Machine Learning Interview Questions and Answers

1) What is the difference between Parametric and Non-Parametric Algorithms?

***Parametric models**:*

- ✓ These algorithms assume a fixed, predefined structure for the model, such as linear or polynomial relationships.
- ✓ They rely on a finite number of parameters (e.g., weights in Linear Regression).
- ✓ They are computationally efficient, making them faster to train.
- ✓ However, they are less flexible and may underperform on complex datasets if the assumptions about the data's structure are incorrect.
- ✓ **Examples**: Linear Regression, Logistic Regression, and SVM with a linear kernel.

Non-Parametric models:

- ✓ These algorithms do not assume any specific structure or distribution for the data.
- ✓ They are more flexible and capable of capturing complex patterns since the model adapts as more data becomes available.
- ✓ However, they require more data to generalize well and are computationally expensive because they often store the entire dataset.
- ✓ **Examples**: k-NN, Decision Trees, Random Forest, and SVM with RBF kernel.

2) Difference between convex and non-convex cost function; what does it mean when a cost function is non-convex?

***Convex*:**

- ✓ A convex function has a bowl-shaped curve where any line drawn between two points on the curve lies above or on the curve.
- ✓ It has a single global minimum, which makes optimization straightforward since gradient descent will always converge to that minimum.
- ✓ Example: Mean Squared Error (MSE) in Linear Regression.

Non-Convex:

- ✓ A non-convex function has a curve with multiple local minima and maxima, meaning it is not bowl-shaped.
- ✓ The presence of multiple minima makes optimization challenging since gradient descent might get stuck in a local minimum instead of reaching the global minimum.
- ✓ Example: Cost functions in deep learning (e.g., neural networks), which are typically non-convex due to the high-dimensional and complex structure of the parameter space.

3) How do you decide when to go for deep learning for a project?

Deciding to use deep learning depends on the complexity of the problem, the data type, and available resources. Deep learning is ideal for solving complex tasks involving unstructured data like images, videos, or text because of its ability to automatically extract meaningful features. However, it requires large datasets to perform well and significant computational power, like GPUs, for training. For smaller datasets or structured data, traditional machine learning models are often more practical and efficient. Additionally, deep learning models are less interpretable, which might be a limitation for applications requiring transparency, such as healthcare or finance. If resources and data size permit, and the problem demands state-of-the-art performance, deep learning can be a strong choice.

4) Give an example of when False positive is more crucial than false negative and vice versa?

- ✓ **False Positive is More Crucial:** In fraud detection systems, flagging a legitimate transaction as fraudulent (false positive) can inconvenience customers and damage the user experience. This is more critical in high-value scenarios, such as large business transactions, where trust is paramount.
- ✓ **False Negative is More Crucial:** In medical diagnosis, missing a life-threatening condition like cancer (false negative) is far more severe because it delays treatment and can result in fatal consequences. It's better to flag a condition as positive, even if it requires additional tests to confirm.

5) Why is "Naive" Bayes naive?

Naive Bayes is considered 'naive' because it makes a strong assumption that all features in the dataset are independent of each other, given the class label. This assumption rarely holds true in real-world scenarios, as features often have some level of correlation. Despite this simplification, Naive Bayes performs surprisingly well in many applications, especially in text classification and spam detection, where feature independence is approximately valid. The 'naive' assumption simplifies the computation of probabilities, making the algorithm efficient and easy to implement.

6) Give an example where the median is a better measure than the mean?

The median is a better measure of central tendency than the mean when the data contains outliers or is skewed. For example, consider a dataset of house prices in a city where most houses cost around $300,000, but a few luxury homes are priced at $10 million. The mean would be heavily influenced by these extreme values and may give a misleading impression of the typical house price. In contrast, the median, which represents the middle value of the sorted data, is unaffected by outliers and provides a more accurate representation of the central tendency in such cases.

7) Why KNN is known as a lazy learning technique?

K-Nearest Neighbors (KNN) is called a lazy learning technique because it doesn't learn an explicit model during the training phase. Instead, it simply stores the training data and defers all computation until prediction time. When making predictions, KNN calculates the distance between the query point and all stored data points, identifies the k-nearest neighbors, and predicts based on their labels. This 'lazy' approach contrasts with algorithms like decision trees or logistic regression, which build a model during training and make predictions based on that model.

8) What do you mean by semi supervised learning?

Semi-supervised learning is a type of machine learning that lies between supervised and unsupervised learning. In semi-supervised learning, the model is trained on a small amount of labeled data and a large amount of unlabeled data. The labeled data provides guidance for the model, while the unlabeled data helps the model learn underlying patterns and generalize better. This approach is useful when labeling data is expensive or time-consuming, but there's an abundance of unlabeled data available. It leverages both to improve the model's performance without requiring a large amount of labeled data. ***Example: Image classification.***

9) What is an OOB error and how is it useful?

The Out-of-Bag (OOB) error is an internal validation method used in ensemble learning algorithms like Random Forest. During training, each decision tree in a Random Forest is trained on a bootstrap sample, meaning a random subset of the data is selected with replacement. Some data points are not included in the bootstrap sample and are left out of the training of each tree; these are called 'out-of-

bag' points. The OOB error is calculated by using these out-of-bag points to test the model. This provides an unbiased estimate of the model's performance without needing a separate validation set. It's especially useful when you have limited data and want to make the most of it.

10) In what scenario decision tree should be preferred over random forest?

- ✓ **Interpretability**: When you need to easily explain the model's logic and decisions.
- ✓ **Speed and simplicity**: When computational efficiency is a concern and you don't need the complexity of an ensemble method.
- ✓ **Small datasets**: When you have a small dataset and overfitting is less of a concern, a decision tree might be sufficient.
- ✓ **Less computational resources**: When you need a less resource-intensive solution for prediction and training.

11) Why Logistic Regression is called regression?

Logistic Regression is called 'regression' because it models the relationship between the dependent variable and independent variables using a regression-based approach, even though its output is categorical (binary). The term 'regression' comes from its method of fitting a line (or curve) to data. In logistic regression, the model first calculates a linear combination of the input features (like in linear regression) and then applies a logistic (sigmoid) function to transform this into a probability between 0 and 1. This is used for binary classification. Despite being used for classification, it's called regression because it uses a linear equation to estimate the outcome before applying a transformation.

12) What is No Free Lunch Theorem?

The No Free Lunch (NFL) Theorem essentially states that no single machine learning algorithm works best for every problem. In other words, the performance of an algorithm is highly dependent on the specific dataset and problem it is being applied to. If an algorithm performs well on one type of problem, it doesn't guarantee that it will perform well on another. This means that, for any algorithm, there will always be some problems for which it is the best performer, and others where it will perform poorly. The theorem emphasizes the importance of experimenting with different algorithms and selecting the one that is most suited to the specific characteristics of your data and problem.

13) Imagine you are working with a laptop of 2GB RAM, how would you process a dataset of 10GB?

- ✓ **Use Data Streaming**: Instead of loading the entire dataset into memory, I would process it in chunks by streaming the data in small batches that fit into memory. Libraries like Pandas offer ways to load data in chunks using the chunksize parameter, allowing for efficient memory management.
- ✓ **Data Compression**: I would consider compressing the dataset into a format like CSV.gz or Parquet, which reduces the file size, and then load it in a more efficient, columnar format.
- ✓ **Out-of-Core Learning**: If applicable, I would use out-of-core learning techniques, which allow machine learning algorithms to train on data that doesn't fit in memory by processing it in chunks. Libraries like Scikit-learn and Dask provide out-of-core learning options.
- ✓ **Use a Database**: I would store the data in a database like SQLite or PostgreSQL and perform SQL queries to process the data in smaller, manageable chunks, only loading relevant data at any given time.

- ✓ **Distributed Computing**: If the dataset is large and the resources allow, I could use a distributed framework like Dask or Apache Spark to distribute the workload across multiple nodes and overcome the memory limitations of a single machine.
- ✓ **Increase Swap Space**: While this is not the most efficient option, increasing the swap space (virtual memory) could help when running out of physical RAM, though it can significantly slow down processing due to reliance on the hard disk.
- ✓ **Cloud or External Resources**: If none of the above strategies are sufficient, I would consider using cloud resources (e.g., AWS, Google Cloud) or external servers to handle larger datasets more effectively.

14) What are the main points of difference between Bagging and Boosting?

Bagging focuses on reducing variance and works with parallel models, while Boosting focuses on reducing bias and works with sequential models, adjusting the focus on difficult data points. *Random Forest is a popular example of bagging. Algorithms like AdaBoost, Gradient Boosting, and XGBoost are examples of boosting.*

15) How do you measure the accuracy of a Clustering Algorithm?

The choice of metric depends on whether ground-truth labels are available. External metrics like ARI (Adjusted Rand Index) and NMI (Normalized Mutual Information) are used with labels, while internal metrics like Silhouette Score and Inertia are used when labels are unavailable. Clustering accuracy is more about evaluating structure and separation rather than direct predictions.

- ✓ **Adjusted Rand Index (ARI)**: Measures the similarity between the true labels and the clustering results, adjusted for chance.
- ✓ **Normalized Mutual Information (NMI)**: Evaluates how much information the predicted clusters share with the true labels, normalized to prevent bias.
- ✓ **Silhouette Score**: Measures how well clusters are separated and how cohesive individual clusters are. A score close to 1 indicates well-separated clusters.
- ✓ **Inertia (within-cluster sum of squares)**: Measures the compactness of clusters but does not directly account for separation between them.

16) What is Matrix Factorization and where is it used in Machine Learning?

Matrix Factorization is a way to break a big table of data into smaller pieces to understand it better. Imagine you have a table where rows represent users, columns represent movies, and the entries show how much a user liked a movie. But most of the table is empty because users haven't rated every movie.

Matrix Factorization splits this table into two smaller tables:

1. One table shows users and their preferences (like how much they like action or comedy).
2. The other table shows movies and their features (like how much action or comedy each movie has).

When you multiply these two smaller tables, you can fill in the missing ratings in the big table. This helps recommend movies to users based on their preferences.

It's mostly used in recommendation systems, like Netflix or Spotify, to suggest things you might like, even if you haven't rated or seen them before.

17) What is an Imbalanced Dataset and how can one deal with this problem?

An imbalanced dataset is when one class in a classification problem has far more samples than the other, like 99% legitimate transactions and 1% fraud in fraud detection. This can lead the model to

favor the majority class, giving misleading results. To handle this, you can balance the data by oversampling the minority class (e.g., SMOTE), undersampling the majority class, or using algorithms that handle imbalance well by adjusting class weights. Additionally, you should evaluate the model using metrics like F1-score or ROC-AUC instead of accuracy to ensure fair assessment.

