

# CS 106S Week 4

## Cancer Detection with K-Nearest Neighbors

Ben Yan, Spring 2025



# Welcome to Week 4 of Class!



Spring

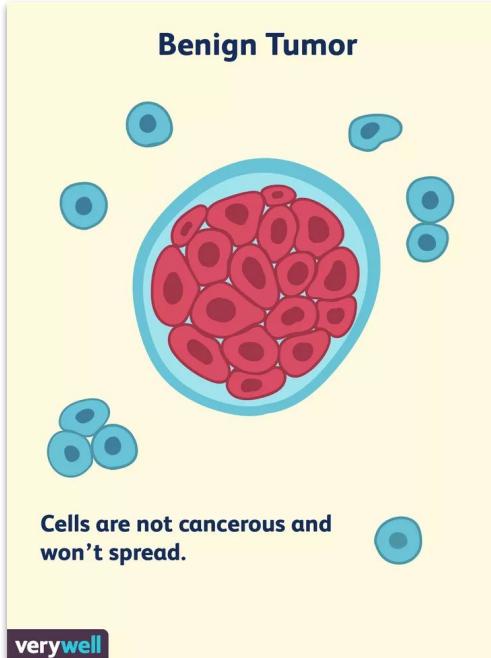
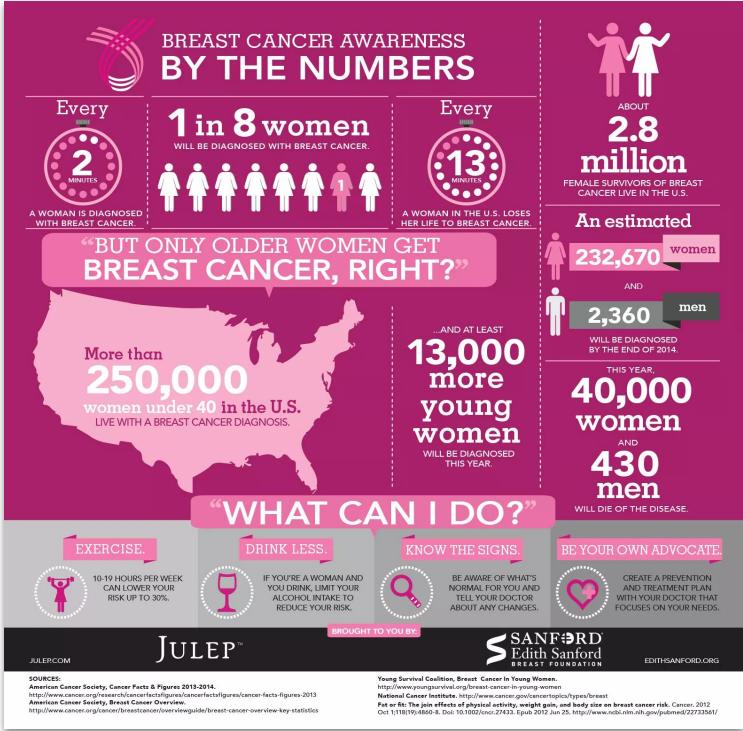


Summer

# Map for Today

- 1 Brief overview of machine learning and its paradigms,  
e.g., supervised vs. unsupervised learning
- 2 Overview of K-nearest neighbors (KNN) algorithm
- 3 project: breast tumor classification with KNN
- 4 implementation & check-off form

# The Problem



# Today's Task

Given medical data about cell growths, can we accurately classify these tumors as **benign** or **malignant**?

Test Sample ID	Correct?	Actual Label	Predicted Label
666942	✓	Benign	Benign
667204	✓	Malignant	Malignant
673637	✓	Benign	Benign
684955	✓	Benign	Benign
688033	✓	Benign	Benign
691628	✓	Malignant	Malignant

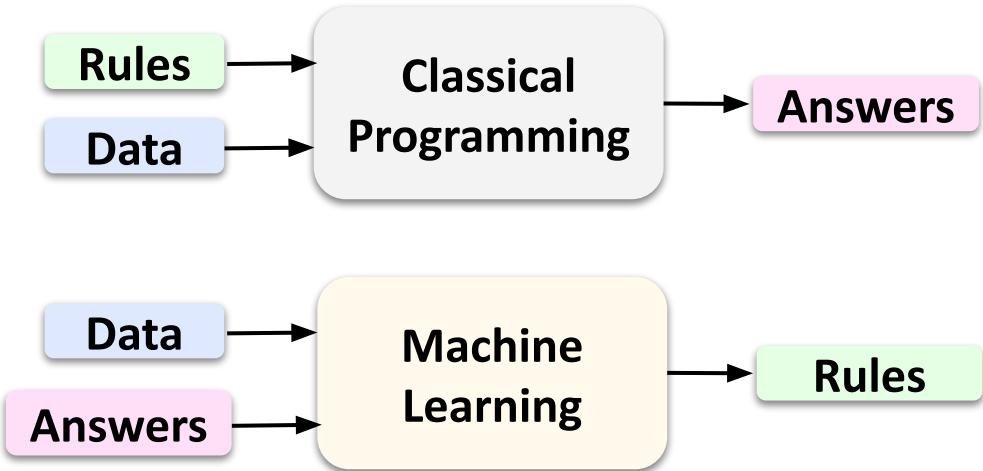
**First, an overview of machine learning**

# Machine Learning

Machine learning is a “field of study that gives computers the ability to learn **without being explicitly programmed**” – Arthur Samuel

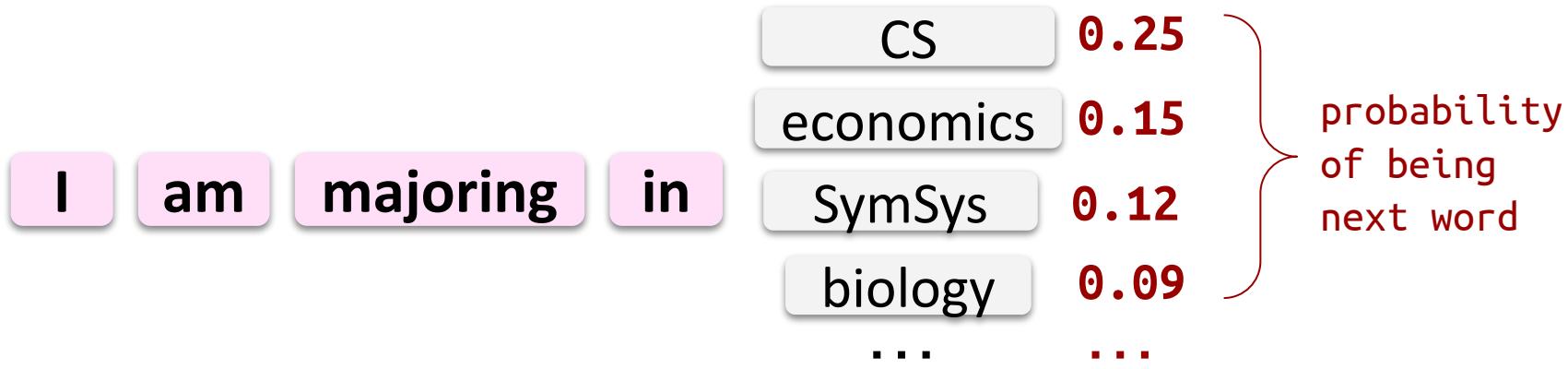
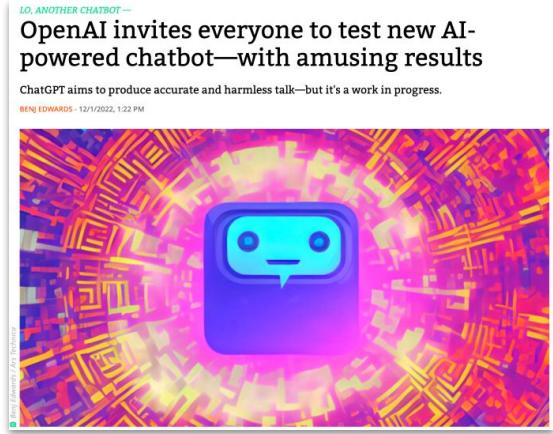


Game-Playing AI  
(AlphaGo)



# Deep Learning

Deep learning (neural networks) requires **very large amounts of data** to learn complex rules, and is the core paradigm behind large language models, or *generative pre-trained transformers*.

