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Machine Learning for *de novo* Molecular Design

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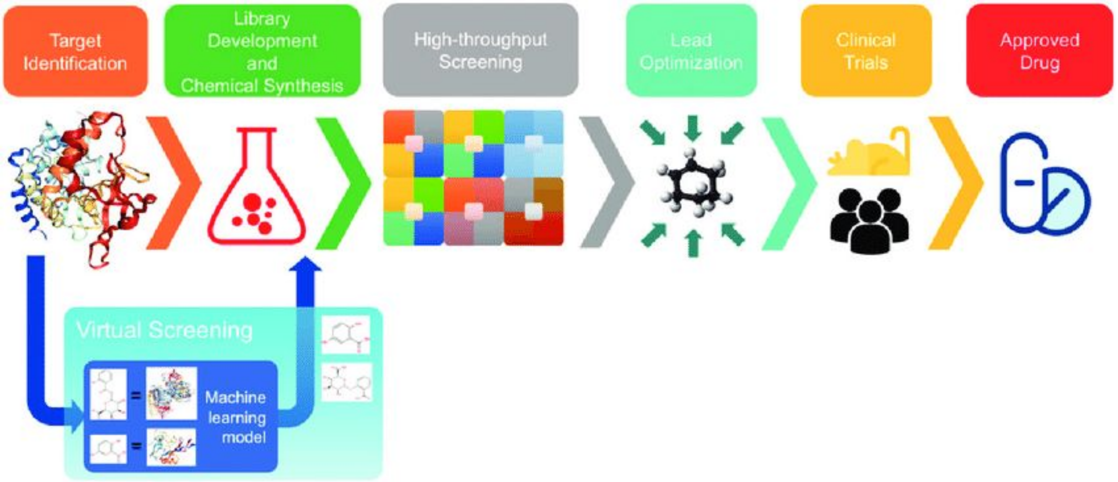
Disclaimer!

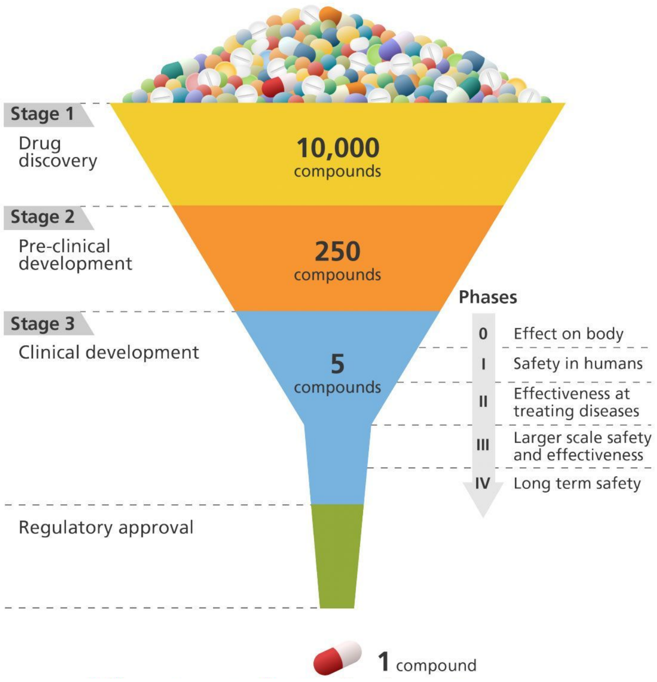
My knowledge in chemistry is very (very) basic…

Why?

The process of discovering new molecules

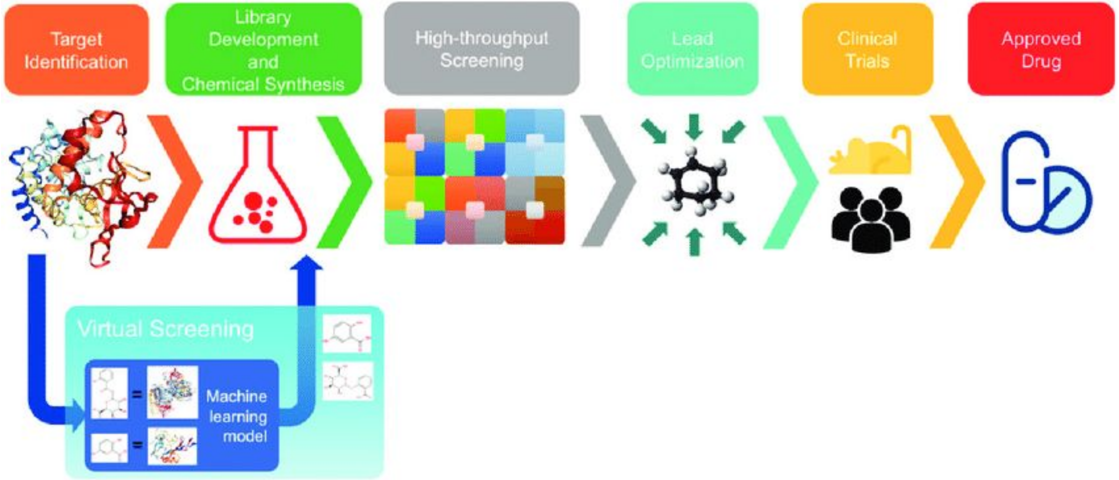
- Pharma: average time discovery – market, 13 years
- Outside pharma: 25 years
- Crucial 1st step: **generate pool of candidates**
- Daunting task (e.g. 10^{23} – 10^{60} drug-like molecules)





