

Artificial Intelligence Driven Drug Discovery

Michelle Gill, PhD

Senior Data Scientist

BenevolentAI

@modernscientist

NYC R Conference

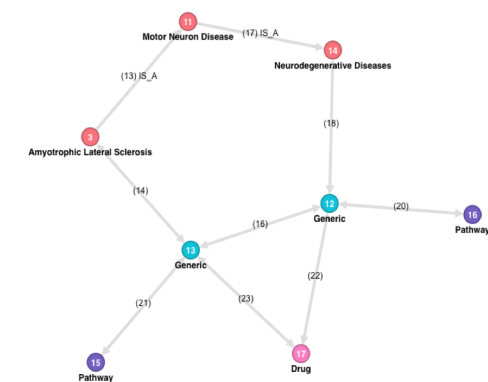
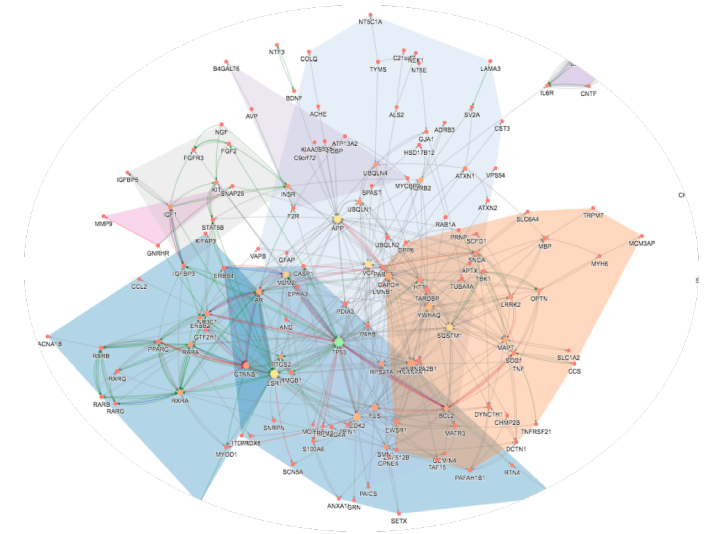
May 10, 2019

BenevolentAI

BenevolentAI

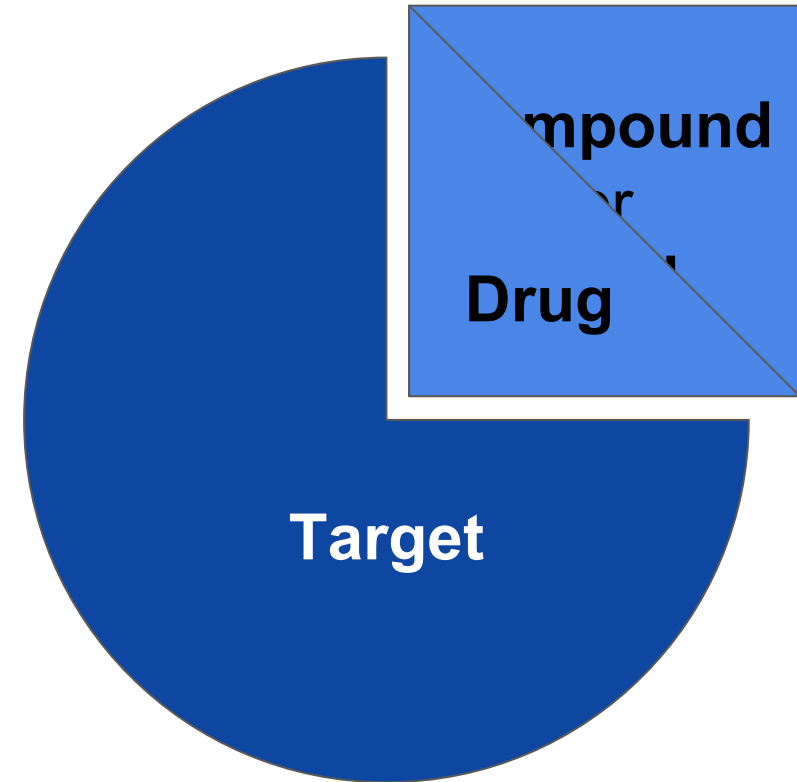
- >200 life scientists, AI scientists, informaticians work side-by-side
- Technology pipeline is **validated by scientific experimentation**
- Only AI company with expertise from **early to late stage drug development process**

Because it matters.

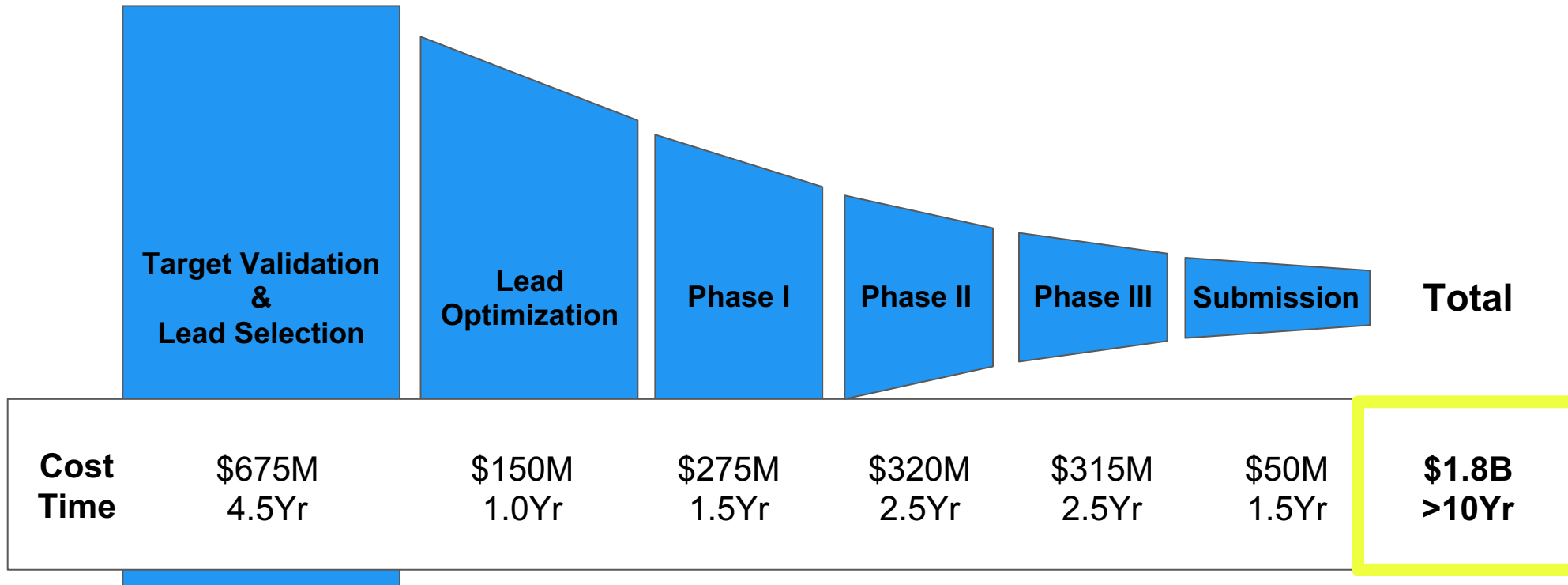


Common Nomenclature

- **Target:** a molecule within an organism that is associated with a disease and the intended destination for a therapy



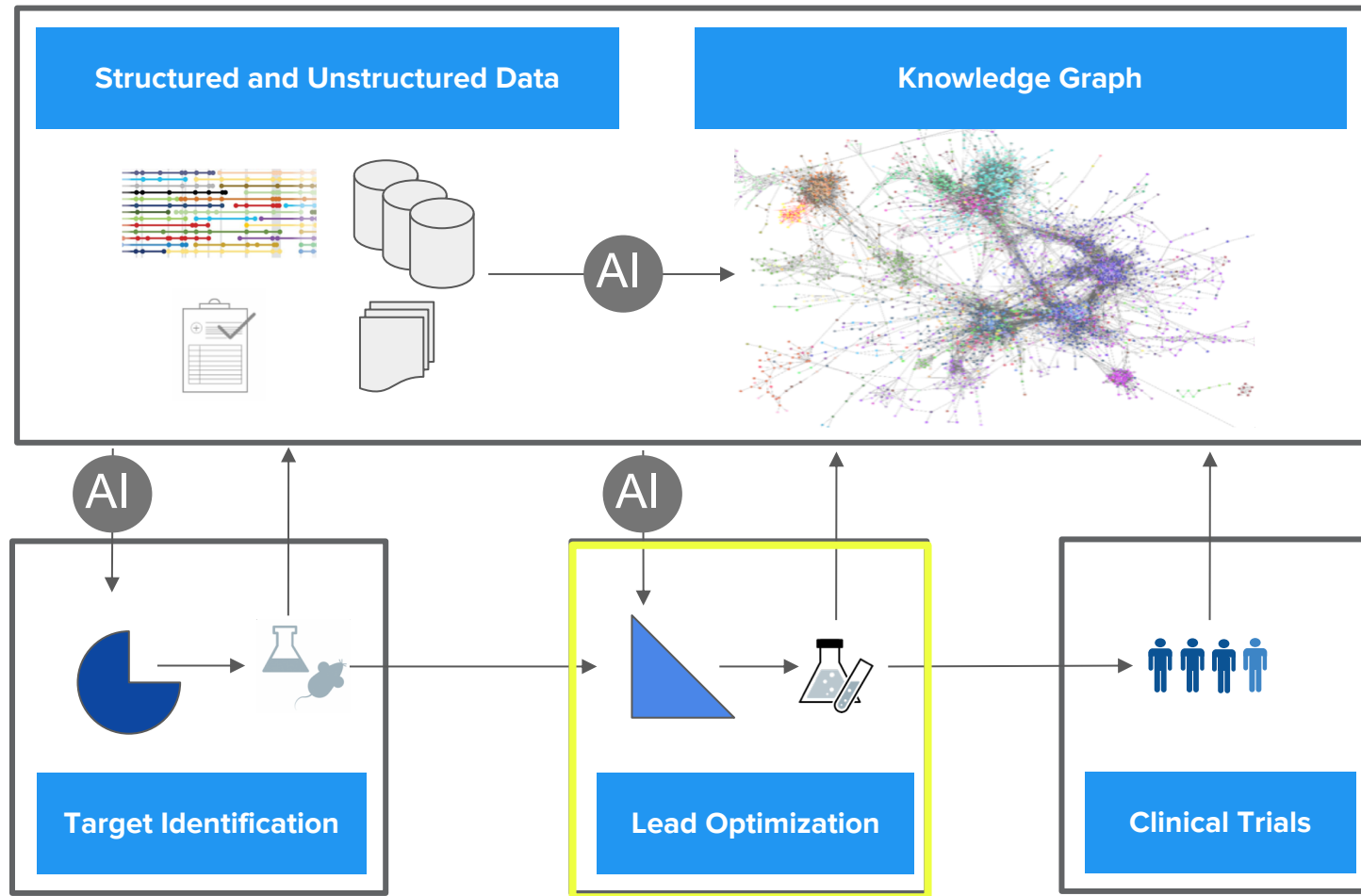
Drug Discovery is an Arduous and Expensive Process



