sheet6_vandeLocht_Beckers_Kalvelage

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1 Sheet 6

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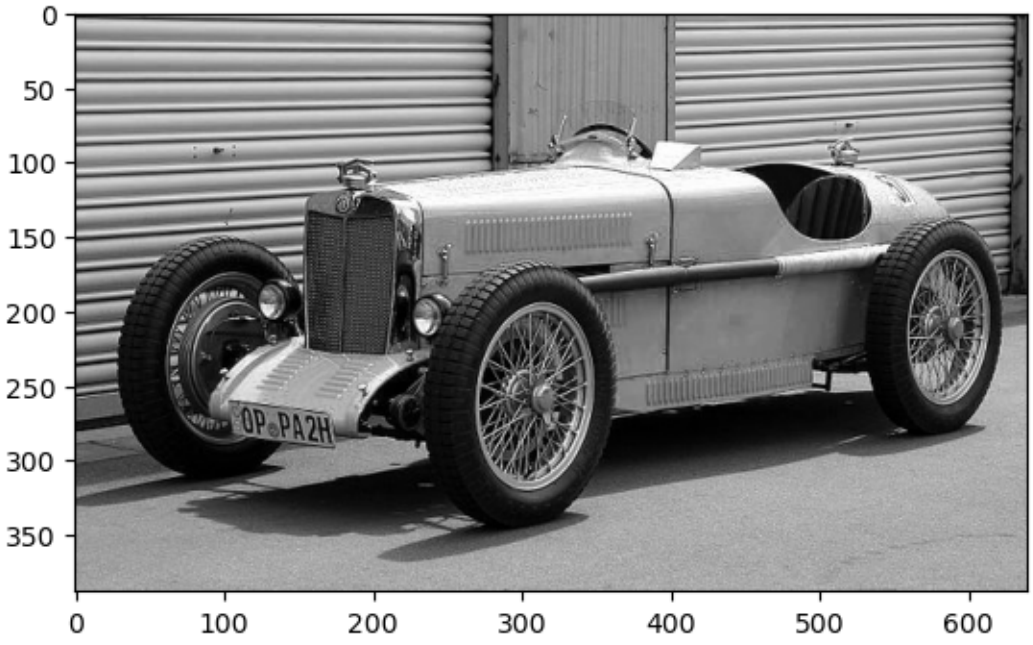
[1]:
```
import matplotlib.pyplot as plt
import matplotlib.colors as colors
import matplotlib.image as mpimg
import numpy as np
```

1.1 Task 1

1.1.1 a)

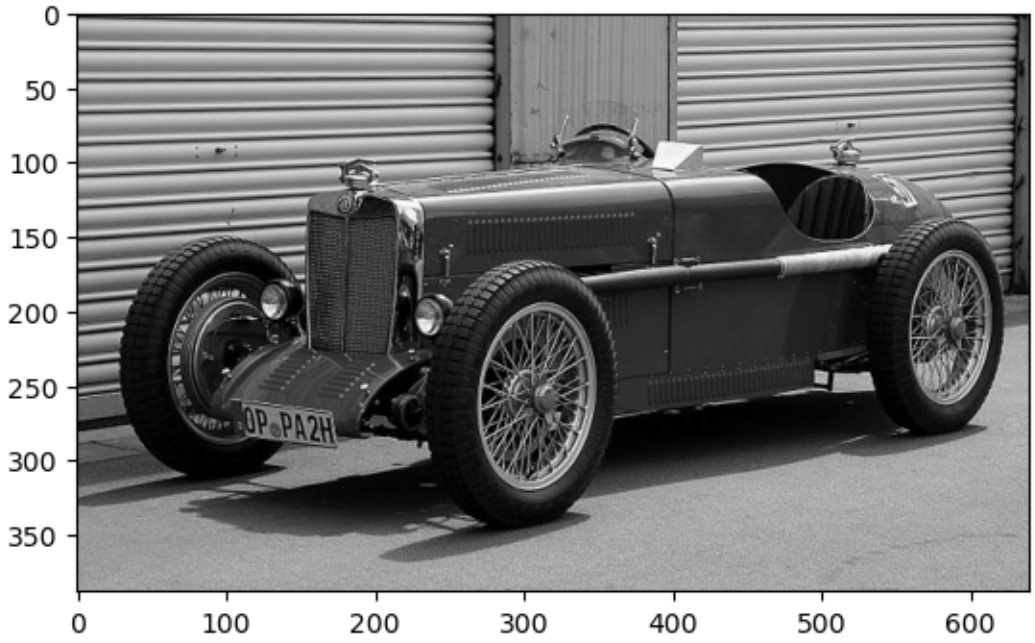
[4]:
```
img = mpimg.imread("oldtimer.png")
img_hsv = colors.rgb_to_hsv(img)
img_rgb = colors.hsv_to_rgb(img_hsv)
plt.imshow(img_hsv[:, :, 2], cmap='gray')
plt.grid(False)
plt.show()
```