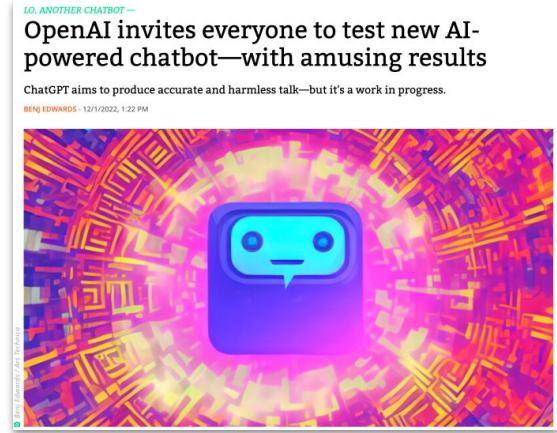


**Next word prediction**—the rule is a **probability distribution** over all possible next words, which is learned from ingesting massive amounts of Internet-based text



# Deep Learning

Deep learning (neural networks) requires **very large amounts of data** to learn complex rules, and is the core paradigm behind large language models, or ***generative pre-trained transformers***.



I am majoring in CS because of

passion 0.45

love 0.35

money! 0.10

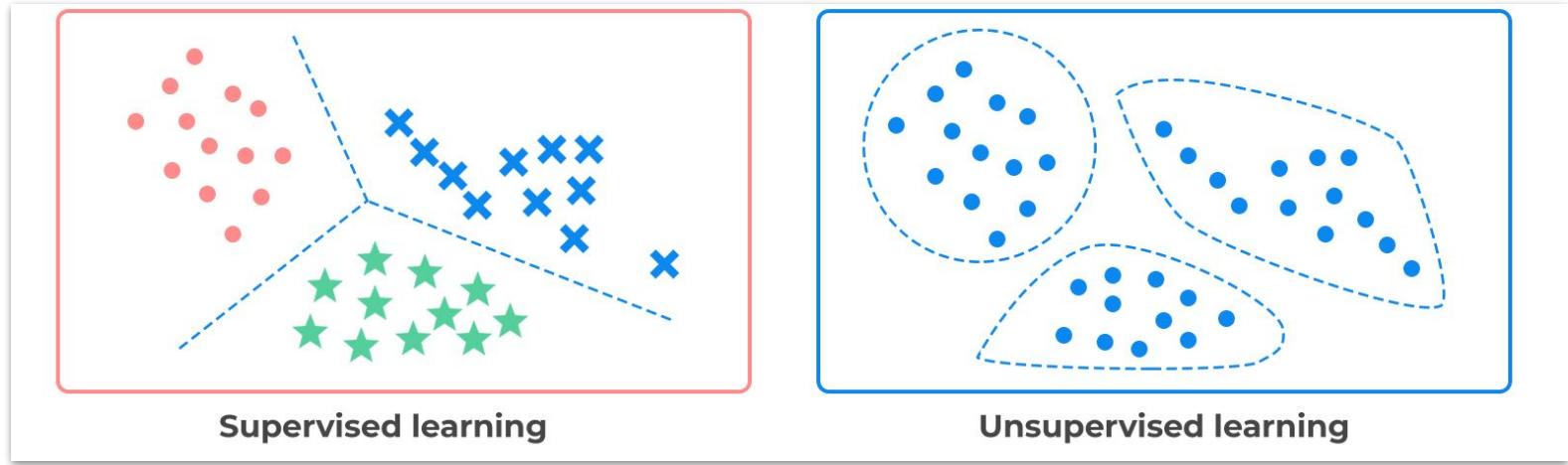
conformity 0.05

...

...

**Next word prediction** – the algorithm, after choosing a word, proceeds to choose the next word from another **learned probability distribution**, and so forth iteratively.

# Supervised vs Unsupervised Learning

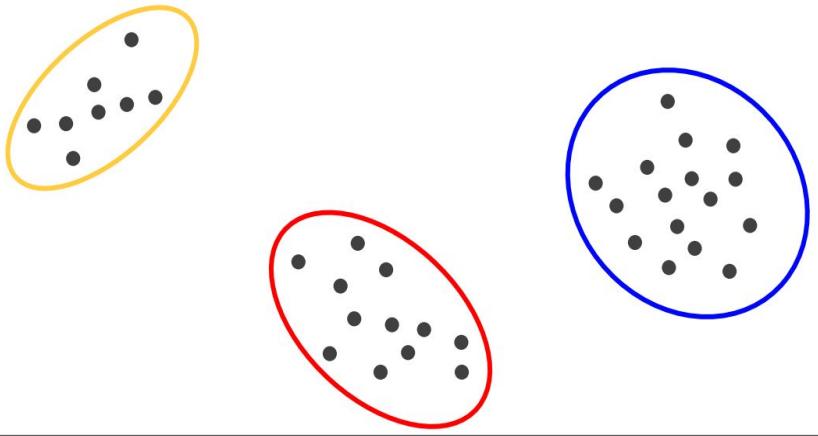


- **Supervised learning** uses **labeled training data** (input features/points and expected outputs) to train an algorithm to predict outputs for new inputs
- **Unsupervised learning** uses **unlabeled data**, and attempts to find patterns/groupings on input features/points without them being explicitly tagged

# Unsupervised Learning: Clustering

A common application of unsupervised learning is **clustering**, which involves grouping a dataset into some number of independent, related clusters.

E,g., Based on locality, we can identify **3 groups** from the (x,y) points below.



Ex. We can **group movies** based on genre.

**tragedy**



**coming-of-age**

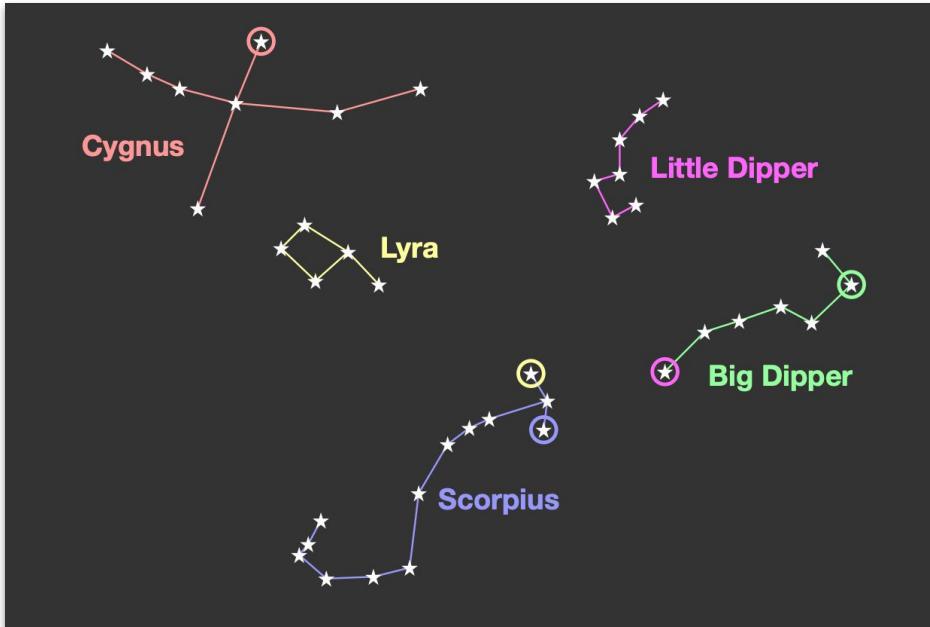


**comedy**



# Clustering Example

## Star Constellations

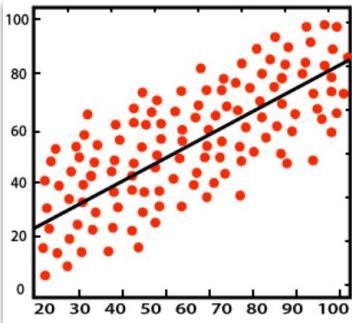


 **Star constellations aren't "real"** – in the sense the lines are imaginary, and the stars aren't actually physically connected.

Instead, they're **clusters / patterns** of stars that we see from Earth. It's a matter of perception.

# Two main types of supervised learning

## Regression



What numerical value is this data point affiliated with?

Avg Temp. Today

51 F

Avg Wind Today

5 mph

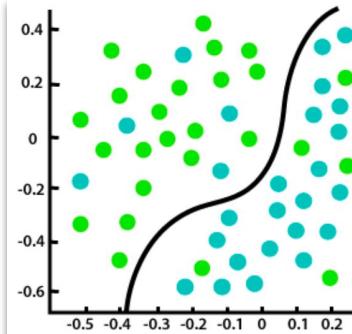
Precip. Today

1 in

Temp (F) Tomorrow

48 F?

## Classification



Which category / label does this data point belong to?

Avg Temp. Today

-3 F

Avg Wind Today

25 mph

Precip. Today

10 in

Weather Type

Sunny

Cloudy

Rainy

Snow



# Our Dataset

	A	B	C	D	E	F
1	666942	1	1	1	1	2
2	667204	7	8	7	6	4
3	673637	3	1	1	1	2
4	684955	2	1	1	1	3

Training: ~630 samples

Testing: ~70 samples

~700 samples (rows) in total

Each row has 11 columns: a sample ID # (col 0), a binary label (last col), and 9 input features (each a value between 1-10) in between.

