3050571 Practical Clin Data Sci

Session 14: Artificial neural network designs

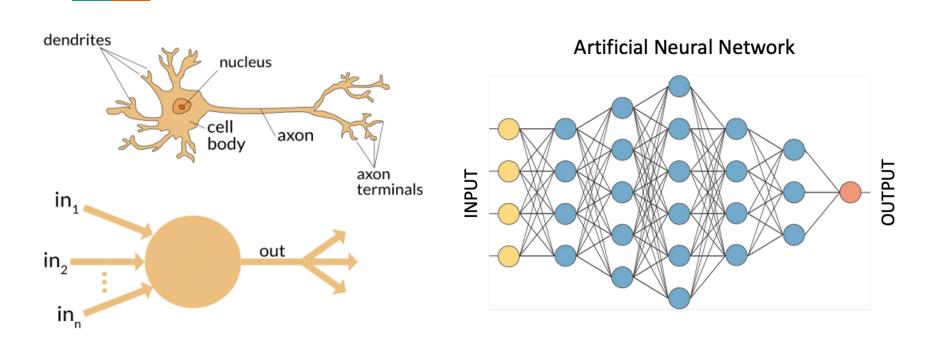
February 29, 2024



Sira Sriswasdi, PhD

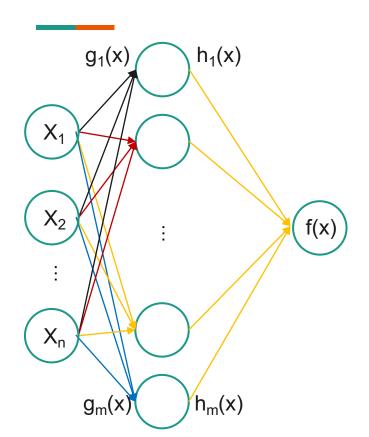
- Research Affairs
- Center of Excellence in Computational Molecular Biology (CMB)
- Center for Artificial Intelligence in Medicine (CU-AIM)

Artificial neural network



Network of simple computation nodes: out = $f(w_1in_1 + w_2in_2 + ... + w_nin_n)$

Calculations inside neural nentwork



Linear neuron input

$$- g_1(x) = w_{1,1}x_1 + \dots + w_{1,n}x_n$$

$$- g_m(x) = w_{m,1}x_1 + \dots + w_{m,n}x_n$$

Sigmoid activation

$$- h_1(x) = \frac{1}{1 + e^{-g_1(x)}}$$

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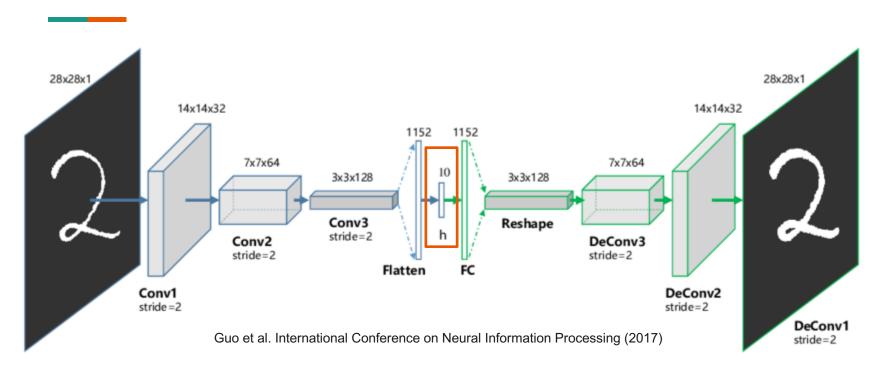
$$h_m(x) = \frac{1}{1 + e^{-g_m(x)}}$$

Linear aggregated output

$$f(x) = u_1 h_1(x) + \dots + u_m h_m(x)$$

Autoencoder

Representation learning via self-reconstruction



Similar to dimensionality reduction

Denoising autoencoder

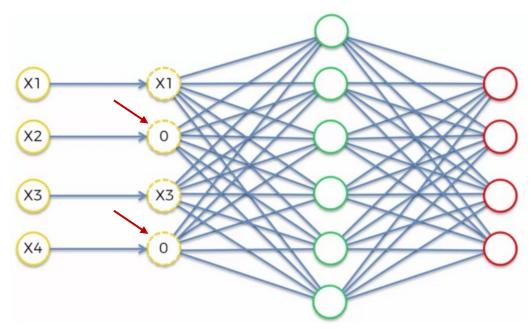


Image from towardsdatascience.com/denoising-autoencoders-explained-dbb82467fc2

- Randomly set some inputs to zero → robust representation

Variational autoencoder (VAE)

