

CORR

April 13, 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 39 columns):

#	Column	Non-Null Count	Dtype
0	Animal ID	149511 non-null	string
1	Name	106260 non-null	string
2	Outcome DateTime	149511 non-null	datetime64[ns]
3	Outcome MonthYear	149511 non-null	string
4	Date of Birth	149511 non-null	datetime64[ns]
5	Outcome Type	149485 non-null	string
6	Outcome Subtype	68443 non-null	string
7	Animal Type	149511 non-null	string
8	Sex upon Outcome	149509 non-null	string
9	Age upon Outcome	149465 non-null	string
10	Breed	149511 non-null	string
11	Color	149511 non-null	string
12	Intake MonthYear	149385 non-null	string

```

13 Intake DateTime      149385 non-null datetime64[ns]
14 Found Location      149385 non-null string
15 Intake Type         149385 non-null string
16 Intake Condition    149385 non-null string
17 Sex upon Intake     149383 non-null string
18 Age upon Intake     149384 non-null string
19 Colors (count)      149511 non-null Int64
20 Color 0             149511 non-null string
21 Color 1             79869 non-null string
22 Color 0 R           135638 non-null Float64
23 Color 0 G           135638 non-null Float64
24 Color 0 B           135638 non-null Float64
25 Color 0 H           135638 non-null Float64
26 Color 0 S           135638 non-null Float64
27 Color 0 V           135638 non-null Float64
28 Color 1 R           78596 non-null Float64
29 Color 1 G           78596 non-null Float64
30 Color 1 B           78596 non-null Float64
31 Color 1 H           78596 non-null Float64
32 Color 1 S           78596 non-null Float64
33 Color 1 V           78596 non-null Float64
34 Age upon Outcome (years) 149465 non-null Float64
35 Male                149509 non-null boolean
36 Female              149509 non-null boolean
37 NeuteredOrSpayed    149509 non-null boolean
38 Adopted             149485 non-null boolean
dtypes: Float64(13), Int64(1), boolean(4), datetime64[ns](3), string(18)
memory usage: 43.1 MB

```

```

[2]: Animal ID   Name   Outcome DateTime Outcome MonthYear Date of Birth \
0    A794011   Chunk  2019-05-08 18:20:00          May 2019   2017-05-02
1    A776359   Gizmo  2018-07-18 16:02:00          Jul 2018   2017-07-12
2    A821648   <NA>  2020-08-16 11:38:00          Aug 2020   2019-08-16
3    A720371   Moose  2016-02-13 17:59:00          Feb 2016   2015-10-08
4    A674754   <NA>  2014-03-18 11:47:00          Mar 2014   2014-03-12

Outcome Type Outcome Subtype Animal Type Sex upon Outcome Age upon Outcome \
0    Rto-Adopt      <NA>      Cat   Neutered Male          2 years
1    Adoption       <NA>      Dog   Neutered Male          1 year
2    Euthanasia     <NA>      Other  Unknown              1 year
3    Adoption       <NA>      Dog   Neutered Male          4 months
4    Transfer       Partner   Cat   Intact Male           6 days

... Color 1 G Color 1 B Color 1 H Color 1 S Color 1 V \
0    ...      1.0      1.0      0.0      0.0      1.0
1    ...      0.44     0.09  0.119444    0.85     0.59
2    ...      <NA>     <NA>    <NA>    <NA>    <NA>

```

```

3 ...      <NA>      <NA>      <NA>      <NA>      <NA>
4 ...      <NA>      <NA>      <NA>      <NA>      <NA>

```

```

      Age upon Outcome (years)  Male Female NeuteredOrSpayed  Adopted
0                2.0      True  False                True    True
1                1.0      True  False                True    True
2                1.0     False  False                False   False
3            0.333333      True  False                True    True
4            0.016438      True  False                False   False

```

[5 rows x 39 columns]

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

```

[3]:      Breed  Count Animal Type  Adopted  Color 0 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 0 R (std dev)  Color 0 G (mean)  Color 0 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 0 B (mean)  Color 0 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

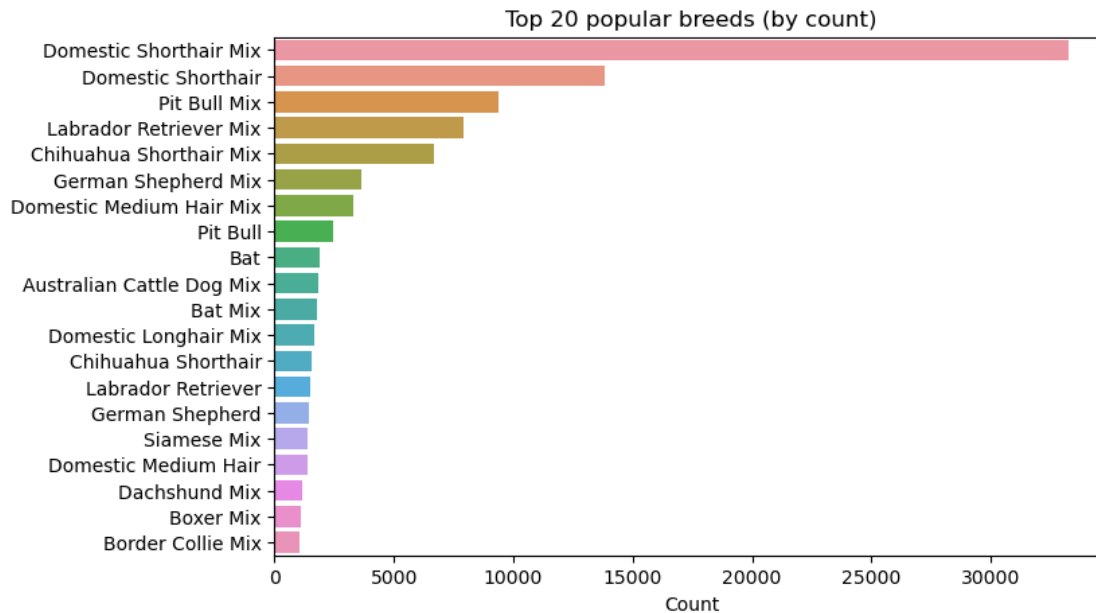
[5 rows x 43 columns]

1 Analysis by breed

1.0.1 Popular breeds

```
[4]: df_breeds_with_info_sorted_by_breed = df_breeds_with_info.sort_values('Count',
    ↪ascending=False)

k = 20
plt.figure(figsize=(8,5))
sns.barplot(
    data=df_breeds_with_info_sorted_by_breed.head(k),
    x='Count',
    y='Breed',
    errorbar=None,
)
plt.xlabel('Count')
plt.ylabel(None)
plt.title(f'Top {k} popular breeds (by count)')
plt.show()
```



```
[5]: n = 25
df_breeds_with_info_sorted_by_breed = df_breeds_with_info.
    loc[df_breeds_with_info.Count >= n]

k = 20

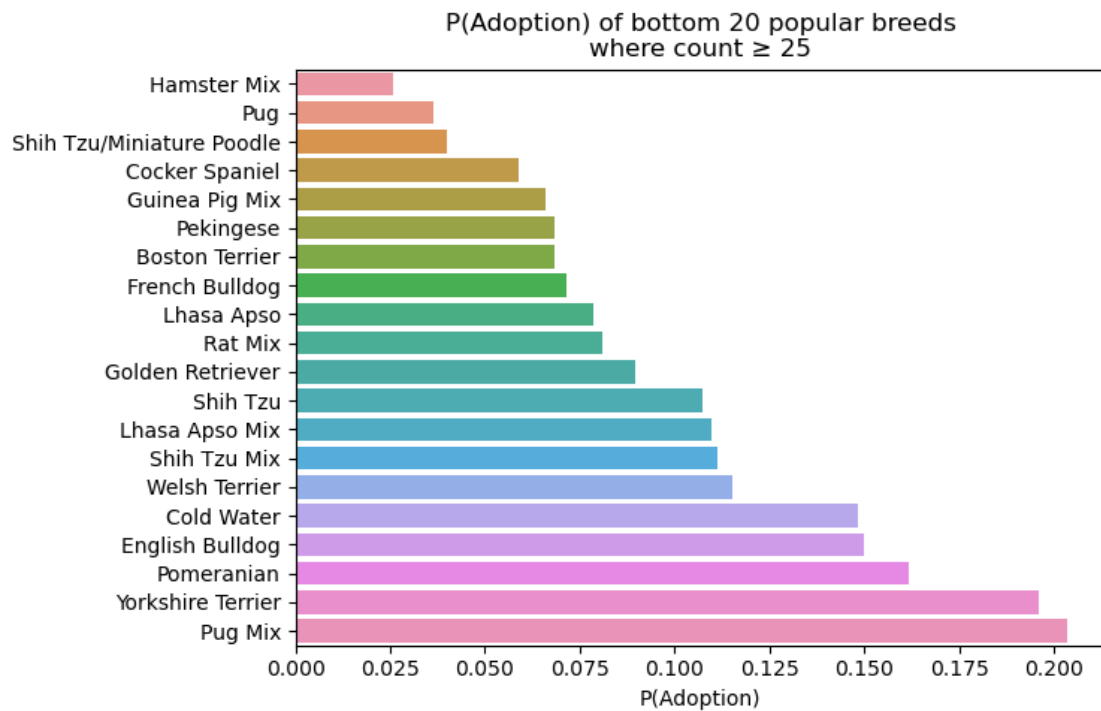
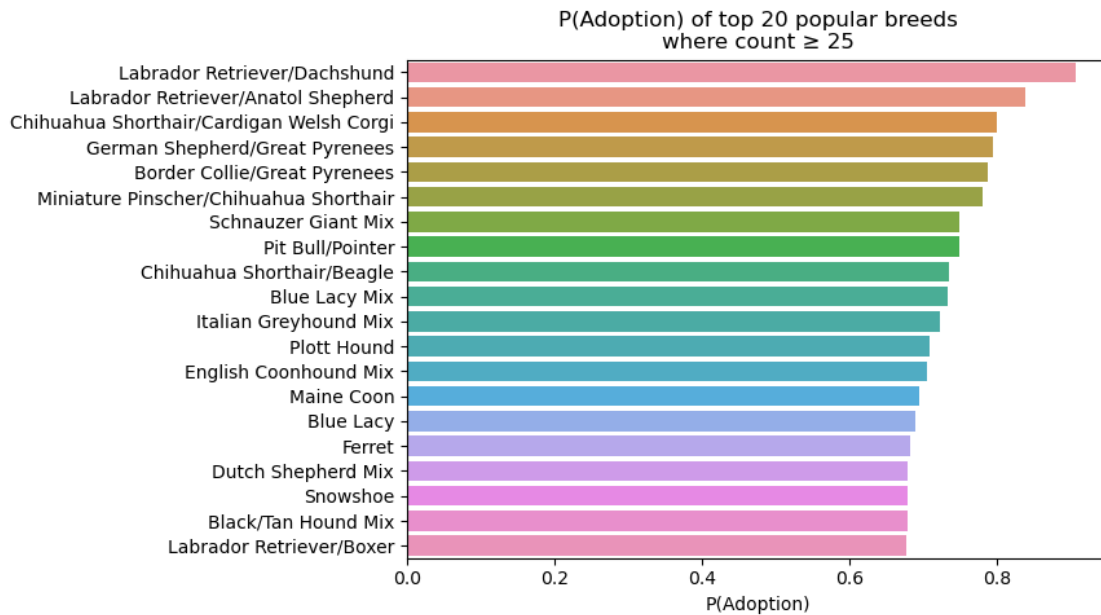
plt.figure(figsize=(7,5))
sns.barplot(
    data=df_breeds_with_info_sorted_by_breed.sort_values('Adopted',
    ascending=False).head(k),
    x='Adopted',
    y='Breed',
    errorbar=None,
)
plt.xlabel('P(Adoption)')
plt.ylabel(None)
plt.title(f'P(Adoption) of top {k} popular breeds\nwhere count {n}')
plt.show()

