Hands-on with One Single Neuron

Code editing by Michela Sperti.

After having learned (at least intuitively) what is learning with neural networks in the previous chapter, we are now ready to understand what their most fundamental component, the neuron, is made of and how it works. In this chapter, we will learn what are the main components of it and how to solve two classical statistical problems (i.e., **linear regression** and **logistic regression**) by using a neural network with just one neuron. To make things a bit more fun, we will do that on real datasets. We will discuss the two models and understand how to implement the two algorithms in **Keras**.

Firstly, we will shortly discuss what a neuron is, its typical structure, and its main characteristics (e.g., the activation function, weights, etc.). Then we will look at how we can formally express it in matrix form (this step is fundamental to obtain optimized codes, exploiting all TensorFlow and numpy functionalities). Finally, we will discuss in detail some code examples in Keras. You can find complete Jupyter notebooks that you can try with the complete code discussed in this chapter at <https://adl.toelt.ai>.

# A short overview of a neuron's structure

Deep learning is based on large and complex networks made of a large number of simple computational units. Companies at the forefront of research are dealing with networks with 160 billion parameters [1]. To put things in perspective, this number is half of the number of stars in our galaxy or 1.5 times the number of people that ever lived. On a basic level, neural networks are a large set of differently interconnected units[[1]](#footnote-1), each performing a specific (and usually relatively easy) computation. They remind me of the game LEGO where you can build very complicated things using elementary and fundamental units.

Due to a biological parallel with the brain [2], those basic units are known as neurons. Each neuron (at least the ones most used and the ones we will used in this book) does a straightforward operation: take a certain number of inputs (real numbers) and calculate an output (also a real number). Remember that the inputs are indicated in this book with (real numbers) with indicating the observation number and indicating the feature index, is the number of input. As an example of input features, you can imagine the age and weight of a person (so we would have ). could be the age and could be the weight of person with index in the dataset. In real life, the number of features can be easily very large (of the order of or higher).

There are several kinds of neurons that have been extensively studied. We will concentrate in this book on the most commonly used one. The neuron we are interested in simply applies a function to a linear combination of all the inputs. In a more mathematical form, given real parameters (with ) and a constant (usually called bias), the neuron will calculate first what is traditionally indicated in literature and in books with :

it will then apply a function to , giving the output

**Note** Practitioners mostly use the following terminology: are called **weights**, **bias**, **input features** and the **activation function**.

Let's summarize the neuron computational steps again.

1. Combine linearly all inputs calculating ;
2. Apply to giving the output .

In the literature, you can find numerous representations for neurons. In Figure 3-1 you can see a graphical representation of the mathematical operations we just discussed to obtain the output from the inputs.

Diagram

Description automatically generated

Figure 3-1. A representation of a single neuron with the operation highlighted. This is also called the computational graph of the a single neuron, or in other words a graphical representation of the operations needed to calculate  from the inputs. In the figure we have considered only one observationa and therefore we have omitted the first index of the inputs for clarity.

Figure 3-1 must be interpreted in this way:

* the inputs are not put in a bubble, simply to distinguish them from nodes that perform an actual calculation.
* The weight's names are typically not written. The expected behaviour is that before passing the inputs to the central bubble (or node), the inputs will be first multiplied by the relative weight. The first input will be multiplied by , by and so on.
* The first bubble (or node) will sum the inputs multiplied by the weights (the for ) and then sum to the result the bias .
* The last bubble (or node) will finally apply to the resulting value the activation function .

All neurons we will deal with in this book will have exactly this structure. Very often an even simpler representation is used, as in Figure 3-2. In such a case, unless otherwise stated, is understood that the output is



Figure 3-2: the following representation is a simplified version of Figure 2-1. Unless otherwise stated it is usually understood that the output is . The weights are often not explicitly reported in the neuron representation. Additionally the observation index is also often omitted for clarity.

## A short introduction to matrix notation

When dealing with big datasets, the number of features is typically large ( will be large) and so it is better to use a vector notation for the features and the weights. The inputs can be indicated with

where we have indicated the vector with a bold-faced . For the weights, we use the same notation

For consistency with formulas that we will use later, to multiply and we will use matrix multiplication notation and therefore we will write

Where indicates the transpose of . can then be written with this vector notation as

and the neuron output as

Let's now summarize the different components that define our neuron and the notation we use in this book:

* 🡪 neuron (and later network) output
* 🡪 activation function (sometime called transfer function) applied to z
* 🡪 weights (vector with components)
* 🡪 bias

## An overview of the most common activation functions

There are many activation functions at our disposal to change the output of our neuron. Remember, an activation function is simply a mathematical function that transforms in the output . Let's have a brief look at the most common ones.

### Identity function

This is the most basic function that you can use. Usually is indicated with . It merely returns the input value unchanged. Mathematically we can write it as

This simple function will come in handy when discussing linear regression with one neuron later in the chapter. Implementing it[[2]](#footnote-2) in Python with NumPy is incredibly trivial

def identity(z):

return z

Chart, line chart

Description automatically generated

Figure 3-3: The identity function

### Sigmoid function

This is a very commonly used function that gives only values between 0 and 1. It is usually indicate with

It is primarily used for classification models where we want to predict the probability as an output (remember that a probability may only assume values between 0 and 1).

