Machine Learning

- Many people imagine that data science is mostly machine learning and that data scientists mostly build and train and tweak machine learning models all day long.
- In fact, data science is mostly turning business problems into data problems and collecting data and understanding data and cleaning data and formatting data, after which machine learning is almost an afterthought.

Modeling

- Before we can talk about machine learning, we need to talk about models.
- What is a model? It's simply a specification of a mathematical (or probabilistic) relationship that exists between different variables.
- For instance, if you're trying to raise money for your social networking site, you might build a business model (likely in a spreadsheet) that takes inputs like "number of users," "ad revenue per user," and "number of employees" and outputs your annual profit for the next several years.
- A cookbook recipe entails a model that relates inputs like "number of eaters" and "hungriness" to quantities of ingredients needed.

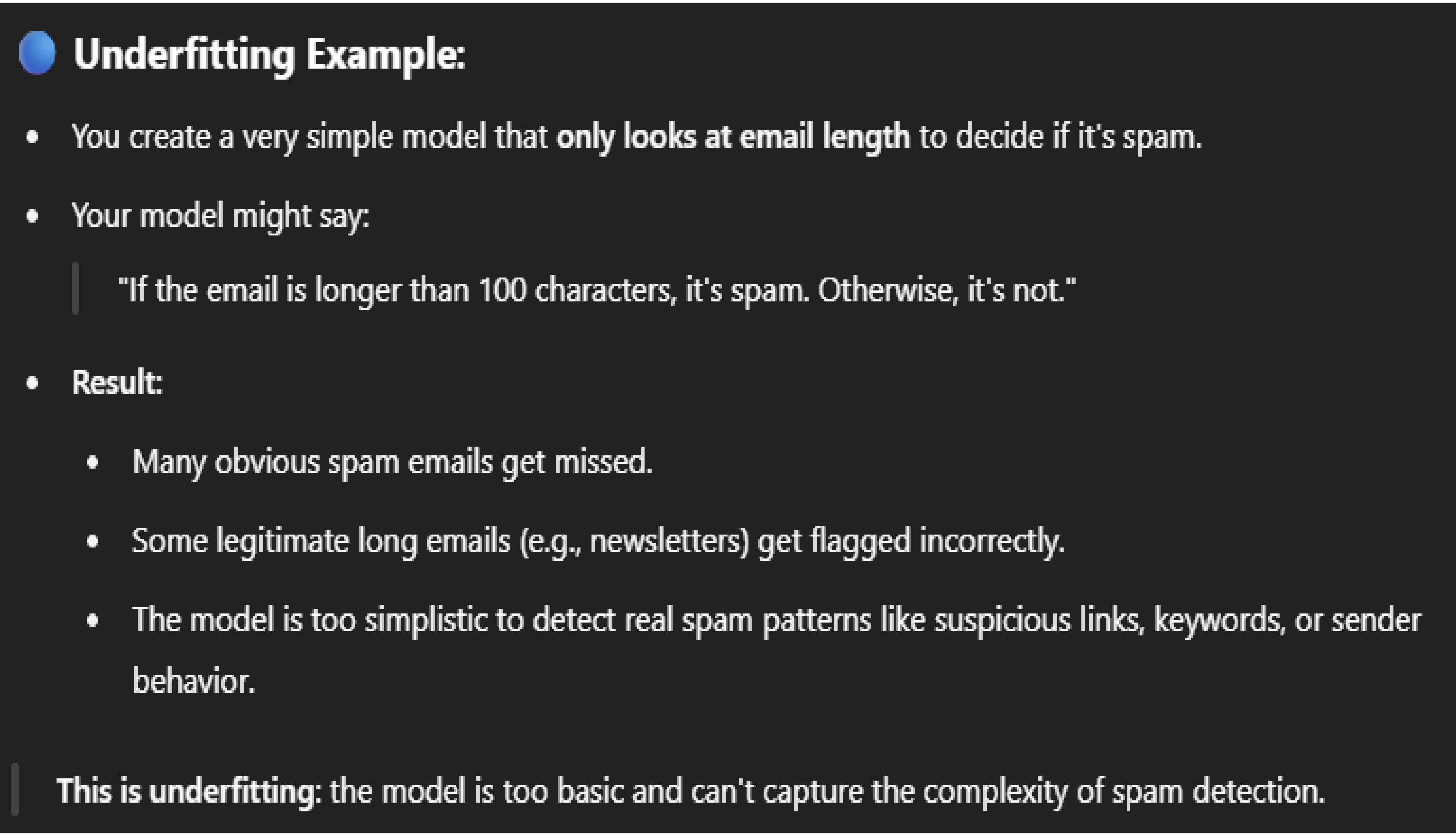
What Is Machine Learning?

- Machine learning refers to creating and using models that are learned from data.
- Our goal will be to **use existing data to develop models** that we can use to **predict** various outcomes for new data, such as:
  - Whether an email message is spam or not
  - Whether a credit card transaction is fraudulent
  - Which advertisement a shopper is most likely to click on
  - Which football team is going to win the Super Bowl

What Is Machine Learning?

- **Supervised models →** in which there is a set of data labeled with the correct answers to learn from
- **Unsupervised models →** in which there are no such labels.
- **Semisupervised →** in which only some of the data are labeled
- **Online →** in which the model needs to continuously adjust to newly arriving data
- **Reinforcement →** in which, after making a series of predictions, the model gets a signal indicating how well it did.
- Before we can do that, we need to better understand the fundamentals of machine learning

Overfitting and Underfitting



🔵 **Underfitting Example:**

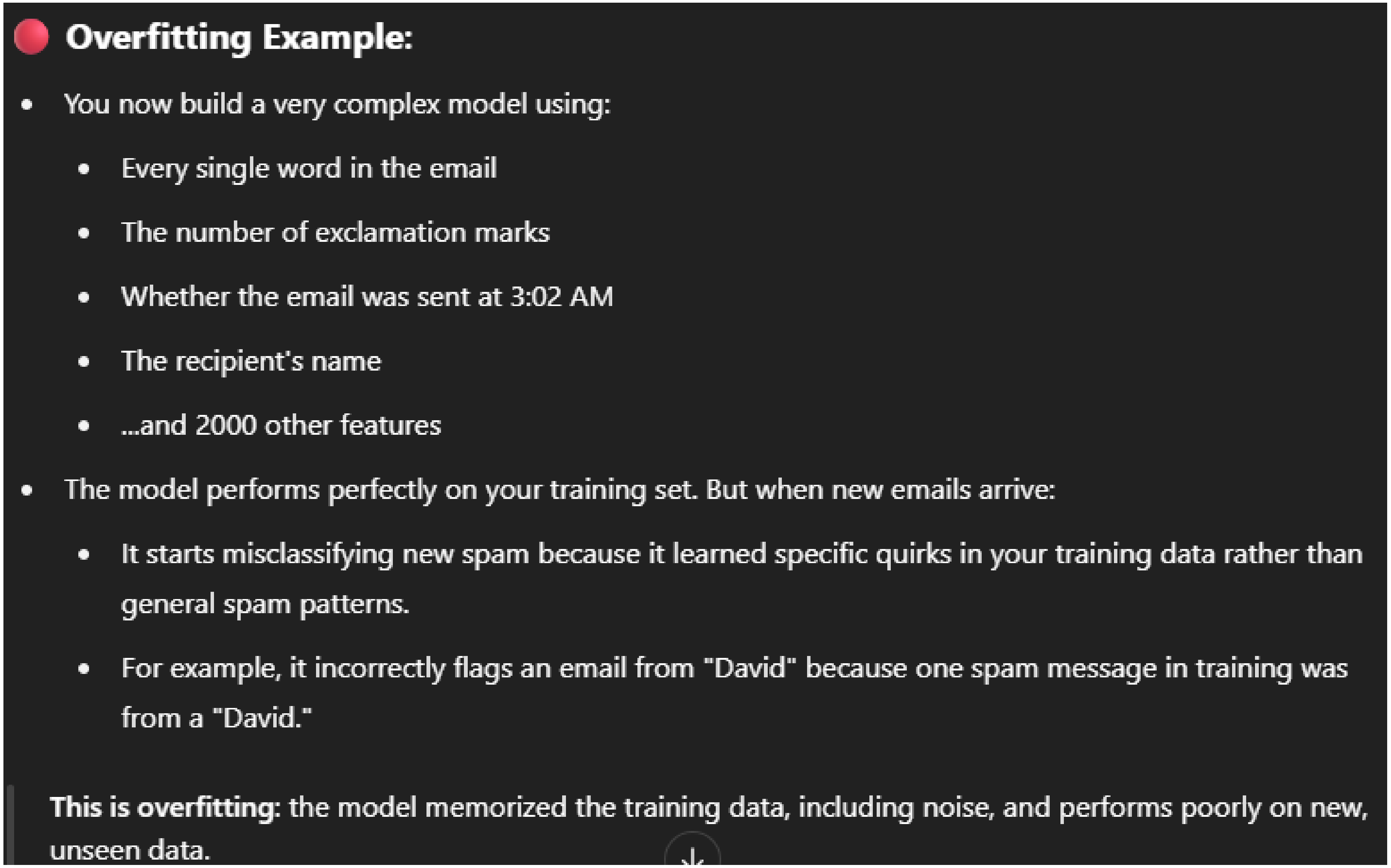
- You create a very simple model that **only looks at email length** to decide if it's spam.
- Your model might say:

  > "If the email is longer than 100 characters, it's spam. Otherwise, it's not."

- **Result:**
  - Many obvious spam emails get missed.
  - Some legitimate long emails (e.g., newsletters) get flagged incorrectly.
  - The model is too simplistic to detect real spam patterns like suspicious links, keywords, or sender behavior.

> **This is underfitting:** the model is too basic and can't capture the complexity of spam detection.

Overfitting and Underfitting

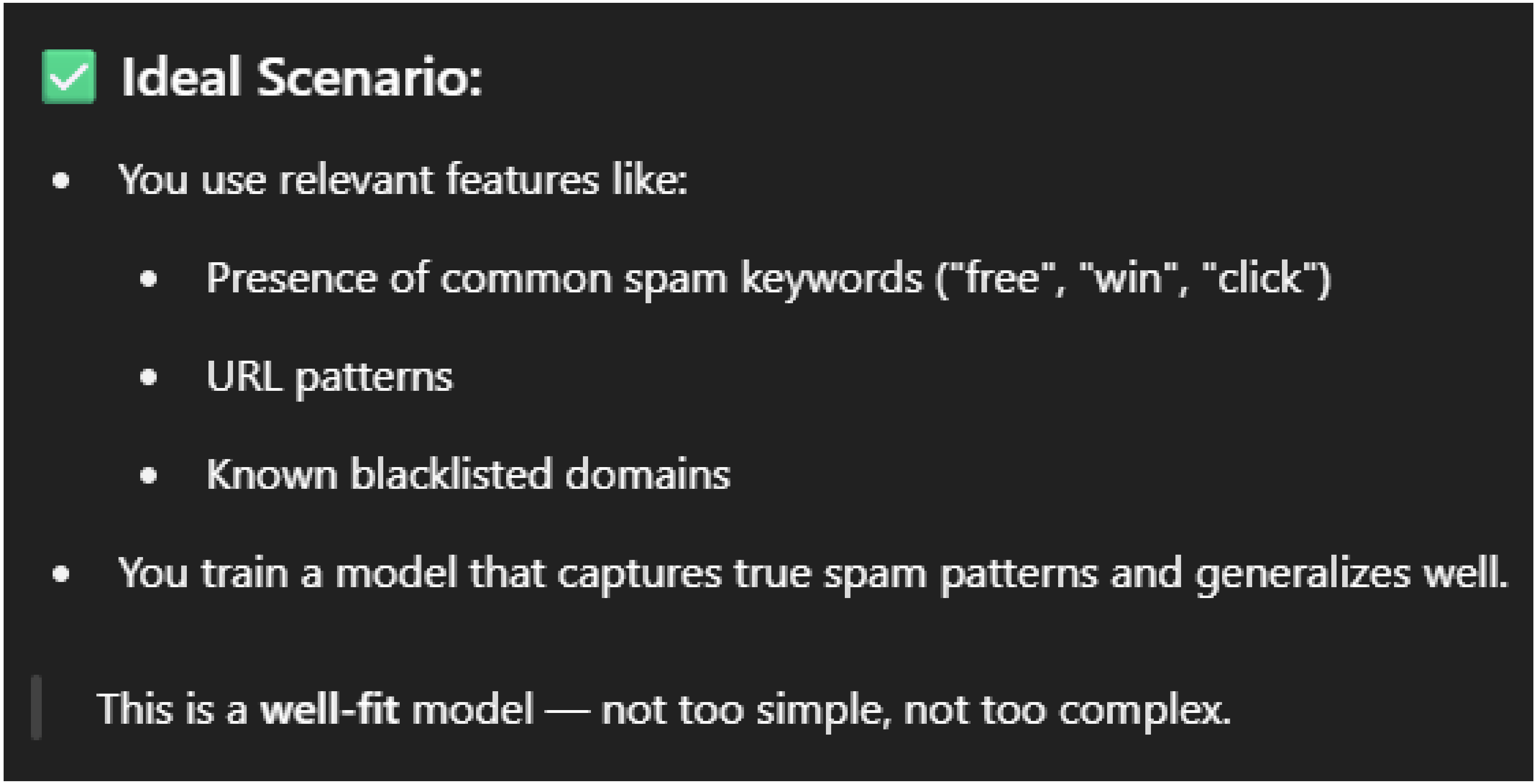


🔴 **Overfitting Example:**

- You now build a very complex model using:
  - Every single word in the email
  - The number of exclamation marks
  - Whether the email was sent at 3:02 AM
  - The recipient's name
  - ...and 2000 other features
- The model performs perfectly on your training set. But when new emails arrive:
  - It starts misclassifying new spam because it learned specific quirks in your training data rather than general spam patterns.
  - For example, it incorrectly flags an email from "David" because one spam message in training was from a "David."

This is overfitting: the model memorized the training data, including noise, and performs poorly on new, unseen data.

Overfitting and Underfitting



✅ Ideal Scenario:

- You use relevant features like:
    - Presence of common spam keywords ("free", "win", "click")
    - URL patterns
    - Known blacklisted domains
- You train a model that captures true spam patterns and generalizes well.

