EDA

November 17, 2025

1 EDA

[2]:
```python
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import sys, os
sys.path.append(os.path.abspath(".."))

from src.EDA import plot_feat_histogram, skew_kurtosis
```

Starting with the essentials: pandas for data manipulation, matplotlib and seaborn for visualization. We'll also define a custom histogram function early on since we'll need it multiple times to explore feature distributions and check for skewness.

1.1 Load the dataset

[3]:
```python
df = pd.read_csv('../data/unprocessed/compas-scores-two-years.csv')
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7214 entries, 0 to 7213
Data columns (total 53 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   id                       7214 non-null   int64
 1   name                     7214 non-null   object
 2   first                    7214 non-null   object
 3   last                     7214 non-null   object
 4   compas_screening_date    7214 non-null   object
 5   sex                      7214 non-null   object
 6   dob                      7214 non-null   object
 7   age                      7214 non-null   int64
 8   age_cat                  7214 non-null   object
 9   race                     7214 non-null   object
 10  juv_fel_count            7214 non-null   int64
 11  decile_score             7214 non-null   int64
 12  juv_misd_count           7214 non-null   int64
 13  juv_other_count          7214 non-null   int64
 14  priors_count             7214 non-null   int64
```

```
 15  days_b_screening_arrest  6907 non-null   float64
 16  c_jail_in                6907 non-null   object
 17  c_jail_out               6907 non-null   object
 18  c_case_number            7192 non-null   object
 19  c_offense_date           6055 non-null   object
 20  c_arrest_date            1137 non-null   object
 21  c_days_from_compas       7192 non-null   float64
 22  c_charge_degree          7214 non-null   object
 23  c_charge_desc            7185 non-null   object
 24  is_recid                 7214 non-null   int64
 25  r_case_number            3471 non-null   object
 26  r_charge_degree          3471 non-null   object
 27  r_days_from_arrest       2316 non-null   float64
 28  r_offense_date           3471 non-null   object
 29  r_charge_desc            3413 non-null   object
 30  r_jail_in                2316 non-null   object
 31  r_jail_out               2316 non-null   object
 32  violent_recid            0 non-null      float64
 33  is_violent_recid         7214 non-null   int64
 34  vr_case_number           819 non-null    object
 35  vr_charge_degree         819 non-null    object
 36  vr_offense_date          819 non-null    object
 37  vr_charge_desc           819 non-null    object
 38  type_of_assessment       7214 non-null   object
 39  decile_score.1           7214 non-null   int64
 40  score_text               7214 non-null   object
 41  screening_date           7214 non-null   object
 42  v_type_of_assessment     7214 non-null   object
 43  v_decile_score           7214 non-null   int64
 44  v_score_text             7214 non-null   object
 45  v_screening_date         7214 non-null   object
 46  in_custody               6978 non-null   object
 47  out_custody              6978 non-null   object
 48  priors_count.1           7214 non-null   int64
 49  start                    7214 non-null   int64
 50  end                      7214 non-null   int64
 51  event                    7214 non-null   int64
 52  two_year_recid           7214 non-null   int64
dtypes: float64(4), int64(16), object(33)
memory usage: 2.9+ MB
```

Loading the raw COMPAS dataset from ProPublica. This contains information about defendants from Broward County, Florida, including their criminal history, demographics, and whether they recidivated. Let's check the structure and see what we're working with.

[4]:
```
df = df[[
    "juv_fel_count", "juv_misd_count",
    "c_charge_degree", "race", "age_cat", "sex",
```

```python
    "priors_count", "days_b_screening_arrest",
    "is_recid", "c_jail_in", "c_jail_out"
]]

# Apply filters one by one
df = df[df["days_b_screening_arrest"] <= 30]
df = df[df["days_b_screening_arrest"] >= -30]
df = df[df["is_recid"] != -1]
df = df[df["c_charge_degree"] != "O"]

# Added a new feature for jail days
df["c_jail_in"] = pd.to_datetime(df["c_jail_in"])
df["c_jail_out"] = pd.to_datetime(df["c_jail_out"])
df["jail_days"] = (df["c_jail_out"] - df["c_jail_in"]).dt.days
df.drop(columns=["c_jail_in", "c_jail_out"], inplace=True)

print(f'df has shape: {df.shape} after filtering')
```

```
df has shape: (6172, 10) after filtering
```

First comes the critical data cleaning step. Following ProPublica's methodology, we apply strict filters to ensure data quality: only cases where screening happened within 30 days of arrest, removing invalid recidivism flags (-1), and excluding minor traffic offenses that wouldn't result in jail time. We also select only the features relevant for our prediction task. These filters are not arbitrary, they're based on the original ProPublica analysis to ensure we're working with reliable, comparable data.

Now, let's begin to inspect some of the remaining data:

1.2 Missing values

[5]:
```python
missing_vals = {}

for cols in df.columns:
    missing_count = df[cols].isnull().sum()
    if missing_count > 0:
        missing_vals[cols] = missing_count

missing_vals
```

[5]:
```
{}
```

Checking for missing values is essential before modeling. Missing data can introduce bias or cause errors during training. If we find any nulls, we'll need to decide whether to impute, drop, or handle them in some other way. An empty dictionary here is good news, it means our filtered data is complete.

1.3 Duplicates

Duplicate rows can artificially inflate patterns and lead to overfitting. Our model might memorize repeated instances rather than learning generalizable patterns. Even a few duplicates can skew results in ways that aren't immediately obvious, so it's important to identify them early.

[6]:
```python
duplicates = df.duplicated().sum()
print(f'The number of duplicate rows in the dataset is: {duplicates}')
```

```
The number of duplicate rows in the dataset is: 2236
```

Duplicates in the COMPAS dataset should not be removed because they are not true duplicates, they represent multiple legitimate assessments for the same individual, often tied to different charges, cases, or parallel risk evaluations. Dropping them would remove real historical records, distort class balance, and reduce the amount of training data, ultimately harming the model's ability to learn meaningful patterns. Retaining these rows preserves the dataset's real-world structure and ensures the model reflects the full assessment history of each person.

1.4 Skewness and Kurtosis of Numerical Features

Understanding the distribution shape of numerical features helps us make informed decisions about transformations. Highly skewed features (especially with high kurtosis) can cause problems for models that assume normality or are sensitive to outliers. Features with extreme skewness might benefit from log transforms, binning, or other preprocessing techniques to improve model performance.

[7]:
```python
for feat in df.select_dtypes(include=['int64', 'float64']).columns:
    print("---")
    skew_kurtosis(df, feat)
```

```
---
Feature: juv_fel_count
 skewness: 19.65
 kurtosis: 644.80
 The feature is positively skewed with high kurtosis.
---
Feature: juv_misd_count
 skewness: 10.93
 kurtosis: 186.13
 The feature is positively skewed with high kurtosis.
---
Feature: priors_count
 skewness: 2.41
 kurtosis: 7.06
 The feature is positively skewed with high kurtosis.
---
Feature: days_b_screening_arrest
 skewness: -2.14
 kurtosis: 16.49
 The feature does NOT exhibit strong positive skewness and high kurtosis.
---
```

```
Feature: is_recid
 skewness: 0.06
 kurtosis: -2.00
 The feature does NOT exhibit strong positive skewness and high kurtosis.
---
Feature: jail_days
 skewness: 6.55
 kurtosis: 60.32
 The feature is positively skewed with high kurtosis.
```

To those features that are positively skewed with high kurtosis, we will later use StandardScaler to standardize the values so regression and distance based models are not impacted by the different scales of values

[8]:
```
df['days_b_screening_arrest'] = df['days_b_screening_arrest'].clip(lower=0)
```

A small but important adjustment: clipping negative values in `days_b_screening_arrest` to zero. Negative values mean the screening happened before the arrest, which doesn't make logical sense for our purposes, so we normalize these edge cases.

