

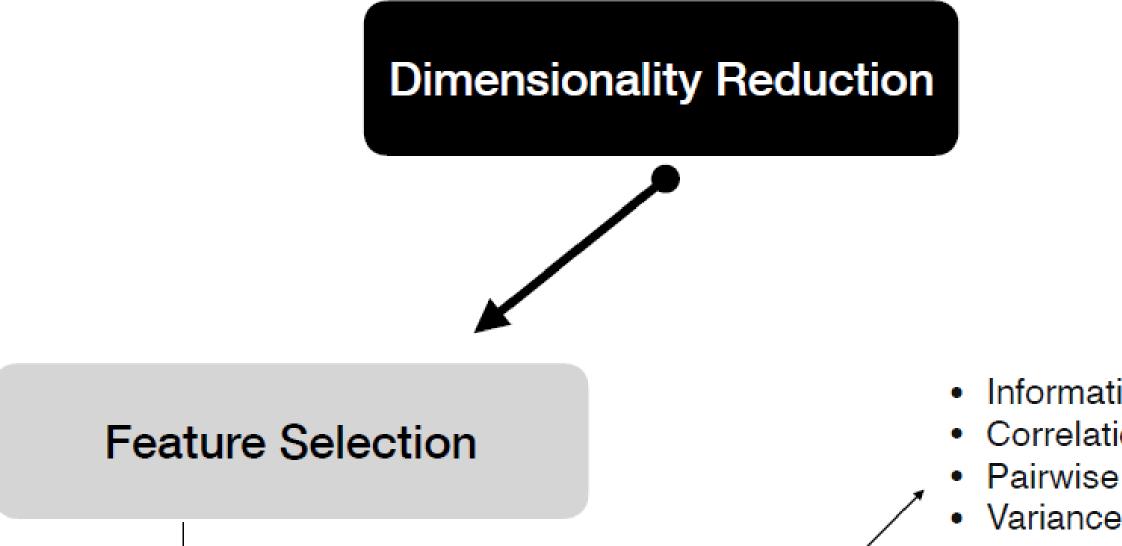
Lecture 28 & 29: Feature Selection Part 2

## Recap

- Feature Selection
  - Unsupervised methods
  - •Filter and wrapper methods



# Feature Selection with Embedded (Intrinsic) methods



- Information gain
- Correlation with target
- Pairwise correlation
- Variance threshold

**Embedded Methods** 

Filter Methods

- L1 (LASSO) regularization
- Decision tree

Wrapper Methods

- Recursive Feature Elimination (RFE)
- Sequential Feature Selection (SFS)
- Permutation importance

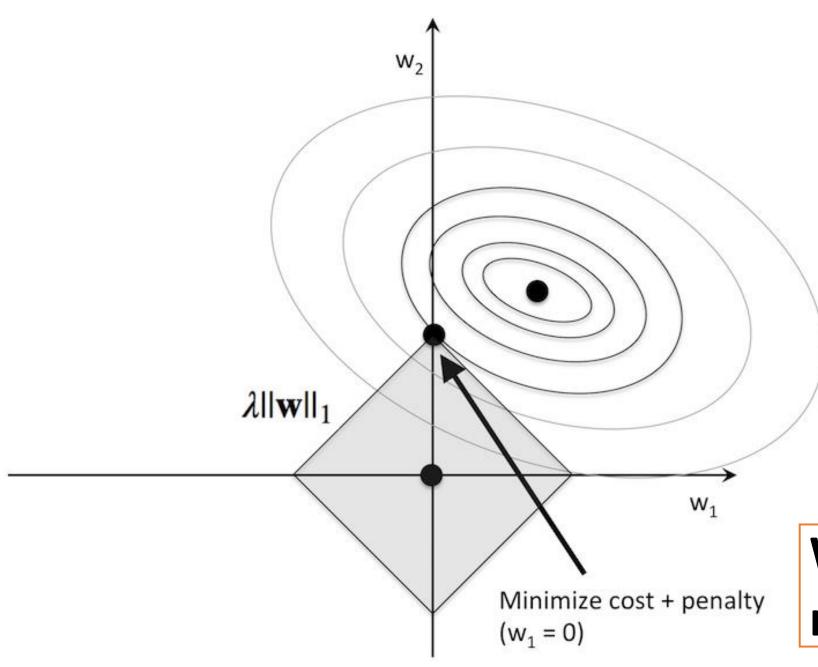
### Embedded methods

- Always supervised
- No separate feature selection
- Feature Selection happens as part of model training
- E.g.:
  - LASSO
  - Feature Importance with Random Forest
- Returns coeff\_ or feature\_importances
- Other non parametric methods do not augur well



Feature Selection with LASSO

## Cost function adjusted for L1 Regularization



$$\arg\min_{w} \nabla_{w} \mathcal{J} + \lambda \nabla_{w} ||w||_{1}$$

$$\nabla_w \mathcal{J} = \frac{2}{m} X^T (Xw - y) \qquad \nabla_w ||w||_1 = \mathbf{1}$$

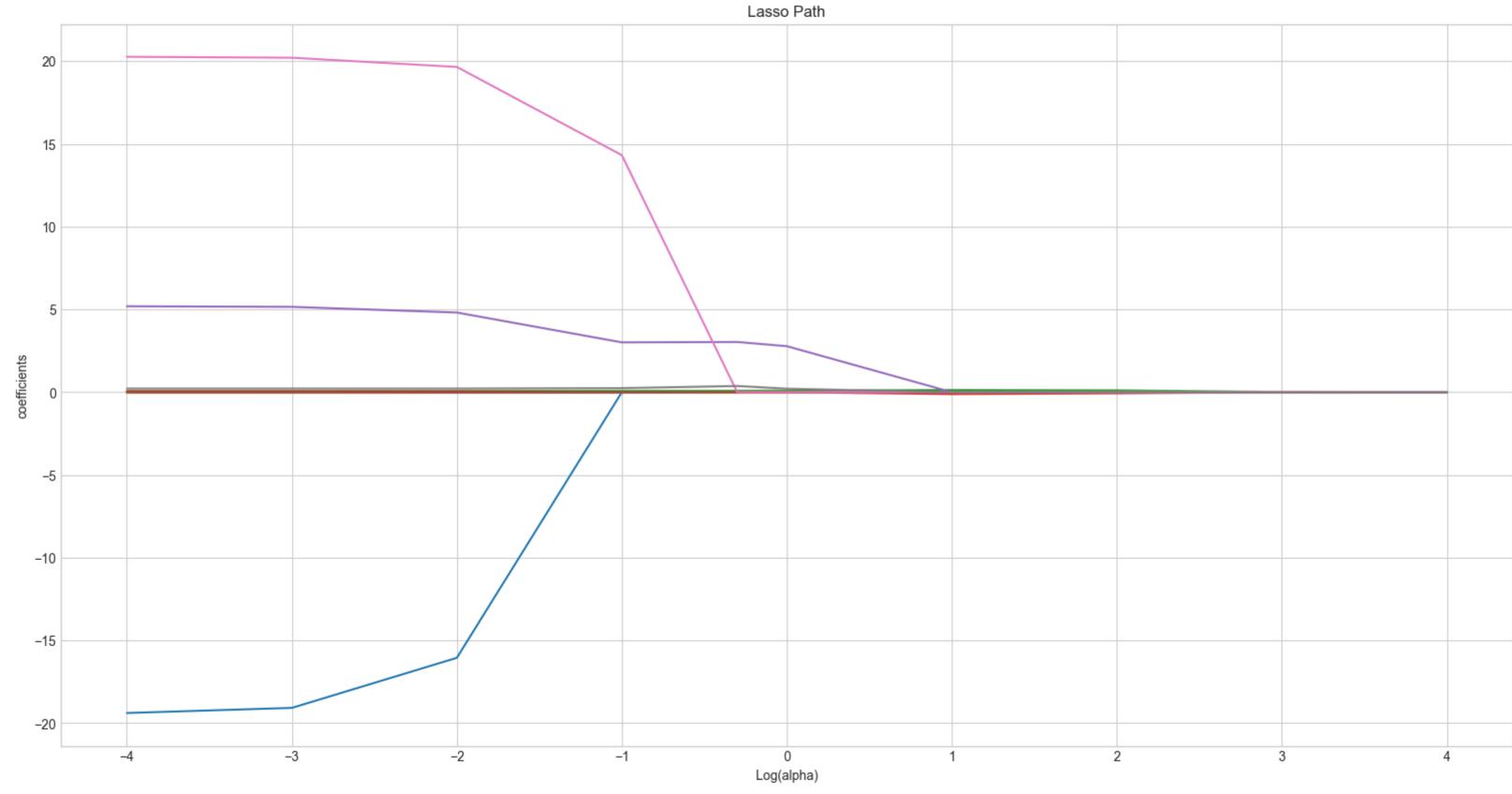
$$\mathbf{w} = \mathbf{w} - \eta \nabla_w \mathcal{J} \qquad \mathbf{w} = \mathbf{w} - \eta \nabla_w \mathcal{J} - \eta \lambda$$

Without regularization

$$\mathbf{w} = (\mathbf{w} - \eta \lambda) - \eta \nabla_w \mathcal{J}$$

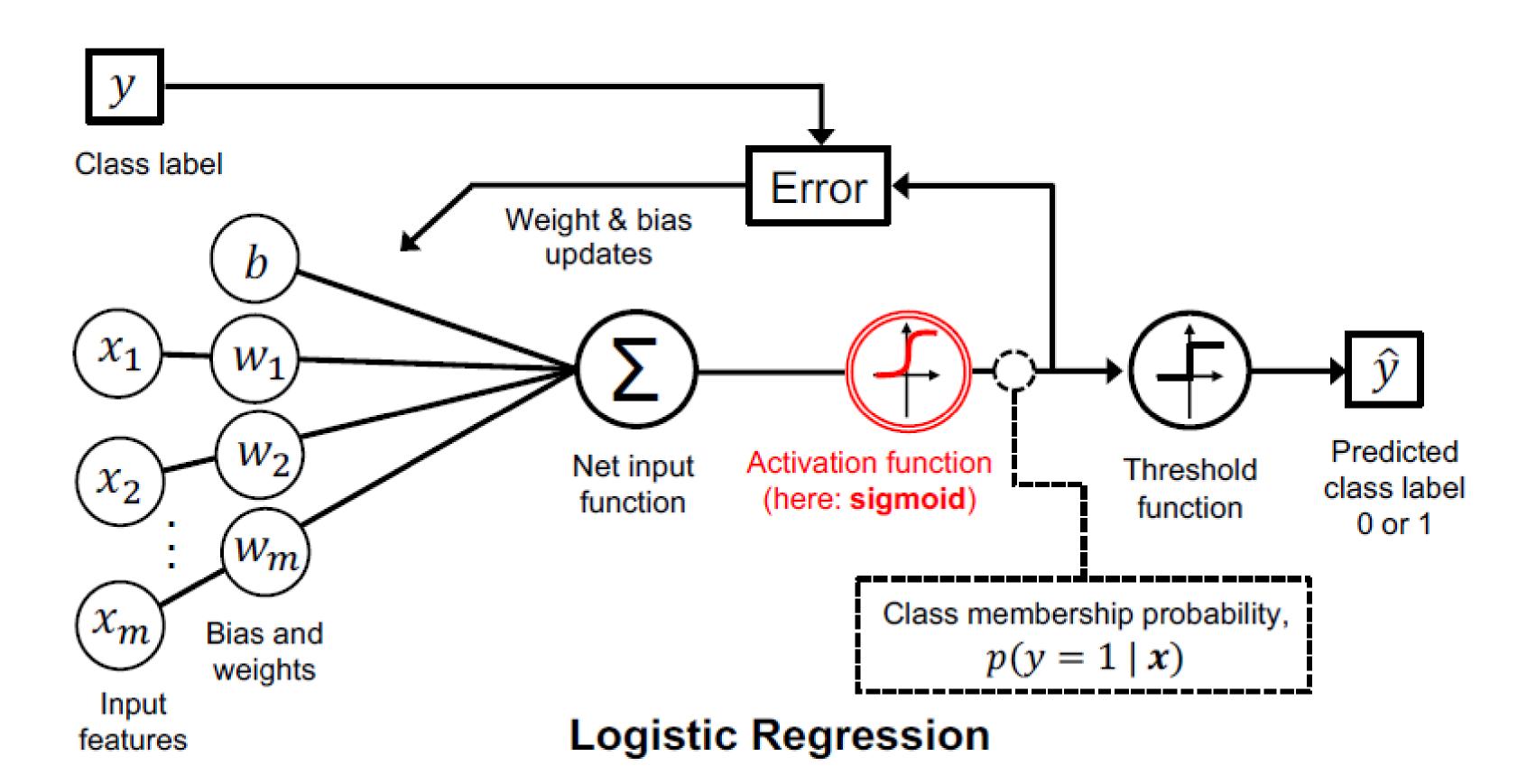
A FIXED small number keeps getting subtracting from a small w. Net effect w becomes 0

