# CNN-Fold: Protein Fold Recognition by Deep Convolutional Neural Networks

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Presented to:
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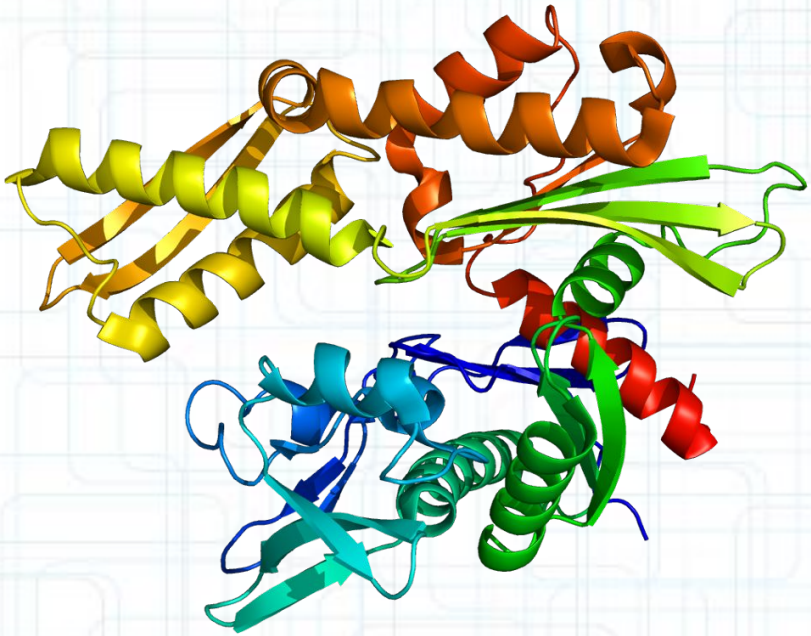
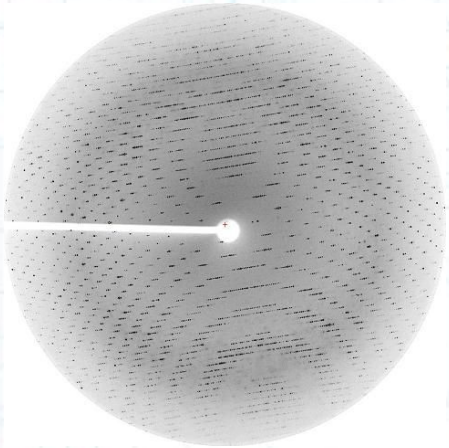
# Motivation

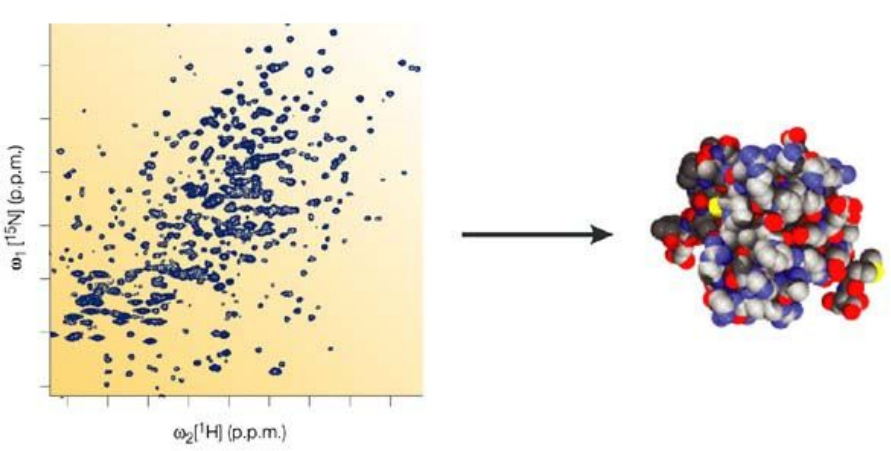
- Proteins structure determines function
  - Medicine
  - Biotechnology
- High discovery rate
- Known to unknown
  - 1:200



# X-Ray Crystallography and NMR Spectroscopy

- X-Ray Crystallography
  - High resolution microscopy
- NMR Spectroscopy
  - Quantum properties of the nucleus



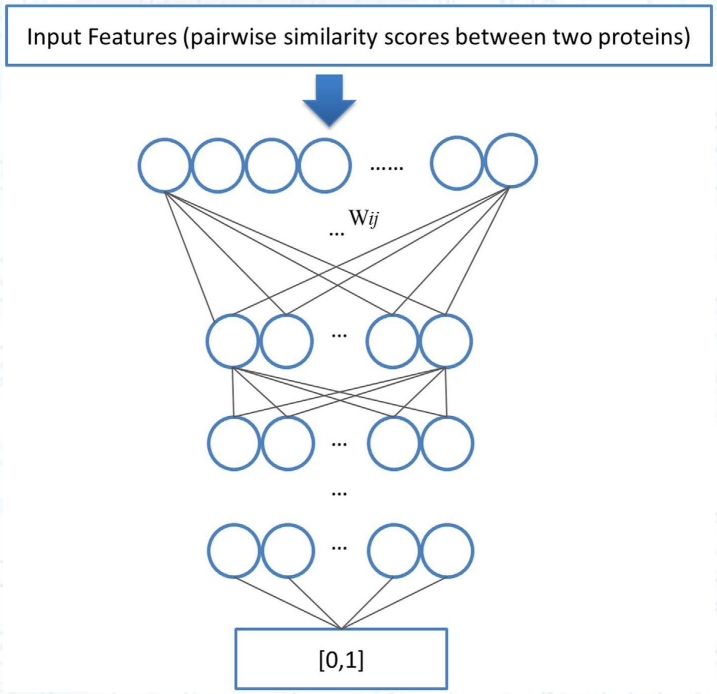


# Machine Learning Techniques

- Support Vector Machines (SVMs)
  - < 50% error rate
- Neural Networks
- Deep Learning
  - Deep Belief networks
  - 84.5% recognition rate

# DN-Fold

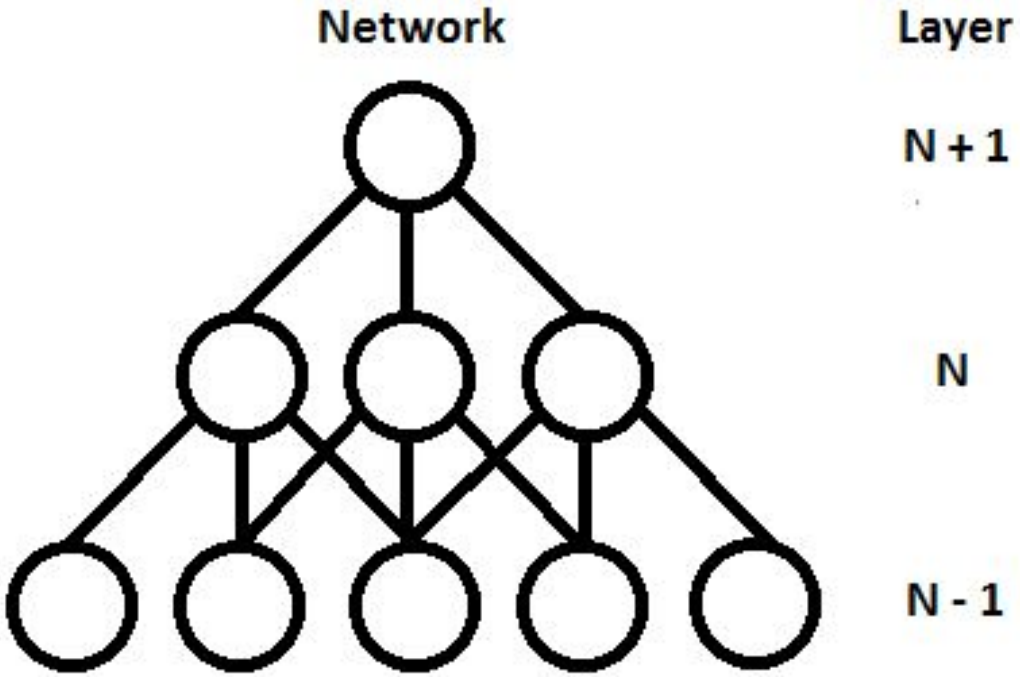
- Deep Belief Networks
  - Restricted Boltzman Machines
  - Generative Autoencoders
- Binary classification problem
  - 976 Proteins
  - (n2-n)
  - Trained and Tested



