Understanding Matrices and Logistic Regression in Neural Networks

In this document, we explore the foundations of matrices in neural networks, logistic regression, forward propagation, and updating weights using stochastic gradient descent. We will implement a basic example in `R` to reinforce learning.

Understanding Matrices in Neural Networks

Matrices enable efficient mathematical operations in neural networks. For a simple model:

$$Z = XW$$

where:

- X is the **input matrix** (containing feature values).
- W is the **weight matrix** (containing learned coefficients).
- Z is the **output before activation**.

Traditional Logistic Regression Notation

In standard **logistic regression**, the equation is expressed using individual predictor variables:

$$Z = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n$$

where:

- β_0 is the **intercept (bias term)**.

- $\beta_1, \beta_2, \ldots, \beta_n$ are the **weights (coefficients) assigned to each feature**.
- $x_1, x_2, \ldots, x_n$ are the **input feature values** (e.g., time spent, pages visited).
- Z is the **linear combination before applying the activation function**.

Once Z is computed, the logistic function (**sigmoid activation**) is applied:

$$\sigma(Z) = \frac{1}{1 + e^{-Z}}$$

{eq-sigmoid-function}

Both forms describe the same underlying concept:

- The **matrix form** ($Z = XW$) is compact and efficient, especially when handling multiple samples.
- The **traditional logistic regression form** explicitly shows the relationship between individual features and their respective weights.

Both representations lead to the same outcome: a **probability prediction** via the sigmoid function.

The term Z in the sigmoid activation function is most commonly referred as the weighted sum of imputs (plus bias)

Herer's a breakdown: In a single neuron, before an activation function is applied, a neuron takes multiple inputs, multiplies each input by a corresponding weight, sums these weighted inputs, and then adds the bias term. So Z represents the linear combination of the inputs to a neuron before any any non-linear transformation is applied.

The concept around activation functions 1. Introducing Non-linearity: this is the most important reason for activation functions. Imagine a neural network without activation functions. Each neuron would simply perform a linear transformation (weighted sum +bias). If you stack multiple layers of linear transformations, the entire network would still be a single linear transformation. Real world data is almost never linearly separable. Problems like image recognition, natural language or complex pattern detection involve highly non-linear relationships. Activation functions introduce non-linearity, allowing neural network to learn and approximate complex, non-linear functions and relationships in the data. You can think of an activation function as determining whether a neuron should "activate" or "fire" and pass its signal to the next layer. It transforms the raw, unbounded weighted sum (Z) into an output that is typically within a specific range, often interpreted as probability or a strength of activation. Sigmoid maps any real number (Z) to a value between 0 and 1. This makes it ideal for output layers in binary classification problems, where the output can be interpreted as a probability.

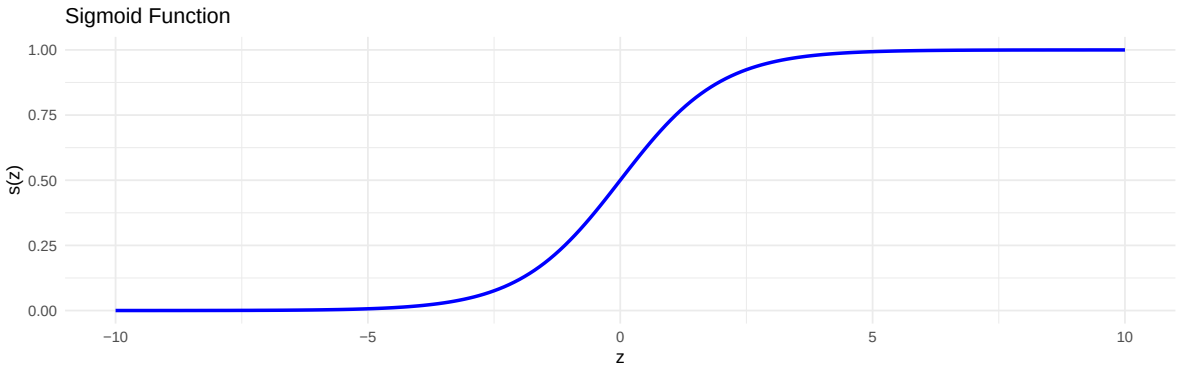
Logistic Regression Model

Logistic regression predicts probabilities using the **sigmoid function**: The sigmoid function is a mathematical function that outputs values between 0 and 1, making it ideal for logistic regression, where we interpret the result as a probability.

$$\sigma(Z) = \frac{1}{1 + e^{-Z}} \tag{1}$$

- Z is the input value (can be any real number)
- e is Euler's number

> **Tip**
>
> If Z is large and positive,$\sigma(z)$ approaches 1 (strong positive probability)
> If z is large and negative,$\sigma(z)$ approaches 0 (strong negative probability)
> when $z = 0$, $\sigma(z) = 0.5$), meaning neutral probability



Forward Propagation & Loss Function

Predictions ($\hat{y}$) are made using:

$$\hat{y} = \sigma(Z)$$

The **binary cross-entropy loss function** quantifies the error between the estimate and the real output provided to the model:

$$L = -\frac{1}{m} \sum_{i=1}^{m} [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)] \tag{2}$$

Updating Weights with Gradient Descent

Since we don't know the optimal values of W, we start with random weights and iteratively update them to minimize the loss function. Now, let's break down the equation further and clarify the partial derivatives.

