COVID-19 Situation in Spain

Libraries

4 cells hidden

Data loading and general overview

First, we will load the csv file from the offical Spanish goverment site which as we said is updated eve

Spanish government website (updated every 24 hours) The data can be automatically downloaded fr
saved in our dataframe called data.

16 cells hidden

Plotting

```
aux = total_s.melt(id_vars="Date", value_vars=("Cases","Infected","TestAc+","Deaths","ICU","H
aux.head()
```

	Date	Description	Count
0	2020-02-20	Cases	0.0
1	2020-02-21	Cases	0.0
2	2020-02-22	Cases	0.0
3	2020-02-23	Cases	0.0
4	2020-02-24	Cases	0.0

```
data_infected = data[data.Date>"20-02-2020"]
```

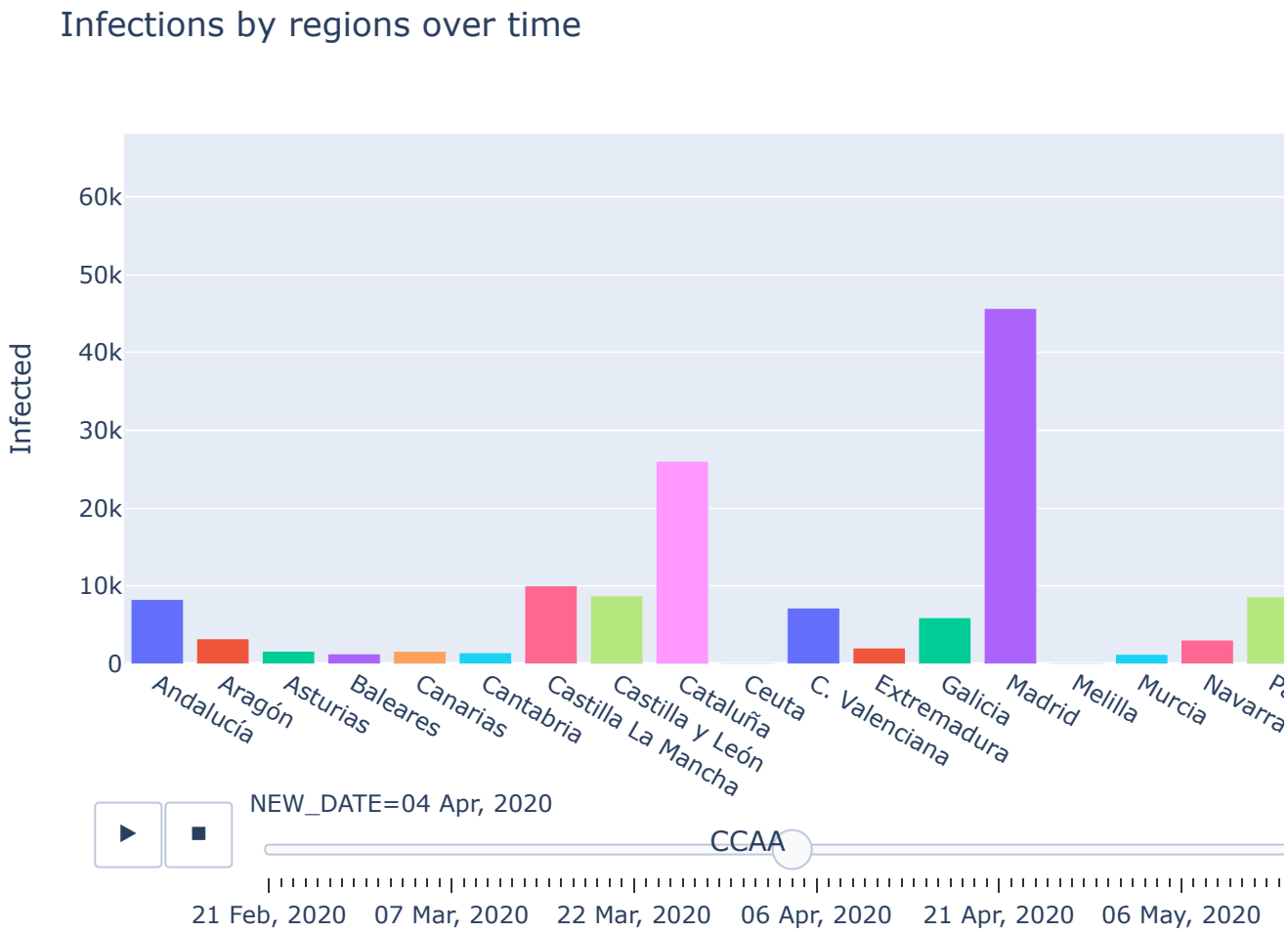
Infections over time

```
fig = px.bar(data_infected, x="CCAA", y="Infected", color="CCAA",
             animation_frame="NEW_DATE", animation_group="CCAA", range_y=[0,data.Infected.ma
fig.show()
```

```
    daily.insert(0,0)

    exec('df_{}["Daily_deaths"] = daily'.format(a))



df_daily_infected = pd.DataFrame({"Date":data.Date.unique(),
                                  "Madrid":df_Madrid["Daily_infected"].values,
                                  "Cataluña":df_Cataluña["Daily_infected"].values,
                                  "Andalucia":df_Andalucía["Daily_infected"].values,
                                  "Castilla La Mancha":df_Castilla_La_Mancha["Daily_infected"]
                                  "Castilla y Leon":df_Castilla_y_León["Daily_infected"].value
                                  "País Vasco":df_País_Vasco["Daily_infected"].values})


aux_i = df_daily_infected.melt(id_vars="Date", value_vars=("Madrid","Cataluña","Andalucia","C
```

Daily infections in Top 6 countries

```
aux_1=aux_i[aux_i.Date>"20-02-2020"]


aux_2=aux_i[aux_i.Date>"18-04-2020"]
fig = px.bar (aux_2, x= "Date", y = "Count", color="CCAA", title= "Daily infections in Spain
fig.show()
```



Analysis of Madrid

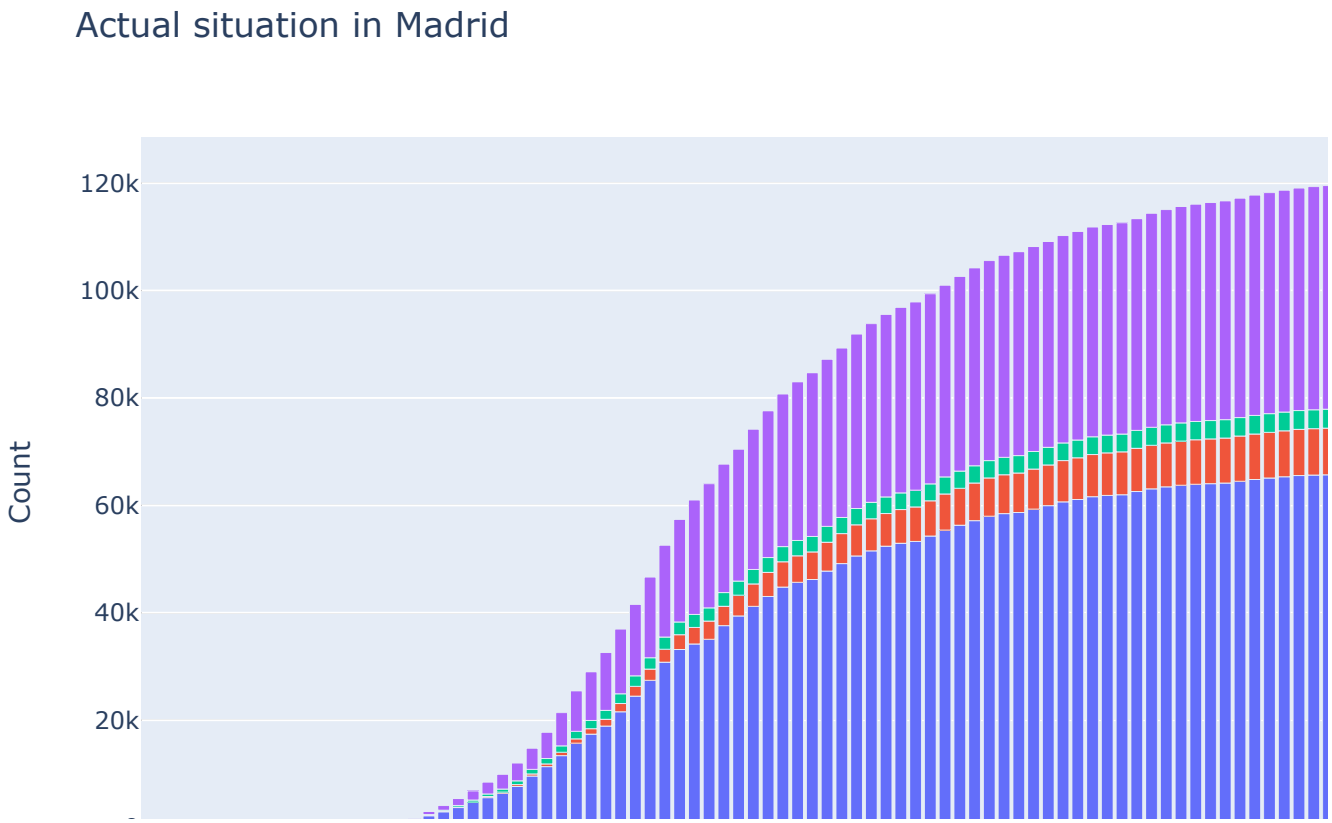
Madrid was the region with the highest number of infections and deaths. In the following graphics we
variables. The cases related to infections were collected in the variable PCR+ (Infected), we can just
Madrid.

```
total_madrid = data[data.CCAA=="Madrid"].groupby("Date")["Date","Infected","Deaths","Hospital
```

```
aux_m = total_madrid.melt(id_vars="Date", value_vars=("Infected","Deaths","ICU","Hospitalizec
```

```
fig = px.bar(aux_m, x= "Date", y = "Count", color="Status", title= "Actual situation in Madri
fig.show()
```

```
 'GA':'Galicia',
 'MD':'Madrid',
 'ML':'Melilla',
 'MC':'Murcia',
 'NC':'Navarra',
 'PV':'País Vasco',
 'RI':'La Rioja'
 }


 d_ccaa = {
 'Andalucía': 'Andalucía',
 'Aragón': 'Aragón',
 'Asturias': 'Principado de Asturias',
 'Baleares': 'Islas Baleares',
 'Canarias': 'Islas Canarias',
 'Cantabria':'Cantabria',
 'Castilla La Mancha': 'Castilla-La Mancha',
 'Castilla y León': 'Castilla y León',
 'Cataluña': 'Cataluña',
 'Ceuta': 'Ceuta y Melilla',
 'C. Valenciana': 'Comunidad Valenciana',
 'Extremadura': 'Extremadura',
 'Galicia': 'Galicia',
 'Madrid': 'Comunidad de Madrid',
 'Melilla': 'Ceuta y Melilla',
 'Murcia': 'Región de Murcia',
 'Navarra': 'Comunidad Foral de Navarra',
 'País Vasco': 'País Vasco',
 'La Rioja': 'La Rioja'
 }


 d_ccaa_id = {
 'Andalucía': "1",
 'Aragón' : "2",
 'Principado de Asturias': "3",
 'Islas Baleares': "4",
 'Islas Canarias': "5",
 'Cantabria': "6",
 'Castilla-La Mancha': "7",
 'Castilla y León': "8",
 'Cataluña': "9",
 'Ceuta y Melilla': "10",
 'Comunidad Valenciana': "11",
 'Extremadura': "12",
 'Galicia': "13",
 'Comunidad de Madrid' : "14",
 'Ceuta y Melilla': "15",
 'Región de Murcia': "16",
 'Comunidad Foral de Navarra': "17",
 'País Vasco': "18",
```




```
for i in data.CCAA.unique():

    a = i.replace(".","")
    a = a.replace(" ","_")

    exec('df_{}=data[data.CCAA == i]'.format(a))

    exec('aux_a = df_{}.Infected.to_list()'.format(a))


    daily=[]
    for i in range(len(aux_a)-1):
        b = aux_a[i+1] - aux_a[i]
        daily.append(b)

    daily.insert(0,0)

    exec('df_{}["Daily_infected"] = daily'.format(a))

    exec('aux_d = df_{}.Deaths.to_list()'.format(a))


    daily=[]
    for i in range(len(aux_d)-1):
        b = aux_d[i+1] - aux_d[i]
        daily.append(b)
```

```
'La Rioja': "19"
}



d_ccaa_population = {
'Andalucía': 8414240,
'Aragón' : 1319291,
'Principado de Asturias': 1022800,
'Islas Baleares': 1149460,
'Islas Canarias': 2153389,
'Cantabria': 581078,
'Castilla-La Mancha': 2032863,
'Castilla y León': 2399548,
'Cataluña': 7675217,
'Ceuta y Melilla': 171264,
'Comunidad Valenciana': 5003769,
'Extremadura': 1067710,
'Galicia': 2699499,
'Comunidad de Madrid' : 6663394,
'Ceuta y Melilla': 171264,
'Región de Murcia': 1493898,
'Comunidad Foral de Navarra': 654214,
'País Vasco': 2207776,
'La Rioja': 316798
}


def get_hex_colors(df, data_to_color, cmap = matplotlib.cm.Reds, log = False):

    '''
    This function takes the following arguments
        1. df:pandas DataFrame with the data.
        2. data_to_color: the column name with data based on which we want to create the colc
        3. cmap: colors you want to plot. You can use this to communicate different messages.
                default is matplotlib.cm.Reds
                more about colormaps: https://matplotlib.org/3.1.1/gallery/color/colormap_ref
        3. log: if data has huge outliers, we can create the color map with a logarithic norm
                default is False.

    '''


    cmap = cmap # define the color pallete you want. You can use Reds, Blues, Greens etc
    my_values = df[data_to_color] # get the value you wan to convert to colors

    mini = min(my_values) # get the min to normalize
    maxi= max(my_values) # get the max to normalize

    LOGMIN = 0.01 # arbitrary lower bound for log scale

    if log:
        norm = matplotlib.colors.LogNorm(vmin=max(mini,LOGMIN), vmax=maxi) # normalize log da
```

```
    else:
        norm = matplotlib.colors.Normalize(vmin=mini, vmax=maxi) # create a color range

    colors = {value:matplotlib.colors.rgb2hex(cmap(norm(value))[:3]) for value in sorted(list

    return colors


def get_hex_colors_2(value, cats):
    '''
    Color paletter used from this website:

    https://colorbrewer2.org/#type=sequential&scheme=Reds&n=9

    The color selection will be based on the percentile each value is in.
    '''
    if value == 0:
        return "#FFFFFF"
    elif value in cats[0]:
        return "#fff5f0"
    elif value in cats[1]:
        return "#fee0d2"
    elif value in cats[2]:
        return "#fcbba1"
    elif value in cats[3]:
        return "#fc9272"
    elif value in cats[4]:
        return "#fb6a4a"
    elif value in cats[5]:
        return "#ef3b2c"
    elif value in cats[6]:
        return "#cb181d"
    elif value in cats[7]:
        return "#a50f15"
    elif value in cats[8]:
        return "#67000d"
    else:
        return "#000000"


df = pd.read_csv("https://covid19.isciii.es/resources/serie_historica_acumulados.csv",delimit


df.rename(columns = {"FECHA":"DATE",
                     "CASOS":"CASES",
                      "PCR+":"TOTAL_INFECTED",
                     "Hospitalizados":"REQUIERED_HOSPITALIZATION",
                     "UCI":"REQUIERED_ADVANCED_CARE",
                     "Fallecidos":"TOTAL_DEATHS"}, inplace = True)

df.fillna(0, inplace = True)
df["CCAA"] = df["CCAA"].map(d_name)
```