18) How do you measure the accuracy of a recommendation engine?

- ✓ **Precision**: Measures how many of the recommended items are relevant (e.g., out of the top 10 recommendations, how many are actually liked by the user).
- ✓ **Recall**: Measures how many of the relevant items are recommended (e.g., out of all items the user likes, how many were recommended).
- ✓ **F1-Score**: A balance between precision and recall.
- ✓ **Mean Average Precision (MAP)**: Evaluates ranking by considering the relevance of recommendations and their order.
- ✓ **Root Mean Square Error (RMSE) or Mean Absolute Error (MAE)**: Used when predicting ratings to measure the difference between predicted and actual ratings.
- ✓ **Hit Rate**: Measures how often a relevant item appears in the top-N recommendations.
- ✓ **Diversity and Novelty**: Evaluates how varied and new the recommendations are to avoid redundancy.

19) What are some ways to make your model more robust to outliers?

To make your model more robust to outliers, you can use techniques like scaling your features with robust methods (e.g., RobustScaler) that are less sensitive to extreme values. Consider using algorithms like tree-based models (e.g., Random Forest, XGBoost) or support vector machines (SVM) with appropriate kernels, as they are inherently less affected by outliers. For regression problems, switch to robust regression techniques like Huber regression or quantile regression. Additionally, detect and handle outliers through methods like the IQR (Interquartile Range) or z-score and either remove, cap, or transform them. Finally, applying log transformation or other nonlinear transformations can help mitigate the impact of outliers in skewed distributions.

20) How can you measure the performance of a dimensionality reduction algorithm on your dataset?

To measure the performance of a dimensionality reduction algorithm, you can evaluate how well the reduced data preserves the structure and information of the original dataset. Common methods include reconstructing the original data from the reduced dimensions and calculating the reconstruction error (e.g., using mean squared error). You can also assess how well the reduced data performs in downstream tasks, like classification or clustering, by comparing metrics such as accuracy or silhouette score before and after dimensionality reduction. Visualization techniques, like plotting 2D or 3D projections, can help analyze whether the reduced data retains separability between classes or clusters.

21) What is Data Leakage? List some ways using which you can overcome this problem.

Data Leakage occurs when information from outside the training dataset leaks into the model during training, giving it an unfair advantage and leading to overly optimistic performance during validation or testing. This results in a model that does not generalize well to unseen data.

Ways to Overcome Data Leakage:

1. **Separate Train-Test Data Properly**: Ensure that no information from the test set influences the training process. Always split the data before any preprocessing.

2. **Avoid Preprocessing on Entire Dataset**: Perform feature scaling, encoding, or transformations only on the training data and then apply the same transformations to the test set.
3. **Handle Temporal Data Carefully**: In time series data, avoid using future information to predict past or present events.
4. **Avoid Target Leakage**: Exclude features created from the target variable, e.g., including future sales data while predicting current sales.
5. **Cross-Validation**: Use techniques like k-fold cross-validation to ensure robust model evaluation without leakage.
6. **Feature Selection**: Perform feature selection only on the training data, not the entire dataset.

22) What is Multicollinearity? How to detect it? List some techniques to overcome Multicollinearity.

Multicollinearity occurs when two or more independent variables in a dataset are highly correlated, meaning they provide redundant information to the model. This can make it difficult for algorithms to determine the individual effect of each variable, leading to unstable coefficients in regression models and reducing interpretability.

How to Detect Multicollinearity:

1. Variance Inflation Factor (VIF): Calculate VIF for each variable. A VIF value greater than 5 or 10 indicates multicollinearity.
2. Correlation Matrix: Check the pairwise correlation coefficients. High correlations (e.g., above 0.8) may indicate multicollinearity.
3. Eigenvalues of the Covariance Matrix: Small eigenvalues indicate multicollinearity.

Techniques to Overcome Multicollinearity:

1. Remove Highly Correlated Variables: Drop one of the variables that are highly correlated.
2. Principal Component Analysis (PCA): Reduce the dimensionality of the dataset by creating uncorrelated components.
3. Regularization Techniques: Use methods like Ridge Regression (L2 regularization) or Lasso Regression (L1 regularization) to penalize large coefficients and reduce multicollinearity.
4. Combine Variables: Merge correlated variables into a single feature, e.g., by averaging or creating interaction terms.
5. Increase Sample Size: More data can help mitigate the impact of multicollinearity on model stability.

23) How do you approach a categorical feature with high cardinality?

A categorical feature with high cardinality refers to a feature in a dataset that is categorical (i.e., it contains discrete, non-numeric values like labels or categories) and has a large number of unique values or levels.

Example:

- A "Country" feature with 200 unique country names.
- A "User ID" or "Product ID" feature with thousands or even millions of unique values.

Why is it a challenge?

1. **Increased Model Complexity:** High cardinality can lead to a large number of features if one-hot encoding is used, which increases the dimensionality of the data.
2. **Overfitting:** Some categories may have very few samples, which can lead to overfitting to those rare categories.

3. **Memory and Computational Overhead:** Large numbers of categories can significantly increase memory usage and computational time.

When dealing with a **categorical feature with high cardinality** (i.e., many unique values), it is important to handle it carefully to avoid overfitting, increased model complexity, or memory issues. Here's how you can approach it:

1. **Frequency Encoding:** Replace categories with their frequency or count in the dataset. For example, assign a value based on how often each category appears.
2. **Target Encoding:** Replace each category with the mean (or other aggregation) of the target variable for that category. Be cautious of data leakage and use cross-validation.
3. **Hash Encoding:** Convert categories to hashed numerical values, reducing dimensionality while maintaining uniqueness.
4. **Clustering Similar Categories:** Group similar categories together based on business logic, domain knowledge, or statistical similarity (e.g., grouping rare categories as "others").
5. **Dimensionality Reduction:** Use techniques like PCA or embeddings (e.g., word embeddings for text-based categories) to represent high-cardinality categories in lower dimensions.
6. **Leave-One-Out Encoding:** Similar to target encoding, but it excludes the current row while calculating the mean for a category to reduce data leakage.
7. **One-Hot Encoding (Selective):** Use this only if the cardinality is moderate, as high cardinality will create a large number of sparse columns, which may increase computational overhead.

24) Explain Pruning in Decision Trees and how it is done?

Pruning in Decision Trees is the process of reducing the size of a decision tree by removing sections of the tree that provide little to no additional predictive power. It is done to prevent overfitting, improve generalization, and make the model simpler and more interpretable.

How Pruning is Done:

1. Pre-Pruning (Early Stopping): Stop the tree's growth early during training by setting constraints such as:
    - Maximum depth of the tree.
    - Minimum number of samples required to split a node.
    - Minimum gain in information (or reduction in impurity) required to make a split.
2. Post-Pruning (Reduced Error Pruning): Grow the tree fully and then prune back unnecessary branches:
    - Evaluate the impact of removing a subtree or branch on validation data.
    - Prune branches that do not reduce the overall error rate or provide marginal improvement.

25) What is ROC-AUC curve? List some of its benefits?

The ROC-AUC curve is a performance metric for classification models, where the ROC curve plots the True Positive Rate (TPR) against the False Positive Rate (FPR) at different thresholds. The AUC (Area Under the Curve) measures the model's ability to distinguish between classes, with a value closer to 1 indicating better performance.

- **Threshold Selection**: It helps you decide the optimal probability threshold for classifying a prediction as positive or negative, depending on the trade-off between **True Positive Rate (TPR)** and **False Positive Rate (FPR)**.

- **Model Comparison**: The **Area Under the Curve (AUC)** provides a single scalar value to compare the performance of different models. A higher AUC indicates a better model in distinguishing between classes.
- **Class Imbalance**: Unlike accuracy, the ROC curve remains effective in assessing performance for imbalanced datasets, as it evaluates TPR and FPR independently of class distribution.
- **Diagnostic Tool**: It helps identify whether the model is biased towards a specific class (e.g., too many false positives or negatives), aiding in model tuning.

26) What are kernels in SVM? Can you list some popular SVM kernels.

In SVM (Support Vector Machines), kernels are techniques used to transform your data into a higher-dimensional space where it is easier to find a dividing line (or hyperplane) between different classes. This allows SVM to classify data that is not easily separable with a straight line in its original form.
Popular SVM Kernels:

1. Linear Kernel: This is used when the data can be separated by a straight line or hyperplane. It's the simplest and most efficient kernel when the data is linearly separable.
2. Polynomial Kernel: Used for data where the relationship between features is non-linear but can be modelled with polynomials (e.g., quadratic or cubic functions). It allows more flexibility in the decision boundary.
3. Radial Basis Function (RBF) Kernel: This is one of the most commonly used kernels because it can handle complex, non-linear data. It works well when there's no clear pattern in how data points are distributed.
4. Sigmoid Kernel: This kernel is inspired by the sigmoid function used in neural networks. It's less common, but may be useful in specific scenarios.

27) What is the difference between Gini Impurity and Entropy? Which one is better and why?

When we build a decision tree, we split the data at each step. To decide where to split, we use measures like Gini Impurity or Entropy.

- Gini Impurity: Think of it as a measure of "mistakes." If we randomly pick a data point and classify it based on the split, Gini tells us the chances of getting it wrong. Lower Gini = better split.
- Entropy: It's a measure of "disorder" or uncertainty in the data. Higher Entropy = more mixed-up data. Lower Entropy = more pure groups (e.g., mostly 0s or 1s).

Both methods help us find splits that make the groups as "pure" as possible. Gini is faster to calculate, while Entropy can give deeper insights. But they often lead to similar results, so many people prefer Gini for its speed.

28) Why does L2 regularization give sparse coefficients?

In the context of machine learning and statistics, sparsity refers to a situation where most of the coefficients (or values) in a dataset or model are zero. It implies that only a few features or variables are actively contributing to the model or dataset, while the rest have no effect.
Actually, L2 regularization does not give sparse coefficients—that's a property of L1 regularization.
L2 Regularization (Ridge Regression)

- L2 regularization adds a penalty proportional to the square of the coefficients to the loss function.
- This shrinks the coefficients toward zero but **does not make them exactly zero**.

- As a result, all features remain in the model, though their impact is reduced.

Key takeaway: L2 regularization **does not produce sparsity**. It's useful when you want to keep all features but reduce their influence to avoid overfitting.