Gradient loss function:

$$dw = \frac{\partial L}{\partial W} = \frac{1}{m} X^T (A - Y) \tag{3}$$

This term represents the gradient, or the slope, of the loss function L with respect to W. Essentially, it tells us:

How much the loss function changes when we slightly change$W$ The direction we should move W to minimize the loss.

Since L depends on W (because changing affects predictions), we need to calculate the rate of change of L concerning W, which is where the partial derivative comes in.

Partial Derivatives Explained A partial derivative calculates how one variable changes while keeping others constant. In our case:

$$\frac{\partial L}{\partial W}$$

measures how much the loss function changes if we make a small adjustment to W. If we visualize the loss function as a mountain, the gradient tells us which direction leads us downhill the fastest (toward lower loss). The gradient gives the best direction for adjusting W, but how far we step in that direction is controlled by the learning rate α

$$W = W - \alpha \cdot \frac{\partial L}{\partial W}$$

Where:

- α is the **learning rate** (a small step size to prevent large jumps)
- $\frac{\partial L}{\partial W}$ is the **gradient**

W is updated gradually with each iteration.

For logistic regression, the gradient of the *binary cross-entropy loss function* with respect to W is:

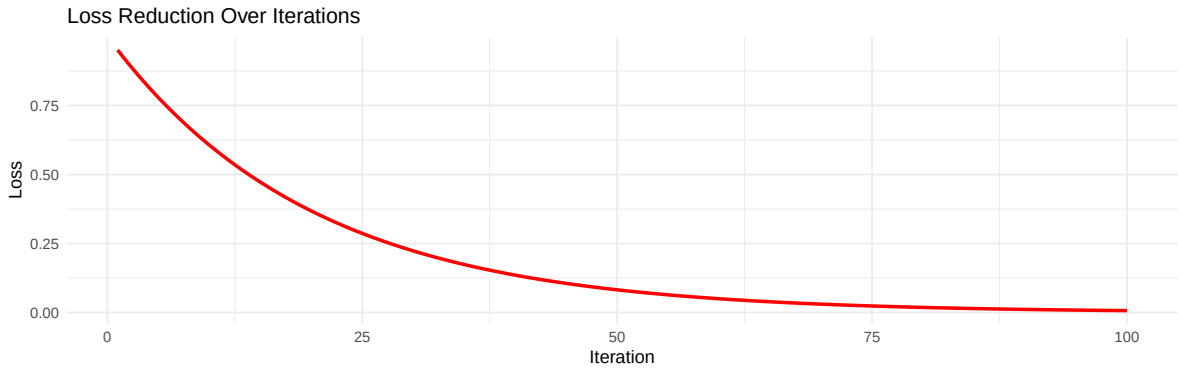
$$\frac{\partial L}{\partial W} = \frac{1}{m} X^T (\hat{y} - y)$$

Where:

- X is the input matrix (features)
- y is the actual target values.

- $\hat{y} = \sigma(XW)$ is the predicted output after applying the sigmoid function.
- $X^T(\hat{y} - y)$ measures the error's contribution to weight updates.

```r
# Example loss reduction over iterations
iterations <- seq(1, 100)
loss_values <- exp(-0.05 * iterations)  # Simulated loss decreasing

# Create dataframe
df <- data.frame(iteration = iterations, loss = loss_values)

# Plot loss reduction
ggplot(df, aes(x = iteration, y = loss)) +
  geom_line(color = "red", size = 1) +
  ggtitle("Loss Reduction Over Iterations") +
  xlab("Iteration") +
  ylab("Loss") +
  theme_minimal()
```



Implementation in R

Scenario: Predicting Whether Someone Will Buy a Product Imagine you're running an online store, and you want to predict whether a customer will buy a product based on two simple features:

- Time spent on the website (in minutes)
- Number of pages visited

We'll create a small dataset with these features and train a logistic regression model using gradient descent to predict whether a customer will buy the product (1) or not (0).

The traditional logistical regression formula would be:

$$Z = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \epsilon_i$$

where:

- β_0 is the **intercept (bias term)**.
- β_1, β_2 are the **weights (coefficients) assigned to each feature**.
- x_{1i}, x_{2i} are the **feature values** for the$i$-th sample.
- ϵ_i is the **error term** accounting for noise in the data.