1.1.2 b)

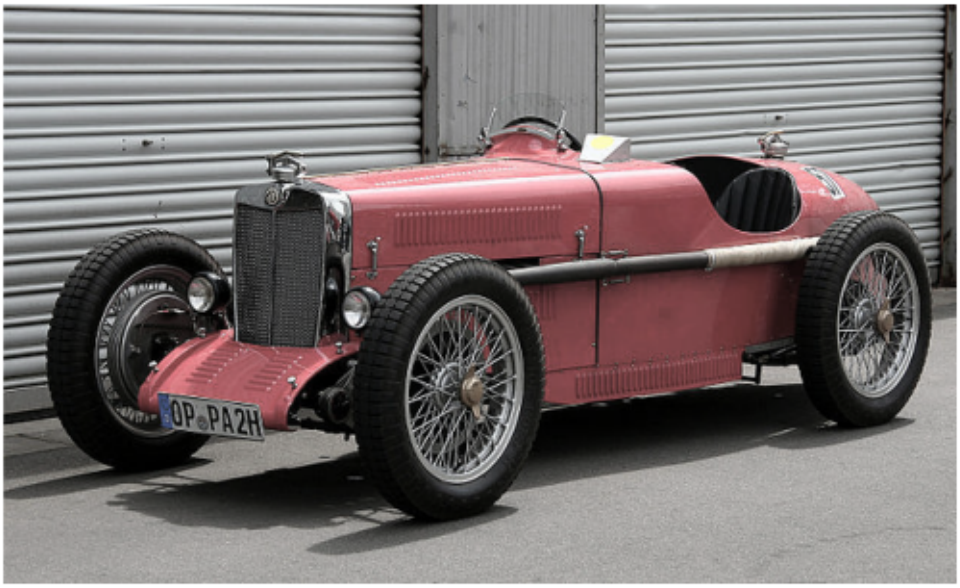
Another way to convert from rgb to grayscale is to just average the three color channels. To represent the human perception of relative brightness we will use the NTSC formula for the conversion.

[6]:
```
img_gray = img[:, :, 0] * 0.299 + img[:, :, 1] * 0.587 + img[:, :, 2] * 0.114
plt.imshow(img_gray, cmap='gray')
plt.grid(False)
plt.show()
```



