

# L08-18-10-31-Supervised-ML

November 12, 2018

## 0.1 Supervised Learning

Machine learning has a few flavors of problems. We can think of it as ways to THINK about a problem. If we can think about a problem in this way, it gives us a framework to solve it. Suppose we have a random variable we can observe like height  $H$ , and a variable we want to predict like gender  $G$ . We know that *height* doesn't determine gender, there are tall women and short men. Lets say we measure somebodys hight as 67 inches and we want a predictor to estimate gender. Suppose we can compute a probability  $P(G|H)$ . Then if we plug in what we know (and assume men and women are equal in the population) ... we have numbers  $A$  and  $B$ .

$$A = P(G = \text{Male}|H = 67), B = P(G = \text{Female}|H = 67)$$

Then if  $A > B$  then it is more probable that the person is male and if  $B > A$  then it is more likely it is a women. We can say this as

$$G^* = \operatorname{argmax}_G P(G|H = 67)$$

So  $G^*$  is formally our best guess. We don't have lots of data on people who are exactly 67 inches tall so we need to flip this a bit using Bayes formula. It follows from  $P(G, H) = P(G|H) * P(H) = P(H|G) * P(G)$

$$P(G|H) = P(H|G) * P(G) / P(H)$$

Now we are going to be told that  $H = 171$  so when we compare  $G = \text{Male}$  and  $G = \text{Female}$ , it doesn't matter what  $P(H)$  is in terms of if  $A > B$  or  $B > A$ . Also we are going to assume  $P(G)$  is equal so again, since it is the same for both sides, it doesn't matter. So all we need to do is compute  $P(H|G)$  which is easier. Why? Because this is the distribution of Men's heights and separately the distribution of Women's heights. We can estimate that somehow (assume normal ... whatever).

```
In [1]: %matplotlib inline
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import sklearn

In [35]: df = pd.read_csv('weight-height.csv')
df.head()
```

```
Out[35]:
```

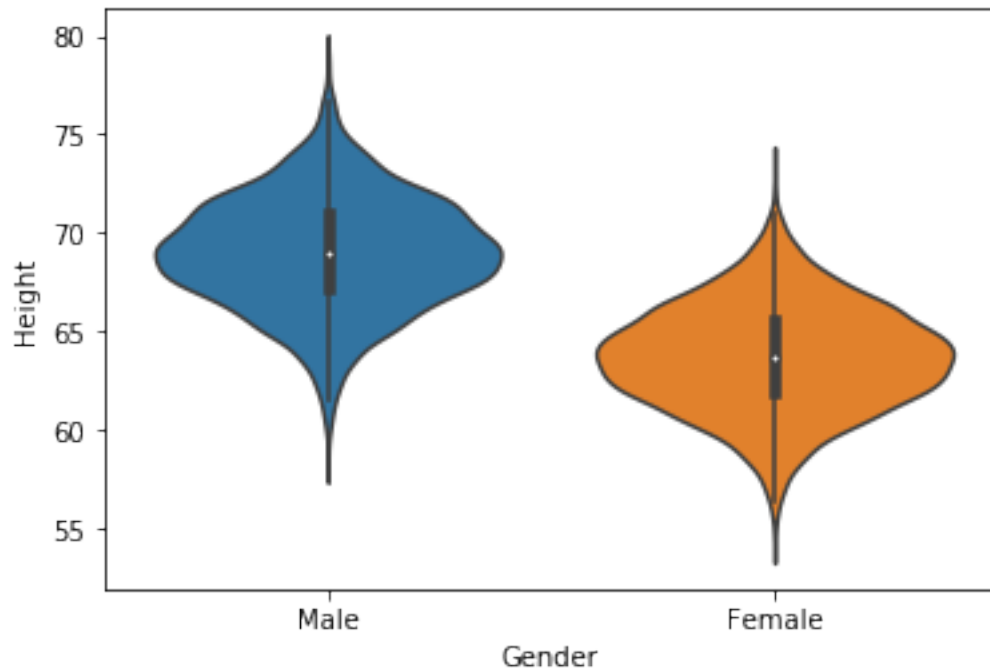
	Gender	Height	Weight
0	Male	73.847017	241.893563
1	Male	68.781904	162.310473
2	Male	74.110105	212.740856
3	Male	71.730978	220.042470
4	Male	69.881796	206.349801

```
In [40]: import seaborn as sns
```

```
In [41]: sns.violinplot(x='Gender', y='Height', data=df[['Gender', 'Height']])
```

```
/opt/tljh/user/lib/python3.6/site-packages/scipy/stats/stats.py:1713: FutureWarning: Using a non-tuple sequence for multidimensional indexing is deprecated; using `tuple` instead. Errors may arise from now.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```