- In JavaScript, we represent each row as an array of numbers.

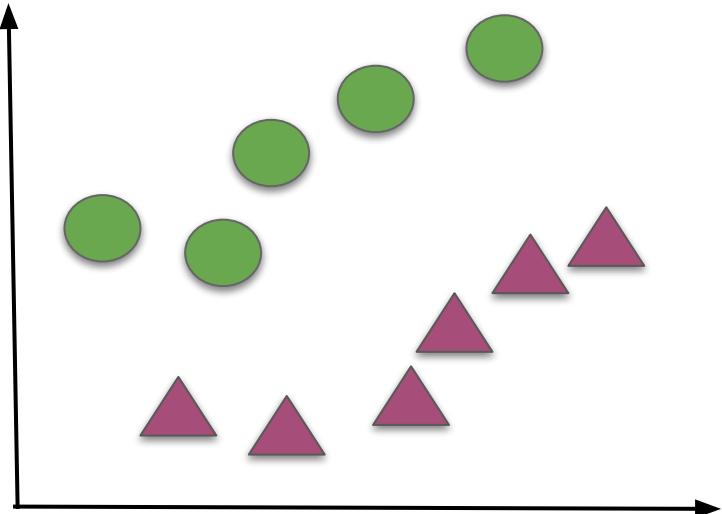
1001	1.0	3.0	4.0	2.0	7.0	6.0	8.0	5.0	1.0	0
------	-----	-----	-----	-----	-----	-----	-----	-----	-----	---

## 9 Input Features

1. Clump Thickness
2. Uniformity of Cell Size
3. Uniformity of Cell Shape
4. Marginal Adhesion
5. Single Epithelial Cell Size
6. Bare Nuclei
7. Bland Chromatin
8. Normal Nucleoli
9. Mitoses

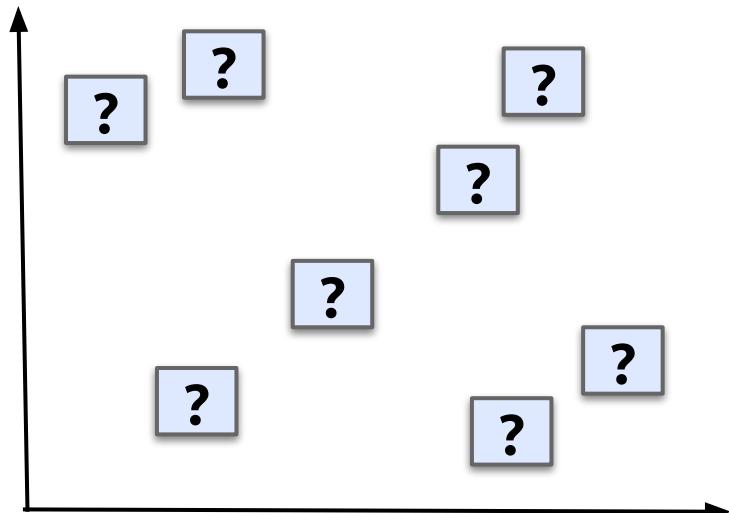
# Training / Testing Split

Training Set



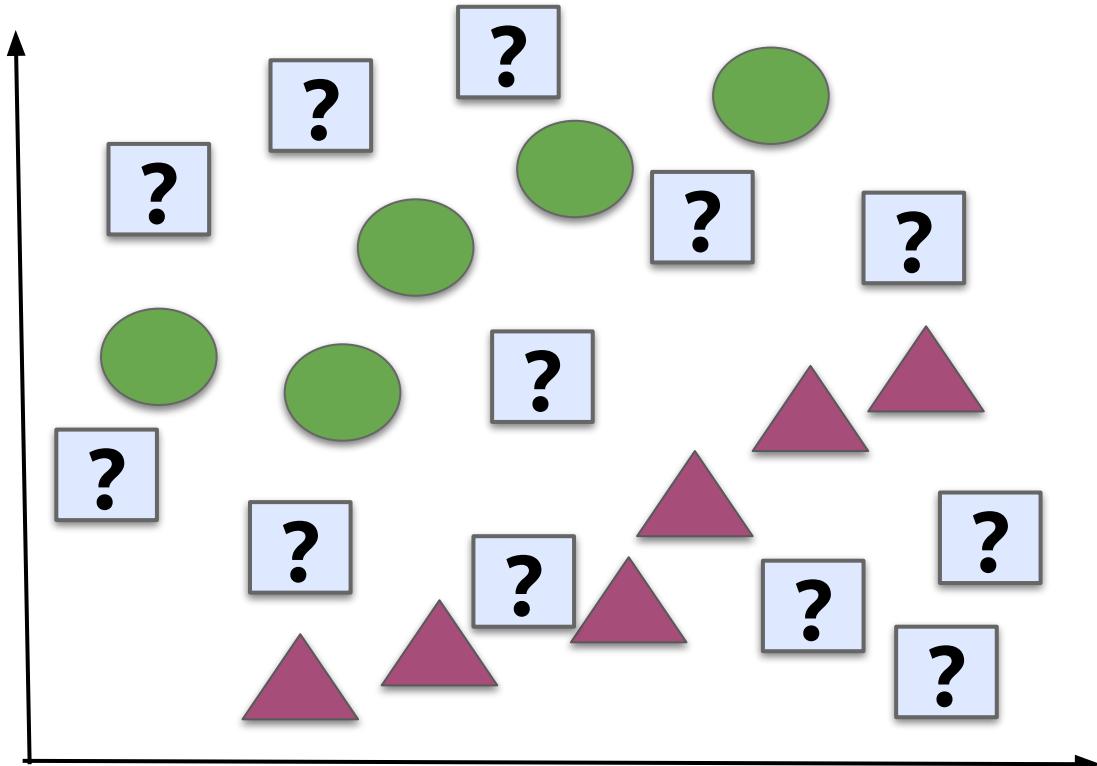
We use this labeled set of tumor samples to train/inform the model

Test Set



We use this to evaluate the model's performance

# How to classify the test set?



## Training Set



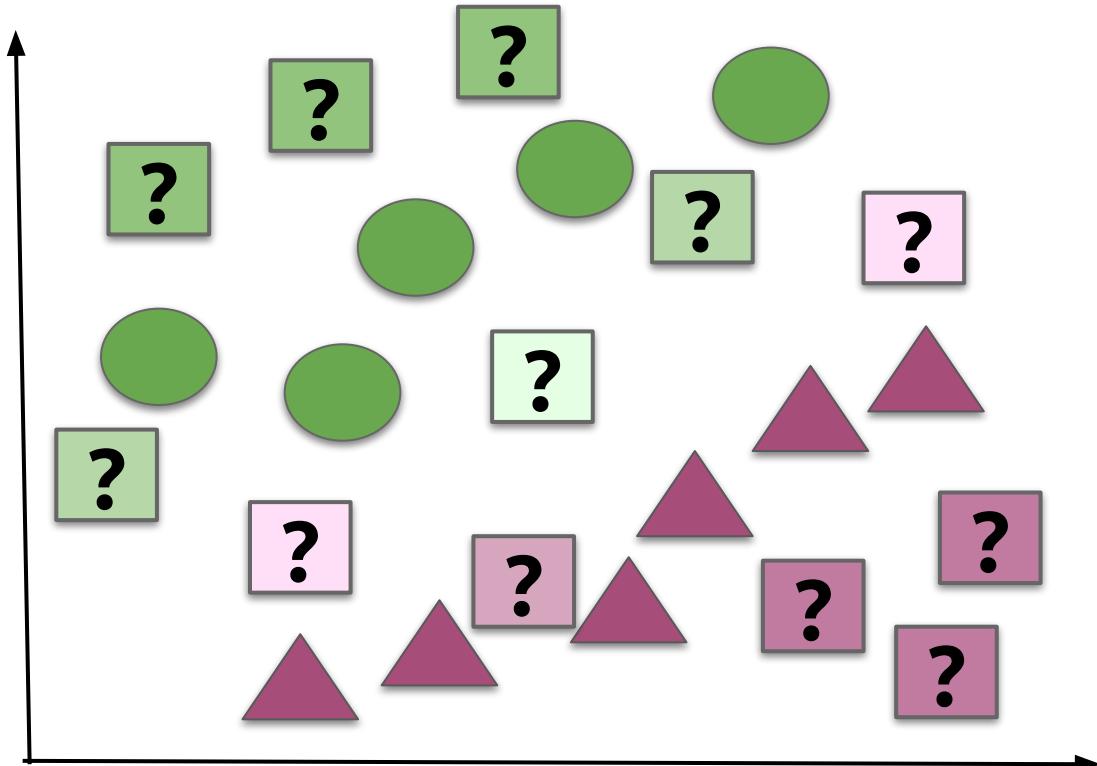
Data points whose **label** the model already knows