The old way and the soon-to-be-old way

- Old way
  - Human experts propose, synthesize and test (*in vitro*)
- Soon-to-be-old way: high throughput virtual screening (HTVS)
  - Predict properties through computational chemistry...
  - ...leverage rapid **ML-based property predictions**



De novo molecular design

- Just existing molecules are explored
- Much time lost evaluating bad leads
- Traverse chemical space more “effectively”: reach **optimal molecules** with **less evaluations** than brute-force screening

> *“De novo molecular design is the process of **automatically proposing novel chemical structures** that **optimally satisfy desired properties**”*

Combinatorial, black-box, stochastic, multi-objective optimization with black-box constraints

Automatically proposing novel chemical structures

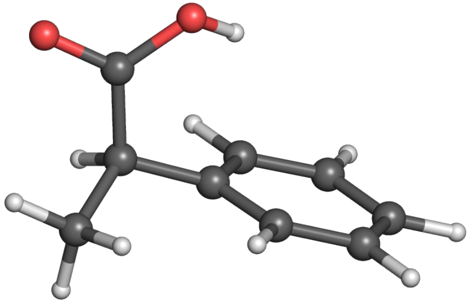
Two main ingredients

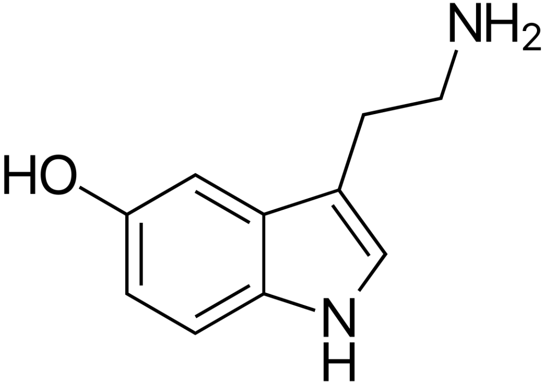
- Molecule representation
- Generative model

Representing molecules

Molecules are **3D QM objects** with: nuclei with defined positions surrounded by electrons described by complex wave-functions

- Digital encoding that serves as input to model
- **Uniqueness and invertibility**
- Trade-off: information lost vs complexity
  - 3D coord. representation (symmetries?)
  - More compact 2D (graph) representation
- 1D, 2D and 3D





1D representations - SMILEs

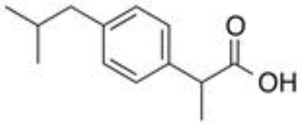
Simplified Molecular Input Line Entry System

Molecule as graph (bond length and conformational info is lost)

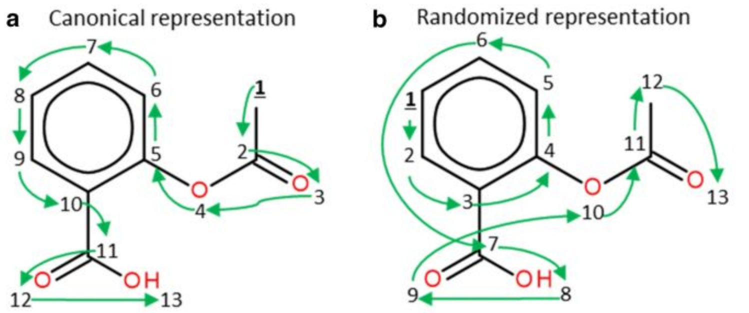
- Graph traversal
- Sequence of ASCII characters
- Non-unique → Canonical SMILES
- One-Hot-Encoding

- Leverage NLP techniques

- SMILE-based methods struggle to generate **valid** molecules
- Valid = valency rules
- Learn spurious grammar rules



Ibuprofen
CC(C)Cc1ccc(cc1)C(C)C(O)=O



CC(=O)Oc1ccccc1C(=O)O

c1cc(c(cc1)C(O)=O)OC(C)=O

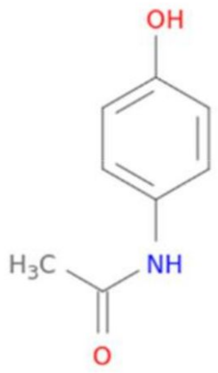
2D representations

- Nodes represent atoms
- Edges represent bonds
- Nodes/Edges have associated features (atom number, bond type, etc.)

