

Lead Optimization Design Cycle in Orion

Matt Geballe

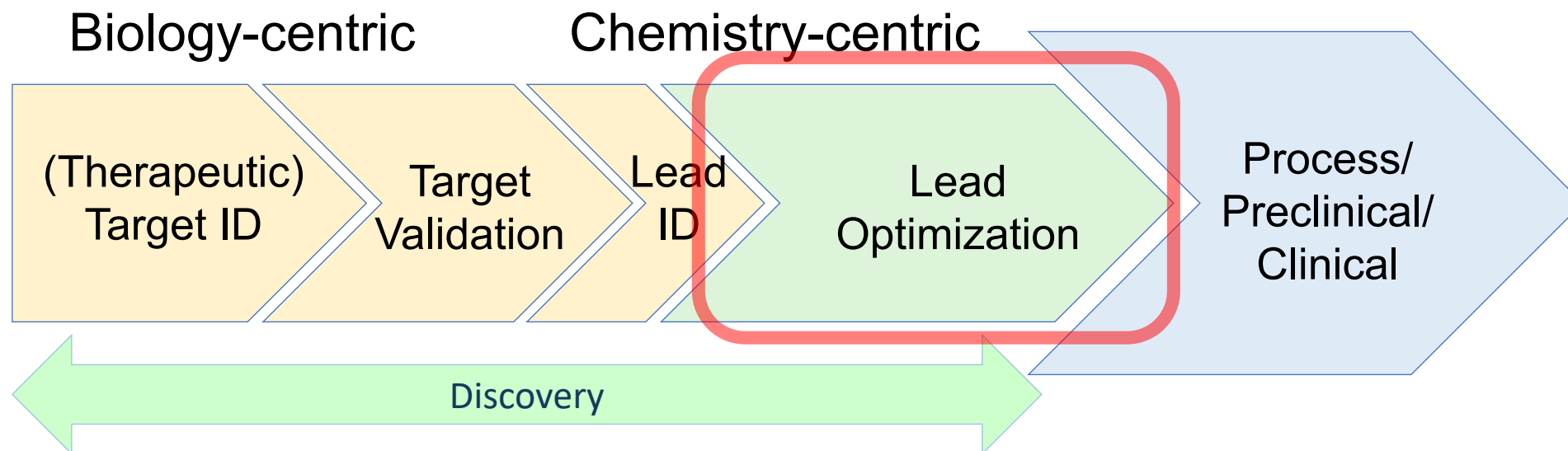
Head of Cheminformatics & Data Science

CUP 2023

Agenda

- Lead Optimization
- Generating Synthetically Accessible Candidates
- Machine Learning and Lead Opt

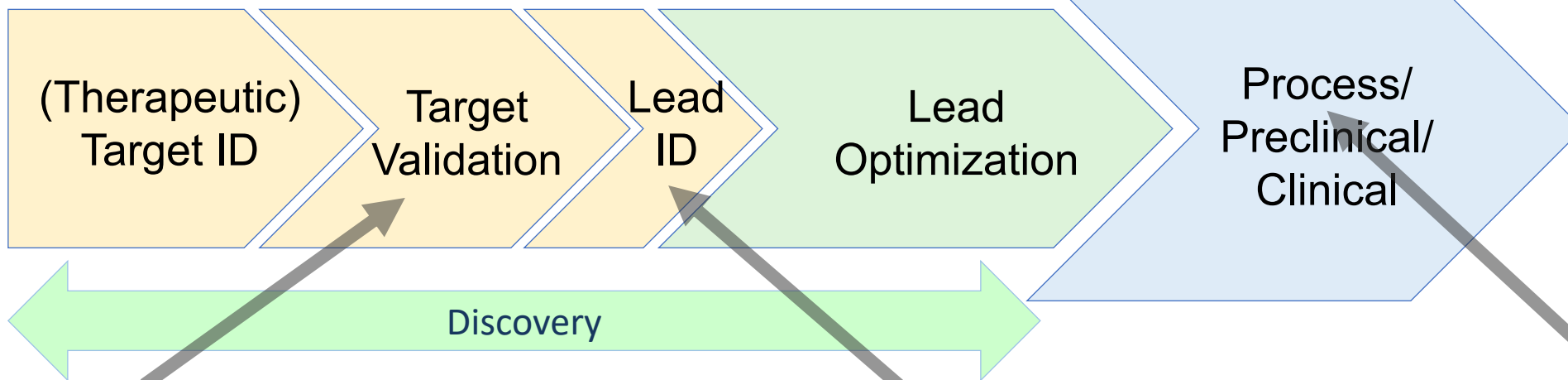
Drug Discovery Process



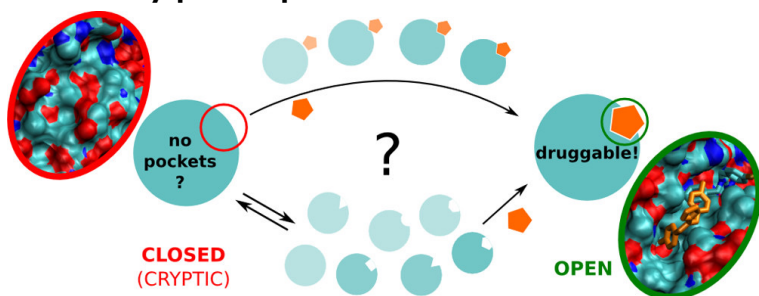
Drug Discovery Process

Biology-centric

Chemistry-centric



Cryptic pocket detection



2D Ligand-Based

Screening by 2D structure and/or fingerprint
([GraphSim Tk](#))

3D Ligand-Based

Search billions of molecules in minutes. Extremely fast screening by shape and chemical-features similarity
([ROCS](#), [FastROCS](#), [FastROCS Plus](#))

3D Structure-Based

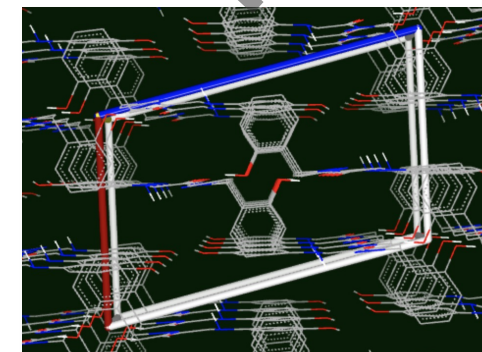
Dock billions of molecules with Gigadock™, for the most rigorous results, and with Gigadock Warp, when speed and affordability matters ([Gigadock](#), [Gigadock Warp](#))

