

Keras hans-on

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自己紹介 > > > カット

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Kerasとは

- TheanoもしくはTensorFlowをエンジンとしたDLのライブラリ
- DLを簡易的に実装したい
- CNN, RNNなどを実装したいときにもオススメ
- CPU/GPU上でのシームレスな実行

<https://keras.io/>


fchollet/keras

keras - Deep Learning library for Python. Convnets, recurrent neural networks, and more. Runs on Theano or TensorFlow.

 [github.com](https://github.com/fchollet/keras) **35 users**



ドキュメントも充実

 **Keras Documentation**

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Keras: Deep Learning library for Theano and TensorFlow

You have just found Keras.

Keras is a high-level neural networks library, written in Python and capable of running on top of either **TensorFlow** or **Theano**. It was developed with a focus on enabling fast experimentation. *Being able to go from idea to result with the least possible delay is key to doing good research.*

Use Keras if you need a deep learning library that:

- Allows for easy and fast prototyping (through total modularity, minimalism, and extensibility).
- Supports both convolutional networks and recurrent networks, as well as combinations of the two.
- Supports arbitrary connectivity schemes (including multi-input and multi-output training).
- Runs seamlessly on CPU and GPU.

Read the documentation at **Keras.io**.

Keras is compatible with: **Python 2.7-3.5**.

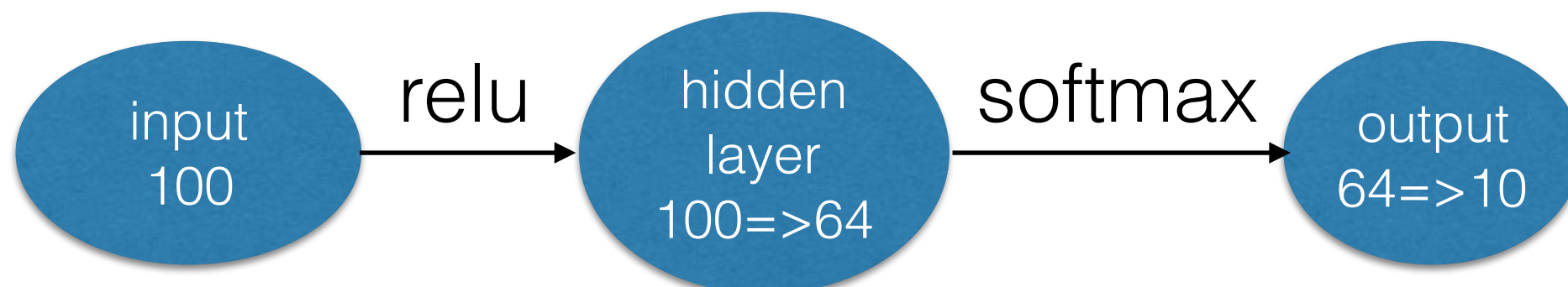
Kerasでの実装

```
from keras.models import Sequential
from keras.layers import Dense, Activation
model = Sequential()
```

addで重ねるだけ！

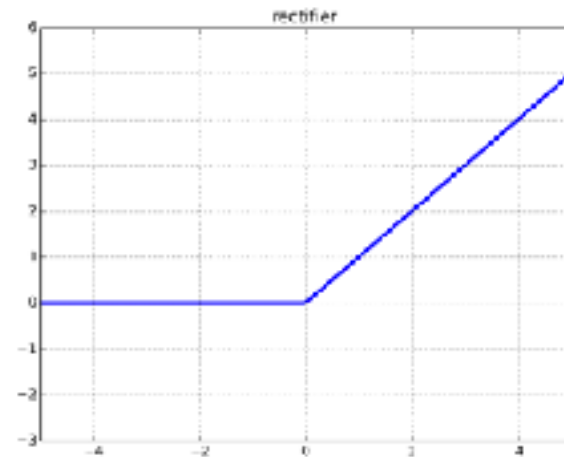
```
model.add( Dense( output_dim=64, input_dim=100 ) )
model.add( Activation( "relu" ) )
model.add( Dense( output_dim=10 ) )
model.add( Activation( "softmax" ) )
```

```
model.compile( loss="categorical_crossentropy",    compileでモデル作成
               optimizer="sgd",
               metrics=[ "accuracy" ] )
```