# Convolutional Neural Networks

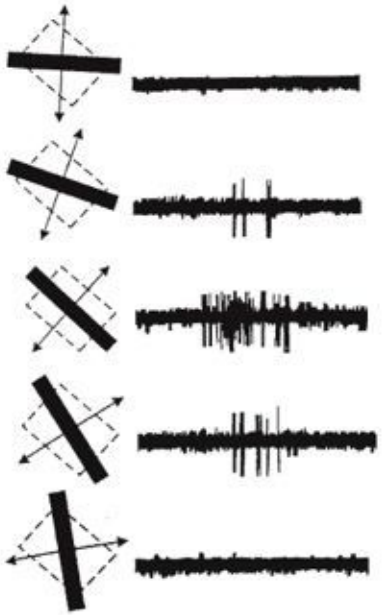
- Receptive Fields
- Surrounding area & Hidden properties
- Fully Connected Deep Neural Network

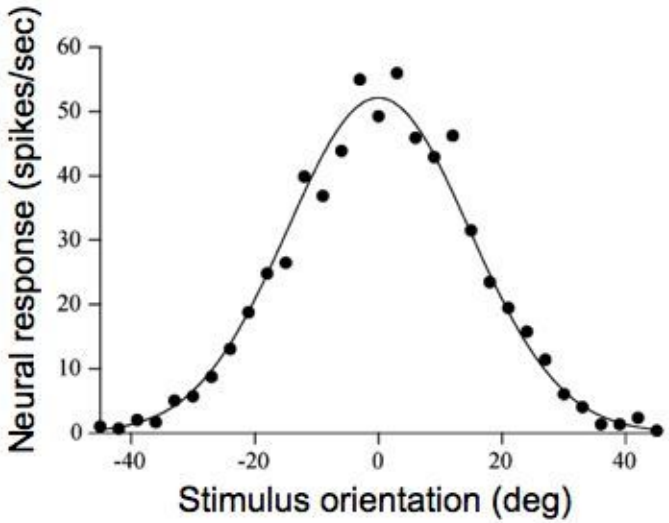
- Images
- Sounds



# Biological Inspiration

## V1 physiology: orientation selectivity

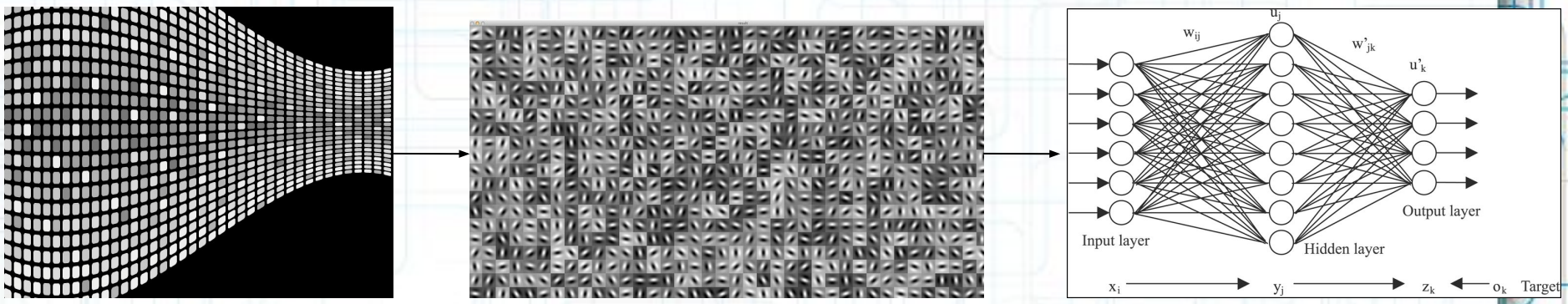





Hubel & Wiesel, 1968

# Convolutional Layers

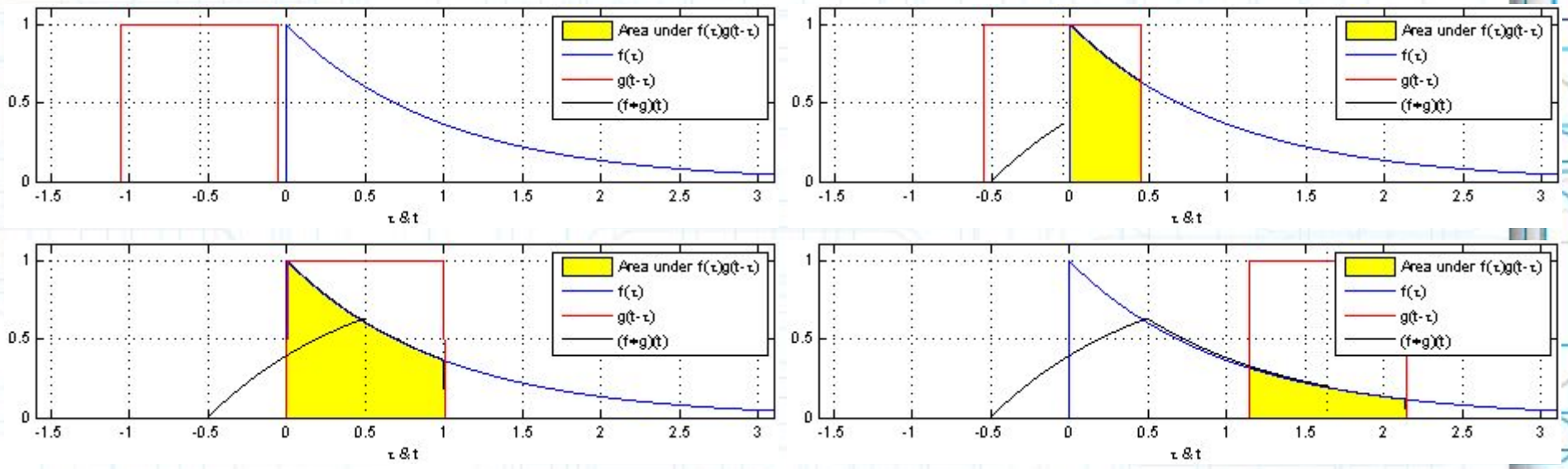
- V1 in the visual cortex
- Input → Eyes
- Filter → V1
- Output → Higher level cortical regions



# Mathematical Convolution

- Multiplying two function mathematically
- Produces an integral

$$\int_{-\infty}^{\infty} \delta(\tau)\, g(t-\tau)\, d\tau = g(t)$$



# Discrete Convolution

- Filters used have discrete stride lengths
- Snapshots taken

| Data Input | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Step 1 | 0.1 | 0.2 | 0.5 | 0.62 | 0.12 | 0.52 | 0.23 | 0.12 | 0.99 | 0.04 | 0.72 | 0.41 | 0.55 | 0.24 | 0.11 | 0.12 |
| Step 2 | 0.1 | 0.2 | 0.5 | 0.62 | 0.12 | 0.52 | 0.23 | 0.12 | 0.99 | 0.04 | 0.72 | 0.41 | 0.55 | 0.24 | 0.11 | 0.12 |
| Step 3 | 0.1 | 0.2 | 0.5 | 0.62 | 0.12 | 0.52 | 0.23 | 0.12 | 0.99 | 0.04 | 0.72 | 0.41 | 0.55 | 0.24 | 0.11 | 0.12 |