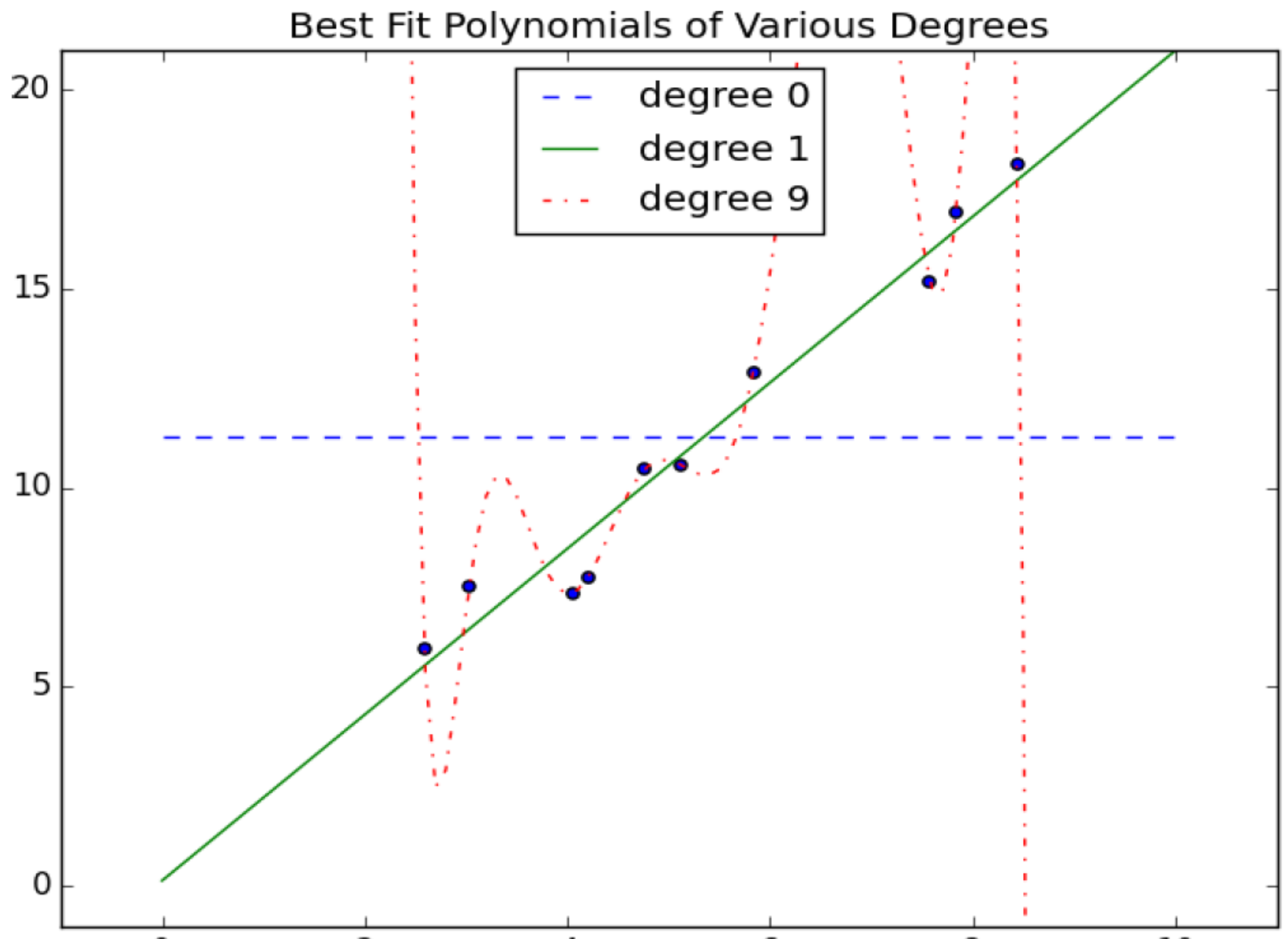
> This is a **well-fit** model — not too simple, not too complex.

Overfitting and Underfitting

- A common danger in machine learning is ***overfitting***—producing a model that performs well on the data you train it on but generalizes poorly to any new data.
- This could involve learning noise in the data. Or it could involve learning to identify specific inputs rather than whatever factors are actually predictive for the desired output.
- The other side of this is ***underfitting***—producing a model that doesn't perform well even on the training data, although typically when this happens you decide your model isn't good enough and keep looking for a better one.

Overfitting and Underfitting

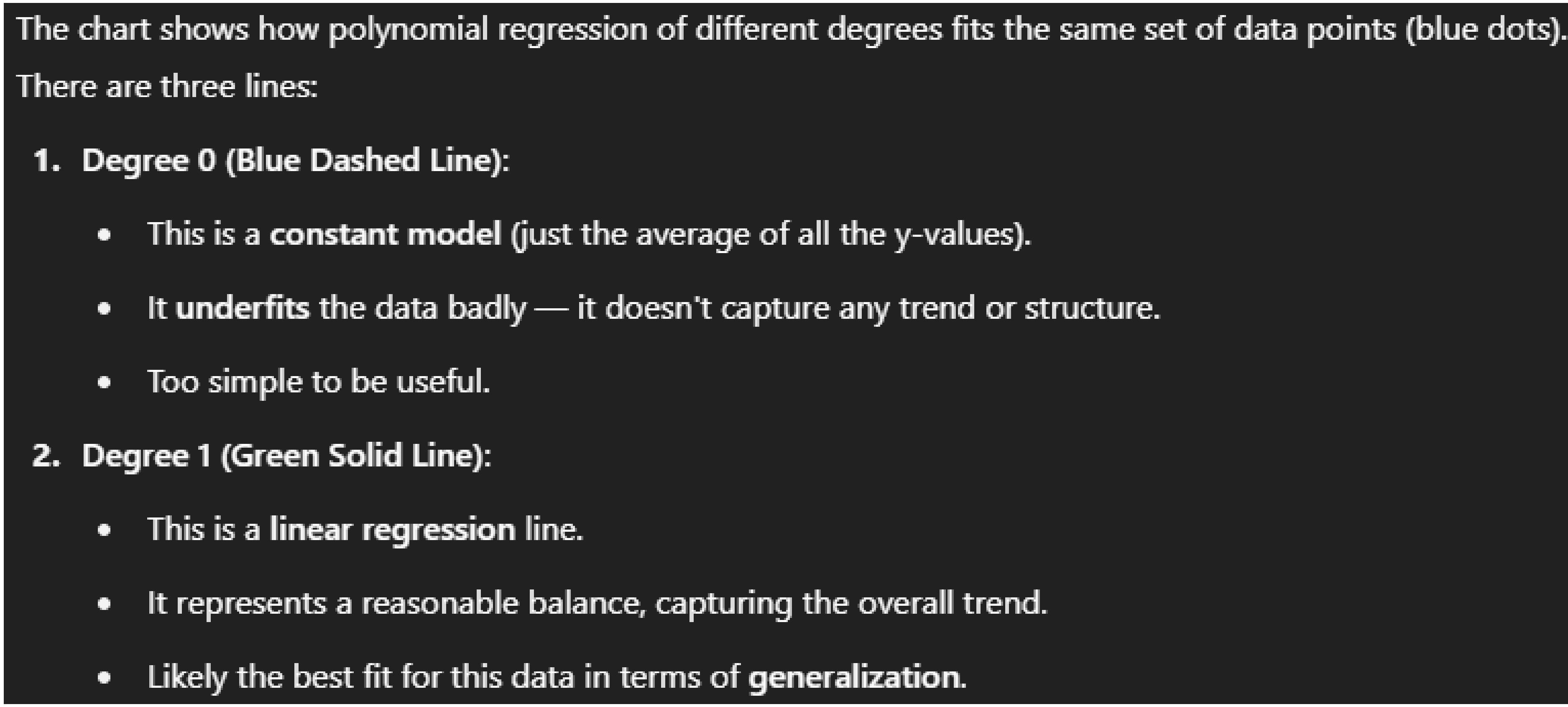
- In the figure, we've fit three polynomials to a sample of data.



Overfitting and underfitting

Overfitting and Underfitting

- In the figure, we’ve fit three polynomials to a sample of data.



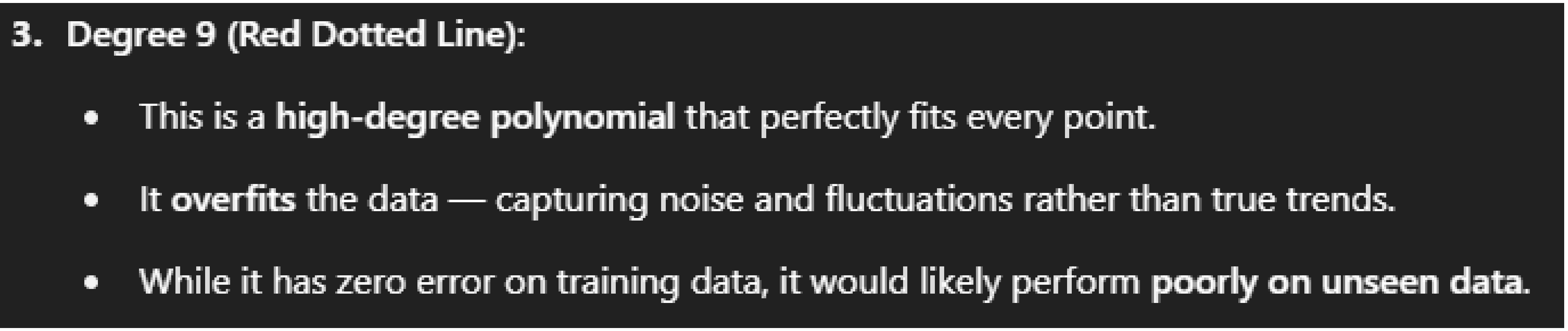
The chart shows how polynomial regression of different degrees fits the same set of data points (blue dots).

There are three lines:

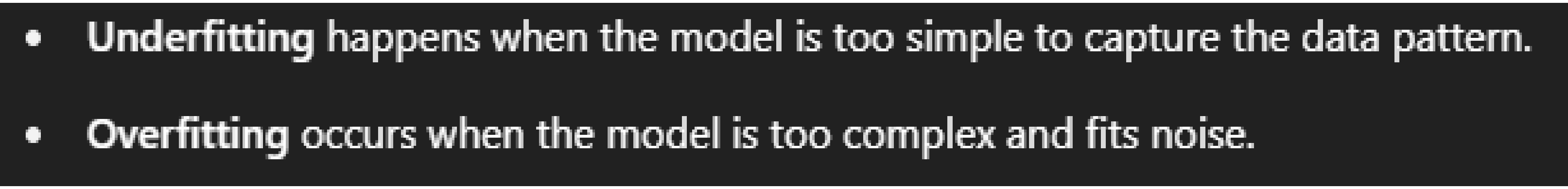
1. **Degree 0 (Blue Dashed Line):**
   - This is a **constant model** (just the average of all the y-values).
   - It **underfits** the data badly — it doesn't capture any trend or structure.
   - Too simple to be useful.
2. **Degree 1 (Green Solid Line):**
   - This is a **linear regression** line.
   - It represents a reasonable balance, capturing the overall trend.
   - Likely the best fit for this data in terms of **generalization**.

Overfitting and Underfitting

- In the figure, we've fit three polynomials to a sample of data.



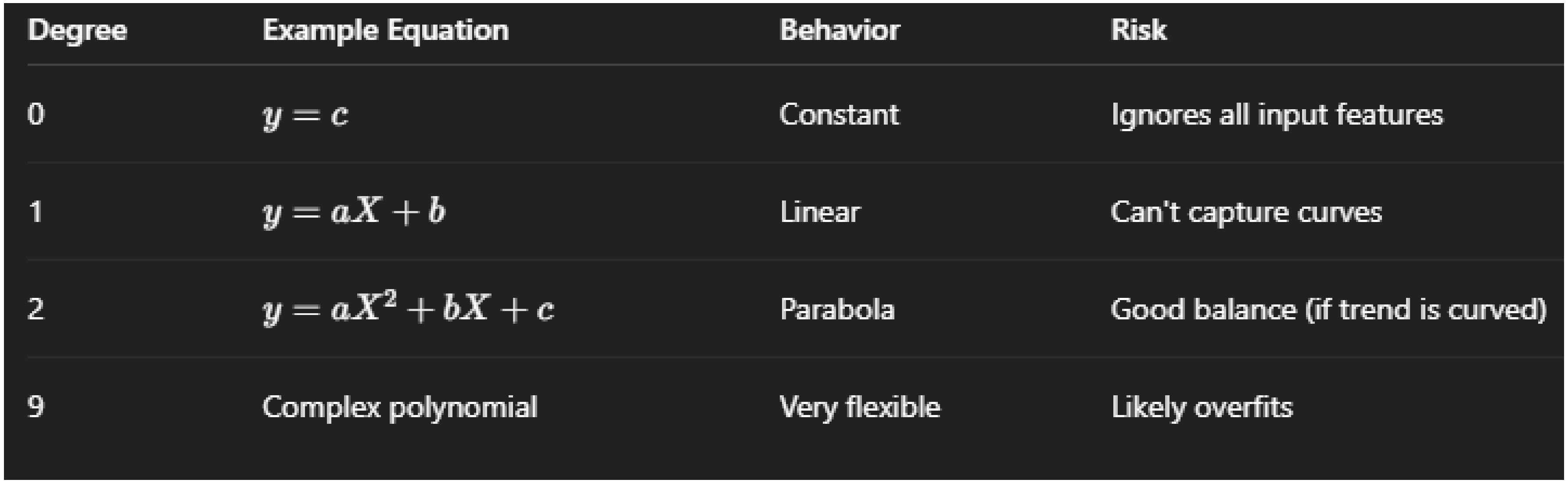
3. Degree 9 (Red Dotted Line):
    - This is a **high-degree polynomial** that perfectly fits every point.
    - It **overfits** the data — capturing noise and fluctuations rather than true trends.
    - While it has zero error on training data, it would likely perform **poorly on unseen data.**



- **Underfitting** happens when the model is too simple to capture the data pattern.
- **Overfitting** occurs when the model is too complex and fits noise.

Overfitting and Underfitting

- In the figure, we've fit three polynomials to a sample of data.



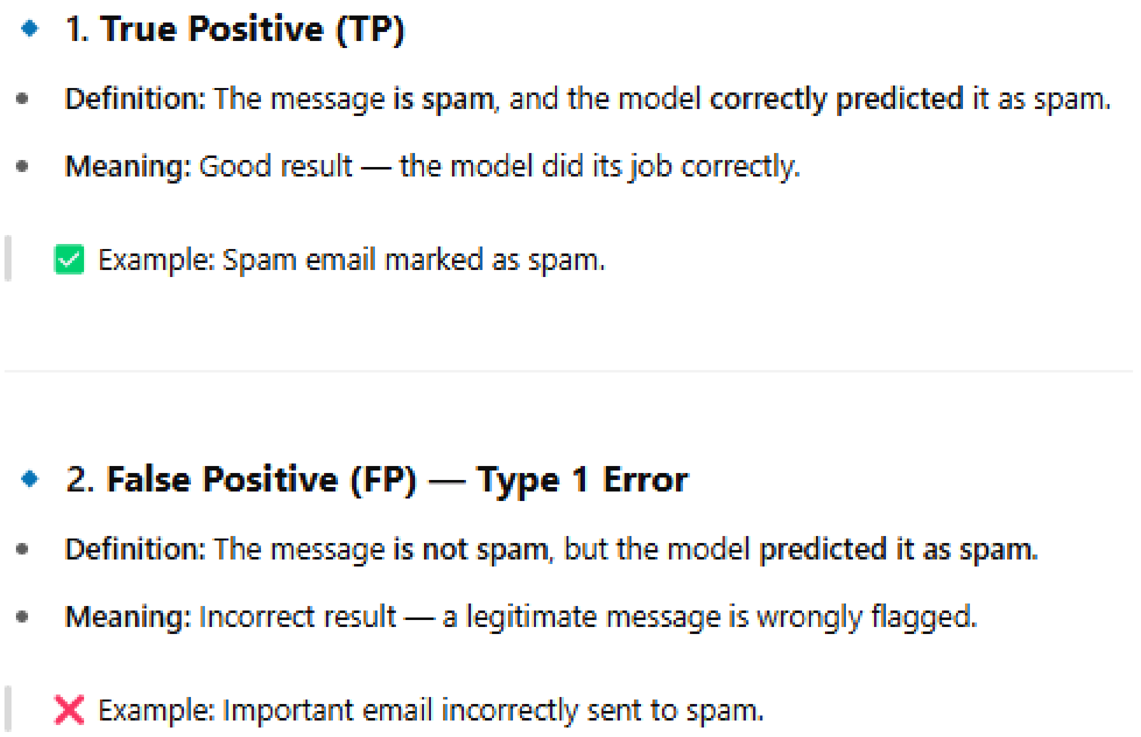
Degree	Example Equation	Behavior	Risk
0	$y = c$	Constant	Ignores all input features
1	$y = aX + b$	Linear	Can't capture curves
2	$y = aX^2 + bX + c$	Parabola	Good balance (if trend is curved)
9	Complex polynomial	Very flexible	Likely overfits

Overfitting and Underfitting

- **Solution**:
- So how do we make sure our models aren't too complex? The most fundamental approach involves **using different data to train the model and to test the model.**
- The simplest way to do this is to **split the dataset**, so that (for example) two-thirds of it is used to train the model, after which we measure the model's performance on the remaining third.

