

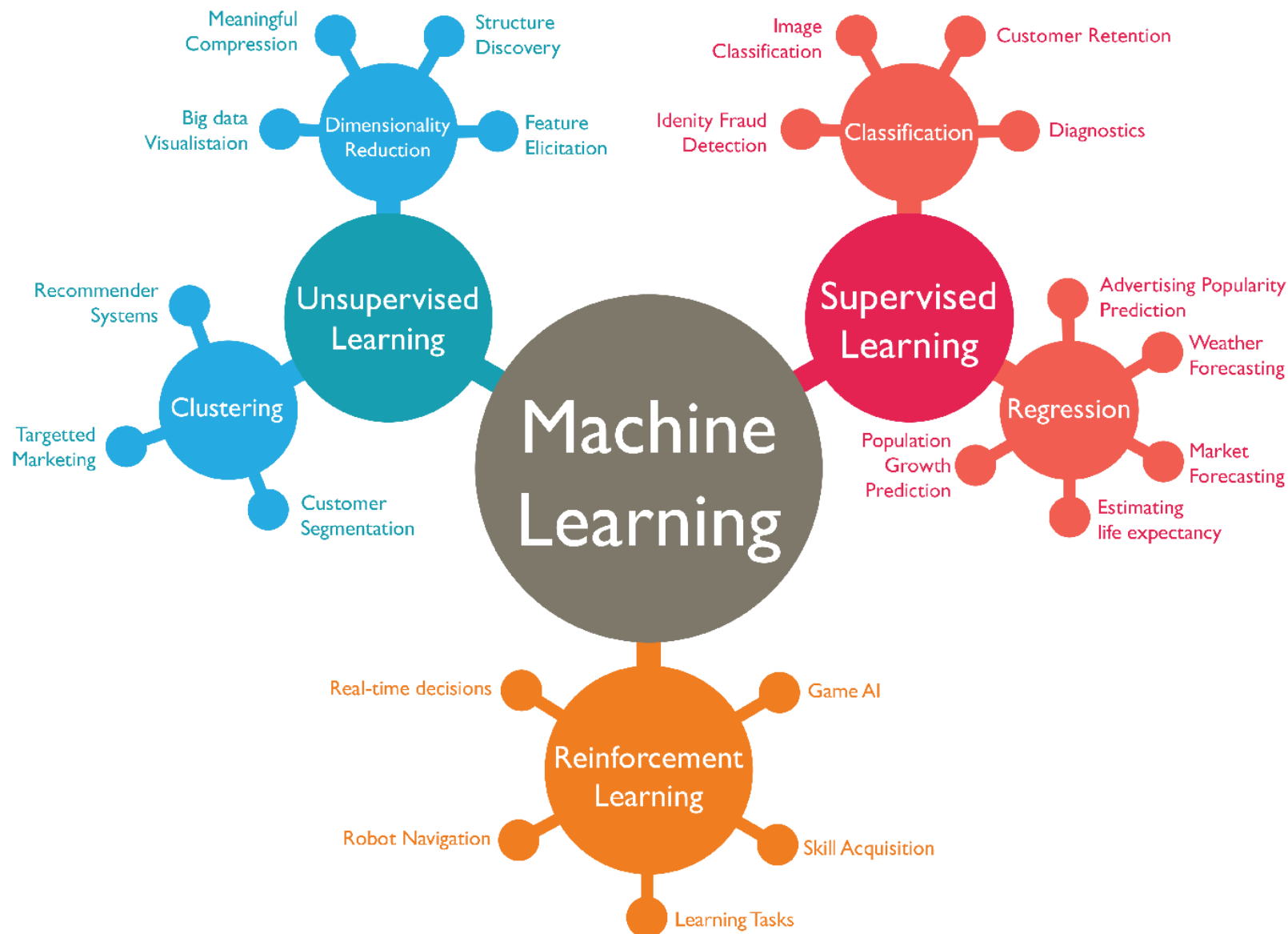
**Machine Learning**

**+**

**Programme Grant Update**

**Science Talk**

# Machine Learning Overview



## General Idea:

- Given a dataset with known labels ...
- “Train” a machine learning model using the dataset ...
- Then used the trained model to make predictions for new data which do not have labels

## Methods:

- Regression
- Random Forests, Support Vector Machines, K-Nearest Neighbor
- Deep Learning (Neural Networks)

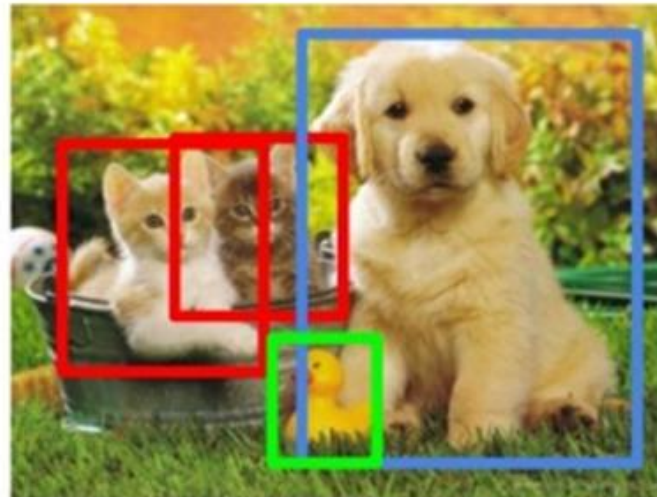
- Image related tasks are the most common problems for machine learning

## Classification



CAT

## Object Detection



CAT, DOG, DUCK

## Segmentation



CAT, DOG, DUCK

# Why These Tasks are Difficult?

What we see:

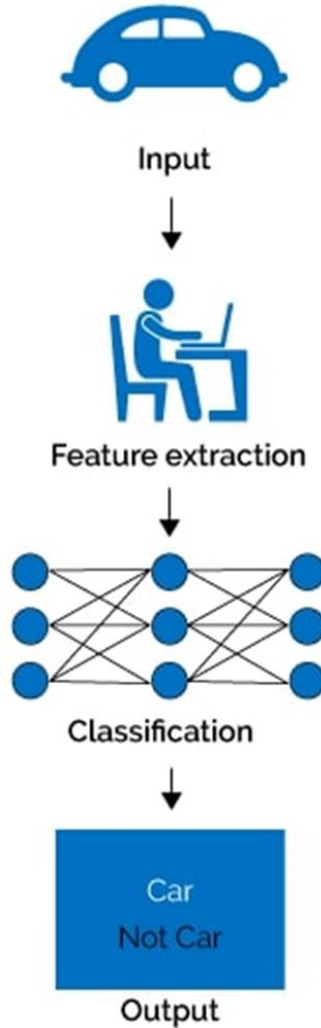


What the computer “sees”:

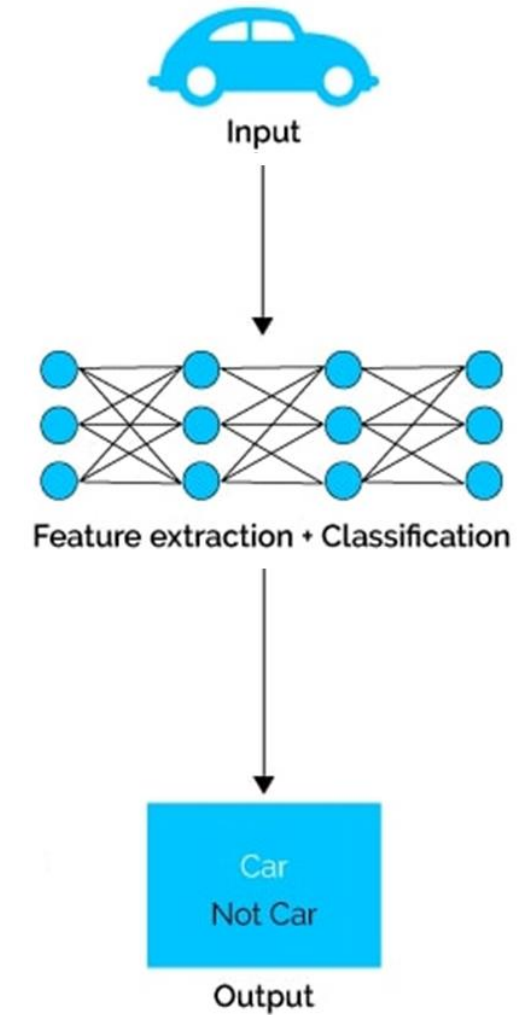
-1	-1	-1	-2	-1	1	0	-3	-2	0	4	-1	-2	-2	0	-1	-1	0	-2	-
-2	2	-1	-3	-2	-1	-1	-3	-2	-3	-1	5	0	-2	-3	1	0	-2	0	-
-3	0	-2	-3	-2	1	0	-4	-2	-3	-2	0	6	1	-3	0	0	0	1	-
-4	-1	-3	-3	-1	0	-1	-4	-3	-3	-2	-2	1	6	-3	0	2	-1	-1	-
-1	-3	-1	-2	-3	-1	-1	-2	-2	-1	0	-3	-3	9	-3	-4	-3	-3	-	-
-2	1	0	-3	-1	0	-1	-2	-1	-2	-1	1	0	0	-3	5	2	-2	0	-
-3	1	-2	-3	-1	0	-1	-3	-2	-2	-1	0	0	2	4	2	5	-2	0	-
-4	-2	-3	-3	-2	0	-2	-2	-3	-3	0	-2	0	-1	-3	-2	-2	6	-2	-
-3	-1	-2	-1	-2	-1	-2	-2	2	-3	-2	0	1	-1	-3	0	0	-2	8	-
2	-3	1	0	-3	-2	-1	-3	-1	3	-1	-3	-3	-3	-1	-3	-3	-4	-3	-
4	-2	2	0	-3	-2	-1	-2	-1	1	-1	-2	-3	-4	-1	-2	-3	-4	-3	-
-2	5	-1	-3	-1	0	-1	-3	-2	-2	-1	2	0	-1	-3	1	1	-2	-1	-
2	-1	5	0	-2	-1	-1	-1	-1	1	-1	-1	-2	-3	-1	0	-2	-3	-2	-
0	-3	0	6	-4	-2	-2	1	3	-1	-2	-3	-3	-3	-2	-3	-3	-3	-1	-
-3	-1	-2	-4	7	-1	-1	-4	-3	-2	-1	-2	-2	-1	-3	-1	-1	-2	-2	-
-2	0	-1	-2	-1	4	1	-3	-2	-2	1	-1	1	0	-1	0	0	0	-1	-
-1	-1	-1	-2	-1	1	5	-2	-2	0	0	-1	0	-1	-1	-1	-1	-2	-2	-
-2	-3	-1	1	-4	-3	-2	11	2	-3	-3	-3	-4	-4	-2	-2	-3	-2	-2	-
-1	-2	-1	3	-3	-2	-2	2	7	-1	-2	-2	-2	-3	-2	-1	-2	-3	2	-
1	-2	1	-1	-2	-2	0	-3	-1	4	0	-3	-3	-3	-1	-2	-2	-3	-3	-
-1	-1	-1	-2	-1	1	0	-3	-2	0	4	-1	-2	-2	0	-1	-1	0	-2	-
-2	2	-1	-3	-2	-1	-1	-3	-2	-3	-1	5	0	-2	-3	1	0	-2	0	-
-3	0	-2	-3	-2	1	0	-4	-2	-3	-2	0	6	1	-3	0	0	0	1	-
-4	-1	-3	-3	-1	0	-1	-4	-3	-3	-2	-2	1	6	-3	0	2	-1	-1	-
-1	-3	-1	-2	-3	-1	-1	-2	-2	-1	0	-3	-3	-3	9	-3	-4	-3	-3	-
-2	1	0	-3	-1	0	-1	-2	-1	-2	-1	1	0	0	-3	5	2	-2	0	-
-3	1	-2	-3	-1	0	-1	-3	-2	-2	-1	0	0	2	4	2	5	-2	0	-
-4	-2	-3	-3	-2	0	-2	-2	-3	-3	0	-2	0	-1	-3	-2	-2	6	-2	-
-3	-1	-2	-1	-2	-1	-2	-2	2	-3	-2	0	1	-1	-3	0	0	-2	8	-
2	-3	1	0	-3	-2	-1	-3	-1	3	-1	-3	-3	-3	-1	-3	-3	-4	-3	-
4	-2	2	0	-3	-2	-1	-2	-1	1	-1	-2	-3	-4	-1	-2	-3	-4	-3	-
-2	5	-1	-3	-1	0	-1	-3	-2	-2	-1	2	0	-1	-3	1	1	-2	-1	-
2	-1	5	0	-2	-1	-1	-1	-1	1	-1	-1	-2	-3	-1	0	-2	-3	-2	-
0	-3	0	6	-4	-2	-2	1	3	-1	-2	-3	-3	-3	-2	-3	-3	-3	-1	-
-3	-1	-2	-4	7	-1	-1	-4	-3	-2	-1	-2	-2	-1	-3	-1	-1	-2	-2	-