- Activation Map

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| **0** | **0** | **0** | 0 | 0 | 0 | 0 |
| **0** | **1** | **1** | 2 | 2 | 2 | 0 |
| **0** | **0** | **2** | 1 | 2 | 2 | 0 |
| 0 | 0 | 2 | 0 | 0 | 1 | 0 |
| 0 | 1 | 2 | 2 | 1 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| **2** | | |
| | | |
| | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | **0** | **0** | **0** | 0 | 0 |
| 0 | 1 | **1** | **2** | **2** | 2 | 0 |
| 0 | 0 | **2** | **1** | **2** | 2 | 0 |
| 0 | 0 | 2 | 0 | 0 | 1 | 0 |
| 0 | 1 | 2 | 2 | 1 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | **-2** | |
| | | |
| | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | **0** | **0** | **0** |
| 0 | 1 | 1 | 2 | **2** | **2** | **0** |
| 0 | 0 | 2 | 1 | **2** | **2** | **0** |
| 0 | 0 | 2 | 0 | 0 | 1 | 0 |
| 0 | 1 | 2 | 2 | 1 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | **-5** |
| | | |
| | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 2 | 2 | 2 | 0 |
| **0** | **0** | **2** | 1 | 2 | 2 | 0 |
| **0** | **0** | **2** | 0 | 0 | 1 | 0 |
| **0** | **1** | **2** | 2 | 1 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | -5 |
| **5** | | |
| | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 2 | 2 | 2 | 0 |
| 0 | 0 | **2** | **1** | **2** | 2 | 0 |
| 0 | 0 | **2** | **0** | **0** | 1 | 0 |
| 0 | 1 | **2** | **2** | **1** | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | -5 |
| 5 | **-1** | |
| | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 2 | 2 | 2 | 0 |
| 0 | 0 | 2 | 1 | **2** | **2** | **0** |
| 0 | 0 | 2 | 0 | **0** | **1** | **0** |
| 0 | 1 | 2 | 2 | **1** | **1** | **0** |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | -5 |
| 5 | -1 | **-1** |
| | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 2 | 2 | 2 | 0 |
| 0 | 0 | 2 | 1 | 2 | 2 | 0 |
| 0 | 0 | 2 | 0 | 0 | 1 | 0 |
| **0** | **1** | **2** | 2 | 1 | 1 | 0 |
| **0** | **0** | **0** | 0 | 0 | 1 | 0 |
| **0** | **0** | **0** | 0 | 0 | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | -5 |
| 5 | -1 | -1 |
| **4** | | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 2 | 2 | 2 | 0 |
| 0 | 0 | 2 | 1 | 2 | 2 | 0 |
| 0 | 0 | 2 | 0 | 0 | 1 | 0 |
| 0 | 1 | **2** | **2** | **1** | 1 | 0 |
| 0 | 0 | **0** | **0** | **0** | 1 | 0 |
| 0 | 0 | **0** | **0** | **0** | 0 | 0 |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | -5 |
| 5 | -1 | -1 |
| 4 | **2** | |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

**(Input * Filter) + Bias**

# Producing an Activation Map

**Input (with a pad of 1) (7x7x1)**

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 1 | 2 | 2 | 2 | 0 |
| 0 | 0 | 2 | 1 | 2 | 2 | 0 |
| 0 | 0 | 2 | 0 | 0 | 1 | 0 |
| 0 | 1 | 2 | 2 | **1** | **1** | **0** |
| 0 | 0 | 0 | 0 | **0** | **1** | **0** |
| 0 | 0 | 0 | 0 | **0** | **0** | **0** |

**Filter F0 (3x3x1)**

| | | |
|---|---|---|
| **-1** | **1** | **1** |
| **-1** | **-1** | **0** |
| **-1** | **0** | **1** |

**Output (3x3x1)**

| | | |
|---|---|---|
| 2 | -2 | -5 |
| 5 | -1 | -1 |
| 4 | 2 | **0** |

**Bias B0 (1x1x1)**

| |
|---|
| 1 |

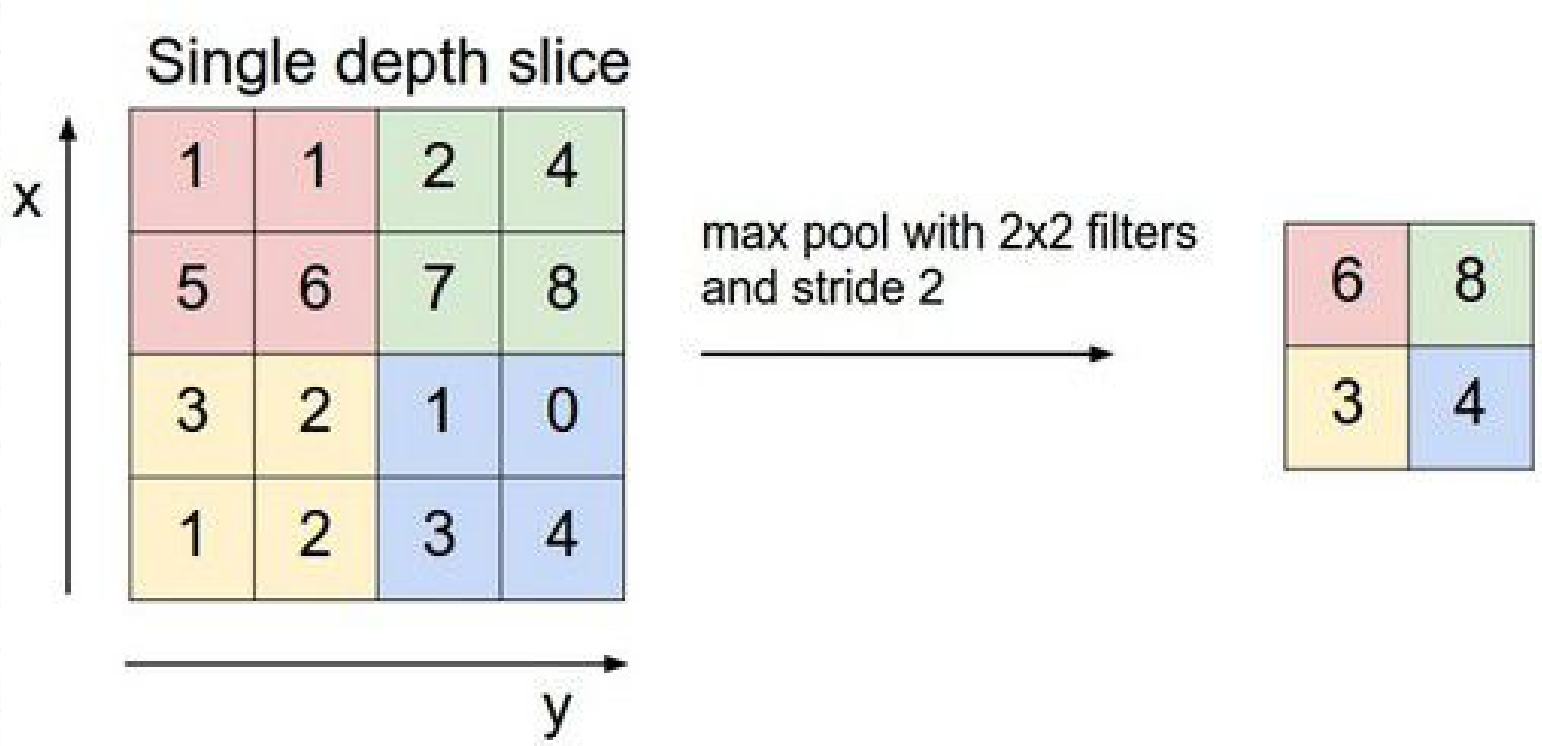
**(Input * Filter) + Bias**

# Convolutional Network Parameters

- Parameters and their effects
  - Kernel Size
  - Stride length
  - Number of Filters
  - Depth of classifying network
- Optional layers and features
  - Downsampling
  - Dropout technique

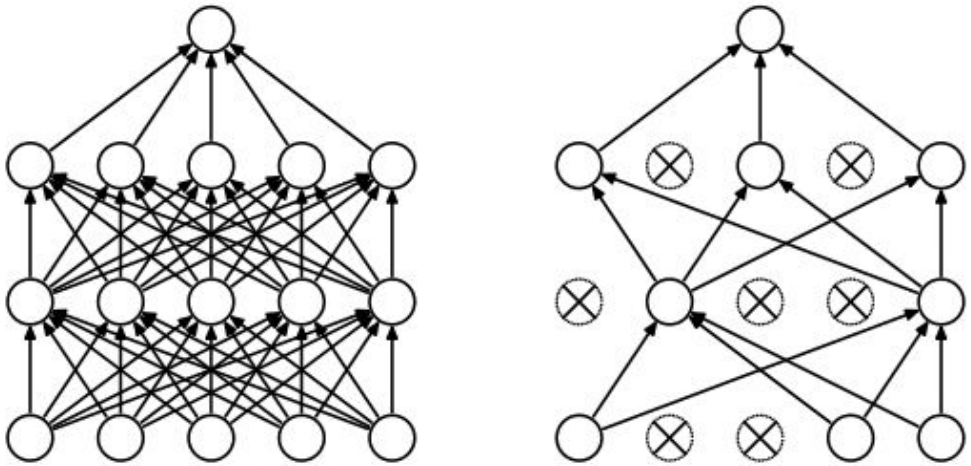
# The Downsampling Layer

- Decrease computational complexity



# Dropout Technique

- Temporarily disable neurons
- Prevents overfitting
- Only used in dense layers



(a) Standard Neural Net

(b) After applying dropout.