```
Out[41]: <matplotlib.axes._subplots.AxesSubplot at 0x7f7301d86a20>
```



```
In [42]: df[['Height', 'Gender']].groupby("Gender").describe()
```

```
Out[42]:
```

	Height	count	mean	std	min	25%	50%
Gender							
Female	5000.0	63.708774	2.696284	54.263133	61.894441	63.730924	
Male	5000.0	69.026346	2.863362	58.406905	67.174679	69.027709	

	75%	max
Gender		
Female	65.563565	73.389586
Male	70.988744	78.998742

```
In [43]: male_heights = (df[df['Gender']=='Male']['Height']).values
        female_heights = (df[df['Gender']=='Female']['Height']).values
```

```
In [45]: print(male_heights.mean(),male_heights.std())
        print(female_heights.mean(),female_heights.std())
```

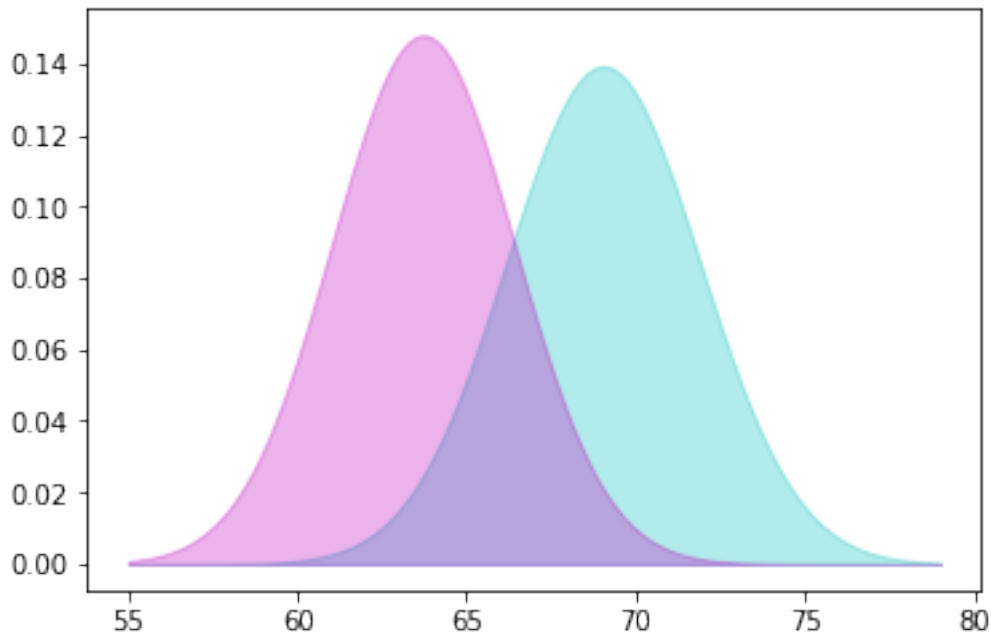
```
69.02634590621741 2.863075878119538
63.70877360342507 2.696014373880709
```

```
In [47]: from scipy import stats
        rv_male = stats.norm(loc=male_heights.mean(), scale=male_heights.std())
        rv_female = stats.norm(loc=female_heights.mean(), scale=female_heights.std())
```