L1 Regularization (Lasso Regression)

- L1 regularization adds a penalty proportional to the absolute value of the coefficients to the loss function.
- This can shrink some coefficients exactly to **zero**, effectively **removing less important features** from the model.
- This happens because the penalty for L1 regularization creates a sharp, "pointy" constraint boundary (in contrast to the rounded boundary in L2).

Key takeaway: L1 regularization **produces sparse coefficients** and is often used for feature selection.

29) List some ways using which you can improve a model's performance?

- Engineer better features or remove irrelevant ones.
- Tune hyperparameters using Grid Search or Random Search.
- Use regularization (L1/L2) to prevent overfitting.
- Apply cross-validation for reliable evaluation.
- Increase training data or use data augmentation.
- Experiment with ensemble methods (e.g., Random Forest, XGBoost).
- Handle class imbalance with resampling or weighted loss functions.
- Optimize decision thresholds for better classification results.

30) Can PCA be used to reduce the dimensionality of a highly nonlinear dataset?

PCA is primarily a linear dimensionality reduction technique, meaning it works best when the dataset's variance is captured in linear combinations of features. For highly nonlinear datasets, PCA may not effectively capture complex structures or relationships.

In such cases, nonlinear techniques like t-SNE, UMAP, or Kernel PCA (which uses kernels to handle nonlinearity) are better suited. However, PCA can still be a good preprocessing step to remove noise or reduce dimensions before applying more complex methods.

31) What's the difference between probability and likelihood?

To summarize, probability is about predicting outcomes given parameters, while likelihood is about estimating parameters given observed outcomes.

32) What cross-validation technique would you use on a time series data set?

Time series data is special because the order of the data points (e.g., past, present, future) matters. You can't shuffle the data randomly, as you would in regular cross-validation, because it would mix up the time sequence. Instead, you use methods that respect the timeline:

1. Walk-Forward Validation

- Start with a small chunk of data for training (e.g., January) and test on the next chunk (e.g., February).
- Then expand the training set (e.g., January + February) and test on the next chunk (e.g., March).

- Repeat this process until you cover the whole dataset.
  This way, you simulate how a model would make predictions in the real world—always using the past to predict the future.

2. Rolling Window Validation

- Instead of growing the training set, keep the training set size fixed.
- For example, train on January and test on February, then slide the window forward: train on February and test on March.
  This helps test how the model performs across different time periods.

33) Why do we always need the intercept term in a regression model??

The intercept in a regression model is the starting point of the line (or curve) that the model fits. It shows what the outcome (target variable) would be if all the input features (independent variables) are zero. Here's why it's important:

- Why include it? If we don't include the intercept, the model will assume the line starts at zero, which may not match the real-world data. For example, predicting someone's salary based only on their years of experience—does someone with zero experience always earn $0? Not necessarily.
- What happens without it? Without an intercept, the model can't shift up or down to better fit the data. This can lead to bad predictions.

In simple terms, the intercept lets the model start at the right place, making predictions more accurate.

34) Which Among These Is More Important Model Accuracy or Model Performance?

Model accuracy refers to how often the model makes correct predictions. It's a straightforward metric but may not always reflect the true effectiveness of a model, especially in cases of imbalanced datasets.

Model performance is a broader concept that includes metrics like precision, recall, F1 score, ROC-AUC, and more. It evaluates how well the model meets the specific goals of the task. For example, in a healthcare application, recall (sensitivity) might be more important than accuracy because identifying all positive cases (e.g., a disease) is critical.

35) What is active learning and where is it useful?

Active learning is a machine learning technique where the model actively selects the most informative data points from an unlabeled dataset for labeling by a human or another oracle. Instead of training on all available data, the model focuses on data that is likely to improve its performance the most.

Where it's useful:

Active learning is particularly useful when labeled data is scarce, expensive, or time-consuming to obtain. For example, in medical imaging, where expert annotations are required, active learning can reduce labeling efforts by focusing on ambiguous or high-value cases. Similarly, it's used in applications like fraud detection or sentiment analysis, where certain data points are more complex or uncertain.

36) Why is Ridge Regression called Ridge?

Ridge Regression is called "Ridge" because it introduces a ridge (or a penalty) to the regression coefficients by adding an L2 regularization term to the cost function. This term is the square of the magnitude of coefficients, which helps shrink them toward zero without making them exactly zero, unlike Lasso regression.

The name "ridge" reflects the fact that this technique constrains the coefficients to lie within a certain boundary, forming a ridge-like structure in the optimization space. This helps prevent overfitting and makes the model more robust, especially when dealing with multicollinearity or high-dimensional datasets.

37) State the differences between causality and correlation?

Causality refers to a relationship where one variable directly influences another. For example, smoking causes an increased risk of lung cancer. **Correlation**, on the other hand, measures the statistical association between two variables but does not imply one causes the other. For instance, ice cream sales and drowning incidents may be correlated because both increase in summer, but one does not cause the other.

38) Does it make any sense to chain two different dimensionality reduction algorithms?

Yes, chaining two dimensionality reduction algorithms can make sense in certain scenarios. For instance, you might first use **Principal Component Analysis (PCA)** to reduce dimensionality by capturing most of the variance in the data, followed by a method like **t-SNE** or **UMAP** for further reducing dimensions while preserving local structures. This approach can help in visualizing high-dimensional data effectively or preparing data for clustering.

39) If a Decision Tree is underfitting the training set, is it a good idea to try scaling the input features?

Scaling input features is not effective for decision trees because they are not sensitive to the scale of the features. If a decision tree is underfitting, the issue is usually with the model's complexity, such as a shallow tree. In such cases, adjusting hyperparameters like increasing the tree depth or reducing the minimum sample size for splits would be more helpful.

40) How do we interpret weights in linear models?

In linear models, the weights (or coefficients) represent the relationship between the input features and the target variable. Specifically, they indicate how much change in the target variable is expected for a one-unit change in the corresponding feature, while holding other features constant.
Here’s how you interpret them:

1. **Positive Weights:** A positive weight means that as the feature increases, the predicted value of the target variable also increases.
2. **Negative Weights:** A negative weight indicates that as the feature increases, the predicted value of the target variable decreases.
3. **Magnitude of the Weight**: The larger the magnitude of the weight (whether positive or negative), the stronger the influence that feature has on the prediction.
4. **Intercept (Bias Term):** The intercept term is the predicted value when all features are zero. It is a baseline prediction in the absence of any features.

For example, if you have a linear regression model predicting house prices, and the weight for the "size of the house" feature is 1000, this means that for every additional square foot of house size, the predicted house price increases by 1000 units, assuming all other features remain the same.

41) Why is it important to scale the inputs when using SVMs?

When using Support Vector Machines (SVMs), it is crucial to scale the inputs because SVMs are sensitive to the scale of the features. This is due to the fact that SVMs rely on calculating the distance between data points (e.g., using the dot product) to find the optimal hyperplane. If the features have

different scales, the SVM model may give disproportionate importance to features with larger scales, potentially leading to suboptimal performance.
Scaling the data ensures that each feature contributes equally to the model, preventing features with larger values from dominating the optimization process. Common scaling techniques include Standardization (subtracting the mean and dividing by the standard deviation) or Min-Max Scaling (rescaling the features to a fixed range, typically [0, 1]). Proper scaling leads to better convergence, faster training, and more accurate models in SVM classification or regression tasks**.**

42) How will you do feature selection using Lasso Regression?

Lasso Regression (Least Absolute Shrinkage and Selection Operator) is a regularization technique that helps in feature selection by adding a penalty to the loss function, proportional to the absolute values of the model coefficients. This penalty encourages the model to shrink less important feature coefficients toward zero, effectively eliminating them from the model.
Here's how Lasso helps in feature selection:

1. **Fit a Lasso Model:** You start by training a Lasso regression model on your dataset. The L1 penalty term in the Lasso algorithm forces the coefficients of some features to become exactly zero.
2. **Evaluate the Coefficients:** After training, the coefficients of the features that are not important for the model will be shrunk to zero. These features can be safely removed from the model.
3. **Select Features:** Features with non-zero coefficients are considered significant and are retained. Features with zero coefficients are excluded from the model.
4. **Tune the Regularization Parameter (Alpha):** The strength of the penalty is controlled by the regularization parameter alpha. A larger value of alpha leads to more features being shrunk to zero, while a smaller value allows more features to remain in the model. You can perform cross-validation to find the optimal alpha value.

43) What is the difference between loss function and cost function?

In machine learning, a loss function measures the error for a single training example, indicating how well the model's prediction matches the actual label for that data point. On the other hand, a cost function is an aggregate measure, typically the average (or sum) of the loss function applied across the entire training dataset, providing a global evaluation of the model's performance. Essentially, while the loss function evaluates individual data points, the cost function evaluates the model’s overall performance across all examples.

44) What is the difference between standard scaler and minmax scaler? What you will do if there is a categorical variable?

The Standard Scaler standardizes features by removing the mean and scaling to unit variance, i.e., it transforms the data to have a mean of 0 and a standard deviation of 1. This is useful when the data follows a normal distribution or when you want to account for outliers.
The Min-Max Scaler scales the features to a specified range, typically [0, 1], by subtracting the minimum value of the feature and dividing by the range (max - min). This is useful when the features have different units or when we need to ensure all features are on the same scale.
For categorical variables, they should be encoded into numerical values before scaling. This can be done using techniques such as One-Hot Encoding (for nominal categories) or Label Encoding (for ordinal categories), depending on the nature of the variable.

45) What are some advantages and Disadvantages of regression models and tree-based models?

Regression models are efficient for simple, linear relationships, while tree-based models are more flexible and capable of capturing complex patterns but may be more prone to overfitting and computationally intensive.

46) What are some important hyperparameters for XGBOOST?

- n_estimators: The number of boosting rounds (trees) to build. More trees generally lead to better performance but increase the risk of overfitting.
- learning_rate (eta): Controls the contribution of each tree to the final prediction. Lower values make the model more robust but require more trees to converge.
- max_depth: The maximum depth of each tree. Deeper trees can capture more complex patterns, but they can also lead to overfitting.

47) Difference between R and Adjusted R Squared values in ML?

1. R-squared (R^2):

- What it is: It measures the proportion of the variance in the dependent variable that is explained by the independent variables in the model. It ranges from 0 to 1, where 1 means the model perfectly explains the variance in the data.
- Issue: As you add more features to a model, R^2 will always increase, even if the additional features are irrelevant or don't improve the model. This means that a model with more predictors might look better simply because it has more variables, even if those variables aren't truly useful.