Correctness

- Imagine building a model to make a binary judgment.
- Is this email spam? Should we hire this candidate? Is this air traveler secretly a terrorist?
- Given a set of labeled data and such a predictive model, every data point lies in one of four categories:



🔹 **1. True Positive (TP)**

- **Definition:** The message **is spam**, and the model **correctly predicted** it as spam.
- **Meaning:** Good result — the model did its job correctly.

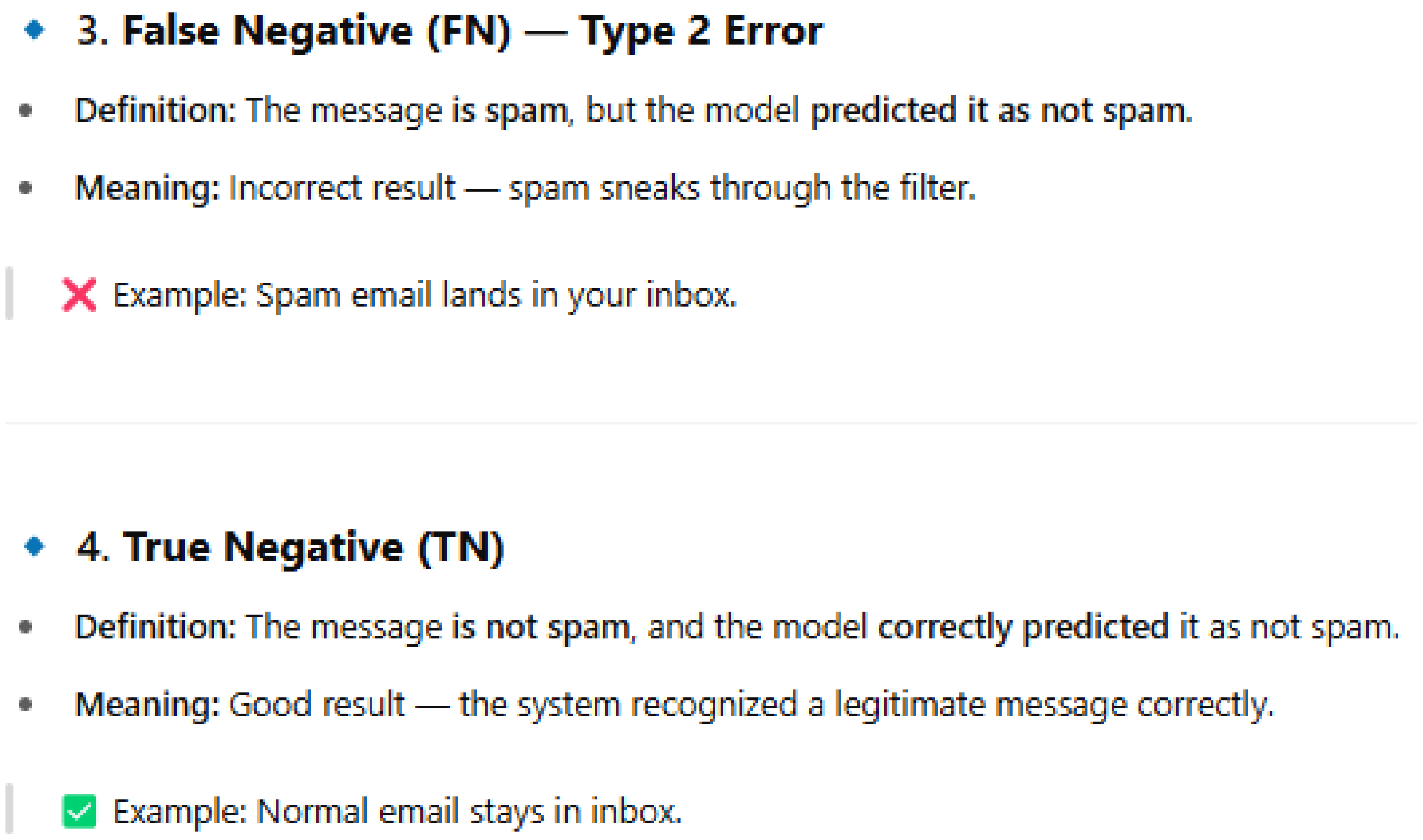
> ✅ Example: Spam email marked as spam.

🔹 **2. False Positive (FP) — Type 1 Error**

- **Definition:** The message **is not spam**, but the model **predicted it as spam.**
- **Meaning:** Incorrect result — a legitimate message is wrongly flagged.

> ❌ Example: Important email incorrectly sent to spam.

Correctness



🔹 **3. False Negative (FN) — Type 2 Error**

- **Definition:** The message is spam, but the model **predicted it as not spam.**
- **Meaning:** Incorrect result — spam sneaks through the filter.

> ❌ Example: Spam email lands in your inbox.

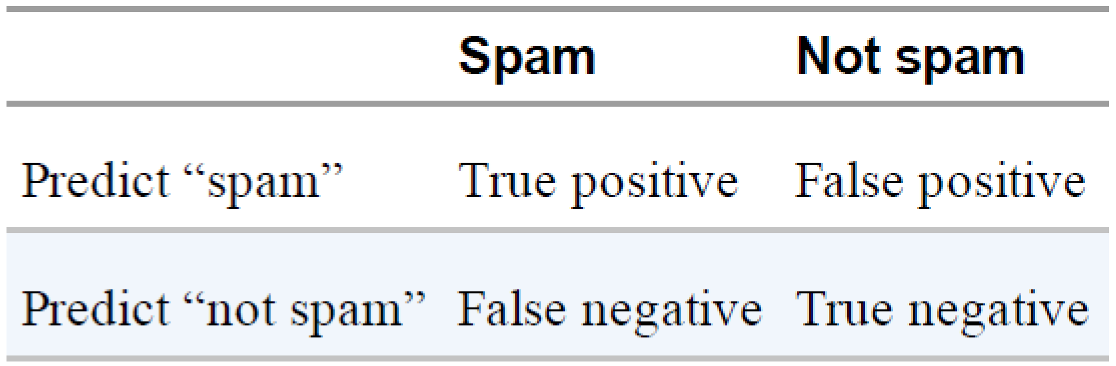
🔹 **4. True Negative (TN)**

- **Definition:** The message **is not spam**, and the model **correctly predicted** it as not spam.
- **Meaning:** Good result — the system recognized a legitimate message correctly.

> ✅ Example: Normal email stays in inbox.

Confusion matrix

- We often represent these as counts in a confusion matrix:



	Spam	Not spam
Predict “spam”	True positive	False positive
Predict “not spam”	False negative	True negative

Confusion Matrix

- Let’s see how our leukemia test fits into this framework.
- These days approximately 5 babies out of 1,000 are named Luke.
- And the lifetime prevalence of leukemia is about 1.4%, or 14 out of every 1,000 people.
- If we believe these two factors are independent and apply my “Luke is for leukemia” test to 1 million people, we’d expect to see a confusion matrix like:

	Leukemia	**No leukemia**	**Total**
“Luke”	70	4,930	5,000
Not “Luke”	13,930	981,070	995,000
Total	14,000	986,000	1,000,000

Accuracy

- We can then use these to compute various statistics about model performance.
- ***Accuracy*** is defined as the **fraction of correct predictions:**

```
def accuracy(tp: int, fp: int, fn: int, tn: int) -> float:
    correct = tp + tn
    total = tp + fp + fn + tn
    return correct / total
assert accuracy(70, 4930, 13930, 981070) == 0.98114
```

- That seems like a pretty impressive number.
- But clearly this is not a good test, which means that we probably shouldn’t put a lot of credence in raw accuracy.

Precision

- It’s common to look at the combination of precision and recall.
- **What is Precision?**
- Precision is defined as the **ratio of correctly classified positive samples (True Positive) to a total number of classified positive samples** (either correctly or incorrectly).
- Precision = True Positive/True Positive + False Positive
- Precision = TP/TP+FP

```
def precision(tp: int, fp: int, fn: int, tn: int) -> float:
    return tp / (tp + fp)
assert precision(70, 4930, 13930, 981070) == 0.014
```

- Precision helps us to visualize the reliability of the machine learning model in classifying the model as positive.

Recall

- **What is Recall?**
- The recall is calculated as the **ratio between the numbers of Positive samples correctly classified as Positive to the total number of Positive samples.**
- The recall measures the model's ability to detect **positive samples.**
- Recall = True Positive/True Positive + False Negative
- Recall = TP/TP+FN

```
def recall(tp: int, fp: int, fn: int, tn: int) -> float:
    return tp / (tp + fn)
assert recall(70, 4930, 13930, 981070) == 0.005
```

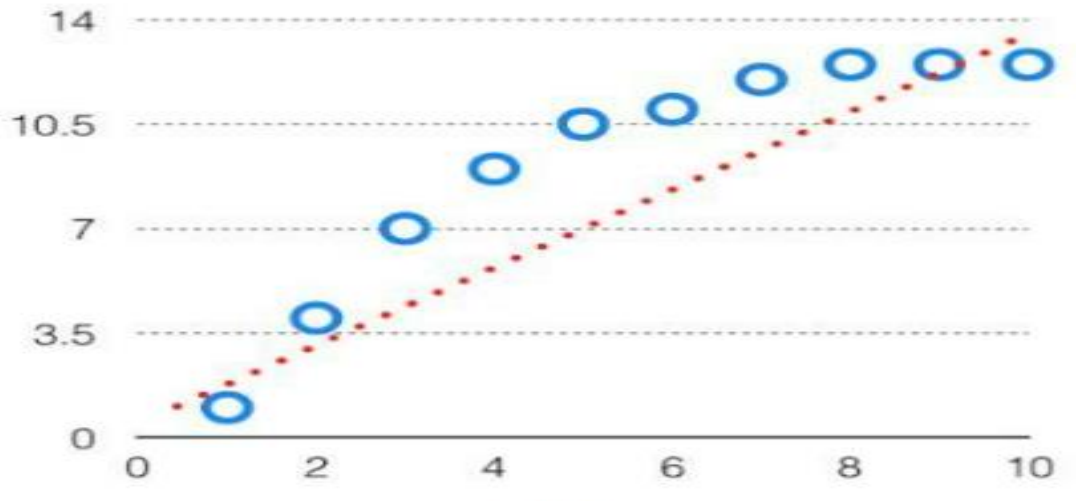
F1-Score

```
def f1_score(tp: int, fp: int, fn: int, tn: int) -> float:
    p = precision(tp, fp, fn, tn)
    r = recall(tp, fp, fn, tn)
    return 2 * p * r / (p + r)
```

- This is the *harmonic mean* of precision and recall and necessarily lies between them.
- Tradeoff between precision and recall. A model that predicts “yes” when it’s even a little bit confident will probably have a high recall but a low precision; a model that predicts “yes” only when it’s extremely confident is likely to have a low recall and a high precision.

Bias

- It is important to understand **prediction errors** (bias and variance) when it comes to accuracy in any machine learning algorithm.
- The bias is known as the **difference between the prediction of the values by the ML model and the correct value.**
- Being high in biasing gives a **large error** in training as well as testing data.

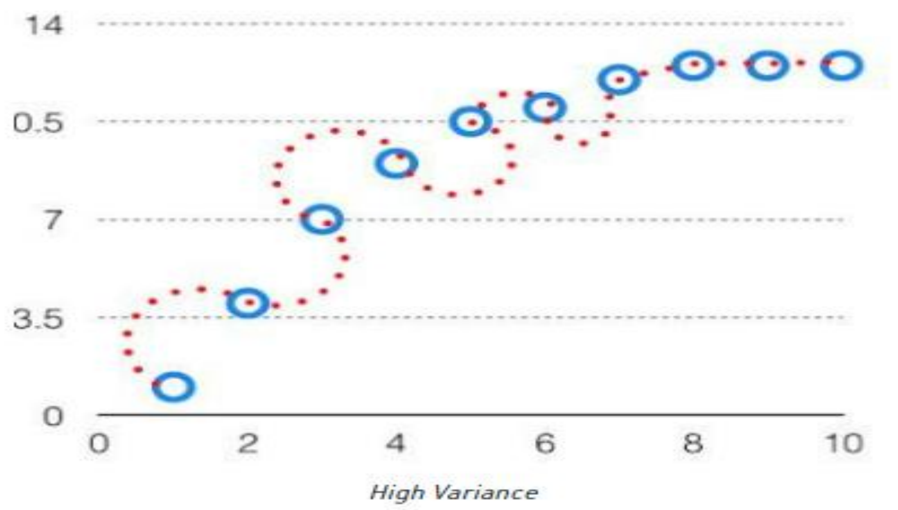


HighBias

- Its recommended that an algorithm should always **be low biased to avoid the problem of underfitting.**
- By high bias, the data predicted is in a straight line format, thus not fitting accurately in the data in the data set.
- Such fitting is known as **Underfitting of Data**.

Variance

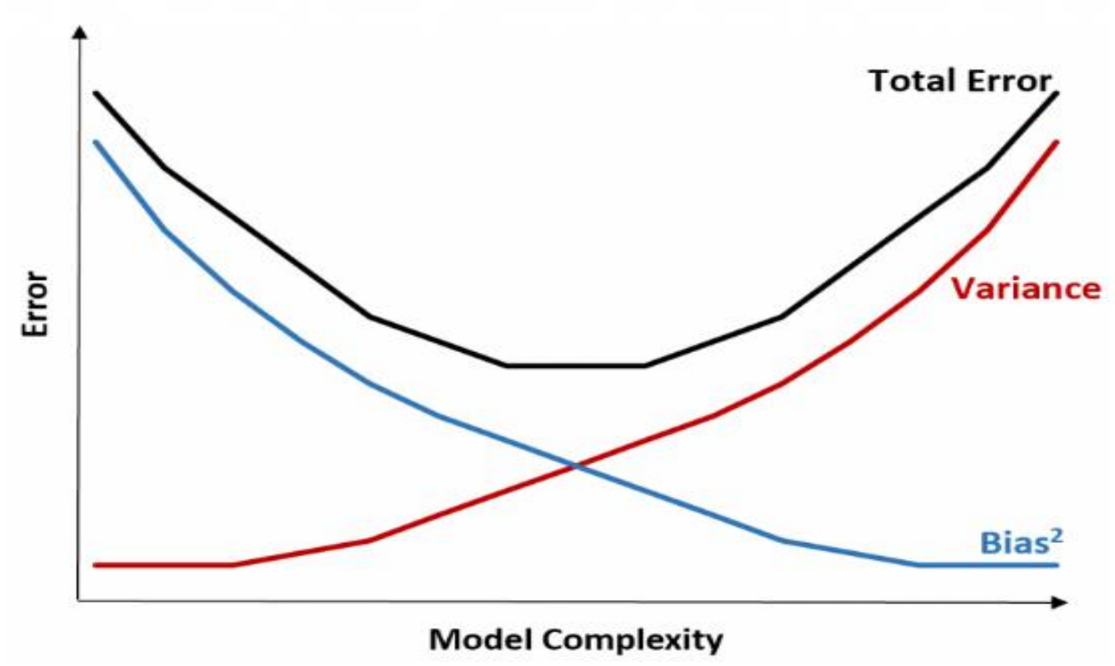
- The variance of the model refers to the **amount by which our model would change if we estimated it using a different training set.**
- The model with high variance has a **very complex fit** to the training data and thus is not able to fit accurately on the data which it hasn't seen before.
- As a result, such models perform very well on training data but has high error rates on test data.
- When a model is high on variance, it is then said to as **Overfitting of Data.**
- Overfitting is fitting the training set accurately via complex curve.
- **While training a data model variance should be kept low.**



- The high variance data looks as above.