plt.figure(figsize=(7,5))
sns.barplot(
    data=df_breeds_with_info_sorted_by_breed.sort_values('Adopted',
    ascending=True).head(k),
    x='Adopted',
    y='Breed',
    errorbar=None,
```

```

)
plt.xlabel('P(Adoption)')
plt.ylabel(None)
plt.title(f'P(Adoption) of bottom {k} popular breeds\nwhere count {n}')
plt.show()

```



1.0.2 Correlating with every variable

There isn't much correlation appearing yet

```
[6]: 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())

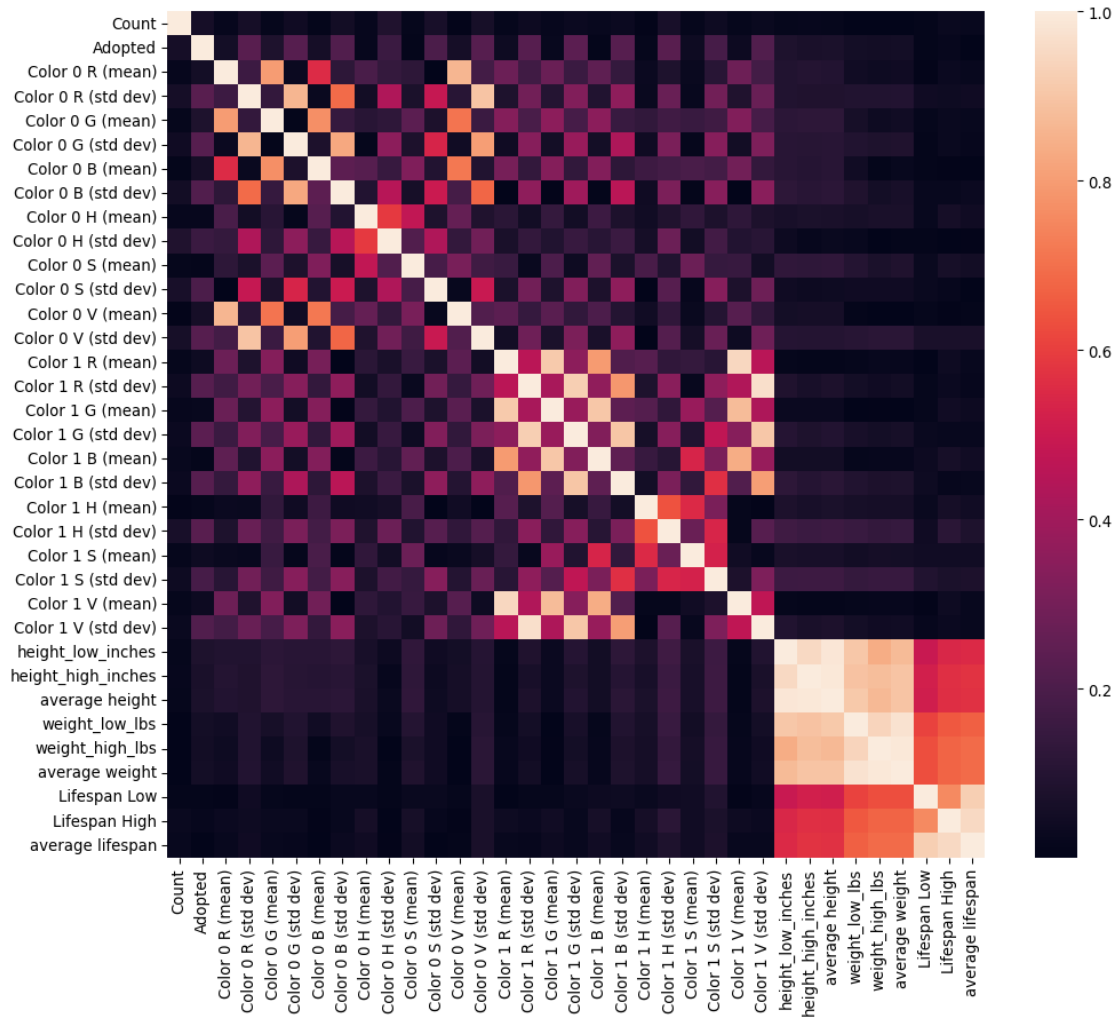
def score(df, var1, var2):
    print(f'Corr({var1}, {var2})    {df[var1][var2]}')

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_13396/4118066584.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.

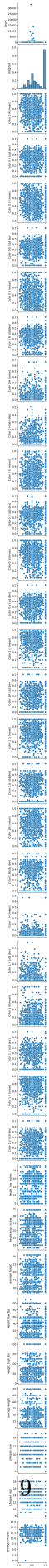
```
df_breeds_with_info_corr = df_breeds_with_info.corr()

Corr(Adopted, Color 0 B (mean))    -0.057521961020765885
Corr(Adopted, Color 0 B (std dev)) -0.21220098425344674
Corr(Adopted, Color 0 V (mean))    -0.05892713325516749
Corr(Adopted, Color 0 V (std dev)) -0.22375794566214077
Corr(Adopted, average height)      0.07520172186737319
Corr(Adopted, height_low_inches)    0.08043859187253975
Corr(Adopted, height_high_inches)   0.06827302387620472
Corr(Adopted, Lifespan Low)         0.011194168083224364
```



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

```
[7]: <seaborn.axisgrid.PairGrid at 0x7fc2a1da80d0>
```

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.

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

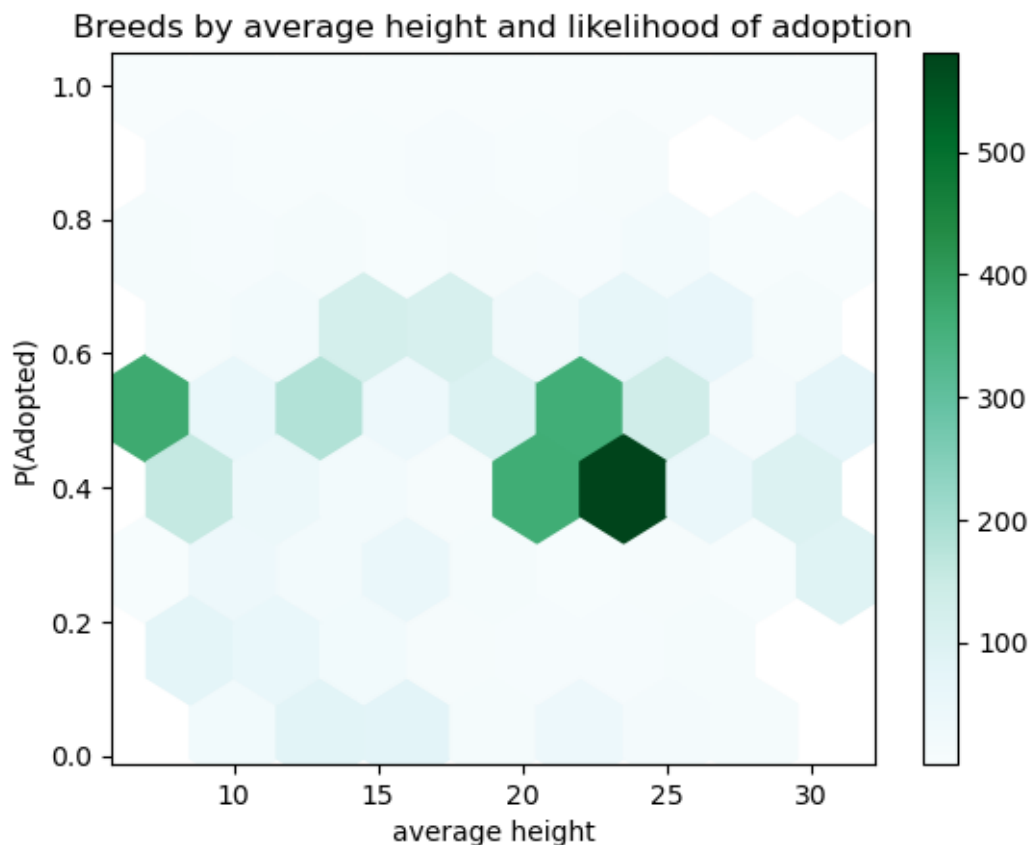
y_data = df_hl['Adopted'].astype(dtype=int)
x_data = df_hl['average height'].astype(dtype=float)

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

	precision	recall	f1-score	support
0	0.53	0.41	0.46	21173
1	0.50	0.62	0.55	20347
accuracy			0.51	41520
macro avg	0.52	0.51	0.51	41520
weighted avg	0.52	0.51	0.51	41520

```
[9]: df_breeds_with_info.plot.hexbin(x='average height', y='Adopted', gridsize=8, \
    ↪C='Count')
plt.ylabel("P(Adopted)")
plt.title("Breeds by average height and likelihood of adoption")
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)

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

Colors

<StringArray>

```
[      'Brown Tabby',      'White',      'Gray',
      'Buff',      'Orange Tabby',      'Brown',
      'Black',      'Blue',      'Calico',
      'Tricolor',      'Brown Brindle',      'Tan',
      'Chocolate',      'Red',      'Blue Tick',
      'Tortie',      'Sable',      'Cream Tabby',
```