- It is difficult to come up with a set of “strict rules” to define image content
- Such tasks require the use of more sophisticated learning algorithms

## Machine Learning



## Deep Learning



## **Simple Neural Networks:**

- Used on 1-Dimensional Data

## **Convolutional Neural Networks:**

- Used on 2D or 3D Data (Images, Volumes, Videos)

## **Recurrent Neural Networks:**

- Used on Sequential Data (Text, Time-Series)



## Simple Neural Networks:

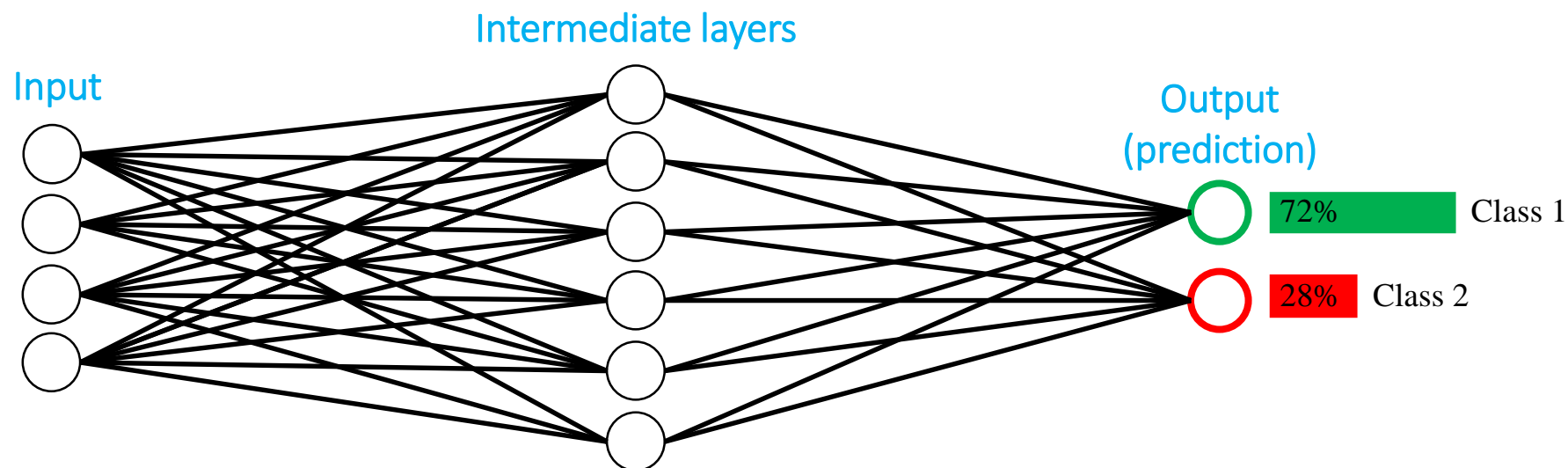
- Used on 1-Dimensional Data

## Convolutional Neural Networks:

- Used on 2D or 3D Data (Images, Volumes, Videos)

## Recurrent Neural Networks:

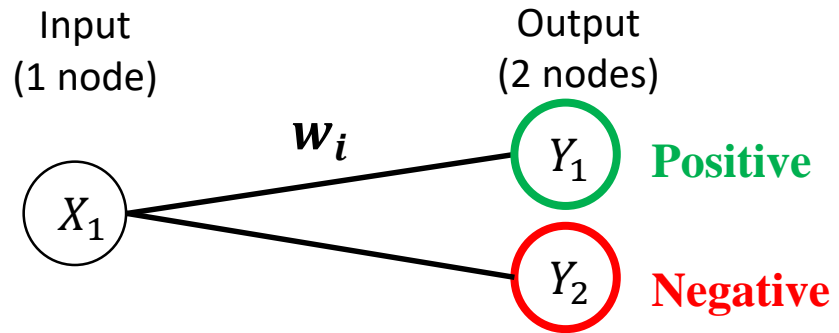
- Used on Sequential Data (Text, Time-Series)



- Given some **input** data,
- **Transform** the data through **intermediate** layers (number can be  $N \geq 0$  layers) (we can also have as many nodes as we want for the intermediate layers),
- So the **output** becomes the probability of being in each class

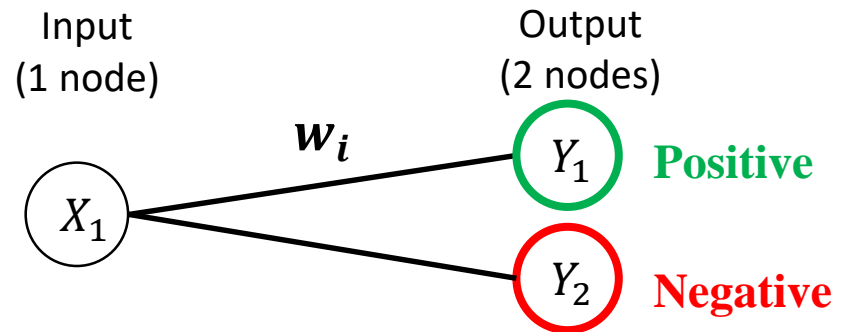
# How Transformations are Performed?

Starting with a (very) simple neural network:



# How Transformations are Performed?

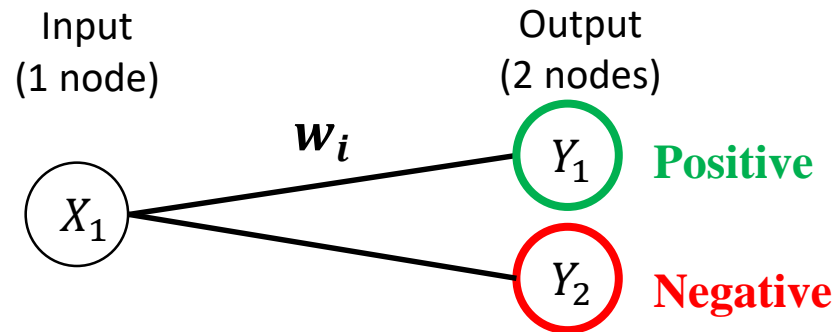
Starting with a (very) simple neural network:



**TASK:** given a single number at the input ( $X_1$ ), predict if its **positive** or **negative** (at the output,  $Y$ ).

# How Transformations are Performed?

Starting with a (very) simple neural network:



**TASK:** given a single number at the input ( $X_1$ ), predict if its **positive** or **negative** (at the output,  $Y$ ).

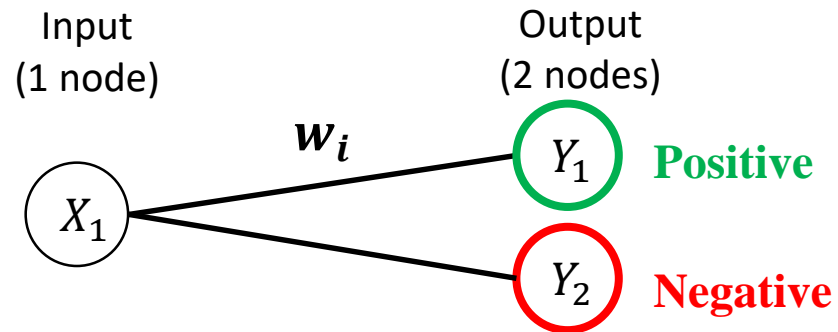
Ideally:

If  $x \geq 0$ , we would want  $[Y_1 \ Y_2] = [1 \ 0]$  (or any  $Y_1 > Y_2$ )

If  $x < 0$ , we would want  $[Y_1 \ Y_2] = [0 \ 1]$  (or any  $Y_1 < Y_2$ )

# How Transformations are Performed?

Starting with a (very) simple neural network:



**TASK:** given a single number at the input ( $X_1$ ), predict if its **positive** or **negative** (at the output,  $Y$ ).

Ideally:

If  $x \geq 0$ , we would want  $[Y_1 \ Y_2] = [1 \ 0]$  (or any  $Y_1 > Y_2$ )

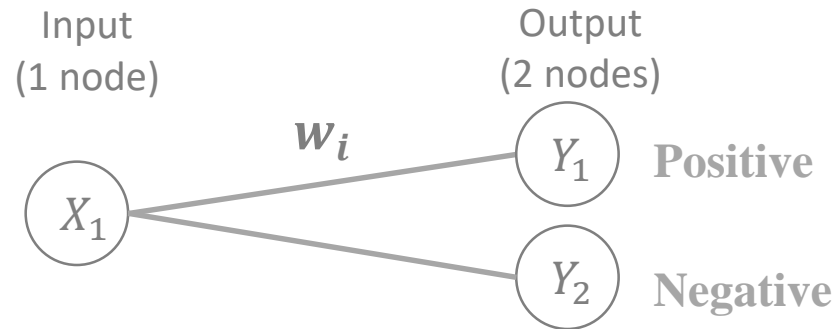
If  $x < 0$ , we would want  $[Y_1 \ Y_2] = [0 \ 1]$  (or any  $Y_1 < Y_2$ )

To transform the input (1 node) to the output (2 nodes), we can perform a matrix multiplication:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

# How Transformations are Performed?

Starting with a (very) simple neural network:



**TASK:** given a single number at the input ( $X_1$ ), predict if its **positive** or **negative** (at the output,  $Y$ ).

