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"matplotlib.pyplot and seaborn are used for visualization.\n",
"%matplotlib inline ensures that plots are displayed within the notebook.\n",
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    "import numpy as np\n",
    "import matplotlib.pyplot as plt\n",
    "import seaborn as sns\n",
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"# Set matplotlib to display inline\n",
"$matplotlib inline\n"
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"Load your dataset and handle any potential file loading errors.\n",
"\m"
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"Dataset loaded successfully\n"

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"# Load the dataset\n",

"try:\n",

" of = pd.read_csv('Healthcare Providers.csv')\n",

" print(\"Dataset loaded successfully\")\n",

"except FileNotEoundError:\n",

" print(\"Error: File not found. Please check the file path.\")\n",

"# Step 2: Subset the Data (first 30 rows)\n",

"df_subset = df.head(30)"
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"Display basic information about the dataset to understand its structure.\n",
"df.info() provides information about the dataset, including column names, non-null counts, and data types.\n",
"df.head() displays the first few rows of the dataset to give a preview of the data.\n"
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Last Name/Organization Name of the Provider
First Name of the Provider
Middle Initial of the Provider
Credentials of the Provider
Gender of the Provider
Entity Type of the Provider
Street Address 1 of the Provider
Street Address 2 of the Provider
City of the Provider
Zip Code of the Provider
State Code of the Provider
Country Code of the Provider
Provider Type
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                               MCPCS Drug Indicator
Number of Services
Number of Medicare Beneficiaries
                               Number of Distinct Medicare Beneficiary/Per Day Services
Average Medicare Allowed Amount
Average Submitted Charge Amount
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" 25 Average Medicare Payment Amount
" 26 Average Medicare Standardized Amount
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20 WASHINGTON AVE STE 212 \\n",
5746 N BROADWAY ST NAN \\n",
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                                                                CS Code

HCPCS Description

\n",
99223 Initial hospital inpatient care, typically 70 ... \n",
GG202 Screening mammography, bilateral (2-view study... \n",
99348 Established patient home visit, typically 25 m... \n",
81002 Urinalysis, manual test \n",
96372 Injection beneath the skin or into muscle for ... \n",
                                   HCPCS Drug Indicator Number of Services Number of Medicare Beneficiaries \n,
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"Greek and handle any missing values in the dataset.\n",
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"df.dropna() removes rows with missing values. You might choose to fill missing values instead depending on the dataset.\n",
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"This step selects numerical columns and plots their distributions using histograms and KDE plots.\n"
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   "numerical features - ...
"\n",
"if numerical features:\n",
" for feature in numerical features:\n",
" plt.figure(figsize=(10, 6))\n",
" sns.histplot(df[feature], kde=True)\n",
" plt.title(f'Distribution of (feature)')\n",
" plt.xlabel(feature)\n",
" plt.ylabel(feature)\n",
" plt.show()\n",
"else:\n",
""else:\n",
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"This step selects categorical columns and plots their value counts.\n"

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"\n".
     "categorical_features = dr_subset.serec_ac_per...
"\n",
"# Step 4: Plot Count Plots for Selected Categorical Features\n",
"if categorical_features:\n",
" for feature in categorical features:\n",
" plt.figure(figsize=(l0, 6))\n",
" sns.countplot(y=df_subset[feature], order=df_subset[feature].value_counts().index)\n",
    plt.title(f'Count Plot of (feature)')\n",
" plt.xlabel('Count')\n",
" plt.xlabel(feature)\n",
" plt.ylabel(feature)\n",
" plt.show()\n",
"else:\n",
                print(\"No categorical features found in the dataset.\")"
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"if numerical features:\n",
" plt.figure(figsize=(12, 7))\n",
" correlation_matrix = df[numerical_features].corr()\n",
" sns.heatmap(correlation matrix, annot=True, cmap='coolwarm', linewidths=0.2)\n",
" plt.fitle('Correlation Matrix')\n",
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"# Pairplot to visualize relationships between numerical features\n",
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" sns.pairplot(df[numerical features])\n",
" plt.title('Pairplot of Numerical Features')\n",
" plt.show()\n",
"else:\n",
" print(\"Not enough numerical features for pairplot.\")\n"
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"if 'feature1' in df.columns and 'feature2' in df.columns:\n",
" plt.figure(figsize=(10, 6))\n",
" sns.scatterplot(x='feature1', y='feature2', data=df)\n",
" plt.xilele'(scatter Plot of feature1 vs feature2')\n",
" plt.xlabel('feature1')\n",
" plt.xlabel('feature2')\n",
" plt.show()\n",
"else:\\n",
" print(\"Scatter plot features 'feature1' and 'feature2' not found in the dataset.\")\n"
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