

CORR

April 19, 2023

```
[1]: import matplotlib
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import seaborn as sns
import statsmodels.api as sm
import scipy.stats as st
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.model_selection import train_test_split

%matplotlib inline
```

```
[2]: df_out = pd.read_pickle('df_out.pkl')
df_breeds = pd.read_pickle('df_breeds.pkl')
df_out_with_breeds_info = pd.read_pickle('df_out_with_breeds_info.pkl')
df_breeds_with_info = pd.read_pickle('df_breeds_with_info.pkl')
df_out.info()
df_out.head()
```

<class 'pandas.core.frame.DataFrame'>

RangeIndex: 149511 entries, 0 to 149510

Data columns (total 41 columns):

#	Column	Non-Null Count	Dtype
0	index	149511 non-null	Int64
1	Animal ID	149511 non-null	string
2	Name	106260 non-null	string
3	Outcome DateTime	149511 non-null	datetime64[ns]
4	Outcome MonthYear	149511 non-null	string
5	Date of Birth	149511 non-null	datetime64[ns]
6	Outcome Type	149485 non-null	string
7	Outcome Subtype	68443 non-null	string
8	Animal Type	149511 non-null	string
9	Sex upon Outcome	149509 non-null	string
10	Age upon Outcome	149465 non-null	string
11	Breed	149511 non-null	string
12	Color	149511 non-null	string

```

13 Intake MonthYear      147980 non-null string
14 Intake DateTime      147980 non-null datetime64[ns]
15 Found Location       147980 non-null string
16 Intake Type          147980 non-null string
17 Intake Condition     147980 non-null string
18 Sex upon Intake      147978 non-null string
19 Age upon Intake      147979 non-null string
20 Years in animal center 147980 non-null Float64
21 Colors (count)      149511 non-null Int64
22 Color 0              149511 non-null string
23 Color 1              79869 non-null string
24 Color 0 R            135638 non-null Float64
25 Color 0 G            135638 non-null Float64
26 Color 0 B            135638 non-null Float64
27 Color 0 H            135638 non-null Float64
28 Color 0 S            135638 non-null Float64
29 Color 0 V            135638 non-null Float64
30 Color 1 R            78596 non-null Float64
31 Color 1 G            78596 non-null Float64
32 Color 1 B            78596 non-null Float64
33 Color 1 H            78596 non-null Float64
34 Color 1 S            78596 non-null Float64
35 Color 1 V            78596 non-null Float64
36 Age upon Outcome (years) 149465 non-null Float64
37 Male                 149509 non-null boolean
38 Female               149509 non-null boolean
39 NeuteredOrSpayed     149509 non-null boolean
40 Adopted              149485 non-null boolean
dtypes: Float64(14), Int64(2), boolean(4), datetime64[ns](3), string(18)
memory usage: 45.6 MB

```

```

[2]:      index Animal ID      Name      Outcome DateTime Outcome MonthYear \
0    61546   A659834  Dudley  2013-10-01 09:31:00      Oct 2013
1    50833   A664235    <NA>  2013-10-01 10:39:00      Oct 2013
2    93227   A664236    <NA>  2013-10-01 10:44:00      Oct 2013
3   109856   A664237    <NA>  2013-10-01 10:44:00      Oct 2013
4    12697   A664223   Moby  2013-10-01 11:03:00      Oct 2013

      Date of Birth      Outcome Type Outcome Subtype Animal Type Sex upon Outcome \
0    2013-07-23      Adoption      Foster      Dog      Neutered Male
1    2013-09-24      Transfer      Partner      Cat      Unknown
2    2013-09-24      Transfer      Partner      Cat      Unknown
3    2013-09-24      Transfer      Partner      Cat      Unknown
4    2009-09-30  Return to Owner      <NA>      Dog      Neutered Male

      ... Color 1 G Color 1 B Color 1 H Color 1 S Color 1 V \
0    ...      <NA>      <NA>      <NA>      <NA>      <NA>

```

1	...	1.0	1.0	0.0	0.0	1.0
2	...	1.0	1.0	0.0	0.0	1.0
3	...	1.0	1.0	0.0	0.0	1.0
4	...	<NA>	<NA>	<NA>	<NA>	<NA>

	Age upon Outcome (years)	Male	Female	NeuteredOrSpayed	Adopted
0	0.166667	True	False	True	True
1	0.019231	False	False	False	False
2	0.019231	False	False	False	False
3	0.019231	False	False	False	False
4	4.0	True	False	True	False

[5 rows x 41 columns]

```
[3]: df_breeds_with_info.head()
```

	Breed	Count	Animal Type	Adopted	Color O R (mean)	\
0	Domestic Shorthair Mix	33260	Cat	0.461425	0.439476	
1	Domestic Shorthair	13808	Cat	0.553158	0.451115	
2	Pit Bull Mix	9406	Dog	0.431427	0.513666	
3	Labrador Retriever Mix	7913	Dog	0.546063	0.409771	
4	Chihuahua Shorthair Mix	6689	Dog	0.483181	0.609789	

	Color O R (std dev)	Color O G (mean)	Color O G (std dev)	\
0	0.412274	0.322711	0.323957	
1	0.412934	0.331264	0.324532	
2	0.403283	0.418784	0.381554	
3	0.421755	0.329495	0.388036	
4	0.370759	0.493648	0.361854	

	Color O B (mean)	Color O B (std dev)	...	\
0	0.286948	0.413041	...	
1	0.293482	0.413847	...	
2	0.476534	0.439715	...	
3	0.181561	0.323025	...	
4	0.356013	0.369441	...	

	CKC Subgroup	height_low_inches	\
0	11-A: Pointing Dogs	21.0	
1	11-A: Pointing Dogs	21.0	
2	4-B: Bull-and-Terrier Breeds	17.0	
3	11-C: Retrievers and Waterdogs	21.0	
4	12-A: Americas and Caribbean Breeds	5.0	

	height_high_inches	average height	weight_low_lbs	weight_high_lbs	\
0	26.0	23.5	45.0	70	
1	26.0	23.5	45.0	70	

2	22.0	19.5	30.0	75
3	25.0	23.0	55.0	80
4	10.0	7.5	1.0	7

	average weight	Lifespan Low	Lifespan High	average lifespan
0	57.5	10	12	11.0
1	57.5	10	12	11.0
2	52.5	10	12	11.0
3	67.5	10	12	11.0
4	4.0	14	16	15.0

[5 rows x 45 columns]

```
[4]: def animalsLongerThan(days_limit):
      years_limit = days_limit / 365.25
      return df_out_with_breeds_info.loc[df_out_with_breeds_info["Years in animal_
      center"] > years_limit]
```

```
[5]: sns.histplot(
      data=df_out,
      x='Years in animal center',
      hue='Outcome Type'
    )
plt.show()
```

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
  pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
```

```

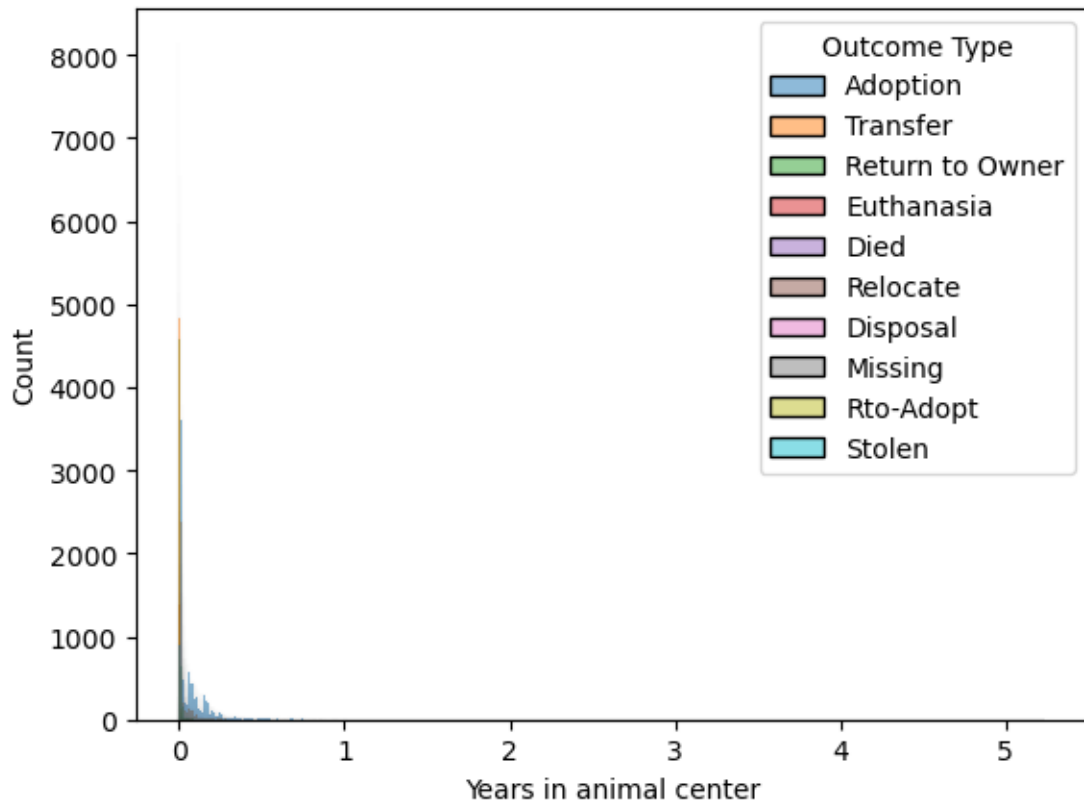
Index constructor will not infer numeric dtypes when passed object-dtype
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packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
    pd.Index(widths, name="widths"),

```

```

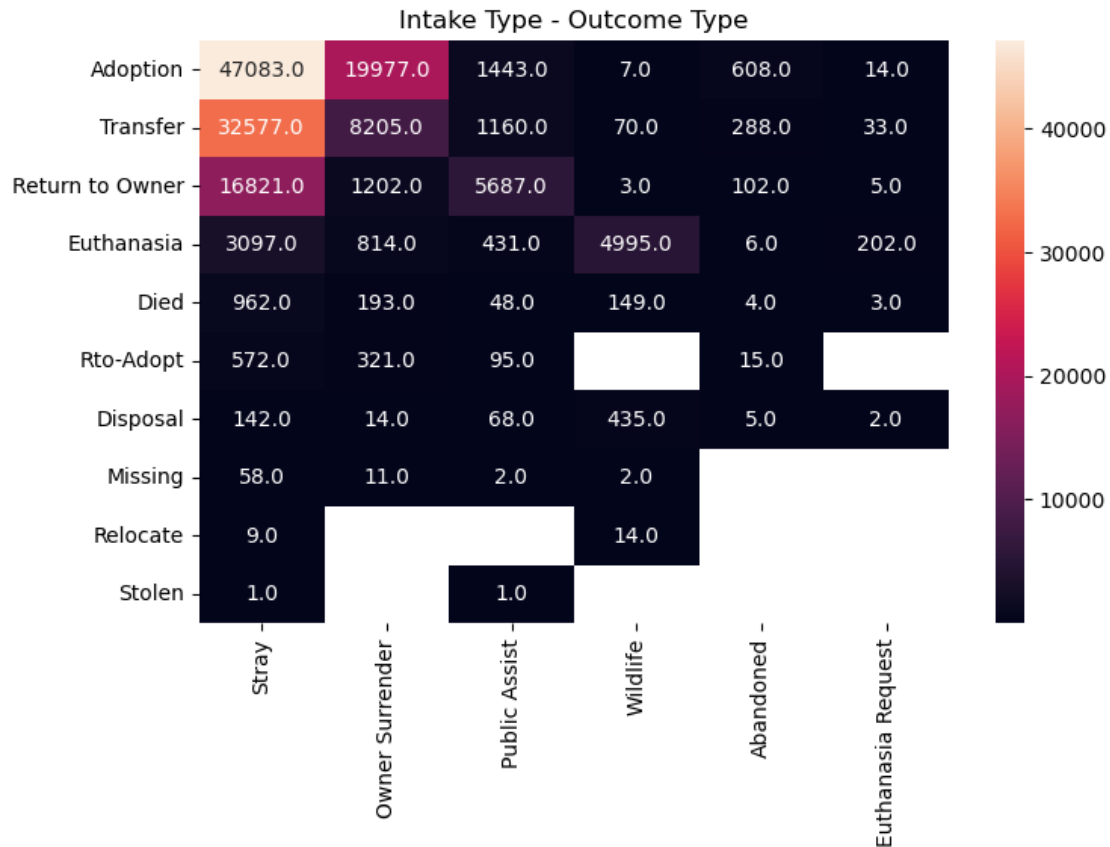
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
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    pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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    pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
    pd.Index(widths, name="widths"),

```



```
[6]: df_intake_outcome_type = pd.DataFrame()
df_intake_outcome_type_grouped = df_out[["Intake Type", "Outcome Type"]].
    ↪value_counts()
for (intake_type, outcome_type), count in df_intake_outcome_type_grouped.
    ↪items():
    df_intake_outcome_type.at[outcome_type, intake_type] = int(count)

plt.figure(figsize=(8,5))
sns.heatmap(data=df_intake_outcome_type, annot=True, fmt="0")
plt.title("Intake Type - Outcome Type")
plt.show()
```



1 Analysis by breed

```
[7]: def breeds(df_animals):
    df_breeds_filtered = pd.DataFrame(columns=['Breed', 'Count'])

    copy_columns = [column for column in df_breeds_with_info.columns if column_
↳not in df_breeds.columns]

    for breed, loc in df_animals.groupby("Breed").groups.items():
        df_out_filtered_breed = df_animals.loc[loc]
        df_breeds_filtered.at[breed, 'Breed'] = breed
        df_breeds_filtered.at[breed, 'Count'] = df_out_filtered_breed.shape[0]
        df_breeds_filtered.at[breed, 'Adopted'] = df_out_filtered_breed.Adopted.
↳mean()

        df_breeds_with_info_row = df_breeds_with_info.loc[df_breeds_with_info.
↳Breed == breed]
        for column in copy_columns:
```



```

        df_breeds_filtered.at[breed, column] =
↪df_breeds_with_info_row[column].values[0]

    return df_breeds_filtered

```

1.0.1 Popular breeds

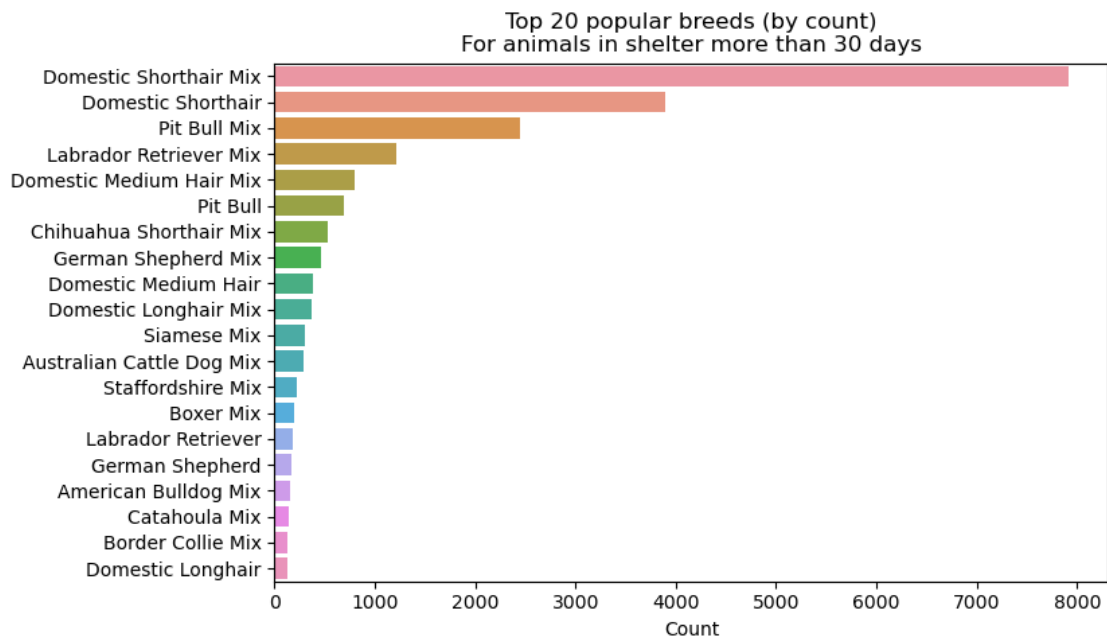
```

[8]: days_limit = 30

df_breeds_filtered = breeds(animalsLongerThan(days_limit))
df_breeds_filtered.sort_values('Count', ascending=False, inplace=True)

k = 20
plt.figure(figsize=(8,5))
sns.barplot(
    data=df_breeds_filtered.head(k),
    x='Count',
    y='Breed',
    errorbar=None,
)
plt.xlabel('Count')
plt.ylabel(None)
plt.title(f'Top {k} popular breeds (by count)\nFor animals in shelter more than
↪{days_limit} days')
plt.show()

```



```

[9]: days_limit = 30
df_breeds_filtered = breeds(animalsLongerThan(days_limit))

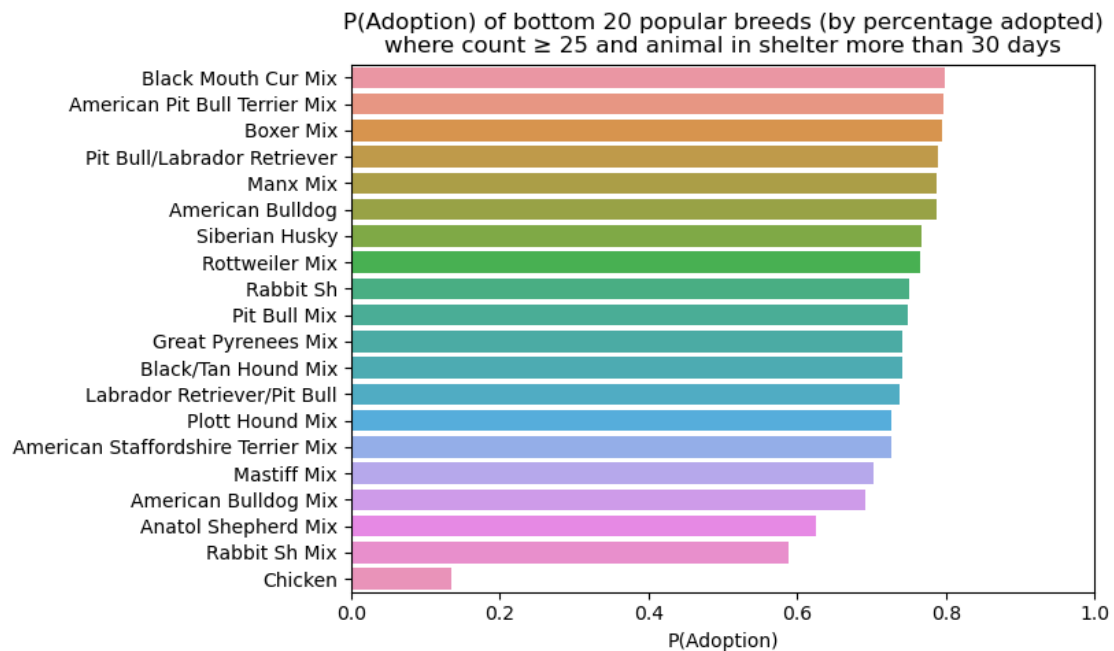
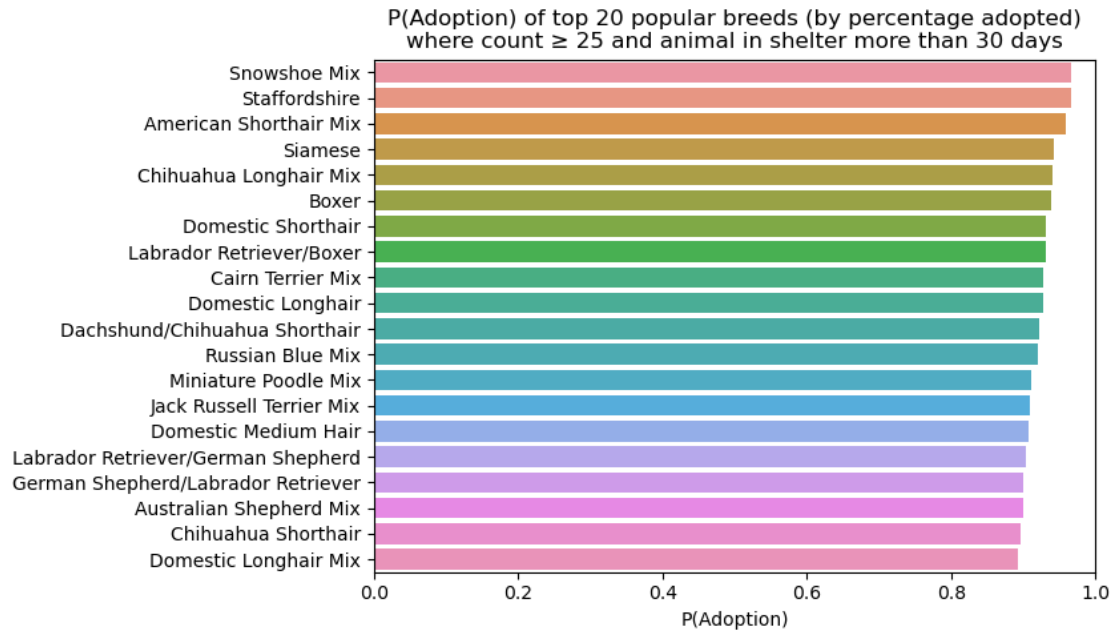
n = 25
df_breeds_filtered = df_breeds_filtered.loc[df_breeds_filtered.Count >= n]

k = 20

plt.figure(figsize=(7,5))
ax = sns.barplot(
    data=df_breeds_filtered.sort_values('Adopted', ascending=False).head(k),
    x='Adopted',
    y='Breed',
    errorbar=None,
)
ax.set_xlim(0, 1)
plt.xlabel('P(Adoption)')
plt.ylabel(None)
plt.title(f'P(Adoption) of top {k} popular breeds (by percentage_
↳adopted)\nwhere count {n} and animal in shelter more than {days_limit}_
↳days')
plt.show()

plt.figure(figsize=(7,5))
ax = sns.barplot(
    data=df_breeds_filtered.sort_values('Adopted', ascending=True).head(k).
↳sort_values('Adopted', ascending=False),
    x='Adopted',
    y='Breed',
    errorbar=None,
)
ax.set_xlim(0, 1)
plt.xlabel('P(Adoption)')
plt.ylabel(None)
plt.title(f'P(Adoption) of bottom {k} popular breeds (by percentage_
↳adopted)\nwhere count {n} and animal in shelter more than {days_limit}_
↳days')
plt.show()

```



1.0.2 Correlating with every variable

There isn't much correlation appearing yet