Ideally:

If  $x \geq 0$ , we would want  $[Y_1 \ Y_2] = [1 \ 0]$  (or any  $Y_1 > Y_2$ )

If  $x < 0$ , we would want  $[Y_1 \ Y_2] = [0 \ 1]$  (or any  $Y_1 < Y_2$ )

To transform the input (1 node) to the output (2 nodes), we can perform a matrix multiplication:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

*How do we choose which  $w$ 's get our desired  $Y$ 's ?*

# Training the Neural Network – An Optimization Problem

Equation from last slide:

$$[X_1][w_1 \quad w_2] = [Y_1 \quad Y_2]$$

- Set up an optimization problem to solve the values of **w**'s.



# Training the Neural Network – An Optimization Problem

Equation from last slide:

$$[X_1][w_1 \quad w_2] = [Y_1 \quad Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

Equation from last slide:

$$[X_1][w_1 \quad w_2] = [Y_1 \quad Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

Sample Training Set:

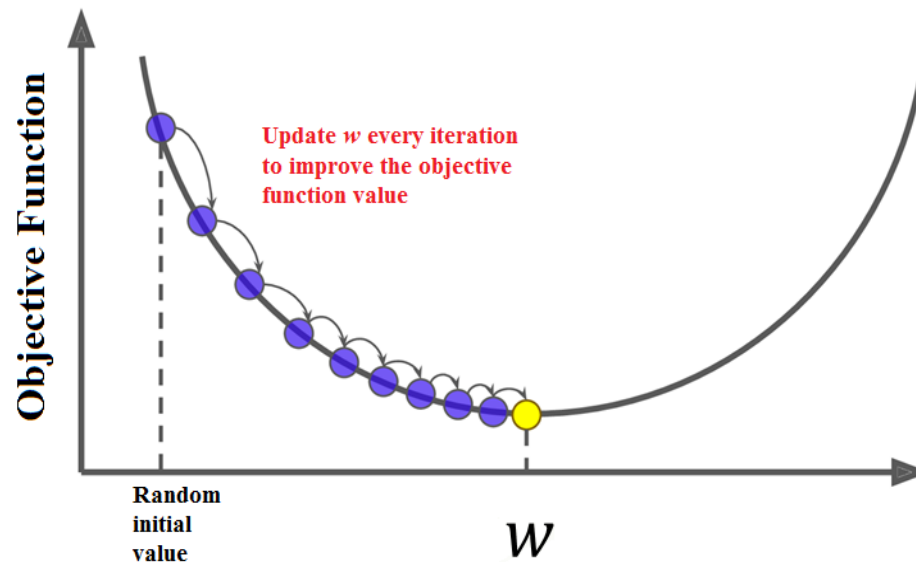
$X$ :	[3]		[-2]		[1]		[5]		[-1]		[-3]		[-2]		[2]		[1]	
$Y$ :	[1	0]	[0	1]	[1	0]	[1	0]	[0	1]	[0	1]	[0	1]	[1	0]	[1	0]

# Training the Neural Network – An Optimization Problem

Equation from last slide:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

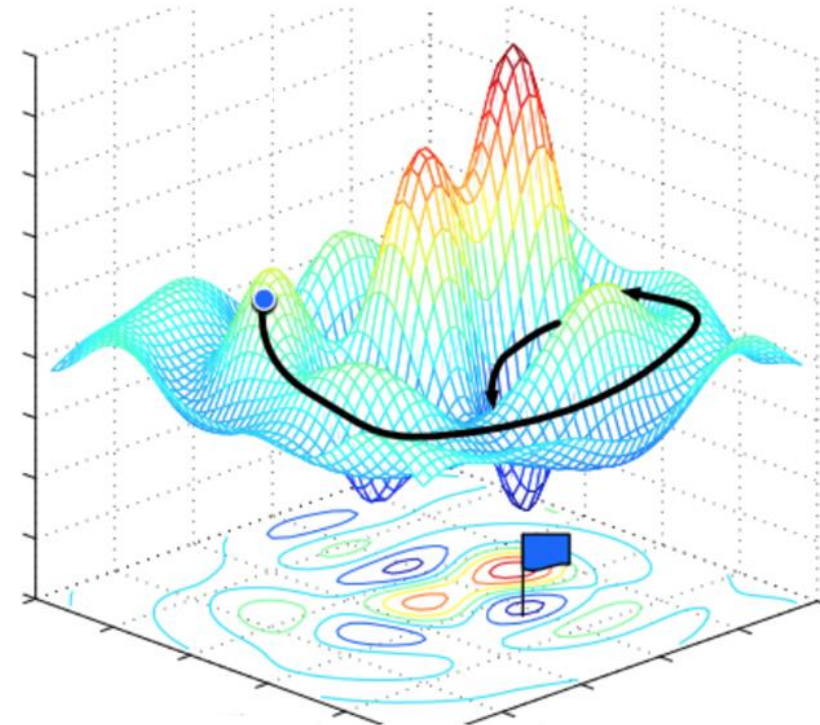
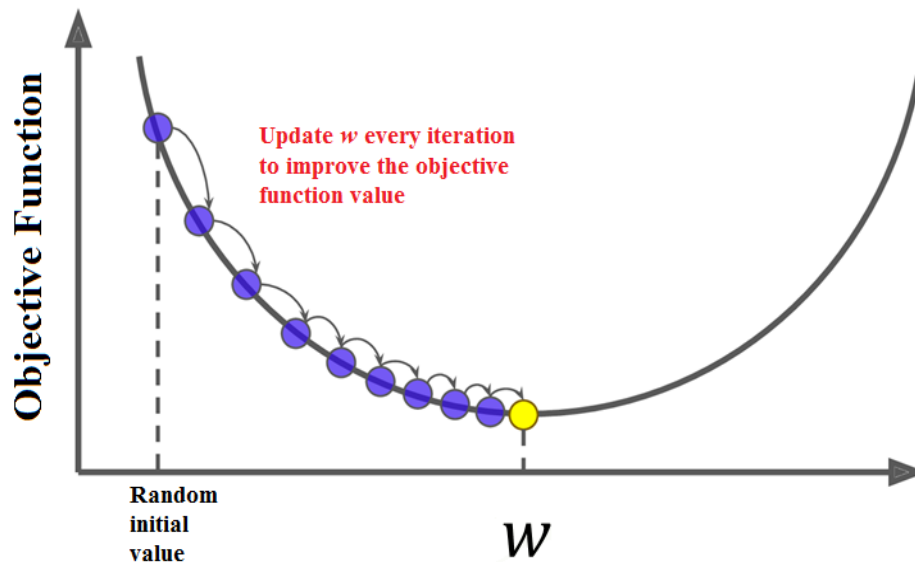


# Training the Neural Network – An Optimization Problem

Equation from last slide:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.



Equation from last slide:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

- Set up an optimization problem to solve the values of  $\mathbf{w}$ 's.
- Train the neural network with lots of  $\mathbf{X}$ 's and  $\mathbf{Y}$ 's so it can incrementally update  $\mathbf{w}$ 's with gradient descent each iteration.

This simple problem has many solutions for  $\mathbf{w}$ , e.g.  $[\mathbf{w}_1 \ \mathbf{w}_2] = [0.6 \ 0.4]$ (or any  $w_1 > w_2$ ).

Equation from last slide:

$$[X_1][w_1 \quad w_2] = [Y_1 \quad Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

This simple problem has many solutions for  $w$ , e.g.  $[w_1 \quad w_2] = [0.6 \quad 0.4]$  (or any  $w_1 > w_2$ ).

If we input  $X = 1$  and  $X = -1$ :

$$\begin{aligned} [1][0.6 \quad 0.4] &= [0.6 \quad 0.4] \quad (Y_1 > Y_2, \text{higher value for positive}) \\ [-1][0.6 \quad 0.4] &= [-0.6 \quad -0.4] \quad (Y_1 < Y_2, \text{higher value for negative}) \end{aligned}$$

Equation from last slide:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

This simple problem has many solutions for  $w$ , e.g.  $[w_1 \ w_2] = [0.6 \ 0.4]$  (or any  $w_1 > w_2$ ).

If we input  $X = 1$ :

$$[1][0.6 \ 0.4] = [0.6 \ 0.4]$$

Equation from last slide:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

This simple problem has many solutions for  $w$ , e.g.  $[w_1 \ w_2] = [0.6 \ 0.4]$  (or any  $w_1 > w_2$ ).

If we input  $X = 1$ :

$$[1][0.6 \ 0.4] = [0.6 \ 0.4]$$

$$\text{normalize: } \left[ \frac{e^{0.6}}{e^{0.6} + e^{0.4}} \quad \frac{e^{0.4}}{e^{0.6} + e^{0.4}} \right] = [0.550 \ 0.450]$$



# Training the Neural Network – An Optimization Problem

Equation from last slide:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

- Set up an optimization problem to solve the values of  $w$ 's.
- Train the neural network with lots of  $X$ 's and  $Y$ 's so it can incrementally update  $w$ 's with gradient descent each iteration.

This simple problem has many solutions for  $w$ , e.g.  $[w_1 \ w_2] = [0.6 \ 0.4]$  (or any  $w_1 > w_2$ ).

If we input  $X = 1$  and  $X = -1$ :

$$[1][0.6 \ 0.4] = [0.6 \ 0.4]$$

$$\text{normalize: } \left[ \frac{e^{0.6}}{e^{0.6} + e^{0.4}} \quad \frac{e^{0.4}}{e^{0.6} + e^{0.4}} \right] = [0.550 \ 0.450]$$

$$[-1][0.6 \ 0.4] = [-0.6 \ -0.4]$$

$$\text{normalize: } \left[ \frac{e^{-0.6}}{e^{-0.6} + e^{-0.4}} \quad \frac{e^{-0.4}}{e^{-0.6} + e^{-0.4}} \right] = [0.450 \ 0.550]$$

For our neural network:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

We have weights of:

$$[w_1 \ w_2] = [0.6 \ 0.4]$$

- What is our output if the input is  $X_1 = 0$ ?

