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## Check adjusted do #arabian_peninsula_d ####################################	ara ara ara ara ara ara ara dj['mv_perc'] = arak ataframe ## adj  ######## taframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	abian_peninsula_adj['m_cellular subscriptions'] + \ abian_peninsula_adj['m_parliament seats (f)'] + \ abian_peninsula_adj['m_malaria cases'] + \ abian_peninsula_adj['m_international trade'] + \ abian_peninsula_adj['m_tuberculosis mortality']  bian_peninsula_adj.loc[: , 'mv_sum'] / 12 * 100 datasets/arabian_peninsula.xlsx", ", riter:
# Imputation for nu. ####################################	ll values per Catego ################  wes for Economic Ind ################  capita column #####  e without null value  ng data set  an_peninsula[economic	######################################
<pre>## Impute missing va # soft coding mean GNI_imputation = ara # filling GNI per ca arabian_peninsula_aa  #################################</pre>	for SYR abian_peninsula.loc  apita SYR with GNI_ dj.fillna(value = inplace = inplace = ###################################	<pre>apita ##  [['PSE', 'YEM'],['gni per capita']].mean()  imputation in the arabian_peninsula_adj data frame    GNI_imputation,    True)  ###################################</pre>
<pre># subset the existing InternationalTrade_c ]].copy()  # drop the missing internationalTrade_c  ## Impute missing value # soft coding mean internationalTrade ame</pre> ## filling International	ng data set dropped = arabian_pe rows with dropna dropped = International Trace poian_peninsula.loc[ conal trade indicator	rade ['PSE', 'YEM'],['international trade']].mean()  r for SYR with IT_imputation in the arabian_peninsula_adj data
######### Parliamed ## Create data framed # subset the existing	<pre>inplace =  ##################  int seats (f) column  e without null value  ing data set</pre>	True)  ###################################
<pre># soft coding value: FemParl_OMN_imputat: FemParl_QAT_imputat: FemParl_SAU_imputat:  # fill values for Off arabian_peninsula_act arabian_peninsula_ac</pre>	ion = 2.33  # https ion = 9.76  # https ion = 19.87  # https MN, QAT, SAU dj.loc['OMN','parliadj.loc['QAT','parliadj.loc['SAU','parliaddj.loc['SAU','par	t Seats held by Women ##  s://www.ipu.org/parliament/OM s://www.ipu.org/parliament/QA s://www.ipu.org/parliament/SA  ament seats (f)'] = FemParl_OMN_imputation ament seats (f)'] = FemParl_QAT_imputation ament seats (f)'] = FemParl_SAU_imputation  ###################################
# drop the missing and malariacases_dropped # Impute value for a malaria_mortality_in # fill null values arabian_peninsula_ad ######## Tubercule # subset the existing tuberculosis_mortal:	d = arabian_peninsularows with dropna d = malariacases_dr  Malaria mputation = 0  for measles immuniza dj['malaria cases']  cosis Mortality ##### ing data set	<pre>.fillna( value = malaria_mortality_imputation,</pre>
<pre># Impute value for stuberculosis_mortal: s = 2) # fill null values</pre>	<pre>ity_dropped = tuber tuberculosis mortal: ity_imputation = re for tuberculosis mortal dj['tuberculosis mortal Immunization ######;</pre>	<pre>ound(arabian_peninsula['tuberculosis mortality'].median(), nds rtality. rtality'].fillna( value = tuberculosis_mortality_imputation,</pre>
# drop the missing measles_immunization # Impute value for measles_immunization # fill null values arabian_peninsula_ad  # Outlier Flagging p	n_dropped = arabian_ rows with dropna n_dropped = measles measles immunization n_imputation = roun for measles immuniza dj['measles immuniza per Category	nd(arabian_peninsula['measles immunization'].mean(), ndigits =
	<pre>peninsula_adj: or\ or\ l or\ in col: insula_adj['o_'+col] ####################################</pre>	] = O ###################################
#set outlier flags  for index, col in a:  #Internet Users if arabian_penin arabian_peninsul arabian_peninsul arabian_peninsul arabian_peninsul arabian_peninsul arabian_peninsul	holds for outliers ernet_high = 35 ernet_upper_middle = lular_high = 100  rabian_peninsula_ad;  Outlier nsula_adj.loc[ index , insula_adj.loc[ index , insula_adj.loc[ index ins	<pre># set according to statistical analysis (boxplot) = 16  # set according to statistical analysis (boxplot)</pre>
