

Feature Distribution and Plotting

Univariate and Bivariate analysis of features

Importing Libraries

In [1]:

```
import numpy as np
import pandas as pd
from IPython.display import display
import matplotlib.pyplot as plt
import seaborn as sns

import warnings
warnings.filterwarnings("ignore", category = UserWarning)

# Importing visualizations code visuals.py
import visuals as vs

# Pretty display for notebooks
%matplotlib inline
```

Loading data set

In [2]:

```
# Load the Covid-19 dataset
data = pd.read_csv('owid-covid-data.csv')

# Splitting features and label
cases = data['new_cases']
features = data.drop('new_cases', axis = 1)

# Success - Displaying the records
display(features)

# Success
print("Covid-19 dataset has {} data points.".format(data.shape[0]))
```

	iso_code	continent	location	date	total_cases	total_deaths	new_deaths	total_
0	AFG	Asia	Afghanistan	2019-12-31	0.0	0.0	0.0	
1	AFG	Asia	Afghanistan	2020-01-01	0.0	0.0	0.0	
2	AFG	Asia	Afghanistan	2020-01-02	0.0	0.0	0.0	
3	AFG	Asia	Afghanistan	2020-01-03	0.0	0.0	0.0	
4	AFG	Asia	Afghanistan	2020-01-04	0.0	0.0	0.0	
...
26129	NaN	NaN	International	2020-02-28	705.0	4.0	0.0	
26130	NaN	NaN	International	2020-02-29	705.0	6.0	2.0	
26131	NaN	NaN	International	2020-03-01	705.0	6.0	0.0	
26132	NaN	NaN	International	2020-03-02	705.0	6.0	0.0	
26133	NaN	NaN	International	2020-03-10	696.0	7.0	1.0	

26134 rows × 33 columns

Covid-19 dataset has 26134 data points.

In [3]:

```
# Setting plotting figures
sns.set(rc={"figure.figsize":(18, 7)})
```

Univariate Analysis of Features

We will be doing univariate distribution and plotting of each and every features given in the dataset.

Seaborn library is used for distribution and plotting of data. For non-numerical data column we will be using `.countplot()` function which takes data column as input parameter. For numerical data we will be using `distplot()` function which also takes data column as input parameter, and then plot the distributed data.

Histograms

A histogram is a plot that lets you discover, and show, the underlying frequency distribution of a set of continuous data. This allows the inspection of the data for its underlying distribution (e.g., normal distribution), outliers, skewness, etc.

Kernel Density Estimation

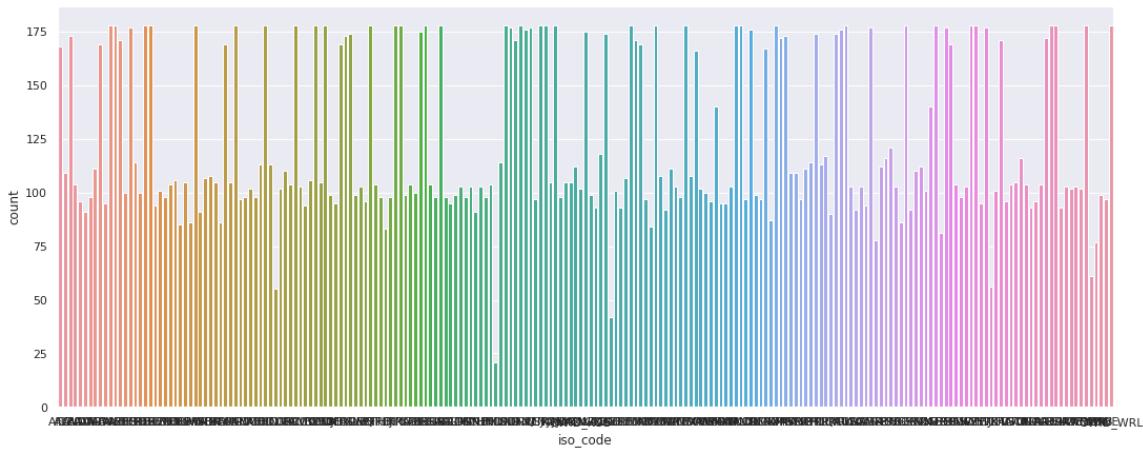
Kernel density estimation is a really useful statistical tool. It's a technique that let's you create a smooth curve given a set of data. Kernel density estimation (KDE) is a non-parametric way to estimate the probability density function of a random variable. KDE is mostly used for numerical data, in the section of numerical data you will find a curve line with histograms, the curve line show KDE.

In [4]:

```
sns.countplot(features["iso_code"])
```

Out[4]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc700bbfc18>
```

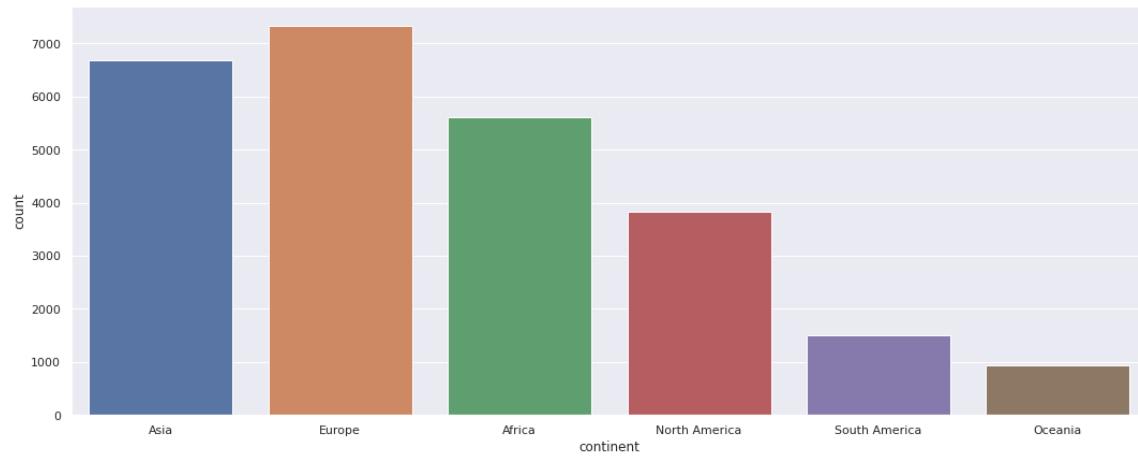


In [5]:

```
sns.countplot(features["continent"])
```

Out[5]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc7484ae978>
```

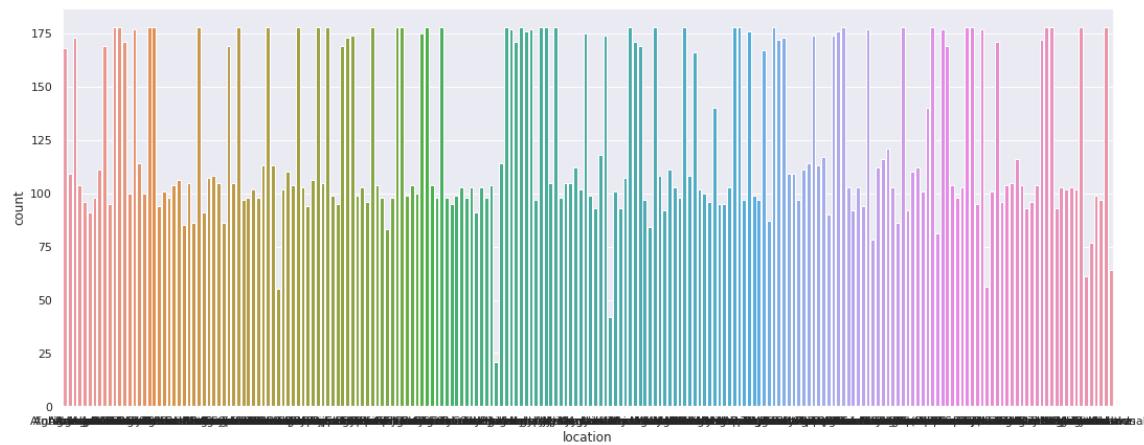


In [6]:

```
sns.countplot(features["location"])
```

Out[6]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fde53be0>
```

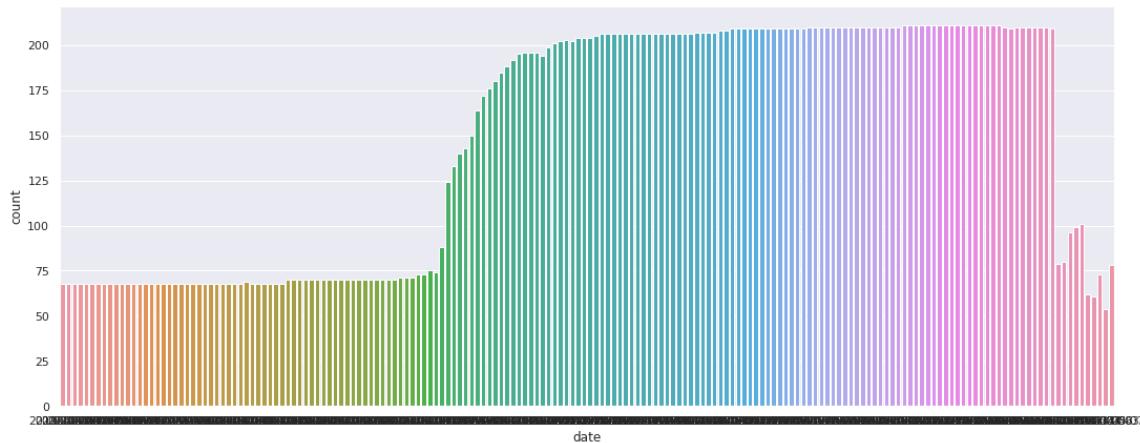


In [7]:

```
sns.countplot(features["date"])
```

Out[7]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fde4ab70>
```

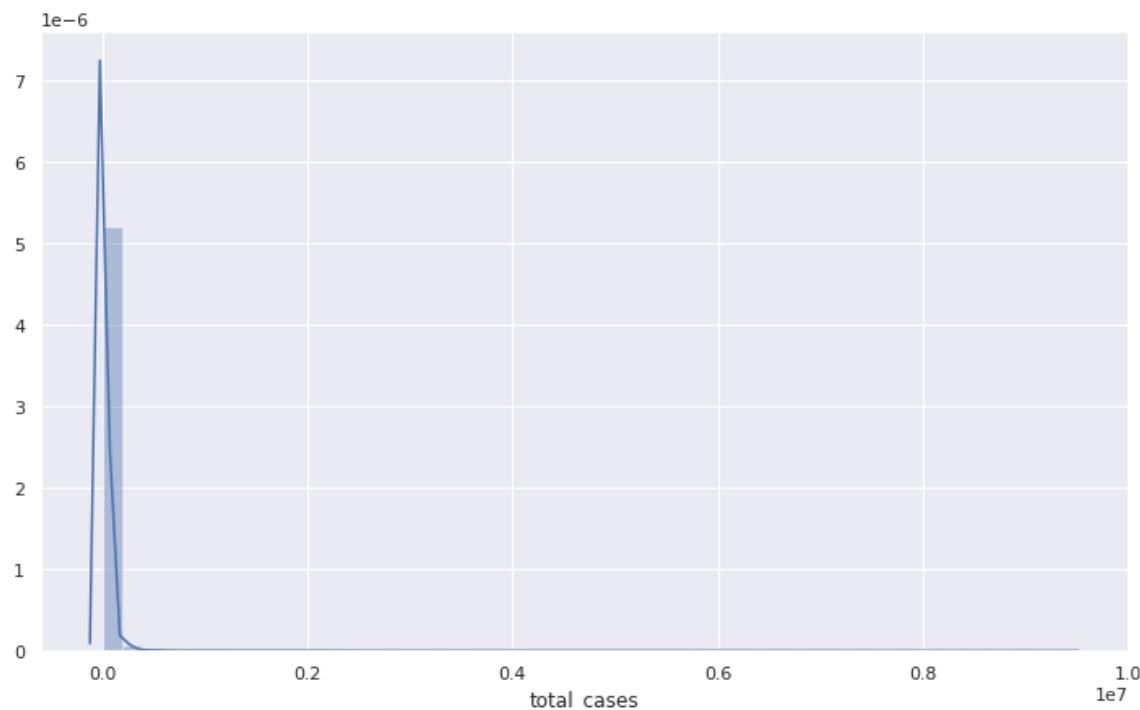


In [8]:

```
sns.set(rc={"figure.figsize":(12, 7)})  
sns.distplot(features["total_cases"])
```

