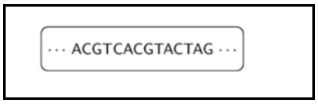
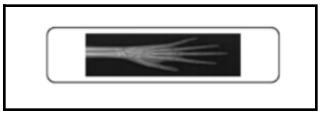
DL applications applied BioInformatics

	Input Data	Research Avenues
Omics - genomics 	Sequencing (DNA-seq, RNA-seq) Features from genomics sequence Contact map (distance of amino acid pairs in 3D structure) Microarray gene expression	Protein structure - 1 dimensional structure protein - Contact map - Structure model quality assessment Gene expression regulation - Splice junction - Genetic variants - Sequence specificity Protein classification - Subcellular classification Anomaly classification - Cancer
Biomedical Imaging 	Magnetic resonance image (MRI) Positron emission tomography (PET) Histopathology image Volumetric electron microscopy image Retinal image	Anomaly classification - Gene expression pattern Segmentation - Cell structure - Neuronal structure - Vessel map - Brain tumor Recognition - Cell nuclei - Finger joint - Anatomical structure Brain decoding
Biomedical Signal processing	—---	—---

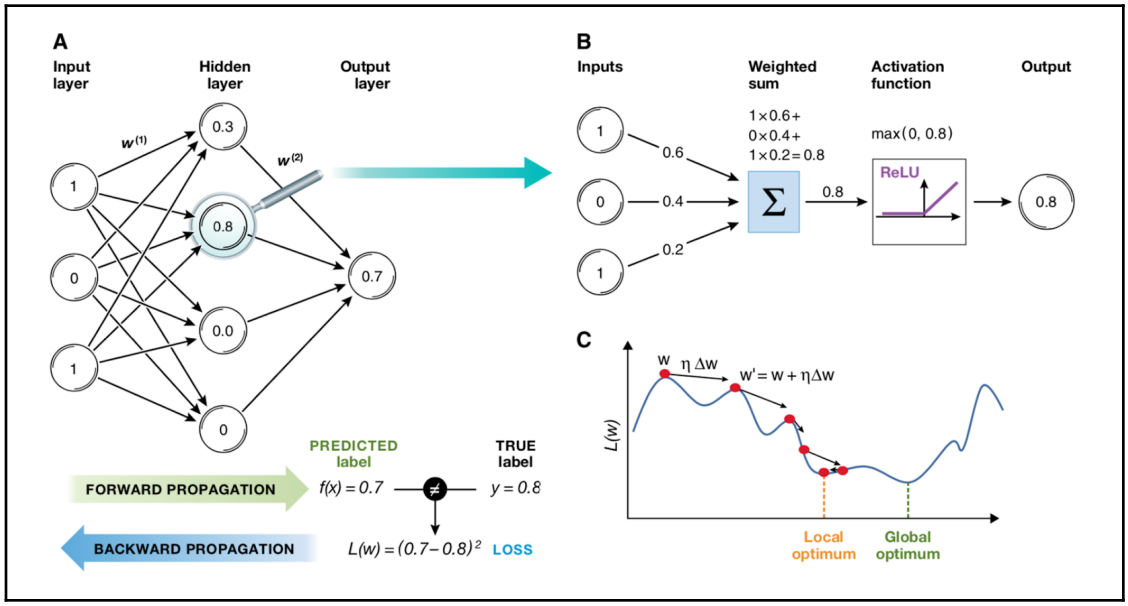
Categorization of Deep Learning

	Omics	Biomedical Imaging	Biomedical SP
Deep NN	Protein structure Gene expression regulation Protein classification Anomaly classification	Anomaly classification Segmentation Recognition Brain decoding	—-
Convolutional NN - CNN	Gene expression regulation	Anomaly classification Segmentation Brain decoding	—-
Recurrent NN - RNN	Protein structure Gene expression regulation Protein classification		—-
Emergent architectures	Protein structure	Segmentation	