Combined 3D Ligand- and Structure-Based

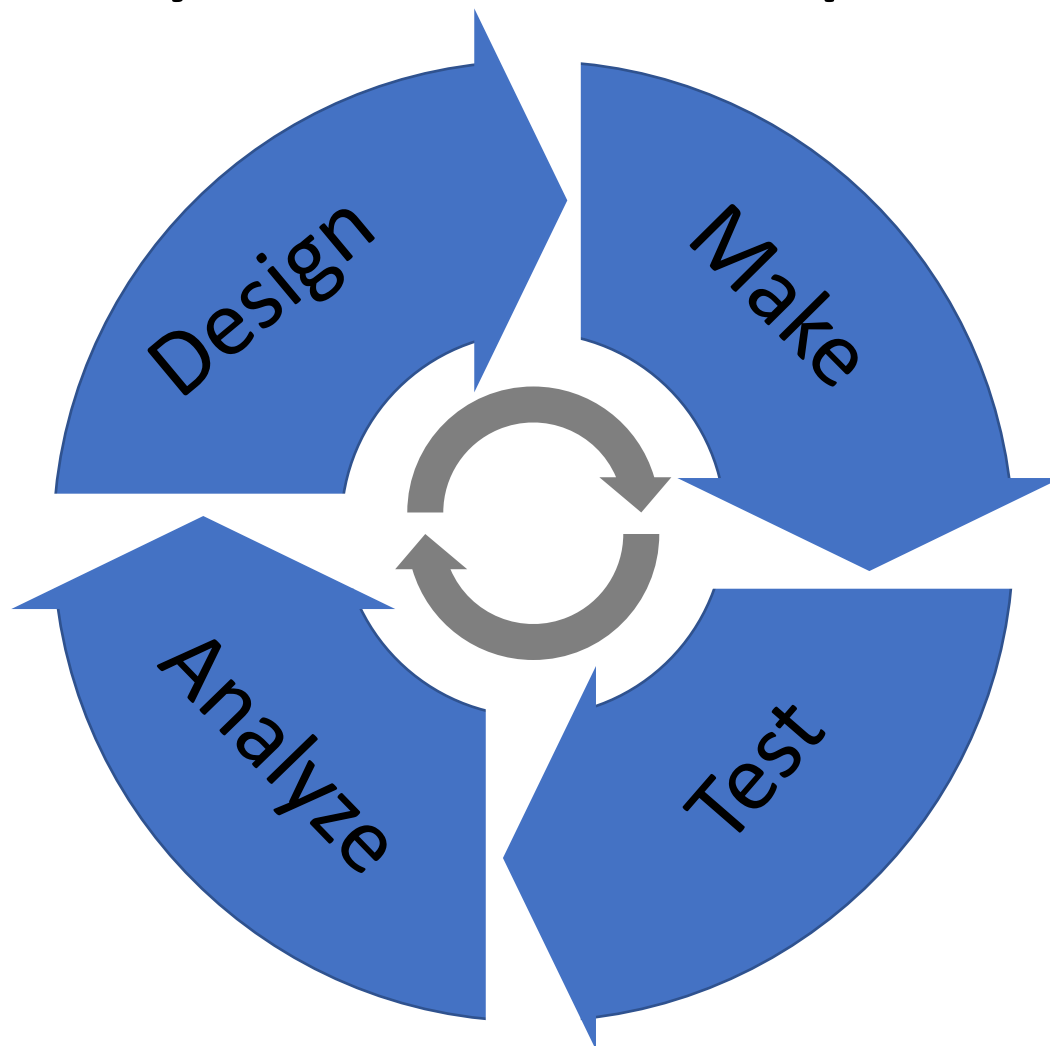
Ready-to-use workflows that combine the best of 3D ligand- and structure-based methods ([FastROCS Plus](#), [Gigadock Warp](#))

Property Calculation and Filter

Calculate molecular properties and filter out undesirables ([FILTER](#))



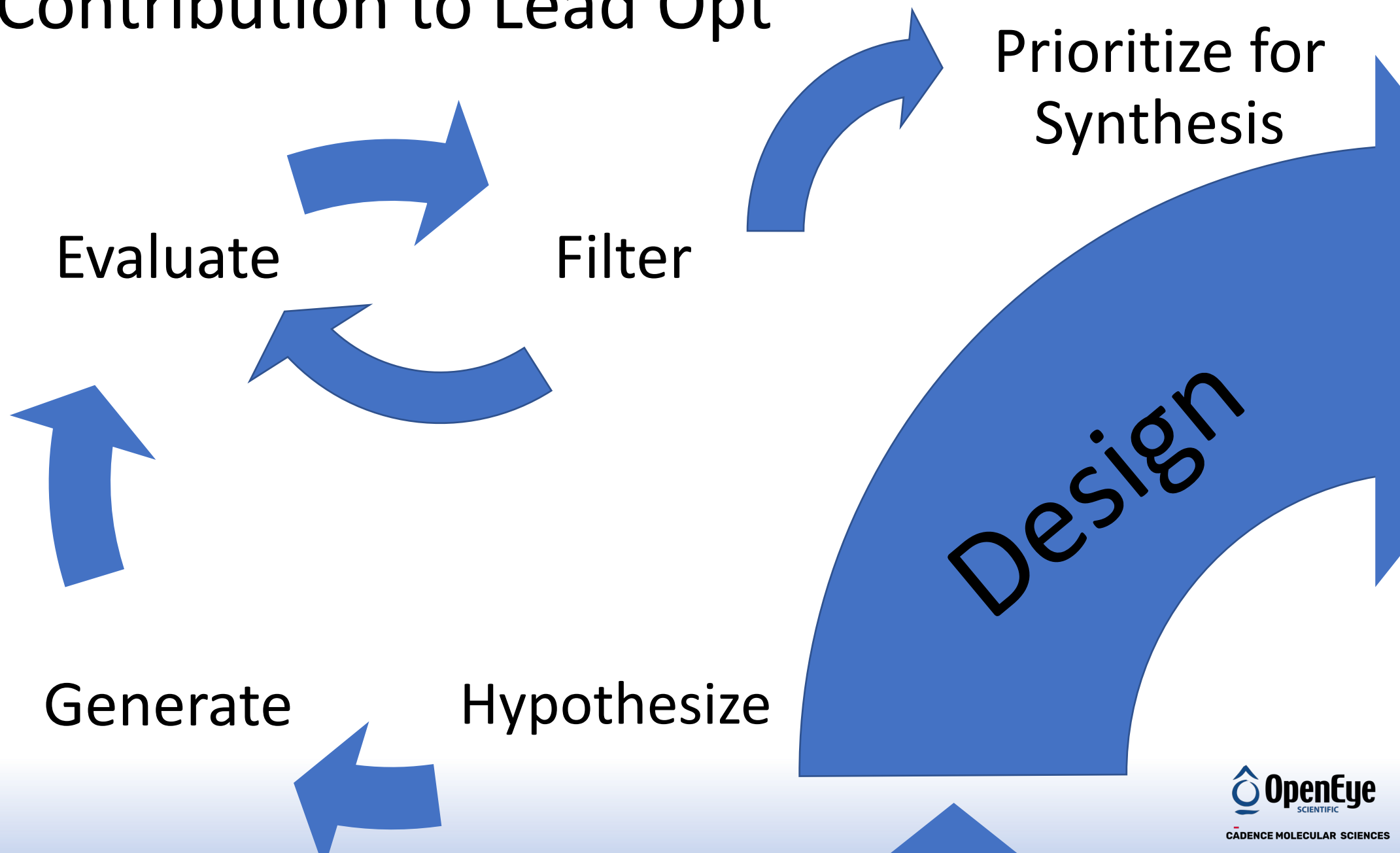
DMTA Cycle in Lead Optimization



- Multiple goals
 - Affinity, ADME-Tox, (Permeability), (Solubility) Selectivity, Synthesizability
 - Priorities shift over Time
- Cycle Time
 - Sequential Process
 - Timelines

Schneider, P., Walters, W.P., Plowright, A.T. *et al.* Rethinking drug design in the artificial intelligence era. *Nat Rev Drug Discov* **19**, 353–364 (2020). <https://doi.org/10.1038/s41573-019-0050-3>