Daily infections in Spain (Top 6)

Daily deaths in Top 6 countries

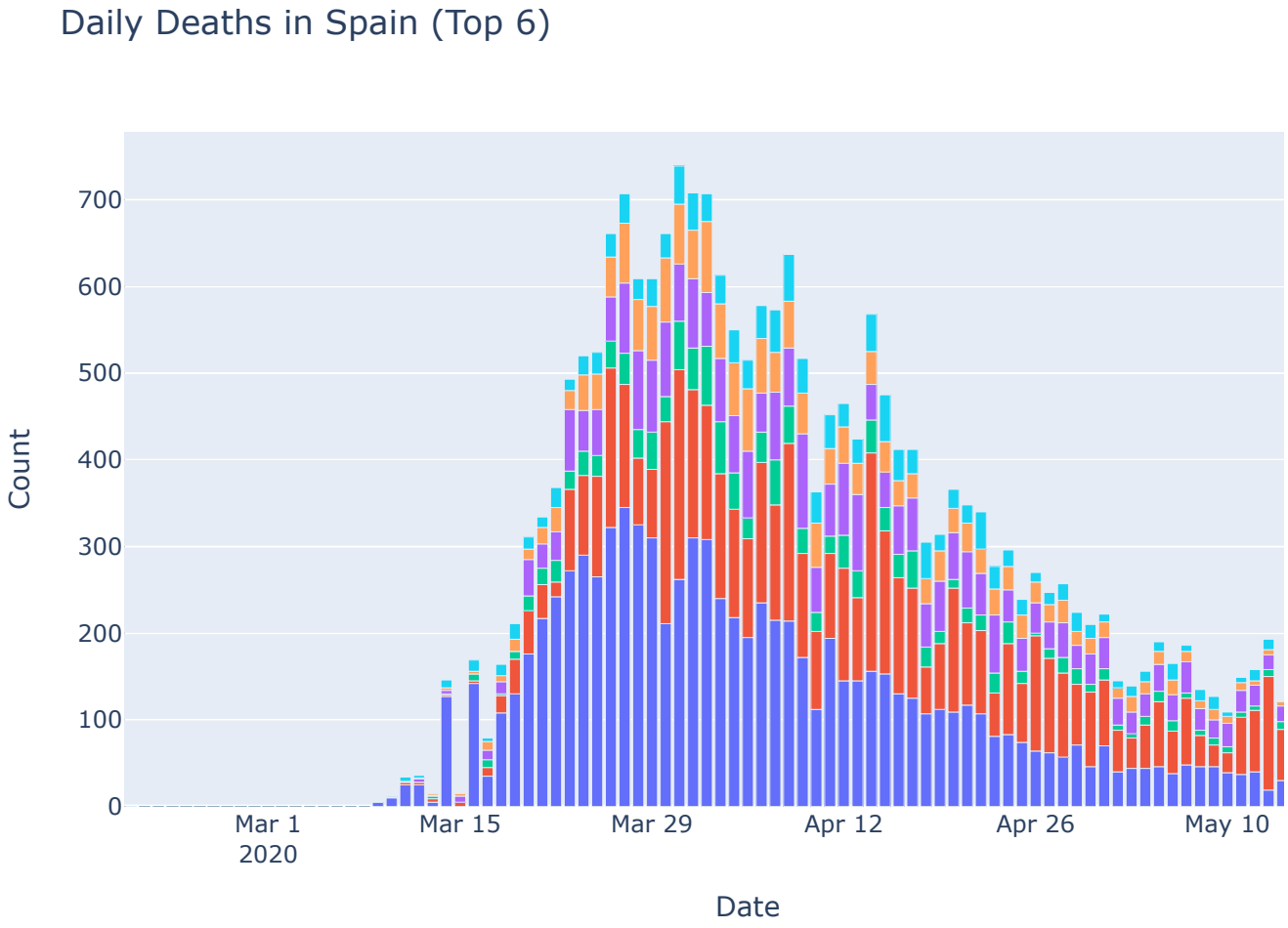
```
df_daily_fatalities = pd.DataFrame({"Date":data.Date.unique(),
                                    "Madrid":df_Madrid["Daily_deaths"].values,
                                    "Cataluña":df_Cataluña["Daily_deaths"].values,
                                    "Valencia":df_C_Valenciana["Daily_deaths"].values,
                                    "Castilla La Mancha":df_Castilla_La_Mancha["Daily_deaths"].v
                                    "Castilla y Leon":df_Castilla_y_León["Daily_deaths"].values,
                                    "País Vasco":df_País_Vasco["Daily_deaths"].values})
```

```
aux_f = df_daily_fatalities.melt(id_vars="Date", value_vars=("Madrid","Cataluña","Valencia",'
```

```
fig = px.line (aux_f, x= "Date", y = "Count", color="CCAA", title= "Daily Death in Spain (Top
fig.show()
```

```
data_to_color = "TOTAL_DEATHS"
cats, bins =  pd.qcut(df[data_to_color].unique()[np.argsort(df[data_to_color].unique())], q =
cats = cats.unique()

#-------------------------------------------------------------------------------

# value we will iterate in order to create the styledict
ccaas = list(df["id"].unique())
dates = list(df["DATE_for_Folium"].unique())

# create the color dict and color column
df["COLORS"] = df[data_to_color].apply(get_hex_colors_2, args = [cats]) # we create a colum i

# creates the styledict for the map
styledict = {}

# iterate the populate the styledict
for ccaa in ccaas:
    styledict[str(ccaa)] = {date: {'color': df[(df["id"] == ccaa) & (df["DATE_for_Folium"] ==
                                   'opacity': 0.6} for date in dates}

# creates and renders the Folium map
m = folium.Map(location=(40, 0), tiles='OpenStreetMap', zoom_start=6)

g = TimeSliderChoropleth(
    gdf.set_index("id").to_json(), # get's the coordinates for each id
    styledict = styledict # styledict contains for each id the timestamp and the color to plc
)

m.add_child(g)

#-----------------------------------------------------------------------------------------
# Let's create a legend for folium
# https://nbviewer.jupyter.org/gist/talbertc-usgs/18f8901fc98f109f2b71156cf3ac81cd

from branca.element import Template, MacroElement

template = """
{% macro html(this, kwargs) %}

<!doctype html>
<html lang="en">
<head>
  <meta charset="utf-8">
  <meta name="viewport" content="width=device-width, initial-scale=1">
  <title>jQuery UI Draggable - Default functionality</title>
  <link rel="stylesheet" href="//code.jquery.com/ui/1.12.1/themes/base/jquery-ui.css">

  <script src="https://code.jquery.com/jquery-1.12.4.js"></script>
  <script src="https://code.jquery.com/ui/1.12.1/jquery-ui.js"></script>
```

```
fig = px.bar (aux_f, x= "Date", y = "Count", color="CCAA", title= "Daily Deaths in Spain (Top
fig.show()
```



Mapping with chloropleth

```
d_name = {
'AN':'Andalucía',
'AR':'Aragón',
'AS':'Asturias',
'IB':'Baleares',
'CN':'Canarias',
'CB':'Cantabria',
'CM':'Castilla La Mancha',
'CL':'Castilla y León',
'CT':'Cataluña',
'CE':'Ceuta',
'VC':'C. Valenciana',
'EX':'Extremadura',
'GA':'Galicia'
```

```
df["CCAA_for_Folium"] = df["CCAA"].map(d_ccaa)
df["id"] = df["CCAA_for_Folium"].map(d_ccaa_id)

df["Population"] = df["CCAA_for_Folium"].map(d_ccaa_population)
```

```
df["CCAA"].isnull().sum()
```

```
0
```

```
def correct_date(date_str):
    list_dates = date_str.split("/")
    day = list_dates[0]
    month = list_dates[1]
    year = list_dates[2]

    if len(day) == 1:
        day = "0" + day
    if len(month) == 1:
        month = "0" + month

    return "/".join([day, month, year])
```

```
df["NEW_DATE"] = df["DATE"].apply(correct_date)
```

```
df["DATE"] = pd.to_datetime(df["NEW_DATE"], format='%d/%m/%Y')

df["DATE_for_Folium"] = (df["DATE"].astype(int)// 10**9).astype('U10')

df = df[["id", "CCAA", "CCAA_for_Folium", "DATE", "DATE_for_Folium", "TOTAL_INFECTED", "REQU
df["id"].astype(np.int16)
df.head()
```

```
PATH_GEO_JSON = 'shapefiles_ccaa_espana.geojson'
gdf = gpd.read_file(PATH_GEO_JSON)
gdf["id"] = gdf["name_1"].map(d_ccaa_id) # create a numerical id for each ccaa
gdf = gdf[["id", "shape_leng","shape_area","geometry"]] # extract the id and the geometry (cc
gdf["geometry"] = gdf["geometry"].simplify(0.1, preserve_topology = False)
gdf["id"].astype(int)
gdf.head()
```

