**[HMM - Current Genomics 2009 .pdf](https://l.facebook.com/l.php?u=https%3A%2F%2Fcdn.fbsbx.com%2Fv%2Ft59.2708-21%2F13286575_10209883216347794_1281296062_n.pdf%2FHMM-Current-Genomics-2009.pdf%3Foh%3D36af49dc806eb554f225e719097f58e6%26oe%3D5748CC7C%26dl%3D1&h=yAQE7Myks)**

**[(ML 14.1) Markov models - motivating examples](https://www.facebook.com/l.php?u=https%3A%2F%2Fwww.youtube.com%2Fwatch%3Fv%3D7KGdE2AK_MQ&h=5AQF1T5S-&s=1" \t "_blank)**

[Introduction to Markov models, using intuitive examples of applications, and motivating the concept of the Markov chain.](https://www.facebook.com/l.php?u=https%3A%2F%2Fwww.youtube.com%2Fwatch%3Fv%3D7KGdE2AK_MQ&h=5AQF1T5S-&s=1" \t "_blank)

[youtube.com](https://www.facebook.com/l.php?u=https%3A%2F%2Fwww.youtube.com%2Fwatch%3Fv%3D7KGdE2AK_MQ&h=5AQF1T5S-&s=1" \t "_blank)

<https://www.youtube.com/watch?v=7KGdE2AK_MQ>

[http://toolkit.tuebingen.mpg.de/hhpred](http://toolkit.tuebingen.mpg.de/hhpred" \t "_blank)

**[HHpred - Homology detection & structure prediction by HMM-HMM comparison](http://l.facebook.com/l.php?u=http%3A%2F%2Ftoolkit.tuebingen.mpg.de%2Fhhpred&h=uAQF9k7A2&s=1" \t "_blank)**

[toolkit.tuebingen.mpg.de](http://l.facebook.com/l.php?u=http%3A%2F%2Ftoolkit.tuebingen.mpg.de%2Fhhpred&h=uAQF9k7A2&s=1" \t "_blank)

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1160169/>

**[The HHpred interactive server for protein homology detection and structure prediction](http://l.facebook.com/l.php?u=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpmc%2Farticles%2FPMC1160169%2F&h=2AQF6A_ye&s=1" \t "_blank)**

[HHpred is a fast server for remote protein homology detection and structure prediction and is the first to implement pairwise comparison of profile hidden Markov models (HMMs). It allows to search a wide choice of databases, such as the PDB, SCOP, Pfam, ...](http://l.facebook.com/l.php?u=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpmc%2Farticles%2FPMC1160169%2F&h=2AQF6A_ye&s=1" \t "_blank)

[ncbi.nlm.nih.gov](http://l.facebook.com/l.php?u=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpmc%2Farticles%2FPMC1160169%2F&h=2AQF6A_ye&s=1" \t "_blank)

[http://hmmer.org](http://hmmer.org/)

**[HMMER](http://l.facebook.com/l.php?u=http%3A%2F%2Fhmmer.org%2F&h=KAQEfDbH0&s=1" \t "_blank)**

[HMMER is used for searching sequence databases for sequence homologs, and for making sequence alignments. It implements methods using probabilistic models called profile hidden Markov models (profile HMMs).](http://l.facebook.com/l.php?u=http%3A%2F%2Fhmmer.org%2F&h=KAQEfDbH0&s=1" \t "_blank)

[hmmer.org](http://l.facebook.com/l.php?u=http%3A%2F%2Fhmmer.org%2F&h=KAQEfDbH0&s=1" \t "_blank)

<https://en.wikipedia.org/wiki/HMMER>

**[HMMER - Wikipedia, the free encyclopedia](https://www.facebook.com/l.php?u=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FHMMER&h=UAQHG0BSf&s=1" \t "_blank)**

[HMMER is a free and commonly used software package for sequence analysis written by Sean Eddy.[1] Its general usage is to identify homologous protein or nucleotide sequences. It does this by comparing a profile-HMM to either a single sequence or a database of sequences. Sequences that score signific...](https://www.facebook.com/l.php?u=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FHMMER&h=UAQHG0BSf&s=1" \t "_blank)

[en.wikipedia.org](https://www.facebook.com/l.php?u=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FHMMER&h=UAQHG0BSf&s=1" \t "_blank)

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3125773/>

**[HMMER web server: interactive sequence similarity searching](http://l.facebook.com/l.php?u=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpmc%2Farticles%2FPMC3125773%2F&h=kAQHANHr2&s=1" \t "_blank)**

[HMMER is a software suite for protein sequence similarity searches using probabilistic methods. Previously, HMMER has mainly been available only as a computationally intensive UNIX command-line tool, restricting its use. Recent advances in the software, ...](http://l.facebook.com/l.php?u=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpmc%2Farticles%2FPMC3125773%2F&h=kAQHANHr2&s=1" \t "_blank)

[ncbi.nlm.nih.gov](http://l.facebook.com/l.php?u=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpmc%2Farticles%2FPMC3125773%2F&h=kAQHANHr2&s=1" \t "_blank)