[9]:
```
df.head()
```

[9]:
```
   juv_fel_count  juv_misd_count c_charge_degree              race  \
0              0               0               F             Other
1              0               0               F  African-American
2              0               0               F  African-American
5              0               0               M             Other
6              0               0               F         Caucasian

           age_cat   sex  priors_count  days_b_screening_arrest  is_recid  \
0  Greater than 45  Male             0                      0.0         0
1          25 - 45  Male             0                      0.0         1
2     Less than 25  Male             4                      0.0         1
5          25 - 45  Male             0                      0.0         0
6          25 - 45  Male            14                      0.0         1

   jail_days
0          0
1         10
2          1
5          1
6          6
```

Quick sanity check. Let's preview the first few rows to make sure our filtering worked as expected and the data looks reasonable.

[10]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 6172 entries, 0 to 7213
```

```
Data columns (total 10 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   juv_fel_count            6172 non-null   int64
 1   juv_misd_count           6172 non-null   int64
 2   c_charge_degree          6172 non-null   object
 3   race                     6172 non-null   object
 4   age_cat                  6172 non-null   object
 5   sex                      6172 non-null   object
 6   priors_count             6172 non-null   int64
 7   days_b_screening_arrest  6172 non-null   float64
 8   is_recid                 6172 non-null   int64
 9   jail_days                6172 non-null   int64
dtypes: float64(1), int64(5), object(4)
memory usage: 530.4+ KB
```

1.5 Convert data types

All datatypes seems correct and appropiate. Hence, there's no need for conversion

1.6 Data Analysis (EDA)

[11]:
```
df["age_cat"].value_counts().sort_index()
```

[11]:
```
age_cat
25 - 45            3532
Greater than 45    1293
Less than 25       1347
Name: count, dtype: int64
```

Time to explore the data! Let's start by understanding the demographic and criminal history distributions. Age categories first are we dealing mostly with young offenders or an older population? This matters because age is often correlated with recidivism risk.

[12]:
```
df["race"].value_counts().sort_index
```

[12]:
```
<bound method Series.sort_index of race
African-American    3175
Caucasian           2103
Hispanic             509
Other                343
Asian                 31
Native American       11
Name: count, dtype: int64>
```

[13]:
```
race_counts = df["race"].value_counts()
for race in race_counts.index:
        percentage = (race_counts[race] / df.shape[0] * 100)
```

```
        print(f"{race} defendants: {percentage:.2f}%")
```

```
African-American defendants: 51.44%
Caucasian defendants: 34.07%
Hispanic defendants: 8.25%
Other defendants: 5.56%
Asian defendants: 0.50%
Native American defendants: 0.18%
```

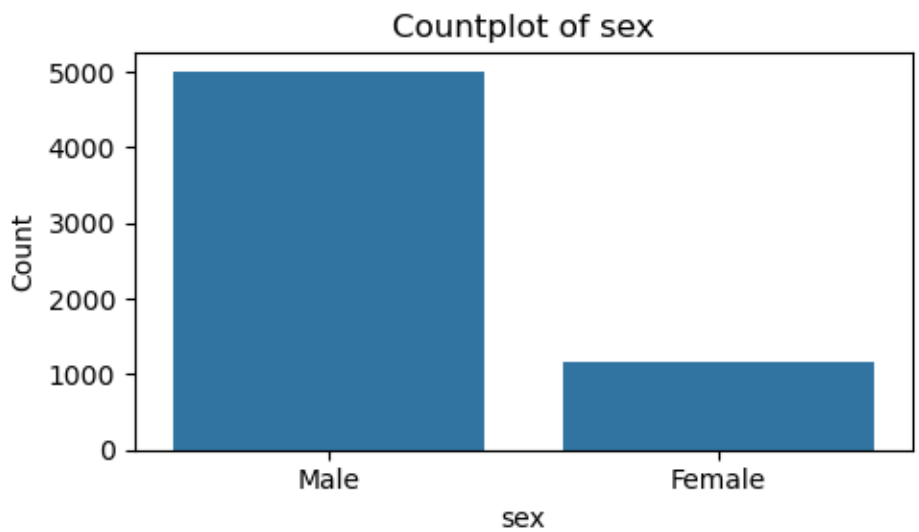
Understanding racial composition is crucial for this dataset. The COMPAS algorithm has been controversial partly due to concerns about racial bias, so we need to know the demographic breakdown. Calculating percentages gives us a clearer picture than raw counts.

[14]:
```
df["sex"].value_counts().sort_index()
```

[14]:
```
sex
Female    1175
Male      4997
Name: count, dtype: int64
```

[15]:
```
gender_counts = df["sex"].value_counts()
for gender in gender_counts.index:
        percentage = (gender_counts[gender] / df.shape[0] * 100)
        print(f"{gender} defendants: {percentage:.2f}%")

plt.figure(figsize=(5, 3))
sns.countplot(x="sex", data=df)
plt.title("Countplot of sex")
plt.xlabel("sex")
plt.ylabel("Count")
plt.tight_layout()
plt.show()
```

```
Male defendants: 80.96%
Female defendants: 19.04%
```



Gender distribution is another demographic factor to examine. Criminal justice data typically shows strong gender imbalances, with males being overrepresented. Let's visualize this to confirm the pattern in our dataset.

[16]:
```
pd.crosstab(df["sex"], df["race"])
```

[16]:

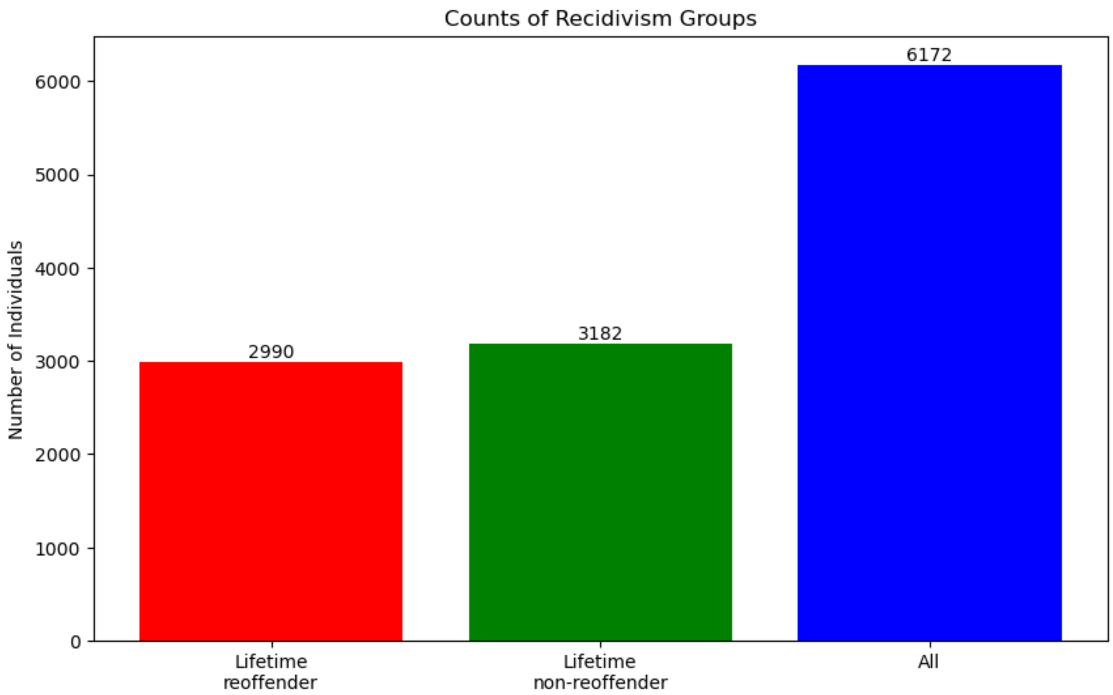
race	African-American	Asian	Caucasian	Hispanic	Native American	Other
sex						
Female	549	2	482	82	2	58
Male	2626	29	1621	427	9	285

A crosstab helps us see the intersection of gender and race—understanding these demographic intersections can reveal important patterns or potential biases in the data.

[17]:
```
reoff_lifetime = df[df["is_recid"] == 1]
no_reoff_lifetime = df[df["is_recid"] == 0]
```

[18]:
```
counts = {
    "Lifetime\nreoffender": len(reoff_lifetime),
    "Lifetime\nnon-reoffender": len(no_reoff_lifetime),
    "All": len(df)
}