2. Adjusted R-squared:

- What it is: It adjusts the R^2 value by taking into account the number of predictors in the model. It penalizes the addition of irrelevant predictors. This means that if you add features that don't improve the model, Adjusted R^2 will decrease.
- Why it matters: Adjusted R^2 gives a more realistic measure of how well the model fits the data, especially when comparing models with different numbers of predictors. It helps prevent overfitting by discouraging the addition of unnecessary features.

In short:

- R^2 tells you how well your model explains the variance but can be misleading with many predictors.
- Adjusted R^2 provides a more reliable metric by adjusting for the number of predictors in the model, making it a better choice when comparing models with different numbers of features.

Example:

- R^2 could be 0.95 (indicating 95% of variance is explained), but after adding irrelevant features, it might still increase to 0.96 even though the model doesn't improve much.
- Adjusted R^2 might stay at 0.95 or drop slightly if those extra features don't improve the model's ability to explain the data.

48) What are the different evaluation metrics for a regression model?

1. Mean Absolute Error (MAE)

MAE measures the average of the absolute differences between predicted and actual values. It tells you how much, on average, the predictions are off by, without considering whether the prediction is over or under the actual value.

Example:
If your house price prediction model gives the following predictions and actual values:

- Predicted: [200K, 300K, 400K]
- Actual: [210K, 290K, 410K]

The absolute errors are:

- |200K - 210K| = 10K
- |300K - 290K| = 10K
- |400K - 410K| = 10K

MAE = (10K + 10K + 10K) / 3 = 10K
This means, on average, the model's predictions are off by 10K.

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2. Mean Squared Error (MSE)
MSE squares the difference between actual and predicted values, which penalizes larger errors more than smaller ones. It's sensitive to outliers, meaning that if you make a large error, it will have a bigger impact on the MSE.
Example:
Using the same predictions and actual values:

- Predicted: [200K, 300K, 400K]
- Actual: [210K, 290K, 410K]

The squared errors are:

- $(200K - 210K)^2 = 100K^2$
- $(300K - 290K)^2 = 100K^2$
- $(400K - 410K)^2 = 100K^2$

MSE = $(100K^2 + 100K^2 + 100K^2) / 3 = 100K^2$
The MSE is $100K^2$, and since squaring magnifies larger errors, it's more sensitive to extreme values.

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3. Root Mean Squared Error (RMSE)
RMSE is the square root of MSE. It gives the error value in the same units as the target variable (e.g., if you're predicting prices, the RMSE will be in dollars, not squared dollars). It helps interpret the error more easily.
Example:
If MSE = $100K^2$, then
RMSE = $\sqrt{100K^2} = 10K$
This means the model's average error is 10K.

---

4. R-squared (R^2)
R^2 tells you how much of the variation in the actual values can be explained by the model. It ranges from 0 to 1, where 1 means the model perfectly explains the variation in the target variable.
Example:
Suppose the R^2 of a model is 0.9, which means the model explains 90% of the variation in the actual values. If your model's R^2 is low (e.g., 0.1), it means the model doesn't explain much of the data's variation, and it's probably a poor fit.

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5. Adjusted R-squared
Adjusted R^2 adjusts the R^2 score by penalizing for adding more predictors to the model. It's useful when comparing models with a different number of predictors, as adding irrelevant features can artificially inflate R^2.

Example:
If you have a model with two features and another with five, Adjusted R^2 helps to determine whether the additional features actually improve the model or not. If the model with five features has a much lower Adjusted R^2, it may indicate that those extra features are unnecessary.

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6. Mean Absolute Percentage Error (MAPE)
MAPE measures the percentage difference between the predicted and actual values. It's a good metric when you want to understand error in relative terms, i.e., how big is the error compared to the actual value.
Example:
For the same house prices:

- Predicted: [200K, 300K, 400K]
- Actual: [210K, 290K, 410K]

The percentage errors are:

- |(200K - 210K) / 210K| × 100 = 4.76%
- |(300K - 290K) / 290K| × 100 = 3.45%
- |(400K - 410K) / 410K| × 100 = 2.44%

MAPE = (4.76% + 3.45% + 2.44%) / 3 = 3.55%
This means that, on average, the model's predictions are off by about 3.55%.

49) What are the different evaluation metrics for a classification model?

For evaluating classification models, key metrics include Accuracy, which measures the proportion of correct predictions but is unreliable for imbalanced datasets. Precision focuses on correctly predicted positives, useful when false positives are costly, while Recall emphasizes detecting all actual positives, critical when false negatives are serious. The F1 Score balances Precision and Recall, ideal for imbalanced datasets. ROC-AUC evaluates the model's ability to distinguish classes across thresholds, and Log Loss penalizes incorrect probabilistic predictions, measuring confidence in predictions. Choose metrics based on the problem—e.g., Precision for spam detection or Recall for medical diagnoses.
Example Usage:

- Use Accuracy for balanced datasets.
- Use Precision or Recall for imbalanced datasets, depending on whether false positives or false negatives are more critical.
- Use F1 Score when balancing Precision and Recall is important.
- Use ROC-AUC for threshold-independent evaluation and comparison.

50) List some of the drawbacks of a Linear model?

Linear models, while simple and interpretable, have several drawbacks. They assume a linear relationship between input features and the target variable, which may not hold in real-world scenarios, limiting their ability to capture complex patterns. They are sensitive to multicollinearity and outliers, which can distort predictions. Linear models also struggle with high-dimensional data, as irrelevant or highly correlated features can negatively impact performance. Additionally, they require feature scaling for optimal performance and cannot handle non-linear relationships unless transformed or combined with other techniques like polynomial features.

51) What do you mean by Bias variance tradeoff?

The **Bias-Variance Tradeoff** is a fundamental concept in machine learning that describes the balance between two sources of error in a model:

1. **Bias**: The error due to overly simplistic assumptions in the model. High bias leads to underfitting, where the model fails to capture the underlying patterns in the data.
2. **Variance**: The error due to sensitivity to small fluctuations in the training data. High variance leads to overfitting, where the model captures noise instead of the actual signal.

The tradeoff lies in finding the right balance: reducing bias usually increases variance and vice versa. A well-performing model minimizes both bias and variance to achieve optimal generalization on unseen data.

52) What is the difference between Type 1 and Type 2 error?

- Type 1 Error (False Positive): Rejecting the null hypothesis when it is actually true. For example, concluding that a new drug is effective when it actually isn't. This error focuses on mistakenly identifying an effect or relationship that doesn't exist.
- Type 2 Error (False Negative): Failing to reject the null hypothesis when it is actually false. For example, concluding that a new drug is not effective when it actually works. This error overlooks a real effect or relationship.

In short, **Type 1 error relates to detecting a false effect**, while **Type 2 error relates to missing a true effect**.

53) How can you determine which features are the most important in your model?

- **Feature Importance (Tree-Based Models):** Algorithms like Random Forest, XGBoost, and Gradient Boosting provide feature importance scores based on how much each feature reduces impurity (Gini or entropy) or impacts model performance.
- **Coefficients (Linear Models):** In linear models, such as Linear Regression or Logistic Regression, the absolute values of coefficients indicate feature importance, assuming the features are scaled.
- **Permutation Importance:** Randomly shuffle the values of each feature and measure the drop in model performance to determine its importance.
- **SHAP Values:** SHAP (SHapley Additive exPlanations) provides a more interpretable method to measure the impact of each feature on the predictions.
- **Recursive Feature Elimination (RFE):** Iteratively removes less important features while evaluating model performance to identify key features.
- **Domain Knowledge:** Combining model-based methods with domain expertise ensures important features are correctly interpreted.

54) How would you differentiate between Multilabel and MultiClass classification?

Multilabel Classification: In multilabel classification, each instance can belong to multiple classes simultaneously. For example, in a movie genre prediction system, a single movie can be classified as both "Action" and "Comedy." The output is typically represented as a binary vector where each position corresponds to a label.

Multiclass Classification: In multiclass classification, each instance belongs to only one class out of multiple possible classes. For example, in handwritten digit recognition, each image represents one digit (0–9). The output is typically a single label indicating the class.

56) When should we use Precision-Recall (PR) curve?

- **Recall is important** (e.g., catching as many positive cases as possible, like fraud or disease detection).
- **The dataset is imbalanced**, meaning one class (e.g., positive cases) is much rarer than the other (e.g., negative cases).

This is because the PR curve focuses specifically on the positive class, making it more informative in these scenarios compared to the ROC curve, which considers both classes equally and can be misleading with imbalanced data.

57) When should we go for ROC curve?

1. **Balanced datasets**: The classes in the dataset are relatively balanced, so both true positives and true negatives are equally important.
2. **Overall performance**: You want to evaluate the model's ability to distinguish between classes, considering both sensitivity (recall) and specificity.
3. **When all thresholds matter**: The ROC curve is helpful if you're exploring a wide range of decision thresholds for classification.

For example:

- **Spam detection**: If false positives (misclassifying a valid email as spam) and false negatives (missing a spam email) are equally important, the ROC curve is suitable.
- **Credit scoring**: Where predicting both good and bad credit decisions matters equally.

58) When should we go for the precision metric?

You should go for the **precision metric** when **false positives** (incorrect positive predictions) are more critical than false negatives. Precision focuses on the proportion of true positive predictions out of all positive predictions the model makes.

Scenarios where precision is important:

1. **Spam detection**:
    - If marking a legitimate email as spam (false positive) would harm user experience, precision is crucial to ensure flagged emails are truly spam.
2. **Medical diagnosis**:
    - In cases where a positive diagnosis leads to invasive or expensive procedures (e.g., cancer detection), you want high precision to minimize unnecessary treatments for healthy individuals.
3. **Fraud detection**:
    - For predicting fraudulent transactions, wrongly classifying a genuine transaction as fraud (false positive) could inconvenience customers. Precision ensures flagged transactions are truly fraudulent.

In summary, use **precision** when **false positives have a high cost** or significant negative consequences.

59) When should we go for the recall metric?

You should prioritize the recall metric when false negatives (missing positive cases) are more critical than false positives. Recall focuses on identifying all actual positive cases, even if it means tolerating some false positives.

Scenarios where recall is important:

1. Medical diagnosis:

- In diseases like cancer or COVID-19, missing a positive case (false negative) could lead to severe consequences. High recall ensures all potential cases are flagged for further testing or treatment.

2. Fraud detection:
    - Detecting fraudulent transactions is critical. Missing fraudulent cases (false negatives) could result in financial losses. High recall ensures most fraud cases are captured.
3. Search and rescue operations:
    - Identifying all potential survivors or missing persons in a disaster is crucial. Missing someone (false negative) could be life-threatening, so recall becomes a priority.