```
[10]: df_breeds_with_info_corr = df_breeds_with_info.corr()

plt.figure(num=None, figsize=(12, 10), dpi=96, facecolor='w', edgecolor='k')
sns.heatmap(data=df_breeds_with_info_corr.abs())

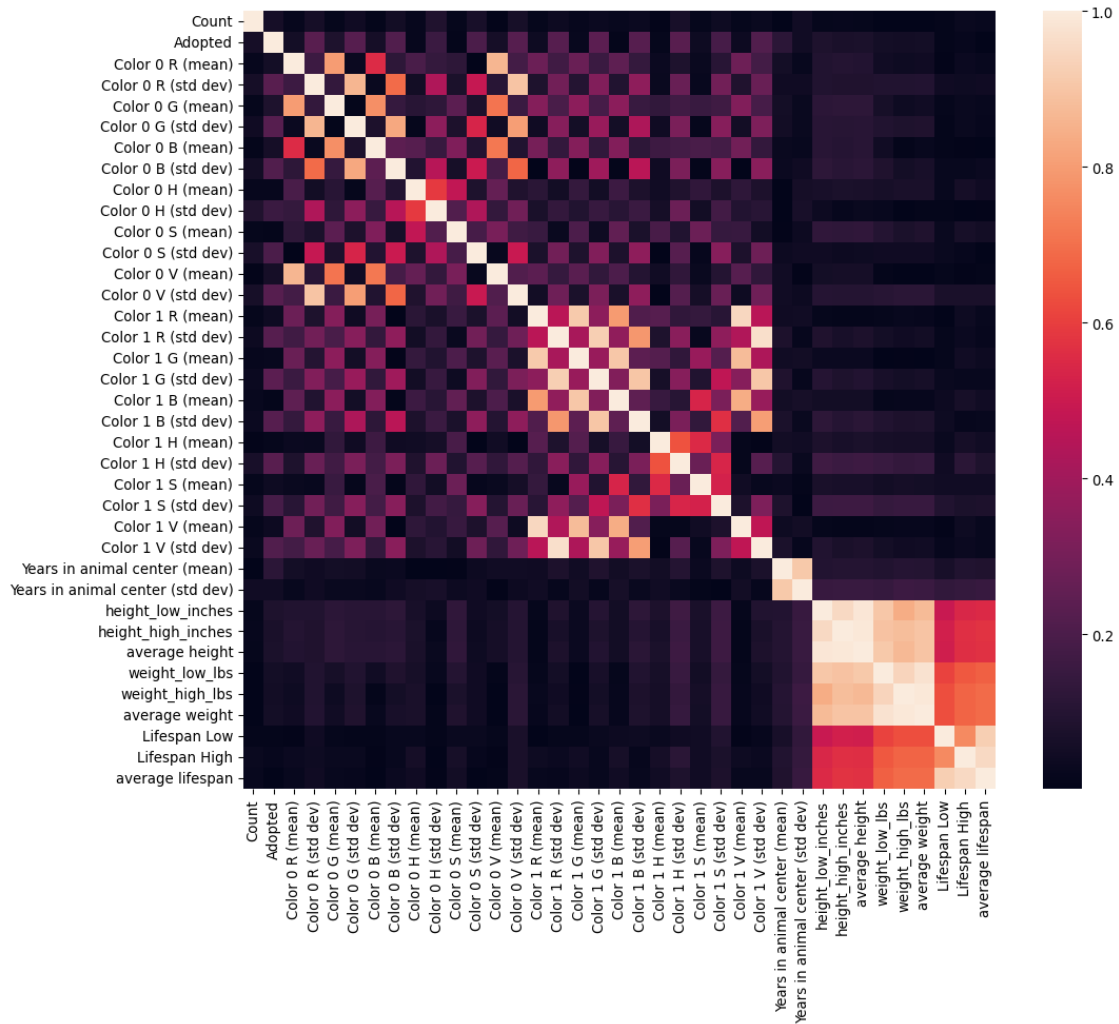
def score(df, var1, var2):
    print(f'Corr({var1}, {var2})    {df[var1][var2]}')

score(df_breeds_with_info_corr, 'Adopted', 'Color 0 B (mean)')
score(df_breeds_with_info_corr, 'Adopted', 'Color 0 B (std dev)')
score(df_breeds_with_info_corr, 'Adopted', 'Color 0 V (mean)')
score(df_breeds_with_info_corr, 'Adopted', 'Color 0 V (std dev)')
score(df_breeds_with_info_corr, 'Adopted', 'average height')
score(df_breeds_with_info_corr, 'Adopted', 'height_low_inches')
score(df_breeds_with_info_corr, 'Adopted', 'height_high_inches')
score(df_breeds_with_info_corr, 'Adopted', 'Lifespan Low')
```

/tmp/ipykernel_83309/4118066584.py:1: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of numeric_only to silence this warning.

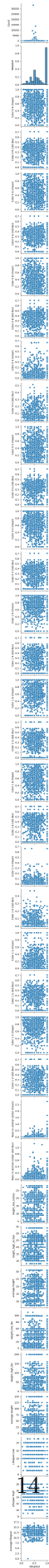
```
df_breeds_with_info_corr = df_breeds_with_info.corr()

Corr(Adopted, Color 0 B (mean))    -0.05752196102076516
Corr(Adopted, Color 0 B (std dev)) -0.21220098425344627
Corr(Adopted, Color 0 V (mean))    -0.05892713325516757
Corr(Adopted, Color 0 V (std dev)) -0.2237579456621404
Corr(Adopted, average height)      0.07520172186737102
Corr(Adopted, height_low_inches)    0.08043859187254204
Corr(Adopted, height_high_inches)   0.06827302387620375
Corr(Adopted, Lifespan Low)         0.011194168083226583
```



```
[11]: sns.pairplot(data=df_breeds_with_info, x_vars=['Adopted'])
```

```
[11]: <seaborn.axisgrid.PairGrid at 0x7f2fc8f65180>
```



1.1 Height ~ adopted?

Is the average height of a breed correlated with likelihood of an animal from that breed being adopted? The Pearson correlation coefficient was $\text{Corr}(\text{Adopted}, \text{average height}) = 0.2286839421877296$.

This section analyzes this by breed and also by individual animal.

See also: toward the end of this notebook, there are histograms that compare many variables with adoption likelihood.

```
[12]: days_limit = 30

df_out_with_breeds_info_filtered = animalsLongerThan(days_limit)

df_hl = df_out_with_breeds_info[['average height', 'Adopted']].dropna()

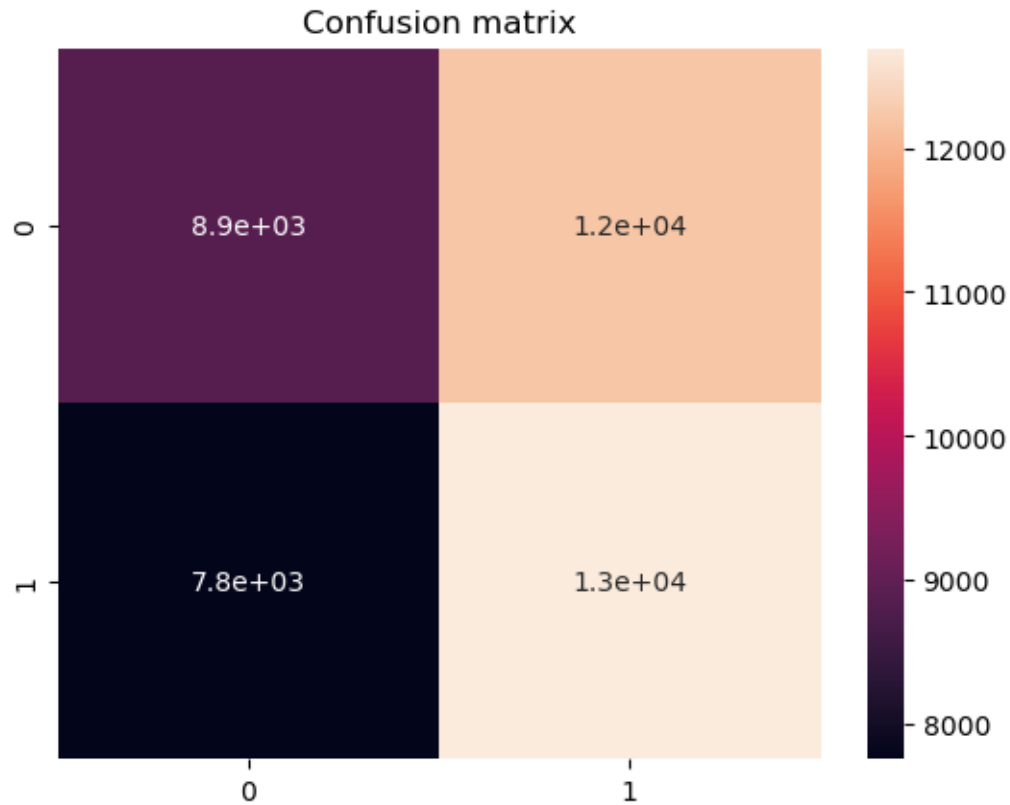
y_data = df_hl['Adopted'].astype(dtype=int)
x_data = df_hl['average height'].astype(dtype=float)

x_data = x_data.values.reshape(-1,1)

x_training_data, x_test_data, y_training_data, y_test_data = \
    ↪train_test_split(x_data, y_data, test_size = 0.3)
model = LogisticRegression()
model.fit(x_training_data, y_training_data)
y_test_pred = model.predict(x_test_data)

sns.heatmap(data=confusion_matrix(y_test_data, y_test_pred), annot=True)
plt.title("Confusion matrix")
plt.show()

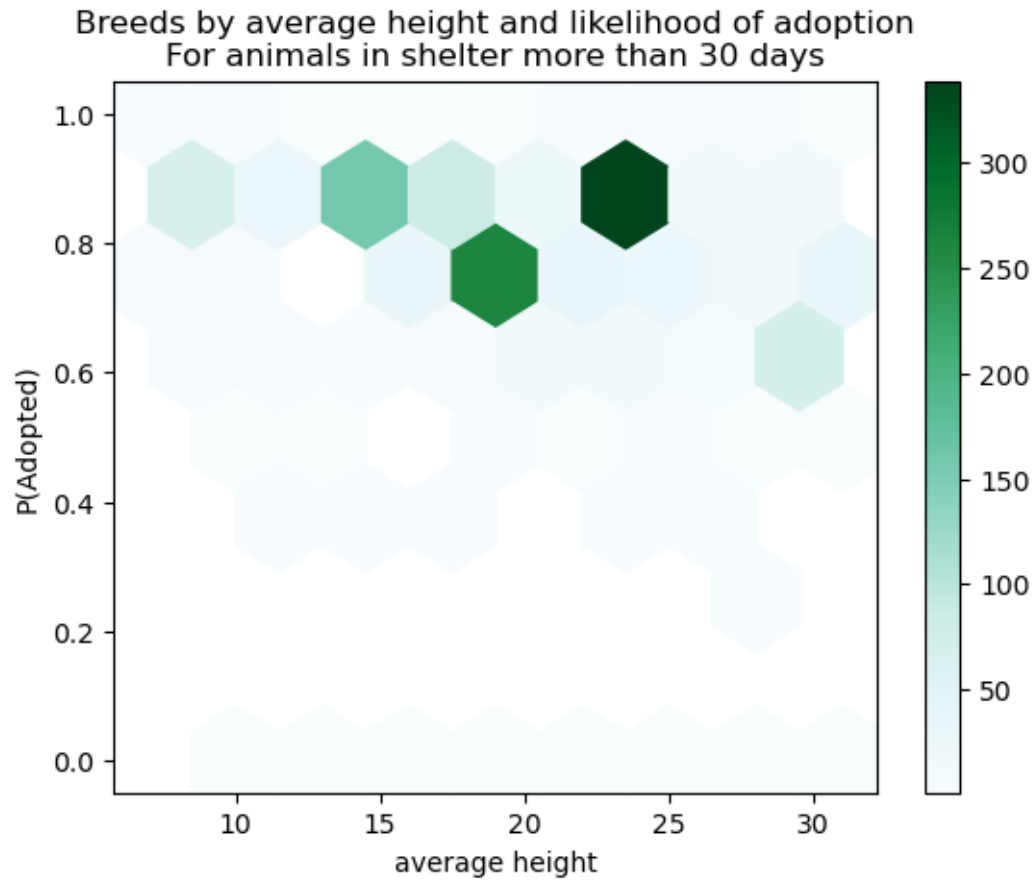
print("Classification report")
print(classification_report(y_test_data, y_test_pred))
```



Classification report

	precision	recall	f1-score	support
0	0.53	0.42	0.47	21069
1	0.51	0.62	0.56	20451
accuracy			0.52	41520
macro avg	0.52	0.52	0.52	41520
weighted avg	0.52	0.52	0.51	41520

```
[13]: days_limit = 30
df_breeds_filtered = breeds(animalsLongerThan(days_limit))
df_breeds_filtered.plot.hexbin(x='average height', y='Adopted', gridsize=8,
    ↪C='Count')
plt.ylabel("P(Adopted)")
plt.title(f"Breeds by average height and likelihood of adoption\nFor animals in
    ↪shelter more than {days_limit} days")
plt.show()
```

I think with all this analysis on height ~ adoption, I don't find a strong correlation between the two.

2 Analysis by individuals

2.1 Color

(results)

```
[14]: print('Colors')
      print(df_out_with_breeds_info['Color 0'].unique())
      print(df_out_with_breeds_info['Color 1'].unique())
```

Colors

<StringArray>

```
[
      'Black',      'Orange',      'White',
      'Red',        'Tortie',      'Gray',
      'Silver',     'Blue',       'Torbie',
      'Orange Tabby', 'Brown',     'Apricot',
      'Brown Tabby', 'Blue Tabby', 'Blue Point',
```

```

        'Calico',      'Brown Brindle',      'Tan',
        'Chocolate',      'Yellow',      'Black Tabby',
        'Lilac Point',      'Cream Tabby',      'Buff',
        'Tricolor',      'Liver',      'Cream',
        'Fawn',      'Blue Merle',      'Red Merle',
        'Tortie Point',      'Calico Point',      'Brown Merle',
        'Silver Tabby',      'Black Smoke',      'Lynx Point',
        'Sable',      'Gold',      'Seal Point',
        'Black Brindle',      'Blue Cream',      'Brown Tiger',
        'Red Tick',      'Flame Point',      'Blue Tick',
        'Gray Tabby',      'Green',      'Blue Tiger',
        'Yellow Brindle',      'Chocolate Point',      'Blue Smoke',
        'Ruddy',      'Black Tiger',      'Pink',
        'Liver Tick',      'Agouti',      'Silver Lynx Point',
        'Orange Tiger',      'Cream Tiger',      'Unknown']
Length: 60, dtype: string
<StringArray>
[
    <NA>,      'White',      'Brown',      'Brown Brindle',
    'Tricolor',      'Tan',      'Black',      'Blue',
    'Cream',      'Buff',      'Blue Merle',      'Blue Tabby',
    'Gray',      'Orange Tabby',      'Black Smoke',      'Brown Merle',
    'Red Tick',      'Orange',      'Red Merle',      'Silver',
    'Red',      'Chocolate',      'Yellow',      'Seal Point',
    'Black Brindle',      'Brown Tabby',      'Blue Cream',      'Liver',
    'Gold',      'Tortie',      'Blue Tick',      'Gray Tabby',
    'Yellow Brindle',      'Apricot',      'Brown Tiger',      'Pink',
    'Lynx Point',      'Black Tabby',      'Cream Tabby',      'Flame Point',
    'Gray Tiger',      'Calico',      'Blue Tiger',      'Green',
    'Chocolate Point',      'Tortie Point',      'Silver Tabby',      'Liver Tick',
    'Calico Point',      'Fawn',      'Lilac Point',      'Blue Point',
    'Agouti',      'Black Tiger']
Length: 54, dtype: string

```

```

[15]: def bigCorr_bernoulli(df, independent, dependent):
        numerator = (
            df[[independent, dependent]].groupby(independent).value_counts()
        )

        denominator = (
            df[[independent]].groupby(independent).value_counts()
        )

        return (numerator.div(denominator))[:,True]

[16]: def bigCorr_bernoulli_custom_colors_2(df_out_colors_1, df_out_colors_2):
        df_out_colors_2_color_0 = df_out_colors_2[['Color 0', 'Adopted']].
        ↪rename(columns={'Color 0': 'Color'})

```