plt.figure(figsize=(10, 6))
plt.bar(counts.keys(), counts.values(), color=["red", "green", "blue",␣
 ↪"orange", "purple"])

plt.title("Counts of Recidivism Groups")
plt.ylabel("Number of Individuals")
```

```
plt.xticks(rotation=0)

for i, v in enumerate(counts.values()):
    plt.text(i, v + 50, str(v), ha='center', fontsize=10)

plt.show()
```

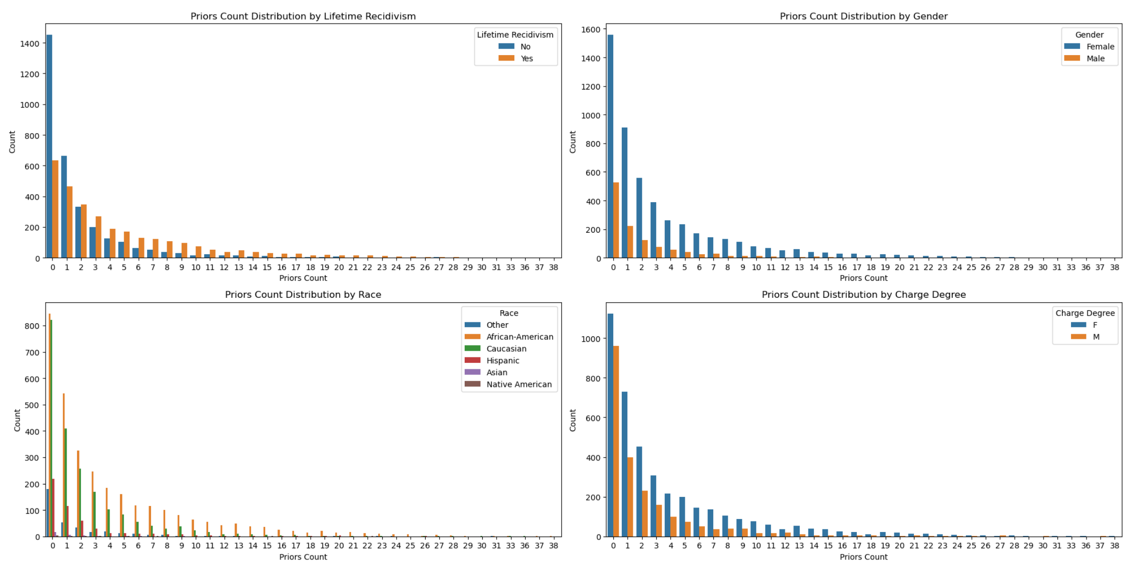


Now for the key question: what's our class balance? Splitting the dataset into recidivists and non-recidivists tells us how imbalanced our target variable is. This will heavily influence our modeling approach if one class dominates, we'll need special techniques to avoid a model that just predicts the majority class.

Prior convictions are one of the strongest predictors of recidivism. Let's create a comprehensive view showing how `priors_count` relates to recidivism, and how it's distributed across gender, race, and charge degree. These multi-dimensional views help us understand if certain groups have systematically different criminal histories, which could indicate bias or real underlying patterns we need to account for.

[19]:
```
fig, axes = plt.subplots(2, 2, figsize=(20, 10))
axes = axes.flatten()

sns.countplot(data=df, x="priors_count", hue="is_recid", ax=axes[0])
axes[0].set_title("Priors Count Distribution by Lifetime Recidivism")
axes[0].set_xlabel("Priors Count")
axes[0].set_ylabel("Count")
```

```
axes[0].legend(title="Lifetime Recidivism", labels=["No", "Yes"])

sns.countplot(data=df, x="priors_count", hue="sex", ax=axes[1])
axes[1].set_title("Priors Count Distribution by Gender")
axes[1].set_xlabel("Priors Count")
axes[1].set_ylabel("Count")
axes[1].legend(title="Gender", labels=["Female", "Male"])

sns.countplot(data=df, x="priors_count", hue="race", ax=axes[2])
axes[2].set_title("Priors Count Distribution by Race")
axes[2].set_xlabel("Priors Count")
axes[2].set_ylabel("Count")
axes[2].legend(title="Race")

sns.countplot(data=df, x="priors_count", hue="c_charge_degree", ax=axes[3])
axes[3].set_title("Priors Count Distribution by Charge Degree")
axes[3].set_xlabel("Priors Count")
axes[3].set_ylabel("Count")
axes[3].legend(title="Charge Degree")


plt.tight_layout()
plt.show()
```



Across all demographic and case-related groups, the distribution of prior offenses is highly right-skewed, with the majority of individuals having 0–2 prior offenses and a long tail extending toward higher prior counts.

Recidivists consistently show higher prior counts than non-recidivists, reinforcing the strong relationship between criminal history and risk of reoffending. Males tend to have more priors than females, and racial groups show distinct patterns, with African-American individuals exhibiting a heavier concentration in higher prior categories. Charge degree (felony vs misdemeanor) also correlates with prior count, as felony cases tend to involve individuals with more extensive histories.

Overall, these distributions confirm that priors_count is a highly informative predictive feature, but also one that reflects structural differences across groups—important to consider when evaluating fairness.

Before we engineer more complex features, let's encode our categorical variables. Using one-hot encoding with `drop_first=True` converts categories like race, sex, and age into binary columns while avoiding multicollinearity (the dummy variable trap). This encoded dataset will serve as our baseline for modeling and help us visualize correlations between all features.

[20]:
```python
# One-hot encode categorical features
df_encoded = df.copy()

# Convert categorical features to category dtype for proper encoding
categorical_cols = ['c_charge_degree', 'race', 'age_cat', 'sex',␣
↪'priors_category', 'jail_time_category']
for col in categorical_cols:
    if col in df_encoded.columns:
        df_encoded[col] = df_encoded[col].astype(str)

# Apply one-hot encoding with drop_first=True to avoid multicollinearity
df_encoded = pd.get_dummies(df_encoded, drop_first=True, dtype=int)

print(f"Encoded dataset shape: {df_encoded.shape}")
print(f"\nColumn names after encoding:")
print(df_encoded.columns.tolist())
print(f"\nFeature count: {len(df_encoded.columns)}")

df_encoded.head()
```

```
Encoded dataset shape: (6172, 15)

Column names after encoding:
['juv_fel_count', 'juv_misd_count', 'priors_count', 'days_b_screening_arrest',
'is_recid', 'jail_days', 'c_charge_degree_M', 'race_Asian', 'race_Caucasian',
'race_Hispanic', 'race_Native American', 'race_Other', 'age_cat_Greater than
45', 'age_cat_Less than 25', 'sex_Male']

Feature count: 15
```

[20]:
```
   juv_fel_count  juv_misd_count  priors_count  days_b_screening_arrest  \
0              0               0             0                      0.0
1              0               0             0                      0.0
2              0               0             4                      0.0
5              0               0             0                      0.0
```