## Lasso path

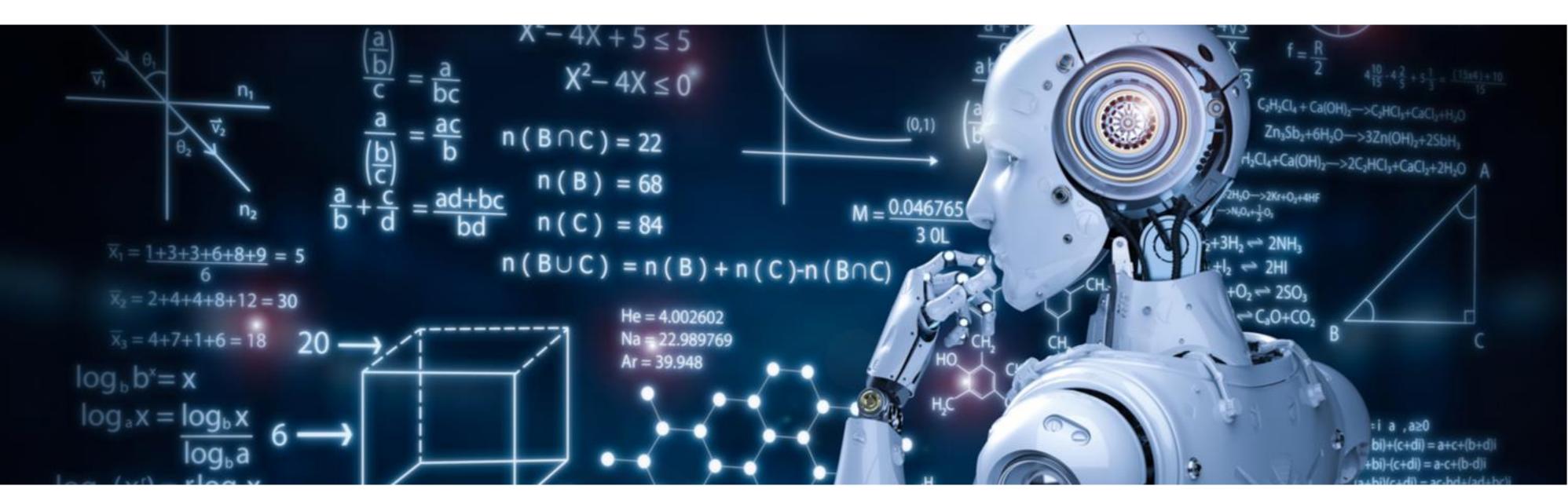




$$\arg\min_{w} \nabla_{w} \mathcal{J} + \lambda \nabla_{w} \|w\|_{1}$$



$$-\sum_{i=1}^{\infty} \left[ y^{(i)} \log \left( \sigma(z^{(i)}) \right) + \left( 1 - y^{(i)} \right) \log \left( 1 - \sigma(z^{(i)}) \right) \right] + \lambda ||w||_{1}$$



## Feature Selection with Decision Tree & Random Forest

#### Sample Tree:

2 Features : X1 & X2

2 Classes : Class1 & Class2



- A feature is important if
  - If used many times for splitting
  - Each split on the feature is high in the tree
  - Split produces lot of decrease in impurity at each node

#### Sample Tree:

2 Features : X1 & X2

2 Classes : Class1 & Class2

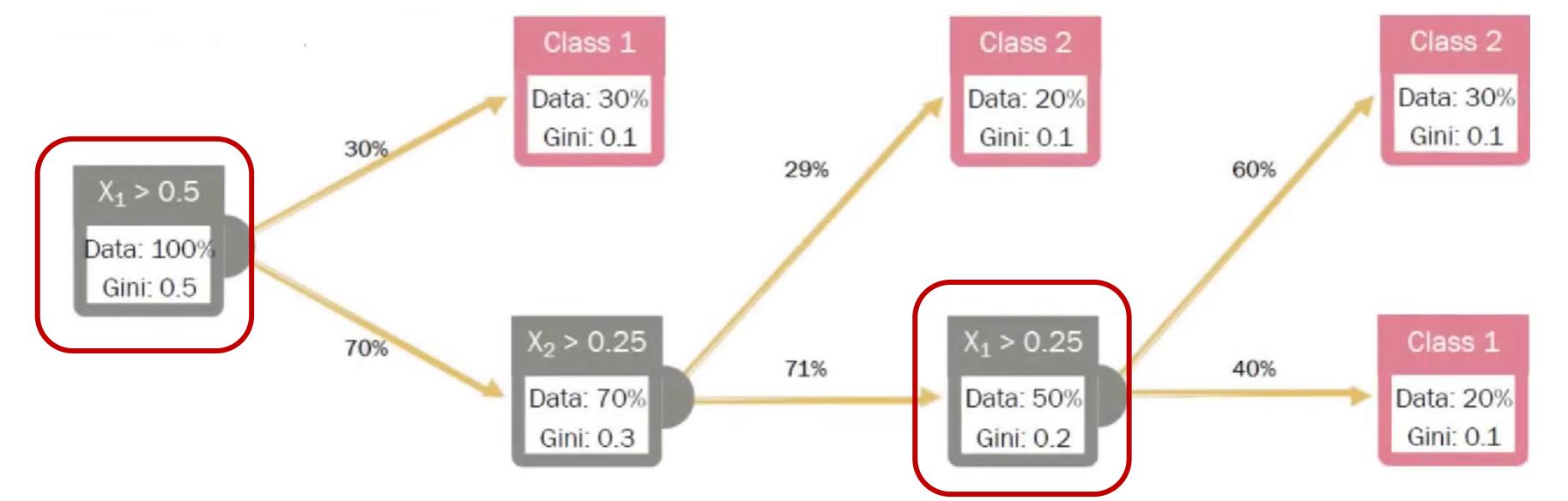


Node Importance

$$ni_{j} = \frac{N_{j}}{N} \left( Gini_{j} - \mathbb{E}[Gini_{j-children}] \right)$$

• Feature Importance

$$fi_i = \frac{\sum_{j \in feature-inodes} ni_j}{\sum_{j \in allnodes} ni_j}$$



• Decrease in impurity for X1 at top:

$$0.5 - (0.7 \times .3 + 0.3 \times 0.1)$$

- Impurity in parent node impurity in child node
- Weighed by the ratio of data N\_in/N

$$\frac{100}{100}[0.5 - (0.7 \times .3 + 0.3 \times 0.1)]$$

• How many times?

$$\frac{100}{100}[0.5 - (0.7 \times .3 + 0.3 \times 0.1)] + \frac{50}{100}[0.2 - (0.3 \times 0.1 + 0.2 \times 0.1)]$$

• Normalized Feature Importance = Sum of this feature importance divided by sum of all feature importance

## Feature Importance in DT/RF summary

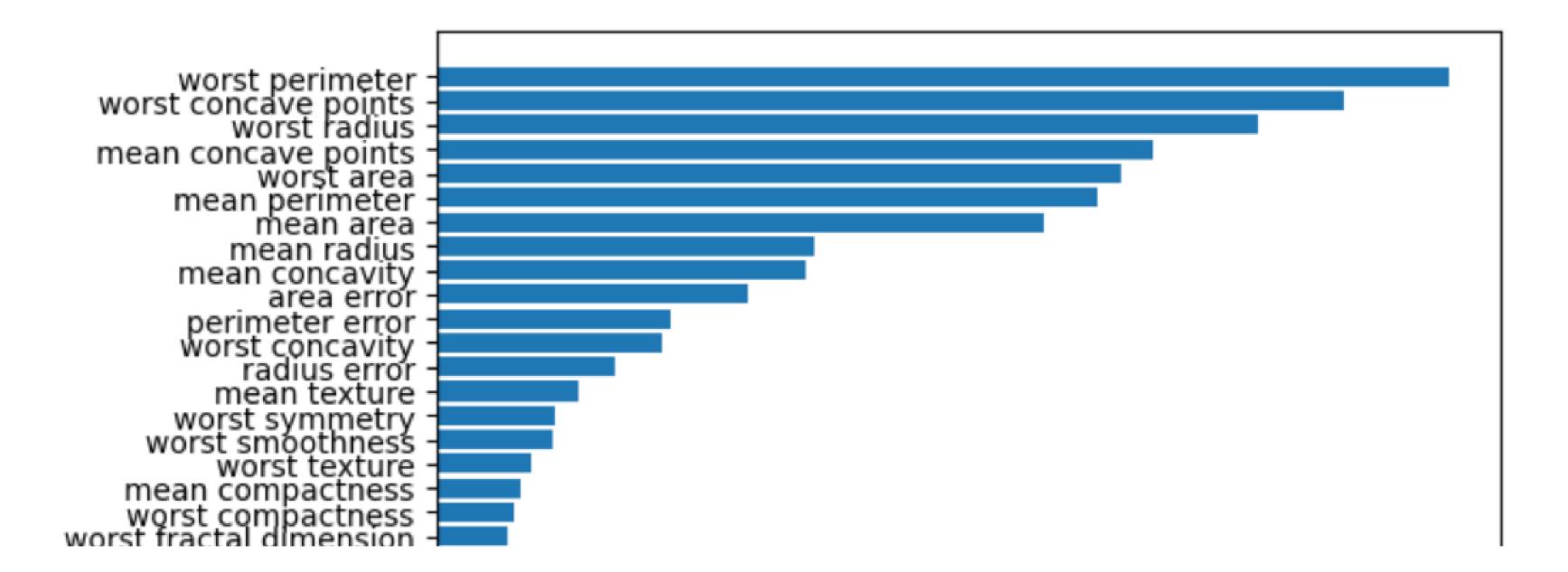
- Node Importance: Mean decrease in entropy/impurity from a parent node to child nodes after a feature split
  - Weighted by tree location (num examples at node)
  - for a given feature
    - for each tree
      - compute impurity decrease (Gini, Entropy)
      - weight by number of examples at that node
      - averaged over all trees
  - normalize importances so that sum of feature importances sum to 1

## Sklearn code

```
sorted_idx = model_best_rf.feature_importances_.argsort()
plt.barh(dataset.feature_names[sorted_idx], model_best_rf.feature_importances_[sorted_idx])
plt.xlabel("Random Forest Feature Importance")

$\square 0.3s$
```

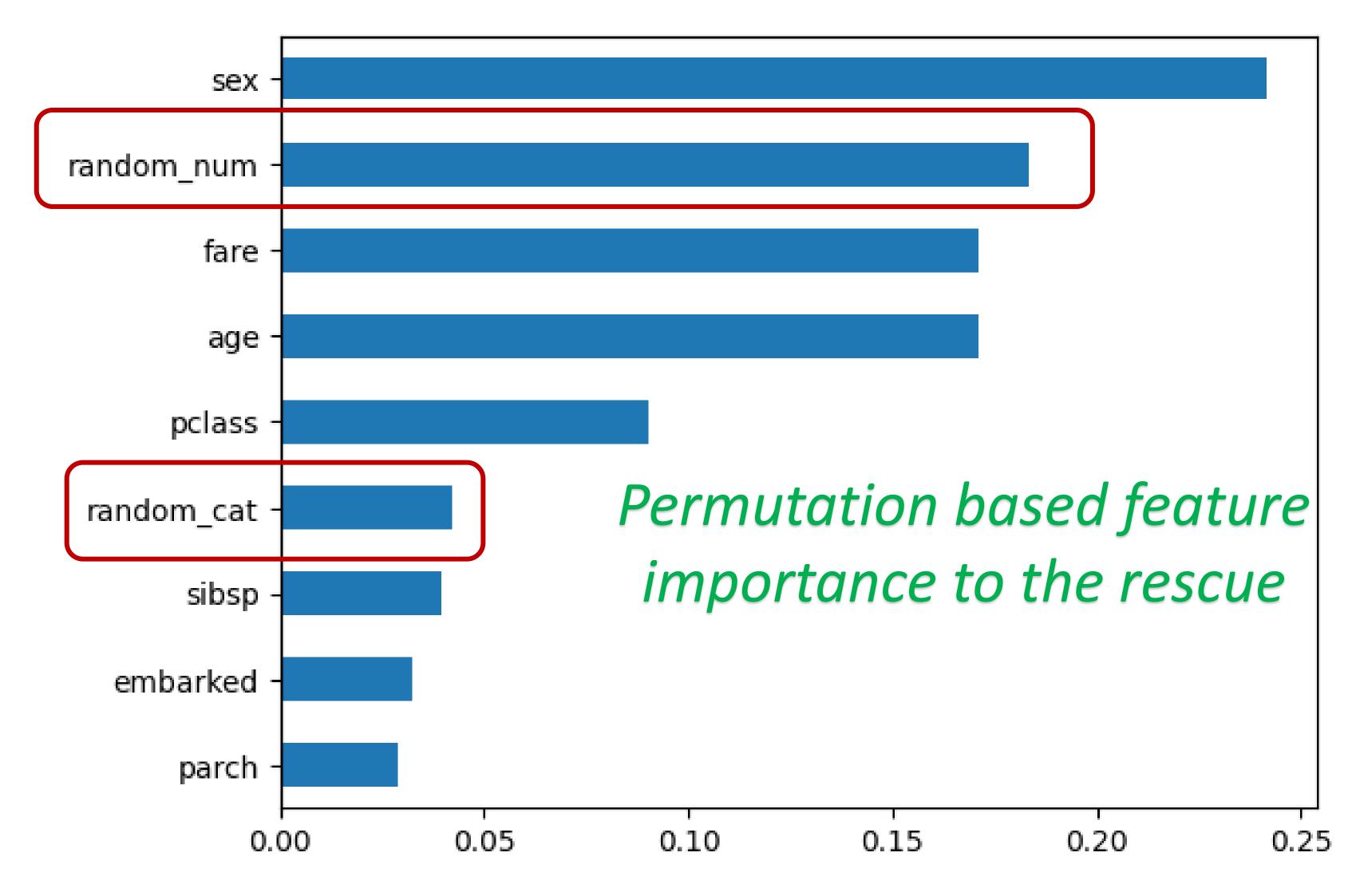
Text(0.5, 0, 'Random Forest Feature Importance')