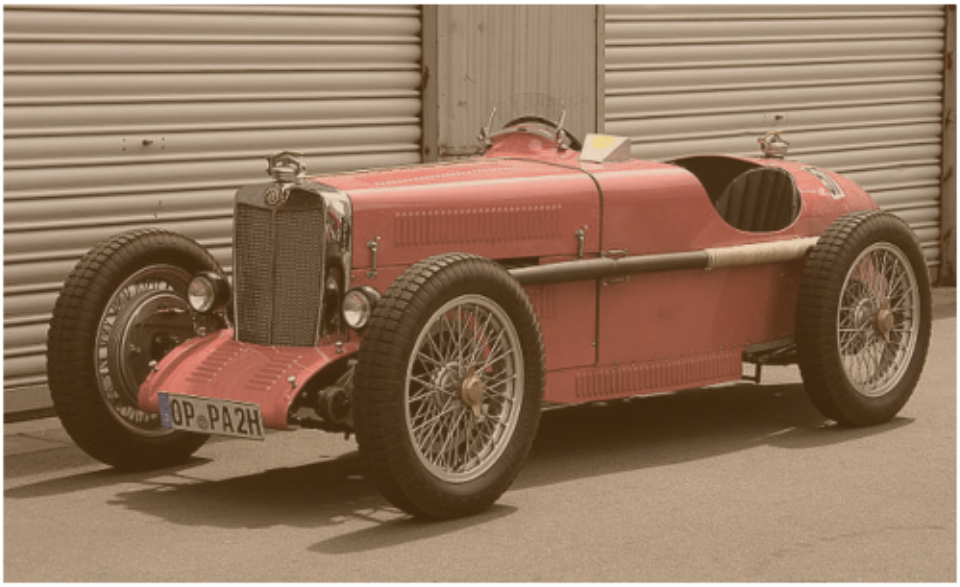
1.1.3 c)

[8]:
```
img_hsv_lowsat = np.copy(img_hsv)
img_hsv_lowsat[:, :, 1] = img_hsv[:, :, 1] * 0.5
img_rgb_lowsat = colors.hsv_to_rgb(img_hsv_lowsat)
plt.imshow(img_rgb_lowsat)
plt.axis('off')
plt.show()
```



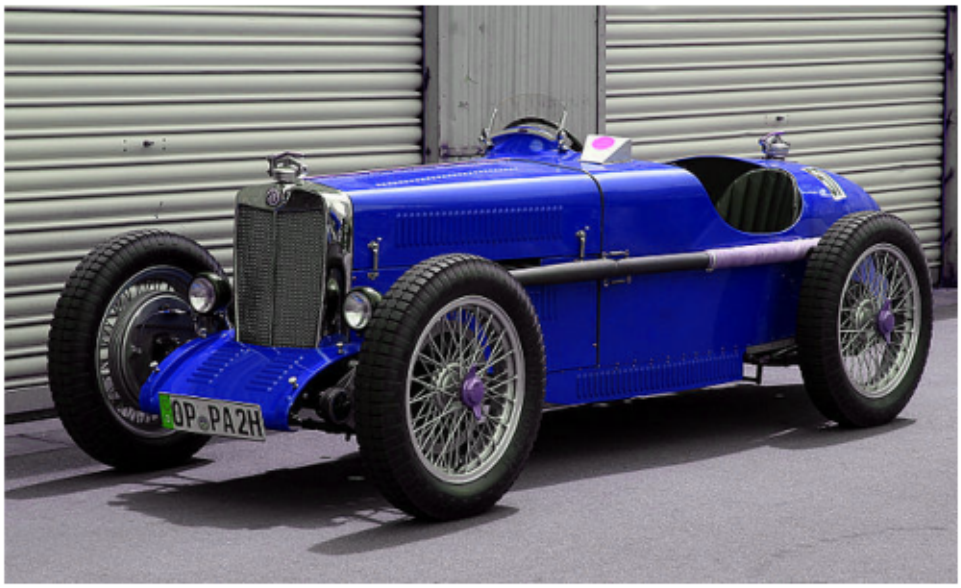
1.1.4 d)

[10]:
```
brown = np.ones_like(img_rgb_lowsat) * [205/255, 127/255, 50/255]
img_aged = 0.70 * img_rgb_lowsat + 0.30 * brown
plt.imshow(img_aged)
plt.axis('off')
plt.show()
```