CADD Contribution to Lead Opt



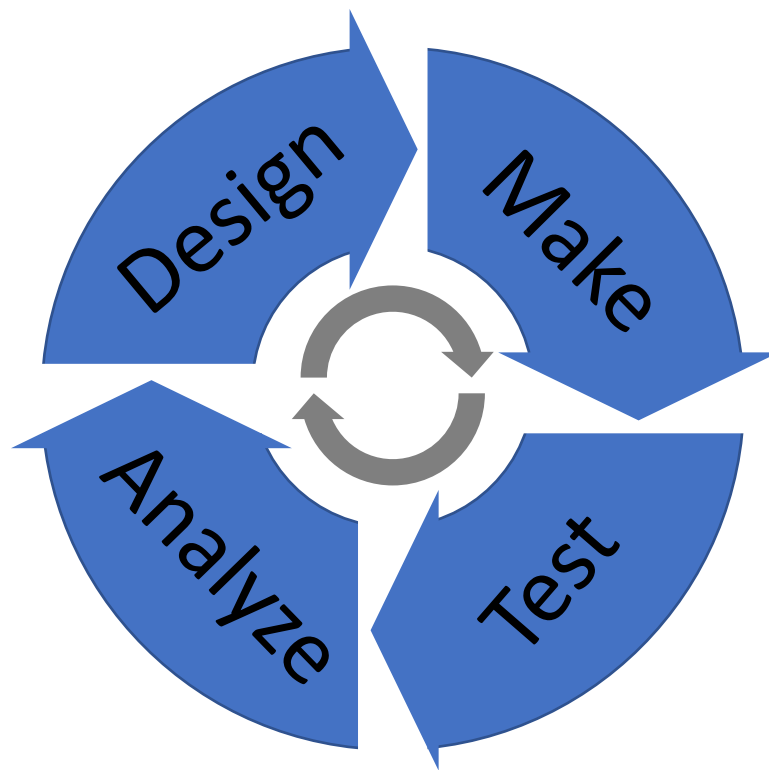
Lead Opt as (too?) Simple Math

Cycle Success $\propto P_{Design}P_{Make}P_{Test}P_{Analyze}$



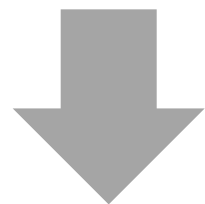
Lead Opt as (too?) Simple Math

Cycle Success $\propto P_{Design} P_{Make} \cancel{P_{Test}} P_{Analyze}$



Lead Opt as (too?) Simple Math

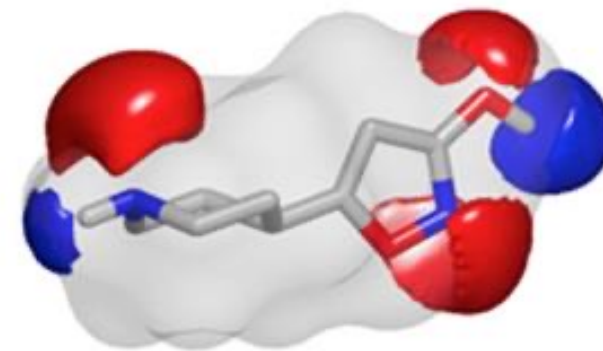
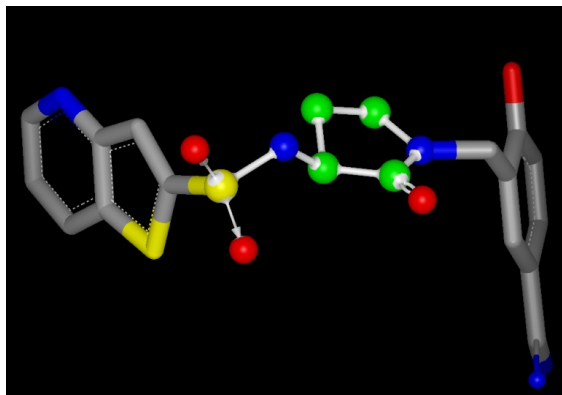

$$\text{Cycle Success} \propto P_{Design} P_{Make} \cancel{P_{Test}} P_{Analyze}$$



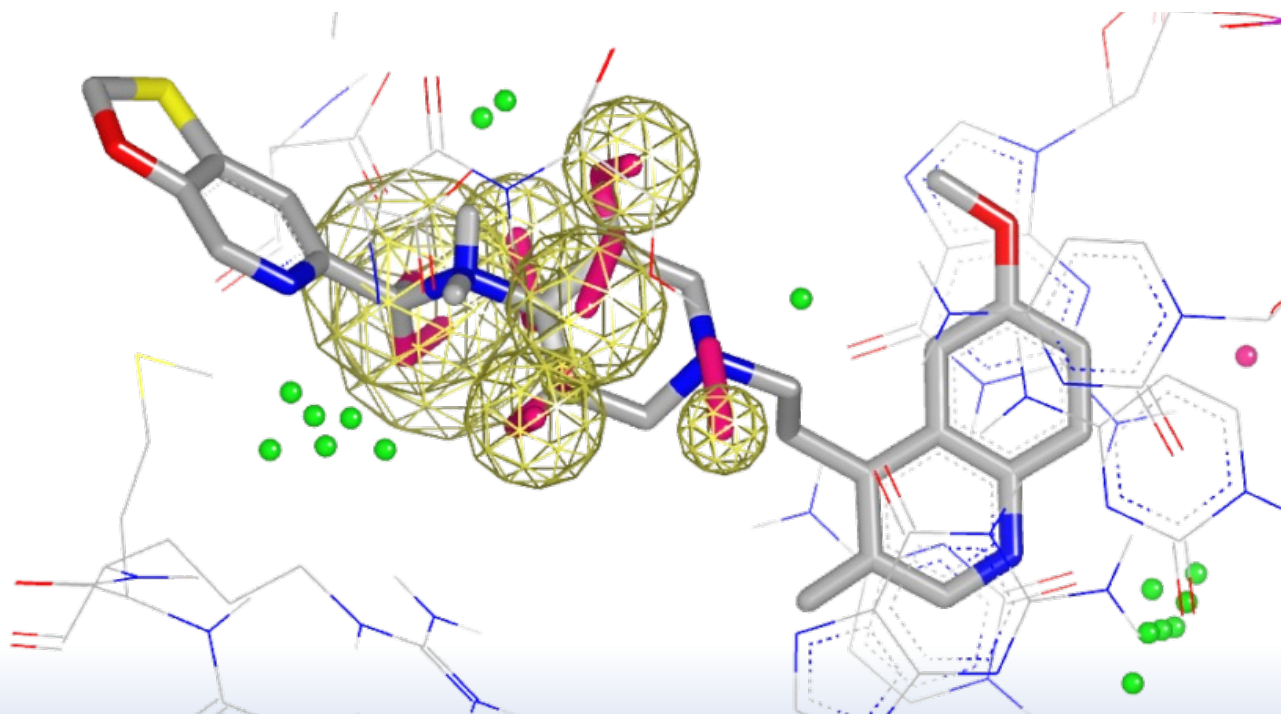
$$\text{LeadOpt Success} \propto P_{Improve} P_{Make}$$

Traditional OpenEye Apps/TKs for Lead Opt

- BROOD
- EON
- FreeForm



- SZMAP/GamePlan
- POSIT



What Orion Brings to the Lead Opt Table

- Platform
 - Central Data Management
 - Scaling Compute Capacity
 - UI for Analysis & Collaboration
- Foundational OE Tools
- New Tools
 - Generating Accessible Candidates
 - ML Models
 - Induced Fit Docking
 - Affinity Prediction



Agenda

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- Machine Learning and Lead Opt

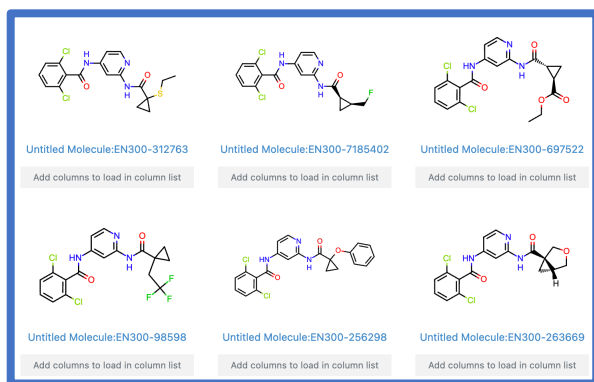
Consider Synthetic Effort at the Beginning