Instead of writing the equation explicitly for each feature, we can use matrix multiplication:

$$Z = XW + \epsilon$$

Where:

- X is the **input matrix** containing feature values.
- W is the **weight matrix** (vector of coefficients).
- ϵ is the **error term**.

Expanding this in **matrix notation**:

$$\begin{bmatrix} Z_1 \\ Z_2 \\ Z_3 \\ \vdots \\ Z_m \end{bmatrix} = \begin{bmatrix} 1 & x_{11} & x_{21} \\ 1 & x_{12} & x_{22} \\ 1 & x_{13} & x_{23} \\ \vdots & \vdots & \vdots \\ 1 & x_{1m} & x_{2m} \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \vdots \\ \epsilon_m \end{bmatrix}$$

Where:

- Each row in X represents **one sample**, including a **bias term (1), feature 1, and feature 2**.
- The column vector W contains the **learned parameters** $(\beta_0, \beta_1, \beta_2)$.
- The error term ϵ accounts for **random noise in predictions**.

We have data from 5 customers, we will create a matrix for this: Each row in X represents a customer. First column = Bias term (always 1). Second column = Time spent on the website. Third column = Number of pages visited. y contains whether the customer bought the product (1) or not (0).

```
 # Real-world dataset (Time spent & Pages visited)
X <- matrix(c(
  1, 5, 2,
  1, 15, 5,
  1, 20, 7,
  1, 2, 1,
  1, 30, 10
), ncol=3, byrow=TRUE)

y <- c(0, 1, 1, 0, 1)  # Labels
```

As a recapitulation, we use the *sigmoid* function to predict the expected output of any specific combination of minutes in the website and pages visited. We will create a function for this:

```
# Sigmoid function
sigmoid <- function(z) {
  return(1 / (1 + exp(-z)))
}
```

The *loss function* will tell us how far our predicted value is from the actual value, we will also create a function for this:

```
# Loss function (binary cross-entropy)
loss_function <- function(y, y_hat) {
  return(-mean(y * log(y_hat) + (1 - y) * log(1 - y_hat)))
}
```

Now we create a function to calculate the *gradient descent*

```
gradient_descent <- function(X, y, learning_rate = 0.01, iterations = 50) {
  m <- nrow(X)
  W <- runif(ncol(X))  # Initialize weights randomly
  for (i in 1:iterations) {
    Z <- X %*% W   # Compute Z values for all samples
    y_hat <- sigmoid(Z)  # Apply sigmoid function to all samples
    gradient <- t(X) %*% (y_hat - y) / m  # Compute gradient for weight updates
```

```
    W <- W - learning_rate * gradient  # Update weights
  }
  return (W)
}
```

Just for learning purposes, we will create a new version of the gradient descent function where we store the results of each iteration, so we can visualize it later:

```
# Gradient Descent Implementation (Tracking Progress)
gradient_descent_progress <- function(X, y, learning_rate = 0.01, iterations = 50) {
  m <- nrow(X)
  W <- runif(ncol(X))  # Initialize weights randomly
  progress <- data.frame(Iteration = integer(),
                         Weight1 = numeric(), Weight2 = numeric(),
                         Z1 = numeric(), Z2 = numeric(), Z3 = numeric(), Z4 = numeric(), Z5 =
                         y_hat1 = numeric(), y_hat2 = numeric(), y_hat3 = numeric(), y_hat4 =
                         Grad1 = numeric(), Grad2 = numeric())  # Tracking all five samples

  for (i in 1:iterations) {
    Z <- X %*% W   # Compute Z values for all samples
    y_hat <- sigmoid(Z)  # Apply sigmoid function to all samples
    gradient <- t(X) %*% (y_hat - y) / m  # Compute gradient for weight updates
    W <- W - learning_rate * gradient  # Update weights

    # Store results for all five samples
    progress <- rbind(progress, data.frame(
      Iteration = i,
      Weight1 = W[2], Weight2 = W[3],
      Z1 = Z[1], Z2 = Z[2], Z3 = Z[3], Z4 = Z[4], Z5 = Z[5],
      y_hat1 = y_hat[1], y_hat2 = y_hat[2], y_hat3 = y_hat[3], y_hat4 = y_hat[4], y_hat5 = y
      Grad1 = gradient[2], Grad2 = gradient[3]
    ))
  }

  return(progress)
}
```

At the beginning, the weights are random.

Over each iteration, the values change towards better predictions.

