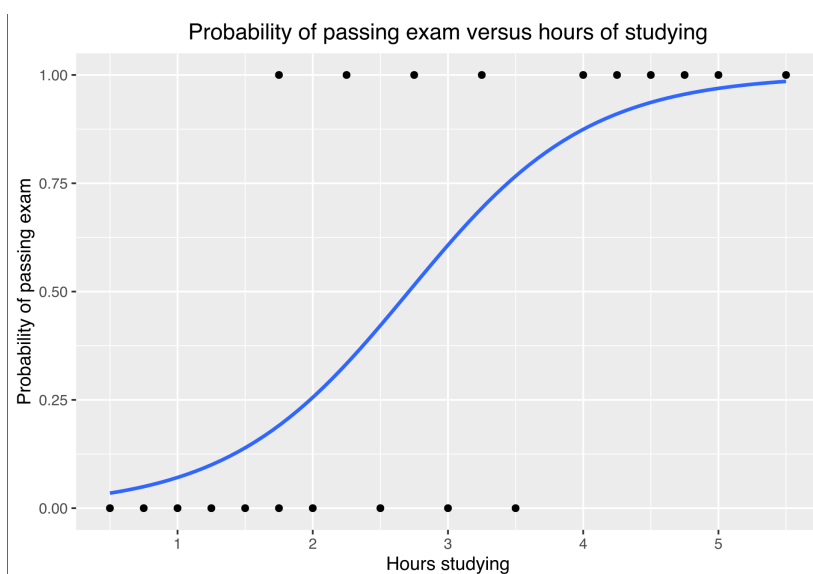


Logistic Regression

- The first classifier we will discuss in this class is **Logistic Regression**.
- In Linear Regression, we fit a line to data.
- In a simple (two-class) Logistic Regression we will fit a curve to the probability that the data comes from one **class**
- Many AI models are complicated versions of logistic regression models.



Logistic Function

Logistic Regression addresses the problem of estimating a probability model, $P(Y = 1|x)$.

The logistic regression model uses a function for the probability model, called the logistic function:

$$P(Y = 1 | x) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x)}}$$

In [1]:

```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score
```

In [2]:

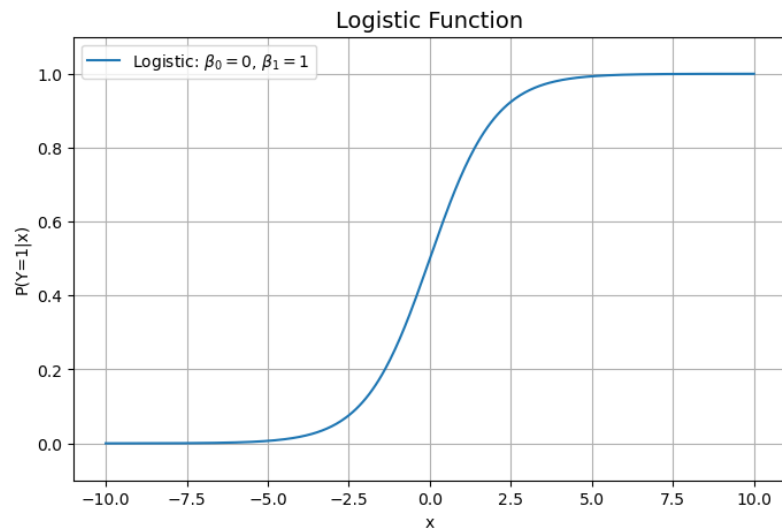
```
def logistic(x, beta0=0, beta1=1):
    p = 1 / (1 + np.exp(-(beta0 + beta1 * x)))
    return p

# Generate a range of x values
x = np.linspace(-10, 10, 400)

# Parameters
beta0 = 0 # Intercept
beta1 = 1 # Slope

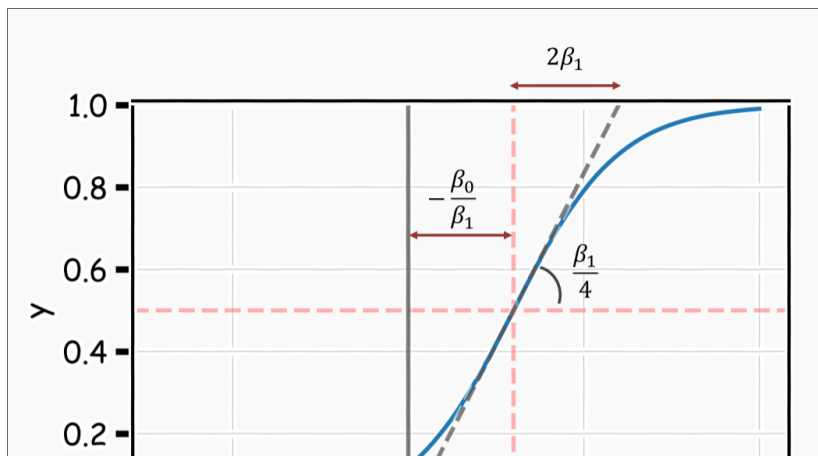
# Compute logistic values
y = logistic(x, beta0, beta1)

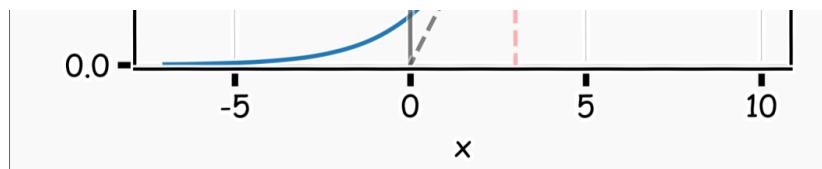
# Plot
plt.figure(figsize=(8, 5))
plt.plot(x, y, label=fr'Logistic: $\beta_0={beta0}$, $\beta_1={beta1}$')
plt.title("Logistic Function", fontsize=14)
plt.xlabel("x")
plt.ylabel("P(Y=1|x)")
plt.grid(True)
plt.legend()
plt.ylim(-0.1, 1.1)
plt.show()
```



The probability model will predict $P(Y = 1|x)$ with an S-shaped curve:

- β_0 shifts the curve right or left by $c = \frac{-\beta_0}{\beta_1}$
- β_1 controls the steepness the S-shaped curve. Distance from $\frac{1}{2}$ to almost 1 or $\frac{1}{2}$ to almost 0 to $\frac{1}{2}$ is $\frac{2\beta_1}{4}$
- if β_1 is positive, then the predicted $P(Y = 1|x)$ goes from zero for small values of x to one for large values of x if β_1 is negative, then the predicted $P(Y = 1|x)$ goes from one for small values of x to zero for large values of x





- It's useful to rewrite the logistic regression model, in terms of odds. This is called the **logit** function by statisticians and in economics

$$\text{logit}(P(Y = 1 | x)) = \ln\left(\frac{P(Y = 1 | x)}{1 - P(Y = 1 | x)}\right) = \beta_0 + \beta_1 x$$

- The ratio shown is the **odds** ratio between the probability of $Y = 1$ with the probability $Y = 0$, where Y can only be 1 or 0
- A one unit change in x is associated with an e^{β_1} change in the odds that $Y = 1$.
- What happens with the odds ratio is 1, i.e., $P(Y = 1) = 0.5$?
- Since $P(Y = 0) = 1 - P(Y = 1) = 0.5$,

$$\ln\left(\frac{P(Y = 1)}{1 - P(Y = 1)}\right) = \ln(1) = 0 = \beta_0 + \beta_1 x$$