Prioritize for
Synthesis

Evaluate

Filter

Design



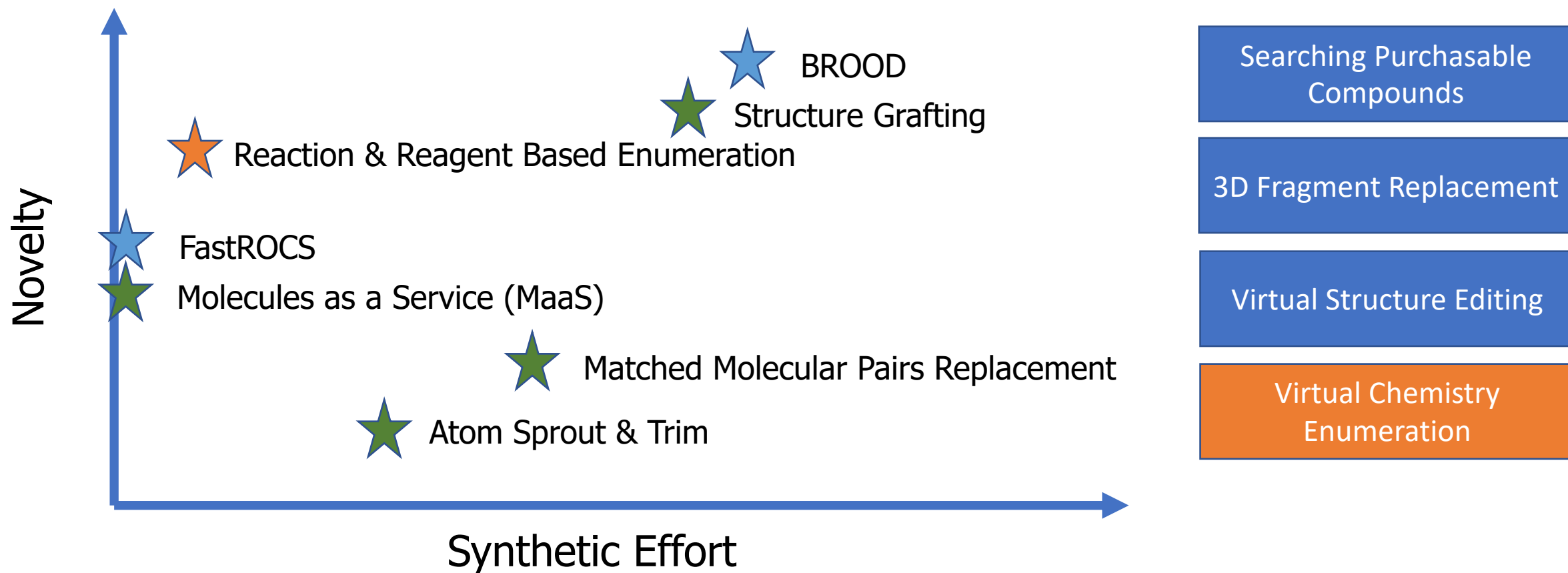
↑↑↑ Focused Library
Generation

P_{Make}

Generate

Hypothesize

Library Generation – “Ideas” on Demand



All methods have push-button execution and capability to build customizable databases/libraries

Building the Foundation – Moieties

Shared definition of **MOIETIES** for all higher-level data structures to use:

<MOIETY>

Suzuki Boronics

Aldehydes

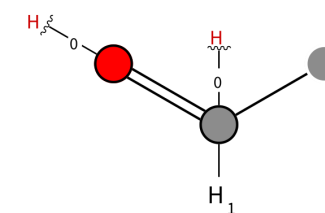
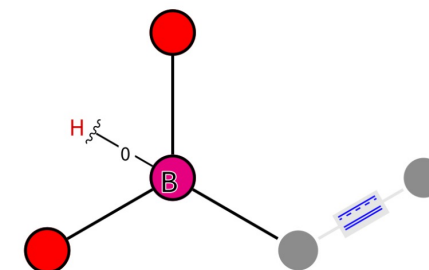
Alkyl bromide

...

[BD3]([#6]=,:[#6])(-O)-O

[OD1]=[CD2H]-[#6]

CBr



Moieties

Visualization created with: <https://smarts.plus/>

Building the Foundation – Reagent Types

Qualifies compounds as **REAGENT TYPE**
based on **MOIETIES** present and/or absent:

<REAGENT_TYPES>

Reaction: **Suzuki_cross_coupling**; Reagent: **Suzuki_boronics**

suzuki_boronics = 1

acetal = 0

acid_chlorides = 0

aldehydes = 0

amidines = 0

amines_aliphatic_primary = 0

amines_aromatic_primary = 0

arylbromide = 0

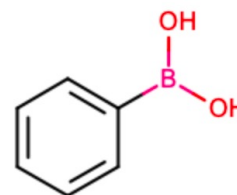
carboxylic_acids = 0

chloroformates = 0

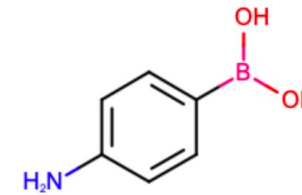
...etc.

Reagent Types

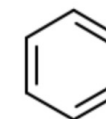
Moieties



Yes



No



No

Building the Foundation – Reaction Definitions

Define **REACTION** by list of classified reagents, SMIRKS to specify transformations of reagents to product structures

<REACTIONS>

Suzuki_cross_coupling

[c!\$(c:c=O):1]-[Cl,Br:2].[BD3:3](#[6:4]=,:[#6])(-[O:5]) [O:6]>>[#6:4]-[c:1]

<REAGENTS>

Aryl_bromides

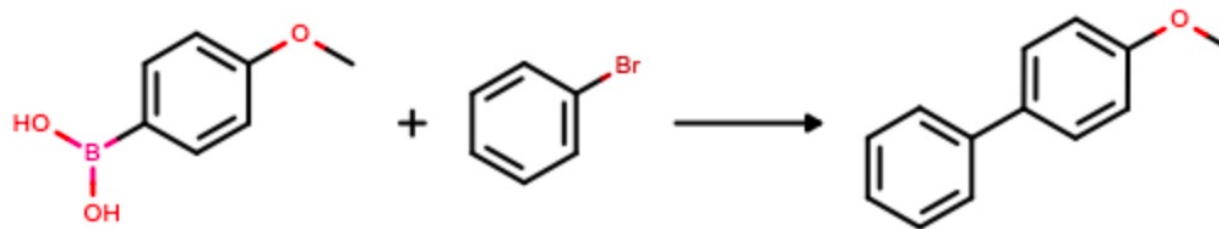
Suzuki_boronics

</REAGENTS>

Reaction Definitions

Reagent Types

Moieties



Definitions for half-reactions (single reagent processing) and retro-transforms are also present


Reaction/Reagent-Based Enumeration

Chemical Moiety Definitions

Reaction: Suzuki cross coupling

Reaction: Buchwald-Hartwig

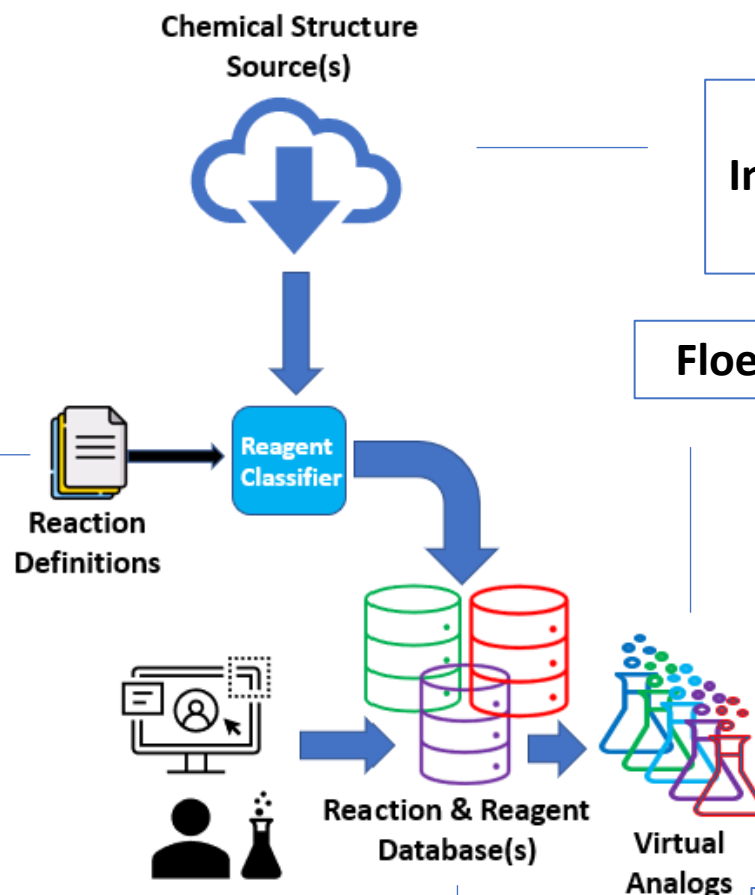
Reaction: Amide Synthesis



Reaction Description

- Reaction Name
- Transformation SMIRKS
- Depiction SMIRKS
- Reactants
 - Amine
 - Acid
- Amine constraints
- Acid constraints
- Reagent half-reactions
- Retro reaction transformation(s)