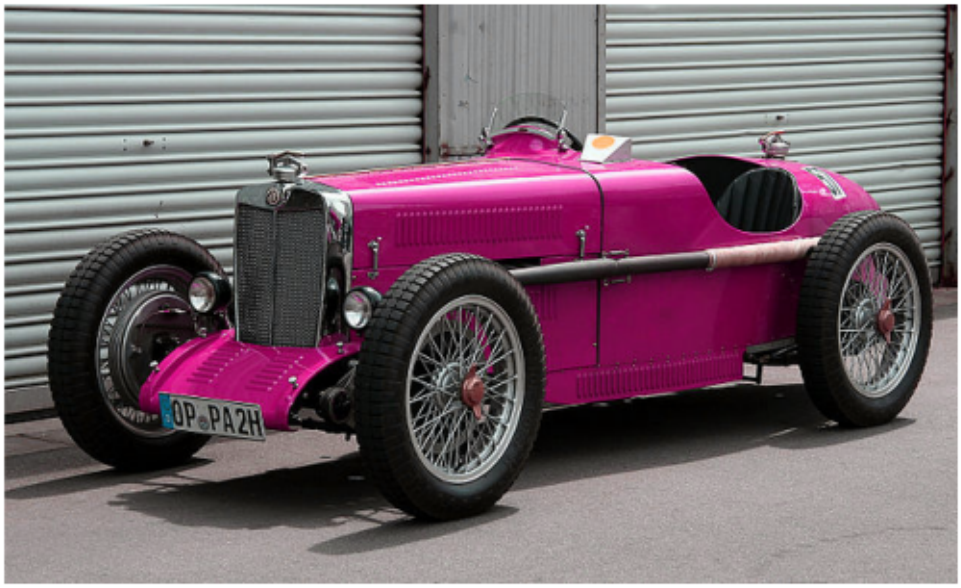


1.1.5 e)

[11]:
```
img_hsv_blue = np.copy(img_hsv)
img_hsv_blue[:, :, 0] = np.mod(img_hsv_blue[:, :, 0] + 240/360, 1)
img_rgb_blue = colors.hsv_to_rgb(img_hsv_blue)
plt.imshow(img_rgb_blue)
plt.axis('off')
plt.show()
```



[12]:
```
img_hsv_pink = np.copy(img_hsv)
img_hsv_pink[:, :, 0] = np.mod(img_hsv_pink[:, :, 0] + 330/360, 1)
img_rgb_pink = colors.hsv_to_rgb(img_hsv_pink)
plt.imshow(img_rgb_pink)
plt.axis('off')
plt.show()
```



1.2 Task 2

1.2.1 a) A straightforward way to find out if test subjects intuitively interpret darker or lighter colors as representing higher values would be to ask them to interpret plots without a legend. Why do the authors instead decide to show legends and evaluate response times?

The authors chose to use the response time method instead of the direct report method (showing an unlabeled visualization) as participants might try to answer consistently across trials even with diffrent background colours. The implicit nature of the response time method reduces this participant demand characteristic. Furthermore the authors wanted to study colormaps in the way they are typically presented, thus with legends or labels.

1.2.2 b) When interpreting visualizations, accuracy should be at least as important as response times.

How do the authors account for that in their experiments?

The authors took accuracy into account by telling the participants that they would be notified eacht time they make a mistake and periodically would be notified of their accuracy. Thus the participant had a motivation to answer accurately. Both the response time and the accuracy were recorded.

1.2.3 c) Authors observe that neither the hypothesis of a“dark-is-more”bias nor a“contrast-is-more”bias could convincingly explain all available experimental results. What explanation do they propose instead?

The authors propose that variations in perceived opacity are a more consistent explanation for their findings. They argue that differences in opacity perception can influence how individuals

interpret visualizations, impacting the perceived magnitude of values. This explanation captures the nuances of how colors are interpreted in a more comprehensive manner than the "dark-is-more" or "contrast-is-more" hypotheses, which failed to account for certain experimental results.