```

    df_out_colors_2_color_1 = df_out_colors_2[['Color 1', 'Adopted']].
    ↪rename(columns={'Color 1': 'Color'})

    numerator = (
        df_out_colors_2_color_0.groupby('Color').value_counts().add(
            df_out_colors_2_color_1.groupby('Color').value_counts(),
            fill_value=0
        )
    )

    denominator = (
        df_out_colors_2_color_0[['Color']].groupby('Color').value_counts().add(
            df_out_colors_2_color_1[['Color']].groupby('Color').value_counts(),
            fill_value=0
        )
    )

    return (numerator.div(denominator))[:,True]

def bigCorr_bernoulli_custom_colors_1_or_2(df_out_colors_1, df_out_colors_2):
    df_out_colors_1_color_0 = df_out_colors_1[['Color 0', 'Adopted']].
    ↪rename(columns={'Color 0': 'Color'})
    df_out_colors_2_color_0 = df_out_colors_2[['Color 0', 'Adopted']].
    ↪rename(columns={'Color 0': 'Color'})
    df_out_colors_2_color_1 = df_out_colors_2[['Color 1', 'Adopted']].
    ↪rename(columns={'Color 1': 'Color'})

    numerator = (
        df_out_colors_1_color_0.groupby('Color').value_counts().add(
            df_out_colors_2_color_0.groupby('Color').value_counts().add(
                df_out_colors_2_color_1.groupby('Color').value_counts(),
                fill_value=0
            ),
            fill_value=0
        )
    )

    denominator = (
        df_out_colors_1_color_0[['Color']].groupby('Color').value_counts().add(
            df_out_colors_2_color_0[['Color']].groupby('Color').value_counts().
            ↪add(
                df_out_colors_2_color_1[['Color']].groupby('Color').
            ↪value_counts(),
                fill_value=0
            ),
            fill_value=0
        )
    )

```

```

    )
)

return (numerator.div(denominator))[:,True]

```

[17]: *# This is copied from prep.ipynb*

```

from math import pi

# colors.csv was compiled from these wikipedia articles
# https://en.wikipedia.org/wiki/List_of_colors:_A-F
# https://en.wikipedia.org/wiki/List_of_colors:_G%E2%80%93M
# https://en.wikipedia.org/wiki/List_of_colors:_N%E2%80%93Z
# Then the "-" character was replaced with "0"
df_colors = pd.read_csv('colors.csv')
df_colors = df_colors.convert_dtypes(infer_objects=True)
df_colors['Name'] = df_colors['Name'].str.lower()
df_colors['Red (RGB)'] = pd.to_numeric(df_colors['Red (RGB)'].str.replace('%', ' '),
    ↪).div(100)
df_colors['Green (RGB)'] = pd.to_numeric(df_colors['Green (RGB)'].str.
    ↪replace('%', ' ').div(100)
df_colors['Blue (RGB)'] = pd.to_numeric(df_colors['Blue (RGB)'].str.
    ↪replace('%', ' ').div(100)
df_colors['Hue (HSL/HSV)'] = pd.to_numeric(df_colors['Hue (HSL/HSV)'].str.
    ↪replace('°', ' ').div(360)
df_colors['Satur. (HSL)'] = pd.to_numeric(df_colors['Satur. (HSL)'].str.
    ↪replace('%', ' ').div(100)
df_colors['Light (HSL)'] = pd.to_numeric(df_colors['Light (HSL)'].str.
    ↪replace('%', ' ').div(100)
df_colors['Satur. (HSV)'] = pd.to_numeric(df_colors['Satur. (HSV)'].str.
    ↪replace('%', ' ').div(100)
df_colors['Value (HSV)'] = pd.to_numeric(df_colors['Value (HSV)'].str.
    ↪replace('%', ' ').div(100)
df_colors.head()

def colorInfo(color):
    color = color.lower()
    words = [color] if color.count(' ') == 0 else [color] + color.split(' ')
    for word in words:
        try:
            items = df_colors.loc[df_colors.Name == word]
            if len(items) > 0:
                return items
        except:
            continue

```

```

for word in words:
    try:
        items = df_colors.loc[df_colors.Name.str.contains(word)]
        if len(items) > 0:
            return items
    except:
        continue

return None

def rgb(color):
    info = colorInfo(color)
    if info is None: return (None, None, None)
    r = info['Red (RGB)'].values[0]
    g = info['Green (RGB)'].values[0]
    b = info['Blue (RGB)'].values[0]
    return (r, g, b)

```

[18]: `from math import floor`

```

def color_dataframes(days_limit):
    df_out_filtered = animalsLongerThan(days_limit)
    df_out_colors_1 = df_out_filtered.loc[(df_out_filtered['Color 0'].notna()
    ↪ == True) & (df_out_filtered['Color 1'].notna() == False)]
    df_out_colors_2 = df_out_filtered.loc[(df_out_filtered['Color 0'].notna()
    ↪ == True) & (df_out_filtered['Color 1'].notna() == True)]
    return df_out_colors_1, df_out_colors_2

def chartColorAdoptionLikelihood(df_colors, color_relation, days_limit):
    disclaimer = f"For animals in shelter more than {days_limit} days"

    # Wilson confidence interval
    # https://en.wikipedia.org/wiki/Binomial_proportion_confidence_interval

    alpha = 0.01
    z = st.norm.ppf(1 - (alpha / 2))
    n = df_colors.Count
    p = df_colors.Adopted
    p_center = (1 / (1 + ((z ** 2) / n))) * (p + ((z ** 2) / (2 * n)))
    p_halfextent = (z / (1 + ((z ** 2) / n))) * (((p * (1 - p)) / (n)) + ((z
    ↪ ** 2) / (4 * (n ** 2)))) * (1/2)
    p_low = p_center - p_halfextent
    p_high = p_center + p_halfextent

    colors = [rgb(color) for color in df_colors.index]
    colors = [color if color[0] != None else '0.3' for color in colors]

```

```

plt.figure(num=None, figsize=(5, 12), dpi=96, facecolor='w', edgecolor='k')
plt.title(f'Probability of an animal with this {color_relation} color being_
↳adopted ({floor(100 * (1 - alpha))}% confidence)\n{n{disclaimer}}')
ax = df_colors.Adopted.plot.barh(x='Color', xerr=[p_low, p_high], ecolor='0.
↳5', color=colors)
ax.set_xlim(0, 1)
plt.show()
print(f'{len(df_colors)} colors')
print()

def colors_single(days_limit):
    df_out_colors_1, df_out_colors_2 = color_dataframes(days_limit)
    colors_adopted = bigCorr_bernoulli(df_out_colors_1, 'Color 0', 'Adopted')
    colors_count = df_out_colors_1['Color 0'].value_counts()
    df_colors = pd.DataFrame(index=colors_count.index)
    df_colors = df_colors.assign(Color=colors_count.index, Count=colors_count,
↳Adopted=colors_adopted)
    df_colors.sort_values(by='Adopted', ascending=False, inplace=True)
    chartColorAdoptionLikelihood(df_colors, 'single', days_limit)

def colors_mixed(days_limit):
    df_out_colors_1, df_out_colors_2 = color_dataframes(days_limit)
    colors_adopted = bigCorr_bernoulli_custom_colors_2(df_out_colors_1,
↳df_out_colors_2)
    colors_count = df_out_colors_2['Color 0'].value_counts().
↳add(df_out_colors_2['Color 1'].value_counts(), fill_value=0)
    df_colors = pd.DataFrame(index=colors_count.index)
    df_colors = df_colors.assign(Color=colors_count.index, Count=colors_count,
↳Adopted=colors_adopted)
    df_colors.sort_values(by='Adopted', ascending=False, inplace=True)
    chartColorAdoptionLikelihood(df_colors, 'mixed', days_limit)

def colors_singleOrMixed(days_limit):
    df_out_colors_1, df_out_colors_2 = color_dataframes(days_limit)
    colors_adopted = bigCorr_bernoulli_custom_colors_1_or_2(df_out_colors_1,
↳df_out_colors_2)
    colors_count = df_out_colors_1['Color 0'].value_counts().
↳add(df_out_colors_2['Color 0'].value_counts(), fill_value=0).
↳add(df_out_colors_2['Color 1'].value_counts(), fill_value=0)
    df_colors = pd.DataFrame(index=colors_count.index)
    df_colors = df_colors.assign(Color=colors_count.index, Count=colors_count,
↳Adopted=colors_adopted)
    df_colors.sort_values(by='Adopted', ascending=False, inplace=True)
    chartColorAdoptionLikelihood(df_colors, 'single or mixed', days_limit)

```

```
colors_single(5)
colors_single(10)
colors_single(30)
colors_mixed(5)
colors_mixed(10)
colors_mixed(30)
colors_singleOrMixed(5)
colors_singleOrMixed(10)
colors_singleOrMixed(30)
```

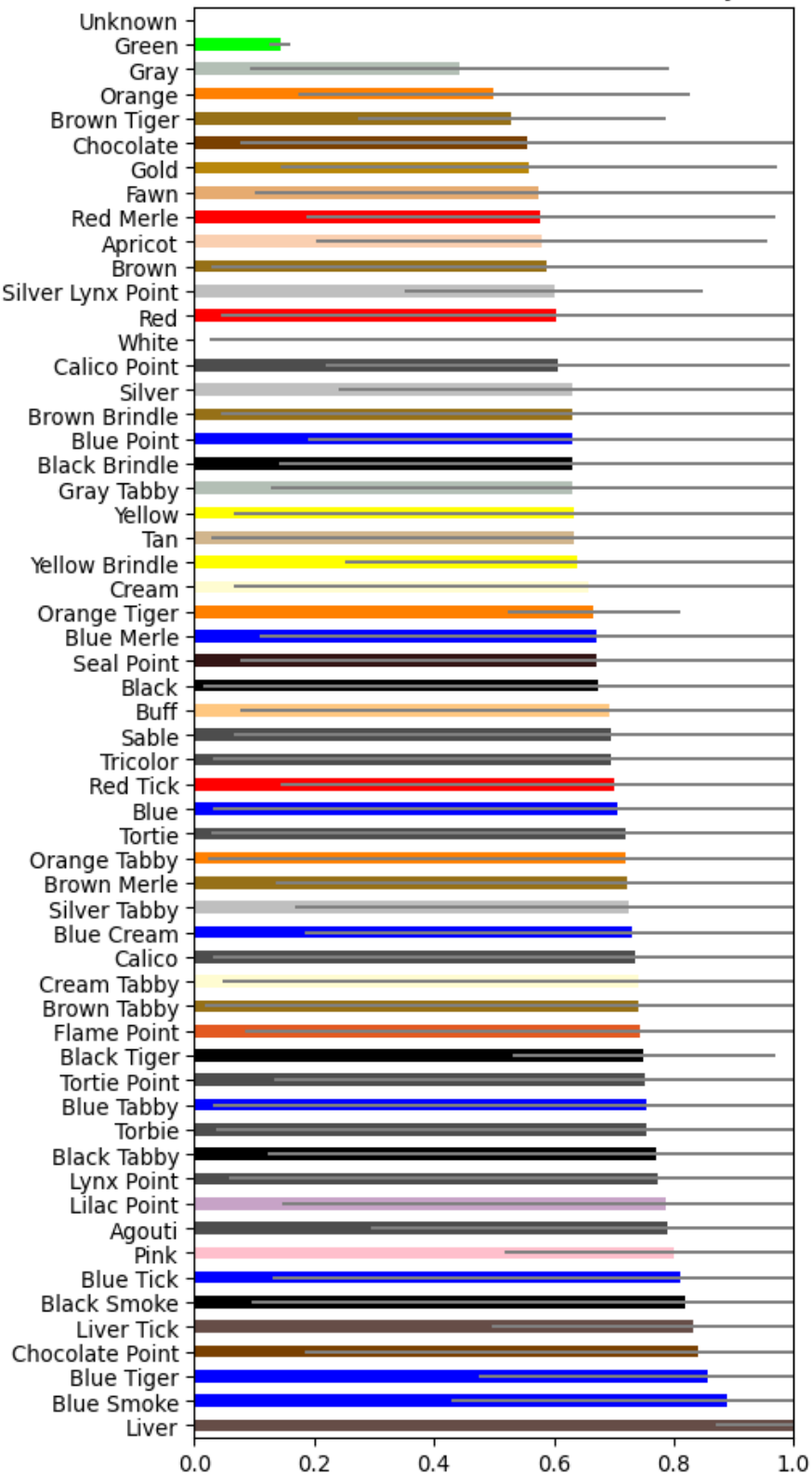
```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in
reduce
```

```
    return umr_minimum(a, axis, None, out, keepdims, initial, where)
```

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in
reduce
```

```
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

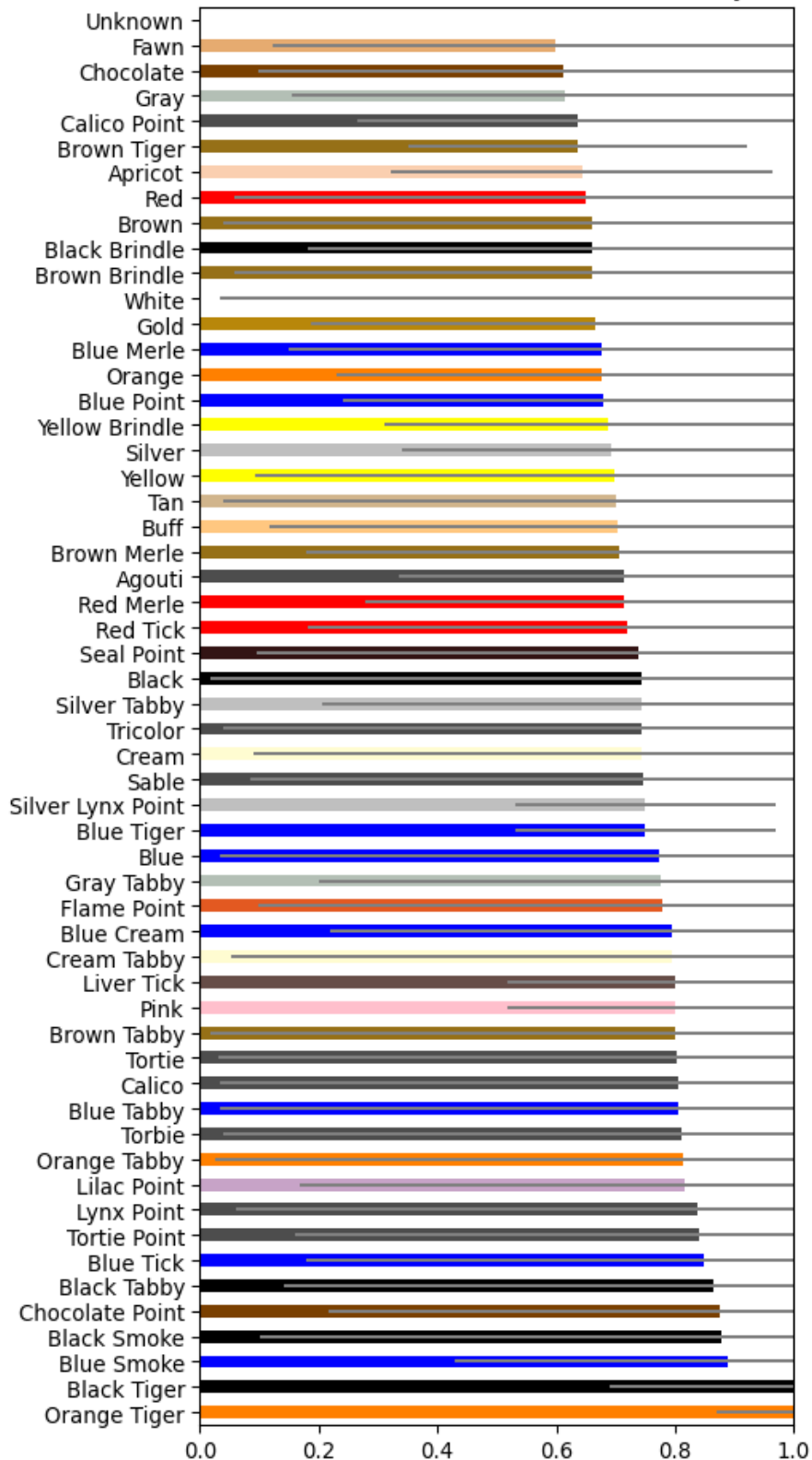
Probability of an animal with this single color being adopted (99% confidence)
For animals in shelter more than 5 days



58 colors

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_minimum(a, axis, None, out, keepdims, initial, where)  
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

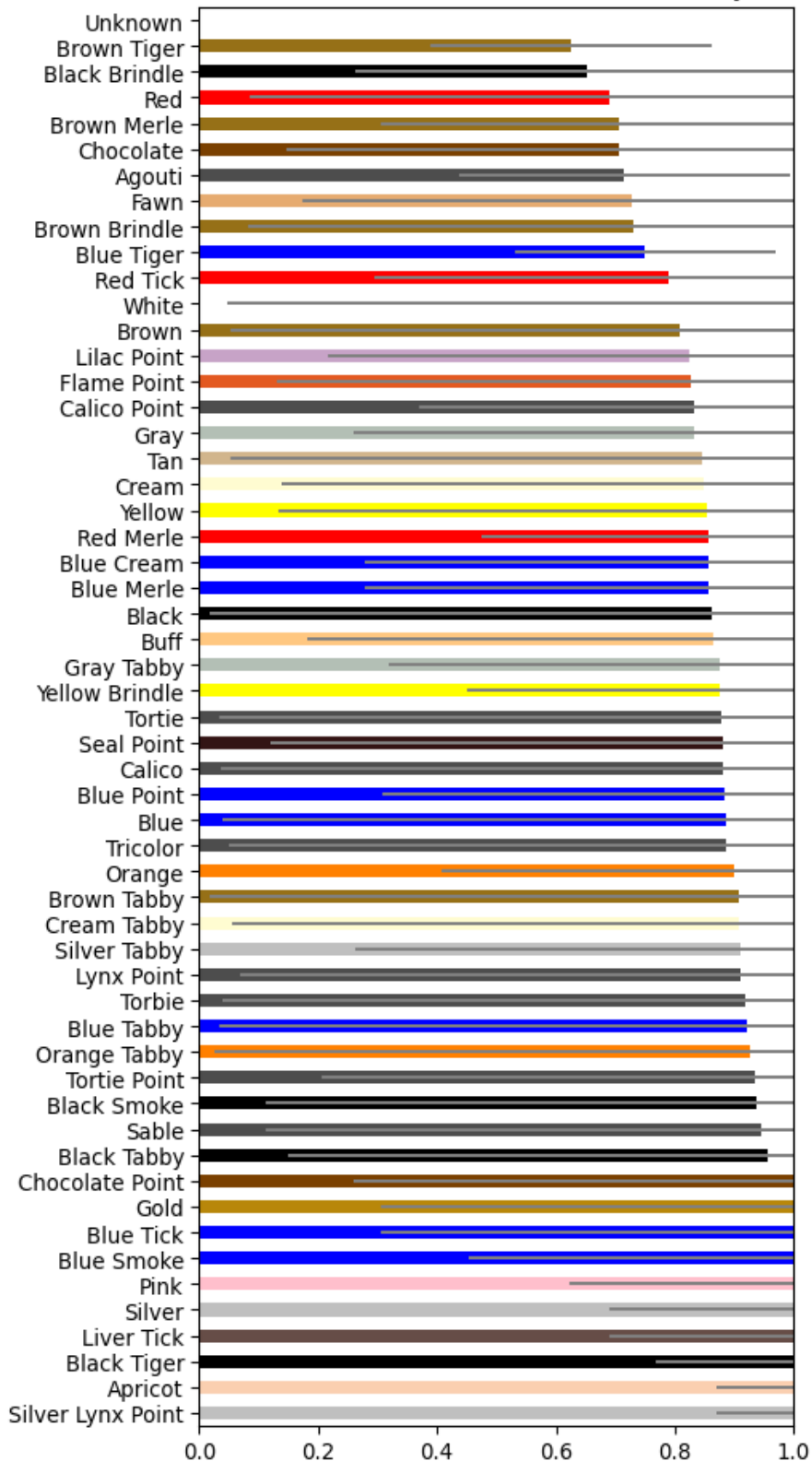
Probability of an animal with this single color being adopted (99% confidence)
For animals in shelter more than 10 days



56 colors

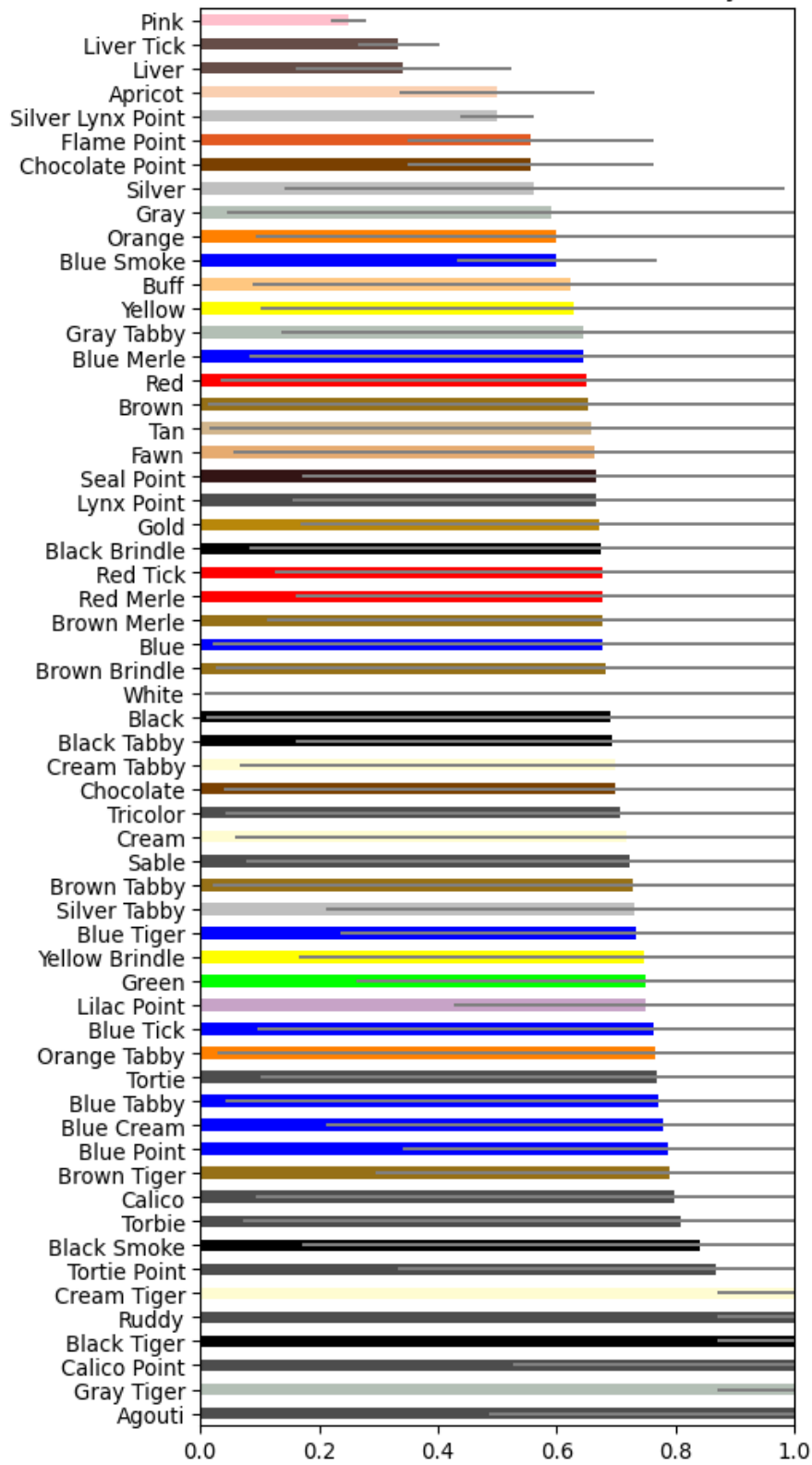
```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_minimum(a, axis, None, out, keepdims, initial, where)  
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