## Economic Indicate  #define upper thresh threshold_upper_GNI threshold_upper_Int threshold_upper_Pari  #define lower thresh threshold_lower_GNI threshold_lower_Int threshold_lower_Pari  #set outlier flags  for index, col in as	holds for outliers = 60000  # 8  Trade = 130  # 8  ISeats = 26  # 8  holds for outliers = 0  # 8  Trade = 45  # 8  ISeats = 0  # 8	######################################
#GNI Outlier  if arabian_penin arabian_peninsul arabian_pen  #International elif arabian_pen arabian_peninsul arabian_peninsul arabian_peninsul arabian_peninsul	nsula_adj.loc[ index , insula_adj.loc[ index , insula_	<pre>x , 'gni per capita'] &gt; threshold_upper_GNI or\   'gni per capita'] &lt; threshold_lower_GNI: ex , 'o_gni per capita'] = 1  dex , 'international trade'] &gt; threshold_upper_IntTrade or\   'international trade'] &lt; threshold_lower_IntTrade: ex , 'o_international trade'] = 1</pre>
######################################	######################################	<pre># set according to statistical analysis (boxplot) # set according to statistical analysis (boxplot) # set according to statistical analysis (boxplot)</pre>
threshold_lower_tube threshold_lower_tube threshold_lower_meas threshold_lower_life threshold_lower_fere  #set outlier flags  for index, col in as  #malaria cases if arabian_penin arabian_peninsus arabian_peninsus	erculosis_c = 5 erculosis_m = 0 sles = 79 e_exp = 72 tility = 1.45  rabian_peninsula_adg  outlier nsula_adj.loc[index, insula_adj.loc[index,	<pre># set according to external research (WHO, 2020) # set according to statistical analysis (boxplot) # set according to statistical analysis (histogram) # set according to statistical analysis (boxplot) # set according to statistical analysis (boxplot)  j.loc[:,:].iterrows():  x , 'malaria cases'] &gt; threshold_upper_malaria or\ 'malaria cases'] &lt; threshold_lower_malaria: ex , 'o_malaria cases'] = 1</pre>
### ### ##############################	ninsula_adj.loc[ inda la_adj.loc[ index , insula_adj.loc[ index ortality outlier ninsula_adj.loc[ index , insula_adj.loc[ inde	<pre>dex , 'tuberculosis cases'] &gt; threshold_upper_tuberculosis_c 'tuberculosis cases'] &lt; threshold_lower_tuberculosis_c: ex , 'o_tuberculosis cases'] = 1  dex , 'tuberculosis mortality'] &gt; threshold_upper_tuberculosis 'tuberculosis mortality'] &lt; threshold_lower_tuberculosis_m: ex , 'o_tuberculosis mortality'] = 1  dex , 'measles immunization'] &gt; threshold_upper_measles or\     'measles immunization'] &lt; threshold_lower_measles: ex , 'o_measles immunization'] = 1  dex , 'life expectancy'] &gt; threshold_upper_life_exp or\     'life expectancy'] &lt; threshold_lower_life_exp: ex , 'o_life expectancy'] = 1  dex , 'fertility'] &gt; threshold_upper_fertility or\     'fertility'] &lt; threshold_lower_fertility: ex , 'o fertility'] = 1</pre>
######################################	######################################	<pre>####################################</pre>
######################################	######################################	<pre>ll values'] = 1 #low number of missing values, identified by ####################################</pre>
	arak arak arak arak arak	<pre>bian_peninsula_adj['o_gni per capita'] + \ bian peninsula adj['o measles immunization'] + \</pre>
######################################	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ",
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ######################### # Export Adjusted Da with pd.ExcelWriter</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ######################### # Export Adjusted Da with pd.ExcelWriter</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
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<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
<pre>arabian_peninsula_ac ###################################</pre>	arak arak arak arak age of outliers dj['o_perc'] = arabs ######## ataframe  ("./_datasets/saved_ engine = "openpyxl' mode = "a") as wa	bian_peninsula_adj['o_tuberculosis cases'] + \ bian_peninsula_adj['o_internet users'] + \ bian_peninsula_adj['o_life expectancy'] + \ bian_peninsula_adj['o_cellular subscriptions'] + \ bian_peninsula_adj['o_parliament seats (f)'] + \ bian_peninsula_adj['o_malaria cases'] + \ bian_peninsula_adj['o_international trade'] + \ bian_peninsula_adj['o_tuberculosis mortality'] + \ bian_peninsula_adj['o_null values']  ian_peninsula_adj.loc[: , 'o_sum'] / 13 * 100 datasets/arabian_peninsula.xlsx", ", riter:
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# If you want to display the plots, please change plt.close() to plt.show() on line 446, 484, 521 #(plots were first saved individally, then added as as group for the PDF) # setting figure size fig, ax = plt.subplots(figsize = [16, 100], sharex = True, # sharing x-axis between visualizations sharey = True) # sharing y-axis between visualizations) # PLOT 1: Internet users plt.subplot(18, 2, 1) #18 rows, 2 columns, spot 1 # Boxplot for internet users sns.boxplot(x = 'internet users', y = 'Income Group', orient = 'h', color = 'skyblue', data = arabian\_peninsula) # titles and labels plt.title(label = "Figure 1:\n Distribution of Internet Users by Income Group", pad = 20.0)plt.xlabel(xlabel = 'Internet Users') plt.ylabel(ylabel = 'Frequency') # PLOT 2: cellular subscriptions plt.subplot(18, 2, 2) #18 rows, 2 columns, spot 2 # Boxplot for cellular subscriptions orient = 'h', color = 'skyblue', data = arabian peninsula) # titles, labels, and formatting plt.title(label = "Figure 2:\n Distribution of Cellular Subscriptions by Income Group", pad = 20.0)plt.xlabel(xlabel = 'Cellular Subscriptions') # PLOT 3: GNI per capita without imputed values plt.subplot(18, 2, 3) #18 rows, 2 columns, spot 3 # histogram for GNI per capita without imputed values sns.distplot(a = GNI\_dropped['gni per capita'], bins = 'fd', hist = True, kde = True, rug = False, color = 'gray') # histogram for GNI per capita with imputed values sns.distplot(a = arabian\_peninsula\_adj['gni per capita'], bins = 'fd', hist = True, kde = True, rug = False, color = 'deepskyblue') # titles, labels, and formatting plt.title(label = """Figure 4:\nGNI per Capita Distribution\n(With/without imputation of missing valu es)""", pad = 10.0) plt.xlabel(xlabel = 'GNI per Capita [USD]') plt.ylabel(ylabel = 'Frequency') plt.xlim(0.0, 70000) #plt.ylim(0.0, 0.00004) # legend plt.legend(labels = ['original distribution', 'imputed distribution']) # PLOT 4: GNI per capita outliers plt.subplot(18, 2, 4) #19 rows, 2 columns, spot 4 # boxplot 1 = 'gni per capita', # x-variable sns.boxplot(x = None, # optional y-variable hue = None, # optional categorical feature # horizontal or vertical orient = 'h', data = arabian\_peninsula\_adj, # DataFrame where features exist color = 'skyblue') # formatting plt.title(label = "Figure 5:\nGNI per Capita Outliers", pad = 10.0)plt.xlabel(xlabel = 'GNI per capita [USD]') # PLOT 5: International Trade without imputed values plt.subplot(18, 2, 5) #18 rows, 2 columns, spot 5 # histogram for International Trade without imputed values sns.distplot(a = InternationalTrade\_dropped['international trade'], bins = 'fd', hist = True, kde = True, rug = False, color = 'gray') # histogram for International Trade with imputed values sns.distplot(a = arabian\_peninsula\_adj['international trade'], bins = 'fd', hist = True, kde = True, rug = False, color = 'deepskyblue') # titles, labels, and formatting plt.title(label = """Figure 6:\nInternational Trade Distribution\n(With/without imputation of missing values)""", = 10)pad plt.xlabel(xlabel = 'International Trade [% of GDP]') plt.ylabel(ylabel = 'Frequency') plt.xlim(40, 150) plt.ylim(0.0, 0.02)# legend plt.legend(labels = ['original distribution', 'imputed distribution']) # PLOT 6: parliament seats without imputed values plt.subplot(18, 2, 6) #18 rows, 2 columns, spot 6 # histogram for parliament seats without imputed values sns.distplot(a = parliamentF dropped['parliament seats (f)'], bins = 'fd', hist = True, kde = True, rug = False, color = 'gray') # histogram for parliament seats with imputed values sns.distplot(a = arabian peninsula adj['parliament seats (f)'], bins = 'fd', hist = True, kde = True, rug = False, color = 'deepskyblue') # titles, labels, and formatting plt.title(label = """Figure 7: $\n$ Parliament Seats Held by Women Distribution $\n$ (With/without imputation of missing values)""", pad = 10)plt.xlabel(xlabel = 'Percentage of Parliament Seats Held by Women') plt.ylabel(ylabel = 'Frequency') plt.xlim(0.0, 40)plt.ylim(0.0, 0.06) # legend plt.legend(labels = ['original distribution', 'imputed distribution']) # PLOT 7: Literacy Rate Analysis (boxplot & table on census years) # Set figure size plt.subplot(18, 2, 7) #18 rows, 2 columns, spot 7 # Create DF of Census Dates per Country literacy rate = arabian peninsula.loc[:,['country']].copy() literacy rate['census date'] = [2010, 2010, 2011, 1997, 2009, 2015, 2011, 1943, 2010, 2017, 2015, 2010, 2004, 2011, 2004] literacy rate.sort values(by = 'census date', ascending = **False**) # Develop a boxplot for Census Date sns.boxplot(x = 'census date', # x-variable = None, # optional y-variable hue = None, # optional categorical feature orient = 'h', # horizontal or vertical color = 'skyblue', data = literacy rate) # DataFrame where features exist # Format and Display the plot plt.axvline(x = 2003,color = "red", linestyle= '--') plt.title(label = """Figure 8:\nBoxplot of Census Year per Country in Arabian Peninsula""") plt.xlabel(xlabel = 'Census Year') # PLOT 8: Malaria Cases impution # Set figure size plt.subplot(18, 2, 8) #18 rows, 2 columns, spot 8 #plot distribution histogram for table without NaN values sns.distplot(a = malariacases dropped['malaria cases'], bins = 2, hist = True, kde = **True**, # activating kde rug = False, color = 'gray') # titles, labels, and formatting plt.title(label = "Figure 12:\nMalaria Cases Distribution\n(With/without imputation of missing value s)") plt.xlabel(xlabel = 'Malaria Cases') plt.ylabel(ylabel = 'Frequency') # histogram for Tuberculosis mortalitY (with imputation) sns.distplot(a = arabian peninsula adj['malaria cases'], bins = 2, hist = True, kde = **True**, # activating kde rug = **False**, color = 'deepskyblue') # this adds a legend plt.legend(labels = ['original distribution', 'imputed distribution']) # PLOT 9: Malaria Cases Outliers # Set figure size plt.subplot(18, 2, 9) #18 rows, 2 columns, spot 9 # developing a boxplot for Malaria Cases sns.boxplot(x = 'malaria cases', # x-variable = None, # optional y-variable hue = None, # optional categorical feature orient = 'h', # horizontal or vertical data = arabian\_peninsula\_adj, # DataFrame where features exist color = "skyblue") # formatting and displaying the plot plt.title(label = 'Figure 13:\n Malaria Cases Outliers') plt.xlabel(xlabel = 'Malaria Cases') # PLOT 10: Tuberculosis Cases Outliers # setting figure size plt.subplot(18, 2, 10) #18 rows, 2 columns, spot 10 # Developing a boxplot for Tuberculosis Cases sns.boxplot(x = 'tuberculosis cases', # x-variable = None, # optional y-variable hue = None, # optional categorical feature orient = 'h', # horizontal or vertical data = arabian\_peninsula\_adj, # DataFrame where features exist color = "skyblue") # Adding a line to signify an outlier threshold plt.axvline(x = 5,color = 'red', linestyle= '--') # Formatting and displaying the plot plt.title(label = 'Figure 14:\nTuberculosis Cases Outliers') plt.xlabel(xlabel = 'Tuberculosis Cases') # PLOT 11: Tuberculosis Mortality Distribution # setting figure size plt.subplot(18, 2, 11) #18 rows, 2 columns, spot 11 # histogram for Tuberculosis Mortality Distribution sns.distplot(a = tuberculosis\_mortality\_dropped['tuberculosis mortality'], bins = 2, hist = True, kde = **False**, rug = False, color = 'gray') # titles and labels plt.title(label = "Figure 15:\nDistribution of Tuberculosis Mortality") plt.xlabel(xlabel = 'Tuberculosis Mortality') plt.ylabel(ylabel = 'Frequency') #vertical lines for mean and median plt.axvline(x = tuberculosis\_mortality\_dropped['tuberculosis mortality'].mean(), color = 'maroon') plt.axvline(x = tuberculosis\_mortality\_dropped['tuberculosis mortality'].median(), color = 'darkorange') #legend plt.legend(labels = ['mean', 'median']) #PLOT 12: Tuberculosis Mortality Distribution Imputed plt.subplot(18, 2, 12) #18 rows, 2 columns, spot 12 # histogram for Tuberculosis mortalitY (without NaN) sns.distplot(a = tuberculosis\_mortality\_dropped['tuberculosis mortality'], bins = 2, hist = True, kde = **True**, # activating kde rug = **False**, color = 'gray') # histogram for Tuberculosis mortality (with imputation) sns.distplot(a = arabian peninsula adj['tuberculosis mortality'], bins = 2, hist = True, kde = **True**, # activating kde rug = **False**, color = 'deepskyblue') # titles, labels, and formatting plt.title(label = "Figure 16:\nTuberculosis Mortality Distribution\n(With/without imputation of missi ng values)") plt.xlabel(xlabel = 'Tuberculosis Mortality') plt.ylabel(ylabel = 'Frequency') # this adds a legend plt.legend(labels = ['original distribution', 'imputed distribution']) **#PLOT 13:** Tuberculosis Mortality Outliers plt.subplot(18, 2, 13) #18 rows, 2 columns, spot 13 # developing a boxplot for Tuberculosis Mortality sns.boxplot(x = 'tuberculosis mortality', # x-variable У = None, # optional y-variable # optional categorical feature hue = None, # horizontal or vertical orient = 'h', data = arabian peninsula adj, # DataFrame where features exist color = "skyblue") # formatting and displaying the plot plt.title(label = 'Figure: 17:\nTuberculosis Mortality Outliers') plt.xlabel(xlabel = 'Tuberculosis Mortality') #PLOT 14: Measles immunization Mean / Median check. plt.subplot(18, 2, 14) #18 