```
6              0                0            14                        0.0

   is_recid  jail_days  c_charge_degree_M  race_Asian  race_Caucasian  \
0         0          0                  0           0               0
1         1         10                  0           0               0
2         1          1                  0           0               0
5         0          1                  1           0               0
6         1          6                  0           0               1

   race_Hispanic  race_Native American  race_Other  age_cat_Greater than 45  \
0              0                     0           1                        1
1              0                     0           0                        0
2              0                     0           0                        0
5              0                     0           1                        0
6              0                     0           0                        0

   age_cat_Less than 25  sex_Male
0                     0         1
1                     0         1
2                     1         1
5                     0         1
6                     0         1
```

1.7 Feature Engineering

[21]:
```python
# Total juvenile offenses
df_encoded['total_juv_offenses'] = df_encoded['juv_fel_count'] +␣
 ↪df_encoded['juv_misd_count']

# Has juvenile record (binary indicator)
df_encoded['has_juv_record'] = (df_encoded['total_juv_offenses'] > 0).
 ↪astype(int)

# Age x Priors interaction (high-risk combination)
# Young offenders with many priors are particularly high-risk
df_encoded['young_with_priors'] = ((df_encoded['age_cat_Less than 25'] == 1) &␣
 ↪(df_encoded['priors_count'] > 2)).astype(int)

print("Engineered features created:")
print(f"- total_juv_offenses: {df_encoded['total_juv_offenses'].describe()}")
print(f"- has_juv_record: {df_encoded['has_juv_record'].value_counts()}")
print(f"- young_with_priors: {df_encoded['young_with_priors'].value_counts()}")

df_encoded.head()
```

```
Engineered features created:
- total_juv_offenses: count    6172.000000
```

```
mean          0.150518
std           0.706840
min           0.000000
25%           0.000000
50%           0.000000
75%           0.000000
max          20.000000
Name: total_juv_offenses, dtype: float64
- has_juv_record: has_juv_record
0    5664
1     508
Name: count, dtype: int64
- young_with_priors: young_with_priors
0    5929
1     243
Name: count, dtype: int64
```

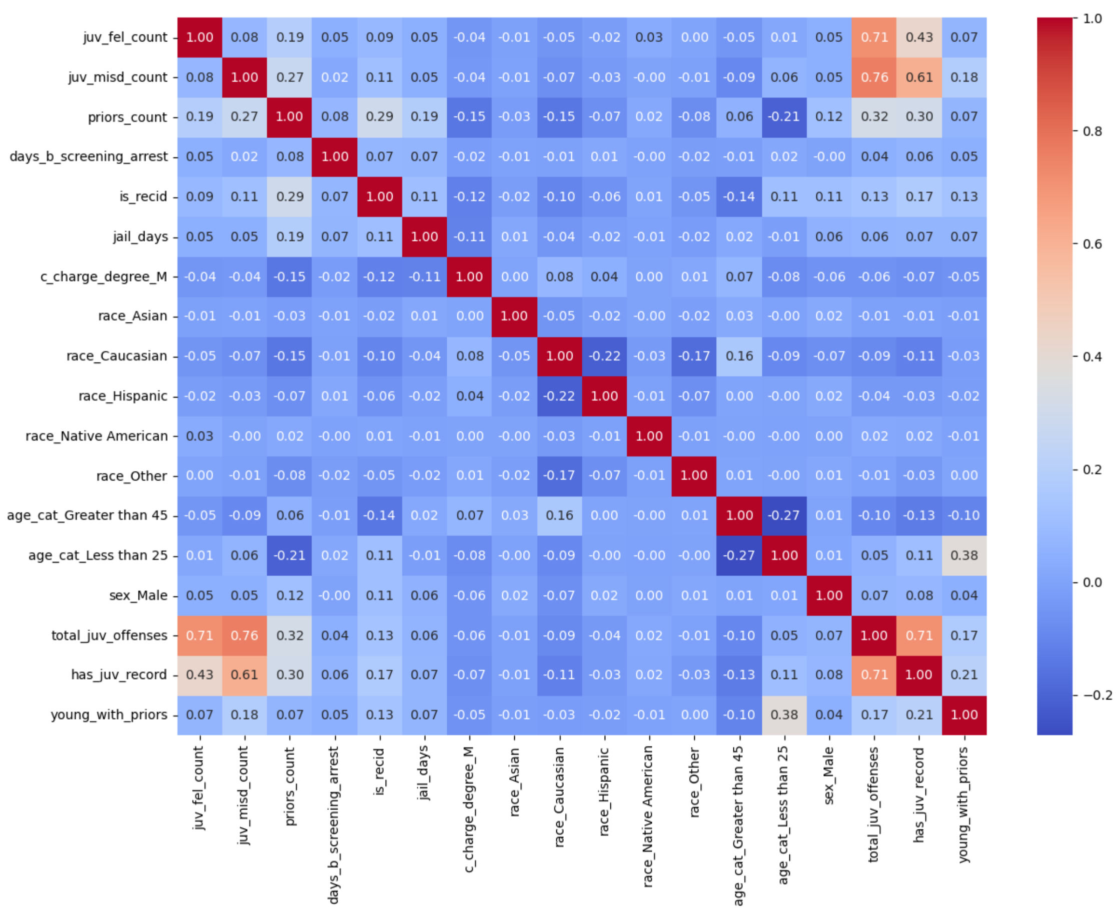
[21]:

```
   juv_fel_count  juv_misd_count  priors_count  days_b_screening_arrest  \
0              0               0             0                      0.0
1              0               0             0                      0.0
2              0               0             4                      0.0
5              0               0             0                      0.0
6              0               0            14                      0.0

   is_recid  jail_days  c_charge_degree_M  race_Asian  race_Caucasian  \
0         0          0                  0           0               0
1         1         10                  0           0               0
2         1          1                  0           0               0
5         0          1                  1           0               0
6         1          6                  0           0               1

   race_Hispanic  race_Native American  race_Other  age_cat_Greater than 45  \
0              0                     0           1                        1
1              0                     0           0                        0
2              0                     0           0                        0
5              0                     0           1                        0
6              0                     0           0                        0

   age_cat_Less than 25  sex_Male  total_juv_offenses  has_juv_record  \
0                     0         1                   0               0
1                     0         1                   0               0
2                     1         1                   0               0
5                     0         1                   0               0
6                     0         1                   0               0