```

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

```

```

[12]: df_out_colors_1 = df_out.loc[(df_out['Color 0'].notna() == True) &
    ↪(df_out['Color 1'].notna() == False)]
df_out_colors_2 = df_out.loc[(df_out['Color 0'].notna() == True) &
    ↪(df_out['Color 1'].notna() == True)]

```

```

[13]: 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]

```

```

[14]: def bigCorr_bernoulli_custom_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_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]

```

```

[15]: # 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('%', '0')).div(100)
df_colors['Green (RGB)'] = pd.to_numeric(df_colors['Green (RGB)'].str.replace('%', '0')).div(100)
df_colors['Blue (RGB)'] = pd.to_numeric(df_colors['Blue (RGB)'].str.replace('%', '0')).div(100)
df_colors['Hue (HSL/HSV)'] = pd.to_numeric(df_colors['Hue (HSL/HSV)'].str.replace('°', '0')).div(360)
df_colors['Satur. (HSL)'] = pd.to_numeric(df_colors['Satur. (HSL)'].str.replace('%', '0')).div(100)
df_colors['Light (HSL)'] = pd.to_numeric(df_colors['Light (HSL)'].str.replace('%', '0')).div(100)
df_colors['Satur. (HSV)'] = pd.to_numeric(df_colors['Satur. (HSV)'].str.replace('%', '0')).div(100)
df_colors['Value (HSV)'] = pd.to_numeric(df_colors['Value (HSV)'].str.replace('%', '0')).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)

```

```

[16]: def chartColorAdoptionLikelihood(df_colors, color_relation):

    # 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 ({(1 - alpha):%} confidence)')
    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():
    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')

def colors_mixed():
    colors_adopted = bigCorr_bernoulli_custom_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')

def colors_singleOrMixed():
    colors_adopted = bigCorr_bernoulli_custom_colors_1_or_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')

colors_single()
colors_mixed()
colors_singleOrMixed()

# TODO 5: make an outcome chart like this for mixed and solid+mixed
# like the bar charts were made for just the Adopted percentage earlier
df_colors_outcomes = df_out_colors_1[['Outcome Type', 'Color 0']]
plt.figure(num=None, figsize=(5, 12), dpi=96, facecolor='w', edgecolor='k')
plt.title('Probability of an animal with this solid color having a certain
    ↪outcome')
sns.histplot(
    data=df_colors_outcomes,
    y='Color 0',
    hue='Outcome Type',

```



```
multiple='fill',  
)
```

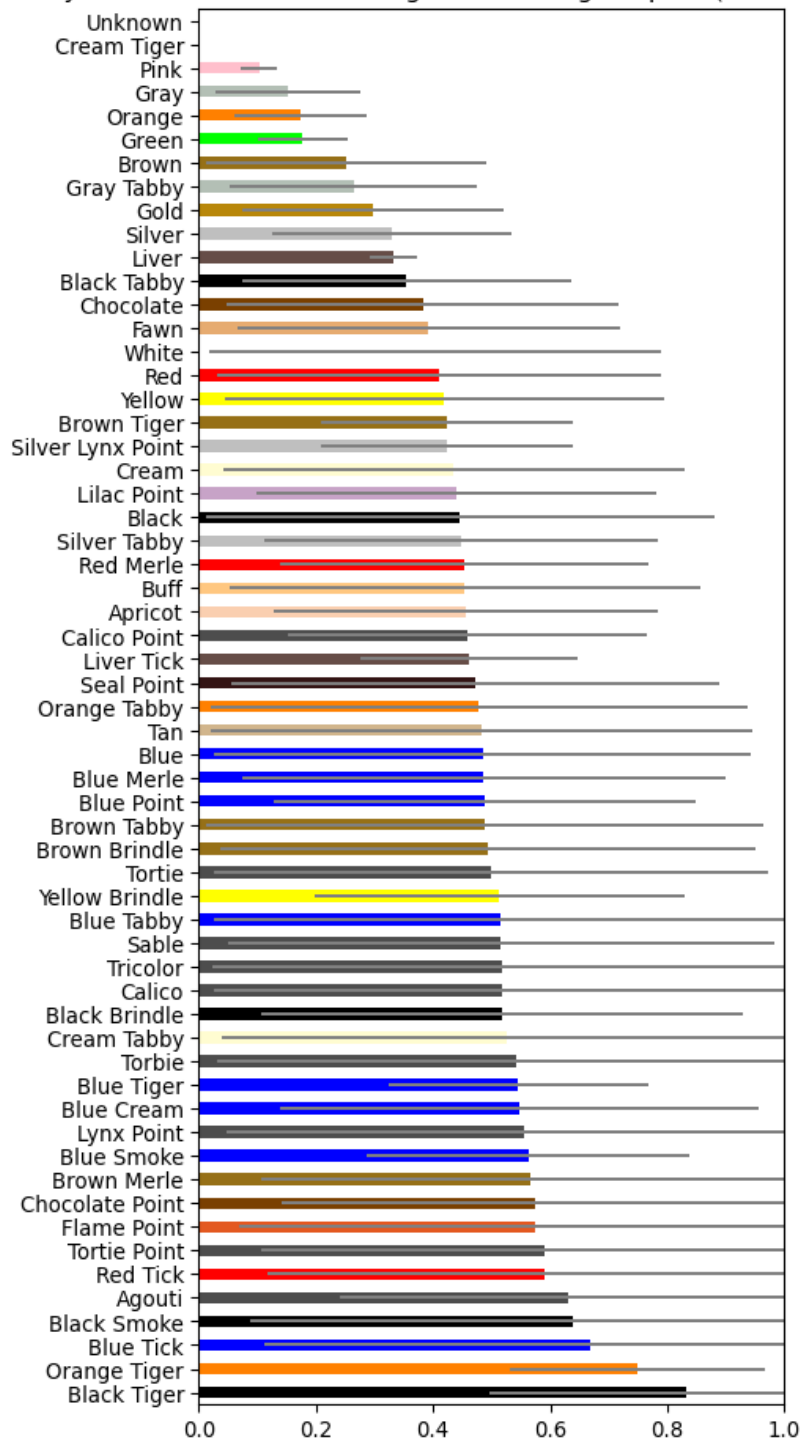
```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-  
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in  
reduce
```

```
    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
```

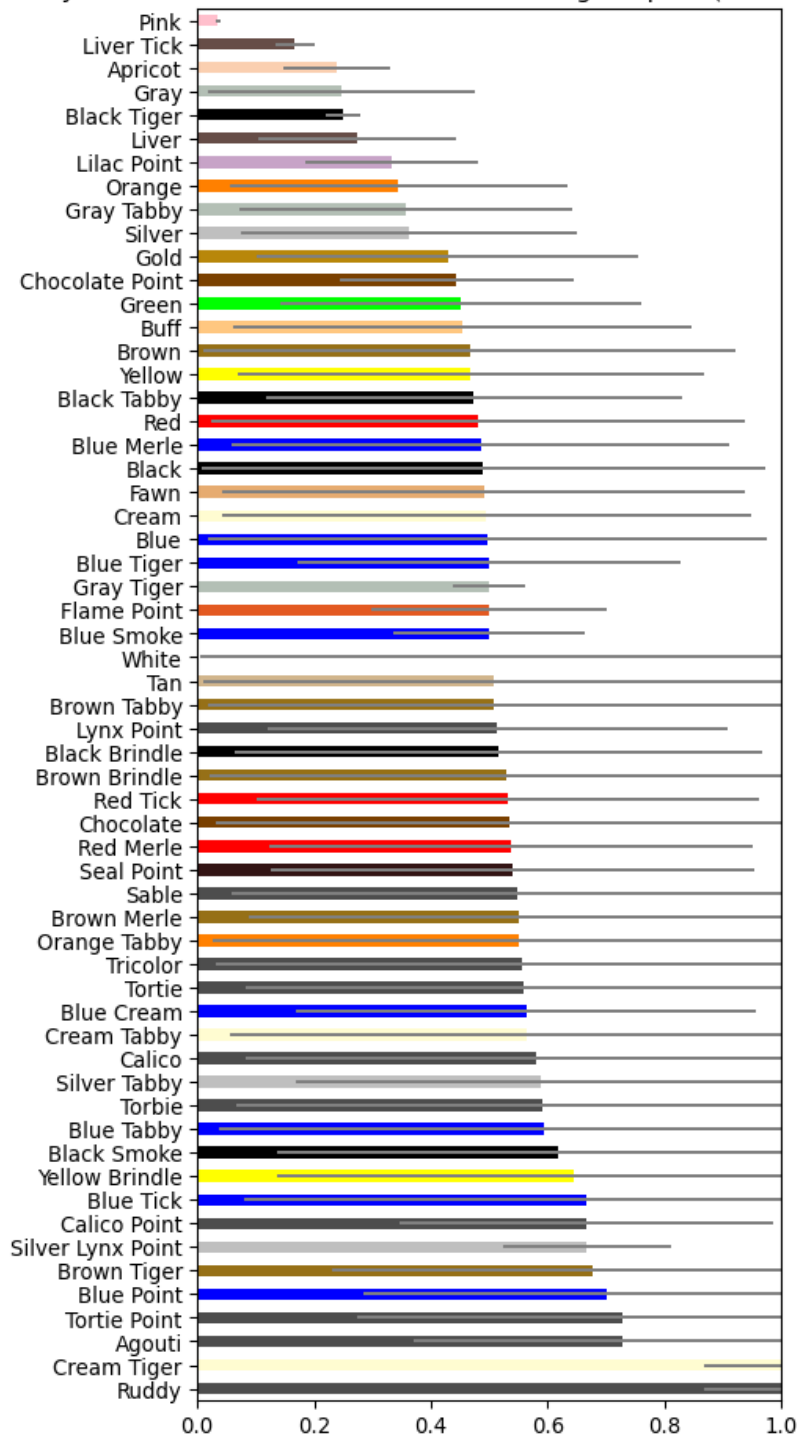
```
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

Probability of an animal with this single color being adopted (99.000000% confidence)



59 colors

Probability of an animal with this mixed color being adopted (99.000000% confidence)



59 colors

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

```
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in reduce
```