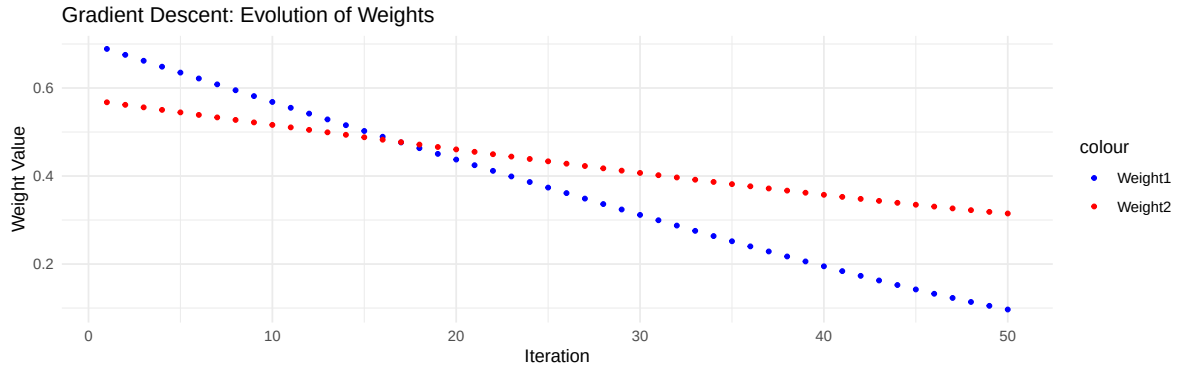
- Z values show the raw linear transformation before activation.

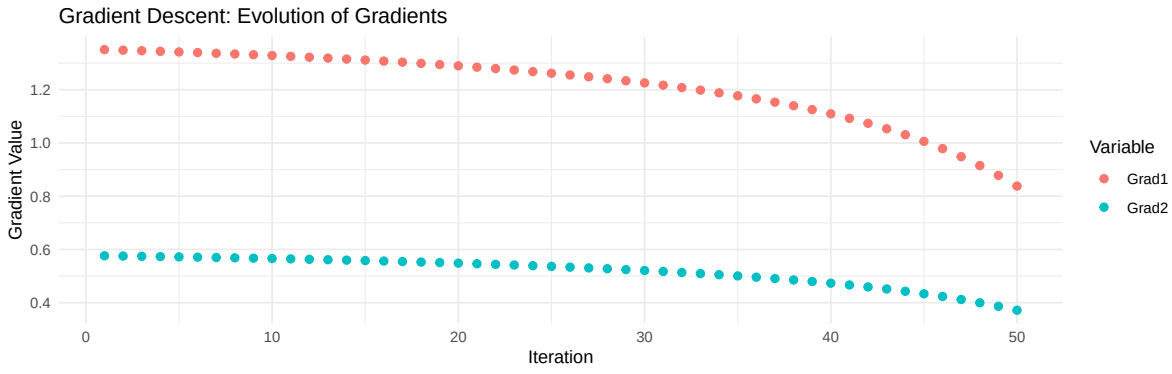
- $\hat{y}$ (y_hat) tracks how probabilities evolve as weights adjust.
- Gradient values indicate how weights update to minimize the loss.

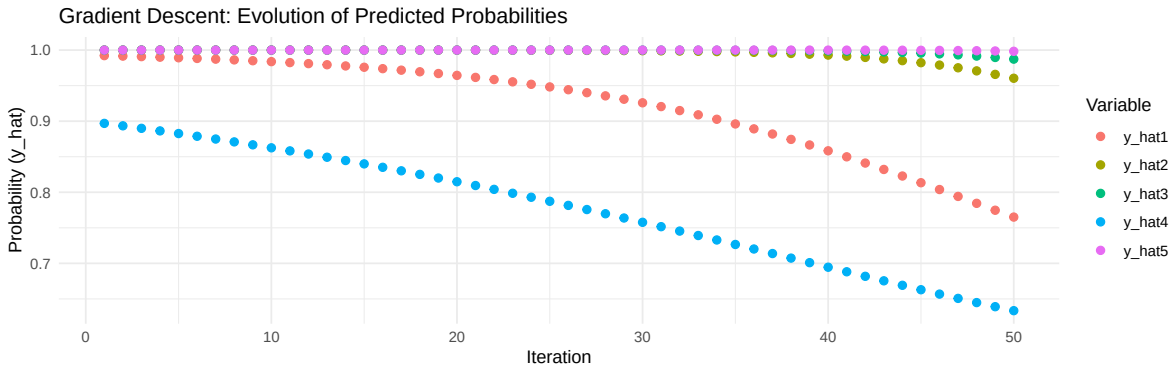
If you increase iterations, you'll see further refinement.

