# Using a Neural Network to Predict **Drug-Kinase Affinities**

By Marcus Schubert

### Introduction

- DREAM Challenge
- Convolutional Neural Network
  - Image recognition
- Kinases cause diseases

#### **General Neural Network**

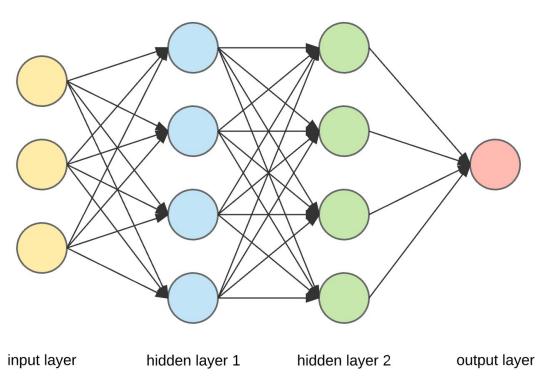
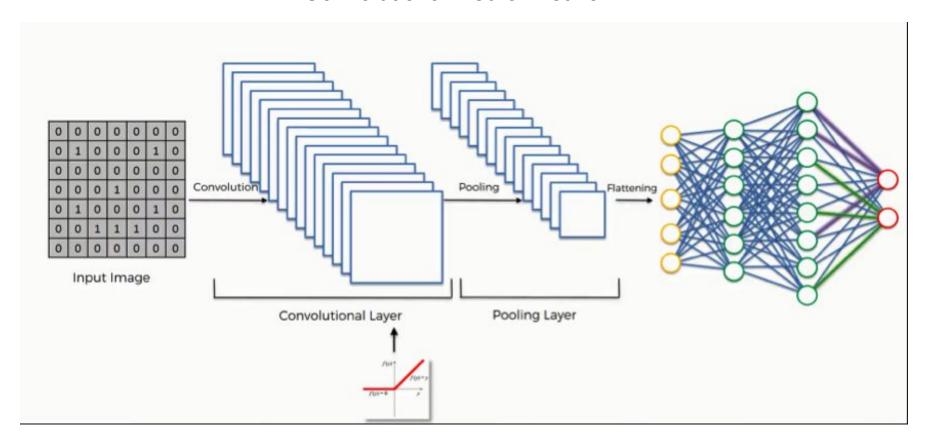


Figure 1: A visual representation of the three layers of a neural network. In the hidden layers, calculations are performed on input from a database or user, which influences an output value.

#### **Convolutional Neural Network**



#### Review of Literature

- https://www.synapse.org/#!Synapse:syn15667962/wiki/
  - DREAM Challenge
- https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5959832/
  - How to use keras for medical image analysis
- <a href="https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1005678">https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1005678</a>
  - Pilot project
- https://www.ebi.ac.uk/chembl/
  - Source for inchls
- https://www.uniprot.org/
  - Source for protein sequences
- - Keras tutorial
- https://drugtargetcommons.fimm.fi/
  - Drug-Kinase interaction dataset

### **Problem Statement**

Do neural networks offer practical benefits in predicting drug-kinase interactions?

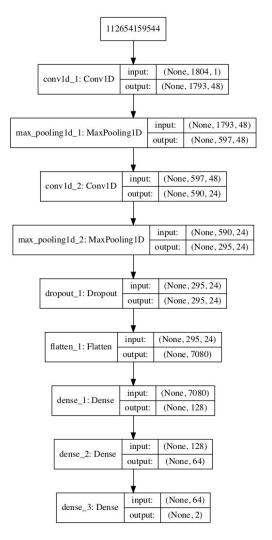
#### Methods

- Dataset (Drug Target Commons)
  - ~6,000,000 interactions
- Python
- SQLite
- IC50 values
  - Concentration to inhibit 50%
- ChEMBL
  - Standard InChl
- Uniprot
  - Amino acid sequence

```
con = sqrres.connect( datapase.sqrres)
cur = con.cursor()
cur.execute("DROP TABLE IF EXISTS proteins;")
cur.execute("CREATE TABLE IF NOT EXISTS proteins(protein id, protein sequence);")
cur.execute("SELECT DISTINCT target id FROM t INNER JOIN compounds on t.compound id = compounds.compound id;")
protein ids = cur.fetchall()
count = 0
for i in protein ids:
    count+=1
        response = urllib.request.urlopen("https://www.uniprot.org/blast/?about="+i[0]+"-1")
        html = response.read()
        htmlstr = html.decode("utf-8")
        asstart = htmlstr.find("SV=")
        asend = htmlstr.find("</textarea>")
        result = htmlstr[asstart+5:asend]
        result = "ASERROR"
    if (asend == -1 or asstart == -1):
        result = "ASERROR"
    to db=(i[0], result)
    cur.execute("INSERT INTO proteins (protein id, protein sequence) VALUES (?, ?);", to db)
    print (count)
con.commit()
con.close()
```

#### Methods

- Change dataset size
  - Amino acid sequence length
  - InChl length
  - IC50 value
- Number of CNN layers (default = 1)
- Number of kernels & length (default= 32 kernels, 8 long)
- Dropout (default = 0.2)
- IC50 cutoff (default = 200 M)