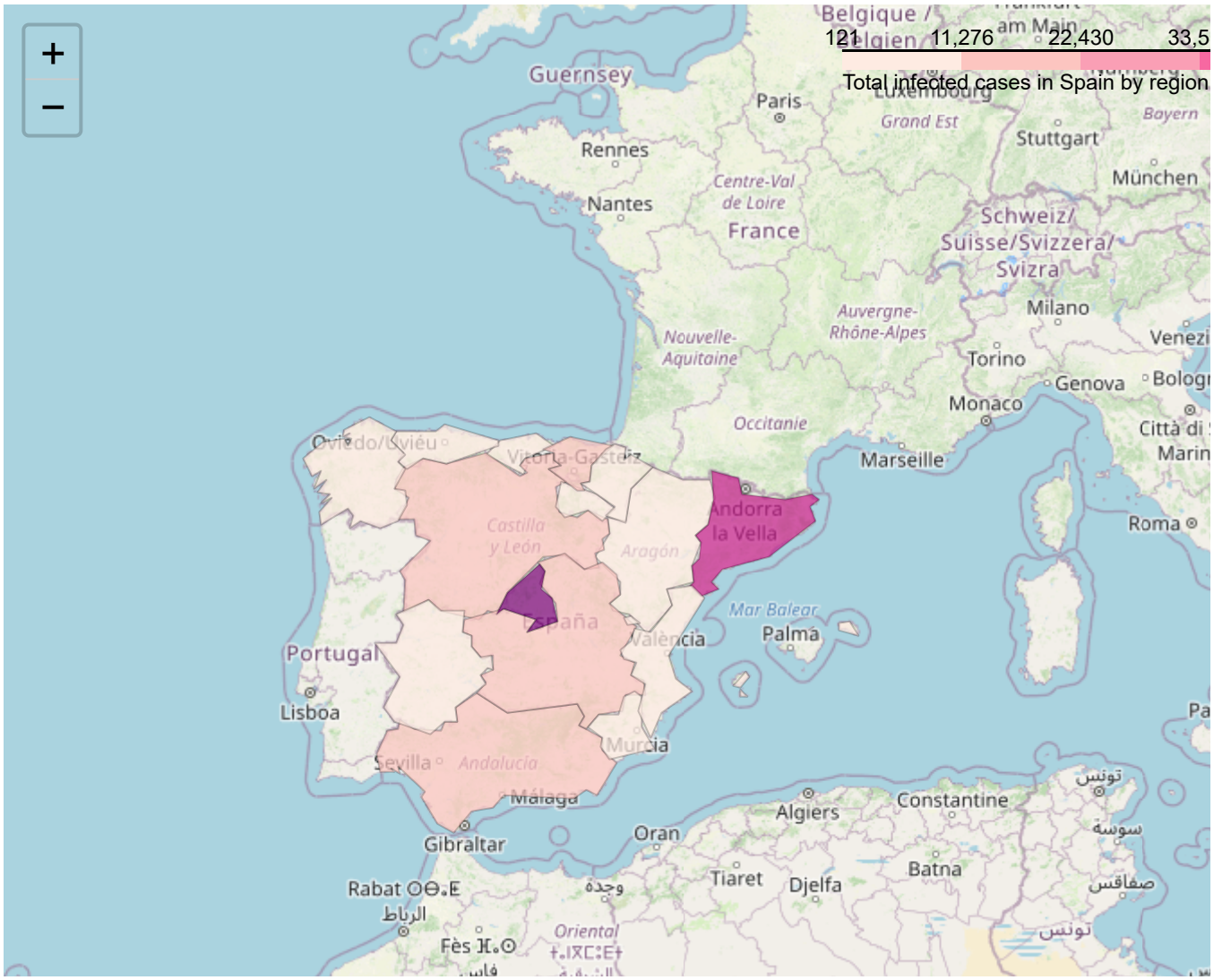
Infections

```
m = folium.Map(location = (40, 0), zoom_start = 5.5)
```

```
      <script>
      $( function() {
        $( "#maplegend" ).draggable({
                        start: function (event, ui) {
                            $(this).css({
                                right: "auto",
                                top: "auto",
                                bottom: "auto"
                            });
                        }
                    });
    });

      </script>
    </head>
    <body>


    <div id='maplegend' class='maplegend'
        style='position: absolute; z-index:9999; border:2px solid grey; background-color:rgba(255
         border-radius:6px; padding: 10px; font-size:14px; right: 20px; bottom: 20px;'>

    <div class='legend-title'>Legend</div>
    <div class='legend-scale'>
      <ul class='legend-labels'>
        <li><span style='background:#FFFFFF;opacity:0.6;'></span>No cases</li>
        <li><span style='background:#fff5f0;opacity:0.6;'></span>1 Quantile</li>
        <li><span style='background:#fee0d2;opacity:0.6;'></span>2 Quantile</li>
        <li><span style='background:#fcbba1;opacity:0.6;'></span>3 Quantile</li>
        <li><span style='background:#fc9272;opacity:0.6;'></span>4 Quantile</li>
        <li><span style='background:#fb6a4a;opacity:0.6;'></span>5 Quantile</li>
        <li><span style='background:#ef3b2c;opacity:0.6;'></span>6 Quantile</li>
        <li><span style='background:#cb181d;opacity:0.6;'></span>7 Quantile</li>
        <li><span style='background:#a50f15;opacity:0.6;'></span>8 Quantile</li>
        <li><span style='background:#67000d;opacity:0.6;'></span>9 Quantile</li>
        <li><span style='background:#000000;opacity:0.6;'></span>Other</li>
      </ul>
    </div>
    </div>

    </body>
    </html>

    <style type='text/css'>
      .maplegend .legend-title {
        text-align: left;
        margin-bottom: 5px;
        font-weight: bold;
        font-size: 90%;
        }
      .maplegend .legend-scale ul {
```

```
      margin: 0;
      margin-bottom: 5px;
      padding: 0;
      float: left;
      list-style: none;
      }
    .maplegend .legend-scale ul li {
      font-size: 80%;
      list-style: none;
      margin-left: 0;
      line-height: 18px;
      margin-bottom: 2px;
      }
    .maplegend ul.legend-labels li span {
      display: block;
      float: left;
      height: 16px;
      width: 30px;
      margin-right: 5px;
      margin-left: 0;
      border: 1px solid #999;
      }
    .maplegend .legend-source {
      font-size: 80%;
      color: #777;
      clear: both;
      }
    .maplegend a {
      color: #777;
      }
  </style>
  {% endmacro %}"""

  macro = MacroElement()
  macro._template = Template(template)

  m.get_root().add_child(macro)
```

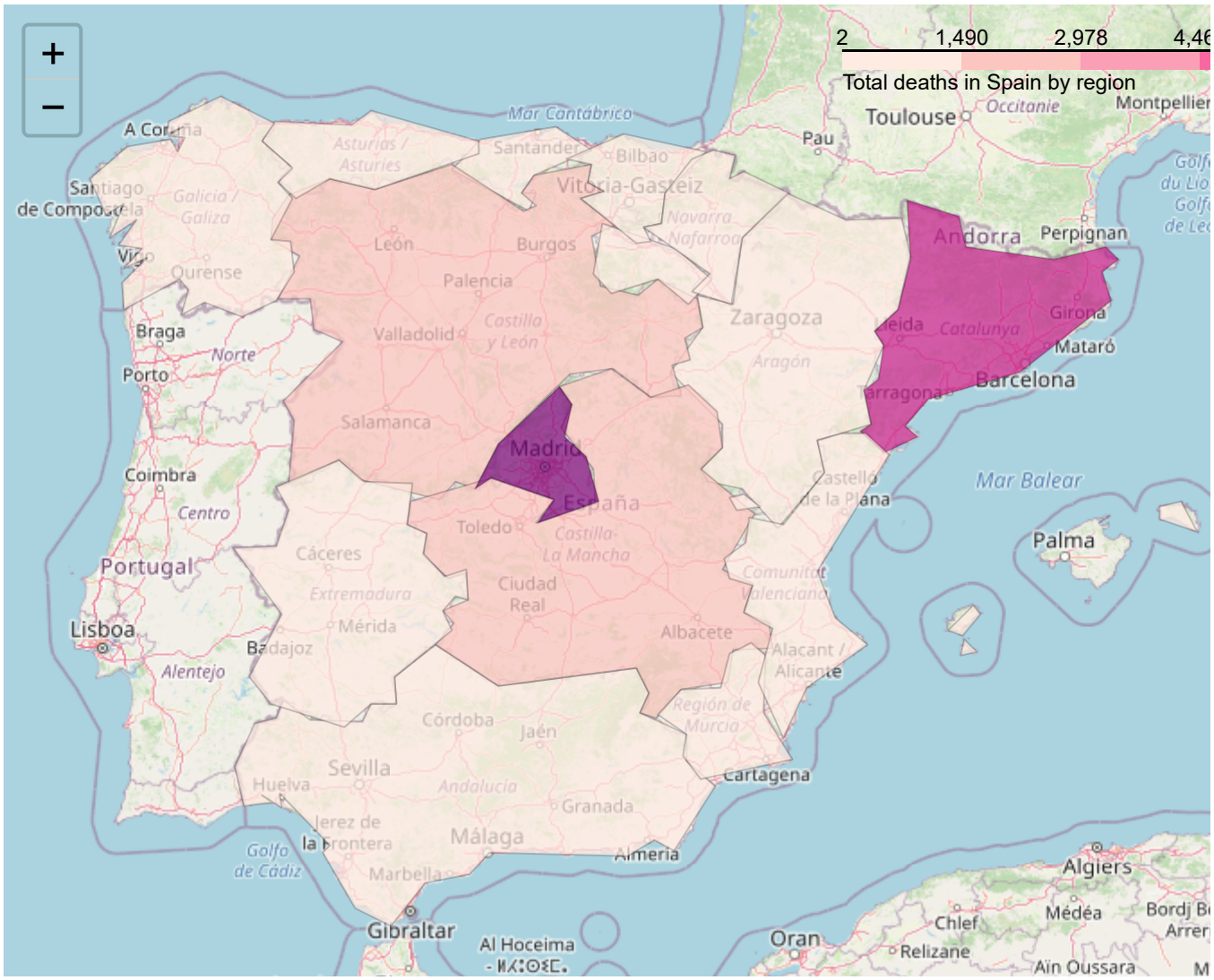
```
folium.Choropleth(
    geo_data = gdf,
    name = 'choropleth',
    data = df[df["DATE"] == max(df["DATE"])],
    columns = ['id', 'TOTAL_INFECTED'],
    key_on='feature.properties.id',
    fill_color='RdPu',
    fill_opacity=0.7,
    line_opacity=0.2,
    legend_name = 'Total infected cases in Spain by region'
).add_to(m)

m
```



Deaths

```
m = folium.Map(location = [40, 0], zoom_start = 5.5)
```

```
m = folium.Map(location = [40, 0], zoom_start = 5.5)

folium.Choropleth(
    geo_data = gdf,
    name = 'choropleth',
    data = df,
    columns = ['id', 'TOTAL_DEATHS'],
    key_on='feature.properties.id',
    fill_color='RdPu',
    fill_opacity=0.7,
    line_opacity=0.2,
    legend_name = 'Total deaths in Spain by region'
).add_to(m)

m
```

