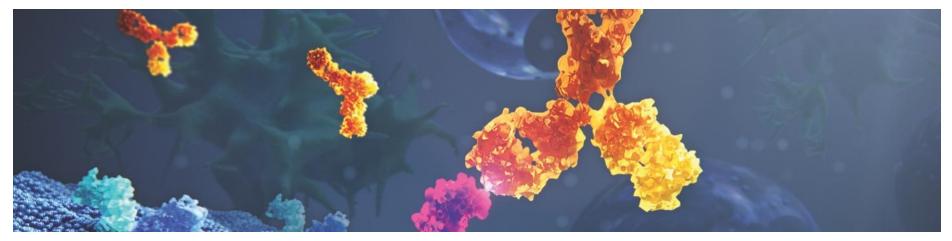


SMILES, RNNs and RDKit, - To the molecular universe and beyond

Esben Jannik Bjerrum, Molecular Al Group

RDKit UGM 2019

Company Restricted 25 – September – 2019



Outline

- Artificial Neural Networks 0=>120mph
 - RNNs, SMILES, LSTM
- Combining elements for molecular tasks
 - Encoders (QSAR task)
 - Generators (de novo design task)
 - Autoencoders and Heteroencoders (Both)
- Conditional Recurrent Neural Networks (cRNNs)
 - Generated Molecules
 - Control of Properties
 - Limitiations



Artificial Neurons

Input

0.1

1

-0.9

weights

20

-1

-2

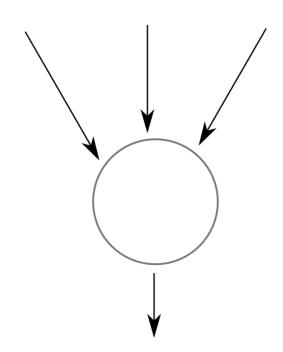
Weighted sum

$$20*0.1 + -1*1 + -2*-0.9 = 2.8$$

Activation Function

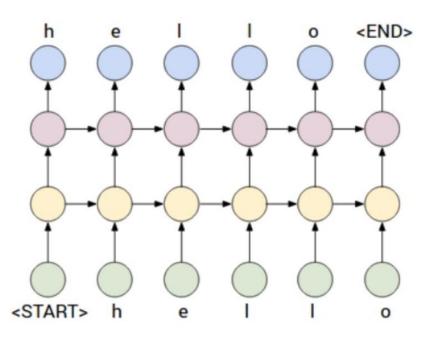
Output

0.992





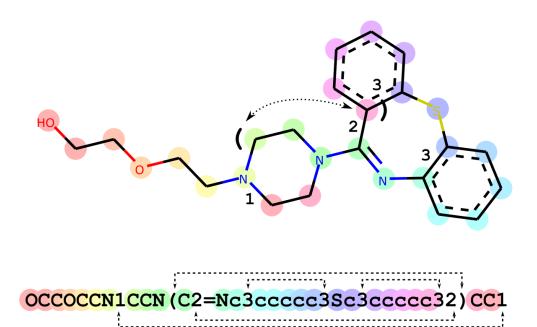
Recurrent Neural Networks (RNN)



- Sequences of features as inputs
- •The same task for every element of a sequence, with the output being affected by the previous computations
- •Modeling of sequences such as text, tweets, time series etc.



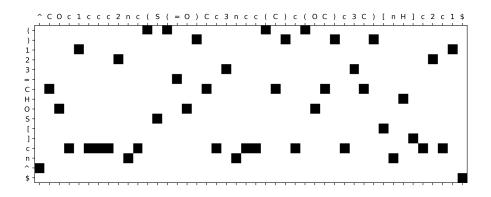
SMILES, a Chemical Language and Information System





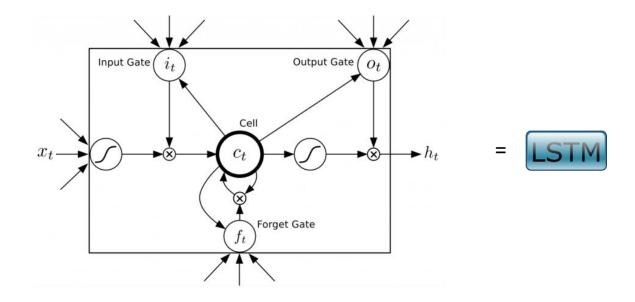
One hot encoding

- Neural Networks learns on vectors, matrices or tensors.
- One-hot encoding with a defined vocabulary converts SMILES strings into 2D matrices