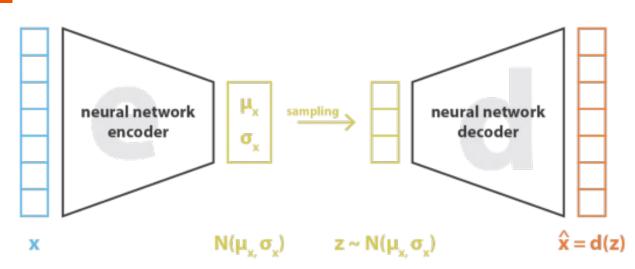
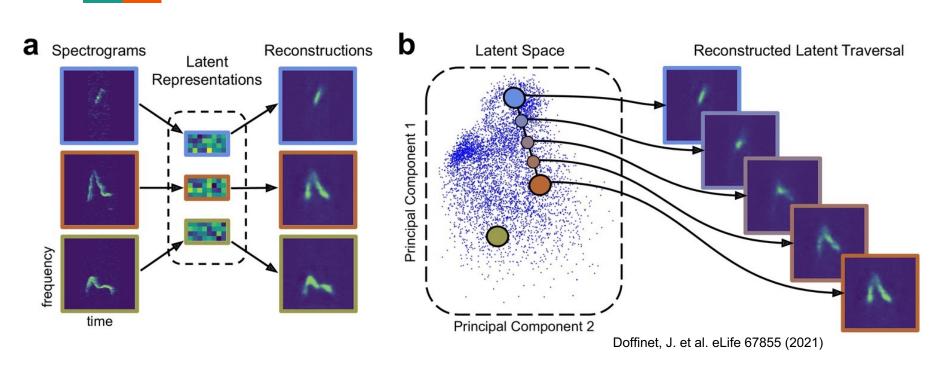


Image from www.jeremyjordan.me/variational-autoencoders/

- Learned representation = parameters for distribution
- Decoder is robust to small changes in the representation
 - Smooth representation space

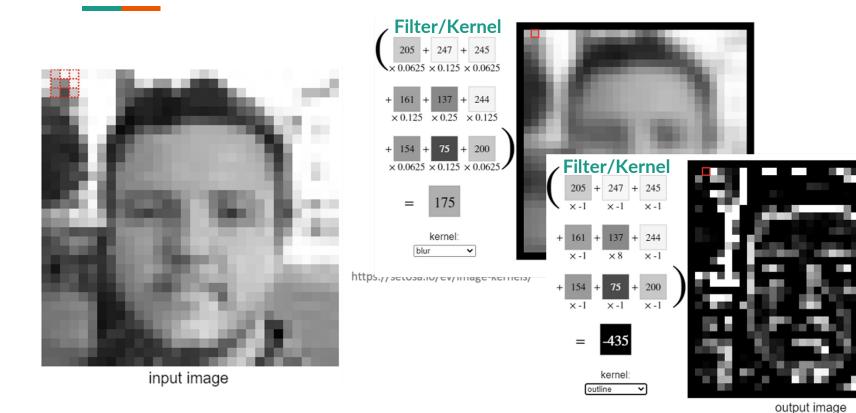
VAE generates smoother representation space



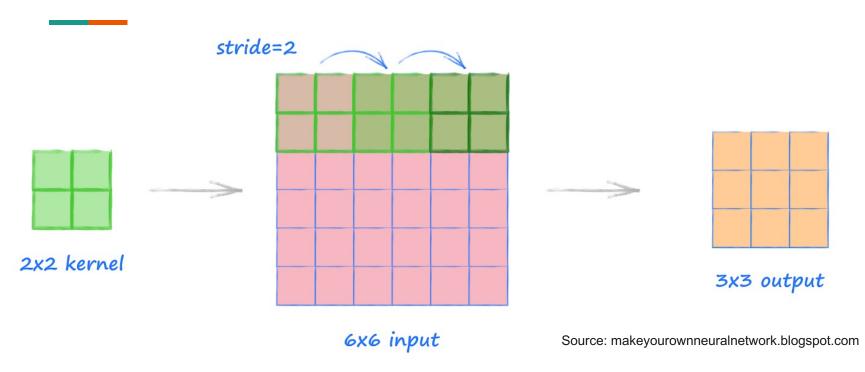
VAE learn representation distribution, not just individual vectors

Convolutional neural network

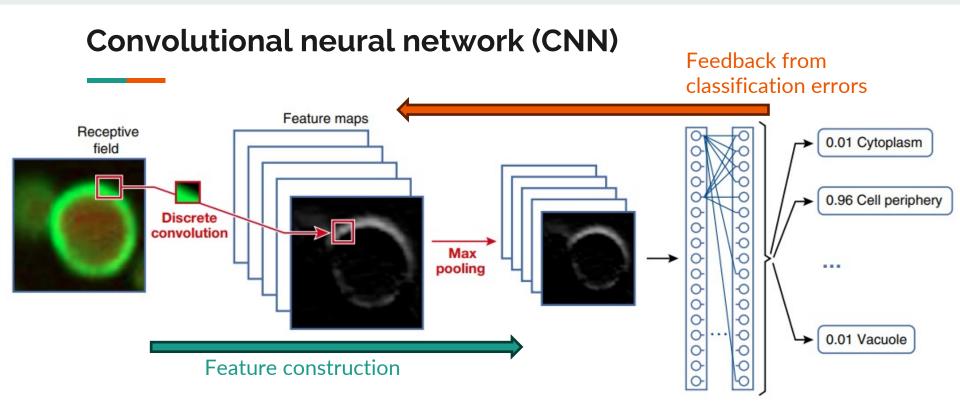
Extracting contextual pattern with filter