## Test Set

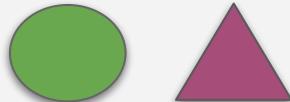


Data points whose **label** the model doesn't know

# Maybe like this:



## Training Set



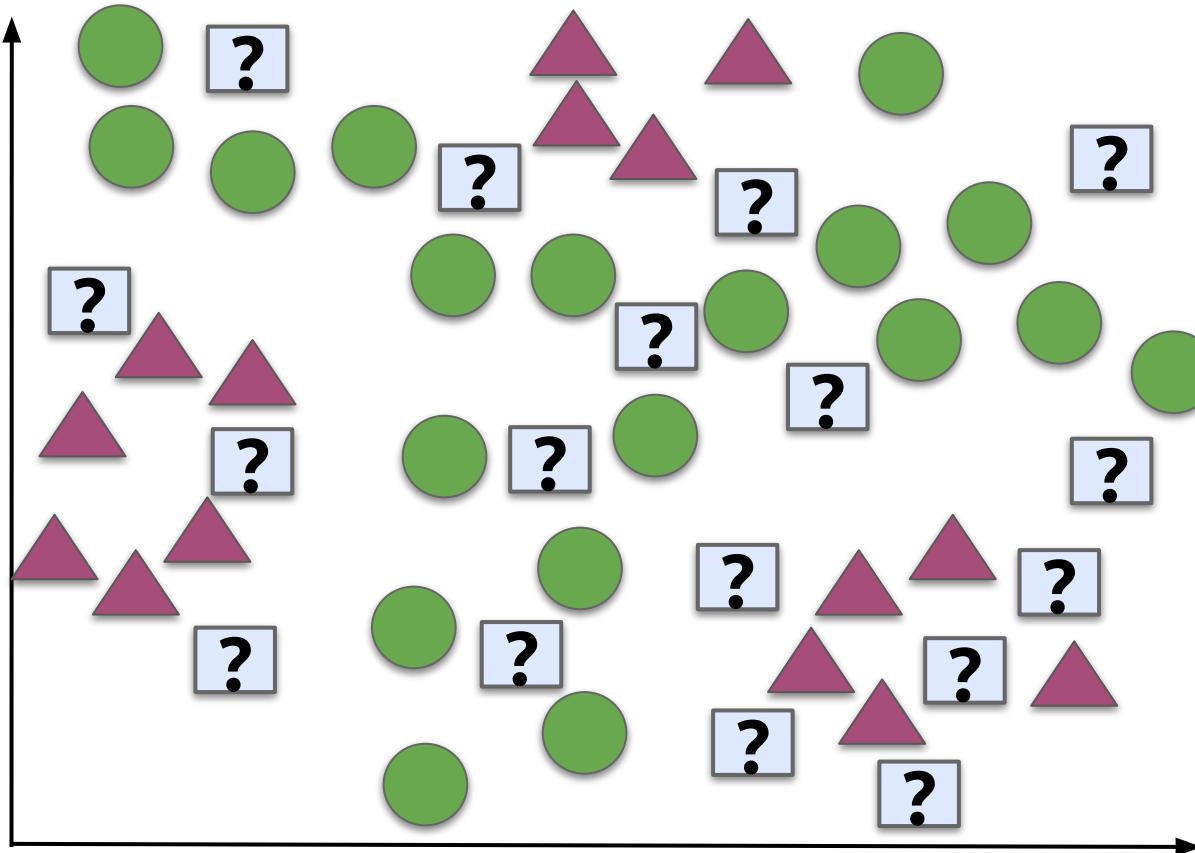
Data points whose **label** the model already knows