The calculation can be written in this form using NumPy functions

s = np.divide(1.0, np.add(1.0, np.exp(-z)))

**Note** It is very useful to know that if we have two NumPy arrays, A and B, the following are equivalent: A/B is equivalent to np.divide(A,B), A+B is equivalent to np.add(A,B), A-B is equivalent to np.subtract(A,B) and A\*B is equivalent to np.multiply(A,B). In case you know object-oriented programming, we say that in NumPy basic operations like /, \*, + and - are **overloaded**. Note also that all those four basic operations in NumPy act element by element.

We can write the sigmoid function in a more readable (at least for humans) form as

def sigmoid(z):

s = 1.0 / (1.0 + np.exp(-z))

return s

As stated above 1.0 + np.exp(-z) is equivalent to np.add(1.0, np.exp(-z)) and 1.0 / (np.add(1.0, np.exp(-z))) to np.divide(1.0, np.add(1.0, np.exp(-z))). I want to draw your attention to another point in the formula. np.exp(-z) will have the dimensions of z (usually a vector that will have a length equal to the number of observations), while 1.0 is a scalar (a one-dimensional entity). How can Python sum the two? What happens is what is called **broadcasting**. Python, subject to certain constraints, "broadcast" the smaller array (in this case, the 1.0) across the larger one so that at the end, the two have the same dimensions. In this case, the 1.0 becomes an array of the same dimensions of z, all filled with 1.0. This is an important concept to understand, as it is very useful. You do not have to transform numbers in arrays, for example. Python will take care of it for you. The rules on how broadcasting works in other cases are rather complex and go beyond this book's scope. However, it is important to know that Python is doing something in the background.

Chart, histogram

Description automatically generated

Figure 3-4: The sigmoid activation function is a s-shaped function that goes from 0 to 1.

The sigmoid activation function (that you can see in Figure 3-4) is especially used for models where we must predict the probability as an output, as logistic regression (remember that a probability may only assume values between 0 and 1). Note that in Python, if is big enough, it can happen that the function returns exactly 0 or 1 (depending on the sign of ) for rounding errors. In classification problems we will calculate or very often, and therefore this can be a source of errors in Python since it will try to calculate that is not defined. For example, you can start seeing nan appearing while calculating the cost function (more on that later).

Although should never be exactly 0 or 1, while programming in Python the reality can be quite different. It may happen that due to a very big (positive or negative) Python will round the results to exactly 0 or 1. This may give you errors while calculating the cost function for classification since we will need to calculate and and therefore Python will try to calculate that is not defined. This may happen, for example, if we don't correctly normalize our input data or if we don't correctly initialize our weights. For the moment is important to remember that although mathematically everything seems under control, the reality while programming can be more difficult. Is something that is good to keep in mind while debugging models that for example gives nan as a result for the cost function.

### Tanh or hyperbolic tangent Activation Function

The hyperbolic tangent is also a s-shaped curve that goes from -1 to 1:

Figure 3-5: The tanh (or hyperbolic function) is a s-shaped curve that goes from -1 to 1.

Chart, rectangle

Description automatically generated

In Python this can be easily implemented

def tanh(z):

return np.tanh(z)

### ReLU (Rectified Linear Unit) Activation Function

The ReLu has the following formula

Figure 3-6: the ReLU function

Shape

Description automatically generated with low confidence

It is interesting to spend a few moments to see how we can implement it in a smart way in Python. Note that when we will start using tensorflow we will have it already implemented for us but is very instructive to see how different Python implementation can make a difference when implementing complex deep learning models.

In Python you can implement the ReLU function in several ways. Listed below are 4 different ways (try to understand why they work before going on)

1. np.maximum(x, 0, x)
2. np.maximum(x, 0)
3. x \* (x > 0)
4. (abs(x) + x) / 2

The four methods have very different execution speed. Let's generate a numpy array with elements

x = np.random.random(10\*\*8)

and let's measure the time needed by the four different versions of the ReLU function when applied to it. Let the following code run

x = np.random.random(10\*\*8)

print("Method 1:")

%timeit -n10 np.maximum(x, 0, x)

print("Method 2:")

%timeit -n10 np.maximum(x, 0)

print("Method 3:")

%timeit -n10 x \* (x > 0)

print("Method 4:")

%timeit -n10 (abs(x) + x) / 2

The results are

Method 1:  
2.66 ms ± 500 µs per loop (mean ± std. dev. of 7 runs, 10 loops each)  
Method 2:   
6.35 ms ± 836 µs per loop (mean ± std. dev. of 7 runs, 10 loops each)  
Method 3:   
4.37 ms ± 780 µs per loop (mean ± std. dev. of 7 runs, 10 loops each)  
Method 4:  
8.33 ms ± 784 µs per loop (mean ± std. dev. of 7 runs, 10 loops each)

The difference is stunning. The method 1 is 4 times faster than the method 4. The numpy library is highly optimized, with many routines written in C. But knowing how to code efficiently still makes a difference and can have a great impact. Why np.maximum(x, 0, x) is faster than np.maximum(x, 0)? The first version update x in place, without creating a new array. This can save a lot of time, especially when the arrays are big. If you don't want to (or can't) update the input vector in place, you can still use the np.maximum(x, 0) version.