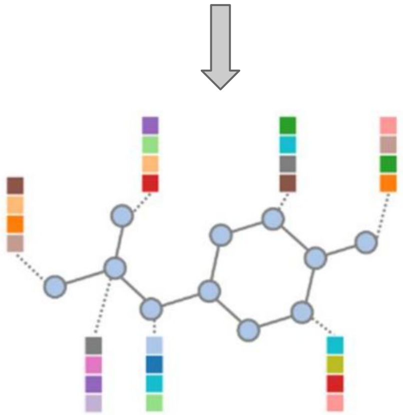
- Capture connectivity!
- Symmetry invariant representation

- More difficult to generate than sequences
- Taylored algorithms that work with graphs (composing transformations on graphs, symmetries?)

- Graph Neural Nets!



Acetaminophen



3D representations

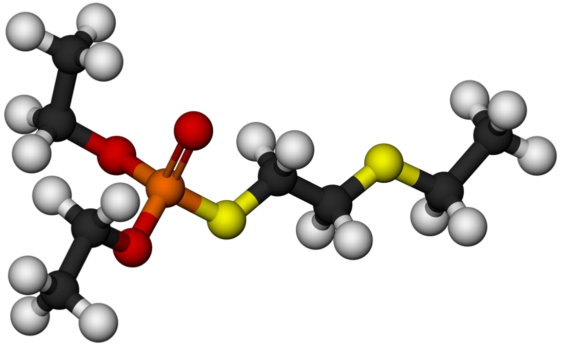
- 3D point clouds

$$\mathcal{M} = \{x_i, r_i\}_{i=1}^{p}$$ where x_i are features and r_i are coordinates.

- Minimal information lost (conformational preferences, bond lengths, etc.)

- Symmetries?
- Too many degrees of freedom

- Generation: sequentially choose pair of atoms, relative position, bond length and angles



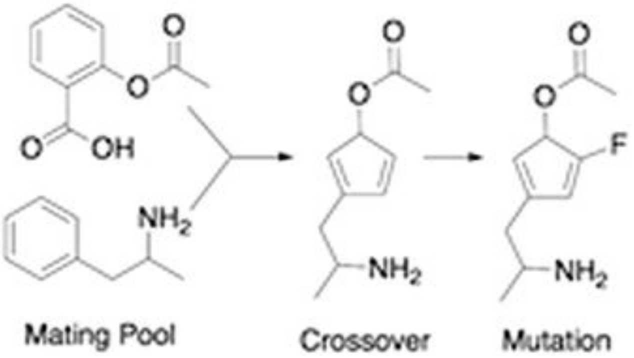
How to generate molecules?

Myriad of different ways. A useful distinction:

- Gradient-free methods
- Gradient-based methods

Gradient Free Methods

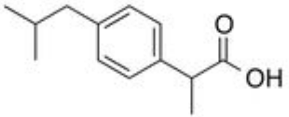
- Graph-based genetic algorithms
    - Mutations and crossover on a pool of candidates
    - Elitist natural selection rule
- Yoshikawa et. al. propose using SMILES
    - Population of SMILES
    - Grammatical Evolution
- Many more...



Gradient Based Methods

- Recurrent Neural Networks
- (Variational) Autoencoders
- Normalizing Flows
- Generative Adversarial Networks (GANs)

Recurrent Neural Networks



Ibuprofen
CC(C)Cc1ccc(cc1)C(C)C(O)=O

- Work on sequences (SMILES)

- Goal: given training sequences → learn to generate new sequences that resemble those of training.

- Sequence: $S_{1:T} = (S_1, \ldots, S_T)$ where $S_i \in \mathcal{V}$

- Training: maximum likelihood, equiv to minimize loss function:

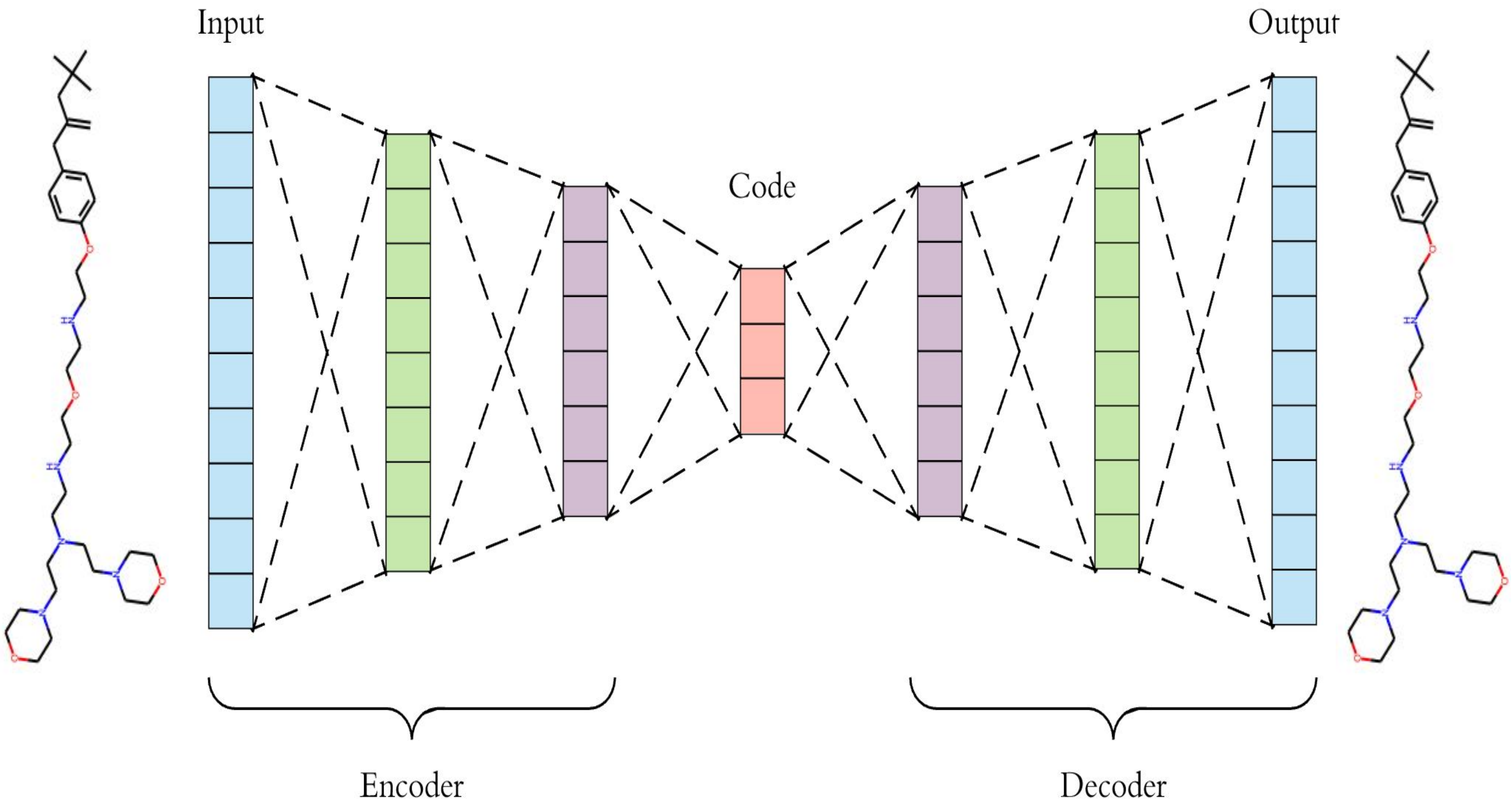
$$L^{MLE} = -\sum_{s\in\mathcal{T}} \sum_{t=2}^{T} \log \pi_\theta(s_t | S_{1:T-1})$$

- Generation: sequentially sample from multinomial dist.

- Thermal rescaling

$$\hat{p}_i \propto \exp(\frac{p_i}{T})$$

(Variational) Autoencoders



Variational Autoencoders

- Goal: learn probabilistic latent variable model for data generation

$$z \sim p(z)$$
$$x \sim p_\theta(x|z)$$

- We want to maximize $p(x) = \int p_\theta(x|z)p(z)dz$; instead maximize

$$\log p(\boldsymbol{x}) \geq \mathrm{E}_{z\sim q_\phi(z|\boldsymbol{x})}\left[\log \frac{p_\theta(\boldsymbol{x}|z)\,p(z)}{q_\phi(\mathbf{z}\,|\,\boldsymbol{x})}\right]$$

- RHS is equal to

$$\mathbb{E}_{z\sim q_\phi(z|x)}[\log p_{\theta(x|z)}] - D_{KL}[q_\phi(z|x), p(z)]$$