In summary:
Use recall when missing positives has a high cost or critical implications.

60) How can you address multicollinearity in a regression model?

- **Remove variables**: Drop one of the highly correlated predictors.
- **Combine variables**: Use principal component analysis (PCA) to create uncorrelated components.
- **Regularization**: Use techniques like Lasso or Ridge regression, which penalize large coefficients and reduce multicollinearity.
- **Feature selection**: Use domain knowledge or statistical methods to select the most relevant features.

61) How would you decide if a new feature improves a model?

Scenario: You add a feature to predict customer churn but aren't sure if it's helpful.
Answer:
Compare models with and without the feature using metrics like **Adjusted R-squared** (for regression) or **AUC-ROC** (for classification).
Perform a **feature importance analysis**.

62) What statistical test would you use to determine if a categorical variable impacts a numerical variable?

Scenario: You want to check if a customer's region impacts their annual spending.
Answer:
Use **ANOVA (Analysis of Variance)** to compare the means of the numerical variable (annual spending) across multiple categories of the categorical variable (regions).
If significant, follow up with **post hoc tests** like Tukey's HSD to identify which groups differ.

63) What statistical test would you use to determine if two categorical variables are associated?

Scenario: You want to check if gender affects product preference.
Answer:
Use the **Chi-square test of independence** to determine if there is a significant association between the two categorical variables (e.g., gender and product type).
If the expected frequency is low, use **Fisher's Exact Test**.

64) When would you use a correlation test, and which type?

Scenario: You want to check the relationship between hours studied and exam scores.

Answer:

- Use **Pearson's correlation** if both variables are continuous and normally distributed.
- Use **Spearman's rank correlation** if the relationship is monotonic but not linear or data isn't normally distributed.

65) What does random state signify and what is the difference between the random states used in train test split and in algorithms?

The random_state in machine learning is a seed value used to ensure reproducibility of random processes. By setting the random_state, you make sure that your results can be reproduced because the random number generation will follow the same sequence every time the code runs.

Why is this distinction important?

- Setting the random_state in **train-test split** ensures you always evaluate the model on the same data split.
- Setting the random_state in the **algorithm** ensures the model itself is consistent in its training behavior, even if you re-run the code multiple times.

66) What are NumPy and Pandas? Why are they used?

- **NumPy** is a library for numerical computations in Python. It provides support for arrays, matrices, and fast mathematical operations.
- **Pandas** is a library for data manipulation and analysis, offering structures like **DataFrames** for working with tabular data.
- **Use Case:** NumPy is best for numerical computation, while Pandas is ideal for data cleaning, manipulation, and analysis.

67) What is the difference between a NumPy array and a Python list?

- **NumPy Array:** Fixed size, homogeneous data, faster operations due to vectorization, and occupies less memory.
- **Python List:** Can store heterogeneous data, dynamic in size, but slower for numerical operations.

68) How do you check for missing values in a Pandas DataFrame? How do you handle them?

- To check: df.isnull() or df.isnull().sum().
- To handle:
  - Replace with a value: df.fillna(value)
  - Drop rows/columns: df.dropna()
  - Impute: Replace with mean, median, or mode.

69) How do you select specific rows and columns from a Pandas DataFrame?

- Using .loc[]: Select rows/columns by labels.
  Example: df.loc[2, 'ColumnName']
- Using .iloc[]: Select rows/columns by position.
  Example: df.iloc[2, 1]
- Boolean indexing: df[df['ColumnName'] > 10]

Key Differences in Real-Time Use

- **.loc[]:** Best for labeled datasets (e.g., selecting rows with meaningful names like "Day1" or columns like "Sales").
- **.iloc[]:** Best when working with raw datasets (e.g., extracting by numeric positions for rows and columns).

When to Use Which

- Use **.loc[]** if your data has meaningful labels (e.g., timestamps, product names).
- Use **.iloc[]** for generic or numerical indexing, especially in exploratory or automated tasks.

70) How do you concatenate two DataFrames in Pandas?

- Use pd.concat([df1, df2], axis=0) for row-wise concatenation.
- Use pd.concat([df1, df2], axis=1) for column-wise concatenation.

71) How do you sort a Pandas DataFrame?

- Use df.sort_values() for sorting by values.
  Example: df.sort_values(by='ColumnName', ascending=True)
- Use df.sort_index() for sorting by index.

72) What is the difference between .at[] and .iat[]?

- .at[]: Access a single element using label-based indexing.
- .iat[]: Access a single element using integer-based indexing.

```
df.at[2, 'ColumnName']   # Label-based
df.iat[2, 1]             # Position-based
```

73) What are the limitations of XGBoost compared to Random Forest?

- **Complexity:** XGBoost requires careful hyperparameter tuning, while Random Forest works well with default parameters.
- **Training Time:** XGBoost can be slower on very large datasets compared to Random Forest.
- **Overfitting Risk:** XGBoost can overfit if not regularized properly.

74) What is the difference between overfitting in XGBoost and Random Forest?

- **XGBoost:** More prone to overfitting due to its sequential nature and ability to learn complex patterns. Regularization techniques like lambda and alpha help reduce overfitting.
- **Random Forest:** Less prone to overfitting because it averages multiple uncorrelated trees, reducing variance.

75) When should you use a t-test vs. a chi-square test?

t-test:

- Use when comparing means of two groups (numerical data).
- Example: Comparing average test scores between two schools.

Chi-Square Test:

- Use when comparing categorical data or testing independence.
- Example: Checking if gender (male/female) is independent of purchasing behavior (yes/no).

76) When would you use a Z-test instead of a t-test?

 Z-test:

- Use when the population standard deviation is known and the sample size is large (n > 30).
- Example: Testing whether the average height of a population differs from a known value.

 t-test:

- Use when the population standard deviation is unknown and the sample size is small.
- Example: Comparing average grades of two small classes.

77) What are some different supervised, unsupervised and semi supervised ml algorithms?

Supervised learning algorithms require labeled data and are used for tasks like classification and regression. Examples include **Linear Regression**, **Logistic Regression**, **Support Vector Machines (SVM)**, **Decision Trees**, **Random Forests**, and **Neural Networks**. These algorithms predict outcomes based on labeled input-output pairs.

Unsupervised learning algorithms, on the other hand, work with unlabeled data to find hidden patterns or groupings in the dataset. Examples include **K-Means Clustering**, **Hierarchical Clustering**, **DBSCAN**, **Principal Component Analysis (PCA)**, and **Autoencoders**. These are used in tasks like clustering, dimensionality reduction, and anomaly detection.

Semi-supervised learning algorithms leverage a mix of labeled and unlabeled data, which is useful when labeling data is expensive or time-consuming. Examples include **Self-training algorithms**, **Label Propagation**, and models like **Generative Adversarial Networks (GANs)** or **Semi-Supervised SVMs**. These algorithms are commonly applied in tasks like fraud detection and medical image classification, where labeled data is sparse.

78) What are the major differences between K-Means Clustering, Hierarchical Clustering, DBSCAN?

K-Means clustering is a partition-based algorithm that divides data into k predefined clusters by minimizing the distance between data points and their centroids. It's fast but sensitive to outliers and requires the number of clusters to be set in advance. Hierarchical clustering, on the other hand, builds a tree-like structure of clusters (dendrogram) either through agglomerative (bottom-up) or divisive (top-down) methods. It doesn’t require specifying k but is computationally expensive and sensitive to noise. DBSCAN (Density-Based Spatial Clustering of Applications with Noise) focuses on identifying dense regions in the data and can find clusters of arbitrary shapes, making it robust to noise and outliers without needing a predefined k. The key differences lie in K-Means requiring k to be defined, Hierarchical providing a hierarchy of clusters, and DBSCAN being ideal for irregular clusters and handling outliers well.

79) Explain SVM?

Support Vector Machine (SVM) is a supervised learning algorithm used for classification and regression that works by finding the optimal hyperplane (boundary) to separate data into classes. It maximizes the margin between the nearest data points of each class, called support vectors, ensuring better generalization. For example, if you classify fruits like apples and oranges based on features like weight and sweetness, SVM draws the best line separating the two classes. For non-linear data, SVM uses a kernel trick to transform data into higher dimensions, making it separable. While SVM is effective for small, clean datasets, it struggles with large or noisy datasets.

80) Explain the difference between p-value and critical value?

Both p-value and critical value are used to decide whether to reject or fail to reject the null hypothesis. The p-value is a probability calculated after performing a test, while the critical value is a fixed threshold that determines the range of values for rejecting or not rejecting the null hypothesis.

The critical value helps determine whether your **test statistic** (e.g., z-score or t-score) falls into the rejection region:

- If the test statistic is beyond the critical value: Reject Null Hypo.
- If the test statistic is within the critical value: Fail to reject Null Hypo.

The p-value represents **how extreme your test results are under the assumption that H0H_0H0 is true**. You compare the p-value to your significance level (α\alphaα) to make a decision:

- If p-value<α: Reject Null Hypo.
- If p-value≥α: Fail to reject Null Hypo.

81) What is a Confidence Interval?

A **confidence interval** (CI) is a range of values that is used to estimate an unknown population parameter (like the mean or proportion) based on a sample from that population.

- **The interval gives you a range**: We don't know the exact value of the population parameter, but we can estimate it with a certain level of confidence.
- **The confidence level** tells you how confident you can be that the population parameter lies within that range. Common confidence levels are **90%**, **95%**, and **99%**.

82) What is a Dendrogram? How it is related to agglomerative clustering?

A dendrogram is a tree-like visualization used to represent hierarchical clustering. It shows how individual data points are grouped into clusters in a step-by-step manner. It's widely used in unsupervised learning to identify natural groupings in data.

Why is a Dendrogram Useful?

1. **Visualizes Relationships:**
   "It helps us visualize relationships between data points and how they group together. For example, we can see which data points are similar and which are very different."
2. **Determining the Number of Clusters:**
   "By cutting the dendrogram at a certain height, we can decide how many clusters are appropriate for the data. This is useful when the number of clusters isn't predefined."

Agglomerative clustering is the algorithm used to group data hierarchically, while a dendrogram is the visual representation of the clustering process. They're related because the dendrogram illustrates how clusters are merged at different stages of agglomerative clustering.

83) What is Agglomerative Clustering?

Agglomerative clustering is a type of **hierarchical clustering** algorithm that works in a **bottom-up approach**, meaning:

- Each data point starts as its **own individual cluster**.
- Gradually, pairs of clusters are **merged** based on their **similarity** or **distance (like Euclidean, Manhattan, or Cosine similarity)**.
- This process continues until all data points belong to a **single cluster** (or until a desired number of clusters is formed).