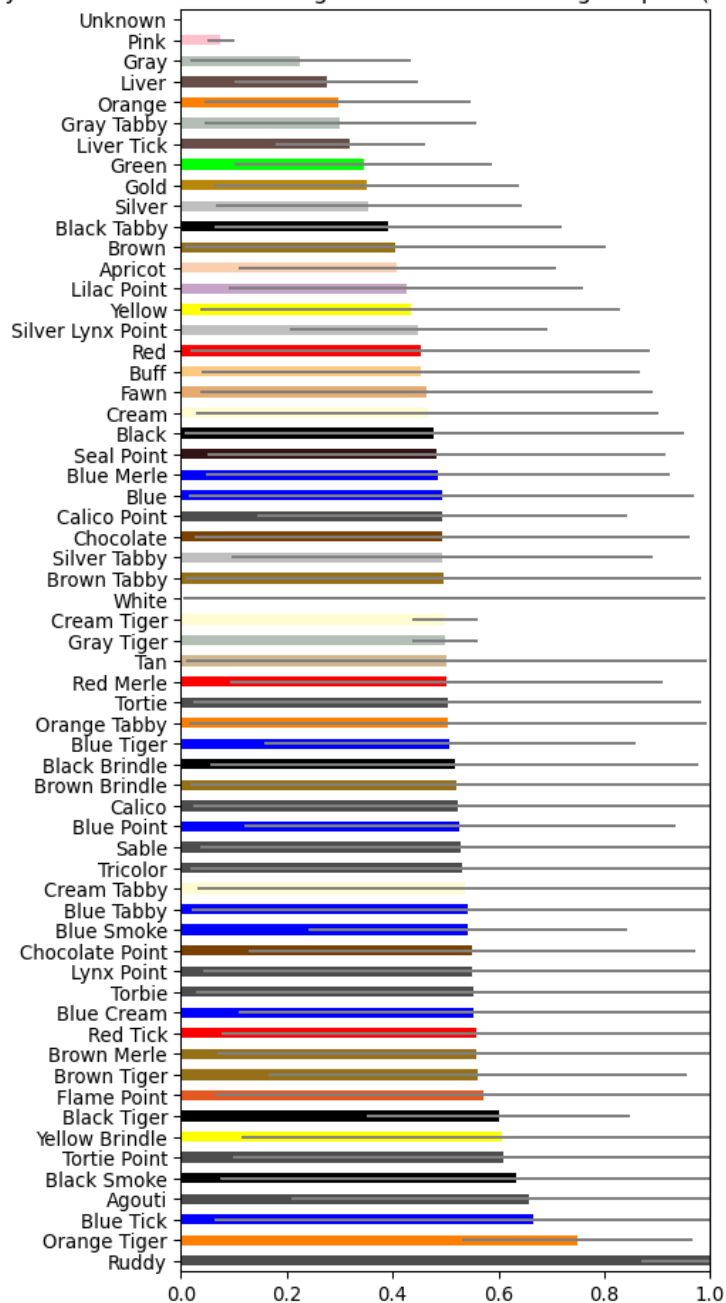
```
    return umr_minimum(a, axis, None, out, keepdims, initial, where)
```

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

```
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in reduce
```

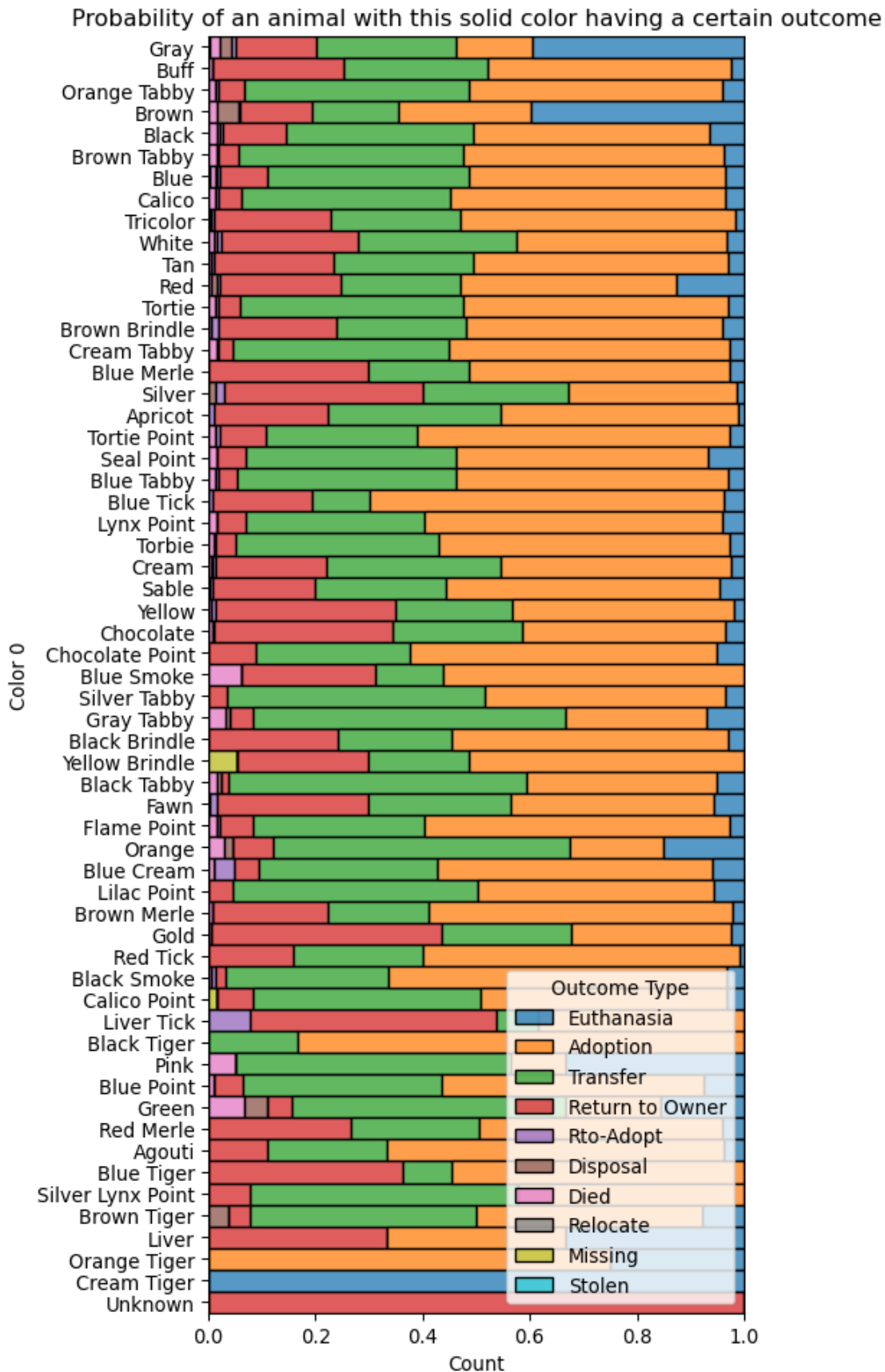
```
    return umr_maximum(a, axis, None, out, keepdims, initial, where)
```

Probability of an animal with this single or mixed color being adopted (99.000000% confidence)



61 colors

```
[16]: <AxesSubplot:title={'center': 'Probability of an animal with this solid color  
having a certain outcome'}, xlabel='Count', ylabel='Color 0'>
```



2.2 Sex

```
[17]: # 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
```

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?

```
[18]: df_out_1 = df_out.assign(Adopted=df_out.Adopted.fillna(False))
df_out_with_breeds_info_1 = df_out_with_breeds_info.assign(Adopted=df_out.
  ↪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],
    ['Color 0 H', 0.1],
    ['Color 0 S', 0.1],
    ['Color 0 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)

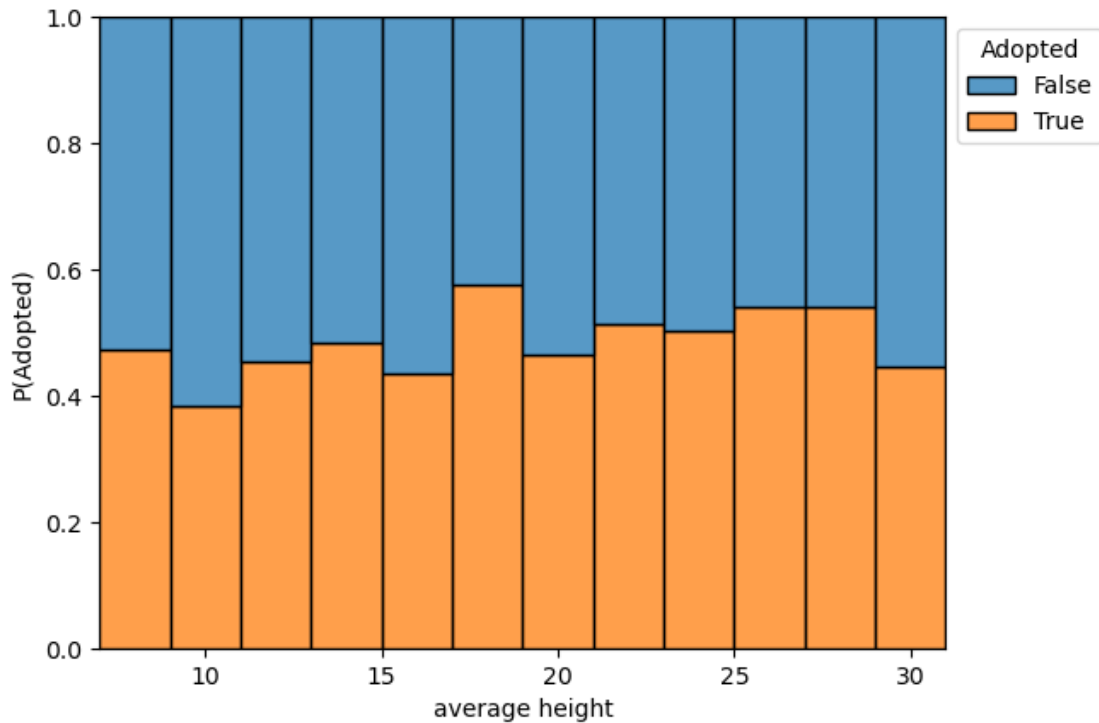
```

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
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    pd.Index(widths, name="widths"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
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    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
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```
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
```