rows, 2 columns, spot 14 # Histogram sns.distplot(a = measles immunization dropped['measles immunization'], bins = 'fd', hist = True, kde = False, rug = False, color = 'gray') # Titles and labels plt.title(label = "Figure 18:\nDistribution of Measles Immunization") plt.xlabel(xlabel = 'Measles Immunization') plt.ylabel(ylabel = 'Frequency') # Vertical lines for mean and median plt.axvline(x = measles\_immunization\_dropped['measles immunization'].mean(), color = 'maroon') plt.axvline(x = measles immunization dropped['measles immunization'].median(), color = 'darkorange') # Legend plt.legend(labels = ['mean', 'median']) **#PLOT 15:** Measles Imputation NaN Values Distribution plt.subplot(18, 2, 15) #18 rows, 2 columns, spot 15 # Histogram for Tuberculosis mortalitY (without NaN) sns.distplot(a = measles immunization dropped['measles immunization'], bins = 'fd', hist = True, kde = **True**, # activating kde rug = **False**, color = 'gray') # Histogram (with imputation) sns.distplot(a = arabian peninsula adj['measles immunization'], bins = 'fd', hist = True, kde = **True**, # activating kde rug = **False**, color = 'deepskyblue') # Titles, labels, and formatting plt.title(label = "Figure 19:\n Measles Immunization Distribution\n(With/without imputation of missin g values)") plt.xlabel(xlabel = 'Measles Immunization') plt.ylabel(ylabel = 'Frequency') # This adds a legend plt.legend(labels = ['original distribution', 'imputed (mean) distribution']) # PLOT 16: Measles Imputation Outliers plt.subplot(18, 2, 16) #18 rows, 2 columns, spot 16 # Developing a boxplot for Measles Immunization sns.boxplot(x = 'measles immunization', # x-variable y = None, # optional y-variable
hue = None, # optional categorical feature
orient = 'h', # horizontal or vertical data = arabian\_peninsula\_adj, # DataFrame where features exist color = "skyblue") # Adding a line to signify an outlier threshold plt.axvline(x = 79,color = 'red', linestyle= '--') # Formatting and displaying the plot plt.title(label = 'Figure 20:\nMeasles Immunization Outliers') plt.xlabel(xlabel = 'Measles Immunization') # PLOT 17: Life Expectancy Outliers plt.subplot(18, 2, 17) #18 rows, 2 columns, spot 17 # Developing a boxplot for life expectancy sns.boxplot(x = 'life expectancy', # x-variable = None, # optional y-variable hue = None, # optional categorical feature
orient = 'h', # horizontal or vertical data = arabian\_peninsula\_adj, # DataFrame where features exist color = "skyblue") # Formatting and displaying the plot plt.title(label = 'Figure 21:\nLife Expectancy Outliers') plt.xlabel(xlabel = 'Life Expectancy Age') # PLOT 18: Life Expectancy Outliers plt.subplot(18, 2, 18) #18 rows, 2 columns, spot 18 # Developing a boxplot for life expectancy sns.boxplot(x = 'fertility', # x-variable= None, # optional y-variable hue = None, # optional categorical feature
orient = 'h', # horizontal or vertical data = arabian\_peninsula\_adj, # DataFrame where features exist color = "skyblue") # Formatting and displaying the plot plt.title(label = 'Figure 22:\nFertility Outliers') plt.xlabel(xlabel = 'Fertility Rate') # If you want to display the plots, please change plt.close() to plt.show() at the bottom of the cell plt.close() # PLOT 19: Correlation Aids Deaths, HIV Cases, ART Coverage compared to Populations. #Copy the dataset to determine the correlation. correlation\_hiv\_aids\_coverage = arabian\_peninsula.loc[ : , ['hiv cases', 'aids deaths','art coverage', 'population']].copy() # Dropping null-values (because this cannot be compared) correlation\_hiv\_aids\_coverage = correlation\_hiv\_aids\_coverage.dropna(axis = 0) #Convert data to the right percentage. correlation\_hiv\_aids\_coverage['art coverage'] = correlation hiv aids coverage['art coverage'] /100 # Plot the correlation. # Size for the population  $marker\_size = [10, 15, 20, 25, 30]$ = 'hiv cases', # x-axis feature sns.lmplot(x = 'art coverage', # y-axis feature = 'aids deaths', legend\_out = False, # formats legend if hue != None scatter = True, # renders a scatter plot

fit\_reg = False, # renders a regression line
aspect = 2, # aspect ratio for plot