\$1.8B and >10 Years to Bring a Drug to Market

Source: *Developability assessment as an early de-risking tool for biopharmaceutical development*, J. Zurdo, 2013, DOI: 10.4155/pbp.13.3

Our Journey from Data to Drugs with Machine Learning



Exploring the Compound Universe is Challenging

- Compound space is large (10^{20} - 10^{60} , depending on definition) and discrete



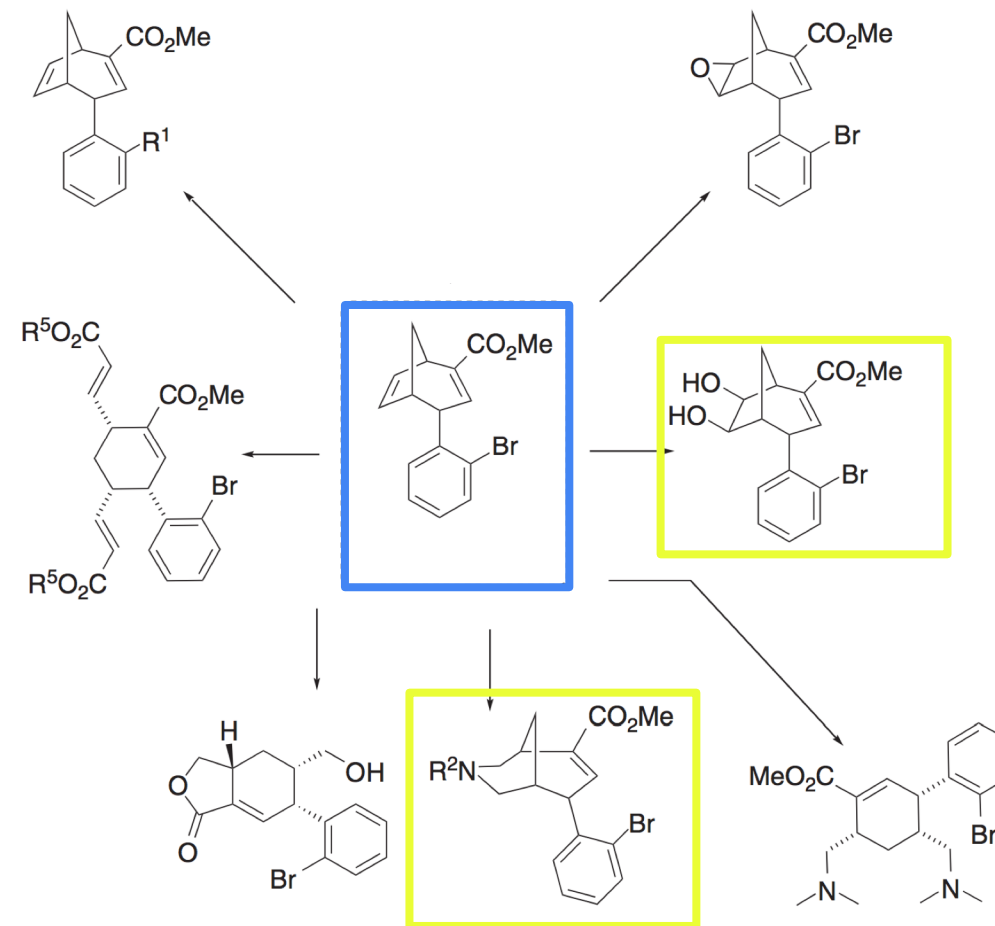
Exploring the Compound Universe is Challenging

- Compound space is large (10^{20} - 10^{60} , depending on definition) and discrete
- Often interested only in regions of compound space



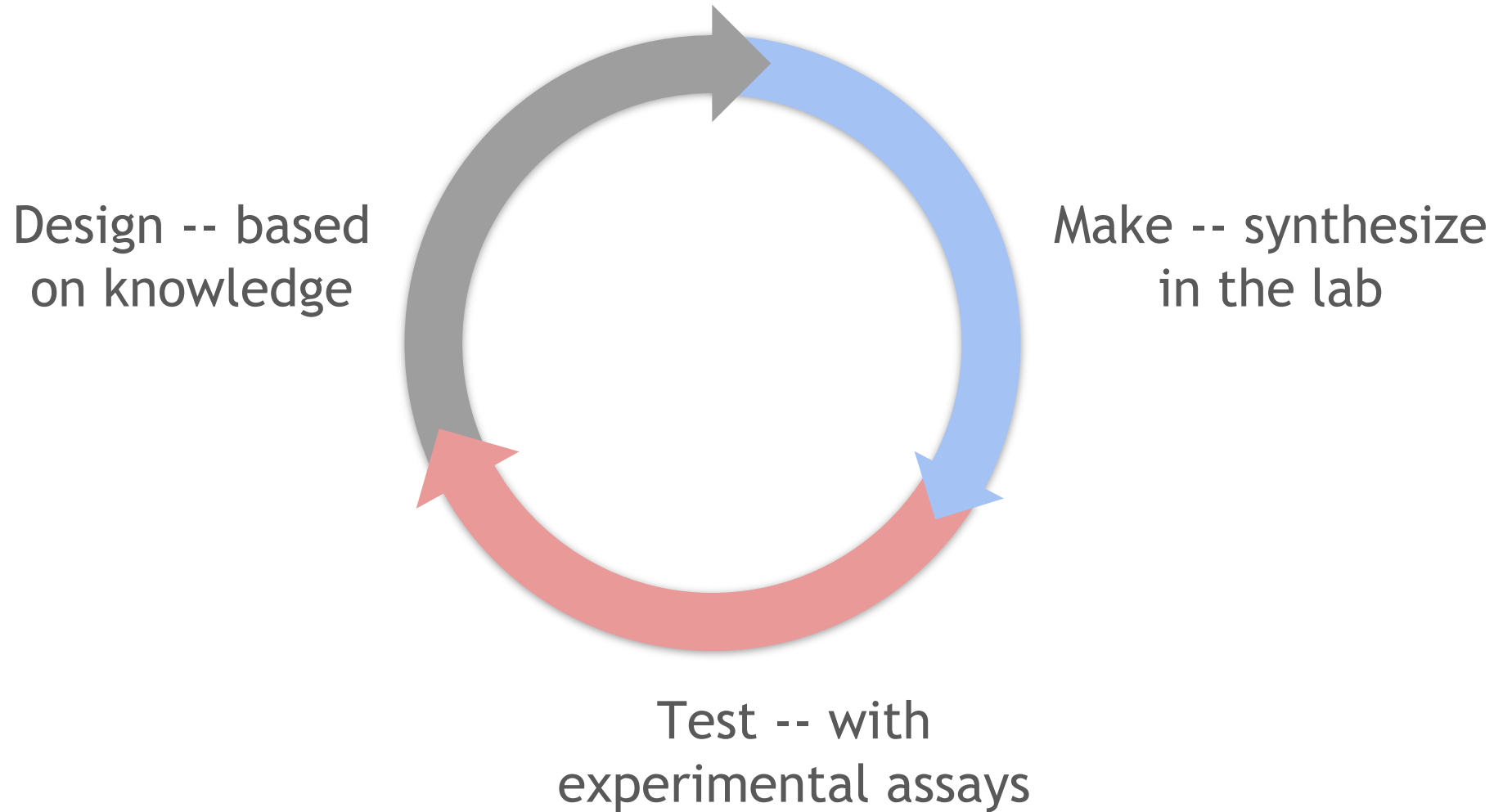
Exploring the Compound Universe is Challenging

