Deep Learning for Computational Drug Poteover Dovid Koes



Dodavid koes

Intelligent Systems Program Al Forum October 19, 2018





THE BIOPHARMACEUTICAL RESEARCH AND DEVELOPMENT PROCESS

BASIC RESEARCH	DRUG DISCOVERY	PRE- CLINICAL		CLINICAL TRIALS		F RE	DA VIEW	POST-APPROVAL RESEARCH & MONITORING
			PHASE I	PHASE II	PHASE III			PHASE IV
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								OVED CINE
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			SUB SUB	NUMBER OF VOLUNTE	ERS	A/BL ^A	APPR	
			TENS	HUNDREDS	THOUSANDS	ND	FD/	

Source: Pharmaceutical Research and Manufacturers of America (<u>http://phrma.org</u>)



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PHASE II	PHASE III				PHASE IV
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HUNDREDS	THOUSANDS	ND		FD,	

Source: Pharmaceutical Research and Manufacturers of America (<u>http://phrma.org</u>)



- 1. Does the compound do what you want it to?
- 2. Does the compound **not** do what you **don't** want it to?
- 3. Is what you want it to do the right thing?





Target Identification

Screening



Compounds

Hits







Lead Identification

Lead Optimization









Target Identification

Virtual





Compounds

Hits







Structure Based Drug Design

Affinity Prediction Pose Prediction **Binding Discrimination**



Virtual Screening



Lead Optimization



Structure Based Drug Design

Affinity Prediction Pose Prediction **Binding Discrimination**



Virtual Screening



Lead Optimization





Drug Discovery Funnel



http://pharmit.csb.pitt.edu



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Drug Discovery Funnel

$$egin{array}{rll} {
m gauss}_1(d) &= w_{{
m guass}_1} e^{-(d/0.5)^2} \ {
m gauss}_2(d) &= w_{{
m guass}_2} e^{-((d-3)/2)^2} \ {
m repulsion}(d) &= \left\{ egin{array}{c} w_{{
m repulsion}} d^2 & d < 0 \ 0 & d \geq 0 \end{array}
ight.$$

$$ext{hydrophobic}(d) \;=\; \left\{egin{array}{cc} w_{ ext{hydrophobic}} & d \ 0 & d \ w_{ ext{hydrophobic}}(1.5-d) & d \ w_{ ext{hydrophobic}}(1.5-d) & o \end{array}
ight.$$

$$\mathrm{hbond}(d) \;=\; \left\{egin{array}{cc} w_\mathrm{hbond} & d < -0. \ 0 & d > 0 \ w_\mathrm{hbond}(-rac{10}{7}d) & otherwind \end{array}
ight.$$























Protein-Ligand Scoring



Computational and Systems Biology

Pose Prediction

Binding Discrimination

Affinity Prediction







The **universal approximation theorem** states that, under reasonable assumptions, a feedforward **neural network** with a finite number of nodes **can approximate any continuous** function to within a given error over a bounded input domain.











Deep Learning







At last — a computer program that can beat a champion Go player PAGE 484 **ALL SYSTEMS GO**

CONSERVATION SONGBIRDS A LA CARTE Illegal harvest of millions of Mediterranean birds PAGE 452

RESEARCH ETHICS SAFEGUARD TRANSPARENCY Don't let openness backfire on individual PAGE 459

POPULAR SCIENCE WHEN GENES GOT 'SELFISH' Dawkins's calling card forty years on PAGE 462

Vol. 529, No. 758 9 770028 083095

⇒ NATURE.COM/NATUR







Deep Learning







At last – a computer program that can beat a champion Go player PAGE 48 **ALL SYSTEMS GO**

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POPULAR SCIENCE WHEN GENES GOT 'SELFISH' > NATURE.COM/NA









Convolutional Neural Networks

Convolutional Filters



-1	-1	-1
0	0	0
1	1	1

-1	0	1	-1	-1	-1
-1	0	1	-1	8	-1
-1	0	1	-1	-1	-1





Protein-Ligand Representation



(R,G,B) pixel



Protein-Ligand Representation



- (R,G,B) pixel \rightarrow
- (Carbon, Nitrogen, Oxygen,...) voxel

The only parameters for this representation are the choice of **grid resolution**, **atom density**, and **atom types**.



Cons

- coordinate frame dependent
- pairwise interactions not explicit



Why Grids?

Pros

- clear spatial relationships
- amazingly parallel
- easy to interpret





Data Augmentation



2000





Data Augmentation



2000





Optimized Models



Default2018









Default2017

Pose Results

Redocked Pose

Default2017

Pose Results

Crossdocked Pose

Vina 12 10 8 6 2 Spearman = 0.473, RMSE = 1.8870 10 12 8 \mathbf{O} Experiment Experiment

But what is it learning?