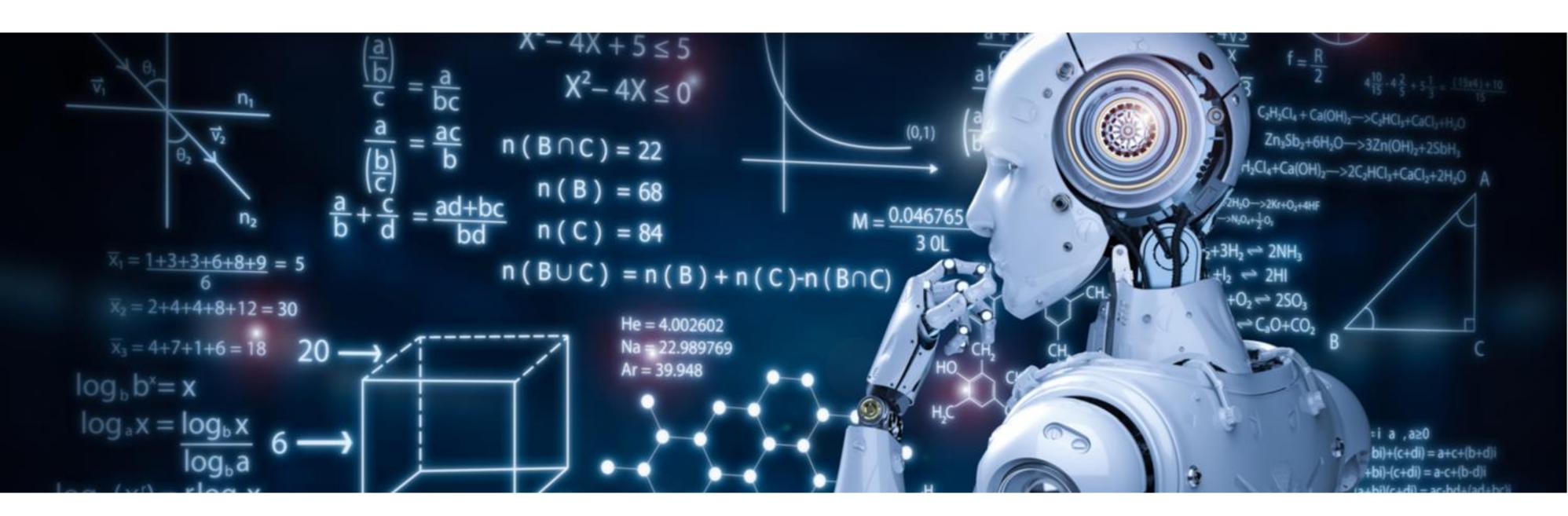


## Problems with Tree based Feature Importance

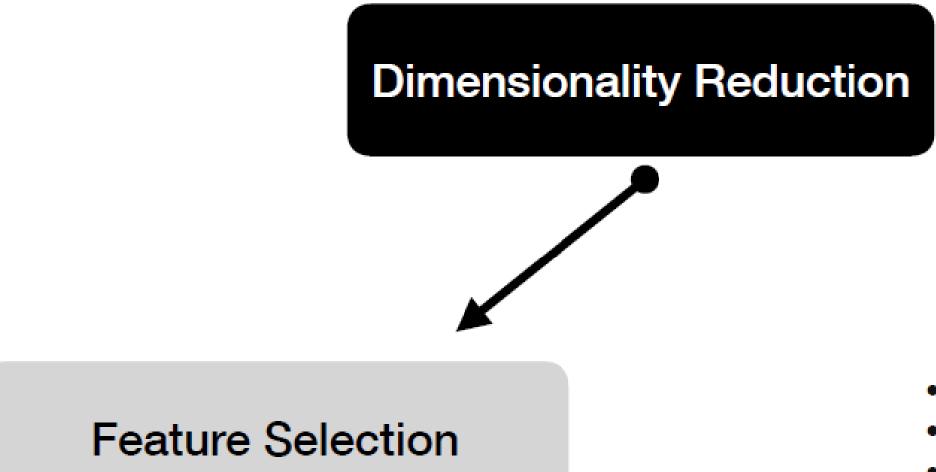
- Inflated feature importance for numerical feature
- Inflated feature importance for categorical feature with high cardinality

| рс | lass | sex    | age  | sibsp | parch | fare    | embarked | random_cat | random_num | survived |
|----|------|--------|------|-------|-------|---------|----------|------------|------------|----------|
|    | 3.0  | male   | 32.0 | 0.0   | 0.0   | 56.4958 | S        | 0          | -2.553921  | 1        |
|    | 2.0  | male   | 27.0 | 0.0   | 0.0   | 26.0000 | S        | 0          | 0.963879   | 0        |
|    | 3.0  | male   | 35.0 | 0.0   | 0.0   | 7.8958  | S        | 0          | 0.536653   | 0        |
|    | 3.0  | female | 26.0 | 1.0   | 1.0   | 22.0250 | S        | 2          | 0.323079   | 1        |
|    | 3.0  | male   | 33.0 | 0.0   | 0.0   | 8.6542  | S        | 1          | 0.884045   | 0        |
|    |      |        |      |       |       |         |          |            |            |          |





## Wrapper methods



- **Filter Methods**
- **Embedded Methods**
- Wrapper Methods

- Information gain
- Correlation with target
- Pairwise correlation
- Variance threshold
- ...
- L1 (LASSO) regularization
- Decision tree
- ...
- Recursive Feature Elimination (RFE)
- Sequential Feature Selection (SFS)
- Permutation importance

## Wrapper methods

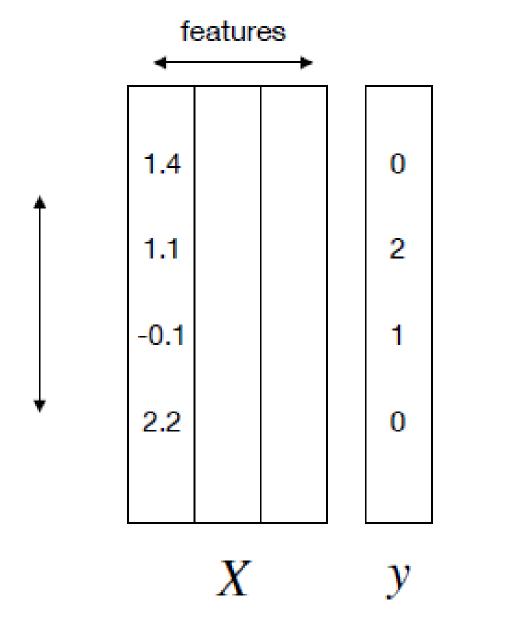
- General working
  - Wrap any algorithm to measure metrics
  - Make slight changes and run the algorithm again
  - •The quantum of "slight changes" gives idea of feature importance
- E.g.:
  - RFE
  - Permutation Importance
  - Selective Feature Selection

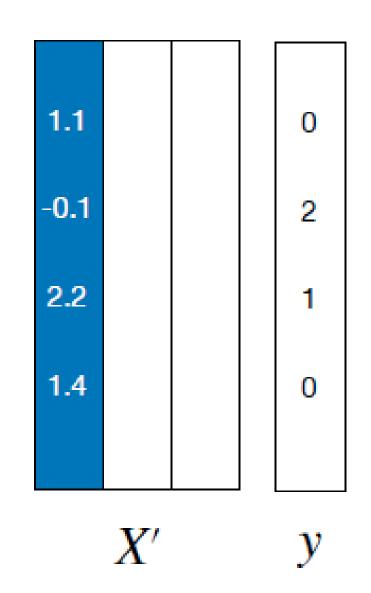


# Permutation based feature importance

## Permutation importance

model.fit(X\_train, y\_train), model.score(X\_test)



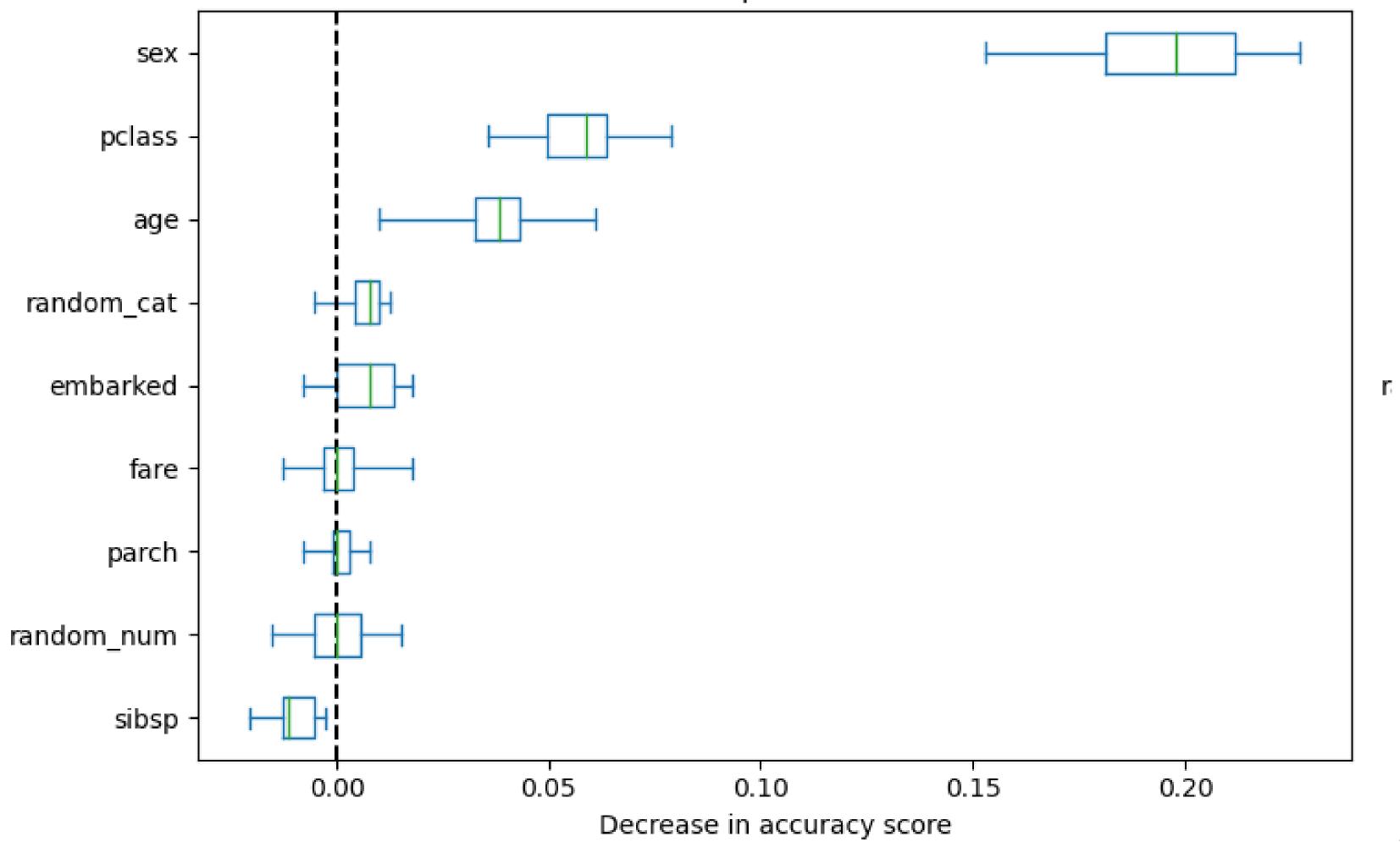


feature importance = baseline performance – shuffled dataset performance

## Permutation importance

- Train a baseline model
- Record model performance (any metric) on test dataset
- For each feature column in test dataset,
  - Shuffle that feature column alone, everything else unchanged
  - Observe performance and compare to original feature importance =
     baseline performance – shuffled dataset performance
- Do the shuffling for training dataset also & record feature importance