It’s commonly used in scenarios where understanding the **hierarchical structure** or relationship between data points is important, such as **gene expression analysis**, **market segmentation**, or **document clustering**.

- **Hierarchical Nature**: Unlike k-means, agglomerative clustering doesn’t require the number of clusters to be pre-defined.
- **Versatility**: It works well with different types of data (numerical, categorical) by choosing appropriate distance metrics.
- **Computational Complexity**: It can be computationally expensive for large datasets because it requires calculating distances between all points/clusters.
- **Interpretability**: The dendrogram makes it easier to understand the structure and relationships in the data.

84) What are Eigenvectors and Eigenvalues?

- Think of eigenvectors as **special directions** or **axes** in your data.
- When you apply a transformation (like rotation or scaling) to data, eigenvectors are the directions that **do not change** during the transformation.
- Instead of changing direction, they only get **stretched** or **compressed** (scaled up or down).

Real-life analogy: Imagine you're holding a rubber band and stretching it in different directions. In some directions, the rubber band doesn't bend, it just gets longer or shorter. Those directions are like eigenvectors.

- Eigenvalues are the **scaling factors** that tell you **how much** an eigenvector is stretched or compressed.
- In other words, they indicate the magnitude (size) of the stretching/compression along the eigenvector.

Real-life analogy: If you're stretching the rubber band along one of its eigenvector directions, the eigenvalue tells you how much longer or shorter the band becomes.

- Eigenvectors are **directions**, and eigenvalues are **magnitudes**.
- Together, they describe how a transformation (like PCA or data rotation) acts on the data.

85) How does PCA works?

Principal Component Analysis (PCA) is a dimensionality reduction technique that transforms high-dimensional data into a lower-dimensional form while preserving as much variance (information) as possible. It starts by **standardizing the data** to ensure all features are on the same scale. Next, the **covariance matrix** is computed to understand how the features vary with respect to each other. Then, **eigenvectors** (directions of maximum variance) and **eigenvalues** (amount of variance explained by each direction) are calculated. The **top eigenvectors** with the largest eigenvalues are selected to form the **principal components**, which capture the most important patterns in the data. Finally, the data is **projected** onto these principal components, reducing the dataset's dimensionality.

For example, imagine a dataset of 1000 students with features like height, weight, and shoe size. PCA could reduce this 3-dimensional dataset into 2 dimensions, keeping the major patterns like overall size and proportions, explaining most of the data's variance while discarding less important variations.

- "We start by standardizing the data."
- "Next, we calculate the covariance matrix to understand the relationships between features."
- "Then, we find the eigenvectors (directions) and eigenvalues (variances) of this matrix."
- "We select the top eigenvectors with the largest eigenvalues to form the principal components."
- "Finally, we project the data onto these components, reducing the dimensionality."

86) How does LDA works?

Linear Discriminant Analysis (LDA) is a dimensionality reduction technique used for supervised learning, particularly when the goal is to **separate classes** in the data. Unlike PCA, which focuses on retaining variance, LDA aims to **maximize the separability between different classes** while reducing the dimensionality of the dataset. It starts by **calculating the mean of each class** and then **computing the within-class and between-class scatter matrices**. These matrices capture the spread of data within each class and the spread between classes, respectively. The next step is to **compute the eigenvectors and eigenvalues** of the scatter matrices, and select the top eigenvectors with the largest eigenvalues, which correspond to the directions that maximize class separability. Finally, the data is **projected onto these eigenvectors**, transforming it into a lower-dimensional space where the classes are more distinguishable.

For example, in a dataset of flower species with features like petal and sepal length, LDA could reduce the dimensionality of the dataset while enhancing the separability of the species, making it easier for classification algorithms to distinguish between them. LDA is particularly useful in **classification tasks** where the goal is to improve the performance of models by reducing overfitting and increasing the computational efficiency while keeping the class separability intact.

- **Standardize the data** to ensure that each feature has a mean of zero and a standard deviation of one.
- **Compute the class means** for each class in the dataset. These are the averages of the feature values for each class.
- **Calculate the within-class scatter matrix** to measure the spread of data points within each class.
- **Calculate the between-class scatter matrix** to measure the spread of the class means from the overall mean of the data.
- **Compute the eigenvectors and eigenvalues** of the scatter matrices. These eigenvectors represent the directions of maximum class separability, and the eigenvalues represent the magnitude of separation.
- **Select the top eigenvectors** with the largest eigenvalues. These eigenvectors define the most significant directions for class separability.
- **Project the data onto these eigenvectors**, reducing the dimensionality while enhancing the distinction between classes.

87) Why did you choose XGBoost over other boosting algorithms?

We chose XGBoost for our customer churn prediction model because of its superior performance on structured/tabular data, faster training time, and its built-in regularization, which helps prevent overfitting. Given that we had a large dataset, the speed and efficiency of XGBoost allowed us to handle it effectively. Additionally, XGBoost's ability to handle missing values and the advanced tree-pruning mechanism made it a great fit for our task.

88) How does XGBoost handle overfitting?

XGBoost handles overfitting through multiple mechanisms:

- **Regularization:** Both L1 and L2 regularization are used to penalize large coefficients, which helps control overfitting.
- **Early Stopping:** XGBoost can stop training when the validation error stops improving, reducing the risk of overfitting.
- **Subsampling and Column Subsampling:** Randomly using subsets of data and features to prevent the model from relying too heavily on any one feature or sample.

89) How XGBoost differs from Gradient Boosting?

- **Regularization:** XGBoost includes **L1** and **L2 regularization** (a key feature that GB does not have), which helps prevent overfitting by penalizing large coefficients.
- **Parallelization:** Unlike traditional gradient boosting, which builds trees sequentially, XGBoost can process trees in parallel, speeding up training time.
- **Handling Missing Data:** XGBoost has an efficient way of handling missing data (it can learn the best direction for missing values during training).
- **Tree Pruning:** XGBoost uses a more sophisticated tree pruning technique, called **max_depth and min_child_weight**, to reduce overfitting and enhance performance.

90) How does XGBoost works?

- **Step 1:** Like GB, start by fitting an initial weak model.
- **Step 2:** Calculate the residuals (errors) from the initial model.
- **Step 3:** Add subsequent trees to minimize the residuals using a **second-order approximation** (this is where the "extreme" part comes in). XGBoost uses **second-order gradients** (i.e., both gradients and Hessians) to make updates, whereas GB only uses first-order gradients.
- **Step 4:** Use the same idea of **additive learning**: Sequentially add trees to reduce the errors of previous trees. But XGBoost does this in a more regularized and efficient manner.

91) What are the key Hyperparameters in XGBoost?

- **Learning Rate (eta):** Similar to GB, controls how much each tree contributes.
- **Number of Trees (n_estimators):** Number of trees to build.
- **Max Depth (max_depth):** Maximum depth of each tree.
- **Subsample and Column Subsample:** To introduce randomness and reduce overfitting.
- **Regularization (alpha and lambda):** L1 (Lasso) and L2 (Ridge) regularization to reduce overfitting.
- **Gamma:** Minimum loss reduction required to make a further partition. It's used to control overfitting.

92) How does Gradient Boosting works?

- **Step 1:** Like GB, start by fitting an initial weak model.
- **Step 2:** Calculate the residuals (errors) from the initial model.
- **Step 3:** Add subsequent trees to minimize the residuals using a second-order approximation (this is where the "extreme" part comes in). XGBoost uses second-order gradients (i.e., both gradients and Hessians) to make updates, whereas GB only uses first-order gradients.
- **Step 4:** Use the same idea of additive learning: Sequentially add trees to reduce the errors of previous trees. But XGBoost does this in a more regularized and efficient manner.

- **Gradient Boosting** builds trees sequentially, where each new tree corrects the errors of the previous trees.
- **Residuals** or errors are used to train each successive tree.
- The aim is to **reduce the overall error** and improve the model's accuracy with each new tree.

93) What are the different columns in the TUI Project?

For predicting why once active and engaged customers in TUI are not actively engaging now, you'd likely focus on identifying behavioral, demographic, and transactional features. These columns could represent various aspects of the customer journey, usage patterns, and engagement metrics. Here's a possible list of columns that could be part of the dataset:

1. Customer Demographics

- **Customer_ID**: Unique identifier for each customer.
- **Age**: Age of the customer.
- **Gender**: Gender of the customer.
- **Location**: Geographical location of the customer (could be region, city, etc.).
- **Subscription_Type**: Type of subscription (e.g., Basic, Premium, Family Plan).
- **Customer_Tenure**: Duration the customer has been with TUI (in months/years).
- **Income_Level**: Income bracket or estimate of the customer (if available).

2. Engagement Data

- **Last_Login_Date**: Date of the last time the customer logged in or accessed the subscription.
- **Average_Session_Duration**: Average time spent on the platform during a session.
- **Interaction_Frequency**: How often the customer interacts with the platform (e.g., monthly, weekly).
- **Content_Viewed**: Types of content the customer typically engages with (e.g., travel packages, promotions, etc.).
- **Clicks_Per_Visit**: Average number of clicks per visit.
- **Views_on_Promotions**: How many times the customer has interacted with promotional content or offers.

3. Customer Activity

- **Booking_Frequency**: How often the customer books a trip or interacts with the booking system.
- **Booking_Value**: Average value of the bookings made by the customer.
- **Booking_Changes**: Frequency of changes or cancellations in bookings.
- **Promotions_Redeemed**: Number of promotional offers or discounts the customer has used.

4. Product Features Usage

- **Mobile_App_Usage**: Whether the customer uses the mobile app to book or interact with services.
- **Website_Usage**: Whether the customer interacts primarily through the website.
- **Subscription_Upgrade_Downgrade**: Whether the customer upgraded or downgraded their subscription level.

5. Behavioral Data

- **Recency**: How recently the customer has engaged with the service.
- **Frequency**: How often the customer engages with TUI's offerings.
- **Monetary**: The total amount spent by the customer over their lifetime with TUI.

6. Customer Support Data

- **Support_Tickets_Raised**: Number of customer support tickets raised by the customer.
- **Customer_Support_Satisfaction**: Satisfaction rating after resolving issues (if available).
- **Complaints**: Number of complaints raised in the last X months (could indicate dissatisfaction).