1.2.4 d) Do all experimental results in the paper agree with their proposed explanation? If not, what is the exception and what do they mention as a potential reason for it?

Not all results align perfectly with the opacity-based explanation. An exception was observed with the gray color scale, where the anticipated opacity effect was weaker or absent. The authors suggest that this might be due to the unique perceptual characteristics of gray, which lacks the hue variations present in other color scales, potentially reducing the impact of perceived opacity.

1.2.5 e) Authors propose an "Opacity Variation Index" whose definition relies on the CIELAB color space. Do you see a reason for preferring CIELAB over alternatives such as RGB or XYZ for this purpose?

The authors likely chose the CIELAB color space for defining their Opacity Variation Index because it is specifically designed to reflect perceptual differences more accurately than RGB or XYZ. CIELAB is structured to be perceptually uniform, meaning that changes in its parameters (lightness, a, *b*) correspond more closely to the way humans perceive differences in color and opacity, making it a more appropriate choice for this context.

1.2.6 f) Several plots include error bars that represent standard errors of the means. Please explain how that differs from the standard deviation of the measurements. Use additional sources of information if needed.

One such plot is figure 8. The standard error of the means describes the standard deviation of the mean in repeated samples from a population, in this case it could be the mean of each participants. The standard deviation itself is the square root of the mean of each data points distance from the mean.Wikipedia: Standard deviation. The standard error is calculated by dividing the standard deviation of a sample through the sqaure root of the sample size. Statology: standard deviation vs standard error.

1.3 Task 3

1.3.1 a) Design a color map that could be used to visualize the aggregate statistics of vehicles sold in Germany in a given year, grouped by the vehicle's manufacturer. Each sample point should have a color that reflects the manufacturer type and the number of vehicles sold in that year. Decide on a suitable color scheme and create a color legend that illustrates it. Justify your choices.

Assumptions: - vehicles are further divided into subtypes - all (sufficiently big/important) manufacturers in the world are represented if they have sold to germany - car brands dont have a **unique** generally accepted distinctive color associated with them > This can have different reasons: too many manufacturers, too much overlap in used colors, changes in branding over time

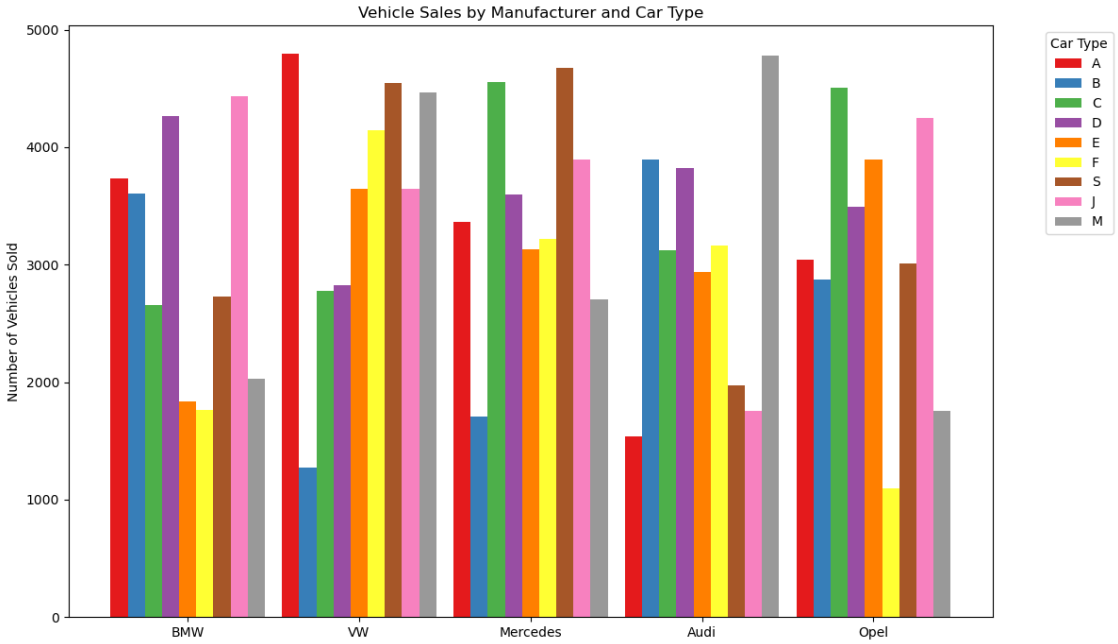
Under these assumptions i would go with a bar chart with the x-axis having the manufacturers (sorted by no. of vehicles sold) and the y-axis showing the no. of cars sold. For the amount of vehicles types we went with the passenger car classification system of the European Commision