58 reactions currently defined,
custom definitions possible but
non-trivial

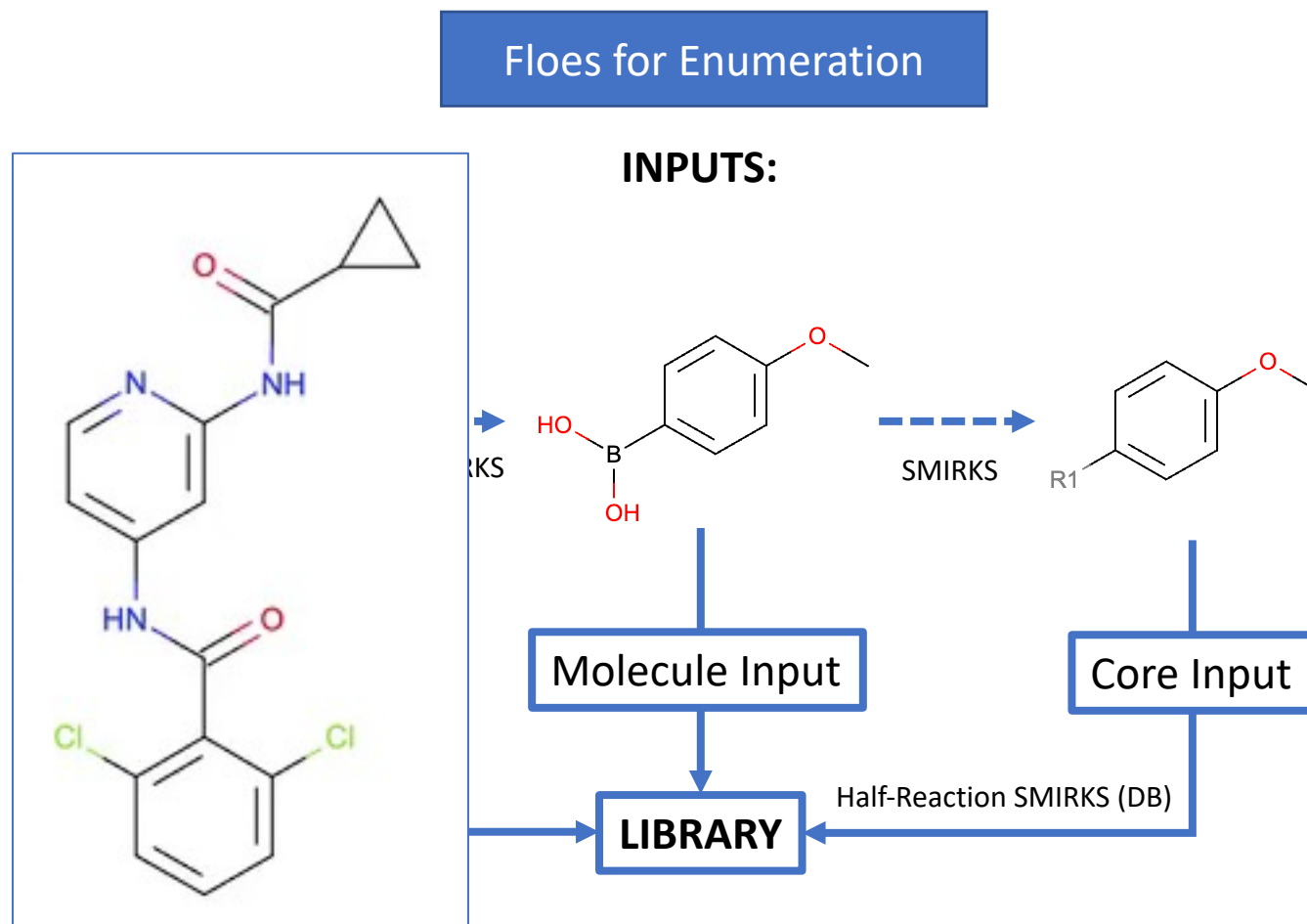
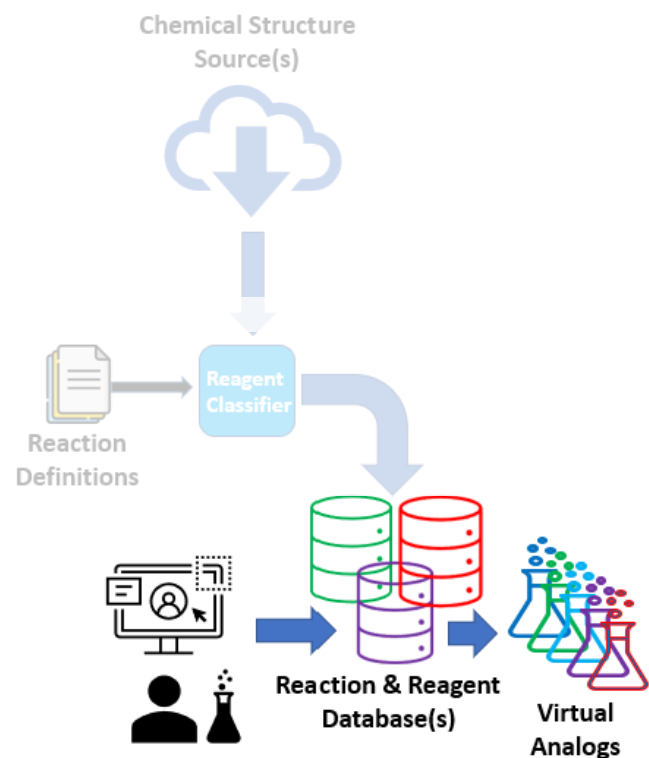


Can use SMILES or .sdf files of
In-house building blocks, vendor catalogs,
or ZINC tranches

Floes available for focused library generation

Default database available
Tools for building databases included

Reaction/Reagent-Based Enumeration



Filtering and Visualization with Orion

The screenshot displays the Orion software interface, which is used for filtering and visualizing molecular data. The interface is divided into several sections:

- Top Bar:** Shows 'Active Datasets' (1), 'Filters' (0/2), 'Records' (All: 13499, Passing Filters: 13499, Selected: 0), a search bar, and options for 'Data Handling', 'Layout', and 'Discussion Boards'.
- Left Sidebar:** Contains navigation icons for 'OpenEye', 'Demonstration - Focused Library', 'Data', '3D', 'Analyze', 'Floe', 'Sources', and 'System'.
- SCATTER View:** A scatter plot showing 'XLogP (Calculated)' on the y-axis (ranging from 0 to 6) versus 'Molecular Weight (Calculated)' on the x-axis (ranging from 350 to 700). The plot contains a dense cloud of blue circular data points.
- SPREADSHEET View:** A table displaying molecular data. The columns include 'Product', 'ProductSmiles', 'Hydrogen-bon...', 'Molecular Weig...', 'Rotatable Bond...', and 'XLogP (Calca...'. The table shows three rows of data, each with a molecular structure icon and a search icon.
- DATA & COLUMNS Panel:** Located on the right, it includes 'Properties', 'R Groups', and 'Regression' options. Under 'Available properties', several properties are listed with checkboxes: XLogP (checked), Complexity, MMFF Internal Energy, TPSA, Lipinski Violations (checked), Abbvie Bioavailability Score, Heavy Atom Count, Chiral Centers, and Hydrogen-bond Acceptors (checked). There are 'Deselect' and 'Select All' buttons, and a 'Calculate' button at the bottom.
- FLOES Panel:** A small panel at the bottom right with a 'JOBS' tab. It contains the text: 'No floes tagged as Analyze-enabled [bar chart icon]. Mark some floes in the Floe list as Analyze-enabled [bar chart icon]'.