For our neural network:

$$[X_1][w_1 \ w_2] = [Y_1 \ Y_2]$$

We have weights of:

$$[w_1 \ w_2] = [0.6 \ 0.4]$$

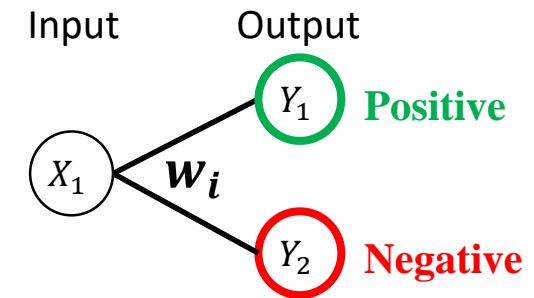
- What is our output if the input is  $X_1 = 0$ ?

$$[X_1][w_1 \ w_2] = [0][0 \ 0]$$

$$[Y_1 \ Y_2] = \left[ \frac{e^0}{e^0 + e^0} \quad \frac{e^0}{e^0 + e^0} \right] = [0.5 \ 0.5]$$

# Coding the Example in Python

```
# import the packages we will be needing  
import tflearn
```

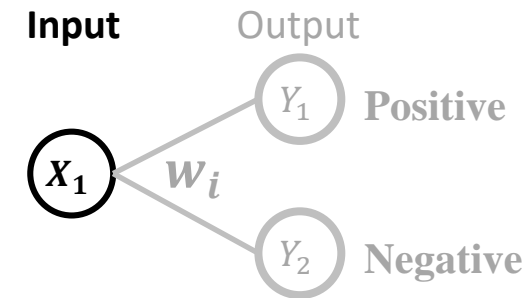


# Coding the Example in Python

```
# import the packages we will be needing  
import tflearn
```

```
# define the input layer (1 node)
```

```
X_i = tflearn.input_data(shape=[None, 1])
```

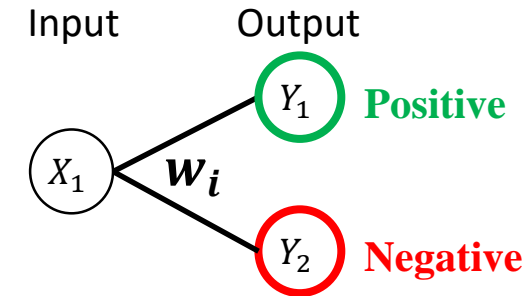


# Coding the Example in Python

```
# import the packages we will be needing  
import tflearn
```

```
# define the input layer (1 node)  
X_i = tflearn.input_data(shape=[None, 1])
```

```
# define the output layer (2 nodes), softmax normalizes values between 0/1  
Y_j = tflearn.fully_connected(X_i, n_units=2, activation='softmax')
```

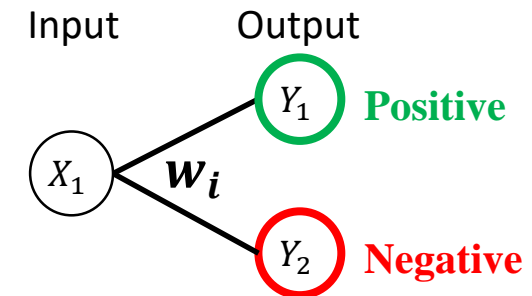


# Coding the Example in Python

```
# import the packages we will be needing  
import tflearn
```

```
# define the input layer (1 node)  
X_i = tflearn.input_data(shape=[None, 1])
```

```
# define the output layer (2 nodes), softmax normalizes values between 0/1  
Y_j = tflearn.fully_connected(X_i, n_units=2, activation='softmax')
```



**We don't need to define  $w_i$**

# Coding the Example in Python

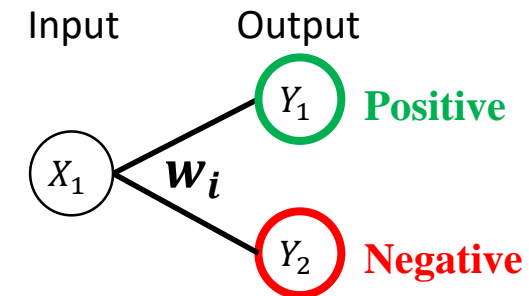
```
# import the packages we will be needing  
import tflearn
```

```
# define the input layer (1 node)  
X_i = tflearn.input_data(shape=[None, 1])
```

```
# define the output layer (2 nodes), softmax normalizes values between 0/1  
Y_j = tflearn.fully_connected(X_i, n_units=2, activation='softmax')
```

```
# set up optimization problem (sgd = stochastic gradient descent)  
optimization_problem = tflearn.regression(Y_j, optimizer="sgd")
```

```
# initialize variables w_i with random values to provide a starting point for optimization  
model = tflearn.DNN(optimization_problem)
```





# Coding the Example in Python

```
# import the packages we will be needing
import tflearn
```

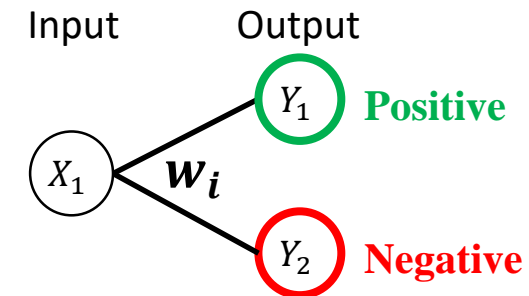
```
# define the input layer (1 node)
X_i = tflearn.input_data(shape=[None, 1])
```

```
# define the output layer (2 nodes), softmax normalizes values between 0/1
Y_j = tflearn.fully_connected(X_i, n_units=2, activation='softmax')
```

```
# set up optimization problem (sgd = stochastic gradient descent)
optimization_problem = tflearn.regression(Y_j, optimizer="sgd")
```

```
# initialize variables w_i with random values to provide a starting point for optimization
model = tflearn.DNN(optimization_problem)
```

```
# train the model (assuming we have some data) for 100 iterations, update w every iteration
model.fit(data, label, n_epoch=100)
```



# Coding the Example in Python

```
# import the packages we will be needing
import tflearn
```

```
# define the input layer (1 node)
X_i = tflearn.input_data(shape=[None, 1])
```

```
# define the output layer (2 nodes), softmax normalizes values between 0/1
Y_j = tflearn.fully_connected(X_i, n_units=2, activation='softmax')
```

```
# set up optimization problem (sgd = stochastic gradient descent)
optimization_problem = tflearn.regression(Y_j, optimizer="sgd")
```

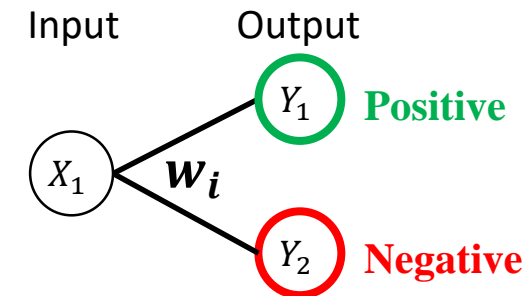
```
# initialize variables w_i with random values to provide a starting point for optimization
model = tflearn.DNN(optimization_problem)
```

```
# train the model (assuming we have some data) for 100 iterations, update w every iteration
model.fit(data, label, n_epoch=100)
```

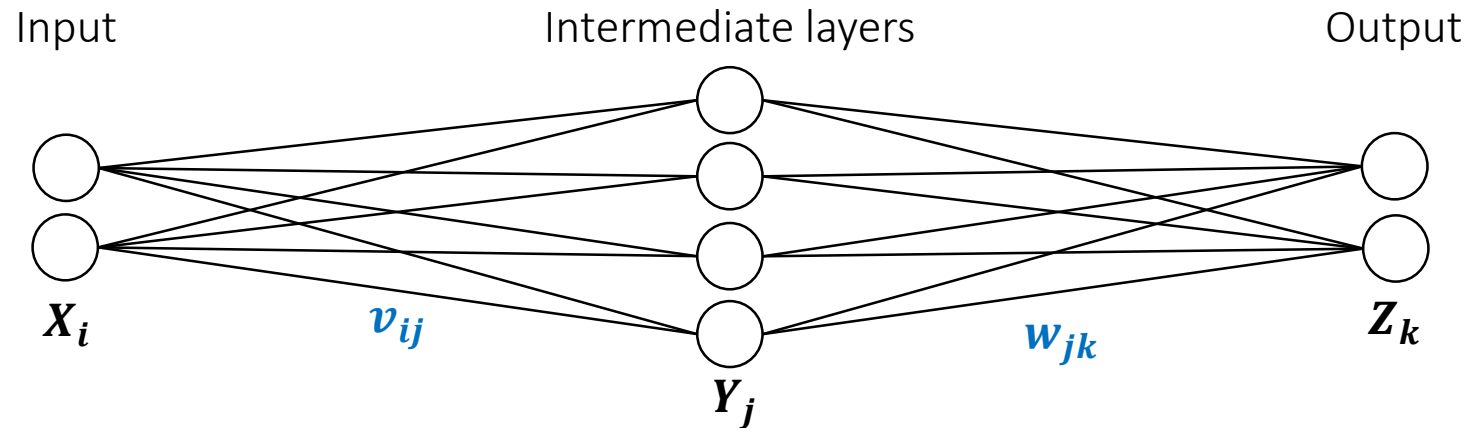
```
# make a prediction
```

```
print( model.predict([[1]]) )    # should get Y1 > Y2 (output = [Y1, Y2])
```

```
print( model.predict([[-1]]) )   # should get Y1 < Y2 (output = [Y1, Y2])
```



# More Complicated Neural Network



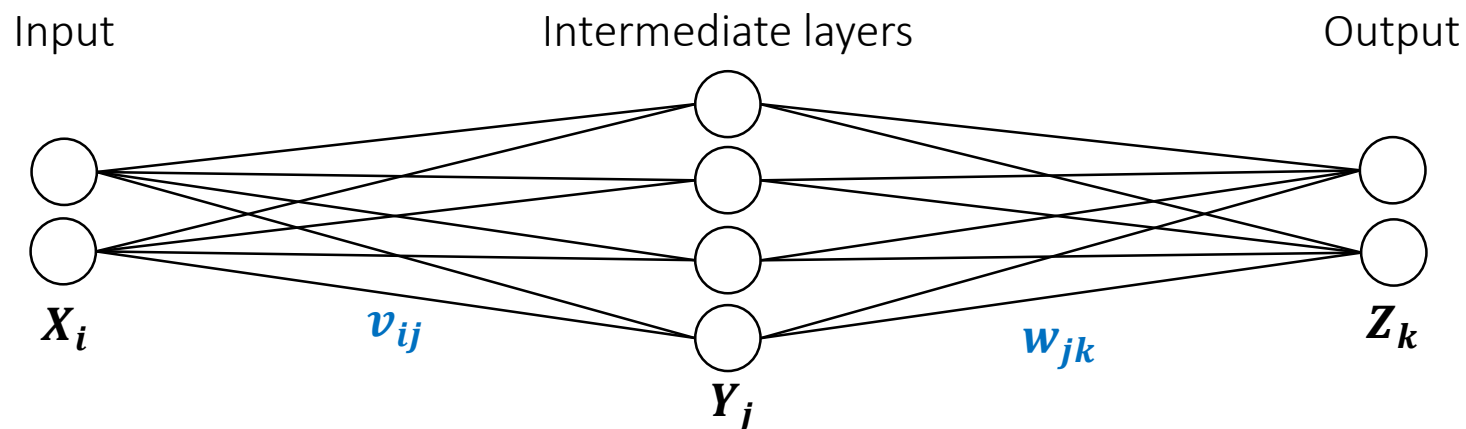
To map  $X_i \rightarrow Y_j$ :

$$\begin{bmatrix} X_1 & X_2 \end{bmatrix} \begin{bmatrix} v_{11} & v_{12} & v_{13} & v_{14} \\ v_{21} & v_{22} & v_{23} & v_{24} \end{bmatrix} = \begin{bmatrix} Y_1 & Y_2 & Y_3 & Y_4 \end{bmatrix}$$