# Dataset

- Derived from the SCOP database
- Proteins
  - Family (555)
  - Superfamily (434)
  - Fold (321)
- Sequence, profile, family alignment and structural information
- 84 data points

```
#1aca-d1aca 1abra-d1abra
-1 1:0.86 2:2.51 3:0.698011213320252 4:0.012914
0.87636911684164 9:0.868627475071523 10:0.45240
 14:0.935274598806304 15:0.439352251735332 16:0
860465 20:0.169767441860465 21:-0.4307829160924
3255813953488 28:-0.198450938723838 29:0.136046
8604651162791 35:2.63905732961526 36:0.06976744
2686904762 42:0.526592567947394 43:0.1916390388
0.553370683027986 48:0.262824274759729 49:0.503
 53:0.427663172777061 54:0.761204462628882 55:0
767253 59:0.71073499382554 60:0.470352794231018
```

# Models

- Generated 11 simi-random networks
- Varying kernels, strides, classifying networks

| Model Number | Network Architecture |
|---|---|
| Model 1 | C21K2S1-D100-D30-O1_30 |
| Model 2 | C21K4S1-D100-D30-O1_30 |
| Model 3 | C42K8S1-D100-D30-O1_30 |
| Model 4 | C42K2S2-D150-D35-O1_30 |
| Model 5 | C63K4S2-D150-D35-O1_30 |
| Model 6 | C63K8S2-D150-D35-O1_30 |
| Model 7 | C84K4S2-D150-D25-O1_30 |
| Model 8 | C84K8S2-D150-D25-O1_30 |
| Model 9 | C105K16S2-D150-D25-O1_30 |
| Model 10 | C105K2S2-D150-D25-O1_30 |
| Model 11 | C84K2S2-D100-D100-D30-O1_30 |

# Model Selection

- Initial testing on a randomized test set
- Chose the top 3 networks to train and test

```
Examples labeled as 0 classified by model as 0: 38582 times
Examples labeled as 0 classified by model as 1: 56221 times
Examples labeled as 1 classified by model as 0: 164 times
Examples labeled as 1 classified by model as 1: 583 times

==========================Scores========================================
 Accuracy:  0.4099
 Precision: 0.503
 Recall:    0.5937
 F1 Score:  0.5446
========================================================================
```

# Results

- Overall CNNs did not outperform DN-Fold
- Provided comparable results to past methods
- Data format
- Label balance

| Network | Family | | Superfamily | | Fold | |
|---|---|---|---|---|---|---|
| | Top 1 | Top 5 | Top 1 | Top 5 | Top 1 | Top 5 |
| C63K8S2-D150-D35-O1 | 25.4 | 51.7 | 3.7 | 66.4 | 4.1 | 46.3 |
| C84K4S2-D150-D25-O1 | 33.2 | 56.8 | 8.1 | 67.9 | 15 | 58.5 |
| C105K16S2-D150-D25-O1 | 24.1 | 37.8 | 5.6 | 42.4 | 10 | 36.2 |

| Network | Family | | Superfamily | | Fold | |
|---|---|---|---|---|---|---|
| | Top 1 | Top 5 | Top 1 | Top 5 | Top 1 | Top 5 |
| PSI-Blast [18] | 71.2 | 72.3 | 27.4 | 27.9 | 4 | 4.7 |
| THREADER [19] | 49.2 | 58.9 | 10.8 | 24.7 | 14.6 | 37.7 |
| CNN-FOLD | 33.2 | 56.8 | 8.1 | 67.9 | 15 | 58.5 |
| DN-FOLD [1] | 84.5 | 91.2 | 61.5 | 76.5 | 33.6 | 60.7 |

# Conclusions

- Tasked with CNNs applied to DN-Fold Dataset
- Lacked spacial properties
- More filters not always good

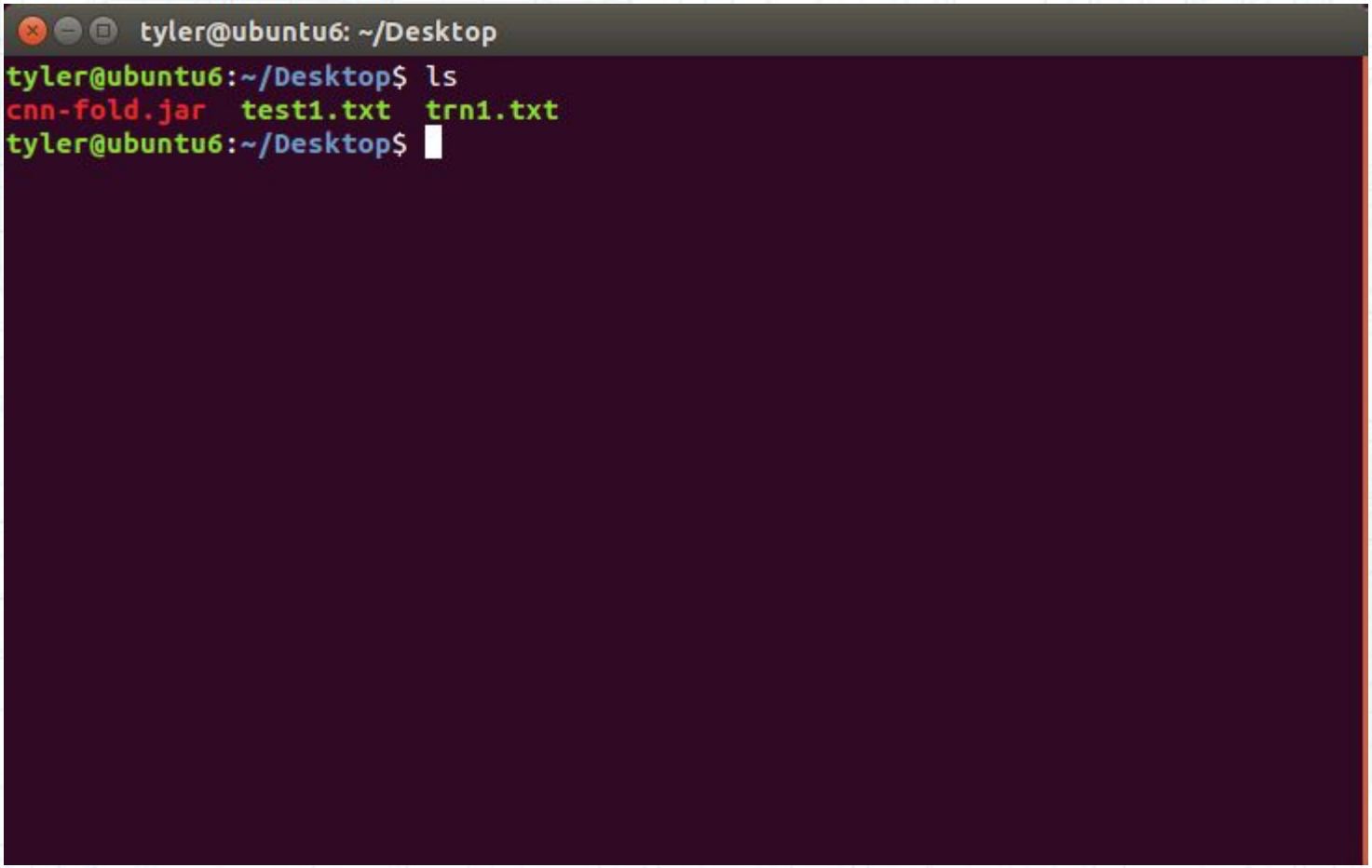
# CNN-Fold

- Program written to obtain results
- Specify CNN-Fold, DN-Fold, Command, or Json network architectures
- Train and Test modes
- Saves trained networks
- Download