Convolutional operation

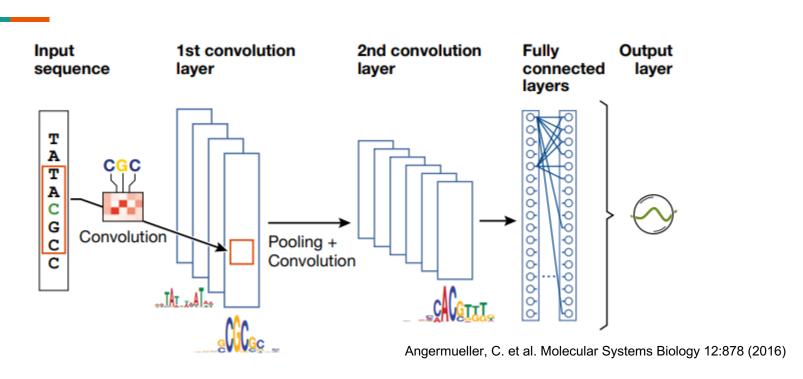


Linear combination of values in nearby pixels – applied throughout



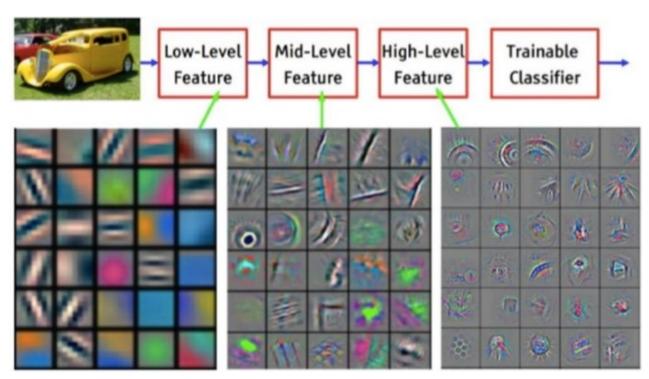
Instead of using human-define filters to extract contextual pattern, CNN learns the best filters from the data

Convolution for DNA sequences



- Motif = contextual pattern on DNA sequence

Hierarchical feature assembly inside CNN



Source: Zeiler and Fergus (2013)

Some CNN designs

Vanishing and exploding gradient problems

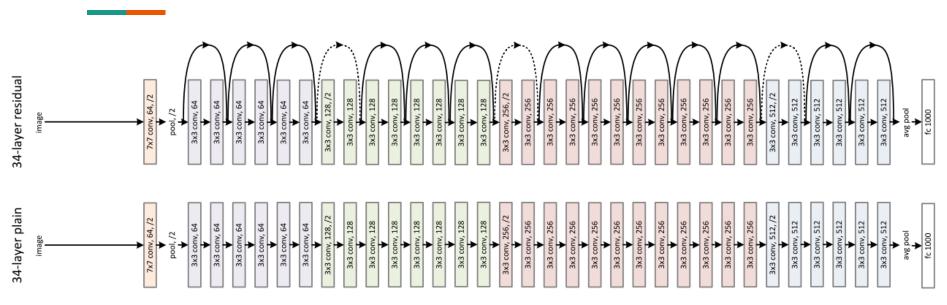
Gradient:
$$\frac{\delta L}{\delta w_{i,j}} = \frac{\delta L}{\delta f} \frac{\delta f}{\delta h_i} \frac{\delta h_i}{\delta g_i} \frac{\delta g_i}{\delta w_{i,j}} = (f(x) - y) \cdot u_i \cdot g_i(x) (1 - g_i(x)) x_j$$

The number of multiplicative terms scales with the number of layers

What would happen if all values are << 1 or >> 1?

- Gradient became very small → No weight update
- Gradient became very large → Unstable

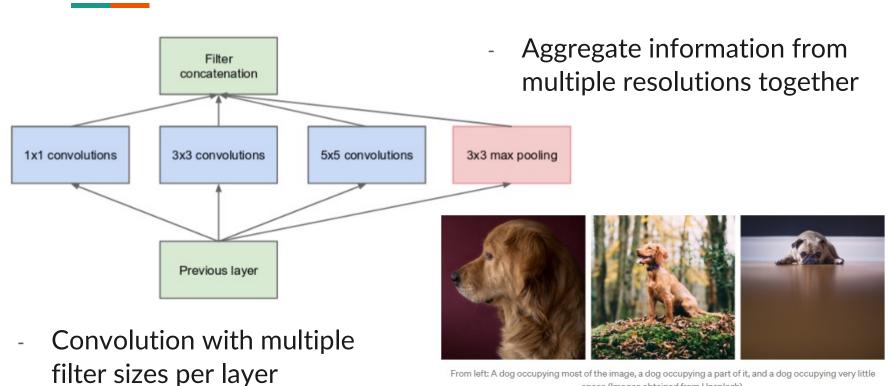
Residual network (ResNet)