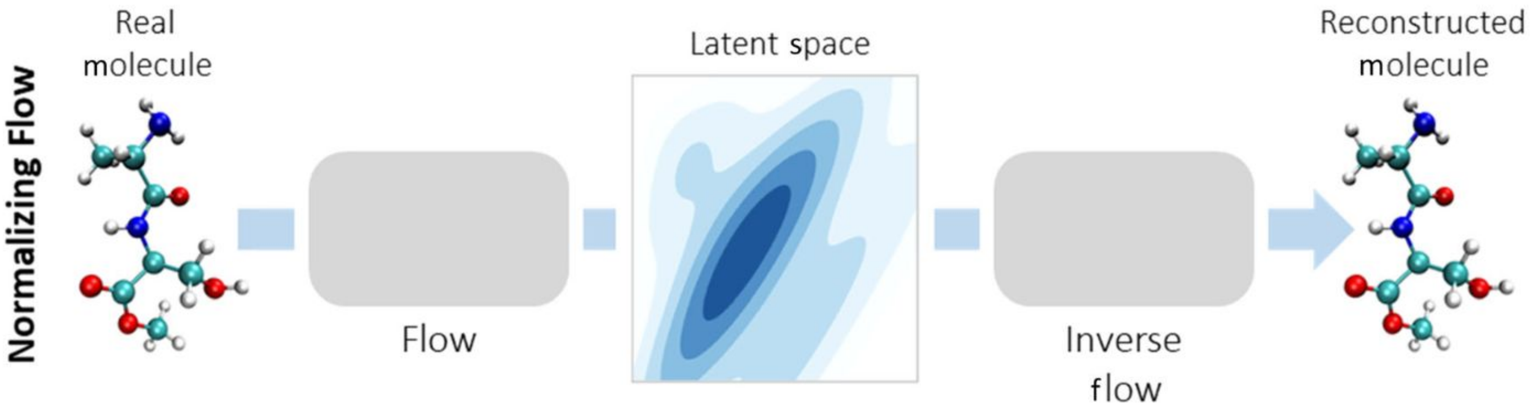
Variational Autoencoders

- Typically: $p(z)$ independent standard normal dist. and $q_\phi(z|x)$ factorized multivar. normal
- Mean and variance functions of encoder parameterized through CNN.
- Decoder normally RNN

- Training
  - Encode each training sample x into z
  - Decode z into x’
  - Minimize loss function

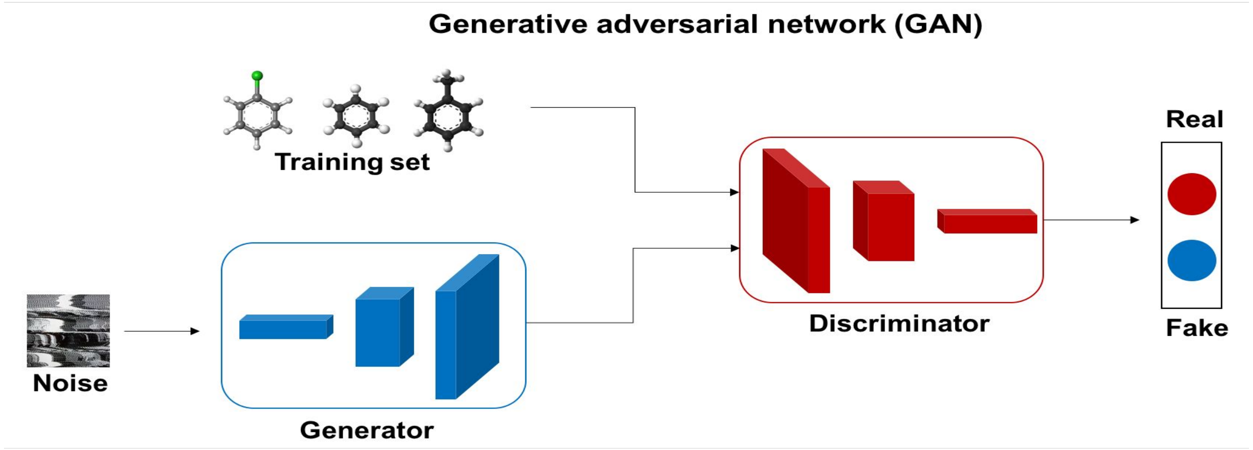
- Generation
  - Get point in latent space z
  - Decode z sampling $x \sim p_\theta(x|z)$

Normalizing Flows



- Learn series of parametric bijective transformations of probability distributions
- Allows (easy) calculation of exact likelihood.
- Deep NN with bijective layers

Generative Adversarial Networks



- Generator: generate molecule from Gaussian noise
- Discriminator: distinguish real from fake molecules
- Train to compete against each other

$$\min_{G}\max_{D} V(D,G) = \mathbb{E}_{x \in p_{\mathrm{d}}(x)}\left[\log D(x)\right] + \mathbb{E}_{z \in p_{z}(z)}\left[\log\left(1 - D\left(G\left(z\right)\right)\right)\right]$$

Recall that…

"De novo molecular design is the process of ***automatically proposing novel chemical structures*** *that* ***optimally satisfy desired properties****"*

Combinatorial, black-box, stochastic, multi-objective optimization with black-box constraints