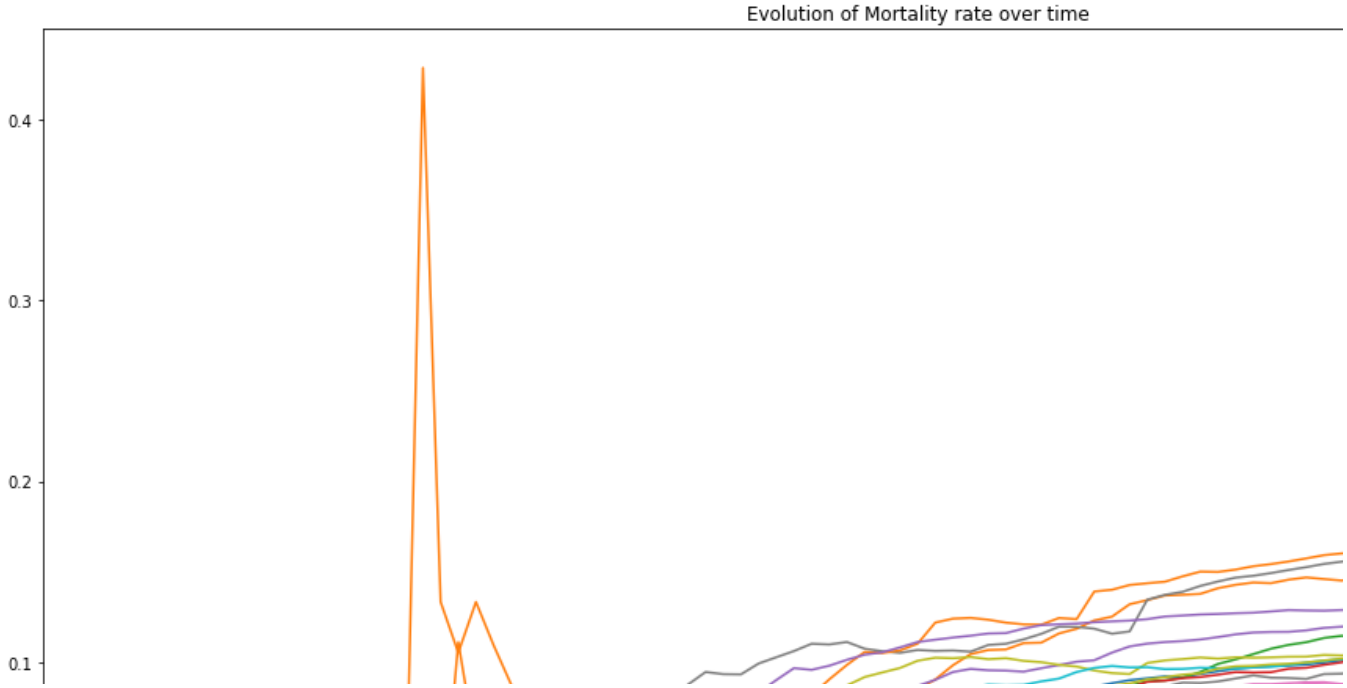


Deaths time slider

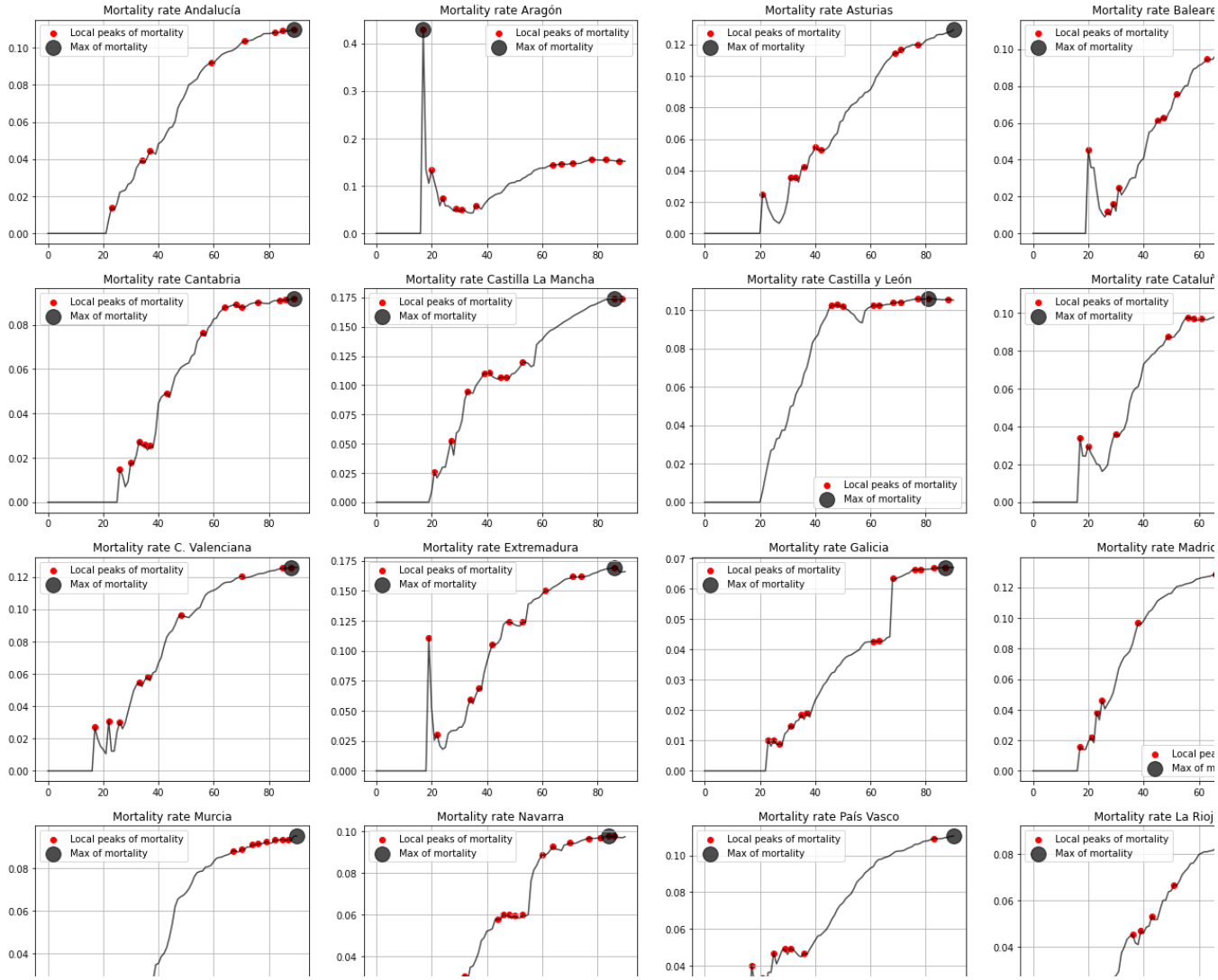
Mortality rate

```
df["Infected_1000h"] = df["TOTAL_INFECTED"]/(df["Population"]/1000)
df["Mortality_rate"] = df["TOTAL_DEATHS"] / df["TOTAL_INFECTED"]
df.fillna(0, inplace = True)
df.tail()
```

```
plt.figure(figsize = (20, 10))

for ccaa in sorted(list(df["CCAA"].unique())):

    x = df["DATE"].unique()
    y = df[df["CCAA"] == ccaa]["Mortality_rate"]

    plt.plot(x, y, label = ccaa)
    plt.title("Evolution of Mortality rate over time")
    plt.legend()
    plt.xticks(rotation=90)
```




```
x = [day for day in range(len(df["DATE"].unique()))]

fig, axes = plt.subplots(nrows=4, ncols=5, figsize=(30,20))
# plt.setp(axes, ylim=(0 ,max(df["Mortality rate"])))
ccaas = list(df["CCAA"].unique())

i = 0

for col_axes in axes:
    for ax in col_axes:
        if i < len(ccaas):
            ccaa = ccaas[i]
            y = df[df["CCAA"] == ccaa]["Mortality_rate"].values

            ipeaks, _ = find_peaks(y)

            ax.plot(x, y, color = "k", alpha = 0.7)
            ax.scatter(ipeaks, np.array(y)[ipeaks], color = "red", label = "Local peaks of mo
            ax.scatter(x[list(y).index(np.max(y))], np.max(y), color = "k", marker = "o", alp

            ax.set_title("Mortality rate {}".format(ccaa))
            ax.legend()
            ax.grid()
            i += 1

fig.delaxes(axes[3, 4])
```