$$x = -\frac{\beta_0}{\beta_1}$$

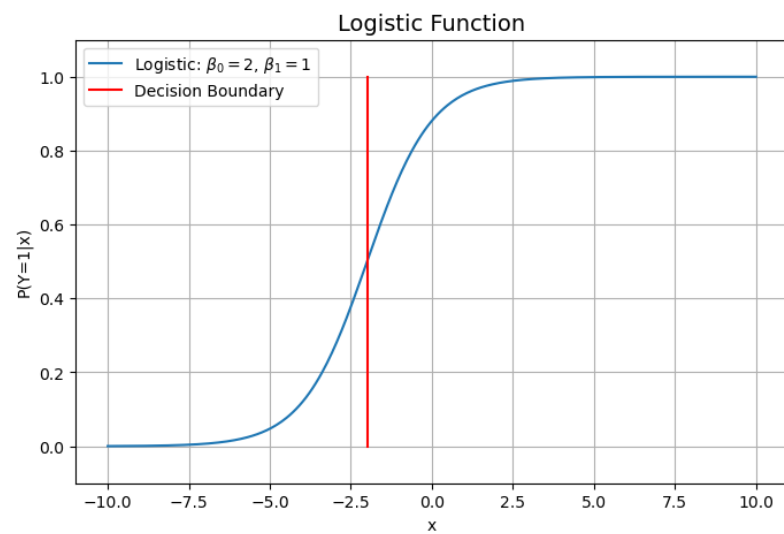
In [3]:

```
# Generate a range of x values
x = np.linspace(-10, 10, 400)

# Parameters
beta0 = 2 # Intercept
beta1 = 1 # Slope
c = -beta0 / beta1 # x value where P(Y=1/x) = 0.5
# Compute logistic values
y = logistic(x, beta0, beta1)

# Plot
plt.figure(figsize=(8, 5))
plt.plot(x, y, label=fr'Logistic: $\beta_0$={beta0}$, $\beta_1$={beta1}$')
plt.plot([c, c], [0, 1], 'r-', label = 'Decision Boundary') # Point where P(Y=1/x) = 0.5
plt.title("Logistic Function", fontsize=14)
plt.xlabel("x")
```

```
plt.ylabel("P(Y=1|x)")
plt.grid(True)
plt.legend()
plt.ylim(-0.1, 1.1)
plt.show()
```



Probability mass function for logistic regression

- In logistic regression, the response variable Y is binary, taking values in

$$Y \in \{0, 1\}$$

- We define

$$P(Y = 1 \mid x) = p \quad \text{and} \quad P(Y = 0 \mid x) = 1 - p$$

- p is modeled using the logistic function:

$$p = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x)}}$$

- The probability mass function (PMF) of a Bernoulli random variable can be written compactly as

$$P(Y = y \mid x) = p^y(1 - p)^{1-y}, \quad \text{for } y \in \{0, 1\}$$

- This expression encodes both possible outcomes in a single formula. Specifically:
 - If $y = 1$

$$P(Y = 1 \mid x) = p^1(1 - p)^0 = p$$

- If $y = 0$

$$P(Y = 0 \mid x) = p^0(1 - p)^1 = 1 - p$$

- The notation $P(Y = y)$ means *the probability that the random variable Y takes the specific observed value y* . Since y can only be 0 or 1, this single expression

$$P(Y = y) = p^y(1 - p)^{1-y}$$

automatically selects the correct probability term depending on whether the observed outcome was 0 or 1.

Likelihood for Logistic Regression

- Given a dataset $\{(x_i, y_i)\}_{i=1}^N$ with $y_i \in \{0, 1\}$ and

$$p_i = P(Y_i = 1 \mid x_i) = \sigma(\beta_0 + \beta_1 x_i) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x_i)}}$$

- the Likelihood of the parameter vector $\beta = (\beta_0, \beta_1)$ is

$$L(\beta \mid x_{1:N}, y_{1:N}) = \prod_{i=1}^N p_i^{y_i} (1 - p_i)^{1-y_i}$$

- Taking the logarithm yields the log-likelihood:

$$\ell(\beta) = \ln L(\beta) = \sum_{i=1}^N [y_i \ln(p_i) + (1 - y_i) \ln(1 - p_i)]$$