An implementation could look like this

def relu(z):

return np.maximum(z, 0)

Remember when optimizing your code even small changes may make a huge difference. In deep learning programs the same chunk of code will be repeated millions and billions of times, so even a small improvement will have a huge impact on the long run. Spending time in optimizing your code is a necessary step that will pay off.

### Leaky ReLU

The Leaky ReLU (also known as Parametric Rectified Linear Unit) is given by the formula

with a parameter typically of the order of 0.01.

Figure 3-7: The Leaky ReLU activation function with . This value has been chosen to make the difference between and more marked. Usually smaller values for are used. But testing with your model is required to find the best value.

Chart

Description automatically generated with medium confidence

In Python this can be for example implemented if the relu(z) function have already been defined as

def lrelu(z, alpha):

return relu(z) - alpha \* relu(-z)

### Swish activation function

Recently Ramachandran, Zopf and Le from Google Brain [4] studied a new activation function that show great promise in the deep learning world that they called Swish. It is defined as

Figure 3-8: the Swish activation function for three different values of the parameter

Chart

Description automatically generated

where is a learnable parameter. Their studies have shown that simply replacing ReLU activation functions with Swish improves classification accuracy on ImageNet by 0.9%, that in today's deep learning world is a lot. You can find more information on ImageNet here

<http://www.image-net.org/>

Imagenet is a large database of images that is often used to benchmark new network architectures or algorithm, as in this case networks with a different activation function.

### Other activation functions

There are many other activation functions, but those are rarely used. As a reference here are some additional ones. The list is by no means comprehensive and should serve the purposes of giving you an idea of the variety of activation functions that can be used when developing neural networks.

* ArcTan
* Exponential Linear unit (ELU)
* Softplus

Practitioners uses almost always only two activation functions: the sigmoid and the ReLU (with probably the ReLU in the lead). With both you can achieve good results, and both can, given a complex enough network architecture, approximate any nonlinear function[[3]](#footnote-3). Remember that when using TensorFlow you will not have to implement them by yourself. TensorFlow will offer an efficient implementation for you to use. But is important to know how each activation function behave to understand when to use which one.

Now we have briefly discussed all the necessary components that you need to use the neuron on some real problem. Let’s see firstly how to implement a neuron in Keras and then how to perform linear and logistic regression with it.

# How to implement a neuron in Keras

Building a network with one single neuron in Keras is really straightforward and can be done with

model = keras.Sequential([

layers.Dense(1, input\_shape = [...])

])

The Sequential class groups a linear stack of layers into a tf.keras.Model. In this straightforward case, we need just one layer made by one single neuron, defined by the command layers.Dense which specifies 1 unit (neuron) inside a layer and the shape of our input dataset. The Dense class implements densely connected neural networks' layers (more on that in the next chapters).

In the next paragraphs, you will see two practical examples of how you use this simple approach, choosing the right activation function and the proper loss function, to solve two different problems, namely linear regression and logistic regression.

## Python implementation tips: loops and NumPy

As you have just seen, Keras does all the dirty job for you. Of course, you can also implement the neuron from scratch, using Python standard functionalities such as lists and loops, but those tends to be very slow as the number of variables and observations grows. A good rule of thumb is to avoid loops when possible and use NumPy (or TensorFlow) methods as often as possible.

It is easy to understand how fast NumPy can be (and how slow loops are). Let's start by creating two standard lists of random numbers in Python with elements in each:

import random

lst1 = random.sample(range(1, 10\*\*8), 10\*\*7)

lst2 = random.sample(range(1, 10\*\*8), 10\*\*7)

The actual values are not relevant for our purposes. We are simply interested in how fast Python can multiply two lists element by element. The time reported was measured on a 2017 Microsoft surface laptop and will vary greatly depending on the hardware where the code runs on. We are not interested in the absolute values, but only on how much faster NumPy is in comparison with standard Python loops. In case you are using a Jupyter notebook, it is useful to know how to time Python code in a cell. To do this, we can use a "magic command". Those commands start (in a Jupyter notebook) usually with %% or with %. A good idea is to check the official documentation to better understand how they work (<http://ipython.readthedocs.io/en/stable/interactive/magics.html>).

Coming back to our test, let us measure how much time a standard laptop takes to multiply element by element the two lists with standard loops. Using the code

%%timeit

ab = [lst1[i]\*lst2[i] for i in range(len(lst1))]

gives us the following result (note that on your computer, you will probably get different numbers):

2.06 s ± 326 ms per loop (mean ± std. dev. of 7 runs, 1 loop each)

The code needed roughly 2 seconds averaged over 7 runs. Now let's try to do the same multiplication, but this time using NumPy

%%timeit

out2 = np.multiply(list1\_np, list2\_np)

Where we have first converted the two lists to numpy arrays with the following code

import numpy

list1\_np = np.array(lst1)

list2\_np = np.array(lst2)

This time we get the following results

20.8 ms ± 2.5 ms per loop (mean ± std. dev. of 7 runs, 10 loops each)

The NumPy code needed only 21 ms, or in other words, was roughly 100 times faster than the code with standard loops. NumPy is faster for two reasons: the underlying routines are written in C, and it uses vectorized code as much as possible to speed up calculations on a large amount of data.