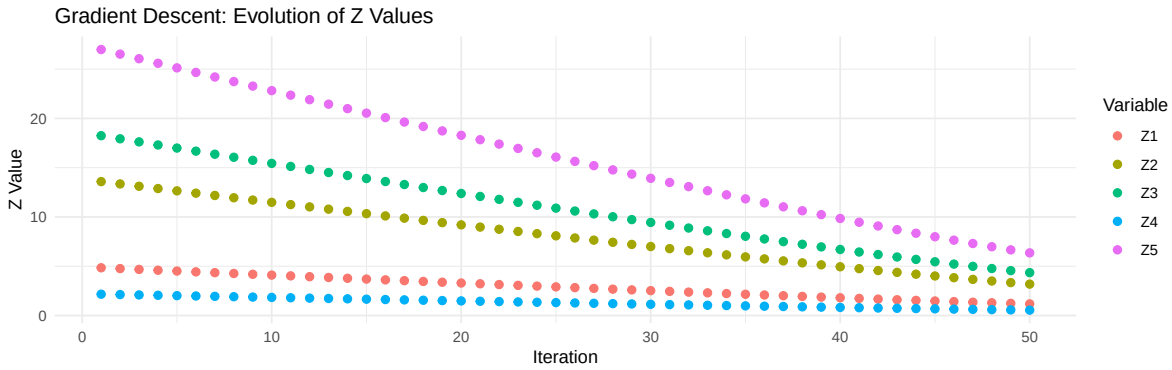
```
# Train Model
set.seed(2)
progress_df <- gradient_descent_progress(X, y)

print(head(progress_df))
```

```
  Iteration   Weight1   Weight2       Z1       Z2       Z3       Z4       Z5
1         1 0.6888648 0.5675639 4.843405 13.58712 18.24565 2.162957 26.98937
2         2 0.6753759 0.5618110 4.760556 13.35190 17.93135 2.126398 26.52269
3         3 0.6619085 0.5560680 4.677836 13.11703 17.61753 2.089897 26.05672
4         4 0.6484633 0.5503354 4.595251 12.88254 17.30422 2.053458 25.59151
5         5 0.6350416 0.5446137 4.512808 12.64845 16.99143 2.017082 25.12707
6         6 0.6216444 0.5389033 4.430512 12.41477 16.67920 1.980774 24.66346
     y_hat1    y_hat2    y_hat3    y_hat4 y_hat5    Grad1     Grad2
1 0.9921814 0.9999987 1.0000000 0.8968733      1 1.350927 0.5762460
2 0.9915118 0.9999984 1.0000000 0.8934425      1 1.348884 0.5752916
3 0.9907866 0.9999980 1.0000000 0.8899173      1 1.346747 0.5742961
4 0.9900013 0.9999975 1.0000000 0.8862965      1 1.344512 0.5732572
5 0.9891514 0.9999968 1.0000000 0.8825790      1 1.342173 0.5721731
6 0.9882318 0.9999959 0.9999999 0.8787636      1 1.339725 0.5710413
```









Understanding the Learned Weights

After running gradient descent, we obtained the following learned weights:

```
set.seed(2)
# Gradient Descent Implementation (Track Progress)
gradient_descent <- function(X, y, learning_rate = 0.01, iterations = 50) {
```

```
  m <- nrow(X)
  W <- runif(ncol(X))  # Initialize weights randomly
  for (i in 1:iterations) {
    Z <- X %*% W   # Compute Z values for all samples
    y_hat <- sigmoid(Z)  # Apply sigmoid function to all samples
    gradient <- t(X) %*% (y_hat - y) / m  # Compute gradient for weight updates
    W <- W - learning_rate * gradient  # Update weights
  }
  return (W)
}
W <- gradient_descent(X, y)
print(W)
```

```
           [,1]
[1,] 0.01567795
[2,] 0.09666904
[3,] 0.31485151
```

These correspond to:

- W_0 **Bias term** (Intercept).
- W_1 **Effect of Time Spent on probability of purchasing**.
- W_2 **Effect of Pages Visited on probability of purchasing**.A positive value increases probability, while a negative value decreases probability.

To predict whether a new customer will buy a product, we use the following equation:

$$Z = W_0 + W_1 \cdot \text{Time Spent} + W_2 \cdot \text{Pages Visited}$$

Once we calculate$Z$, we apply the **sigmoid activation function**:

$$\sigma(Z) = \frac{1}{1 + e^{-Z}}$$

where $\sigma(Z)$ represents the **probability** that the customer will buy.