Out[8]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fdfe9a20>
```

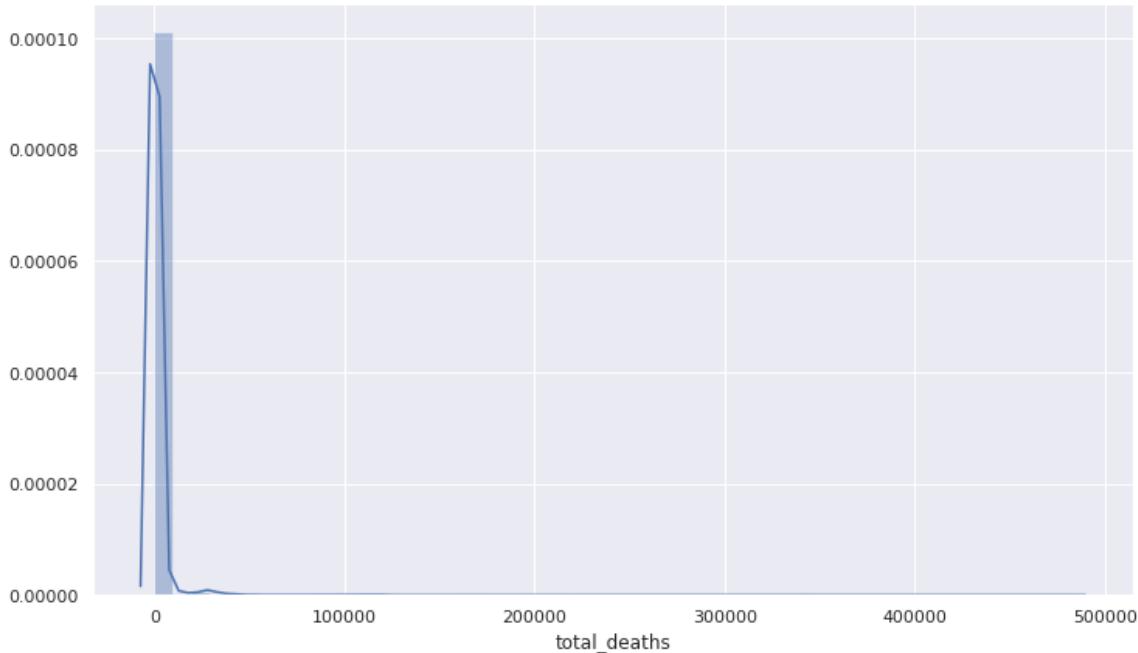


In [9]:

```
sns.distplot(features["total_deaths"])
```

Out[9]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fdf84cc0>
```

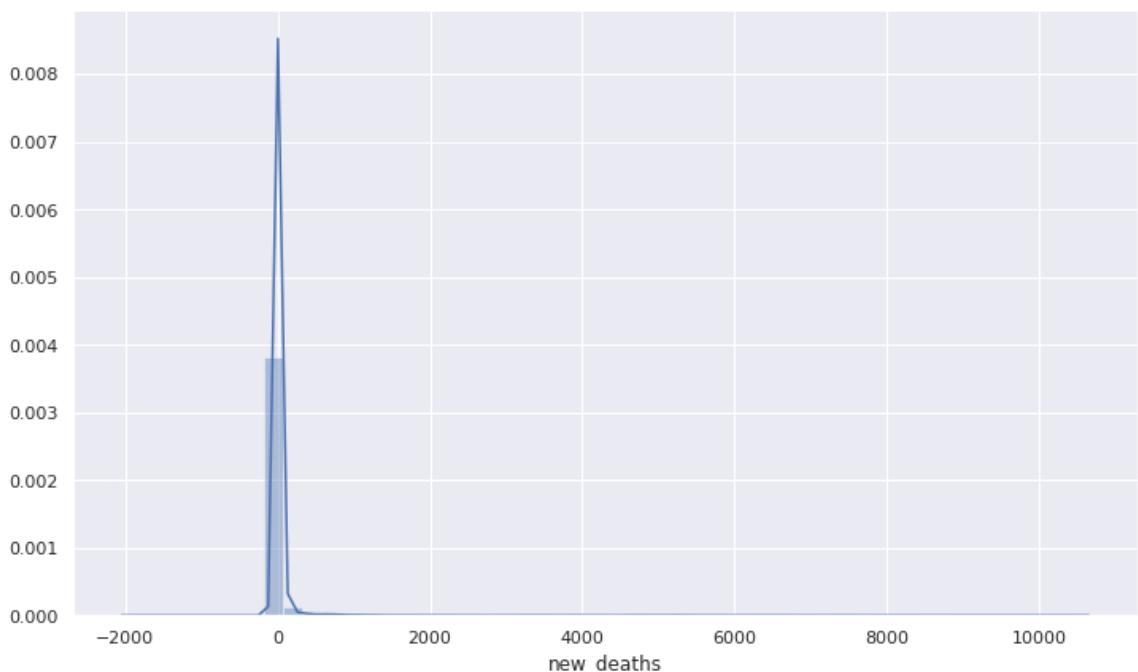


In [10]:

```
sns.distplot(features["new_deaths"])
```

Out[10]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb756080>
```

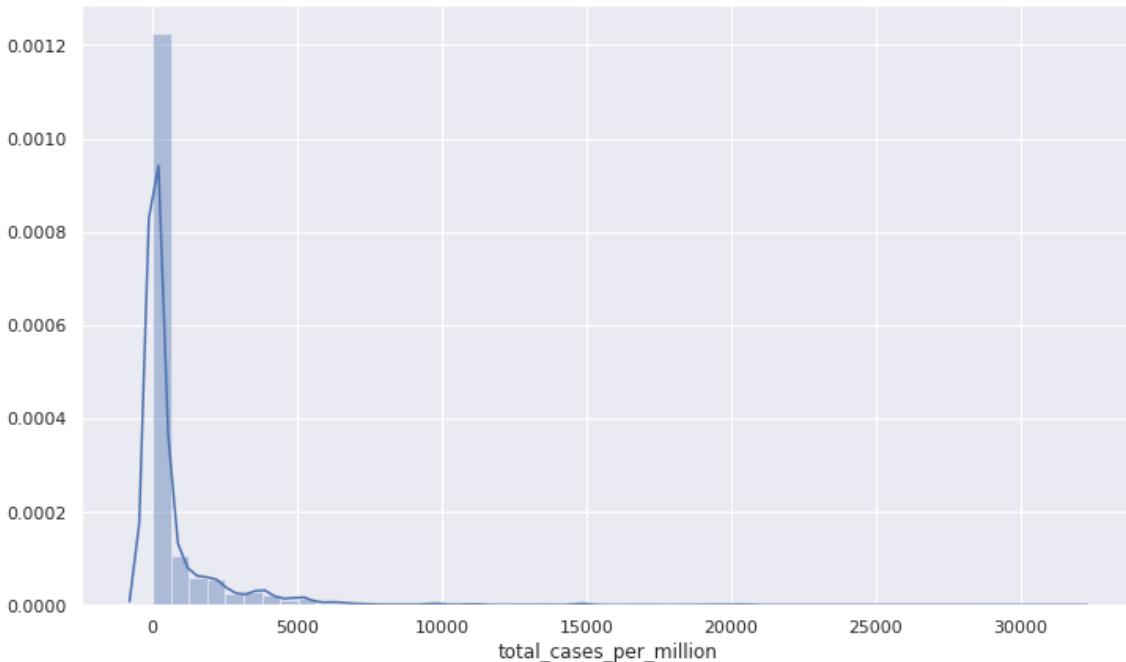


In [11]:

```
sns.distplot(features["total_cases_per_million"])
```

Out[11]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb668588>
```

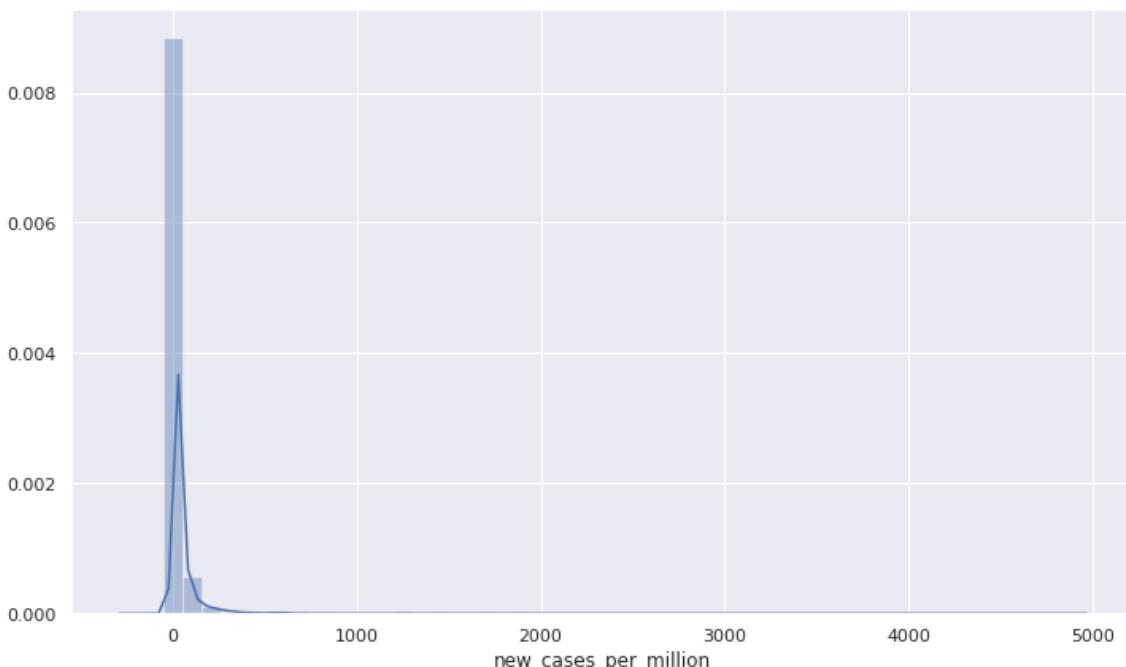


In [12]:

```
sns.distplot(features["new_cases_per_million"])
```

Out[12]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb64a828>
```

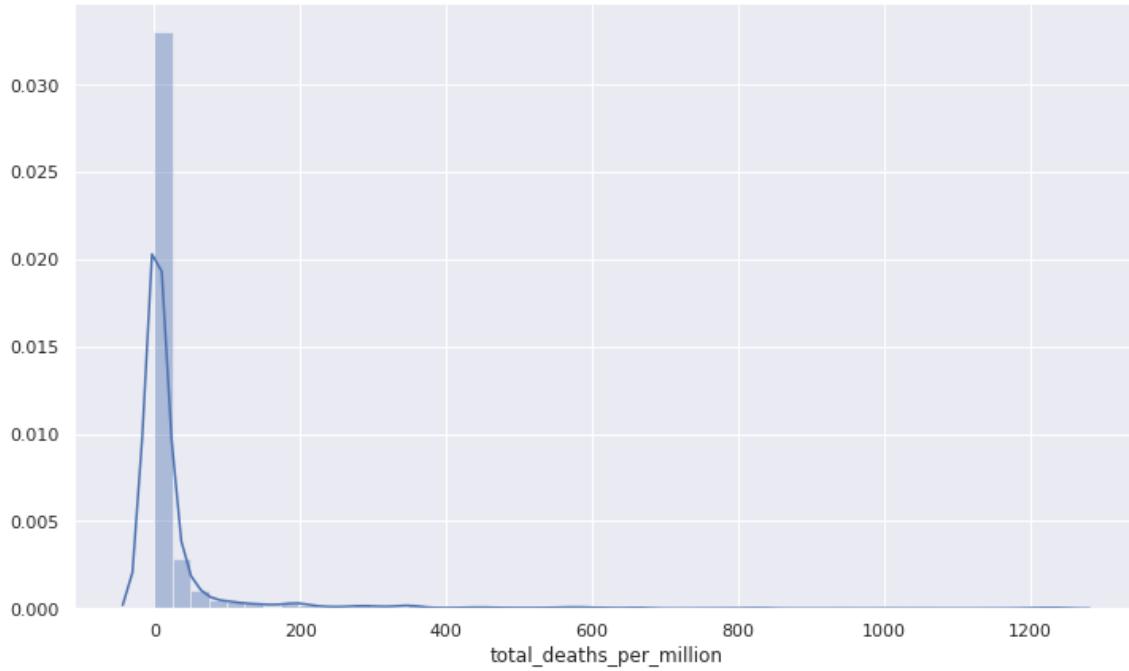


In [13]:

```
sns.distplot(features["total_deaths_per_million"])
```

Out[13]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb48ac50>
```

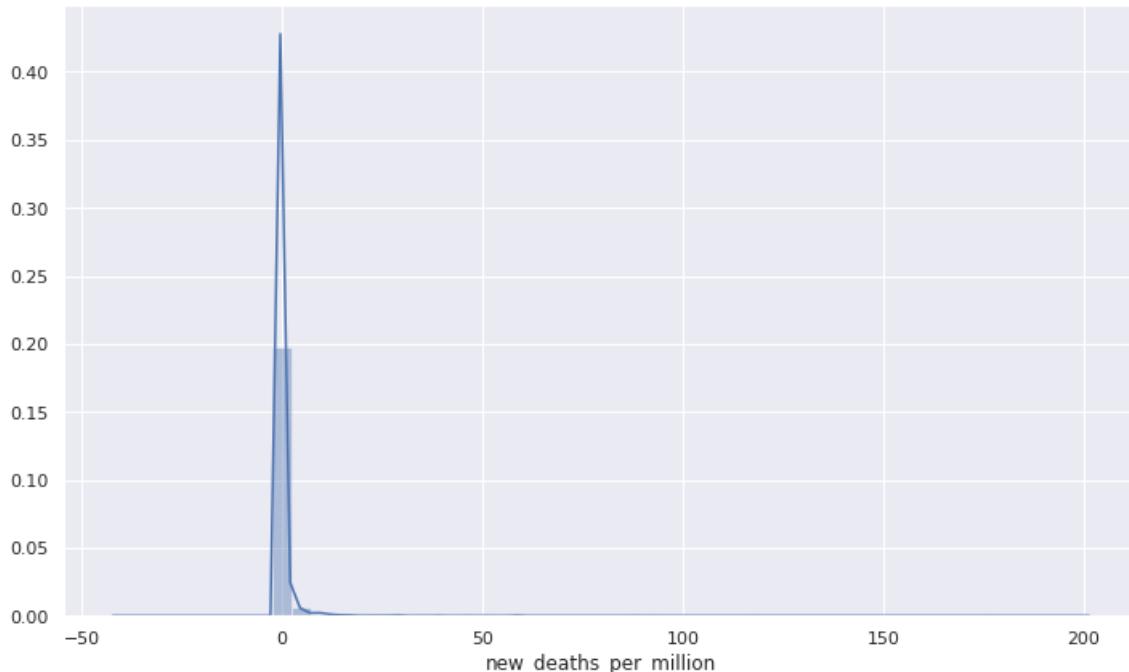


In [14]:

```
sns.distplot(features["new_deaths_per_million"])
```

Out[14]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb48a8d0>
```

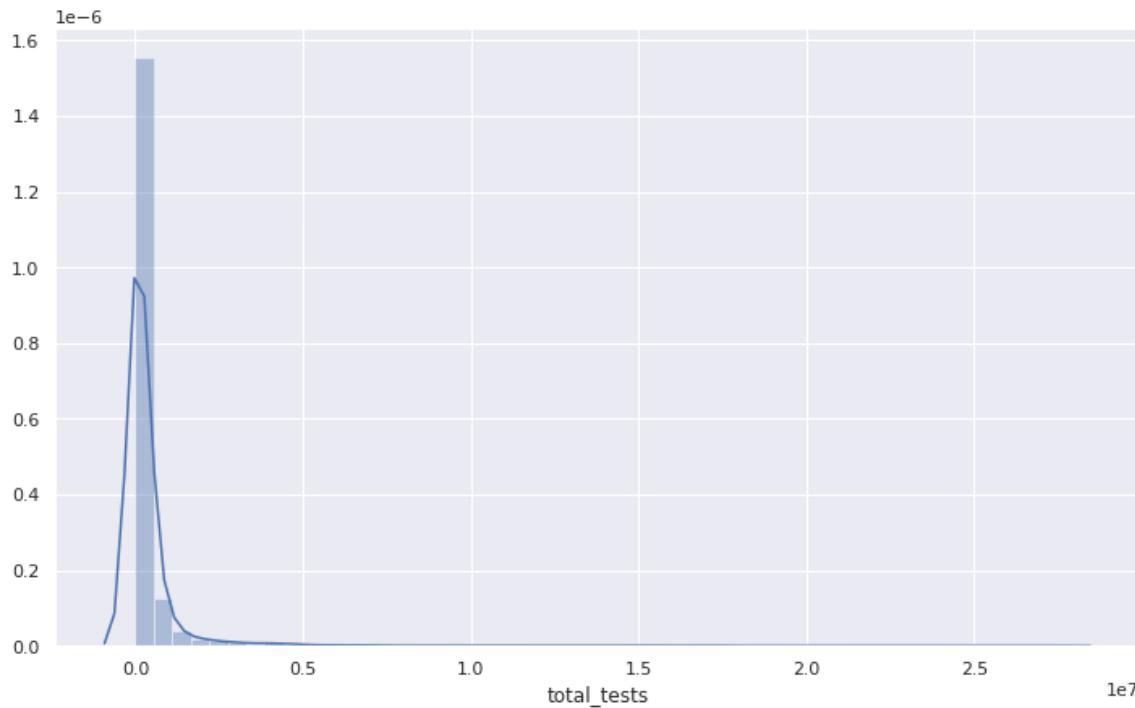


In [15]:

```
sns.distplot(features["total_tests"])
```

Out[15]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fe04d940>
```

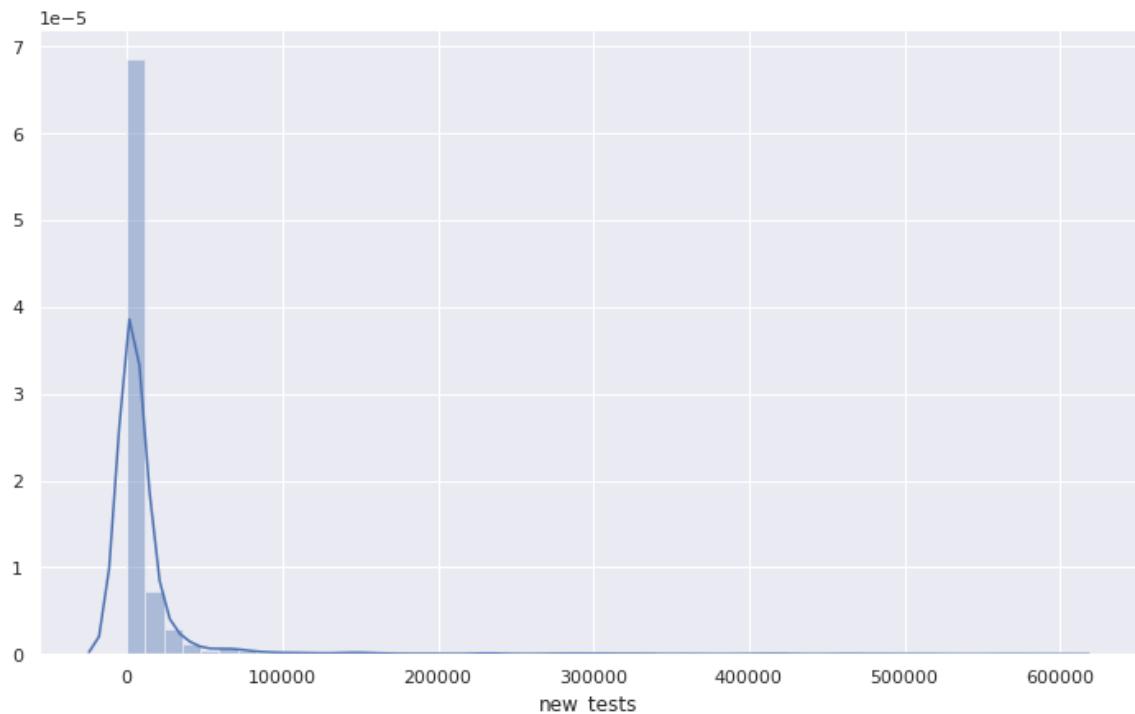


In [16]:

```
sns.distplot(features["new_tests"])
```

Out[16]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb25f0b8>
```

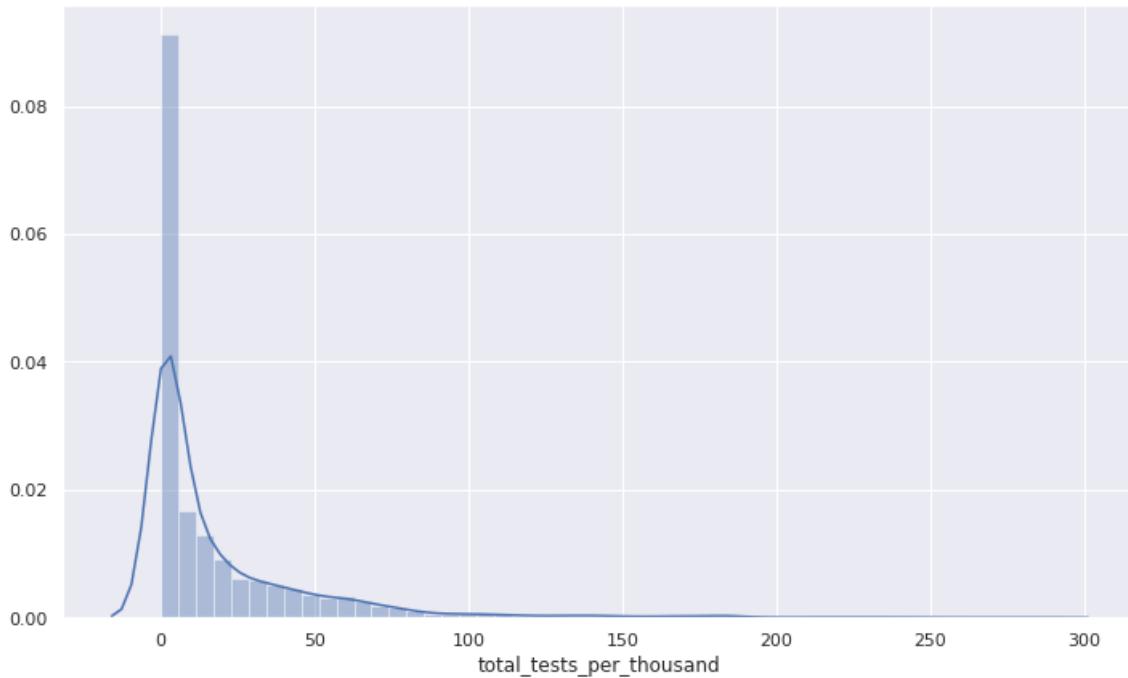


In [17]:

```
sns.distplot(features["total_tests_per_thousand"])
```

Out[17]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb133e48>
```

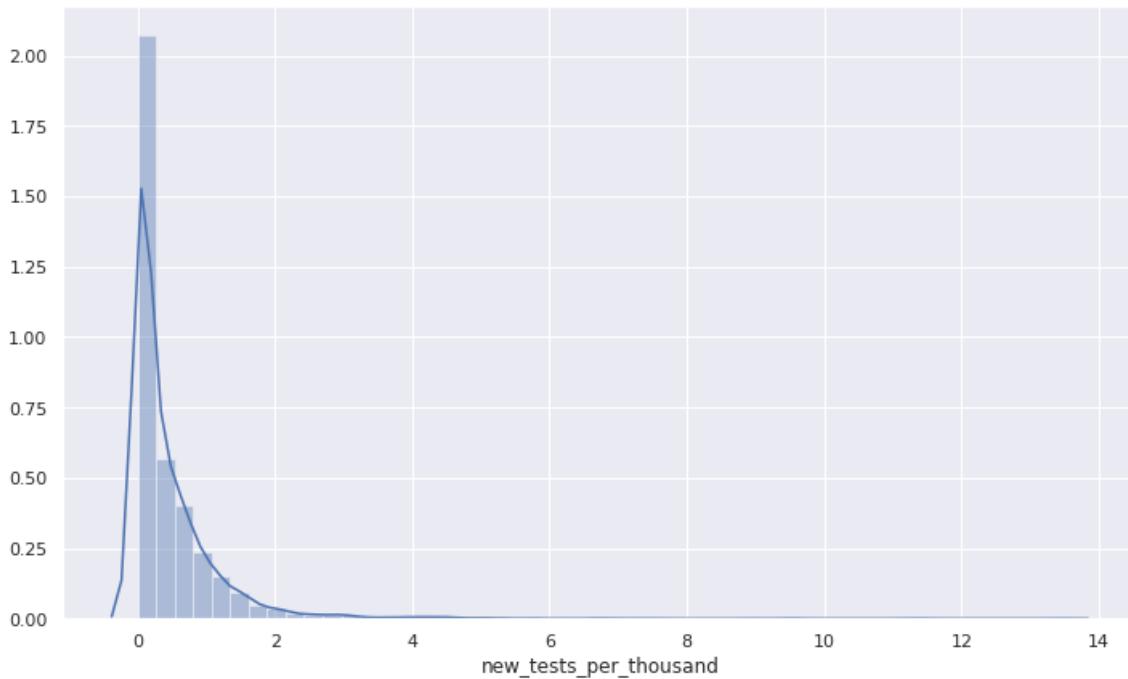


In [18]:

```
sns.distplot(features["new_tests_per_thousand"])
```

Out[18]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fb026eb8>
```

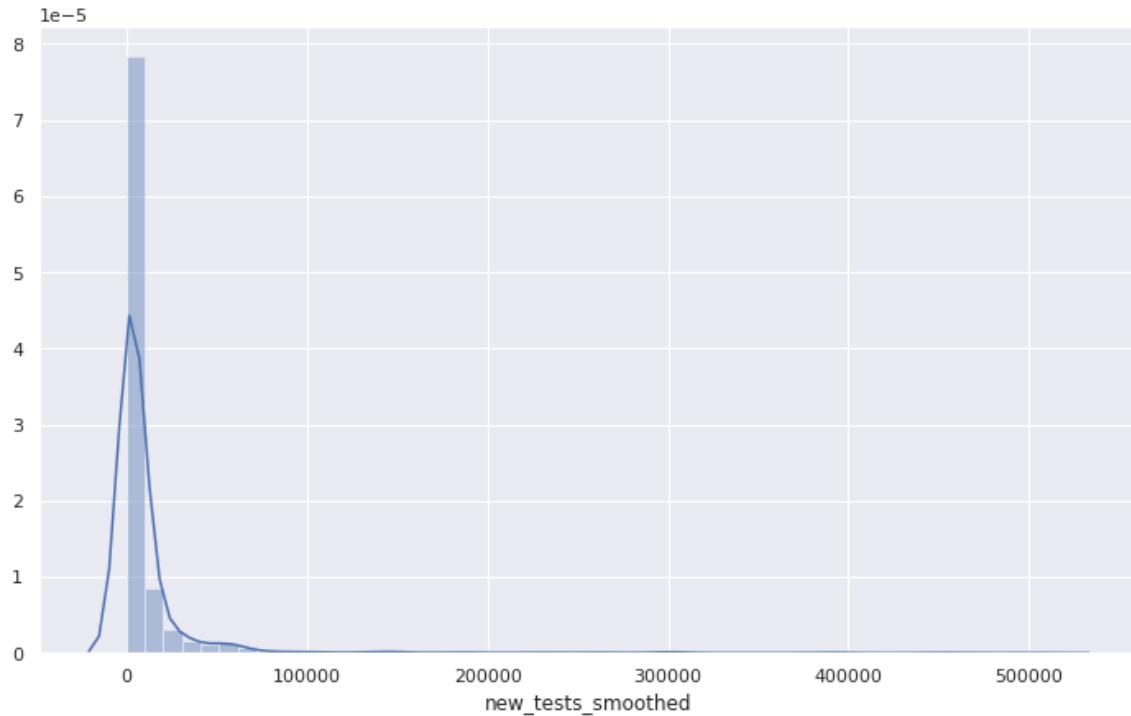


In [19]:

```
sns.distplot(features["new_tests_smoothed"])
```

Out[19]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6faf874a8>
```

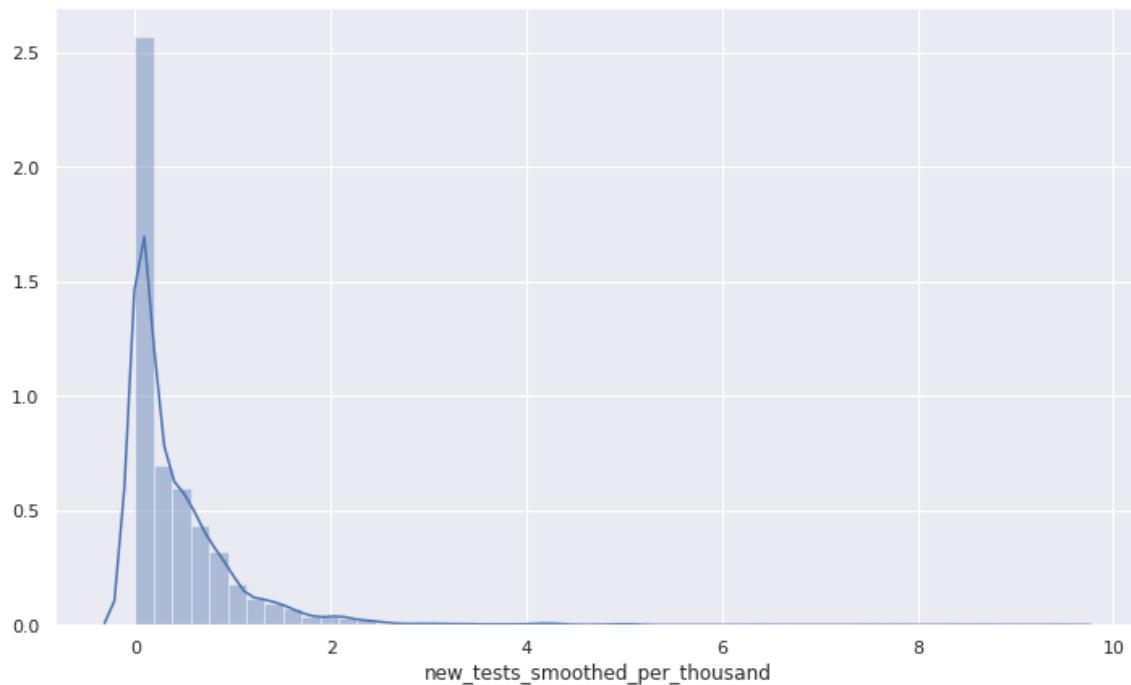


In [20]:

```
sns.distplot(features["new_tests_smoothed_per_thousand"])
```

Out[20]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fae7bac8>
```

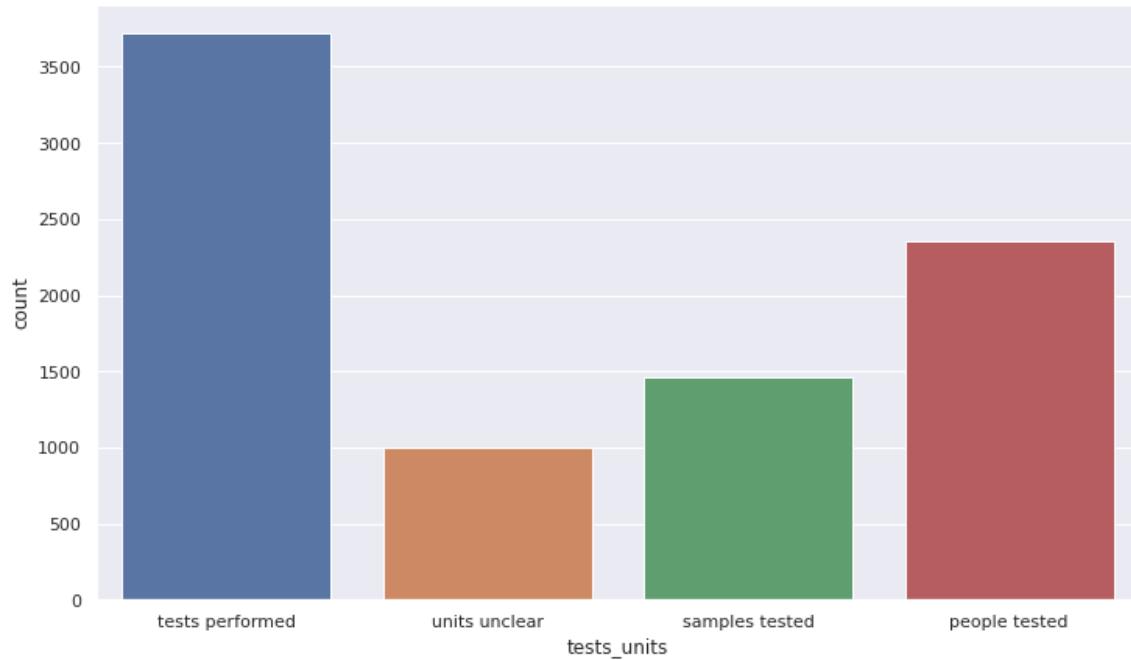


In [21]:

```
sns.countplot(features["tests_units"])
```

Out[21]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fadff8d0>
```

