Deep Learning

in Biomedical Data Science



Hussein Mohsen CBB752 Spring 2019

- Image Color Restoration
- Image Captioning
- Object Classification
- Robotics
- Self-driving Cars
- Machine Translation
- Speech Recognition
- Text Generation
- Handwriting Generation
- Music Composition
- & more

handwriting generation





We've trained an unsupervised language model that can generate coherent paragraphs and perform rudimentary reading comprehension, machine translation, question answering, and summarization — all without task-specific training:

blog.openai.com/better-languag ...

We've trained a large-scale unsupervised language model which generates coherent paragraphs of text, achieves state of the art performance on many language modeling benchmarks, and performs rudimentary reading comprehension, machine translation, question answering, and summarization —





DeepMind's new AI just beat top human pro-gamers at Starcraft II for the first time



[https://thispersondoesnotexist.com]

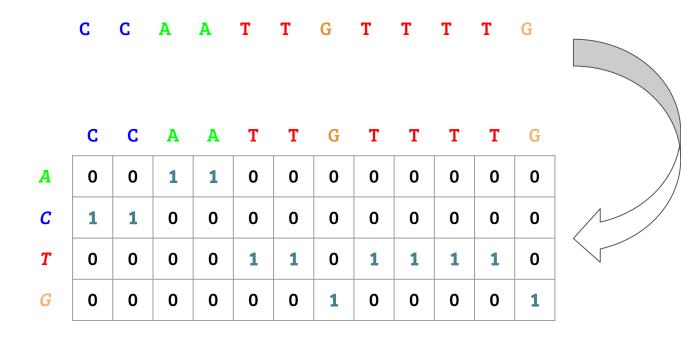
0:38 312K views

9:03 AM - 14 Feb 2019

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One-Hot Encoding of Sequences



Biomedical Data Science

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Convolutional neural network architectures for predicting DNA-protein binding 👌 Haoyang Zeng, Matthew D. Edwards, Ge Liu, David K. Gifford 🐱 Bioinformatics, Volume 32, Issue 12, 15 June 2016, Pages i121-i127, https://doi.org/10.1093/bioinformatics/btw255

Published: 11 June 2016

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Abstract

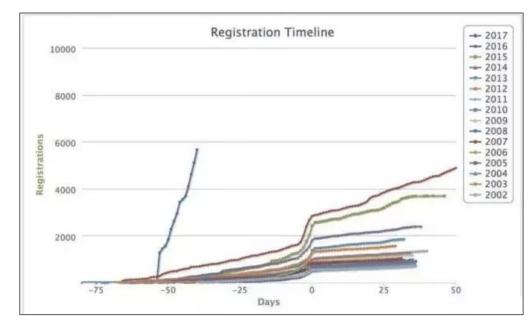
2016

Motivation: Convolutional neural networks (CNN) have outperformed conventional methods in modeling the sequence specificity of DNA-protein binding. Yet inappropriate CNN architectures can yield poorer performance than simpler models. Thus an in-depth understanding of how to match CNN architecture to a given task is needed to fully harness the power of CNNs for computational biology applications.

Results: We present a systematic exploration of CNN architectures for predicting DNA sequence binding using a large compendium of transcription

Biomedical Data Science

 DeepBind, DeepFold, DeepSEA, DeepCNF, DeepVariant, DeepMotif, DeepLNC, DeepCpG, DeepCyTOF, DeepChrome, DeepWAS, DeepSplice, and other methods



NeurIPS Registration Timeline [2002-17] @lxbrun

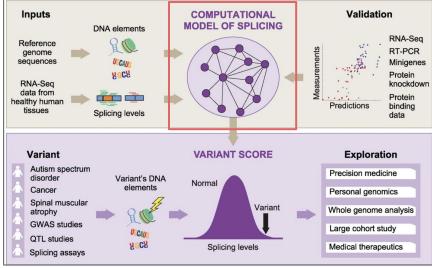
Biomedical Data Science

- Prediction of RNA Splicing
- 1393 sequence features as input
- Fully-connected neural networks
- RNA-seq from *Illumina Human Body Map* 2.0 project
- Assessment of >650,000 SNPs effect on splicing regulation from the NCBI database of genetic variation (*dbSNP*) and Human Gene Mutation Database (*HGMD*)