Probability of an animal with this single color being adopted (99% confidence)
For animals in shelter more than 30 days



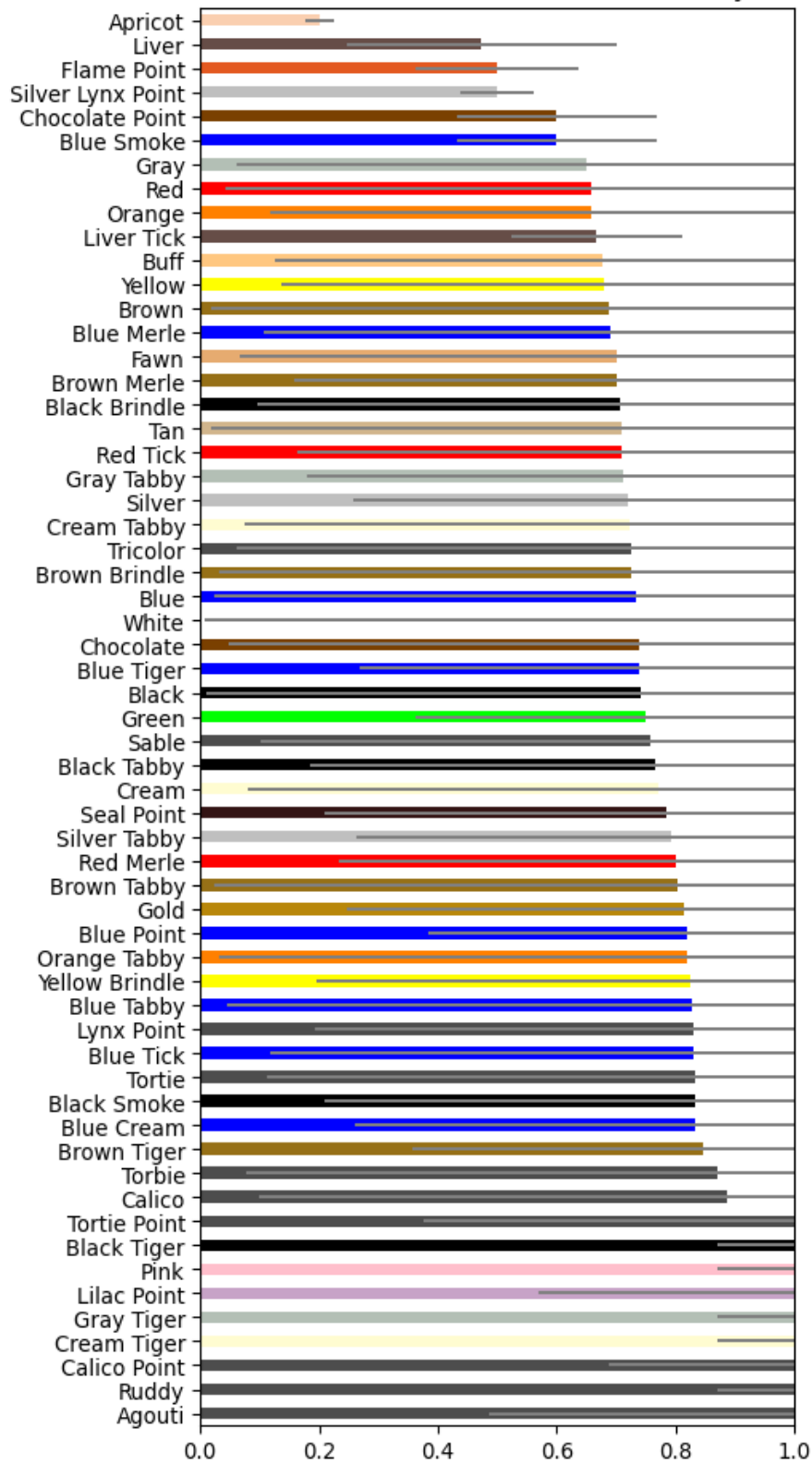
55 colors

Probability of an animal with this mixed color being adopted (99% confidence)
For animals in shelter more than 5 days



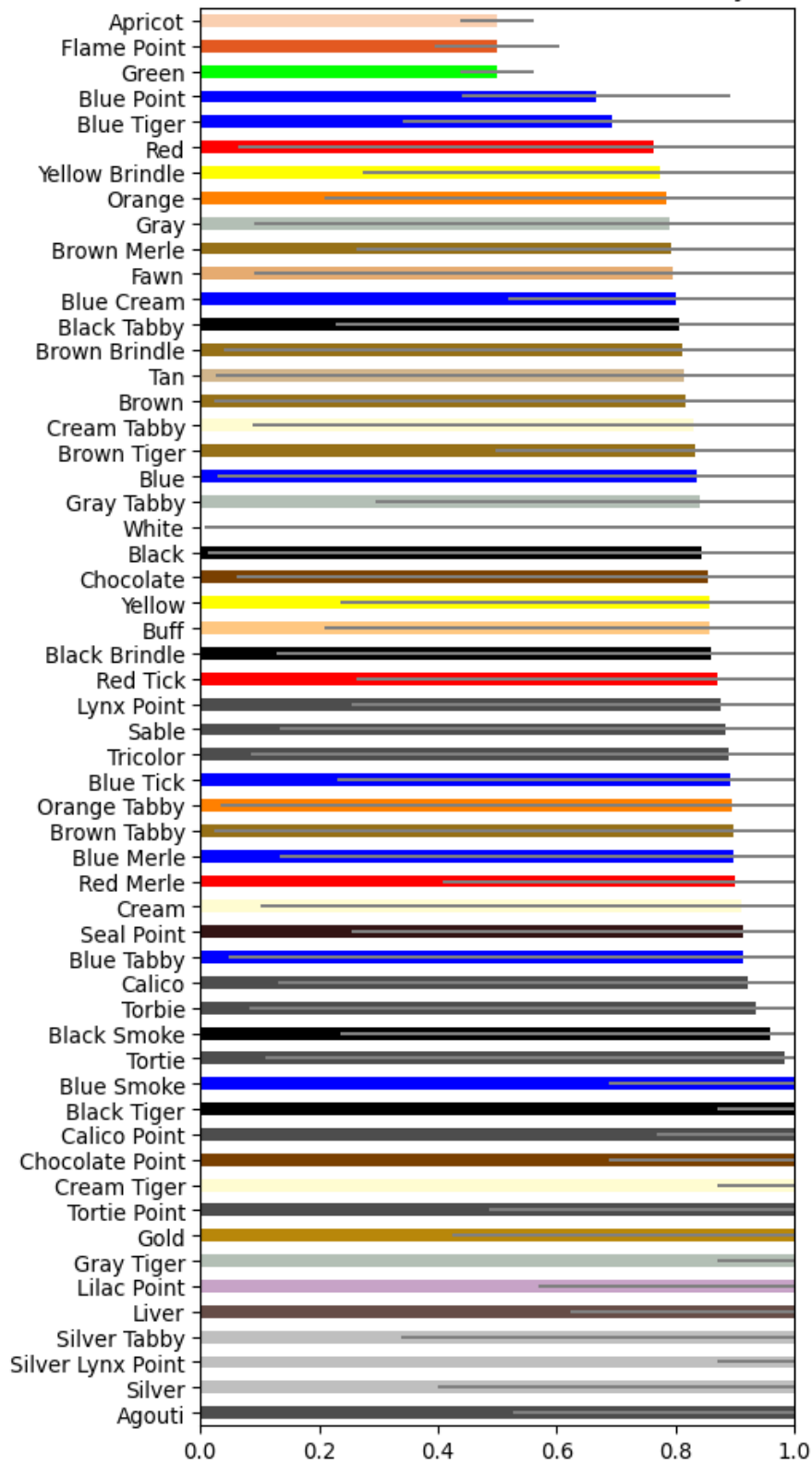
59 colors

Probability of an animal with this mixed color being adopted (99% confidence)
For animals in shelter more than 10 days



59 colors

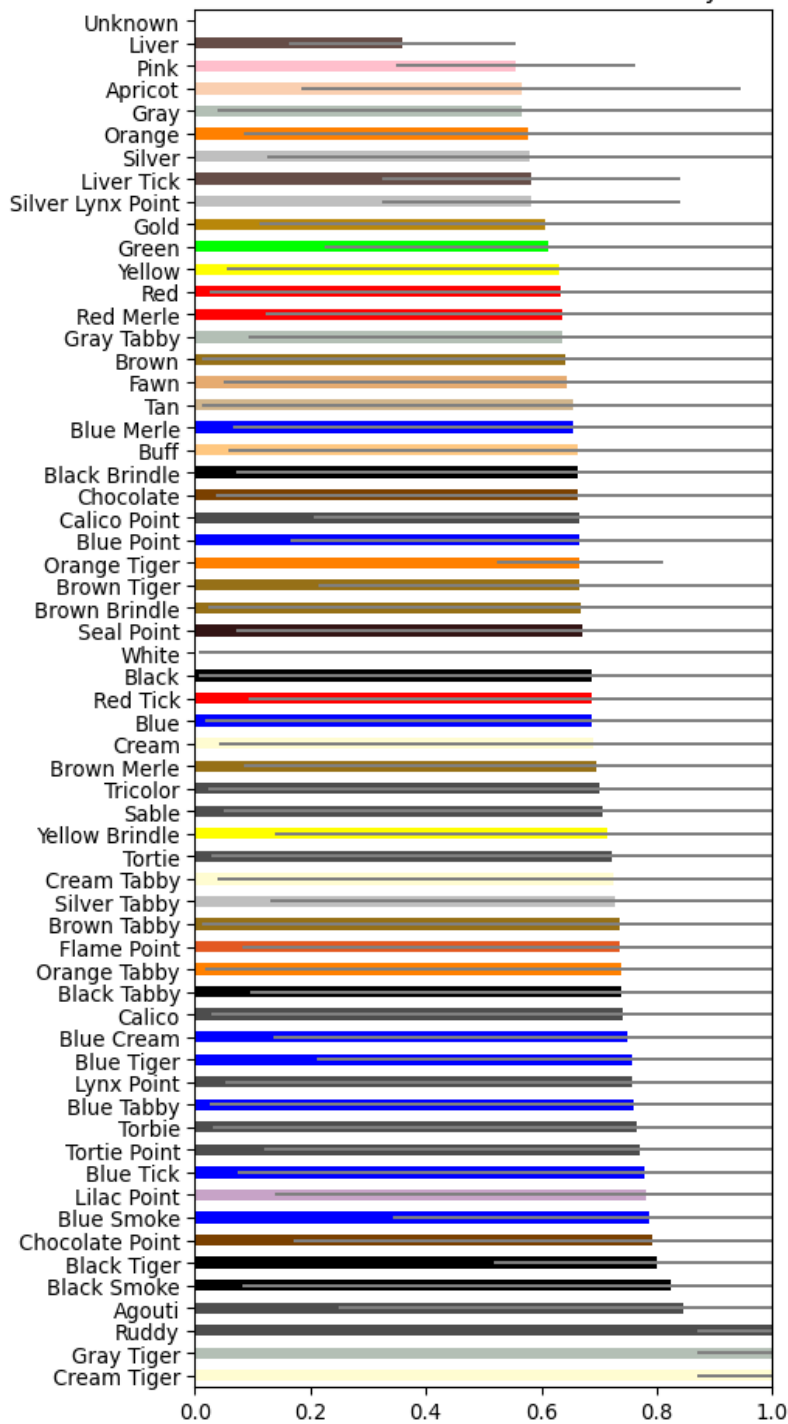
Probability of an animal with this mixed color being adopted (99% confidence)
For animals in shelter more than 30 days



56 colors

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_minimum(a, axis, None, out, keepdims, initial, where)  
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

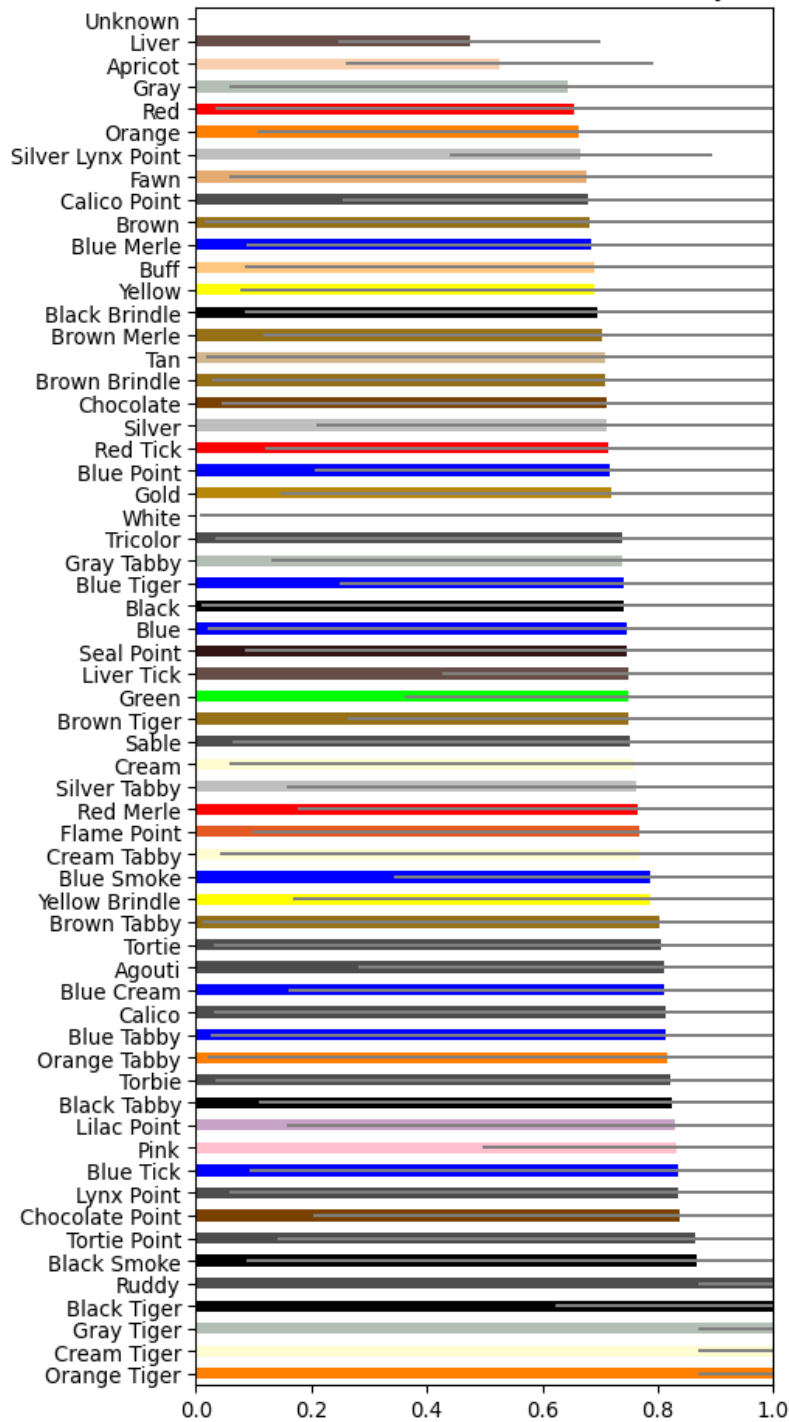
Probability of an animal with this single or mixed color being adopted (99% confidence)
For animals in shelter more than 5 days



61 colors

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_minimum(a, axis, None, out, keepdims, initial, where)  
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