data = correlation\_hiv\_aids\_coverage, scatter\_kws={'s':marker\_size})# DataFrame where features exist # Formatting and displaying the plot plt.title(label = 'Figure 10:\nCorrelation HIV Cases, Treatment, Aids Deaths') plt.xlabel(xlabel = 'Hiv Cases % of population') plt.ylabel(ylabel = 'Art Coverage % of population') # Reset size for x axis plt.xticks([0.09, 0.10, 0.11]) # If you want to display the plots, please change plt.close() to plt.show() at the bottom of the cell plt.close() ########################## Environment Plot # PLOT 20: CO2 per Top 10 Countries for all regions # Set figure size fig, ax = plt.subplots(figsize=[15, 8]) splot = sns.barplot(data=all regions.sort values(by='co2 emissions', ascending=False).head(n = 11), x='country', y='co2 emissions', orient='v', color='grey') for p in splot.patches: splot.annotate(format(p.get\_height(), '.0f'),  $(p.get_x() + p.get_width() / 2., p.get_height()),$ ha='center', va='center', xytext=(0, 6),textcoords='offset points') # titles, labels, and formatting plt.title(label=""" Figure 9:\nTop 10 Countries in terms of CO2 Emissions per Capita""") plt.xlabel(xlabel='Country') plt.xticks(rotation=30) splot.spines['right'].set visible(False) splot.spines['top'].set\_visible(False) splot.spines['left'].set visible(False) splot.axes.yaxis.set visible(False) # If you want to display the plots, please change plt.close() to plt.show() at the bottom of the cell plt.close() 3. Obscure Findings 3.1 Null Values Figure 3.1 displays the count of null values in the region before dropping or imputations. It is remarkable that PSE and SYR, the countries with a long-lasting history of war, have the most missing values, while CYP and TUR, the two countries which are members/candidates for the EU, have the least missing values. Thus, we flagged these countries as outliers. Outlier 12 United Arab Emirates Frag West Bank and Gaza Syrian Arab Regulatic Figure 3.1: Null values per Country in Arabian Peninsula # Barplot for Null Values per Country (change plt.close() to plt.show to display plot) # If you want to display the plots, please change plt.close() to plt.show() at the bottom of the cell # Set figure size fig, ax = plt.subplots(figsize=[15, 8]) splot = sns.barplot(data=all\_regions\_flagged.loc[arabian\_peninsula\_country\_codes, :].sort\_values(by='mv \_perc', ascend ing=False), x='country', y='mv perc', orient='v', palette='mako') for p in splot.patches: splot.annotate(format(p.get\_height(), '.0f'), (p.get\_x() + p.get\_width() / 2., p.get\_height()), ha='center', va='center', xytext=(0, 6),textcoords='offset points') # labels, and formatting plt.xlabel(xlabel='Country') plt.xticks(rotation=30) plt.ylabel(ylabel='Null % of Total Indicators') plt.axhline(y=31, color='red') plt.axhline(y=14, color='red') splot.spines['right'].set visible(False) splot.spines['top'].set visible(False) splot.spines['left'].set visible(False) splot.axes.yaxis.set\_visible(False) # Save plot as image plt.savefig( fname='./ images/jupyter-exports/null-values-country.png') # If you want to display the plots, please change plt.close() to plt.show() plt.close() 3.2 Accuracy Many of the organizations that collect data rely on government reported information. Due to instability in many of the countries in the Arabian Peninsula, not much information is available. The majority of data gathered are estimates, or collected from the latest census, which varies from 1963 to 2018, making it incomparable. Furthermore, the Weighted Average aggregation method renders some inaccuracy as the weights are unknown and many of the original and external sources consider the most recent reported values. Figure 3.3 exemplifies the difference between weighted average to more recent data, showing that weighted averages increase outliers. Most Recent Year (2017) WA Aggregation Method (1960 to 2020) High income High income Upper middle income Upper middle income Income Group Lower middle income Lower middle income Low income 30 60 Internet Users Internet Users Figure 3.2: Weighted Average Aggregation Criticism In [ ]: # WA Aggregation Method Analysis (change plt.close() to plt.show to display plot) # If you want to display the plots, please change plt.close() to plt.show() at the bottom of the cell # Prepare Data # Import internet\_users original data internet df = pd.read csv(filepath or buffer = "./ datasets/evidence/internet users.csv", = 2) # Join Income Group to internet users internet df = internet df.merge(income group, how = 'inner', left on='Country Code', right on='Code') # Set index to country code and drop unnecessary columns internet df.set index('Code', inplace = True) internet\_df.drop(['Unnamed: 65', 'Country Code'], axis = 1, inplace = True) # Boxplots of Internet Users # Set figure size fig, ax = plt.subplots(figsize = [15, 7]) # Plot the first graph: weighted average plt.subplot(1, 2, 1) # Boxplot for internet