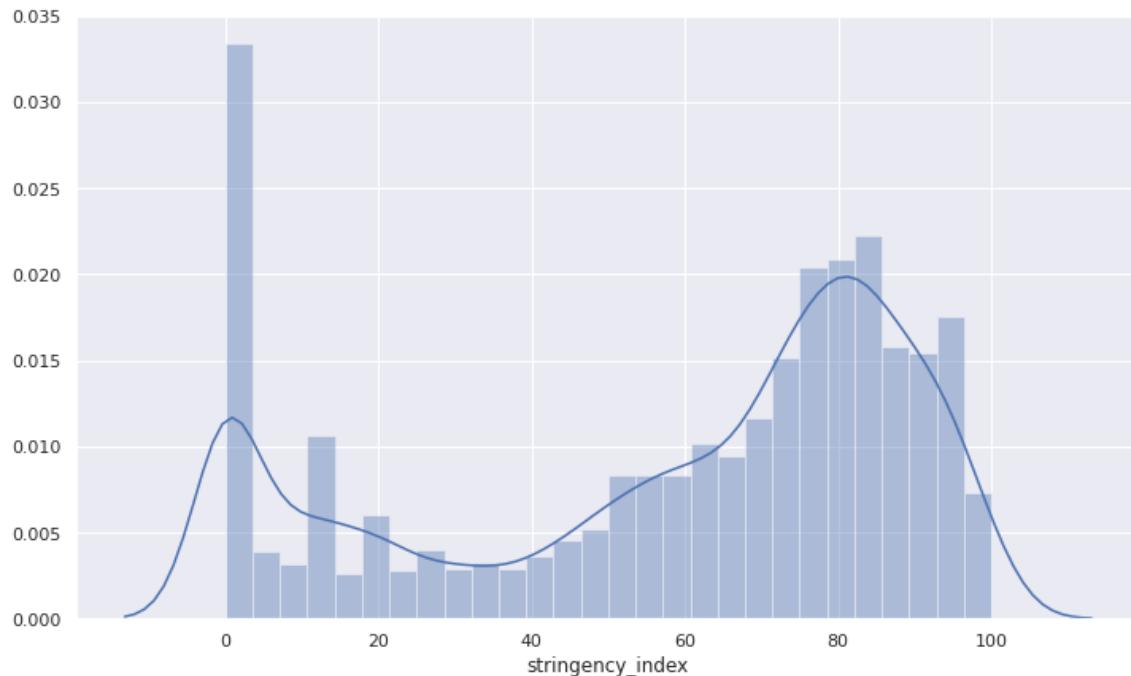


In [22]:

```
sns.distplot(features["stringency_index"])
```

Out[22]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fad98780>
```

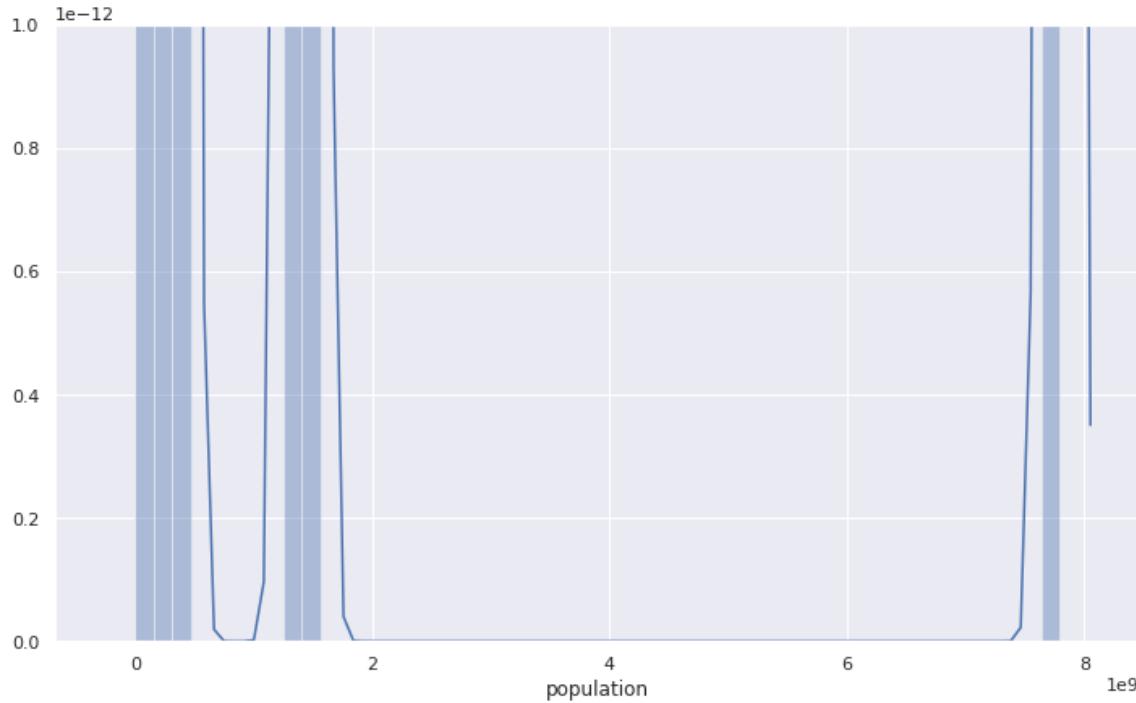


In [23]:

```
sns.distplot(features["population"])
```

Out[23]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fad222e8>
```

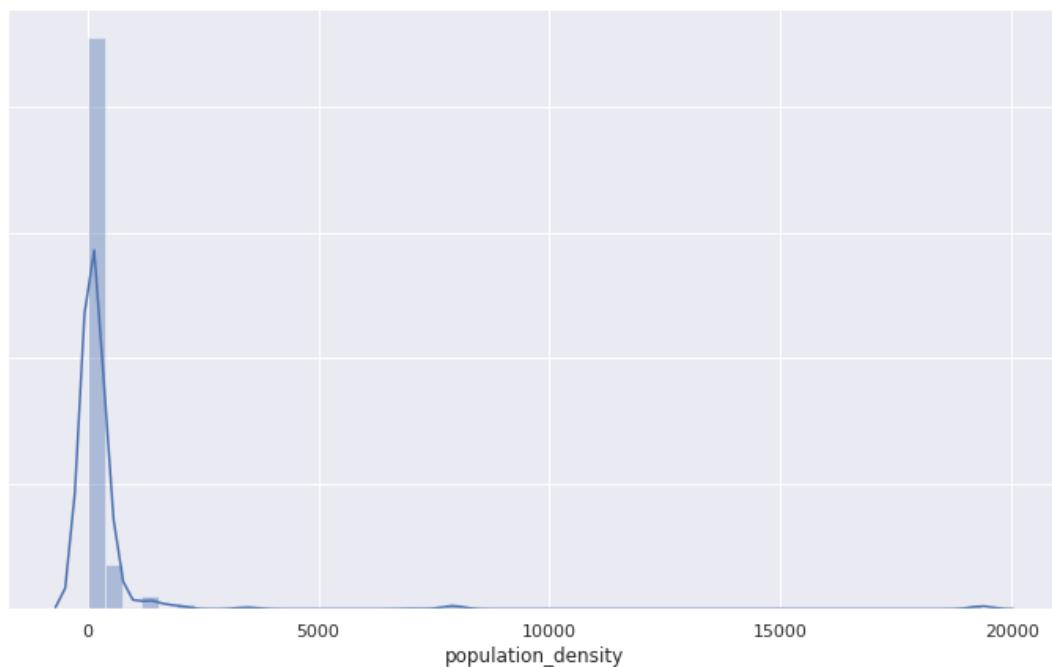


In [24]:

```
sns.distplot(features["population_density"])
```

Out[24]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fabd8518>
```

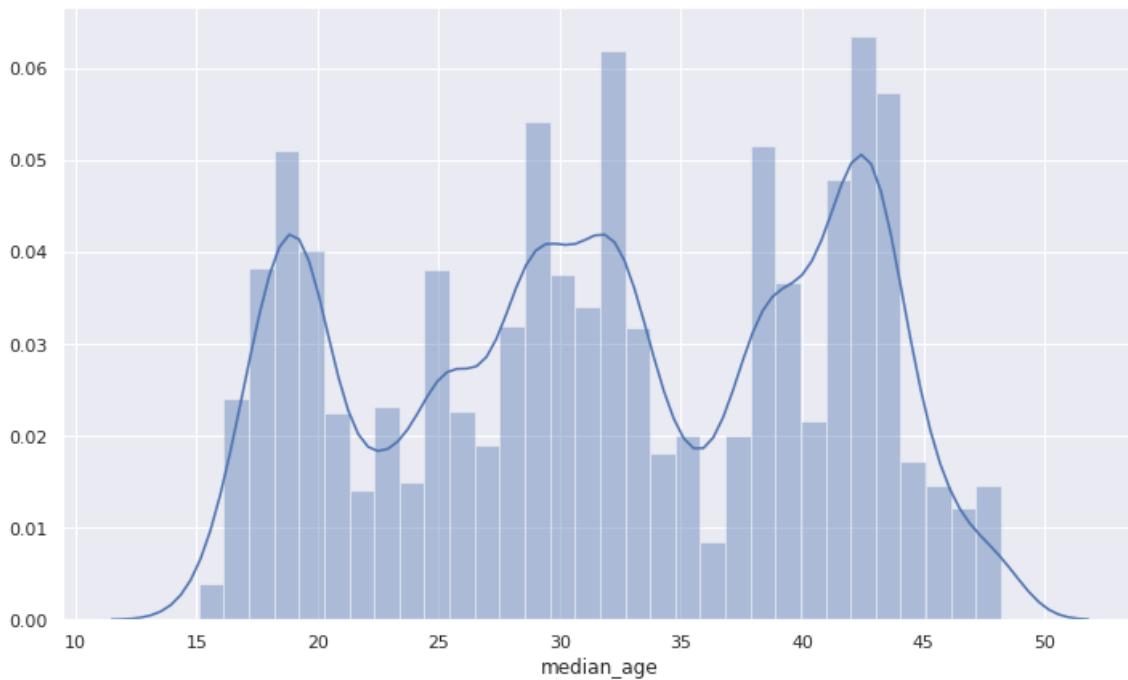


In [25]:

```
sns.distplot(features["median_age"])
```

Out[25]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6faec8588>
```