   young_with_priors
0                  0
```

```
1                         0
2                         1
5                         0
6                         0
```

Now for feature engineering! Rather than just using the raw features, we can create more informative ones. Combining juvenile felonies and misdemeanors gives us total juvenile offense count. Creating binary indicators (like `has_juv_record`) simplifies the signal for models. The `young_with_priors` interaction feature captures a high-risk combination—young defendants with extensive criminal histories are particularly likely to reoffend. These engineered features can help our models detect patterns that might be missed with raw data alone.

[22]:
```python
corr = df_encoded.corr()
plt.figure(figsize=(14, 10))
sns.heatmap(corr, cmap="coolwarm", annot=True, fmt=".2f")
plt.show()
```

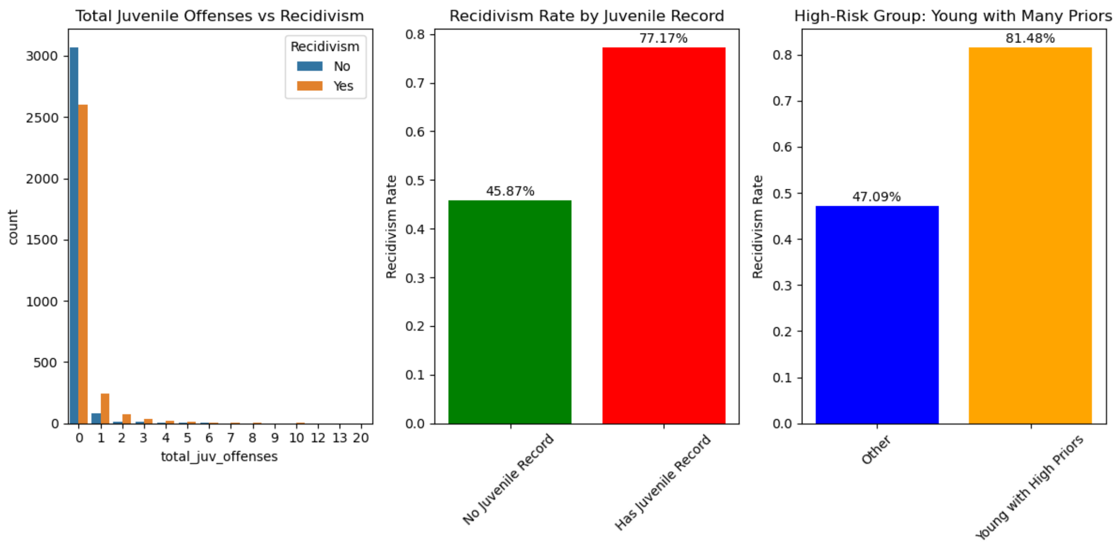


A correlation heatmap gives us the big picture of feature relationships. Which features are strongly correlated with `is_recid`? Are any features highly correlated with each other (potential multicollinearity issues)? This visual guide helps prioritize which features to focus on and identify redundancies.

The correlation heatmap reveals that most features in the dataset are weakly correlated, with only a few clusters showing moderate relationships. Juvenile offense variables (e.g., `juv_fel_count`, `juv_misd_count`) correlate naturally with `total_juv_offenses`, and `priors_count` correlates moderately with `has_juv_record` and `young_with_priors`. These patterns are expected because these features measure related aspects of an individual's criminal history. Importantly, none of the predictors show strong correlation with the target variable (`is_recid`), meaning there is no evidence of data leakage. The correlations instead reflect meaningful structure: criminal history variables cluster together, categorical encodings remain isolated, and no future-information or outcome-based features accidentally feed into the model.

1.8 Visualize Engineered Features

[23]:
```python
# Visualize engineered features' relationship with recidivism
fig, axes = plt.subplots(1, 3, figsize=(12, 6))
axes = axes.flatten()

# Total juvenile offenses vs recidivism
sns.countplot(data=df_encoded, x='total_juv_offenses', hue='is_recid',␣
 ↪ax=axes[0])
axes[0].set_title('Total Juvenile Offenses vs Recidivism')
axes[0].legend(title='Recidivism', labels=['No', 'Yes'])

# Has juvenile record vs recidivism rate
juv_recid = df_encoded.groupby('has_juv_record')['is_recid'].mean()
axes[1].bar(['No Juvenile Record', 'Has Juvenile Record'], juv_recid.values,␣
 ↪color=['green', 'red'])
axes[1].set_title('Recidivism Rate by Juvenile Record')
axes[1].set_ylabel('Recidivism Rate')
for i, v in enumerate(juv_recid.values):
    axes[1].text(i, v + 0.01, f'{v:.2%}', ha='center')
axes[1].tick_params(axis='x', rotation=45)

# Young with priors indicator
young_priors_recid = df_encoded.groupby('young_with_priors')['is_recid'].mean()
axes[2].bar(['Other', 'Young with High Priors'], young_priors_recid.values,␣
 ↪color=['blue', 'orange'])
axes[2].set_title('High-Risk Group: Young with Many Priors')
axes[2].set_ylabel('Recidivism Rate')
for i, v in enumerate(young_priors_recid.values):
    axes[2].text(i, v + 0.01, f'{v:.2%}', ha='center')
axes[2].tick_params(axis='x', rotation=45)

plt.tight_layout()
plt.show()
```



Let's validate our feature engineering by visualizing how these new features relate to recidivism. Do defendants with juvenile records really have higher recidivism rates? Is the "young with high priors" group truly high-risk? These plots confirm whether our feature engineering intuitions are supported by the data—if they show strong patterns, our engineered features are worth including in the model.

These plots show a strong relationship between juvenile criminal history and the likelihood of adult recidivism. Individuals with more juvenile offenses are disproportionately represented among recidivists, with the distribution showing that even a small number of early offenses significantly increases the chance of reoffending. The second chart highlights this more clearly: adults with a juvenile record recidivate at a rate of about 77%, compared to only 46% for those without one. Finally, the high-risk subgroup plot shows that individuals who were young at the time of assessment and had multiple prior offenses have the highest recidivism rates—over 81%, making them the most at-risk category. Overall, the figures indicate that early criminal involvement specially persistent juvenile offending is one of the strongest predictors of long-term reoffending risk.

1.9 Saving DataFrame as Parquet

[24]:
```
# Save the processed and encoded dataframe
df_encoded.to_parquet('../data/processed/compas_processed.parquet',␣
    ↪index=False, engine='fastparquet')

print(f"Saved processed data with {df_encoded.shape[0]} rows and {df_encoded.
    ↪shape[1]} features")
print(f"Target variable distribution:")
print(df_encoded['is_recid'].value_counts())
print(f"\nProcessed data saved to: data/processed/compas_processed.parquet")
```

```
Saved processed data with 6172 rows and 18 features
Target variable distribution:
```

```
is_recid
0    3182
1    2990
Name: count, dtype: int64

Processed data saved to: data/processed/compas_processed.parquet
```

With our EDA complete and features engineered, it's time to save our work. The processed dataset gets saved as a parquet file, a compressed, efficient format that preserves data types perfectly. This becomes the input for our modeling notebook, ensuring we have a clean, reproducible pipeline. Everything we've learned from the EDA (class imbalance, feature relationships, distributions) will inform our modeling decisions next.

modeling

November 17, 2025

1 Modelling

[158]:
```
import os

import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier
from imblearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
from lightgbm import LGBMClassifier
from sklearn.ensemble import ExtraTreesClassifier, StackingClassifier,␣
↪StackingClassifier
from xgboost import XGBClassifier
from catboost import CatBoostClassifier

from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.metrics import classification_report
from sklearn.compose import ColumnTransformer
import pickle
from sklearn import clone