To map  $Y_j \rightarrow Z_k$ :

$$\begin{bmatrix} Y_1 & Y_2 & Y_3 & Y_4 \end{bmatrix} \begin{bmatrix} w_{11} & w_{12} \\ w_{21} & w_{22} \\ w_{31} & w_{32} \\ w_{41} & w_{42} \end{bmatrix} = \begin{bmatrix} Z_1 & Z_2 \end{bmatrix}$$

# More Complicated Neural Network



To map  $X_i \rightarrow Y_j$ :

$$\begin{bmatrix} X_1 & X_2 \end{bmatrix} \begin{bmatrix} v_{11} & v_{12} & v_{13} & v_{14} \\ v_{21} & v_{22} & v_{23} & v_{24} \end{bmatrix} = \begin{bmatrix} Y_1 & Y_2 & Y_3 & Y_4 \end{bmatrix}$$

To map  $Y_j \rightarrow Z_k$ :

$$\begin{bmatrix} Y_1 & Y_2 & Y_3 & Y_4 \end{bmatrix} \begin{bmatrix} w_{11} & w_{12} \\ w_{21} & w_{22} \\ w_{31} & w_{32} \\ w_{41} & w_{42} \end{bmatrix} = \begin{bmatrix} Z_1 & Z_2 \end{bmatrix}$$

Transformations are done with  
matrix multiplications

**Mid Session Break**

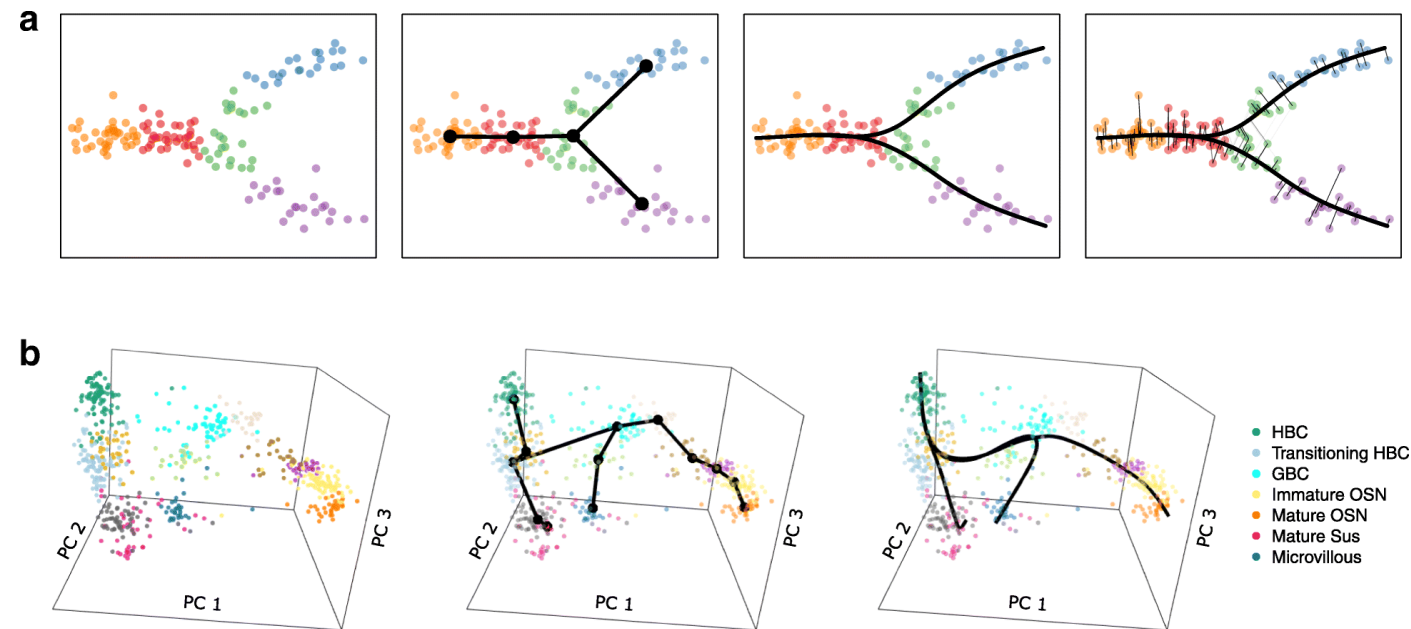
## **Background:**

- Hypertension contributes to increased risk of stroke and heart attack
- Early detection of hypertension may aid the development of preventative measures
- We aim to identify trends and early indicators for hypertension to quantify progression in a population-wide dataset

- In a population-level cohort (such as the UK Biobank), participants fit into different stages of disease progression and represent the entire healthy-to-disease scale
- Build a pseudo-temporal model using cross-sectional data to study the changes/progression of various biomarkers in patients from healthy to diseased
- Assign a score (0 to 1) to reflect the degree of disease, in our case the severity of hypertension
- “Trajectory inference” is the main method used

# Trajectory Inference

- Pseudo-temporal modelling to score patients based on their disease progression
- Fits patients on “trajectories” of disease progression
- Each trajectory may relate to changes in different combinations of biomarkers
- Trajectory inference 2 main steps:
  - Dimensionality reduction of features
  - Connect each patient in the reduced dimensional space to form a minimum spanning tree

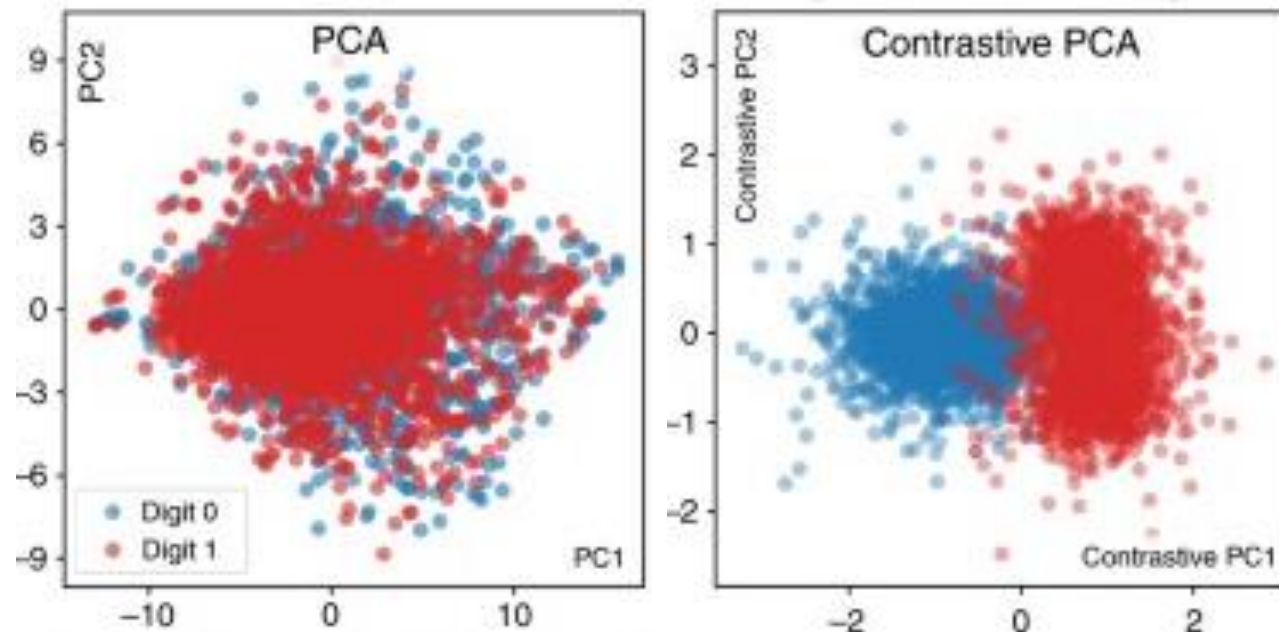




## Contrastive Trajectory Inference (cTI)

---

- “Contrastive” trajectory inference method to improve separation of pre-defined groups
- Incorporate prior information (background/between/diseased) during the dimensionality reduction step of trajectory inference



## Contrastive Trajectory Inference (cTI) – Dimensionality Reduction

---

- Contrastive PCA (cPCA) for dimensionality reduction:

### PCA:

- Standard PCA is done by first computing the covariance matrix ( $cov$ )
- Then perform eigen decomposition on the covariance matrix to transform features into a reduced representation

### cPCA:

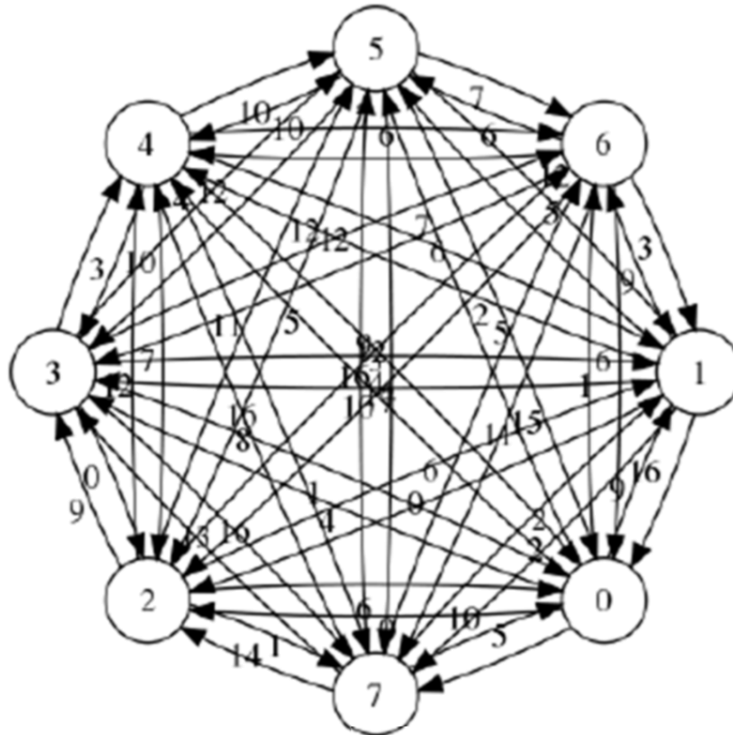
- cPCA is performed by computing a weighted sum between the covariance of the background ( $cov_b$ ) and diseased ( $cov_d$ ) group over a range of  $\alpha$ 's (~100 values from  $10^{-2}$  to  $10^2$ ):

$$cov = cov_d - \alpha \times cov_b$$

- Perform eigen decomposition for each of these resulting covariance matrices
- Determine the optimal  $\alpha$  using K-means clustering to find the value which produces the best clustering tendency of the background and disease groups in the reduced space

## Contrastive Trajectory Inference (cTI) – Trajectory Construction

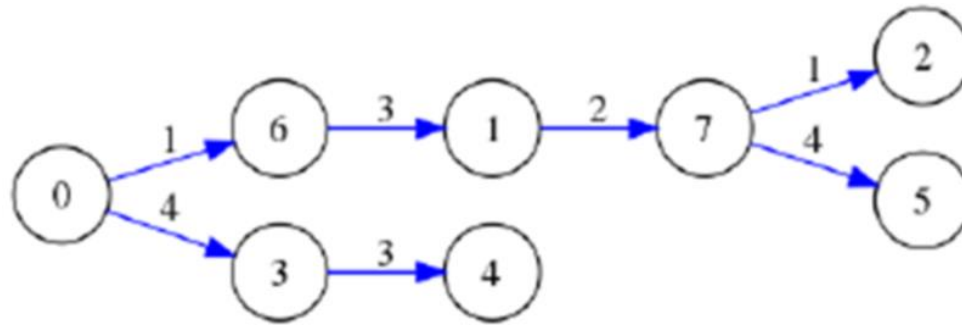
- Consider each individual as a “node” in a complete graph in the contrastive principle component space (cPC)
- Edge of the graph are defined by the Euclidean distance between nodes in the cPC space
- Define “*root node*” as the node with the smallest overall distance in the cPC space from all nodes in the population



