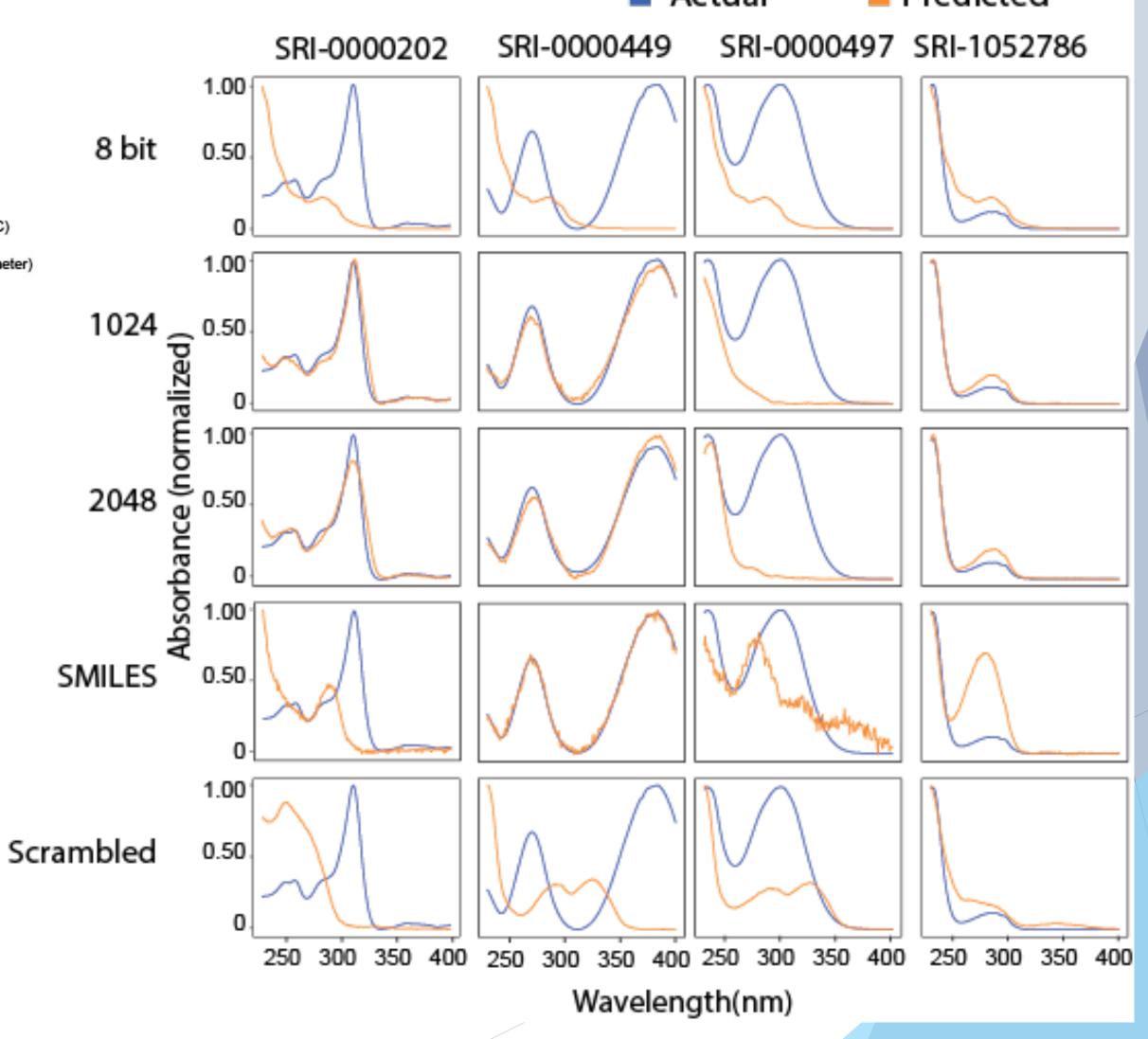






- Potential use in predicting:
- Chemistry-in-a-box analytical
- Assay interference for novel libraries
- Predicting color
- Predicting phototoxicity
- 70:15:15 (train: test: validation)
- SMILES Median RMSE = 0.166
- predictions better than DFT RMSE ~0.3-0.4





Funding: DARPA (HR0011-19-C-0108; PI: P. Madrid)

## The Future of Computational Toxicology

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We have the technology to create massive numbers of molecules

Molecule design becomes autonomous

We have the tools to predict toxicology and physicochemical properties faster

Integrated design-make-test cycles becomes a reality

Al can help us learn from the data we have for predicting impact on human and other targets

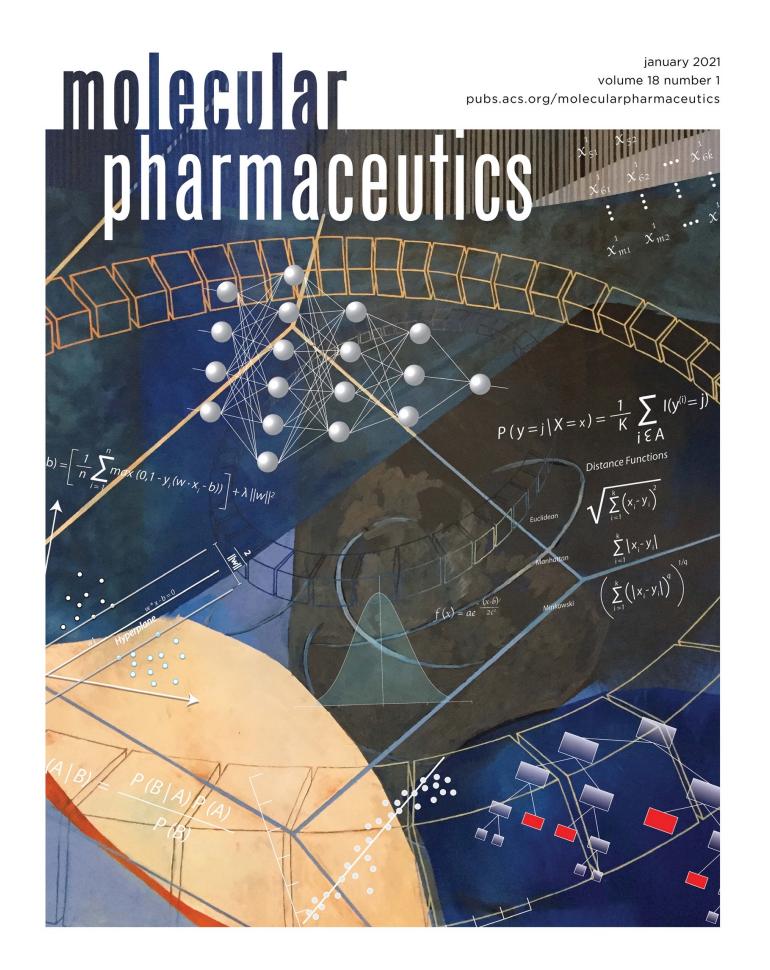




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