Deep learning

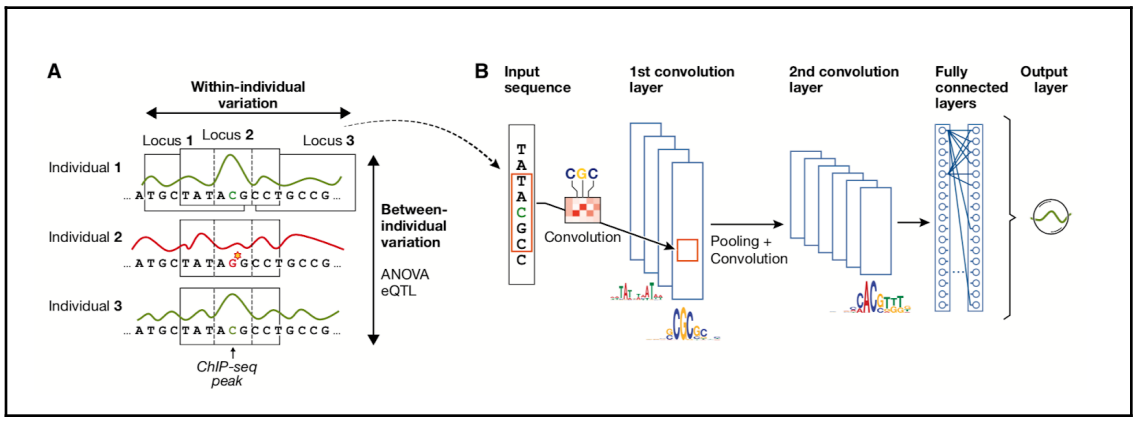
Artificial Neural Network for the brain McCulloch and Pitts 1943, Farley and Clark 1954

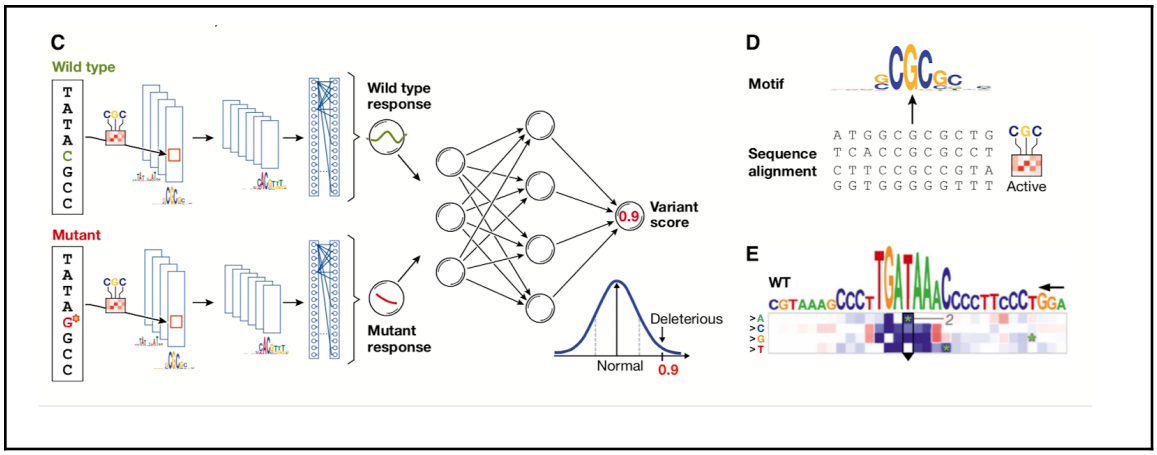
Deep Learning for Computational Biology: Christof Angermueller et al