AliphaticCarbon

OxygenDonorAcceptor

OxygenAcceptor

| 2×| 2×| 2×32

Convolution 3×3×3

Rectified Linear Unit

| 2×| 2×| 2×64

Max Pooling 2×2×2

6x6x6x64

Convolution x3x3 \mathbf{M}

Rectified Linear Unit

6×6×6×128

Pseudo-Huber Loss Softmax+Logistic Loss

Fully Connected

Fully Connected

Computational and Systems Biology

https://research.googleblog.com/2015/06/inceptionism-going-deeper-into-neural.html

$\frac{\partial L}{\partial A} = \sum_{i \in G_A} \frac{\partial L}{\partial G_i} \frac{\partial G_i}{\partial D} \frac{\partial D}{\partial A}$

$\frac{\partial L}{\partial A} = \sum_{i \in G_A} \frac{\partial L}{\partial G_i} \frac{\partial G_i}{\partial D} \frac{\partial D}{\partial A}$

















Iterative Refinement





Iterative Refinement







Iterative Refinement







Generative Modeling



Discriminative Model

Features X -



Computational and Systems Biology





Generative Model

Features X







Generative Model





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Generative Model





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→ Features X



True Examples





Generator





True Examples







Generator







Generative Adversarial Networks https://arxiv.org > stat 🔻

by IJ Goodfellow - 2014 - Cited by 4339 - Related articles Jun 10, 2014 - Submission history. From: Ian Goodfellow [view email] [v1] Tue, 10 Jun 2014 18:58:17 GMT (1257kb,D). Which authors of this paper are ...









Generative Adversarial Networks https://arxiv.org > stat 🔻

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PROGRESSIVE GROWING OF GANS FOR IMPROVED QUALITY, STABILITY, AND VARIATION

Tero Karras **NVIDIA**

Timo Aila **NVIDIA**





Samuli Laine **NVIDIA**

Jaakko Lehtinen NVIDIA Aalto University



https://youtu.be/G06dEcZ-QTg



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Generative Models

Generative models approximate a data distribution directly. They can map samples from one distribution (noise or input data) to realistic samples from an output distribution of interest.



noise sample

generated receptor & ligand grid





Autoencoding



Encoder





Automatic Chemical Design Using a Data-Driven Continuous Representation of Molecules

Hirzel[†], Ryan P. Adams^{∇I}, and Alán Aspuru-Guzik^{*‡⊥} (1)









http://people.eecs.berkeley.edu/~pathak/context_encoder/

Context Encoding





receptor grid

Computational and Systems Biology

Context Encoding





generated ligand grid







Receptor-Conditional Ligand-Variational Model





Receptor-Conditional Ligand-Variational Model





Receptor-Conditional Ligand-Variational Model





Model Architecture

 $n_{evels} = 3$ $conv_per_level = 3$ $n_{filters} = 32$ width_factor = 2 $n_latent = 1024$



ligand input density 19 x 24 x 24 x 24	3 convolutions 32 x 24 x 24 x 24	average pooling 32 x 12 x 12 x 12	3 convolutions 64 x 12 x 12 x 12	

Computational and Systems Biology































Atom Fitting $a^* = \arg\min ||d - D(a)||_2^2 + \lambda E(a)$ a






Atom Fitting $a^* = \arg\min ||d - D(a)||_2^2 + \lambda E(a)$ a









Conditioning on the Receptor







Conditioning on the Receptor





Iterpolating



Two atom toy system





Iterpolating



Two atom toy system





LALRNN Removing the third dimension



Chomsky Hierarchy



http://www.cs.appstate.edu/~dap/classes/2490/chapter11print.html

Turing machines that might loop

Turing machines that always accept or reject

Turing machines that use only as much tape as the input takes

Nondeterministic pushdown automata

Deterministic pushdown automata

Finite automata

An Introduction to **FORMAL LANGUAGES** and AUTOMATA







Balanced Parentheses $S \rightarrow \varepsilon$ $S \rightarrow (S)$ $S \rightarrow SS$

((())))()(())() () () () ()

Grammars

- Palindromes
 - $S \rightarrow \varepsilon$ $S \rightarrow aSa$ $S \rightarrow bSb$