7. Subscription Data

- **Subscription_Renewal_Status**: Whether the customer renewed their subscription.
- **Subscription_Expiration**: The date their subscription is set to expire or has expired.
- **Subscription_Engagement_Plan**: Specific engagements or goals tied to the customer's subscription.

8. Promotions and Offers

- **Promo_Code_Used**: Whether the customer has used promo codes in the last X months.
- **Discount_Availability**: Whether discounts were available for the customer, and if they engaged with them.

9. Churn Indicators (Target Variable)

- **Inactive_for_X_Days**: Whether the customer has been inactive for a set number of days.
- **Churned**: Whether the customer is considered "churned" or not. This could be derived from their activity over time.

94) Explain the Humerus Fracture Classification Project (Densenet169)?

1. **Input Layer:**
   The model takes X-ray images of the humerus bone as input, typically resized to a fixed dimension like 224x224 pixels.
2. **Convolution Layer (Initial Block):**
   An initial convolutional layer with a small filter (e.g., 7x7) extracts low-level features like edges and textures.
3. **Batch Normalization and ReLU Activation:**
   Batch normalization stabilizes training, and ReLU (Rectified Linear Unit) introduces non-linearity to help the network learn complex patterns.
4. **Pooling Layer (MaxPooling):**
   A pooling layer reduces the spatial dimensions of the image, retaining important features while decreasing computational load.
5. **Dense Blocks (Core of DenseNet):**
   DenseNet169 contains **4 dense blocks**, where each block has multiple convolutional layers. These layers are connected **densely** (all previous layers' outputs are passed as inputs to every subsequent layer), promoting feature reuse and improving gradient flow.
6. **Growth Rate (Feature Expansion):**
   Each layer in the dense block adds a fixed number of new features (growth rate), allowing the network to gradually learn more detailed and diverse patterns.
7. **Transition Layers (Between Dense Blocks):**
   Transition layers with convolution and pooling reduce the feature dimensions between dense blocks to prevent overfitting and control model size.
8. **Global Average Pooling (GAP):**
   Instead of fully connected layers, DenseNet uses GAP to reduce the feature map to a single value per feature, significantly lowering the parameter count and preventing overfitting.
9. **Fully Connected (Classification) Layer:**
   The GAP layer output is fed to a dense (fully connected) layer with softmax activation to predict the probability of each class (e.g., fracture or no fracture).
10. **Loss Function (Cross-Entropy):**
    The model calculates the cross-entropy loss during training to measure the difference between predicted probabilities and actual labels.
11. **Optimization (Backpropagation):**
    The network uses an optimizer like Adam or SGD to update weights by minimizing the loss during backpropagation.
12. **Pre-Trained Weights (Transfer Learning):**
    DenseNet169 is pre-trained on a large dataset like ImageNet, allowing the network to leverage learned features and adapt them to the fracture classification task.
13. **Fine-Tuning:**
    Only the last few layers (classification head) are retrained on the X-ray dataset, while earlier layers remain frozen to retain generalized features.

14. **Evaluation Metrics:**
    The model's performance is evaluated using metrics like accuracy, precision, recall, and F1-score on validation data.
15. **Deployment:**
    Once trained and validated, the model is deployed using platforms like AWS SageMaker for real-time predictions on new X-ray images.

Summary for Interview:
"DenseNet169 works by densely connecting layers in blocks to maximize feature reuse and improve gradient flow. It starts with basic convolution, pooling, and dense blocks, transitions between these blocks using pooling, and finally uses global average pooling and a classification layer to predict fracture or no fracture. We leveraged pre-trained weights for feature extraction and fine-tuned the last layers on our X-ray dataset, achieving a robust and efficient model for deployment."

95) Explain the working of Gradient Descent algorithm?

Gradient Descent (GD) is an optimization algorithm used in machine learning to minimize the **cost function**, which measures the overall error between the model's predictions and the actual values across the entire dataset. Its goal is to find the optimal values of the model's parameters (like weights and biases) that result in the best predictions. Gradient Descent works iteratively by calculating the gradient (or slope) of the cost function with respect to each parameter and updating the parameters in the opposite direction of the gradient to reduce the error. This process continues until the gradient approaches zero, indicating the minimum cost (or loss). GD is crucial for training models like linear regression, logistic regression, and neural networks, ensuring they learn meaningful patterns from data and make accurate predictions.
An **optimizer** in TensorFlow is an algorithm used to minimize the loss function by adjusting the weights of the neural network during training. Common optimizers include **Gradient Descent**, **Adam**, **RMSprop**, etc. Optimizers are crucial for the learning process.
E.g.)
optimizer = tf.keras.optimizers.Adam(learning_rate=0.001)
model.compile(optimizer=optimizer, loss='categorical_crossentropy', metrics=['accuracy'])

96) What is TensorFlow, and how is it different from other machine learning frameworks?

TensorFlow is an open-source machine learning framework developed by Google that is widely used for deep learning tasks. It provides an ecosystem for developing, training, and deploying machine learning models. TensorFlow uses data flow graphs to represent computations, where nodes represent mathematical operations and edges represent data (tensors).
Differences from other ML frameworks:

- **PyTorch:** Unlike TensorFlow, which uses static computation graphs (TensorFlow 1.x), PyTorch is dynamic, making it more flexible and easier to debug.
- **Keras:** Keras is a high-level API that runs on top of TensorFlow, making it easier to build neural networks. Keras focuses on simplicity, while TensorFlow provides more flexibility and scalability.

97) Explain ARIMA model in detail?

The **ARIMA** model stands for **Autoregressive Integrated Moving Average**. It is one of the most popular models for **time series forecasting**, especially for univariate data. Let's break it down step-by-step to understand its components and concepts.

1. Components of ARIMA

ARIMA is composed of three main parts:

A: Autoregressive (AR)

- **What it means**: AR uses the relationship between a data point and its previous values (lags).
- **Example**: Predicting today's stock price based on the prices from the last 3 days.

I: Integrated

- **What it means**: Differencing the data to make it stationary (remove trends).
- **Example**: If the original series is Yt=[10,12,15,20] Y_t = [10, 12, 15, 20] Yt=[10,12,15,20], first-order differencing gives:
  Yt′=[2,3,5] Y_t' = [2, 3, 5]Yt′=[2,3,5], where Yt′=Yt−Yt−1Y_t' = Y_t - Y_{t-1}Yt′=Yt−Yt−1.
- **Why it's needed**: Many time series are non-stationary, so differencing helps stabilize the mean.

MA: Moving Average

- **What it means**: MA uses past forecast errors to improve the current prediction.
- **Example**: If yesterday's forecast underestimated by 5 units, today's forecast can adjust for that.

2. How ARIMA Works

ARIMA combines AR, I, and MA components to model a time series:

1. **Autoregression (AR):** Uses lagged values to predict the current value.
2. **Differencing (I):** Makes the data stationary.
3. **Moving Average (MA):** Adjusts predictions using past errors.

3. ARIMA Hyperparameters (p, d, q)

- p: Number of AR terms (lags).
- d: Number of differences needed to make the series stationary.
- q: Number of MA terms (errors).

How to determine (p, d, q):

- p: Use the **Partial Autocorrelation Function (PACF)** plot to identify the significant lags.
- d: Check stationarity using **ADF test** or observe differencing results.
- q: Use the **Autocorrelation Function (ACF)** plot to find significant error terms.

4. When to Use ARIMA

- When your data is **univariate** (a single time series).
- When there is **no strong seasonality** (otherwise, use SARIMA).
- When patterns are **linear** and predictable.

A **univariate time series** means that the dataset contains **only one variable** (or feature) being observed or measured over time. Each data point in the series represents the value of this single variable at a specific point in time. Example, imagine you're tracking daily temperatures in a city. The temperature is the only variable being recorded.

The **ARIMA model** predicts **future values** of a time series based on its **past values** (autoregression), **past errors** (moving average), and by transforming the data to remove trends or seasonality (integration). Essentially, it forecasts what the next value(s) in the time series will be, given the observed historical data.

98) Explain SARIMA model in detail?

SARIMA (Seasonal AutoRegressive Integrated Moving Average) is an extension of the ARIMA model that incorporates **seasonality** into the forecasting process. It is used when the time series data exhibits clear **seasonal patterns** that repeat at regular intervals, such as daily, monthly, or yearly cycles.

When is SARIMA Used?

SARIMA is used when:

- The data has **seasonal patterns**, like sales increasing during holidays or website traffic spiking every weekend.
- ARIMA is insufficient because it cannot capture these repeating patterns.

Example:

- Monthly sales data of a store showing spikes every December due to holiday shopping.
- SARIMA will model this **seasonal behavior** in addition to trends and other patterns in the data.

Working Principle of SARIMA

SARIMA extends ARIMA by adding **seasonal components** to handle periodic patterns. It works through these steps:

1. **Seasonal Differencing (S):** Removes seasonal trends by differencing data at the seasonal lag.
    - Example: If sales spike every 12 months, subtract the value from 12 months ago to remove the seasonal effect.
2. **Seasonal AR (P):** Uses past seasonal values to predict future seasonal behavior.
    - Example: Sales in December this year are likely influenced by sales in December of previous years.
3. **Seasonal MA (Q):** Accounts for past seasonal forecasting errors.
    - Example: Adjusting December sales predictions based on how accurate last December's predictions were.
4. **Seasonal Integration (D):** Makes seasonal data stationary by applying differencing at the seasonal level.

The SARIMA model is represented as:

SARIMA(p, d, q)(P, D, Q, s)

Where:

- **p, d, q:** Non-seasonal ARIMA parameters.
- **P, D, Q:** Seasonal ARIMA parameters.
- **s:** Seasonal period (e.g., 12 for monthly data with yearly seasonality).

Key Intuition:

SARIMA applies **seasonality-aware modeling** for the entire dataset, not just one month. It identifies and uses patterns for each time step (month, day, etc.) based on the defined seasonal period (s). The **seasonal period (s)** is defined based on the frequency at which a **seasonal pattern repeats** in your time series data. It depends on the time intervals in your dataset and how often the same pattern is observed.

99) What Are ACF and PACF Plots?

1. ACF (Autocorrelation Function) Plot:

- Represents: The correlation between a time series and its lagged values.
- Purpose: Shows how current values are related to past values over different time lags.
- Key Idea: It measures the strength and direction of the relationship between a time series and its past observations.

2. PACF (Partial Autocorrelation Function) Plot:

- Represents: The correlation between a time series and its lagged values, after removing the effects of intermediate lags.
- Purpose: Identifies the direct impact of a lagged observation on the current value without being influenced by correlations from shorter lags.