users sns.boxplot(x = 'internet users', = 'Income Group', orient = 'h', color = 'skyblue', data = all regions.loc[arabian peninsula country codes, :]) # titles and labels plt.title(label = """WA Aggregation Method (1960 to 2020)""", pad = 20.0)plt.xlabel(xlabel = 'Internet Users') plt.ylabel(ylabel = 'Income Group') # Plot the second graph: cellular subscriptions plt.subplot(1, 2, 2) # Boxplot for cellular subscriptions = '2017', sns.boxplot(x = 'Income Group', orient = 'h', = 'skyblue', color data = internet df.loc[arabian peninsula country codes, '2017':]) # titles, labels, and formatting plt.title(label = """Most Recent Year (2017)""", pad = 20.0)plt.xlabel(xlabel = 'Internet Users') plt.ylabel(ylabel = 'Income Group') #compile and display the plot plt.tight layout(pad = 5.0)# If you want to display the plots, please change plt.close() to plt.show() plt.close() 3.3 Correlations Figure 3.3 suggests three obscure correlations between indicators: 1. The high correlation between GNI per capita and CO2 emissions (0.9) is driven by the significant oil reserves, and the correlated energy production in the region (Al-mulali, 2011). 2. The strong negative correlation between life expectancy and fertility (-0.79) refers to the evolutionary trade-off between reproduction and body maintenance. Fertility comes at the cost of the mother: the process of birthing and raising many children is demanding and can have negative effects on womens' health and lifespan (Liefbroer, et al., 2015). 3. The identified positive correlation between malaria cases and tuberculosis mortality (0.92) cannot be verified by external sources. We assume, the correlation formed due to the high numbers of Yemen in both indicators, a country reported as an outlier within the health section. - 1.0 - 0.8 -0.48 0.9 0.55 0.58 -0.24 co2 emissions -0.58 0.62 -0.481 -0.45-0.66 -0.79 -0.510.05 -0.28- 0.6 gni per capita 0.9 -0.58 1 0.68 -0.26-0.45 1 -0.370.69 0.59 0.66 -0.61 -0.65 measles immunization - 0.4 1 -0.4 -0.62 0.56 -0.38 0.68 tuberculosis cases - 0.2 0.58 -0.66 0.68 0.69 -0.4 1 0.71 0.72 -0.38 -0.51 -0.79 0.59 0.71 0.56 -0.71 -0.83 -0.62 1 life expectancy - 0.0 cellular subscriptions -0.51 0.66 -0.350.72 0.56 1 -0.38-0.371 - -0.2 parliament seats (f) -0.25 -0.61 0.56 -0.38 -0.71 -0.38 -0.37 1 -0.18 0.92 malaria cases - -0.4 -0.28 -0.38 1 international trade 0.62 -0.65 0.68 0.92 tuberculosis mortality -0.3 -0.51 -0.83-0.37 - -0.6 uberculosis mortality internet users cellular subscription ьe Figure 3.3: Correlation Heat map for considered indicators. In [ ]: # Heatmap for considered indicators (change plt.close() to plt.show to display plot) # If you want to display the plots, please change plt.close() to plt.show() at the bottom of the cell # Create list of considered indicators for easy referencing considered indicators = ['co2 emissions', 'fertility', 'gni per capita', 'measles immunization', 'tuberculosis cases', 'internet users', 'life expectancy', 'cellular subscriptions', 'parliament seats (f)', 'malaria cases', 'international trade', 'tuberculosis mortality'] # converting correlation matrix into a DataFrame cons\_indicators\_corr = arabian\_peninsula\_adj.loc[:, considered\_indicators].corr(method = 'pearson').rou nd(decimals = 2)# specifying plot size (making it bigger) fig, ax = plt.subplots(figsize=(12,12)) # developing a spicy heatmap sns.heatmap(data = cons\_indicators\_corr, # the correlation matrix = 'mako', cmap robust = True, square = True, = True, annot linecolor = 'black', linewidths = 0.25)# title and displaying the plot plt.title(""" Linear Correlation Heatmap for Considered Indicators # If you want to display the plots, please change plt.close() to plt.show() plt.close() 4. Representative Country

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# Display only Arabian Peninsula and World Figures # Canadia Town on the Arabian peninsula and World Figures # Set column names for the transposed data frame # Arabia Town World columns = ("AR", "MED") # set column names for the transposed data frame # Arabia Town World columns = ("AR", "MED") # set column names for the transposed data frame # Arabia Town World columns = ("AR", "MED") # add the indicator names as a column # Arabia Town World Interest (100 = 0, column = 'considered indicators ## # Calculate difference to world and rank indicators ## # Calculates the average distranse abusen world and region # # Calculates the average distranse abusen world and region # # Calculates the average distranse abusen world and region # # Calculates the average distranse abusen world and region # # Calculates the average distranse abusen world and region # # Calculates the average distranse abusen world and region # # Calculates the average distranse abusen # # Calculates the average distranse abusen # # World Note: "# Arabia Town Town Town Town Town Town Town Town