```
In [52]: heights = np.linspace(55,79,1000)
        male_probs = rv_male.pdf(heights)
        female_probs = rv_female.pdf(heights)
```

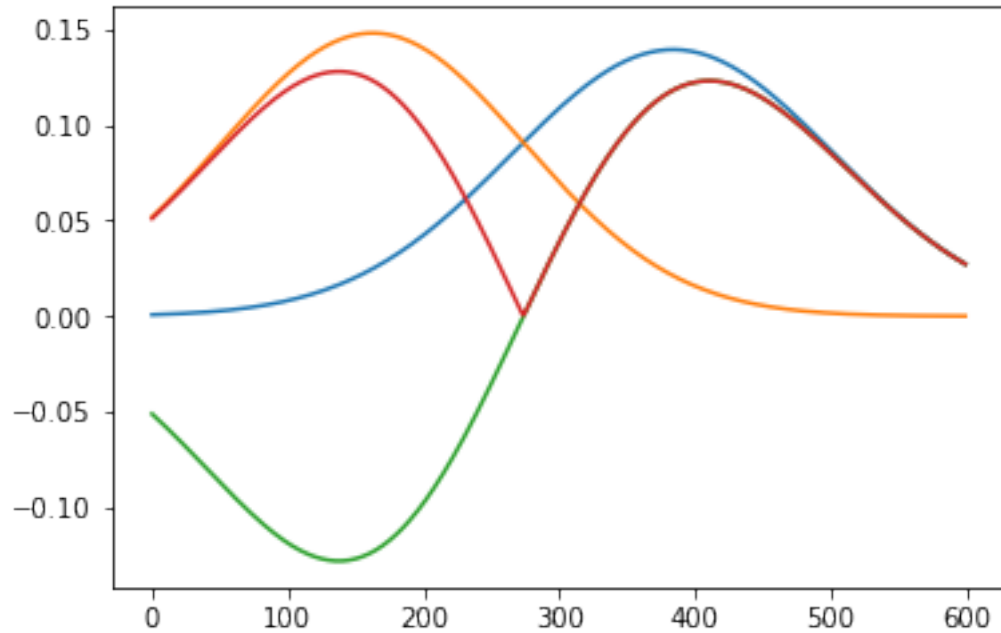
```
In [59]: plt.fill_between(heights, male_probs, color='c', alpha=0.3)
        plt.fill_between(heights, female_probs, color='m', alpha=0.3)
```

```
Out[59]: <matplotlib.collections.PolyCollection at 0x7f7301b17eb8>
```



```
In [72]: plt.plot(male_probs[200:-200])
plt.plot(female_probs[200:-200])
plt.plot(male_probs[200:-200]-female_probs[200:-200])
plt.plot(np.abs(male_probs[200:-200]-female_probs[200:-200]))
```

```
Out[72]: [<matplotlib.lines.Line2D at 0x7f7301810e80>]
```

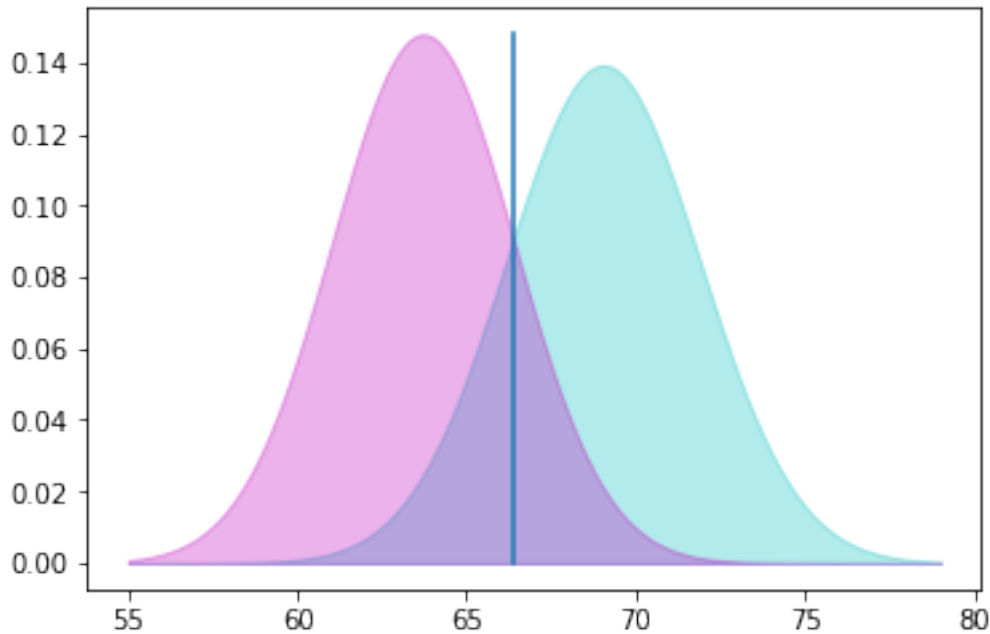


```
In [74]: threshold = heights[200:-200][np.argmin(np.abs(male_probs[200:-200]-female_probs[200:-200]))]
threshold
```