**Note** Vectorized code refers to operations performed on multiple components of a vector (or a matrix) at the same time (in one statement). Passing matrices to NumPy functions is an excellent example of **vectorized code**. NumPy will perform operations on big chunks of data simultaneously, obtaining much better performance than standard Python loops since the latter must operate on one element at a time. Note that part of the excellent performance NumPy shows is also due to the underlying routines being written in C.

While training deep learning models, you will find yourself doing this kind of operation over and over. Such a speed gain will make the difference between having a model that can be trained and one that will never give you a result.

# Linear regression with one single neuron

In this section we will understand how to build your first model in Keras and how to use it to solve one of the most basic statistical problems. You can, of course, perform linear regression quickly by applying traditional math formulas or using dedicated functions such as those found in Scikit-learn. For example, you can find the complete implementation of linear regression from scratch with NumPy, using the analytical formulas (http://adl.toelt.ai/single\_neuron/Linear\_regression\_with\_numpy.html) in the online version of the book. However, it is very instructive to follow this example, since it gives a practical grasp of how the building blocks of Deep Learning architectures (i.e. neurons) work.

If you remember we have said many times that NumPy is highly optimized to perform several parallel operations simultaneously. To get the best performance possible is essential to write our equations in matrix form and feed the matrices to NumPy. In this way, our code will be as efficient as possible. Remember: avoid loops at all costs whenever possible.

## The dataset for our real case example

To make things a bit more interesting, let's use an instructive dataset. We will use the so-called radon data set [3]. Radon is a radioactive gas that enters homes through contact points with the ground. It is a carcinogen that is the primary cause of lung cancer in non-smokers. Radon levels vary significantly from household to household. The dataset mentioned above contains measured radon levels in U.S. homes by county and state. The **activity** label is the measured radon concentration in pCi/L (we can refer to it as the **target** variable, i.e., the one we want to predict using a linear regression model). Important features are:

* floor (the floor of the house in which the measurement was taken),
* county (the U.S. county in which the house is located), and
* uppm (a measurement of uranium level of the soil by county).

This dataset fits a classical regression problem well since it contains a continuous variable (radon activity) to predict. The model which we will build is made of one neuron and will fit a linear function to the different features.

We do not need for our example to understand or study the features. Our goal here is to understand how to build a linear regression model with what we have learned. Generally, in a Machine Learning project, you would first study your input data, check their distribution, quality, missing values, and so on. But we will skip this part here to concentrate on the implementation with Keras.

**Note** In machine learning, the variable we want to predict is usually called the **target variable**.

Now, let us have a look at our data. We will skip all the import and load details for simplicity, and we will concentrate on the fundamental steps of our code, such as dataset preparation, model creation, and performance evaluation. Remember you can find the complete code on the online version of the book. We start by checking how many observations we have

num\_counties = len(county\_name)

num\_observations = len(radon\_features)

print('Number of counties included in the dataset: ', num\_counties)

print('Number of total samples: ', num\_observations)

The code will give the following results

Number of counties included in the dataset: 85

Number of total samples: 919

So, we have 919 different measurements of radon activity in 85 distinct counties. Now, let us use the command radon\_features.head() which will give the following table as output (the first 5 lines of the pandas dataframe)

floor county log\_uranium\_ppm pcterr

0 1 0 0.502054 9.7

1 0 0 0.502054 14.5

2 0 0 0.502054 9.6

3 0 0 0.502054 24.3

4 0 1 0.428565 13.8

We have 4 features (floor, county, log\_uranium\_ppm, pcterr) that we will use as predictors of radon activity.

### Dataset splitting

In any machine learning project, to check how the model generalize to unseen data one need to split the dataset into different subsets[[4]](#footnote-4). To simply explain the concept: when you build a machine learning model, you first need to train the model, and then you have to test it (i.e., verify the model's performances on data never seen before). The most used way to do this is to split the dataset into two subsets: 80% of the original dataset to train the model (the more data you have, the better your model will perform) and the remaining 20% to test it[[5]](#footnote-5).

The following code will split the dataset randomly in two parts with the following proportions: 80/20.

np.random.seed(42)

rnd = np.random.rand(len(radon\_features)) < 0.8

train\_x = radon\_features[rnd] # training dataset (features)

train\_y = radon\_labels[rnd] # training dataset (labels)

test\_x = radon\_features[~rnd] # testing dataset (features)

test\_y = radon\_labels[~rnd] # testing dataset (labels)

print('The training dataset dimensions are: ', train\_x.shape)

print('The testing dataset dimensions are: ', test\_x.shape)

The above code will give as output the following lines

The training dataset dimensions are: (733, 4)

The testing dataset dimensions are: (186, 4)

We will use 733 observations to train our linear regression model, and we will then evaluate it on the remaining 186 observations.