Source: medium.com

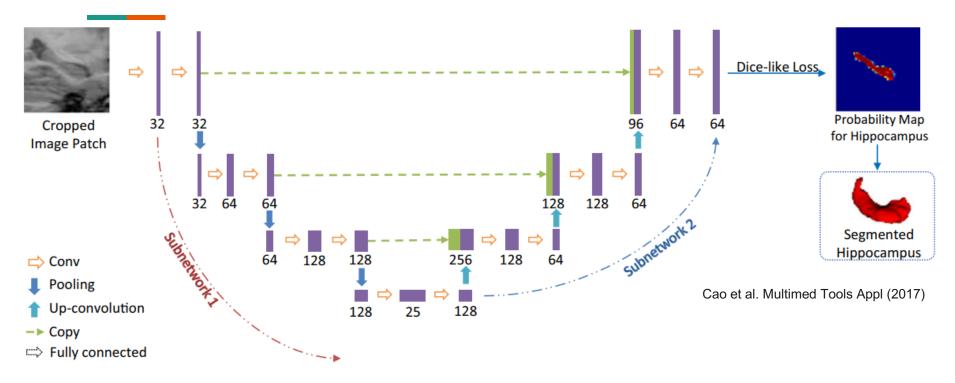
- Adding skip connections jumping over blocks of convolutional layers
- Reduce the number of terms in gradient of early weights

Inception = multi-resolution layer



From left: A dog occupying most of the image, a dog occupying a part of it, and a dog occupying very little space (Images obtained from Unsplash).

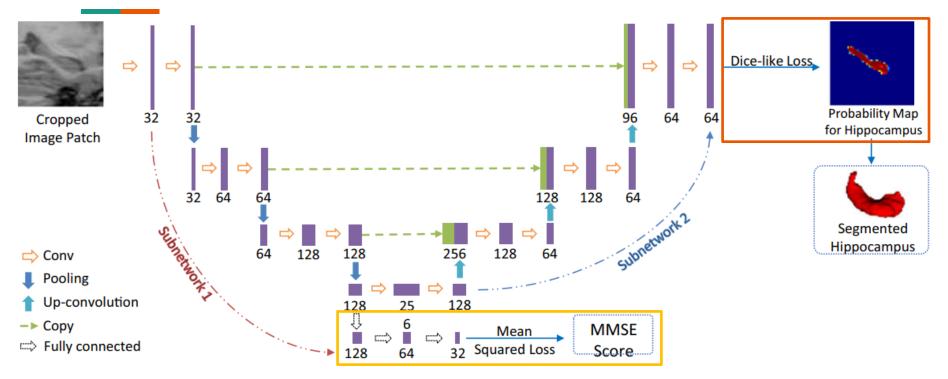
U Net = producing image from image



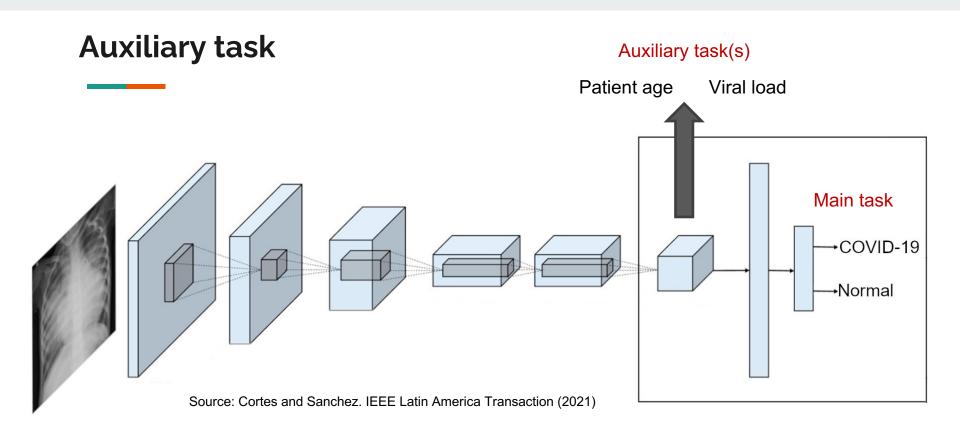
- Make prediction for every pixel → output size = input size