import pyarrow as pa

from imblearn.over_sampling import SMOTE
```

We start by importing all the tools we'll need for this classification challenge. Since we're dealing with recidivism prediction (a binary classification problem), we bring in multiple algorithms to compare from simple logistic regression to complex ensemble methods. Importantly, we include `SMOTE` because we will purposefully undersample our dataset so that it has class imbalance, and we'll need to handle that carefully to avoid biased predictions.

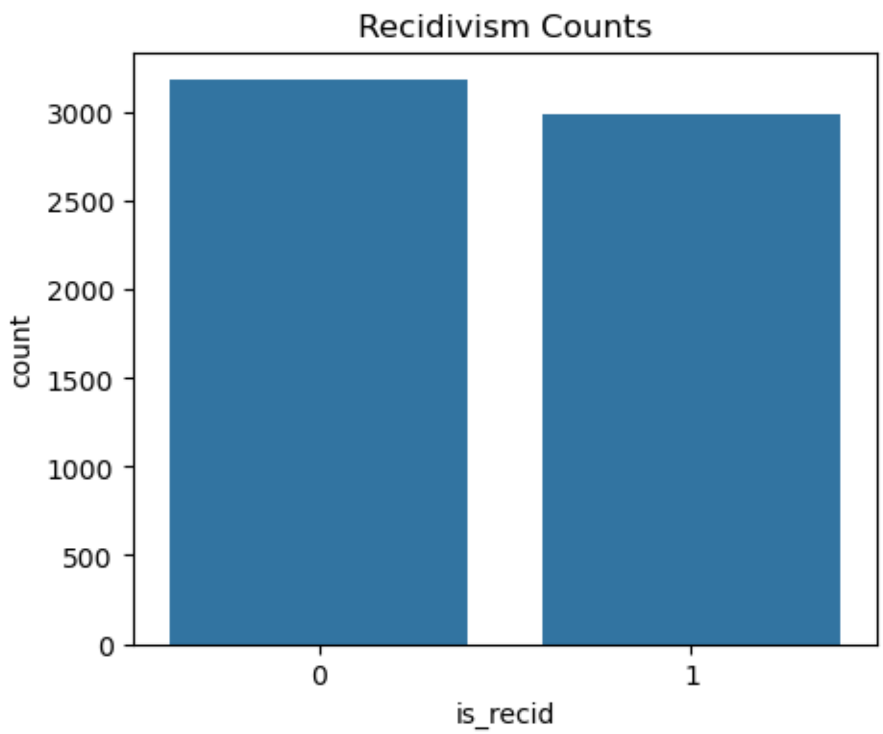
1.1 Load the Processed Data

[159]:
```
# Ensure pyarrow is available and use it as the parquet engine to avoid␣
↪ArrowKeyError
df_encoded = pd.read_parquet('../data/processed/compas_processed.parquet',␣
↪engine='fastparquet')
df_encoded.head()
```

[159]:
```
   juv_fel_count  juv_misd_count  priors_count  days_b_screening_arrest  \
0              0               0             0                      0.0
1              0               0             0                      0.0
2              0               0             4                      0.0
3              0               0             0                      0.0
4              0               0            14                      0.0

   is_recid  jail_days  c_charge_degree_M  race_Asian  race_Caucasian  \
0         0          0                  0           0               0
1         1         10                  0           0               0
2         1          1                  0           0               0
3         0          1                  1           0               0
4         1          6                  0           0               1

   race_Hispanic  race_Native American  race_Other  age_cat_Greater than 45  \
0              0                     0           1                        1
1              0                     0           0                        0
2              0                     0           0                        0
3              0                     0           1                        0
4              0                     0           0                        0

   age_cat_Less than 25  sex_Male  total_juv_offenses  has_juv_record  \
0                     0         1                   0               0
1                     0         1                   0               0
2                     1         1                   0               0
3                     0         1                   0               0
4                     0         1                   0               0

   young_with_priors
0                  0
1                  0
2                  1
3                  0
4                  0
```

Loading the processed dataset that we prepared in the EDA notebook. This data already has our engineered features (like `criminal_severity` and `priors_category`) and all categorical variables are one-hot encoded. By using the parquet format, we get fast loading and preserve data types. Let's verify the structure looks correct before proceeding.

[160]:
```
plt.figure(figsize=(5,4))
sns.countplot(x='is_recid', data=df_encoded)
plt.ylabel('count')
plt.xlabel('is_recid')
plt.title('Recidivism Counts')
plt.show()
```



Here we can see that the class 0 and class 1 is balanced

1.2 Simulate Undersampling of the Recidivists Group to Artificially Achieve Imbalance

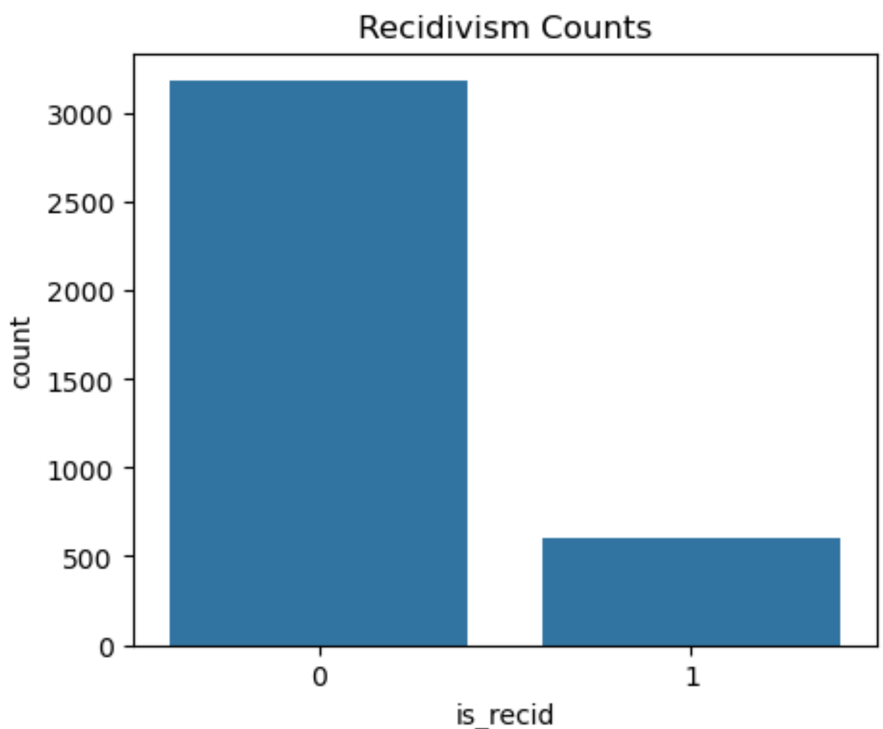
[161]:
```
positive = df_encoded[df_encoded["is_recid"] == 1]       # recidivists
negative = df_encoded[df_encoded["is_recid"] == 0]       # non-recidivists

positive_small = positive.sample(frac=0.20, random_state=42)

df_imbalanced = pd.concat([positive_small, negative], axis=0).sample(frac=1)
df_imbalanced["is_recid"].value_counts()
```

[161]:
```
is_recid
0    3182
1     598
```

```
Name: count, dtype: int64
```

To simulate a more challenging real-world scenario and rigorously test our imbalance handling techniques, I'm artificially creating a stronger class imbalance. By undersampling the recidivist class to just 20% of its original size, we'll have far fewer positive examples. This will force our SMOTE implementation and class weighting strategies to work harder if they perform well here, they'll definitely handle the original imbalance.

[162]:
```
plt.figure(figsize=(5,4))
sns.countplot(x='is_recid', data=df_imbalanced)
plt.ylabel('count')
plt.xlabel('is_recid')
plt.title('Recidivism Counts')
plt.show()
```



Visualizing the new imbalance confirms we have a significant disparity—the minority class (recidivists) is now heavily outnumbered. This is intentional and realistic: in many criminal justice applications, recidivism rates can be relatively low, making the prediction task more difficult but also more important to get right. Now we're ready to split the data and build our modeling pipeline.

[163]:
```
X = df_imbalanced.drop("is_recid", axis=1)
y = df_imbalanced["is_recid"]
print(X.shape, y.shape)
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪stratify=y, random_state=100)

print(X_train.columns)
```

```
(3780, 17) (3780,)
Index(['juv_fel_count', 'juv_misd_count', 'priors_count',
       'days_b_screening_arrest', 'jail_days', 'c_charge_degree_M',
       'race_Asian', 'race_Caucasian', 'race_Hispanic', 'race_Native American',
       'race_Other', 'age_cat_Greater than 45', 'age_cat_Less than 25',
       'sex_Male', 'total_juv_offenses', 'has_juv_record',
       'young_with_priors'],
      dtype='object')
```

Now we separate features from the target and create our train-test split. Using stratification is crucial here, it ensures both our training and test sets maintain the same class imbalance ratio, preventing any data leakage and ensuring fair evaluation. The 80-20 split gives us enough data to train complex models while reserving sufficient samples for testing. Let's also check what features we're working with.

[164]:
```
scale_feats = ["juv_fel_count", "juv_misd_count", "priors_count", "jail_days"]

preprocess = ColumnTransformer(
    transformers=[
        ('num', StandardScaler(), scale_feats),
    ],
    remainder='passthrough'
)
```

Some of our features (like `priors_count` and `jail_days`) are on very different scales than our binary one-hot encoded features. Distance-based algorithms like SVM and KNN are sensitive to these scale differences, so we need to standardize them. I'm using a ColumnTransformer to selectively scale only the continuous features while leaving the binary features as-is. This preprocessing will be embedded in our pipeline to prevent data leakage.

1.3 Batch Definition of Classification Models

[165]:
```
stacking_estimators = [
    ('svm_rbf', SVC(kernel='rbf', class_weight='balanced', probability=True)),
    ('logreg', LogisticRegression(class_weight='balanced')),
    ('knn', KNeighborsClassifier())
]



models = {
    "Logistic Regression": LogisticRegression(class_weight="balanced",␣
↪random_state=100),
```