## Column Drop Variant of permutation importance

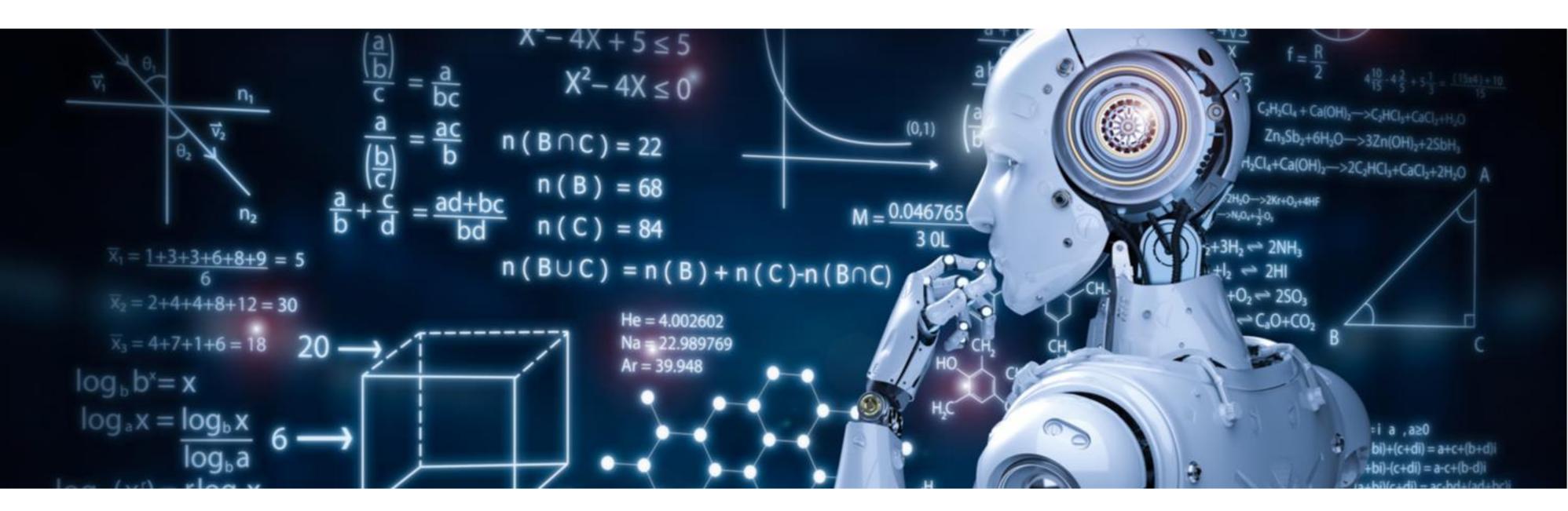
- Train a baseline model
- Record model performance (any metric) on test dataset
- For each feature column in test dataset,
  - Drop column
  - Fit model
  - Compare test data set performance to original
- Accurate but very expensive

Fixes the random\_cat issue as well

## Wrapper methods general features (except as noted)

- Permutation importance is model agnostic
  - No need for coeff\_ or feature\_importance implementation
    - (this is not applicable to other wrapper methods)
- Feature Importance is specific to model

- Permutation importance is flexible, can use any metric
- Feature importance is tied to impurity measure
- Permutation importance is easy to understand
- Feature importance is slightly tricky



## Recursive Feature Elimination

#### RFE

- Suppose you have number (or range) of features in mind
- Algorithm
  - Fit model to dataset
  - Eliminate feature with lowest coefficient (or lowest feature importance)
  - Repeat steps until desired features is reached
- Can be applied along with cross validation
- Comprehensive but expensive

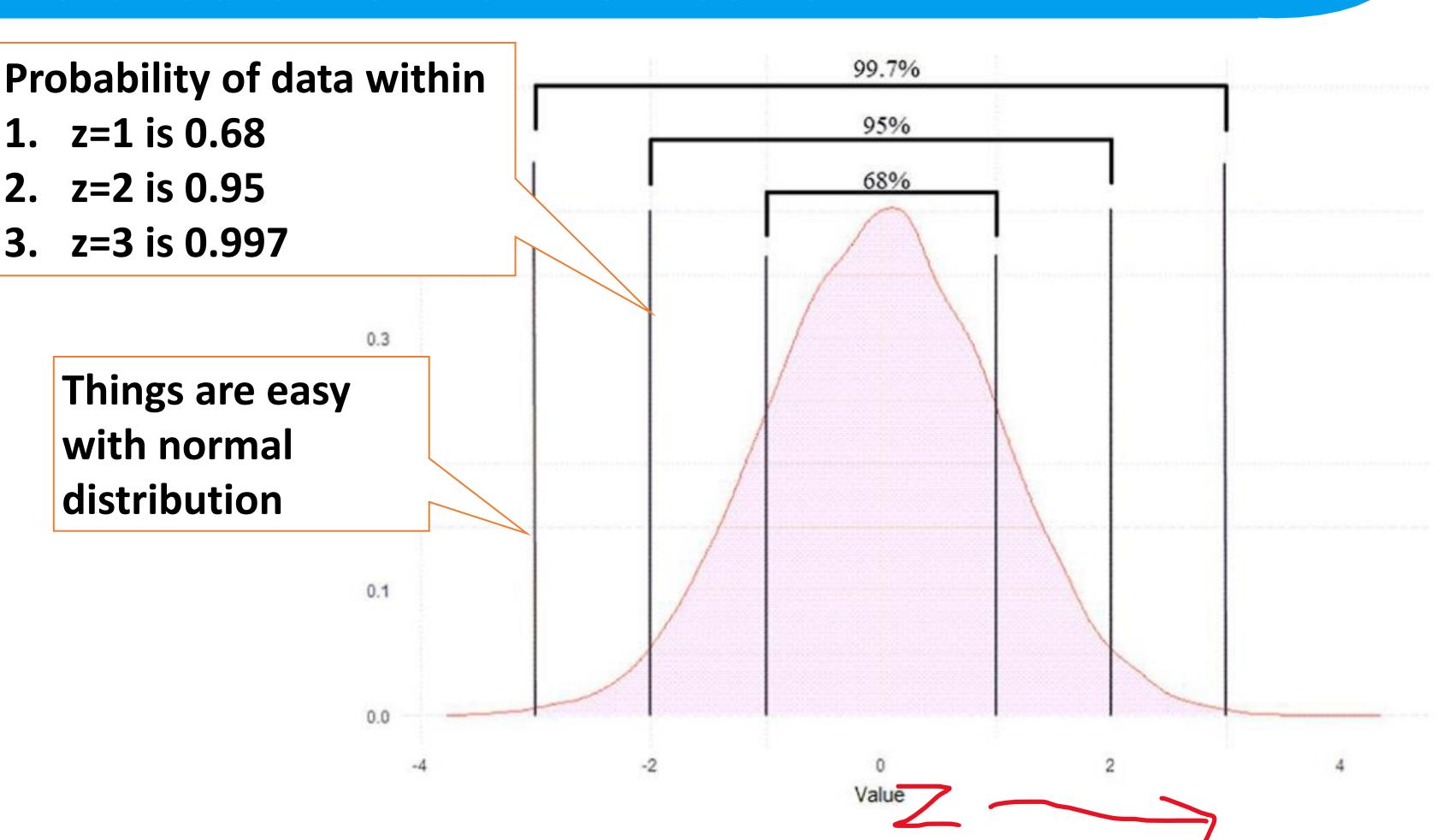
Why repeat steps?
Why not delete all low coefficient features at the outset?



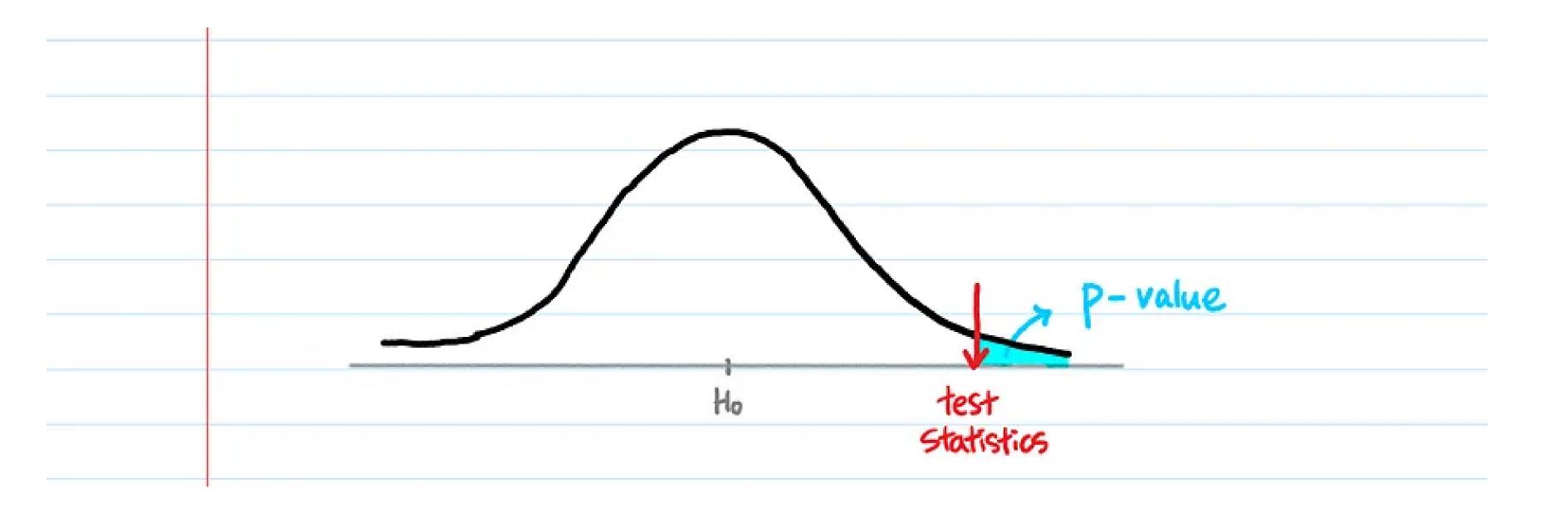
## Feature Selection with Chi Squared Test

## **Dimensionality Reduction** Information gain Correlation with target Feature Selection Pairwise correlation Variance threshold Chi-Squared ANOVA Filter Methods L1 (LASSO) regularization **Embedded Methods** Decision tree Wrapper Methods Recursive Feature Elimination (RFE) Sequential Feature Selection (SFS) Permutation importance

## Standard Normal Distribution



## Standard Normal distribution and p-values

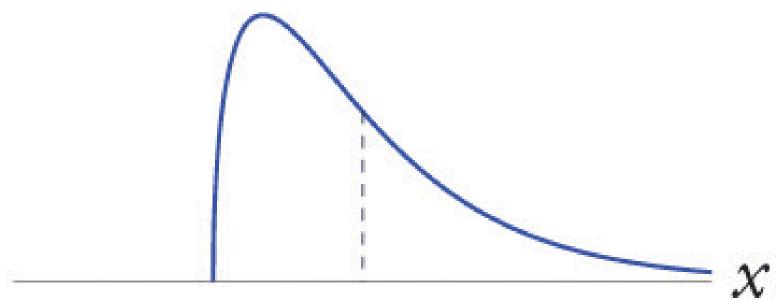


$$\bullet P(X > k)$$

## Why normal distribution?

Not everything follows normal distribution





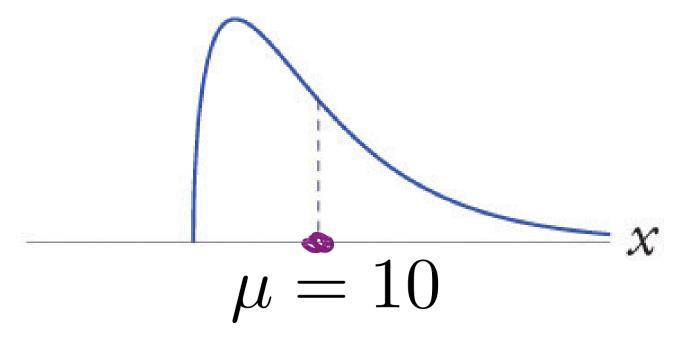
- Accidents on road follow Poisson distribution
- Volcanic eruption, asteroid strike: exponential distribution
- Why do we keep talking about normal distribution?
- The answer is in Central Limit theorem

## Central Limit Theorem (CLT)

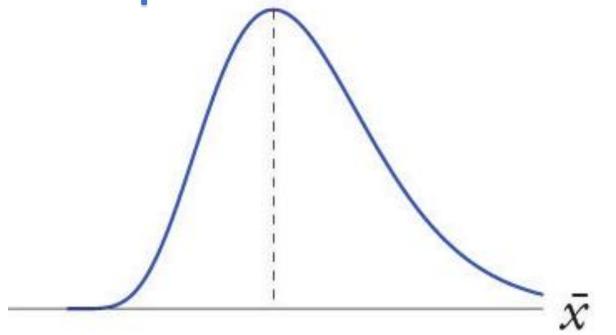
- Most fundamental to inferential statistics
- Aside: What is inferential statistics versus descriptive statistics?
- •CLT provides mechanism to apply normal distribution to everything

## Central Limit Theorem – Sampling distribution of mean

## Population distribution



Sampling distribution of sample mean with n=5

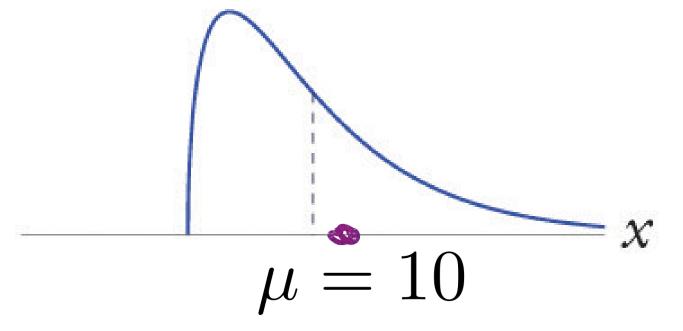


## Sample size n = 5

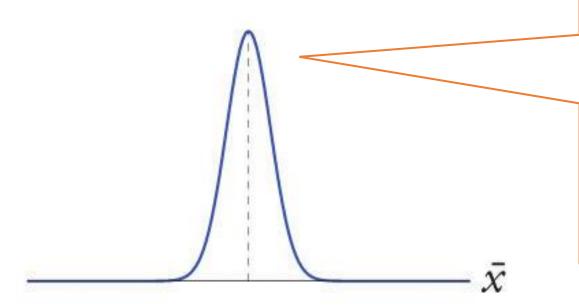
| Sampling | Mean |
|----------|------|
| 1        | 7.5  |
| 2        | 9.5  |
| 3        | 11   |
| 4        | 9    |
| 5        | 11.5 |
| 6        | 10.5 |
| 7        | 9.75 |
| 8        | 9    |
| 9        | 9.25 |
| 10       | 9.8  |