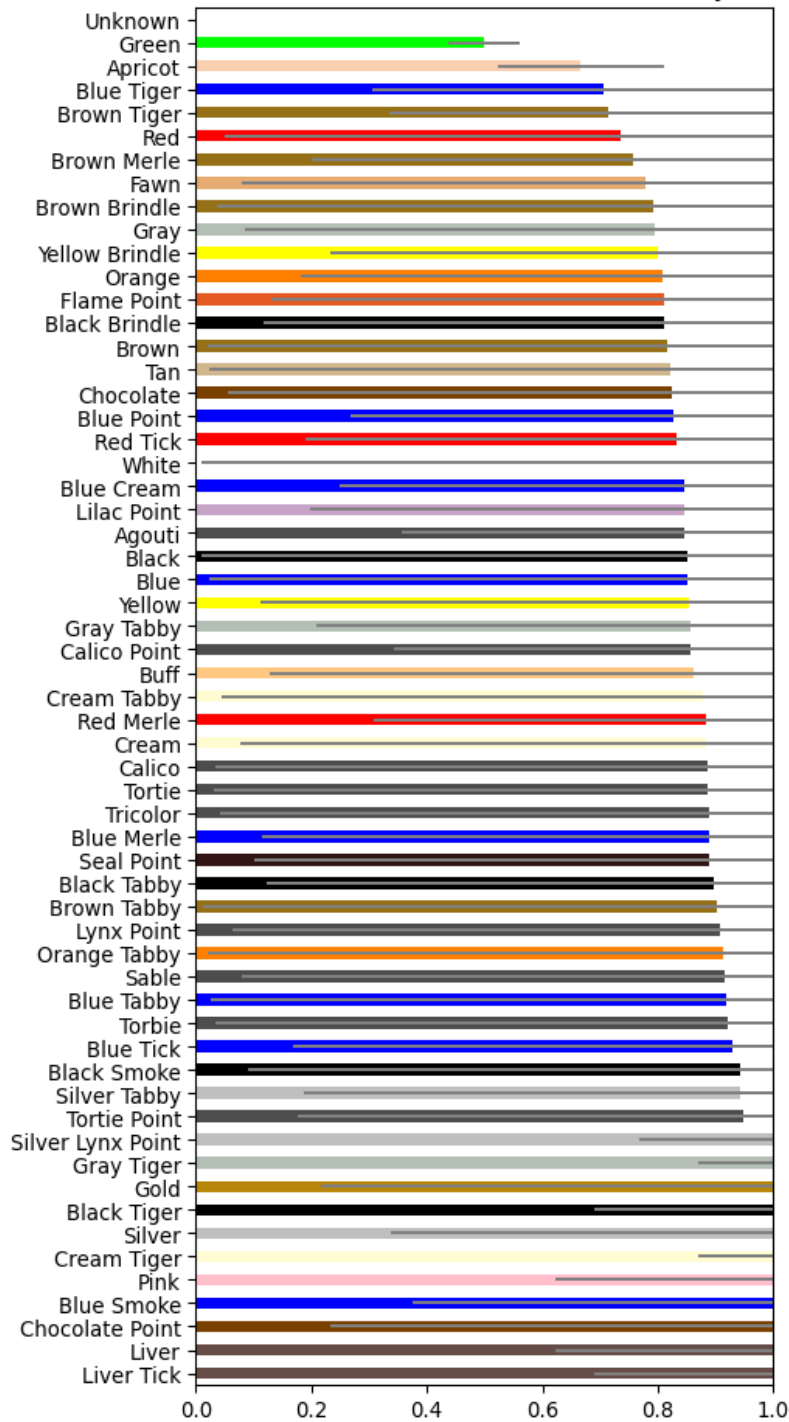
Probability of an animal with this single or mixed color being adopted (99% confidence)
For animals in shelter more than 10 days



61 colors

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_minimum(a, axis, None, out, keepdims, initial, where)  
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in  
reduce  
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

Probability of an animal with this single or mixed color being adopted (99% confidence)
For animals in shelter more than 30 days



59 colors

2.2 Sex

```
[19]: # TODO 6: regress sex against adoption likelihood
# Please make 3 bar charts:
# - "Sex upon Outcome" (neutered male, spayed female, intact male, intact
  ↪ female)
# - male or female
# - neutered/spayed or intact
# Also please construct the 95% confidence interval and make it the error bars
# see the earlier cell in the section on color for an example of how to do this
days_limit = 5
confidence = 95
df = animalsLongerThan(days_limit)
df = df[['Sex upon Intake', 'Sex upon Outcome', 'Adopted']]
df = df.dropna()
df['NeuteredOrSpayed_Intake'] = (df['Sex upon Intake'].str.contains("Neuter")) |
  ↪ (df['Sex upon Intake'].str.contains("Spay"))
df['NeuteredOrSpayed_Outcome'] = (df['Sex upon Outcome'].str.
  ↪ contains("Neuter")) | (df['Sex upon Outcome'].str.contains("Spay"))
df['NeuteredOrSpayed_InCenter'] = df['NeuteredOrSpayed_Outcome'] &
  ↪ df['NeuteredOrSpayed_Intake']

plt.figure(figsize=(7,3))
ax=sns.barplot(
    data=df,
    y='Sex upon Intake',
    x='Adopted',
    estimator='mean',
    errorbar=('ci', confidence)
)
ax.set_xlim(0,1)
plt.title(f'P(Adoption | Sex [intake]) ({confidence}% confidence interval)\nFor
  ↪ animals in center more than {days_limit} days')
plt.xlabel("P(Adoption)")
plt.show()

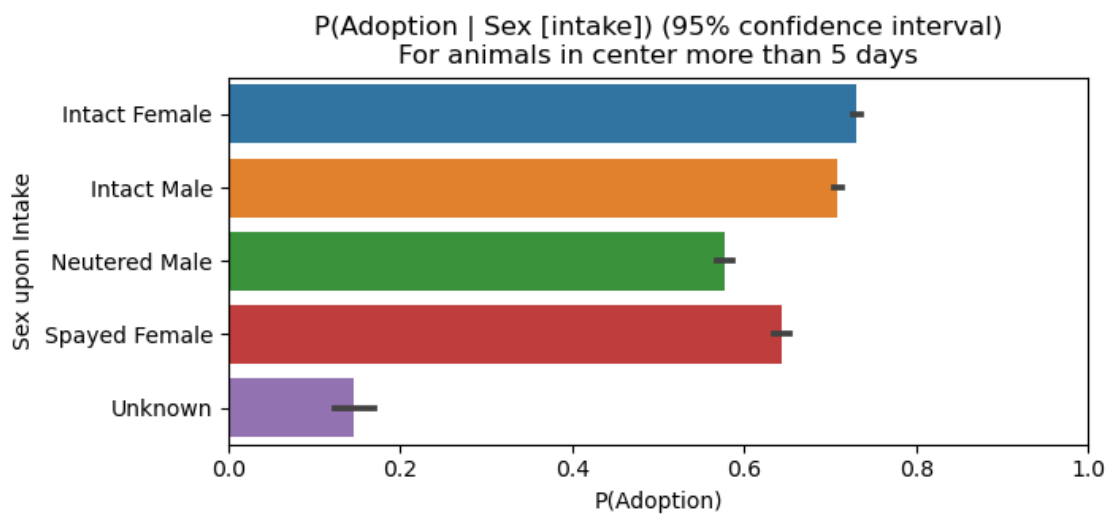
plt.figure(figsize=(7,3))
ax=sns.barplot(
    data=df,
    y='Sex upon Outcome',
    x='Adopted',
    estimator='mean',
    errorbar=('ci', confidence)
)
ax.set_xlim(0,1)
plt.title(f'P(Adoption | Sex [outcome]) ({confidence}% confidence
  ↪ interval)\nFor animals in center more than {days_limit} days')
```

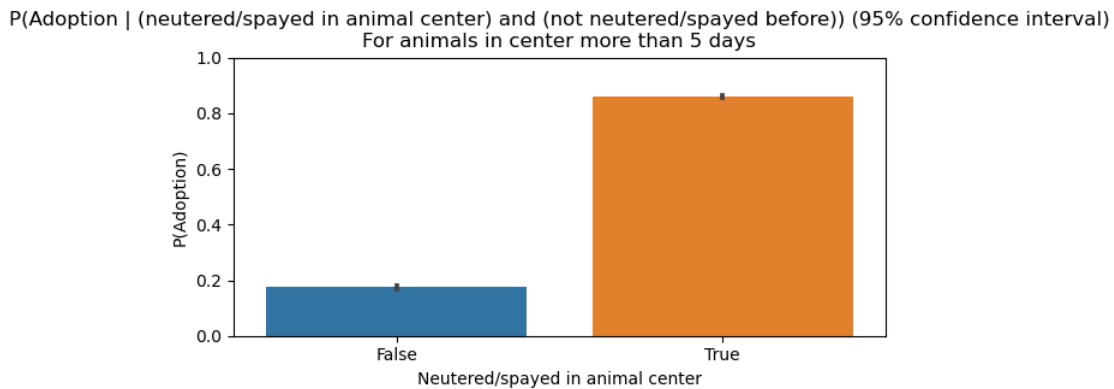
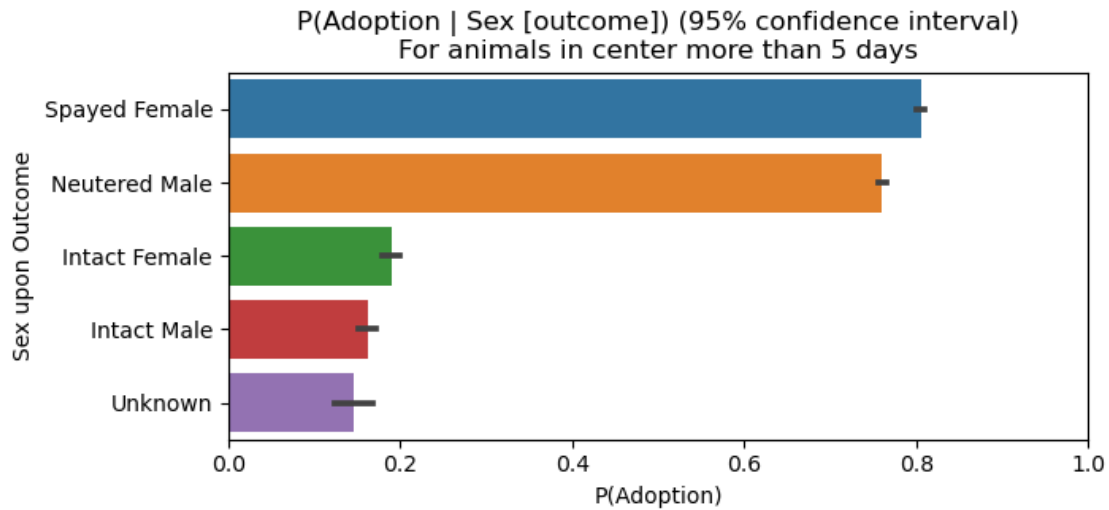
```

plt.xlabel("P(Adoption)")
plt.show()

plt.figure(figsize=(7,3))
ax=sns.barplot(
    data=df.loc[(df['NeuteredOrSpayed_Intake'] == False) & (df['Sex upon_
    ↪Outcome'] != 'Unknown')],
    x='NeuteredOrSpayed_InCenter',
    y='Adopted',
    estimator='mean',
    errorbar=('ci', confidence)
)
ax.set_ylim(0,1)
plt.title(f'P(Adoption | (neutered/spayed in animal center) and (not neutered/
    ↪spayed before)) ({confidence}% confidence interval)\nFor animals in center_
    ↪more than {days_limit} days')
plt.xlabel("Neutered/spayed in animal center")
plt.ylabel("P(Adoption)")
plt.show()

```





2.3 Breed characteristics

This analysis considers individual animals and looks for correlations between characteristics of their breed and their outcome.

It looks like the animals belonging to a breed with an average height around 20-25 (inches?) are more likely to be adopted than others, and animals between 5-12 inches are less likely than others to be adopted.

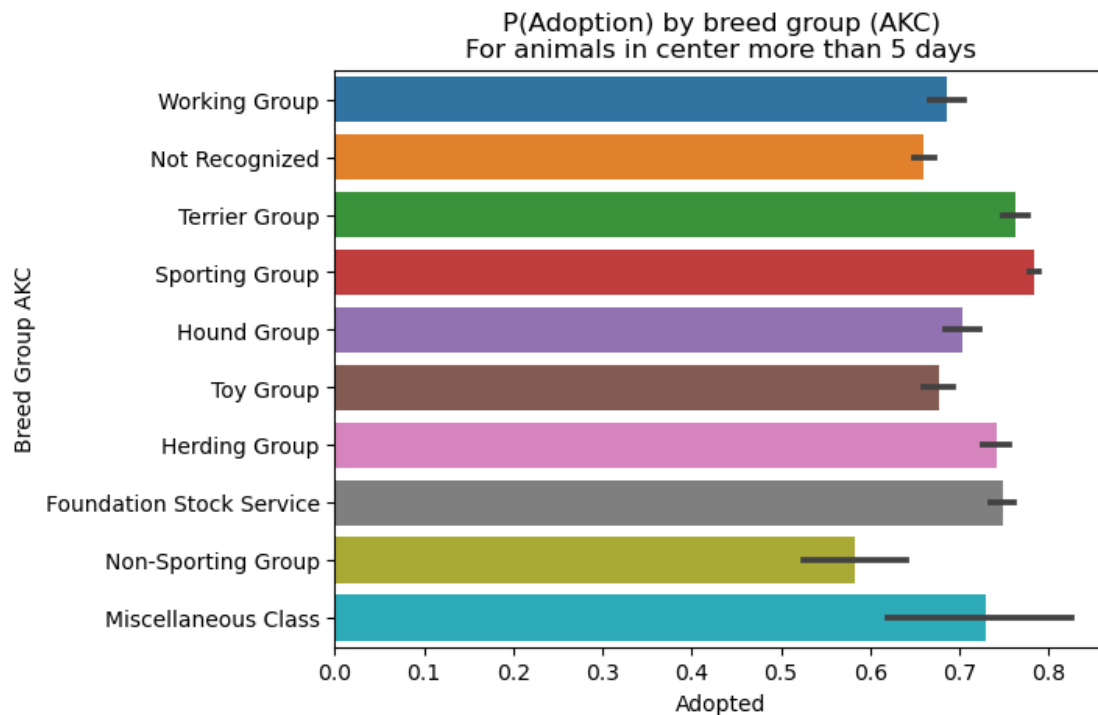
TODO 7: interpret the other graphs. Why are the different lifespan variables distributed the way they are, and why are they distributed differently compared to each other?

```
[20]: day_limit = 10
df_out_1 = animalsLongerThan(day_limit)
df_out_1 = df_out_1.assign(Adopted=df_out_1.Adopted.fillna(False))
```

```

ax=sns.barplot(data=df_out_1,
               y='Breed Group AKC',
               x='Adopted',
               estimator="mean")
plt.title(f"P(Adoption) by breed group (AKC)\nFor animals in center more than_{days_limit} days")
plt.show()

```



```

[21]: day_limit = 10
df_out_1 = animalsLongerThan(day_limit)
df_out_1 = df_out_1.assign(Adopted=df_out_1.Adopted.fillna(False))
df_out_with_breeds_info_1 = df_out_with_breeds_info.assign(Adopted=df_out_1.
    ↳ Adopted.fillna(False))

def correlo_histogram(df, independent, dependent, binwidth):
    print(f'{independent} ~ {dependent}')
    # TODO 8: add error bars when the dependent variable is "Adopted"
    # (see how the confidence interval was constructed in the previous cell
    # for regression by color)

    ax=sns.histplot(data=df,
                    x=independent,
                    hue=dependent,

```

```

        multiple='fill',
        binwidth=binwidth)
sns.move_legend(ax, 'upper left', bbox_to_anchor=(1,1))
plt.ylabel(f"P({dependent})")
plt.show()

independent_vars_breeds_info = [
    ['average height', 2],
    ['Est. lifespan remaining', 1],
    ['average lifespan', 1],
    ['Lifespan Low', 1],
    ['Lifespan High', 1],
]

independent_vars_individuals = [
    ['Age upon Outcome (years)', 1],
    ['Years in animal center', 0.25],
    ['Color O H', 0.1],
    ['Color O S', 0.1],
    ['Color O V', 0.1],
]

for [independent, binwidth] in independent_vars_breeds_info:
    for dependent in ['Adopted', 'Outcome Type']:
        correlo_histogram(df_out_with_breeds_info_1, independent, dependent,
        ↪binwidth)

for [independent, binwidth] in independent_vars_individuals:
    for dependent in ['Adopted', 'Outcome Type']:
        correlo_histogram(df_out_1, independent, dependent, binwidth)

```

average height ~ Adopted

```

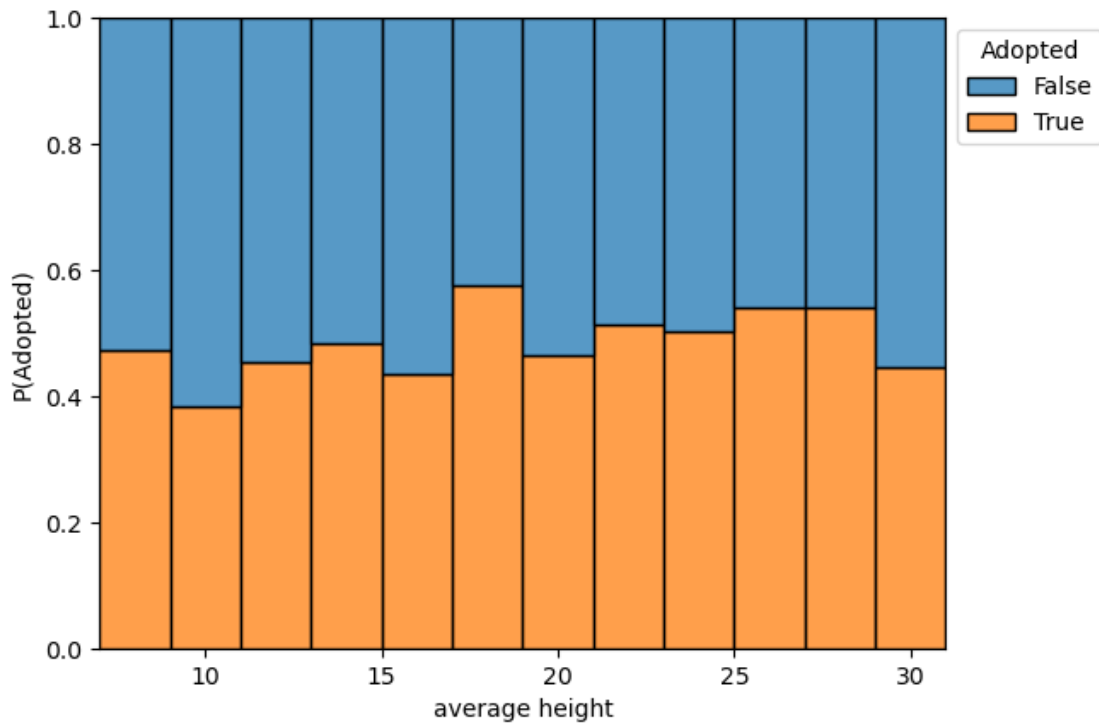
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
    pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
    pd.Index(widths, name="widths"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
    pd.Index(edges, name="edges"),

```

```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
pd.Index(widths, name="widths"),

```



average height ~ Outcome Type

```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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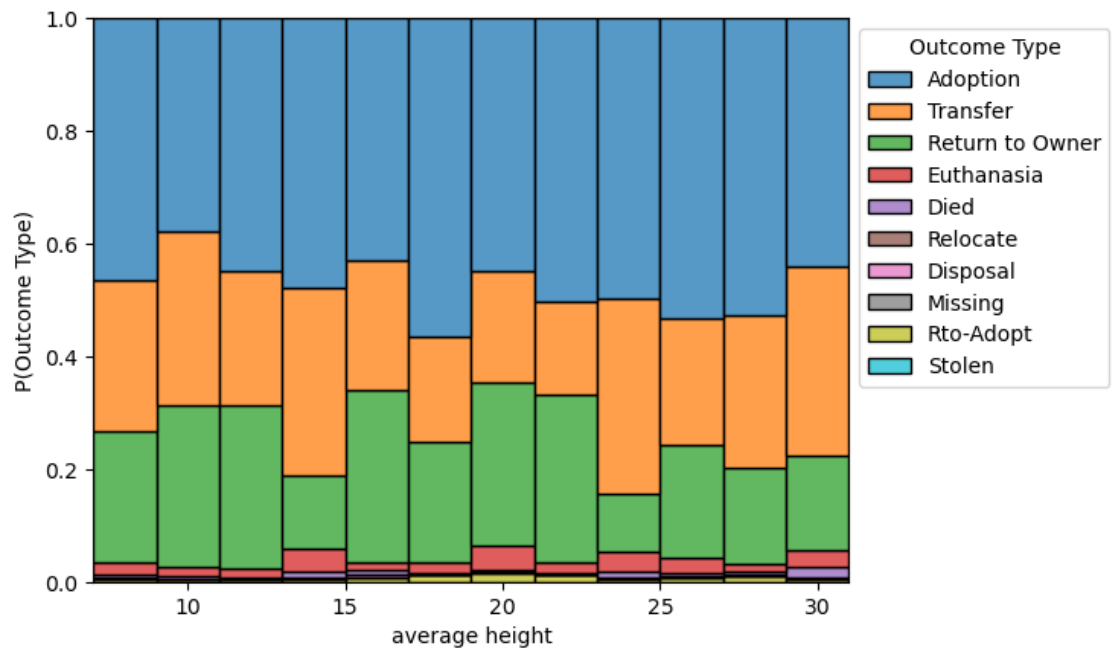
```