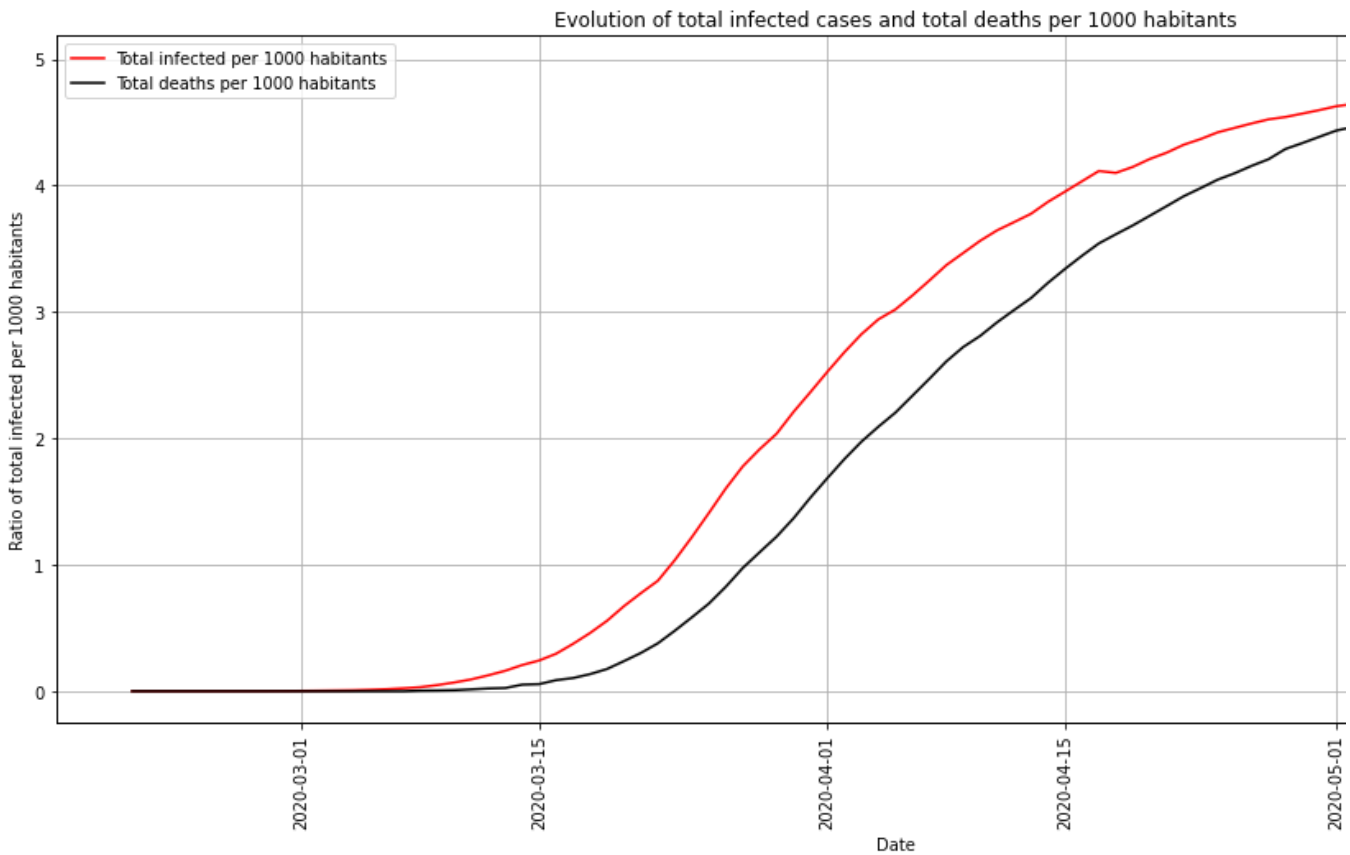


create the pivot table of total cases

```
total_df = df.set_index("DATE").resample("D")[["TOTAL_INFECTED", "REQUIERED_HOSPITALIZATION",
total_df = total_df[total_df["Population"] > 0]
total_df["TOTAL_INFECTED_1000H"] = total_df["TOTAL_INFECTED"]/(total_df["Population"]/1000)
total_df["TOTAL_DEATHS_1000H"] = total_df["TOTAL_DEATHS"]/(total_df["Population"]/1000)

# get the data
x = list(total_df.index)
y_1 = list(total_df["TOTAL_INFECTED_1000H"]) # 1 axis
y_2 = list(total_df["TOTAL_DEATHS_1000H"]) # 2 axis

# create the figures
fig, ax = plt.subplots(figsize = (15, 7))
plot1 = ax.plot(x, y_1, color = "r", label = "Total infected per 1000 habitants") # plot the
plt.xticks(rotation=90) # rotate the date

ax2 = ax.twinx() # create a secondary axis
plot2 = ax2.plot(x, y_2, color = "k", label = "Total deaths per 1000 habitants") # plot the s
fig.tight_layout()
plt.title("Evolution of total infected cases and total deaths per 1000 habitants")
```

```
plt.title("Evolution of total infected cases and total deaths per 1000 habitants")

# create a common legend
lns = plot1 + plot2
labs = [l.get_label() for l in lns]
ax.legend(lns, labs, loc=0)

# prettify
ax.grid()
ax.set_xlabel("Date")
ax.set_ylabel("Ratio of total infected per 1000 habitants")
ax2.set_ylabel("Ratio of total deaths per 1000 habitants")
```

```
Text(998.875, 0.5, 'Ratio of total deaths per 1000 habitants')
```



8 of March manifestation

On 8 of March, the goverment allowed a massive manifestationa all over the country for the internati

By that time, there where already some informed cases, but, we only know what we know. Now, since days to incubate in your body, this means that a person who was on the manifestation and begin to h likely that was already infected or got infected. Let's make this shift in infected cases and see the res

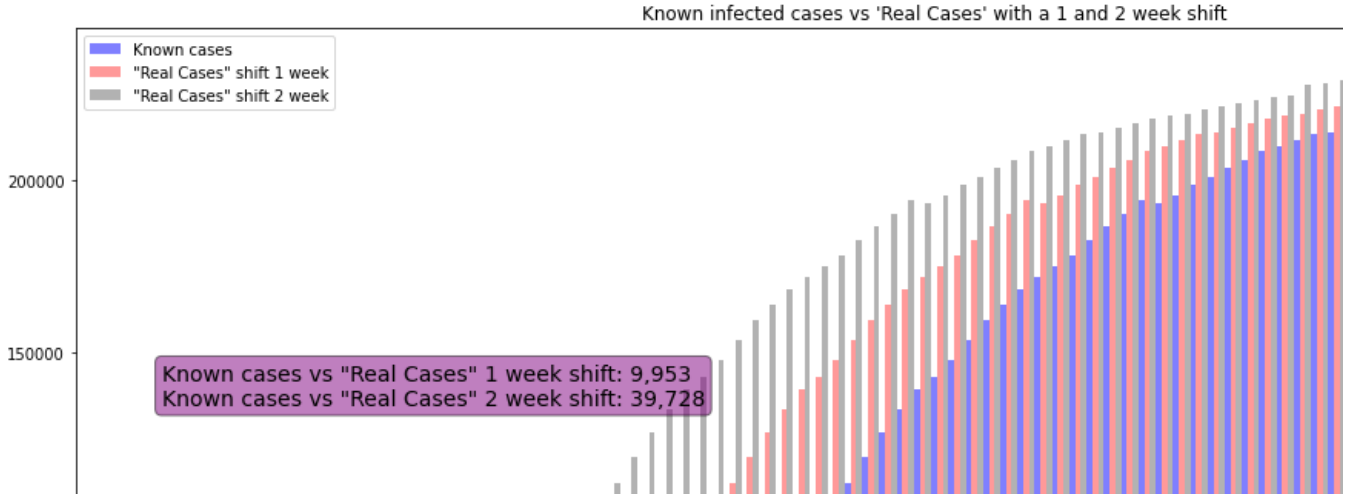
As you can see, when the manifestation was held, it is likely that there was around between 10k anc than the official 1006 cases.

```
total_df["SHIFT_7_DAYS"] = total_df["TOTAL_INFECTED"].shift(-7)
total_df["SHIFT_14_DAYS"] = total_df["TOTAL_INFECTED"].shift(-14)
```

Known infected cases vs 'Real Cases' with a 1 and 2 week shift

```
x = np.array([x for x in range(len(total_df.index))])
y_informed = total_df["TOTAL_INFECTED"]
y_real_7_days = total_df["SHIFT_7_DAYS"]
y_real_14_days = total_df["SHIFT_14_DAYS"]
width = np.min(np.diff(x))/3

fig = plt.figure(figsize = (20, 10))

ax = fig.add_subplot(111)
ax.bar(x - width, y_informed, width, color = 'b', label = 'Known cases', alpha = 0.5)
ax.bar(x, y_real_7_days, width, color = 'r', label = '"Real Cases" shift 1 week', alpha = 0.4
ax.bar(x + width, y_real_14_days, width, color='k', label = '"Real Cases" shift 2 week', alph
ax.set_xlabel('Days since first infected case.')

plt.title("Known infected cases vs 'Real Cases' with a 1 and 2 week shift")
plt.axvline(x=17, lw = 1, alpha = 0.3, ymax = 0.4, color = "purple")
plt.annotate("8 March manifestation held", xy= (15, 80000), color = "purple")

textstr = '\n'.join((
    r'Known cases vs "Real Cases" 1 week shift: {:,.0f}'.format(total_df.iloc[17]["SHIFT_7_DA
    r'Known cases vs "Real Cases" 2 week shift: {:,.0f}'.format(total_df.iloc[17]["SHIFT_14_D

props = dict(boxstyle='round', facecolor='purple', alpha=0.5)

# place a text box in upper left in axes coords
ax.text(0.05, 0.6, textstr, transform=ax.transAxes, fontsize=14,
        verticalalignment='top', bbox=props)

plt.legend()
```

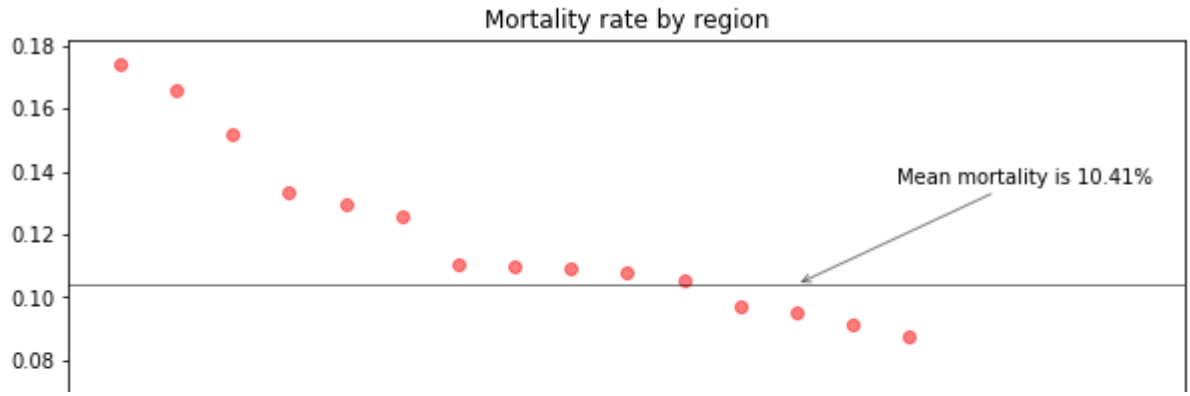
```
<matplotlib.legend.Legend at 0x7fa53a6eaeb8>
```



Mortality rate by region

```
short_df = df[df["DATE"] == max(df["DATE"])][["CCAA", "Mortality_rate"]].sort_values("Mortali
x = short_df["CCAA"]
y = short_df["Mortality_rate"]

mean_y = np.mean(y)
mean_y

plt.figure(figsize = (10, 5))
plt.scatter(x, y, c= "red", alpha = 0.5)
plt.title("Mortality rate by region")

plt.xticks(rotation=90)
plt.axhline(mean_y, c = "k", alpha = 0.5, lw = 1)
plt.annotate('Mean mortality is {}%'.format(round(mean_y * 100, 2)),
             xy=(12, mean_y),
             xycoords='data',
             xytext=(50, 50),
             textcoords='offset points',
             arrowprops=dict(arrowstyle="->", color = "k", alpha = 0.5),
             color = "k")
```

```
Text(50, 50, 'Mean mortality is 10.41%')
```



General Analysis over the time

Data Load

```
infected = pd.read_csv('ccaa_covid19_casos_long.csv')
uci_beds = pd.read_csv('ccaa_camas_uci_2017.csv')
recovered = pd.read_csv('ccaa_covid19_altas_long.csv')
death = pd.read_csv('ccaa_covid19_fallecidos_long.csv')
hospitalized = pd.read_csv('ccaa_covid19_hospitalizados_long.csv')
masks = pd.read_csv('ccaa_covid19_mascarillas.csv')
uci = pd.read_csv('ccaa_covid19_uci_long.csv')
national = pd.read_csv('nacional_covid19.csv')
age_range = pd.read_csv('nacional_covid19_rango_edad.csv')
gdf = gpd.read_file('shapefiles_ccaa_espana.geojson')
```

Coordinates for mapping each CCAA

```
locations = {'Andalucía':[37.38,-5.97],
             'Aragón':[41.64,-0.88],
             'Asturias':[43.36,-5.85],
             'Baleares':[39.57,2.65],
             'Canarias':[28.09,-15.41],
             'Cantabria':[43.46,-3.8],
             'Castilla La Mancha':[38.98,-3.92],
             'Castilla y León':[41.65,-4.77],
             'Cataluña':[41.39,2.17],
             'Ceuta':[35.89,-5.34],
             'C. Valenciana':[39.37,-0.8],
             'Extremadura':[39.71,-6.16],
             'Galicia':[43.12,-8.46],
             'Madrid':[40.49,-3.71],
             'Melilla':[35.29,-2.95],
             'Murcia':[38.00,-1.48],
             'Navarra':[42.66,-1.64],
```

```
             'Navarra':[42.83, 1.64],
             'País Vasco':[43.23,-2.85],
             'La Rioja':[42.27,-2.51]}
```