## Central Limit Theorem – Sampling distribution of mean

## Population distribution



# Sampling distribution of sample mean with n=30



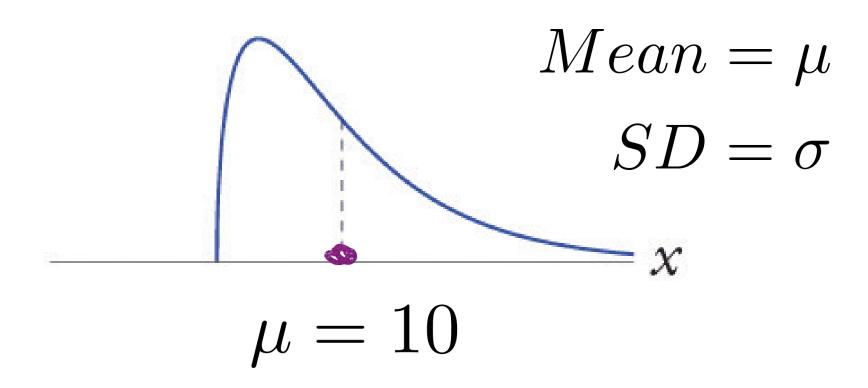
Sampling distribution approximates normal distribution when n>=30

## Sample size n = 30

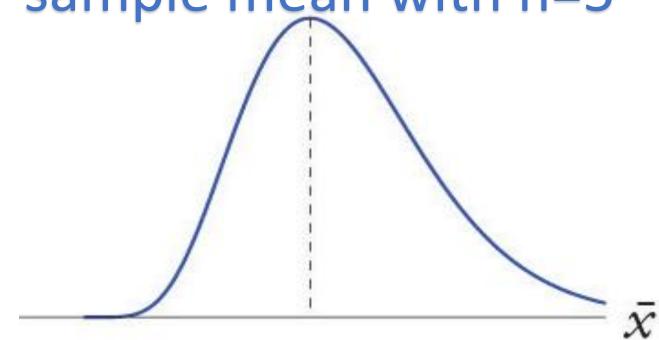
| Sampling | Mean  |
|----------|-------|
| 1        | 7.5   |
| 2        | 9.5   |
| 3        | 11    |
| 4        | 12    |
| 5        | 11.5  |
| 6        | 10.5  |
| 7        | 9.75  |
| 8        | 10    |
| 9        | 10.25 |
| 10       | 9.8   |

#### Central Limit Theorem – Sampling distribution of mean

#### Population distribution



Sampling distribution of sample mean with n=5



#### Sampling distribution of sample mean with n=30

$$Mean = \mu_s$$

$$SD = \frac{\sigma}{\sqrt{n}}$$

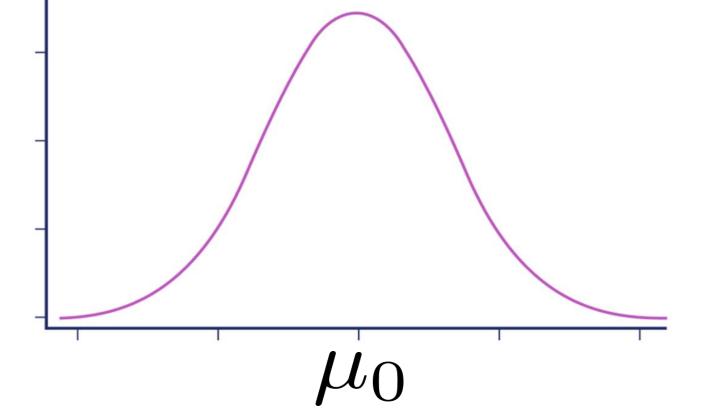
$$z \sim \mathcal{N}(\mu, \frac{\sigma}{\sqrt{n}})$$

#### Made in India iPhone 15 battery life

- •iPhone 15 has mean battery life  $~\mu_0$  & variance  $\sigma_0$
- Population has some unknown distribution

$$X \sim Unknown(\mu_0, \sigma_0)$$

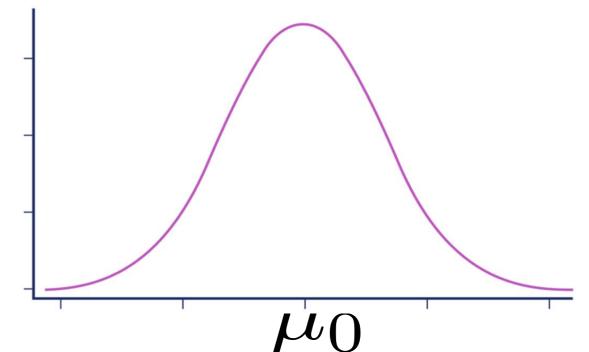
- How was population mean & variance found?
  - Draw samples (each of size >= 30) 10 times in population
  - Sampling distribution of mean battery life is gaussian

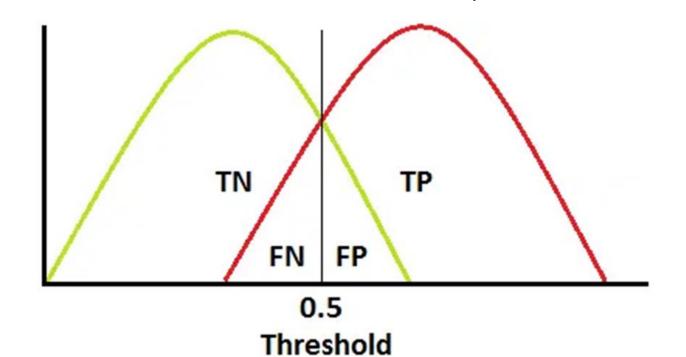


$$Y \sim \mathcal{N}(\mu_0, \frac{\sigma_0}{\sqrt{n}})$$

#### Made in China v/s India iPhone battery life

• Historical sampling distribution from China  $Y \sim \mathcal{N}(\mu_0, \frac{\sigma_0}{\sqrt{\gamma}})$ 





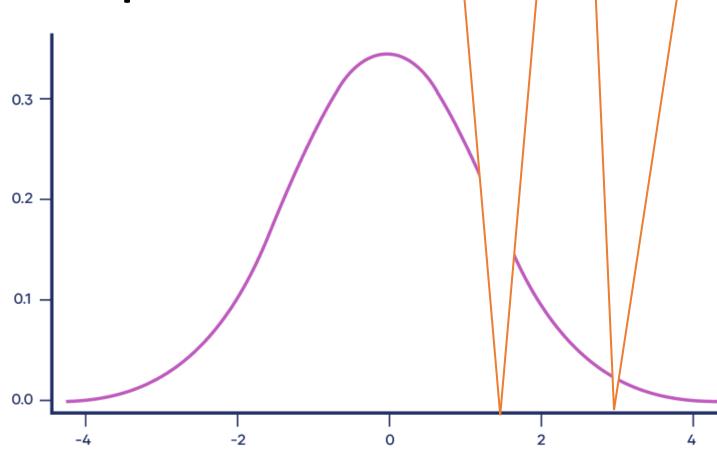
- •v/s distribution of Made in India
- Where is the mean of new distribution?
- •Should new distribution exactly align with historical distribution? What is confidence interval (CI)?  $(\mu_0 \pm \frac{\sigma_0}{\sqrt{n}})$
- CI relation to TP/TN Type 1 Type2

#### Clinical Trial of a new cancer medicine

- Current medicine has some efficacy
- Efficacy of current medicine decided by equation/past data
- Central Limit Theorem "sort of" gives bell curve (t distribution)
  - New medicine efficacy based on n samples
    - •(n-1 degrees of freedom)

$$z \sim \mathcal{N}(\mu, \frac{\sigma}{\sqrt{n}})$$

$$t_{n-1} \sim \mathcal{T}(\mu, \frac{\sigma}{\sqrt{n}})$$



T-score (no. standard deviations from the mean)

New

medicine

is here

Mean efficacy

#### T Distribution

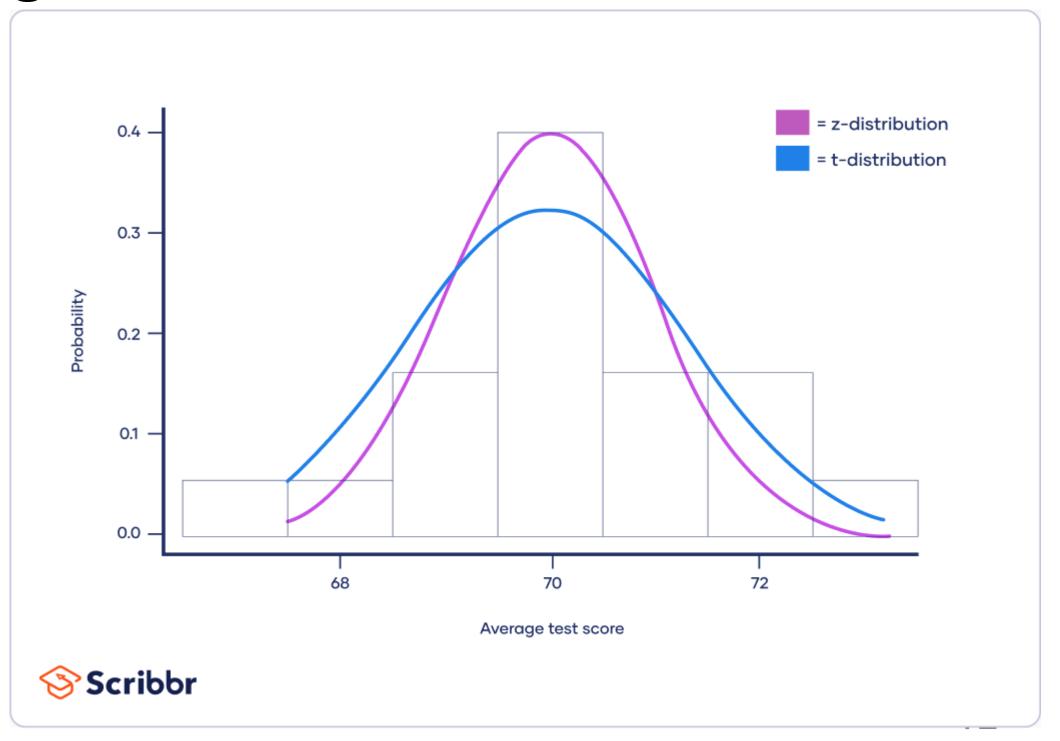
- Adjusted normal distribution for small sample sizes
- Number of samples = Degrees of freedom