Multitasking

Simultaneous segmentation & classification

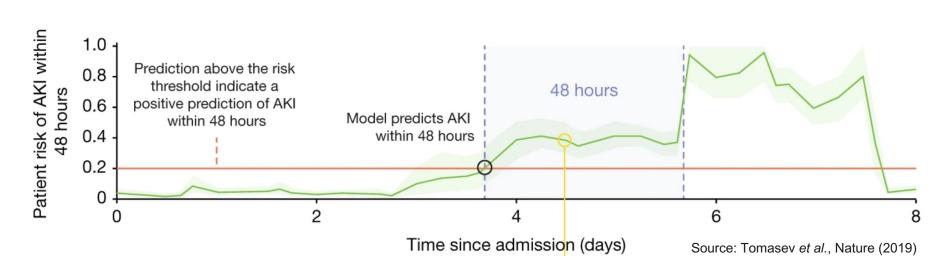


- Combine gradients from both tasks



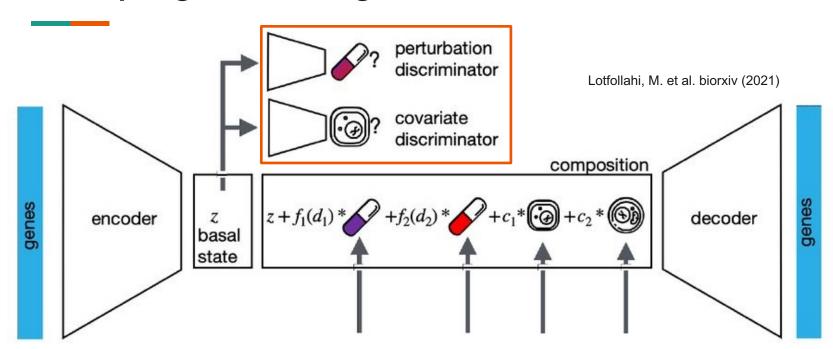
Encourage the learned representation to include more information

Acute kidney injury prediction



- Main task: Occurrence of acute kidney injury within 48 hours
- Auxiliary tasks: Maximal values of 7 key lab tests within 48 hours
 - Provide more feedback on what the model gets wrong

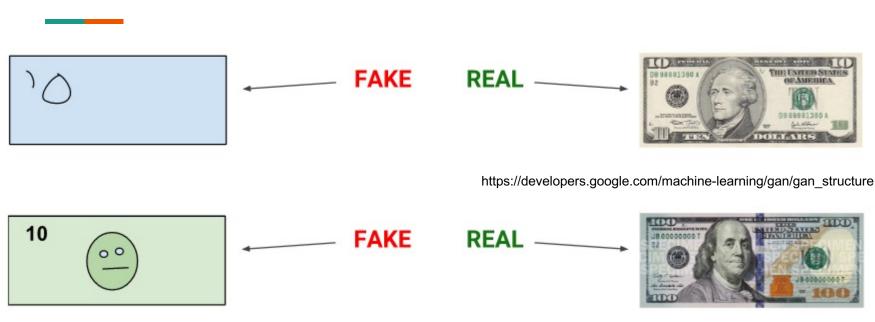
Decoupling / debiasing



- Deconvolute cell basal state from perturbation and covariate
- Update weights in the opposite direction of gradient

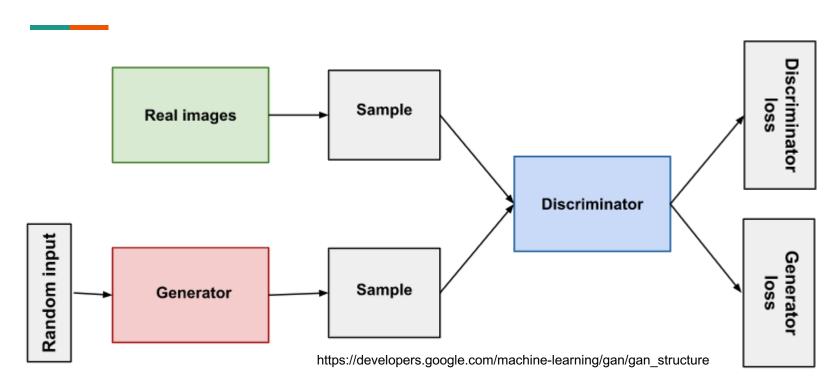
Generative model

Why generative model?



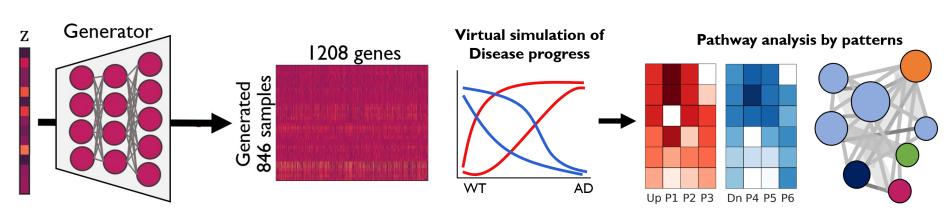
Models that generate realistic data can tell us about the underlying mechanisms of the system

Generative adversarial network (GAN)