## Test Set

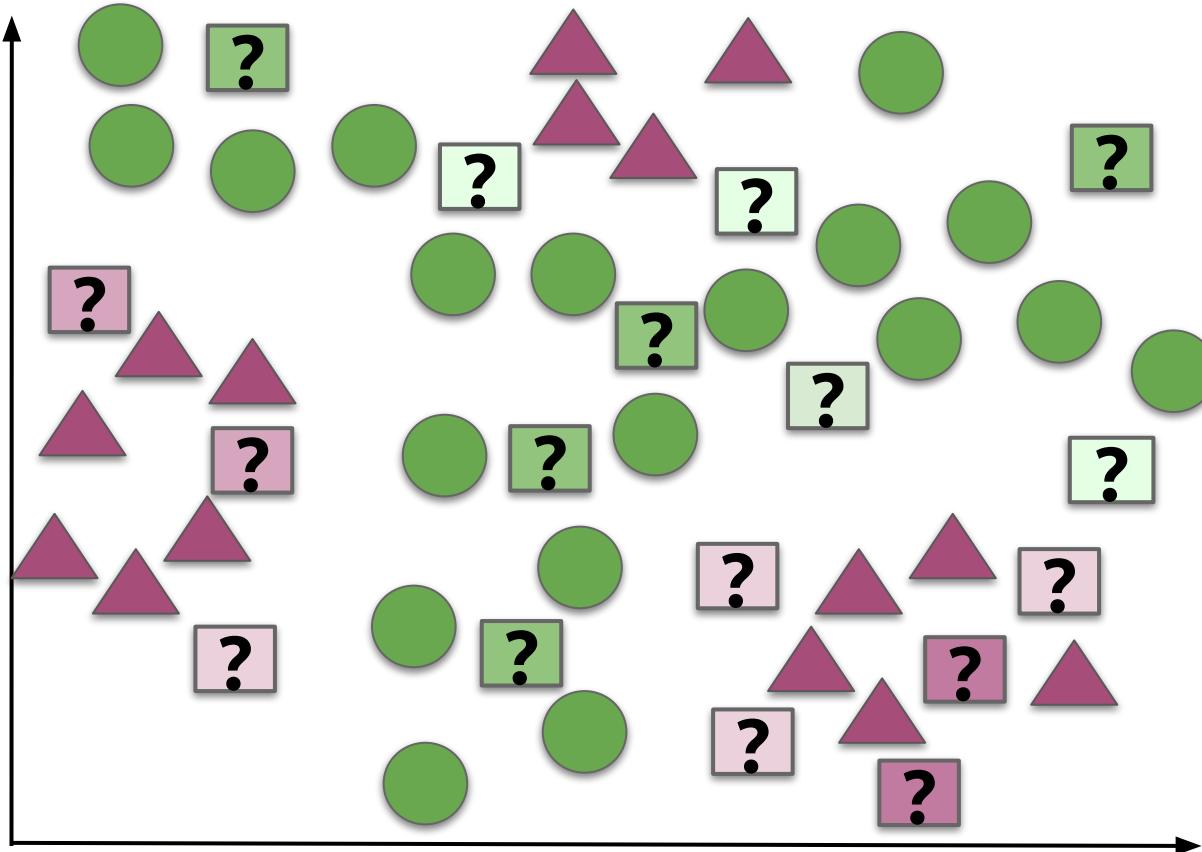


Data points whose **label** the model doesn't know

# How about this one? Oof



# Maybe like this:



## Training Set



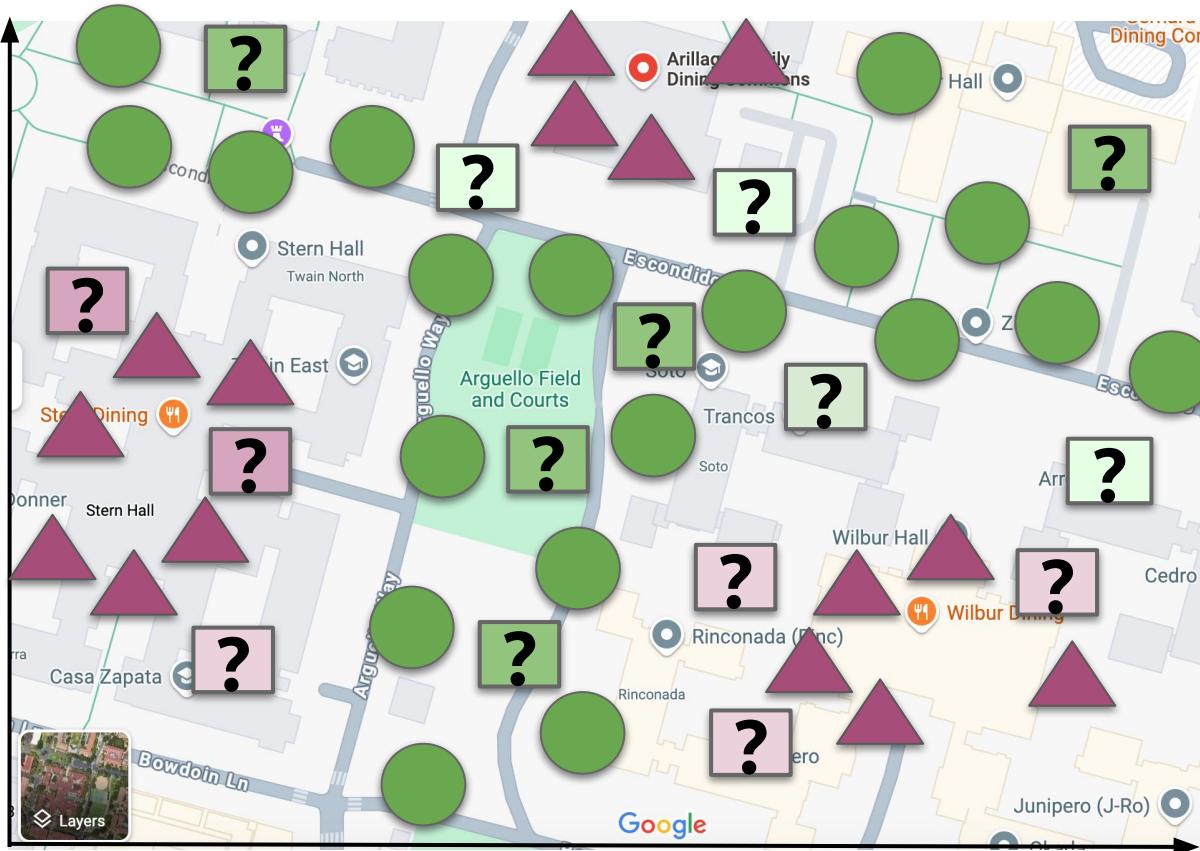
Data points whose **label** the model already knows

## Test Set



Data points whose **label** the model doesn't know

# Real data doesn't look like that...



Within a dining hall,  
or the surrounding  
tables outside

Not within a dining  
hall area

## Training Set



Data points whose **label**  
the model already knows

## Test Set



Data points whose **label**  
the model doesn't know

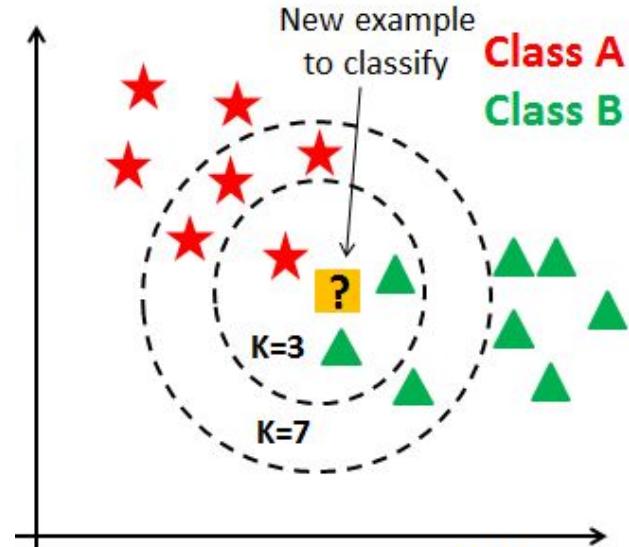
# K-Nearest Neighbors Algorithm

**Guiding Principle:** Use **locality / proximity** in the dataset to predict new points!

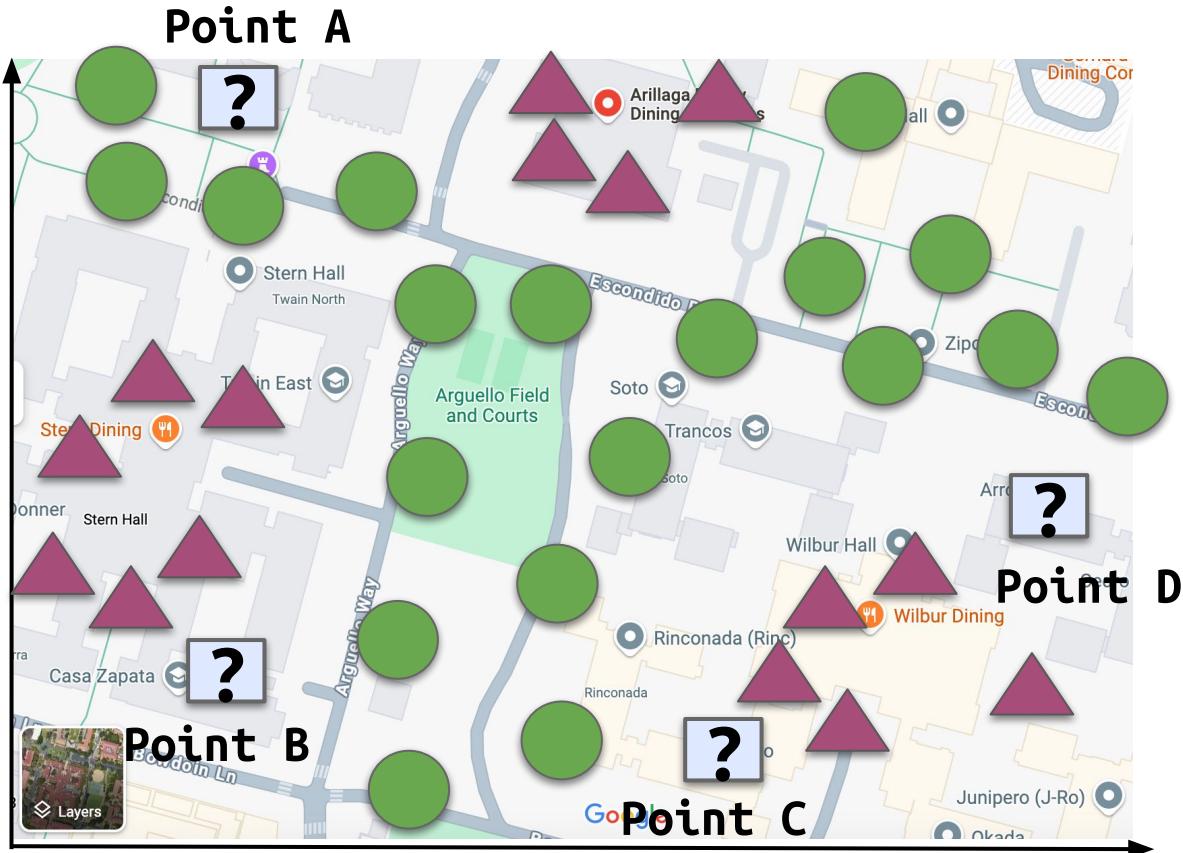
- Points with the **same label** are likely to be **close to each other**
- Points with **different labels** are likely to be **far away** from each other

For each test sample / point to classify:

1. Calculate distance between test sample and every training point.
2. Pick the K training points with the smallest distances to the test sample (i.e. its “nearest neighbors”)
3. Of those K points, do a vote: how many are classified as **malignant** vs. **benign**?
4. Majority wins: pick the majority label