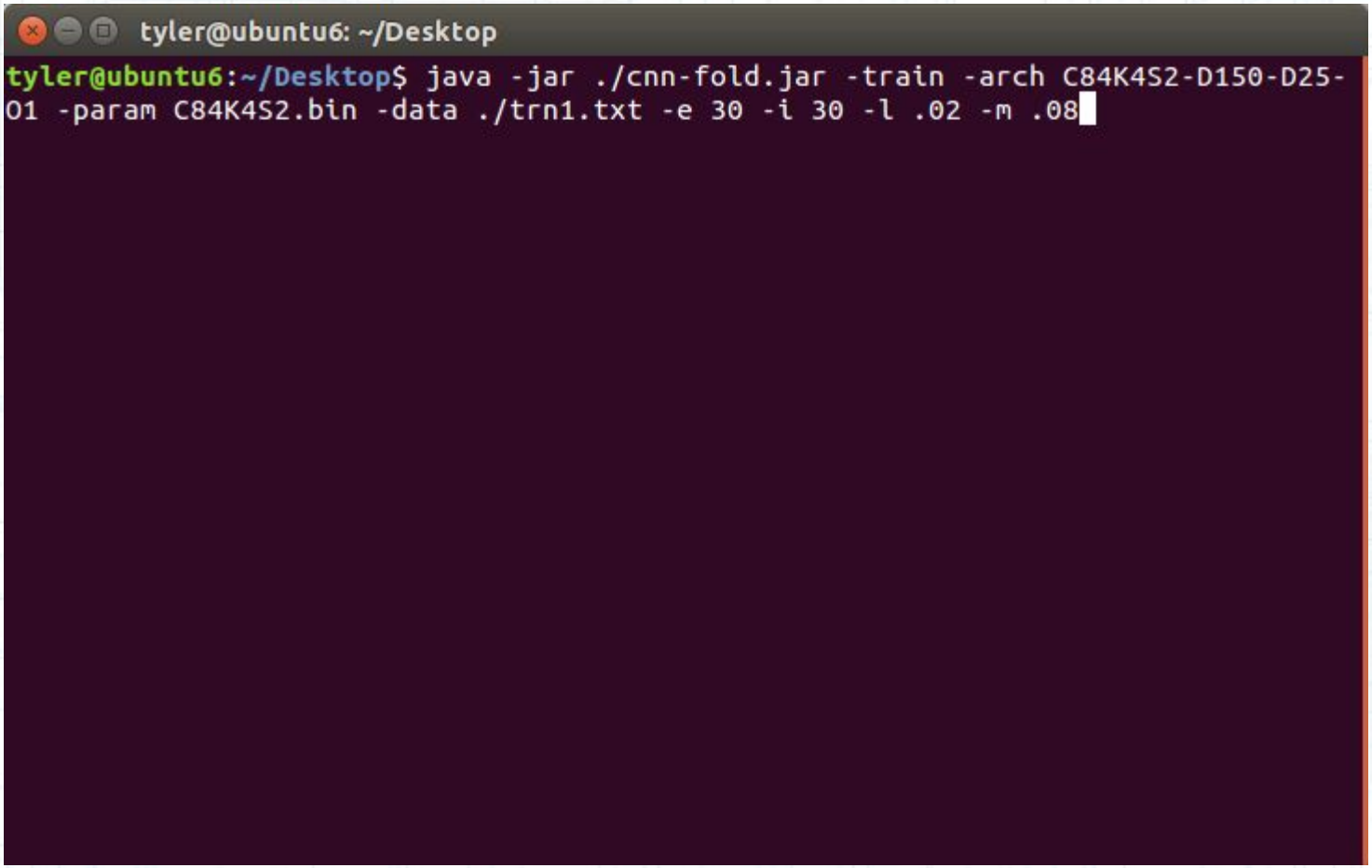
```
.der builder = new NeuralNetConfiguration.Builder()
 .seed(System.currentTimeMillis())
 .iterations(iter)
 .learningRate(learningRate)
 .momentum(momentum)
 .optimizationAlgo(OptimizationAlgorithm.STOCHASTIC_GRADIENT_
 .list(numLayers);

 for(int i = 0; i < numLayers; i++){
     if(layerConf[i][0] == CONVOLAYER){
         convo = true;
         builder.layer(currentLayer++, new ConvolutionLayer.
                 .stride(1,layerConf[i][3])
                 .nIn(1).nOut(layerConf[i][1])//input is 1 b
```