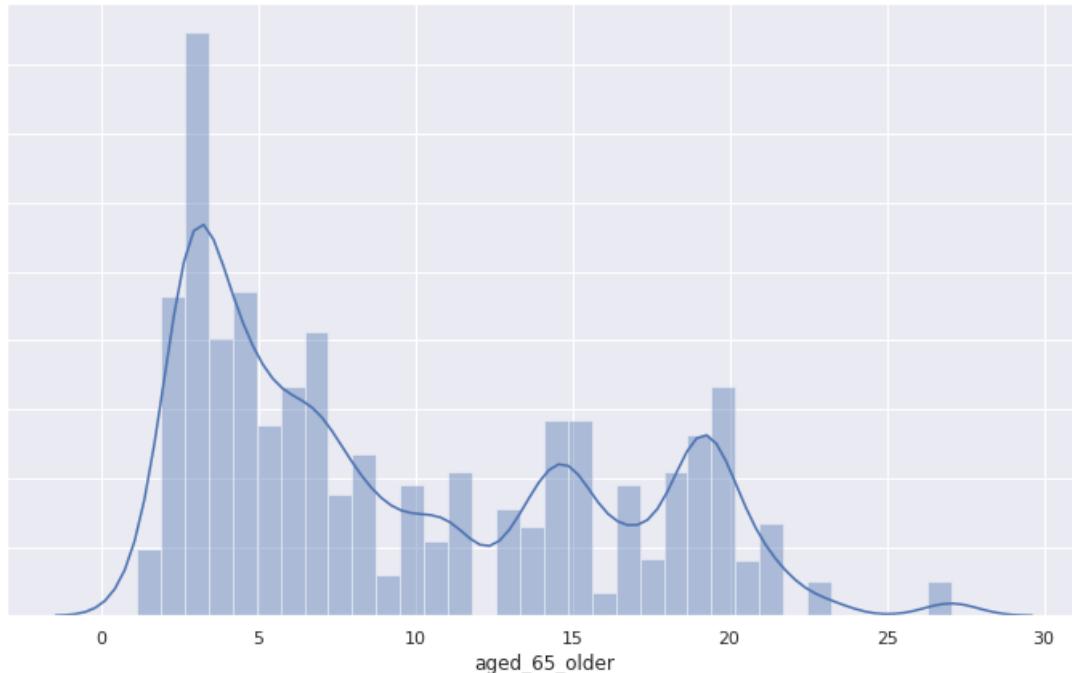


In [26]:

```
sns.distplot(features["aged_65_older"])
```

Out[26]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6faa23b70>
```

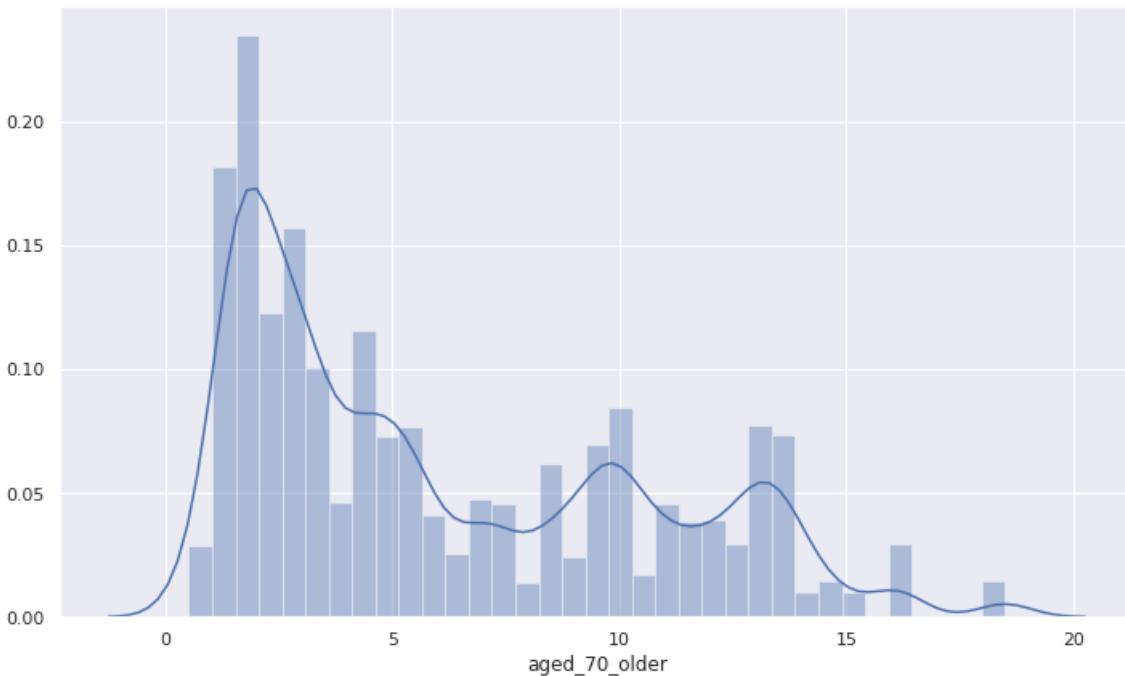


In [27]:

```
sns.distplot(features["aged_70_older"])
```

Out[27]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6faa374e0>
```

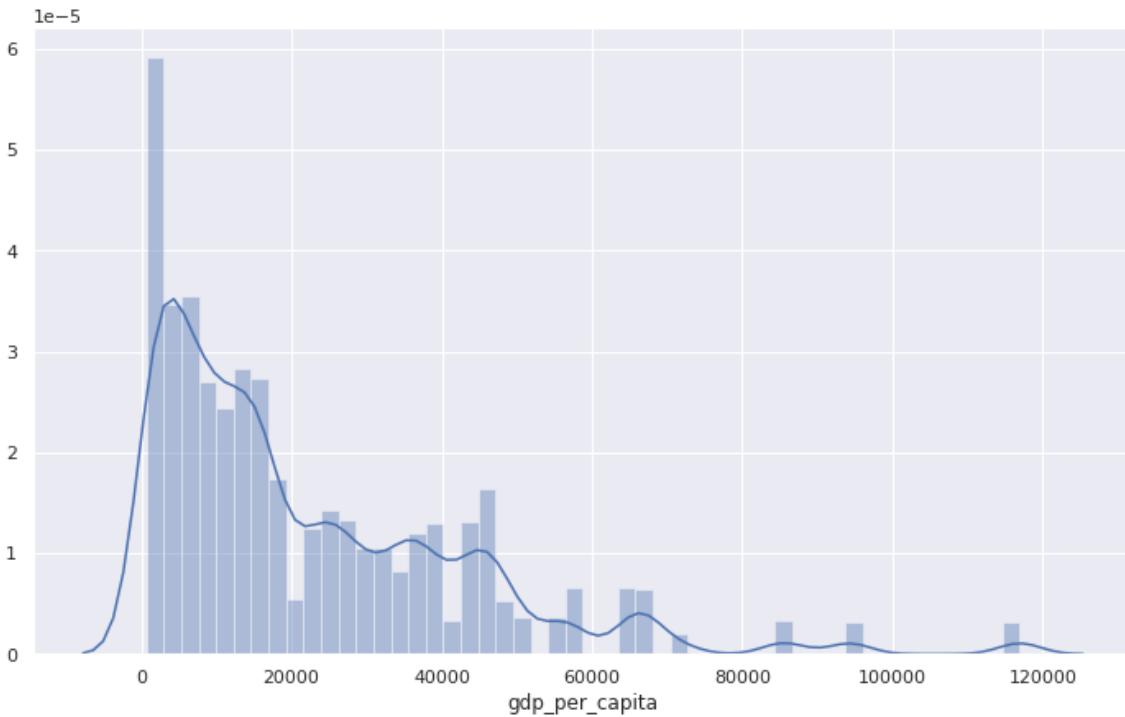


In [28]:

```
sns.distplot(features["gdp_per_capita"])
```

Out[28]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa9586d8>
```

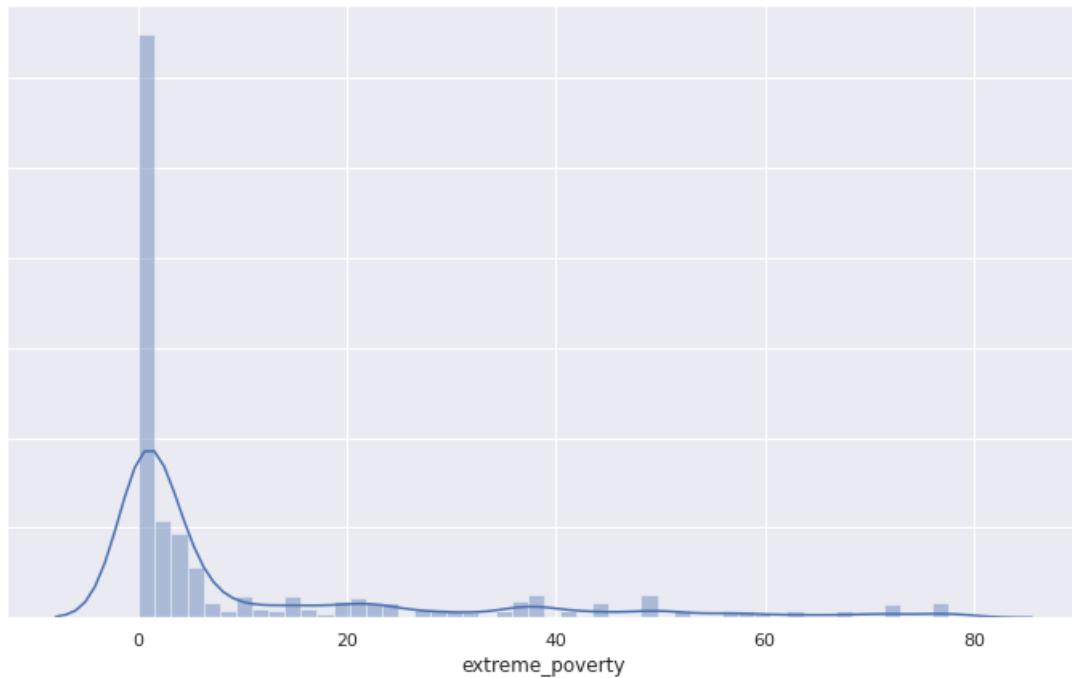


In [29]:

```
sns.distplot(features["extreme_poverty"])
```

Out[29]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa812eb8>
```