# Linear regression model

Keep in mind that using a one neuron model is an overkill for a linear regression task. We could solve linear regression exactly without the need of using gradient descent or a similar optimization algorithm. As already mentioned you can find an exact regression solution example, implemented with NumPy library, in the book's online version.

Given that our dataset (as previously discussed) can be expressed as a matrix () and the label we want to predict as a column vector (), when we employ one neuron to perform linear regression, we simply try to find the best weights () that appear in the following equation:

The weights and bias need to be chosen so that that the network output is as similar as possible to the expected target variable.

If you remember how a neuron is structured, you can easily see that for the neuron to give as output a linear combination of the inputs, we need to use the **identity activation function**. How can we measure how close are the neuron’s outputs to the target variables? The difference is measured by the Mean Squared Error (MSE) function.

where the sum is over all observations. This is the typical loss function chosen in a regression problem. By minimizing with respect to the weights and bias, we can find their optimal values.

Minimizing will be done with an optimizer. If you remember from last chapter, Gradient Descent is the most basic example of an optimizer and could be used to solve this problem. Since is not available out of the box in TensorFlow 2.5 we will use the RMSProp optimizer for practical reasons. Don’t worry if you don’t know how it works. Just think that it is simply a more intelligent version of the GD algorithm. We will learn how it works in details in the next chapters.

### Keras implementation

If you have no experience with Keras you can consult the appendices of this book. There you will find an introduction to Keras that will give you enough information to be able to understand the following discussion.

Implementing what we discussed with Keras is straightforward. The following function builds the one neuron model for linear regression.

def build\_model():

model = keras.Sequential([

layers.Dense(1, input\_shape = [len(train\_x.columns)])

])

optimizer = tf.keras.optimizers.RMSprop(

learning\_rate = 0.001)

model.compile(loss = 'mse',

optimizer = optimizer,

metrics = ['mse'])

return model

Let analyze what this code does.

* First of all, we defined the net structure with the keras.Sequential class, adding one layer[[6]](#footnote-6) made of one neuron (layers.Dense) and with input dimensions equal to the number of features used to build the model. The activation function is the one set by default, i.e. the identity function.
* Then, we defined the optimizer (tf.keras.optimizers.RMSprop) setting the learning rate to 0.001. The optimizer is the algorithm that Keras will use to minimize the cost function. We use in this example the RMSprop algorithm.
* Finally, we compile the model (i.e. we configure the model for training), setting its loss function (i.e. the cost function to be minimized), its optimizer and the metric to be calculated during performances evaluation (model.compile). The function returns the built model as one single Python object.

**The Learning rate** is a very important parameter for the optimizer. In fact, it strongly influences the convergence of the minimization process. It is a common and good behavior to try different learning rate values and see how the model's convergence changes.

Now, let us apply the build\_model function and have a look at the model summary

model = build\_model()

model.summary()

The above code gives the following output

Model: "sequential"

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Layer (type) Output Shape Param #

==============================================================

dense (Dense) (None, 1) 5

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Total params: 5

Trainable params: 5

Non-trainable params:

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Thus, we have 5 parameters to be trained, i.e. the weights associated to the 4 features plus the bias.

## Model's Learning Phase

Training our neuron means finding the weights and biases that minimize the chosen cost function (the MSE in our case). The **minimization process** is iterative; therefore, it is necessary to decide when to stop it. For this example, we will simply set a fixed number of epochs. We will train the model for 1000 epochs, and we will then look at the results in terms of the MSE.

EPOCHS = 1000

history = model.fit(

train\_x, train\_y,

epochs = EPOCHS, verbose = 0

)

As you can see, training the model in Keras is straightforward. It is enough to apply the fit method to our model object. fit takes as inputs the training data and the number of epochs.

The cost function clearly decreases for a while and then stays almost constant. That is a good sign indicating that the cost function has reached a minimum. That does not mean that our model is good or that it will give good predictions. This tells us only that learning has somehow worked. A very good way to immediately visualize the loss function decrease is by plotting the **cost function vs. number of epochs**. This can be seen for our case in Figure 3-8.

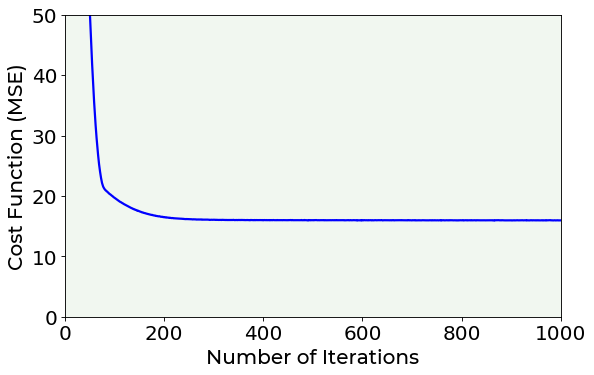


Figure 3-8. The cost function behaviour during the model training applied to the radon dataset with a learning rate of 0.001.