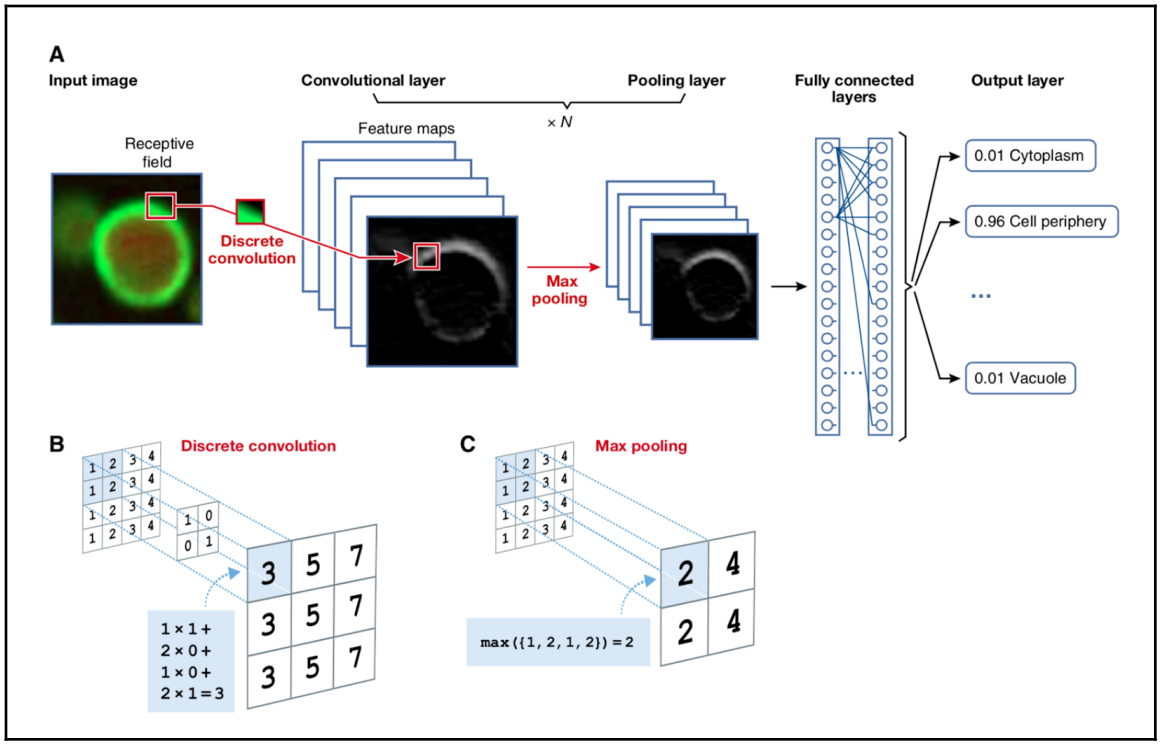
Deep Learning Neural Networks for predicting molecular trains from DNA sequencing

- Christof Angermueller et al

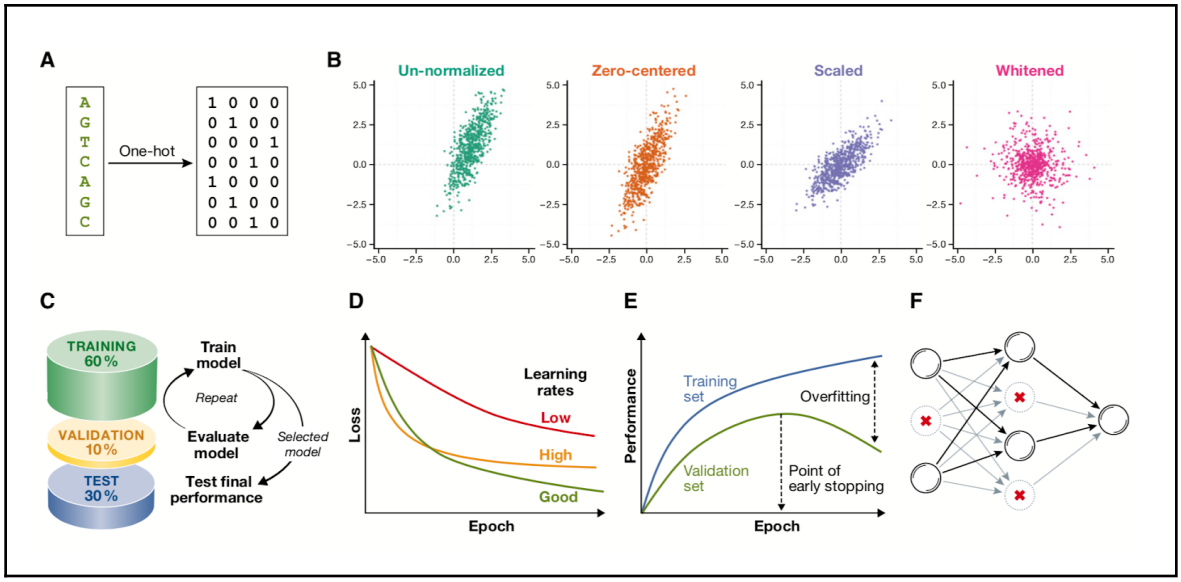




Convolutional Neural Networks



Data normalization for and pre-processing into neural networks



Hyperparameters

	Range	Default value
Learning rate		
Batch size		
Momentum rate		
Weight initialization		
Per-parameter adaptive learning rate methods		
Batch normalization		
Learning rate decay		
Activation function		
Dropout rate		
L1, L2 regularization		