# CNN-Fold Demo



# CNN-Fold Demo



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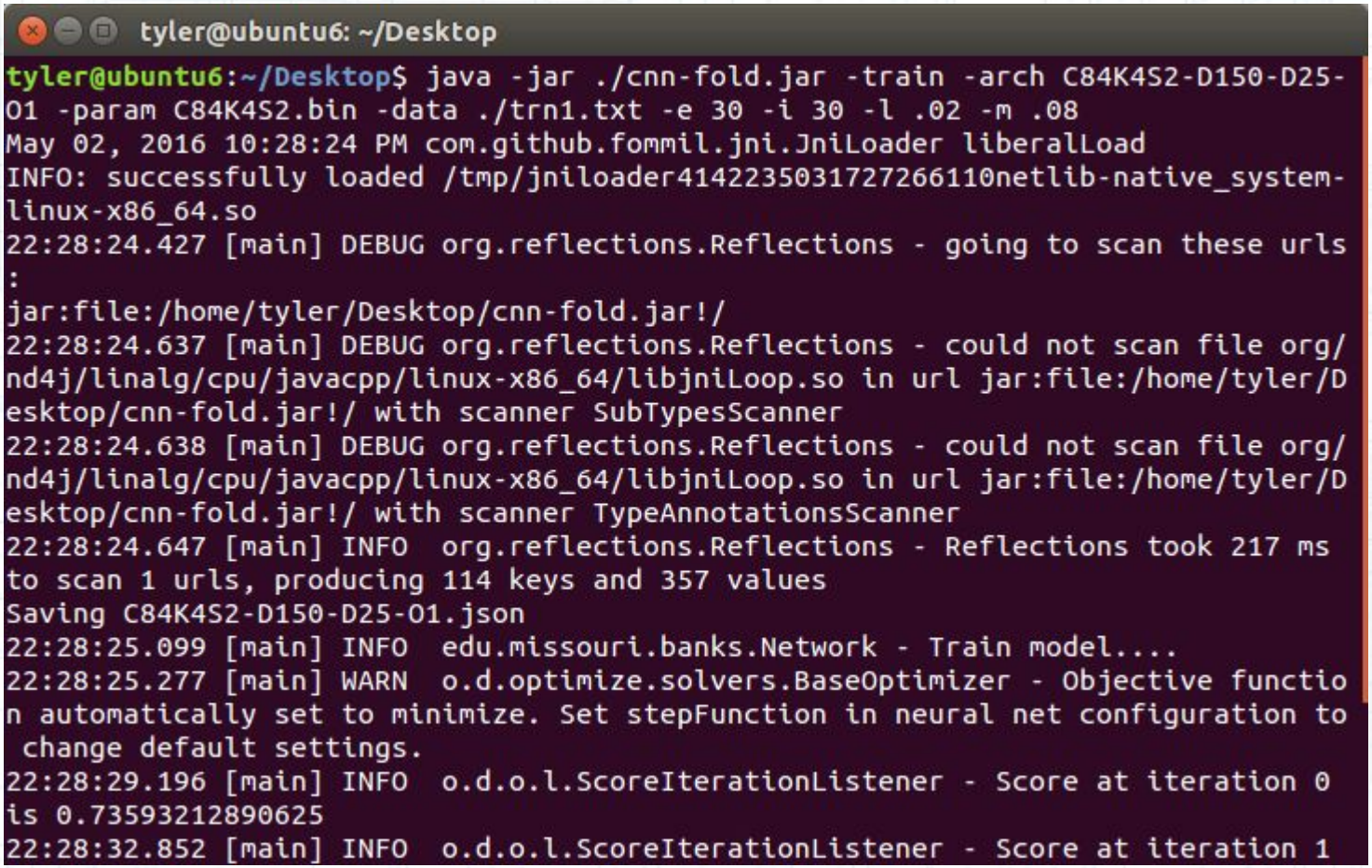
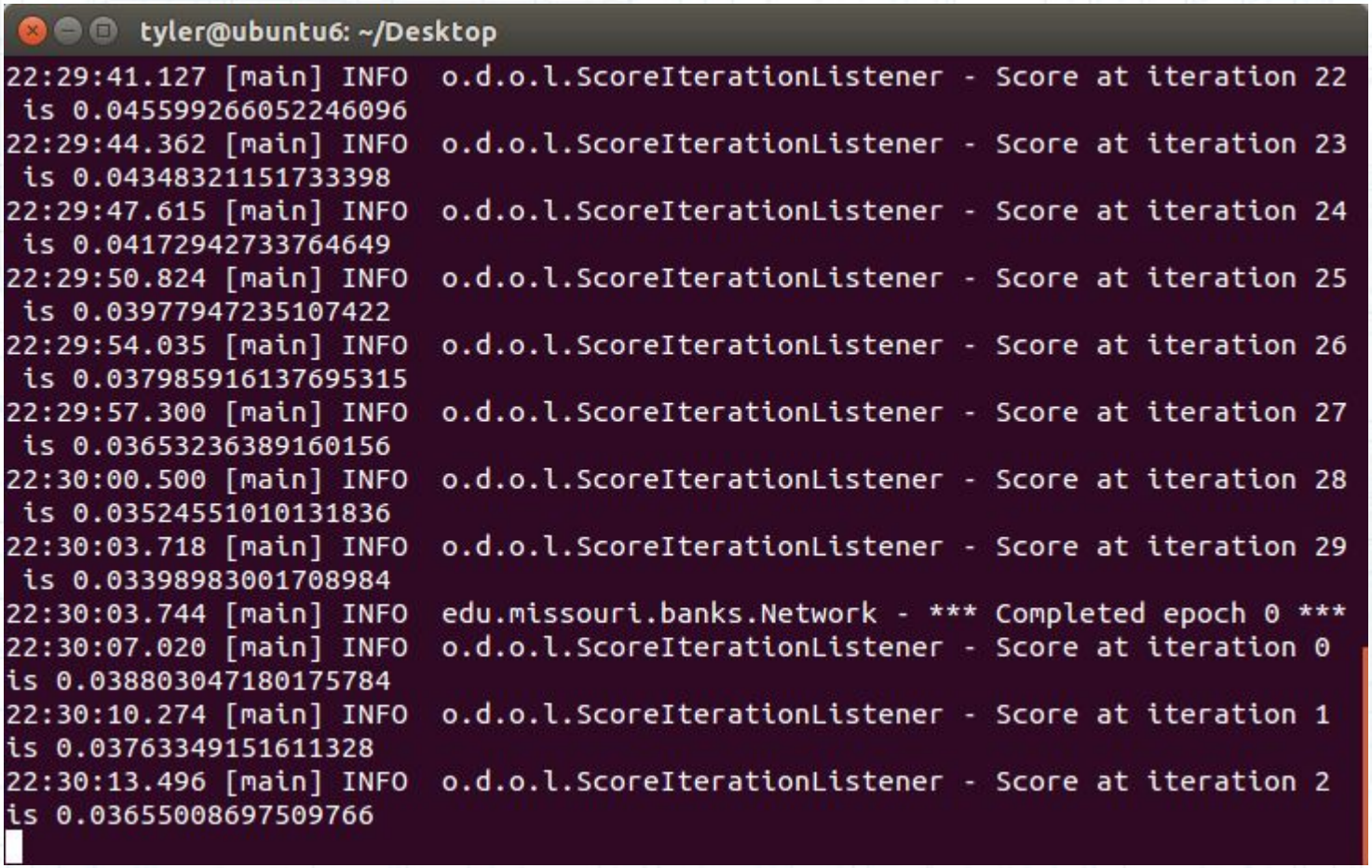
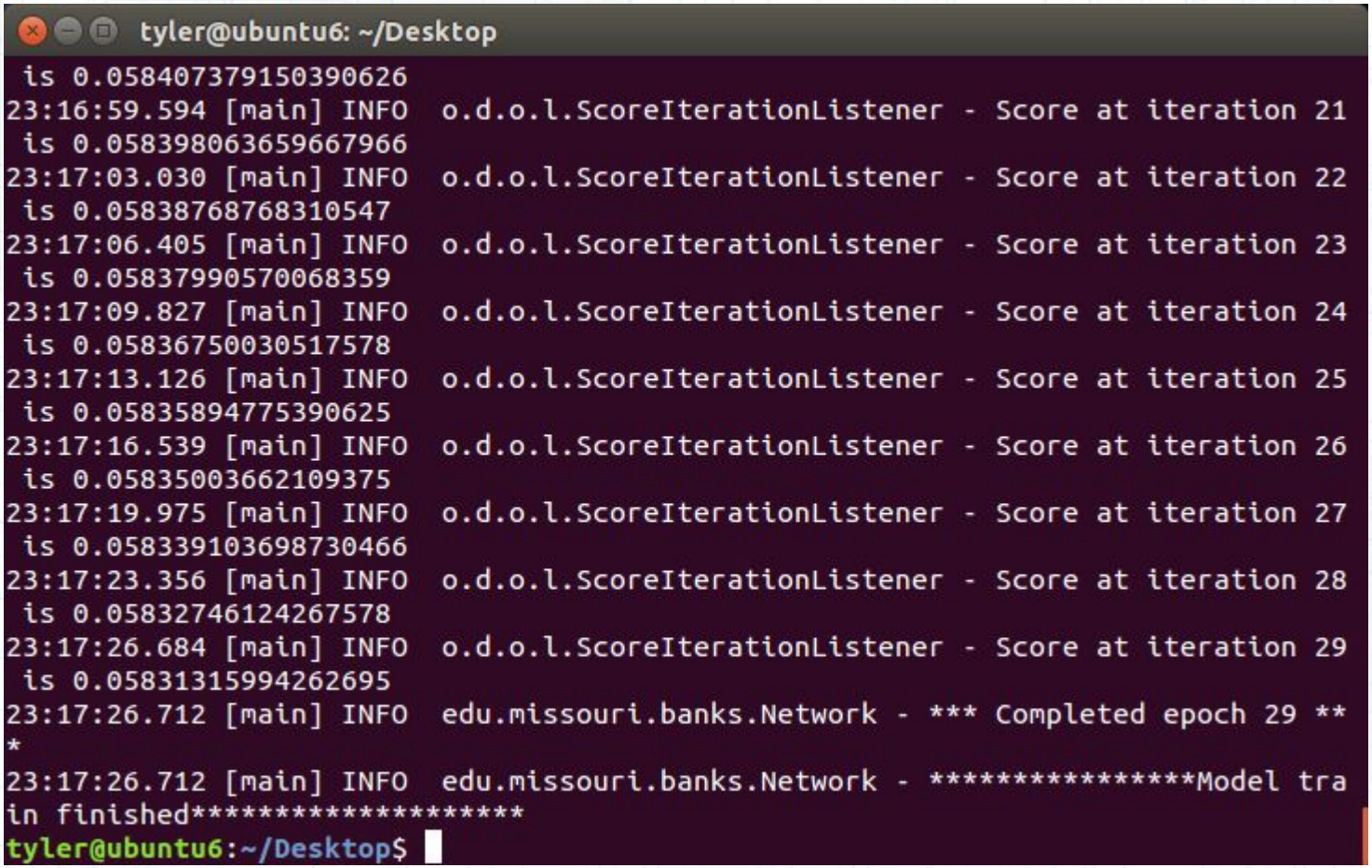