# KNN (K=3): Campus Map Example



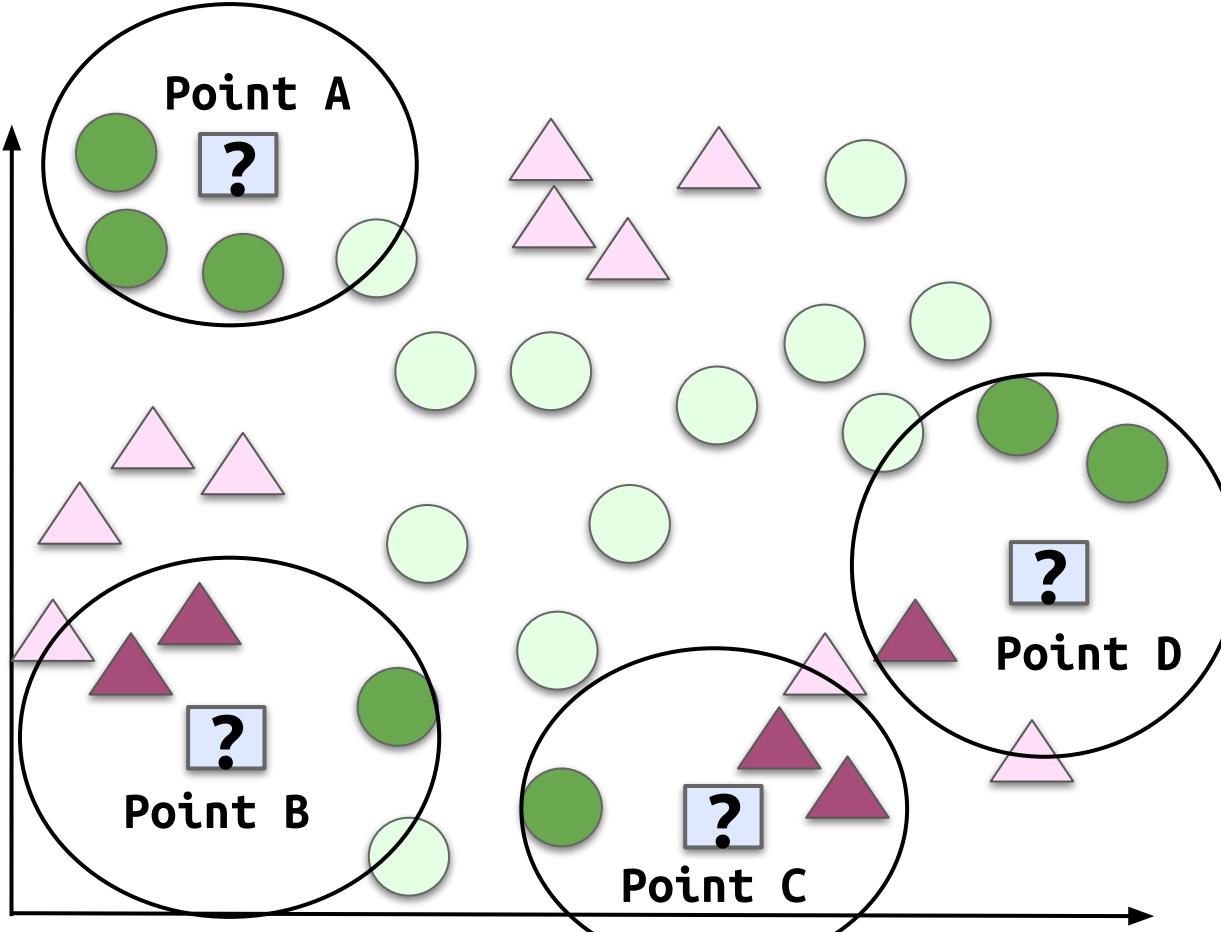
**Point A**  
3 Nearest  
Neighbors  
**Predict**

**Point B**  
3 Nearest  
Neighbors  
**Predict**

**Point C**  
3 Nearest  
Neighbors  
**Predict**

**Point D**  
3 Nearest  
Neighbors  
**Predict**

# For each point, get nearest neighbors



**Point A**

3 Nearest  
Neighbors

Predict



**Point B**

3 Nearest  
Neighbors

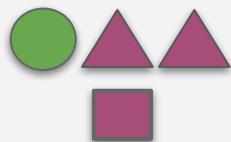
Predict



**Point C**

3 Nearest  
Neighbors

Predict



**Point D**

3 Nearest  
Neighbors

Predict



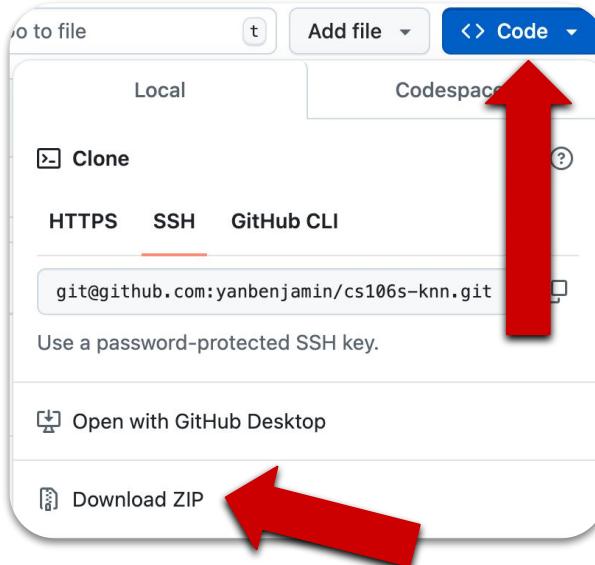
# Let's get started!



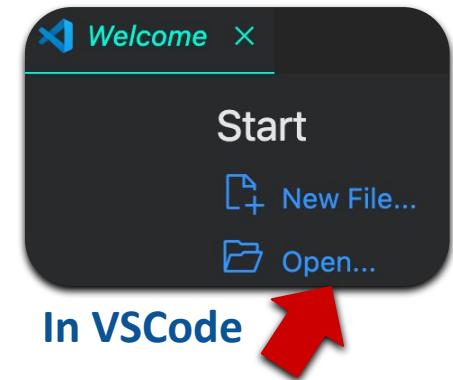
- 1 Navigate to Week 4 of the Schedule section of **cs106s.stanford.edu**

Also, at this link:

<https://github.com/yanbenjamin/cs106s-knn>



- 2 Click the bright “Code” button, then click “Download ZIP”



- 3 Unzip the download (clicking .zip file should do the trick) and open the folder / files in your editor

# Array Methods

`arr.push(element)`

Adds element to end of array.

`arr.pop()`

Removes and returns last element.

`arr.slice(start,finish)`

Returns subarray beginning at index **start** and ending **just before finish**



```
> let arr = [1,2,3];
> arr.push(4);
// arr is now [1,2,3,4]
> newArr = arr.slice(0,2);
// newArr is [1,2]
```

# Object Methods

To **create an object** / dictionary in JS, you list a sequence of **key-value pairs**, enclosed in curly braces.

```
let bratAlbum = {
  "name": "Brat",
  "artist": "Charli XCX",
  "year": 2024
}
```



You can lookup **values** via their **keys**!

```
bratAlbum["artist"] \\ "Charli XCX"
/* alternative syntax */
bratAlbum.year \\ 2024
```

[Link to JavaScript Guide!](#)

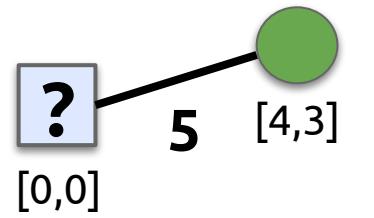


# 3 Milestones for KNN Task

You'll want to work in the `classify.js` file; there's 3 functions to write, each accompanied by tips and documentation! See `index.html` in Chrome for results.

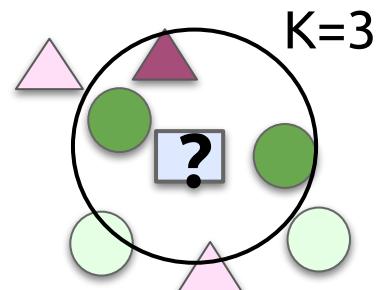
## 1 `calculateDistance(testSample, trainSample)`

Computes the Euclidean **distance** between a test sample and a training sample, i.e.  $\sqrt{\text{sum of squared differences over indices}}$



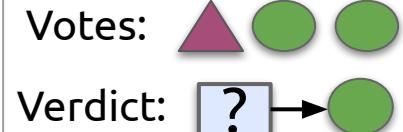
## 2 `findNearestPoints(testSample, trainSamples, K)`

Computes distance of each `trainSample` with `testSample`, determining the `K` closest training samples and returning them.



## 3 `predictSample(testSample, trainSamples, K)`

Among the `K` closest samples, count how many are benign (label 0) and malignant (label 1). Return the majority label / "vote".



# JavaScript: Sorting

Recall: JavaScript is a “vibes”-based language ✨🔥



```
> let arr = [3,2,1];
> arr.sort();
> console.log(arr)
[1, 2, 3]
```

Okay makes sense



```
> let arr = [200,60,3,1000];
> arr.sort();
> console.log(arr)
[1000, 200, 3, 60]
```

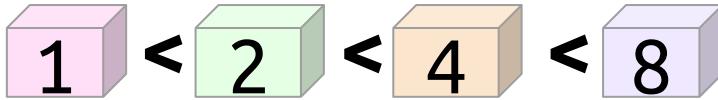
um excuse me what the actual-

**Everything is a string** if you have the willpower! JavaScript interprets and sorts the inputs alphabetically, as though they are strings, so “200” < “3”, “3” < “60”

# We gotta teach JavaScript how to sort 😞



```
> let arr = [200,60,3,1000];  
> arr.sort((a,b) => (a - b));  
> console.log(arr)  
[3, 60, 200, 1000] Okay slay
```



Sorting is really just knowing **how to compare items**

This is a **comparison function**, written here like lambda functions in Python, i.e.

```
lambda a,b: a - b
```

A **comparison function** should return:

- Negative (<0) if **a** goes before **b**
- Positive (>0) if **a** goes after **b**
- 0 if **a** has the same ordering as **b**

In Milestone 2, we have to sort an array of point objects from **lowest to highest distance**, e.g.,

```
arr = [{"distance": 1.2, "id": 7, "label": 0},  
       {"distance": 3.7, "id": 9, "label": 1}, ...]
```

→ **How should we sort?**

```
arr.sort((pointA, pointB) => (pointA.distance - pointB.distance));
```



This is negative when **pointA** has lower distance ✓, positive when **pointA** has higher distance ✓, and zero when they have equal distance ✓.