$$z \sim \mathcal{N}(\mu, \frac{\sigma}{\sqrt{n}})$$

z statistic follows from this

t statistic follows from this

$$t_{n-1} \sim \mathcal{T}(\mu, \frac{o}{\sqrt{n}})$$



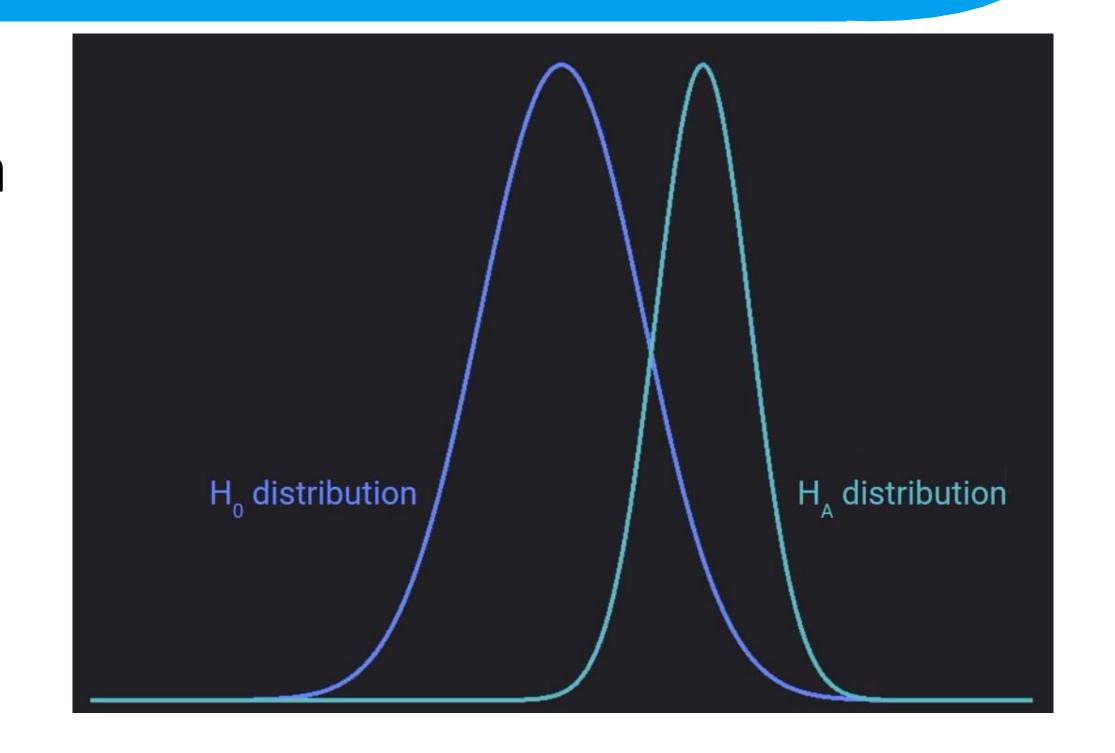
#### Intro to Hypothesis Test

- Null hypothesis Ho,
- Alternate hypothesis Ha

$$z \sim \mathcal{N}(\mu_0, \frac{\sigma_0}{\sqrt{n}})$$

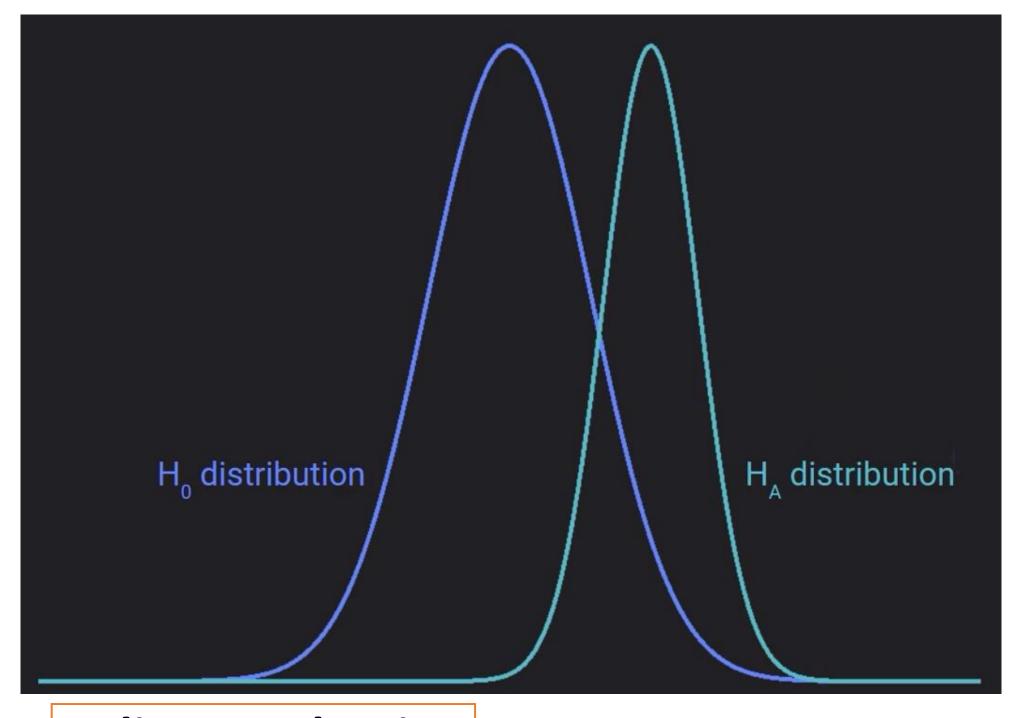
$$t_{n-1} \sim \mathcal{T}(\mu_0, \frac{\sigma_0}{\sqrt{n}})$$

Convert x to z or t



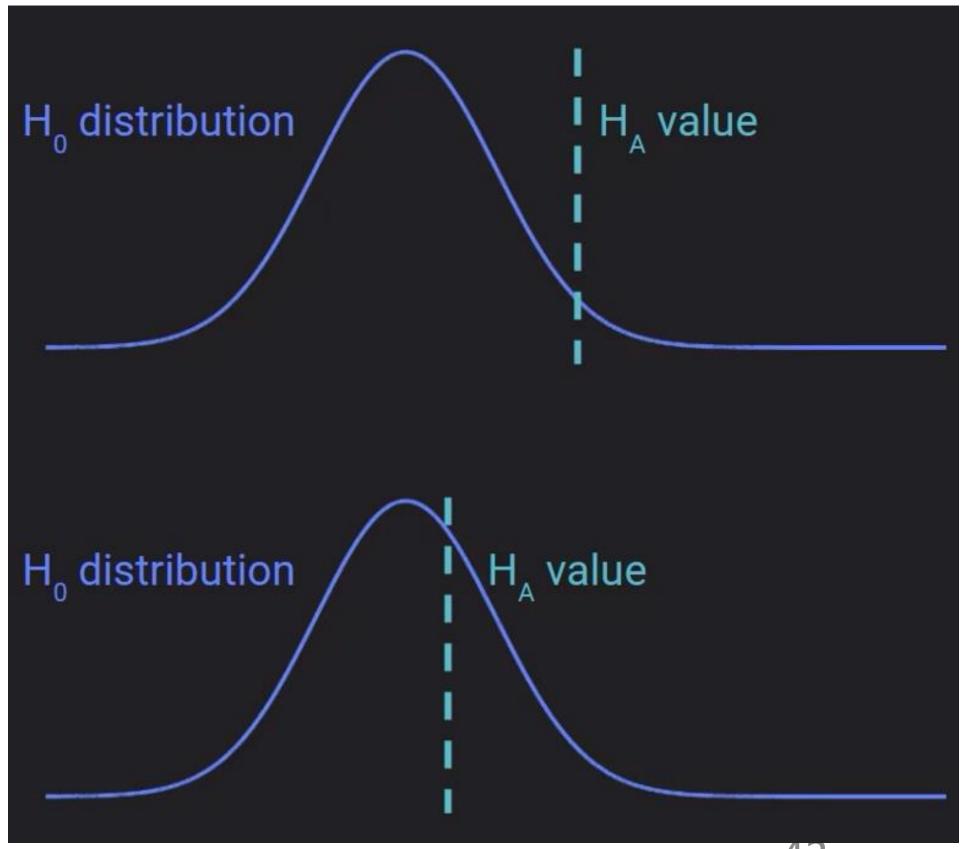
$$t_{n-1} = \frac{x - \mu_0}{\sigma / \sqrt{n}}$$

#### Intro to p-values in Hypothesis Test



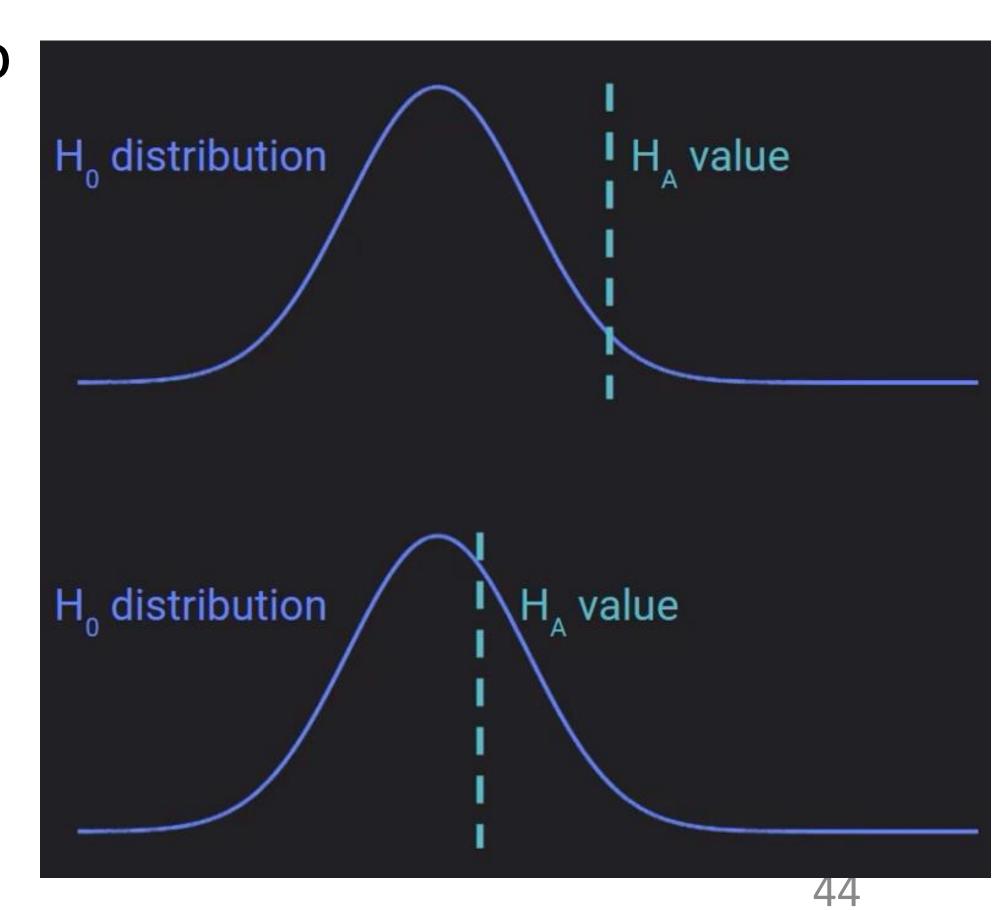
Indicates what is the probability value >= t-statistic

$$t_{n-1} = \frac{x - \mu}{\sigma / \sqrt{n}}$$



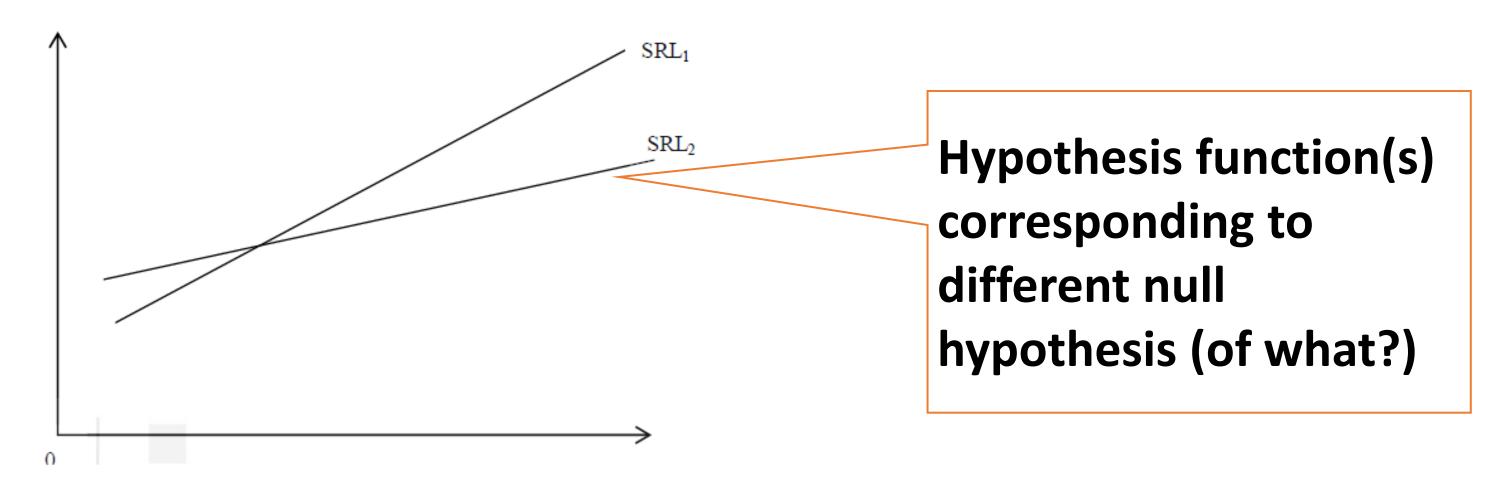
# p-values in Hypothesis Test

- How likely for the Ha value to occur if Ho is true?
- What is the probability of observing a value of Ha larger than current value if there was no true effect?
- P(Ha | Ho)
- Definite Integral
  - Lookup table or coding



# Regression - Population versus Sample View

- Sample Regression Functions
  - Different Regression Line/Plane/Hyperplane



- Difference between lines values of coefficients
- Distribution of coefficients

$$\hat{y} = h(x) =$$

$$w_1 TV + w_2 radio +$$

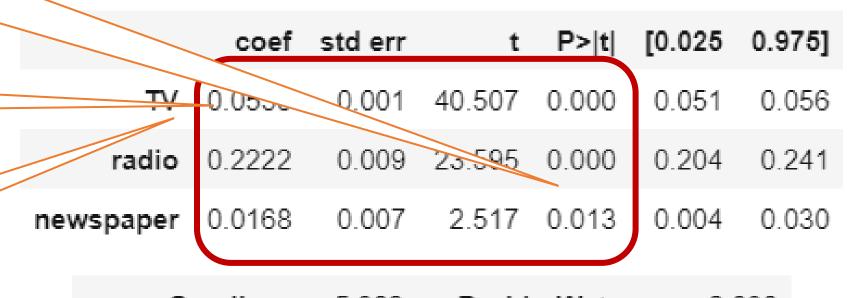
$$w_3 new spaper$$

P value tells us total probability of given value under null hypothesis

Null Hypothesis is coefficient = 0

Alternate
Hypothesis is
coefficient not 0

|                   | OLS Regre        | ession Results               |           |
|-------------------|------------------|------------------------------|-----------|
| Dep. Variable:    | sales            | R-squared (uncentered):      | 0.982     |
| Model:            | OLS              | Adj. R-squared (uncentered): | 0.982     |
| Method:           | Least Squares    | F-statistic:                 | 3566.     |
| Date:             | Sun, 28 Mar 2021 | Prob (F-statistic):          | 2.43e-171 |
| Time:             | 13:42:33         | Log-Likelihood:              | -423.54   |
| No. Observations: | 200              | AIC:                         | 853.1     |
| Df Residuals:     | 197              | BIC:                         | 863.0     |
| Df Model:         | 3                |                              |           |
| Covariance Type:  | nonrobust        |                              |           |