## Contrastive Trajectory Inference (cTI) – Pseudo Time Score Calculation

---

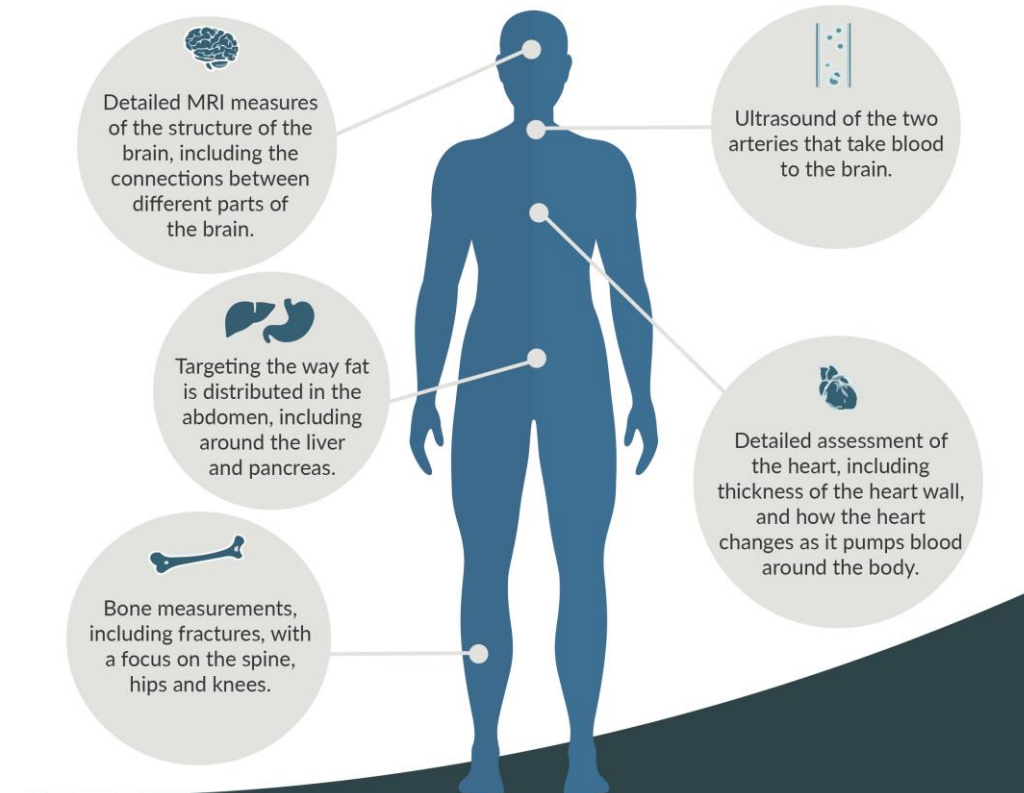
- Construct a minimum spanning tree which minimizes the overall distance between all nodes
- Find the shortest path between each node and the root node
- The disease (pseudo time) score is the normalized distance along the shortest path



- UK Biobank has around 500,000 participants from the general population
- 100,000 of these participants are planned to undergo medical imaging (cardiac MRI + brain MRI + carotid ultrasound)
- UK Biobank contains ~15,000 features for each patient
- Imaging patient dataset contains **~30,000** participants with **~2,000** imaging features
- Aim:
  - Investigate the progression/change in features from the normotensive population to the hypertensive population

**Find more details below on the scans we do when you visit the imaging centre**

The assessment lasts about 4-5 hours and involves imaging the heart, brain, abdomen and bones plus the collection of more information about health and lifestyle, and a donation of blood.



## Data Pre-Processing

---

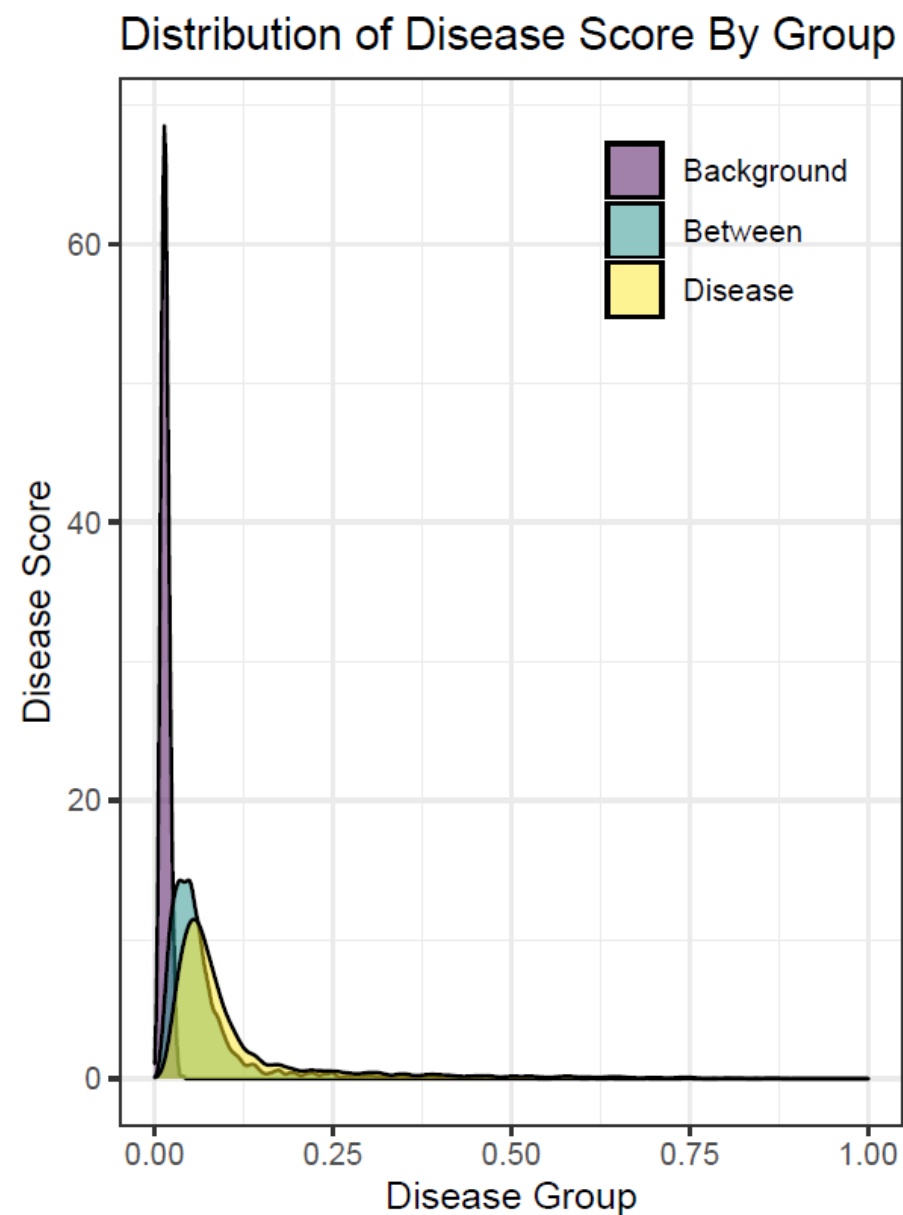
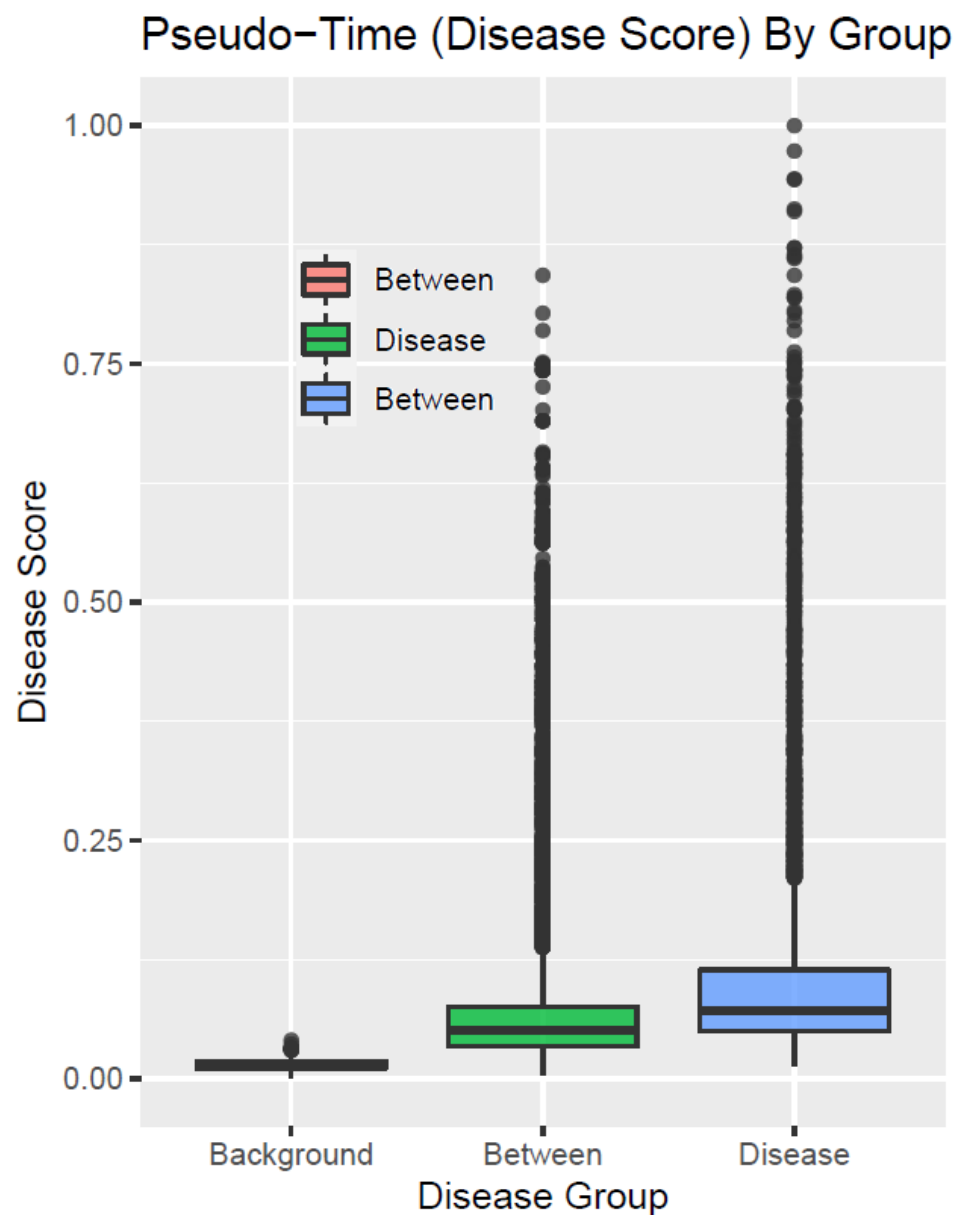
- Filter out patients without blood pressure readings
- Filter out variables which are not related to imaging/baseline measures
- Remove participants who have already experienced a heart attack, angina or stroke before the time of imaging
- Filter columns/rows with too many missing values
- Remove outliers
- Perform z-score normalization
- Adjust for age/sex