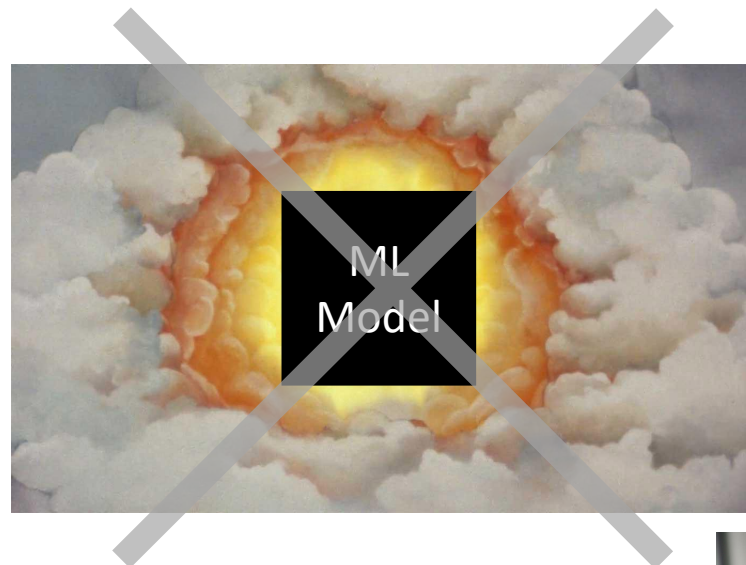
	Product	ProductSmiles	Hydrogen-bon...	Hydrogen-bon...	Molecular Weig...	Rotatable Bond...	XLogP (Calca...
0	ttitled Molec...	CCOc1c(cccc1...	3	2	448.27	6	4.61
1	ttitled Molec...	CN(CCCC(=O)...	5	2	527.44	9	4.14
2	ttitled Molec...	CN(C)c1[nH]c...	4	3	469.32	5	4.14

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Machine Learning in the Lead Opt Context

- Paucity of (Good, Local) Data
 - Prefer simpler models
 - Explore global & local models
 - Beware overfitting
- Good ML Hygiene
 - Domain of Applicability
 - Confidence/Error Bars
 - Explainable Predictions
- Utility in Lead Opt:
 - Tools for assessing “modelability”
 - Filtering and Prioritization



Unlikely

“Cleanliness becomes more important when godliness is unlikely.”
— P. J. O’Rourke



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Model Building in Orion

- Model Building Floes shipped in 2022
- Floe to prepare data
- Floes to train Models
- Floes to apply Models for prediction
- Pre-trained Solubility model



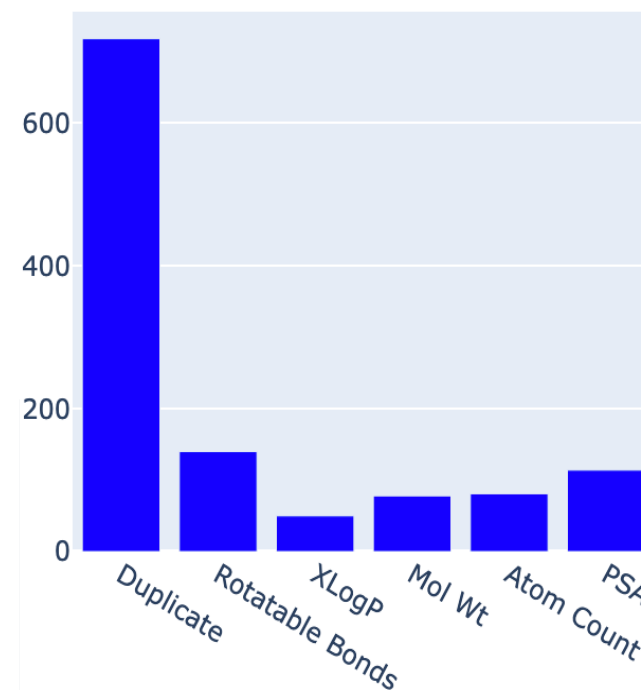
Training Data Pre-Processing

- Molecule standardization
- Simple property distributions
- Duplicate handling
- Response (or class) distribution