 Omnibus:
 5.982
 Durbin-Watson:
 2.038

 Prob(Omnibus):
 0.050
 Jarque-Bera (JB):
 7.039

 Skew:
 -0.232
 Prob(JB):
 0.0296

Kurtosis: 3.794 Cond. No. 12.6

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# Viewing hypothesis test from generative ML perspective

- p values & statistical significance
- Machine Learning
  - Training is not a strict Ho, but a foundation
  - Each X\_test record is sample from different dist (RV)
  - Each X\_test record is the mean of the RV
  - Prediction on each X\_test is different Ha

ML looks for optimal threshold

TN TP

FN FP

0.5

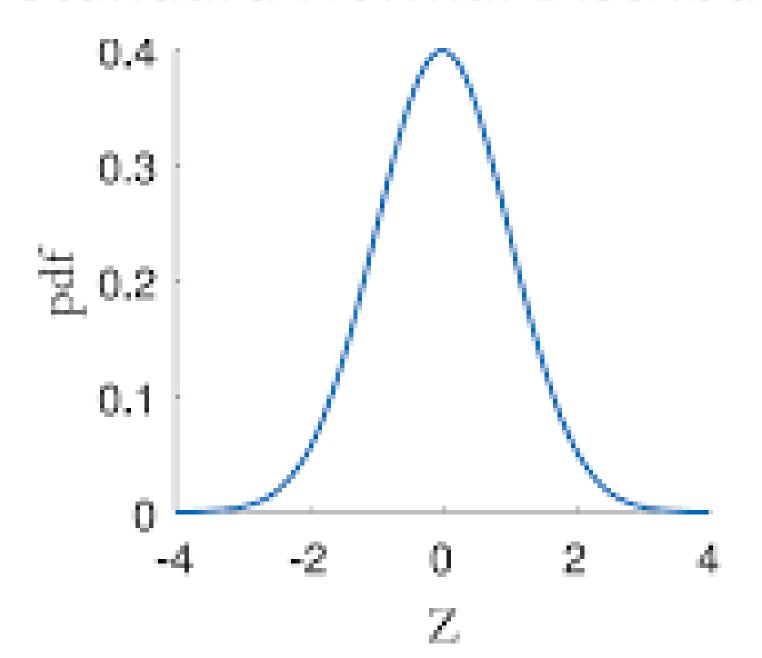
Threshold

Hypothesis testing looks for conservative threshold for a given p-value

#### Chi-squared Distribution

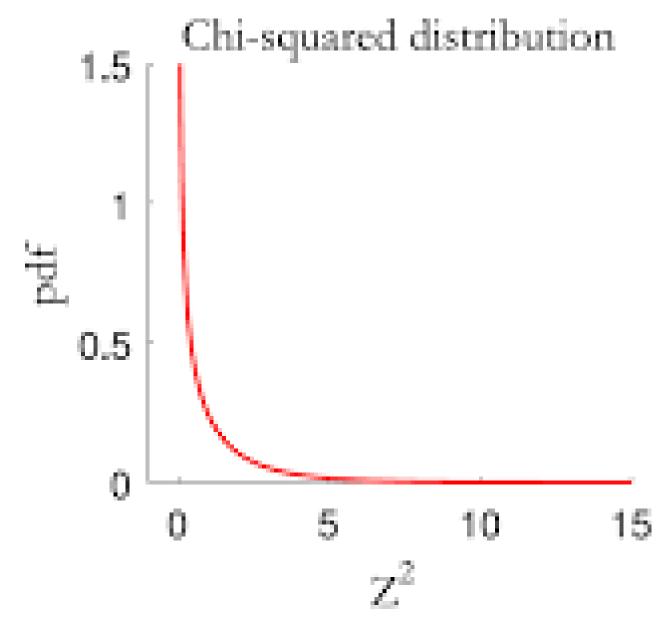
$$Z \sim N(0,1)$$

#### Standard Normal Distribution





#### **Chi-Squared Distribution**

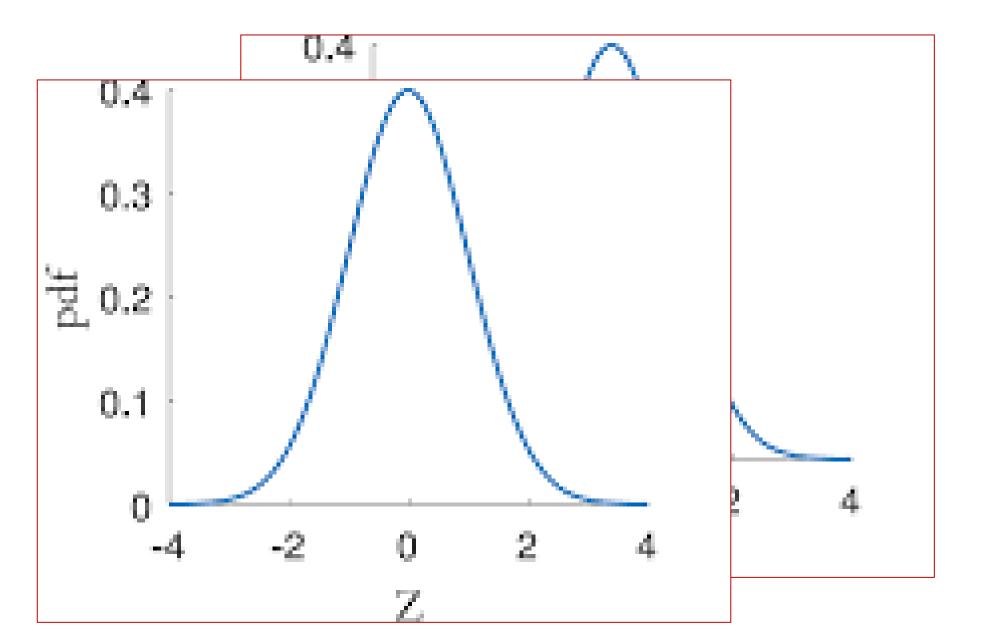


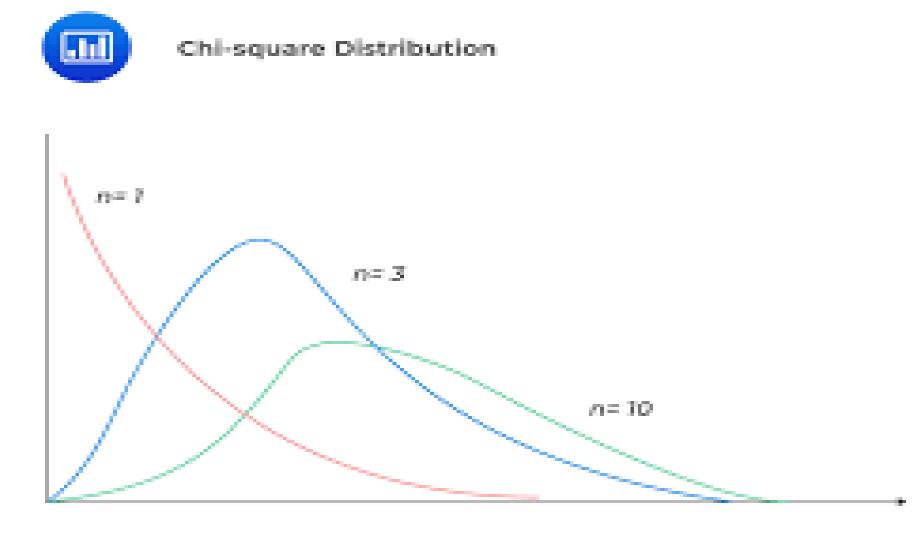
#### Chi-squared Distribution with two degrees of freedom

•Two random var  $Z_1, Z_2$  with std normal distribution

$$Z_1 \sim N(0,1)$$
  $Z_2 \sim N(0,1)$ 

$$Q = Z_1^2 + Z_2^2 \sim \chi_2^2$$

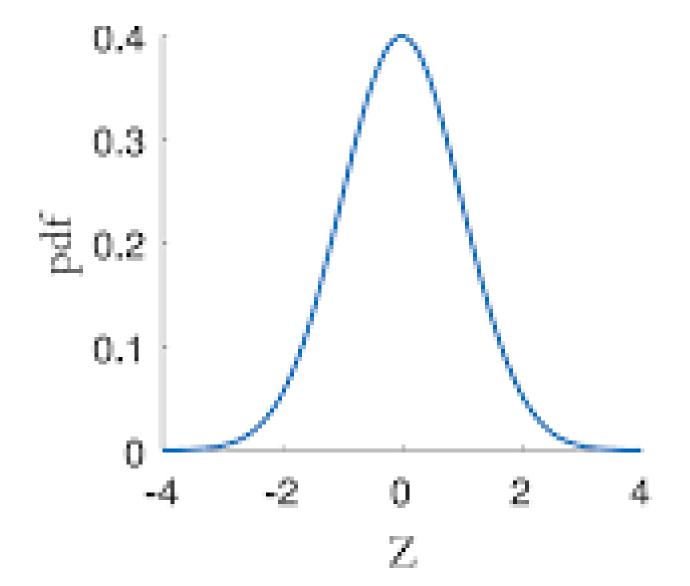




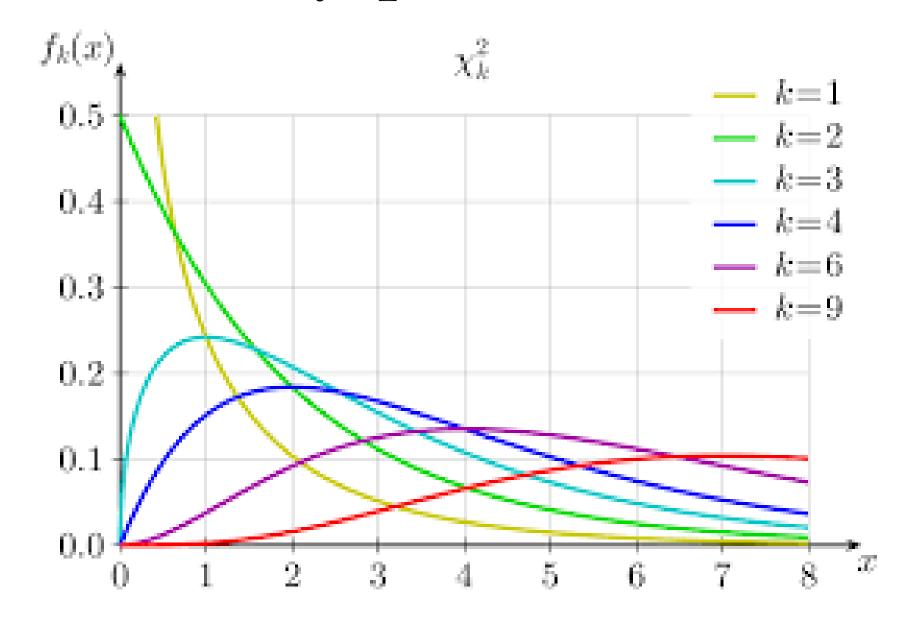
# Chi-squared Distribution with n degrees of freedom

•n random var  $Z_1,..Z_n$  with std normal distribution

$$Z_1 \sim N(0,1)$$
  $Z_n \sim N(0,1)$ 



$$Q = \sum_{i=1}^{n} Z_i^2 \sim \chi_n^2$$



### Revisiting the contingency table for independence

- Titanic dataset
  - Sex & Survived (x & y)

| se      | x fem | ale r | nale |     |
|---------|-------|-------|------|-----|
| survive | d     |       |      |     |
| (       | 0     | 91    | 479  | 570 |
|         | 1 2   | 235   | 109  | 344 |
| a Tot   | al 3  | 26    | 588  | 914 |

|          | Female | Male | Total |
|----------|--------|------|-------|
| Survived | 0.1    | 0.52 | 0.62  |
| Not      | 0.26   | 0.12 | 0.38  |
| Survived |        |      |       |
| Total    | 0.36   | 0.64 | 1     |

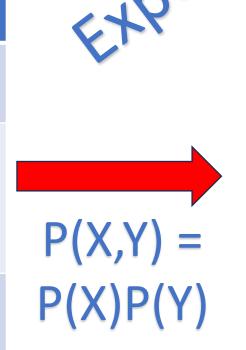
|                 | Female | Male | Total |
|-----------------|--------|------|-------|
| Survived        | .22    | 0.4  | 0.62  |
| Not<br>Survived | 0.14   | 0.25 | 0.38  |
| Total           | 0.36   | 0.64 | 1     |