```

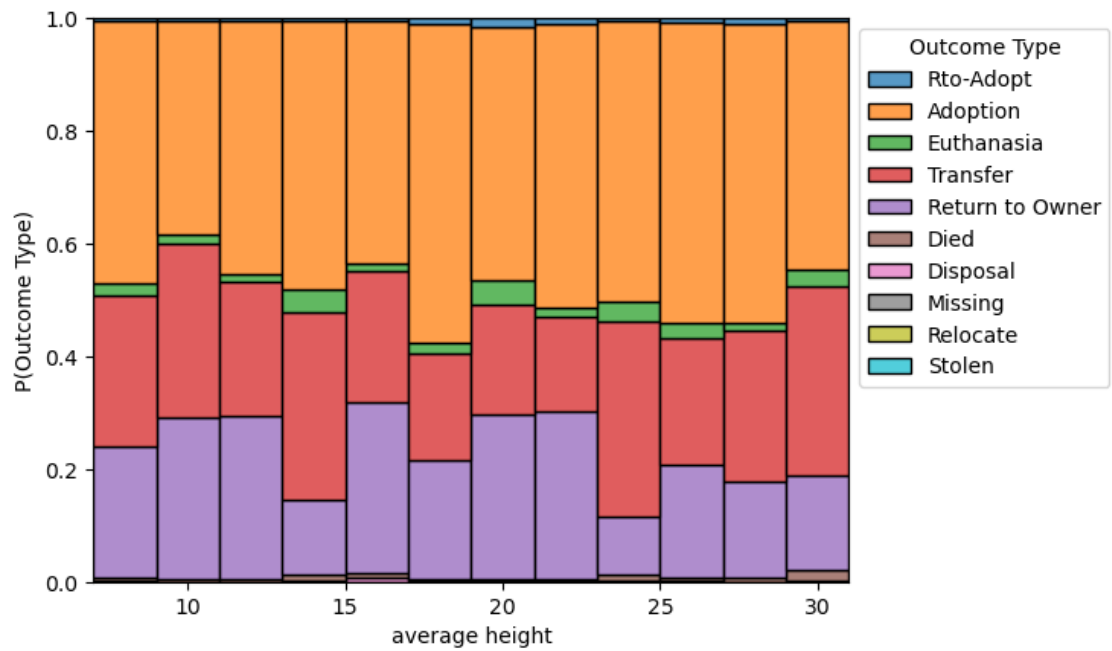
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
    pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
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/home/isaac/miniconda3/envs/cs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

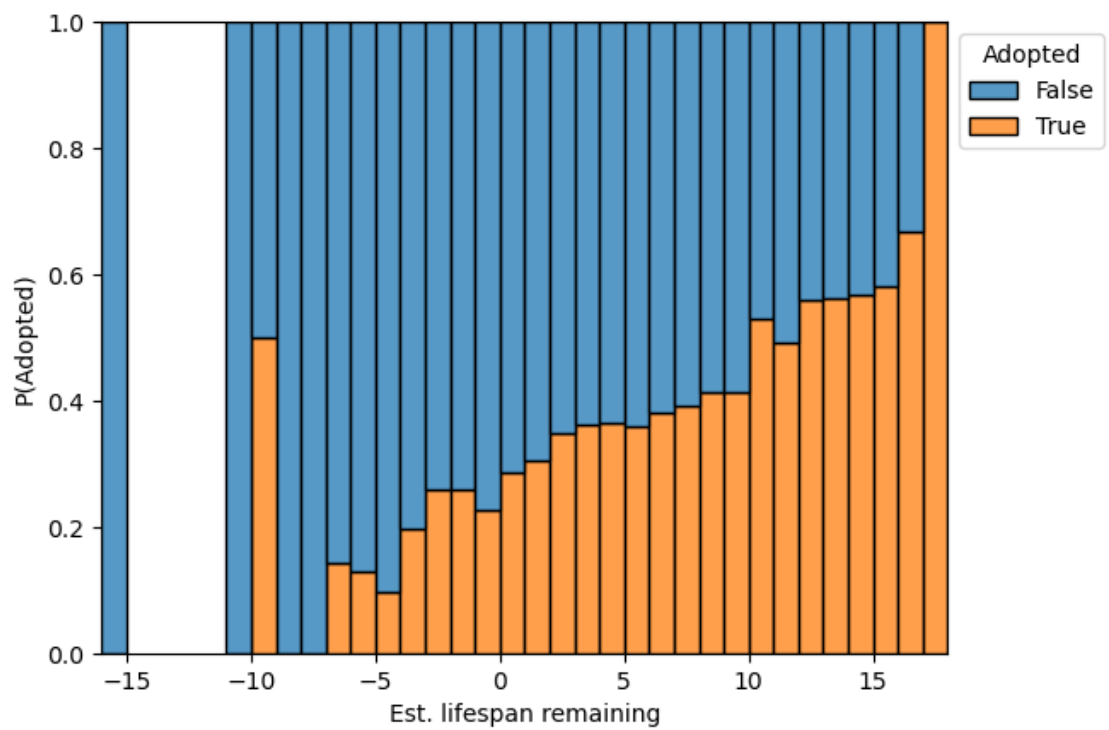
```

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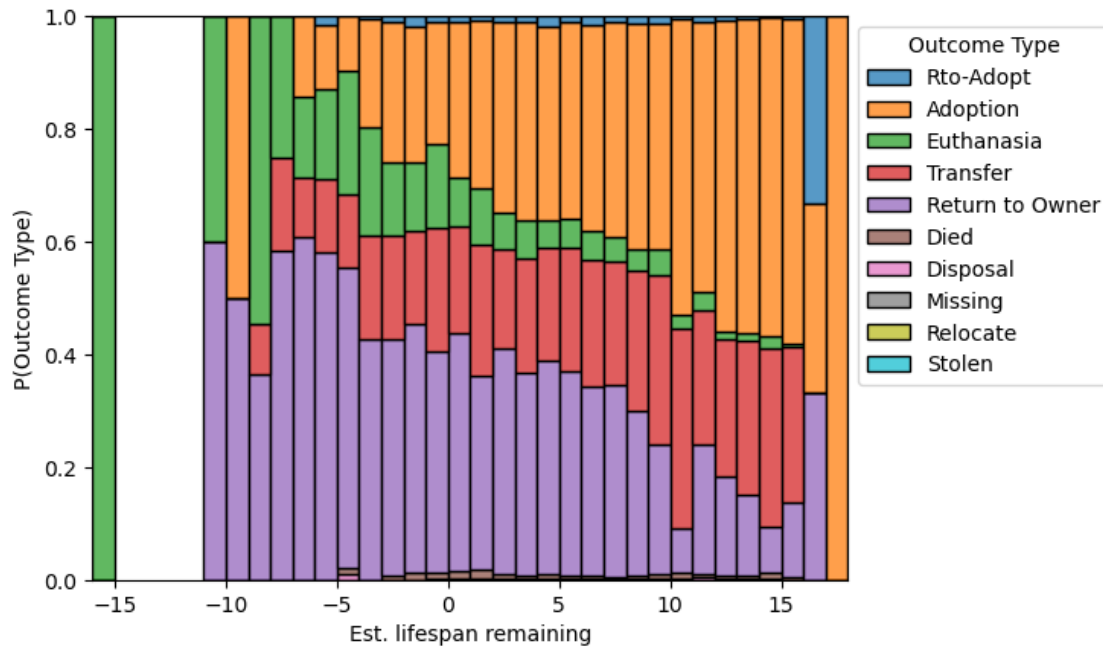
```



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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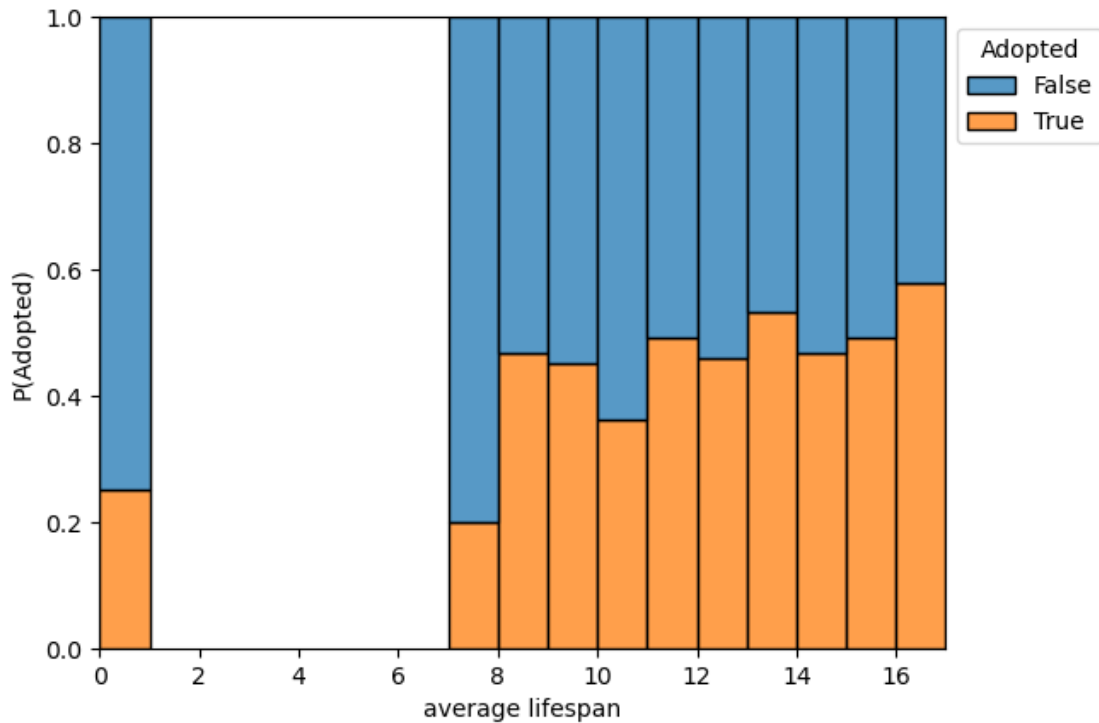
```
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```

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



average lifespan ~ Outcome Type

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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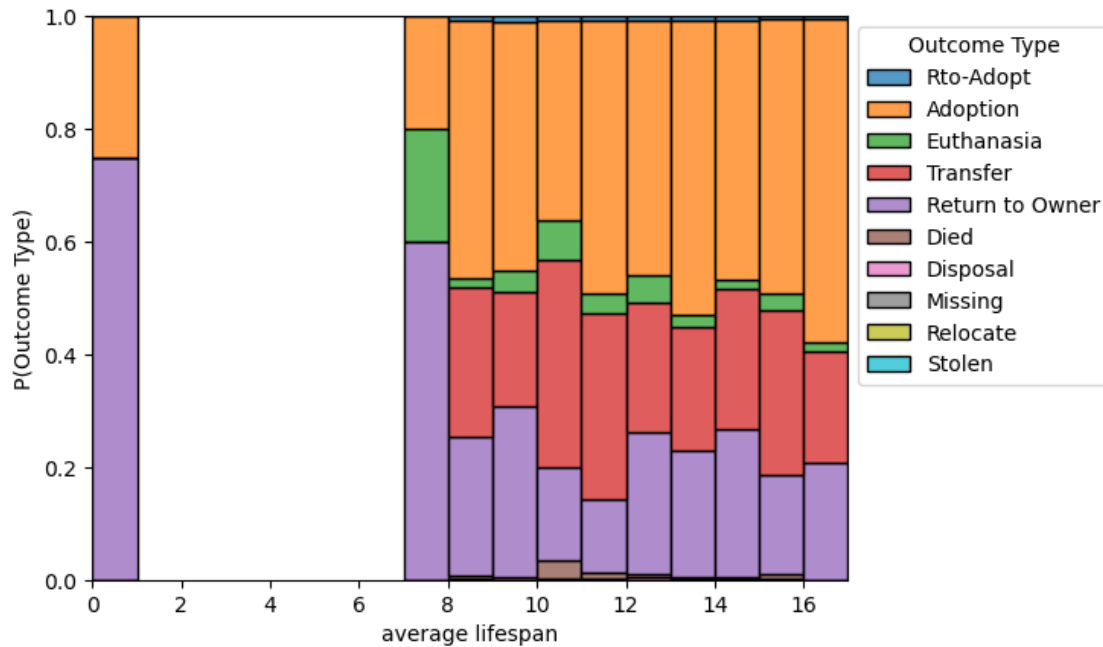
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packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
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    pd.Index(widths, name="widths"),

```

```

/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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sequences (matching Series behavior)
    pd.Index(widths, name="widths"),

```

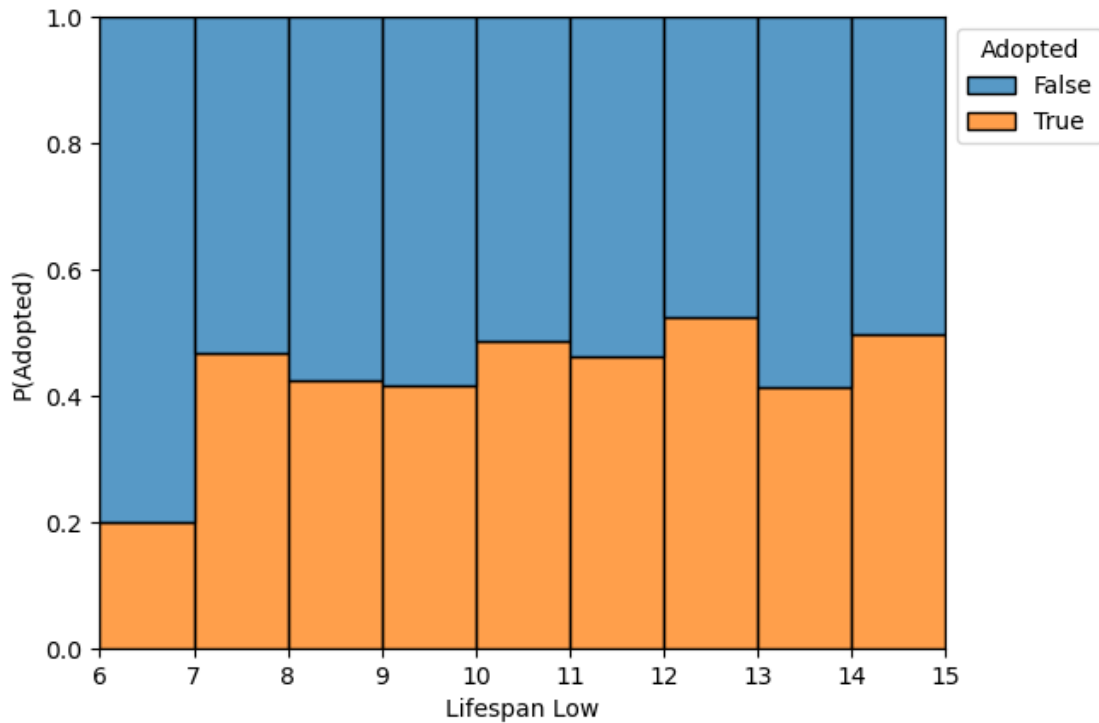



Lifespan Low ~ Adopted

```

/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
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    pd.Index(widths, name="widths"),

```



Lifespan Low ~ Outcome Type

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

```

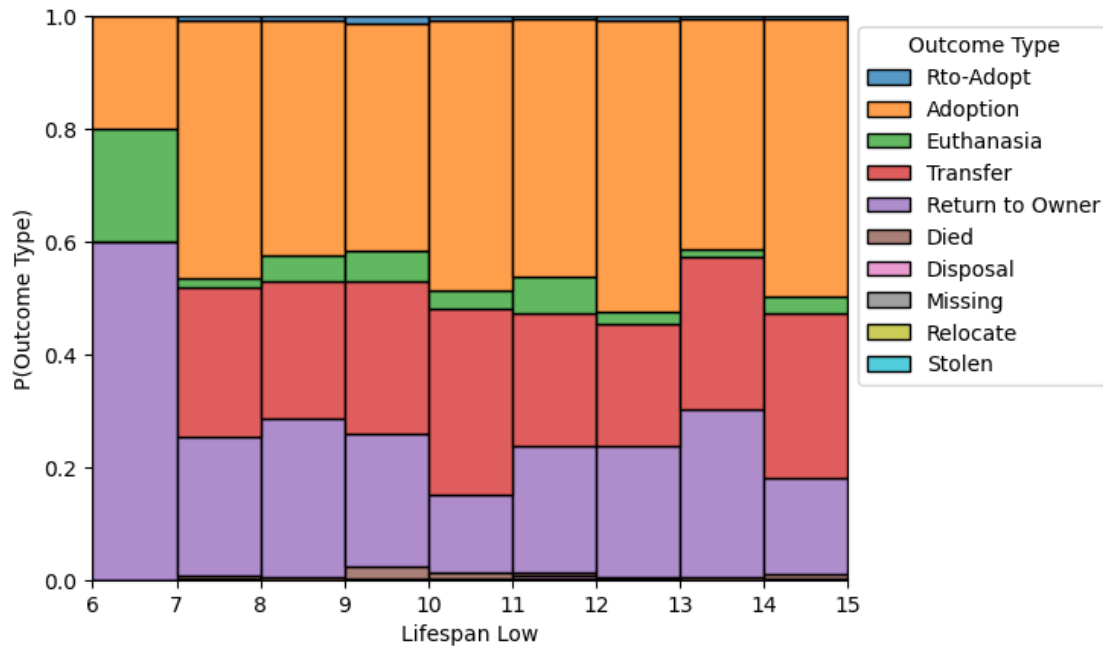
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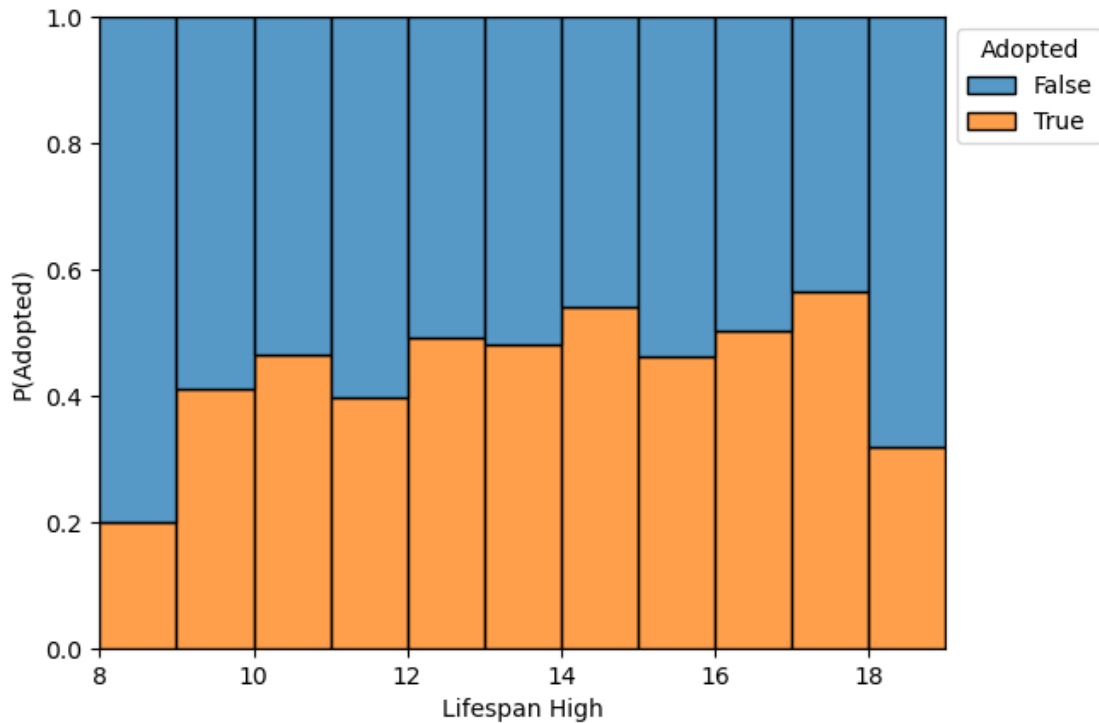


Lifespan High ~ Adopted

```

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Lifespan High ~ Outcome Type

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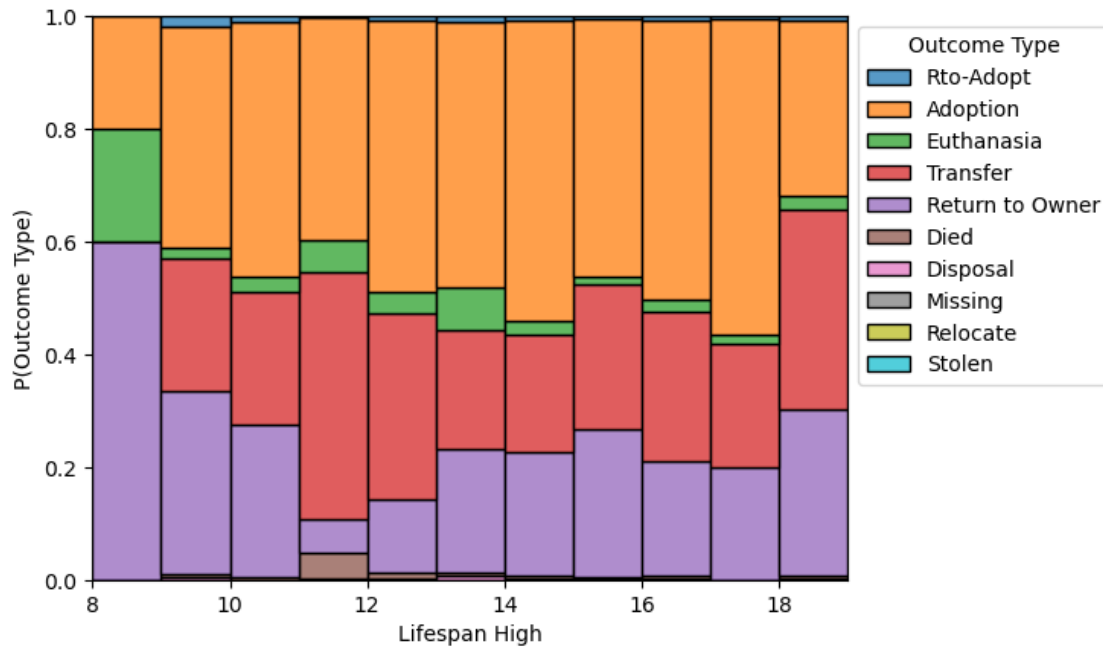
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Age upon Outcome (years) ~ Adopted

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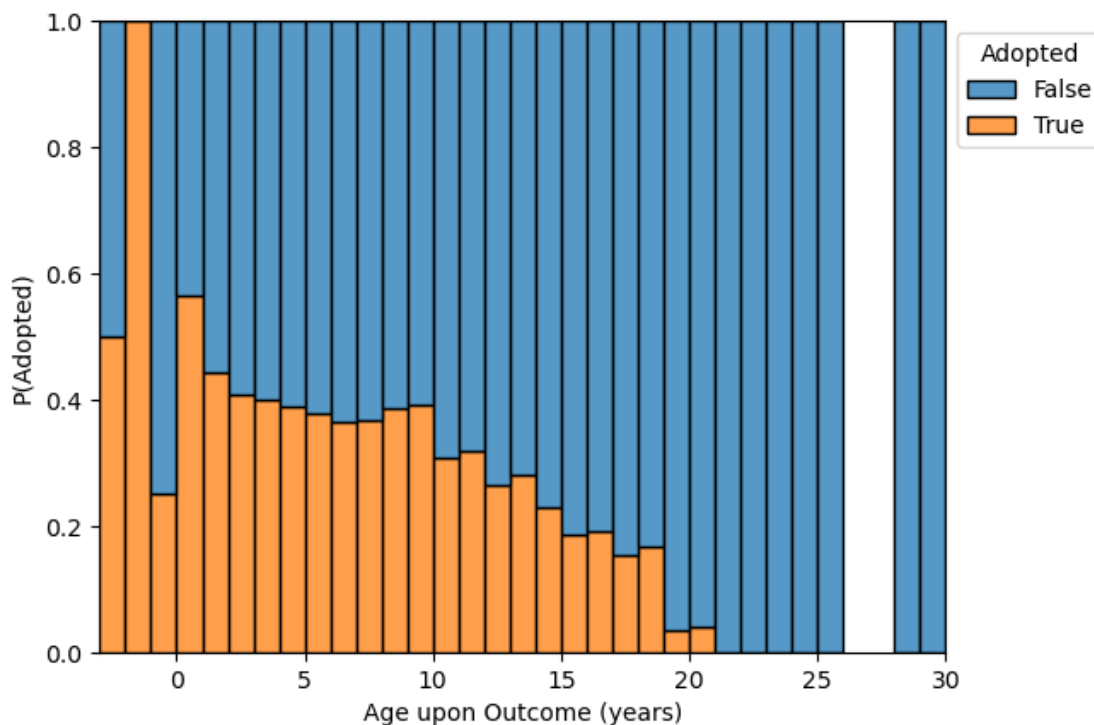
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Age upon Outcome (years) ~ Outcome Type

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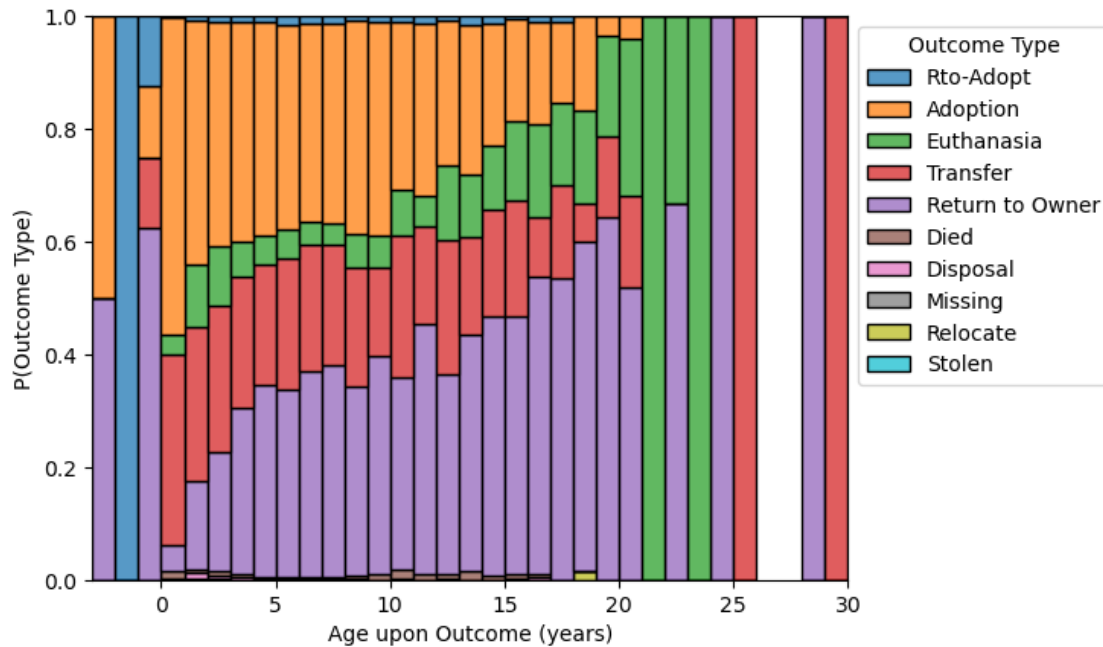
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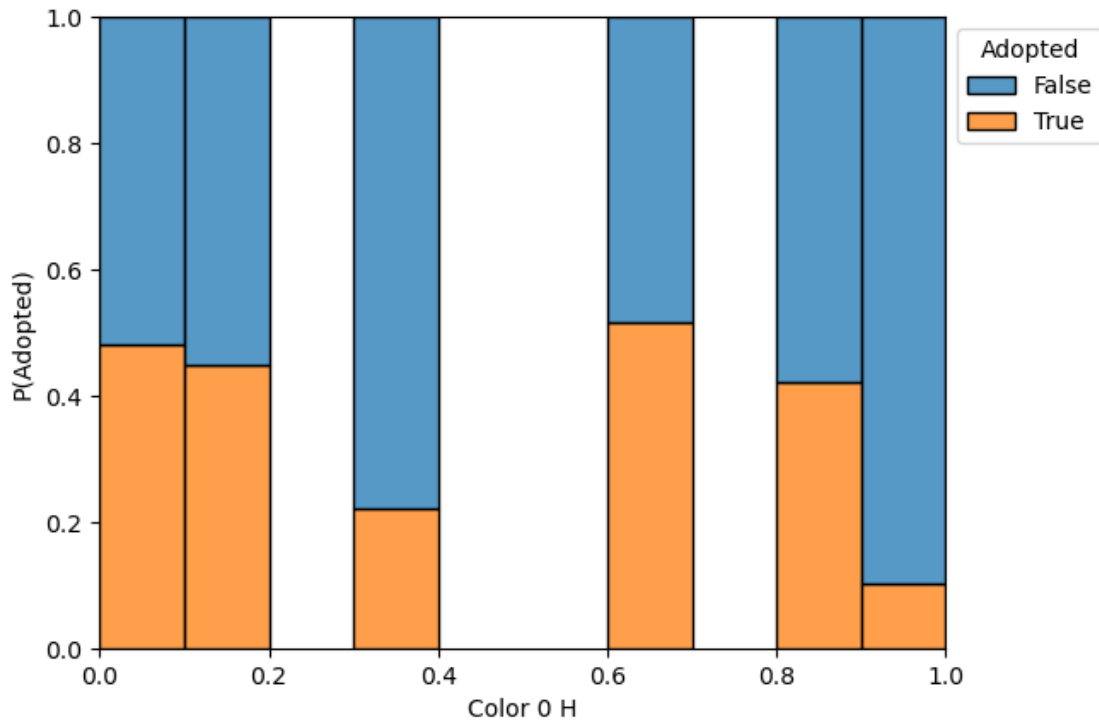


