corr

April 1, 2023

```python
[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

     %matplotlib inline
```

```python
[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_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 32 columns):
 #   Column             Non-Null Count   Dtype
---  ------             --------------   -----
 0   Animal ID          149511 non-null  string
 1   Name               106260 non-null  string
 2   DateTime           149511 non-null  datetime64[ns]
 3   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  Colors (count)     149511 non-null  Int64
 13  Color 0            149511 non-null  string
 14  Color 1            79869 non-null   string
 15  Color 0 R          135638 non-null  Float64
 16  Color 0 G          135638 non-null  Float64
```

```
17  Color 0 B                 135638 non-null  Float64
18  Color 0 H                 135638 non-null  Float64
19  Color 0 S                 135638 non-null  Float64
20  Color 0 V                 135638 non-null  Float64
21  Color 1 R                 78596 non-null   Float64
22  Color 1 G                 78596 non-null   Float64
23  Color 1 B                 78596 non-null   Float64
24  Color 1 H                 78596 non-null   Float64
25  Color 1 S                 78596 non-null   Float64
26  Color 1 V                 78596 non-null   Float64
27  Age upon Outcome (years)  149465 non-null  Float64
28  Male                      149509 non-null  boolean
29  Female                    149509 non-null  boolean
30  NeuteredOrSpayed          149509 non-null  boolean
31  Adopted                   149485 non-null  boolean
dtypes: Float64(13), Int64(1), boolean(4), datetime64[ns](2), string(12)
memory usage: 35.1 MB
```

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

  Outcome Subtype Animal Type Sex upon Outcome Age upon Outcome  … \
0            <NA>         Cat    Neutered Male          2 years  …
1            <NA>         Dog    Neutered Male           1 year  …
2            <NA>       Other          Unknown           1 year  …
3            <NA>         Dog    Neutered Male         4 months  …
4         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 32 columns]
```

1 Analysis by breed

There isn't much correlation appearing yet

```
[3]: 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_13237/4118066584.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
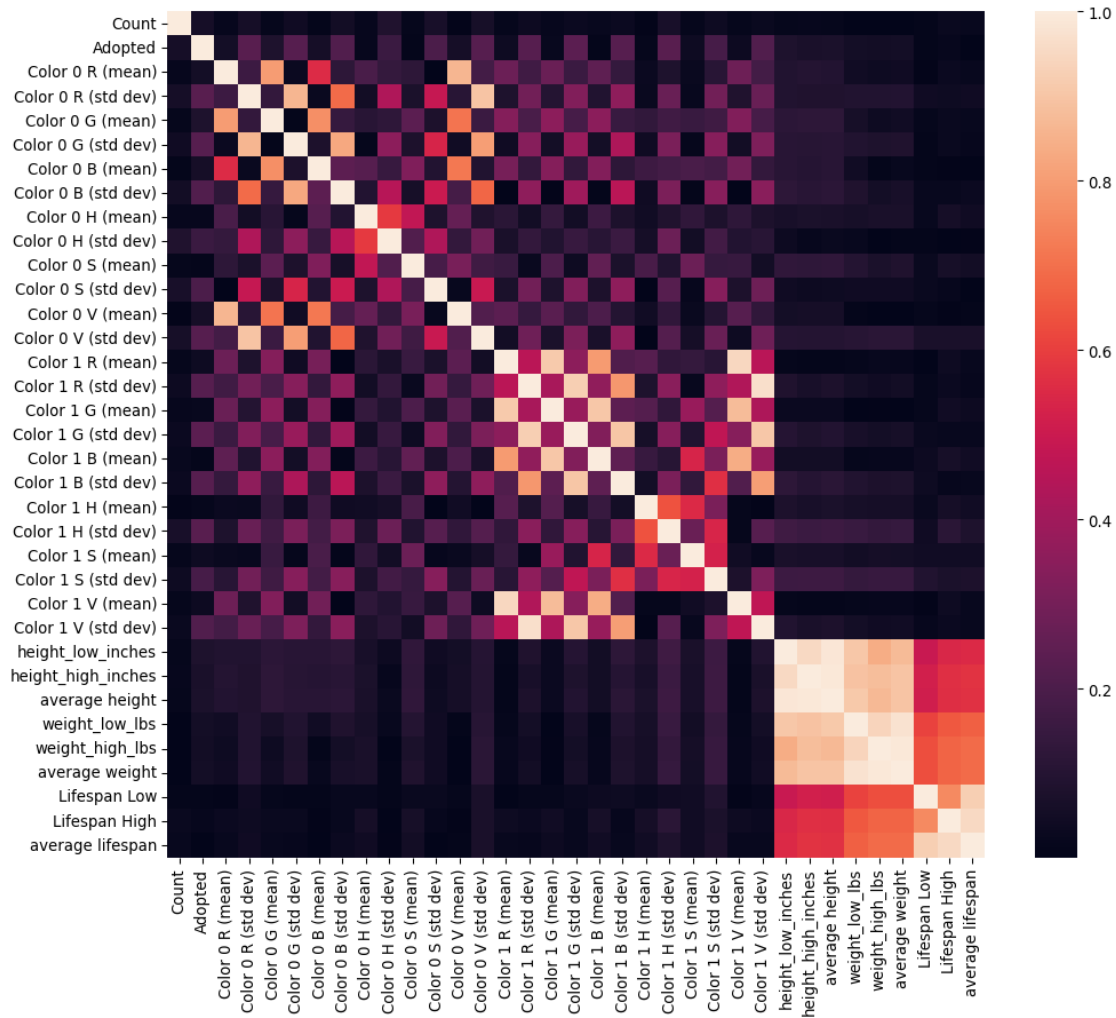
```
[4]: sns.pairplot(data=df_breeds_with_info, x_vars=['Adopted'])
```

```
[4]: <seaborn.axisgrid.PairGrid at 0x7f2263f54730>
```
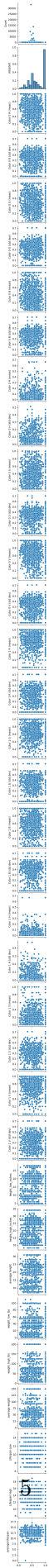
1.1 Height ~ adopted?

Is the average height of a breed correlated with its likelihood of being adopted? The Pearson correlation coefficient was Corr(Adopted, average height) 0.2286839421877296.

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

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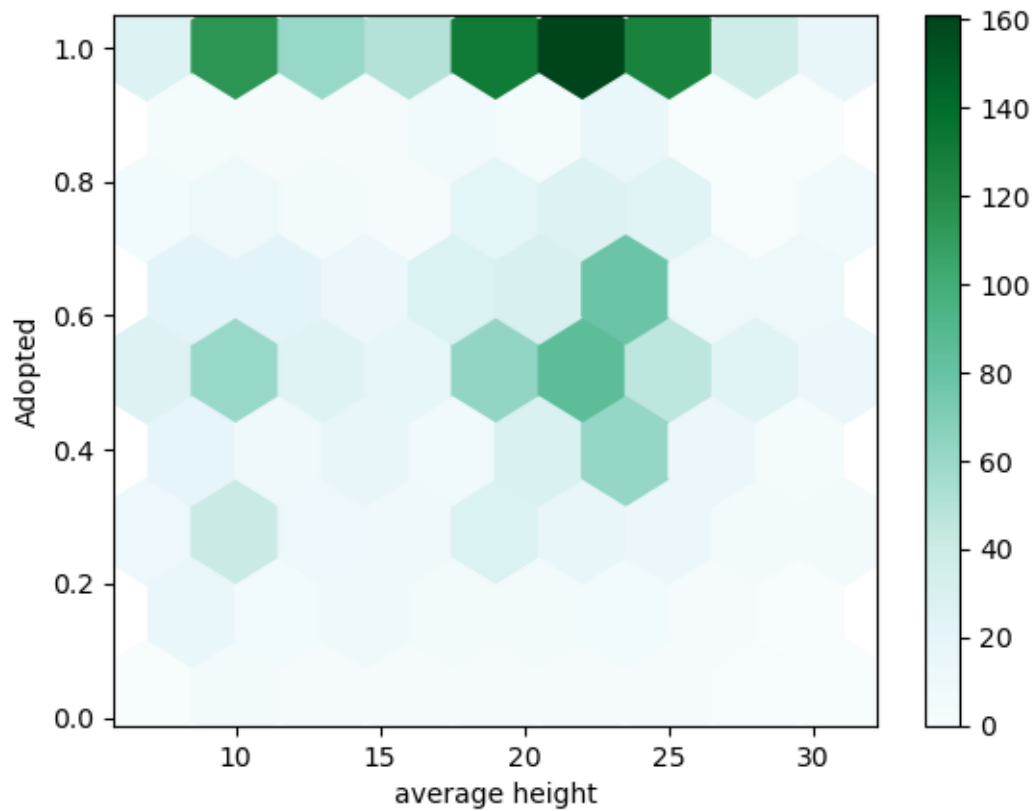


```
[6]: sns.jointplot(
         x=df_breeds_with_info['average height'].astype(dtype=float),
         y=df_breeds_with_info.Adopted.astype(dtype=float),
         kind='reg')
```

```
[6]: <seaborn.axisgrid.JointGrid at 0x7f2263f54640>
```
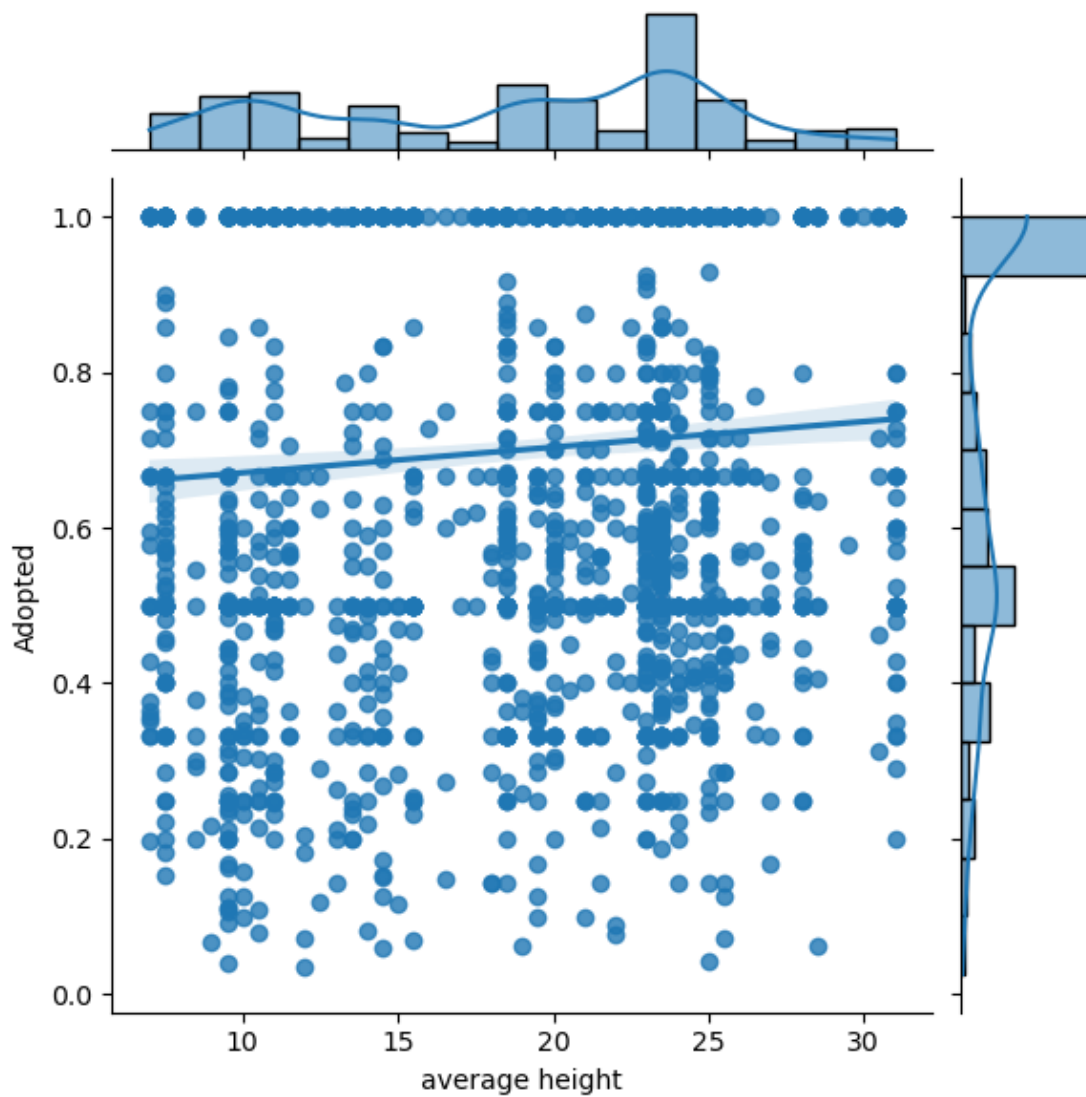
2 Analysis by individuals

2.1 Color

(results)

```
[7]: 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
```

```
[8]: 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)]
```

```
[11]: 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]
```

```
[9]: 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() +
            df_out_colors_2_color_1.groupby('Color').value_counts()
        )

        denominator = (
            df_out_colors_2_color_0[['Color']].groupby('Color').value_counts() +
            df_out_colors_2_color_1[['Color']].groupby('Color').value_counts()
        )

        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() +
            df_out_colors_2_color_0.groupby('Color').value_counts() +
            df_out_colors_2_color_1.groupby('Color').value_counts()
        )

        denominator = (
            df_out_colors_1_color_0[['Color']].groupby('Color').value_counts() +
            df_out_colors_2_color_0[['Color']].groupby('Color').value_counts() +
            df_out_colors_2_color_1[['Color']].groupby('Color').value_counts()
        )

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

```
[12]: def chartColorAdoptionLikelihood(df_colors, color_relation):
          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')
          df_colors.Adopted.plot.barh(x='Color')
          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() +␣
       ↪df_out_colors_2['Color 1'].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, 'mixed')

      def colors_singleOrMixed():
          colors_adopted = bigCorr_bernoulli_custom_colors_1_or_2()
          colors_count = df_out_colors_1['Color 0'].value_counts() +␣
       ↪df_out_colors_2['Color 0'].value_counts() + df_out_colors_2['Color 1'].
       ↪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 or mixed')

      colors_single()
      colors_mixed()
      colors_singleOrMixed()

      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',
)
```

Probability of an animal with this single color being adopted

12
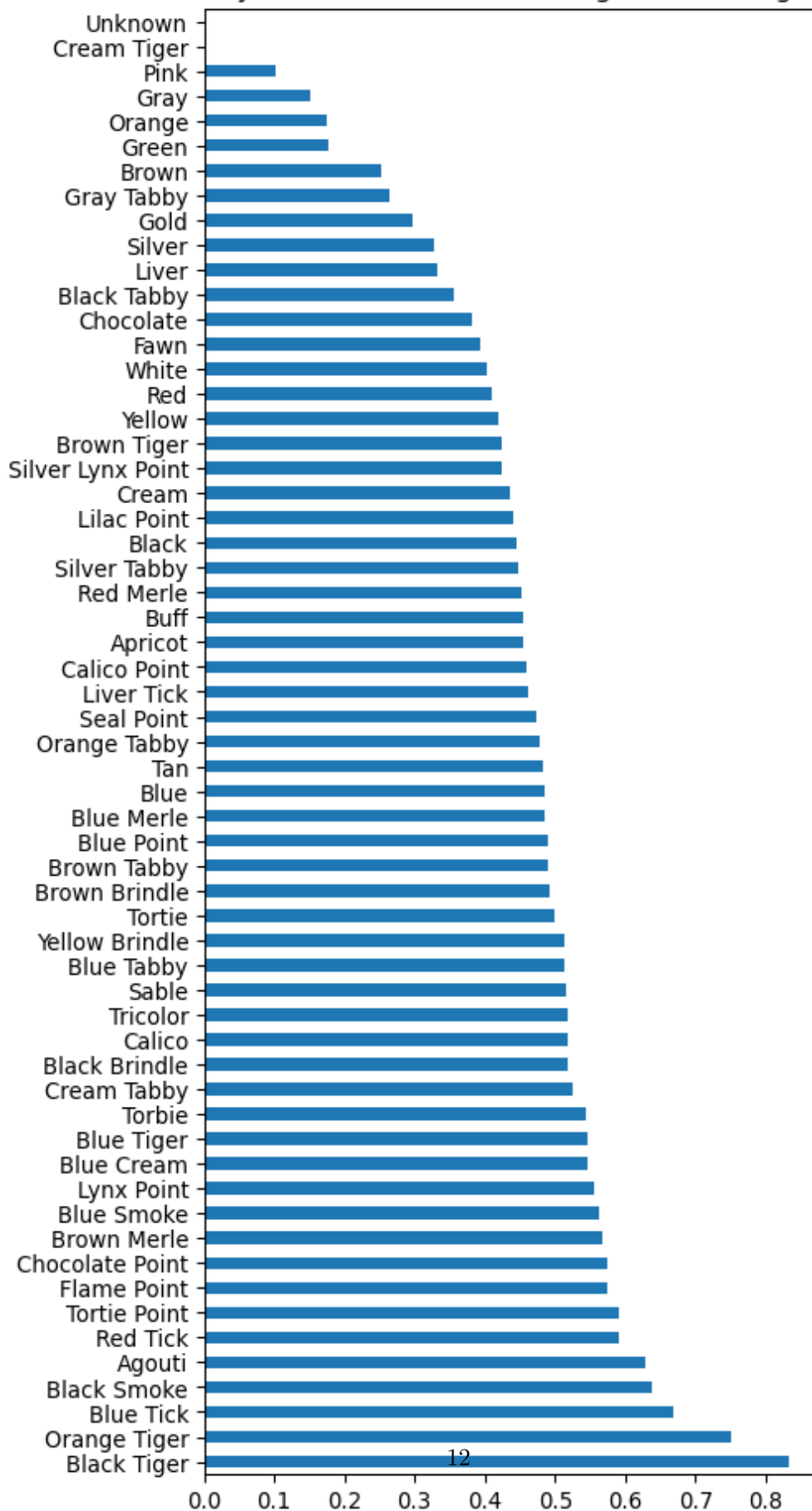
59 colors

Probability of an animal with this mixed color being adopted

14

59 colors

Probability of an animal with this single or mixed color being adopted
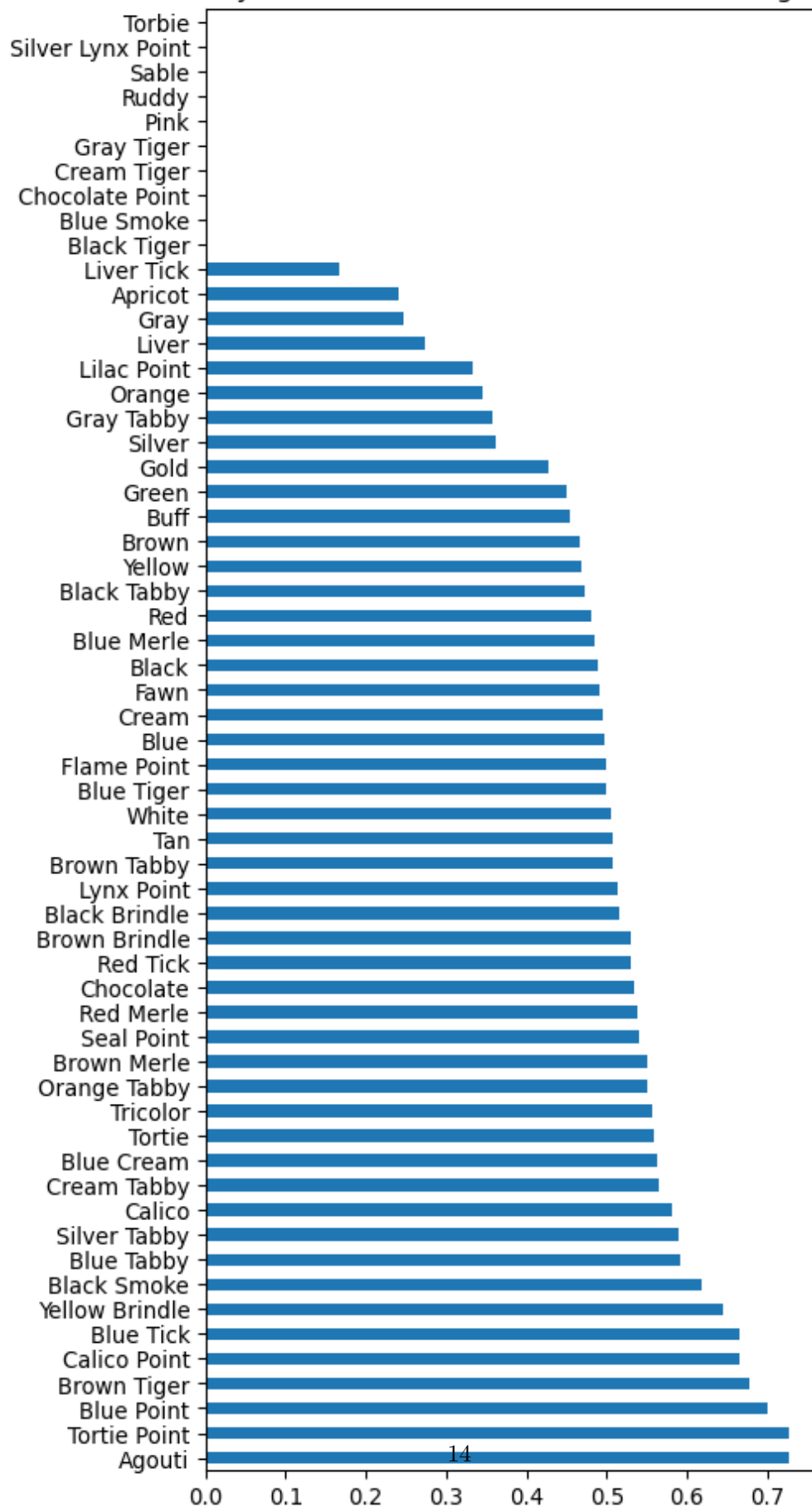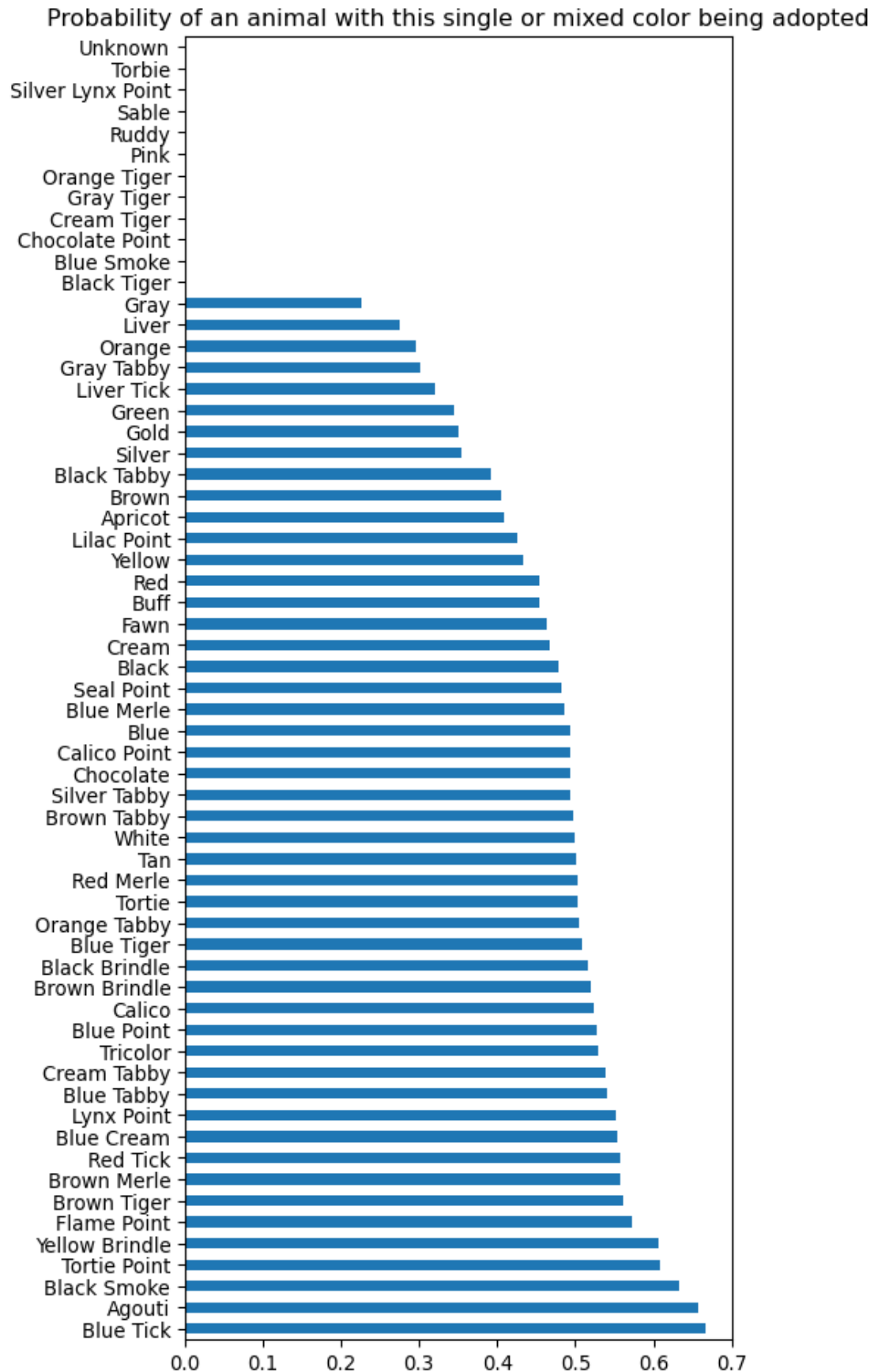
61 colors

[12]: <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
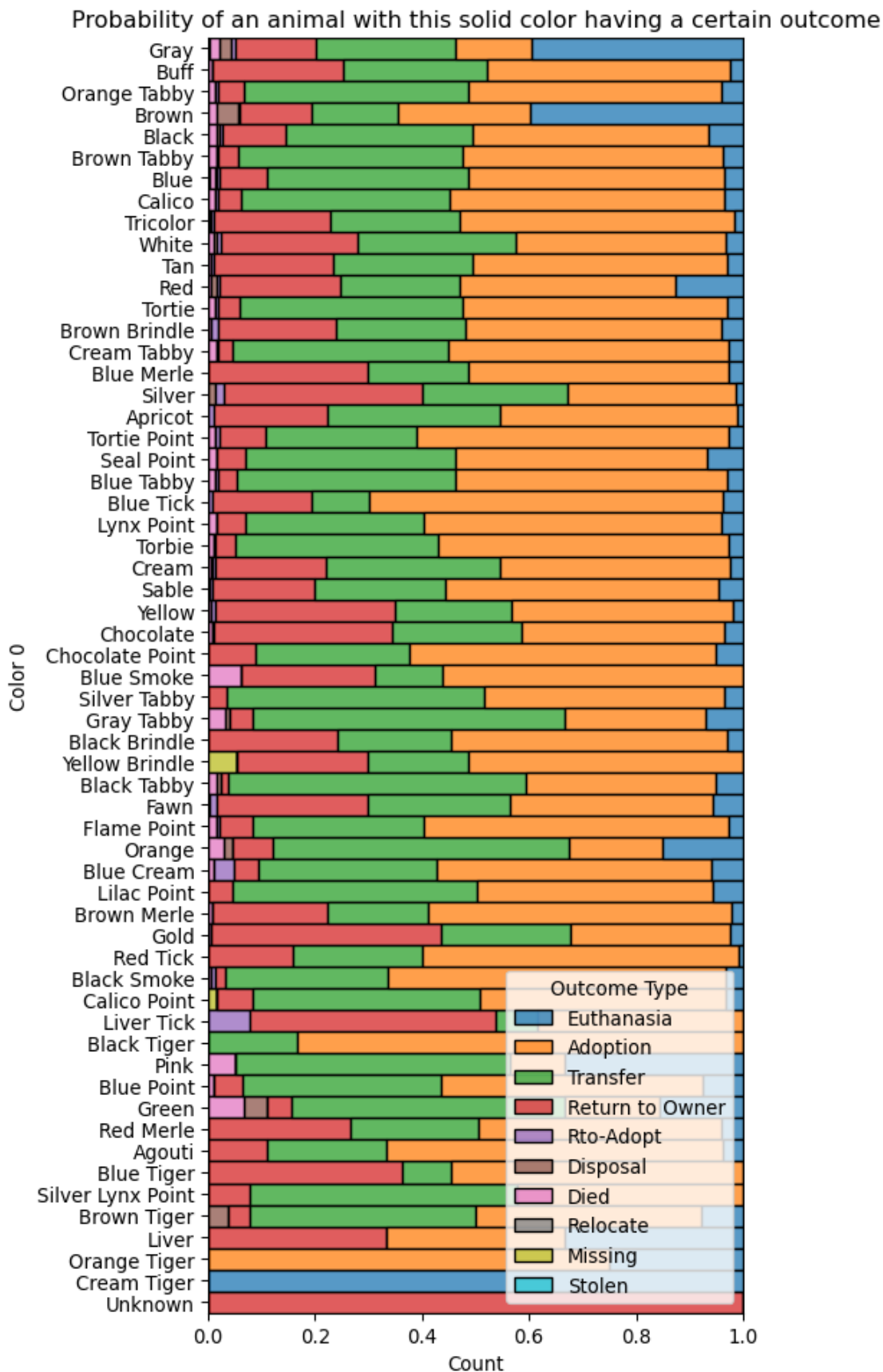
```
[13]: df_out.plot.hexbin(x='Color 0 H', y='Color 0 V', gridsize=5)
      df_out.plot.hexbin(x='Color 0 H', y='Color 0 S', gridsize=5)
      df_out.plot.hexbin(x='Color 0 S', y='Color 0 V', gridsize=5)
```

[13]: <AxesSubplot:xlabel='Color 0 S', ylabel='Color 0 V'>
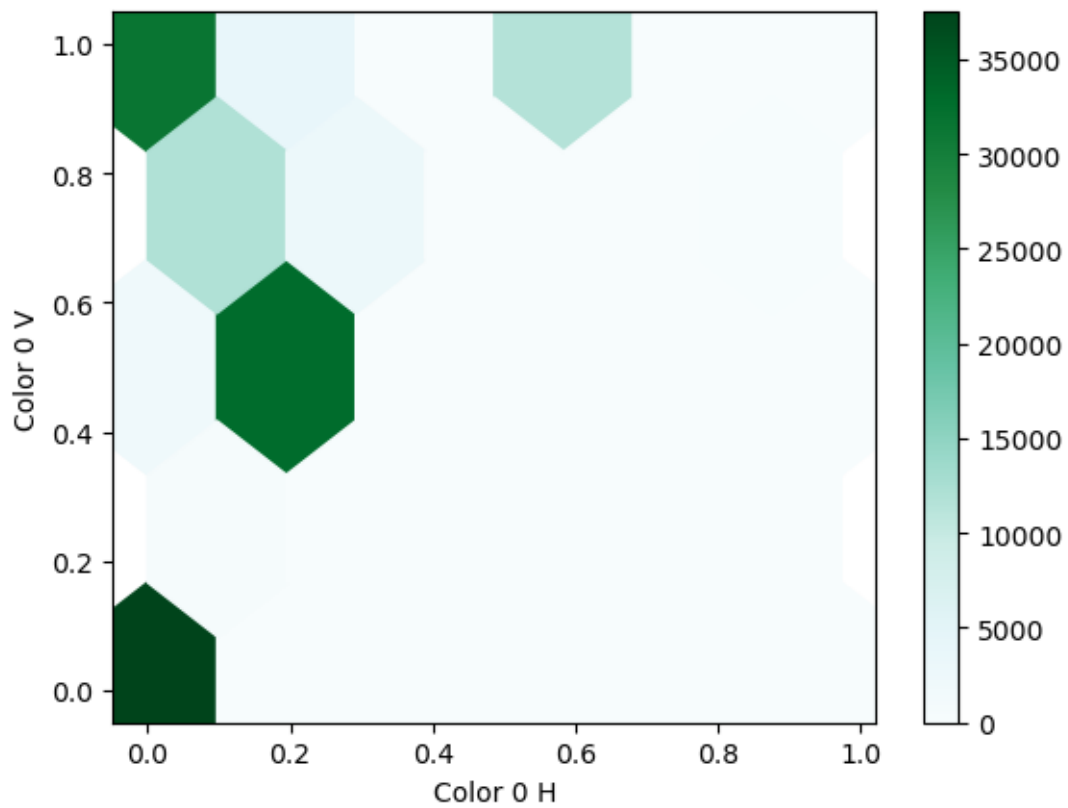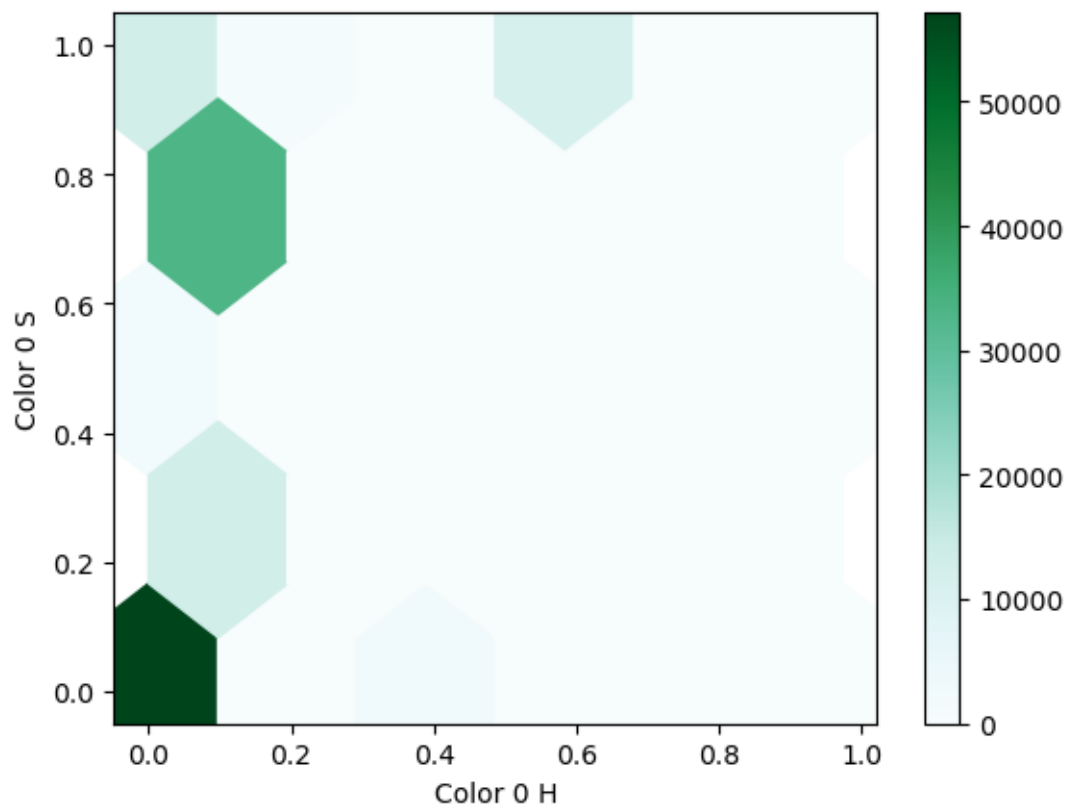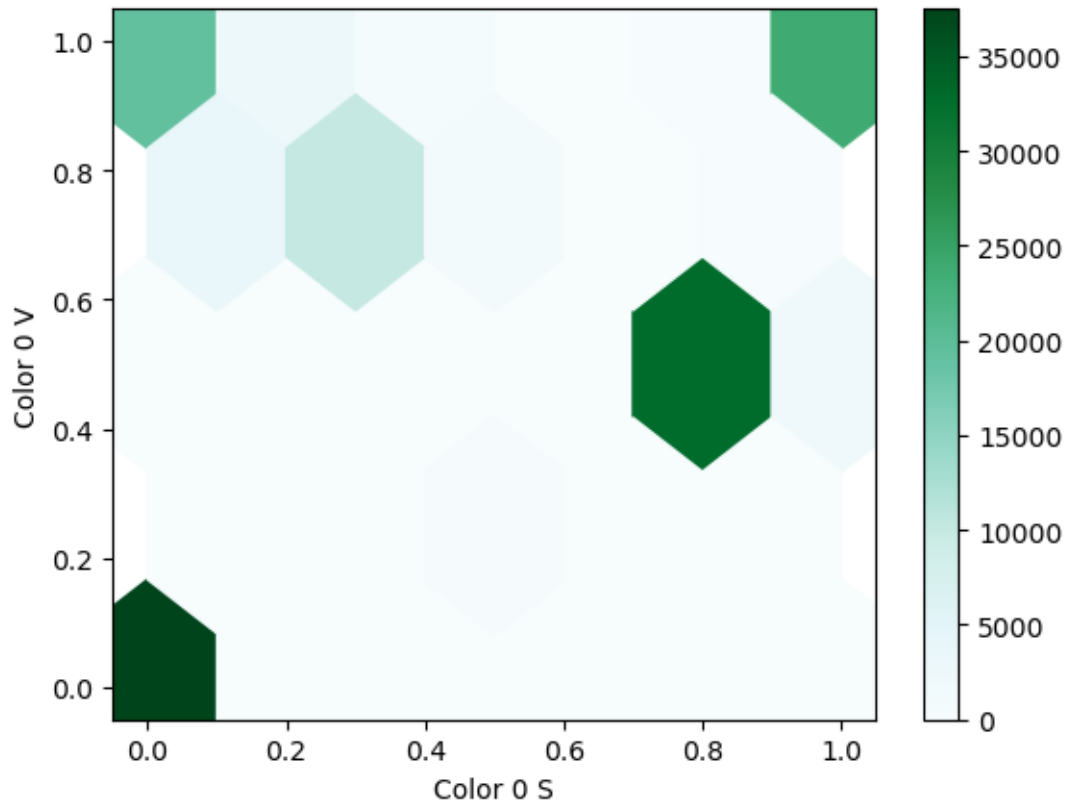
2.2 Breed characteristics

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: 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?

```
[14]: 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}')
          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
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)
  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"),
/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
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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
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"),
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Est. lifespan remaining ~ Adopted
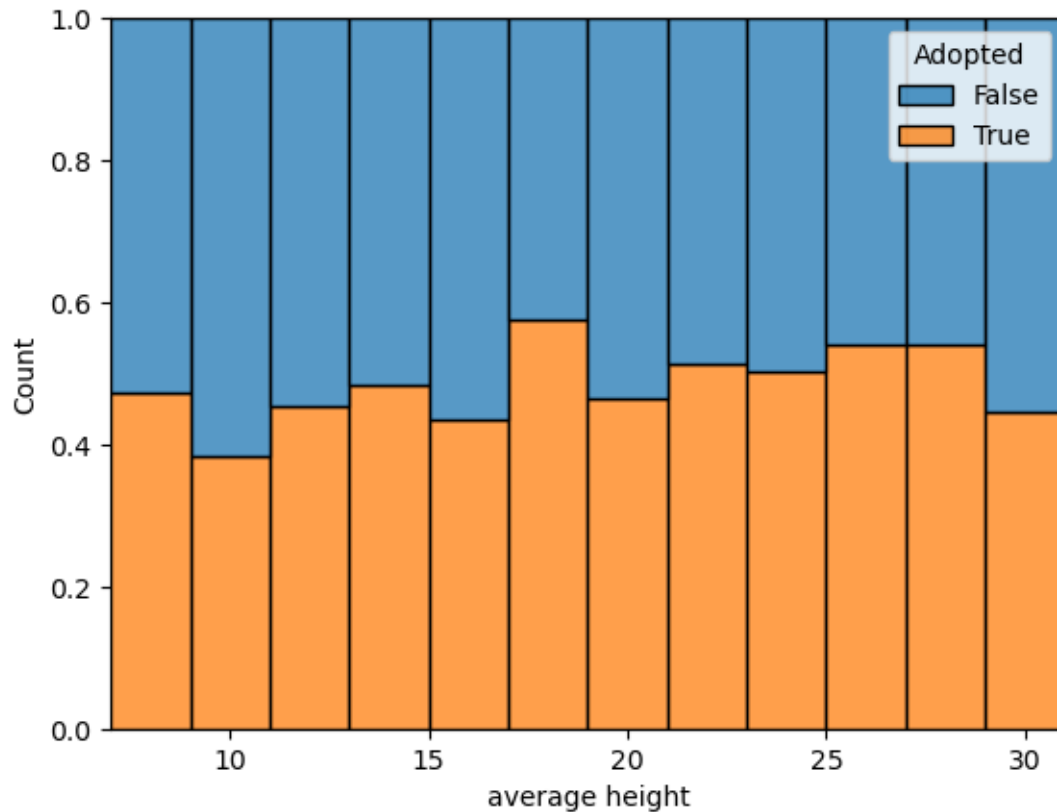
Est. lifespan remaining ~ Outcome Type

average lifespan ~ Adopted

```
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average lifespan ~ Outcome Type

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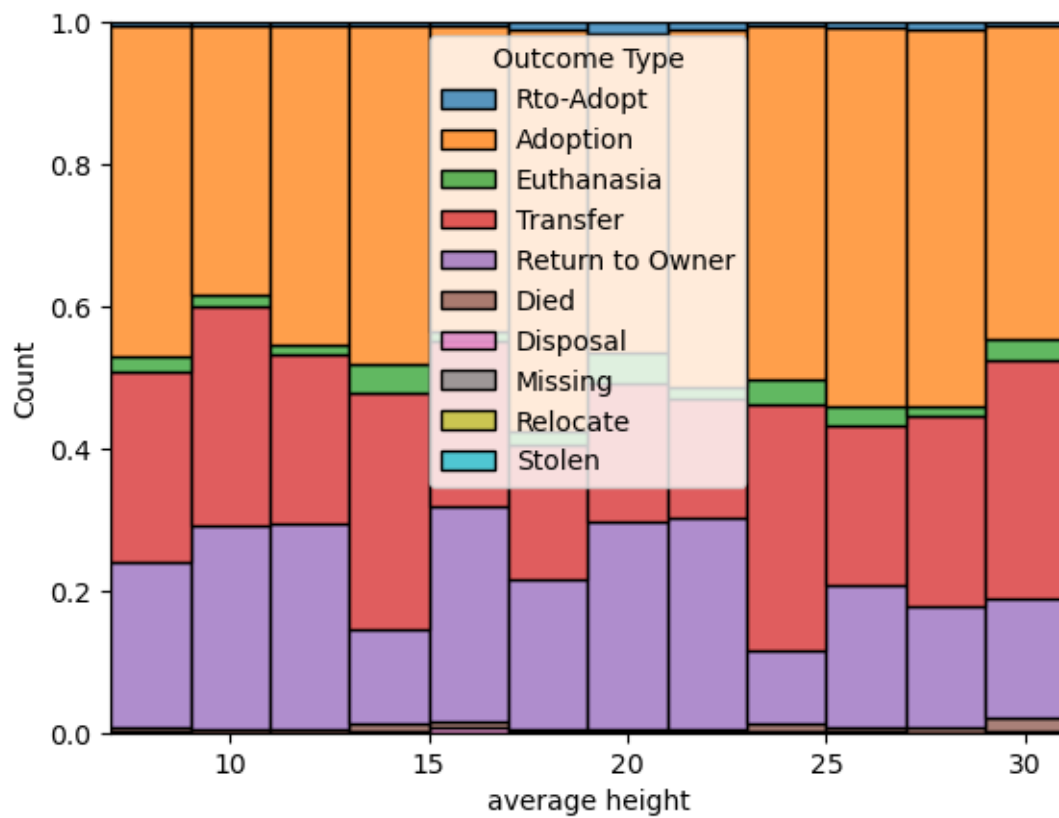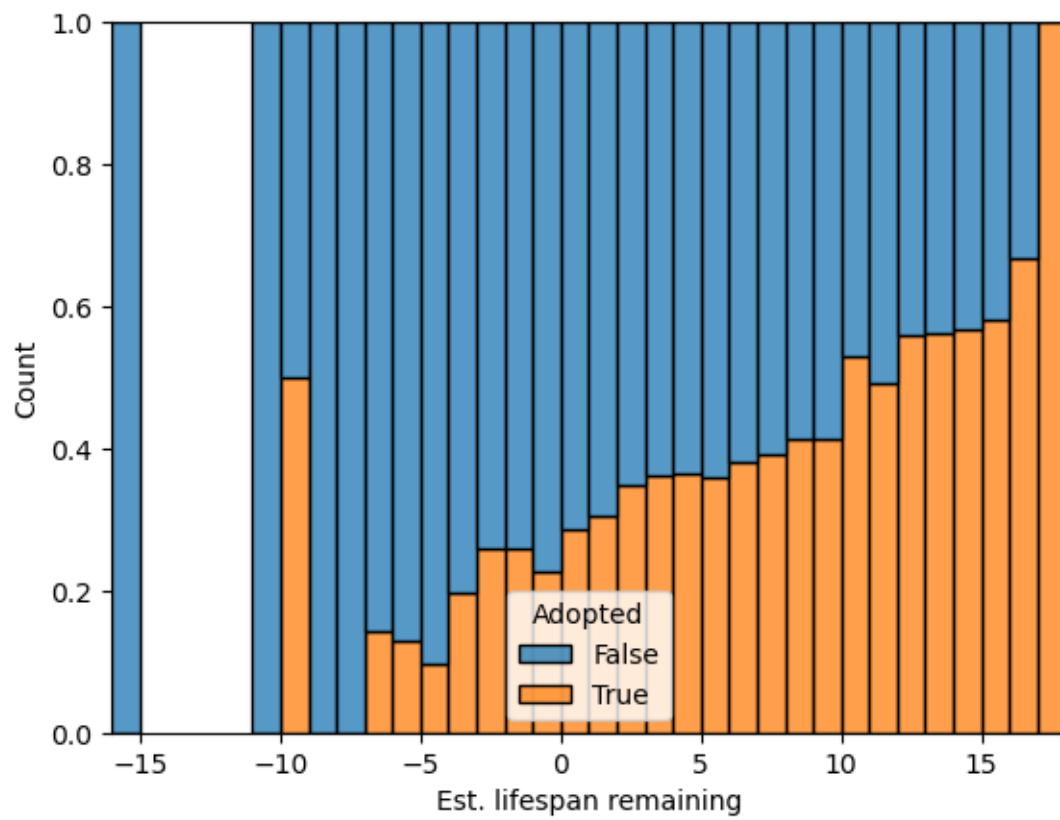
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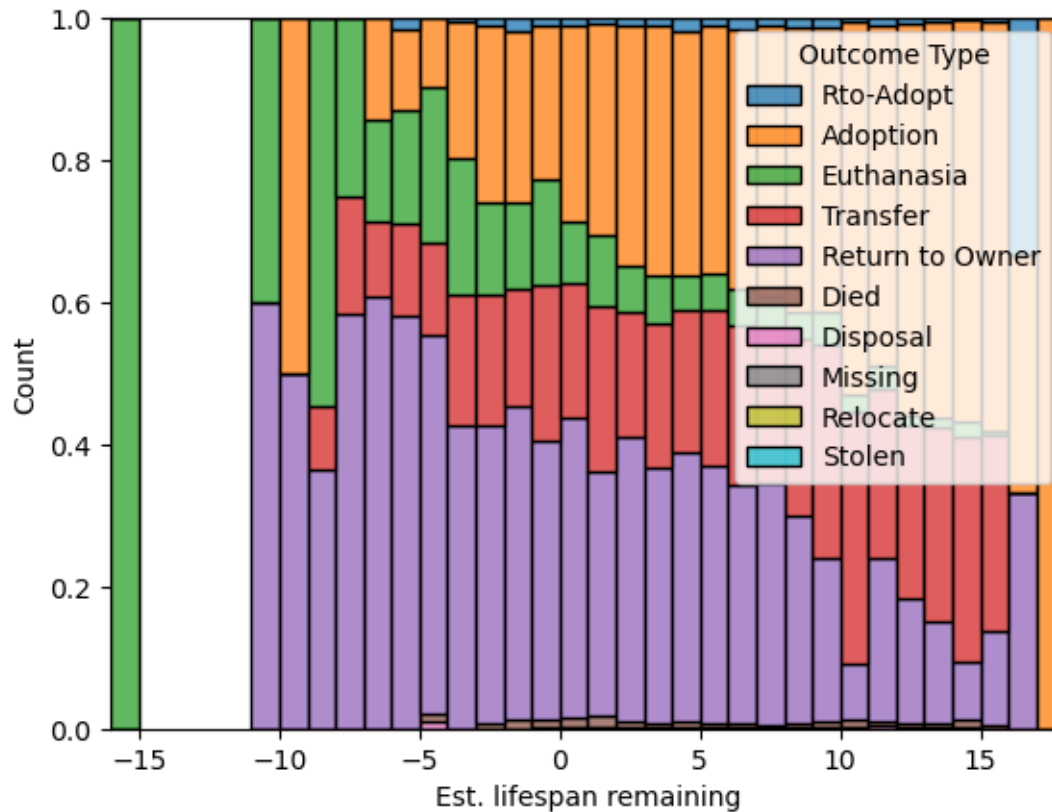
Lifespan Low ~ Adopted

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Lifespan Low ~ Outcome Type

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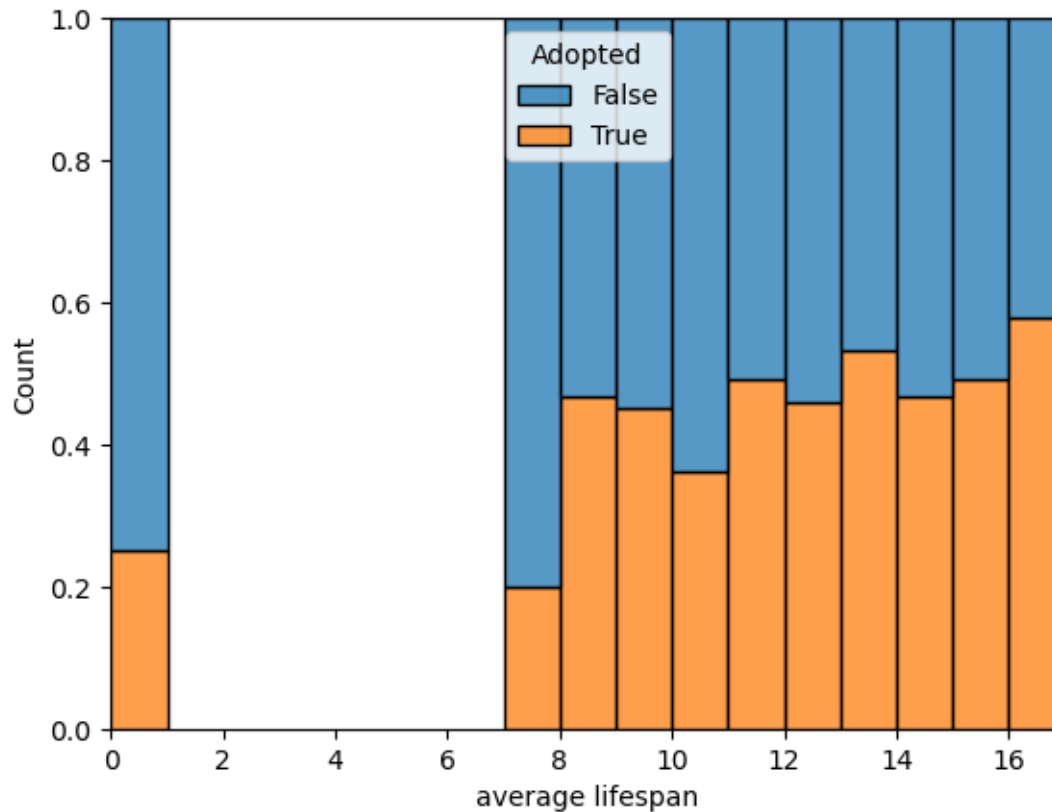
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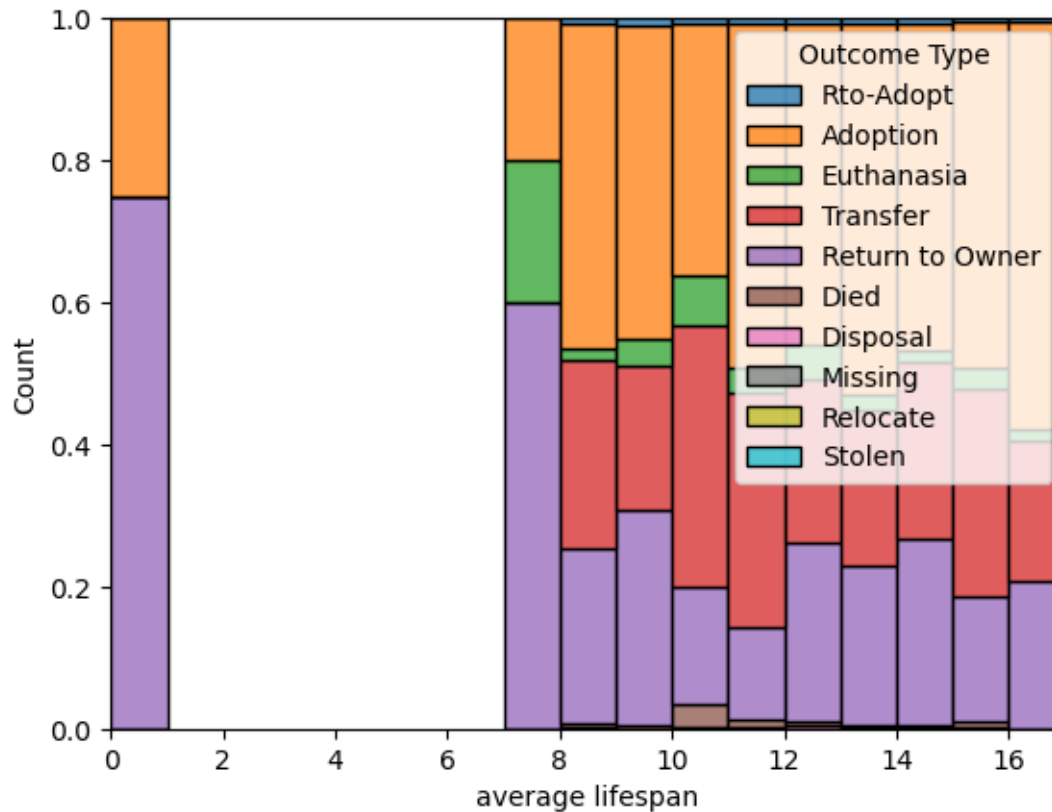
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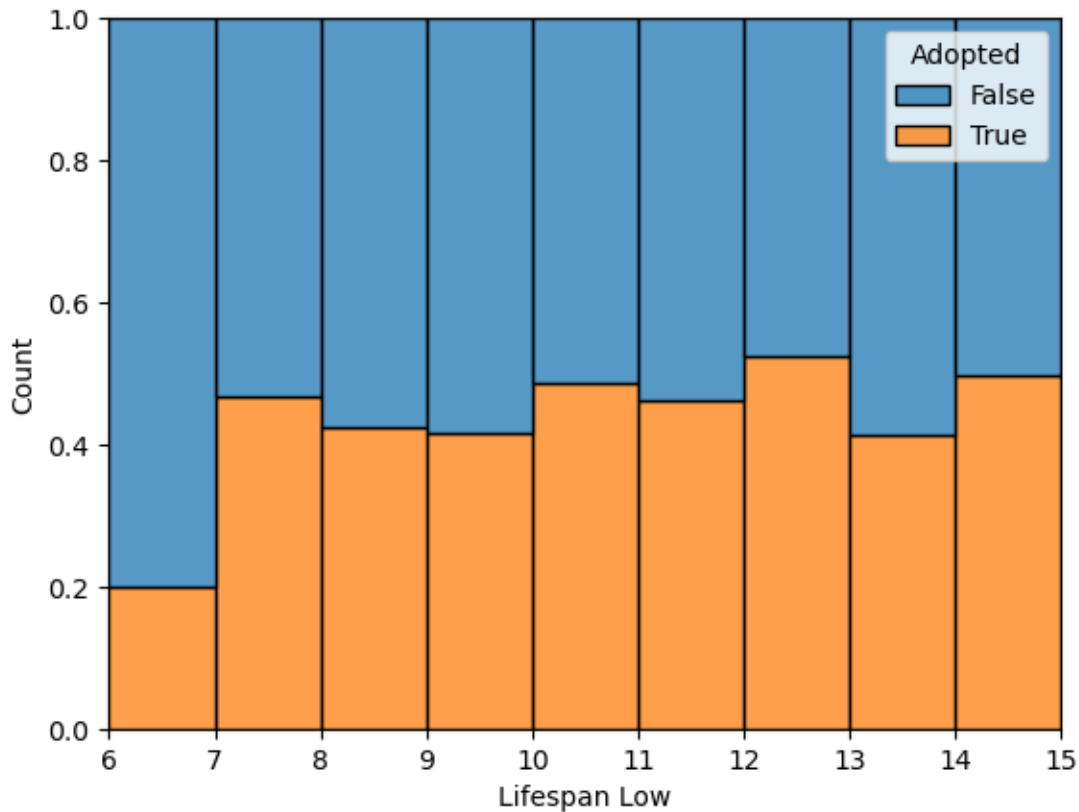
Lifespan High ~ Adopted

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Lifespan High ~ Outcome Type

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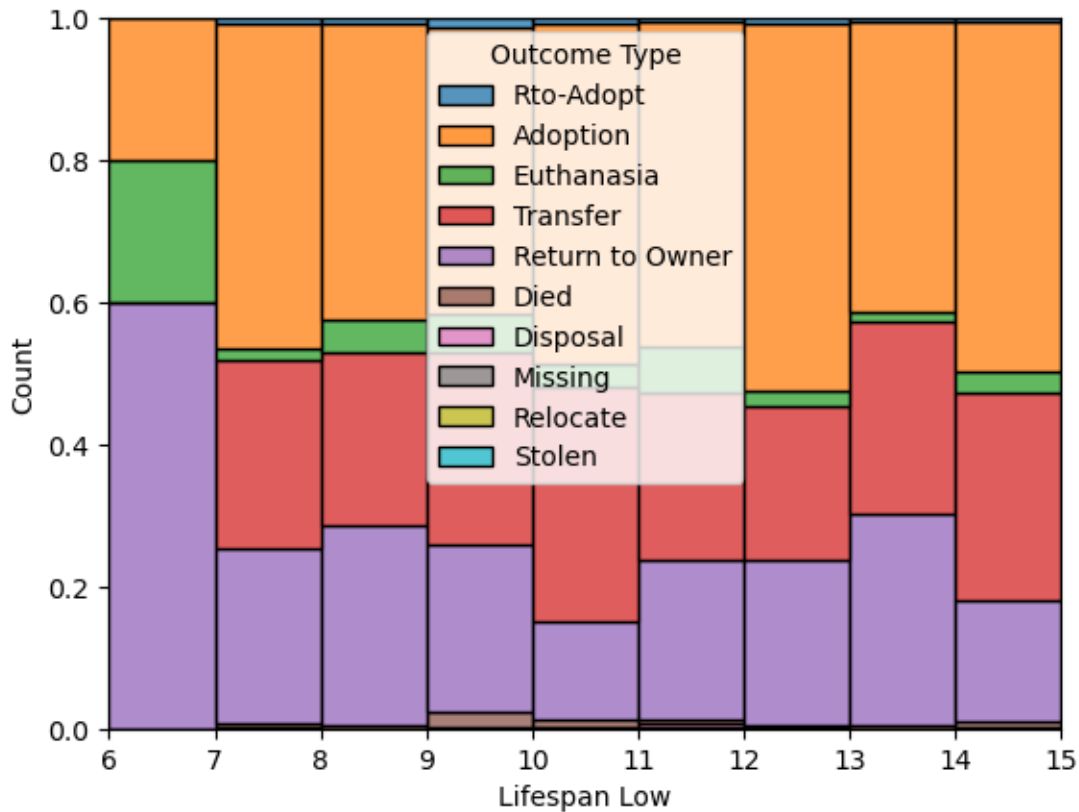
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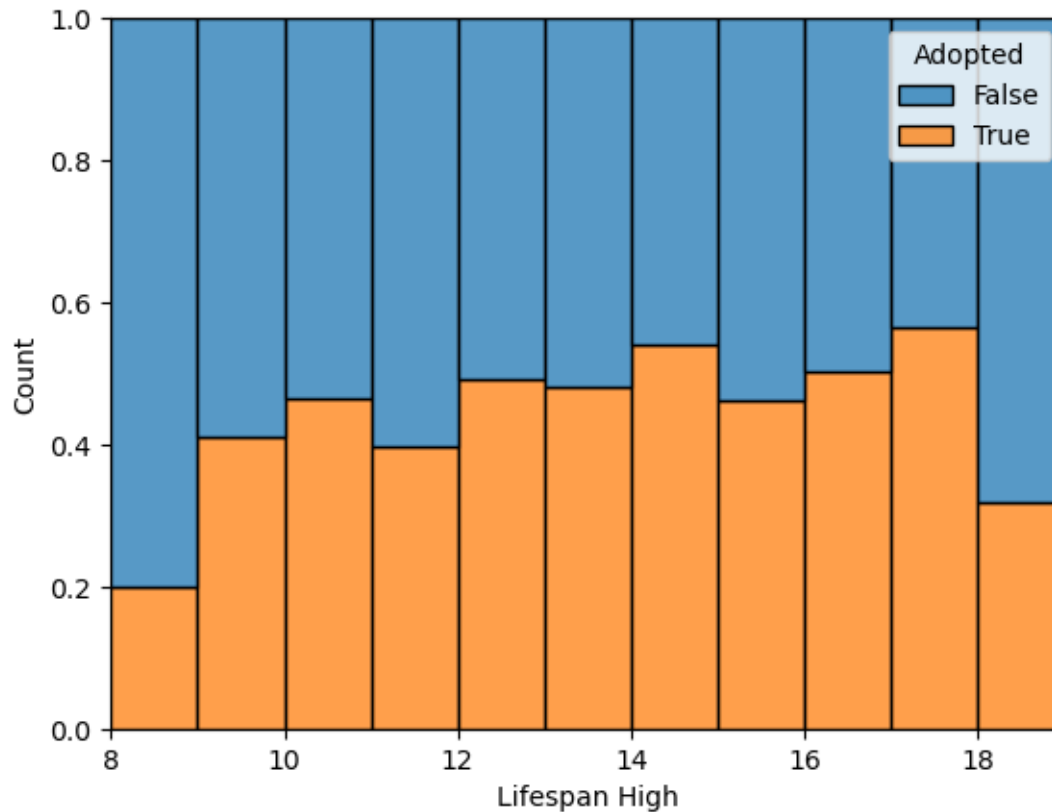
Age upon Outcome (years) ~ Adopted

```
/home/isaac/miniconda3/envs/cse3380/lib/python3.10/site-
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Age upon Outcome (years) ~ Outcome Type

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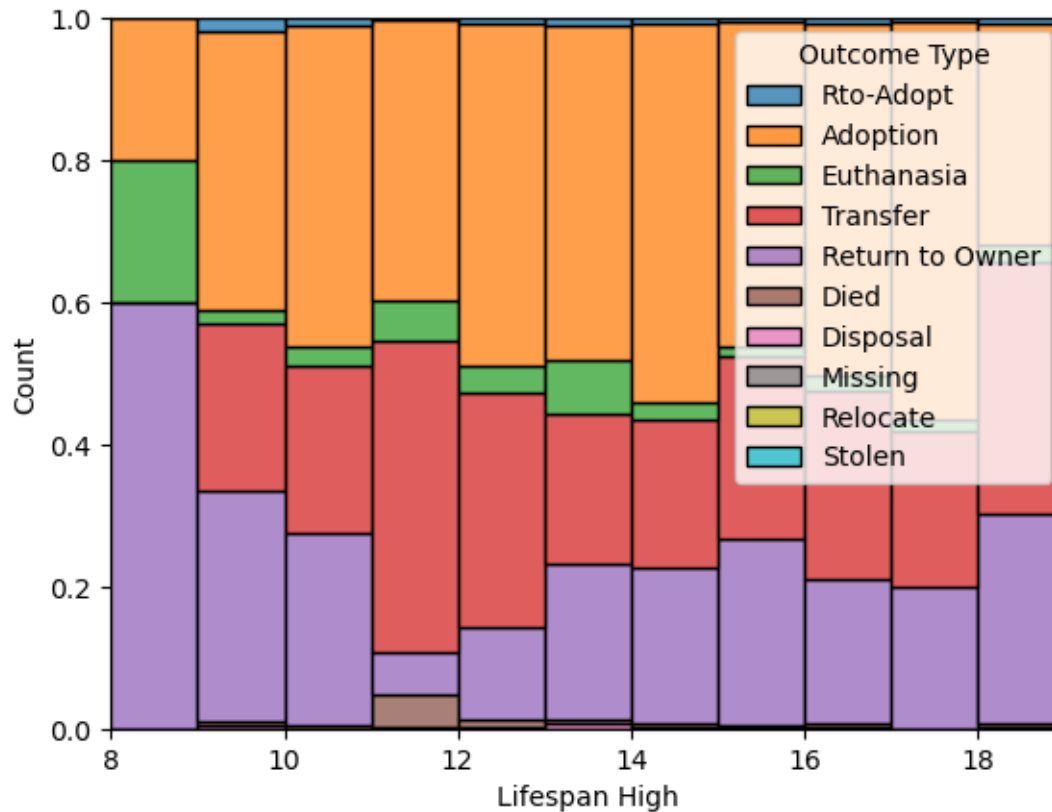
41

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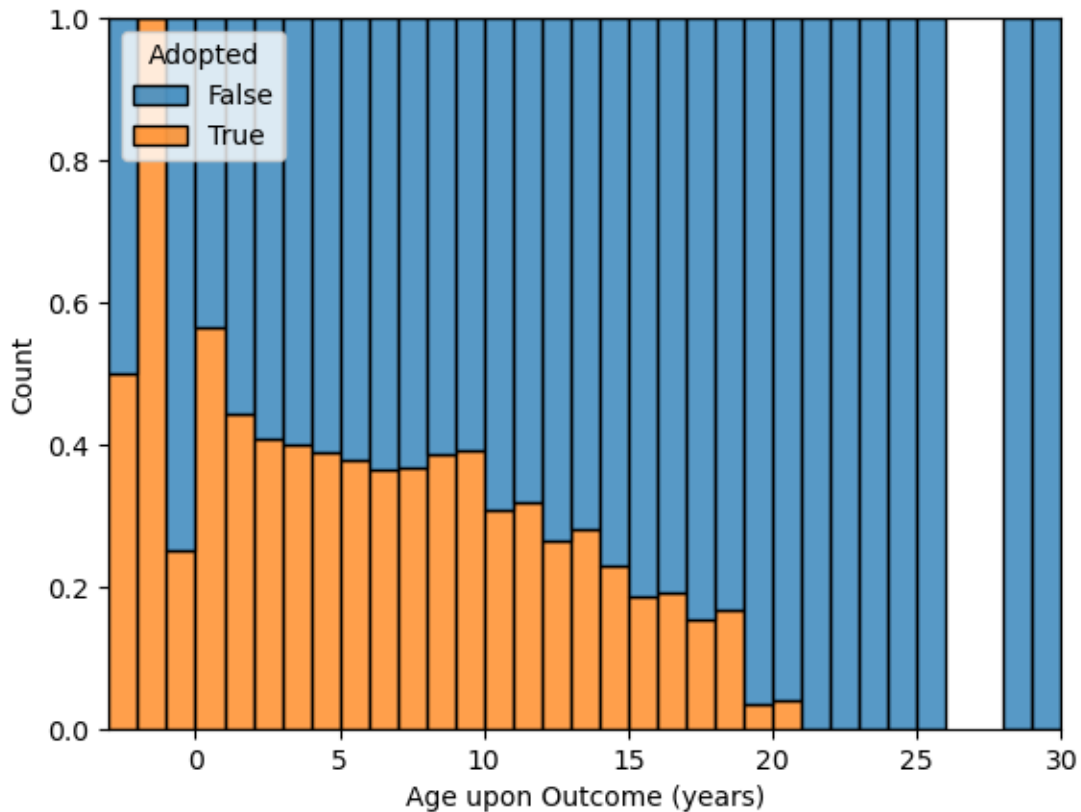
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Color 0 H ~ Adopted

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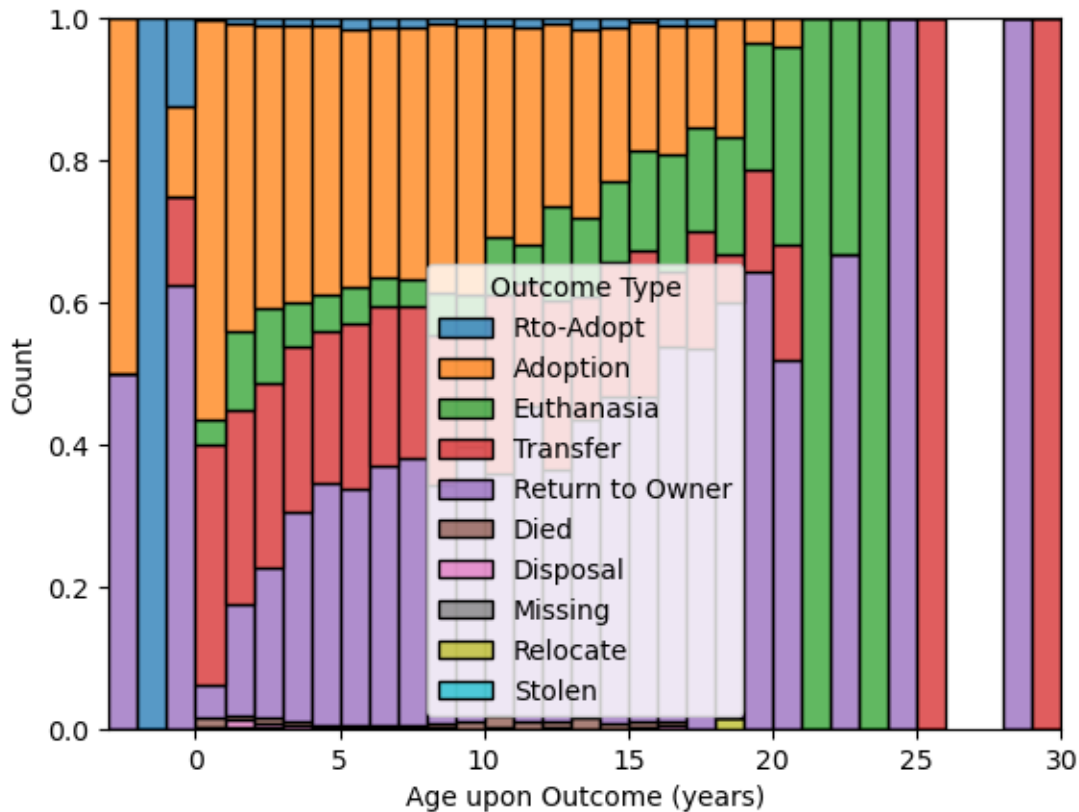
Color 0 H ~ Outcome Type

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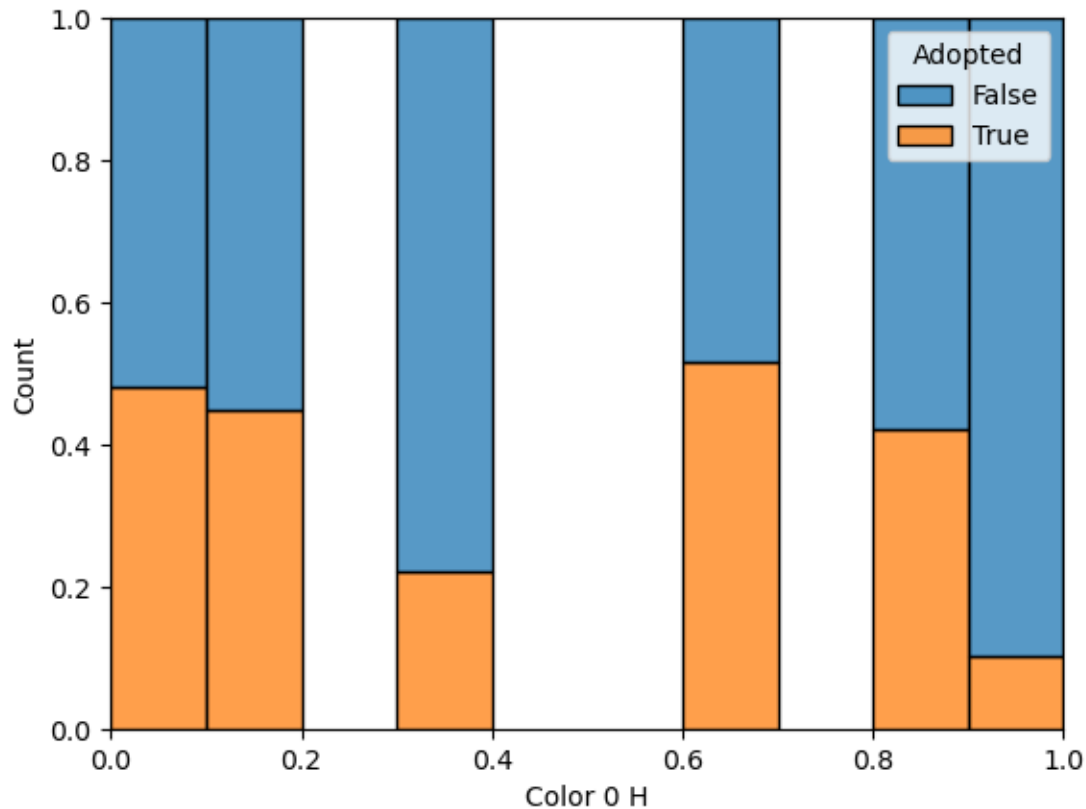
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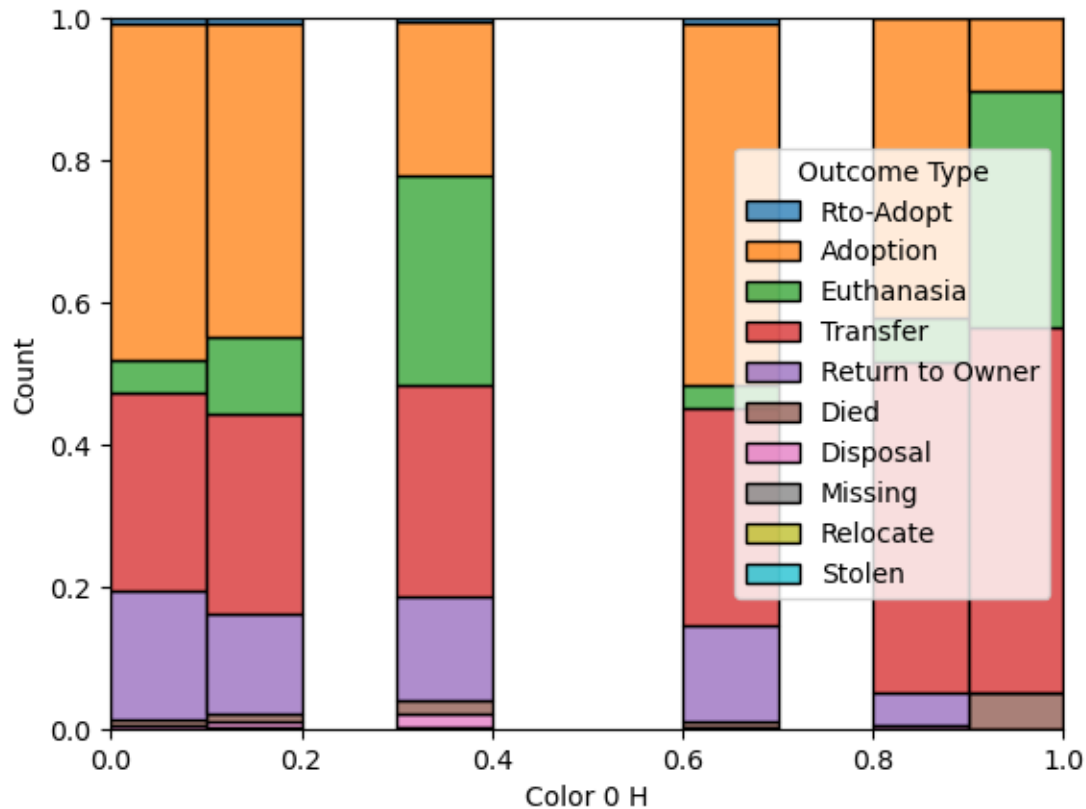
Color 0 S ~ Adopted