Loss Function

- In machine learning, the term loss function is used to refer to some measure of error that you are trying to minimize. If you have a probability model, as in Logistic Regression, the loss function is simply the **negative log-Likelihood**

$$-\ell(\beta) = -\ln L(\beta) = -\sum_{i=1}^N [y_i \ln(p_i) + (1 - y_i) \ln(1 - p_i)]$$

- As mentioned in the video lecture, in machine learning this is called negative cross-entropy.
- How do we minimize this? Differentiate, equate to zero and solve for it!
- Or, stick into some numerical procedure (gradient descent usually) to find the minimum

An example of real data:

Diabetes Prediction Example

Pima Indians Diabetes Study

In [4]:

```
#col_names = ['pregnant', 'glucose', 'bp', 'skin', 'insulin', 'bmi', 'pedigree', 'age', 'label']  
# load dataset  
pima = pd.read_csv("../data/diabetes.csv")
```

In [5]:

```
pima.head()
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

In [6]:

```
pima.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
#   Column                Non-Null Count  Dtype
---  -
0   Pregnancies            768 non-null    int64
1   Glucose                 768 non-null    int64
2   BloodPressure           768 non-null    int64
3   SkinThickness           768 non-null    int64
4   Insulin                 768 non-null    int64
5   BMI                     768 non-null    float64
6   DiabetesPedigreeFunction 768 non-null    float64
7   Age                     768 non-null    int64
8   Outcome                 768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [7]:

```
#I grabbed a list of all the columns
cols = pima.columns
```

In [8]:

```
#Examine how many of each outcome
pima["Outcome"].value_counts()
```

Out[8]:

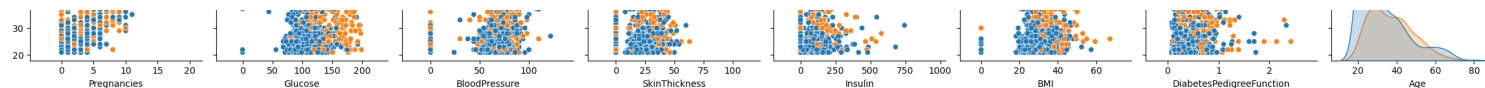
```
Outcome
0    500
1    268
Name: count, dtype: int64
```


- I always like to take a first glance at all the data. This works for continuous valued data, and works if you have fewer than 10 variables.

In [9]:

```
sns.pairplot(pima, hue="Outcome", height=3);  
plt.show()
```



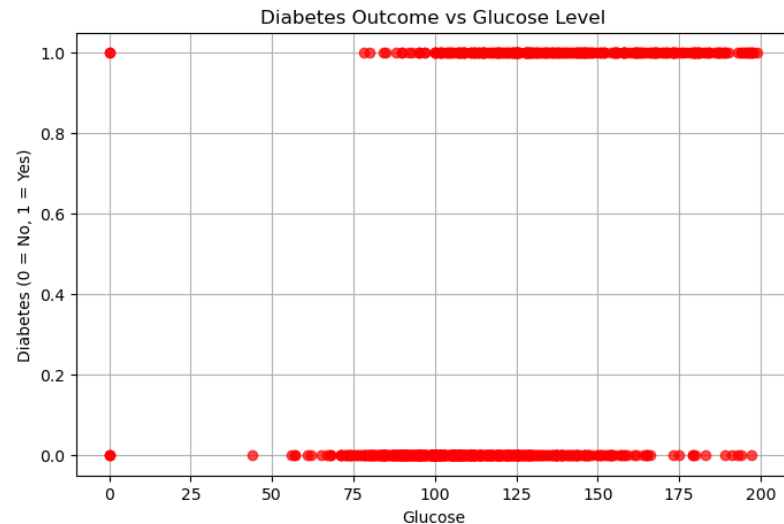


In [10]:

```
diabetes = pima['Outcome']
predictors = pima['Glucose']
```

In [11]:

```
plt.figure(figsize=(8,5))
plt.plot(predictors, diabetes, 'ro', alpha=0.7)
plt.xlabel('Glucose')
plt.ylabel('Diabetes (0 = No, 1 = Yes)')
plt.title('Diabetes Outcome vs Glucose Level')
plt.grid(True)
```



- First step is always to set aside some data for testing after we train the model.