Simultaneous training of generator and discriminator

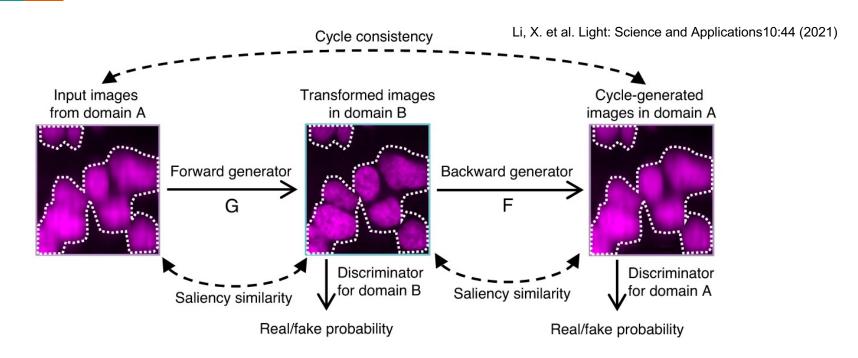
Knowledge from simulated data



Park, J. et al. PLoS Computational Biology 16:e1008099 (2020)

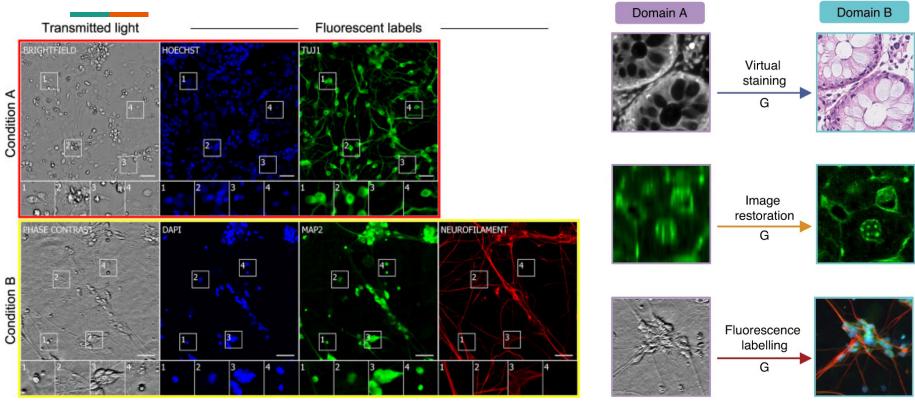
- Train a generator with data from small-scale experiment
- Simulate time-course gene expression profiles
- Perform usual bioinformatics analyses to infer biological knowledge

Cycle GAN for transforming image



Generate sharpened image from blurry image and back

Virtual staining

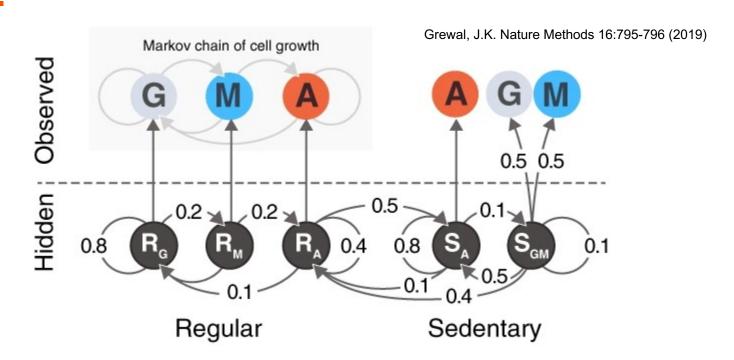


Christiansen, E.M. et al. Cell 173:792-803.e19 (2018)

Li, X. et al. Light: Science and Applications10:44 (2021)

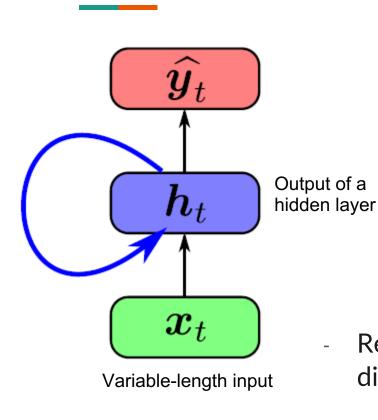
Recurrent neural network

Hidden Markov Model



- Sequence of observations, each generated from a model

Recurrent neural network



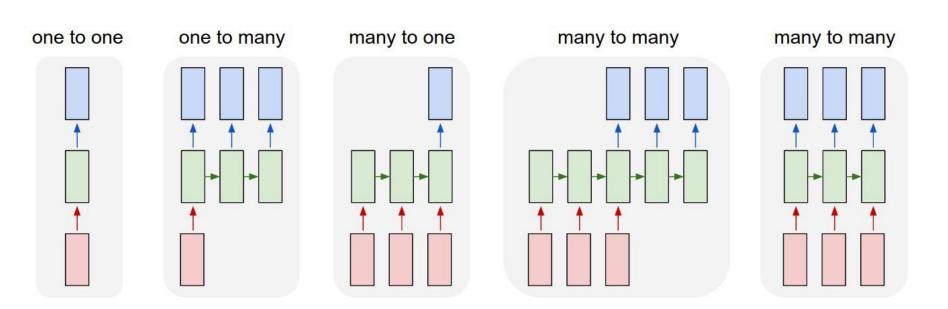
Shared weights!
$$h_1 = f(\boldsymbol{u} \cdot x_1 + \boldsymbol{v} \cdot h_0 + c)$$