```
    "SVM Linear": SVC(kernel='linear', random_state=100,␣
↪class_weight="balanced"),
    "SVM RBF": SVC(kernel='rbf', random_state=100, class_weight="balanced"),
    "K-Nearest Neighbors": KNeighborsClassifier(n_neighbors=5),
    "Decision Tree": DecisionTreeClassifier(class_weight="balanced",␣
↪random_state=100),
    "Random Forest": RandomForestClassifier(class_weight="balanced",␣
↪random_state=100),
    "Extra Trees": ExtraTreesClassifier(class_weight="balanced",␣
↪random_state=100),
    "Gradient Boosting": GradientBoostingClassifier(random_state=100),
    "lightGBM": LGBMClassifier(class_weight="balanced", random_state=100,␣
↪verbose=-1),
    "xgboost": XGBClassifier(scale_pos_weight= (y_train == 0).sum() / (y_train␣
↪== 1).sum(), random_state=100, verbose=0),
    "catboost": CatBoostClassifier(class_weights=[1, (y_train == 0).sum() /␣
↪(y_train == 1).sum()], random_state=100, verbose=0),
    "stacking": StackingClassifier(
        estimators=stacking_estimators,
        final_estimator=LogisticRegression(random_state=100)
    )
}
```

Instead of committing to one algorithm upfront, I'm defining a diverse set of 12 classifiers. From simple linear models to complex ensembles. Each model is configured with class imbalance handling: most use `class_weight='balanced'` which automatically adjusts weights inversely proportional to class frequencies. XGBoost and CatBoost have their own syntax for this. The stacking classifier is interesting, it combines predictions from multiple strong learners (SVM, LogReg, KNN) to potentially capture different aspects of the data. Now we'll see which approach works best for our recidivism prediction task.

[166]:
```
params = {
    "Logistic Regression": {
        'model__C': [0.01, 0.1, 1, 10, 100]
    },
    "SVM Linear": {
        'model__C': [0.01, 0.1, 1, 10, 100]
    },
    "SVM RBF": {
        'model__C': [0.01, 0.1, 1, 10, 100],
        'model__gamma': ['scale', 'auto']
    },
    "K-Nearest Neighbors": {
        'model__n_neighbors': [3, 5, 7, 9]
    },
    "Decision Tree": {
        'model__max_depth': [None, 5, 10, 15],
```

```
        'model__min_samples_split': [2, 5, 10]
    },
    "Random Forest": {
        'model__n_estimators': [50, 100, 200],
        'model__max_depth': [None, 5, 10],
        'model__min_samples_split': [2, 5, 10]
    },
        "Extra Trees": {
        'model__n_estimators': [50, 100, 200],
        'model__max_depth': [None, 5, 10],
        'model__min_samples_split': [2, 5, 10]
    },
    "Gradient Boosting": {
        'model__n_estimators': [50, 100, 200],
        'model__learning_rate': [0.01, 0.1, 0.2],
        'model__max_depth': [3, 5, 7]
    },
    "lightGBM": {
        'model__n_estimators': [50, 100, 200],
        'model__learning_rate': [0.01, 0.1, 0.2],
        'model__max_depth': [3, 5, 7]
    },
    "xgboost": {
        'model__n_estimators': [50, 100, 200],
        'model__learning_rate': [0.01, 0.1, 0.2],
        'model__max_depth': [3, 5, 7]
    },
    "catboost": {
        'model__iterations': [50, 100, 200],
        'model__learning_rate': [0.01, 0.1, 0.2],
        'model__depth': [3, 5, 7]
    },
    "stacking": {
        'model__final_estimator__C': [0.01, 0.1, 1, 10, 100]
    }
}


for model_name, estimator in models.items():
    pipe = Pipeline(steps=[
        ('smote', SMOTE(random_state=42)),
        ('preprocess', clone(preprocess)),
        ('model', estimator)
    ])

    gs = GridSearchCV(
        estimator=pipe,
```

```python
        param_grid=params[model_name],
        cv=5,
        scoring='f1',
        n_jobs=-1,
    )

    gs.fit(X_train, y_train)
    pickle.dump(gs, open(f'../models/{model_name}_gridsearch.pkl', 'wb'))
```

```
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
```

```
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/xgboost/training.py:183: UserWarning: [14:41:00] WARNING:
/Users/runner/miniforge3/conda-bld/xgboost-
split_1754001896909/work/src/learner.cc:738:
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/xgboost/training.py:183: UserWarning: [14:41:00] WARNING:
/Users/runner/miniforge3/conda-bld/xgboost-
split_1754001896909/work/src/learner.cc:738:
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/xgboost/training.py:183: UserWarning: [14:41:00] WARNING:
/Users/runner/miniforge3/conda-bld/xgboost-
split_1754001896909/work/src/learner.cc:738:
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/xgboost/training.py:183: UserWarning: [14:41:00] WARNING:
/Users/runner/miniforge3/conda-bld/xgboost-
split_1754001896909/work/src/learner.cc:738:
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/xgboost/training.py:183: UserWarning: [14:41:00] WARNING:
/Users/runner/miniforge3/conda-bld/xgboost-
split_1754001896909/work/src/learner.cc:738:
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/xgboost/training.py:183: UserWarning: [14:41:00] WARNING:
/Users/runner/miniforge3/conda-bld/xgboost-
split_1754001896909/work/src/learner.cc:738:
Parameters: { "verbose" } are not used.

  bst.update(dtrain, iteration=i, fobj=obj)
```

Here's where the magic happens. For each model, I'm creating a complete Pipeline: SMOTE first (to generate synthetic minority class samples), then preprocessing (to scale features), then the model itself. This order is critical, SMOTE only sees training data within each CV fold, preventing data leakage. We use GridSearchCV to systematically test different hyperparameters with 5-fold cross-validation, optimizing for F1 score (which balances precision and recall—important for imbalanced data). Each optimized model gets saved so we can load them later without retraining. This will take several minutes since we're training 12 models with multiple hyperparameter combinations each.

[167]:
```
models = {}
results = {}
pipelines = {}

folder = "../models"

# Load all models from folder
for file in os.listdir(folder):
    if file.endswith(".pkl"):
        model_name = file.replace(".pkl", "")
        with open(os.path.join(folder, file), "rb") as f:
            models[model_name] = pickle.load(f)

for model_name, gs in models.items():
    best_model = gs.best_estimator_ if hasattr(gs, "best_estimator_") else gs

    y_pred = best_model.predict(X_test)
    report = classification_report(y_test, y_pred, output_dict=True)

    results[model_name] = report
    pipelines[model_name] = best_model
```

```
/opt/miniconda3/envs/portfolio/lib/python3.11/site-
packages/sklearn/utils/validation.py:2749: UserWarning: X does not have valid
feature names, but LGBMClassifier was fitted with feature names
  warnings.warn(
```

Now that all models are trained and saved, let's load them back and evaluate their performance on our held-out test set. For each model, we extract the best estimator found by GridSearch, make predictions, and generate a detailed classification report with precision, recall, and F1 scores for both classes. By storing everything in dictionaries, we can easily compare all 12 models side-by-side in the next steps. This is the moment of truth, which approach best predicts recidivism?

[168]:
```
rows = []
for model_name, report in results.items():
    for label, metrics in report.items():
        if label in ["0", "1"]:
            rows.append({
                "model": model_name,
                "class": label,
                "precision": metrics["precision"],
```