aa babbab abbaabba Arithmetic

- E ::= id
 - num + E E * E E
 - E
 - 3 * 5 + 4 (3 + 4) * 5



University of Pittsburgh

Section	Formal Grammar						
	ATOMS						
3.1	atom ::= bracket_atom aliphatic_organic aromatic_organic '*'						
	ORGANIC SUBSET ATOMS						
3.1.5	aliphatic organic ::= $ B' C' N' O' S' P' F' C ' Br' I'$						
3.5	aromatic organic ::= 'b' 'c' 'n' 'o' 's' 'n'						
5.5	$\frac{1}{ppacket atoms} = \frac{p + c + n + o + s + p}{ppacket atoms}$						
211	bracket atom u = "" is atoma? sumbal shira!? heavint? sharga? slass? ""						
3.1.1	bracket_atom ::= [isotope? symbol chiral? ncount? charge? class?]						
3.1.1	symbol := element_symbols aromatic_symbols '*'						
3.1.4	isotope ::= NUMBER						
3.1.1	element_symbols ::=						
	'H' 'He'						
	'Li' 'Be' 'B' 'C' 'N' 'O' 'F' 'Ne'						
	'Na' 'Mg' 'Al' 'Si' 'P' 'S' 'Cl' 'Ar'						
	'K' 'Ca' 'Sc' 'Ti' 'V' 'Cr' 'Mn' 'Fe' 'Co' 'Ni' 'Cu' 'Zn' 'Ga' 'Ge' 'As' 'Se' 'Br' 'Kr'						
	'Rb' 'Sr' 'Y' 'Zr' 'Nb' 'Mo' 'Tc' 'Ru' 'Rh' 'Pd' 'Ag' 'Cd' 'In' 'Sn' 'Sb' 'Te' 'I' 'Xe'						
	'Cs' 'Ba' 'Hf' 'Ta' 'W' 'Re' 'Os' 'Ir' 'Pt' 'Au' 'Hg' 'Tl' 'Pb' 'Bi' 'Po' 'At' 'Rn'						
	'Fr' 'Ra' 'Rf' 'Db' 'Sg' 'Bh' 'Hs' 'Mt' 'Ds' 'Rg'						
	l'La'l'Ce'l'Pr'l'Nd'l'Pm'l'Sm'l'Eu'l'Gd'l'Tb'l'Dv'l'Ho'l'Er'l'Tm'l'Yb'l'Lu'						
	l'Ac'l'Th'l'Pa'l'U' l'Np'l'Pu'l'Am'l'Cm'l'Bk'l'Cf'l'Es'l'Em'l'Md'l'No'l'Lr'						
3.5	aromatic symbols $:= c' n' c' n' s' s' s' as'$						
5.5							
3.0	chiral ::= '@'						
5.5							
	.@IBT. .@IB5. .@IB3. .@IB59. .@IB30.						
	'@OH1' '@OH2' '@OH3' '@OH29' '@OH30'						
	HYDROGENS						
3.1.2	hcount ::= 'H'						
	CHARGE						
3.1.3	charge ::= '-'						
	'-' DIGIT						
	'+'						
	'+' DIGIT						
	'' *deprecated*						
	'++' *deprecated*						
	ATOM CLASS						
317	class ::= ':' NUMBER						
5.1.7							
22202	bonds And CHAINS						
3.2, 3.9.3							
3.4							
3.3	branched_atom ::= atom ringbond* branch*						
	branch ::= '(' chain ')'						
	'(' bond chain ')'						
	'(' dot chain ')'						
	chain ::= branched_atom						
	chain branched_atom						
	chain bond branched_atom						
	chain dot branched_atom						
3.7	dot ::= '.'						
	SMILES STRINGS						
3 10	smiles "= chain terminator						
5.10	terminator : SDACE TAR LINESEED CADDIACE DETURN END OF STRING						

SMILES



clcccclN





Push Down Automata

Balanced Parentheses

If input is) and (is on stack top, then (is popped and nothing is pushed to stack.



If input is (, what's on stack top doesn't matter and a (is pushed to stack.

 $|\varepsilon|$





Bottom Up Parsing

A PDA can be implemented with a parse table

	action			goto	
state	ident	+	\$	E	Т
0	s3			g1	g2
1			а		
2		s4	r2		
3		r3	r3		
4	s3			g 5	g2
5			r1		



while(true) s = state on top of stack a = current input token shift if(action[s][a] == sN)push N a = next input token reduce else if (action[s][a] == rR)remove rhs of rule R from stack X = lhs of rule RN = state on top of stack push goto[N][X] accept :-) else if(action[s][a] == a) return success error else return failure





The NN Part

Implement every state as its own neural network that calculates a function of the input in the context of the parse (encoder) or outputs a syntactically correct string according to the rules of the grammar (generator)



Reduce State *n* stack states state (pushed)



The NN Part

Implement every state as its own neural network that calculates a function of the input in the context of the parse (encoder) or outputs a syntactically correct string according to the rules of the grammar (generator)

Shift State



Reduce State







U \mathbf{G} G A G G G

GGGAGAAUUGUCCC ((((...)))))

clcccclN

Does it work???

	state		()	S	
$S \rightarrow$	0	s6	s1		g5	
0 7.	1	s6	s1	s7	g4	
$S \rightarrow ()$	2	s6	s1	s11	g3	
\mathcal{O} $()$	3	s10	s2	s9		
$S \rightarrow (S)$	4	s10	s2	s8		
U (U)	5	s10	s2			
$S \rightarrow S(S)$	6	Redu				
U / U(U)	7	Reduce $S \rightarrow ()$				
$S \rightarrow S$	8	Reduce $S \rightarrow (S)$				
0 70.	9	Reduce $S \rightarrow S(S)$				
$S \rightarrow S()$	10	Reduce $S \rightarrow S$.				
\mathcal{O}	11	Reduce $S \rightarrow S()$				
	12	END				



GRU Encoder











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G github.com/gnina

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