- Compound space is large (10^{20} - 10^{60} , depending on definition) and discrete
- Often interested only in regions of compound space
- Identify compound which binds to target, then use local exploration to improve other properties
- **One solution:** learn search policies or **generative algorithms** to create novel and optimal compounds in regions of interest



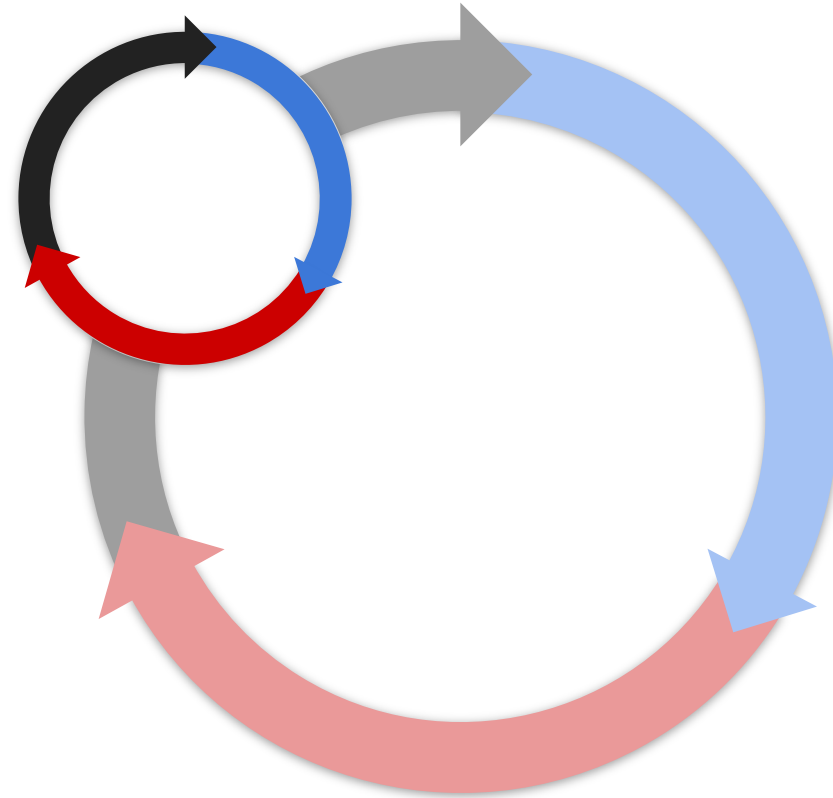
How can we efficiently explore the
compound universe in a property driven
way?