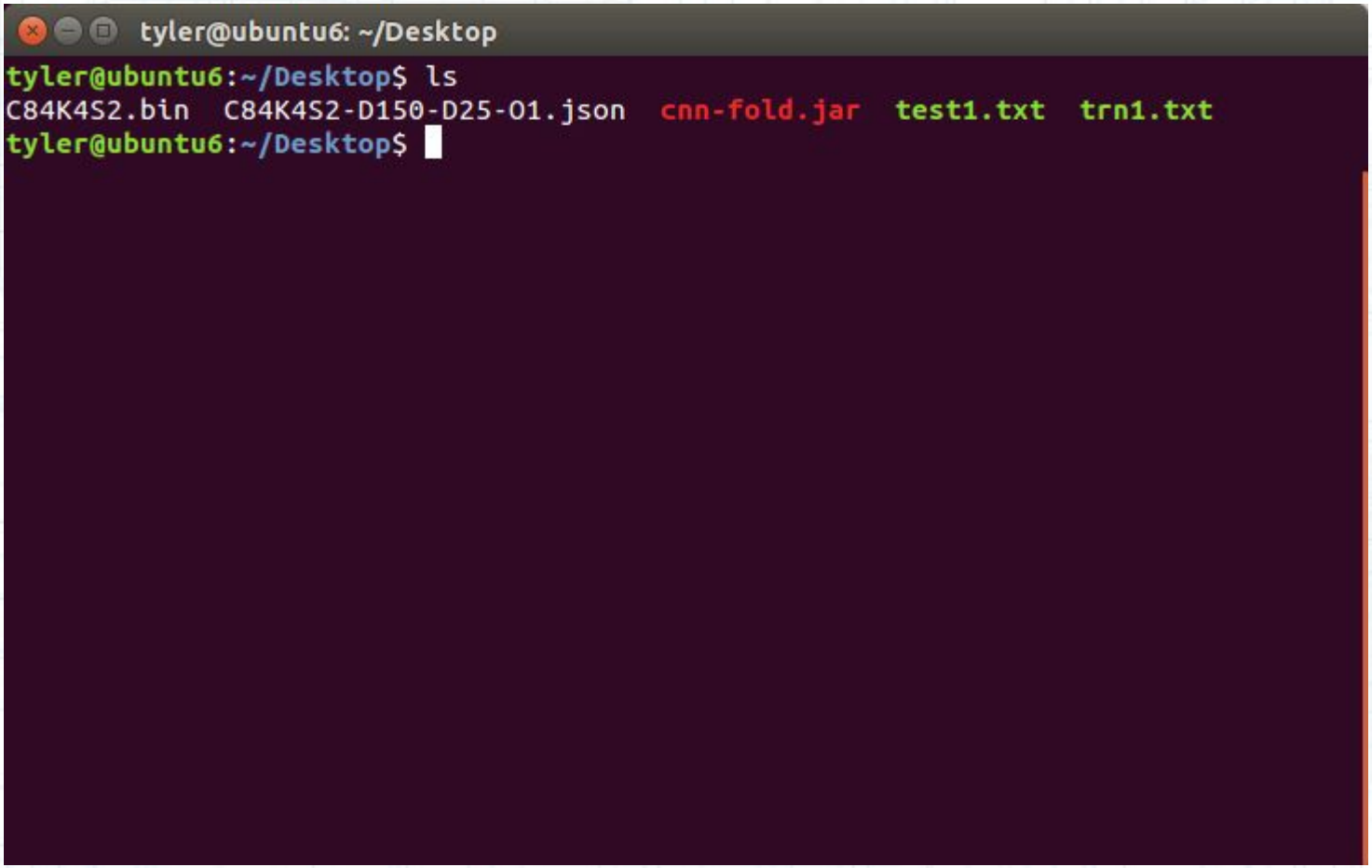
# CNN-Fold Demo



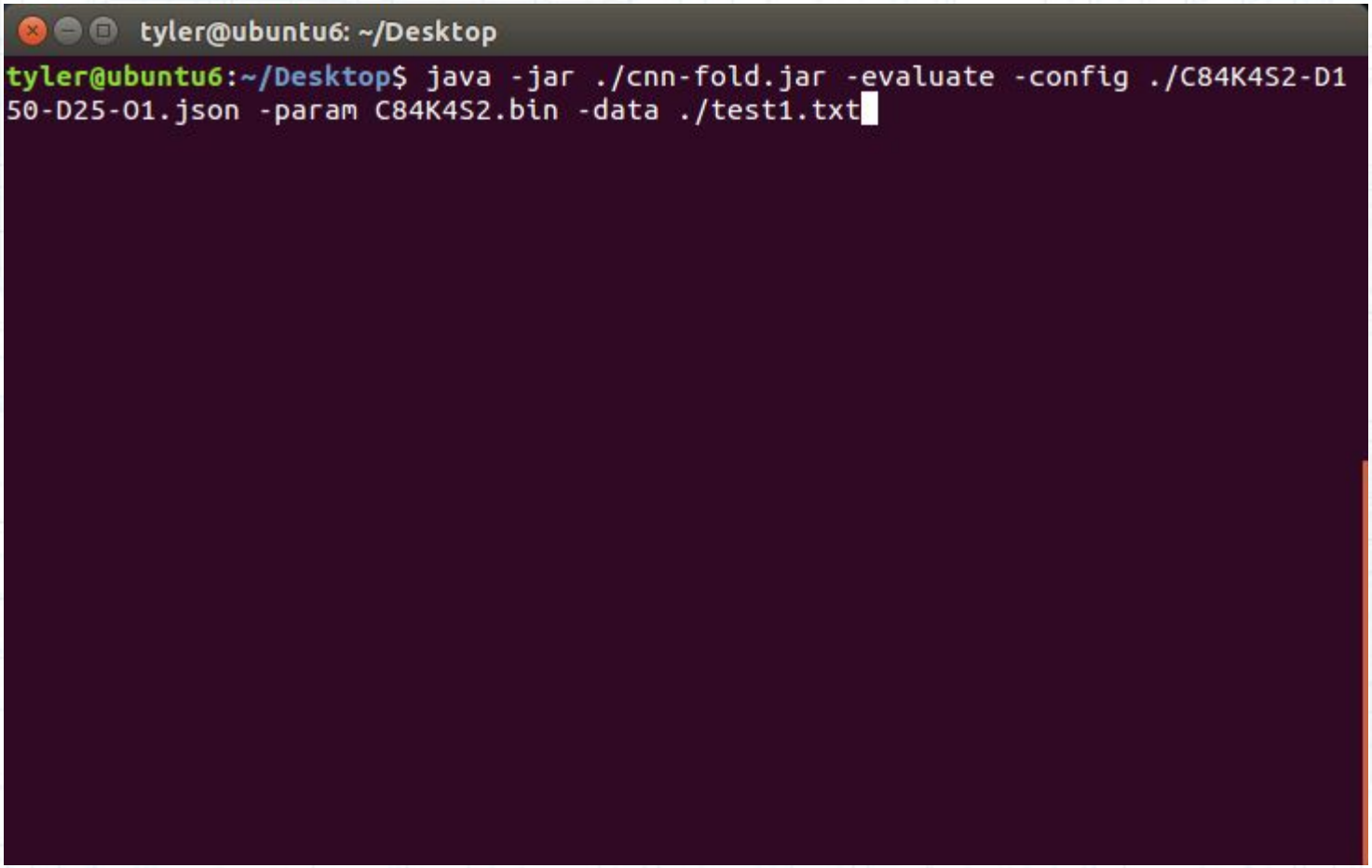
# CNN-Fold Demo



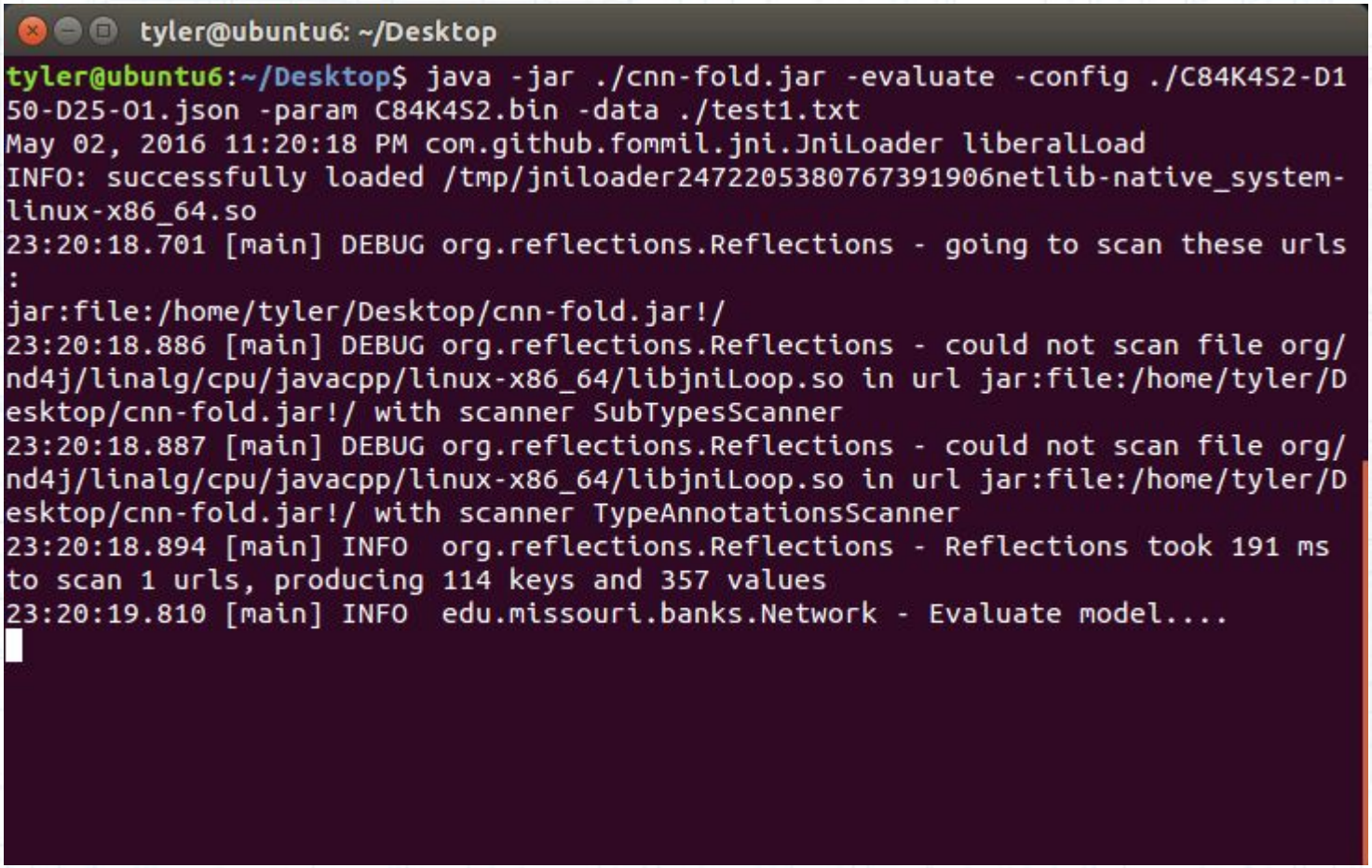
# CNN-Fold Demo



# CNN-Fold Demo



# CNN-Fold Demo



# CNN-Fold Demo

```
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=========================Scores========================================
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=======================================================================
```
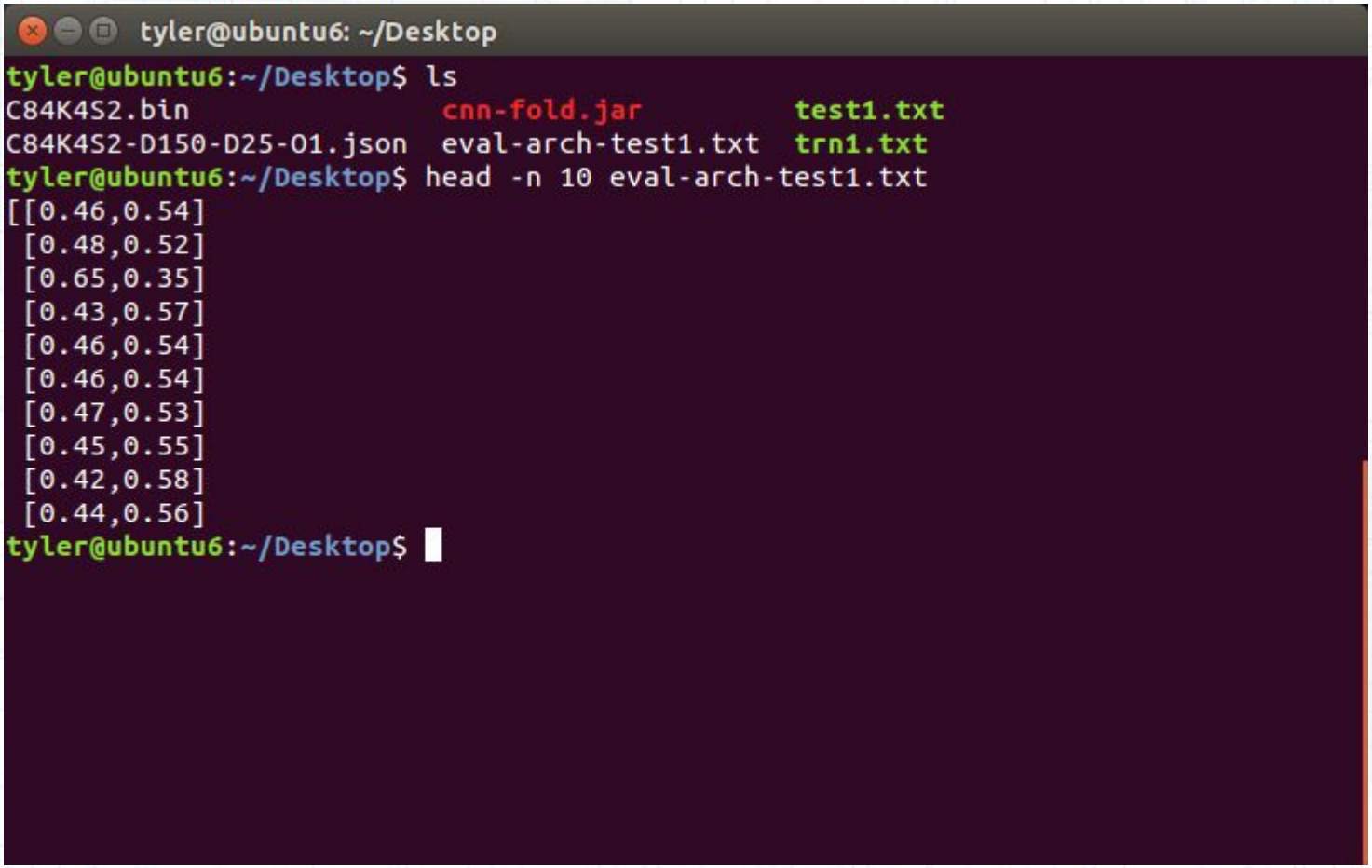

# CNN-Fold Demo



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```
C84 Results
Family: The protein list size is: 555
Top1:184 Top5:315
Top1_acc:0.331531531531532 Top5_acc:0.567567567567568

Fold: The protein list size is: 321
Top1:26 Top5:218
Top1_acc:0.080968847352025 Top5_acc:0.679127725856698

SuperFamily: The protein list size is: 434
Top1:65 Top5:254
Top1_acc:0.149769585253456 Top5_acc:0.585253456221198
```

# Future Work

- Additional methods of conveying proteins
  - Mimic image or sound
  - Data normalization
- CNN-Fold
  - Generalized input
  - Additional command line parameters

Thank you!

# Image Reference


- Protein - https://commons.wikimedia.org/wiki/File:Protein_HSPA8_PDB_1atr.png
- X Ray - http://chemwiki.ucdavis.edu/Core/Analytical_Chemistry/Instrumental_Analysis/Diffraction/X-ray_Crystallography
- NMR - http://www.nature.com/horizon/proteinfolding/background/figs/technology_f3.html
- DNN - Jo, Taeho, et al. "Improving Protein Fold Recognition by Deep Learning Networks." Scientific reports 5 (2015).
- Filter - http://eric-yuan.me/fake-cnn/
- Random data- http://www.thesearchagents.com/2013/06/google-wants-to-collect-our-data-to-show-us-what-we-want-why-do-our-governments-want-it/
- Convolution gif - https://upload.wikimedia.org/wikipedia/commons/b/b9/Convolution_of_spiky_function_with_box2.gif
- Downsampling – deeplearning4j.org
- Dropout - Srivastava et. al.