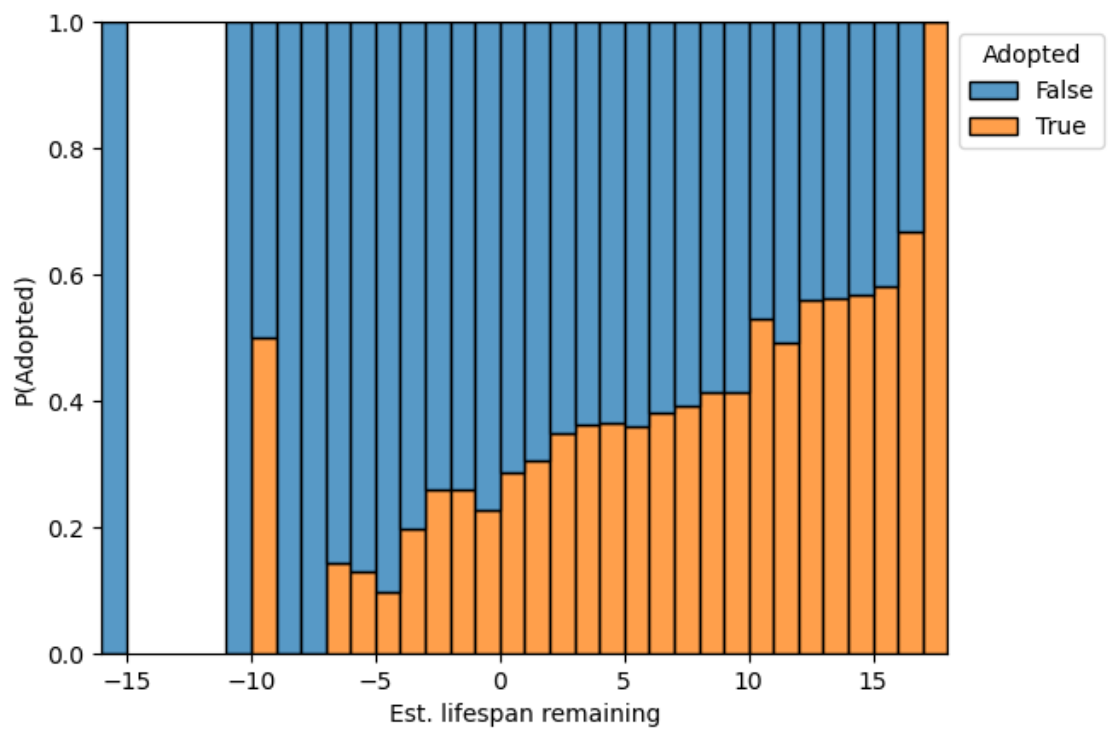
```

    pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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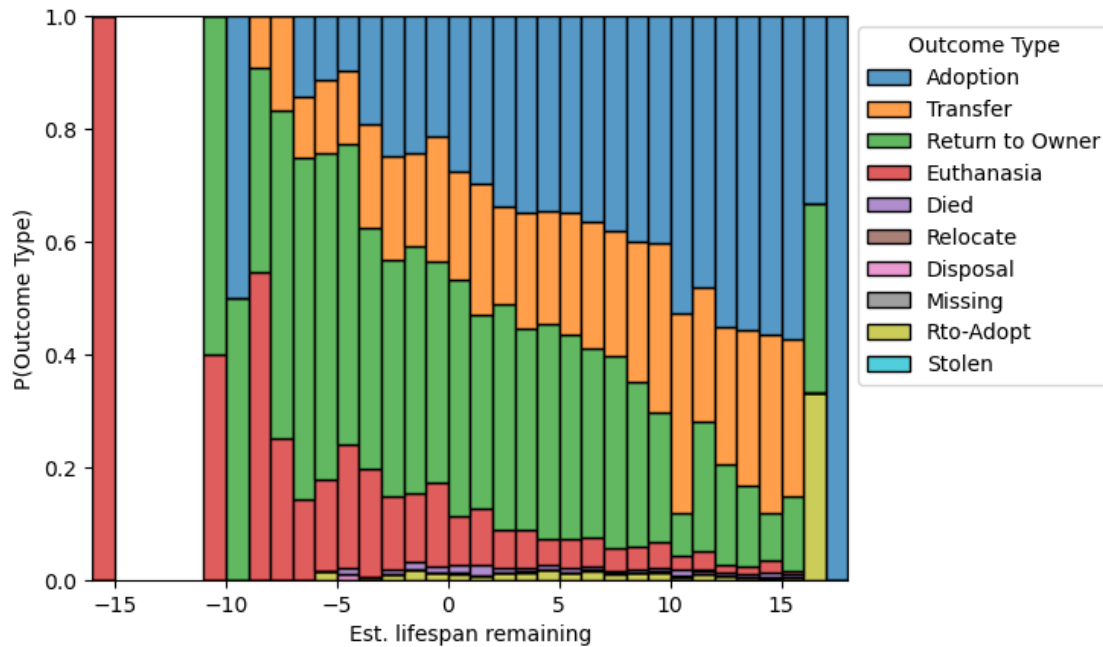
```

Est. lifespan remaining ~ Adopted

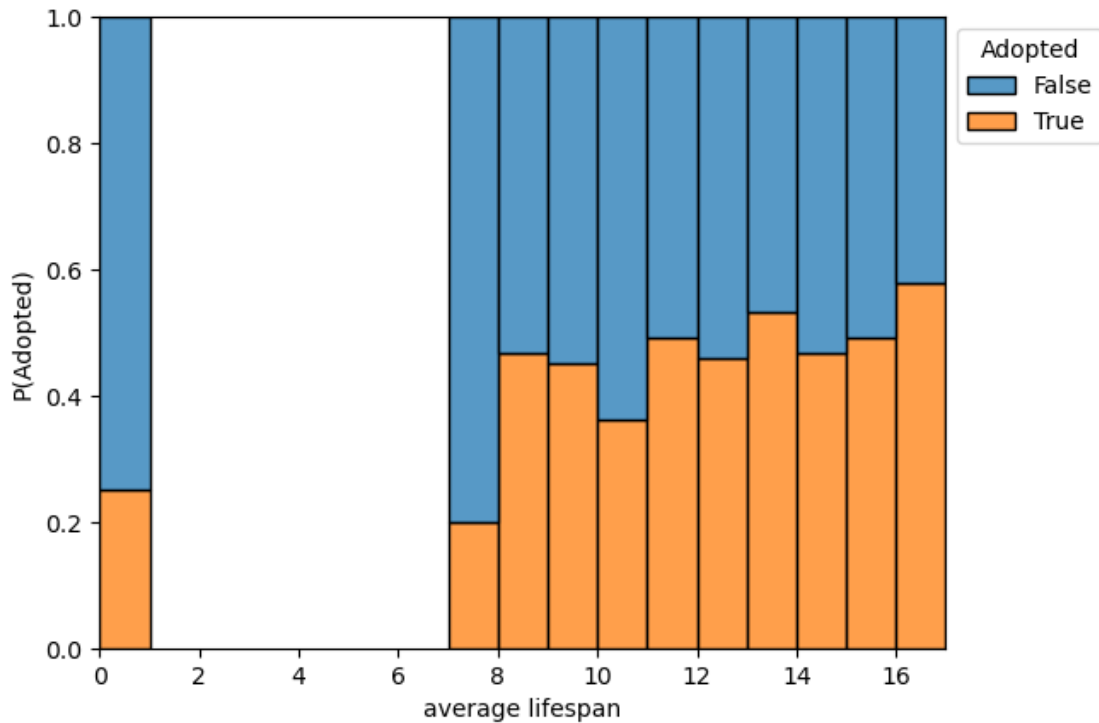


Est. lifespan remaining ~ Outcome Type



average lifespan ~ Adopted

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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average lifespan ~ Outcome Type

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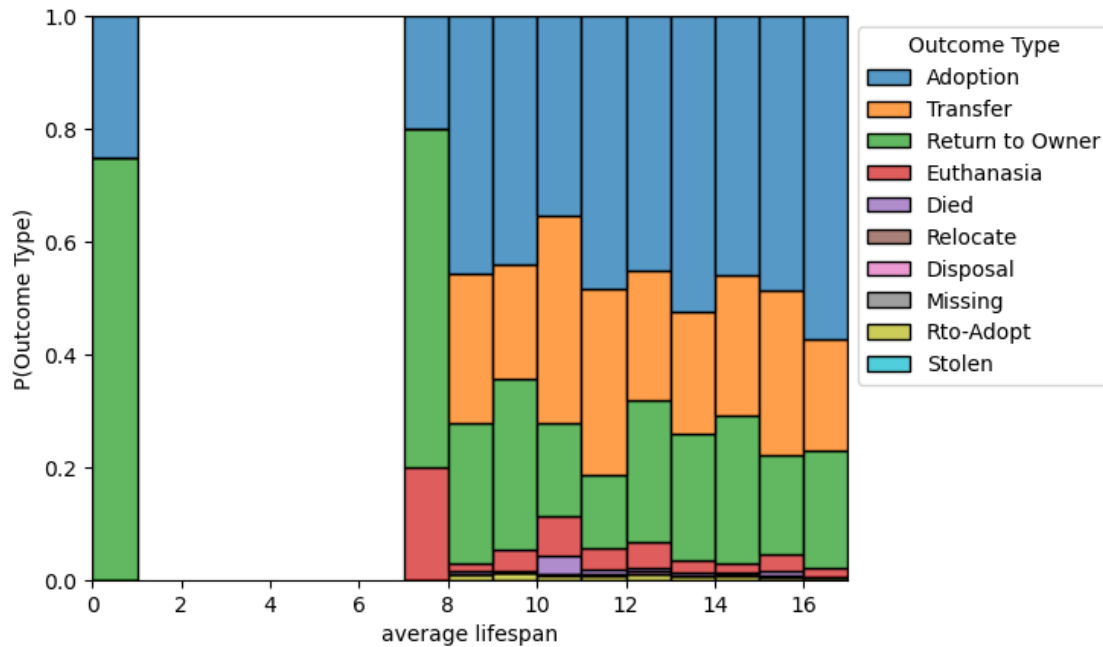
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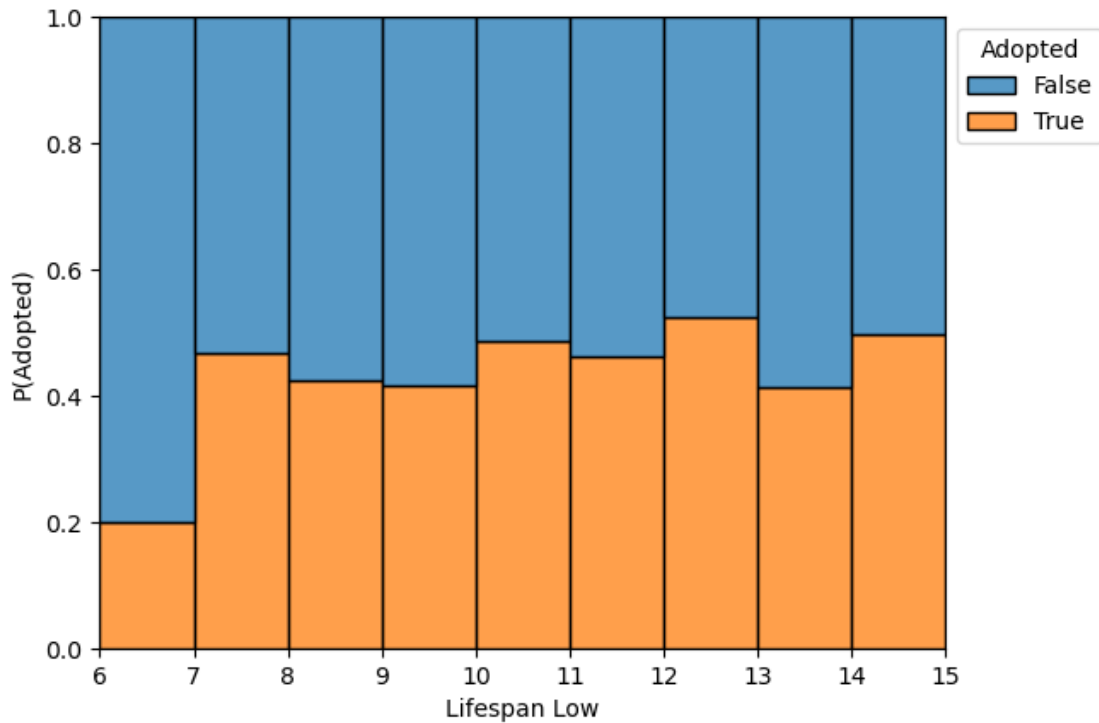


Lifespan Low ~ Adopted

```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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Lifespan Low ~ Outcome Type

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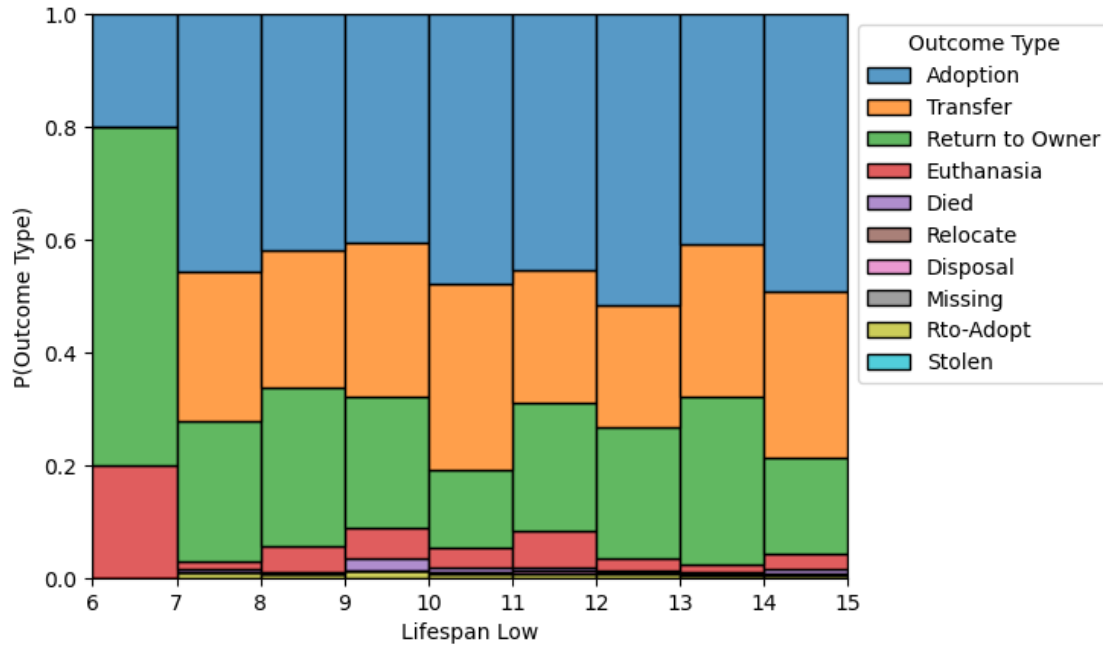
```



```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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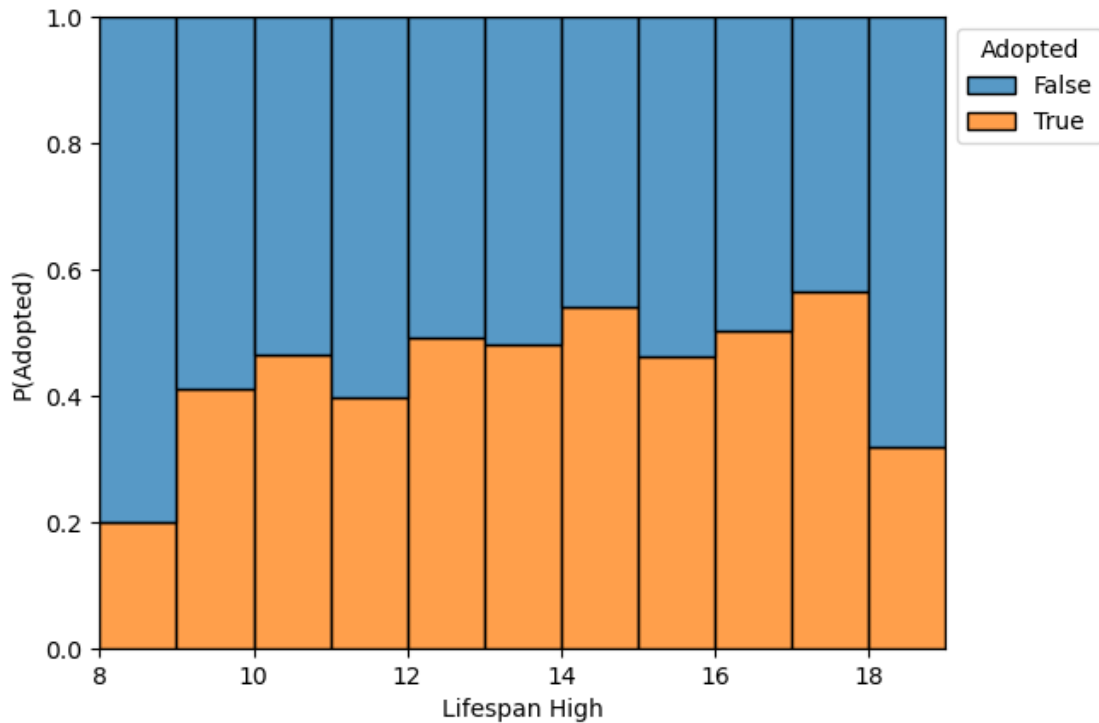


Lifespan High ~ Adopted

```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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Lifespan High ~ Outcome Type

```
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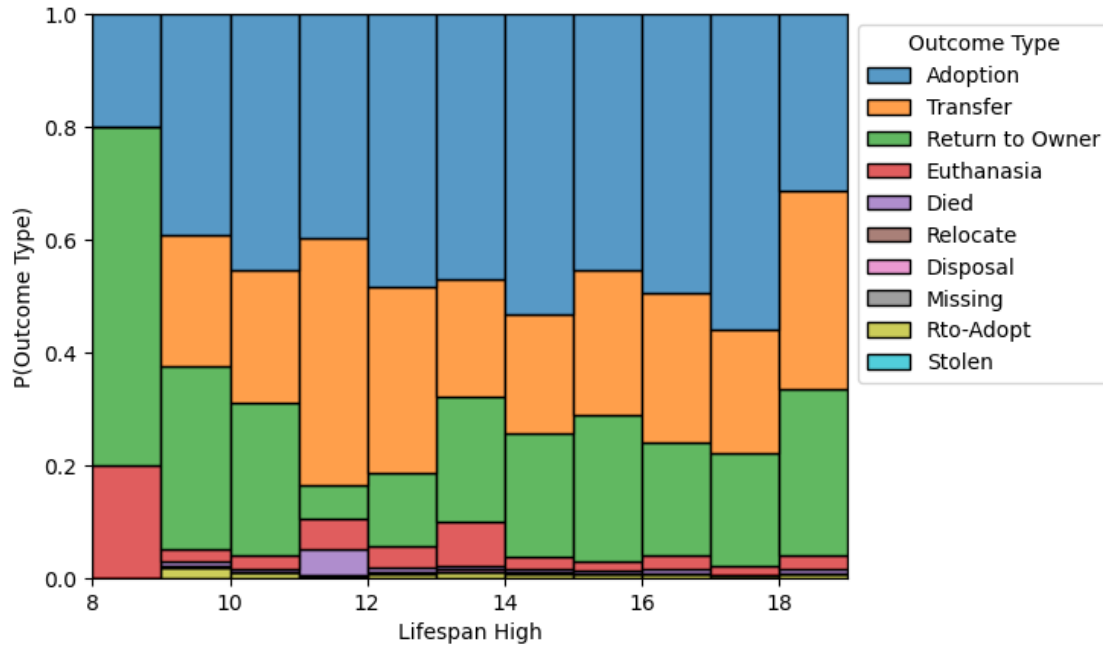
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Age upon Outcome (years) ~ Adopted