Color 0 H ~ Adopted

```

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Color 0 H ~ Outcome Type

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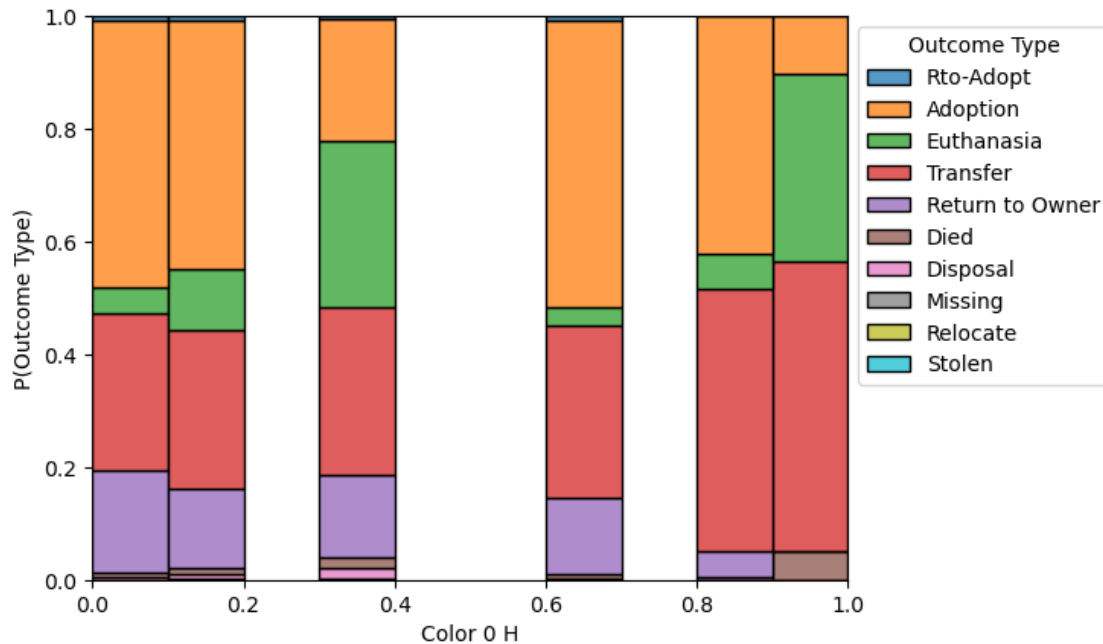
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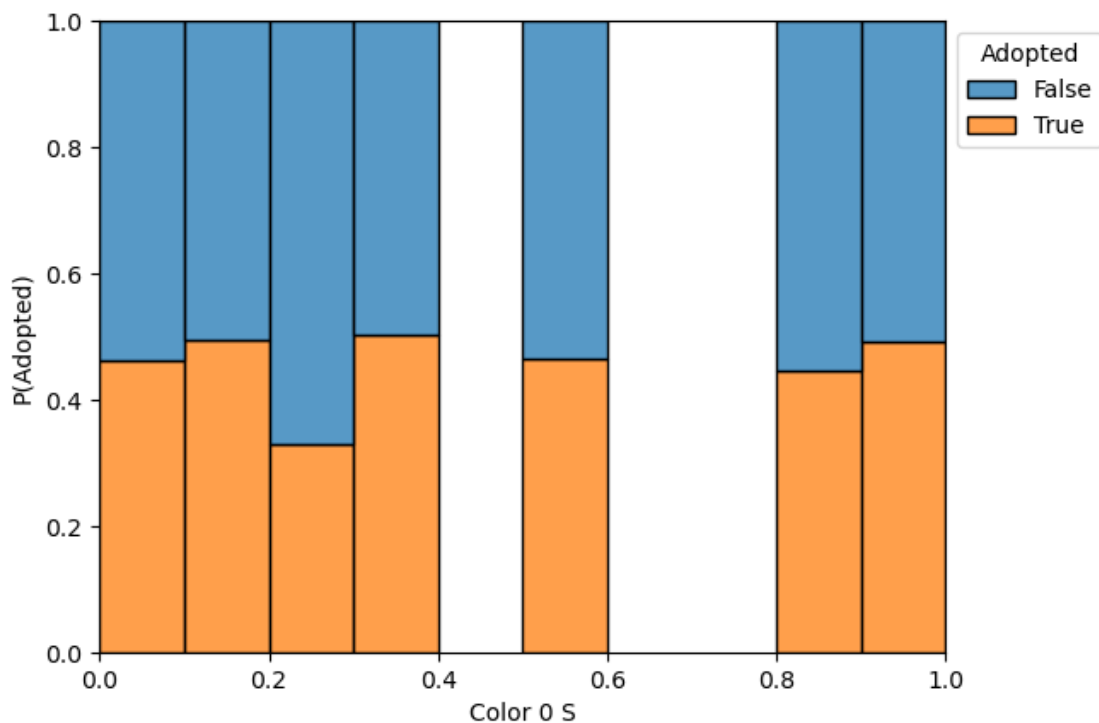



Color 0 S ~ Adopted

```

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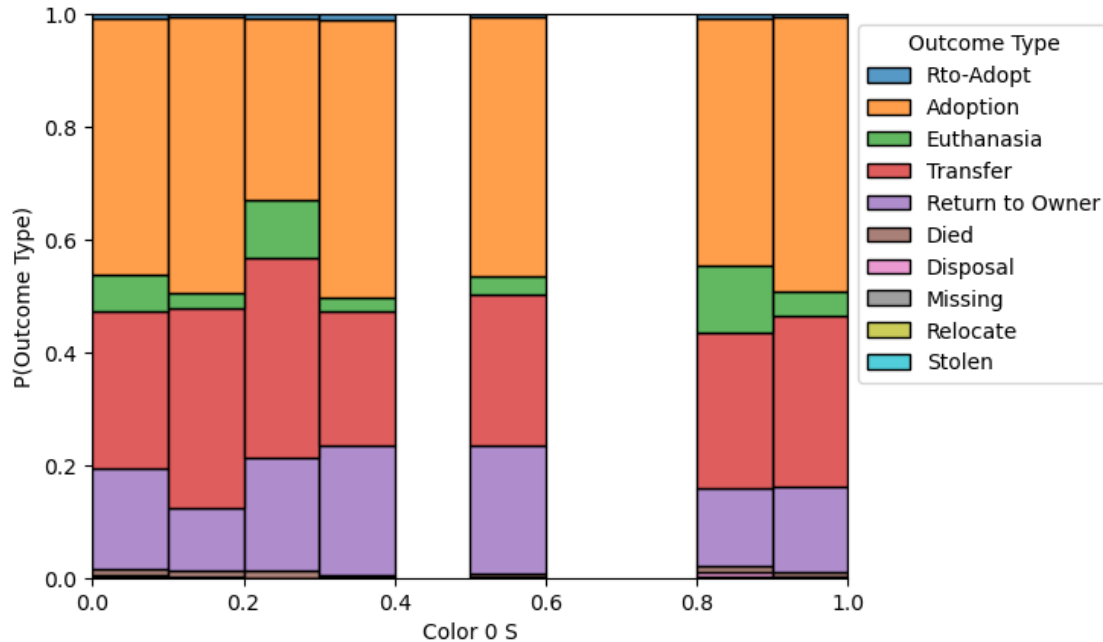
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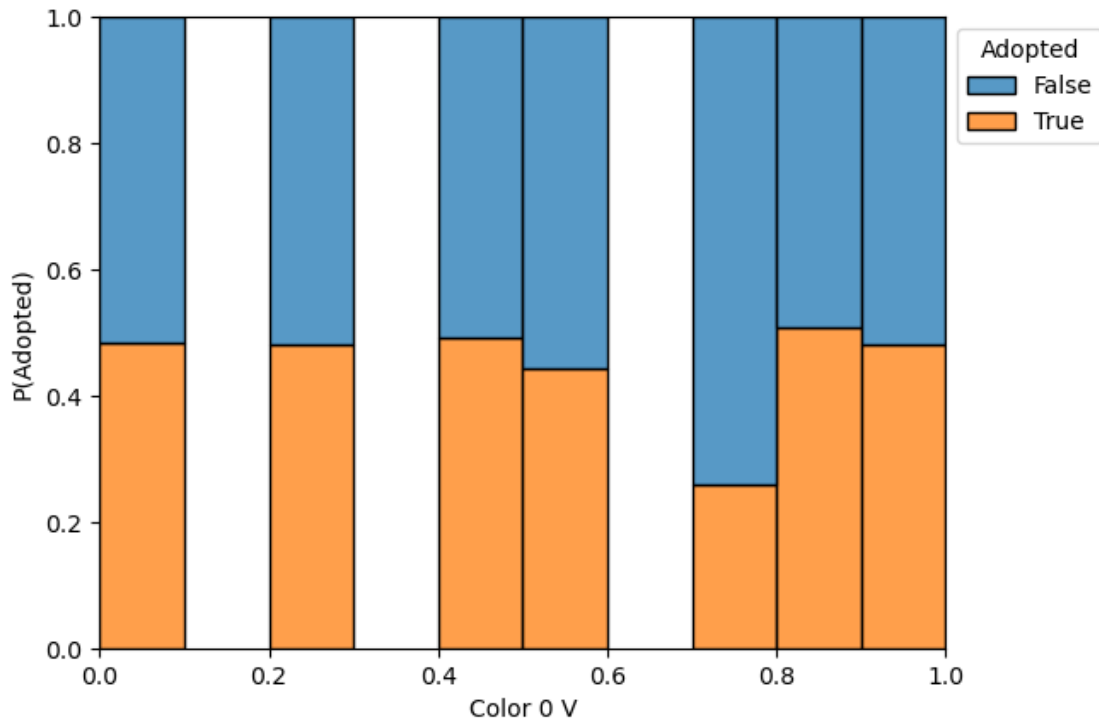


Color 0 V ~ Adopted

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Color 0 V ~ Outcome Type

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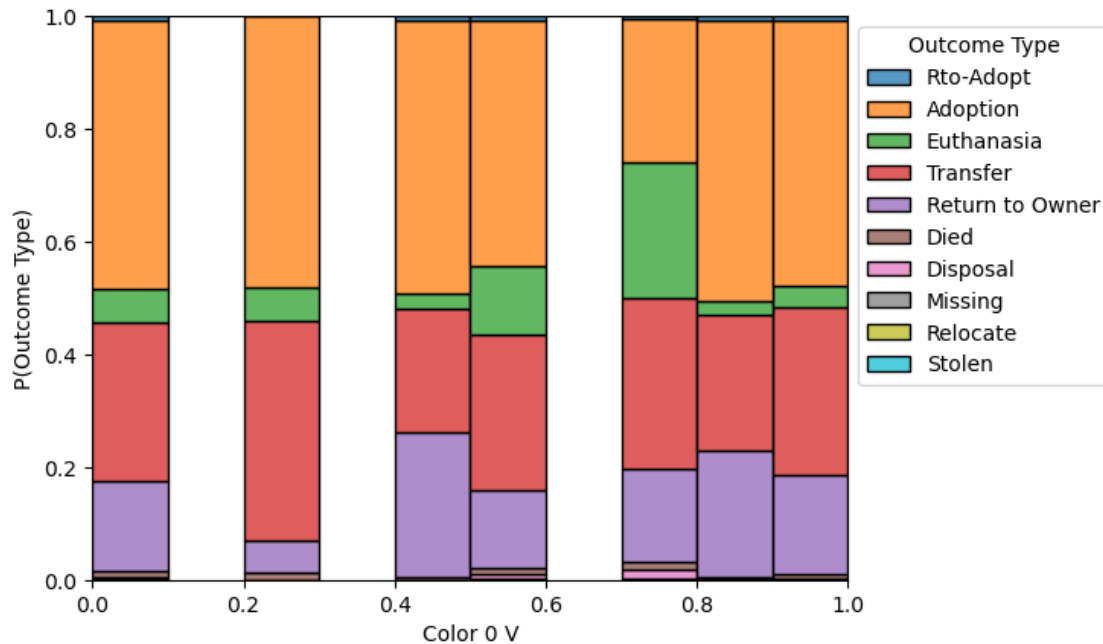
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```

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

```
[19]: df_al = df_out.dropna(how='all',axis=0)
df_al['Age upon Outcome (years)'] = df_al['Age upon Outcome (years)'].fillna(0)
df_al['Adopted'] = df_al['Adopted'].fillna(False)

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)
```

```

model = LogisticRegression()
model.fit(x_training_data, y_training_data)
# predictions = model.predict(x_test_data)
print(confusion_matrix(y_test_data, model.predict(x_test_data)))
print(classification_report(y_test_data, model.predict(x_test_data)))

```

```

[[14954  8618]
 [10069 11213]]

```

	precision	recall	f1-score	support
0	0.60	0.63	0.62	23572
1	0.57	0.53	0.55	21282
accuracy			0.58	44854
macro avg	0.58	0.58	0.58	44854
weighted avg	0.58	0.58	0.58	44854

The precision of 0.60 with a large support could be useful.