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Color 0 S ~ Outcome Type

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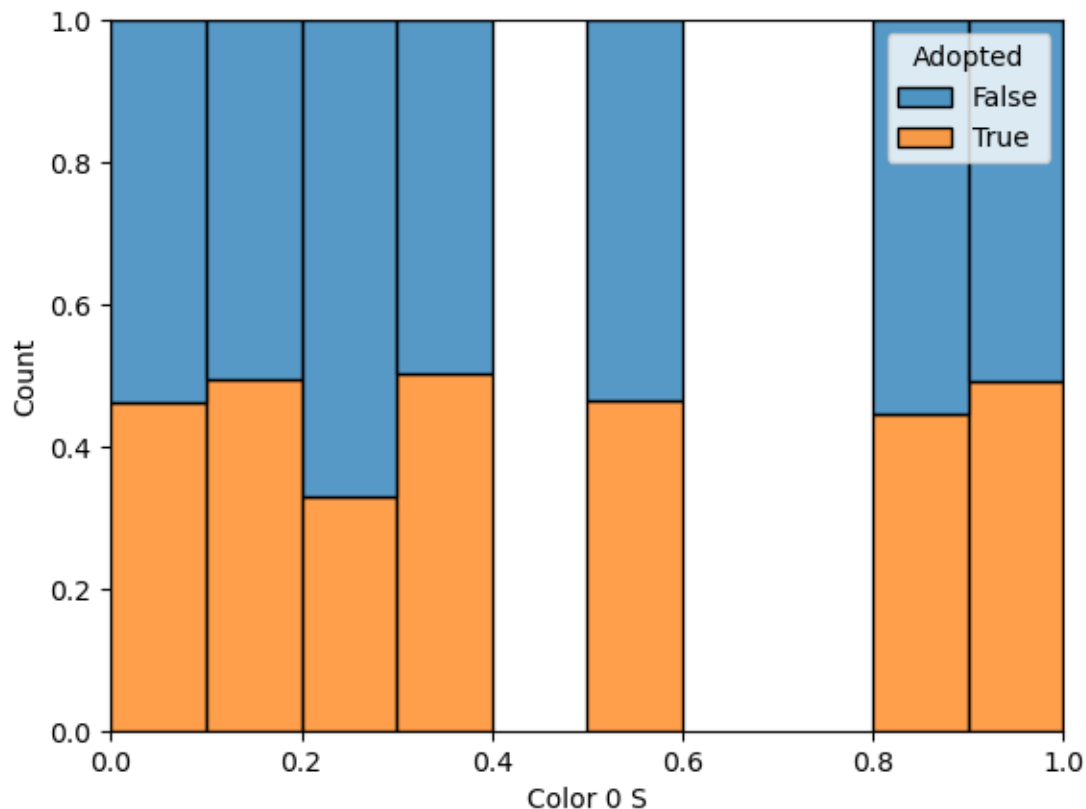
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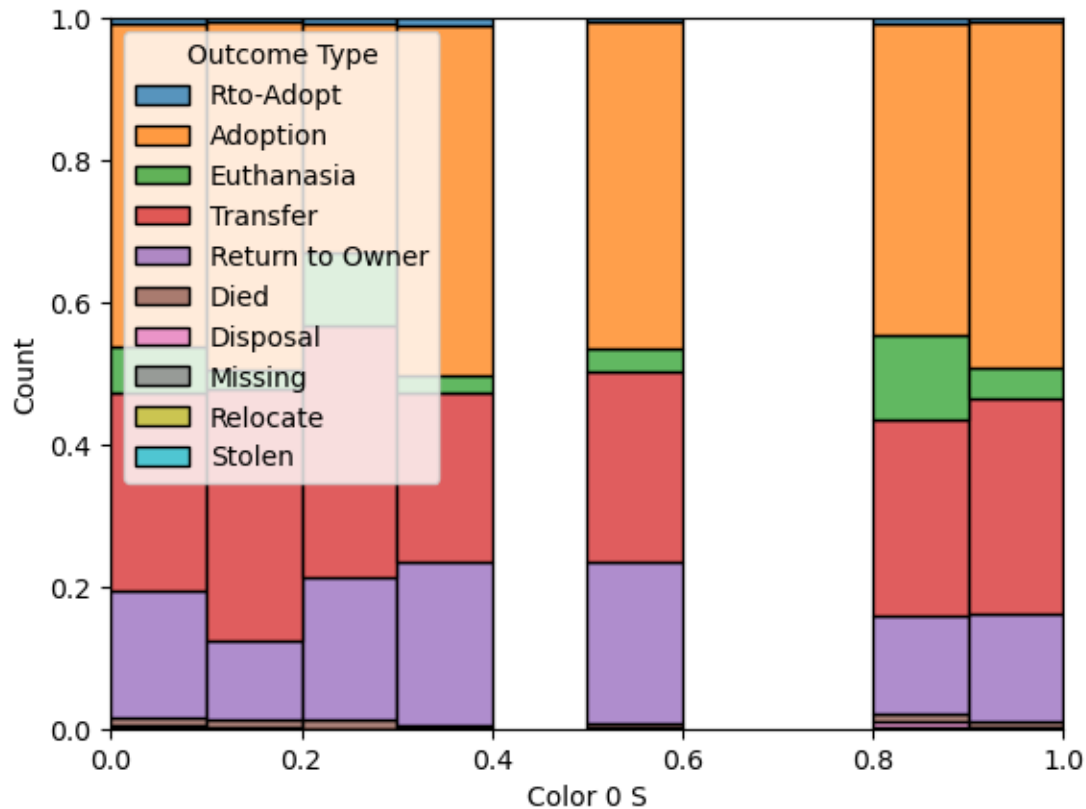
Color 0 V ~ Adopted

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Color 0 V ~ Outcome Type

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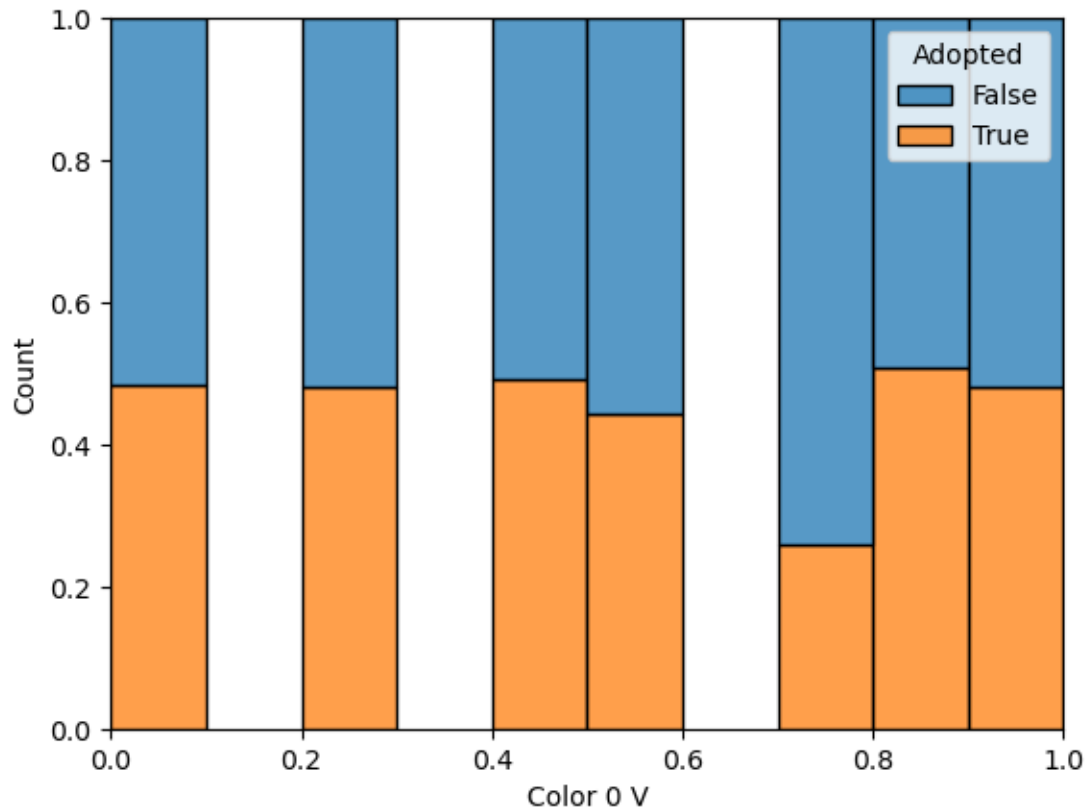
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