The Bias-Variance Tradeoff

- The bias-variance tradeoff refers to the tradeoff that takes place when we choose to lower bias which typically increases variance, or lower variance which typically increases bias.
- The following chart offers a way to visualize this tradeoff·



The Bias-Variance Tradeoff

- The **total error decreases** as the complexity of a model increases but only up to a certain point.
- **Past a certain point**, variance begins to increase and total error also begins to increase.
- In practice, we only **care about minimizing the total error of a model**, not necessarily minimizing the variance or bias.
- It turns out that the way to minimize the total error is to **strike the right balance between variance and bias.**
- In other words, we want a model that is **complex enough to capture the true relationship** between the explanatory variables and the response variable, but not overly complex such that it finds patterns that don't really exist.
- When a **model is too complex, it overfits the data**.
- But when a model is **too simple, it underfits the data**. This happens because it **assumes the true relationship** between the explanatory variables and the response variable is more simple than it actually is.
- The way to pick optimal models in machine learning is to **strike the balance between bias and variance such that we can minimize the test error of the model on future unseen data.**

Feature Extraction and Selection

- As has been mentioned, when your data doesn’t have enough features, your model is likely to underfit.
- And when your data has too many features, it’s easy to overfit.
- *But what are features, and where do they come from?*
- Features are whatever inputs we provide to our model.
- If you want to predict someone’s salary based on her years of experience, then years of experience is the only feature you have.

Feature Extraction and Selection

- Things become more interesting as your data becomes more complicated.
- Imagine trying to build a spam filter to predict whether an email is junk or not.
- Most models won’t know what to do with a raw email, which is just a collection of text.
- You’ll have to extract features. For example:
  - Does the email contain the word Gun?
  - How many times does the letter d appear?
  - What was the domain of the sender?
- The answer to a question like the first question here is simply a yes or no, which we typically encode as a 1 or 0.
- The second is a number.
- And the third is a choice from a discrete set of options.

Feature Extraction and Selection

- Pretty much always, we'll extract features from our data that fall into one of these three categories.
- What's more, the types of features we have constrain the types of models we can use.
  - The Naive Bayes classifier is suited to yes-or-no features, like the first one in the preceding list.
  - Regression models, require numeric features (which could include dummy variables that are 0s and 1s).
  - Decision trees, can deal with numeric or categorical data.

k-Nearest Neighbors: The Model

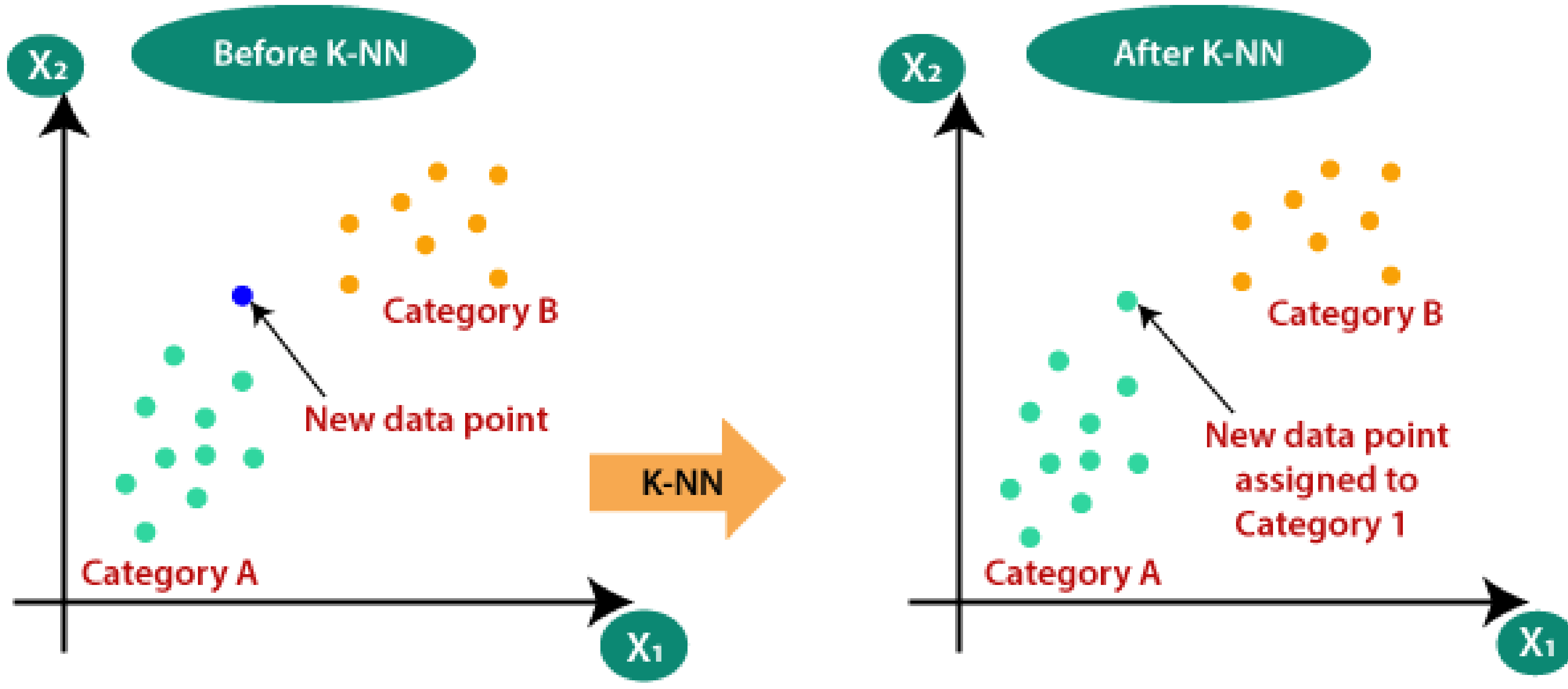
What is k-Nearest Neighbors?

- k-NN is a machine learning algorithm that helps make predictions based on the idea that similar things are close together.
- It is a Supervised Classification or Regression Method

How It Works:

- **Pick a number "k"** (how many neighbors to look at).
- **Measure the distance** between your data point and all others in the dataset (usually with Euclidean distance—think of it as drawing a straight line).
- **Find the k closest points.**
- **Look at their labels** (e.g., "cat," "dog," "spam," "not spam").
- **Predict** the most common label among those neighbors.

k-Nearest Neighbors: The Model



k-Nearest Neighbors: The Model

- **Pros:**
- Very simple and intuitive
- No training phase (it's a lazy learner)
- **Cons:**
- Slow with large datasets
- Doesn’t work well with irrelevant features or very different scales
- Neglects a lot of information, since the prediction for each new point depends only on the handful of points closest to it.

k-Nearest Neighbors: The Model

📊 Sample Dataset

Point	Feature 1 (X)	Feature 2 (Y)	Label
A	1	2	Red
B	2	3	Red
C	3	1	Blue
D	6	5	Blue
E	7	7	Blue

k-Nearest Neighbors: The Model

🎯 Goal:

Classify a **new point P** = (3, 3) using **k** = **3** neighbors.

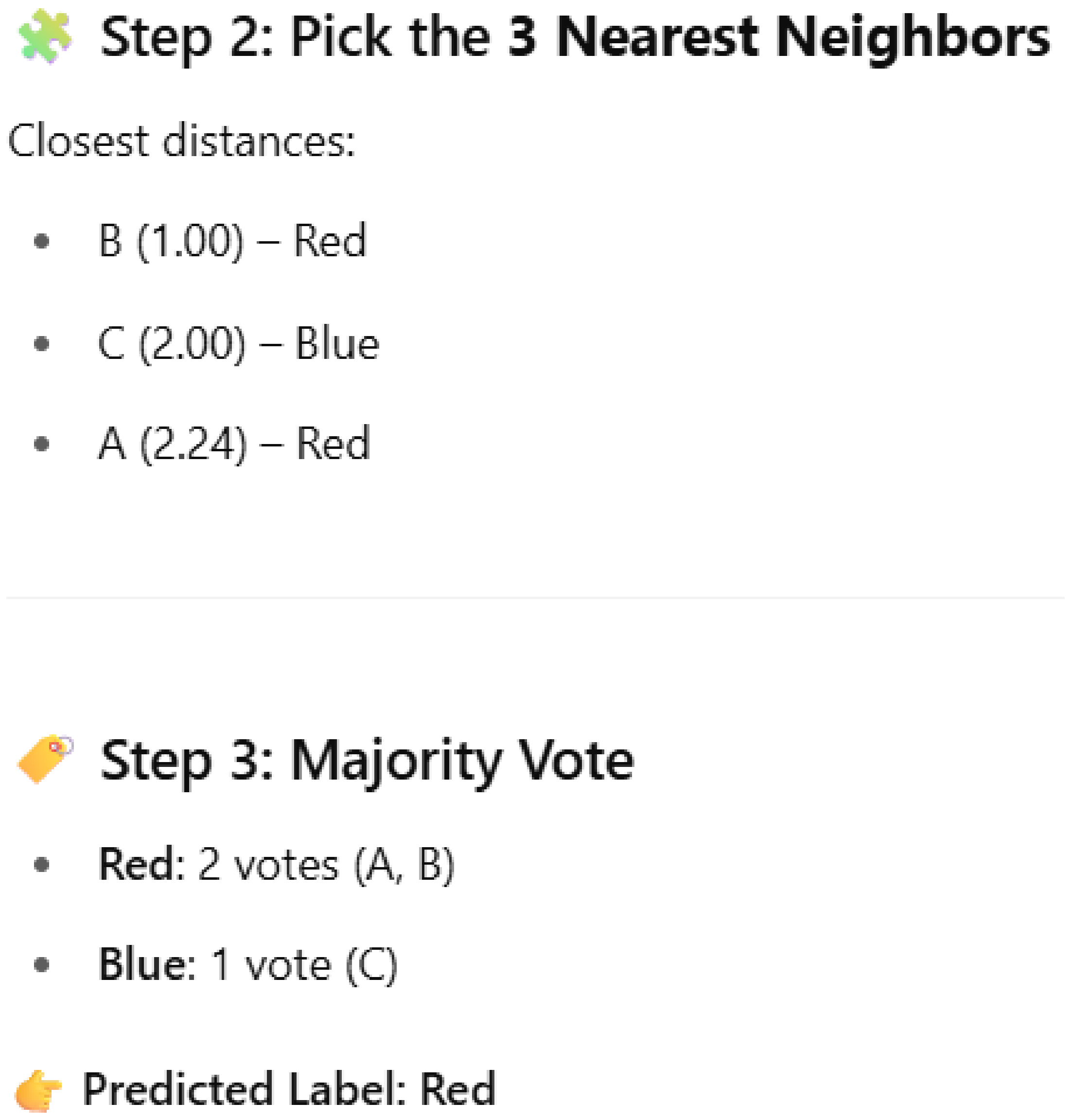
🧮 Step 1: Calculate Euclidean Distance

Euclidean distance formula:

$$\text{distance} = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$$

Point	Coordinates	Distance to P(3,3)	Label
A	(1, 2)	$\sqrt{[(3-1)^2 + (3-2)^2]} = \sqrt{5} \approx 2.24$	Red
B	(2, 3)	$\sqrt{[(3-2)^2 + (3-3)^2]} = \sqrt{1} = 1.00$	Red
C	(3, 1)	$\sqrt{[(3-3)^2 + (3-1)^2]} = \sqrt{4} = 2.00$	Blue
D	(6, 5)	$\sqrt{[(3-6)^2 + (3-5)^2]} = \sqrt{13} \approx 3.61$	Blue
E	(7, 7)	$\sqrt{[(3-7)^2 + (3-7)^2]} = \sqrt{32} \approx 5.66$	Blue

k-Nearest Neighbors: The Model



🧩 Step 2: Pick the **3 Nearest Neighbors**

Closest distances:

- B (1.00) – Red
- C (2.00) – Blue
- A (2.24) – Red

🏷️ Step 3: Majority Vote

- **Red**: 2 votes (A, B)
- **Blue**: 1 vote (C)

👉 **Predicted Label: Red**

The Model : Code Snippet

- Creating a classifier:

```
from typing import NamedTuple
from scratch.linear_algebra import Vector, distance
class LabeledPoint(NamedTuple):
   point: Vector
   label: str
def knn_classify(k: int, labeled_points: List[LabeledPoint], new_point: Vector) -> str:
   # Order the labeled points from nearest to farthest.
   by_distance = sorted(labeled_points, key=lambda lp:
   distance(lp.point, new_point))
   # Find the labels for the k closest
   k_nearest_labels = [lp.label for lp in by_distance[:k]]
   # and let them vote.
   return majority_vote(k_nearest_labels)
```

The Model : Code Snippet

```
def majority_vote(labels: List[str]) -> str:
    """Assumes that labels are ordered from nearest to farthest."""
    vote_counts = Counter(labels)
    winner, winner_count = vote_counts.most_common(1)[0]
    num_winners = len([count for count in vote_counts.values() if count
    == winner_count])
    if num_winners == 1:
            return winner # unique winner, so return it
    else:
            return majority_vote(labels[:-1]) # try again without the
    farthest
    # Tie, so look at first 4, then 'b'
assert majority_vote(['a', 'b', 'c', 'b', 'a']) == 'b'
```

The Model : KNN Program

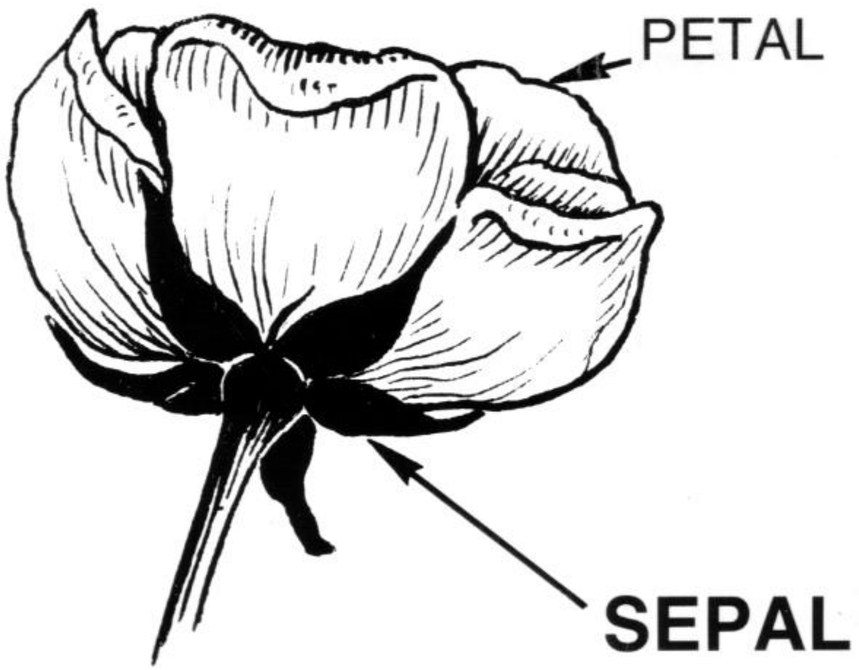
```
from typing import List, NamedTuple
from collections import Counter
import math
# ---------- Data Structures ----------
class LabeledPoint(NamedTuple):
    point: List[float]
    label: str
# ---------- Euclidean Distance Function ----------
def distance(p1: List[float], p2: List[float]) -> float:
    return math.sqrt(sum((x - y) ** 2 for x, y in zip(p1, p2)))
# ---------- Tie-Breaking Majority Vote ----------
def majority_vote(labels: List[str]) -> str:
    """Assumes labels are ordered from nearest to farthest."""
    vote_counts = Counter(labels)
    winner, winner_count = vote_counts.most_common(1)[0]
      num_winners = len([count for count in vote_counts.values() if count ==
winner_count])
    if num_winners == 1:
        return winner  # Unique winner
    else:
        return majority_vote(labels[:-1])  # Remove farthest and retry
```

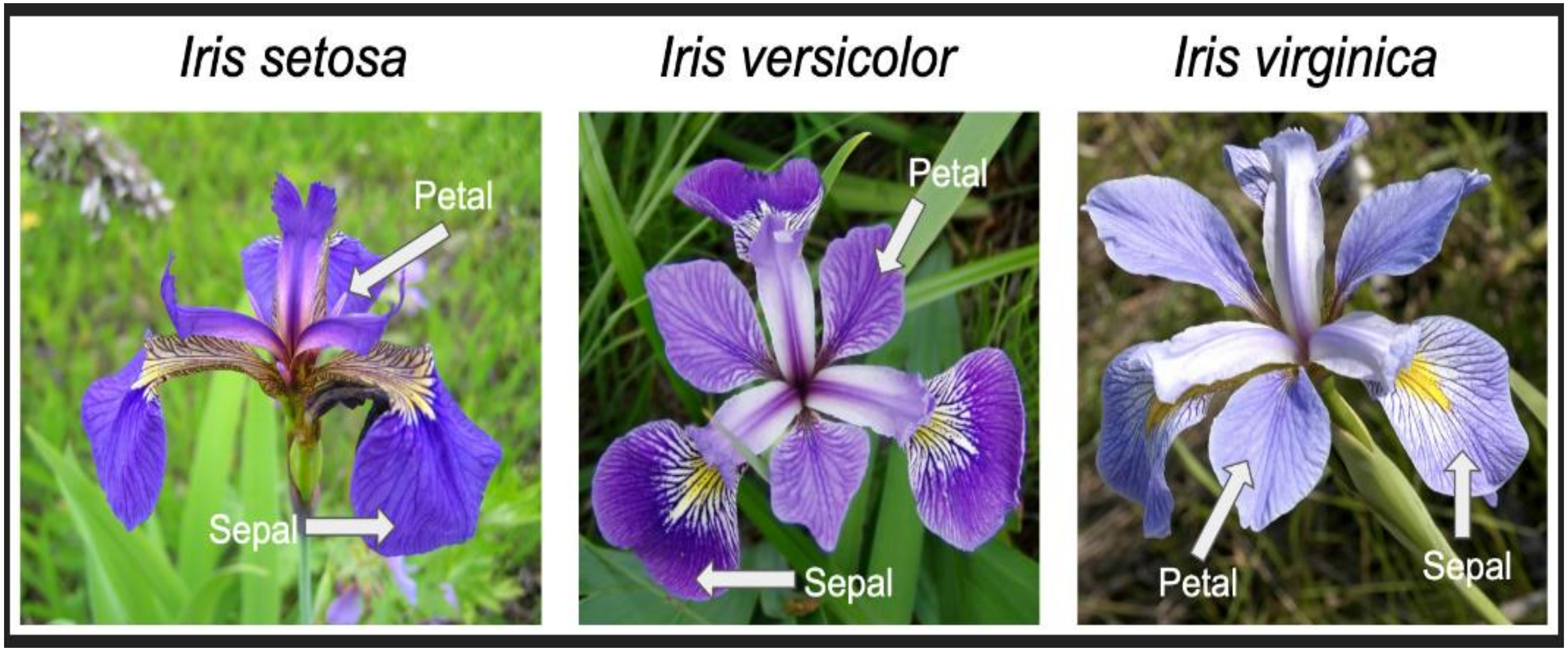
The Model : KNN Program

```
# ---------- k-NN Classifier ----------
def knn_classify(k: int, labeled_points: List[LabeledPoint], new_point: List[float]) -> str:
    # Sort points by distance from new_point
    by_distance = sorted(labeled_points, key=lambda lp: distance(lp.point, new_point))
    # Get labels of the k closest
    k_nearest_labels = [lp.label for lp in by_distance[:k]]
    # Let them vote
    return majority_vote(k_nearest_labels)
# ---------- Example Usage ----------
if __name__ == "__main__":
    # Example dataset (2D points)
    data = [
        LabeledPoint([1.0, 2.0], "A"),
        LabeledPoint([2.0, 3.0], "A"),
        LabeledPoint([3.0, 3.0], "B"),
        LabeledPoint([6.0, 5.0], "B"),
        LabeledPoint([7.0, 8.0], "C")
    ]
    # New point to classify
    new_point = [3.5, 3.5]
    # Classify with k=3
    k = 3
    predicted_label = knn_classify(k, data, new_point)
    print(f"Predicted label for {new_point} with k={k} is: {predicted_label}")
```

Example Iris Dataset

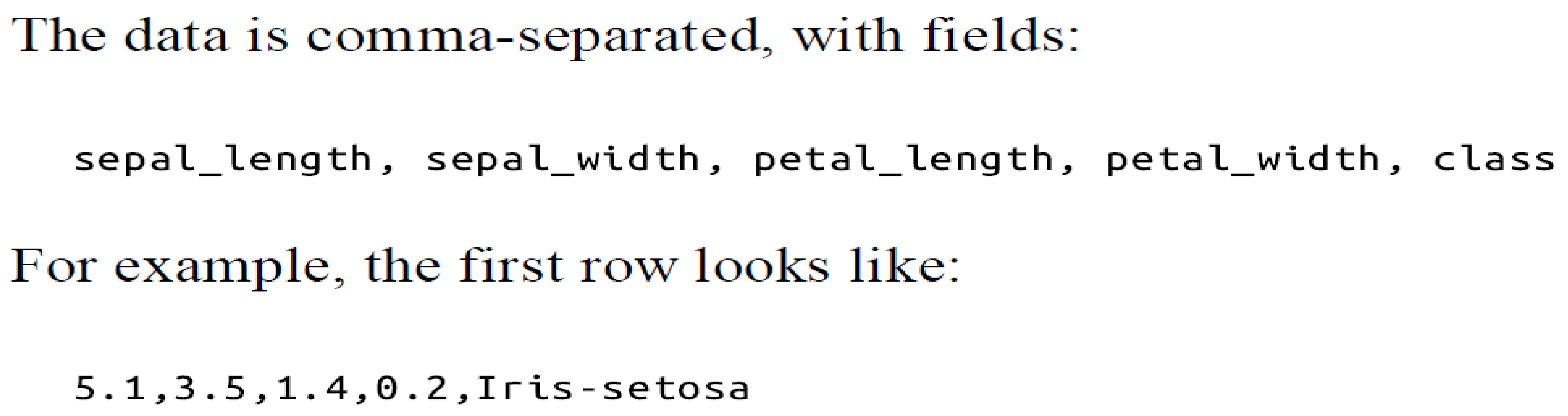
The Iris dataset is a staple of machine learning. It contains a bunch of measurements for 150 flowers representing three species of iris. For each flower we have its petal length, petal width, sepal length, and sepal width, as well as its species. You can download it from https://archive.ics.uci.edu/ml/datasets/iris:




Iris setosa
Petal
Sepal
Iris versicolor
Petal
Sepal
Iris virginica
Petal
Sepal

Example: The Iris Dataset

```
import requests
data = requests.get( "https://archive.ics.uci.edu/ml/machine-learningdatabases/ iris/iris.data")
with open('iris.dat', 'w') as f:
        f.write(data.txt)
```



The data is comma-separated, with fields:

```
sepal_length, sepal_width, petal_length, petal_width, class
```

For example, the first row looks like:

```
5.1,3.5,1.4,0.2,Iris-setosa
```

Example: The Iris Dataset: Code Snippet

- Build a model that can predict the class (that is, the species) from the first four measurements.

```
from typing import Dict
import csv
from collections import defaultdict
def parse_iris_row(row: List[str]) -> LabeledPoint:
    """“ sepal_length, sepal_width, petal_length, petal_width, class """
    measurements = [float(value) for value in row[:-1]]
    # class is e.g. "Iris-virginica"; we just want "virginica"
    label = row[-1].split("-")[-1]
    return LabeledPoint(measurements, label)
with open('iris.data') as f:
    reader = csv.reader(f)
    iris_data = [parse_iris_row(row) for row in reader]
    # We'll also group just the points by species/label so we can plot them
points_by_species: Dict[str, List[Vector]] = defaultdict(list)
for iris in iris_data:
    points_by_species[iris.label].append(iris.point)
```

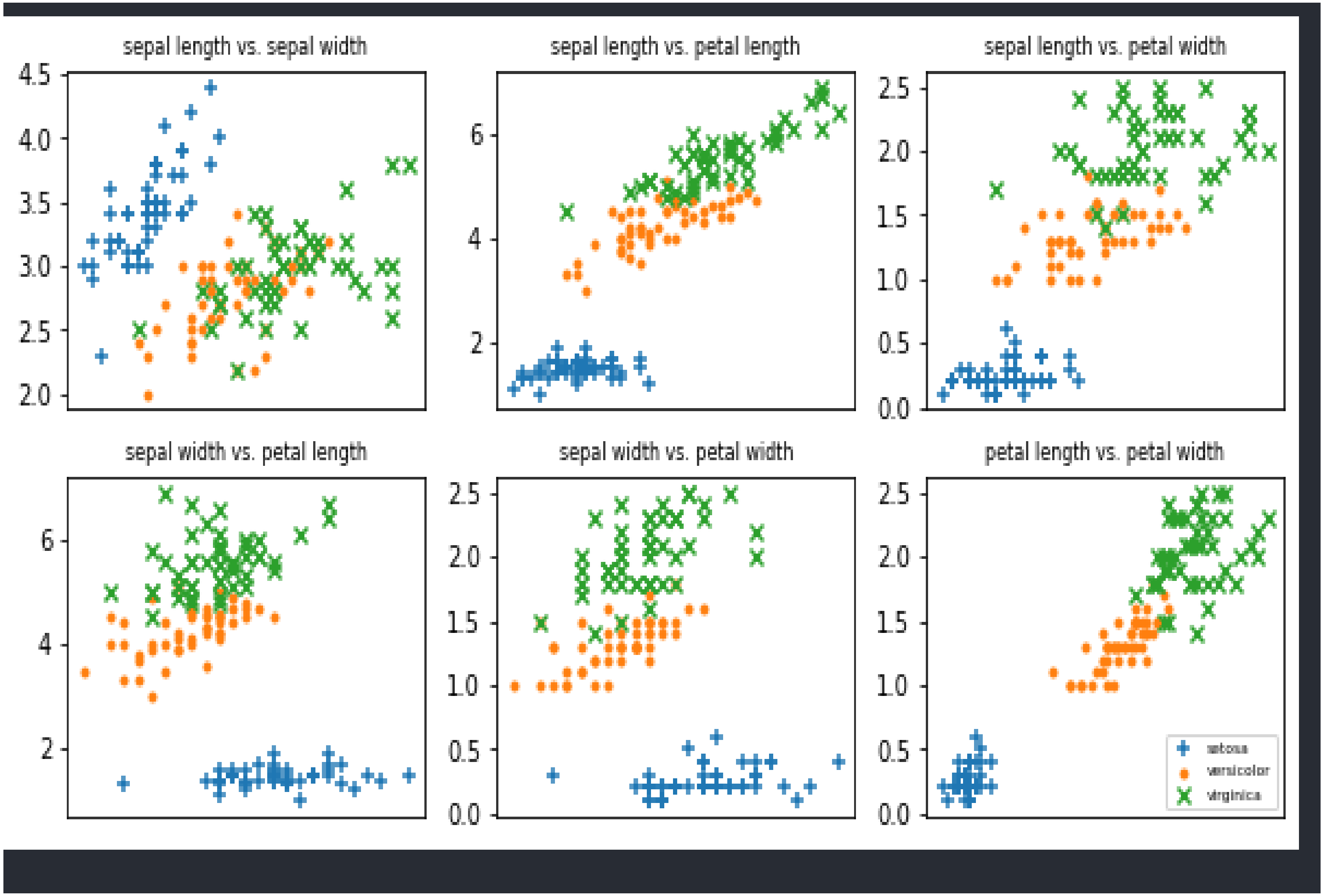
Example: The Iris Dataset Code Snippet

```
import random
from scratch.machine_learning import split_data
random.seed(12)
iris_train, iris_test = split_data(iris_data, 0.70)
assert len(iris_train) == 0.7 * 150
assert len(iris_test) == 0.3 * 150
from typing import Tuple
# track how many times we see (predicted, actual)
confusion_matrix: Dict[Tuple[str, str], int] = defaultdict(int)
num_correct = 0
for iris in iris_test:
    predicted = knn_classify(5, iris_train, iris.point)
    actual = iris.label
    if predicted == actual:
            num_correct += 1
    confusion_matrix[(predicted, actual)] += 1
pct_correct = num_correct / len(iris_test)
print(pct_correct, confusion_matrix)
```

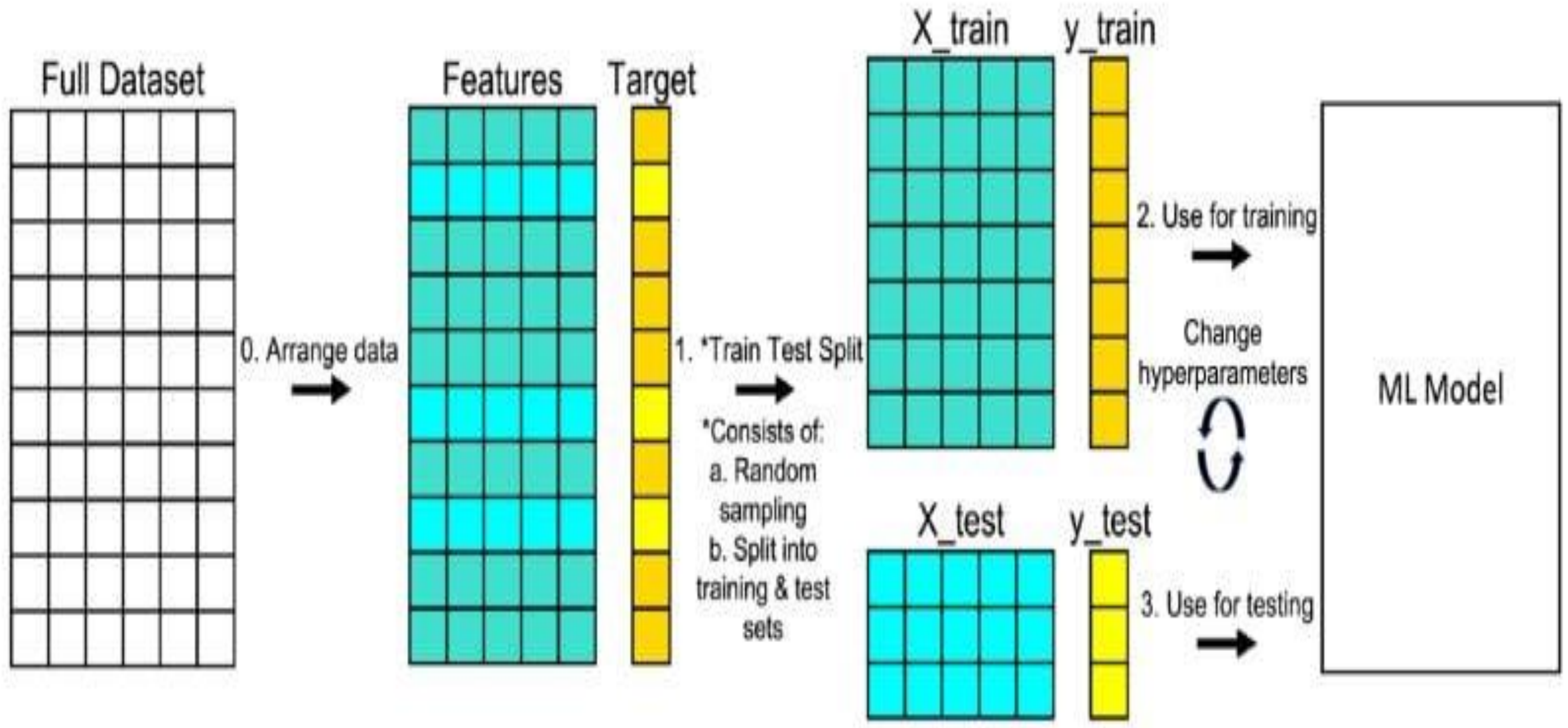
Example: The Iris Dataset: Code Snippet

```
from matplotlib import pyplot as plt
metrics = ['sepal length', 'sepal width', 'petal length', 'petal width']
pairs = [(i, j) for i in range(4) for j in range(4) if i < j]
marks = ['+', '.', 'x'] # we have 3 classes, so 3 markers
fig, ax = plt.subplots(2, 3)
for row in range(2):
    for col in range(3):
        i, j = pairs[3 * row + col]
        ax[row][col].set_title(f"{metrics[i]} vs {metrics[j]}", fontsize=8)
        ax[row][col].set_xticks([])
        ax[row][col].set_yticks([])
        for mark, (species, points) in zip(marks,
        points_by_species.items()):
        xs = [point[i] for point in points]
        ys = [point[j] for point in points]
        ax[row][col].scatter(xs, ys, marker=mark, label=species)
ax[-1][-1].legend(loc='lower right', prop={'size': 6})
plt.show()
```

Example: The Iris Dataset



Example: The Iris Dataset



KNN Implementation using Libraries

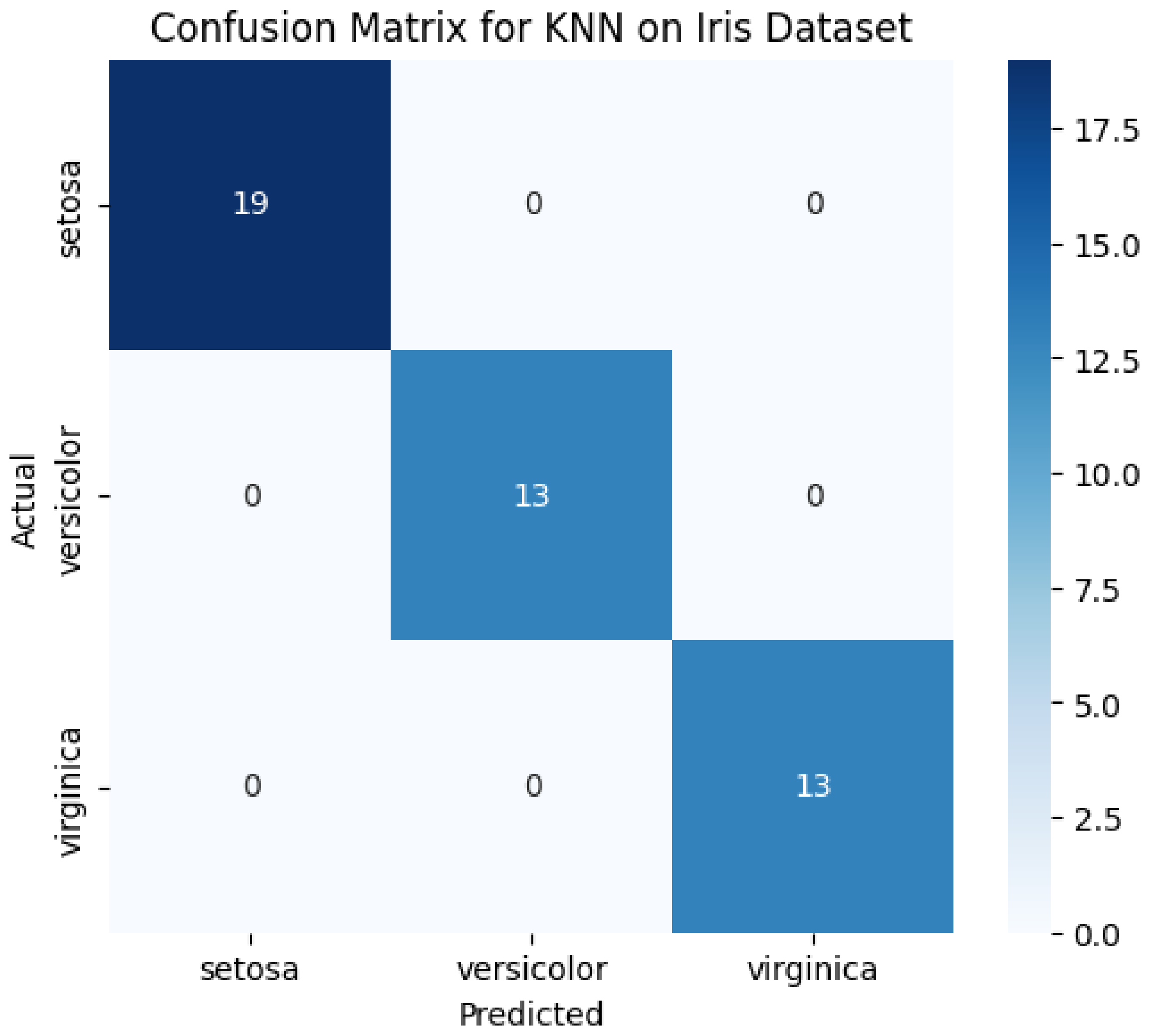
```
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns

# Step 1: Load the Iris dataset
iris = load_iris()
X = iris.data  # Features: sepal length, sepal width, etc.
y = iris.target  # Labels: 0=setosa, 1=versicolor, 2=virginica
target_names = iris.target_names

# Step 2: Split into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.3, random_state=42)
```

KNN Implementation using Libraries

```python
# Step 3: Create and train KNN model
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(X_train, y_train)

# Step 4: Predict
y_pred = knn.predict(X_test)

# Step 5: Accuracy and confusion matrix
acc = accuracy_score(y_test, y_pred)
print(f"Accuracy: {acc:.2f}")

# Confusion Matrix
cm = confusion_matrix(y_test, y_pred)

# Step 6: Visualize confusion matrix
plt.figure(figsize=(6, 5))
sns.heatmap(cm, annot=True, cmap="Blues", fmt='d',
            xticklabels=target_names, yticklabels=target_names)
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.title("Confusion Matrix for KNN on Iris Dataset")
plt.show()
```

Example: The Iris Dataset

```
Accuracy: 1.00
```



The Curse of Dimensionality

- The **curse of dimensionality** refers to a set of problems and challenges that arise when working with **high-dimensional data** (i.e., data with many features or variables)
- The k-nearest neighbors algorithm runs into trouble in higher dimensions.
  - ❖ **Data Sparsity**: In high-dimensional space, data points are very far apart. Models struggle to find patterns, and overfitting becomes likely.
  - ❖ **Distance Metrics** Become Useless Algorithms
  - ❖ **Computational Cost**: More features = more computations. High-dimensional data increases time complexity and memory usage for many algorithms.
  - ❖ **Overfitting** Risk Models can easily find patterns in high dimensions that are just noise.

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The Curse of Dimensionality

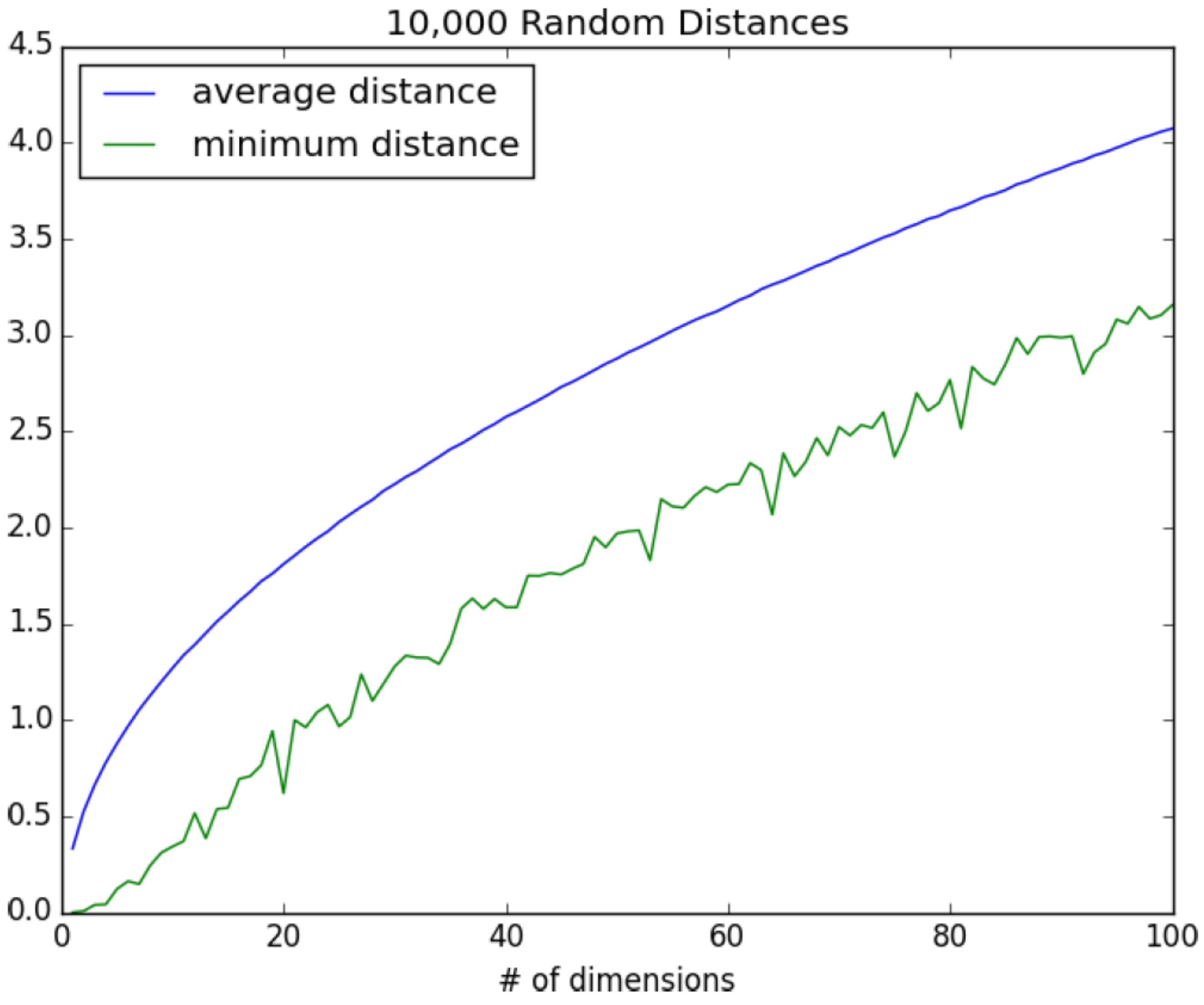
- One way to see this is by rand**omly generating pairs of points in the d-dimensional** “unit cube” in a variety of dimensions, and calculating the distances between them.
- For every dimension from 1 to 100, we’ll compute 10,000 distances and use those to compute the average distance between points and the minimum distance between points in each dimension.

The Curse of Dimensionality

- Generating random points should be second nature by now:

```
def random_point(dim: int) -> Vector:
        return [random.random() for _ in range(dim)]

def random_distances(dim: int, num_pairs: int) -> List[float]:
        return [distance(random_point(dim), random_point(dim)) for _ in
range(num_pairs)]

import tqdm
dimensions = range(1, 101)
avg_distances = []
min_distances = []
random.seed(0)
for dim in tqdm.tqdm(dimensions, desc="Curse of Dimensionality"):
    distances = random_distances(dim, 10000) # 10,000 random pairs
    avg_distances.append(sum(distances) / 10000) # track the average
    min_distances.append(min(distances)) # track the minimum
```

The Curse of Dimensionality

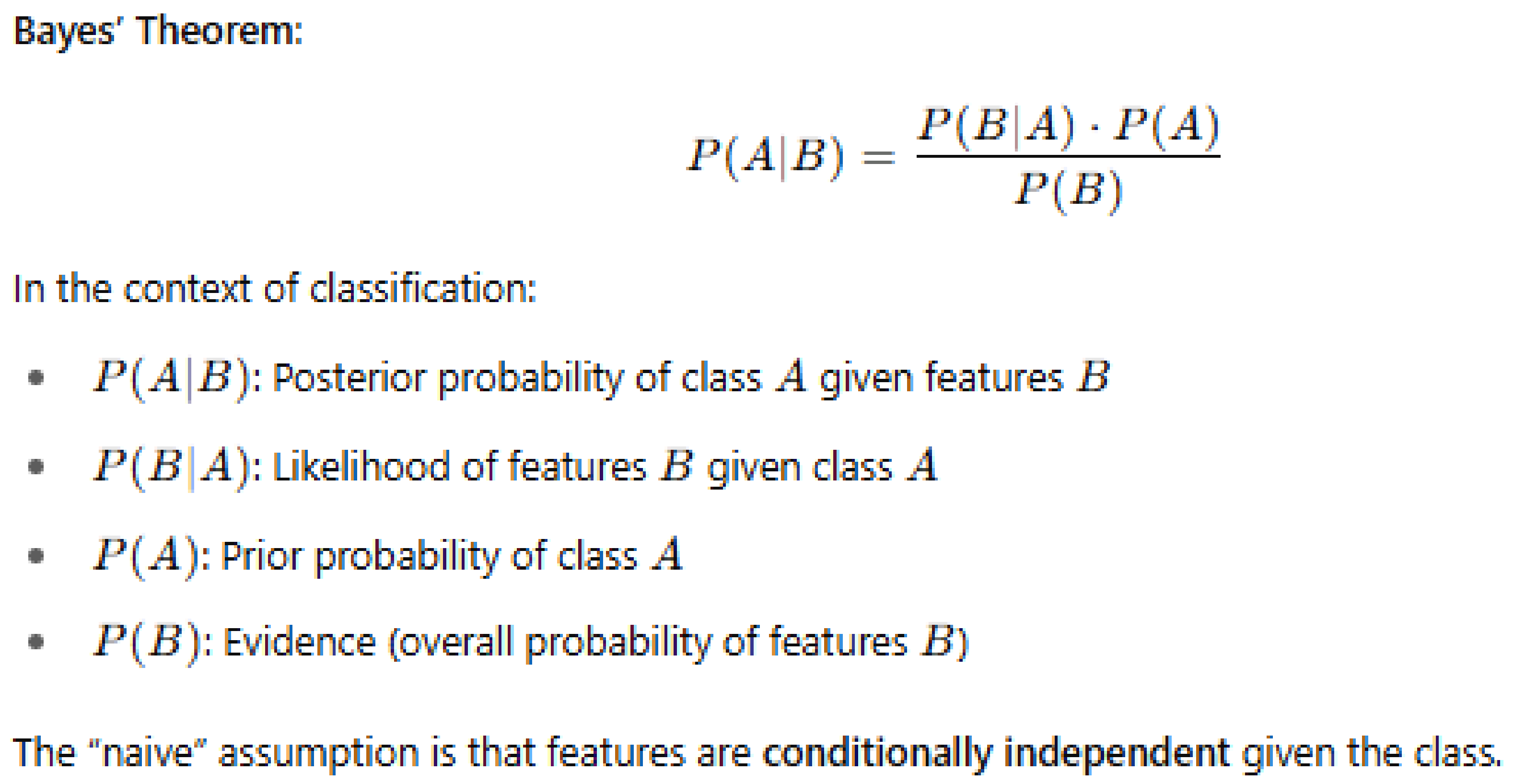


The Curse of Dimensionality

- In low-dimensional datasets, the closest points tend to be much closer than average.
- But two points are close only if they’re close in every dimension, and every extra dimension—even if just noise—is another opportunity for each point to be farther away from every other point.
- When you have a lot of dimensions, it’s likely that the closest points aren’t much closer than average, so two points being close doesn’t mean very much.

Naive Bayes

- Naive Bayes is a family of simple probabilistic classifiers based on **Bayes' Theorem**, with a strong (naive) assumption of independence between features.
- Supervised Machine Learning



Bayes' Theorem:

$$P(A|B) = \frac{P(B|A) \cdot P(A)}{P(B)}$$

In the context of classification:

- $P(A|B)$: Posterior probability of class A given features B
- $P(B|A)$: Likelihood of features B given class A
- $P(A)$: Prior probability of class A
- $P(B)$: Evidence (overall probability of features B)

The "naive" assumption is that features are **conditionally independent** given the class.