Example Calculation Let's take a new customer who spends **12 minutes** on the website and visits **4 pages**. We calculate Z as:

$$Z = 0.01567795 + (0.09666904 \times 12) + (0.31485151 \times 4)$$

Applying the *learned weights*, the prediction follows:

$$Z = 2.435112$$

Applying the *sigmoid* function:

$$\sigma(2.435112) = \frac{1}{1 + e^{-2.435112}}$$

Approximating:

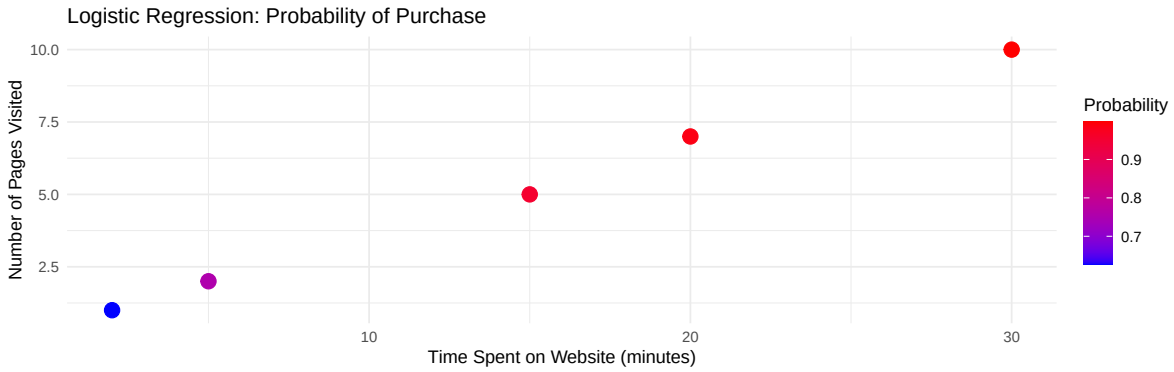
$$\sigma(2.435112) \approx 0.91$$

Thus, the model predicts **91% probability** that this customer **will buy** the product.

Let's see the predictions calculated in `r` over the same data we used for training:

```r
# Function to predict probability based on learned weights
predict_probability <- function(X, W) {
  return(sigmoid(X %*% W))
}
```

```r
# Get predictions
predicted_probs <- predict_probability(X, W)

# Create dataframe for plotting
df <- data.frame(TimeSpent = X[,2], PagesVisited = X[,3], Probability = predicted_probs)

# Plot results
ggplot(df, aes(x = TimeSpent, y = PagesVisited, color = Probability)) +
  geom_point(size = 4) +
  scale_color_gradient(low = "blue", high = "red") +
  ggtitle("Logistic Regression: Probability of Purchase") +
  xlab("Time Spent on Website (minutes)") +
  ylab("Number of Pages Visited") +
  theme_minimal()
```



We apply gradient descent to learn optimal weights and predict whether future customers will buy by minimizing the loss function iteratively.

Cat /Non-cat exercise

We are going to use the cat/non-cat dataset from `kaggle` package to see how to use these maths to find out if a given image is a cat or not a cat. The cat dataset comes in `hdf5`format so we will need to install a couple of libraries to load it.

Now we load the datasets for our model. You can download the data from cat/non-cat

Data Loading and Preprocessing for Image Classification

Before we can feed our "cat/non-cat" image data into our logistic regression model, we need to load it and transform it into a format that our matrix-based gradient descent implementation can efficiently process. Image data, especially raw pixel values, requires several crucial preprocessing steps to make it suitable for machine learning algorithms.

1. **Loading the HDF5 Dataset**

Our image dataset is stored in HDF5 (`.h5`) files, a format optimized for storing large arrays of numerical data. The dataset is conveniently split into two files: `train_catvsnoncat.h5` for training and `test_catvsnoncat.h5` for evaluation. Within each file, the image pixel data is typically stored under a key like `train_set_x` (or `test_set_x`), and their corresponding labels under `train_set_y` (or `test_set_y`).

We use the `h5read()` function from the `rhdf5` package to extract these specific datasets from the HDF5 files.

```r
library(rhdf5)
test_data_file_path <- file.path("data", "test_catvsnoncat.h5")
train_data_file_path <- file.path("data", "train_catvsnoncat.h5")

# Load training and test data
train_dataset <- h5read(train_data_file_path, "train_set_x")
train_labels <- h5read(train_data_file_path, "train_set_y")

# Load test data
test_dataset <- h5read(test_data_file_path, "test_set_x")
test_labels <- h5read(test_data_file_path, "test_set_y")
```

Raw image data is inherently multi-dimensional (e.g., `64 pixels height x 64 pixels width x 3 color channels for RGB`).

By looking at the dimensions of the datasets we can see that we have 209 images in the train dataset and 50 in the test dataset:

```r
dim(test_dataset)
```

```
[1]  3 64 64 50
```

```r
dim(train_dataset)
```

```
[1]   3  64  64 209
```

If we want to extract the data for the first cat image (the first cat image is the third image in the train dataset), for example:

```r
# Extract the third image (which is a 3D array)
first_cat_image_raw <- train_dataset[,,,3]
dim(first_cat_image_raw)
```

```
[1]  3 64 64
```

This will give us a 3X64x64 matrix

To get just the first channel (Red) for the first image:

```
# Extract the Red channel (1st channel)
first_cat_image_red_channel_raw <- train_dataset[1,,,3]
dim(first_cat_image_red_channel_raw)
```

```
[1] 64 64
```