The Compound Design Cycle



De novo Design mimics the Compound Design Cycle

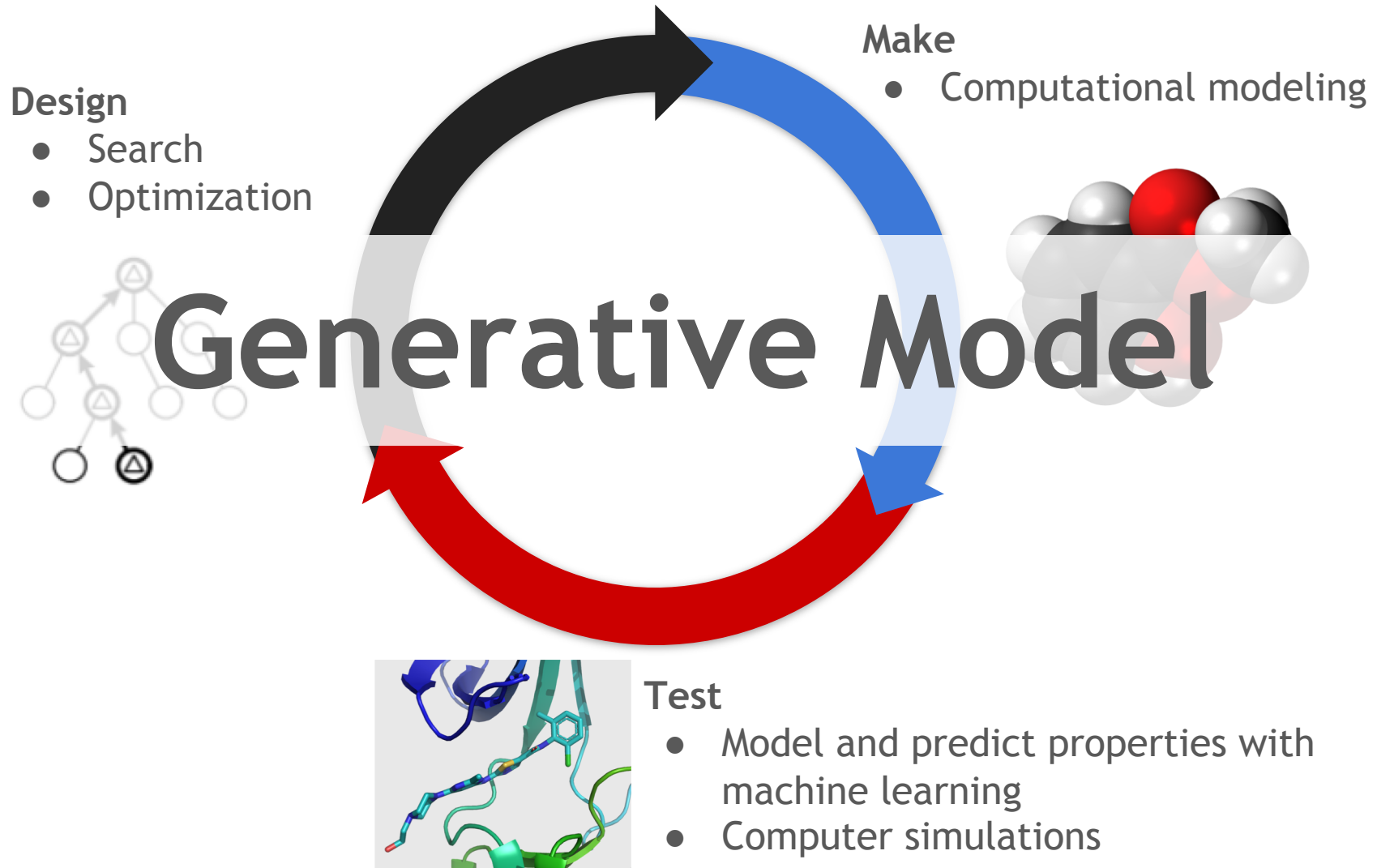
De novo Design



Make

Test

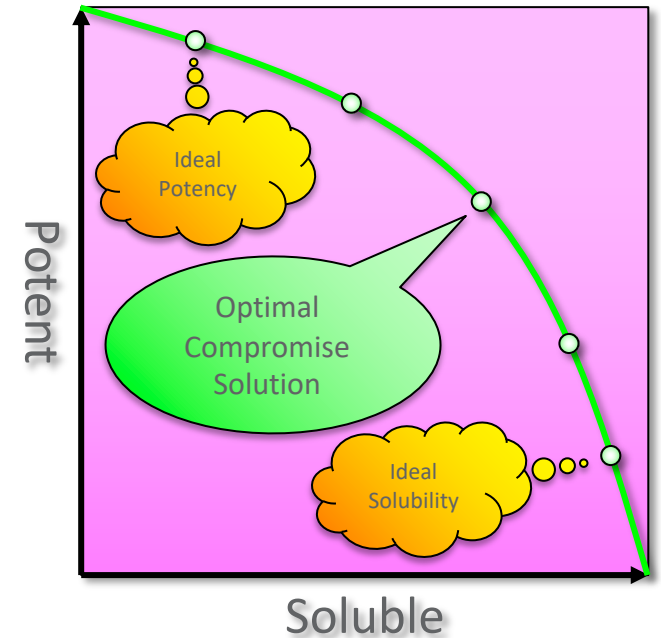
De novo Design



Multi-Parameter Objective Optimization

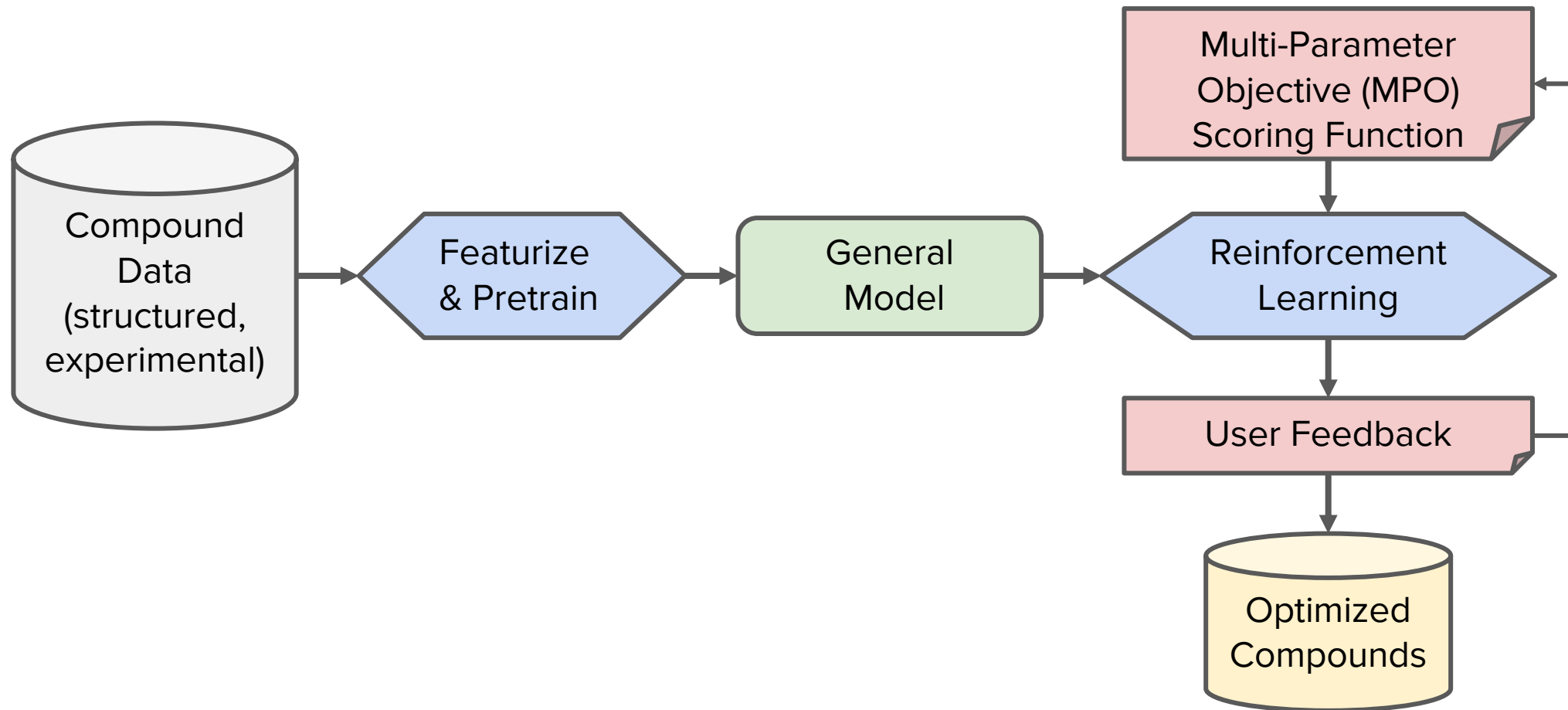
Focus on multiple properties:

- Affinity -- binds to target well
- Toxicity -- isn't harmful to organism
- Selectivity -- binds to only the desired target



Drug design is inherently a multi-objective optimization problem

Learning to Generate the Best Compounds



Aside: machine learning has a long history
in chemistry

Machine Learning & Chemistry: Long Time Acquaintances

Analytica Chimica Acta, 248 (1991) 1–30
Elsevier Science Publishers B V , Amsterdam

1

Review

Neural networks: A new method for solving chemical problems or just a passing phase?

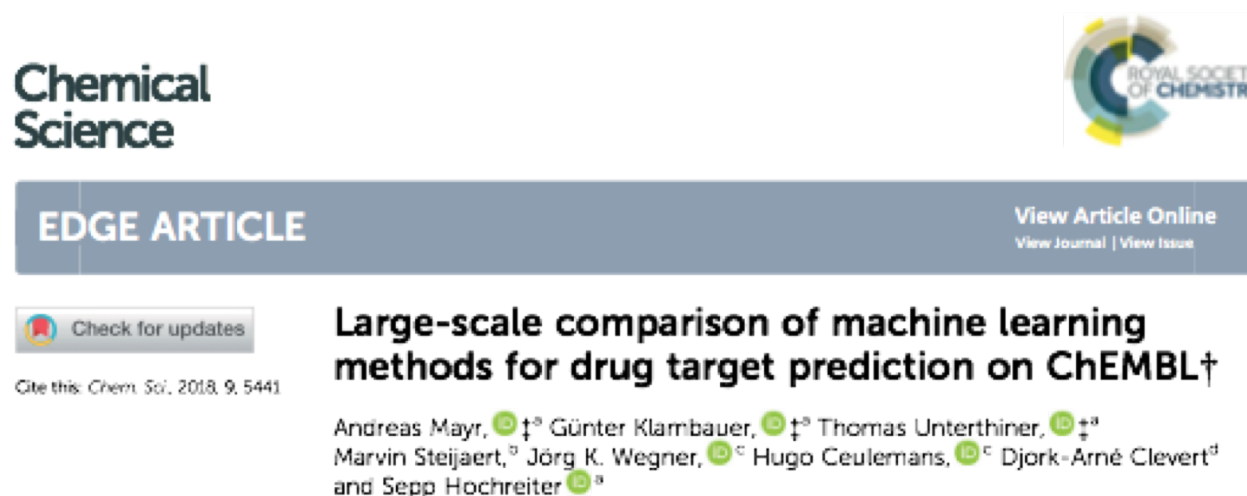
J. Zupan ^{*.1} and J. Gasteiger

Organisch-chemisches Institut, Technische Universität München, D-8046 Garching (Germany)

(Received January 1991)

Feed-forward neural networks have decades of history in computational chemistry

Machine Learning & Chemistry: Long Time Acquaintances



The image shows a screenshot of a journal article page from Chemical Science, published by the Royal Society of Chemistry. The article is an 'EDGE ARTICLE' and is titled 'Large-scale comparison of machine learning methods for drug target prediction on ChEMBL†'. The authors listed are Andreas Mayr, Günter Klambauer, Thomas Unterthiner, Marvin Steijaert, Jörg K. Wegner, Hugo Ceulemans, Djork-Arné Clevert, and Sepp Hochreiter. The page includes a 'Check for updates' button, a citation reference 'Cite this: Chem. Sci., 2018, 9, 5441', and links to 'View Article Online', 'View Journal', and 'View Issue'.

Chemical Science

ROYAL SOCIETY OF CHEMISTRY














EDGE ARTICLE

View Article Online
View Journal | View Issue

Check for updates

Cite this: *Chem. Sci.*, 2018, 9, 5441

Large-scale comparison of machine learning methods for drug target prediction on ChEMBL†

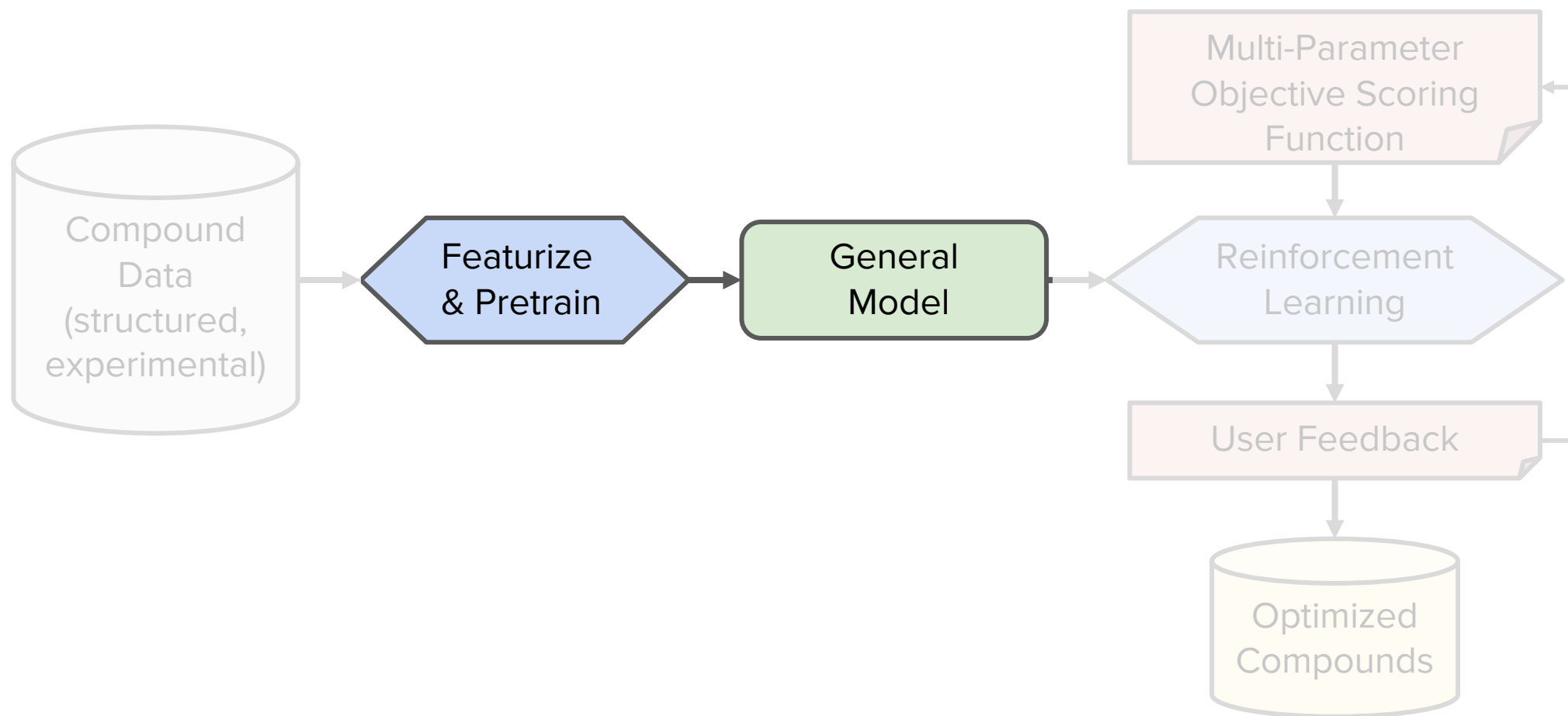
Andreas Mayr,   Günter Klambauer,   Thomas Unterthiner,  
Marvin Steijaert,   Jörg K. Wegner,   Hugo Ceulemans,   Djork-Arné Clevert[‡]
and Sepp Hochreiter 

(Received January 2018)

Feed-forward neural networks have decades of history in computational chemistry

Large chemical datasets have fueled recent successes with deep neural networks

Learning to Generate the Best Compounds



How can neural networks be used to
predict compounds?