## Data Label Definition

---

- Define blood pressure groups
  - Background:  $< 120/80$  (both)
  - Disease:  $> 160/100$  (either)
  - Between: Any patient otherwise
- Tightening “background” group definition
  - Remove patients already diagnosed with high blood pressure
  - Remove patients on blood pressure medication
  - Remove patients that had a high blood pressure reading at any stage (3 visits)
- The final data frame has **27,338** (participants) with **1,086** (features)
- Distribution of samples: background = 1,380, Between = 21,759, Disease = 4,199

# Main Results – Pseudotime Score



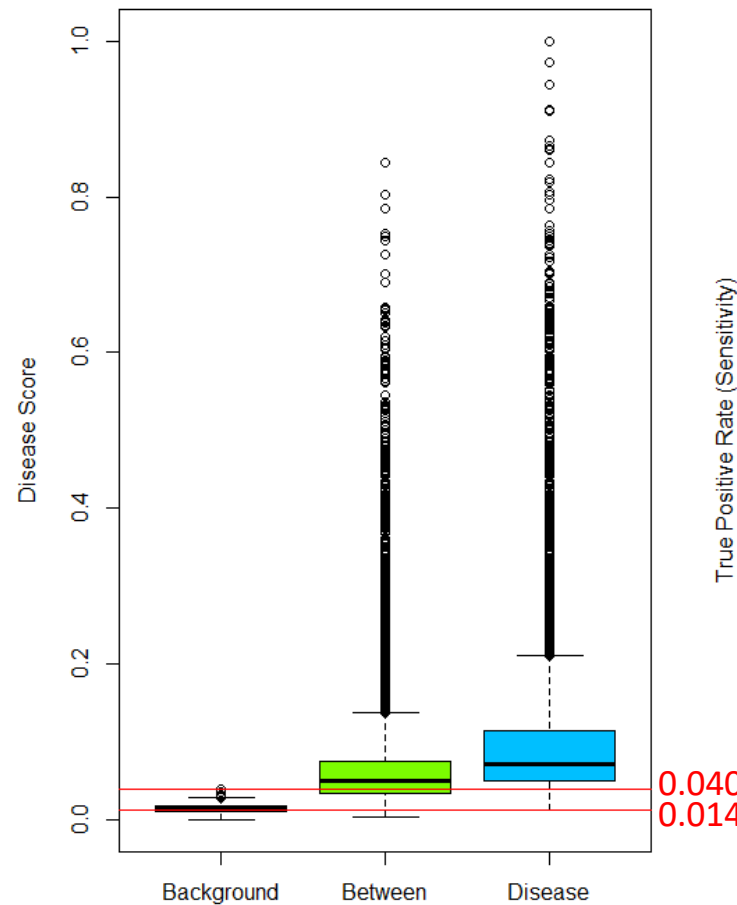


## Evaluating the Accuracy of the cTI Model

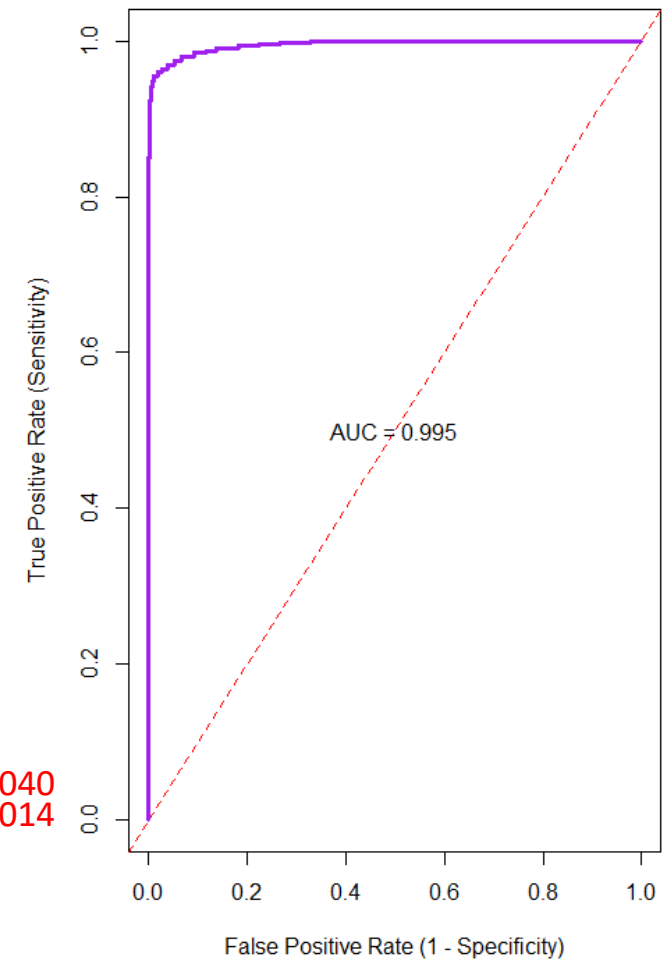
- AUC of 99.5% for distinguishing between “background” and “diseased”
- Sensitivity = 96.4%
- Specificity = 97.2%
- Optimal threshold = 0.027

		Ground Truth	
		Background	Disease
Prediction	Background	96.4	2.8
	Disease	3.6	97.2

Distribution of Disease Scores Between Groups

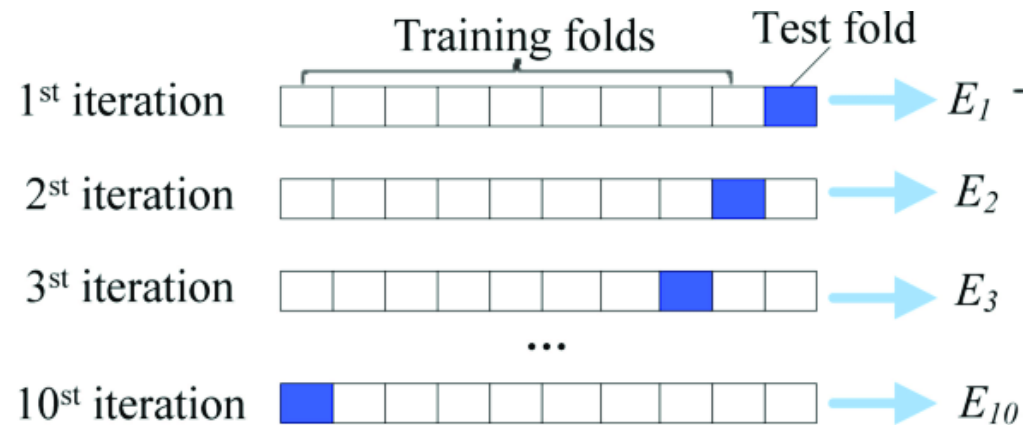


ROC (Receiver Operating Characteristic) Curve



## Evaluating the Stability of the cTI Model

- Run the cTI model on 100% of the data to produce the set of baseline disease scores
- Split dataset into 90:10 splits
- Run cTI on 90% of the data to generate disease, ignore the 10% left out
- Compare the scores generated from the subset dataset with those obtained from the full dataset



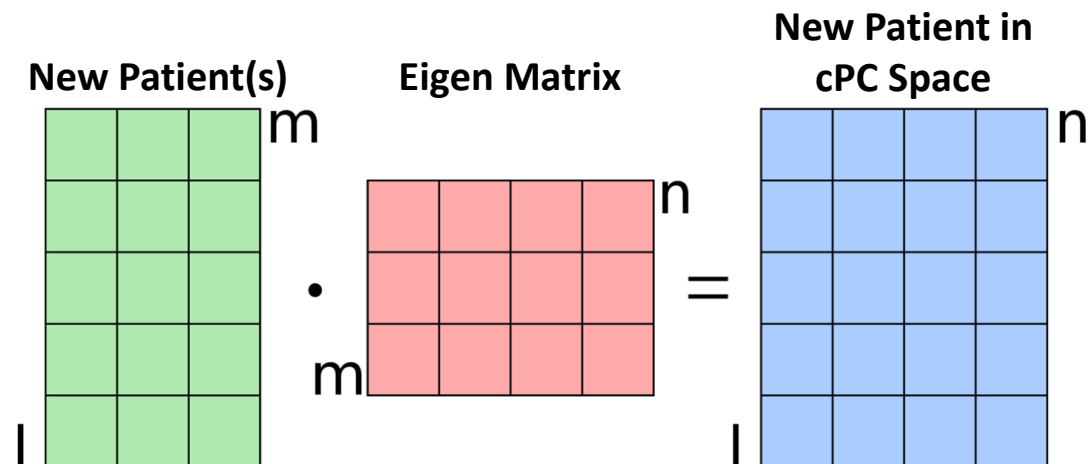
- Repeat this for every 90:10 split (10-fold cross validation)
- Overall 10-fold validation resulted in an **RMSE of 0.04 (sd = 0.004)**

- Place new patient in the current trajectory map from the existing cTI model
  - cTI generates a reduced representation (cPC) for the existing data
  - Transform new patient into the existing cPC space of the current cTI model
  - “Infer” the disease score as the score of the patient in the existing model with the smallest distance from a new patient in the cPC space
- Advantages:
  - Don’t need to re-run cTI model
  - Nearest neighbor is easy to quantify when there are only ~15 cPCs

## Implementation of cPC Transformation

- Equation of transformation in/out of the cPC space:
  - $X_{cPC} = X * Eig(cov_d - \alpha \times cov_b)$  (matrix multiplication with the most optimal  $\alpha$ )
  - The eigen matrix above is generated when building the cTI model, and can be stored as an intermediary value
  - New patients can be mapped into the cPC space with:

$$X_{cPC\ New} = X_{New} * Eig(cov_d - \alpha \times cov_b)$$



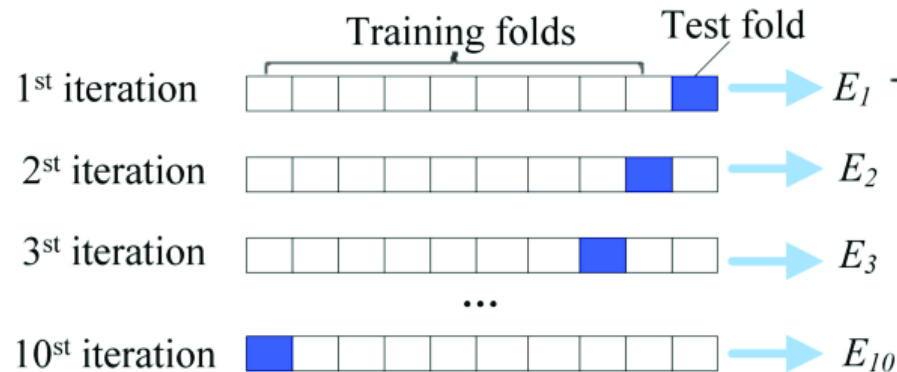
## Implementation of cPC Transformation

---

- The transformed data for the new patient can then be compared with  $X_{cPC}$  to find the sample in the existing model with the closest Euclidean distance
- Disease score can then be inferred directly from the nearest existing sample