Le't see the first 10 pixels of that channel:

```
first_cat_image_red_channel_raw[1:10,1:10]
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
 [1,]   52   5f   5e   60   63   5e   62   65   67    6d
 [2,]   59   68   61   62   63   60   62   69   69    6e
 [3,]   64   6e   6e   65   6d   67   6a   73   70    70
 [4,]   6a   74   77   6f   74   72   6d   79   77    73
 [5,]   76   78   7a   72   7d   7d   71   77   7c    75
 [6,]   79   7e   80   76   7c   81   7c   7a   81    7c
 [7,]   77   7e   83   7d   7b   7f   83   80   86    85
 [8,]   85   80   84   81   7c   80   85   83   87    88
 [9,]   84   82   83   88   82   7f   87   86   86    88
[10,]   82   7d   7e   83   85   7f   84   8c   8a    89
```

We can see that we have hexadecimal values, so we will need to convert them to numeric:

```
# Convert character (hex) values to numeric integers ---
# 'strtoi()' converts string representations of numbers in a given base
#(here, 16 for hexadecimal) to integers. We apply it directly to the entire array, preservin
original_train_dims <- dim(train_dataset)
original_test_dims <- dim(test_dataset)

train_dataset <- array(strtoi(as.vector(train_dataset), base = 16), dim = original_train_dim
test_dataset <- array(strtoi(as.vector(test_dataset), base = 16), dim = original_test_dims)
```

Let's see the Red channel of the image again to see if its numeric now:

```
dim(train_dataset)
```

```
[1]   3  64  64 209
```

```r
first_cat_image_red_channel_raw <- train_dataset[1,,,3]
first_cat_image_red_channel_raw[1:10,1:10]
```

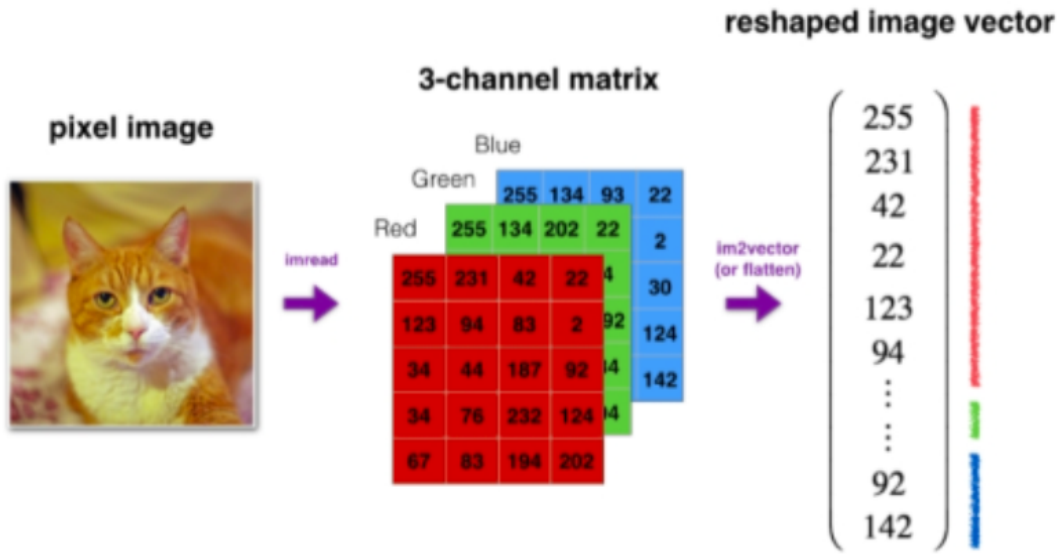
```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
 [1,]   82   95   94   96   99   94   98  101  103   109
 [2,]   89  104   97   98   99   96   98  105  105   110
 [3,]  100  110  110  101  109  103  106  115  112   112
 [4,]  106  116  119  111  116  114  109  121  119   115
 [5,]  118  120  122  114  125  125  113  119  124   117
 [6,]  121  126  128  118  124  129  124  122  129   124
 [7,]  119  126  131  125  123  127  131  128  134   133
 [8,]  133  128  132  129  124  128  133  131  135   136
 [9,]  132  130  131  136  130  127  135  134  134   136
[10,]  130  125  126  131  133  127  132  140  138   137
```

Now we can display the Red channel as a grayscale image

```r
 # Normalize pixel values (0-255 to 0-1) for plotting
first_cat_image_red_channel_normalized <- first_cat_image_red_channel_raw / 255
# For a single channel, higher values will appear brighter.
plot(as.raster(first_cat_image_red_channel_normalized),
     main = "First Image: Red Channel Only (Grayscale)")
```

2. **Flattening the Images**

As we have seen, the image data is multi-dimensional, however, our logistic regression model, which operates on linear combinations of features, expects each image to be represented as a single, flat vector of features.