arabia_vw_world.column = ["AP", "Wint"]  # add tha indicator names as a column arabia_vw_world.innert (loc = 0, column = 'considered indicators', value = considered_indicator  ## Calculate difference to world and rank indicators ##  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Calculate the swrapp distance between world and region  ## Distance of the swrapp distance between the swrapp distance in the swrapp
arabla_vs_world('evg difference') = abe((arabla_vs_world.loo(); "AP") = arabla_vs_world.loo(); "AP") = arabla_vs_world.loo(); "AP") = arabla_vs_world.loo(); "AP") = arabla_vs_world('rank') = arabla_vs_world.loo('; ';').sort_values (by = 'rank') = arabla_vs_world.loo('; ';').sort_values (by = 'rank') = arabla_vs_world.loo('; ';').sort_values (by = 'rank') = arabla_vs_world.sort_values (by = 'rank') = arabla_vs_w
# If you want to display the plots, please change plt.close() to plt.show() at the bottom of the set figure size fig. ax = plt.subplots(figsize=[15, 8]) plt.subplot(1, 1, 1)  # lst row, lst column, lst space splot = sns.barplot(data=arabia_vs_world.sort_values(by='rank', ascending=True),
x='avg difference', y= 'considered indicators', orient='h', palette='mako')  for p in splot.patches: splot.annotate("%.2f" % p.get_width(), (p.get_x() + p.get_width(),
(p.get_x()) + p.get_width(),
splot.spines['top'].set_visible(False) splot.spines['top'].set_visible(False) splot.spines['bottom'].set_visible(False) splot.axes.xaxis.set_visible(False)  # Save plot as image #plt.savefig(fname='./_images/jupyter-exports/indicator_rank.png')  # If you want to display the plots, please change plt.close() to plt.show() plt.close()  6. Conclusion  Our region shines in diversity. Some countries face on-going civil war, others are economically prosperous due to their reserves.  We explored 41 indicators and determined that only 12 revealed meaningful insights (chapter 2). This was due to a variobscure findings regarding null values, data accuracy, and indicator correlations (chapter 3).  Afterwards, we determined Oman as the best representative of the Arabian Peninsula based on a statistical analysis rearound each indicator mean (chapter 4).  Lastly, we compared & contrasted the mean of each indicator for both the Arabian Peninsula and the world. We identific differentiating indicators for the Arabian Peninsula (chapter 5):  1. Tuberculosis mortality 2. Tuberculosis mortality 2. Tuberculosis cases 3. CO2 emissions 4. GNI per capita 5. Parliament seats held by women  These indicators should be closely monitored by the countries of the region to develop future strategies for the triple by
# IF you want to display the plots, please change plt.close() to plt.show() plt.close()  6. Conclusion  Our region shines in diversity. Some countries face on-going civil war, others are economically prosperous due to their reserves.  We explored 41 indicators and determined that only 12 revealed meaningful insights (chapter 2). This was due to a variobscure findings regarding null values, data accuracy, and indicator correlations (chapter 3).  Afterwards, we determined Oman as the best representative of the Arabian Peninsula based on a statistical analysis rearound each indicator mean (chapter 4).  Lastly, we compared & contrasted the mean of each indicator for both the Arabian Peninsula and the world. We identific differentiating indicators for the Arabian Peninsula (chapter 5):  1. Tuberculosis mortality 2. Tuberculosis cases 3. CO2 emissions 4. GNI per capita 5. Parliament seats held by women  These indicators should be closely monitored by the countries of the region to develop future strategies for the triple by
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<ol> <li>Tuberculosis cases</li> <li>CO2 emissions</li> <li>GNI per capita</li> <li>Parliament seats held by women</li> </ol> These indicators should be closely monitored by the countries of the region to develop future strategies for the triple be compared to the region to develop future strategies for the triple be countries.
These indicators should be closely monitored by the countries of the region to develop future strategies for the triple by