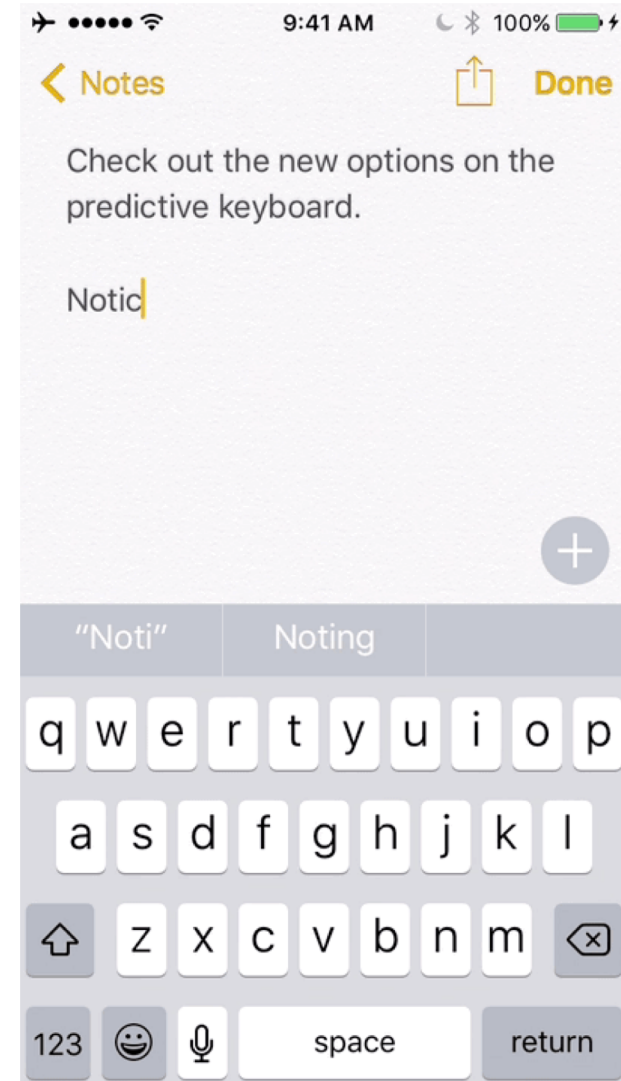
Language Models

Predict probability of next word in a sentence

Chemistry is _____?

amazing
difficult

potato
compares

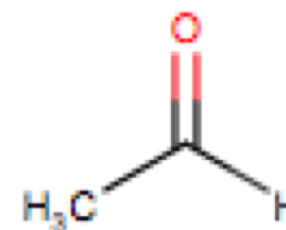


Language Models for Chemistry?

Chemistry → is → ?

Use SMILES!

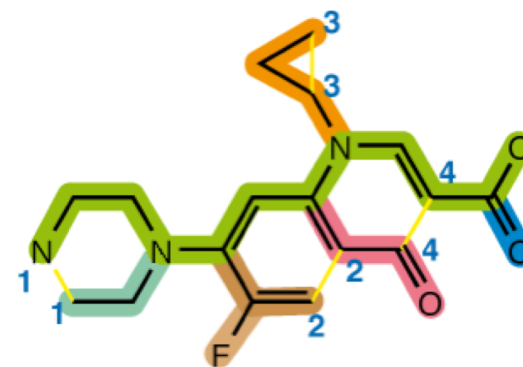
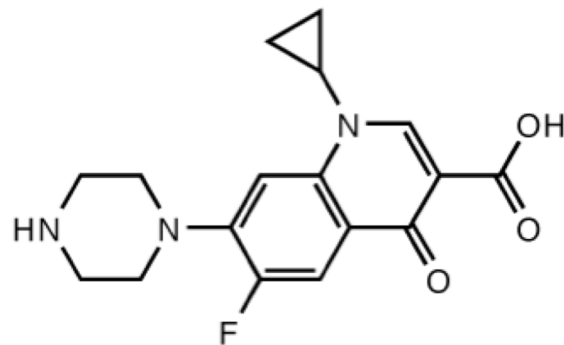
C → C → = → ?



Predict the probability of next character

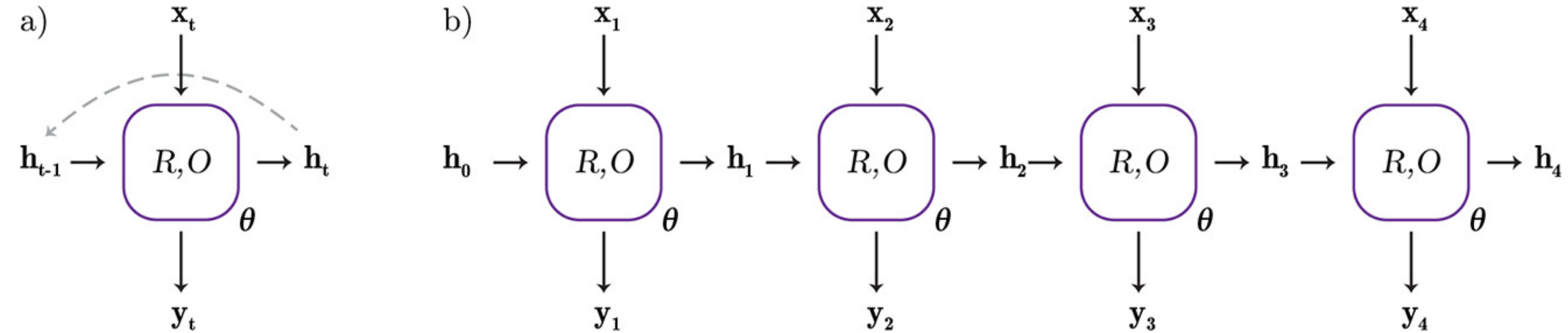
Featurizing Compounds with SMILES

- Simplified Molecular Input Line-Entry System (SMILES)
- Symbolic string obtained from depth-first traversal of a compound graph
- Multiple variations -- standardization is challenging
- Chemical rules must be obeyed for validity

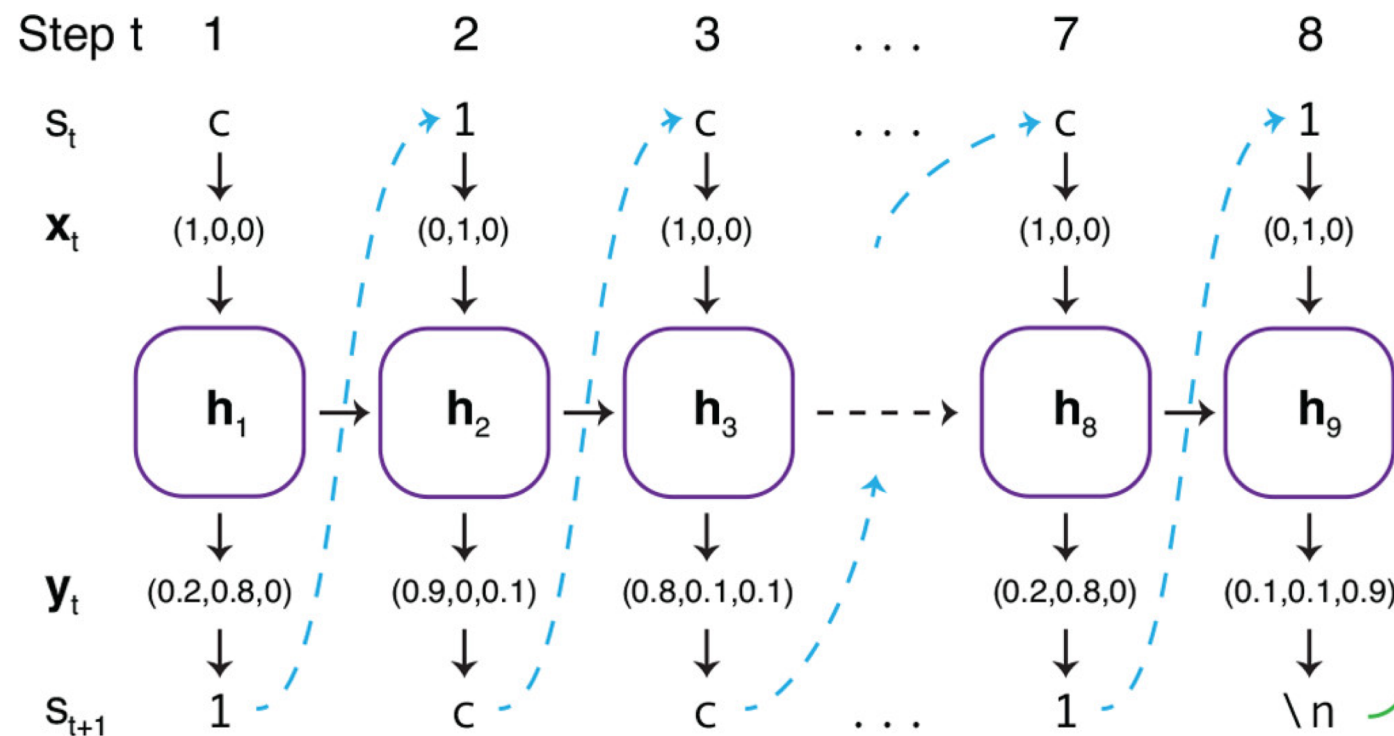


N1CCN(CC1)C(C(F)=C2)=CC(=C2C4=O)N(C3CC3)C=C4C(=O)O

Recurrent Neural Networks (RNNs)