Generate molecules that optimally satisfy desired properties

- Goal: learn valid molecules with **desirable properties**
- Infeasible to measure properties experimentally for every generated molecule…
- Infeasible to use computational chemistry to compute properties…
- **Prediction**: quantitative structure-activity relationship (QSAR)
- Done usually in separate datasets
- Many models depending on property, representation, etc.
  - Molecular Descriptors
  - SMILEs
  - Graphs

Using properties to guide generation

1. Reinforcement Learning coupled with sequence generator

- A time t, state is $(s_0, \ldots, s_t)$
- Action is next token $a_t = s_{t+1}$
- After taking action, a reward R_t is perceived
- Goal, learn policy $\pi_\theta(a|s)$

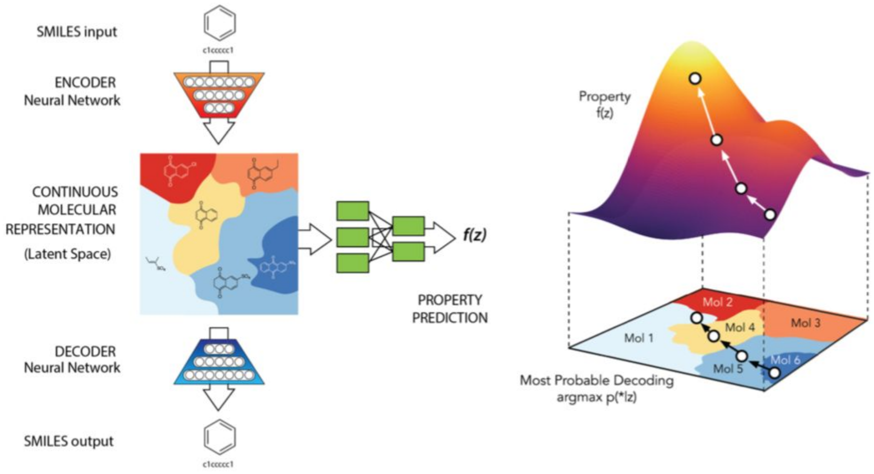
$$\mathbf{max}_\theta \, \mathbb{E}[\textstyle\sum_{i=1}^{T} R_i \,|\, s_0, \theta]$$

- The only non-zero reward is $R_T$which is equal to the property prediction

Using properties to guide generation

2. Optimization with VAE

- Learn map from latent space to property (e.g. through GP)
- Optimize that map (gradient ascent, bayesian optimization, etc.)



Issues/Thoughts

- Multi-objective optimization
    - Many properties to be optimized (depending even on different stakeholders!)
    - Drug discovery: **high binding affinity to biological target**, low toxicity, solubility, synthetically accessible, stability, economical costs!
    - Commonly: predict properties independently and combine predictions in loss function.
    - Also, hold properties constant implicitly through structural constraints.
    - **Decision theory**: **multi-attribute utilities** to incorporate different objectives for different stakeholders into the generative process

Issues/Thoughts

- Uncertainty quantification
    - Models rely on predictions to generate promising molecules
    - Accuracy of these models is key
    - In small data regimes… models tend to be less accurate.
    - Incorporate uncertainty quantification into generative process! (**Bayesian inference**)
    - Exploration vs exploitation (**Bayesian optimization**)
    - **Bayesian decision theory**