Looking at Figure 3-8, you can notice that, after 400 epochs, the cost function remains almost constant in its value, indicating that a minimum has been reached.

Since we are doing a linear regression, we are interested in the coefficients of the linear equation. Those are the weights of our neuron. The first four are the linear regression coefficients, while the last one is the bias term. You can compare these numbers with the ones obtained by performing linear regression with traditional math formulas and using NumPy library in the online version of the book. To get the weights in Keras you can simply use the get\_weights() call.

weights = model.get\_weights() # return a numpy list of weights

print(weights)

which returns

[array([[-6.6795307e-01],

[ 2.7279984e-03],

[ 2.8733387e+00],

[-2.0828046e-01]], dtype=float32),

array([4.2394686], dtype=float32)]

Those are the weights we were expecting.

## Model's performance evaluation on unseen data

Now, to know if the model you have just trained is suited to be applied to unseen data, you must check its performances over a dataset containing only unseen data (the test set). Then, predicted radon activity values are compared with real values (test\_y) by simply plotting **predictions vs. true values as can be seen in Figure 3-9**. A perfect model will show points distributed over the black solid line present in the plot. The less precise our predictions are, the most spread the points will be around the diagonal.

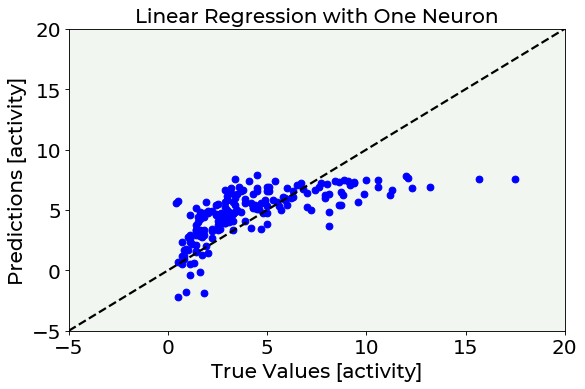


Figure 3-9. The predicted target value vs. measured target value for our model, applied to our testing data.

If you have followed so far, congratulations! You just built your very first neural networks, with just one neuron but still a neural network!

# Logistic regression with one single neuron

Now let’s try to solve with one single neuron a classification problem. The logistic regression is a classical and probably the simplest classification algorithm. We will consider here a binary classification problem: that means we will deal with the problem of recognizing two classes only (that we will label as 0 or 1). We will need an activation function different from the one we used for linear regression, and a different cost function to minimize and a slight modification of the output of our neuron. Our goal is to be able to build a model that can predict if a certain new observation is of one of two classes. The neuron should give as output the probability of the input to be of class 1. We will then classify our observation as of class 1 if or of class 0 if .

It is very instructive to compare this example with the one about linear regression, since they both are applications of the one neuron model, used to solve different tasks. You should try to pay attention to similarities and differences with the linear regression model discussed previously. You are going to see how simple is using Keras in this case and how, changing a few things (as activation and loss function), you can easily obtain a different model that can solve a different problem.

## The dataset for the classification problem

As in the linear regression example, we will use a dataset taken from the real world, to make things more interesting. We will employ the BCCD Dataset, a small-scale dataset for blood cells classification. The dataset can be downloaded from its GitHub repository [8]. For this dataset, two Python scripts have been developed to make preparation of the data easier. All the code can be found in the online version of the book. In the example, a slightly modified version of the two scripts will be used. Remember we are not really interested at this point in how the data looks like or how it is cleaned. You should focus on how to build the model with Keras.

The dataset contains three kind of labels:

1. Red Blood Cell (**RBC**)
2. White Blood Cell (**WBC**)
3. Platelets

To make it a binary classification problem, we will consider only **RBC** and **WBC** types. The model which will be trained is made of one neuron and will predict if an image contains an **RBC** or a **WBC** type using as features the xmin, xmax, ymin and ymax variables.

For simplicity, as in the linear regression example, we will skip all the import and load details and we will concentrate on the fundamental steps of our code, such as dataset preparation, model creation and performances evaluation. You can find the complete code on the online version of the book. Note that the greatest differences between this case and the linear regression lie in the chosen activation and cost function.

Let us have a look at our data:

num\_observations = len(bccd\_features)

print('Number of total samples: ', num\_observations)

The above lines of code return

Number of total samples: 4527

And let us display the first lines of our data

bccd\_features.head()

which prints to the screen

xmin xmax ymin ymax

0 192 292 376 473

1 301 419 320 424

2 433 510 273 358

3 434 528 368 454

4 507 574 381 454

The dataset is made of 4527 observations, 1 target column (cell\_type) and 4 features (xmin, xmax, ymin, ymax). When working with images, it is always useful to get an idea of how they look. You can see an example in Figure 3-10.

Immagine che contiene testo

Descrizione generata automaticamente

Figure 3-10. A sample image from the BCCD dataset.

Note that the features we will employ in our example are not the pixel values of the image, but the location of the edges of the bounding box of the cell; in fact, for each image, we only have 4 values (xmin, xmax, ymin and ymax).