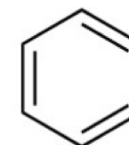


Probing Compound Space with RNNs

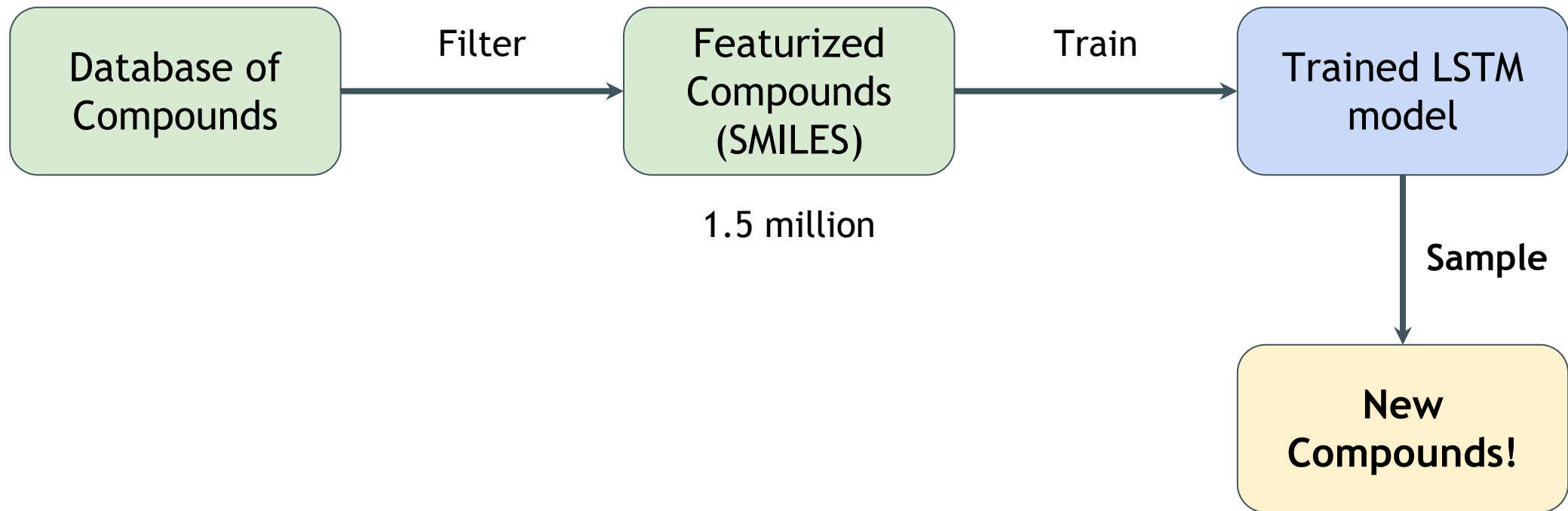


- Network is a character-level LSTM with initial embedding layer and teacher forcing
- Trained with SMILES representations of compounds from database