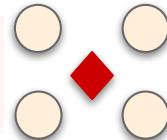


# Optional Extension: K-Means

Code is in the **extensions.js** file. The challenging task is to classify the samples **without any training data or labels**—see the documentation for more details!

## 1 calculateAverage(points)

Computes the average (i.e. center) of an array of points, e.g.,  
for input points = [[0,0,0],[2,4,6]], it should return [1,2,3].



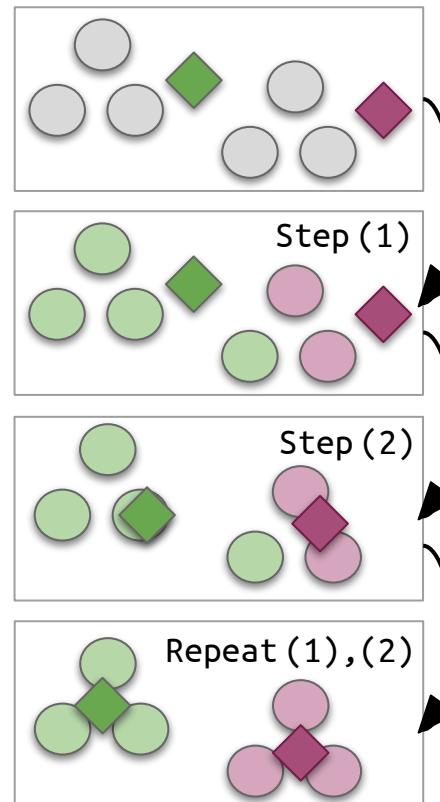
## 2 KMeans(testSamples, numIterations)

The core idea is dividing the sample points into K=2 clusters / groups, keeping track of which samples are in which group, and each group's center, e.g.,

**benignPoints** = [sample1, sample3,...],      **benignCenter** = avg of benignPoints  
**malignantPoints** = [sample2, sample5,...],      **malignantCenter** = avg of malignantPoints

We repeatedly refine the groupings / point assignments with these steps:

- (1) For each testSample, assign it to **benignPoints** if closer to **benignCenter** than **malignantCenter**; otherwise, assign it to **malignantPoints**
- (2) Recalculate the **benign/malignant** centers based on the new assignments.
- (3) Repeat steps (1) and (2) over multiple iterations.



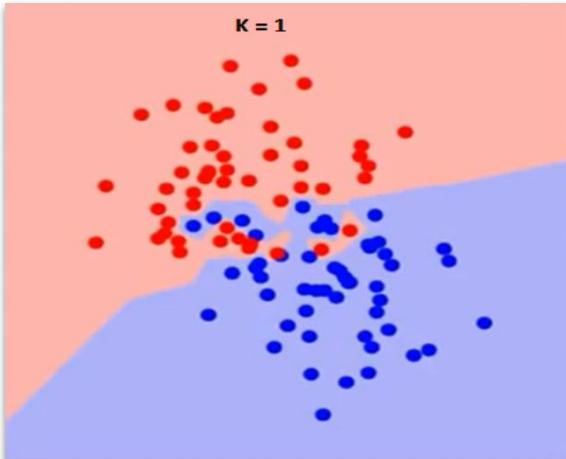
# KNN Predictions

Test Sample ID	Correct?	Actual Label	Predicted Label	K-Nearest Neighbors (K=3)		
666942	✓	Benign	Benign	1059552	1156272	1164066
667204	✓	Malignant	Malignant	1223793	1228152	1296572
673637	✓	Benign	Benign	128059	1133136	1043999
684955	✓	Benign	Benign	1136142	1036172	1067444
688033	✓	Benign	Benign	1190485	1204242	1214092
691628	✓	Malignant	Malignant	314428	1102573	1096800
693702	✓	Benign	Benign	1190485	1204242	1214092
704097	✓	Benign	Benign	1320077	1344449	1035283
704168	✗	Benign	Malignant	1096800	1115282	1253955
706426	✓	Malignant	Malignant	1168736	1185609	1174428
709287	✓	Malignant	Malignant	1205138	1231387	1193544
718641	✓	Benign	Benign	1136142	1185610	1155546
721482	✗	Benign	Malignant	1091262	1148278	1185609
730881	✓	Malignant	Malignant	1176881	1189266	1171710
733639	✓	Benign	Benign	169356	1177027	1197270
733639	✓	Benign	Benign	1177027	1197270	1198641

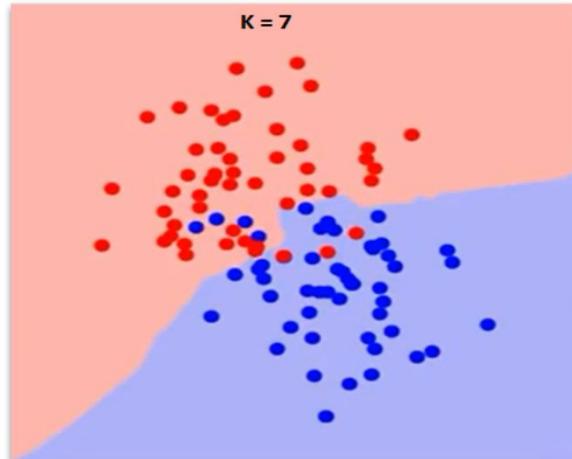
# What value of K is best?

**Case-Specific:** Depends on dataset! Just have to try out different values

**Low K** – Very sensitive to noise, but advantage is selectivity (looking just at the closest possible / most similar points)



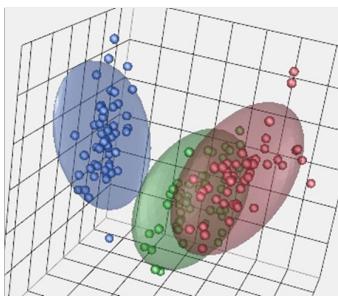
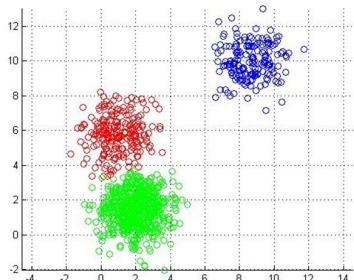
**High K** – Smoother decision boundaries, but at a trade-off of diminishing locality and what qualifies as a nearest neighbor



# Further resources

- More on KNN and classification broadly from CS231N [course notes](#)
- Related algorithms and techniques:

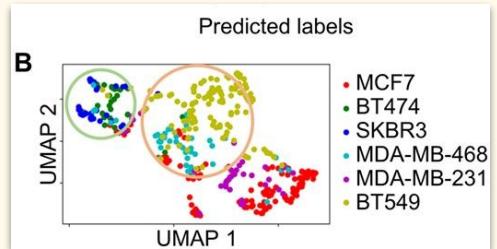
## More on K-means Clustering



## Image-based KNN

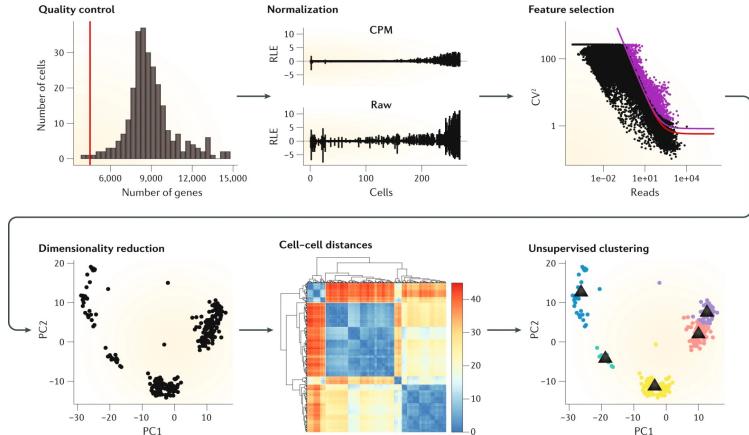


- Real world connection: “Deep learning-based classification of breast cancer cells using transmembrane receptor dynamics” ([Kim et al. 2022](#)) applies deep learning to assess the metastatic potential of breast cancer cells