<keras.callbacks.History at 0x19edd279550>

Using 60,000 Interactions

Using 600,000 Interactions

```
batch size = 128
epochs = 3
model.fit(X_train, y_train,
      batch size=batch size,
      epochs=epochs,
      verbose=1,
      validation data=(X test, y test))
Train on 47990 samples, validate on 11998 samples
Epoch 1/3
47990/47990 [============== ] - 23s 486us/step - loss: 0.4755 - acc: 0.7760 - val loss: 0.4295 - val
 acc: 0.7985
Epoch 2/3
acc: 0.8081
Epoch 3/3
acc: 0.8157
```

```
batch_size = 128
epochs = 1
model.fit(X_train, y_train,
    batch_size=batch_size,
    epochs=epochs,
    verbose=1,
    validation_data=(X_test, y_test))
```

#### Using 1 Convolutional Layer

#### Using 2 Convolutional Layers

```
batch size = 128
epochs = 3
model.fit(X train, y train,
     batch size=batch size,
     epochs=epochs,
     verbose=1,
     validation data=(X test, y test))
Train on 47990 samples, validate on 11998 samples
Epoch 1/3
acc: 0.8023
Epoch 2/3
acc: 0.8156
Epoch 3/3
<keras.callbacks.History at 0x2c1a38ed400>
```

```
batch_size = 128
epochs = 3
model.fit(X_train, y_train,
    batch_size=batch size,
    epochs=epochs,
    verbose=1,
    validation_data=(X_test, y_test))
```

<keras.callbacks.History at 0x2cla2fc4b00>

Using 8 kernels

batch size = 128

epochs = 3

acc: 0.8177

<keras.callbacks.History at 0x172cc323ba8>

#### Using 32 kernels

<keras.callbacks.History at 0x2c1a38ed400>

```
| batch_size = 128

epochs = 3

model.fit(X_train, y_train,

batch_size=batch_size,

epochs=epochs,

verbose=1,

validation_data=(X_test, y_test))
```

Dropout .4 Dropout .2

```
batch size = 128
                                                                                         batch size = 128
epochs = 3
                                                                                          epochs = 3
model.fit(X train, y train,
                                                                                          model.fit(X_train, y_train,
       batch_size=batch_size,
                                                                                                  batch size=batch size,
       epochs=epochs,
                                                                                                  epochs=epochs,
       verbose=1,
                                                                                                  verbose=1,
       validation data=(X test, y test))
                                                                                                  validation_data=(X_test, y_test))
Train on 47990 samples, validate on 11998 samples
                                                                                          Train on 47990 samples, validate on 11998 samples
Epoch 1/3
                                                                                          Epoch 1/3
47990/47990 [=========] - 24s 490us/step - loss: 0.4738 - acc: 0.7792 - val loss: 0.4297 - val
                                                                                          47990/47990 [============= ] - 23s 480us/step - loss: 0.4503 - acc: 0.7872 - val loss: 0.4060 - val
acc: 0.7942
                                                                                           _acc: 0.8023
Epoch 2/3
                                                                                          Epoch 2/3
47990/47990 [=========] - 26s 551us/step - loss: 0.4158 - acc: 0.8022 - val loss: 0.3923 - val
                                                                                          acc: 0.8156
acc: 0.8094
Epoch 3/3
                                                                                          Epoch 3/3
                                                                                          47990/47990 [============= ] - 28s 580us/step - loss: 0.3947 - acc: 0.8113 - val_loss: 0.3819 - val
                                                                                           acc: 0.8157
acc: 0.8183
                                                                                          <keras.callbacks.History at 0x2c1a38ed400>
<keras.callbacks.History at 0x19aa02439b0>
```

IC50 Cutoff = 50

batch size = 128

acc: 0.8533

IC50 Cutoff = 200

acc: 0.8157

<keras.callbacks.History at 0x2cla38ed400>

47990/47990 [============] - 25s 514us/step - loss: 0.3109 - acc: 0.8563 - val loss: 0.3166 - val

```
batch size = 128
epochs = 3
model.fit(X_train, y_train,
    batch size=batch size,
    epochs=epochs,
    verbose=1,
    validation data=(X test, y test))
Train on 47990 samples, validate on 11998 samples
Epoch 1/3
_acc: 0.8023
Epoch 2/3
acc: 0.8156
Epoch 3/3
```

- IC50 cutoff = 800
- 2 kernels, each 1 long
- 2 nodes on Dense layer
- 607 Parameters

```
batch size = 128
epochs = 3
model.fit(X train, y train,
    batch size=batch size,
    epochs=epochs,
    verbose=1,
    validation data=(X test, y test))
Train on 47990 samples, validate on 11998 samples
cc: 0.7055
Epoch 2/3
cc: 0.7152
Epoch 3/3
cc: 0.7216
```

### Discussion

- More data means less accuracy, but more practical benefits
- Amount of layers / kernels no significant impact
- Only changing many parameters made significant impact

### Conclusion

#### Conclusion

- Problem statement is confirmed
- Accuracy of about .8 means neural net is practical to use

#### Applications

- Can be used to save time + money on research
- Protein inhibitors used to treat a variety of diseases
  - Kinases control cell & protein activity
  - Kinases cause diseases such as cancer

## Acknowledgements

 Thank you to Mr. Simon for being my mentor and for the rest of the SRP staff for

# Questions?