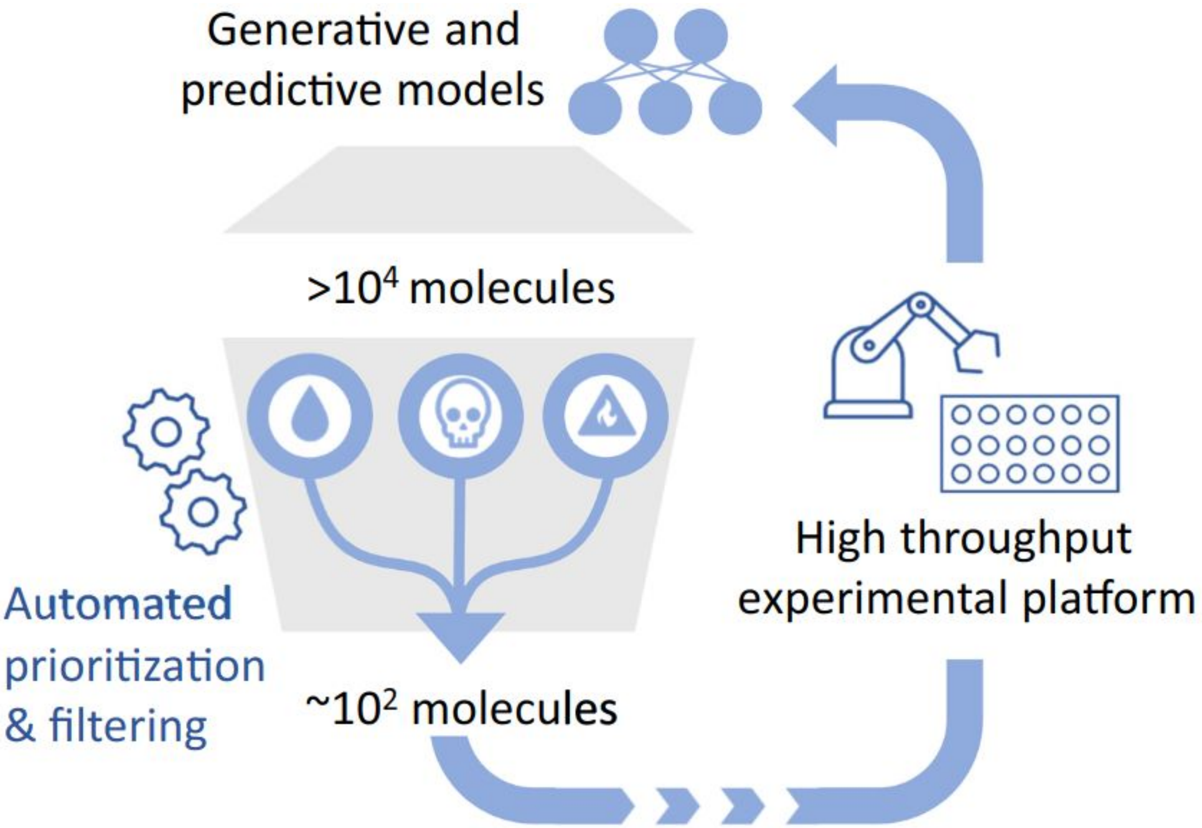
Issues/Thoughts

- Synthesizability
  - Generated molecules must be easy to synthesize
  - This concept is hard to define!
  - Methods to automatically evaluate synthesizability without human intervention
  - Rather than molecules, generate synthetic pathways (learn reactions)

Other relevant fields

- Graph based deep learning
- Geometric deep learning
- Combinatorial black-box optimization
- Heuristic search algorithms
- Reinforcement Learning

The dream - Closing the loop


Generative and predictive models
$>10^4$ molecules
Automated prioritization & filtering
$\sim10^2$ molecules
High throughput experimental platform

The reality?

- More likely: computer-aided molecular design
- Interpretability
  - Prediction is not enough, we need understanding (?).
  - Chemist need to derive an actionable hypothesis from model output.
  - If chemist sees, e.g. structural elements responsible for toxicity, she might have ideas on how to modify molecule to diminish toxicity
  - Interpretable representations: molecular descriptors…?
  - Interpretable methods to determine **causality between structure presence and property** (**causal inference, counterfactual inference**)

References

Bilodeau, C., Jin, W., Jaakkola, T., Barzilay, R., & Jensen, K. F. (2022). Generative models for molecular discovery: Recent advances and challenges. Wiley Interdisciplinary Reviews: Computational Molecular Science, e1608.

Meyers, J., Fabian, B., & Brown, N. (2021). De novo molecular design and generative models. Drug Discovery Today, 26(11), 2707-2715.

Elton, D. C., Boukouvalas, Z., Fuge, M. D., & Chung, P. W. (2019). Deep learning for molecular design—a review of the state of the art. Molecular Systems Design & Engineering, 4(4), 828-849.

Gallego, V., Naveiro, R., Roca, C., Ríos Insua, D., & Campillo, N. E. (2021). AI in drug development: a multidisciplinary perspective. Molecular Diversity, 25(3), 1461-1479.

Yoshikawa, N., Terayama, K., Sumita, M., Homma, T., Oono, K., & Tsuda, K. (2018). Population-based de novo molecule generation, using grammatical evolution. Chemistry Letters, 47(11), 1431-1434.

Thanks!