gather symbols c1ccccc1\n

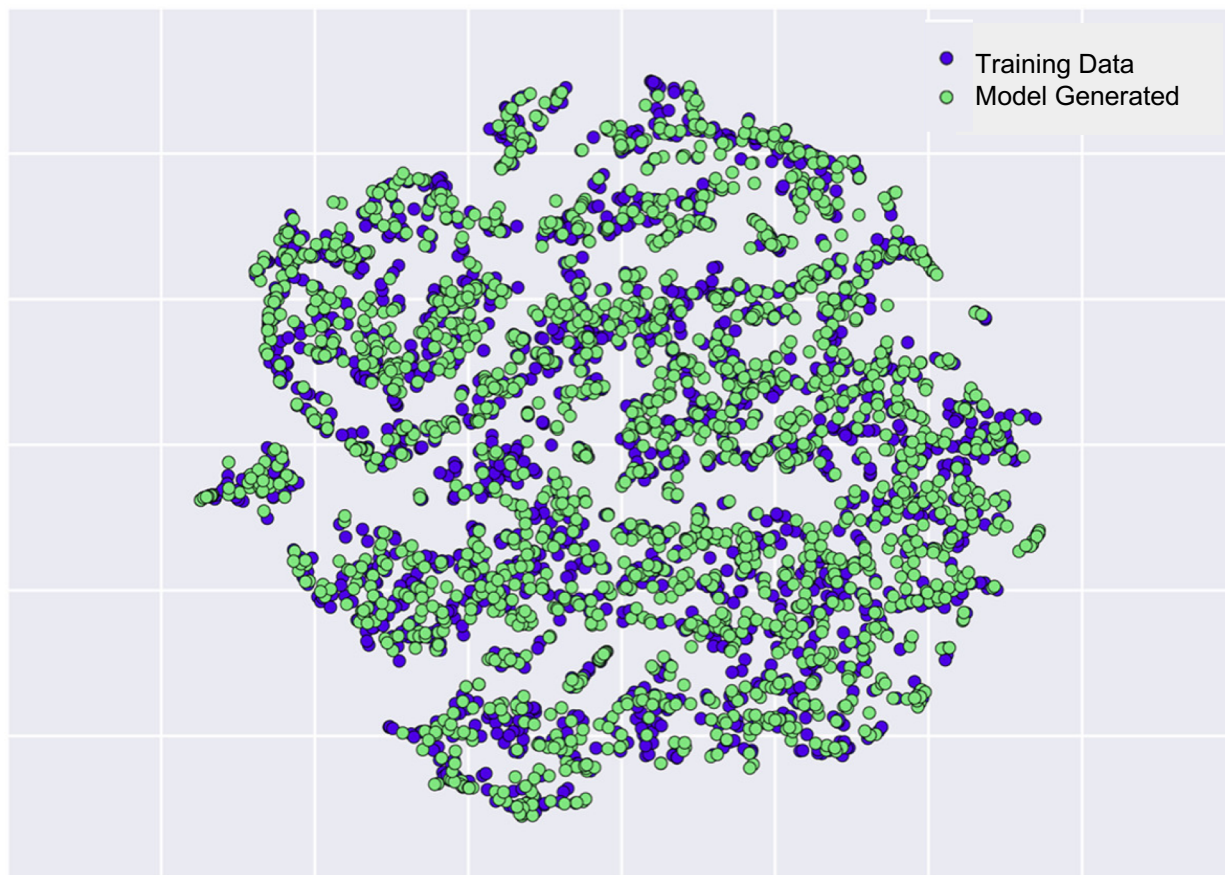


Probing Compound Space with RNNs



Probing Compound Space with RNNs

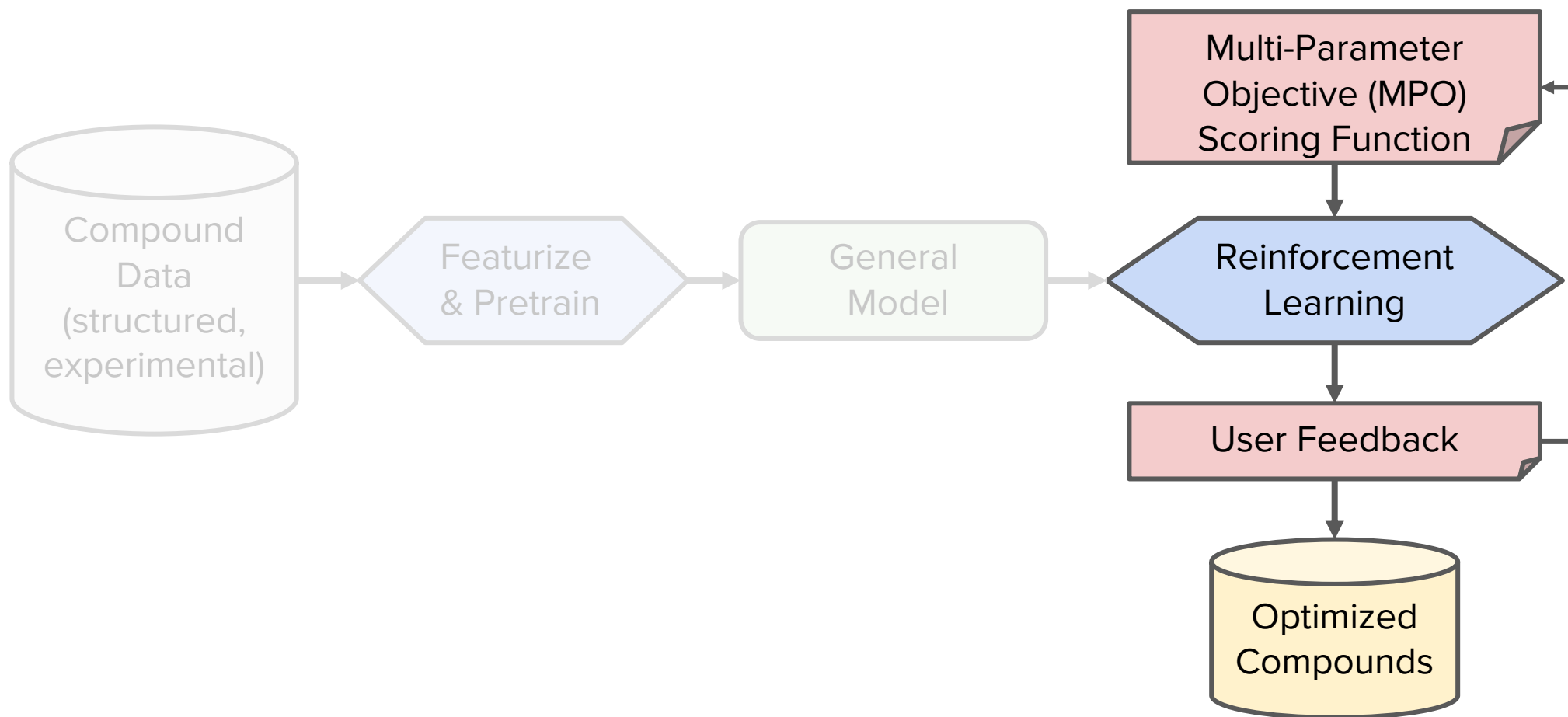
t-SNE of Compound Properties



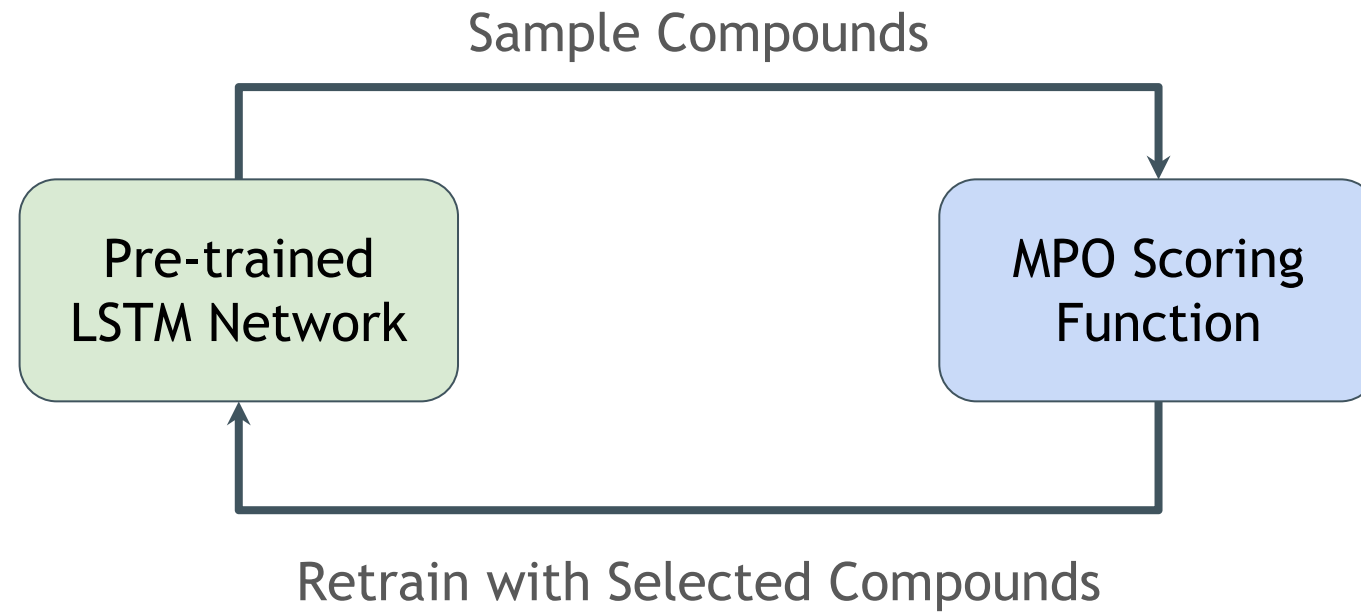
- Distribution of physical properties in training data as reproduced by sampling from model
- SMILES strings produced are:

95% valid
90% novel

Learning to Generate the Best Compounds



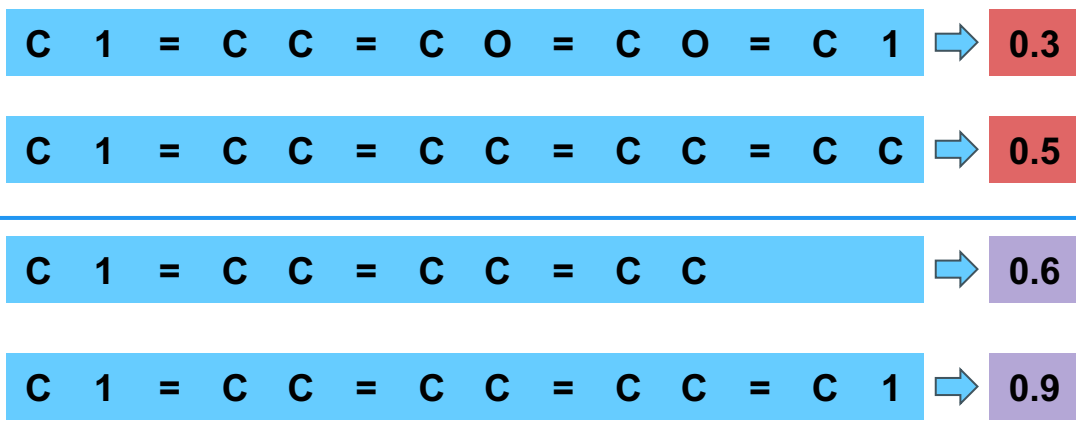
Reinforcement Learning (RL) Rounds



Model Refinement with RL and User Feedback

Compounds from Model

Score



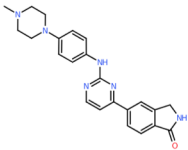
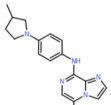
1. Sample compounds from retrained model and score according to MPO
2. Select best compounds for another round of retraining or to present to user