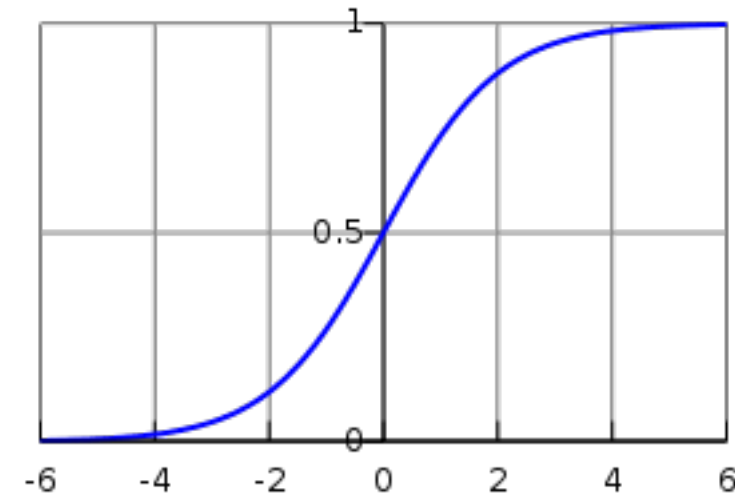


ちょっとだけ補足

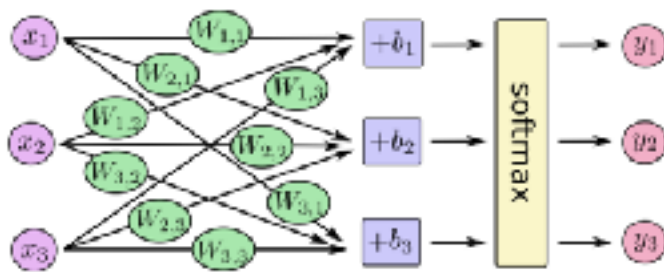
relu



sigmoid



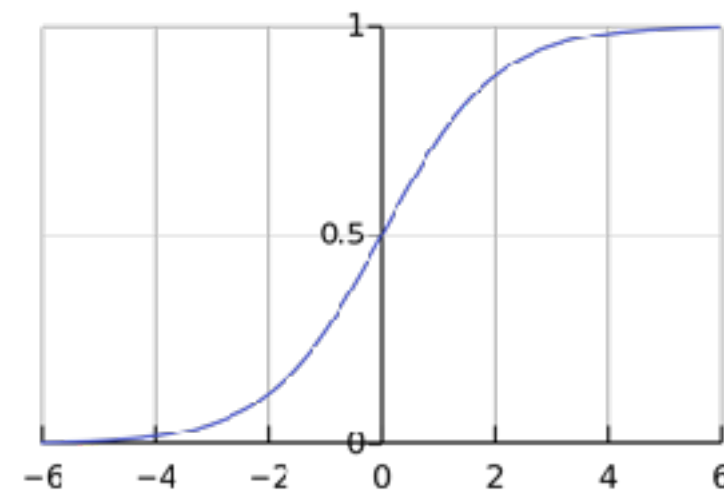
You can picture our softmax regression as looking something like the following, although with a lot more x s. For each output, we compute a weighted sum of the x s, add a bias, and then apply softmax.



If we write that out as equations, we get:

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \text{softmax} \begin{bmatrix} W_{1,1}x_1 + W_{1,2}x_2 + W_{1,3}x_3 + b_1 \\ W_{2,1}x_1 + W_{2,2}x_2 + W_{2,3}x_3 + b_2 \\ W_{3,1}x_1 + W_{3,2}x_2 + W_{3,3}x_3 + b_3 \end{bmatrix}$$

softmax



modelができたら学習

```
model.fit(X_train, Y_train, nb_epoch=5, batch_size=32)
```

```
# 予測もシンプル
```

```
classes = model.predict_classes(X_test, batch_size=32)
```

```
proba = model.predict_proba(X_test, batch_size=32)
```

今日のネタはとにかです。



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Predicting a Biological Response


Fri 16 Mar 2012 – Fri 15 Jun 2012 (4 years ago)

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Predict a biological response of molecules from their chemical properties

The objective of the competition is to help us build as good a model as possible so that we can, as optimally as this data allows, relate molecular information, to an actual biological response.

We have shared the data in the comma separated values (CSV) format. Each row in this data set represents a molecule. The first column contains experimental data describing an actual biological response; the molecule was seen to elicit this response (1), or not (0). The remaining columns represent molecular descriptors (d1 through d1776), these are calculated properties that can capture some of the characteristics of the molecule - for example size, shape, or elemental constitution. The descriptor matrix has been normalized.

<https://www.kaggle.com/c/bioresponse>

ということでVMにGO

```
$ vagrant up
```

```
$ vagrant ssh
```