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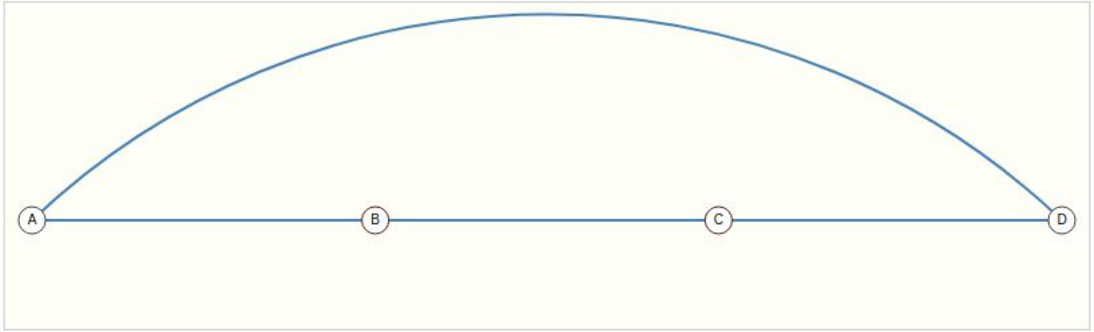
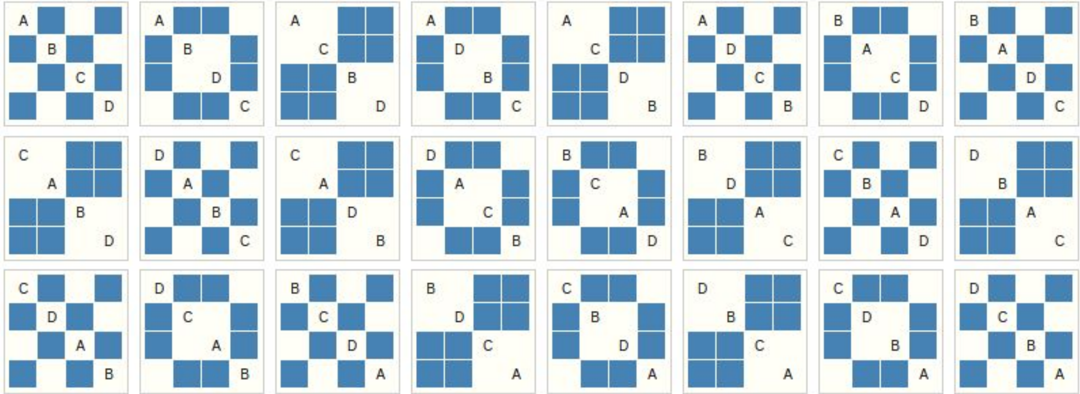
https://roinaveiro.github.io/

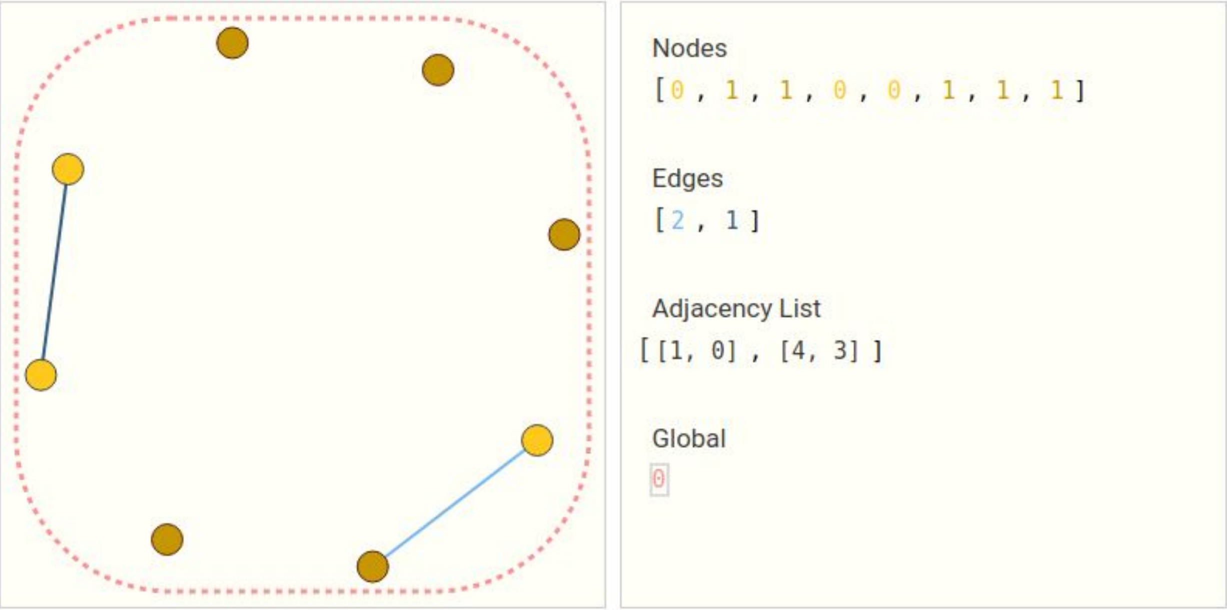
https://github.com/roinaveiro

Adjacency Matrices





Permutation Invariant representation



Nodes

[0 , 1 , 1 , 0 , 0 , 1 , 1 , 1]

Edges

[2 , 1]

Adjacency List

[[1, 0] , [4, 3]]

Global

0

Unconstrained generation

- Goal: learn general distribution of molecules in chemical space
- Evaluated based on chemical validity, novelty, uniqueness

Generation Issues