$$h_2 = f(\boldsymbol{u} \cdot x_2 + \boldsymbol{v} \cdot h_1 + c)$$
...
$$h_t = f(\boldsymbol{u} \cdot x_t + \boldsymbol{v} \cdot h_{t-1} + c)$$

$$\hat{y}_t = \boldsymbol{w} \cdot h_t + b$$

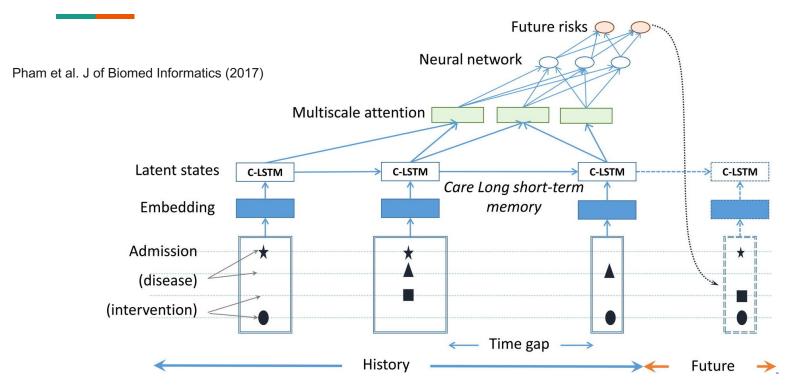
Reuse a single layer (weights) over time with different input

Sequence-to-sequence capability



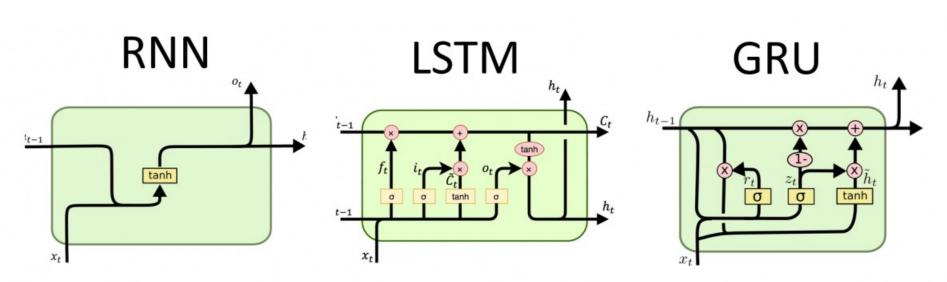
- Handle variable input and output

RNN on medical history



- Aggregate information across time to make prediction

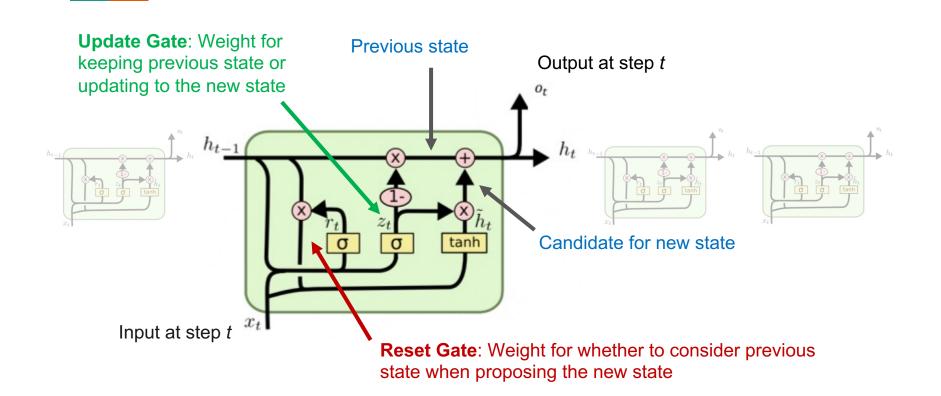
RNN architecture



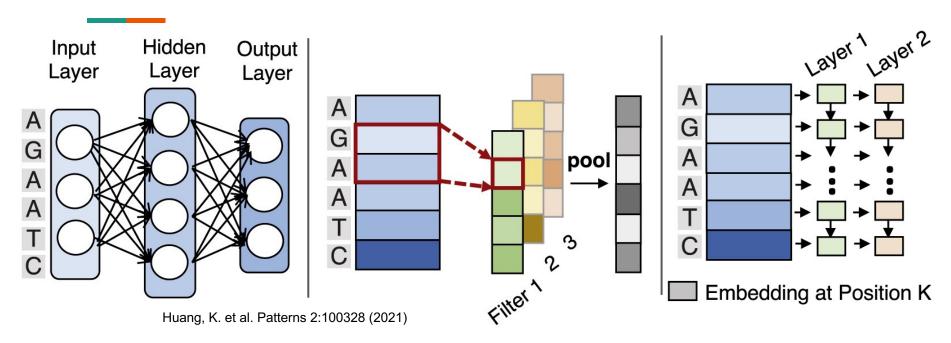
Source: www.linkedin.com/pulse/recurrent-neural-networks-rnn-gated-units-gru-long-short-robin-kalia