# Observed counts to expected counts

| sex      | female | male |     |
|----------|--------|------|-----|
| survived |        |      |     |
| 0        | 91     | 479  | 570 |
| 1        | 235    | 109  | 344 |
| ed Total | 326    | 588  | 914 |

|          | Female     | Male       | Total |
|----------|------------|------------|-------|
| Survived | 0.22 x 570 | 0.4 x 570  | 570   |
| Not      | 0.14 x 344 | 0.25 x 344 | 344   |
| Survived |            |            |       |
| Total    | 0.36       | 0.64       | 1     |

|          | Female | Male | Total |
|----------|--------|------|-------|
| Survived | 0.1    | 0.52 | 0.62  |
| Not      | 0.26   | 0.12 | 0.38  |
| Survived |        |      |       |
| Total    | 0.36   | 0.64 | 1     |



|                 | Female | Male | Total |
|-----------------|--------|------|-------|
| Survived        | .22    | 0.4  | 0.62  |
| Not<br>Survived | 0.14   | 0.25 | 0.38  |
| Total           | 0.36   | 0.64 | 1     |

# Distribution of a single column in contingency table

#### female sex survived

235

326

|          | Female |
|----------|--------|
| Survived | 0.1    |
| Not      | 0.26   |
| Survived |        |
| Total    | 0.36   |

#### Binomial distribution with large n

•
$$p=0.1$$

•n = 326 
$$Z = \frac{X - np}{\sqrt{np(1-p)}} \sim \mathbb{N}(0,1)$$
•p=0.1

$$Z^2 = \frac{(X - np)^2}{np(1-p)}$$

$$Z^{2} = \frac{(X - np)^{2}}{np} + \frac{(n - X - np(1 - p))^{2}}{n(1 - p)}$$

$$Z^2 = \sum_{i} \frac{(o_i - e_i)^2}{e_i}$$

#### Chi-Squared distribution

| sex      | female | male |     |
|----------|--------|------|-----|
| survived |        |      |     |
| 0        | 91     | 479  | 570 |
| 1        | 235    | 109  | 344 |
| Total    | 326    | 588  | 914 |

|          | Female     | Male       | Total |
|----------|------------|------------|-------|
| Survived | 0.22 x 570 | 0.4 x 570  | 570   |
| Not      | 0.14 x 344 | 0.25 x 344 | 344   |
| Survived |            |            |       |
| Total    | 0.36       | 0.64       | 1     |

$$\chi^2 = Z^2 = \sum_{all-cells} \frac{(o_i - e_i)^2}{e_i}$$

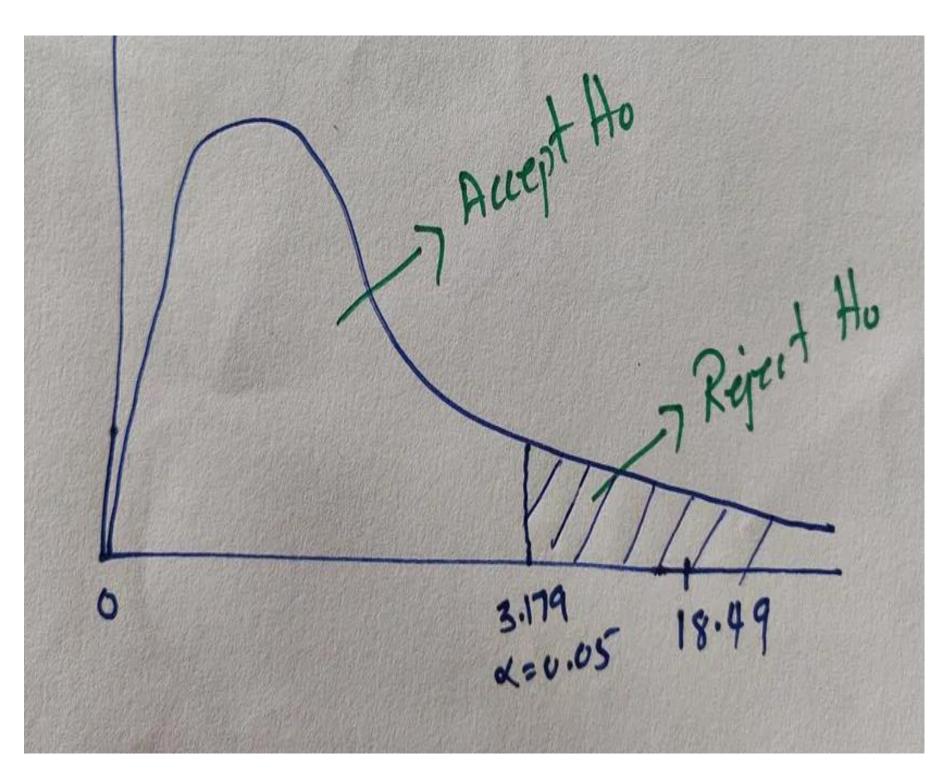
- How many degrees of freedom
- Ho Two features or featuretarget are independent

Ha Features not independent

$$Z_1^2 = \sum_{i \in k} \frac{(o_i - e_i)^2}{e_i} \qquad Z_2^2 = \sum_{i \in k} \frac{(o_i - e_i)^2}{e_i}$$

$$\chi^2 = Z_1^2 + Z_2^2 = \sum_{all-cells} \frac{(o_i - e_i)^2}{e_i}$$
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$$\chi^{2} = Z_{1}^{2} + Z_{2}^{2} + \dots = \sum_{all-cells} \frac{(o_{i} - e_{i})^{2}}{e_{i}}$$



- Ho Two features (or featuretarget) are independent
- Ha Features (or feature-target)
   not independent

- Observed diverges A LOT from expected
- Chi-Squared value increases



# ANOVA

#### ANOVA intuitively from ML perspective

- Categorical Feature: Crime rate = High, Medium, Low
- Numerical target: House price
- Does crime rate have impact on house price?

- Is the price difference between groups a mere chance (noise) or significant enough to be good predictor?
- Quantifying the difference as not significant/significant
- Think of it as lining up all combinations of Ho-Ha between categorical values

$$SSB = \sum_{i=1}^m n_i (ar{x}_i - ar{x})^2$$

$$SSW = \sum_{i=1}^m \sum_{j=1}^n (x_{i,j} - ar{x}_i)^2$$

$$F=rac{SSB/n_1}{SSW/n_2}$$

F-statistic from F distribution Has its own p-values

- •n1, n2 degrees of freedom
- Ho Categorical feature has no variance between groups
- Ha Categorical feature has significant variance between groups

- Ho Categorical target cannot be predicted by a numerical feature
- Ha??

#### Code example in sklearn

```
from sklearn.feature_selection import f_classif

from sklearn.datasets import load_iris
    data = load_iris()
    X = data.data
    y = data.target

# Perform ANOVA
F_scores, p_values = f_classif(X, y)

for feature, F, p in zip(data.feature_names, F_scores, p_values):
```

print(f"Feature: {feature}, F-score: {F}, p-value: {p}")

```
Feature: sepal length (cm), F-score: 119.26450218449871, p-value: 1.6696691907731823e-31 Feature: sepal width (cm), F-score: 49.16004008961098, p-value: 4.492017133311986e-17 Feature: petal length (cm), F-score: 1180.1611822529776, p-value: 2.856776610962102e-91 Feature: petal width (cm), F-score: 960.0071468018025, p-value: 4.169445839445031e-85
```



F-statistic in OLS

$$\hat{y} = h(x) =$$

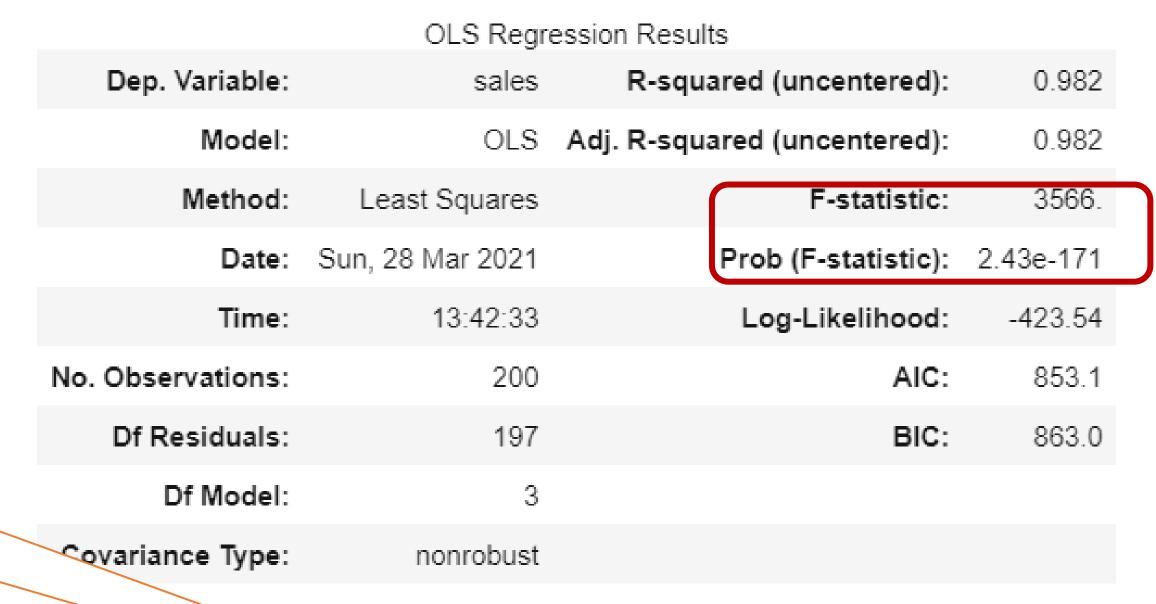
$$w_1 TV + w_2 radio +$$

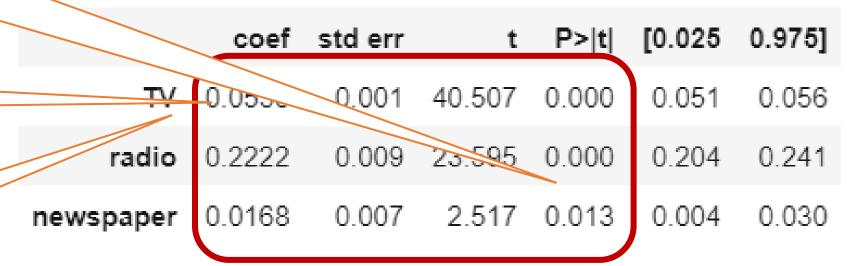
$$w_3 new spaper$$

P value tells us total probability of given value under null hypothesis

Null Hypothesis is coefficient = 0

Alternate
Hypothesis is
coefficient not 0





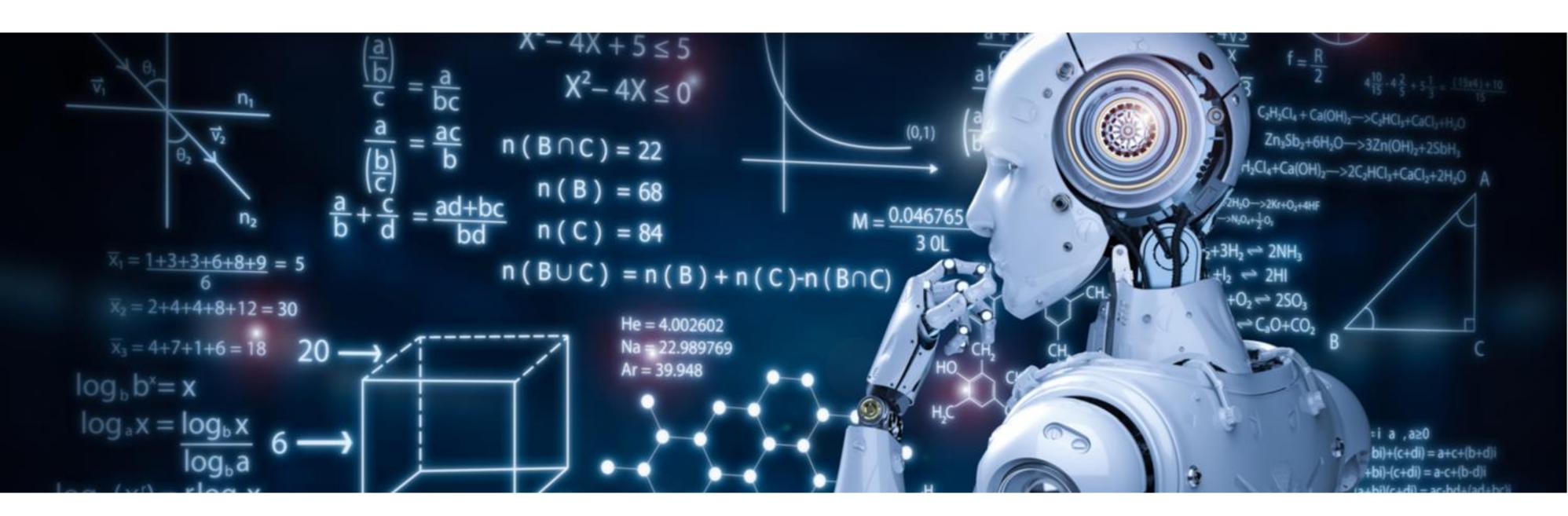
 Omnibus:
 5.982
 Durbin-Watson:
 2.038

 Prob(Omnibus):
 0.050
 Jarque-Bera (JB):
 7.039

 Skew:
 -0.232
 Prob(JB):
 0.0296

Kurtosis: 3.794 Cond. No. 12.6

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F-statistic in OLS

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