which defines 9 distinct types eu vehicle types. Based on this we used the website colorbrewer2 from the slides to look at color schemes for qualitative (nominal) data with 9 classes. The website shows no colorblind safe scheme for this many classes, so the following non-safe scheme was choosen: [‘#e41a1c’,‘#377eb8’,‘#4daf4a’,‘#984ea3’,‘#ff7f00’,‘#ffff33’,‘#a65628’,‘#f781bf’,‘#999999’].

The amount of classes and therefore colors makes the visualization on first glance very confusing. But when focusing on a specific type the colors are sufficiently distinct, so that one can reason about the underlying data. This color scheme was choosen in favor of multiple others which used less saturated colors. This was done as color schemes were harder to tell apart at a glance.

The example chart could still be improved but even as it is now the colors do their job, by helping viewers compare the types more easily against or with each other.

[13]:
```
# Data setup
manufacturers = ['BMW', 'VW', 'Mercedes', 'Audi', 'Opel']
car_types = ["A","B","C","D","E","F","S","J","M"]
colors = ['#e41a1c','#377eb8','#4daf4a','#984ea3','#ff7f00',
          '#ffff33','#a65628','#f781bf','#999999']

# Generate dummy sales data (rows: manufacturers, columns: car types)
np.random.seed(0)
sales_data = np.random.randint(1000, 5000, size=(len(manufacturers),␣
 ↪len(car_types)))

# Create Figure
fig, ax = plt.subplots(figsize=(12, 7))

bar_width = 0.1
indices = np.arange(len(manufacturers))

# Plot bars for each car type (grouped within each manufacturer)
for j in range(len(car_types)):
    # Extract the j-th type sales for all manufacturers
    sales = sales_data[:, j]
    ax.bar(indices + (j - 4) * bar_width, sales, bar_width, color=colors[j],␣
 ↪label=car_types[j] if j == 0 else "")

# Axes and legend
ax.set_xticks(indices)
ax.set_xticklabels(manufacturers)
ax.set_ylabel('Number of Vehicles Sold')
ax.set_title('Vehicle Sales by Manufacturer and Car Type')
ax.legend(car_types, title="Car Type", bbox_to_anchor=(1.05, 1), loc='upper␣
 ↪left')

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



1.3.2 b) In Section 4.2 of the lecture slides, equations are provided to convert from RGB to HSV color space. Derive the inverse mapping, which should convert from HSV to RGB. Please specify intermediate steps. (4P)

[14]:
```
hsv_60 = (60,0.4,0.9)
hsv_180 = (189,0.2,0.6)

# based on the slides and https://cs.stackexchange.com/questions/64549/
 ↪convert-hsv-to-rgb-colors
def hsv_to_rgb(hsv_col):
    (H,S,V) = hsv_col
    # defined in slides
    M = V
    # slides: S = C/V
    C = S * V
    # slides: 1 - m/M = C/M
    m = M - C
    if 60 <= H < 180:
        # between 60 and 180 green is the "main" color
        # we set it to M(ax)
        G = M
        # between 60 and 180 blue is the color with the least impact
        # we set it to m(in)
        B = m
        # slides: (B-R)/C + 2 if green is the "main" color
        R = B - (H/60 - 2) * C
```