- Allow the model to retain / forget information from earlier time points
- Include shortcuts for gradient calculation similar to ResNet

Gated recurrent unit (GRU)



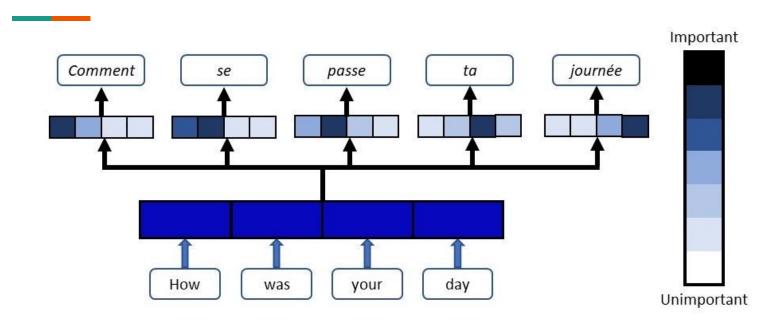
Picking the right model requires domain knowledge



 Choosing the "right" model depends on the interpretation of the task and the underlying mechanisms

Transformer and attention

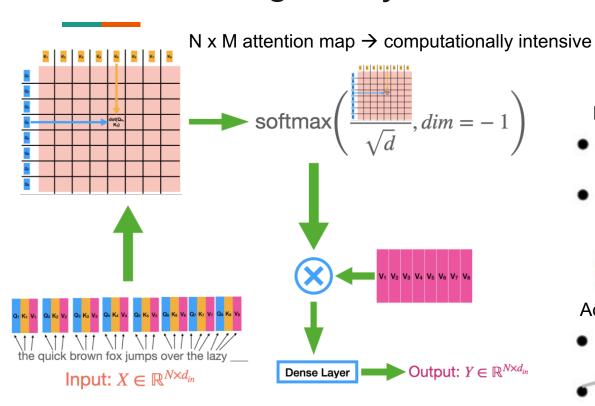
Attention explicitly model the contribution of each input



https://blog.floydhub.com/attention-mechanism/

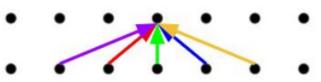
The model learn to estimate contribution directly during training, not as a post-hoc explainability

Attention vs regular layers



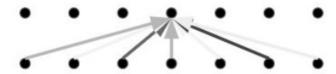
Convolution

Fixed weights regardless of input

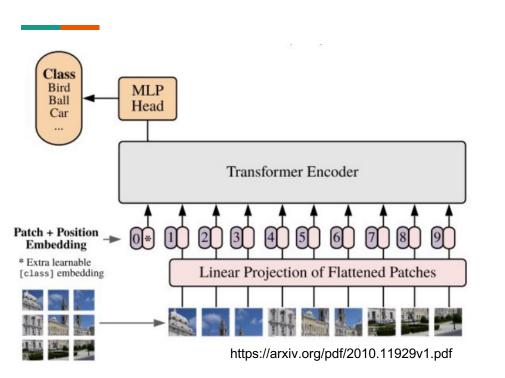


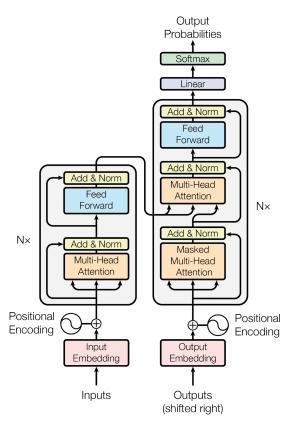
Self-Attention

Adaptive weights depending on input



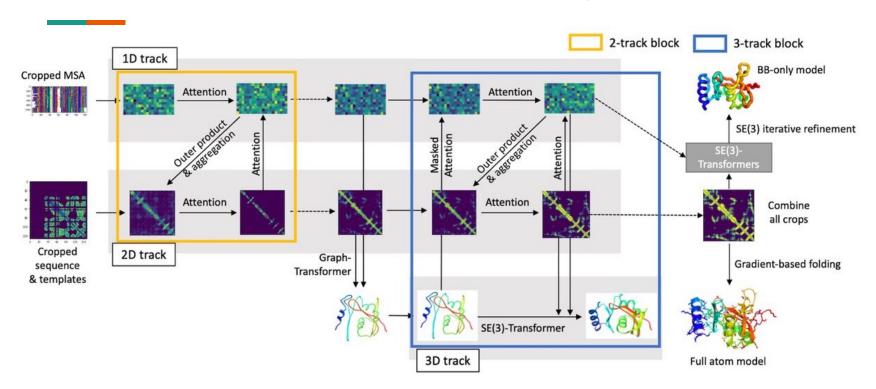
Transformer architecture





Multiple attention layers replace conventional networks

Transformer model for protein folding prediction



Attention is all you need

Any questions?

See you on March 1st