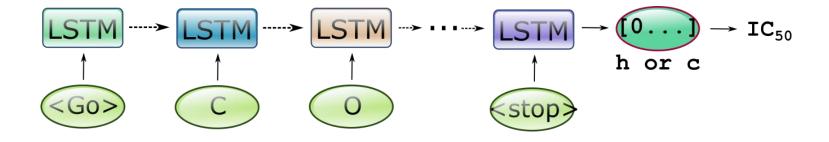


Long Short-Term Memory cells (LSTM)





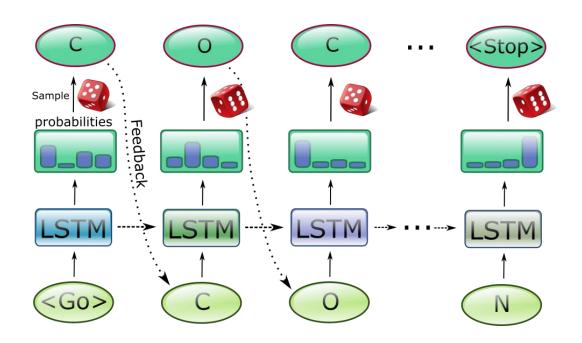
RNNs as an encoder



Internal LSTM states gets changed from step to step. The full sequence influences the final vector used for prediction task. QSAR from raw SMILES possible

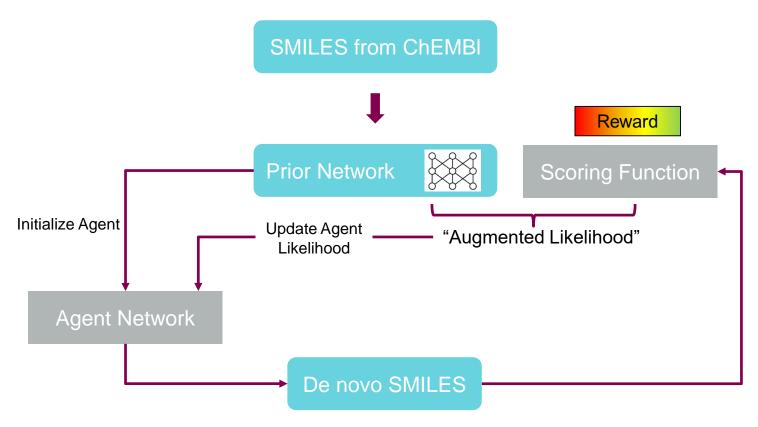


RNNs as generators



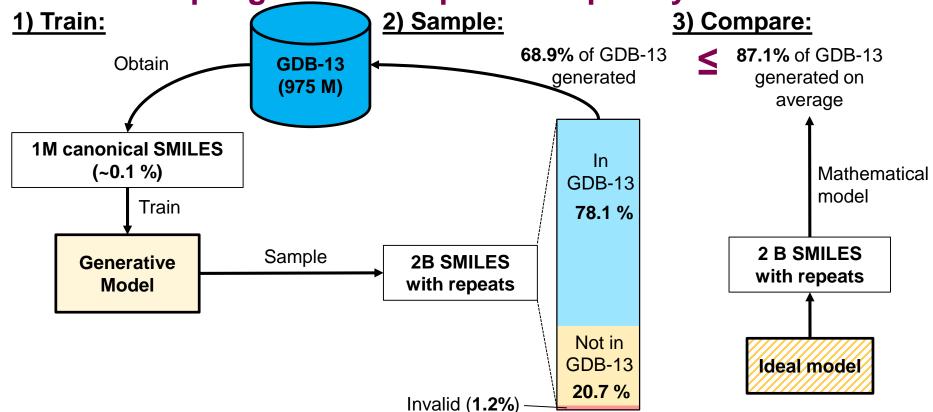


Optimizing molecular generation via reinforcement learning





Are we sampling chemical space completely?

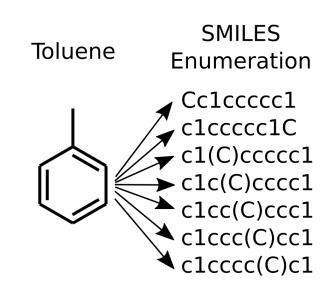


Completeness: 68.9/87.1 = **79%**

⁽¹⁾ Arús-Pous, J.; Blaschke, T.; Ulander, S.; Reymond, J.-L. L.; Chen, H.; Engkvist, O. Exploring the GDB-13 Chemical Space Using Deep Generative Models. *J. Cheminform.* **2019**, *11* (1), 20. https://doi.org/10.1186/s13321-019-0341-z.