In [12]:

```
predictors_train, predictors_test, diabetes_train, diabetes_test = train_test_split(predictors, diabetes, test_size=0.25, random_state=1)
```

- Lets examine how the test and training data are distributed.

In [13]:

```
print(np.sum(diabetes_train == 1), np.sum(diabetes_train == 0))
```

```
print(np.sum(diabetes_test== 1), np.sum(diabetes_test == 0))
```

```
201 375  
67 125
```

- our syntax is sklearn is standard

In [14]:

```
# I need to do a reshape here because I have a single predictor.  
predictors_train.values.reshape(-1,1)  
# this forces it to be a 2D array with one column and many rows.
```

Out[14]:

```
array([[142],
       [ 99],
       [125],
       [195],
       [122],
       [125],
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```

- first lets fit the model

In [15]:

```
lr = LogisticRegression()  
lr.fit(predictors_train.values.reshape(-1,1), diabetes_train)
```

Out[15]:

▼ LogisticRegression ⓘ ?
LogisticRegression()

- Now lets evaluate the model performance. the `score` method returns accuracy for Logistic Regression

In [16]:

```
accuracy_train = lr.score(predictors_train.values.reshape(-1,1), diabetes_train)
accuracy_test = lr.score(predictors_test.values.reshape(-1,1), diabetes_test)
print(f"Training Accuracy: {accuracy_train:.3f}")
print(f"Test Accuracy: {accuracy_test:.3f}")
```

```
Training Accuracy: 0.743
Test Accuracy: 0.760
```

- Is that good?
- Is there anything unusual?

In []:

*Whats the model it generated?

In [17]:

```
beta = list()
beta.append(lr.intercept_[0])
beta.append(lr.coef_[0][0])
print(f"beta0 (intercept): {beta[0]:.3f}")
print(f"beta1 (slope): {beta[1]:.3f}")
```

```
beta0 (intercept): -4.920
beta1 (slope): 0.035
```

In [18]:

```
decision_boundary = -beta[0] / beta[1]
print(f"Decision Boundary (Glucose level where P(Y=1|x)=0.5): {decision_boundary:.3f}")
```

```
Decision Boundary (Glucose level where P(Y=1|x)=0.5): 142.577
```

Confusion Matrix

- A Confusion Matrix provides better insight into classifier performance than simple accuracy
- To obtain a confusion matrix we need predictions from the model

In [19]:

```
diabetes_train_pred = lr.predict(predictors_train.values.reshape(-1,1))
diabetes_test_pred = lr.predict(predictors_test.values.reshape(-1,1))
```

Compute the confusion matrix for the training data

In [20]:

```
cnf_matrix_train = confusion_matrix(diabetes_train, diabetes_train_pred)
print(cnf_matrix_train)
```

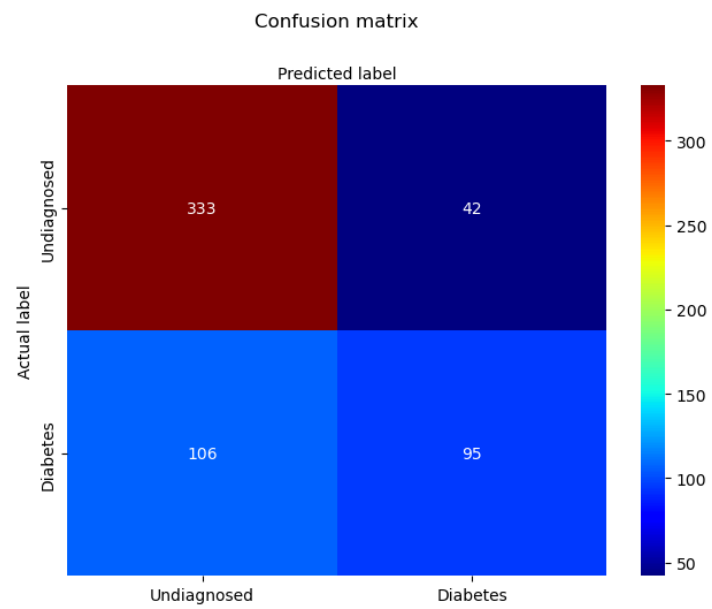
```
[[333  42]
 [106  95]]
```

In [21]:

```
#Never say "Healthy", "Normal", just say "Undiagnosed"
class_names=['Undiagnosed', 'Diabetes'] # name of classes
fig, ax = plt.subplots()
tick_marks = np.arange(len(class_names))
# create heatmap
sns.heatmap(pd.DataFrame(cnf_matrix_train), annot=True, cmap="jet" ,fmt='g')
ax.xaxis.set_label_position("top")
plt.tight_layout()
plt.title('Confusion matrix', y=1.1)
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
plt.xticks(tick_marks+0.5, class_names)
plt.yticks(tick_marks+0.5, class_names)
```

Out[21]:

```
([<matplotlib.axis.YTick at 0x7fa0ad648cd0>,
  <matplotlib.axis.YTick at 0x7fa0ad60e5d0>],
 [Text(0, 0.5, 'Undiagnosed'), Text(0, 1.5, 'Diabetes')])
```

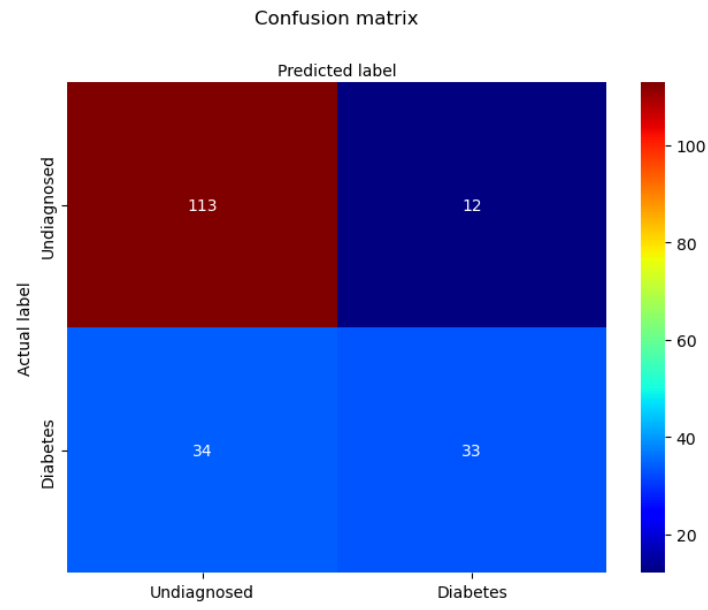


In [22]:

```
cnf_matrix_test = confusion_matrix(diabetes_test, diabetes_test_pred)
#Never say "Healthy", "Normal", just say "Undiagnosed"
class_names=['Undiagnosed','Diabetes'] # name of classes
fig, ax = plt.subplots()
tick_marks = np.arange(len(class_names))
# create heatmap
sns.heatmap(pd.DataFrame(cnf_matrix_test), annot=True, cmap="jet" ,fmt='g')
ax.xaxis.set_label_position("top")
plt.tight_layout()
plt.title('Confusion matrix', y=1.1)
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
plt.xticks(tick_marks+0.5, class_names)
plt.yticks(tick_marks+0.5, class_names)
```

Out[22]:

```
([<matplotlib.axis.YTick at 0x7fa0ac480a50>,
  <matplotlib.axis.YTick at 0x7fa0ac4aa850>],
 [Text(0, 0.5, 'Undiagnosed'), Text(0, 1.5, 'Diabetes')])
```



In []: