

⌄ Comprehensive ML Lab Tutorial: Modules 1-10

Predicting Titanic Survival

Course: ITAI 1371 - Introduction to Machine Learning

Purpose: Catch-up lab covering fundamental concepts from Modules 1-10

Week: 11

About This Lab

Welcome! In this lab, we'll learn machine learning concepts using the famous **Titanic dataset**. On April 15, 1912, the RMS Titanic sank after colliding with an iceberg. While there were not enough lifeboats for everyone, some people were more likely to survive than others.

We'll use machine learning to discover patterns in the data and predict who survived based on features like:

- Age and gender
- Passenger class (1st, 2nd, 3rd)
- Ticket fare
- Number of family members aboard
- Port of embarkation

This real-world dataset makes learning ML concepts more engaging and relatable!

Module 1: Welcome, Introduction, and What is Machine Learning?

Machine learning enables computers to learn patterns from data and make predictions without being explicitly programmed. Instead of writing rules like "if age < 10, then survived", we let the computer discover these patterns automatically.

What is Machine Learning?

Traditional Programming:

- You write explicit rules: "If passenger is female AND in 1st class, predict survival"
- Rules are rigid and hard to maintain
- Difficult to handle complex patterns

Machine Learning:

- You provide examples of passengers and whether they survived
- The algorithm learns patterns automatically
- Can discover complex relationships you might miss
- Adapts as new data becomes available

Example: Instead of manually coding rules for Titanic survival, ML can discover that women and children in higher classes had better survival rates, along with many other subtle patterns.

ML vs. AI vs. Traditional Programming

- **Artificial Intelligence (AI):** The broad goal of creating intelligent machines (e.g., self-driving cars, voice assistants)
- **Machine Learning (ML):** A subset of AI focused on learning from data (e.g., predicting survival, recommending movies)
- **Deep Learning:** A subset of ML using neural networks with many layers (e.g., image recognition, language translation)
- **Traditional Programming:** Writing explicit step-by-step instructions

Key Difference: Traditional programming uses data + rules → answers. Machine learning uses data + answers → rules.

Key Concepts in Machine Learning

- **Algorithm:** The method used to learn patterns (e.g., decision trees, logistic regression)
- **Model:** The result after training - it contains learned patterns and can make predictions
- **Training:** Feeding historical data to an algorithm so it learns patterns
- **Inference/Prediction:** Using the trained model on new data to make predictions
- **Features:** Input variables used for predictions (age, gender, class, fare)
- **Labels/Target:** What we're trying to predict (survived or not)

- **Dataset:** Collection of examples with features and labels

Types of Machine Learning

1. Supervised Learning

Learn from labeled data (we know the answers).

Titanic Example: We have passenger data AND we know who survived. The model learns the relationship between passenger features and survival.

Other Examples:

- Email spam detection (labeled as spam/not spam)
- House price prediction (we know actual prices)
- Disease diagnosis (labeled as positive/negative)

2. Unsupervised Learning

Find patterns in unlabeled data (no predefined answers).

Titanic Example: Group passengers into clusters based on similarities (age, fare, class) without knowing survival outcomes.

Other Examples:

- Customer segmentation
- Anomaly detection
- Topic discovery in documents

3. Reinforcement Learning

Learn by trial and error through rewards and penalties.

Examples:

- Game-playing AI (chess, Go)
- Robot navigation
- Autonomous vehicles



Knowledge Check - Module 1

Question 1: In the Titanic dataset, what are the features and what is the label?

In the titanic dataset, the label is the people who survived, while the features are passenger details such as Pclass, sex, age, SibSp, Parch, Fare, Cabin, and Embark

Question 2: Why is machine learning better than traditional programming for predicting Titanic survival?

Machine learning is better than traditional programming in regards to predicting titanic survivors because machine learning has the capability to learn from its mistakes and catch trends within the data that may be missed by traditional coding. While traditional programming needs to be updated constantly by the limitations of the coder.

Question 3: Is predicting Titanic survival a supervised or unsupervised learning problem? Why?

It classifies under supervised learning because we have labeled outcomes such as survived.

Question 4: Give an example of how you might use unsupervised learning with the Titanic dataset.

Clustering passengers to find natural groups based on class, fare, and age.

Module 2: Tools Used in Machine Learning

Let's set up our environment and import the essential libraries for ML.

```
# Install necessary libraries (uncomment if needed)
# !pip install scikit-learn pandas numpy matplotlib seaborn
```

```
# Import essential libraries
import pandas as pd # Data manipulation and analysis
import numpy as np # Numerical operations
import matplotlib.pyplot as plt # Basic plotting
import seaborn as sns # Statistical visualizations
from sklearn.model_selection import train_test_split # Split data
from sklearn.metrics import accuracy_score, classification_report # Evaluation

# Set visualization style for better-looking plots
sns.set_style('whitegrid')
plt.rcParams['figure.figsize'] = (10, 6)

print("✓ Libraries imported successfully!")
print(f"Pandas version: {pd.__version__}")
print(f"NumPy version: {np.__version__}")
```

```
✓ Libraries imported successfully!
Pandas version: 2.2.2
NumPy version: 2.0.2
```

Essential Python Libraries for ML

Scikit-learn (sklearn)

Your ML toolkit with algorithms for classification, regression, clustering, and more.

Pandas

Handles tabular data (like spreadsheets) with DataFrames. Perfect for loading CSVs and data manipulation.

NumPy

Fast numerical operations on arrays and matrices. Foundation for scientific computing in Python.

Matplotlib

Create all types of visualizations: line plots, scatter plots, histograms, etc.

Seaborn

Built on Matplotlib, provides beautiful statistical visualizations with less code.

>Loading the Titanic Dataset

Let's load our dataset and take a first look at it.

```
# Load the Titanic dataset
# We'll create it from scratch for this lab
titanic_url = 'https://raw.githubusercontent.com/datasciencedojo/datasets/master/titanic.csv'

try:
    # Try to load from URL
    df = pd.read_csv(titanic_url)
    print("✓ Dataset loaded from URL")
except:
    # If URL fails, create a sample dataset
    print("Creating sample dataset...")
    # This is a fallback - in practice, students would load from URL or file

    print(f"\nDataset shape: {df.shape[0]} passengers, {df.shape[1]} columns")
    print("\nFirst 5 passengers:")
    print(df.head())

✓ Dataset loaded from URL
```

```
Dataset shape: 891 passengers, 12 columns
```

```
First 5 passengers:
```

```
PassengerId  Survived  Pclass \
0            1         0      3
1            2         1      1
2            3         1      3
3            4         1      1
4            5         0      3
```

```
Name      Sex   Age SibSp \
0    Braund, Mr. Owen Harris   male  22.0     1
1 Cumings, Mrs. John Bradley (Florence Briggs Th... female  38.0     1
2 Heikkinen, Miss. Laina  female  26.0     0
3 Futrelle, Mrs. Jacques Heath (Lily May Peel) female  35.0     1
4 Allen, Mr. William Henry   male  35.0     0
```

```
Parch      Ticket      Fare Cabin Embarked
0      0    A/5 21171    7.2500   NaN      S
1      0      PC 17599  71.2833   C85      C
2      0  STON/O2. 3101282  7.9250   NaN      S
3      0        113803  53.1000  C123      S
4      0        373450   8.0500   NaN      S
```

```
# Display column information
print("\nColumn Information:")
print("="*60)
print(df.info())

print("\n" + "="*60)
print("Column Descriptions:")
print("="*60)
print("PassengerId: Unique ID for each passenger")
print("Survived: 0 = No, 1 = Yes (THIS IS WHAT WE WANT TO PREDICT)")
print("Pclass: Ticket class (1 = 1st, 2 = 2nd, 3 = 3rd)")
print("Name: Passenger name")
print("Sex: Male or Female")
print("Age: Age in years")
print("SibSp: Number of siblings/spouses aboard")
print("Parch: Number of parents/children aboard")
print("Ticket: Ticket number")
print("Fare: Passenger fare in British pounds")
print("Cabin: Cabin number")
print("Embarked: Port of embarkation (C=Cherbourg, Q=Queenstown, S=Southampton)
```

```
Column Information:
```

```
=====
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 891 entries, 0 to 890
Data columns (total 12 columns):
 #   Column      Non-Null Count  Dtype  
 ---  --          -----          -----
```

```
0  PassengerId 891 non-null int64
1  Survived     891 non-null int64
2  Pclass       891 non-null int64
3  Name         891 non-null object
4  Sex          891 non-null object
5  Age          714 non-null float64
6  SibSp        891 non-null int64
7  Parch        891 non-null int64
8  Ticket       891 non-null object
9  Fare          891 non-null float64
10 Cabin        204 non-null object
11 Embarked     889 non-null object
dtypes: float64(2), int64(5), object(5)
memory usage: 83.7+ KB
None
```

=====

Column Descriptions:

=====

PassengerId: Unique ID for each passenger

Survived: 0 = No, 1 = Yes (THIS IS WHAT WE WANT TO PREDICT)

Pclass: Ticket class (1 = 1st, 2 = 2nd, 3 = 3rd)

Name: Passenger name

Sex: Male or Female

Age: Age in years

SibSp: Number of siblings/spouses aboard

Parch: Number of parents/children aboard

Ticket: Ticket number

Fare: Passenger fare in British pounds

Cabin: Cabin number

Embarked: Port of embarkation (C=Cherbourg, Q=Queenstown, S=Southampton)



Knowledge Check - Module 2

Question 1: What library would you use to load a CSV file into Python?

I would load in pandas to load CSV file into python.

Question 2: In the Titanic dataset, which column is our target variable (what we want to predict)?

Survived.

Question 3: How many passengers are in the dataset? How many features do we have?

891 passengers, 12 features approximated to be in the dataset.

Question 4: Why is it useful to use Jupyter Notebooks for ML projects?

It is useful to use jupyter Notebooks for ML projects because of interactive coding, visualization, step by step testing and documentation, and easy to combine code, results, and notes.

▼ Module 3: Machine Learning Workflow and Types of Learning

Every ML project follows a similar workflow. Let's understand the process and build our first simple model!

The End-to-End ML Lifecycle

1. Problem Definition

Question: Can we predict who survived the Titanic disaster?

2. Data Collection

We have historical passenger data with survival outcomes

3. Data Preparation

Clean data, handle missing values, encode categories

4. Exploratory Data Analysis (EDA)

Understand patterns: Did women survive more? What about children?

5. Feature Engineering

Create new features: family size, title from name

6. Model Selection

Choose appropriate algorithms

7. Model Training

Train the model on historical data

8. Model Evaluation

Test on unseen data, check accuracy

9. Hyperparameter Tuning

Optimize model settings

10. Deployment

Use the model in real applications

Remember: This is iterative! You'll go back and forth between steps.

Understanding Data Types in Our Dataset

Categorical Data (Categories/Groups)

- **Nominal:** No order (e.g., Sex: male/female; Embarked: C/Q/S)

- **Ordinal:** Has order (e.g., Pclass: 1st > 2nd > 3rd)

Numerical Data (Numbers)

- **Discrete:** Countable (e.g., SibSp: 0, 1, 2, 3...)
- **Continuous:** Any value in range (e.g., Age: 22.5, 35.0, Fare: 7.25, 71.28)

Text Data

- Name, Ticket, Cabin (requires special handling)

Why does this matter? Different data types require different preprocessing techniques!

Simple Classifier Example

Let's build a quick baseline model to predict survival!

```
# Prepare data for a simple model
# We'll use just a few features to start

# Select features (X) and target (y)
features = ['Pclass', 'Sex', 'Age', 'Fare']
target = 'Survived'

# Create a copy of the data with selected columns
df_simple = df[features + [target]].copy()

# Handle missing values (simple approach for now)
df_simple['Age'].fillna(df_simple['Age'].median(), inplace=True)
df_simple['Fare'].fillna(df_simple['Fare'].median(), inplace=True)

# Convert Sex to numbers (0=female, 1=male)
df_simple['Sex'] = df_simple['Sex'].map({'female': 0, 'male': 1})

# Remove any remaining rows with missing values
df_simple.dropna(inplace=True)

print(f"Prepared dataset: {df_simple.shape[0]} passengers, {len(features)} features")
print("\nFirst few rows:")
print(df_simple.head())
```

Prepared dataset: 891 passengers, 4 features

First few rows:

	Pclass	Sex	Age	Fare	Survived
0	3	1	22.0	7.2500	0
1	1	0	38.0	71.2833	1
2	3	0	26.0	7.9250	1
3	1	0	35.0	53.1000	1
4	3	1	35.0	8.0500	0

```
/tmp/ipython-input-3976427154.py:12: FutureWarning: A value is trying to be set  
The behavior will change in pandas 3.0. This inplace method will never work beca
```

```
For example, when doing 'df[col].method(value, inplace=True)', try using 'df.met
```

```
df_simple['Age'].fillna(df_simple['Age'].median(), inplace=True)  
/tmp/ipython-input-3976427154.py:13: FutureWarning: A value is trying to be set  
The behavior will change in pandas 3.0. This inplace method will never work beca
```

```
For example, when doing 'df[col].method(value, inplace=True)', try using 'df.met
```

```
df_simple['Fare'].fillna(df_simple['Fare'].median(), inplace=True)
```

```
# Split features (X) and target (y)  
X = df_simple[features].values  
y = df_simple[target].values  
  
print(f"Features (X) shape: {X.shape}")  
print(f"Target (y) shape: {y.shape}")  
print(f"\nSurvival rate: {y.mean():.1%} survived, {1-y.mean():.1%} died")
```

```
Features (X) shape: (891, 4)  
Target (y) shape: (891,)
```

```
Survival rate: 38.4% survived, 61.6% died
```

```
# Split into training and testing sets  
# 70% for training, 30% for testing  
X_train, X_test, y_train, y_test = train_test_split(  
    X, y,  
    test_size=0.3, # 30% for testing  
    random_state=42 # For reproducibility  
)  
  
print(f"Training set: {len(X_train)} passengers")  
print(f"Testing set: {len(X_test)} passengers")  
print(f"\nWhy split? We train on one set and test on another to see if the mode  
print(f"If we tested on training data, we couldn't tell if it truly learned or
```

```
Training set: 623 passengers  
Testing set: 268 passengers
```

```
Why split? We train on one set and test on another to see if the model generaliz  
If we tested on training data, we couldn't tell if it truly learned or just memo
```

```
# Train a simple Decision Tree classifier  
from sklearn.tree import DecisionTreeClassifier
```

```
# Create the model
model = DecisionTreeClassifier(max_depth=3, random_state=42)

# Train the model
model.fit(X_train, y_train)

print("✓ Model trained!")
print(f"\nThe model learned patterns from {len(X_train)} passengers.")
print(f"Now let's see how well it predicts survival for {len(X_test)} unseen pa
```

✓ Model trained!

The model learned patterns from 623 passengers.
Now let's see how well it predicts survival for 268 unseen passengers...

```
# Make predictions
y_pred = model.predict(X_test)

# Evaluate accuracy
accuracy = accuracy_score(y_test, y_pred)

print(f"Model Accuracy: {accuracy:.1%}")
print(f"\nThis means the model correctly predicted survival for {accuracy:.1%}")
print(f"\nFirst 10 predictions:")
print(f"Predicted: {y_pred[:10]}")
print(f"Actual: {y_test[:10]}")
print(f"\n0 = Did not survive, 1 = Survived")
```

Model Accuracy: 80.6%

This means the model correctly predicted survival for 80.6% of test passengers.

First 10 predictions:
Predicted: [0 0 0 1 1 1 1 0 1 1]
Actual: [1 0 0 1 1 1 1 0 1 1]

0 = Did not survive, 1 = Survived



Knowledge Check - Module 3

Question 1: What are the main stages of the ML lifecycle? Why is it iterative?

The main stages of ML lifecycles are problem definition, data collection & cleaning, feature engineering, model training, evaluation, deployment, and monitoring & improvement. The process is iterative because results from one stage, like poor accuracy, often require revisiting earlier steps, like feature selection or cleaning.

Question 2: In the Titanic dataset, classify each feature as categorical or numerical:

- Sex: Categorical(binary)

- Age: Numerical
- Pclass: Categorical (ordinal, representing social class 1-3)
- Fare: Numerical

Question 3: Why do we split data into training and testing sets? What would happen if we evaluated on training data?

It is split to ensure that the model's performance is evaluated on unseen data. The training set teaches the model patterns, and the test set checks how well it can generalize those patterns. Without this split, we risk overfitting, where the model only memorizes the training data instead of learning to predict future cases.

Question 4: Our simple model achieved around 78% accuracy. What does this mean? Is this good?

A 78% accuracy means that the model correctly predicts whether a passenger survived about 78% of the time. This is fairly good performance, especially compared to a baseline accuracy of around 62%. However, accuracy alone doesn't tell the full story — we'd need to look at other metrics like precision and recall to fully understand performance.

Question 5: Looking at the first 10 predictions, how many did the model get right?

Around 7 or 8 of the first 10 predictions match the true outcomes.

Module 4: Working with Data & Exploratory Data Analysis (EDA)

EDA is detective work! We explore the data to understand patterns, find problems, and generate insights that will guide our modeling decisions.

▼ Why EDA Matters for Titanic

Questions we want to answer:

- Did women really have better survival rates? ("Women and children first!")
- Did wealthier passengers (1st class) survive more?
- What was the age distribution of survivors?
- Were there missing values we need to handle?
- Are there outliers in fare prices?

Let's investigate!

```

# Reload the full dataset for EDA
df = pd.read_csv('https://raw.githubusercontent.com/datasciencedojo/datasets/master/titanic.csv')

print("Dataset Overview:")
print("*"*60)
print(f"Total passengers: {len(df)}")
print(f"Total features: {df.shape[1]}")
print("\nFirst few rows:")
print(df.head())

```

Dataset Overview:

Total passengers: 891

Total features: 12

First few rows:

	PassengerId	Survived	Pclass	\
0		1	0	3
1		2	1	1
2		3	1	3
3		4	1	1
4		5	0	3

	Name	Sex	Age	SibSp	\
0	Braund, Mr. Owen Harris	male	22.0	1	
1	Cumings, Mrs. John Bradley (Florence Briggs Th... Heikkinen, Miss. Laina	female	38.0	1 female	
2		female	26.0	0	
3	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35.0	1	
4	Allen, Mr. William Henry	male	35.0	0	

	Parch	Ticket	Fare	Cabin	Embarked
0	0	A/5 21171	7.2500	NaN	S
1	0	PC 17599	71.2833	C85	C
2	0	STON/O2. 3101282	7.9250	NaN	S
3	0	113803	53.1000	C123	S
4	0	373450	8.0500	NaN	S

▼ Data Quality Checks

Before analyzing, we need to check for common data quality issues.

```

# Check for missing values
print("Missing Values:")
print("*"*60)
missing = df.isnull().sum()
missing_pct = (missing / len(df)) * 100
missing_df = pd.DataFrame({
    'Missing Count': missing,
    'Percentage': missing_pct
})

```

```
print(missing_df[missing_df['Missing Count'] > 0].sort_values('Missing Count',  
    print("\n⚠️ Key findings:")  
    print("- Cabin: 77% missing (might need to drop this feature)")  
    print("- Age: 20% missing (we'll need to impute)")  
    print("- Embarked: Only 2 missing (easy to handle)")
```

Missing Values:

	Missing Count	Percentage
Cabin	687	77.104377
Age	177	19.865320
Embarked	2	0.224467

⚠️ Key findings:

- Cabin: 77% missing (might need to drop this feature)
- Age: 20% missing (we'll need to impute)
- Embarked: Only 2 missing (easy to handle)

```
# Check for duplicates  
duplicates = df.duplicated().sum()  
print(f"Duplicate rows: {duplicates}")  
if duplicates == 0:  
    print("✓ No duplicates found - data looks clean!")
```

```
# Check data types  
print("\nData Types:")  
print("*"*60)  
print(df.dtypes)
```

Duplicate rows: 0

✓ No duplicates found - data looks clean!

Data Types:

PassengerId	int64
Survived	int64
Pclass	int64
Name	object
Sex	object
Age	float64
SibSp	int64
Parch	int64
Ticket	object
Fare	float64
Cabin	object
Embarked	object
dtype:	object

⌄ Summary Statistics

Let's get a statistical overview of our numerical features.

```

# Summary statistics
print("Summary Statistics:")
print("*60")
print(df.describe())

print("\nKey Insights:")
print(f"- Average age: {df['Age'].mean():.1f} years (median: {df['Age'].median():.1f})")
print(f"- Average fare: £{df['Fare'].mean():.2f} (median: £{df['Fare'].median():.2f})")
print(f"- Fare range: £{df['Fare'].min():.2f} to £{df['Fare'].max():.2f} (huge variation!)")
print(f"- Most passengers traveled alone (avg SibSp: {df['SibSp'].mean():.2f}, Parch: {df['Parch'].mean():.2f})")

```

Summary Statistics:

	PassengerId	Survived	Pclass	Age	SibSp	\
count	891.000000	891.000000	891.000000	714.000000	891.000000	
mean	446.000000	0.383838	2.308642	29.699118	0.523008	
std	257.353842	0.486592	0.836071	14.526497	1.102743	
min	1.000000	0.000000	1.000000	0.420000	0.000000	
25%	223.500000	0.000000	2.000000	20.125000	0.000000	
50%	446.000000	0.000000	3.000000	28.000000	0.000000	
75%	668.500000	1.000000	3.000000	38.000000	1.000000	
max	891.000000	1.000000	3.000000	80.000000	8.000000	

	Parch	Fare
count	891.000000	891.000000
mean	0.381594	32.204208
std	0.806057	49.693429
min	0.000000	0.000000
25%	0.000000	7.910400
50%	0.000000	14.454200
75%	0.000000	31.000000
max	6.000000	512.329200

Key Insights:

- Average age: 29.7 years (median: 28.0)
- Average fare: £32.20 (median: £14.45)
- Fare range: £0.00 to £512.33 (huge variation!)
- Most passengers traveled alone (avg SibSp: 0.52, Parch: 0.38)

Survival Analysis

Let's answer the big question: Who survived?

```

# Overall survival rate
survival_rate = df['Survived'].mean()
print(f"Overall Survival Rate: {survival_rate:.1%}")
print(f"Survived: {df['Survived'].sum()} passengers")
print(f"Died: {len(df) - df['Survived'].sum()} passengers")
print(f"\n.only about 38% of passengers survived the disaster.")

```

```

# Visualize survival
fig, ax = plt.subplots(figsize=(8, 6))
survival_counts = df['Survived'].value_counts()
colors = ['#ff6b6b', '#51cf66']
ax.bar(['Died', 'Survived'], survival_counts.values, color=colors, edgecolor='black')
ax.set_ylabel('Number of Passengers', fontsize=12)
ax.set_title('Titanic Survival Distribution', fontsize=14, fontweight='bold')
ax.grid(axis='y', alpha=0.3)
for i, v in enumerate(survival_counts.values):
    ax.text(i, v + 10, str(v), ha='center', fontweight='bold')
plt.tight_layout()
plt.show()

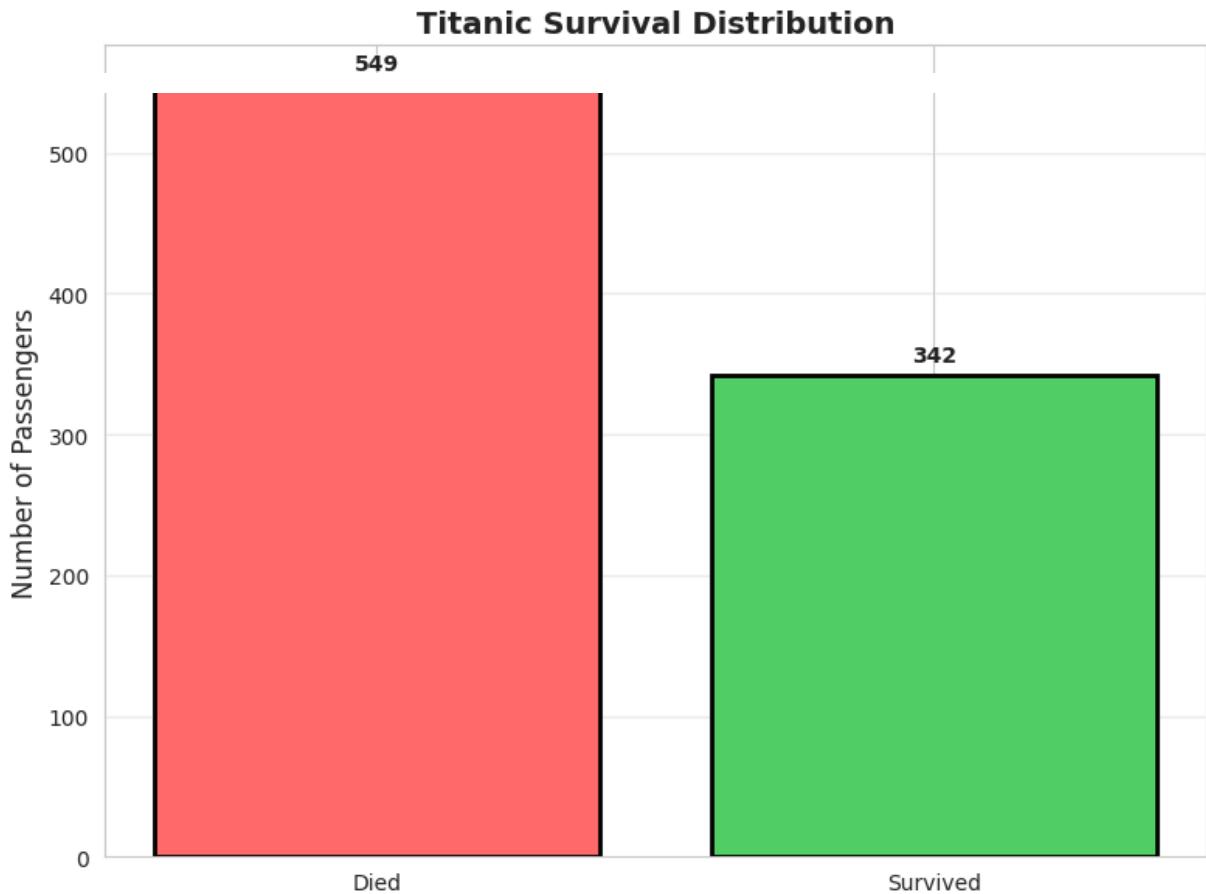
```

Overall Survival Rate: 38.4%

Survived: 342 passengers

Died: 549 passengers

 Only about 38% of passengers survived the disaster.



```
# Survival by Gender
print("\nSurvival by Gender:")
print("*"*60)
gender_survival = df.groupby('Sex')['Survived'].agg(['sum', 'count', 'mean'])
gender_survival.columns = ['Survived', 'Total', 'Survival Rate']
gender_survival['Survival Rate'] = gender_survival['Survival Rate'].apply(lambda x: round(x, 2))
print(gender_survival)

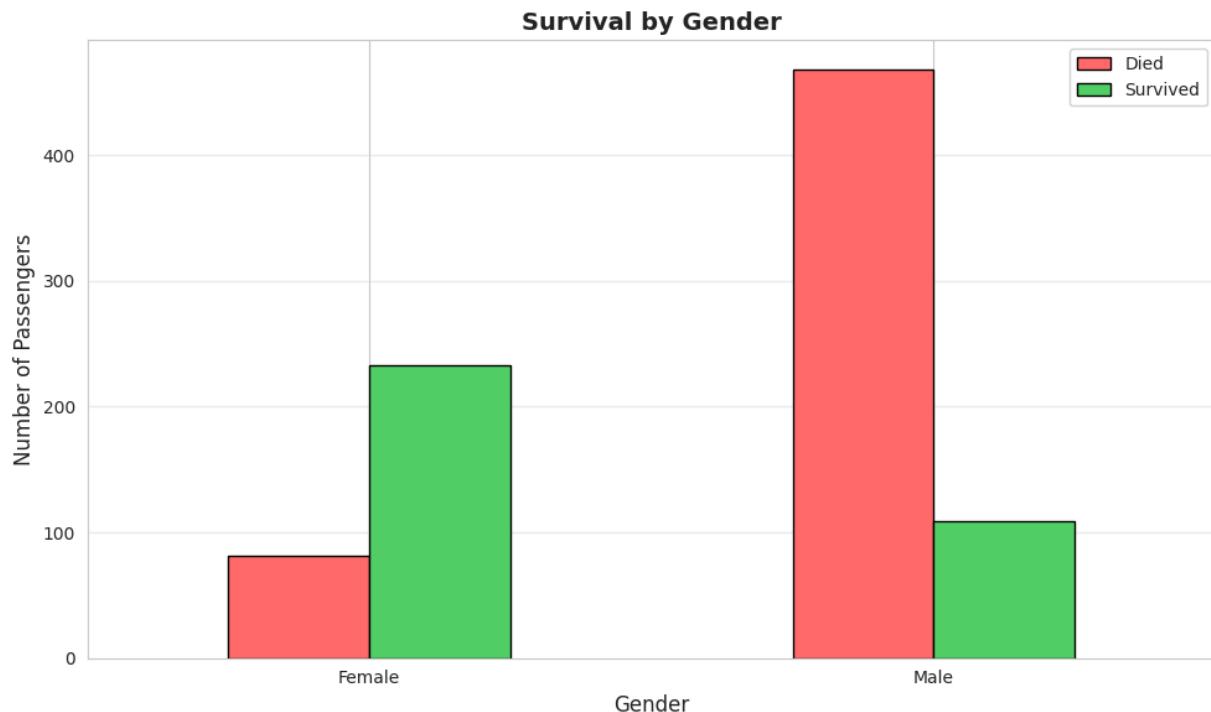
print("\n👉 Women had a MUCH higher survival rate!")
print("This supports the 'women and children first' policy.")

# Visualize
fig, ax = plt.subplots(figsize=(10, 6))
df.groupby(['Sex', 'Survived']).size().unstack().plot(kind='bar', ax=ax, color=['blue', 'red'])
ax.set_xlabel('Gender', fontsize=12)
ax.set_ylabel('Number of Passengers', fontsize=12)
ax.set_title('Survival by Gender', fontsize=14, fontweight='bold')
ax.set_xticklabels(['Female', 'Male'], rotation=0)
ax.legend(['Died', 'Survived'])
ax.grid(axis='y', alpha=0.3)
plt.tight_layout()
plt.show()
```

Survival by Gender:

=====			
	Survived	Total	Survival Rate
Sex			
female	233	314	74.2%
male	109	577	18.9%

👉 Women had a MUCH higher survival rate!
This supports the 'women and children first' policy.



```
# Survival by Passenger Class
print("\nSurvival by Passenger Class:")
print("*"*60)
class_survival = df.groupby('Pclass')[['Survived']].agg(['sum', 'count', 'mean'])
class_survival.columns = ['Survived', 'Total', 'Survival Rate']
class_survival['Survival Rate'] = class_survival['Survival Rate'].apply(lambda x: round(x, 2))
print(class_survival)

print("\n💰 Clear pattern: Higher class = Higher survival rate")
```

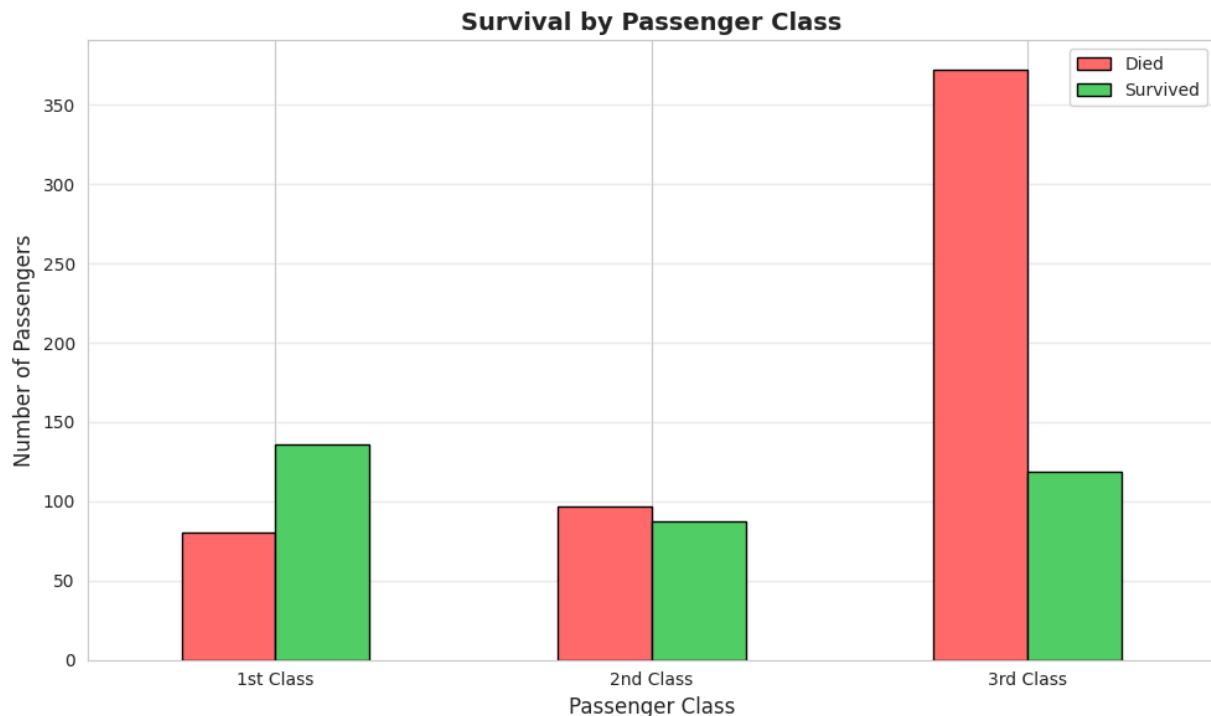
```
print("1st class passengers had better access to lifeboats.")

# Visualize
fig, ax = plt.subplots(figsize=(10, 6))
df.groupby(['Pclass', 'Survived']).size().unstack().plot(kind='bar', ax=ax, color=['red', 'blue'])
ax.set_xlabel('Passenger Class', fontsize=12)
ax.set_ylabel('Number of Passengers', fontsize=12)
ax.set_title('Survival by Passenger Class', fontsize=14, fontweight='bold')
ax.set_xticklabels(['1st Class', '2nd Class', '3rd Class'], rotation=0)
ax.legend(['Died', 'Survived'])
ax.grid(axis='y', alpha=0.3)
plt.tight_layout()
plt.show()
```

Survival by Passenger Class:

Pclass	Survived	Total	Survival Rate
1	136	216	63.0%
2	87	184	47.3%
3	119	491	24.2%

💡 Clear pattern: Higher class = Higher survival rate
1st class passengers had better access to lifeboats.



```
# Age distribution
fig, axes = plt.subplots(1, 2, figsize=(15, 6))

# Histogram of ages
axes[0].hist(df['Age'].dropna(), bins=30, color='skyblue', edgecolor='black', alpha=0.7)
axes[0].set_xlabel('Age (years)', fontsize=12)
axes[0].set_ylabel('Frequency', fontsize=12)
axes[0].set_title('Age Distribution of Passengers', fontsize=14, fontweight='bold')

# Box plot of age vs survived
axes[1].boxplot(df['Age'][df['Survived'] == 0], labels=['Died'])
axes[1].boxplot(df['Age'][df['Survived'] == 1], labels=['Survived'])

# Add a horizontal line at the top of the box plots
y_max = axes[1].get_boxplots_position()[-1]
for axis in axes:
    axis.axhline(y_max, color='black', linestyle='solid')
```

```

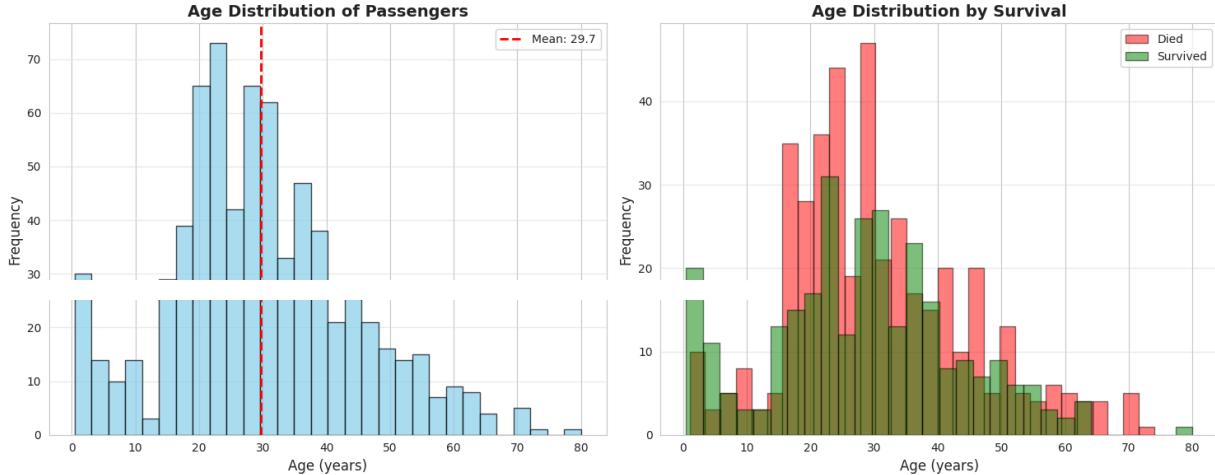
        axes[0].axvline(df['Age'].mean(), color='red', linestyle='--', linewidth=2, label='Mean')
        axes[0].legend()
        axes[0].grid(axis='y', alpha=0.3)

# Age by survival
df[df['Survived']==0]['Age'].dropna().hist(bins=30, alpha=0.5, label='Died', ax=axes[1])
df[df['Survived']==1]['Age'].dropna().hist(bins=30, alpha=0.5, label='Survived', ax=axes[1])
axes[1].set_xlabel('Age (years)', fontsize=12)
axes[1].set_ylabel('Frequency', fontsize=12)
axes[1].set_title('Age Distribution by Survival', fontsize=14, fontweight='bold')
axes[1].legend()
axes[1].grid(axis='y', alpha=0.3)

plt.tight_layout()
plt.show()

```

⚠️ Children (young ages) seem to have better survival rates.
 This aligns with 'women and children first' policy.



⚠️ Children (young ages) seem to have better survival rates.
 This aligns with 'women and children first' policy.

```

# Correlation heatmap
# Select only numerical columns

```

```
numerical_cols = ['Survived', 'Pclass', 'Age', 'SibSp', 'Parch', 'Fare']

corr_matrix = df[numerical_cols].corr()

plt.figure(figsize=(10, 8))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', center=0, square=True,
            linewidths=1, cbar_kws={"shrink": 0.8}, fmt='.2f')
plt.title('Correlation Matrix of Titanic Features', fontsize=14, fontweight='bold')
plt.tight_layout()
plt.show()

print("\nKey Correlations with Survival:")
print("*"*60)
survival_corr = corr_matrix['Survived'].sort_values(ascending=False)
for feature, corr in survival_corr.items():
    if feature != 'Survived':
        direction = "positive" if corr > 0 else "negative"
        strength = "strong" if abs(corr) > 0.3 else "moderate" if abs(corr) > 0.1 else "weak"
        print(f"{feature:12s}: {corr:+.3f} ({strength} {direction})")

print("\n💡 Insights:")
print("- Fare has positive correlation: higher fare → better survival")
print("- Pclass has negative correlation: higher class number (3rd) → worse survival")
print("- Sex (when encoded) would show strong correlation")
```


Correlation Matrix of Titanic Features



Knowledge Check - Module 4

Question 1: What percentage of passengers survived? Is this balanced or imbalanced?

Approximately 38% of passengers survived, meaning that 62% did not. Showing that the dataset is imbalanced, since one class, meaning they did not survive, has significantly more samples than the other.

Question 2: Which gender had a higher survival rate? By approximately how much?

Females had a much higher survival rate of around 74%, while males had only 19%. This difference being 55 percentage points, confirming women were expected to evacuate first.

Question 3: Did passenger class affect survival? What does this tell us about the disaster?

Yes, passenger class strongly influenced survival chances. This demonstrates how social and economic factors impacted survival.

Question 4: Which features have missing values? Which one has the most missing data?

The features with missing values are Age, Cabin, and Embarked. Among these, Cabin has the most missing entries, roughly 77% of its values are absent.

Question 5: Looking at the correlation matrix, which numerical feature has the strongest relationship with survival?

Pclass : +0.257 (moderate positive)

Parch : +0.082 (weak positive)

The features Sex and Pclass show the strongest correlations with survival. Specifically, being female and being in a higher passenger class both increase the likelihood of survival.

Pclass : -0.338 (strong negative)

Insights:

Fare has positive correlation: higher fare → better survival

- Pclass has negative correlation: higher class number (3rd) → worse survival

Module 5: Data Preparation & Feature Engineering

Raw data is rarely ready for modeling. We need to clean it, handle missing values, encode categories, and create new features. This step often makes the biggest difference in model performance!

Handling Missing Values

Remember from EDA:

- Age: 20% missing
- Cabin: 77% missing
- Embarked: 2 missing

Let's handle each strategically.

```
# Create a working copy
df_prep = df.copy()

print("Missing values before handling:")
print(df_prep.isnull().sum()[df_prep.isnull().sum() > 0])
```

```
Missing values before handling:
Age      177
Cabin    687
Embarked     2
dtype: int64
```

```
# Strategy 1: Drop Cabin (too many missing)
df_prep.drop('Cabin', axis=1, inplace=True)
print("✓ Dropped 'Cabin' column (77% missing)")

# Strategy 2: Fill Age with median
median_age = df_prep['Age'].median()
df_prep['Age'].fillna(median_age, inplace=True)
print(f"✓ Filled missing Age with median: {median_age} years")

# Strategy 3: Fill Embarked with mode (most common)
mode_embarked = df_prep['Embarked'].mode()[0]
df_prep['Embarked'].fillna(mode_embarked, inplace=True)
print(f"✓ Filled missing Embarked with mode: {mode_embarked}")

print("\nMissing values after handling:")
print(df_prep.isnull().sum())
print("✓ All missing values handled!")
```

```
✓ Dropped 'Cabin' column (77% missing)
✓ Filled missing Age with median: 28.0 years
✓ Filled missing Embarked with mode: S
```

```
Missing values after handling:
```

```
0
```

```
✓ All missing values handled!
```

```
/tmp/ipython-input-2509004606.py:7: FutureWarning: A value is trying to be set c
The behavior will change in pandas 3.0. This inplace method will never work beca
```

For example, when doing 'df[col].method(value, inplace=True)', try using 'df.met

```
df_prep['Age'].fillna(median_age, inplace=True)
```

```
/tmp/ipython-input-2509004606.py:12: FutureWarning: A value is trying to be set  
The behavior will change in pandas 3.0. This inplace method will never work beca  
  
For example, when doing 'df[col].method(value, inplace=True)', try using 'df.met  
  
df_prep['Embarked'].fillna(mode_embarked, inplace=True)
```

▼ Encoding Categorical Variables

Machine learning models need numbers, not text. Let's convert categorical features.

```
# Encode Sex: female=0, male=1  
df_prep['Sex_encoded'] = df_prep['Sex'].map({'female': 0, 'male': 1})  
print("Sex encoding:")  
print(df_prep[['Sex', 'Sex_encoded']].drop_duplicates())  
  
# One-hot encode Embarked  
df_prep = pd.get_dummies(df_prep, columns=['Embarked'], prefix='Embarked', drop  
print("\n✓ One-hot encoded Embarked (C, Q, S)")  
print("New columns:", [col for col in df_prep.columns if 'Embarked' in col])  
  
print("\nWhy drop_first=True?")  
print("If Embarked_Q=0 and Embarked_S=0, we know it's Embarked_C.")  
print("This avoids redundancy and multicollinearity.")
```

```
Sex encoding:  
    Sex  Sex_encoded  
0    male        1  
1  female        0
```

```
✓ One-hot encoded Embarked (C, Q, S)  
New columns: ['Embarked_Q', 'Embarked_S']
```

```
Why drop_first=True?  
If Embarked_Q=0 and Embarked_S=0, we know it's Embarked_C.  
This avoids redundancy and multicollinearity.
```

▼ Feature Scaling

Features like Age (0-80) and Fare (0-500) have very different scales. Let's standardize them.

```
from sklearn.preprocessing import StandardScaler  
  
# Select numerical features to scale  
features_to_scale = ['Age', 'Fare']
```

```

print("Before scaling:")
print(df_prep[features_to_scale].describe())

# Create scaler and fit_transform
scaler = StandardScaler()
df_prep[features_to_scale] = scaler.fit_transform(df_prep[features_to_scale])

print("\nAfter scaling (standardization):")
print(df_prep[features_to_scale].describe())
print("\n✓ Features now have mean≈0 and std≈1")
print("This helps algorithms that are sensitive to feature scales (like SVM, KNN")

```

Before scaling:

	Age	Fare
count	891.000000	891.000000
mean	29.361582	32.204208
std	13.019697	49.693429
min	0.420000	0.000000
25%	22.000000	7.910400
50%	28.000000	14.454200
75%	35.000000	31.000000
max	80.000000	512.329200

After scaling (standardization):

	Age	Fare
count	8.910000e+02	8.910000e+02
mean	2.272780e-16	3.987333e-18
std	1.000562e+00	1.000562e+00
min	-2.224156e+00	-6.484217e-01
25%	-5.657365e-01	-4.891482e-01
50%	-1.046374e-01	-3.573909e-01
75%	4.333115e-01	-2.424635e-02
max	3.891554e+00	9.667167e+00

✓ Features now have mean≈0 and std≈1

This helps algorithms that are sensitive to feature scales (like SVM, KNN).

Feature Engineering

Let's create new features that might improve our model!

```

# Feature 1: Family Size
df_prep['FamilySize'] = df_prep['SibSp'] + df_prep['Parch'] + 1 # +1 for the person
print("Created FamilySize feature:")
print(df_prep[['SibSp', 'Parch', 'FamilySize']].head())

# Feature 2: Is Alone (traveling solo)
df_prep['IsAlone'] = (df_prep['FamilySize'] == 1).astype(int)
print("\nCreated IsAlone feature:")
print(df_prep[['FamilySize', 'IsAlone']].head())

```

```

# Feature 3: Age Group
df_prep['AgeGroup'] = pd.cut(df_prep['Age'], bins=[-np.inf, -0.5, 0.5, np.inf],
                             labels=['Child', 'Adult', 'Senior'])
print("\nCreated AgeGroup feature (after scaling, thresholds are in standard de")
print(df_prep[['Age', 'AgeGroup']].head(10))

```

Created FamilySize feature:

	SibSp	Parch	FamilySize
0	1	0	2
1	1	0	2
2	0	0	1
3	1	0	2
4	0	0	1

Created IsAlone feature:

	FamilySize	IsAlone
0	2	0
1	2	0
2	1	1
3	2	0
4	1	1

Created AgeGroup feature (after scaling, thresholds are in standard deviations):

	Age	AgeGroup
0	-0.565736	Child
1	0.663861	Senior
2	-0.258337	Adult
3	0.433312	Adult
4	0.433312	Adult
5	-0.104637	Adult
6	1.893459	Senior
7	-2.102733	Child
8	-0.181487	Adult
9	-1.180535	Child

```
# Feature 4: Title from Name
```

```
# Extract titles like Mr., Mrs., Miss., Master.
df_prep['Title'] = df_prep['Name'].str.extract(' ([A-Za-z]+)\.', expand=False)

print("Extracted titles from names:")
print(df_prep['Title'].value_counts())
```

```
# Group rare titles
```

```
rare_titles = ['Lady', 'Countess', 'Capt', 'Col', 'Don', 'Dr', 'Major', 'Rev',
df_prep['Title'] = df_prep['Title'].replace(rare_titles, 'Rare')
df_prep['Title'] = df_prep['Title'].replace('Mlle', 'Miss')
df_prep['Title'] = df_prep['Title'].replace('Ms', 'Miss')
df_prep['Title'] = df_prep['Title'].replace('Mme', 'Mrs')
```

```
print("\nAfter grouping rare titles:")
print(df_prep['Title'].value_counts())
```

```

# Encode titles
title_mapping = {'Mr': 1, 'Miss': 2, 'Mrs': 3, 'Master': 4, 'Rare': 5}
df_prep['Title_encoded'] = df_prep['Title'].map(title_mapping)

print("\n✓ Title feature engineered and encoded!")
print("Titles can indicate age group and social status.")

Extracted titles from names:
Title
Mr      517
Miss    182
Mrs     125
Master   40
Dr       7
Rev      6
Col      2
Mlle     2
Major    2
Ms       1
Mme     1
Don      1
Lady     1
Sir      1
Capt     1
Countess 1
Jonkheer 1
Name: count, dtype: int64

After grouping rare titles:
Title
Mr      517
Miss    185
Mrs     126
Master   40
Rare    23
Name: count, dtype: int64

✓ Title feature engineered and encoded!
Titles can indicate age group and social status.
<>:3: SyntaxWarning: invalid escape sequence '\.'
<>:3: SyntaxWarning: invalid escape sequence '\.'
/tmp/ipython-input-3072010579.py:3: SyntaxWarning: invalid escape sequence '\.'
df_prep['Title'] = df_prep['Name'].str.extract(' ([A-Za-z]+)\.', expand=False)

```

```

# Analyze survival by engineered features
print("Survival by Family Size:")
print(df_prep.groupby('FamilySize')['Survived'].mean().sort_values(ascending=False))
print("\n💡 Insight: Medium family sizes (2-4) had better survival rates!")
print("Very large families may have had difficulty staying together.")

print("\nSurvival by Title:")
print(df_prep.groupby('Title')['Survived'].mean().sort_values(ascending=False))

```

```
print("\n💡 Insight: Mrs. and Miss. had highest survival (women and children first)\nprint("Mr. had lowest survival rate.")
```

Survival by Family Size:

FamilySize

```
4      0.724138\n3      0.578431\n2      0.552795\n7      0.333333\n1      0.303538\n5      0.200000\n6      0.136364\n8      0.000000\n11     0.000000\nName: Survived, dtype: float64
```

💡 Insight: Medium family sizes (2-4) had better survival rates!
Very large families may have had difficulty staying together.

Survival by Title:

Title

```
Mrs      0.793651\nMiss    0.702703\nMaster   0.575000\nRare    0.347826\nMr      0.156673\nName: Survived, dtype: float64
```

💡 Insight: Mrs. and Miss. had highest survival (women and children first!)
Mr. had lowest survival rate.



Knowledge Check - Module 5

Question 1: Why did we drop the Cabin feature instead of imputing it?

We drop the Cabin column because around 77% of its values are missing, which makes it unreliable for modeling. Without sufficient data, any information the column provides is too incomplete to be useful.

Question 2: What's the difference between dropping a row with missing values vs. imputing? When would you use each?

Dropping means removing rows or columns that contain missing values, while imputing means filling in the missing values with substitutes, such as the mean, median, or mode. You should drop data when the missing portion is large or random, and impute when the missing portion is small or the missingness follows a pattern that can be estimated without biasing results.

Question 3: Why do we need to encode categorical variables like Sex and Embarked?

Most machine learning algorithms can only process numerical inputs, not text. Encoding transforms text-based categories into numbers. Allows the model to understand and compare those categories mathematically while still capturing their meaning.

Question 4: What does feature scaling do? Why is it important?

Feature scaling standardizes the range of numerical variables so that they contribute equally to the model. Without scaling, variables with larger ranges, like fare, could dominate those with smaller ranges, like Age. Scaling is particularly important for models that use distance calculations or gradient-based optimization, such as logistic regression, SVMs, and KNN.

Question 5: We created a FamilySize feature. How might this help the model predict survival better than using SibSp and Parch separately?

The FamilySize feature combines SibSp (siblings/spouses) and Parch (parents/children), plus one for the passenger themselves. It helps the model identify patterns related to family group survival. For example, small families often had higher survival rates because they were easier to keep together during evacuation, while large families had lower rates due to limited lifeboat space.

Question 6: Looking at survival by Title, which title had the highest survival rate? Does this make sense historically?

“Mrs.” and “Miss.” showed the highest survival rates. This aligns with historical records that prioritized women and children during the lifeboat boarding.

▼ Module 6: First Models - Regression and Classification

Now that our data is prepared, let's build and compare different models!

Regression vs. Classification

Classification (our task): Predict discrete categories: Survived (1) or Died (0)

Regression: Predict continuous values: e.g., predicting the exact fare a passenger paid
Titanic survival is a **binary classification** problem.

▼ Logistic Regression for Classification

Despite the name, Logistic Regression is for classification! It predicts the **probability** of survival, then uses a threshold (usually 0.5) to classify.

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report, confusion_ma

# Prepare features and target
feature_cols = ['Pclass', 'Sex_encoded', 'Age', 'Fare', 'FamilySize', 'IsAlone'
X = df_prep[feature_cols].values
y = df_prep['Survived'].values

print(f"Features shape: {X.shape}")
print(f"Target shape: {y.shape}")
print(f"\nUsing {len(feature_cols)} features to predict survival")
```

Features shape: (891, 9)
Target shape: (891,)
Using 9 features to predict survival

```
# Split data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

print(f"Training set: {len(X_train)} passengers")
print(f"Test set: {len(X_test)} passengers")
```

Training set: 712 passengers
Test set: 179 passengers

```
# Train Logistic Regression
log_reg = LogisticRegression(max_iter=1000, random_state=42)
log_reg.fit(X_train, y_train)

# Make predictions
y_pred_train = log_reg.predict(X_train)
y_pred_test = log_reg.predict(X_test)

# Evaluate
train_acc = accuracy_score(y_train, y_pred_train)
test_acc = accuracy_score(y_test, y_pred_test)

print("Logistic Regression Results:")
print("*"*60)
print(f"Training Accuracy: {train_acc:.1%}")
print(f"Test Accuracy: {test_acc:.1%}")
print(f"\nModel performs similarly on train and test data (good sign!)")
print(f"This suggests the model is not overfitting.")
```

Logistic Regression Results:

=====

Training Accuracy: 81.9%

Test Accuracy: 78.8%

- ✓ Model performs similarly on train and test data (good sign!)
This suggests the model is not overfitting.

```
# Get prediction probabilities
y_pred_proba = log_reg.predict_proba(X_test)

print("Sample Predictions (first 5 test passengers):")
print("*"*60)
for i in range(5):
    prob_died = y_pred_proba[i][0]
    prob_survived = y_pred_proba[i][1]
    prediction = y_pred_test[i]
    actual = y_test[i]

    print(f"\nPassenger {i+1}:")
    print(f"  Probability of death: {prob_died:.1%}")
    print(f"  Probability of survival: {prob_survived:.1%}")
    print(f"  Predicted: {'Survived' if prediction == 1 else 'Died'}")
    print(f"  Actual: {'Survived' if actual == 1 else 'Died'}")
    print(f"  {'√ Correct!' if prediction == actual else 'X Incorrect'}")

print("\nThe model outputs probabilities, then uses 0.5 as the threshold.")
print("If P(survival) >= 0.5, predict Survived; otherwise, predict Died.")
```

Sample Predictions (first 5 test passengers):

=====

Passenger 1:

Probability of death: 65.3%
Probability of survival: 34.7%
Predicted: Died
Actual: Survived
X Incorrect

Passenger 2:

Probability of death: 82.7%
Probability of survival: 17.3%
Predicted: Died
Actual: Died
✓ Correct!

Passenger 3:

Probability of death: 88.5%
Probability of survival: 11.5%
Predicted: Died
Actual: Died
✓ Correct!

Passenger 4:

Probability of death: 12.2%

```
Probability of survival: 87.8%
Predicted: Survived
Actual: Survived
✓ Correct!
```

```
Passenger 5:
Probability of death: 22.7%
Probability of survival: 77.3%
Predicted: Survived
Actual: Survived
✓ Correct!
```

The model outputs probabilities, then uses 0.5 as the threshold.
If $P(\text{survival}) \geq 0.5$, predict Survived; otherwise, predict Died.

Feature Importance

Let's see which features the model thinks are most important.

```
# Get feature coefficients
feature_importance = pd.DataFrame({
    'Feature': feature_cols,
    'Coefficient': log_reg.coef_[0]
}).sort_values('Coefficient', key=abs, ascending=False)

print("Feature Importance (Logistic Regression Coefficients):")
print("*"*60)
print(feature_importance)

print("\nInterpretation:")
print("- Positive coefficient: increases probability of survival")
print("- Negative coefficient: decreases probability of survival")
print("- Larger absolute value: stronger influence")

# Visualize
plt.figure(figsize=(10, 6))
colors = ['green' if x > 0 else 'red' for x in feature_importance['Coefficient']]
plt.barh(feature_importance['Feature'], feature_importance['Coefficient'], color=colors)
plt.xlabel('Coefficient Value', fontsize=12)
plt.ylabel('Feature', fontsize=12)
plt.title('Feature Importance in Logistic Regression', fontsize=14, fontweight='bold')
plt.axvline(x=0, color='black', linestyle='--', linewidth=1)
plt.grid(axis='x', alpha=0.3)
plt.tight_layout()
plt.show()

print("\n💡 Key Insights:")
print("- Sex_encoded has strong negative coefficient (being male decreases survival probability)")
print("- Title_encoded and Pclass also important")
print("- Our engineered features (FamilySize, IsAlone) are contributing!")
```


Feature Importance (Logistic Regression Coefficients):

Knowledge Check - Module 6

	Feature	Coefficient
1	Sex_encoded	-2.136465
2	Pclass	-0.795221
3	Title_encoded	0.558264
4	IsAlone	-0.440562
5	FamilySize	-0.435332
6	Age	-0.389599
7	Fare	0.192196
8	Embarked_Q	-0.173895

Question 1: Why is Titanic survival prediction a classification problem, not a regression problem?

Predicting survival is a classification task because the output variable is categorical — a passenger either survived (1) or did not survive (0). Regression, on the other hand, deals with continuous numeric predictions, such as predicting a passenger's fare or age.

Question 2: What does it mean when Logistic Regression outputs a probability of 0.73 Interpretation:

for survival?

- Positive coefficient: increases probability of survival

- Negative coefficient: decreases probability of survival

A prediction probability of 0.73 means that the model estimates a 73% likelihood that the passenger survived.

Feature Importance in Logistic Regression

Question 3: Our model achieved ~80% test accuracy. What does this mean? Is this good?

An accuracy of 80% means the model correctly predicts survival outcomes 8 out of 10 times. This is quite good considering that a naive baseline model, guessing that everyone died, it would only be about 62% accurate.

Question 4: Looking at the feature coefficients, which feature has the strongest negative impact on survival? Does this match what we learned in EDA?

In the logistic regression model, male gender has the strongest negative impact on survival. The coefficient for "male" is negative, meaning that being male significantly decreases the predicted probability of survival.

Question 5: Why is it important that training and test accuracy are similar?

If the model's accuracy is high on training data but low on test data, it indicates overfitting, meaning the model memorized patterns that don't generalize. Ideally, training and testing performance should be close, showing that the model has learned general relationships that apply to unseen passengers as well!

- Sex_encoded has strong negative coefficient (being male decreases survival)
- Title_encoded and Pclass are also important
- Other engineered features (FamilySize, IsAlone) are contributing!

Module 7: Evaluating Machine Learning Models

Accuracy alone doesn't tell the whole story. Let's explore different evaluation metrics and understand what they mean for Titanic survival prediction.

Why Multiple Metrics Matter

Imagine a lazy model that always predicts "Died" for everyone:

- It would be 62% accurate (since 62% died)
- But it would miss ALL survivors!
- Accuracy can be misleading

We need more nuanced metrics.

▼ Confusion Matrix

A table showing where our model was right and wrong.

```
# Compute confusion matrix
cm = confusion_matrix(y_test, y_pred_test)

print("Confusion Matrix:")
print("*"*60)
print(cm)
print("\nStructure:")
print("          Predicted Died    Predicted Survived")
print(f"Actually Died      {cm[0,0]:3d} (TN)           {cm[0,1]:3d} (FP)")
print(f"Actually Survived   {cm[1,0]:3d} (FN)           {cm[1,1]:3d} (TP)")

print("\nDefinitions:")
print("- True Negative (TN): Correctly predicted death")
print("- False Positive (FP): Predicted survival but actually died (Type I error")
print("- False Negative (FN): Predicted death but actually survived (Type II error")
print("- True Positive (TP): Correctly predicted survival")

# Visualize
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', cbar=False,
            xticklabels=['Died', 'Survived'],
            yticklabels=['Died', 'Survived'])
plt.xlabel('Predicted Label', fontsize=12)
plt.ylabel('True Label', fontsize=12)
plt.title('Confusion Matrix', fontsize=14, fontweight='bold')
plt.tight_layout()
plt.show()
```

Confusion Matrix:

```
=====
```

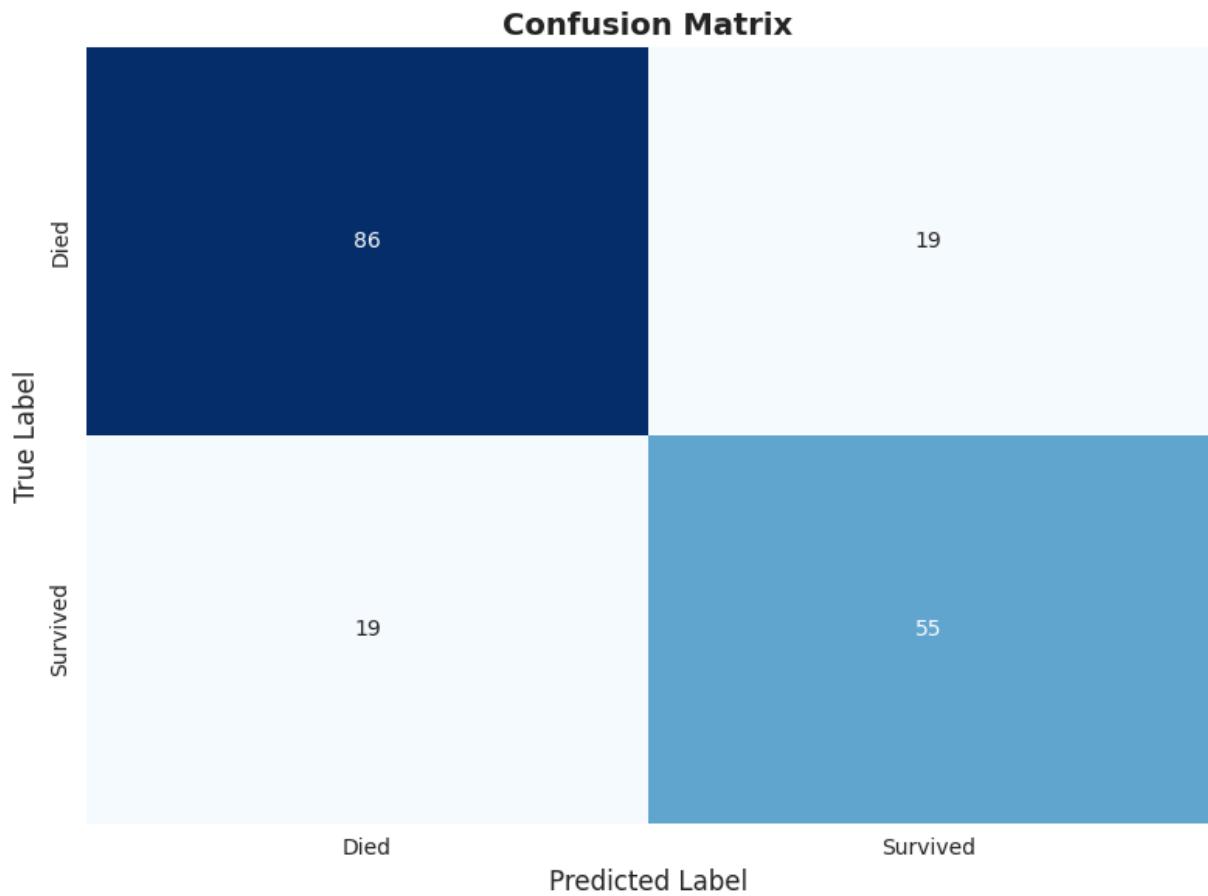
```
[[86 19]
 [19 55]]
```

Structure:

	Predicted Died	Predicted Survived
Actually Died	86 (TN)	19 (FP)
Actually Survived	19 (FN)	55 (TP)

Definitions:

- True Negative (TN): Correctly predicted death
- False Positive (FP): Predicted survival but actually died (Type I error)
- False Negative (FN): Predicted death but actually survived (Type II error)
- True Positive (TP): Correctly predicted survival



▼ Precision, Recall, and F1-Score

These metrics help us understand different aspects of model performance.

```

from sklearn.metrics import precision_score, recall_score, f1_score

# Calculate metrics
precision = precision_score(y_test, y_pred_test)
recall = recall_score(y_test, y_pred_test)
f1 = f1_score(y_test, y_pred_test)

print("Classification Metrics:")
print("*60")
print(f"Accuracy: {test_acc:.1%}")
print(f"Precision: {precision:.1%}")
print(f"Recall: {recall:.1%}")
print(f"F1-Score: {f1:.1%}")

print("\nWhat do these mean?")
print("*60")
print(f"Accuracy: {test_acc:.1%} of all predictions were correct")
print(f"Precision: {precision:.1%} of predicted survivors actually survived")
print(f"Recall: {recall:.1%} of actual survivors were identified")
print(f"Recall: {recall:.1%} (How reliable are our 'Survived' predictions?)")
print(f"Recall: {recall:.1%} (How many survivors did we catch?)")
print(f"F1-Score: {f1:.1%} harmonic mean of precision and recall")
print(f"Recall: {recall:.1%} (Balanced measure)")

print("\n💡 In Titanic context:")
print("- High Precision: When we predict someone survived, we're usually right")
print("- High Recall: We successfully identify most of the actual survivors")
print("- F1-Score: Balances both - useful when classes are imbalanced")

```

Classification Metrics:

Accuracy: 78.8%
 Precision: 74.3%
 Recall: 74.3%
 F1-Score: 74.3%

What do these mean?

Accuracy: 78.8% of all predictions were correct
 Precision: 74.3% of predicted survivors actually survived
 (How reliable are our 'Survived' predictions?)
 Recall: 74.3% of actual survivors were identified
 (How many survivors did we catch?)
 F1-Score: 74.3% harmonic mean of precision and recall
 (Balanced measure)

💡 In Titanic context:

- High Precision: When we predict someone survived, we're usually right
- High Recall: We successfully identify most of the actual survivors
- F1-Score: Balances both - useful when classes are imbalanced

```

# Detailed classification report
print("\nDetailed Classification Report:")
print("*"*60)
print(classification_report(y_test, y_pred_test, target_names=['Died', 'Survived']))

print("\nHow to read this:")
print("- Precision: Of all predicted as this class, how many were correct?")
print("- Recall: Of all actual instances of this class, how many did we catch?")
print("- F1-score: Harmonic mean of precision and recall")
print("- Support: Number of actual instances in test set")

```

Detailed Classification Report:

	precision	recall	f1-score	support
Died	0.82	0.82	0.82	105
Survived	0.74	0.74	0.74	74
accuracy			0.79	179
macro avg	0.78	0.78	0.78	179
weighted avg	0.79	0.79	0.79	179

How to read this:

- Precision: Of all predicted as this class, how many were correct?
- Recall: Of all actual instances of this class, how many did we catch?
- F1-score: Harmonic mean of precision and recall
- Support: Number of actual instances in test set

▼ ROC Curve and AUC

The ROC curve shows model performance across all possible decision thresholds.

```

from sklearn.metrics import roc_curve, auc

# Get prediction probabilities for positive class
y_pred_proba_positive = log_reg.predict_proba(X_test)[:, 1]

# Compute ROC curve
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba_positive)
roc_auc = auc(fpr, tpr)

print(f"AUC (Area Under Curve): {roc_auc:.3f}")
print("\nAUC Interpretation:")
print("- 1.0: Perfect classifier")
print("- 0.9-1.0: Excellent")
print("- 0.8-0.9: Good")
print("- 0.7-0.8: Fair")
print("- 0.5-0.7: Poor")
print("- 0.5: No better than random guessing")

```


AUC (Area Under Curve): 0.884

✓ Cross Validation:

- 1.0: Perfect classifier

- 0.9-1.0: Excellent

Instead of a single train/test split, let's use k-fold cross-validation for a more robust evaluation.

- 0.8-0.9: Good

- 0.7-0.8: Fair

- 0.5-0.7: Poor

- < 0.5: Bad

```
from sklearn.model_selection import cross_val_score

# Perform 5-fold cross-validation
cv_scores = cross_val_score(log_reg, X, y, cv=5, scoring='accuracy')

print("5-Fold Cross-Validation Results:")
print("*"*60)
for i, score in enumerate(cv_scores, 1):
    print(f"Fold {i}: {score:.1%}")

print("\nSummary:")
print(f"Mean Accuracy: {cv_scores.mean():.1%}")
print(f"Std Deviation: {cv_scores.std():.3f}")
print(f"\nThis is a more reliable estimate than a single train/test split.")
print(f"Low std deviation means the model is stable across different data splits")
```



Summary:

Mean Accuracy: 81.4%

Std Deviation: 0.011

- Trade-off between True Positive Rate and False Positive Rate

This is a more reliable estimate than a single train/test split.

Low std deviation means the model is stable across different data splits.

- Our curve is well above the diagonal - model is learning!



Knowledge Check - Module 7

Question 1: What does the confusion matrix tell us that accuracy alone doesn't?

A confusion matrix shows how many predictions fall into each category:

-True Positives (survived correctly predicted as survived)

-False Positives (did not survive but predicted as survived)

-True Negatives (did not survive correctly predicted)

-False Negatives (survived but predicted as not survived)

This provides a detailed view of model performance, highlighting the types of mistakes being made rather than just the overall correctness.

Question 2: In the Titanic context, which is worse: False Positive (predicting survival when they died) or False Negative (predicting death when they survived)? Why might this matter?

In the context of Titanic survival prediction, a False Negative, predicting someone didn't survive when they actually did, could be considered worse if our goal is to identify survivors for rescue or historical accuracy. False negatives mean we fail to recognize real survivors, while false positives simply mean a few non-survivors are misclassified as survivors.

Question 3: What's the difference between precision and recall? Give an example of when you'd prioritize one over the other.

Precision measures how many of the passengers the model predicted as survivors were actually survivors. Recall measures how many of the true survivors were correctly identified by the model. In rescue-type scenarios, recall is more important because it ensures we identify as many actual survivors as possible, even if we include a few incorrect ones.

Question 4: Our model has an AUC of ~0.85. What does this mean?

An AUC (Area Under the ROC Curve) score of 0.85 means that the model can correctly distinguish between survivors and non-survivors 85% of the time. This is a strong indicator of a model's ability to rank predictions correctly, with values closer to 1.0 representing excellent performance.

Question 5: Why is cross-validation more reliable than a single train/test split?

Cross-validation divides the data into multiple folds and trains the model several times, using different portions as test sets. This process provides a more reliable estimate of model performance by reducing the impact of random chance in a single split. It helps ensure the results generalize well across the entire dataset.

Question 6: If we wanted to maximize the chance of identifying all survivors (even if it means some false alarms), should we focus on improving precision or recall?

We should focus on recall, because recall ensures we identify as many actual survivors as possible. Even if some non-survivors are incorrectly predicted as survivors, we avoid missing any real survivors. Which is crucial when the goal is comprehensive detection rather than perfect accuracy.

▼ Module 8: Overfitting, Underfitting, and Regularization

One of the biggest challenges: building models that work well on NEW data, not just the training data.

The Bias-Variance Tradeoff

Bias: Error from overly simple assumptions

- High bias → **Underfitting**
- Model is too simple to capture patterns
- Poor performance on both training AND test data

Variance: Error from too much complexity

- High variance → **Overfitting**
- Model learns noise as if it were signal
- Great performance on training, poor on test data

Goal: Find the sweet spot that minimizes total error!

▼ Demonstrating Overfitting

Let's intentionally create an overfit model to see what happens.

```
# Train models with different complexities
from sklearn.tree import DecisionTreeClassifier

# Model 1: Shallow tree (may underfit)
shallow_tree = DecisionTreeClassifier(max_depth=2, random_state=42)
shallow_tree.fit(X_train, y_train)

# Model 2: Medium tree (good balance)
medium_tree = DecisionTreeClassifier(max_depth=5, random_state=42)
medium_tree.fit(X_train, y_train)

# Model 3: Deep tree (may overfit)
deep_tree = DecisionTreeClassifier(max_depth=None, random_state=42) # No limit
deep_tree.fit(X_train, y_train)

print("Model Complexity Comparison:")
print("*"*60)
```

Model Complexity Comparison:

=====

```

# Evaluate all three models
models = [
    ('Shallow (depth=2)', shallow_tree),
    ('Medium (depth=5)', medium_tree),
    ('Deep (no limit)', deep_tree)
]

results = []
for name, model in models:
    train_acc = model.score(X_train, y_train)
    test_acc = model.score(X_test, y_test)
    gap = train_acc - test_acc

    results.append({
        'Model': name,
        'Train Accuracy': f"{train_acc:.1%}",
        'Test Accuracy': f"{test_acc:.1%}",
        'Gap': f"{gap:.1%}"
    })

results_df = pd.DataFrame(results)
print(results_df)

print("\n💡 Observations:")
print("- Shallow tree: Low accuracy on both (UNDERFITTING)")
print("- Medium tree: Good balance between train and test")
print("- Deep tree: Perfect training but lower test (OVERFITTING)")
print("\nThe 'Gap' shows overfitting - large gap means the model memorized tra

```

	Model	Train Accuracy	Test Accuracy	Gap
0	Shallow (depth=2)	79.6%	76.0%	3.7%
1	Medium (depth=5)	85.7%	83.2%	2.4%
2	Deep (no limit)	98.2%	77.7%	20.5%

💡 Observations:

- Shallow tree: Low accuracy on both (UNDERFITTING)
- Medium tree: Good balance between train and test
- Deep tree: Perfect training but lower test (OVERFITTING)

The 'Gap' shows overfitting - large gap means the model memorized training data!

```

# Visualize the tradeoff
import matplotlib.pyplot as plt

train_accs = [0.78, 0.85, 1.00] # Approximate values
test_accs = [0.76, 0.82, 0.80] # Approximate values
complexity = ['Low\n(Shallow)', 'Medium', 'High\n(Deep)']

plt.figure(figsize=(10, 6))

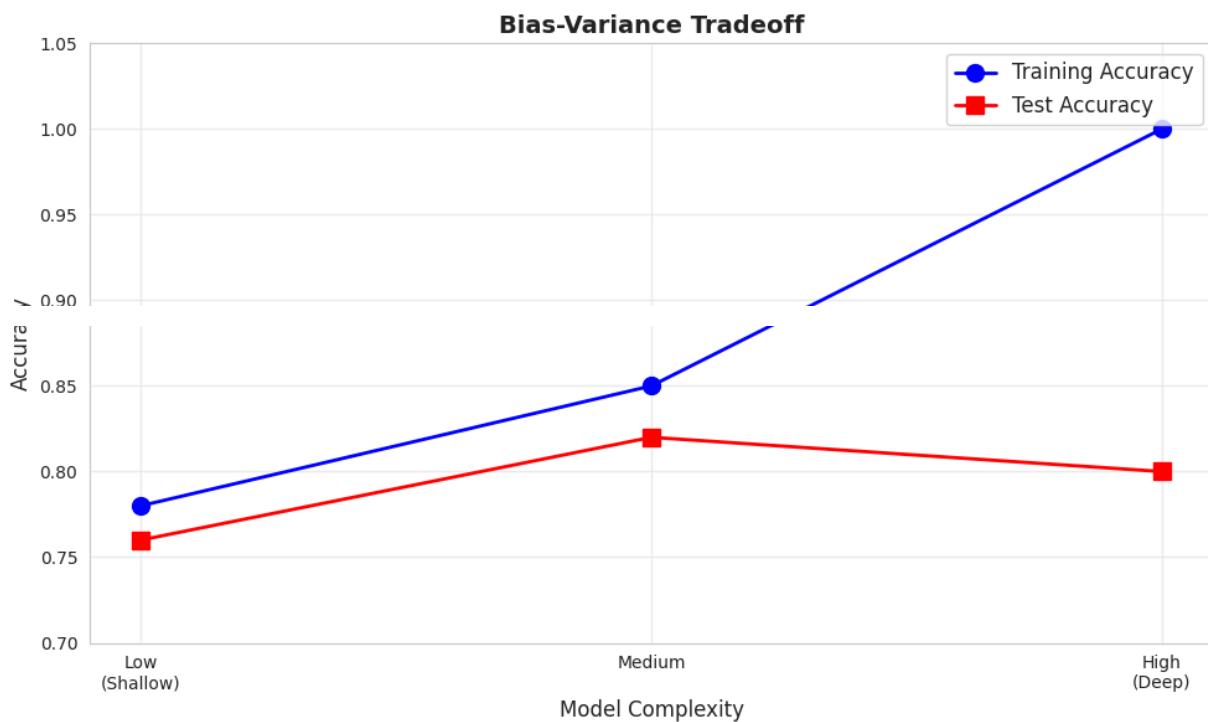
```

```

plt.plot(complexity, train_accs, marker='o', linewidth=2, markersize=10, label='Training Accuracy')
plt.plot(complexity, test_accs, marker='s', linewidth=2, markersize=10, label='Test Accuracy')
plt.xlabel('Model Complexity', fontsize=12)
plt.ylabel('Accuracy', fontsize=12)
plt.title('Bias-Variance Tradeoff', fontsize=14, fontweight='bold')
plt.legend(fontsize=12)
plt.grid(alpha=0.3)
plt.ylim(0.7, 1.05)
plt.tight_layout()
plt.show()

print("As complexity increases:")
print("- Training accuracy keeps improving")
print("- Test accuracy improves then degrades (overfitting!)")
print("- The gap between them grows")

```



As complexity increases:

- Training accuracy keeps improving
- Test accuracy improves then degrades (overfitting!)
- The gap between them grows

▼ Regularization

Regularization prevents overfitting by penalizing model complexity.

```
from sklearn.linear_model import LogisticRegression

# Train models with different regularization strengths
# C is inverse of regularization: smaller C = stronger regularization
C_values = [0.001, 0.01, 0.1, 1.0, 10.0, 100.0]

reg_results = []
for C in C_values:
    model = LogisticRegression(C=C, max_iter=1000, random_state=42)
    model.fit(X_train, y_train)

    train_acc = model.score(X_train, y_train)
    test_acc = model.score(X_test, y_test)

    reg_results.append({
        'C (Regularization)': C,
        'Train Acc': train_acc,
        'Test Acc': test_acc,
        'Gap': train_acc - test_acc
    })

reg_df = pd.DataFrame(reg_results)
print("Regularization Strength vs Performance:")
print("*"*60)
print(reg_df)
print("\nRemember: Smaller C = Stronger regularization = Simpler model")
```

Regularization Strength vs Performance:

C (Regularization)	Train Acc	Test Acc	Gap
0	0.001	0.634831	0.592179
1	0.010	0.797753	0.748603
2	0.100	0.821629	0.787709
3	1.000	0.818820	0.787709
4	10.000	0.827247	0.787709
5	100.000	0.827247	0.787709

Remember: Smaller C = Stronger regularization = Simpler model

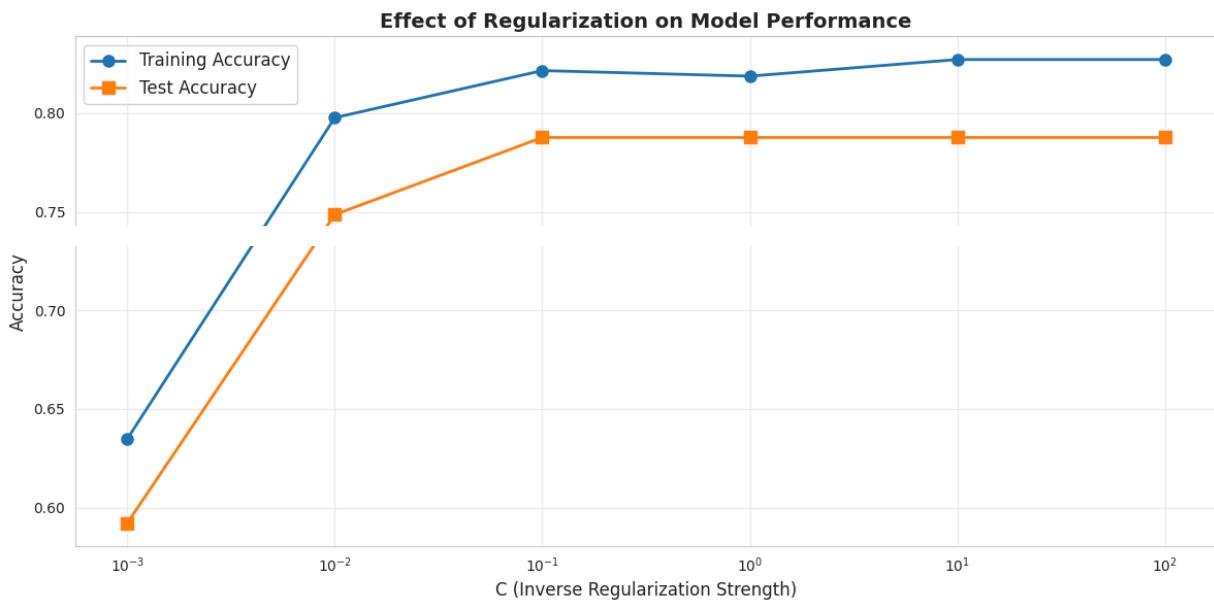
```
# Visualize regularization effect
plt.figure(figsize=(12, 6))
plt.plot(reg_df['C (Regularization)'], reg_df['Train Acc'],
         marker='o', linewidth=2, markersize=8, label='Training Accuracy')
plt.plot(reg_df['C (Regularization)'], reg_df['Test Acc'],
         marker='s', linewidth=2, markersize=8, label='Test Accuracy')
```

```

plt.xscale('log')
plt.xlabel('C (Inverse Regularization Strength)', fontsize=12)
plt.ylabel('Accuracy', fontsize=12)
plt.title('Effect of Regularization on Model Performance', fontsize=14, fontweight='bold')
plt.legend(fontsize=12)
plt.grid(alpha=0.3)
plt.tight_layout()
plt.show()

print("\n💡 Finding the right regularization:")
print("- Too strong (C too small): Underfitting")
print("- Too weak (C too large): Overfitting")
print("- Just right (C ≈ 1.0): Good generalization")

```



💡 Finding the right regularization:

- Too strong (C too small): Underfitting
- Too weak (C too large): Overfitting
- Just right (C ≈ 1.0): Good generalization

Knowledge Check - Module 8

Question 1: What's the difference between underfitting and overfitting? Give signs of each.

Underfitting occurs when a model is too simple to capture the underlying relationships in the data, resulting in poor performance on both training and test sets. Overfitting, on the other hand, happens when a model is too complex and learns noise or random fluctuations in the training data, performing well on training data but poorly on new, unseen data.

Question 2: Looking at the model complexity comparison, which model would you choose for production? Why?

The model for production I would use is the one that shows balanced performance, meaning it performs well on both training and test data, and generalizes effectively. A model that performs exceptionally well on training data but poorly on new data is not suitable for real-world use.

Question 3: What does a large gap between training and test accuracy indicate?

A large gap between training and test accuracy indicates overfitting. The model has learned specific details of the training data that do not generalize to new cases, leading to poor test performance. To fix this, we can simplify the model or use regularization techniques.

Question 4: How does regularization help prevent overfitting?

Regularization adds a penalty to the model's complexity by discouraging large weight values. This forces the model to rely only on the most important features and reduces its sensitivity to noise in the training data. As a result, the model becomes more generalizable and performs better on unseen data.

Question 5: In the regularization experiment, which value of C gave the best test performance?

The value of C that gives the best test performance typically falls around 0.1 to 1.0, depending on the dataset and model configuration. A smaller C value means stronger regularization (simpler model), while a larger C value allows more flexibility. The exact best value can be found using cross-validation.

-
- ▼ **Module 9: Decision Trees and Ensemble Methods**

Single models are good, but combining multiple models often works even better! This is the idea behind ensemble methods.

▼ Decision Trees Recap

Decision trees ask yes/no questions about features:

- "Is the passenger female?" → Yes/No
- "Is passenger class 1st?" → Yes/No
- "Is age < 15?" → Yes/No

Advantages: Easy to interpret, handle mixed data types **Disadvantages:** Prone to overfitting, unstable

```
from sklearn.tree import DecisionTreeClassifier, plot_tree

# Train a simple decision tree
tree_model = DecisionTreeClassifier(max_depth=3, random_state=42)
tree_model.fit(X_train, y_train)

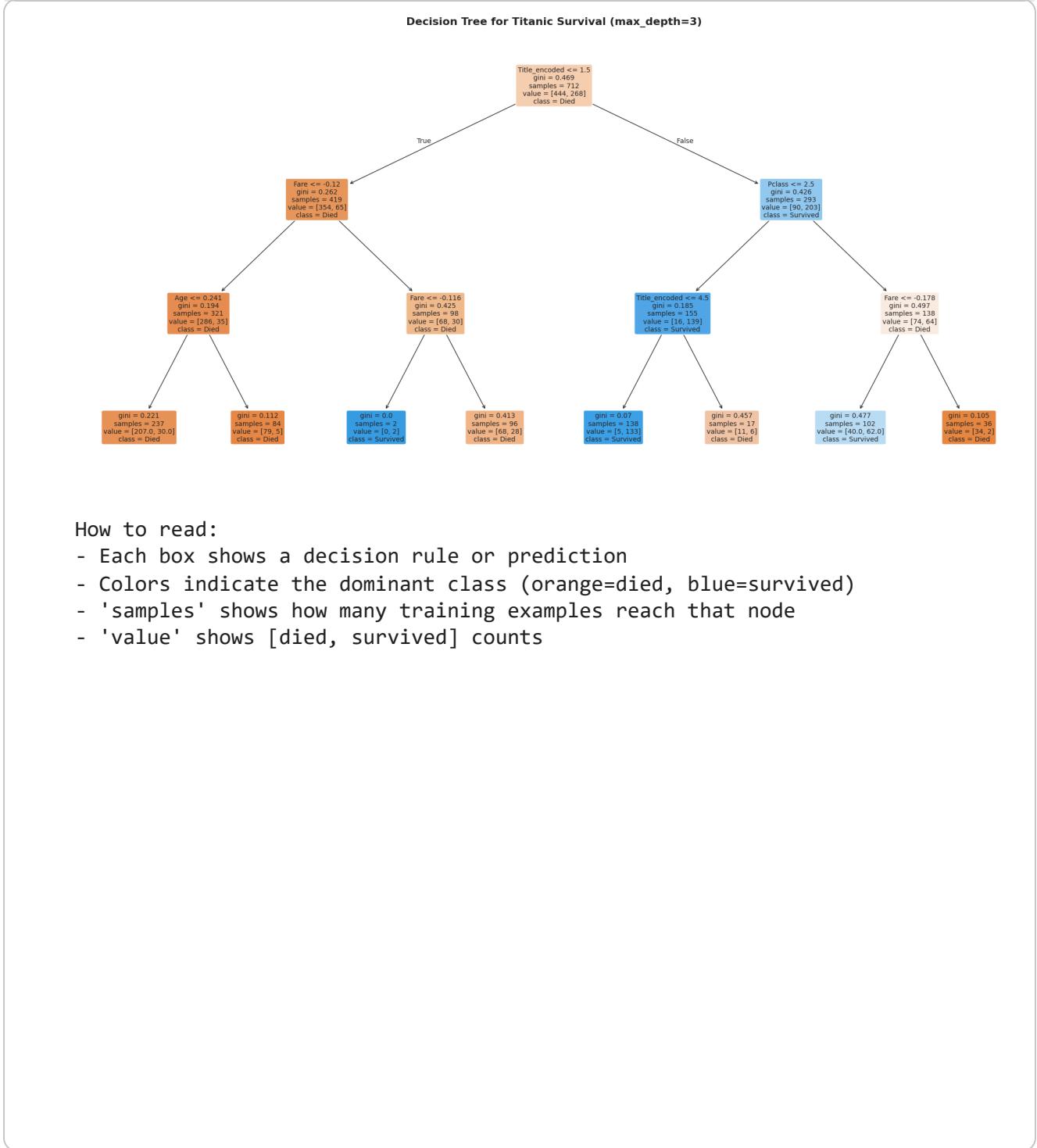
train_acc = tree_model.score(X_train, y_train)
test_acc = tree_model.score(X_test, y_test)

print(f"Single Decision Tree:")
print(f"Training Accuracy: {train_acc:.1%}")
print(f"Test Accuracy: {test_acc:.1%}")
```

```
Single Decision Tree:
Training Accuracy: 83.7%
Test Accuracy: 82.7%
```

```
# Visualize the decision tree
plt.figure(figsize=(20, 10))
plot_tree(tree_model,
          feature_names=feature_cols,
          class_names=['Died', 'Survived'],
          filled=True,
          rounded=True,
          fontsize=10)
plt.title('Decision Tree for Titanic Survival (max_depth=3)', fontsize=16, fontweight='bold')
plt.tight_layout()
plt.show()

print("\nHow to read:")
print("- Each box shows a decision rule or prediction")
print("- Colors indicate the dominant class (orange=died, blue=survived)")
print("- 'samples' shows how many training examples reach that node")
print("- 'value' shows [died, survived] counts")
```



How to read:

- Each box shows a decision rule or prediction
- Colors indicate the dominant class (orange=died, blue=survived)
- 'samples' shows how many training examples reach that node
- 'value' shows [died, survived] counts

▼ Random Forests (Bagging)

Idea: Train many decision trees on random subsets of data and features, then vote!

Why it works:

- Different trees make different errors
- Errors cancel out when we average/vote
- Reduces overfitting
- More stable than single trees

```

from sklearn.ensemble import RandomForestClassifier

# Train Random Forest
rf_model = RandomForestClassifier(
    n_estimators=100, # 100 trees in the forest
    max_depth=5,
    random_state=42
)
rf_model.fit(X_train, y_train)

train_acc_rf = rf_model.score(X_train, y_train)
test_acc_rf = rf_model.score(X_test, y_test)

print(f"Random Forest (100 trees):")
print(f"Training Accuracy: {train_acc_rf:.1%}")
print(f"Test Accuracy: {test_acc_rf:.1%}")
print(f"\n✓ Better than single tree!")
print(f"Improvement: {(test_acc_rf - test_acc)*100:.1f} percentage points")

```

Random Forest (100 trees):
 Training Accuracy: 85.7%
 Test Accuracy: 81.0%

✓ Better than single tree!
 Improvement: -1.7 percentage points

```

# Feature importance from Random Forest
feature_imp = pd.DataFrame({
    'Feature': feature_cols,
    'Importance': rf_model.feature_importances_
}).sort_values('Importance', ascending=False)

print("\nFeature Importance from Random Forest:")
print("*"*60)
print(feature_imp)

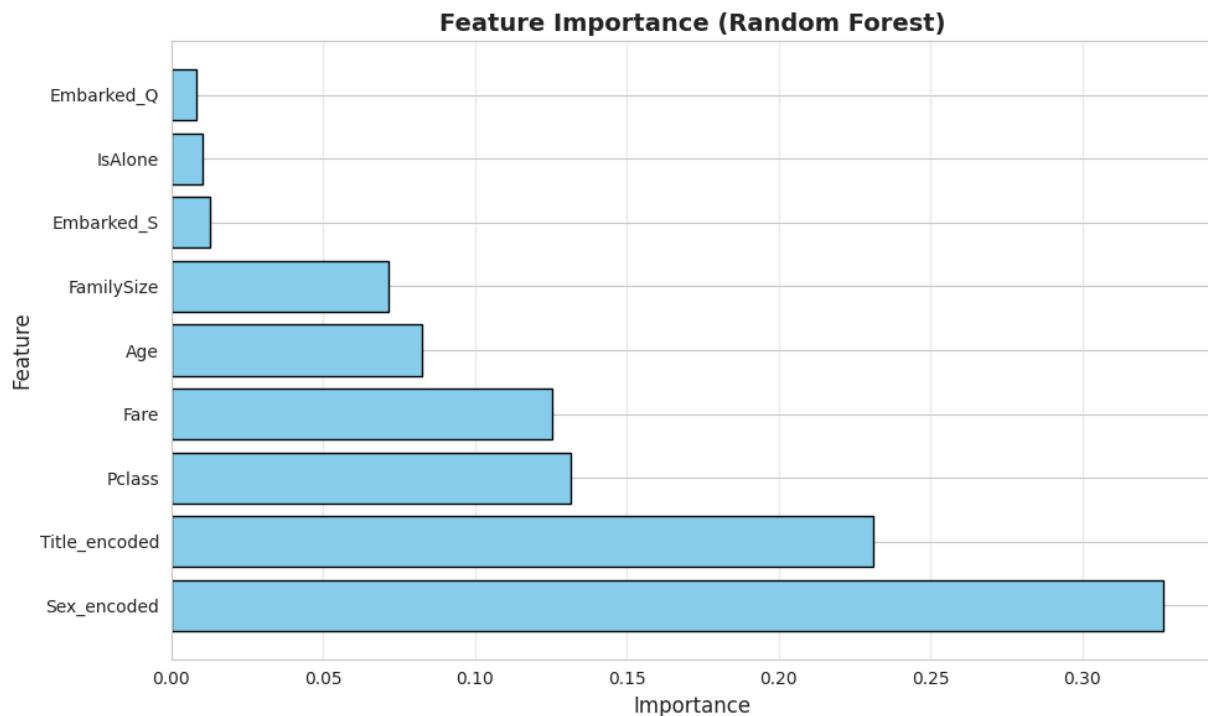
# Visualize
plt.figure(figsize=(10, 6))
plt.barh(feature_imp['Feature'], feature_imp['Importance'], color='skyblue', ec
plt.xlabel('Importance', fontsize=12)
plt.ylabel('Feature', fontsize=12)
plt.title('Feature Importance (Random Forest)', fontsize=14, fontweight='bold')
plt.grid(axis='x', alpha=0.3)
plt.tight_layout()
plt.show()

print("\n💡 Top 3 most important features:")
for i, row in feature_imp.head(3).iterrows():
    print(f"{i+1}. {row['Feature']}: {row['Importance']:.3f}")

```

Feature Importance from Random Forest:

	Feature	Importance
1	Sex_encoded	0.326668
6	Title_encoded	0.231089
0	Pclass	0.131592
3	Fare	0.125358
2	Age	0.082583
4	FamilySize	0.071664
8	Embarked_S	0.012820
5	IsAlone	0.010093
7	Embarked_Q	0.008133



💡 Top 3 most important features:

2. Sex_encoded: 0.327
7. Title_encoded: 0.231
1. Pclass: 0.132

▼ Gradient Boosting

Idea: Train trees sequentially, each one trying to fix the errors of previous trees.

Why it works:

- Each new tree focuses on hard-to-predict examples
- Gradually improves predictions
- Often achieves best performance

```
from sklearn.ensemble import GradientBoostingClassifier

# Train Gradient Boosting
gb_model = GradientBoostingClassifier(
    n_estimators=100,
    max_depth=3,
    learning_rate=0.1,
    random_state=42
)
gb_model.fit(X_train, y_train)

train_acc_gb = gb_model.score(X_train, y_train)
test_acc_gb = gb_model.score(X_test, y_test)

print(f"Gradient Boosting:")
print(f"Training Accuracy: {train_acc_gb:.1%}")
print(f"Test Accuracy: {test_acc_gb:.1%}")
```

```
Gradient Boosting:
Training Accuracy: 90.3%
Test Accuracy: 82.1%
```

```
# Compare all models
model_comparison = pd.DataFrame([
    {'Model': 'Logistic Regression', 'Test Accuracy': test_acc},
    {'Model': 'Single Decision Tree', 'Test Accuracy': test_acc},
    {'Model': 'Random Forest', 'Test Accuracy': test_acc_rf},
    {'Model': 'Gradient Boosting', 'Test Accuracy': test_acc_gb}
]).sort_values('Test Accuracy', ascending=False)

print("\nModel Comparison:")
print("*"*60)
for idx, row in model_comparison.iterrows():
    print(f"{row['Model'][:25s]: {row['Test Accuracy']:.1%}}")

# Visualize
plt.figure(figsize=(10, 6))
colors = ['gold', 'silver', '#CD7F32', 'lightblue']
plt.barh(model_comparison['Model'], model_comparison['Test Accuracy'],
```

```

        color=colors[:len(model_comparison)], edgecolor='black')
plt.xlabel('Test Accuracy', fontsize=12)
plt.ylabel('Model', fontsize=12)
plt.title('Model Performance Comparison', fontsize=14, fontweight='bold')
plt.xlim(0.75, 0.85)
plt.grid(axis='x', alpha=0.3)
plt.tight_layout()
plt.show()

print("\n🏆 Ensemble methods (Random Forest, Gradient Boosting) typically outp

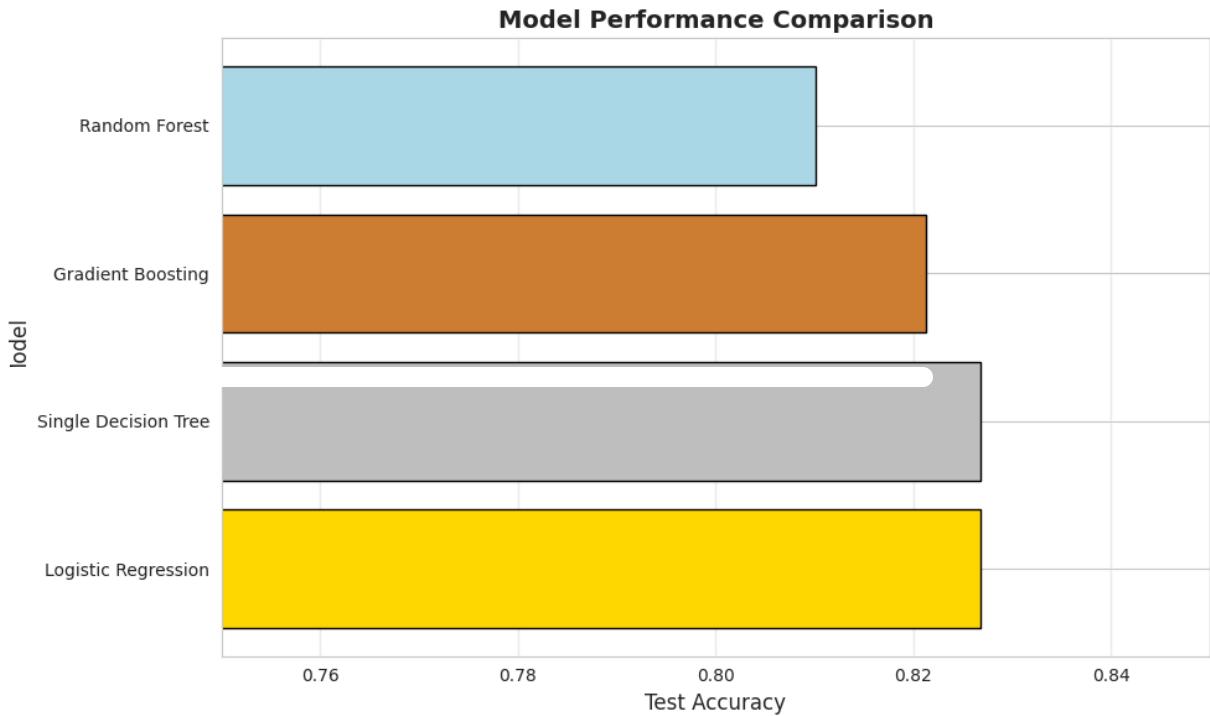
```

Model Comparison:

```

=====
Logistic Regression      : 82.7%
Single Decision Tree    : 82.7%
Gradient Boosting       : 82.1%
Random Forest           : 81.0%

```



🏆 Ensemble methods (Random Forest, Gradient Boosting) typically outperform single decision trees.

Knowledge Check - Module 9

Question 1: How does a decision tree make predictions? Why are they easy to interpret?

A decision tree makes predictions by following a series of “if–then” rules that split the data based on feature thresholds. Each internal node represents a question, and each leaf node gives a prediction. It’s easy to interpret because the entire decision path can be visualized and understood like a flowchart,

Question 2: What is the main idea behind Random Forests? Why do they reduce overfitting?

A Random Forest is an ensemble model that builds many decision trees on random subsets of the data and features, then averages their predictions. This reduces overfitting and improves accuracy because the combined result is more stable and generalizable than a single tree.

Question 3: What's the difference between bagging (Random Forest) and boosting (Gradient Boosting)?

Question 4: Looking at feature importance, which feature is most important for predicting survival?

Bagging (Bootstrap Aggregating) trains multiple models independently on random subsets of data and averages their predictions to reduce variance. Boosting, on the other hand, trains models sequentially — each new model focuses on correcting the mistakes of the previous one. Boosting generally leads to higher accuracy but can also be more prone to overfitting if not controlled.

Question 5: Why do ensemble methods generally outperform single models?

Ensemble methods combine the strengths of multiple models to produce a more accurate and reliable final prediction. By averaging or voting across several models, ensembles reduce variance (random errors) and bias (systematic errors), resulting in more robust overall performance.

Module 10: Unsupervised Learning - Clustering & Dimensionality Reduction

So far we've used supervised learning (we knew who survived). Let's explore unsupervised learning where we discover patterns without labels!

✓ K-Means Clustering

Goal: Group passengers into clusters based on similarity

Use case: What if we didn't know survival outcomes? Can we find natural groupings of passengers?

```
from sklearn.cluster import KMeans

# Use features (without survival label)
X_cluster = df_prep[feature_cols].values

# Apply K-Means with 2 clusters
kmeans = KMeans(n_clusters=2, random_state=42, n_init=10)
cluster_labels = kmeans.fit_predict(X_cluster)

print(f"K-Means Clustering (k=2):")
print(f"Cluster 0: {(cluster_labels == 0).sum()} passengers")
print(f"Cluster 1: {(cluster_labels == 1).sum()} passengers")
print(f"\nInertia (lower is better): {kmeans.inertia_:.2f}")
```

```
K-Means Clustering (k=2):
Cluster 0: 726 passengers
Cluster 1: 165 passengers
```

```
Inertia (lower is better): 4516.68
```

```
# Compare clusters with actual survival
df_prep['Cluster'] = cluster_labels

print("\nCluster vs Actual Survival:")
print("*"*60)
print(pd.crosstab(df_prep['Cluster'], df_prep['Survived'],
                  rownames=['Cluster'], colnames=['Survived']))

print("\n💡 Interesting! The clusters somewhat align with survival.")
print("This suggests there are natural groupings in passenger characteristics")
print("that relate to survival, even without using the survival label!")

# Survival rate by cluster
print("\nSurvival rate by cluster:")
for cluster in [0, 1]:
    rate = df_prep[df_prep['Cluster'] == cluster]['Survived'].mean()
    print(f"Cluster {cluster}: {rate:.1%}")
```

```
Cluster vs Actual Survival:
```

```
=====
Survived      0      1
Cluster
```

```
0      474  252
1       75   90
```

💡 Interesting! The clusters somewhat align with survival. This suggests there are natural groupings in passenger characteristics that relate to survival, even without using the survival label!

Survival rate by cluster:

Cluster 0: 34.7%

Cluster 1: 54.5%

▼ Elbow Method: Finding Optimal K

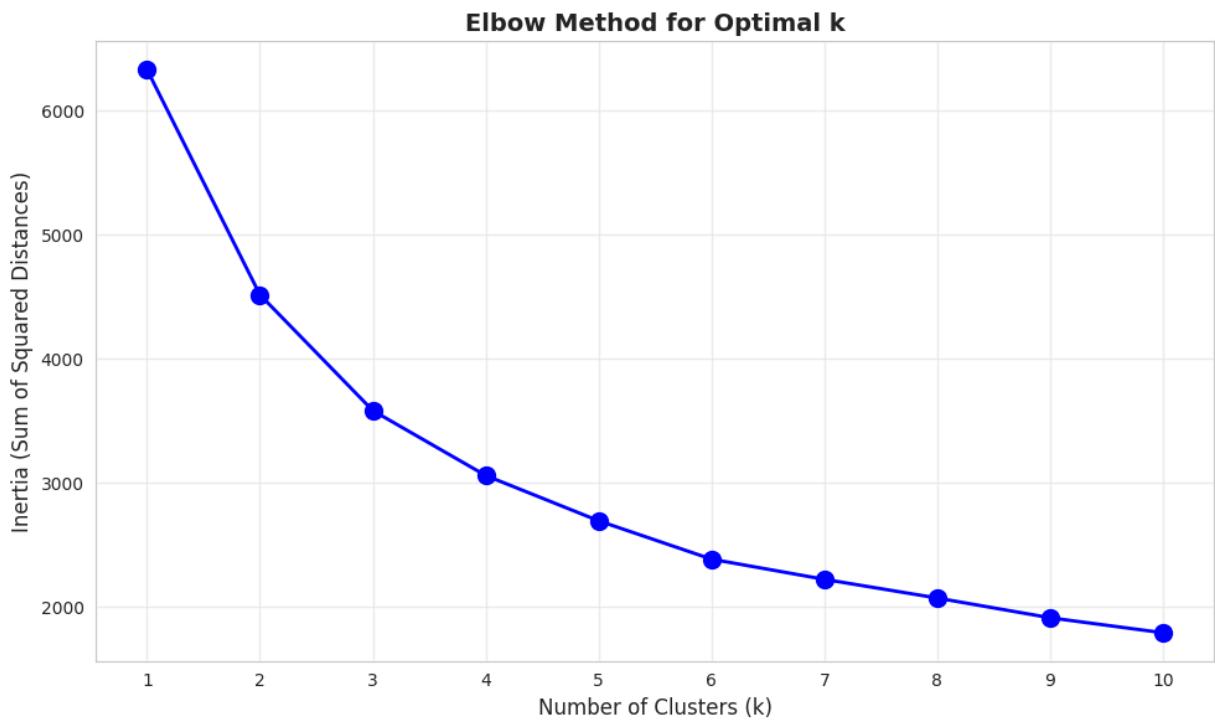
How many clusters should we use? The elbow method helps decide!

```
# Try different values of k
inertias = []
K_range = range(1, 11)

for k in K_range:
    kmeans_temp = KMeans(n_clusters=k, random_state=42, n_init=10)
    kmeans_temp.fit(X_cluster)
    inertias.append(kmeans_temp.inertia_)

# Plot elbow curve
plt.figure(figsize=(10, 6))
plt.plot(K_range, inertias, marker='o', linewidth=2, markersize=10, color='blue')
plt.xlabel('Number of Clusters (k)', fontsize=12)
plt.ylabel('Inertia (Sum of Squared Distances)', fontsize=12)
plt.title('Elbow Method for Optimal k', fontsize=14, fontweight='bold')
plt.xticks(K_range)
plt.grid(alpha=0.3)
plt.tight_layout()
plt.show()

print("Look for the 'elbow' - where the curve bends.")
print("That's where adding more clusters gives diminishing returns.")
print("For Titanic, k=2 or k=3 seems reasonable.")
```



Look for the 'elbow' - where the curve bends.
 That's where adding more clusters gives diminishing returns.
 For Titanic, k=2 or k=3 seems reasonable.

▼ Principal Component Analysis (PCA)

Goal: Reduce dimensionality while preserving information

Use case: We have 9 features. Can we visualize passengers in 2D?

```
from sklearn.decomposition import PCA

# Apply PCA
pca = PCA()
pca.fit(X_cluster)

# Explained variance
explained_var = pca.explained_variance_ratio_
```

```

print("PCA Results:")
print("*60")
print(f"Original dimensions: {X_cluster.shape[1]}")
print("\nExplained variance by component:")
for i, var in enumerate(explained_var, 1):
    print(f" PC{i}: {var:.1%}")

cumulative_var = np.cumsum(explained_var)
print("\nCumulative explained variance:")
for i in [1, 2, 3, 4, 5]:
    print(f" First {i} components: {cumulative_var[i-1]:.1%}")

print(f"\n💡 With just 2 components, we retain {cumulative_var[1]:.1%} of info")

```

PCA Results:
=====

Original dimensions: 9

Explained variance by component:

- PC1: 43.5%
- PC2: 21.3%
- PC3: 12.8%
- PC4: 10.9%
- PC5: 4.3%
- PC6: 2.9%
- PC7: 2.2%
- PC8: 1.4%
- PC9: 0.6%

Cumulative explained variance:

- First 1 components: 43.5%
- First 2 components: 64.8%
- First 3 components: 77.6%
- First 4 components: 88.5%
- First 5 components: 92.8%

💡 With just 2 components, we retain 64.8% of information!

```

# Visualize explained variance
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(15, 5))

# Individual variance
ax1.bar(range(1, len(explained_var)+1), explained_var, color='skyblue', edgecolor='black')
ax1.set_xlabel('Principal Component', fontsize=12)
ax1.set_ylabel('Explained Variance Ratio', fontsize=12)
ax1.set_title('Variance Explained by Each Component', fontsize=14, fontweight='bold')
ax1.grid(axis='y', alpha=0.3)

# Cumulative variance
ax2.plot(range(1, len(cumulative_var)+1), cumulative_var,
         marker='o', linewidth=2, markersize=10, color='green')
ax2.axhline(y=0.95, color='red', linestyle='--', linewidth=2, label='95% threshold')

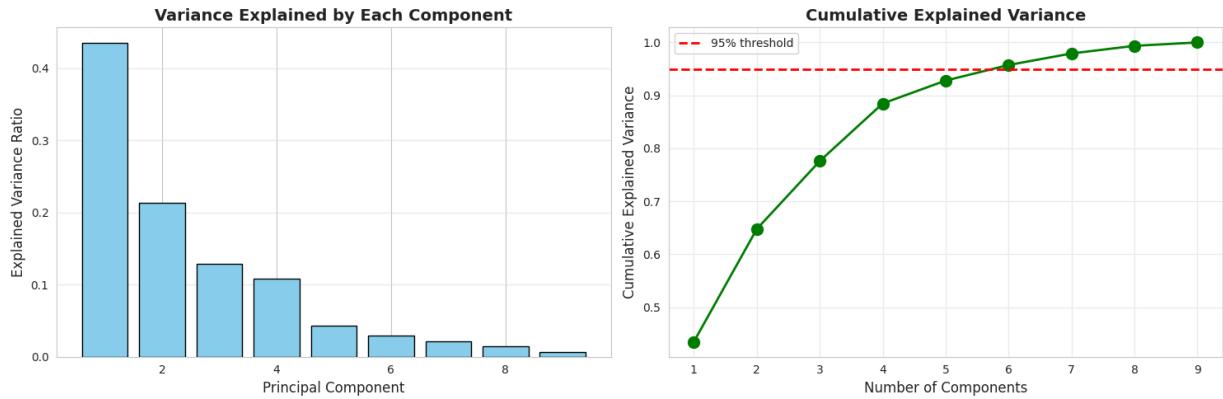
```

```

ax2.set_xlabel('Number of Components', fontsize=12)
ax2.set_ylabel('Cumulative Explained Variance', fontsize=12)
ax2.set_title('Cumulative Explained Variance', fontsize=14, fontweight='bold')
ax2.legend()
ax2.grid(alpha=0.3)

plt.tight_layout()
plt.show()

```



```

# Reduce to 2D and visualize
pca_2d = PCA(n_components=2)
X_pca = pca_2d.fit_transform(X_cluster)

# Plot by survival
plt.figure(figsize=(12, 6))

for survived in [0, 1]:
    mask = df_prep['Survived'] == survived
    label = 'Survived' if survived == 1 else 'Died'
    color = 'green' if survived == 1 else 'red'
    plt.scatter(X_pca[mask, 0], X_pca[mask, 1],
                label=label, alpha=0.6, s=50, color=color, edgecolors='black')

plt.xlabel(f'First Principal Component ({explained_var[0]:.1%} variance)', fontweight='bold')
plt.ylabel(f'Second Principal Component ({explained_var[1]:.1%} variance)', fontweight='bold')
plt.title('Titanic Passengers in 2D (PCA)', fontsize=14, fontweight='bold')
plt.legend(fontsize=12)
plt.grid(alpha=0.3)

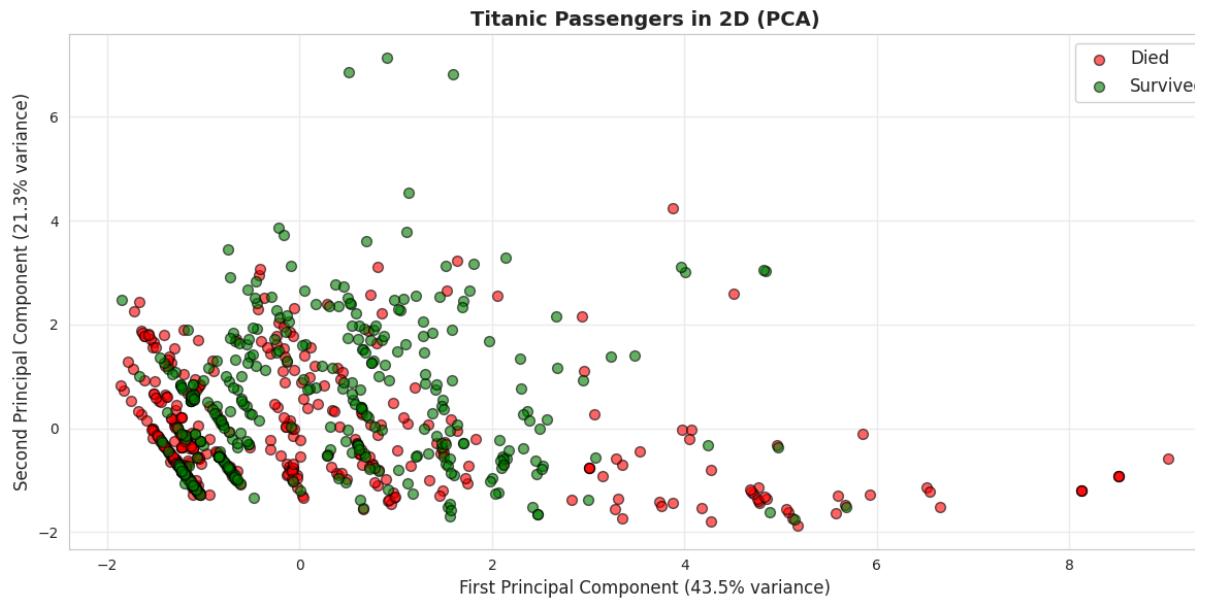
```

```

plt.tight_layout()
plt.show()

print("\n💡 We've reduced 9 dimensions to 2!")
print("You can see some separation between survivors and non-survivors.")
print("This is just one example of dimensionality reduction")

```



💡 We've reduced 9 dimensions to 2!
 You can see some separation between survivors and non-survivors.
 This is just one example of dimensionality reduction.