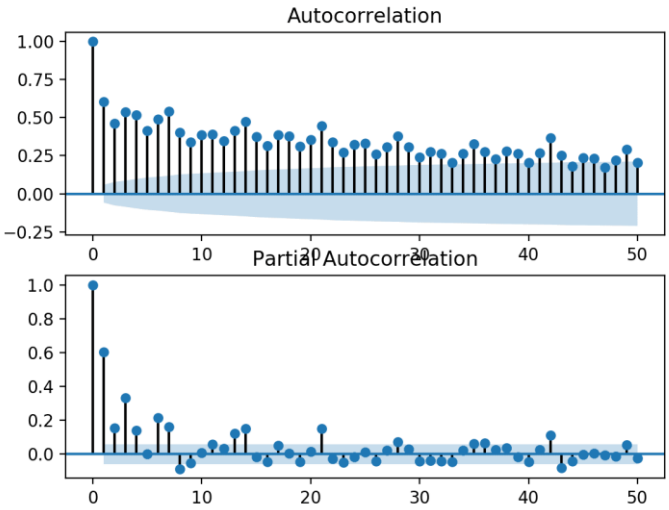
Uses of ACF and PACF Plots

⇒ Model Selection in ARIMA:
  - ACF helps identify the order of MA (q) terms.
  - PACF helps identify the order of AR (p) terms.

⇒ Understand Data Dependencies:
  - Detect whether the data is autocorrelated or has seasonal patterns.
  - Diagnose stationarity (ACF diminishes quickly for stationary data).

⇒ Seasonality Detection:
  - Peaks at seasonal lags (e.g., 12 for monthly data with yearly seasonality).

100) How do you interpret the following ACF, PACF plot?



1. **ACF Plot (Autocorrelation):**
   - The ACF plot does not exhibit a sharp cut-off at any specific lag.
   - Instead, the ACF gradually decreases over time, which suggests non-stationarity in the data.
   - Gradual decay is often a sign that differencing might be required.
2. **PACF Plot (Partial Autocorrelation):**
   - The PACF plot shows a significant spike at lag 1 followed by no significant spikes after that. This indicates that there may be an AR(1) component in the data.

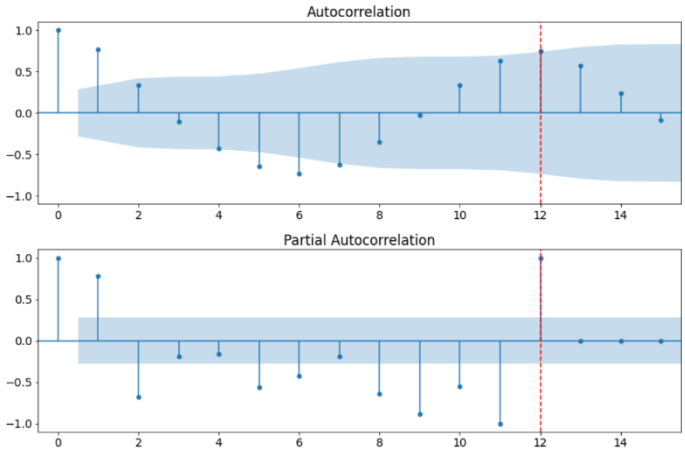
Determining the Orders (p and q):

- For AR (p): Based on the PACF plot, since there is one significant spike at lag 1, the order of p = 1.
- For MA (q): Since the ACF does not show a sharp cut-off and gradually decreases, the MA component isn't clearly determined. However, after differencing to make the data stationary, you can re-evaluate the ACF to determine q.

ACF Plot and Non-Stationarity:

- When the ACF plot has no significant cutoff and instead decays gradually (or very slowly) over lags, it often indicates non-stationarity in the data. This behavior occurs because the data has trends or seasonality that cause high correlations across lags.
- In such cases, differencing (or other transformations) is needed to remove the trend or seasonality and make the data stationary.

To pick the cutoff in ACF and PACF plots, look for the **last lag** where a spike lies **outside the blue confidence bands** (positive or negative). For ACF, this cutoff identifies the order of **MA (q)**, while for PACF, it identifies the order of **AR (p)**. If no clear cutoff is visible and the spikes decay slowly, the data might be non-stationary and need differencing.



In the above plot, the ACF (top plot) shows significant spikes at lags 1, 2, and so on, with a slow decay, indicating possible non-stationarity in the data. The PACF (bottom plot) has a clear significant spike at lag 1 and quickly drops within the confidence interval after lag 1. This suggests an AR(1) process is a good starting point. However, due to the slow decay in the ACF, you might need to difference the data to make it stationary before finalizing the ARIMA model parameters.

In summary, **ACF and PACF plots** are essential tools in deciding the parameters for the ARIMA formula. Once these parameters are identified, they are plugged into the formula, and the model is trained to predict future values.

101) What is a Tensor in TensorFlow?

A **Tensor** is the fundamental building block in TensorFlow. It is a multi-dimensional array or matrix that represents data in the form of n-dimensional arrays (rank-0 tensors are scalars, rank-1 tensors are vectors, rank-2 tensors are matrices, etc.). Tensors flow through TensorFlow operations, which is why it's named TensorFlow.

102) Detailed Theory – 1:

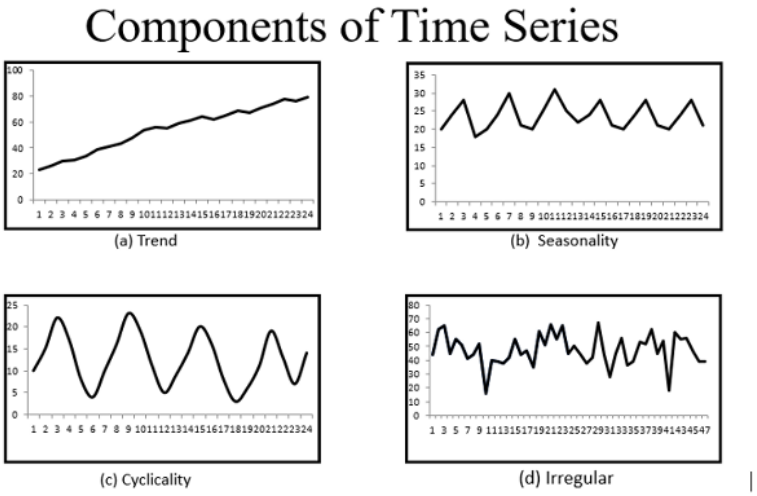
TIME SERIES ANALYSIS:

Time Series Analysis is a method of analyzing data points collected or recorded at specific time intervals, often sequentially. The goal is to identify trends, patterns, and seasonal variations in the data

over time. Unlike other data analyses, it accounts for the temporal structure, meaning that the order of the data matters. Time series analysis is widely used in forecasting (e.g., stock prices, weather predictions, sales forecasting) and anomaly detection (e.g., fraud detection, network monitoring). It is essential because many real-world phenomena are time-dependent, and understanding their temporal behavior helps in making informed decisions and predictions.

Components of Time Series Analysis:

1. **Trend**: The long-term movement in the data, either upward, downward, or stagnant. For example, a steady increase in a company's sales over the years represents a trend.
2. **Seasonality**: Regular, repeating patterns over fixed intervals, like increased ice cream sales in summer or holiday shopping spikes in December.
3. **Cyclic Patterns**: Fluctuations that occur over irregular intervals, often tied to economic cycles, such as booms and recessions.
4. **Irregular/Residual Component**: Random, unpredictable variations in the data that cannot be attributed to trends, seasonality, or cycles.



Stationarity:

Stationarity in time series refers to a property where the statistical characteristics of the data (mean, variance, and autocorrelation) remain constant over time. A stationary time series does not exhibit trends, seasonal effects, or changing variances.

Why It Matters: Stationarity is crucial for time series modeling, as many analytical methods (like ARIMA) assume the data is stationary. If a series is non-stationary, transformations like differencing or detrending are often applied to make it stationary before modeling. Testing for stationarity is a critical step in analyzing and modeling time series data. Here are some commonly used tests to check stationarity:

1. Augmented Dickey-Fuller (ADF) Test

The ADF test checks for the presence of a unit root in a series. If a unit root is present, the series is non-stationary.

Steps in ADF Test:

- Null Hypothesis (H0): The series has a unit root (non-stationary).
- Alternate Hypothesis (H1): The series is stationary.
- If the p-value is less than 0.05, reject the null hypothesis, meaning the series is stationary.
- If the p-value is greater than 0.05, the series is non-stationary.

2. KPSS (Kwiatkowski-Phillips-Schmidt-Shin) Test

The KPSS test is another method to check stationarity. It complements the ADF test.

Steps in KPSS Test:

- Null Hypothesis (H0): The series is stationary.
- Alternate Hypothesis (H1): The series is not stationary.
- A p-value greater than 0.05 means the series is stationary.
- A p-value less than 0.05 means the series is non-stationary.

3. Rolling Statistics

A simple visual method to check stationarity involves plotting the rolling mean and standard deviation of the series over time.

- If the rolling mean and standard deviation are roughly constant over time, the series is stationary.
- If they vary significantly, the series is non-stationary.

A Simple Analogy:

Imagine you're on a treadmill. If you're walking steadily at the same speed (stationary), things are predictable. But if your speed changes unpredictably or you're running uphill (non-stationary), things become harder to manage. Stationarity tests figure out whether you're walking calmly or if the treadmill has unexpected changes.

Removing Non-stationarity from the data:

To remove non-stationarity from a time series, several techniques can be applied. **Differencing** is the most common, where you subtract each value from its previous value to remove trends; if needed, second-order differencing can be applied. **Log Transformation** reduces the magnitude of large values and stabilizes variance by taking the natural logarithm of the data. **Seasonal Differencing** removes seasonality by subtracting values from their counterparts in the previous season (e.g., t minus t-season_length). **Detrending** eliminates trends by fitting a line (like linear regression) and subtracting it from the series. Power transformations like **Square Root** or **Box-Cox** can further stabilize variance. After applying these techniques, recheck stationarity using tests like ADF or KPSS, and proceed to build models such as ARIMA or SARIMA.

Once your time series data is stationary, the next step is to apply **time series forecasting models**. These models use the historical patterns (trend, seasonality, and noise) to predict future values. The choice of the model depends on the nature of the data and the goal of your analysis.

102) Difference between White Noise and Random Walk?

⇒ **White Noise**: Constant mean, constant variance, no correlation. It **is** random, but it follows specific statistical properties.

⇒ **Random Walk**: A series where the next value depends on the previous value, and it usually results in non-stationary behavior with trends over time.