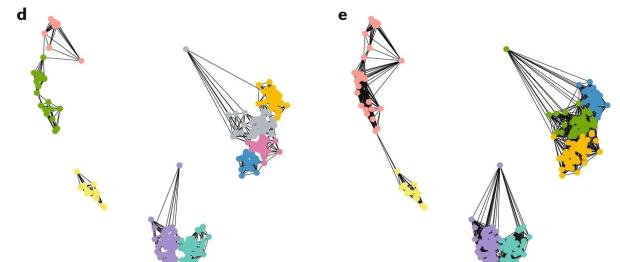
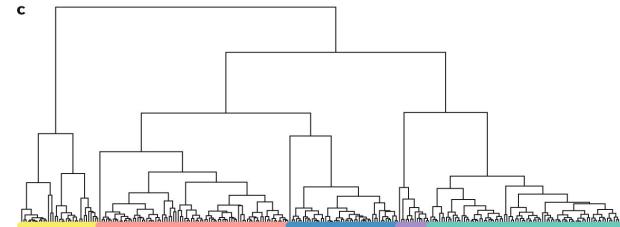
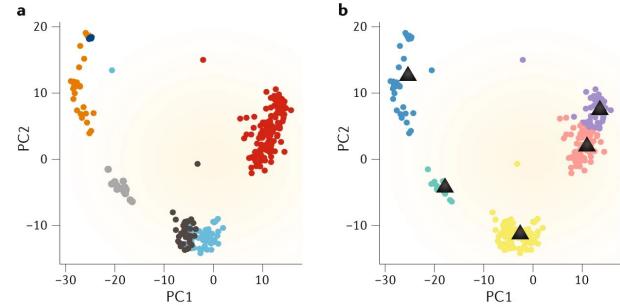


# Further Resources

## clustering scRNA-seq data



Clusters for scRNA sequences reveal  
and categorize **different cell types!**



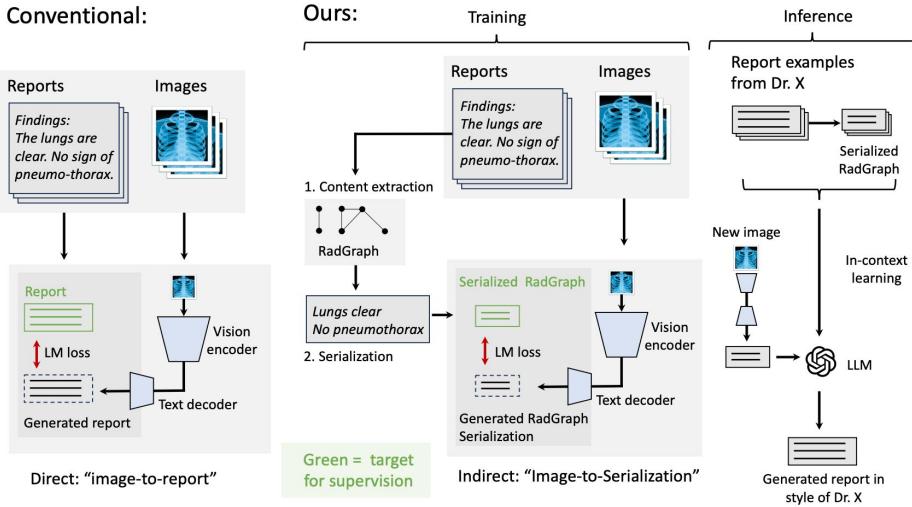
<https://www.nature.com/articles/s41576-018-0088-9/figures/1>  
<https://www.nature.com/articles/s41576-018-0088-9/figures/3>

# Some research I've worked on, '23

Clustering related medical entities in radiology reports—for helping image-to-text models generate **accurate, focused findings** from chest X-rays

Happy to talk more about research on campus / at least my experience with it!

Would also love to hear about other experiences!



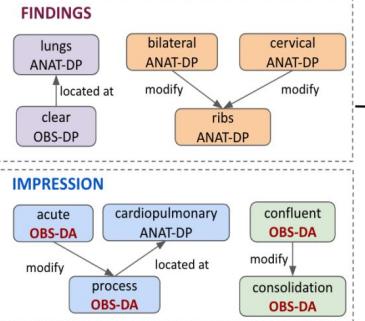
## 1. Clinical Report

**FINDINGS**: The lungs are clear . Incidentally noted are bilateral cervical ribs .

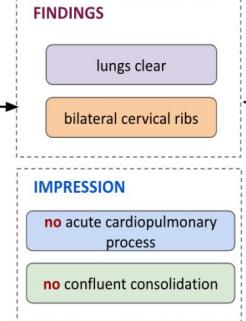
**IMPRESSION** : There is no acute cardiopulmonary process , and no confluent consolidation is present .

Average Token Count: 70.9

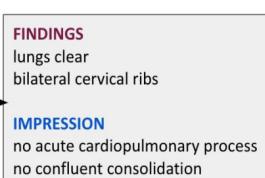
## 2. RadGraph



## 3. Subgraph Serializations



## 4. RadGraph Serialization



Average Token Count: 39.7

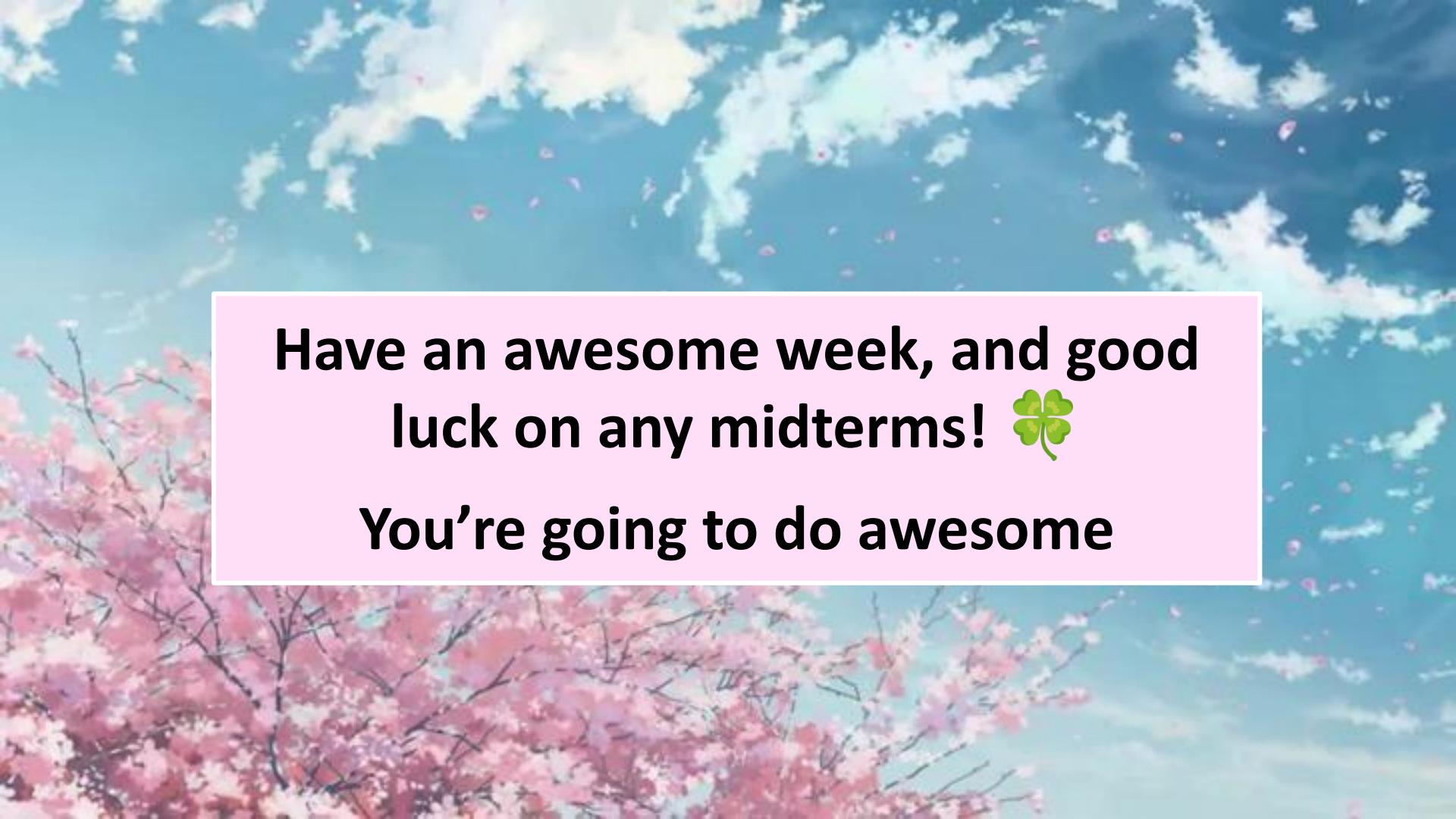
# Check-Off Form

Another **brief check-off form** (< 5 min to complete) for checking attendance!

For today, click the “Check-Off Form” link in the **Week 4** section of [cs106s.stanford.edu](http://cs106s.stanford.edu).

**Thank you so much!**





Have an awesome week, and good  
luck on any midterms! 🍀

You're going to do awesome