```
Out[74]: 66.36336336336336
```

```
In [75]: plt.fill_between(heights, male_probs, color='c', alpha=0.3)
plt.fill_between(heights, female_probs, color='m', alpha=0.3)
plt.plot([threshold,threshold],[0,max([male_probs.max(),female_probs.max()])])
```

```
Out[75]: [<matplotlib.lines.Line2D at 0x7f73017f2860>]
```



This is called the generative approach because we have to model our data well enough to build a probability for it. What if we have multi-dimensional data. This seems extra hard. All we really want to do is fit a function that tells us given an input in inches whether it is male or female. That is a discriminative approach.

## 0.2 Iris Data Sets

Lets think about the Iris data set. Lets say we measure 4 variables of different iris flowers. Lets say there are 3 species (Iris setosa, Iris virginica and Iris versicolor) of this data and we want to classify which species we are looking at. Lets say the species is a random variable  $S$ , and the four attributes are  $W, X, Y, Z$ . Assume we measure  $W, X, Y, Z$  for a particular flower  $F$ . It is not clear that those properties will with 100% certainty. Lets use conditional probability to express our knowledge.

$$P(S|W, X, Y, X)$$

is the probability of a species  $S$  given we measured the other variables. We want to figure out which species it is given the four attributes.

```
In [76]: from sklearn import datasets
iris = datasets.load_iris()
```

```
In [77]: iris_df = pd.DataFrame(data= np.c_[iris['data'], iris['target']],
                                columns= iris['feature_names'] + ['target'])
```

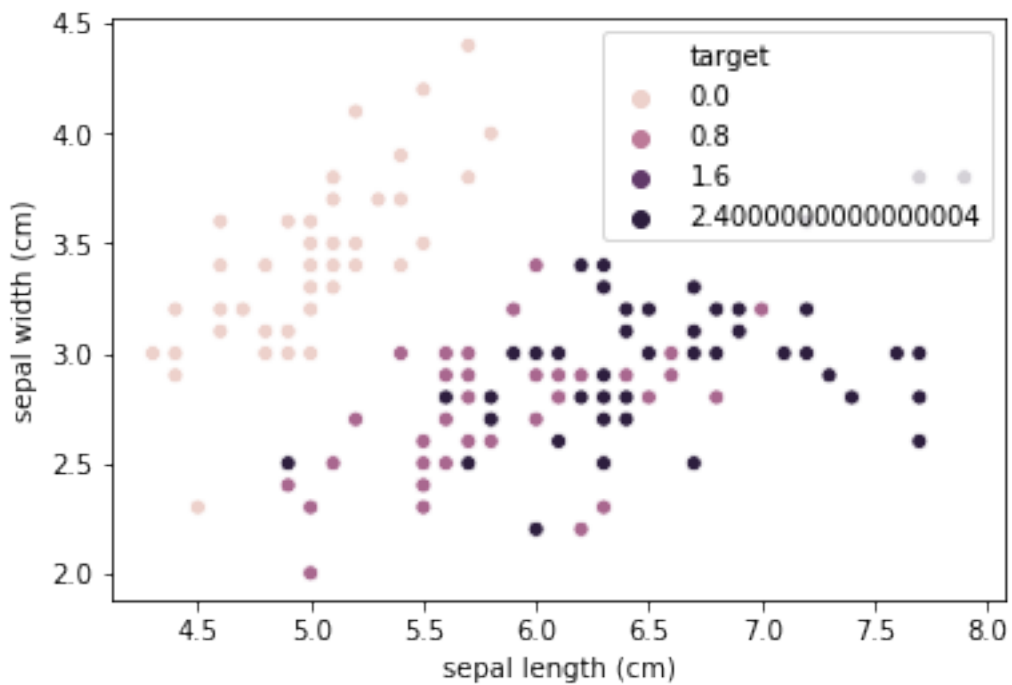
```
In [78]: iris_df.head()
```

```
Out[78]:   sepal length (cm)  sepal width (cm)  petal length (cm)  petal width (cm)  \
0              5.1              3.5              1.4              0.2
```

1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

	target
0	0.0
1	0.0
2	0.0
3	0.0
4	0.0

```
In [81]: ax = sns.scatterplot(x="sepal length (cm)", y="sepal width (cm)", hue="target", data=
```



```
In [82]: from sklearn import neighbors
```

```
In [ ]: n_neighbors = 3
        clf = neighbors.KNeighborsClassifier(n)
```