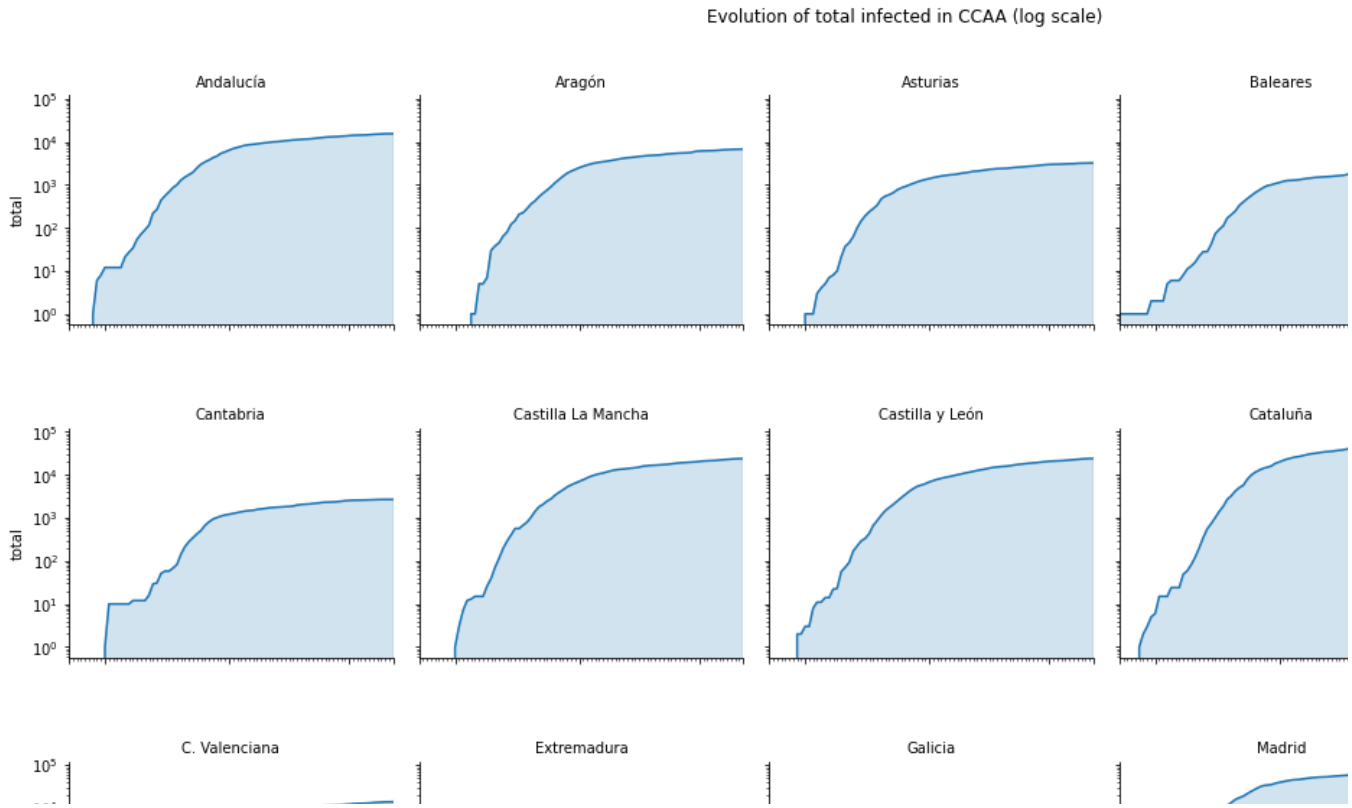
```
def dateplot(x, y, **kwargs):
    ax = plt.gca()
    data = kwargs.pop("data")
    data.plot(x=x, y=y, ax=ax, grid=False, **kwargs)
```

```
infected['fecha'] = pd.to_datetime(infected['fecha'])
hospitalized['fecha'] = pd.to_datetime(hospitalized['fecha'])
uci['fecha'] = pd.to_datetime(uci['fecha'])
recovered['fecha'] = pd.to_datetime(recovered['fecha'])
death['fecha'] = pd.to_datetime(death['fecha'])
```

As the following variables follow an exponential line,the following plots will be displayed using logarit
the lineal trend.

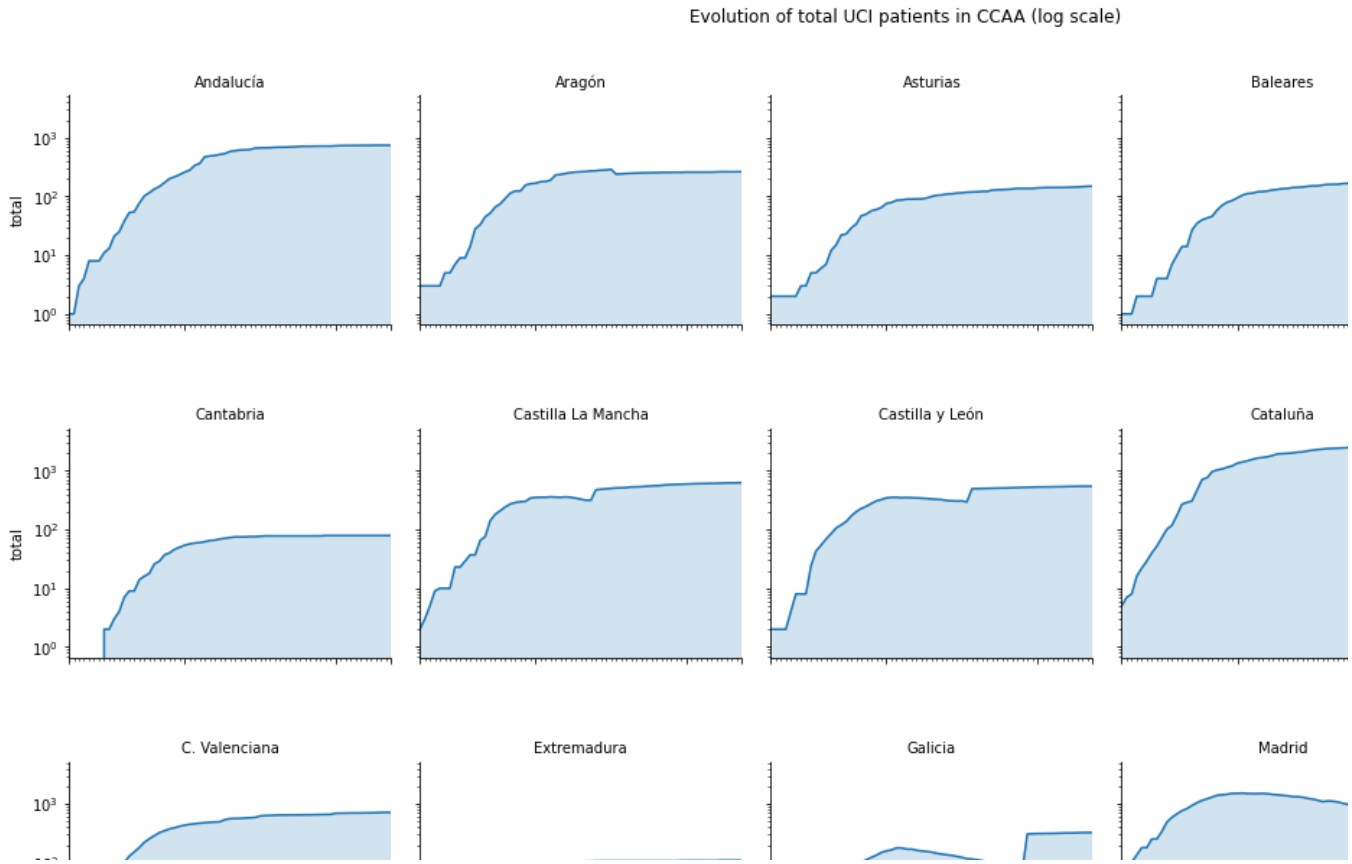
Infected over time

```
infected = infected[infected['CCAA']!= 'Total']
g = sns.FacetGrid(infected, col="CCAA", col_wrap=5, height=3.5)
g = g.map_dataframe(dateplot, "fecha", "total").set(yscale='log')
g = g.map(plt.fill_between, 'fecha', 'total', alpha=0.2).set_titles("{col_name} CCAA")
g = g.set_titles("{col_name}")
plt.subplots_adjust(top=0.92)
g = g.fig.suptitle('Evolution of total infected in CCAA (log scale)')
```



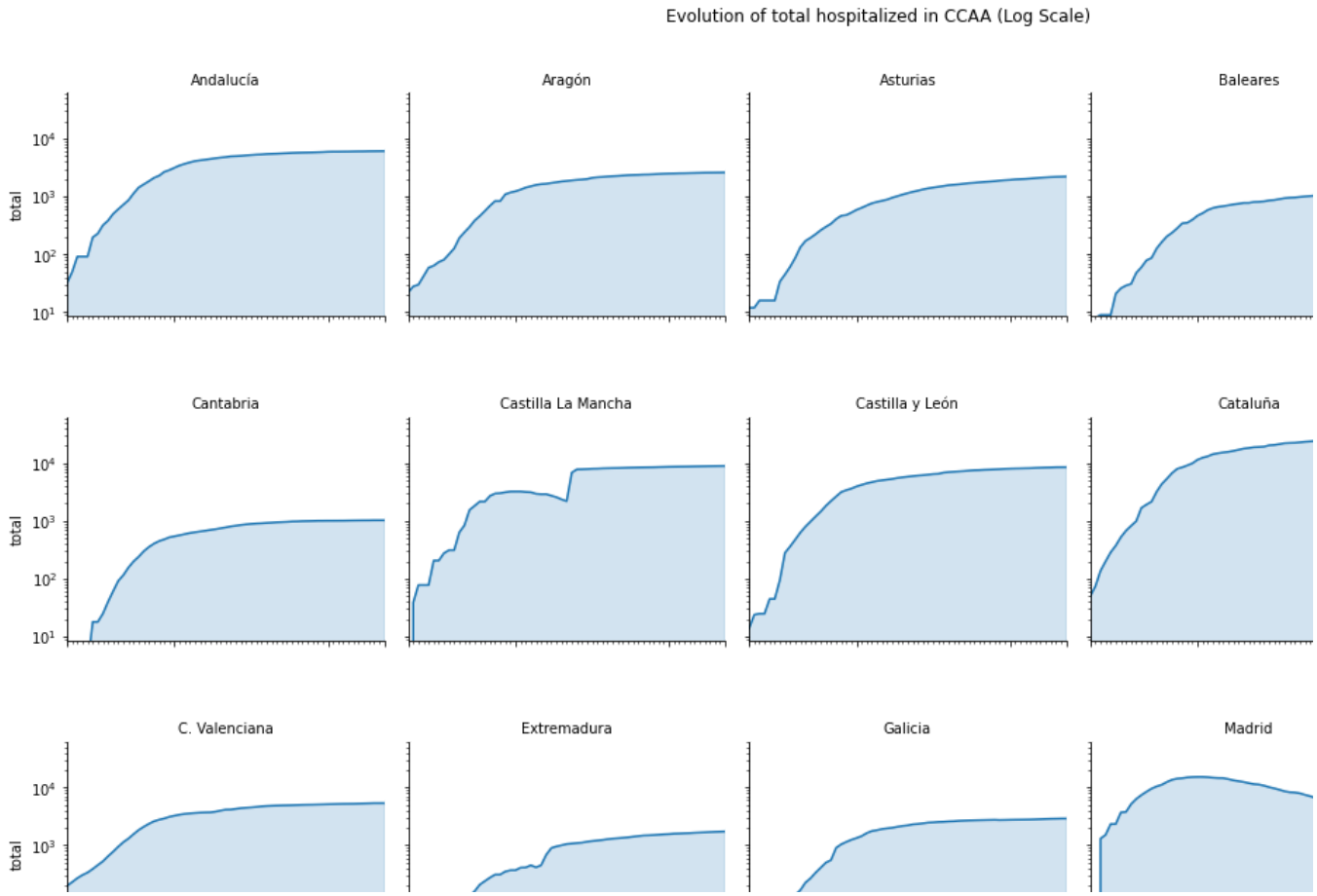
ICU over time

```
uci = uci[uci['CCAA']!= 'Total']
g = sns.FacetGrid(uci, col="CCAA", col_wrap=5, height=3.5)
g = g.map_dataframe(dateplot, "fecha", "total").set(yscale='log')
g = g.map(plt.fill_between, 'fecha', 'total', alpha=0.2).set_titles("{col_name} CCAA")
g = g.set_titles("{col_name}")
plt.subplots_adjust(top=0.92)
g = g.fig.suptitle('Evolution of total UCI patients in CCAA (log scale)')
```