## Dataset splitting

We have already stated, in the linear regression model's section, that in any machine learning project, we have to split the dataset in different subsets. Let’s create a train and a test dataset by splitting the dataset randomly in two parts with a ration of 80/20, as we have already performed for the radon dataset.

np.random.seed(42)

rnd = np.random.rand(len(bccd\_features)) < 0.8

train\_x = bccd\_features[rnd] # training dataset (features)

train\_y = bccd\_labels[rnd] # training dataset (labels)

test\_x = bccd\_features[~rnd] # testing dataset (features)

test\_y = bccd\_labels[~rnd] # testing dataset (labels)

print('The training dataset dimensions are: ', train\_x.shape)

print('The testing dataset dimensions are: ', test\_x.shape)

The above code will give as output the following lines

The training dataset dimensions are: (3631, 4)

The testing dataset dimensions are: (896, 4)

So, we will use 3631 observations to train our logistic regression model and we will then evaluate it on the remaining 896 observations.

Now comes a particularly important point. The labels in our dataset as imported will be 'WBC' or 'RBC' strings (they simply tell you if an image contains white or red blood cells). But we will build our cost function with the assumptions that our class labels are 0 and 1, so we need to change our train\_y and test\_y arrays.

**Note** When doing binary classification remember to check the values of the labels you are using for training. Sometimes using the wrong labels (not 0 and 1) may cost you quite some time in understanding why the model is not learning.

train\_y\_bin = np.zeros(len(train\_y))

train\_y\_bin[train\_y == 'WBC'] = 1

test\_y\_bin = np.zeros(len(test\_y))

test\_y\_bin[test\_y == 'WBC'] = 1

Now all images containing RBC will have a label of 0, and all images containing WBC will have a label of 1.

## Logistic regression model

Our model will be made of one neuron and its goal will be to recognize two classes (labeled as 0 or 1, referring to RBC or WBC inside a cell image). This is a **binary classification problem**.

Differently from linear regression, the **activation function** will be a **sigmoid function** (leading to a different neuron's output) and the **cost function** will be the **cross-entropy** [7]. If you don’t remember what a sigmoid function is, check again the beginning of this chapter. We use it since we want our neuron to output the probability of our observation to be of class 1. Therefore we need an activation function that can assume only values between 0 and 1, otherwise we cannot regard it as a probability. The cross-entropy for one observation is

In presence of more than one observation, the cost function is the sum over all observations

Explaining the cross-entropy loss function goes beyond the scope of this book, but if you are interested you can find it described in many books and websites. For example, you can check [7].

### Keras implementation

The following function builds the one neuron model for logistic regression. The implementation is remarkably similar to that of linear regression. The differences, as already mentioned, are the activation function, the cost function, and the metrics (accuracy in this case, which we will analyze more in detail in the testing phase).

def build\_model():

model = keras.Sequential([

layers.Dense(1, input\_shape = [len(train\_x.columns)], activation = 'sigmoid')

])

optimizer = tf.keras.optimizers.RMSprop(

learning\_rate = 0.001)

model.compile(loss = 'binary\_crossentropy',

optimizer = optimizer,

metrics =

['binary\_crossentropy','binary\_accuracy'])

return model

Now, let us apply the build\_model function and have a look at the model summary

model = build\_model()

model.summary()

The above code gives the following output

Model: "sequential"

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Layer (type) Output Shape Param #

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dense (Dense) (None, 1) 5

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Total params: 5

Trainable params: 5

Non-trainable params: 0

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We have 5 parameters to be trained also in this case, i.e., the weights associated to the 4 features plus the bias.

## Model's learning phase

As in the linear regression example, training our neuron means finding the weights and biases that minimize the cost function. The cost function we chose to minimize in our logistic regression task is the cross-entropy, as we discussed in the previous section.

We start training our model for 500 epochs and we look at the summary in terms of performances (accuracy).

EPOCHS = 500

history = model.fit(

train\_x, train\_y\_bin,

epochs = EPOCHS, verbose = 1

)

In Figure 3-11 you can see the **cost function vs. number of iterations** plot associated to the learning phase.

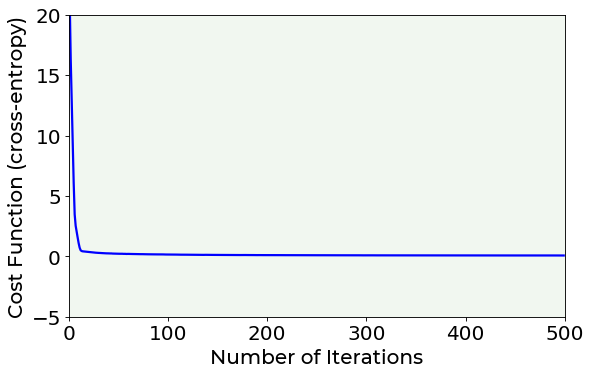


Figure 3-11. The cost function resulting in our model applied to the BCCD dataset with a learning rate of 0.001.

Looking at the previous plot, you can notice that, after 100 epochs, the cost function remains almost constant in its value, indicating that a minimum has been reached.