Enumeration of non-canonical SMILES

- Canonical SMILES ensures a 1:1 relationship between molecule and SMILES
- I go the other way and generate multiple SMILES for the same molecule
- Works as data augmentation =>
 Improves Deep Learning models



Bjerrum, Esben Jannik. 2017. "SMILES Enumeration as Data Augmentation for Neural Network Modeling of Molecules." http://arxiv.org/abs/1703.07076



Random SMILES in practice

```
[1]: from rdkit import Chem
      from rdkit.Chem.Draw import IPythonConsole
[2]: drugname = "Omeprazol"
      mol = Chem.MolFromSmiles("CC1=CN=C(C(=C10C)C)CS(=0)C2=NC3=C(N2)C=C(C=C3)OC")
[3]: print("%i Atoms, %i Rings"%(mol.GetNumAtoms(), Chem.GetSSSR(mol)))
     24 Atoms, 3 Rings
[]: s = set()
     i = 0
      while True:
         1 = len(s)
         smiles = Chem.MolToSmiles(mol, doRandom = True
         s.add(smiles)
         if len(s) > 1:[
             print("\r %i \t %s"% ( len(s), smiles), end = '')
             i = 0
         else:
         if i > 1000:
              break
      print()
      print("Done")
```

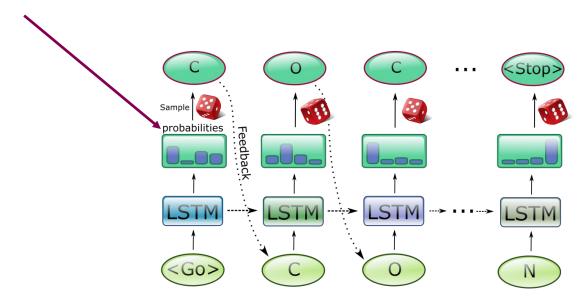
- doRandom flag in Chem.MolToSmiles randomizes all decisions during path traversal
- "Old-style" atom order shuffling gives less SMILES forms

```
ans = list(range(mol.GetNumAtoms()))
np.random.shuffle(ans)
rmol = Chem.RenumberAtoms(mol,ans)
Chem.MolToSmiles(rmol, canonical=False)
```



Finding the sampling probability of a single SMILES

Multiplying the probability for given characters will yield the probability of sampling that exact sequence.

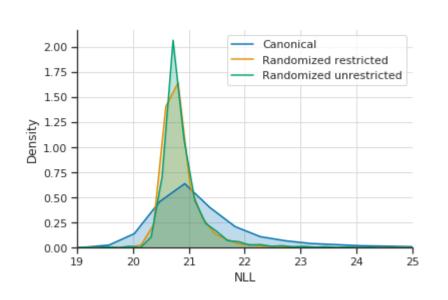


Sum of negative log likelihoods used for numerical stability Low probability => High NLL



SMILES enumeration increases Chemical Space Coverage

More uniform



More Complete

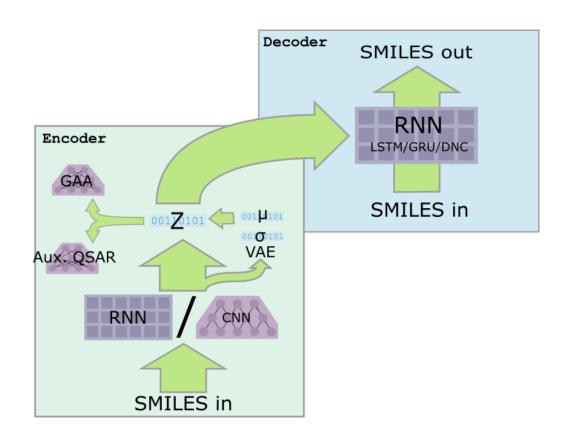
Set	SMILES	Validity	Completeness
1M	Canonical	0.994	0.836
	Randomized	0.999	0.953
10K	Canonical	0.905	0.445
	Randomized	0.974	0.715
1K	Canonical	0.504	0.167
	Randomized	0.812	0.392

GDB-13 is 975 million molecules

Arús-Pous, Josep et al. 2019.