Naive Bayes

- **Types of Naive Bayes Classifiers**

1. **Gaussian Naive Bayes**: Assumes features follow a normal distribution. Used for continuous data.
2. **Multinomial Naive Bayes**: Best for document classification, especially for discrete features (like word counts).
3. **Bernoulli Naive Bayes**: Assumes binary features (e.g., whether a word exists in a document).

Naive Bayes

Domain	Use Case
Marketing	Customer segmentation, email campaign response prediction
Healthcare	Disease diagnosis based on symptoms
Finance	Credit scoring, fraud detection
E-commerce	Predicting customer churn, product recommendation
Natural Language Processing (NLP)	Spam detection, sentiment analysis, topic categorization

Naive Bayes

Advanages

- Fast and efficient, even on large datasets
- Works well with high-dimensional data (e.g., text)
- Performs well with small datasets and requires less training data
- Easy to interpret and implement

Limitations

- Assumes independence of features, which is rarely true in real data
- Struggles with correlated features (can lead to misleading probabilities)
- Poor performance with continuous variables unless assumptions are met (e.g., Gaussian distribution)

Naive Bayes

```
import math

data = [
    ([1, 1, 1], 'yes'),
    ([1, 1, 0], 'yes'),
    ([0, 1, 1], 'no'),
    ([1, 0, 0], 'no')
]
def train_naive_bayes(data):
    class_counts = {'yes': 0, 'no': 0}
    feature_counts = {'yes': [0]*3, 'no': [0]*3}
    total_docs = len(data)

    for features, label in data:
        class_counts[label] += 1
        for i, val in enumerate(features):
            feature_counts[label][i] += val

    return feature_counts, class_counts, total_docs
```

Naive Bayes

```
def predict(features, feature_counts, class_counts, total_docs):
    results = {}
    for c in class_counts:
        log_prob = math.log(class_counts[c] / total_docs)
        total_in_class = class_counts[c]

        for i, val in enumerate(features):
            p = (feature_counts[c][i] + 1) / (total_in_class + 2)
            if val == 1:
                log_prob += math.log(p)
            else:
                log_prob += math.log(1 - p)

        results[c] = log_prob

    return results, max(results, key=results.get)

# Train and predict
feature_counts, class_counts, total_docs = train_naive_bayes(data)
probs, prediction = predict([1, 1, 0], feature_counts, class_counts,
total_docs)
print("Log probabilities:", probs)
print("Prediction:", prediction)
```

Naive Bayes

```
from sklearn.naive_bayes import BernoulliNB
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, classification_report
# Sample dataset: [Fever, Cough, Fatigue], Label
data = [
    [1, 1, 1],  # yes
    [1, 1, 0],  # yes
    [0, 1, 1],  # no
    [1, 0, 0]   # no
]
labels = ['yes', 'yes', 'no', 'no']
# Split into training and test data (optional, here we'll just train and test on all)
X_train = data
y_train = labels
# Initialize and train the Naive Bayes classifier
model = BernoulliNB()
model.fit(X_train, y_train)
# Predict on the same data (for demonstration)
predictions = model.predict(X_train)
# Output results
print("Predictions:", predictions)
print("Accuracy:", accuracy_score(y_train, predictions))
print("Classification Report:\n", classification_report(y_train, predictions))
```

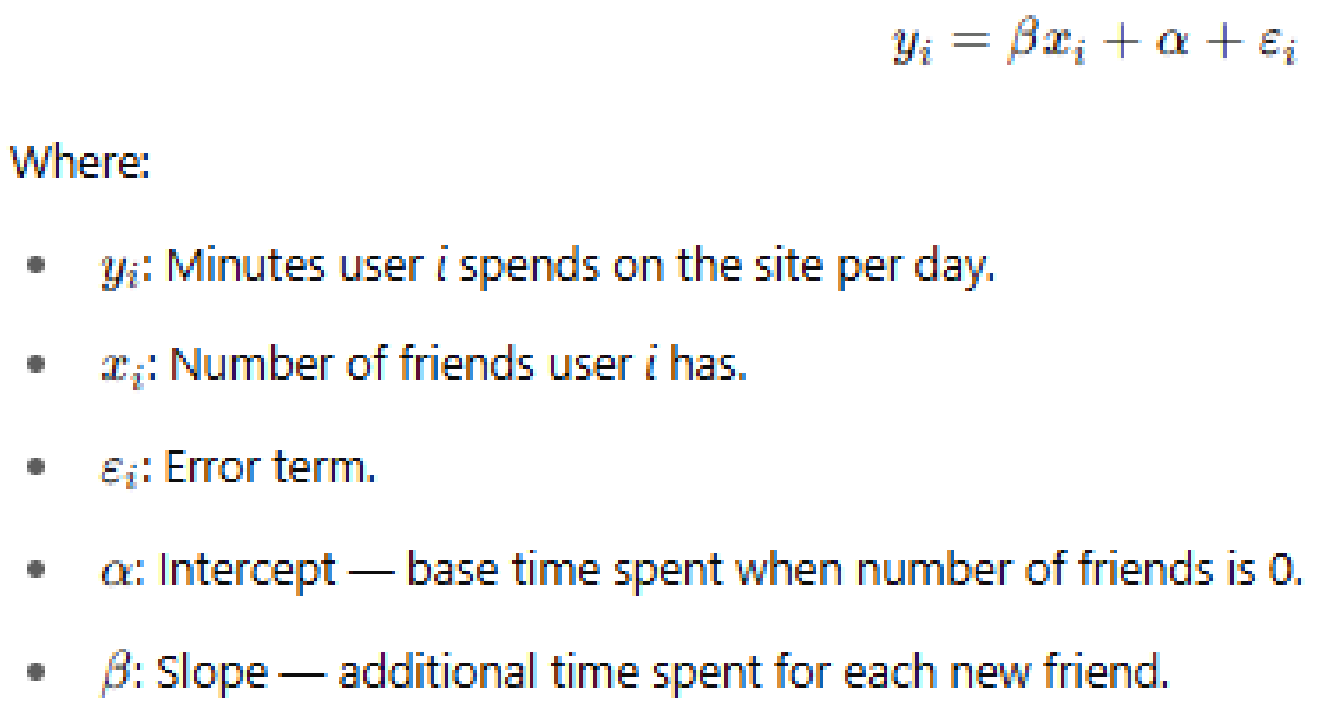
Simple Linear Regression

- We have used the ***correlation*** function to measure the strength of the linear relationship between two variables.
- For most applications, knowing that such a linear relationship exists isn't enough.
- We'll want to understand the nature of the relationship.
- This is where we'll use simple linear regression.

$$\text{correlation}(x, y) = \frac{1}{n-1} \sum \left(\frac{x_i - \bar{x}}{s_x} \cdot \frac{y_i - \bar{y}}{s_y} \right)$$

The Model

- Recall that we were investigating the relationship between a DataSciencester user’s number of friends and the amount of time the user spends on the site each day.
- Let’s assume that you’ve considered that **having more friends causes people to spend more time on the site.**
- The VP of Engagement asks you to **build a model describing this relationship.**

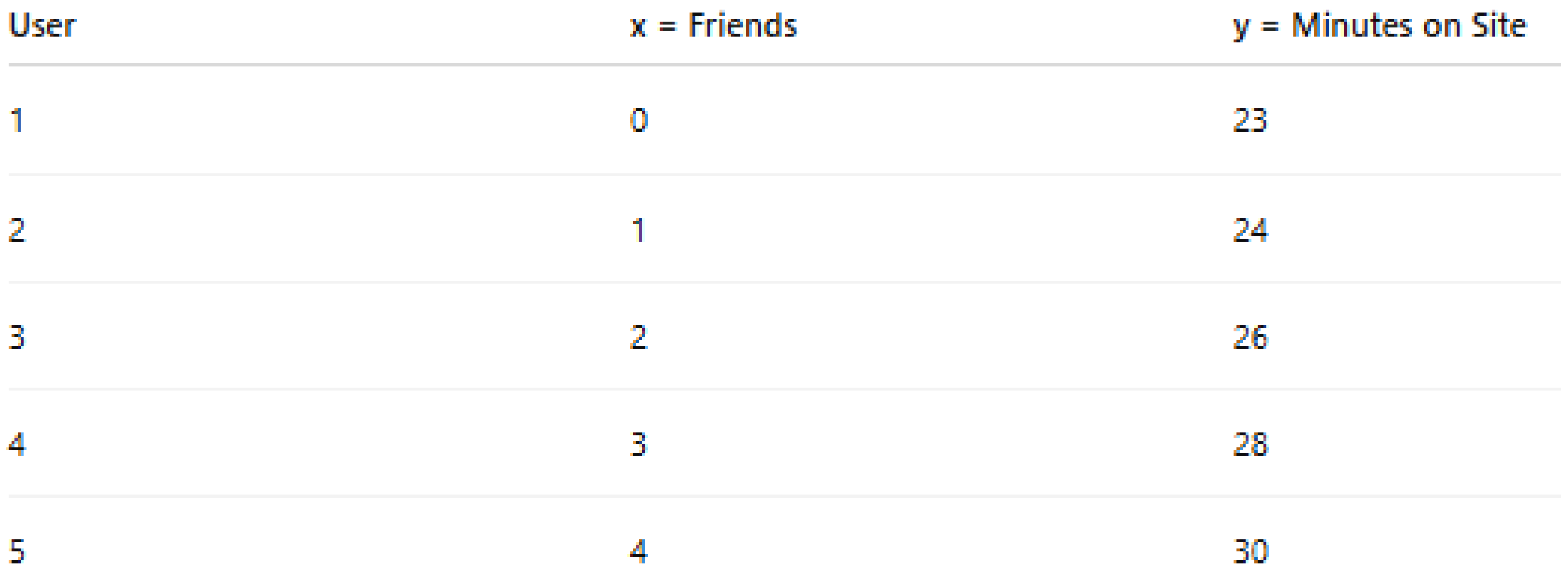


$$y_i = \beta x_i + \alpha + \varepsilon_i$$

Where:

- y_i: Minutes user i spends on the site per day.
- x_i: Number of friends user i has.
- ε_i: Error term.
- α: Intercept — base time spent when number of friends is 0.
- β: Slope — additional time spent for each new friend.

The Model



User	x = Friends	y = Minutes on Site
1	0	23
2	1	24
3	2	26
4	3	28
5	4	30

You can already see there’s a clear linear trend.

The Model : Program/Code Snippet

```
from typing import Tuple
from statistics import mean, stdev
from math import sqrt
```

$$\text{correlation}(x, y) = \frac{1}{n-1} \sum \left(\frac{x_i - \bar{x}}{s_x} \cdot \frac{y_i - \bar{y}}{s_y} \right)$$

```
def correlation(x, y):
    n = len(x)
    mean_x, mean_y = mean(x), mean(y)
    std_x, std_y = stdev(x), stdev(y)
     return sum((x_i - mean_x) * (y_i - mean_y) for x_i, y_i in zip(x, y)) / ((n -
1) * std_x * std_y)
```

least_squares_fit function calculates the best-fit line parameters, alpha and beta.

beta (slope): How much y increases for every 1-unit increase in x.

alpha (intercept): The value of y when x = 0.

```
def least_squares_fit(x, y) -> Tuple[float, float]:
    beta = correlation(x, y) * stdev(y) / stdev(x)
    alpha = mean(y) - beta * mean(x)
    return alpha, beta
```

The Model: Program/Code Snippet

```
x = [0, 1, 2, 3, 4]
y = [23, 24, 26, 28, 30]

alpha, beta = least_squares_fit(x, y)
print(f"alpha = {alpha:.2f}, beta = {beta:.2f}")
```

- alpha = 22.60, beta = 1.80

- **What the Model Means**
  - This gives us the model:
  - y=1.80x+22.60
  - A user with **0 friends** is predicted to spend **22 .60minutes/day**.
  - For **each additional friend**, they spend **1.80 more minutes/day.**

The Model: Program/Code Snippet

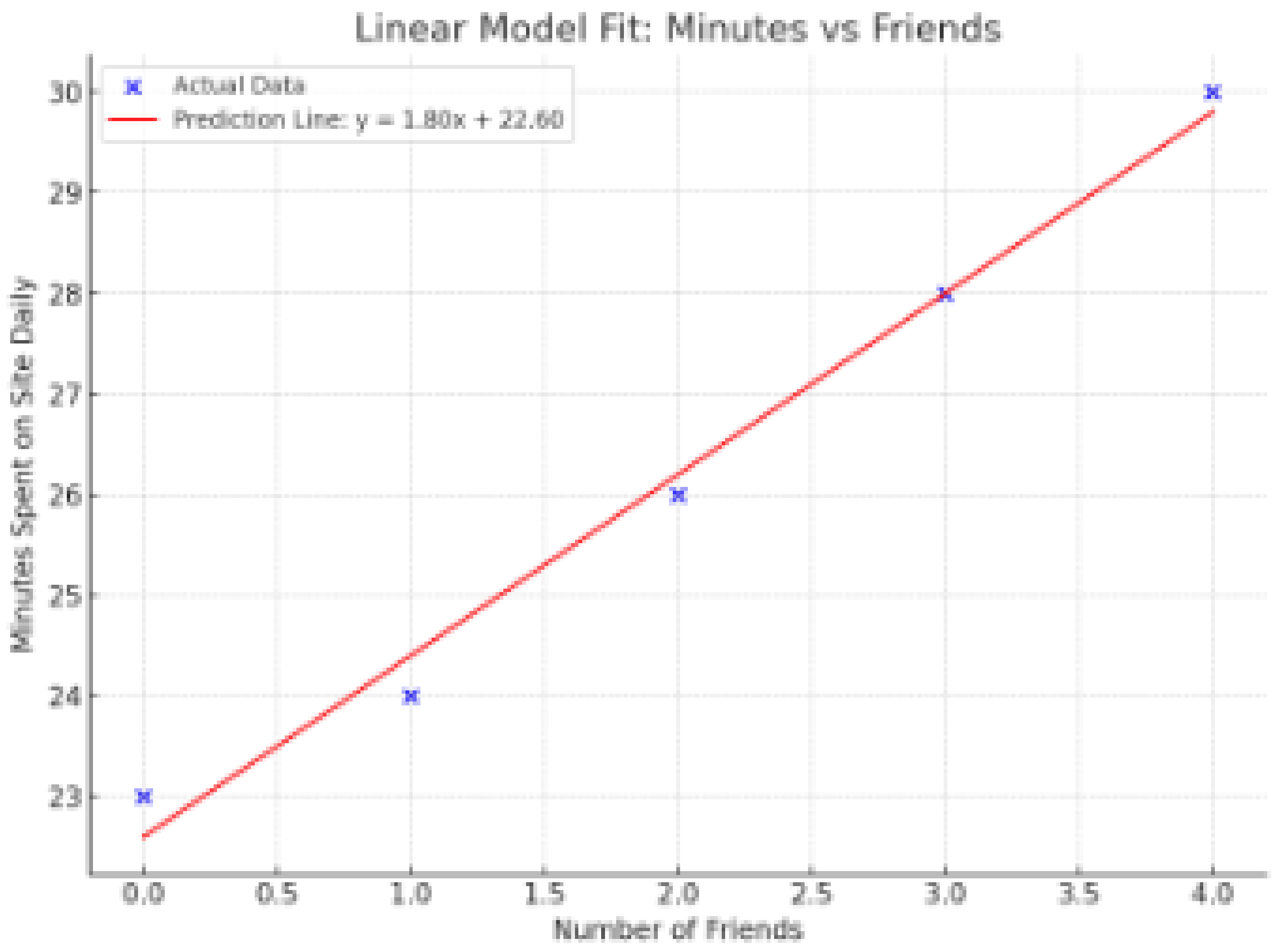
Predicting how many minutes a user with **2 friends** will spend on the site

```
def predict(alpha, beta, x_i):
    return beta * x_i + alpha

prediction = predict(22.60, 1., 2)
print(f"Predicted minutes: {prediction:.2f}")

error = prediction - 26  # = 0.5
```

sum_of_sqerrors function calculates the **total squared error** between your model's predictions and the actual values in your dataset — also known as the **sum of squared errors (SSE)**.

```
def sum_of_sqerrors(alpha, beta, x, y):
    return sum((predict(alpha, beta, x_i) - y_i) ** 2 for x_i, y_i in zip(x, y))

sse = sum_of_sqerrors(alpha, beta, x, y)
print(f"Total Squared Error: {sse:.2f}")
```