## Model's performance evaluation

Now, to know if the model you have just trained is suited to be applied to unseen data, you must check its performances over the test set. Moreover, an **optimizing metric** must be chosen. For a binary classification problem, a classic metric is the **accuracy** which can be understood as a measure of how well the classifier correctly identified the two classes of the dataset. Mathematically it can be calculated as

where the number of cases correctly identified is the sum of all positive samples and negative samples (i.e., all 0s and 1s) that were correctly classified, usually called true positives and true negatives.

To get the accuracy we can run this code (remember we will classify an observation of class 0 if or in class 1 if

test\_predictions = model.predict(test\_x).flatten()

test\_predictions1 = test\_predictions > 0.5

tp = np.sum((test\_predictions1 == 1) & (test\_y\_bin == 1))

tn = np.sum((test\_predictions1 == 0) & (test\_y\_bin == 0))

accuracy\_test = (tp + tn)/len(test\_y)

print('The accuracy on the test set is equal to: ',

int(accuracy\_test\*100), '%.')

The above code prints to the screen

The accuracy on the test set is equal to: 98 %.

With this model we reach an accuracy of 98%. Not bad for a network with just one neuron.

# Conclusions

In this chapter we have looked at many things. You have learned how a neuron is working and what are its main components. You have seen the most used activation functions and how to implement a model with one single neuron in Keras to solve two problems: linear and logistic regression. In the next chapter we will look at how to build neural networks with a large number of neurons and how to train it.

**Note** linear and logistic regression are two classical statistical models that can be implemented in many ways. In this chapter we have used a neural network language to implement them to show the readers how flexible are neural networks, and how, by understanding their inner components, they can be used in many ways.

# Exercises

EXERCISE 1 (linear REGRESSION) (LEVEL: EASY)

Try using only one feature to predict radon activity and see how results change.

exercise 2 (linear regression) (LEVEL: MEDIUM)

Try to change the learning\_rate parameter and see how the model's convergence changes. Then try to reduce the EPOCHS parameter and see when the model cannot reach convergence. Difficulty: medium.

exercise 3 (linear regression) (LEVEL: MEDIUM)

Try to see how model's results change based on the training dataset's size (reduce it and use different sizes comparing the results). Difficulty: medium.

exercise 4 (logistic regression) (LEVEL: MEDIUM)

Try to change the learning\_rate parameter and see how the model's convergence changes. Then try to reduce the EPOCHS parameter and see when the model cannot reach convergence.

exercise 5 (logistic regression) (LEVEL: MEDIUM)

Try to see how model's results change based on the training dataset's size (reduce it and use different sizes comparing the results).

exercise 6 (logistic regression) (LEVEL: HARD)

Try to add to labels Platelets samples and generalize the binary classification model to a multiclass one (3 possible classes). Difficulty: hard.

# References

[1] <https://spectrum.ieee.org/tech-talk/computing/software/biggest-neural-network-ever-pushes-ai-deep-learning>, last accessed 27.12.2017

[2] R. Rojas (1996), Neural Networks: a systematic introduction, Springer-Verlag Berlin Heidelberg

[3] <https://www.tensorflow.org/datasets/catalog/radon>, last accessed 09.01.2021

[4] Lever, Jake, Martin Krzywinski, and Naomi Altman. "Points of significance: model selection and overfitting." (2016): 703.

[5] Srivastava, Nitish, et al. "Dropout: a simple way to prevent neural networks from overfitting." The journal of machine learning research 15.1 (2014): 1929-1958.

[6] Bengio, Yoshua. "Practical recommendations for gradient-based training of deep architectures." Neural networks: Tricks of the trade. Springer, Berlin, Heidelberg, 2012. 437-478.

[7] <https://rdipietro.github.io/friendly-intro-to-cross-entropy-loss/>, last accessed 10.01.2021

[8] <https://www.tensorflow.org/datasets/catalog/bccd>, last accessed 10.01.2021

1. More advanced architecture as convolutional or recurrent neural networks have a structure that is more complex than what is describe here. In this chapter we will describe the neurons used to build so called Feed Forward Neural Networks (FFNN). [↑](#footnote-ref-1)
2. Note that you will not have to implement it yourself in Python. Keras offers already this function, and many more, out of the box. [↑](#footnote-ref-2)
3. Montufar G., Pascanu R., Cho K. and Bengio Y., On the Number of Linear Regions of Deep Neural Networks, thttps://papers.nips.cc/paper/5422-on-the-number-of-linear-regions-of-deep-neural-networks.pdf , last accessed 10th Jan. 2018; Fortuner B., Can neural networks solve any problem?, https://towardsdatascience.com/can-neural-networks-really-learn-any-function-65e106617fc6, last accessed 10th Jan. 2018 [↑](#footnote-ref-3)
4. It is assumed here that you know the reasons and why it is important. [↑](#footnote-ref-4)
5. The ratios 80/20 is simply a convention and you can choose 75/25, 70/30 or anything in between. Normally 80/20 is chosen since you want to have as much training data as possible and enough test data to make your testing reasonable. [↑](#footnote-ref-5)
6. We will discuss at length what layers are in the next chapter. For the moment just ignore it if you don’t understand what it means. [↑](#footnote-ref-6)