SMILES Based Autoencoders



Gómez-Bombarelli, Rafael et al. 2018.

"Automatic Chemical Design Using a
Data-Driven Continuous Representation
of Molecules." ACS Central Science 4(2):
268–76.

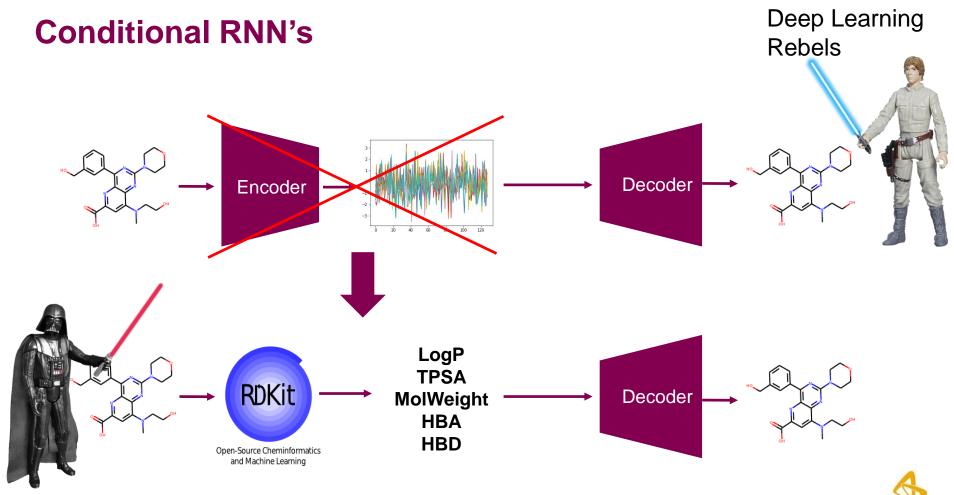
Winter et al. 2018. "Learning Continuous and Data-Driven Molecular Descriptors by Translating Equivalent Chemical Representations." *Chemical Science* 10(6): 1692–1701.

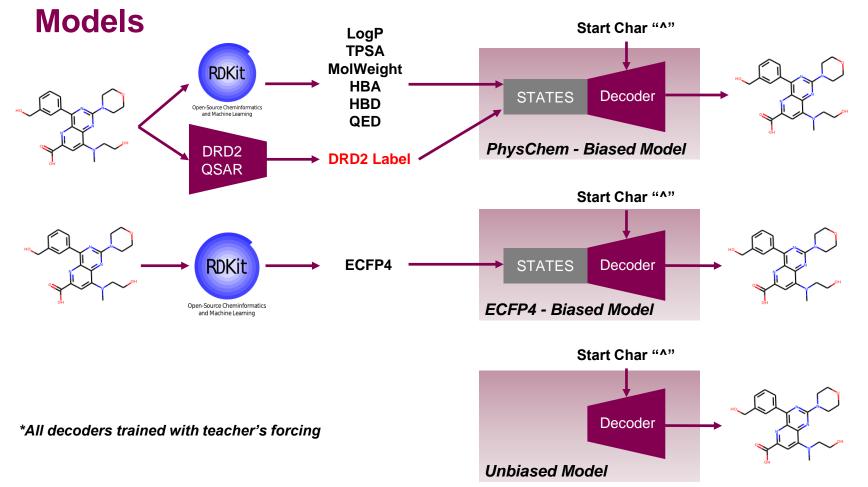
Bjerrum, Esben Jannik, and Boris Sattarov. 2018. "Improving Chemical Autoencoder Latent Space and Molecular De Novo Generation Diversity with Heteroencoders." *Biomolecules*.













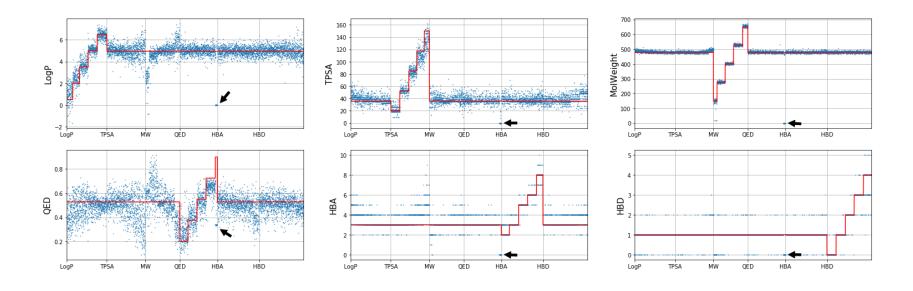
https://chemrxiv.org/articles/Direct Steering of de novo Molecular Generation_using_Descriptor_Conditional_Recurrent Neural_Networks_cRNNs_/9860906