<https://en.wikipedia.org/wiki/HHpred_/_HHsearch>

**[HHpred / HHsearch - Wikipedia, the free encyclopedia](https://www.facebook.com/l.php?u=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FHHpred_%2F_HHsearch&h=BAQHJUKKc&s=1" \t "_blank)**

[HHsearch is an open-source software program for protein sequence searching that is part of the free HH-suite software package.[1]HHpred is a free protein function and protein structure prediction server[2] that is based on HHsearch and HHblits, another program in the HH-suite package. HHpred and HHs...](https://www.facebook.com/l.php?u=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FHHpred_%2F_HHsearch&h=BAQHJUKKc&s=1" \t "_blank)

[en.wikipedia.org](https://www.facebook.com/l.php?u=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FHHpred_%2F_HHsearch&h=BAQHJUKKc&s=1" \t "_blank)

<https://www.youtube.com/playlist?list=PLiaHhY2iBX9hdHaRr6b7XevZtgZRa1PoU>

<https://www.youtube.com/watch?v=He4t7Zekob0>

**[Two+ Minute Papers - How Does Deep Learning Work?](https://www.facebook.com/l.php?u=https%3A%2F%2Fwww.youtube.com%2Fwatch%3Fv%3DHe4t7Zekob0&h=XAQFNsNho&s=1" \t "_blank)**

[Artificial neural networks provide us incredibly powerful tools in machine learning that are useful for a variety of tasks ranging from image classification ...](https://www.facebook.com/l.php?u=https%3A%2F%2Fwww.youtube.com%2Fwatch%3Fv%3DHe4t7Zekob0&h=XAQFNsNho&s=1" \t "_blank)

[youtube.com](https://www.facebook.com/l.php?u=https%3A%2F%2Fwww.youtube.com%2Fwatch%3Fv%3DHe4t7Zekob0&h=XAQFNsNho&s=1" \t "_blank)

<http://playground.tensorflow.org/#activation=tanh&batchSize=10&dataset=circle&regDataset=reg-plane&learningRate=0.03&regularizationRate=0&noise=0&networkShape=4,2,2&seed=0.95445&showTestData=false&discretize=false&percTrainData=50&x=true&y=true&xTimesY=false&xSquared=false&ySquared=false&cosX=false&sinX=false&cosY=false&sinY=false&collectStats=false&problem=classification>

**[Tensorflow — Neural Network Playground](http://l.facebook.com/l.php?u=http%3A%2F%2Fplayground.tensorflow.org%2F%23activation%3Dtanh%26batchSize%3D10%26dataset%3Dcircle%26regDataset%3Dreg-plane%26learningRate%3D0.03%26regularizationRate%3D0%26noise%3D0%26networkShape%3D4%2C2%2C2%26seed%3D0.95445%26showTestData%3Dfalse%26discretize%3Dfalse%26percTrainData%3D50%26x%3Dtrue%26y%3Dtrue%26xTimesY%3Dfalse%26xSquared%3Dfalse%26ySquared%3Dfalse%26cosX%3Dfalse%26sinX%3Dfalse%26cosY%3Dfalse%26sinY%3Dfalse%26collectStats%3Dfalse%26problem%3Dclassification&h=xAQEX_IwX&s=1" \t "_blank)**

[Tinker with a real neural network right here in your browser.](http://l.facebook.com/l.php?u=http%3A%2F%2Fplayground.tensorflow.org%2F%23activation%3Dtanh%26batchSize%3D10%26dataset%3Dcircle%26regDataset%3Dreg-plane%26learningRate%3D0.03%26regularizationRate%3D0%26noise%3D0%26networkShape%3D4%2C2%2C2%26seed%3D0.95445%26showTestData%3Dfalse%26discretize%3Dfalse%26percTrainData%3D50%26x%3Dtrue%26y%3Dtrue%26xTimesY%3Dfalse%26xSquared%3Dfalse%26ySquared%3Dfalse%26cosX%3Dfalse%26sinX%3Dfalse%26cosY%3Dfalse%26sinY%3Dfalse%26collectStats%3Dfalse%26problem%3Dclassification&h=xAQEX_IwX&s=1" \t "_blank)

[playground.tensorflow.org](http://l.facebook.com/l.php?u=http%3A%2F%2Fplayground.tensorflow.org%2F%23activation%3Dtanh%26batchSize%3D10%26dataset%3Dcircle%26regDataset%3Dreg-plane%26learningRate%3D0.03%26regularizationRate%3D0%26noise%3D0%26networkShape%3D4%2C2%2C2%26seed%3D0.95445%26showTestData%3Dfalse%26discretize%3Dfalse%26percTrainData%3D50%26x%3Dtrue%26y%3Dtrue%26xTimesY%3Dfalse%26xSquared%3Dfalse%26ySquared%3Dfalse%26cosX%3Dfalse%26sinX%3Dfalse%26cosY%3Dfalse%26sinY%3Dfalse%26collectStats%3Dfalse%26problem%3Dclassification&h=xAQEX_IwX&s=1" \t "_blank)