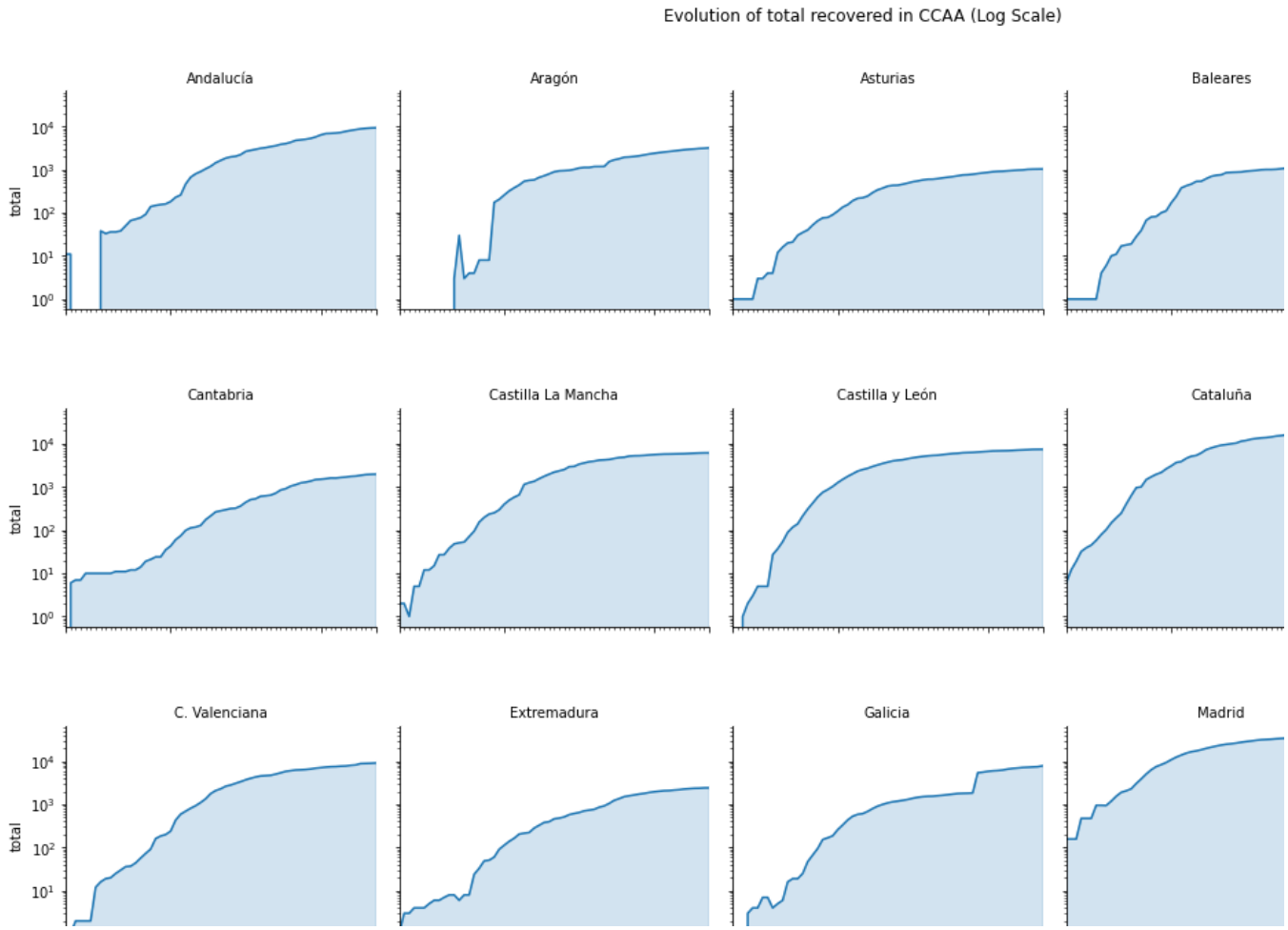
Hospitalized over time

```
hospitalized = hospitalized[hospitalized['CCAA']!= 'Total']
g = sns.FacetGrid(hospitalized, col="CCAA", col_wrap=5, height=3.5)
g = g.map_dataframe(dateplot, "fecha", "total").set(yscale='log')
g = g.map(plt.fill_between, 'fecha', 'total', alpha=0.2).set_titles("{col_name} CCAA")
g = g.set_titles("{col_name}")
plt.subplots_adjust(top=0.92)
g = g.fig.suptitle('Evolution of total hospitalized in CCAA (Log Scale) ')
```



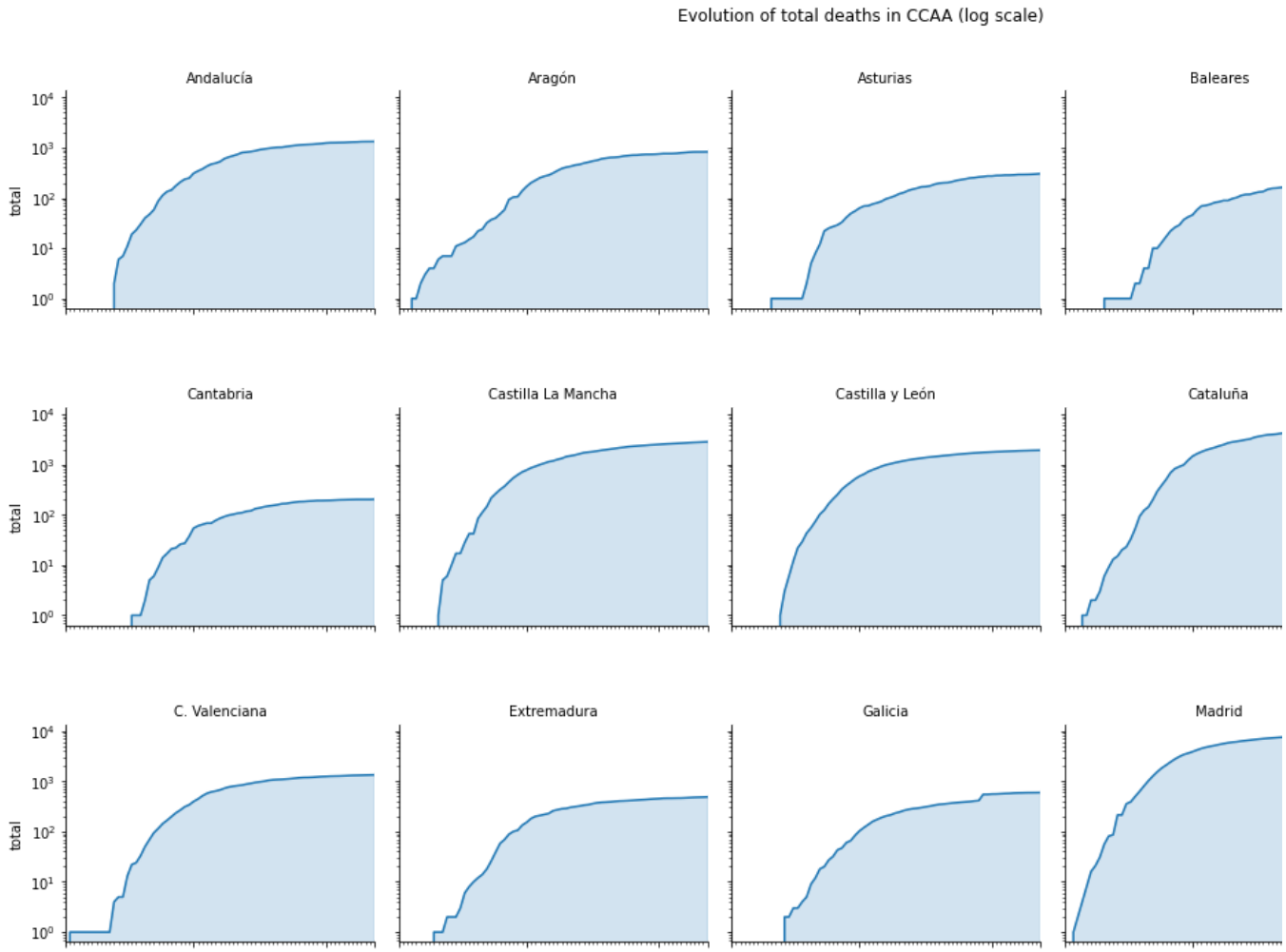
Recovered over time

```
recovered = recovered[recovered['CCAA']!= 'Total']
g = sns.FacetGrid(recovered, col="CCAA", col_wrap=5, height=3.5)
g = g.map_dataframe(dateplot, "fecha", "total").set(yscale='log')
g = g.map(plt.fill_between, 'fecha', 'total', alpha=0.2).set_titles("{col_name} CCAA")
g = g.set_titles("{col_name}")
plt.subplots_adjust(top=0.92)
g = g.fig.suptitle('Evolution of total recovered in CCAA (Log Scale)')
```



Deaths over time

```
death = death[death['CCAA']!= 'Total']
g = sns.FacetGrid(death, col="CCAA", col_wrap=5, height=3.5)
g = g.map_dataframe(dateplot, "fecha", "total").set(yscale='log')
g = g.map(plt.fill_between, 'fecha', 'total', alpha=0.2).set_titles("{col_name} CCAA")
g = g.set_titles("{col_name}")
plt.subplots_adjust(top=0.92)
g = g.fig.suptitle('Evolution of total deaths in CCAA (log scale)')
```



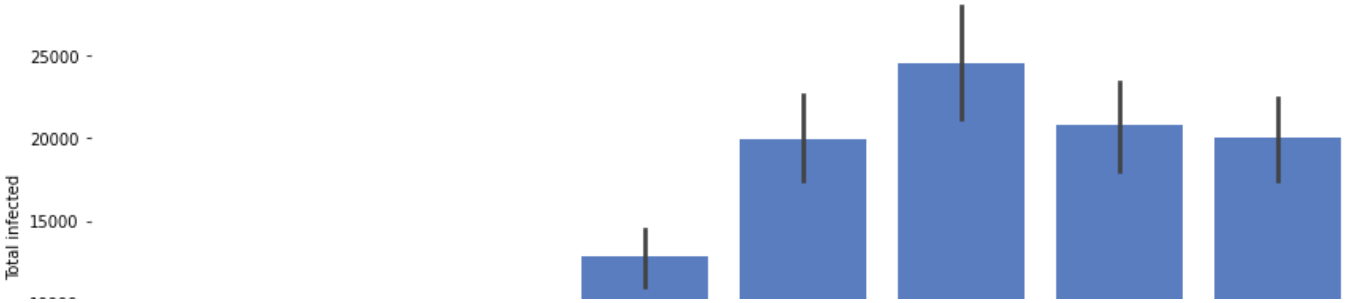
Patient Analysis

As a first aproach, I will compare the effects of COVID-19 in each age group without taking into accou

```
age_range= age_range[age_range['rango_edad']!='Total']
age_range= age_range[age_range['rango_edad']!='80 y +']
no_gender = age_range[age_range['sexo']=='ambos']
```

```
g = sns.catplot(x="rango_edad", y="casos_confirmados", hue="sexo", data=no_gender, kind="bar'
g.despine(left=True)
g.set_ylabels("Total infected")
```

```
<seaborn.axisgrid.FacetGrid at 0x7fa53d6e27b8>
```




```
last = age_range[age_range.iloc[:,0]== age_range.iloc[:,0].max()]
```

In case dataframe format is wrong:

```
for i in range(last['ingresos_uci'].shape[0]):
    if last.iloc[i,5] == 'i':
        last.iloc[i,5] = 0

last['ingresos_uci']= last['ingresos_uci'].astype(int)
```

In order to compare between different categories, we should normalize the data:

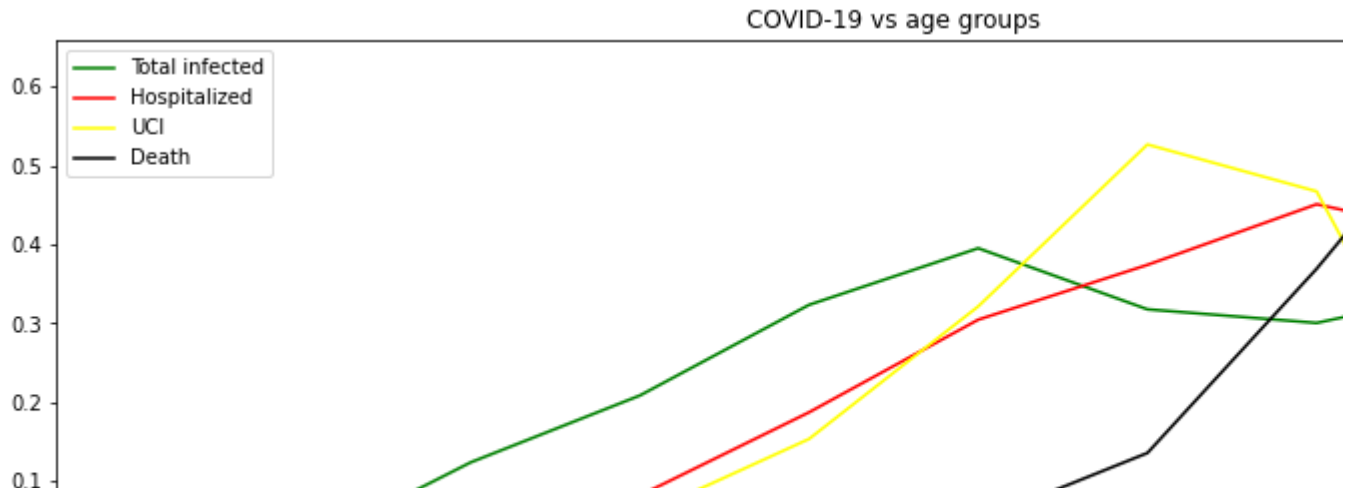
```
last['casos_confirmados'] = last['casos_confirmados'] / np.linalg.norm(last['casos_confirmadc
last['hospitalizados'] = last['hospitalizados'] / np.linalg.norm(last['hospitalizados'])
last['ingresos_uci'] = last['ingresos_uci'] / np.linalg.norm(last['ingresos_uci'])
last['fallecidos'] = last['fallecidos'] / np.linalg.norm(last['fallecidos'])
```

```
last_ambos = last[last['sexo']=='ambos']
last_gender = last[last['sexo']!='ambos']
```

COVID-19 vs age groups

```
plt.figure(figsize=(15,5))
plt.plot(last_ambos['rango_edad'], last_ambos['casos_confirmados'],color = 'green',label='Tot
plt.plot(last_ambos['rango_edad'], last_ambos['hospitalizados'],color = 'red',label='Hospital
plt.plot( last_ambos['rango_edad'], last_ambos['ingresos_uci'],color = 'yellow',label='UCI')
plt.plot( last_ambos['rango_edad'], last_ambos['fallecidos'],color = 'black',label='Death')
plt.title('COVID-19 vs age groups')
plt.legend()
```

```
<matplotlib.legend.Legend at 0x7fa53efb6ef0>
```

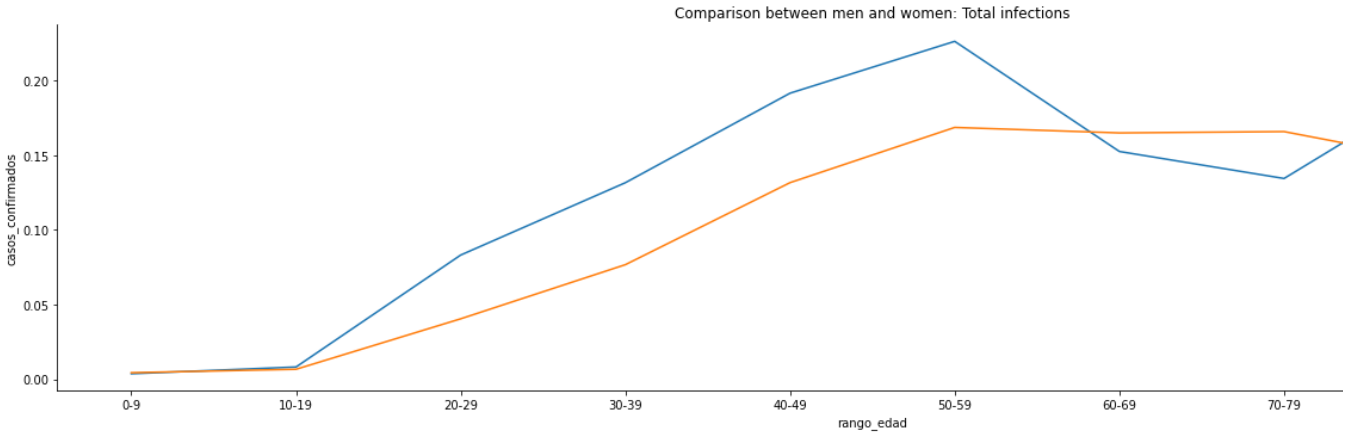


The results are as expected. virus affects mostly older people. We can see that the death´s curve pea
surprising result is the "Total infected" line as the 'peak' goes from 40 to 80 years whick means the di
population.

COVID-19 vs Gender

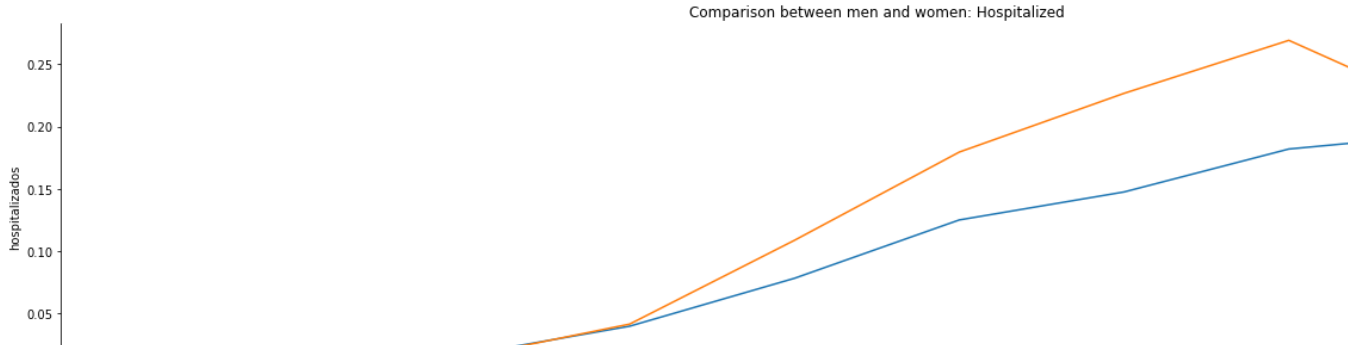
```
plt.figure(figsize= (10,5))
sns.relplot(x='rango_edad',y ='casos_confirmados', hue = 'sexo',kind='line',data = last_gende
plt.title('Comparison between men and women: Total infections')
```

```
Text(0.5, 1.0, 'Comparison between men and women: Total infections')
<Figure size 720x360 with 0 Axes>
```



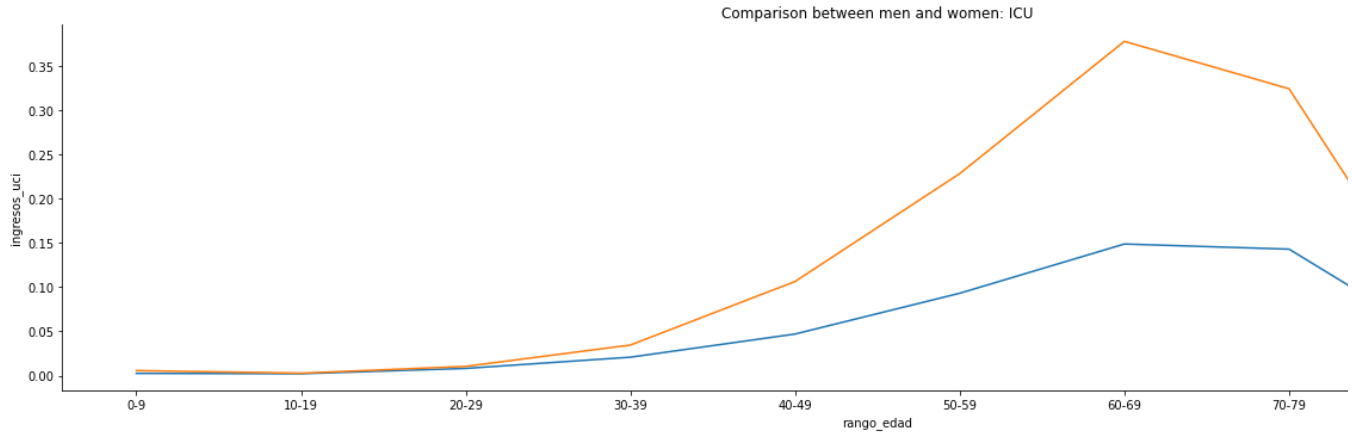

```
plt.figure(figsize= (10,5))
sns.relplot(x='rango_edad',y ='hospitalizados', hue = 'sexo',kind='line',data = last_gender,h
plt.title('Comparison between men and women: Hospitalized')
```

```
Text(0.5, 1.0, 'Comparison between men and women: Hospitalized')
<Figure size 720x360 with 0 Axes>
```



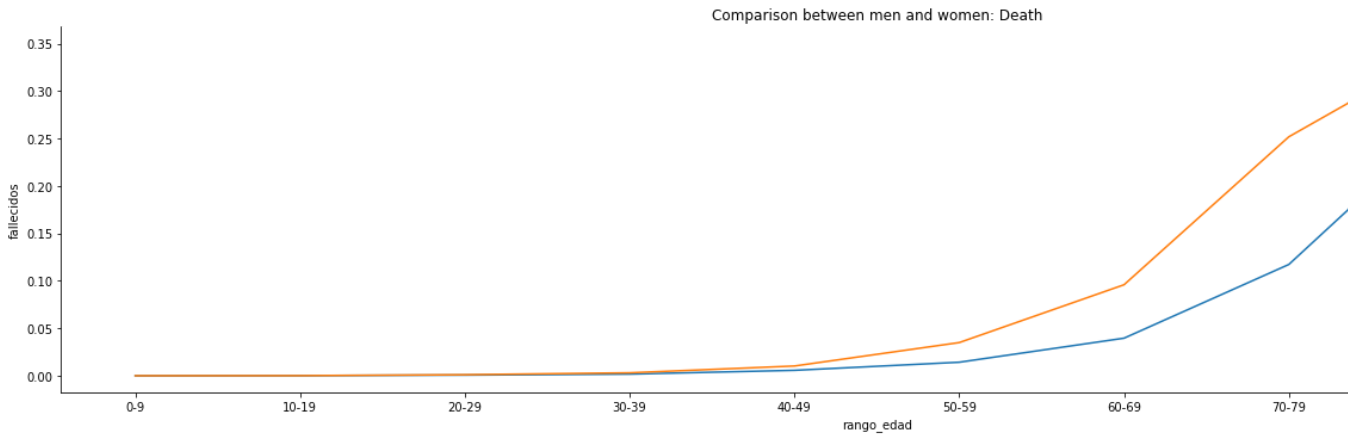

```
plt.figure(figsize= (10,5))
sns.relplot(x='rango_edad',y ='ingresos_uci', hue = 'sexo',kind='line',data = last_gender,hei
plt.title('Comparison between men and women: ICU')
```

```
Text(0.5, 1.0, 'Comparison between men and women: ICU')
<Figure size 720x360 with 0 Axes>
```




```
plt.figure(figsize= (10,5))
sns.relplot(x='rango_edad',y ='fallecidos', hue = 'sexo',kind='line',data = last_gender,heigh
plt.title('Comparison between men and women: Death')
```

```
Text(0.5, 1.0, 'Comparison between men and women: Death')
<Figure size 720x360 with 0 Axes>
```



As we can see, in general the virus is more dangerous in men than woman altough the total infected
60yo. This can be easily explained with the previous chart as the age ranges in which women are mo
less dangerous ages. One the other hand, the are more men than woman infected in the dangerous a