Control of Properties





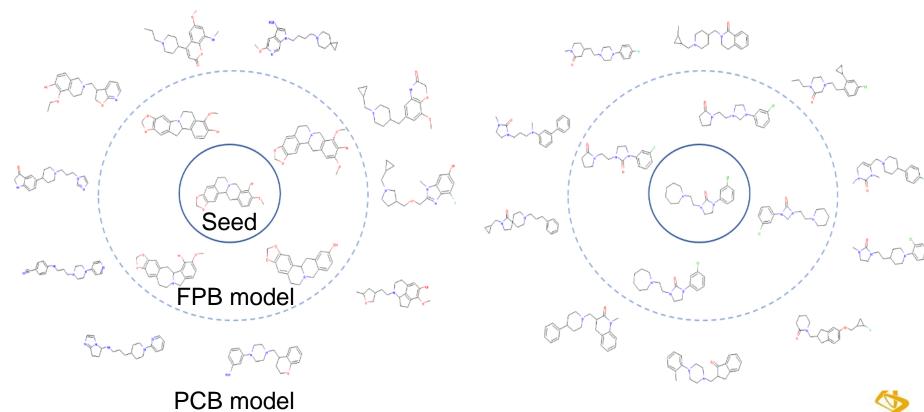
Independent control of properties



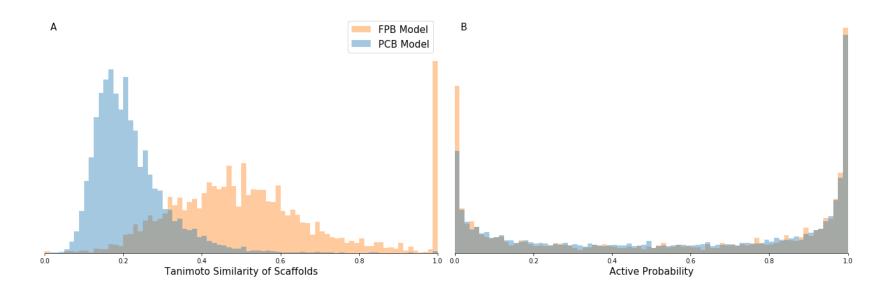
Molecule generation breaks down outside of applicability domain (shown with arrow)



Some molecules generated

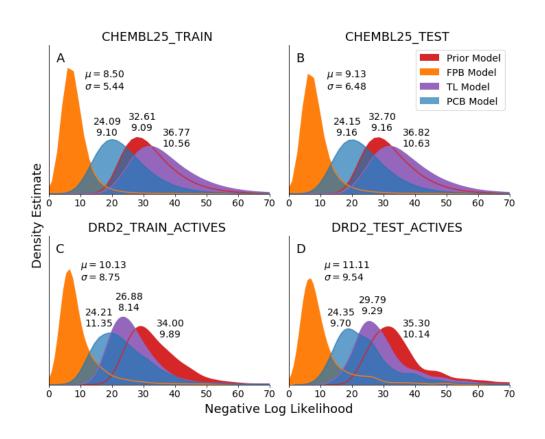


cRNN as Scaffold jumper





Generative probability distributions (neg.log.likelihood)

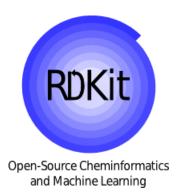


If completely uniform (Dirac distribution)
NLL 0, One SMILES possible
NLL 11, tens of thousands
NLL 24, Billions
NLL 35, Quadrillions



Toolkits – Source code - Links











github.com/MarcusOlivecrona/REINVENT

github.com/Ebjerrum/molvegen









Conclusions

- Using SMILES and RNNs in different architectures can solve many different tasks
- Its fast to develop! RDKit is central for molecular/SMILES handling and LSTM cells are standard in most NN frameworks
- SMILES enumeration tricks gives better performance in many applications, but sampling becomes a bit more "fuzzy"

 Conditioinal Recurrent Neural Networks are a direct inverse QSAR model which have intermediate properties between ideal autoencoders and unbiased RNNs



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Thank you for listening, Feedback, Questions





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