corr

April 13, 2023

[17]:

```python
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

%matplotlib inline
```

[18]:

```python
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_breeks_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
```

[18]:

```
  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]
```

[19]:

```
df_breeds_with_info.head()
```

[19]:

```
                     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]
```

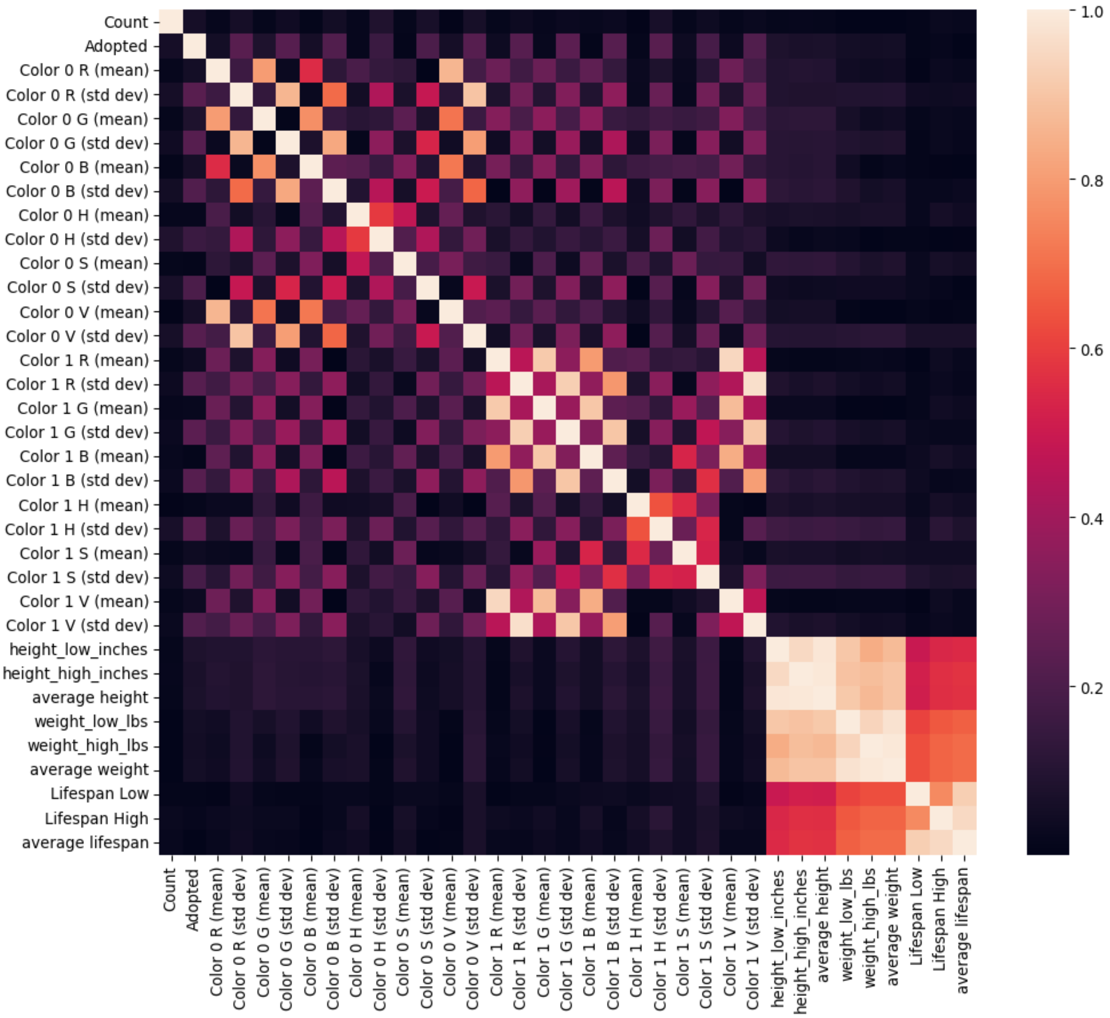
1 Analysis by breed

There isn't much correlation appearing yet

[20]:
```
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')
```

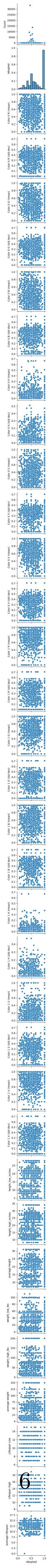
```
/tmp/ipykernel_9684/4118066584.py:1: FutureWarning: The default value of
numeric_only in DataFrame.corr is deprecated. In a future version, it will
default to False. Select only valid columns or specify the value of numeric_only
to silence this warning.
  df_breeds_with_info_corr = df_breeds_with_info.corr()
```

```
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
```



[21]:
```
sns.pairplot(data=df_breeds_with_info, x_vars=['Adopted'])
```

[21]:
```
<seaborn.axisgrid.PairGrid at 0x7f7f2955b220>
```


Count
Adopted
Color 0 R (mean)
Color 0 R (std dev)
Color 0 G (mean)
Color 0 G (std dev)
Color 0 B (mean)
Color 0 B (std dev)
Color 0 H (mean)
Color 0 H (std dev)
Color 0 S (mean)
Color 0 S (std dev)
Color 0 V (mean)
Color 0 V (std dev)
Color 1 R (mean)
Color 1 R (std dev)
Color 1 G (mean)
Color 1 G (std dev)
Color 1 B (mean)
Color 1 B (std dev)
Color 1 H (mean)
Color 1 H (std dev)
Color 1 S (mean)
Color 1 S (std dev)
Color 1 V (mean)
Color 1 V (std dev)
height_low_inches
height_high_inches
average height
weight_low_lbs
weight_high_lbs
average weight
Lifespan Low
Lifespan High
average lifespan
0.0
0.5
1.0
Adopted

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 Corr(Adopted, average height) 0.2286839421877296.

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

[22]:

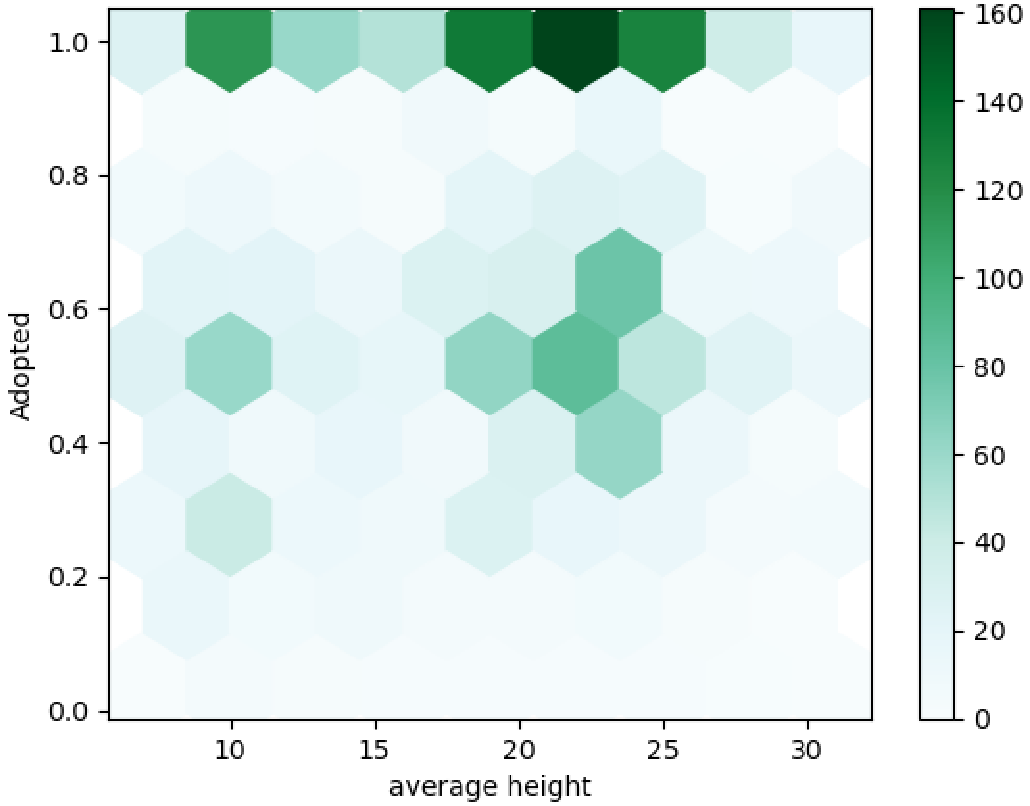
```
# TODO 1: perform logistic regression on the individual animals in␣
 ↪df_out_with_breeds_info
# to regress average_height with Adopted
```

[23]:

```
# TODO 2: make the "Count" column be the weight for the hexbin()
# so that breeds with more animals weigh more heavily than breeds with few␣
 ↪animals.

df_breeds_with_info.plot.hexbin(x='average height', y='Adopted', gridsize=8)
```

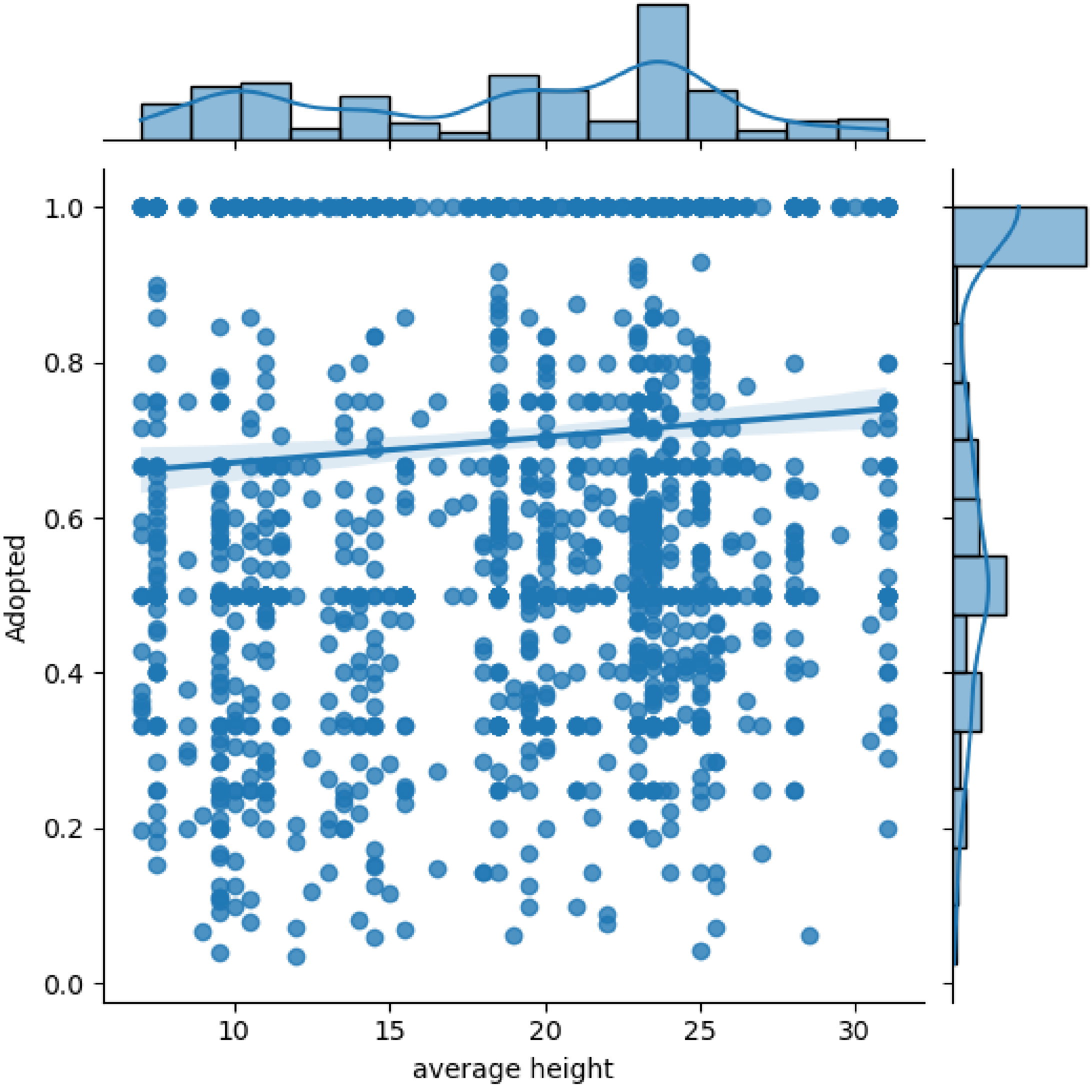
[23]:

```
<AxesSubplot:xlabel='average height', ylabel='Adopted'>
```



```
[24]: # TODO 3: make the "Count" column be the weight for the points and regression␣
       ↪here
      # TODO 4: include Y error bars for the uncertainty in the true value of Adopted␣
       ↪for that breed
      # (see how the confidence interval was constructed in the color regression␣
       ↪later)

      sns.jointplot(
          x=df_breeds_with_info['average height'].astype(dtype=float),
          y=df_breeds_with_info.Adopted.astype(dtype=float),
          kind='reg')
```

```
[24]: <seaborn.axisgrid.JointGrid at 0x7f7f293b31f0>
```



2 Analysis by individuals

2.1 Color

(results)

[25]:

```python
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
```

[26]:
```python
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)]
```

[27]:
```python
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]
```

[28]:
```python
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]
```

[29]:

```
# 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)
```

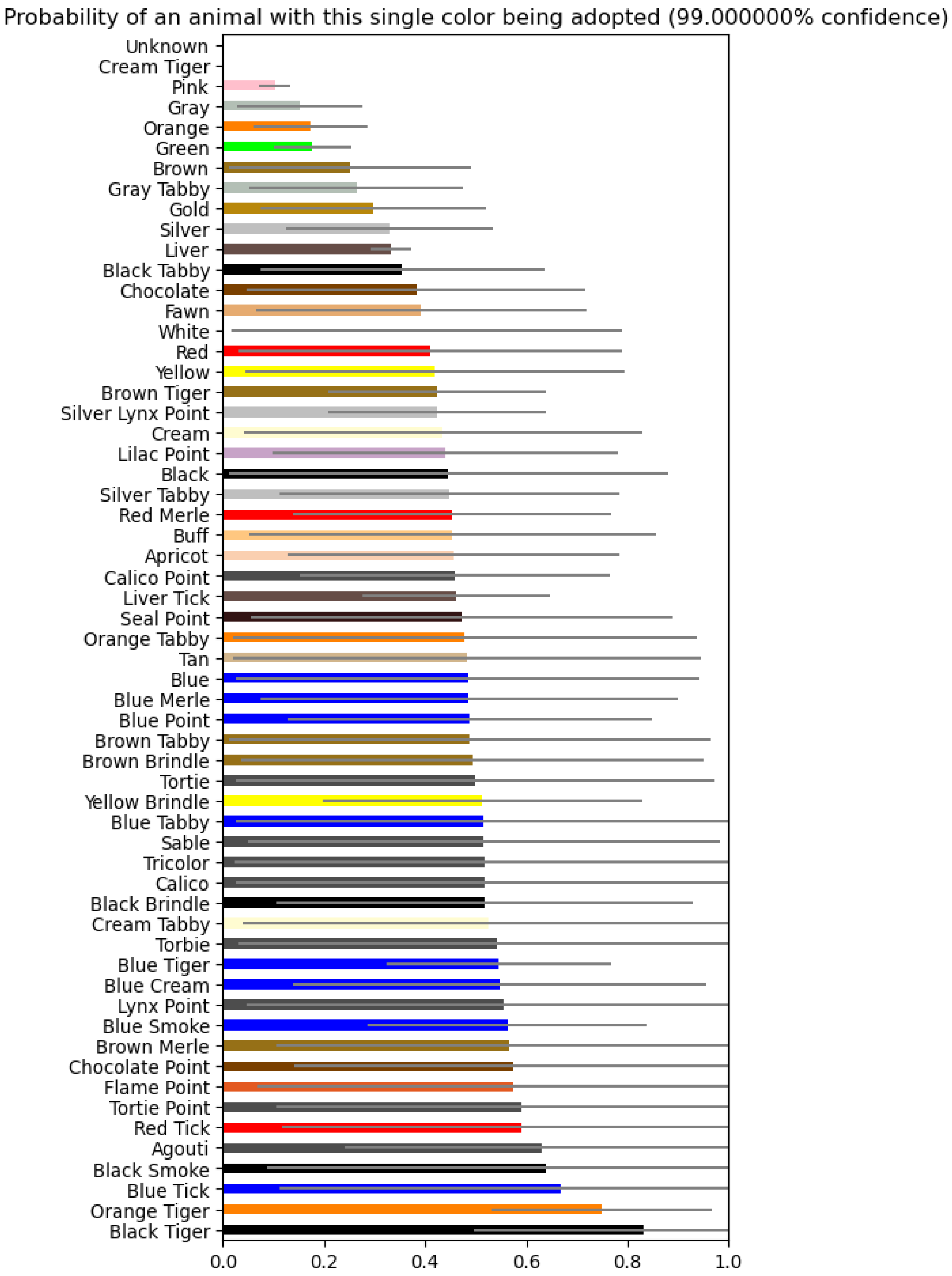
[30]:

```
def chartColorAdoptionLikelihood(df_colors, color_relation):

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

    alpha = 0.01
```

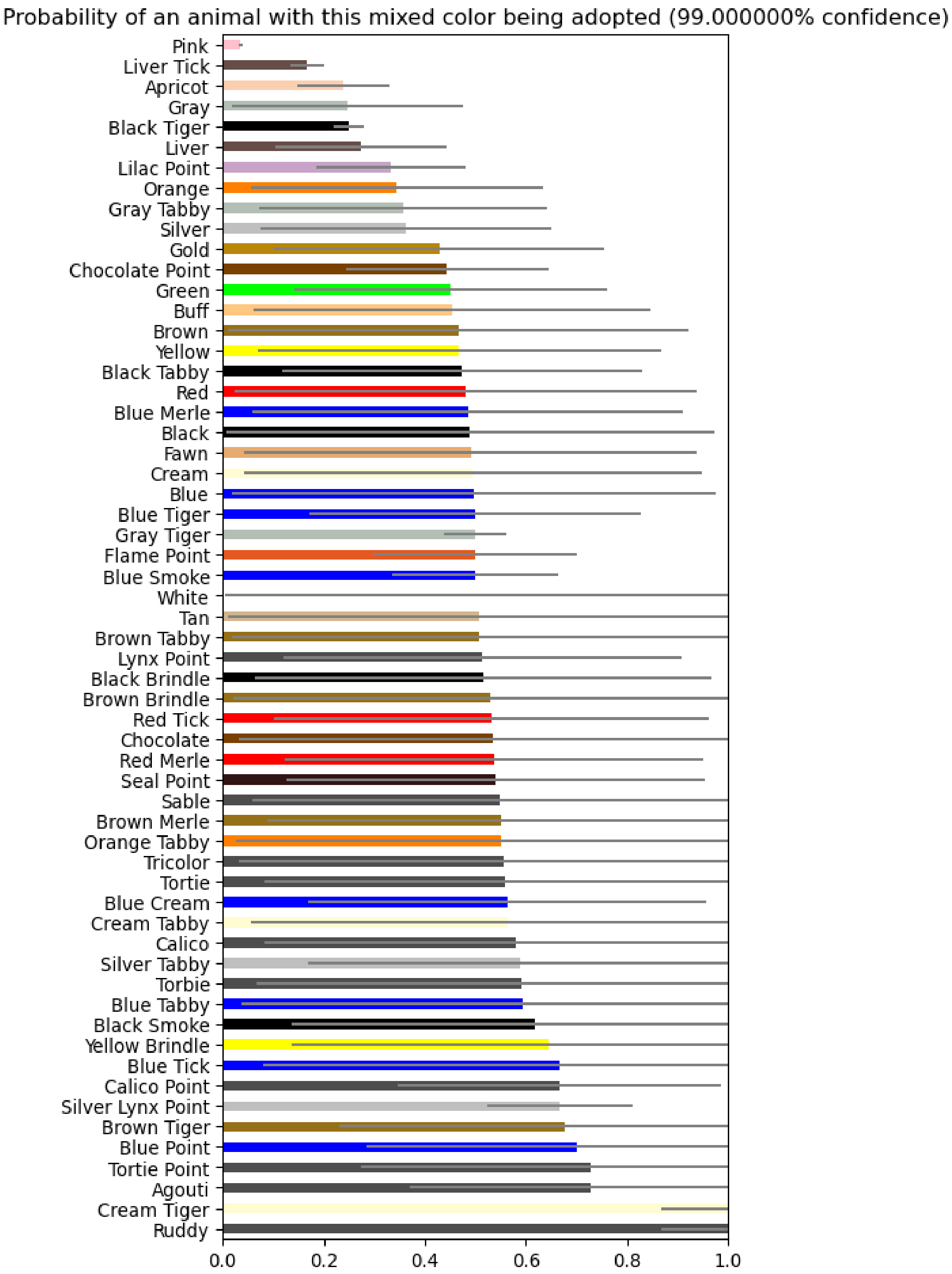
```
    z = st.norm.ppf(1 - (alpha / 2))
    n = df_colors.Count
    p = df_colors.Adopted
    p_center = (1 / (1 + ((z ** 2) / n))) * (p + ((z ** 2) / (2 * n)))
    p_halfextent = (z / (1 + ((z ** 2) / n))) * ((( (p * (1 - p)) / (n) ) + ((z␣
 ↪** 2) / (4 * (n ** 2)))) ** (1/2))
    p_low = p_center - 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)
Unknown
Cream Tiger
Pink
Gray
Orange
Green
Brown
Gray Tabby
Gold
Silver
Liver
Black Tabby
Chocolate
Fawn
White
Red
Yellow
Brown Tiger
Silver Lynx Point
Cream
Lilac Point
Black
Silver Tabby
Red Merle
Buff
Apricot
Calico Point
Liver Tick
Seal Point
Orange Tabby
Tan
Blue
Blue Merle
Blue Point
Brown Tabby
Brown Brindle
Tortie
Yellow Brindle
Blue Tabby
Sable
Tricolor
Calico
Black Brindle
Cream Tabby
Torbie
Blue Tiger
Blue Cream
Lynx Point
Blue Smoke
Brown Merle
Chocolate Point
Flame Point
Tortie Point
Red Tick
Agouti
Black Smoke
Blue Tick
Orange Tiger
Black Tiger
0.0
0.2
0.4
0.6
0.8
1.0

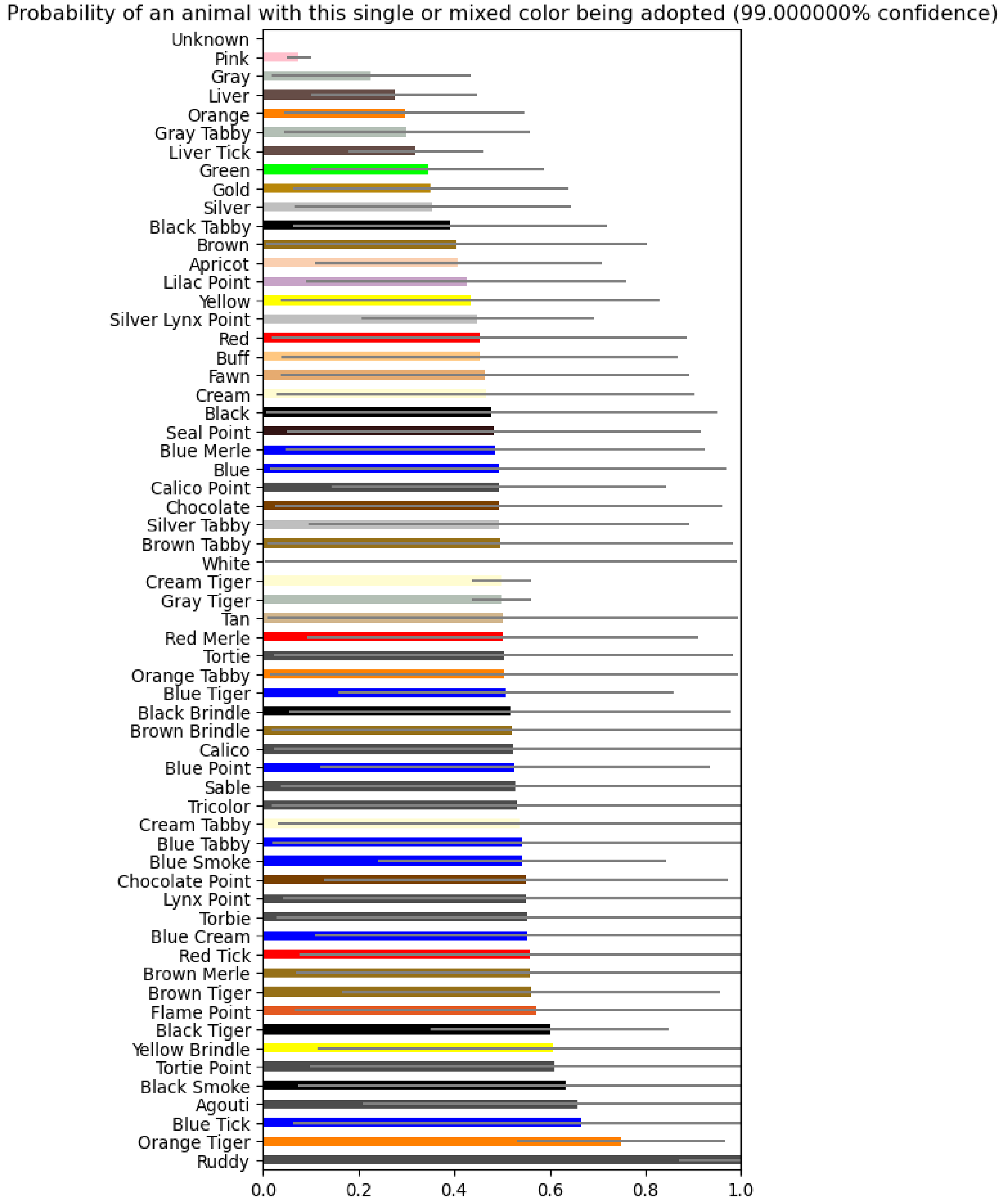
```
59 colors
```



```
59 colors
```

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

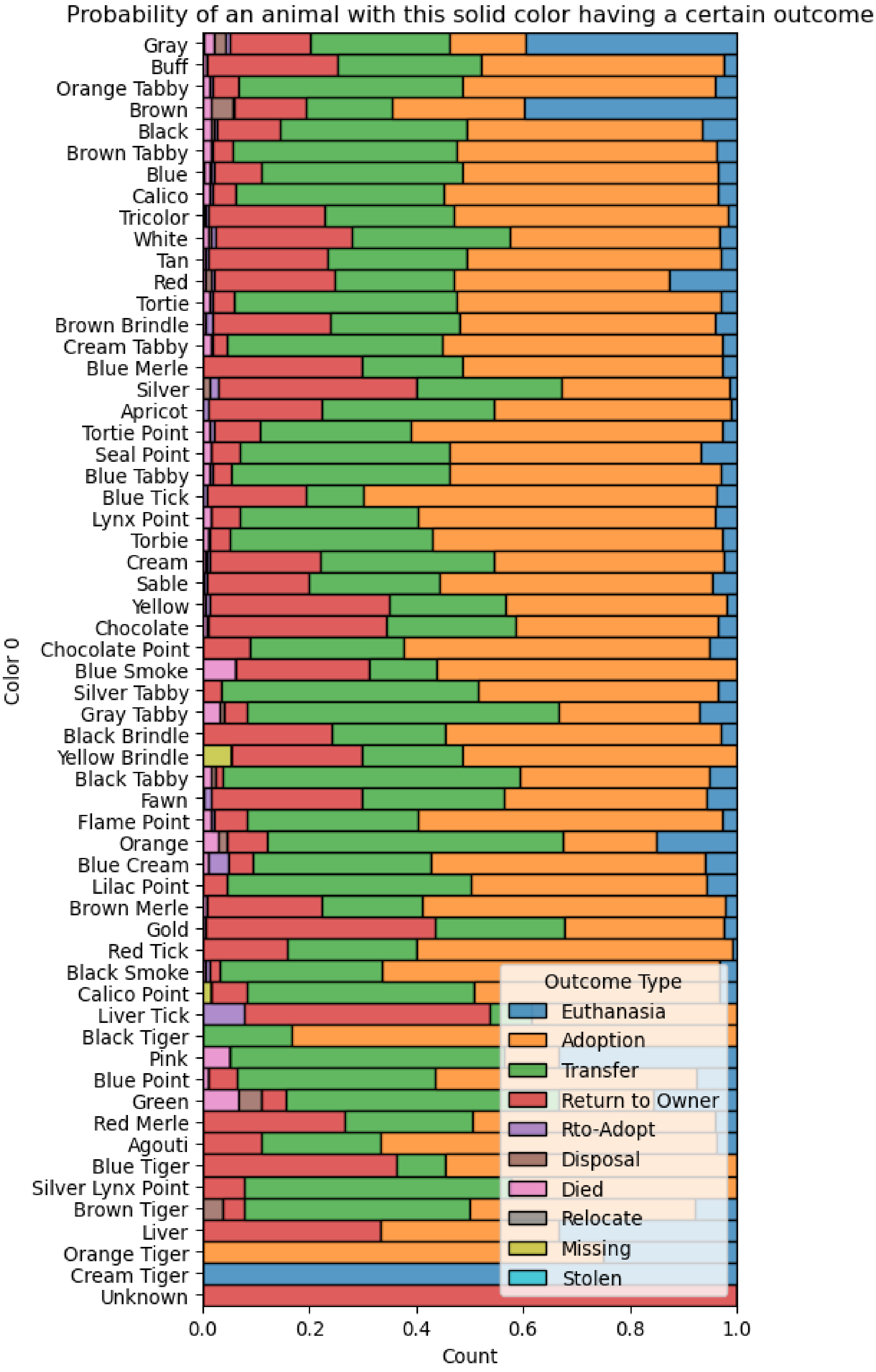
```
packages/numpy/core/_methods.py:44: RuntimeWarning: invalid value encountered in
reduce
  return umr_minimum(a, axis, None, out, keepdims, initial, where)
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/numpy/core/_methods.py:40: RuntimeWarning: invalid value encountered in
reduce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



```
61 colors
```

[30]:

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


Probability of an animal with this solid color having a certain outcome
Color 0
Gray
Buff
Orange Tabby
Brown
Black
Brown Tabby
Blue
Calico
Tricolor
White
Tan
Red
Tortie
Brown Brindle
Cream Tabby
Blue Merle
Silver
Apricot
Tortie Point
Seal Point
Blue Tabby
Blue Tick
Lynx Point
Torbie
Cream
Sable
Yellow
Chocolate
Chocolate Point
Blue Smoke
Silver Tabby
Gray Tabby
Black Brindle
Yellow Brindle
Black Tabby
Fawn
Flame Point
Orange
Blue Cream
Lilac Point
Brown Merle
Gold
Red Tick
Black Smoke
Calico Point
Liver Tick
Black Tiger
Pink
Blue Point
Green
Red Merle
Agouti
Blue Tiger
Silver Lynx Point
Brown Tiger
Liver
Orange Tiger
Cream Tiger
Unknown
0.0
0.2
0.4
0.6
0.8
1.0
Count
Outcome Type
Euthanasia
Adoption
Transfer
Return to Owner
Rto-Adopt
Disposal
Died
Relocate
Missing
Stolen

2.2 Sex

[31]:

```
# 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?

[32]:

```
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)

    sns.histplot(data=df,
                 x=independent,
                 hue=dependent,
                 multiple='fill',
                 binwidth=binwidth)
    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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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"),
```

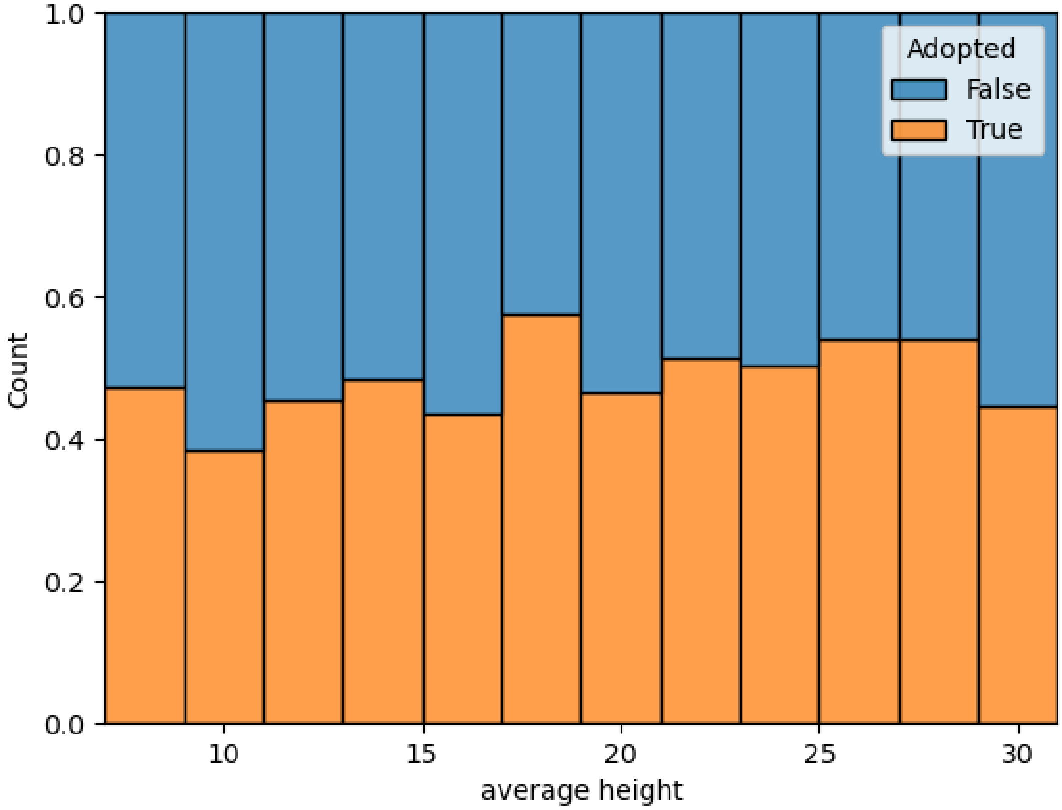

```
average height ~ Outcome Type
```

```
/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)
  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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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
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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
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packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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/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
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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
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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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/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
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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"),
/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(edges, name="edges"),
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  pd.Index(edges, name="edges"),
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packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
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sequences (matching Series behavior)
  pd.Index(widths, name="widths"),
```
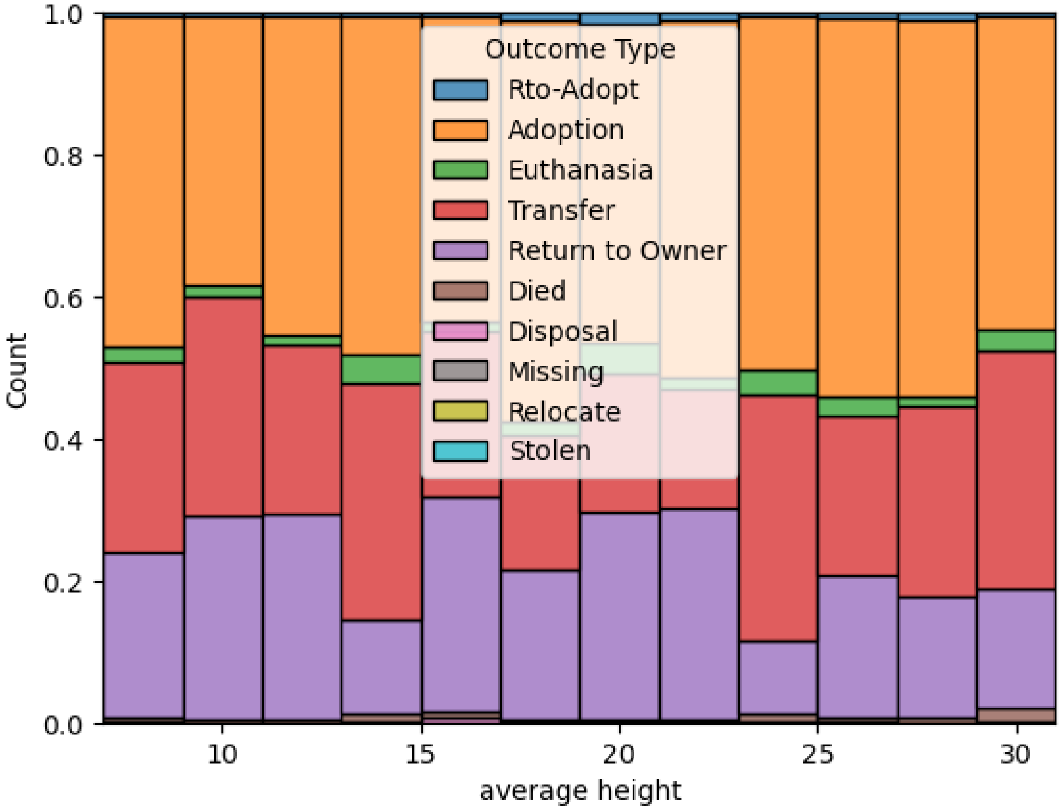
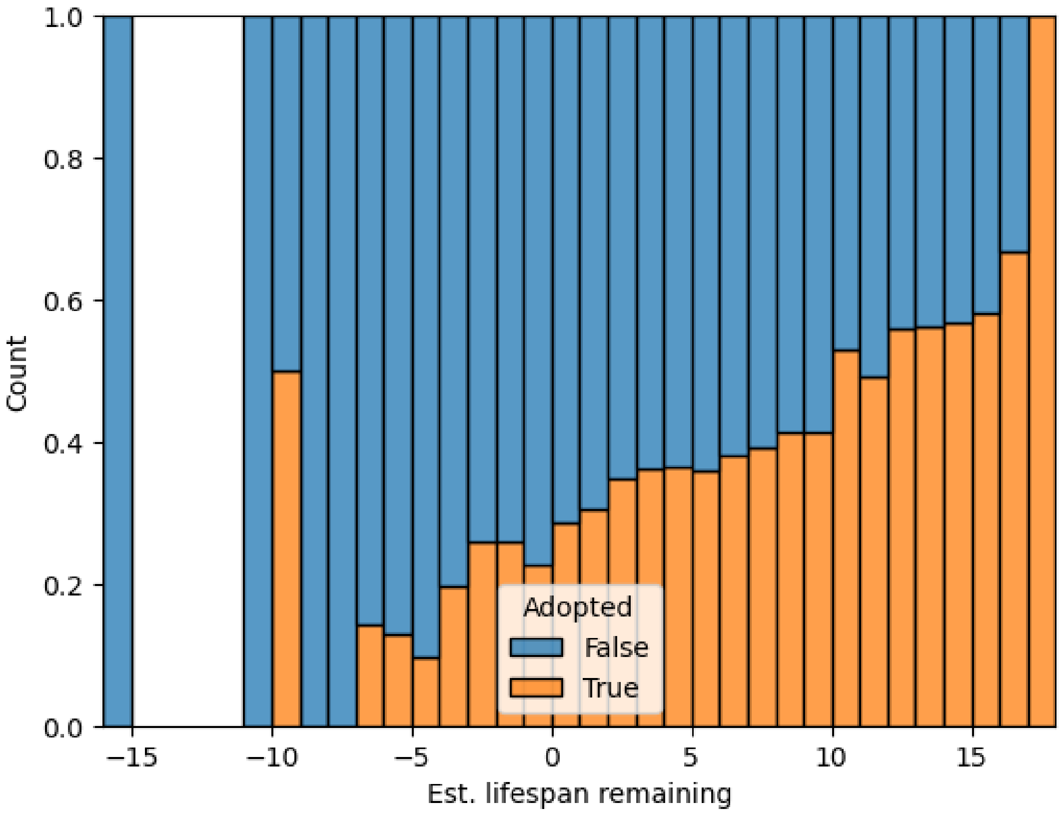
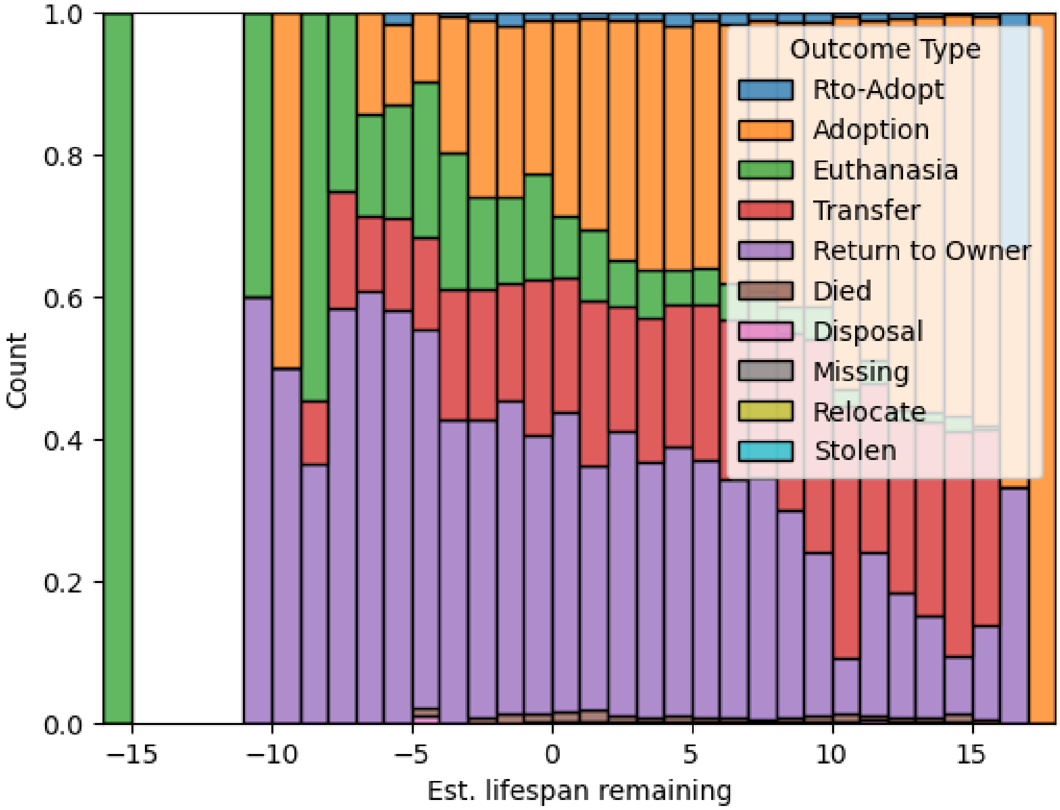



```
Est. lifespan remaining ~ Adopted
```



`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
Index constructor will not infer numeric dtypes when passed object-dtype
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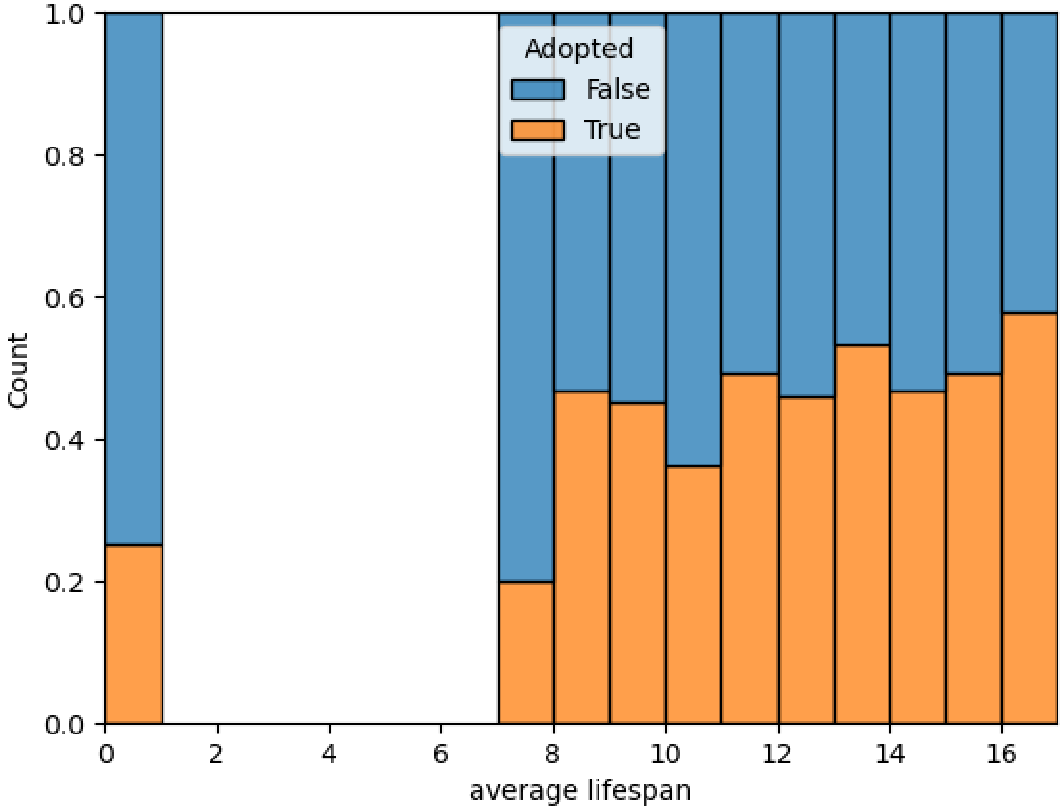

```
average lifespan ~ Outcome Type
```

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

```
/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-
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packages/seaborn/distributions.py:499: FutureWarning: In a future version, the
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
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```

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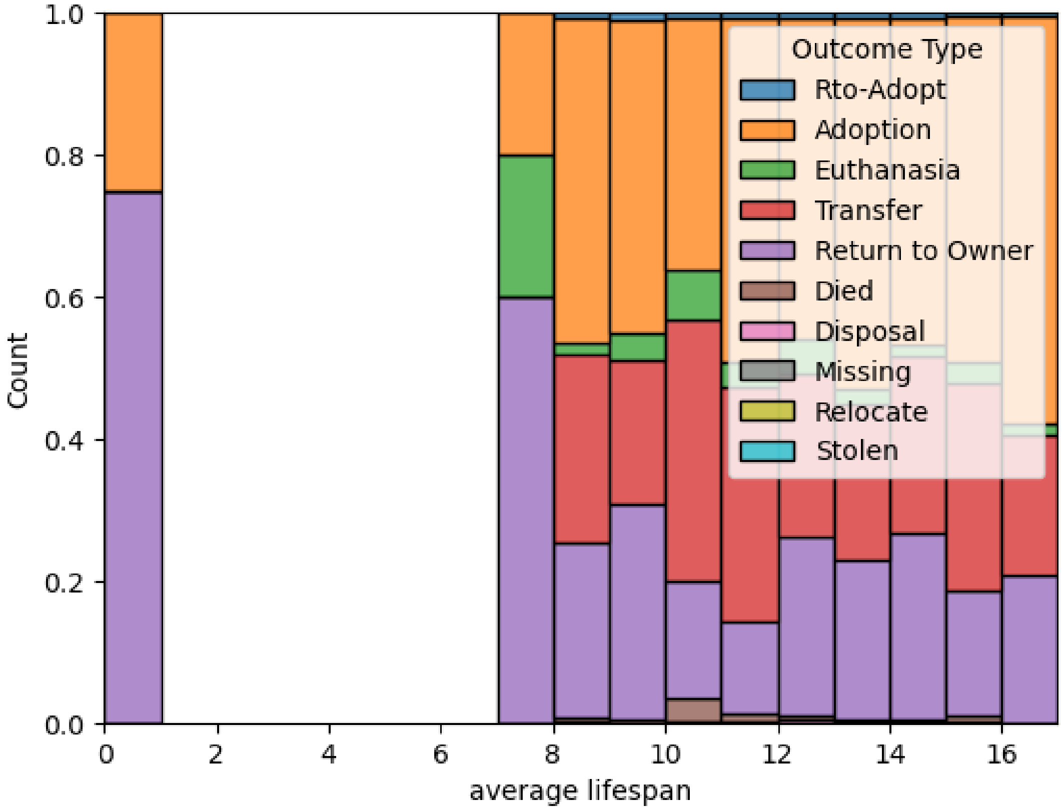
  pd.Index(edges, name="edges"),
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
packages/seaborn/distributions.py:500: FutureWarning: In a future version, the
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
  pd.Index(widths, name="widths"),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



```
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
sequences (matching Series behavior)
  pd.Index(edges, name="edges"),
/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-
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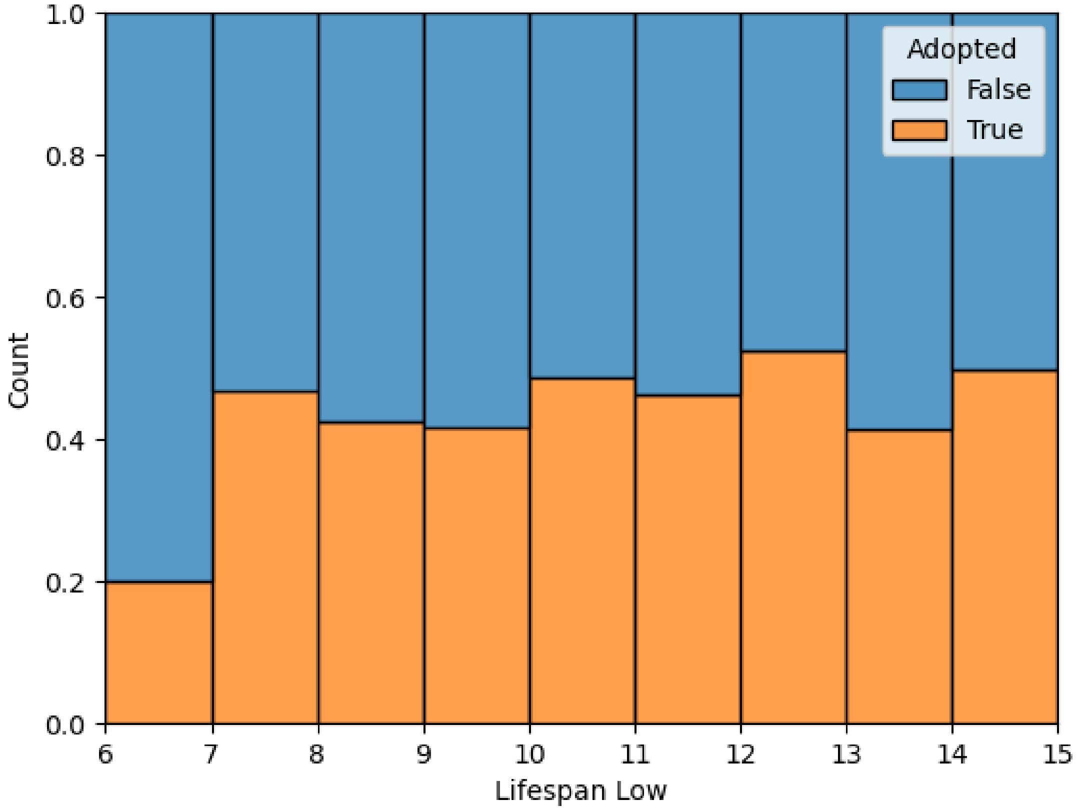
Index constructor will not infer numeric dtypes when passed object-dtype
sequences (matching Series behavior)
  pd.Index(widths, name="widths"),
```



```
Lifespan Low ~ Outcome Type
```

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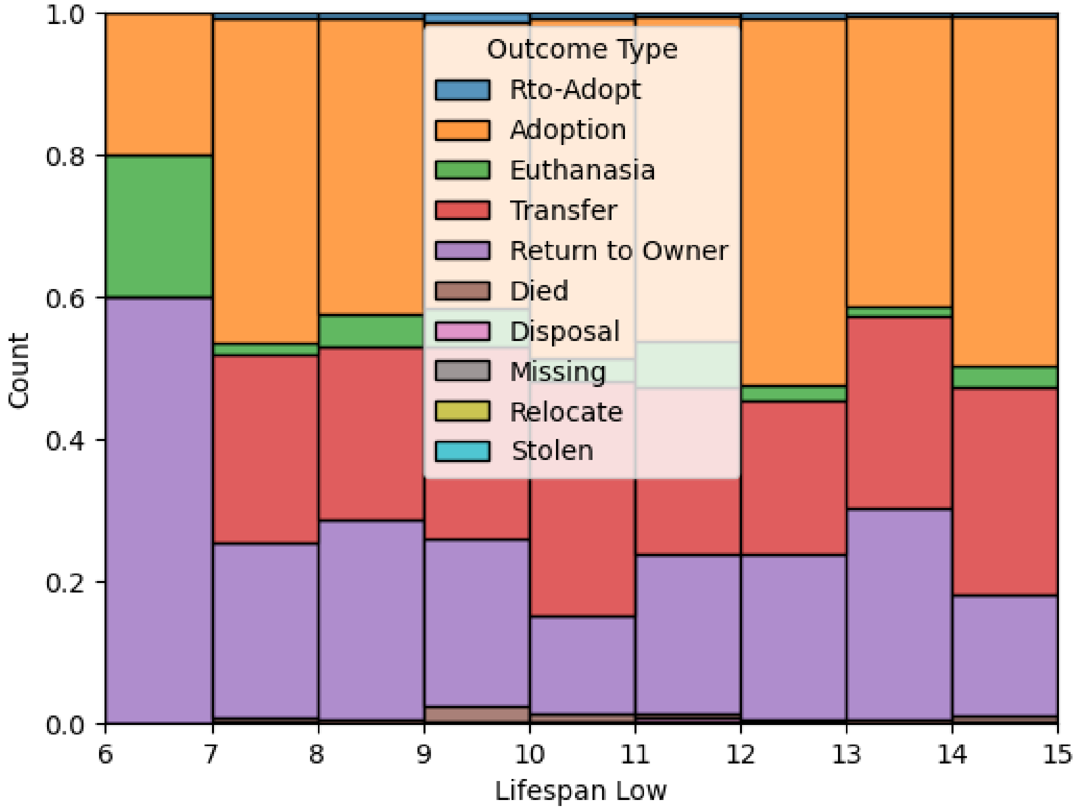

```
Lifespan High ~ Adopted
```

```
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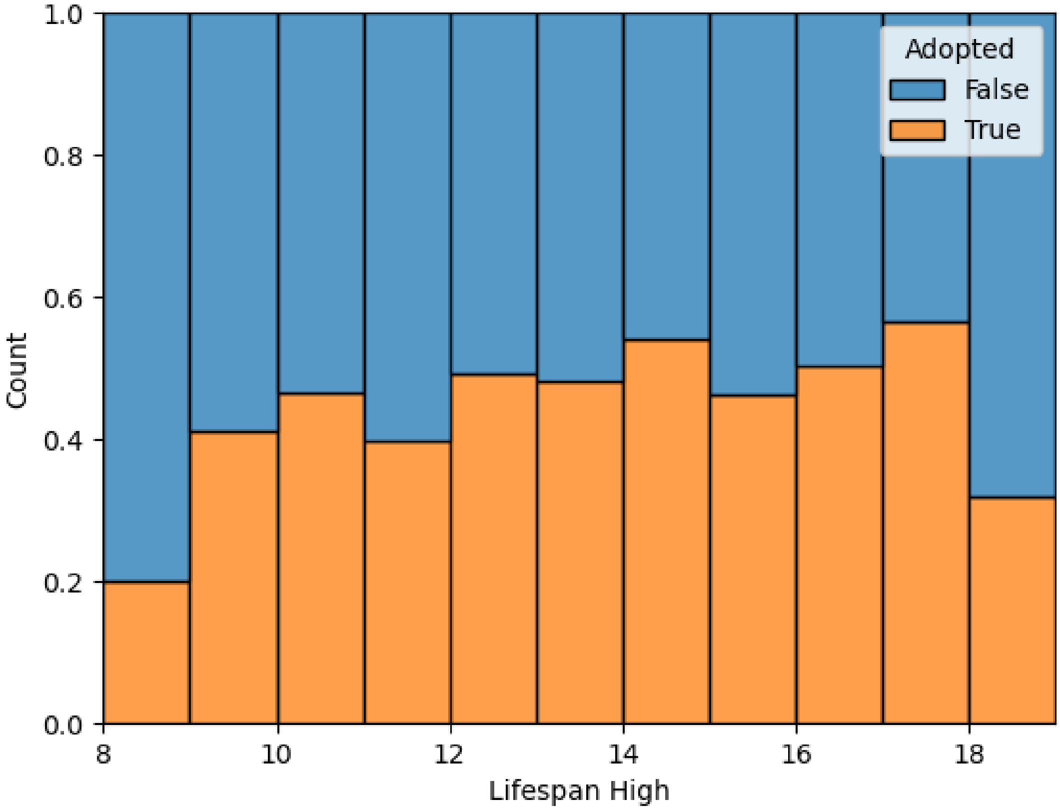

```
Lifespan High ~ Outcome Type
```

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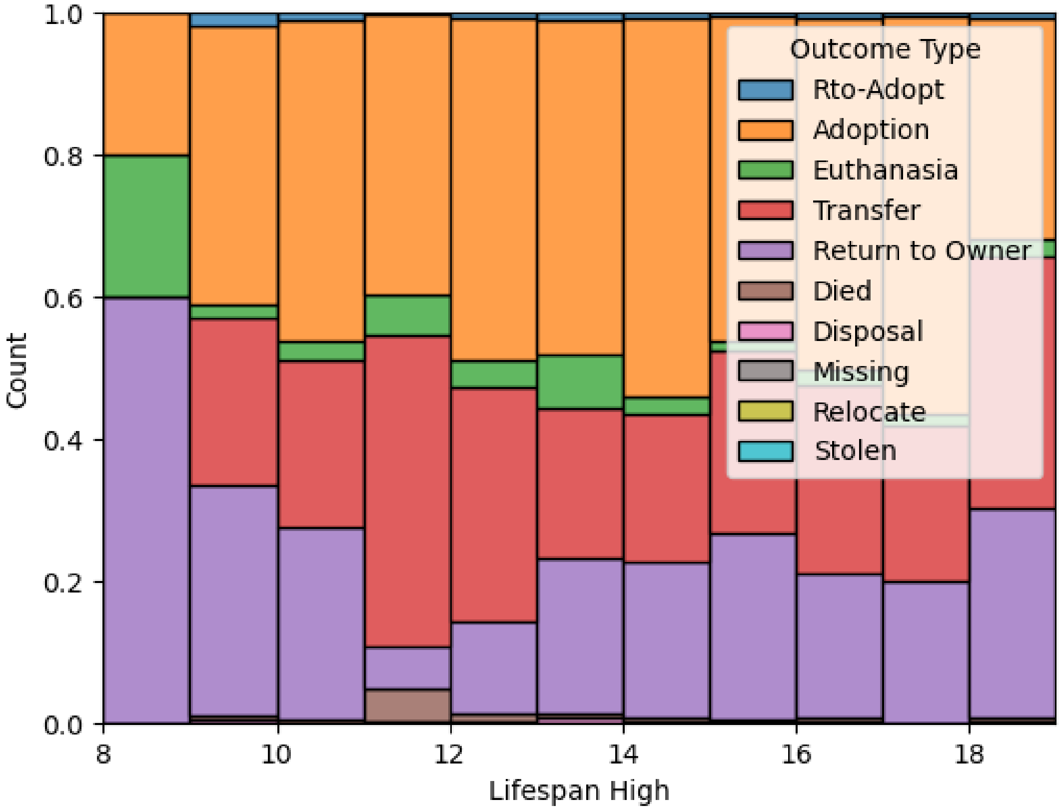

```
Age upon Outcome (years) ~ Adopted
```

```
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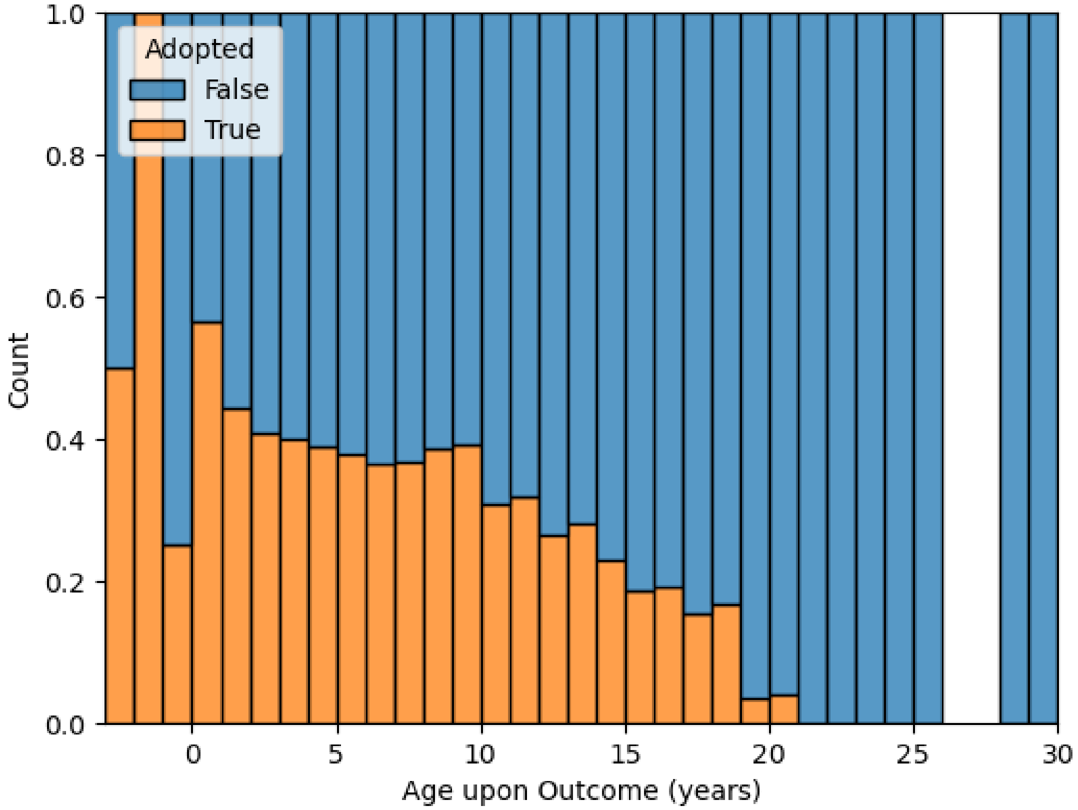

```
Age upon Outcome (years) ~ Outcome Type
```

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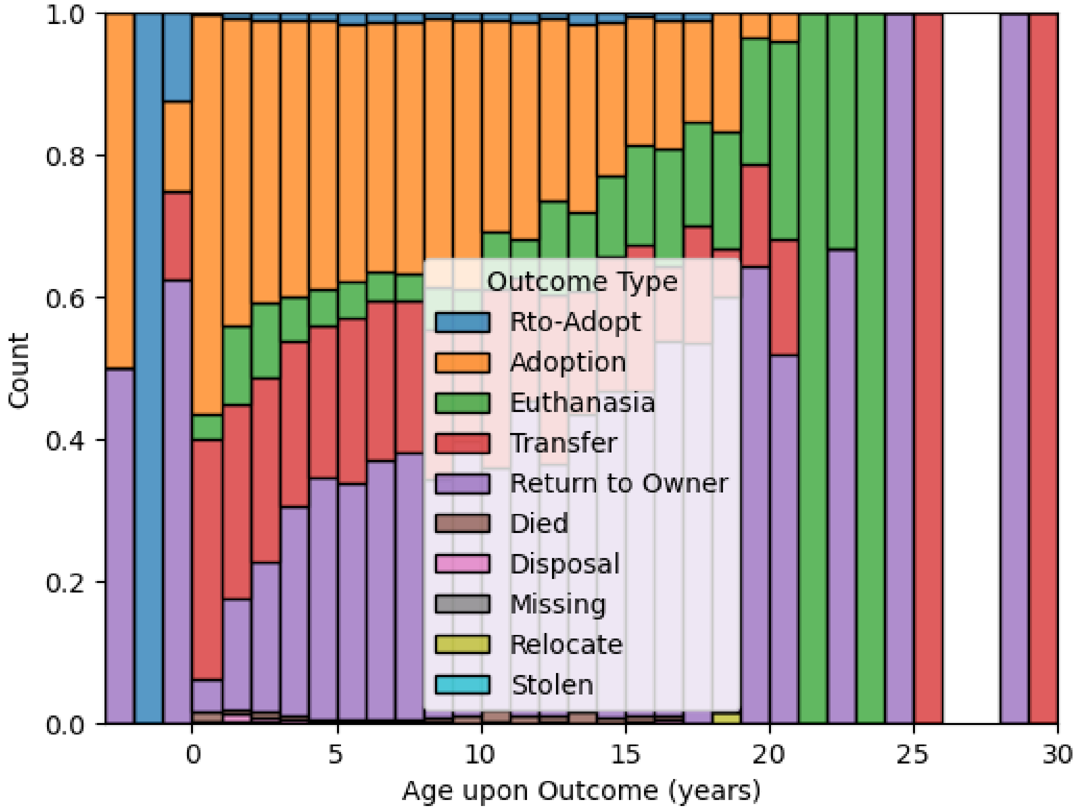

```
Color 0 H ~ Adopted
```

```
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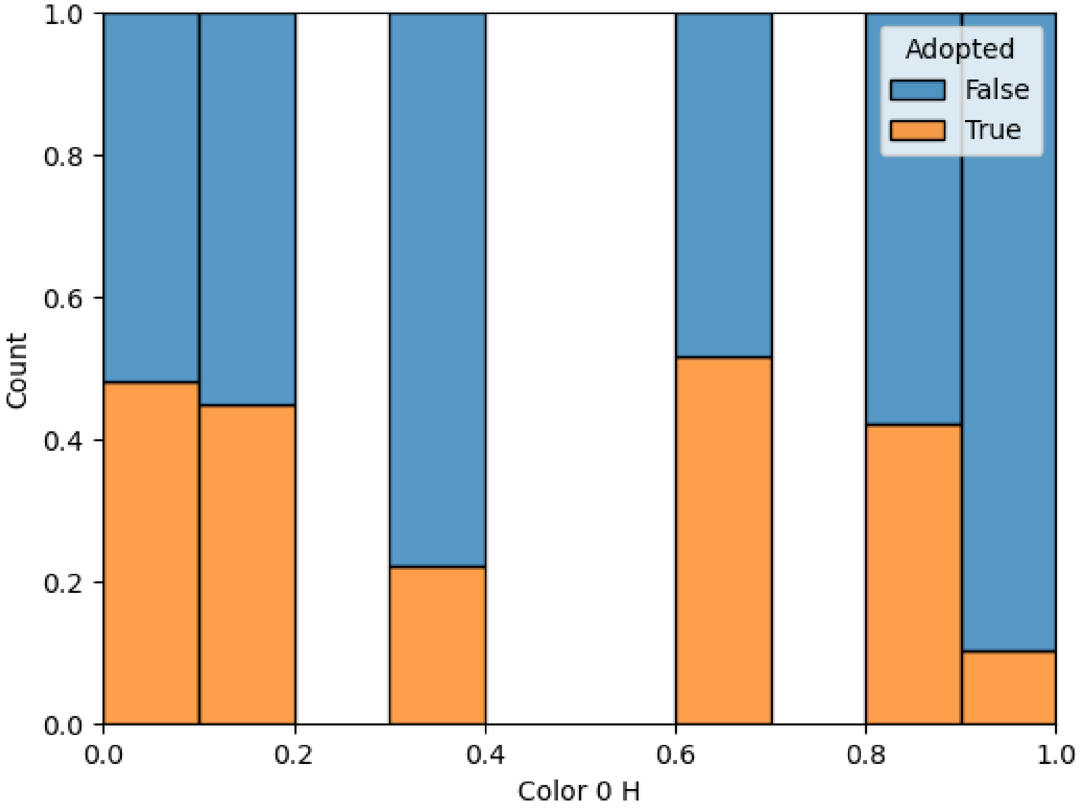

```
Color 0 H ~ Outcome Type
```

```
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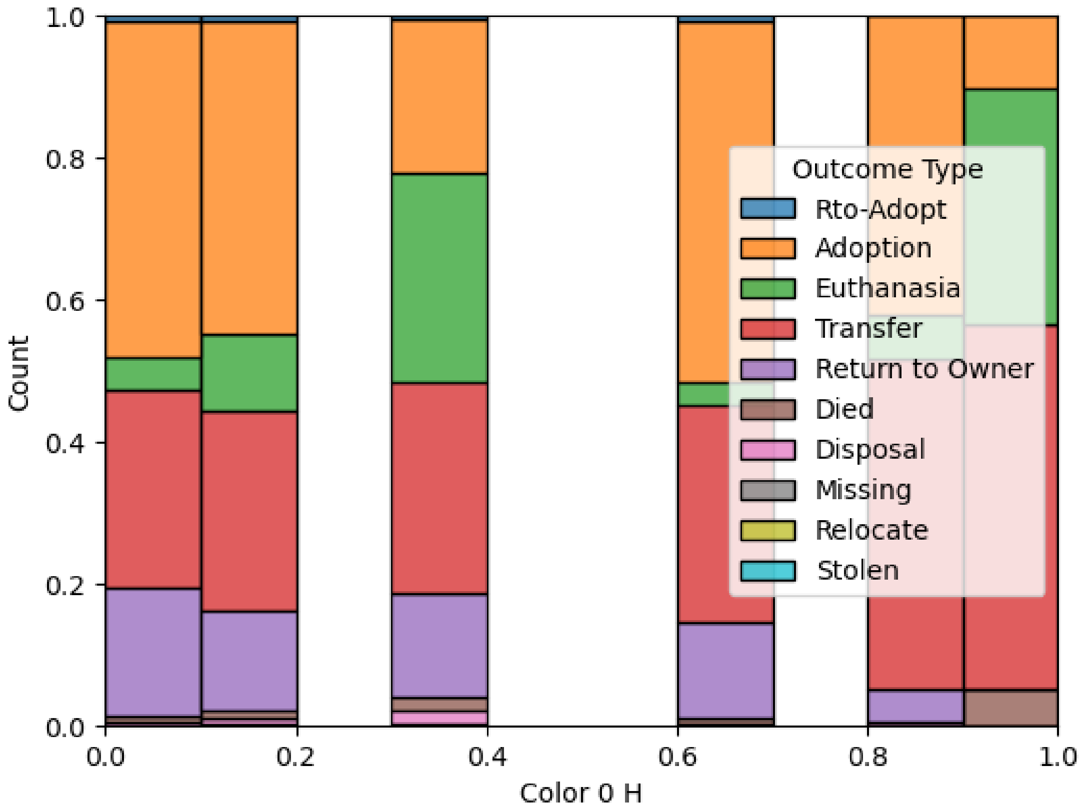

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Color 0 S ~ Adopted
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/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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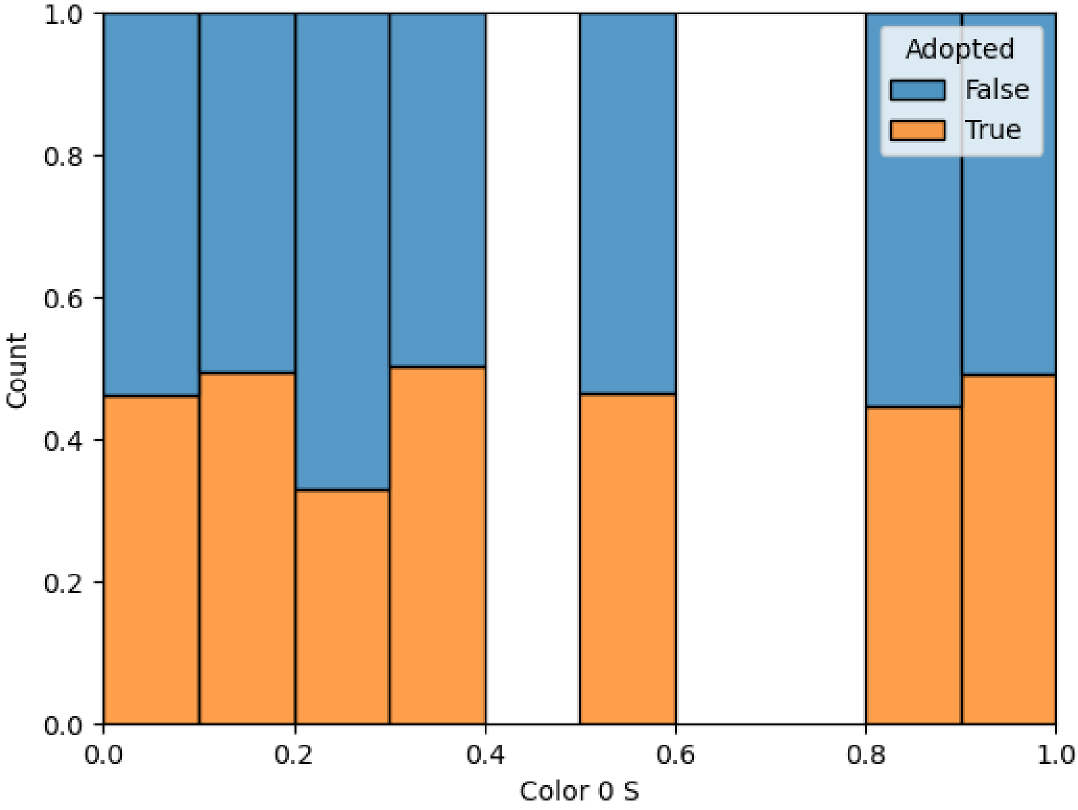

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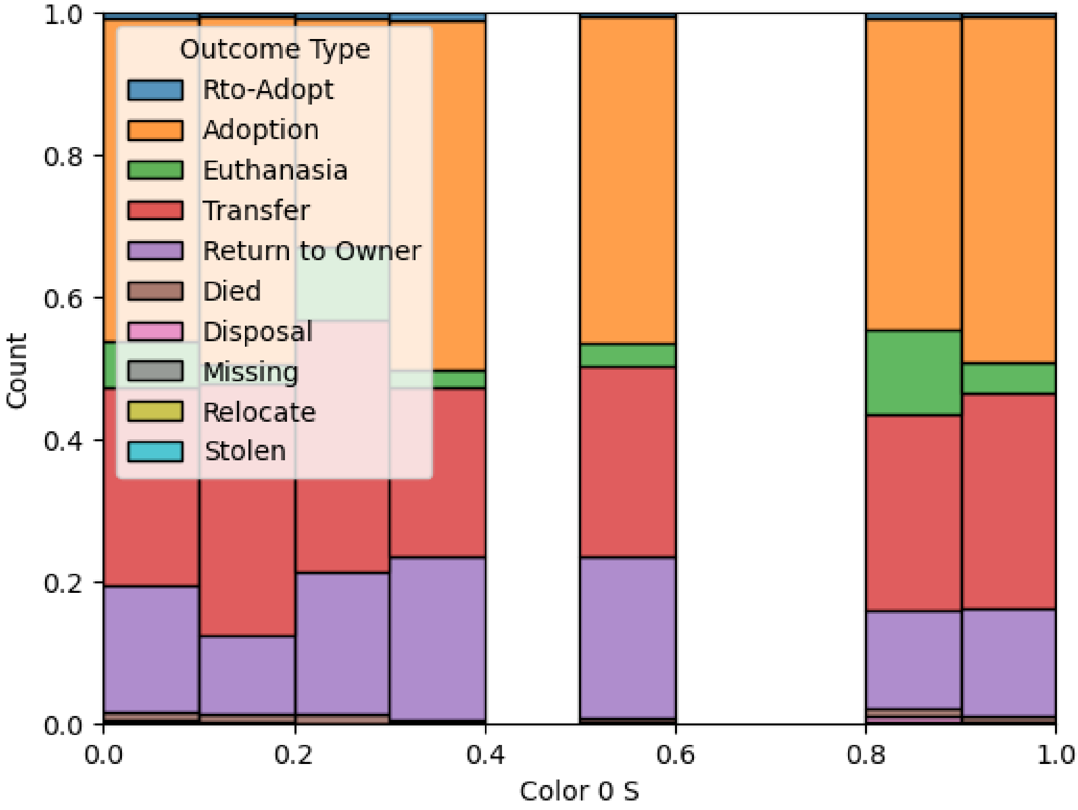

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Color 0 V ~ Adopted
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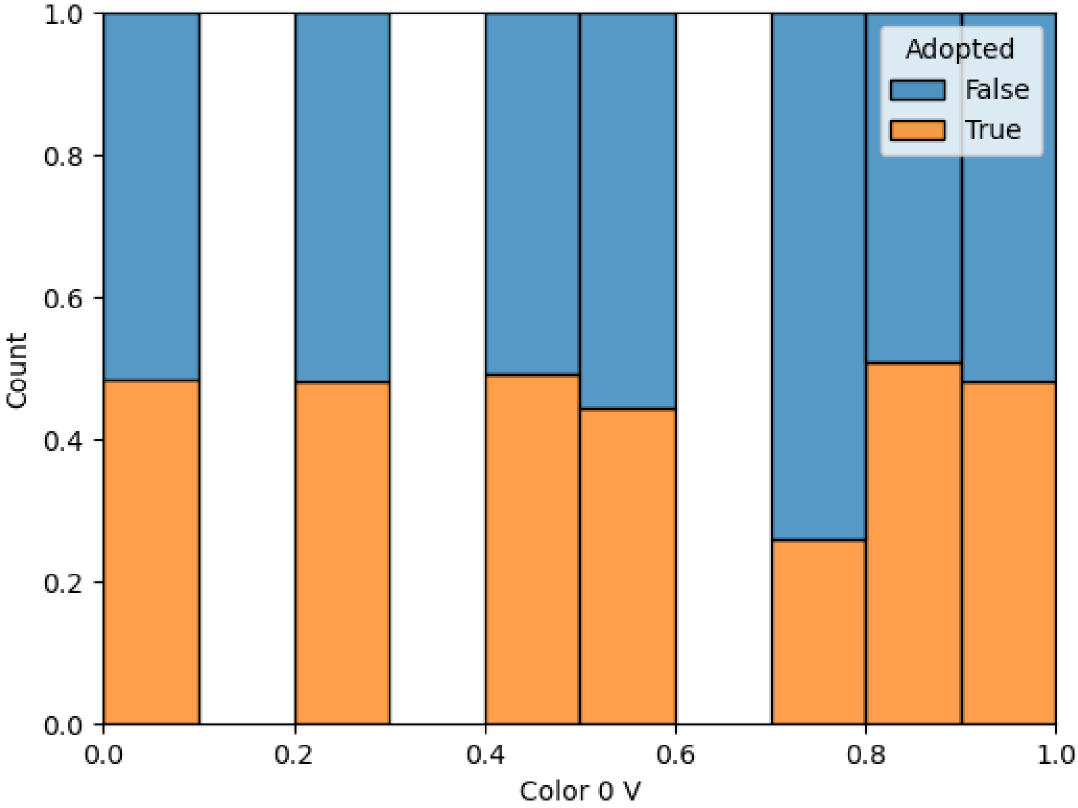

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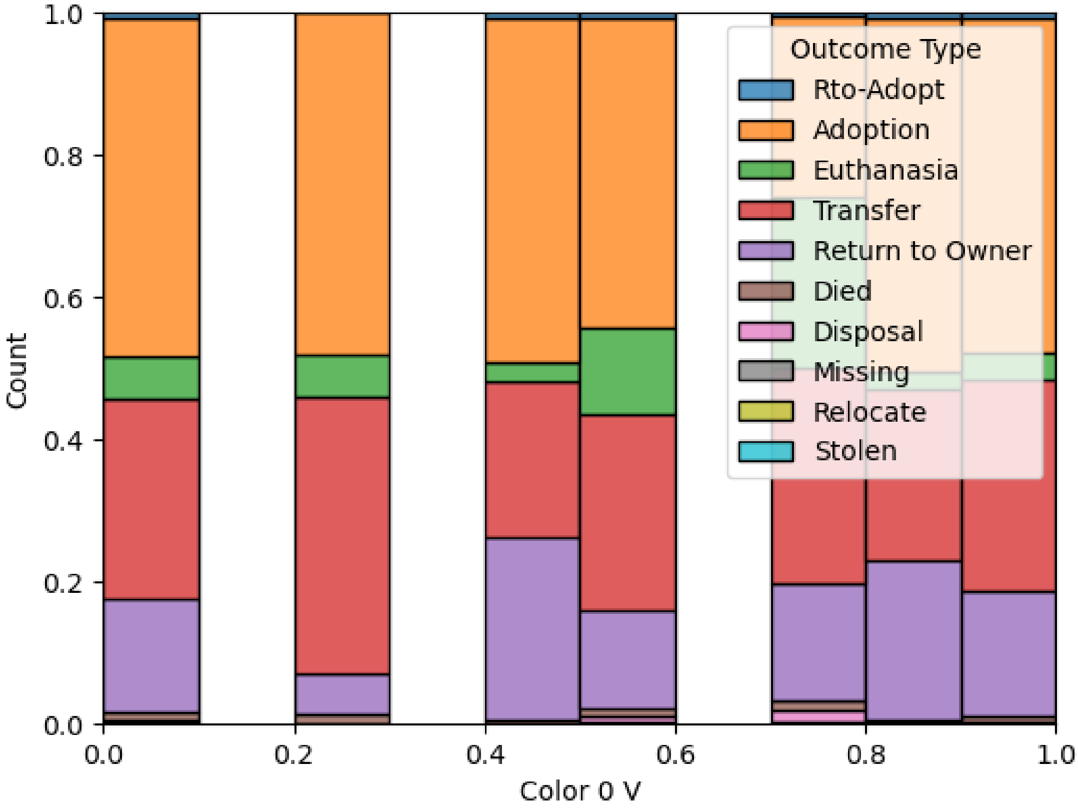
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Relocate
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