Loading packages

In [1]:

```
import numpy as np
import pandas as pd
import glob
```

In [2]:

```
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

In [3]:

```
from pandas.api.types import CategoricalDtype
```

Loading data

In [4]:

```
data= pd.read_pickle("../data/modified_exclusions/pt_replication_modified_exclusions_data
.pkl")
```

In [5]:

```
data.head()
```

Out[5]:

	1	2	3	4	5	6	7	8	9	10	...	Loss_Intuition	Country	Duration_in_seconds	Language	Sample	Duration
0	1.0	0.0	0.0	1.0	1.0	1.0	1.0	0.0	1.0	1.0	...	1.0	Bulgaria	356	Bulgarian	Direct	
1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	...	NaN	Bulgaria	931	Bulgarian	Direct	1
2	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	...	1.0	Bulgaria	462	Bulgarian	Direct	
3	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	1.0	0.0	...	NaN	Bulgaria	412	Bulgarian	Direct	
4	0.0	0.0	0.0	0.0	0.0	1.0	1.0	1.0	1.0	1.0	...	NaN	Bulgaria	490	Bulgarian	Direct	

5 rows × 39 columns

Sample overview

In [6]:

```
sample_size_df = pd.DataFrame(data["Country"].value_counts())
sample_size_df.columns = ["Total n"]
```

In [7]:

```
sample_size_df["Direct n"] = data.loc[data["Sample"]=="Direct", "Country"].value_counts()
sample_size_df["Paid n"] = data.loc[data["Sample"]=="Paid", "Country"].value_counts()
```

In [8]:

```
sample_size_df.loc[sample_size_df["Paid n"].notna(), "Paid n"] = sample_size_df.loc[
    sample_size_df["Paid n"].notna(), "Paid n"].round()
sample_size_df = sample_size_df.loc[:, ["Direct n", "Paid n", "Total n"]]
```

```
sample_size_df.to_excel("../output/Sample Size.xlsx")
sample_size_df.to_csv("../output/Sample Size.csv")
```

Creating long format data frames

Create a vector of original PT proportions

In [9]:

```
original_pt_proportions = pd.Series([0.18, 0.83, 0.20, 0.65, 0.14, 0.73, 0.92, 0.42, 0.9
2, 0.30, 0.22, 0.16, 0.69, 0.18, 0.70, 0.72, 0.17],
                                   index=[str(i) for i in np.arange(1, 18)])
original_pt_proportions
```

Out[9]:

```
1     0.18
2     0.83
3     0.20
4     0.65
5     0.14
6     0.73
7     0.92
8     0.42
9     0.92
10    0.30
11    0.22
12    0.16
13    0.69
14    0.18
15    0.70
16    0.72
17    0.17
dtype: float64
```

Create a dataframe for original PT Proportions

In [64]:

```
original_pt_proportions_df = pd.DataFrame(original_pt_proportions)
original_pt_proportions_df = original_pt_proportions_df.reset_index()
original_pt_proportions_df.columns = ["Item", "Proportion"]
original_pt_proportions_df["Item"] = original_pt_proportions_df["Item"].astype(str)
original_pt_proportions_df["Country"] = "Original"
original_pt_proportions_df.to_csv("../output/original_proportions.csv", index=False)
```

Pivoting the replication data to a long format with response proportions per item per country

In [11]:

```
long_data = data.groupby("Country")[[str(i) for i in np.arange(1, 18)]].mean().reset_ind
ex().melt(id_vars="Country", value_vars=[str(i) for i in np.arange(1, 18)],
                                                                                    var_
name="Item", value_name="Proportion")
```

Creating dataframe combining proportions from the replication and the original

In [12]:

```
long_data_combinded = pd.concat([long_data, original_pt_proportions_df], ignore_index=Tr
ue, sort=True)
```

In [13]:

```
long_data_combinded.tail()
```

Out[13]:

	Country	Item	Proportion
335	Original	13	0.69
336	Original	14	0.18
337	Original	15	0.70
338	Original	16	0.72
339	Original	17	0.17

Data wrangling with the proportions

Create wide dataframe with response proportion per item per country

In [14]:

```
country_proportions = data.groupby("Country")[[str(i) for i in np.arange(1, 18)]].mean()
country_proportions.head()
```

Out[14]:

	1	2	3	4	5	6	7	8	9	10	11	
Country												
Australia	0.446809	0.705674	0.152482	0.524823	0.095745	0.673759	0.695035	0.432624	0.815603	0.340426	0.145390	0.262
Austria	0.198198	0.549550	0.090090	0.414414	0.126126	0.657658	0.828829	0.459459	0.810811	0.378378	0.081081	0.189
Belgium	0.192708	0.645833	0.125000	0.489583	0.072917	0.656250	0.833333	0.510417	0.828125	0.380208	0.135417	0.276
Bulgaria	0.181102	0.566929	0.118110	0.511811	0.125984	0.645669	0.858268	0.598425	0.811024	0.559055	0.165354	0.267
Chile	0.186207	0.565517	0.103448	0.475862	0.096552	0.606897	0.827586	0.558621	0.772414	0.503448	0.165517	0.165

check the extent to which the current proportion of A choices deviate from the original study

In [15]:

```
country_deviations = country_proportions - original_pt_proportions
country_deviations.head()
```

Out[15]:

	1	2	3	4	5	6	7	8	9	10	11	
Country												
Australia	0.266809	-0.124326	-0.047518	-0.125177	-0.044255	-0.056241	-0.224965	0.012624	-0.104397	0.040426	-0.074610	0.102
Austria	0.018198	-0.280450	-0.109910	-0.235586	-0.013874	-0.072342	-0.091171	0.039459	-0.109189	0.078378	-0.138919	0.029
Belgium	0.012708	-0.184167	-0.075000	-0.160417	-0.067083	-0.073750	-0.086667	0.090417	-0.091875	0.080208	-0.084583	0.116
Bulgaria	0.001102	-0.263071	-0.081890	-0.138189	-0.014016	-0.084331	-0.061732	0.178425	-0.108976	0.259055	-0.054646	0.107
Chile	0.006207	-0.264483	-0.096552	-0.174138	-0.043448	-0.123103	-0.092414	0.138621	-0.147586	0.203448	-0.054483	0.005

Quantify how far the original PT proportions were from a 50-50 split

In [16]:

```
original_pt_distance_from_indifference = original_pt_proportions - 0.5
```

Transform the difference in proportion to a difference in effect size, accounting for whether the majority chose option A in the original study. I.e. if the original proportion was less than 0.5 an increase in proportion is treated as decrease in effect and vice versa.

In [17]:

```
country_deviations_signed = country_deviations.copy()
for col in country_deviations:
    if original_pt_distance_from_indifference[col] < 0:
        country_deviations_signed[col] = country_deviations_signed[col]*-1
```

Comparing differences in effect size from the original between countries and between Items

In [18]:

```
country_deviations_signed.mean(1).sort_values()
```

Out[18]:

```
Country
Slovenia         -0.109071
Serbia           -0.103812
Bulgaria         -0.100107
Mainland China   -0.099937
Italy            -0.097360
Hong Kong        -0.095561
USA              -0.093723
Chile            -0.091907
Germany          -0.091047
Australia        -0.085558
Belgium          -0.081528
Ireland          -0.081515
Hungary          -0.078715
Denmark          -0.078627
Sweden           -0.077194
Austria          -0.071060
Spain            -0.069126
UK               -0.065343
Norway           -0.053581
dtype: float64
```

The range for country deviation form the original study is 5%. All countries show a smaller effect than the original study

In [19]:

```
country_deviations_signed.mean(0).sort_values()
```

Out[19]:

```
17   -0.262927
2    -0.217742
16   -0.145438
4    -0.141856
10   -0.130317
9    -0.125516
7    -0.122677
12   -0.090539
```

```
15    -0.085043
8     -0.082913
6     -0.078992
13    -0.074606
1     -0.063367
14     0.001623
5      0.031387
11     0.060408
3      0.074771
dtype: float64
```

Range for items is over 30%, and three items show a greater effect than in the original study

In [20]:

```
country_deviations_signed.std(1)
```

Out[20]:

```
Country
Australia         0.099013
Austria           0.117945
Belgium           0.102024
Bulgaria          0.128943
Chile             0.135769
Denmark           0.104010
Germany           0.096131
Hong Kong         0.084780
Hungary           0.106656
Ireland           0.133570
Italy             0.098792
Mainland China    0.097058
Norway            0.113455
Serbia            0.090144
Slovenia          0.086970
Spain             0.091175
Sweden            0.111519
UK                0.099581
USA               0.123843
dtype: float64
```

The standard deviation in all countries is between 9 and 12%

Creating pivoting the country deviations data to the long form

In [21]:

```
country_deviations_signed_long = country_deviations_signed.reset_index().melt(id_vars="Country",
                                                                                  var_name="Item", value_name="Deviation")
```

In [22]:

```
country_deviations_signed_long["Sample Size"] = data.groupby("Country")[[str(i) for i in np.arange(1, 18)]].count().melt()["value"]
```

In [23]:

```
country_deviations_signed_long["Sign Difference"] = (original_pt_distance_from_indifference.apply(np.sign) == (country_proportions - .5).apply(np.sign)).melt()["value"]
```

In [24]:

```
country_deviations_signed_long["Sign Difference"] = ~country_deviations_signed_long["Sign
Difference"]
```

Item-by-item chisquare tests

In [25]:

```
from scipy.stats import chisquare
```

Analyses by country

Running chisquare tests per item per country, and saving the results in vectors

In [26]:

```
%%time
country_p_values = {}
country_chi_squares = {}
for country in data["Country"].unique():
    item_p_values = {}
    item_chi_squares = {}
    for col in [str(i) for i in np.arange(1, 18)]:
        observations = data.loc[data["Country"] == country, col].value_counts().values
        chi, p = chisquare(observations)
        item_p_values[col] = p
        item_chi_squares[col] = chi
        if col == "17":
            country_p_values[country] = item_p_values
            country_chi_squares[country] = item_chi_squares
```

```
Wall time: 385 ms
```

Creating a dataframe from the results vector

In [27]:

```
p_value_df = pd.DataFrame(country_p_values)
p_value_df = p_value_df.loc[[str(i) for i in np.arange(1, 18)], :]
```

In [28]:

```
chi_square_df = pd.DataFrame(country_chi_squares)
chi_square_df =chi_square_df.loc[[str(i) for i in np.arange(1, 18)], :]
```

Adding the results from the chisquare tests to the long form country deviations

Adding sample size to the long form country deviations

In [29]:

```
country_deviations_signed_long["Sample Size"] = data.groupby("Country")[[str(i) for i in
np.arange(1, 18)]].count().melt()["value"]
```

Checking whether the sign of the effect is the same as in the original study

In [30]:

```
country_deviations_signed_long["Sign Difference"] = (original_pt_distance_from_indifferen
```

```
ce.apply(np.sign) == (country_proportions - .5).apply(np.sign)).melt()["value"]
```

In [31]:

```
country_deviations_signed_long["Sign Difference"] = ~country_deviations_signed_long["Sign Difference"]
```

In [32]:

```
country_deviations_signed_long.head()
```

Out[32]:

	Country	Item	Deviation	Sample Size	Sign Difference
0	Australia	1	-0.266809	282	False
1	Austria	1	-0.018198	111	False
2	Belgium	1	-0.012708	192	False
3	Bulgaria	1	-0.001102	127	False
4	Chile	1	-0.006207	145	False

In [33]:

```
country_deviations_signed_long.tail()
```

Out[33]:

	Country	Item	Deviation	Sample Size	Sign Difference
318	Slovenia	17	-0.250792	202	False
319	Spain	17	-0.272211	199	False
320	Sweden	17	-0.132158	139	False
321	UK	17	-0.161034	290	False
322	USA	17	-0.274444	243	False

Adding p-values

In [34]:

```
p_value_long = p_value_df.reset_index().melt(id_vars="index")
p_value_long.columns = ["Item", "Country", "p-value"]
p_value_long["Item"] = p_value_long["Item"].astype(int)
p_value_long = p_value_long.sort_values(by=["Item", "Country"])
p_value_long = p_value_long.reset_index(drop=True)
```

In [35]:

```
country_deviations_signed_long["p-value"] = p_value_long["p-value"]
```

In [36]:

```
p_value_long.head()
```

Out[36]:

	Item	Country	p-value
0	1	Australia	7.402254e-02
1	1	Austria	2.025980e-10
2	1	Belgium	1.652779e-17
3	1	Bulgaria	6.594603e-13
4	1	Chile	4.120326e-14

	Item	Country	p-value

In [37]:

```
country_deviations_signed_long.head()
```

Out[37]:

	Country	Item	Deviation	Sample Size	Sign Difference	p-value
0	Australia	1	-0.266809	282	False	7.402254e-02
1	Austria	1	-0.018198	111	False	2.025980e-10
2	Belgium	1	-0.012708	192	False	1.652779e-17
3	Bulgaria	1	-0.001102	127	False	6.594603e-13
4	Chile	1	-0.006207	145	False	4.120326e-14

Computing replication rates based on p-values and sign agreement between original study and replication

In [38]:

```
country_deviations_signed_long["Succesful Replication"] = np.nan
country_deviations_signed_long.loc[(country_deviations_signed_long["Sign Difference"] ==
False) & (country_deviations_signed_long["p-value"]<0.05),
                                    "Succesful Replication"] = True
country_deviations_signed_long.loc[(country_deviations_signed_long["Sign Difference"] ==
False) & (country_deviations_signed_long["p-value"]>0.05),
                                    "Succesful Replication"] = False
country_deviations_signed_long.loc[(country_deviations_signed_long["Sign Difference"] ==
True), "Succesful Replication"] = False
country_deviations_signed_long.loc[(country_deviations_signed_long["Item"]=="8"), "Succes
ful Replication"] = np.nan
```

In [39]:

```
country_deviations_signed_long["Succesful Replication"] = country_deviations_signed_long[
"Succesful Replication"].astype(float)
```

In [40]:

```
country_deviations_signed_long.head()
```

Out[40]:

	Country	Item	Deviation	Sample Size	Sign Difference	p-value	Succesful Replication
0	Australia	1	-0.266809	282	False	7.402254e-02	0.0
1	Austria	1	-0.018198	111	False	2.025980e-10	1.0
2	Belgium	1	-0.012708	192	False	1.652779e-17	1.0
3	Bulgaria	1	-0.001102	127	False	6.594603e-13	1.0
4	Chile	1	-0.006207	145	False	4.120326e-14	1.0

Saving country deviations

In [41]:

```
country_deviations_signed_long.to_csv("../output/deviations_from_original_by_country.csv"
, index=False)
```

Exploring item-based replications

Total replication rates across all countries and items

In [42]:

```
country_deviations_signed_long["Succesful Replication"].mean()
```

Out[42]:

```
0.8125
```

Total number of succesful replications

In [43]:

```
country_deviations_signed_long["Succesful Replication"].sum()
```

Out[43]:

```
247.0
```

Total number of attempted replications

In [44]:

```
country_deviations_signed_long["Succesful Replication"].count()
```

Out[44]:

```
304
```

Compute replication rate per item and store the results in a dataframe

In [45]:

```
%%time
replication_rate_by_item = pd.DataFrame(country_deviations_signed_long.groupby("Item")["
Succesful Replication"].mean())
replication_rate_by_item = replication_rate_by_item.loc[[str(i) for i in np.arange(1, 18
)], :]
replication_rate_by_item = replication_rate_by_item.reset_index()
```

```
Wall time: 2.97 ms
```

In [46]:

```
replication_rate_by_item
```

Out[46]:

	Item	Succesful Replication
0	1	0.947368
1	2	0.684211
2	3	1.000000
3	4	0.157895
4	5	1.000000
5	6	1.000000
6	7	1.000000
7	8	NaN
8	9	1.000000
9	10	0.578947
10	11	1.000000

	Item	Succesful Replication
11	12	1.000000
12	13	0.789474
13	14	1.000000
14	15	0.789474
15	16	0.631579
16	17	0.421053

Compute replication rates per country (and continent) and store in a dataframe

In [47]:

```
replication_rate_by_country = pd.DataFrame(country_deviations_signed_long.groupby("Count
ry")["Succesful Replication"].mean()).reset_index()
replication_rate_by_country = replication_rate_by_country.sort_values(by="Succesful Repl
ication", ascending=False)
continents = {"Europe":['Bulgaria', 'Denmark', 'Belgium', 'Ireland', 'UK','Austria', 'Ger
many',
        'Hungary', 'Italy', 'Norway', 'Serbia', 'Slovenia', 'Spain', 'Sweden'],
              "Asia":['Hong Kong', 'Mainland China'],
              "North America": ["USA"],
             "Oceania": ["Australia"],
              "South America":["Chile"]}
replication_rate_by_country["Continent"] = np.nan
for continent in continents.keys():
    replication_rate_by_country.loc[replication_rate_by_country["Country"].isin(continent
s[continent]), "Continent"] = continent
```

In [48]:

```
replication_rate_by_country.head()
```

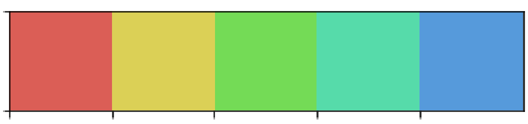
Out[48]:

	Country	Succesful Replication	Continent
17	UK	0.9375	Europe
5	Denmark	0.8750	Europe
8	Hungary	0.8750	Europe
11	Mainland China	0.8750	Asia
12	Norway	0.8750	Europe

Hard-coding colors for the different continents to the dataframe because it makes plotting easier

In [110]:

```
sns.palplot(sns.color_palette("hls", 7)[:5])
```



In [50]:

```
cont_col_dict = dict(zip(replication_rate_by_country["Continent"].unique(), sns.color_pal
ette("hls", 7)[:5]))
replication_rate_by_country["Colour"] = replication_rate_by_country["Continent"].map(cont
_col_dict)
```

Add a row for the replication rate of the pooled data (based on the meta-analytic

Add a row for the replication rate of the pooled data (based on the meta-analytic analyses)

In [51]:

```
pooled_data_row = pd.DataFrame(pd.Series(["Pooled", 15/16, "Pooled", sns.color_palette("
hls", 7)[6]], index=replication_rate_by_country.columns)).transpose()
```

In [52]:

```
replication_rate_by_country = pd.concat([pooled_data_row, replication_rate_by_country]).
reset_index(drop = True)
```

Saving replication rate per country

In [53]:

```
replication_rate_by_country.to_csv("../output/replication_rate_by_country.csv", index=Fal
se)
```

Adding whether a replication was successful to the long data and save the long data

In [54]:

```
long_data["Succesful Replication"] = country_deviations_signed_long["Succesful Replicatio
n"]
long_data.loc[long_data["Succesful Replication"].isna(), "Succesful Replication"] = "NA"
long_data.loc[long_data["Succesful Replication"]==1, "Succesful Replication"] = "Yes"
long_data.loc[long_data["Succesful Replication"]==0, "Succesful Replication"] = "No"
long_data["Sample Size"] = country_deviations_signed_long["Sample Size"]
```

In [55]:

```
long_data.head()
```

Out[55]:

	Country	Item	Proportion	Succesful Replication	Sample Size
0	Australia	1	0.446809	No	282
1	Austria	1	0.198198	Yes	111
2	Belgium	1	0.192708	Yes	192
3	Bulgaria	1	0.181102	Yes	127
4	Chile	1	0.186207	Yes	145

In [56]:

```
long_data.to_csv("../output/proportions_by_country.csv", index=False)
```

Checking the number of effects that are attenuated compared to the original study

In [57]:

```
n_attenuated_effects = (np.sign(country_deviations_signed_long["Deviation"])==-1).sum()
n_attenuated_effects
```

Out[57]:

```
250
```

In [58]:

```
n_total_effects = country_deviations_signed_long.shape[0]
n_total_effects
```

Out[58]:

```
323
```

In [59]:

```
n_attenuated_effects/n_total_effects
```

Out[59]:

```
0.7739938080495357
```

In [60]:

```
n_larger_effects = n_total_effects - n_attenuated_effects
n_larger_effects
```

Out[60]:

```
73
```

In [61]:

```
chisquare([n_larger_effects, n_attenuated_effects])
```

Out[61]:

```
Power_divergenceResult(statistic=96.9938080495356, pvalue=6.954447526227529e-23)
```

Attenuation is significantly more common than would be expected by chance. In other words, sampling variation alone cannot plausible account for the attenuation effect.