```python
                "recall": metrics["recall"],
                "f1": metrics["f1-score"],
                "support": metrics["support"],
            })

result_df = pd.DataFrame(rows)

result_df_minor = result_df[result_df["class"] == "1"] \
    .sort_values("recall", ascending=False)

result_df_minor
```

[168]:

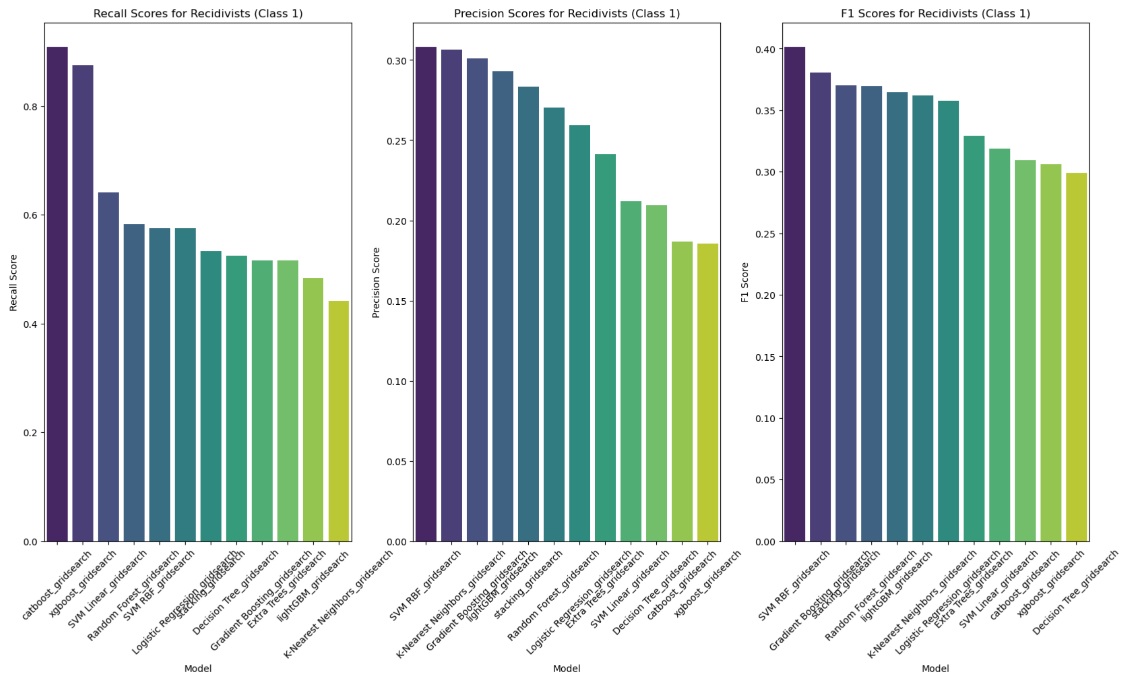
```
                             model class  precision    recall        f1  \
23             catboost_gridsearch     1   0.186644  0.908333  0.309659
17              xgboost_gridsearch     1   0.185512  0.875000  0.306122
15           SVM Linear_gridsearch     1   0.212121  0.641667  0.318841
9         Random Forest_gridsearch     1   0.270270  0.583333  0.369393
3               SVM RBF_gridsearch     1   0.308036  0.575000  0.401163
11  Logistic Regression_gridsearch     1   0.259398  0.575000  0.357513
13             stacking_gridsearch     1   0.283186  0.533333  0.369942
1         Decision Tree_gridsearch     1   0.209302  0.525000  0.299287
5     Gradient Boosting_gridsearch     1   0.300971  0.516667  0.380368
21          Extra Trees_gridsearch     1   0.241245  0.516667  0.328912
19             lightGBM_gridsearch     1   0.292929  0.483333  0.364780
7   K-Nearest Neighbors_gridsearch     1   0.306358  0.441667  0.361775

    support
23    120.0
17    120.0
15    120.0
9     120.0
3     120.0
11    120.0
13    120.0
1     120.0
5     120.0
21    120.0
19    120.0
7     120.0
```

Let's structure the results for easy comparison. I'm focusing on the minority class (recidivists, class 1) because correctly identifying potential recidivists is more critical than identifying non-recidivists, the cost of missing a recidivist (false negative) is typically higher in criminal justice applications. Sorting by recall shows us which models are best at catching recidivism cases, even if it means some false alarms. This table will help us quickly identify our top performers.

[169]:
```
fig, axes = plt.subplots(1, 3, figsize=(20, 10))


sns.barplot(data=result_df_minor, x="model", y="recall", palette="viridis",␣
↪ax=axes[0])
axes[0].set_title("Recall Scores for Recidivists (Class 1)")
axes[0].set_ylabel("Recall Score")
axes[0].set_xlabel("Model")
axes[0].tick_params(axis='x', rotation=45)

sorted_by_precision = result_df_minor.sort_values("precision", ascending=False)
sns.barplot(data=sorted_by_precision, x="model", y="precision",␣
↪palette="viridis", ax=axes[1])
axes[1].set_title("Precision Scores for Recidivists (Class 1)")
axes[1].set_ylabel("Precision Score")
axes[1].set_xlabel("Model")
axes[1].tick_params(axis='x', rotation=45)

sorted_by_f1 = result_df_minor.sort_values("f1", ascending=False)
sns.barplot(data=sorted_by_f1, x="model", y="f1", palette="viridis", ax=axes[2])
axes[2].set_title("F1 Scores for Recidivists (Class 1)")
axes[2].set_ylabel("F1 Score")
axes[2].set_xlabel("Model")
axes[2].tick_params(axis='x', rotation=45)
plt.show()
```

```
/var/folders/n1/k6wd8lyx2b76lr9n8ln2vjch0000gn/T/ipykernel_5262/2436557067.py:4:
FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.barplot(data=result_df_minor, x="model", y="recall", palette="viridis",
ax=axes[0])
/var/folders/n1/k6wd8lyx2b76lr9n8ln2vjch0000gn/T/ipykernel_5262/2436557067.py:11
: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.barplot(data=sorted_by_precision, x="model", y="precision",
palette="viridis", ax=axes[1])
/var/folders/n1/k6wd8lyx2b76lr9n8ln2vjch0000gn/T/ipykernel_5262/2436557067.py:18
: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
```

```
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.barplot(data=sorted_by_f1, x="model", y="f1", palette="viridis",
ax=axes[2])
```



The model comparison shows clear trade-offs between recall, precision, and overall F1 performance for predicting recidivism. CatBoost achieves the highest recall and F1, meaning it catches the most true reoffenders, but it does so by heavily overpredicting recidivism, resulting in very low precision and many false positives. In contrast, SVM RBF delivers the best precision with still-reasonable recall, making it the most balanced and fairness-aligned model—it avoids unnecessarily flagging low-risk individuals while maintaining solid predictive power. Logistic Regression also performs consistently and serves as a strong, interpretable baseline. Overall, if the priority is maximizing public safety through high recall, CatBoost is best, but if fairness, balance, and minimizing false accusations matter, SVM RBF is the more appropriate choice.