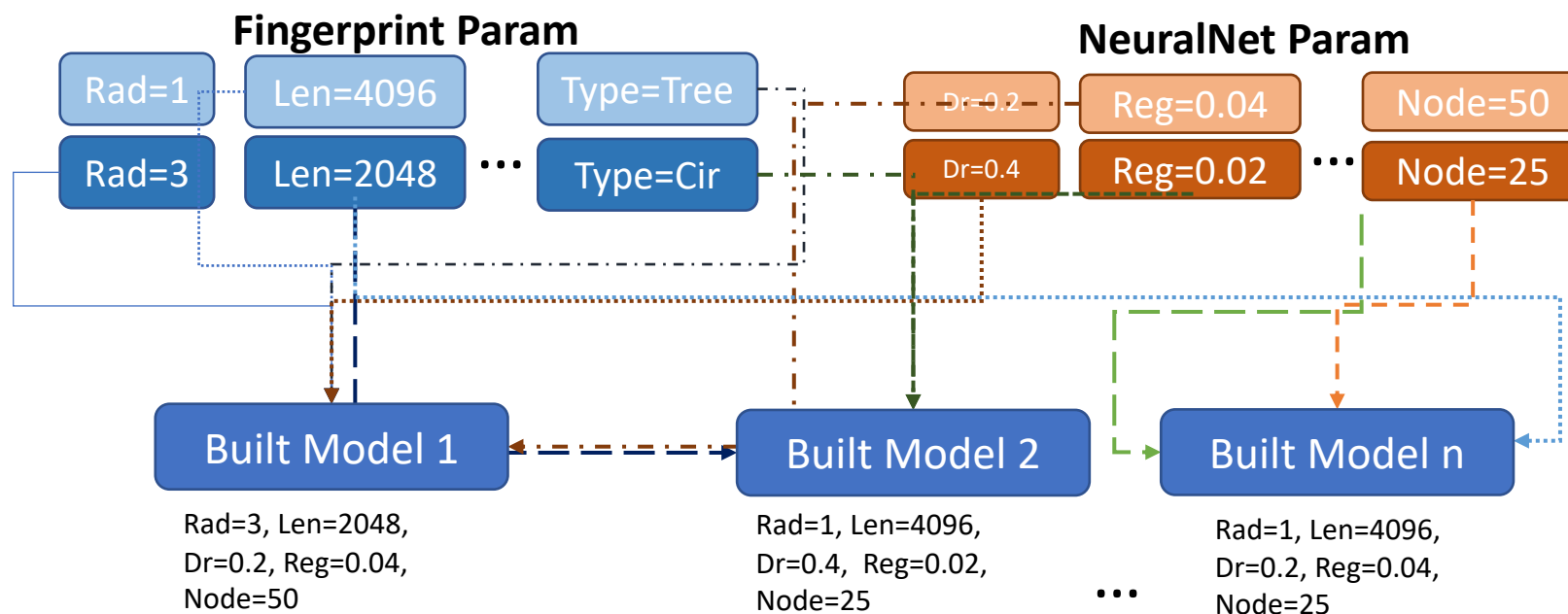


Input

Modified



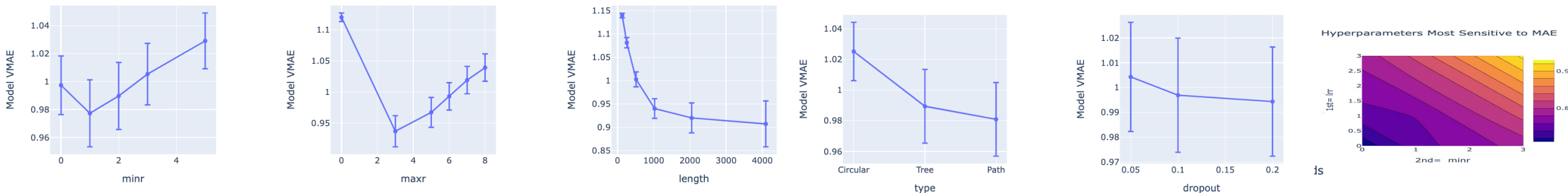
Train Multiple Models



Grid-Based Parameter Search

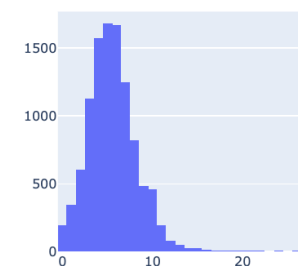
Model Building Floe Report

Summary of Model Hyperparameters on Validation Set



List of Fully-connected Neural Network Models Generated

Model #	Record #	MinRad	MaxRad	Bit-Length	FP-Type	Dropout	Learning Rate	Hidden Layers	Reg Layers	VMAe	VLoss	Link
1	122	0	3	4096	Path	0.4	0.0005	250 150 100	0.04 0.02 0.02	6.99e-01	1.49e+00	Model link
2	126	0	3	4096	Path	0.1	0.0005	250 150 50	0.04 0.02 0.02	7.03e-01	1.56e+00	Model link
3	141	0	3	4096	Path	0.2	0.0005	250 150 100	0.04 0.02 0.02	7.07e-01	1.53e+00	Model link
4	33	1	3	4096	Tree	0.4	0.0005	250 150 100	0.04 0.02 0.02	7.08e-01	1.49e+00	Model link
5	56	1	3	4096	Path	0.1	0.0005	250 150 50	0.04 0.02 0.02	7.14e-01	1.58e+00	Model link
6	128	0	3	4096	Tree	0.4	0.0005	250 150 100	0.04 0.02 0.02	7.16e-01	1.48e+00	Model link
7	86	0	3	4096	Tree	0.1	0.0005	250 150 50	0.04 0.02 0.02	7.19e-01	1.54e+00	Model link
8	58	1	3	4096	Path	0.2	0.0005	250 150 100	0.04 0.02 0.02	7.19e-01	1.56e+00	Model link
9	15	1	3	4096	Tree	0.1	0.001	250 150 100	0.04 0.02 0.02	7.24e-01	1.43e+00	Model link
10	16	1	3	4096	Tree	0.1	0.0005	250 150 100	0.04 0.02 0.02	7.27e-01	1.61e+00	Model link
11	108	0	3	4096	Tree	0.2	0.0005	250 150 100	0.04 0.02 0.02	7.32e-01	1.60e+00	Model link
12	67	0	3	4096	Tree	0.1	0.0005	250 150 100	0.04 0.02 0.02	7.32e-01	1.58e+00	Model link
13	105	0	3	4096	Path	0.4	0.0005	250 150 50	0.04 0.02 0.02	7.35e-01	1.63e+00	Model link

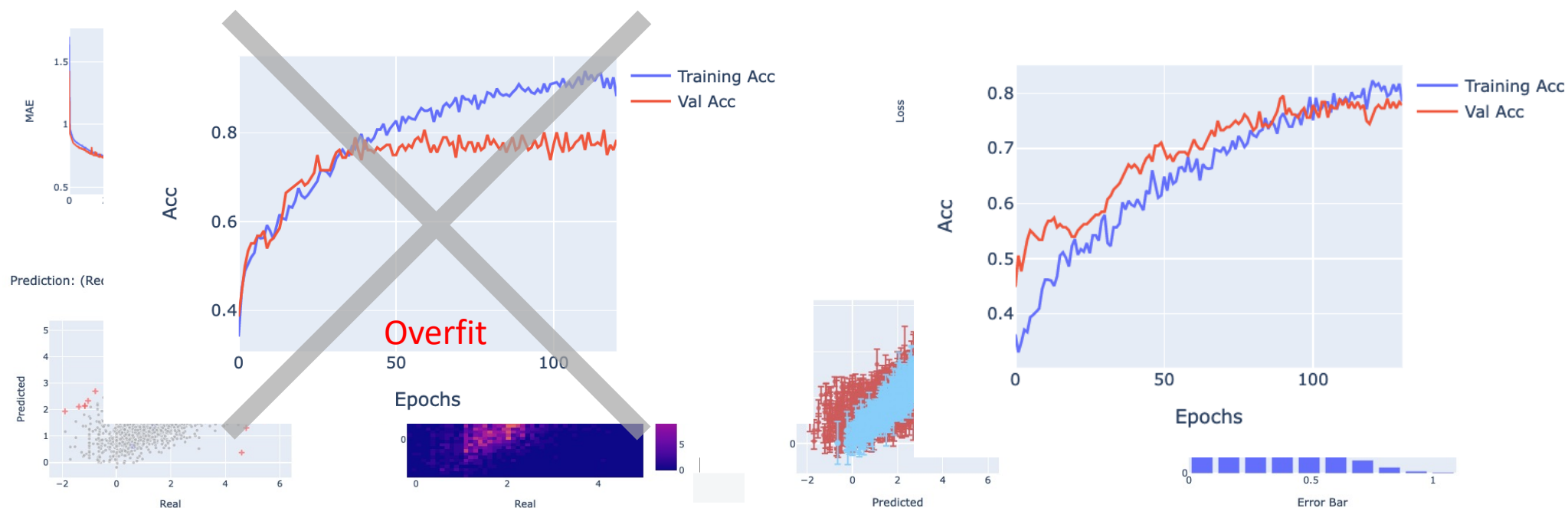


Training: Floe Report and Model Details

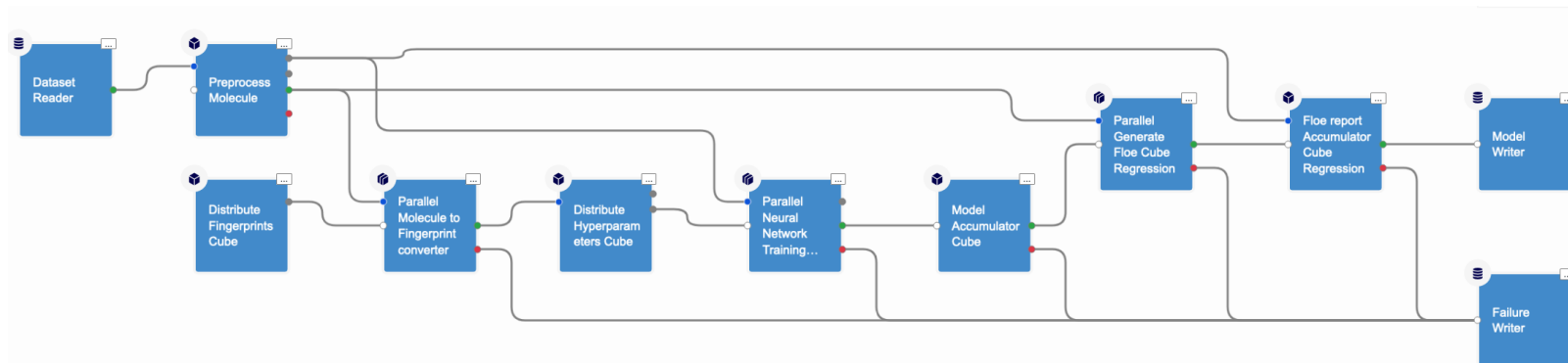
NN Hyperparam and Fingerprint Parameters



Neural Network Epoch Training Plots



Model Building Summary



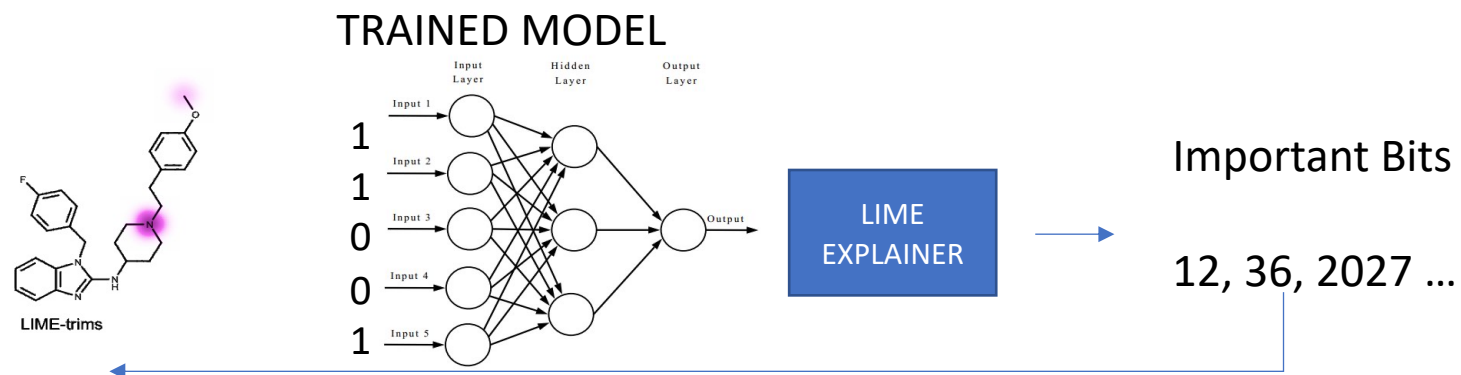
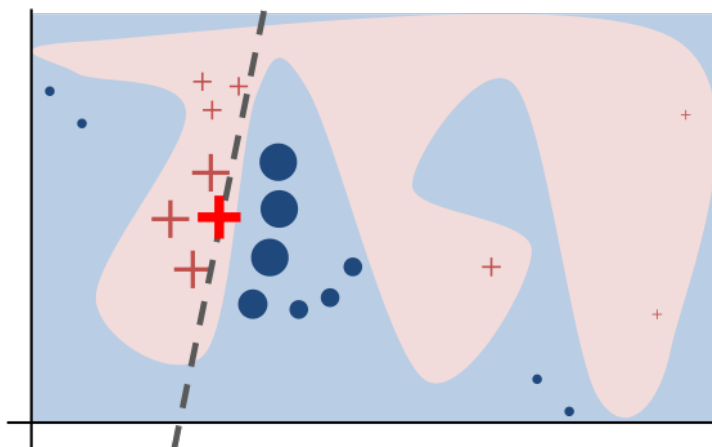
- Input
 - Molecules (or custom feature vectors)
 - Response property
- Training Setup
 - Regression or Classification
 - Automatic Train/Test/Validation splits and cross-validation
- Build Multiple Models (in Parallel)
 - Featurization Parameters (FPs for now)
 - Neural Network hyperparameters
- Comprehensive Floe Report
 - Summary with Model Ranking
 - Individual Model Performance