## Experimental Setup for Evaluating the “Prediction” Method

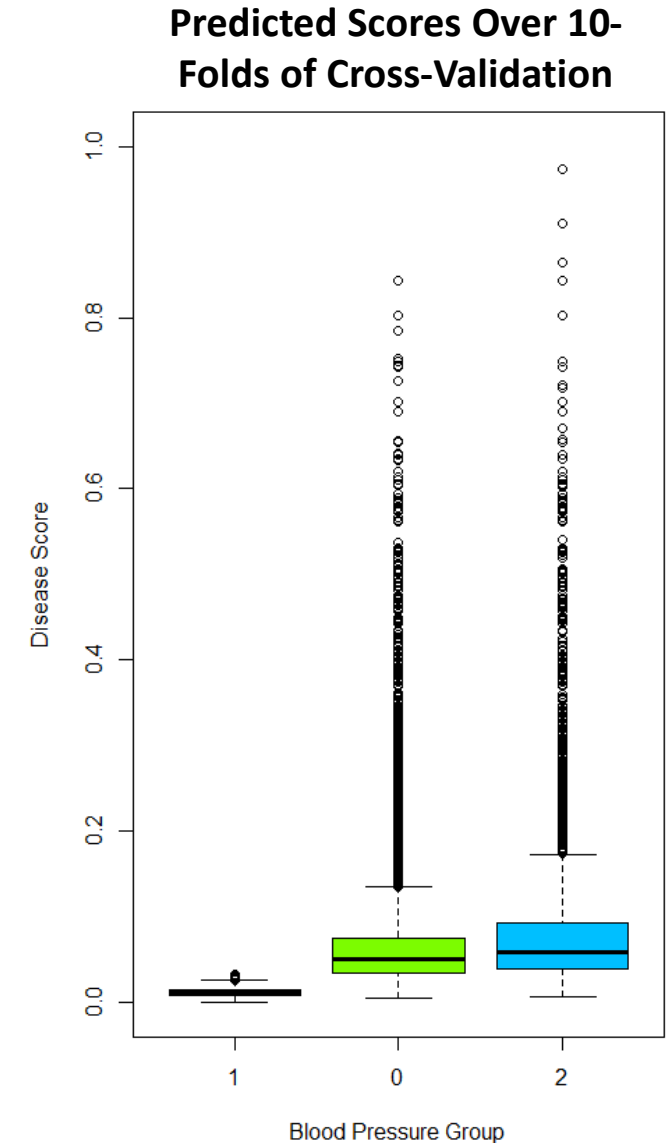
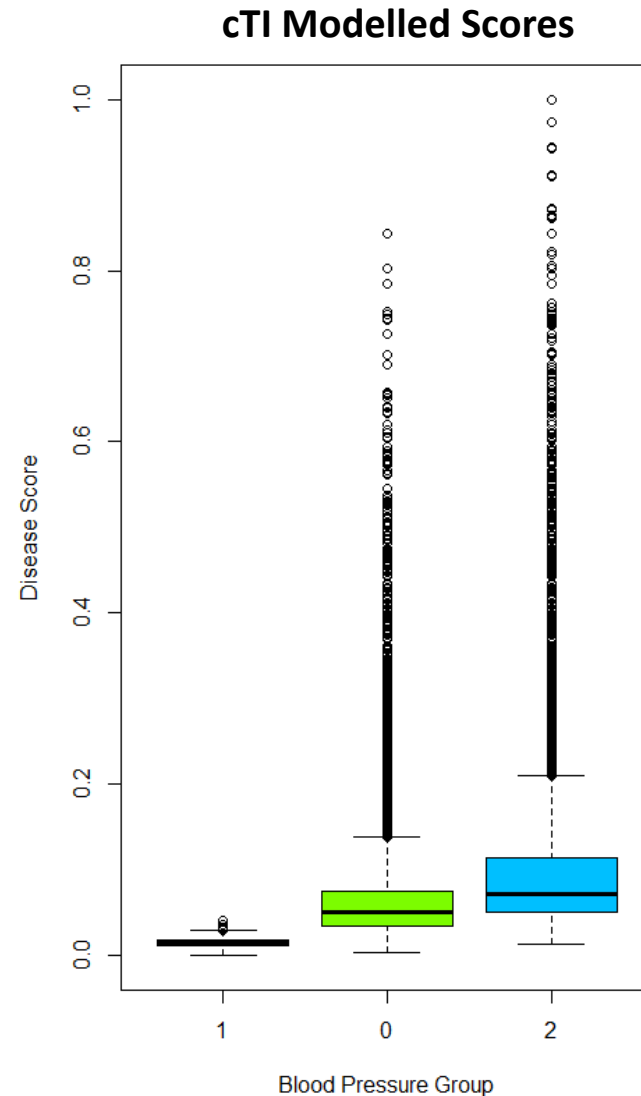
- Run the cTI model on 100% of the data to produce the set of baseline disease scores
- Split the data into 90% (training) and 10% (testing)
- Use the 90% to train the cTI model
- Use the proposed prediction approach to predict the 10% left out



- Compare the predicted scores of the 10% with scores of the same patient in the 100% run
- Repeat this for every 90:10 split (10-fold cross validation)

## Experimental Results for “Prediction” Method

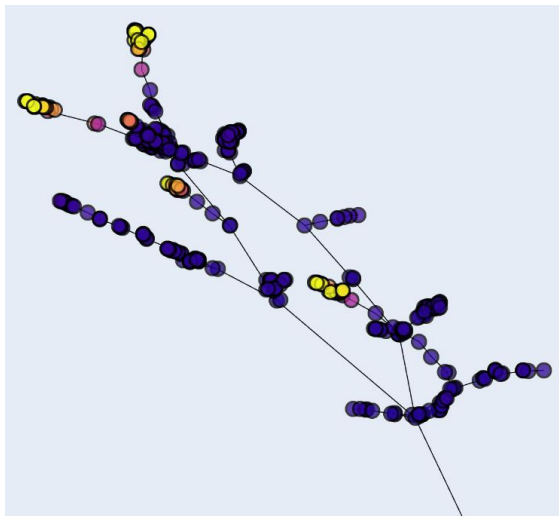
- 10-fold cross validation resulted in an **RMSE of 0.043**
- Errors for each group were:
  - Background = **0.018 RMSE**
  - Between = **0.085 RMSE**
  - Disease = **0.094 RMSE**



# Trajectories – Preliminary Results

- Compute the Laplacian of the matrix representation of the minimum spanning tree
- Perform eigen decomposition on the Laplacian, the coordinates are thus the first two eigen vectors

Zoomed in Section

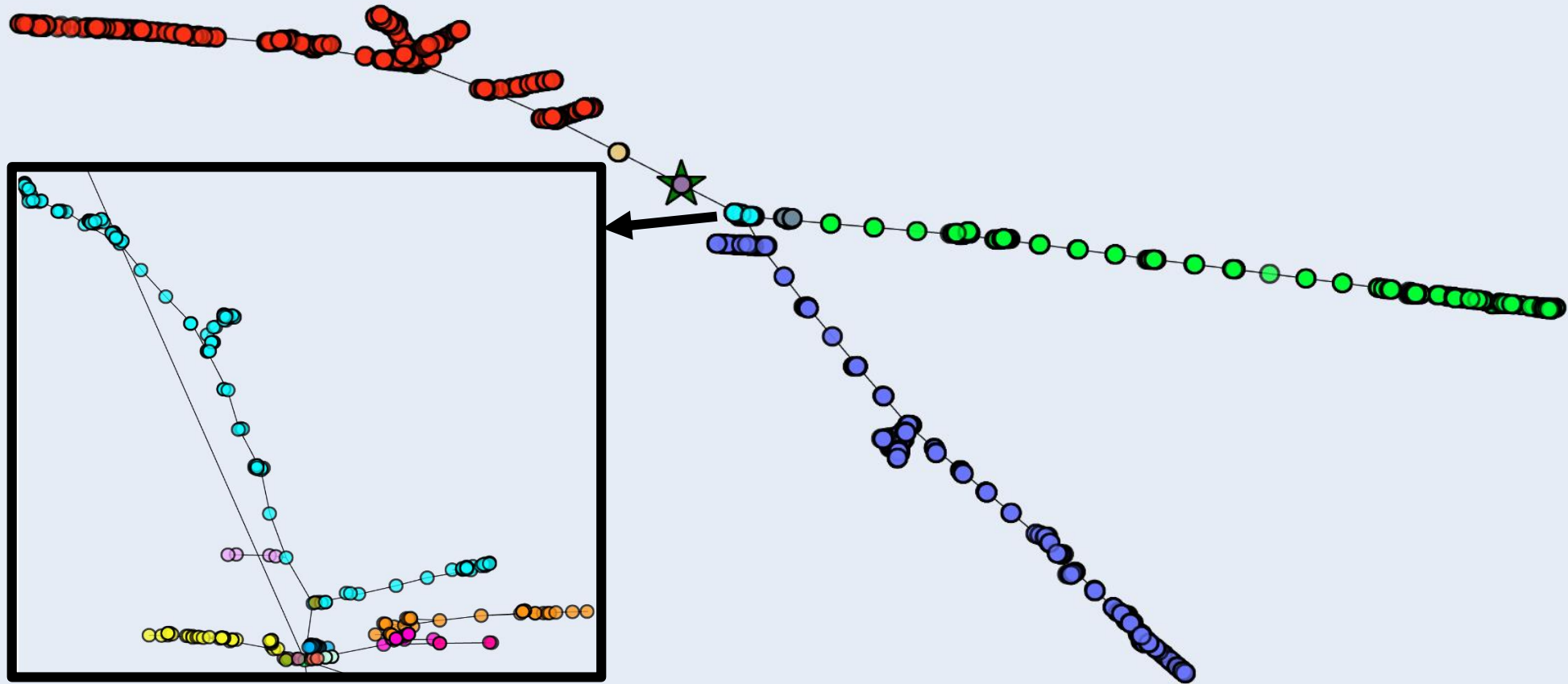




# Trajectories – Preliminary Results

- Color each unique trajectory
- Many “unique” trajectories close to the root node due to low overlap

Disease Trajectory Map of Patients in the UK Biobank



## **Contrastive Trajectory Inference Model:**

- Improve score distribution in the model output

## **Understanding cTI Model:**

- Explore which variables contribute to elevated scores
- Explore the change in these variables from healthy to disease

## **Trajectory Investigation:**

- Develop method to assign patients to a small number of “main” trajectories
- Explore which variables are more significant in different trajectories