```
    elif 180 <= H < 300:
            # between 60 and 180 red is the color with the least impact
            # we set it to m(in)
            R = m
            # between 180 and 300 blue is the "main" color
            # we set it to M(ax)
            B = M
            # slides: (R-G)/C + 4 if blue is the "main" color
            G = R - (H/60 - 4) * C
    else:
        print("Unable to convert")
        R,G,B = 0
    print(R,G,B)
    print(int(R*255),int(G*255),int(B*255))

print("HSV (60,0.4,0.9) to RGB:")
hsv_to_rgb(hsv_60)
print("HSV (180,0.2,0.6) to RGB:")
hsv_to_rgb(hsv_180)
```

```
HSV (60,0.4,0.9) to RGB:
0.9000000000000001 0.9 0.54
229 229 137
HSV (180,0.2,0.6) to RGB:
0.48 0.582 0.6
122 148 153
```

1.4 Task 4

1.4.1 a) Propose a visual encoding of total population and life expectancy over time. Describe and justify your choice of chart type, axis range and scaling, and visualization channels.

I would propose a scatter plot with the years on the X-axis and the life expectancy on the Y-axis which both scale linearly. The scale of each data point is given by the population size. This makes the 3 main data points of year, life expectancy and total population easily visible and enables us to have the timeline on the X-axis. Each compared region will have their own color, to make comparisons easier.

1.4.2 b) Read the dataset and filter/aggregate it so that you can compare the population and life expectancy in different parts of the world, but so that you do not retain more data than can be visualized in a meaningful way with your proposed design. Note that the dataset provides pre-aggregated data at different levels (cf. attribute "Type"). Implement your proposed visualization using a software package of your choice. Take care to keep your plot well-readable, and to include meaningful axis labels and legends. Point out at least two remarkable findings that can be observed in your visualization.

[15]:
```
import plotly.express as px
import pandas as pd

df = pd.read_excel("./WPP2024_GEN_F01_DEMOGRAPHIC_INDICATORS_COMPACT.xlsx")
```

[16]:
```
filtered_df = pd.DataFrame()

filtered_df['Region'] = df['Unnamed: 2']
filtered_df['Type'] = df['Unnamed: 8']
filtered_df['Year'] = df['Unnamed: 10']
filtered_df['Total Population'] = df['Unnamed: 11']
filtered_df['Total Population'] = df['Unnamed: 11']
filtered_df['Life Expectancy at Birth'] = df['Unnamed: 34']
filtered_df = filtered_df.iloc[16:]
filtered_df = filtered_df[filtered_df['Type'] != 'Label/Separator']
filtered_df = filtered_df.fillna(0)
```

```
C:\Users\jovdl\AppData\Local\Temp\ipykernel_24140\3566424737.py:11:
FutureWarning: Downcasting object dtype arrays on .fillna, .ffill, .bfill is
deprecated and will change in a future version. Call
result.infer_objects(copy=False) instead. To opt-in to the future behavior, set
`pd.set_option('future.no_silent_downcasting', True)`
  filtered_df = filtered_df.fillna(0)
```

[17]:
```
# Sadly i got stuck while trying to use ipywidgets
# Thats why the "interactivity" is now here:
# Set type to one of the following: ['World' 'SDG region' 'Development Group'␣
 ↪'Special other' 'Income Group' 'Region' 'Subregion' 'Country/Area']
type = 'Income Group'

type_filtered_df = filtered_df[filtered_df["Type"]== type]
print("Pick out the regions you want to compare from here, after choosing the␣
 ↪correct type:")
print(type_filtered_df["Region"].unique())

regions = ['High-income countries','Low-income countries','Middle-income␣
 ↪countries']

region_filtered_df = type_filtered_df[type_filtered_df['Region'].isin(regions)]
```

```
def show_plot():
    fig = px.scatter(region_filtered_df, x="Year", y="Life Expectancy at␣
 ↪Birth", size="Total Population",
                     color="Region", hover_name="Region", title=f"Gapminder␣
 ↪Data for {type}")
    fig.show()

show_plot()
```

```
Pick out the regions you want to compare from here, after choosing the correct
type:
['High-and-upper-middle-income countries'
 'Low-and-Lower-middle-income countries' 'High-income countries'
 'Low-and-middle-income countries' 'Middle-income countries'
 'Upper-middle-income countries' 'Lower-middle-income countries'
 'Low-income countries' 'No income group available']
```

Finding 1: When looking at the plot above and comparing the following income groups: 'High-income countries','Low-income countries','Middle-income countries' one can see countries with higher income have less outliers where the life expectancy drops for a year or a few years before growing steadily again.

[18]:
```
# Sadly i got stuck while trying to use ipywidgets
# Thats why the "interactivity" is now here:
# Set type to one of the following: ['World' 'SDG region' 'Development Group'␣
 ↪'Special other' 'Income Group' 'Region' 'Subregion' 'Country/Area']
type = 'Development Group'

type_filtered_df = filtered_df[filtered_df["Type"]== type]
print("Pick out the regions you want to compare from here, after choosing the␣
 ↪correct type:")
print(type_filtered_df["Region"].unique())

regions = ['More developed regions','Less developed regions', 'Least developed␣
 ↪countries']

region_filtered_df = type_filtered_df[type_filtered_df['Region'].isin(regions)]

def show_plot():
    fig = px.scatter(region_filtered_df, x="Year", y="Life Expectancy at␣
 ↪Birth", size="Total Population",
                     color="Region", hover_name="Region", title=f"Gapminder␣
 ↪Data for {type}")
    fig.show()

show_plot()
```

```
Pick out the regions you want to compare from here, after choosing the correct
type:
['More developed regions' 'Less developed regions'
 'Least developed countries'
 'Less developed regions, excluding least developed countries'
 'Less developed regions, excluding China']
```

Finding 2: When comparing more developed and less developed regions in the plot above, one can see that the life expectancy of the less developed regions is slowly catching up to the more developed regions. From around a 22-27 year gap in 1950 to a 8-13 year gap in 2023. I found this remarkable as i would have expected that countries that improve their citizens life expectancy would also change from a less to a more developed country as other indicators would also improve.

1.4.3 c) The dataset provides a lot of additional information. Formulate a question out of your own interest that can be answered with this data. Filter and visualize the data accordingly, and report your findings.

In which region did the corona pandemic have the biggest impact on the life expectancy?

[19]:
```
# Sadly i got stuck while trying to use ipywidgets
# Thats why the "interactivity" is now here:
# Set type to one of the following: ['World' 'SDG region' 'Development Group'␣
 ↪'Special other' 'Income Group' 'Region' 'Subregion' 'Country/Area']
type = 'Region'
type_filtered_df = filtered_df[filtered_df["Type"]== type]

regions = ['Africa', 'Asia', 'Europe', 'Latin America and the Caribbean',␣
 ↪'Northern America', 'Oceania' ]
region_filtered_df = type_filtered_df[type_filtered_df['Region'].isin(regions)]

def show_plot():
    fig = px.scatter(region_filtered_df, x="Year", y="Life Expectancy at␣
 ↪Birth", size="Total Population",
                     color="Region", hover_name="Region", title=f"Gapminder␣
 ↪Data for {type}")
    fig.show()

show_plot()
```

When looking at the years 2020 and 2021 one can see the drop in life expectancy that was mostly caused by corona:

- Africa: -0.47
- Asia: -1.235
- Europe: -0.615
- Latin America and the Caribbean: -1.442
- Northern America: -0.54
- Oceania: -0.398

From this we can see that the biggest impact was in Latin America and the Caribbean closely followed by Asia.

This was sadly not directly visible from the visualization, this could be improved by adding a value to the hover information which shows the difference between the current data point and the next or previous year.