Making Predictions

- Predictions in Parallel
 - Take advantage of Orion, predictions can be applied at scale
- Confidence and Domain of Applicability
 - Models retain knowledge of training set property distributions
 - Multiple ways to assess uncertainty (property box, dropout)
 - Train and supply separate Bayesian uncertainty model
 - High/Med/Low assessment with rationale
- Explainable Predictions

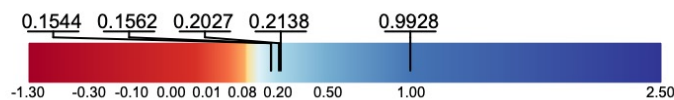
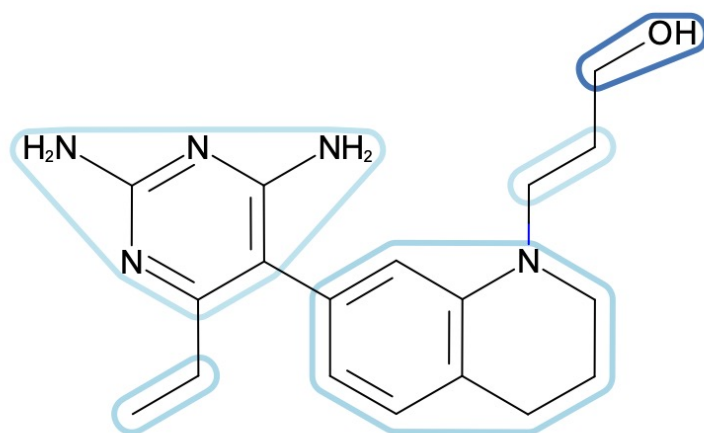
Local Interpretable Model-Agnostic Explanations (LIME)

- **Interpretable:** qualitative understanding between the input variables and the response
- **Local Fidelity:** learns an interpretable model locally around the prediction.



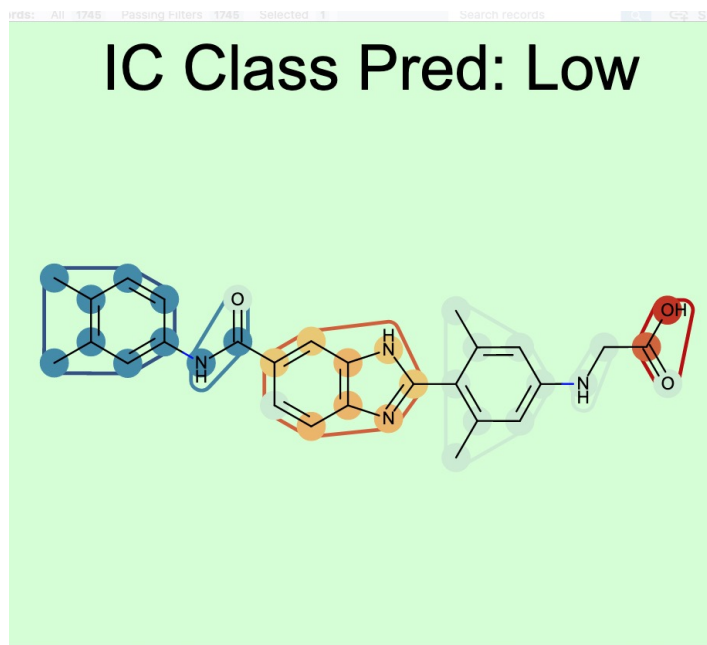
Prediction Explainer Examples

Solubility Pred.: 1.72 log(uM)

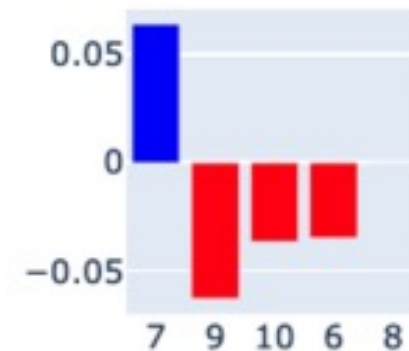
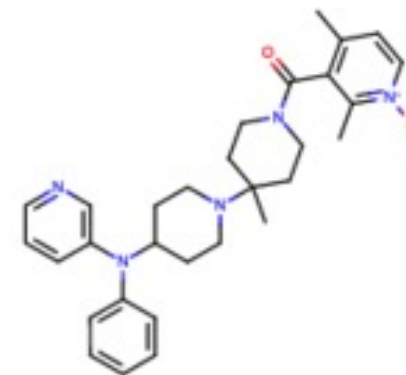


Regression

IC Class Pred: Low



Classification



Custom Feature Vector

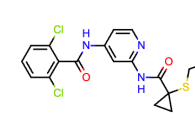
Future Work

- Graph Convolutions
- 3D Representations
- Kriging
- Diffusion
- Distributed Training of Larger Models
- Hyperparameter Optimization
- Advanced Train/Test Splitting
- Model Comparison

And much more...

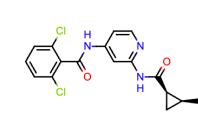
Conclusions

- Orion brings all of OpenEye Lead Opt capabilities into one place
 - Ways to increase $P_{Improve}$ and P_{Make}
- Robust cheminformatic foundation for building synthetically accessible lead opt libraries
- General ML tools to assist in model building with guardrails



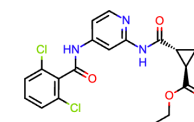
Untitled Molecule:EN300-312763

Add columns to load in column list



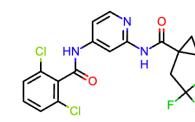
Untitled Molecule:EN300-7185402

Add columns to load in column list



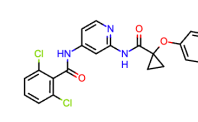
Untitled Molecule:EN300-697522

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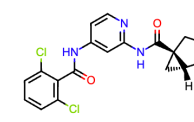
Untitled Molecule:EN300-98598

Add columns to load in column list



Untitled Molecule:EN300-256298

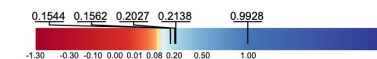
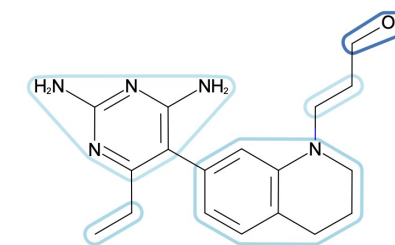
Add columns to load in column list



Untitled Molecule:EN300-263669

Add columns to load in column list

Solubility Pred.: 1.72 log(uM)



Acknowledgements

- Burt Leland
- Sayan Mandal
- David Hamilton
- Cheminformatics & Data Science Group

- Scientific Development Teams
- Cloud Teams
- Geoff Skillman, Ant Nicholls, Bob Tolbert



Open Positions in the Cheminformatics & Data Science Group

Thank You