RESEARCH ARTICLE

The human splicing code reveals new insights into the genetic determinants of disease

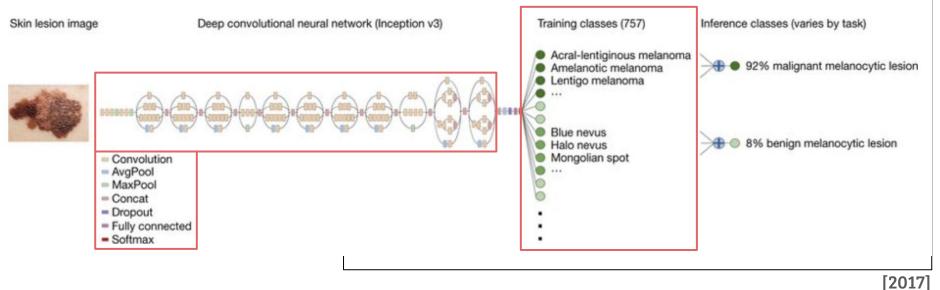
Hui Y. Xiong^{1,2,3,*}, Babak Alipanahi^{1,2,3,*}, Leo J. Lee^{1,2,3,*}, Hannes Bretschneider^{1,3,4}, Daniele Merico^{5,6,7}, Ryan K. C. Yuen^{5,6,7}, Yimin Hua⁸, Serge Gueroussov^{2,7}, Hamed S. Najafabadi^{1,2,3}, Timothy R. Hughes^{2,3,7}, Quaid Morris^{1,2,3,7}, Yoseph Barash^{1,2,9}, Adrian R. Krainer⁸, Nebojsa Jojic¹⁰, Stephen W. Scherer^{3,5,6,7}, Benjamin J. Blencowe^{2,5,7}, Brendan J. Frey^{1,2,3,4,5,7,10,†}



Biomedical Data Science

- Skin cancer classification
- 129,450 clinical images from public

Dermatologist-level classification of skin

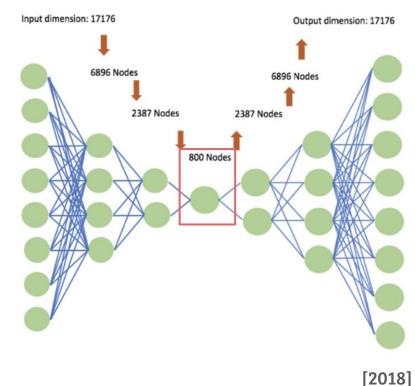


Biomedical Data Science

- Denoising Autoencoder (AE) for genomic data imputation
- | *I* | = | *O* |, bottleneck layer | *B* | << | *I* |, | *O* |
- 17,000+ genes, 269,000+ CpG sites
- Pan-Cancer RNA-seq and DNA Methylation data from The Cancer Genome Atlas (*TCGA*)

A deep learning framework for imputing missing values in

Yeping Lina Qiu^{1,2}, Hong Zheng², Olivier Gevaert^{2,3,*}



9

Challenges

- Interpretability
 - Different from interpretability in Optimization
 - Weight matrix interpretation
 - Input feature prioritization
 - Biologically or clinically-driven
 - Earlier and later layers usually have more importance
- Data availability
- Hyperparamter Optimization
 - Set *before* training
 - Finding suboptimal combinations can be time consuming



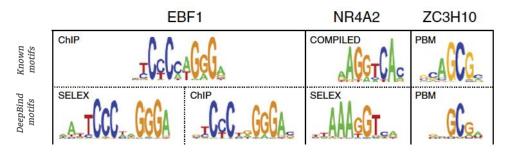
Interpretability

DeepBind

- Interpretability
 - Different from interpretability in Optimization
 - Weight matrix interpretation
 - Input feature prioritization
 - Biologically or clinically-driven
 - Earlier and later layers usually have more importance
- What would happen if the number of convolution filters is quite high?

Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning

Babak Alipanahi^{1,2,6}, Andrew Delong^{1,6}, Matthew T Weirauch^{3–5} & Brendan J Frey^{1–3}



Interpretability

SurvivalNet

- Interpretability
 - Different from interpretability in Optimization
 - Weight matrix interpretation
 - Input feature prioritization
 - Biologically or clinically-driven
 - Earlier and later layers usually have more importance
- 17,000-18,000 features dominated by gene expression and clinical variables
- Why would features be prioritized? What would potential downstream analyses be?

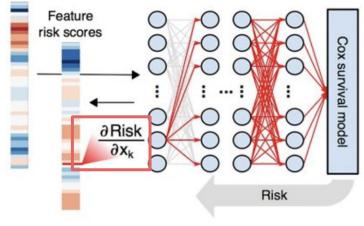
SCIENTIFIC REPORTS

Predicting clinical outcomes from large scale cancer genomic profiles with deep survival models

Received: 23 May 2017 Accepted: 30 August 2017 Published online: 15 September 2017

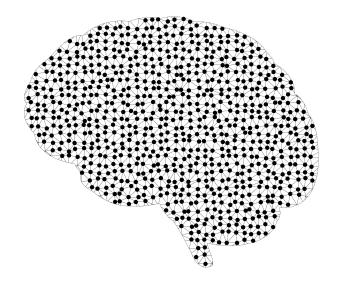
Safoora Yousefi¹, Fatemeh Amrollahi¹, Mohamed Amgad¹, Chengliang Dong², Joshua E. Lawis³, Congzheng Song⁴, David A. Gutman⁵, Sameer H. Halani⁶, Jose Enrique Velazquez Vega⁷, Daniel J. Brat^{7,8} & Lee A. D. Cooperg^{0,1,3,8}

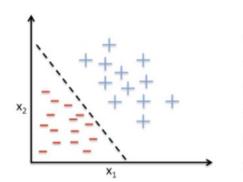
Patient features

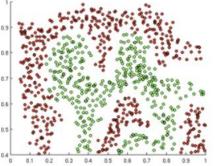


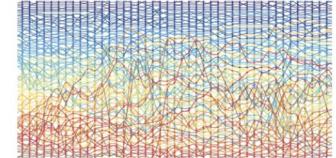
Notes

- Advances in computing
- Availability of large datasets
- Ability to detect highly complex, non-linear patterns
- Ability to predict many outputs at once
- Transfer learning to *transfer* patterns learned by one model to another









Resources

INTERFACE

rsif.royalsocietypublishing.org

Headline review



Cite this article: Ching T *et al.* 2018 Opportunities and obstacles for deep learning in biology and medicine. *J. R. Soc. Interface* **15**: 20170387.

http://dx.doi.org/10.1098/rsif.2017.0387

Opportunities and obstacles for deep learning in biology and medicine

Travers Ching^{1,†}, Daniel S. Himmelstein², Brett K. Beaulieu-Jones³, Alexandr A. Kalinin⁴, Brian T. Do⁵, Gregory P. Way², Enrico Ferrero⁶, Paul-Michael Agapow⁷, Michael Zietz², Michael M. Hoffman^{8,9,10}, Wei Xie¹¹, Gail L. Rosen¹², Benjamin J. Lengerich¹³, Johnny Israeli¹⁴, Jack Lanchantin¹⁷, Stephen Woloszynek¹², Anne E. Carpenter¹⁸, Avanti Shrikumar¹⁵, Jinbo Xu¹⁹, Evan M. Cofer^{20,21}, Christopher A. Lavender²², Srinivas C. Turaga²³, Amr M. Alexandari¹⁵, Zhiyong Lu²⁴, David J. Harris²⁵, Dave DeCaprio²⁶, Yanjun Qi¹⁷, Anshul Kundaje^{15,16}, Yifan Peng²⁴, Laura K. Wiley²⁷, Marwin H. S. Segler²⁸, Simina M. Boca²⁹, S. Joshua Swamidass³⁰, Austin Huang³¹, Anthony Gitter^{32,33} and Casey S. Greene²

Resources

- Neural Networks and Deep Learning by Michael Neilson [http://neuralnetworksanddeeplearning.com/]
- Deep Learning by Ian Goodfellow and Yoshua Bengio and Aaron Courville [http://www.deeplearningbook.org/]
- DeepLearning.ai on Coursera [https://www.coursera.org/deeplearning-ai]

Resources