This step transforms each 3D image array into a 1D vector by concatenating all its pixel values. We then stack these individual vectors to form a 2D matrix, where each row corresponds to a single image (sample) and each column represents a specific pixel feature. This conversion makes the data compatible with standard matrix multiplication operations like $Z = XW$, where X is a `(samples x features)` matrix.

```
# Flattening the images:
# Each image (accessed by the 4th dimension) is converted to a vector.
# 't()' transposes the result to get samples as rows, features (pixels) as columns.
X_train <- t(apply(train_dataset, 4, as.vector))
X_test <- t(apply(test_dataset, 4, as.vector))
dim(X_train)
```

```
[1]   209 12288
```

```
dim(X_test)
```

```
[1]    50 12288
```

3. **Converting Labels to a Matrix (Column Vector)**

The labels (0 for non-cat, 1 for cat) are initially loaded as simple numerical vectors. For consistency and robustness in matrix operations within our gradient descent functions (e.g., calculating `y_hat - y`), it's good practice to explicitly convert these label vectors into single-column matrices. This ensures that matrix multiplication and subtraction behave as expected without unexpected R vector recycling rules.

```
# Converting labels to a matrix (column vector):
# Ensures y_train and y_test are treated as column matrices for consistent
# matrix operations later in the gradient descent.
y_train <- as.matrix(train_labels)
y_test <- as.matrix(test_labels)
dim(y_train)
```

```
[1] 209   1
```

```
dim(y_test)
```

```
[1] 50  1
```

4. Normalizing Pixel Values

Image pixel intensities range from 0 to 255. This step involves dividing all pixel values by 255 (the max value), scaling them down to a standardized range between 0 and 1.

This normalization is critical for several reasons:

- **Numerical Stability:** Machine learning algorithms, especially those that rely on gradient descent, perform much better and converge more reliably when input features are on a similar, small scale. Large input values can lead to extremely large intermediate calculations (Z values) and gradients, potentially causing numerical overflow or instability.
- **Faster Convergence:** Scaling features to a consistent range helps the optimization algorithm find the optimal weights more efficiently. The sigmoid activation function, in particular, has a very flat gradient for very large or very small inputs; normalizing helps keep inputs within the active range of the sigmoid, where gradients are stronger and learning is more effective.

```r
X_train <- X_train/255
X_test <- X_test/255
```

5. Adding a Bias Term (Intercept)

Finally, we add an extra column of 1s to the leftmost side of our feature matrices (`X_train` and `X_test`).

This column represents the **bias term** (or intercept) for our logistic regression model. In the matrix multiplication $Z = XW$, if X includes this column of ones, the first element of the weight vector W will correspond to β_0 (the intercept). This allows the model to learn a baseline probability (or a baseline activation) even if all other feature values are zero. It effectively shifts the decision boundary, giving the model more flexibility to fit the data.

```r
# Prepends a column of '1's to the feature matrices. This allows the model
# to learn an intercept, which is a baseline prediction independent of features.
X_train <- cbind(1, X_train)
X_test <- cbind(1, X_test)

# --- Display Final Dimensions for Verification ---
# These outputs confirm the shape of your data matrices after preprocessing.
cat("--- Final Data Dimensions (after preprocessing) ---\n")
```

```
--- Final Data Dimensions (after preprocessing) ---
```

```r
cat("Dimensions of X_train (samples x (features + bias)):", dim(X_train), "\n")
```

```
Dimensions of X_train (samples x (features + bias)): 209 12289
```

```r
cat("Dimensions of y_train (samples x 1):", dim(y_train), "\n")
```

```
Dimensions of y_train (samples x 1): 209 1
```

```r
cat("Dimensions of X_test (samples x (features + bias)):", dim(X_test), "\n")
```

```
Dimensions of X_test (samples x (features + bias)): 50 12289
```

```r
cat("Dimensions of y_test (samples x 1):", dim(y_test), "\n")
```

```
Dimensions of y_test (samples x 1): 50 1
```

Building the parts of our algorithm

The main steps for building a neural network are:

1. Define the model structure (such as number of input features)
2. Initialize the model's parameters
3. loop:
    1. Calculate current loss (forward propagation)
    2. Calculate current gradient (Backward propagation)
    3. Update parameters (gradient descent)
4. You often build 1-3 separately and integrate them into one function we call model.

Let's start:

For one sample image x_i :

$$z_i = w^T x_i + b$$

the probability of belonging to the cat class will be calculated as:

$$\hat{y}_i = a_i = sigmoid(z_i)$$

where the formula for the *sigmoid* function is:

$$\sigma(Z) = \frac{1}{1 + e^{-Z}}$$

and loss function:

$$L = -\frac{1}{m} \sum_{i=1}^{m} [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$$