User Feedback Sessions

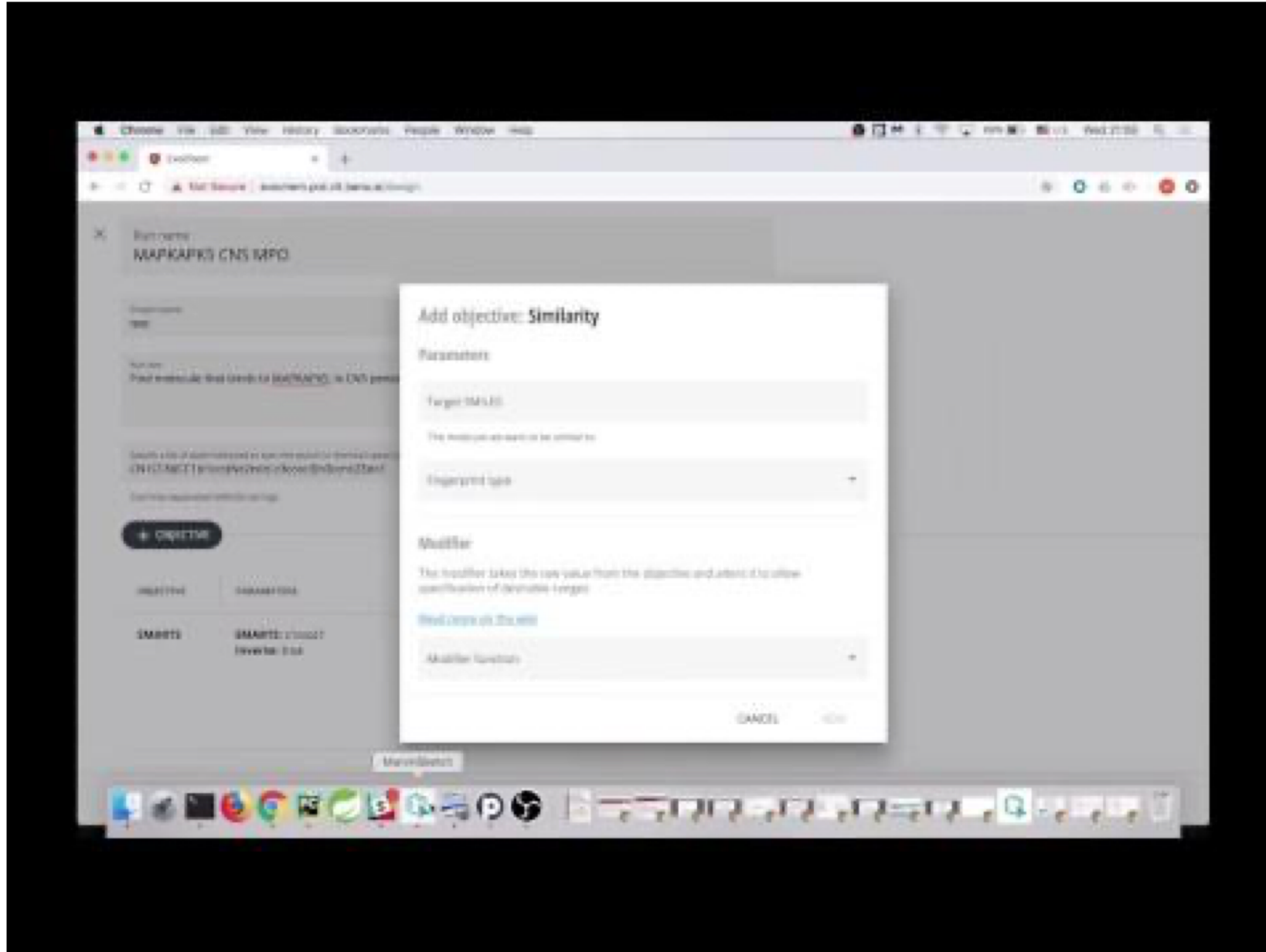
MAPKAPK5 CNS MPO

SEE MPO DETAILS START NEW FROM THIS MPO

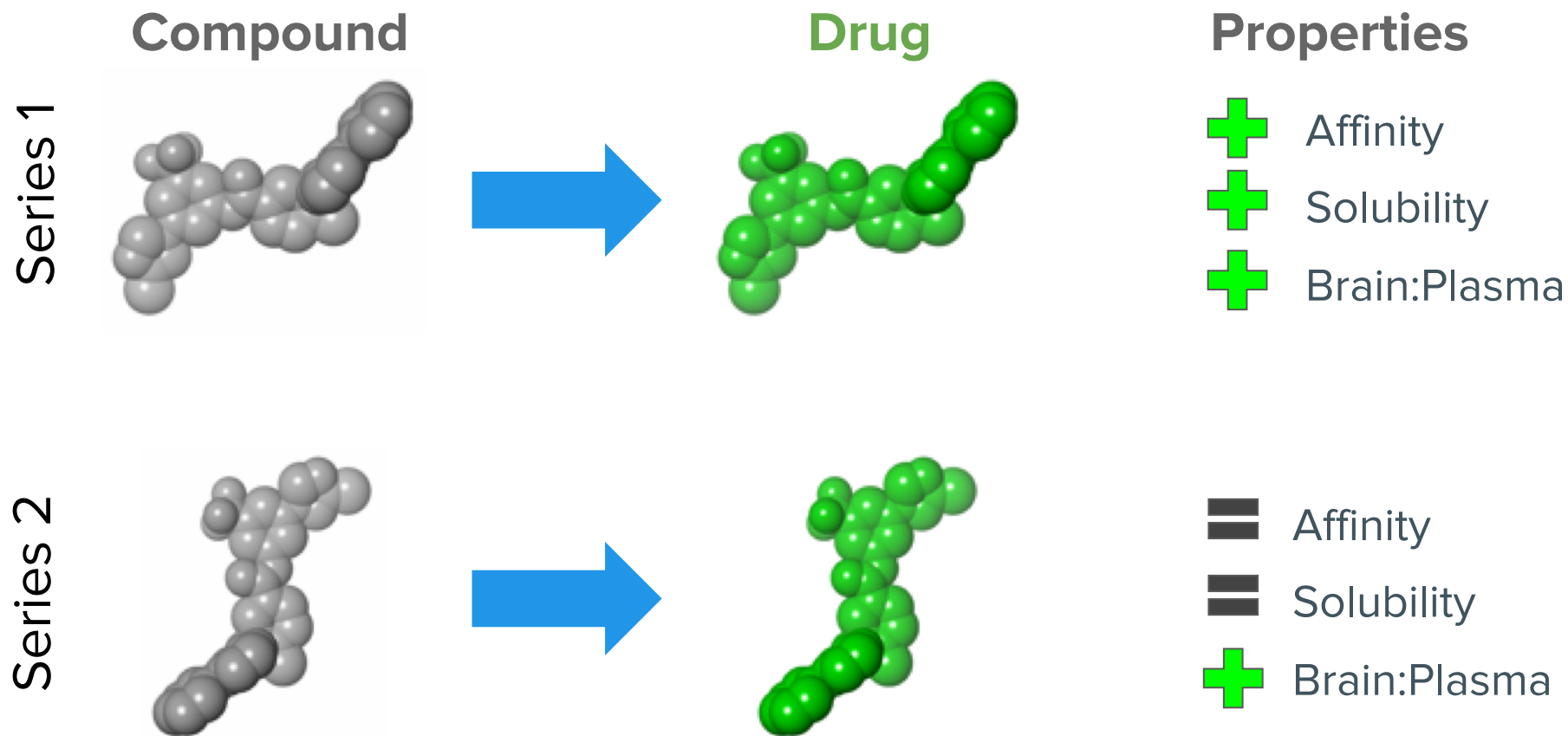
Selected Sent to LiveDesign Not sent to LiveDesign Flagged SEND MOLECULES TO LIVEDESIGN

#	STRUCTURE	SCORE	LOGP	MOLW	MPO PROPERTIES	STATUS
<input type="checkbox"/> 1	<chem>CN1CCN(c2ccc(Nc3nccc(-c4ccc5c(c4)CNC5=O)n3)cc2)CC1</chem> 	0.67	2.88	400.49	CNS Score: 0.92 Handbuilt ML model: 0.82 SMARTS: 0 Similarity: 0.95	FLAG
<input type="checkbox"/> 2	<chem>CC1CCN(c2ccc(Nc3nccc(-c4cnn(C)c4)n4ccnc34)cc2)C1</chem> 	0.63	3.72	373.46	CNS Score: 0.98 Handbuilt ML model: 0.56 SMARTS: 0 Similarity: 1	FLAG

MPO Setup & User Feedback



Finding Drugs for ALS with Generative Models



< 3 months vs industry average of 1.5 - 3 years

External Demonstration of Drugs Designed by ML

- First published validation of compounds optimized by machine learning
- Models fine tuned with transfer learning
- Five highly active drugs produced

Communication

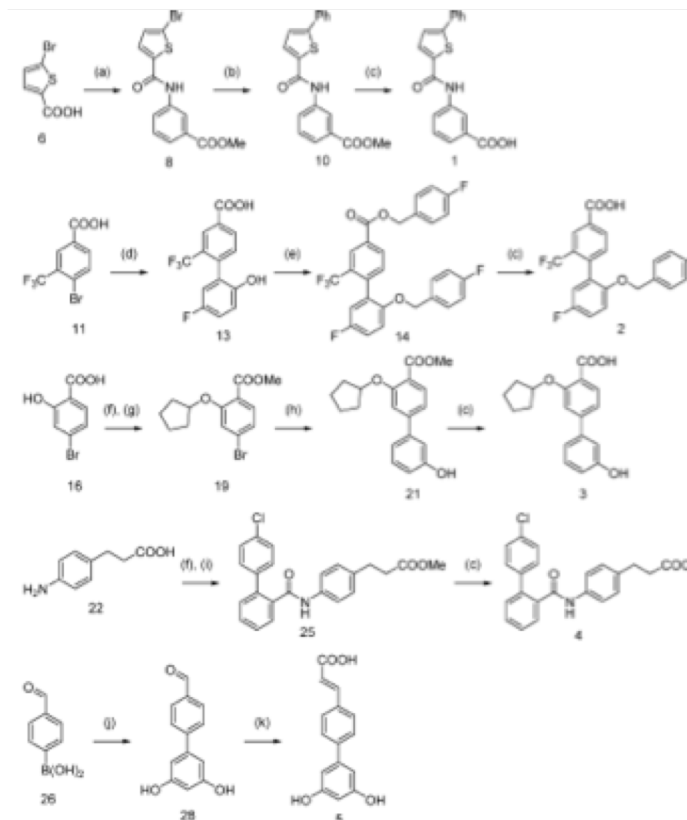
www.molinf.com

molecular
informatics

DOI: 10.1002/minf.201700153

De Novo Design of Bioactive Small Molecules by Artificial Intelligence

Daniel Merk,^[a] Lukas Friedrich,^[a] Francesca Grisoni,^[a, b] and Gisbert Schneider^[a, b]



Benchmarking: How Good is a Generative Model?

Assesses two dimensions:

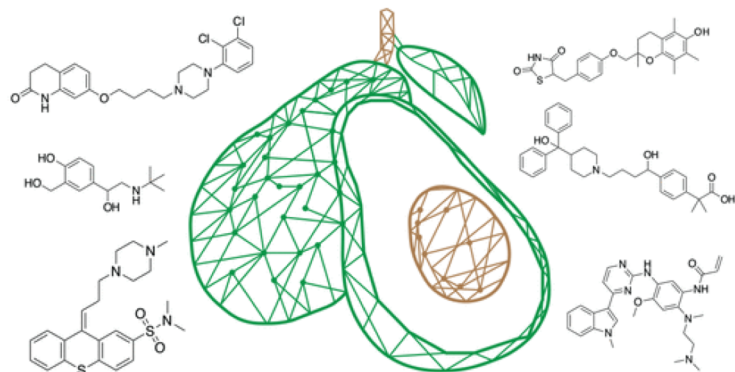
- **Distribution based:** how well a model can learn the chemical distribution of data
- **Goal based:** model generates molecules to satisfy pre-defined goal(s)

GuacaMol: Benchmarking Models for De Novo Molecular Design

Nathan Brown, Marco Fiscato, Marwin H.S. Segler, Alain C. Vaucher

<https://arxiv.org/abs/1811.09621>

Code: <https://github.com/BenevolentAI/guacamol>





BenevolentAI

Because it matters

Acknowledgements

Marwin Segler, Nathan Brown, Dan Neil, Alix Lacoste

Michelle Gill: michelle.gill@benevolent.ai

Twitter: [@modernscientist](https://twitter.com/modernscientist)

Website: <https://benevolent.ai>