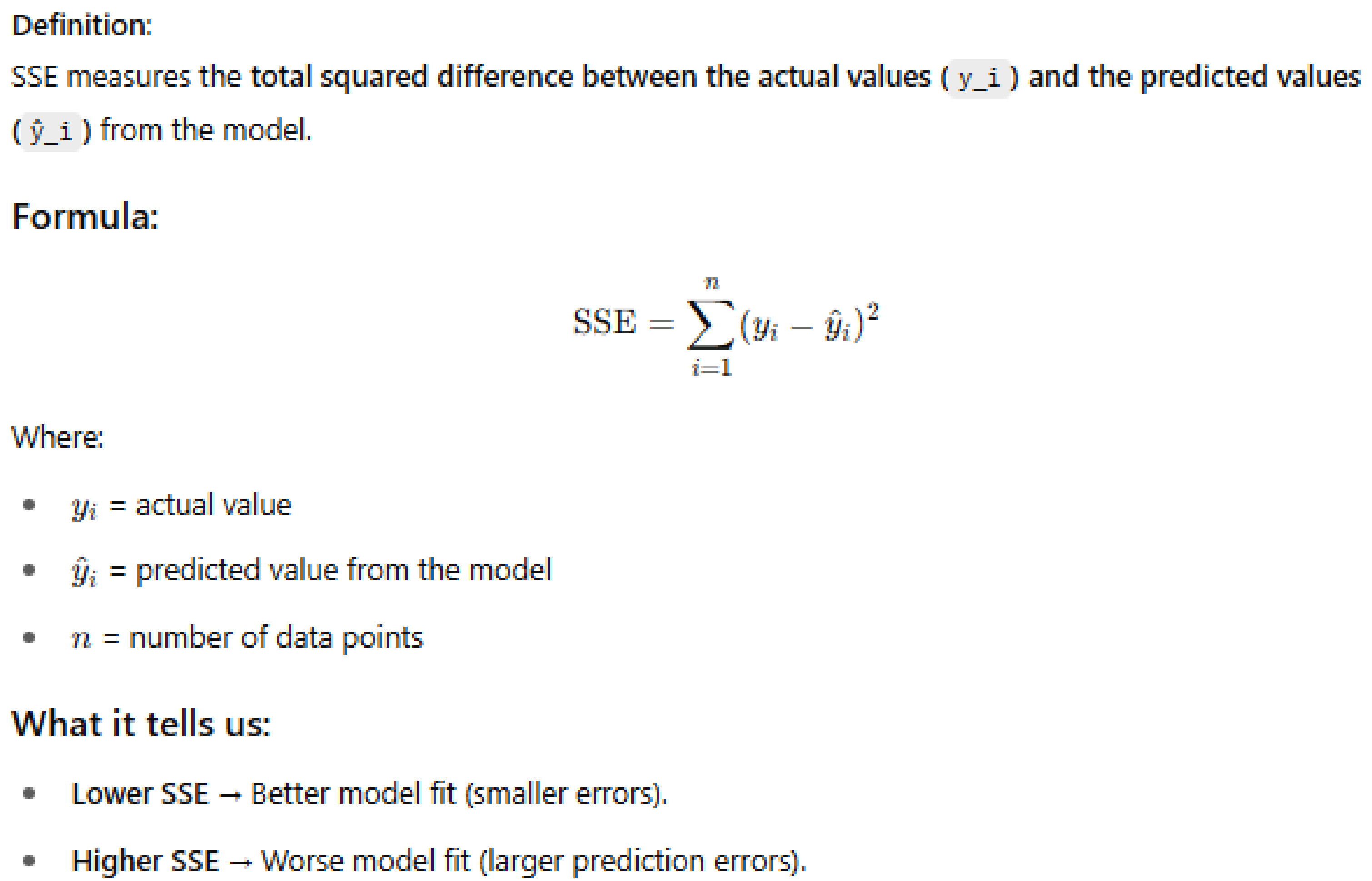
The Model


Linear Model Fit: Minutes vs Friends
Actual Data
Prediction Line: y = 1.80x + 22.60
Minutes Spent on Site Daily
Number of Friends
30
29
28
27
26
25
24
23
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

The Model

SE (Sum of Squared Errors) and **R-squared (R^2)** — two fundamental metrics in linear regression — to understand what each tells us about the quality of a model.

What is SSE (Sum of Squared Errors)?



Definition:

SSE measures the total squared difference between the actual values (`y_i`) and the predicted values (`ŷ_i`) from the model.

Formula:

$$\mathrm{SSE} = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2$$

Where:

- y_i = actual value
- $\hat{y}_i$ = predicted value from the model
- n = number of data points

What it tells us:

- Lower SSE → Better model fit (smaller errors).
- Higher SSE → Worse model fit (larger prediction errors).

The Model

Definition:

R-squared measures the **proportion of the variance in the dependent variable that is explained by the model.** It's a **relative** measure.

Formula:

$$R^2 = 1 - \frac{\text{SSE}}{\text{TSS}}$$

Where:

- **SSE** = Sum of Squared Errors
- **TSS** = Total Sum of Squares

$$\text{TSS} = \sum_{i=1}^{n} (y_i - \bar{y})^2$$

$\bar{y}$ = mean of all y_i

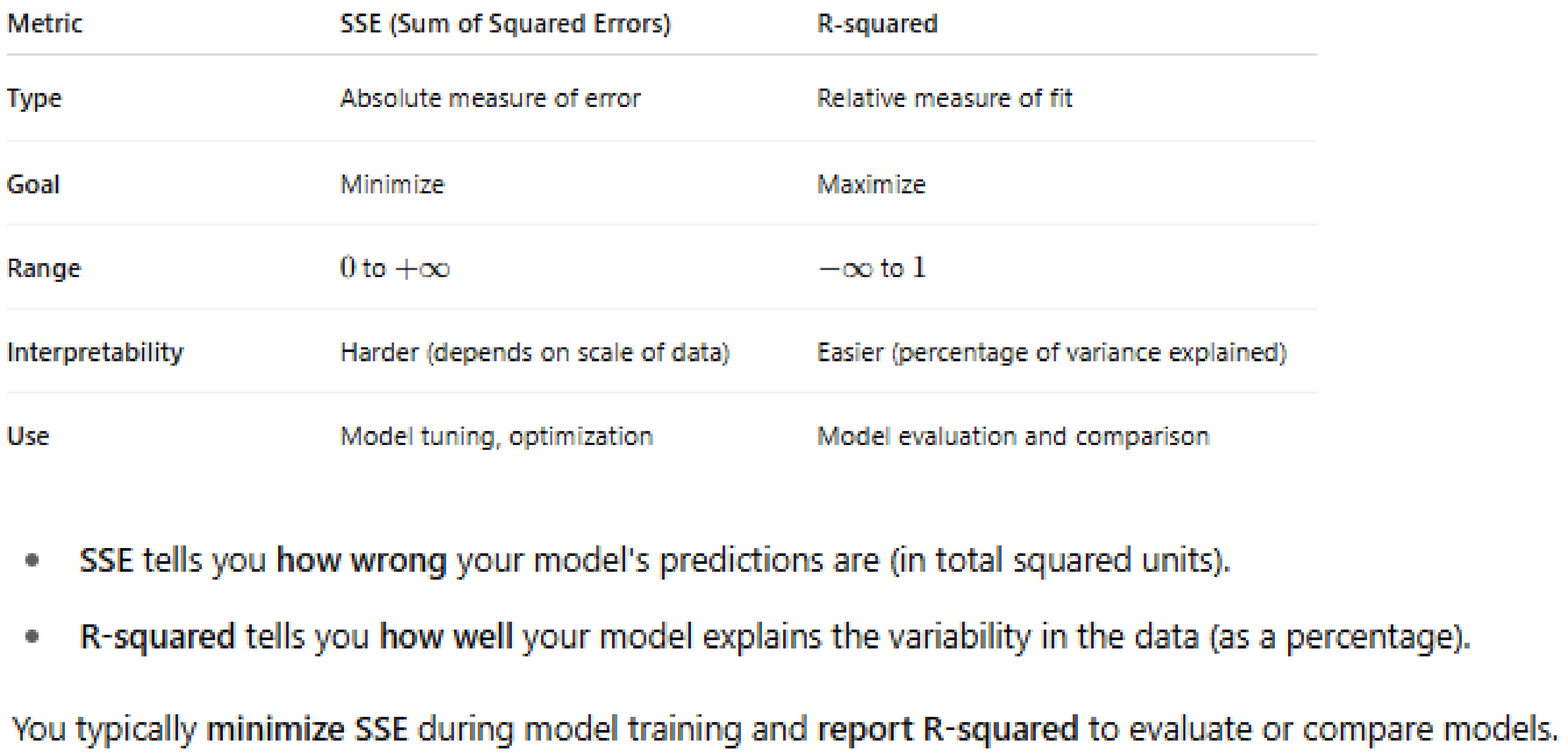
What it tells us:

- $R^2 = 1$ → Perfect fit: model explains **100%** of the variance.
- $R^2 = 0$ → Model explains **none** of the variance (as good as just predicting the mean).
- Can be **negative** if the model is worse than predicting the mean.

The Model

```
from scratch.statistics import de_mean

def de_mean(data: Vector) -> Vector:
    x_bar = mean(data)
    return [x_i - x_bar for x_i in data]

def total_sum_of_squares(y: Vector) -> float:
    """the total squared variation of y_i's from their mean"""
    return sum(v ** 2 for v in de_mean(y))

def r_squared(alpha: float, beta: float, x: Vector, y: Vector) -> float:
    """
    the fraction of variation in y captured by the model, which equals
    1 - the fraction of variation in y not captured by the model
    """
    return 1.0 - (sum_of_sqerrors(alpha, beta, x, y) /
    total_sum_of_squares(y))
rsq = r_squared(alpha, beta, num_friends_good, daily_minutes_good)
assert 0.328 < rsq < 0.330
```

The Model

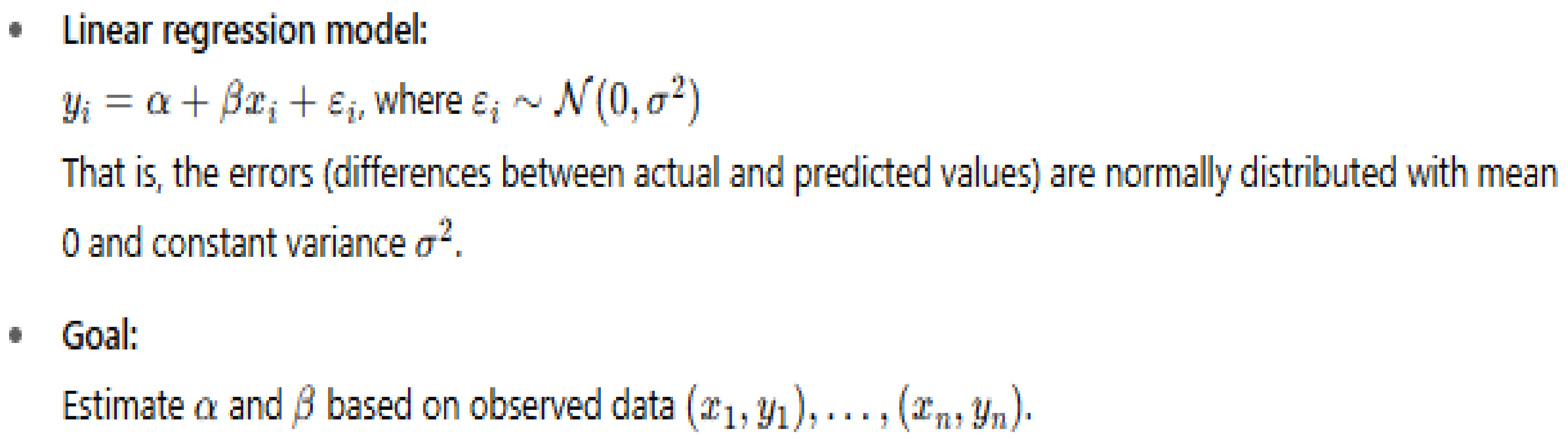


Metric	SSE (Sum of Squared Errors)	R-squared
Type	Absolute measure of error	Relative measure of fit
Goal	Minimize	Maximize
Range	0 to $+\infty$	$-\infty$ to 1
Interpretability	Harder (depends on scale of data)	Easier (percentage of variance explained)
Use	Model tuning, optimization	Model evaluation and comparison

- SSE tells you **how wrong** your model's predictions are (in total squared units).
- **R-squared** tells you **how well** your model explains the variability in the data (as a percentage).

You typically **minimize SSE** during model training and **report R-squared** to evaluate or compare models.

Maximum Likelihood Estimation (MLE).



- Linear regression model:

  $y_i = \alpha + \beta x_i + \varepsilon_i$, where $\varepsilon_i \sim \mathcal{N}(0, \sigma^2)$

  That is, the errors (differences between actual and predicted values) are normally distributed with mean 0 and constant variance σ^2.

- Goal:

  Estimate α and β based on observed data $(x_1, y_1), \ldots, (x_n, y_n)$.

Maximum Likelihood Estimation (MLE) is used in linear regression to estimate the model parameters (like the intercept α, slope β, and possibly error variance $\sigma 2$) because it provides a principled, probabilistic way to find the values that make the observed data most likely under the assumed model.

Maximum Likelihood Estimation (MLE).

1. Likelihood Function for One Data Point

Given one data point (x_i, y_i), the probability of observing y_i given x_i, α, and β, under the assumption of normally distributed errors, is:

$$L(\alpha, \beta \mid x_i, y_i, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(y_i - \alpha - \beta x_i)^2}{2\sigma^2}\right)$$

This expression tells us how *likely* the observed y_i is, given a predicted value $\alpha + \beta x_i$ and a known error variance σ^2.

- $L(\alpha, \beta \mid x_i, y_i, \sigma)$:
  This is the **likelihood function** — the probability (density) of observing the data point (x_i, y_i) given the parameters α, β, and σ.
- α:
  The **intercept** of the linear regression model. It represents the expected value of y when $x = 0$.
- β:
  The **slope** of the regression line. It measures the change in y for a unit change in x.
- x_i:
  The **input (independent variable)** value for the i^{th} observation.
- y_i:
  The **output (dependent variable)** value for the i^{th} observation.
- σ:
  The **standard deviation** of the normally distributed errors. It reflects the variability of the observations around the regression line.

Maximum Likelihood Estimation (MLE).

- $\frac{1}{\sqrt{2\pi\sigma^2}}$:
  This is the **normalization constant** of the normal distribution. It ensures that the total area under the probability density function equals 1.
- $\exp\left(-\frac{(y_i-\alpha-\beta x_i)^2}{2\sigma^2}\right)$:
  This is the **exponential part** of the normal distribution. It decreases as the squared difference between the observed value y_i and the predicted value $\alpha + \beta x_i$ increases.

2. Likelihood of the Whole Dataset

Assuming the data points are independent, the likelihood for the entire dataset is the **product** of the individual likelihoods:

$$L(\alpha, \beta) = \prod_{i=1}^{n} \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(y_i - \alpha - \beta x_i)^2}{2\sigma^2}\right)$$