```
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```

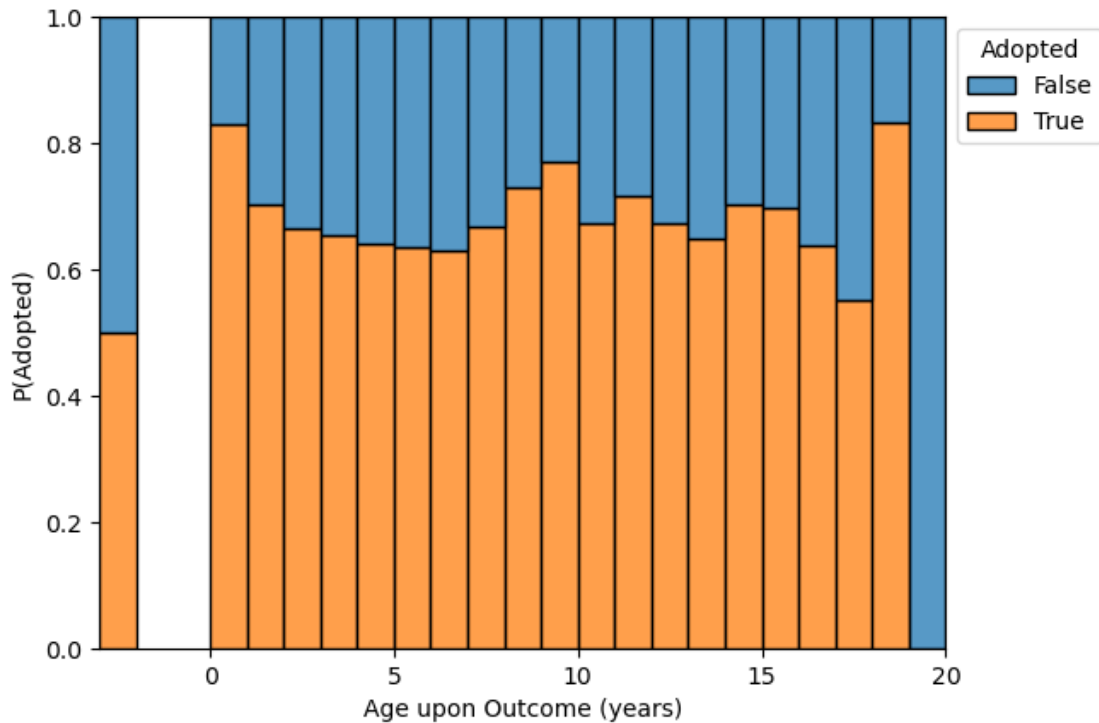
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pd.Index(widths, name="widths"),
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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Age upon Outcome (years) ~ Outcome Type

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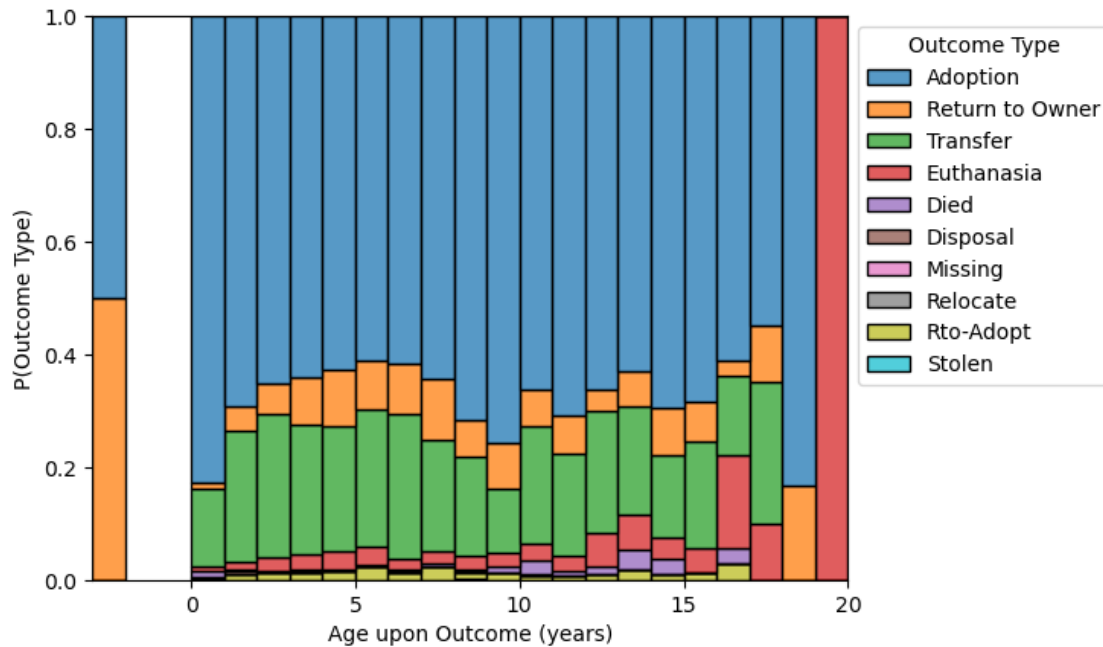
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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Years in animal center ~ Adopted

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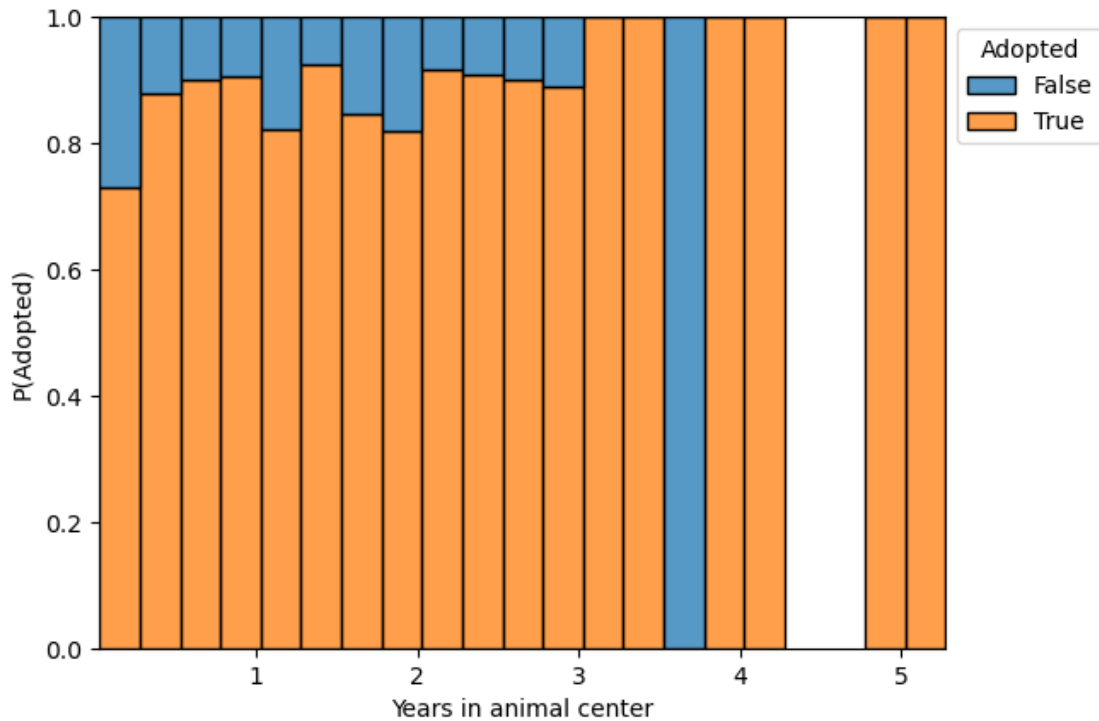
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Years in animal center ~ Outcome Type

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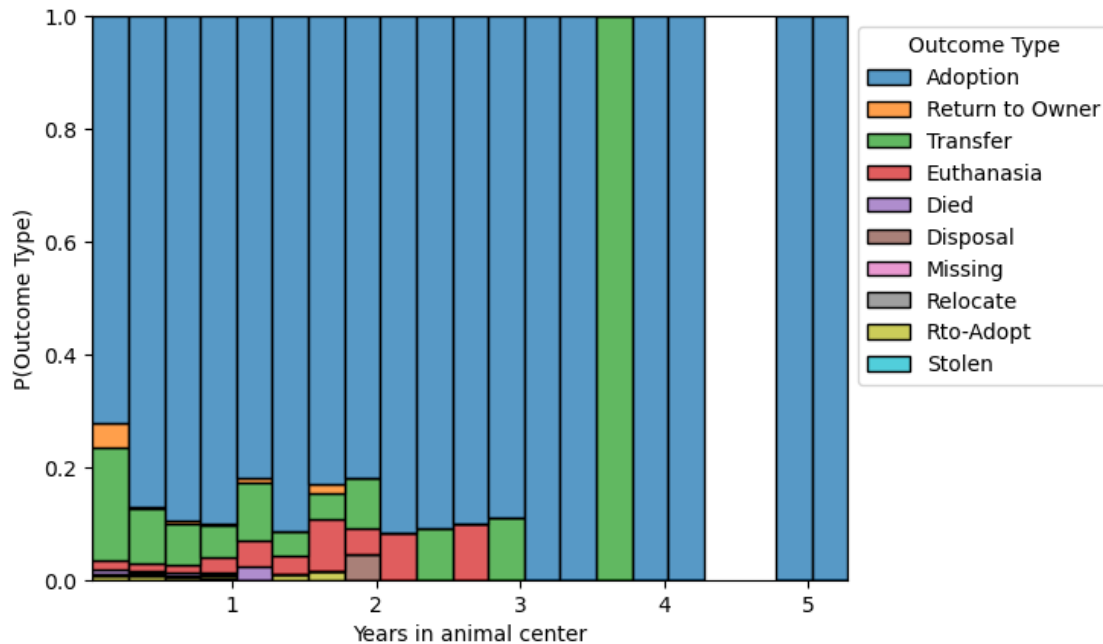
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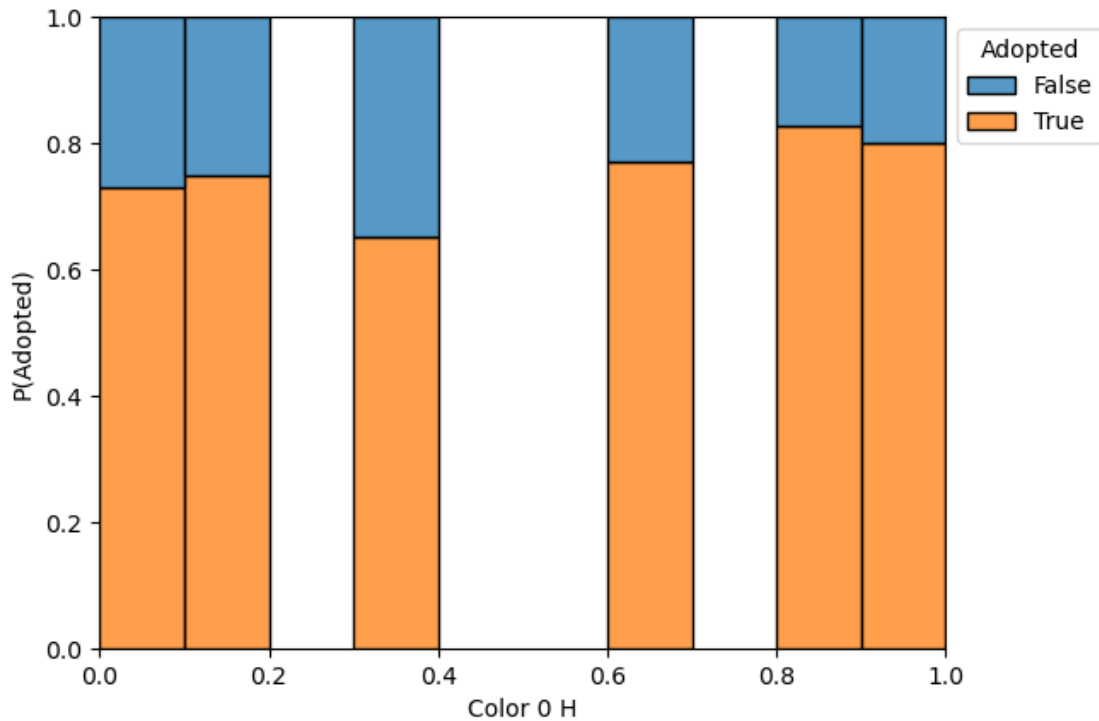


Color 0 H ~ Adopted

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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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Color 0 H ~ Outcome Type

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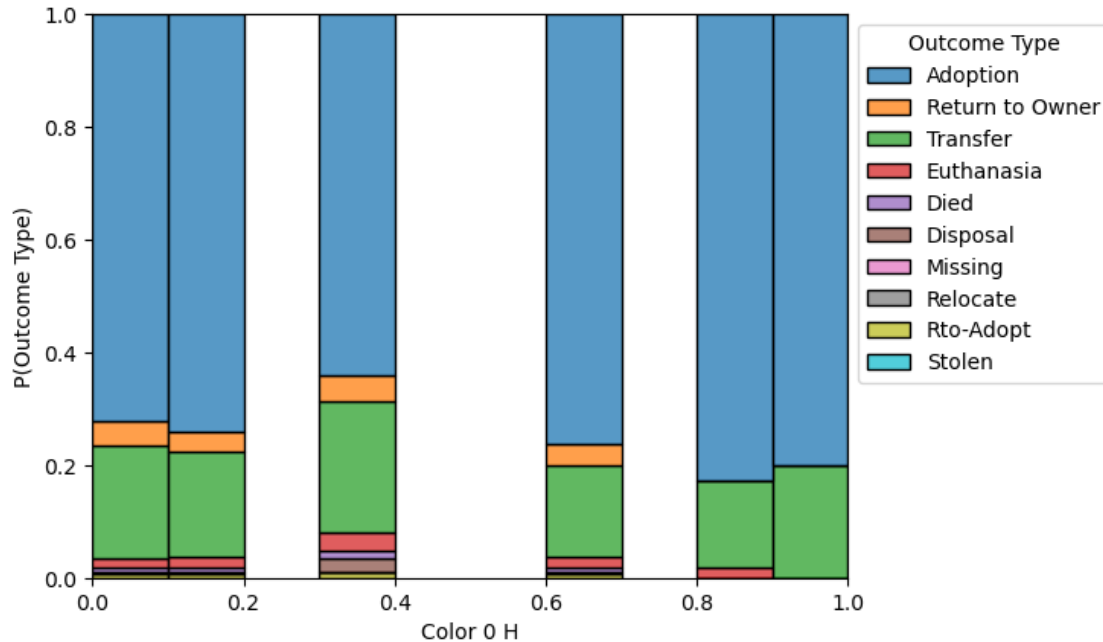
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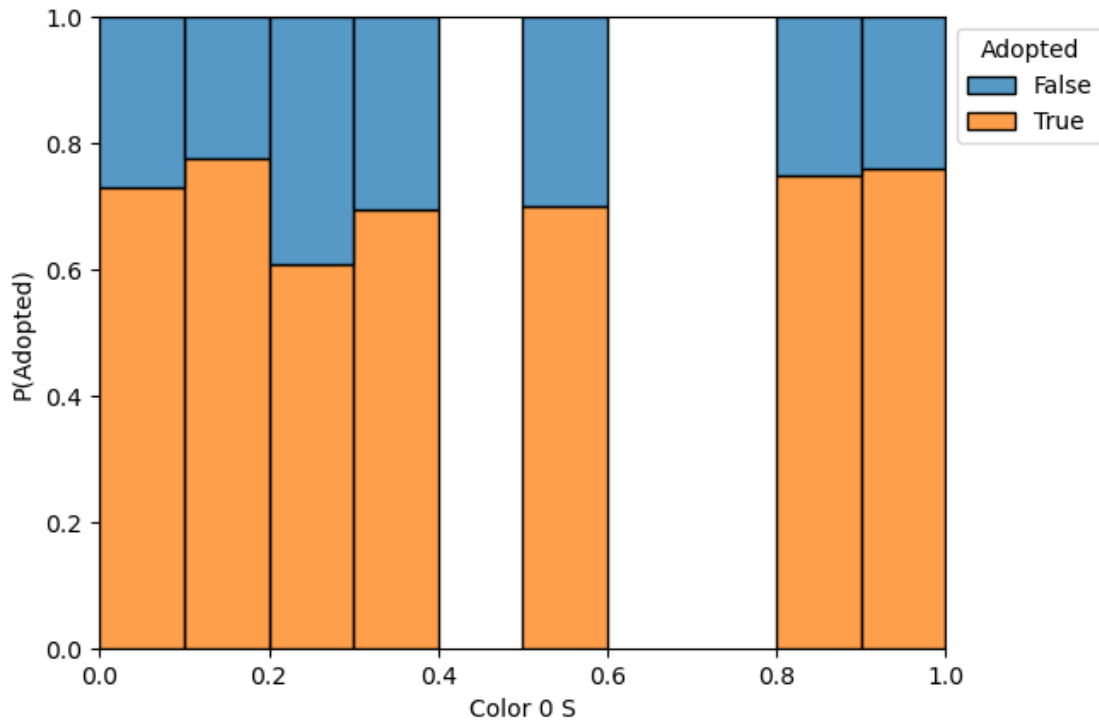


Color 0 S ~ Adopted

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Color 0 S ~ Outcome Type

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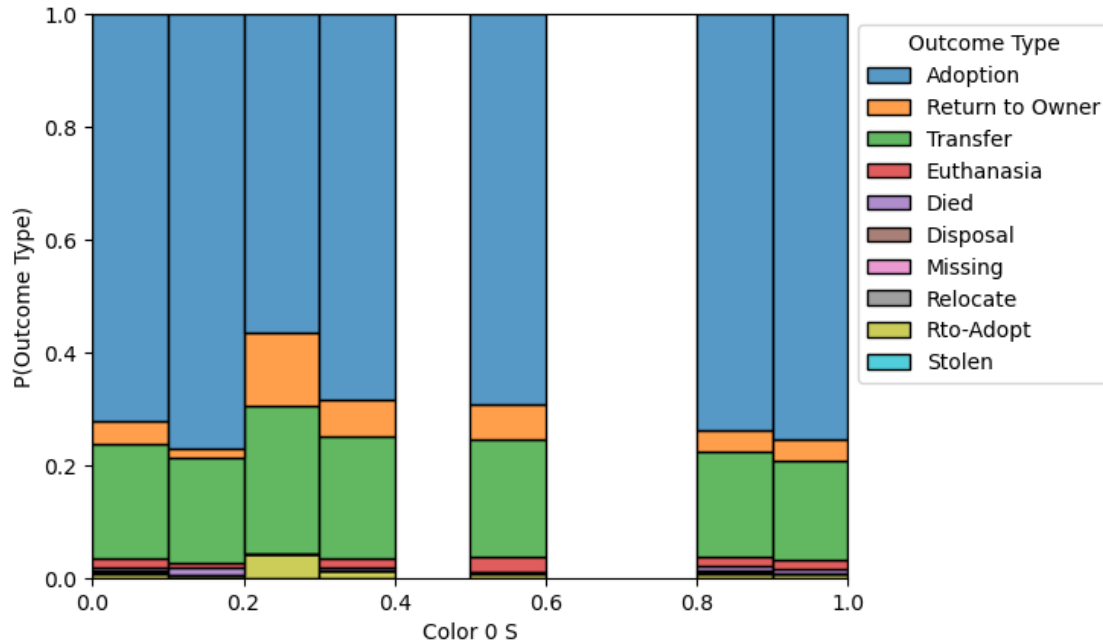
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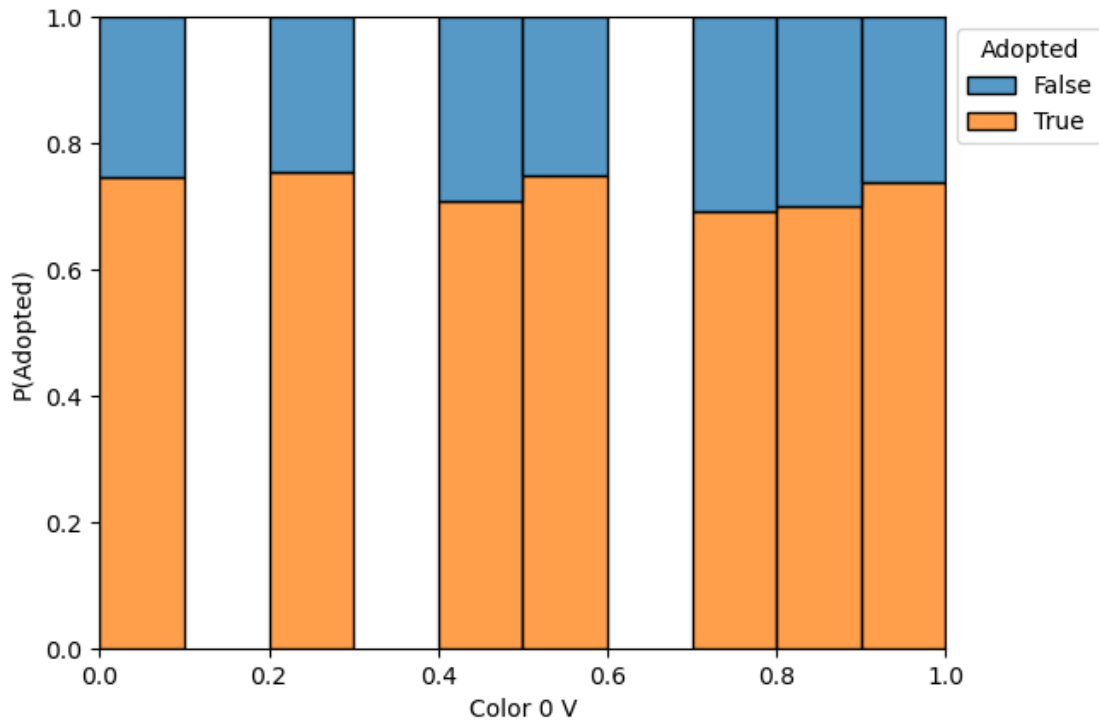
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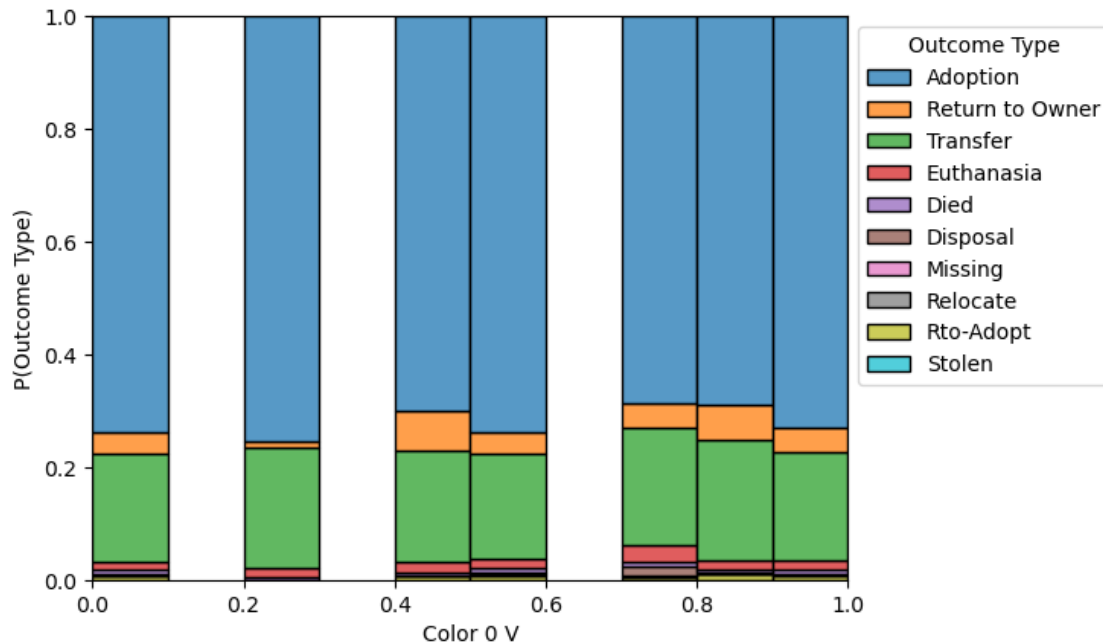
```



```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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```



Based on these charts it seems the strongest indicator of adoption in a pet is its age. The graph 'est lifespan remaining ~ adopted' shows this very strongly as does the graph 'age upon outcome ~ adopted'.

Another correlation in these graphs is in 'average lifespan ~ adoption'. This once again shows that potential adopters favor pets with a lot of years ahead of them.

This seems to imply that the biggest indicator of whether or not an animal will be adopted is its age. Younger pets are more likely to be adopted by a rather strong degree.

2.4 Age

Lets see if we can pull of some logistic regression of age ~ adoption

```
[22]: bins = [0, 1/365.25, 7/365.25, 1/12, 1/2, 1, 2, 5, 10]
labels = ['0-1 days', '1 day - 1 week', '1 week - 1 month', '1-6 months', '0.
↳5-1 years', '1-2 years', '2-5 years', '5-10 years']
df_out_1 = df_out.assign(**{'Time in animal center': pd.cut(df_out['Years in_
↳animal center'], bins, labels=labels, include_lowest=True, right=False)})
df_out_1 = df_out_1[['Adopted', 'Time in animal center', 'Age upon Outcome_
↳(years)']]
df_out_1.dropna(inplace=True)

# sns.histplot(data=df_out_1, x='Age upon Outcome (years)', hue='Years in_
↳animal center', binwidth=1, element='poly', fill=None)

# the histogram is manually made to add more features
```

```
df_out_1 = df_out_1.assign(**{'Age upon Outcome (years)': pd.cut(df_out_1['Age upon Outcome (years)'], 10)})
```

```
[23]: df_out_2 = df_out_1.groupby(['Time in animal center', 'Age upon Outcome (years)']).Adopted.mean()
df_out_2 = df_out_2.reset_index()
df_out_2.dropna(inplace=True)
df_out_2_ageUponOutcome = df_out_2['Age upon Outcome (years)']
df_out_2 = df_out_2.assign(**{'Age upon Outcome (years)': df_out_2['Age upon Outcome (years)'].apply(lambda x: x.left).astype(float) })
df_out_2.info()
df_out_2.describe()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 52 entries, 0 to 74
Data columns (total 3 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   Time in animal center                 52 non-null    category
1   Age upon Outcome (years)             52 non-null    float64
2   Adopted                             52 non-null    Float64
dtypes: Float64(1), category(1), float64(1)
memory usage: 1.7 KB
```

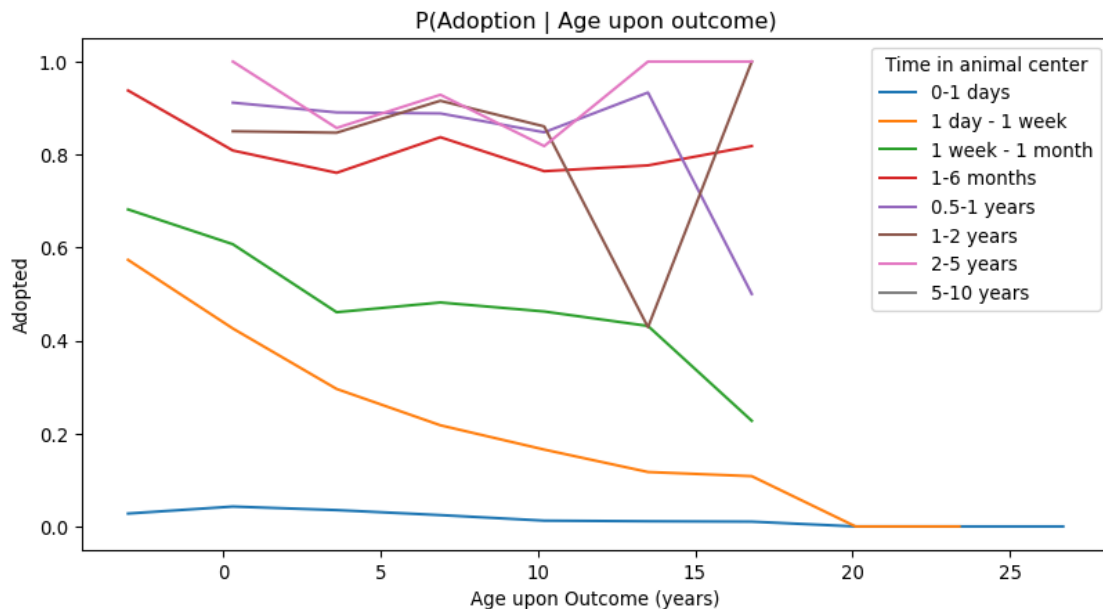
```
[23]:
```

	Age upon Outcome (years)	Adopted
count	52.000000	52.0
mean	9.055154	0.530769
std	7.537376	0.375057
min	-3.033000	0.0
25%	3.600000	0.114832
50%	10.200000	0.590232
75%	13.500000	0.857973
max	26.700000	1.0

```
[24]: # for time, time_loc in df_out_1.groupby('Time in animal center').groups.items():
#     df_out_1_loc = df_out_1.loc[time_loc]
#     i = df_out_2.shape
#     df_out_2.at[]

plt.figure(figsize=(10, 5), dpi=96)
ax=sns.lineplot(data=df_out_2, x='Age upon Outcome (years)', y='Adopted', hue='Time in animal center', errorbar=None)
plt.title('P(Adoption | Age upon outcome)')
# sns.move_legend(ax, 'upper left', bbox_to_anchor=(1,1))
# plt.xticks(ticks=df_out_2['Age upon Outcome (years)'], labels=df_out_2_ageUponOutcome, rotation='vertical')
```

```
plt.show()
```



```
[25]: from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB

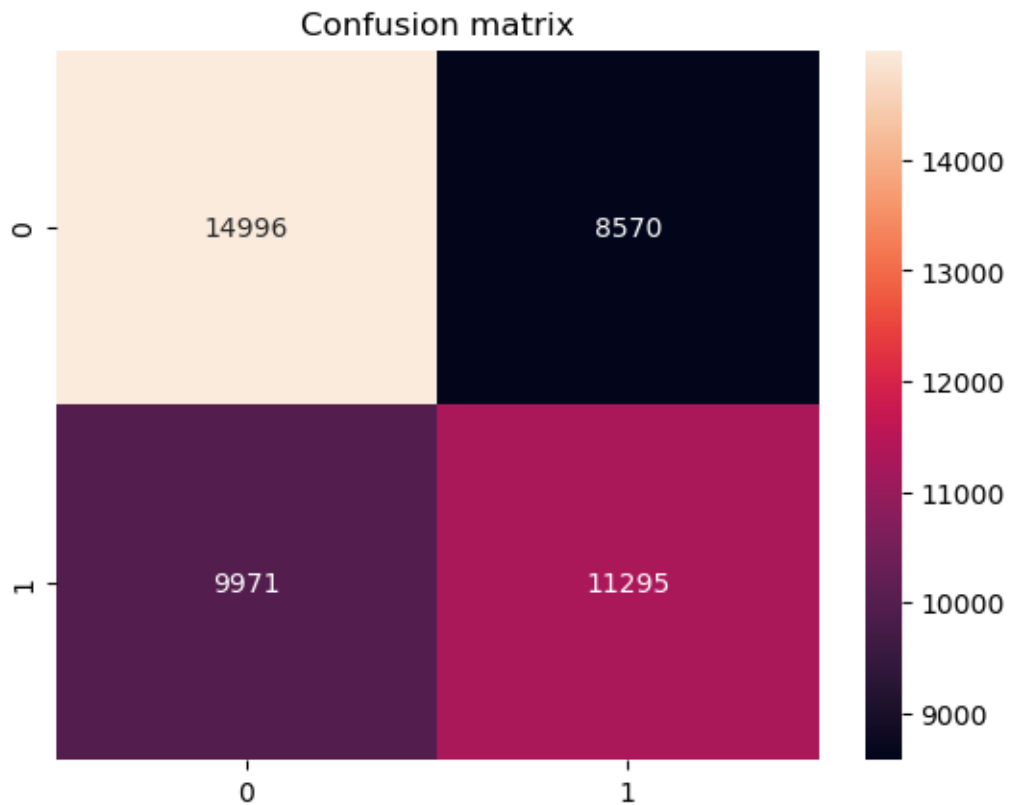
df_al = df_out[['Adopted', 'Age upon Outcome (years)']].dropna()
y_data = df_al['Adopted'].astype(dtype=int)
x_data = df_al['Age upon Outcome (years)'].astype(dtype=float)

x_data = x_data.values.reshape(-1,1)

x_training_data, x_test_data, y_training_data, y_test_data = \
    train_test_split(x_data, y_data, test_size = 0.3)
models = [LogisticRegression, GaussianNB, RandomForestClassifier]
for modelType in models:
    print("Adopted ~ Age upon outcome (years)")
    print(modelType.__name__)
    model = modelType()
    model.fit(x_training_data, y_training_data)
    # predictions = model.predict(x_test_data)
    sns.heatmap(confusion_matrix(y_test_data, model.predict(x_test_data)),
    annot=True, fmt="0")
    plt.title("Confusion matrix")
    plt.show()
    print("Classification report")
```

```
print(classification_report(y_test_data, model.predict(x_test_data)))
print()
```

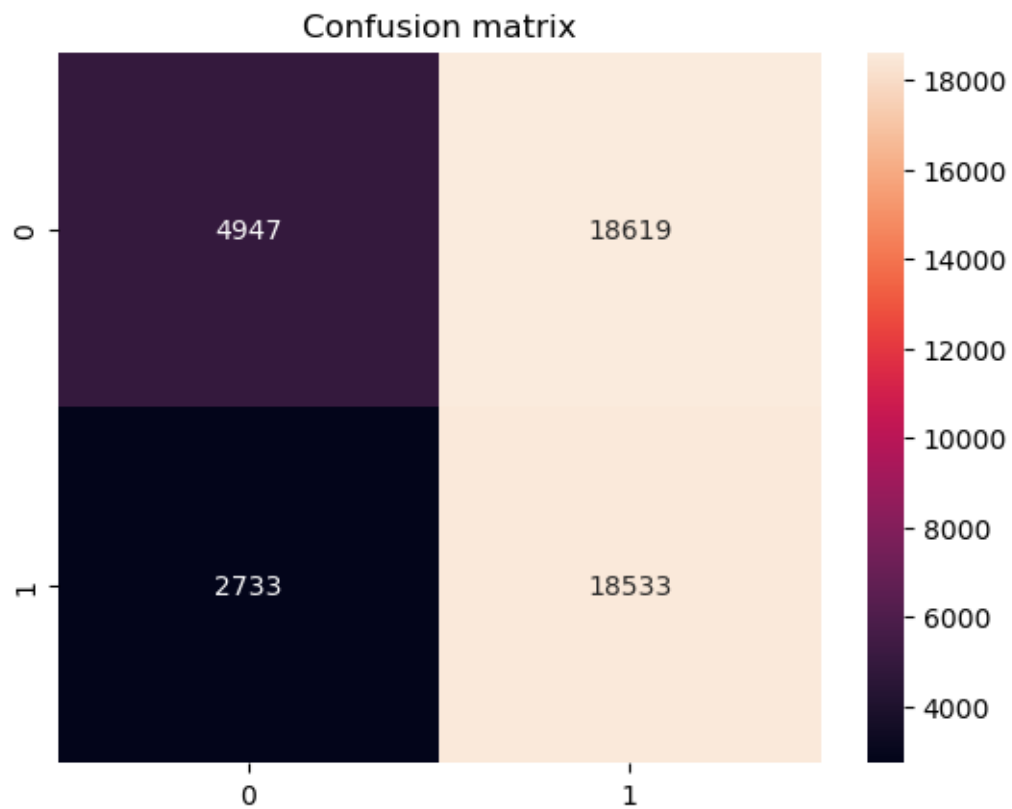
Adopted ~ Age upon outcome (years)
LogisticRegression



Classification report

	precision	recall	f1-score	support
0	0.60	0.64	0.62	23566
1	0.57	0.53	0.55	21266
accuracy			0.59	44832
macro avg	0.58	0.58	0.58	44832
weighted avg	0.59	0.59	0.59	44832

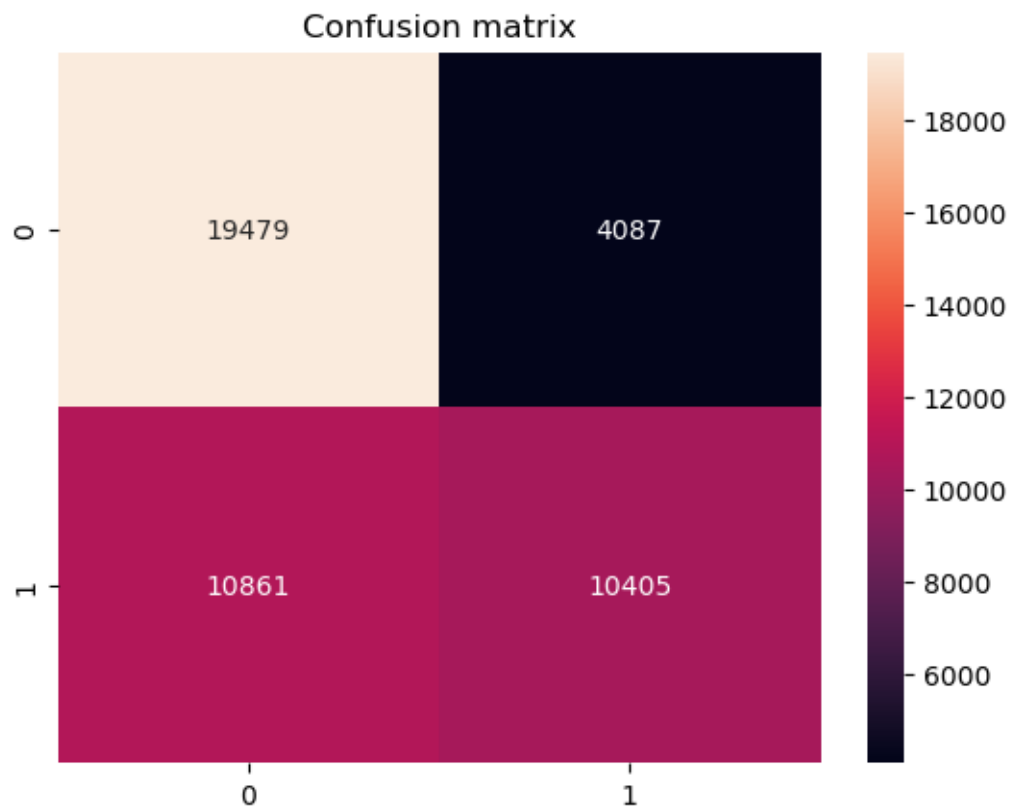
Adopted ~ Age upon outcome (years)
GaussianNB



Classification report

	precision	recall	f1-score	support
0	0.64	0.21	0.32	23566
1	0.50	0.87	0.63	21266
accuracy			0.52	44832
macro avg	0.57	0.54	0.48	44832
weighted avg	0.58	0.52	0.47	44832

Adopted ~ Age upon outcome (years)
 RandomForestClassifier



Classification report

	precision	recall	f1-score	support
0	0.64	0.83	0.72	23566
1	0.72	0.49	0.58	21266
accuracy			0.67	44832
macro avg	0.68	0.66	0.65	44832
weighted avg	0.68	0.67	0.66	44832

They have around 50-70% accuracy.