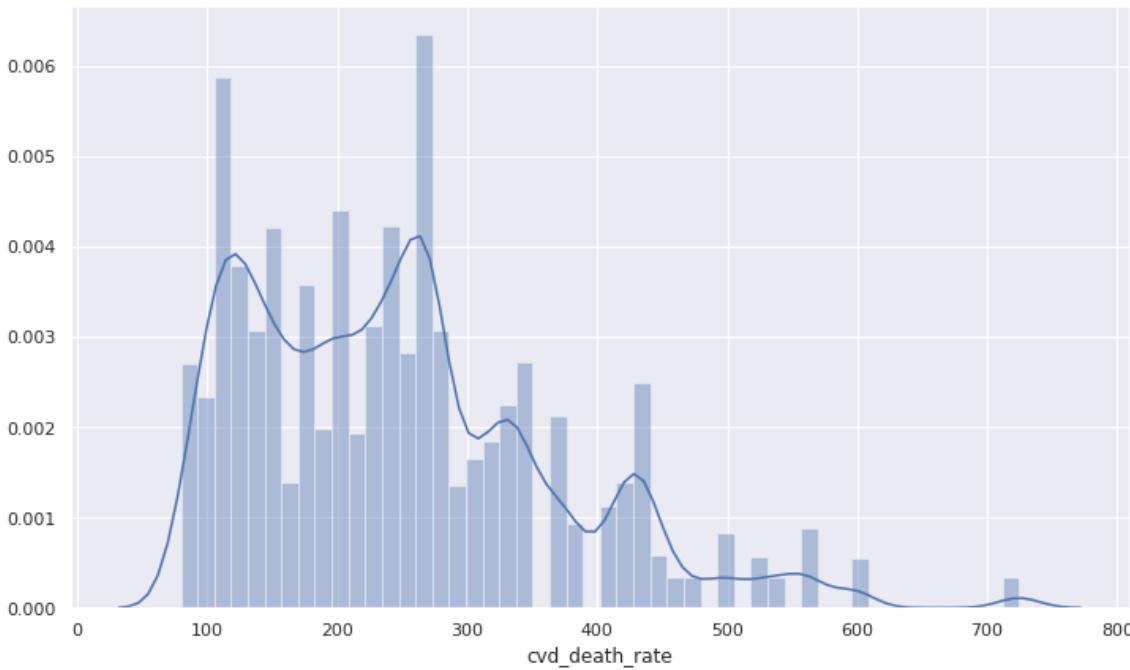


In [30]:

```
sns.distplot(features["cvd_death_rate"])
```

Out[30]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa728320>
```

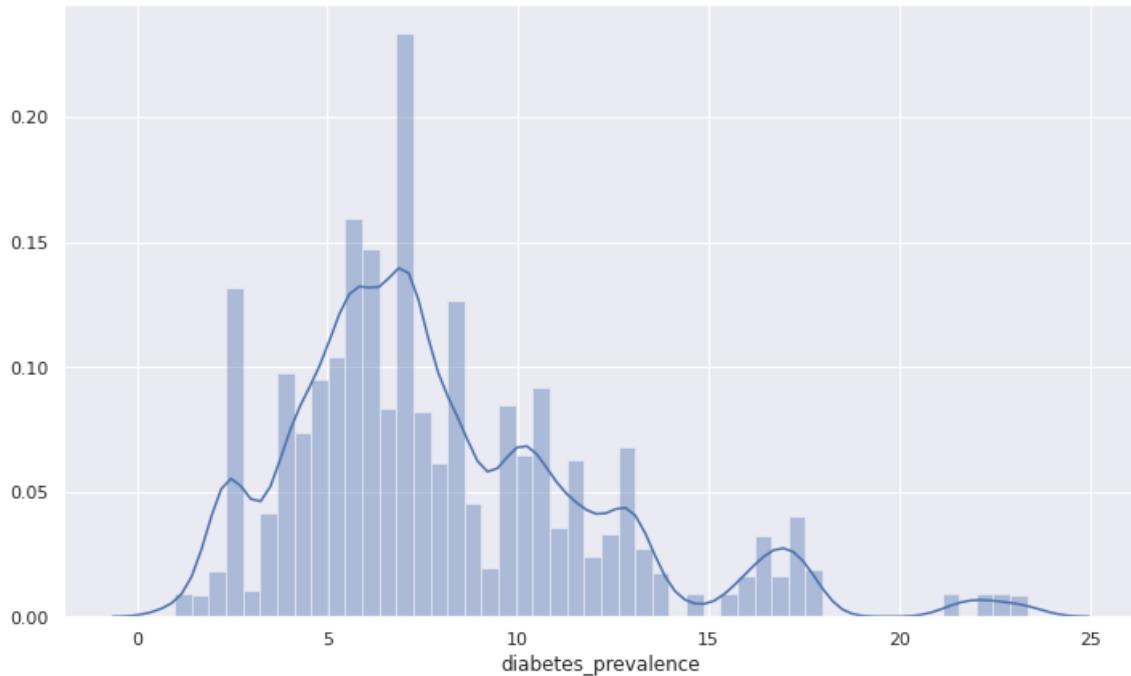


In [31]:

```
sns.distplot(features["diabetes_prevalence"])
```

Out[31]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa5edba8>
```

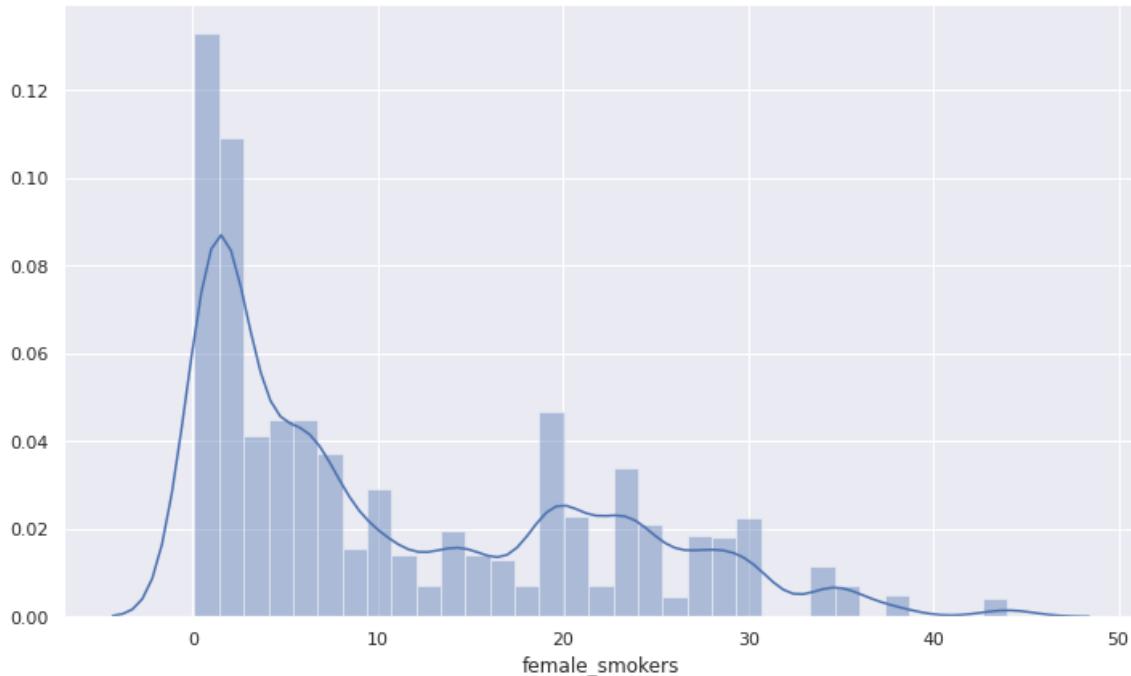


In [32]:

```
sns.distplot(features["female_smokers"])
```

Out[32]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa55e5c0>
```

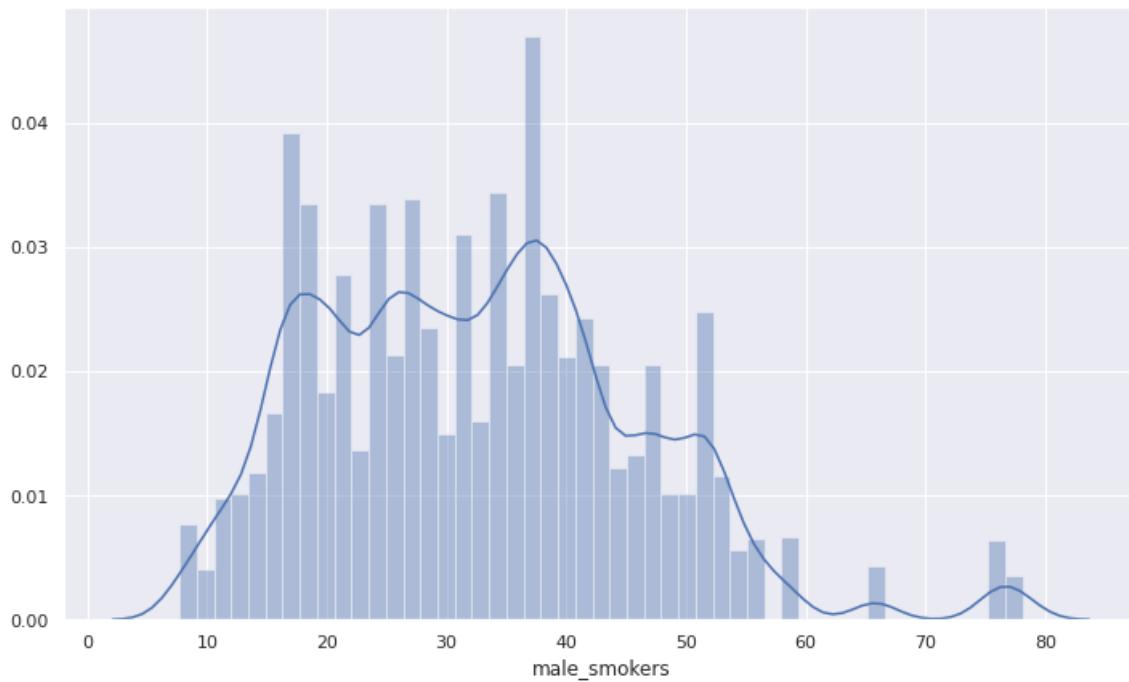


In [33]:

```
sns.distplot(features["male_smokers"])
```

Out[33]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa509e48>
```

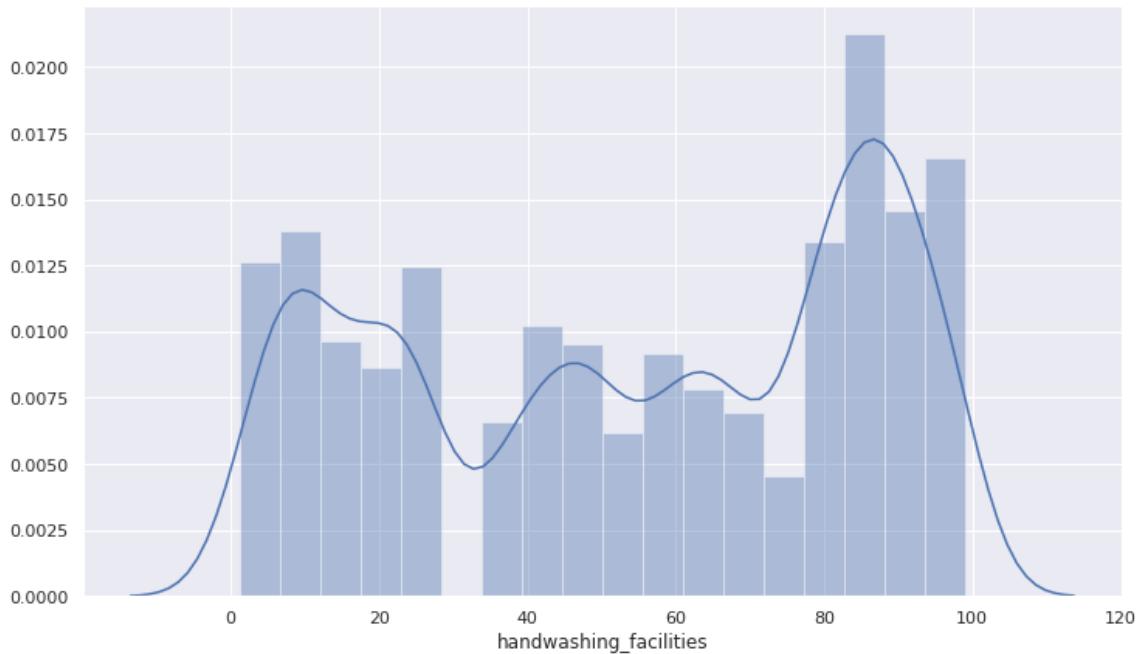


In [34]:

```
sns.distplot(features["handwashing_facilities"])
```

Out[34]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa6f1940>
```

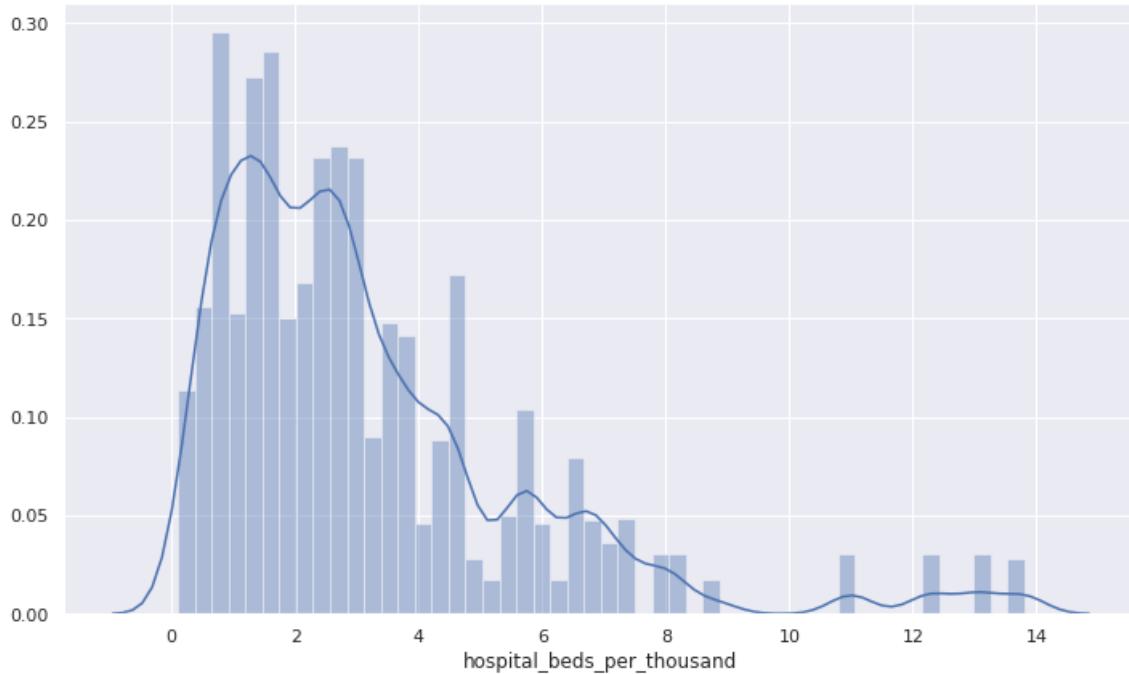


In [35]:

```
sns.distplot(features["hospital_beds_per_thousand"])
```

Out[35]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa364f28>
```

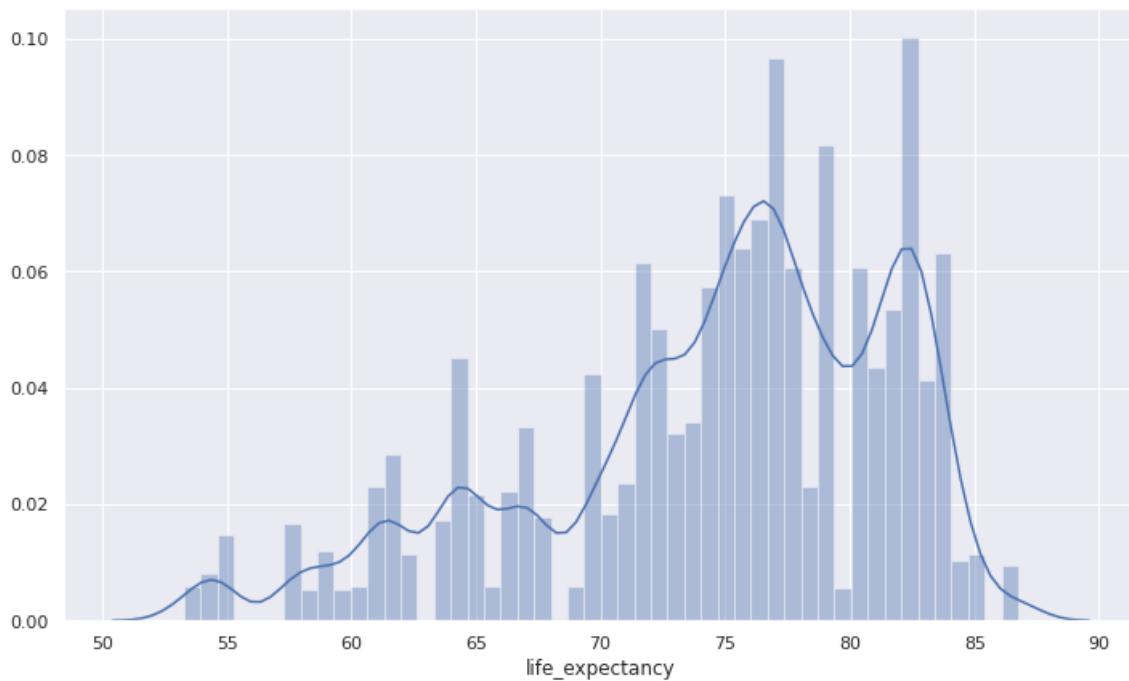


In [36]:

```
sns.distplot(features["life_expectancy"])
```

Out[36]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6fa631320>
```



Bivariate Analysis of Features

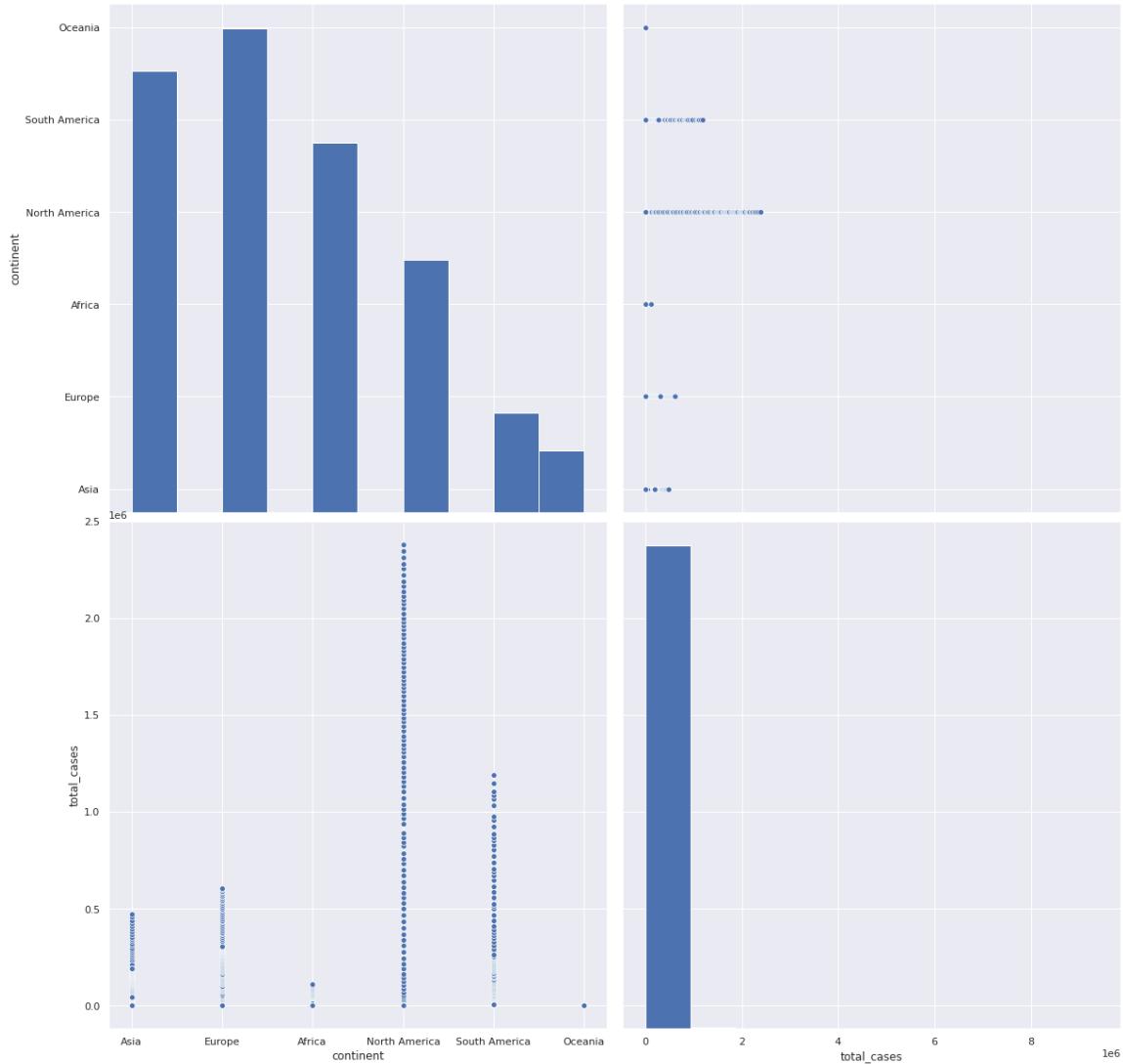
In this section we will do a bivariate of each feature with another one. For this process we will be usng seaborn library's function `pairplot`. The first parameter will be the dataset of features, next parameter will be name of two columns on which we are doing a bivariate analysis, third parameter height is given for figure size

In [41]:

```
sns.pairplot(features, vars=["continent", "total_cases"], height=8)
```

Out[41]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f9a1ef98>
```

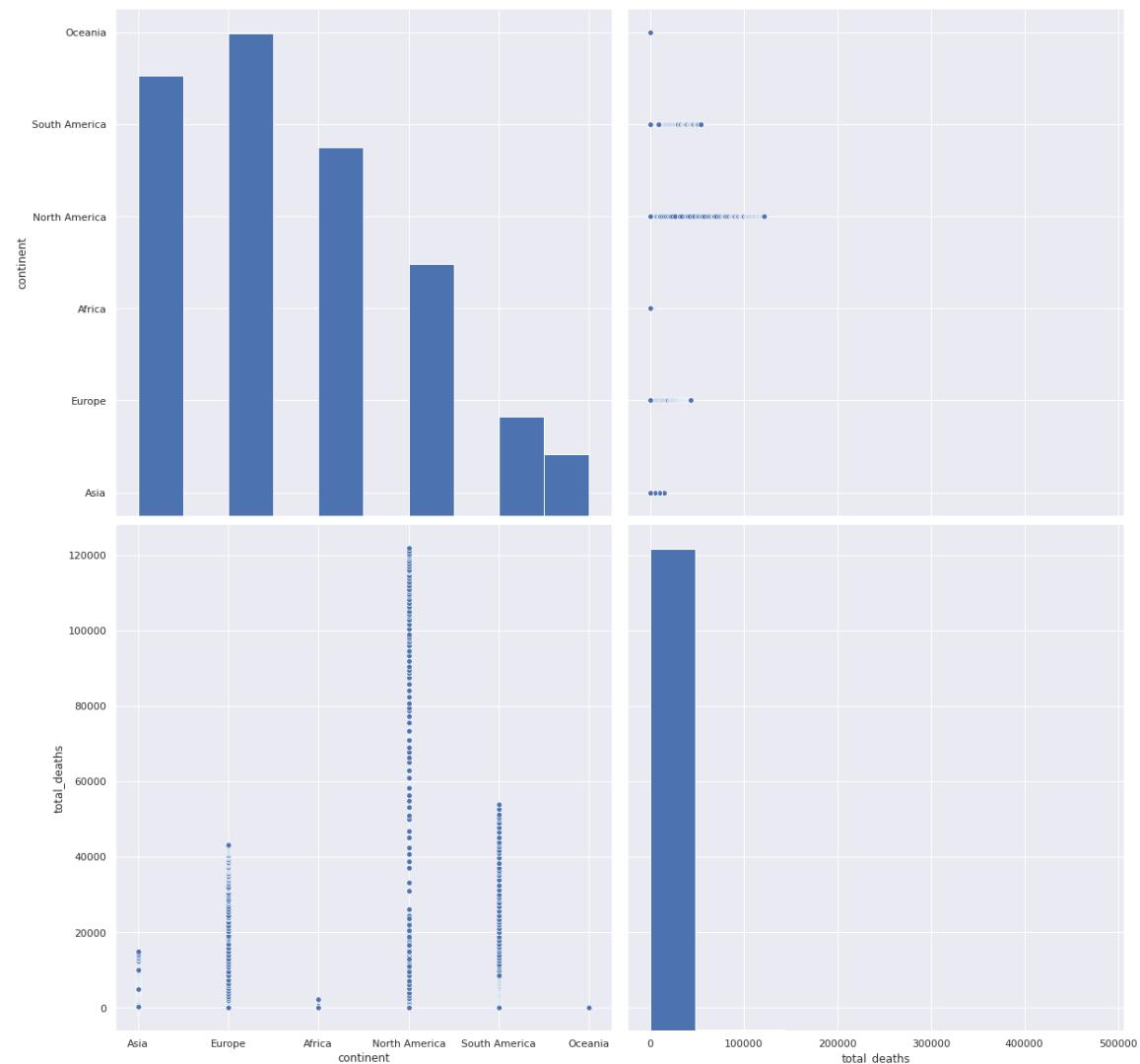


In [42]:

```
sns.pairplot(features, vars=["continent", "total_deaths"], height=8)
```

Out[42]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f930ddd8>
```

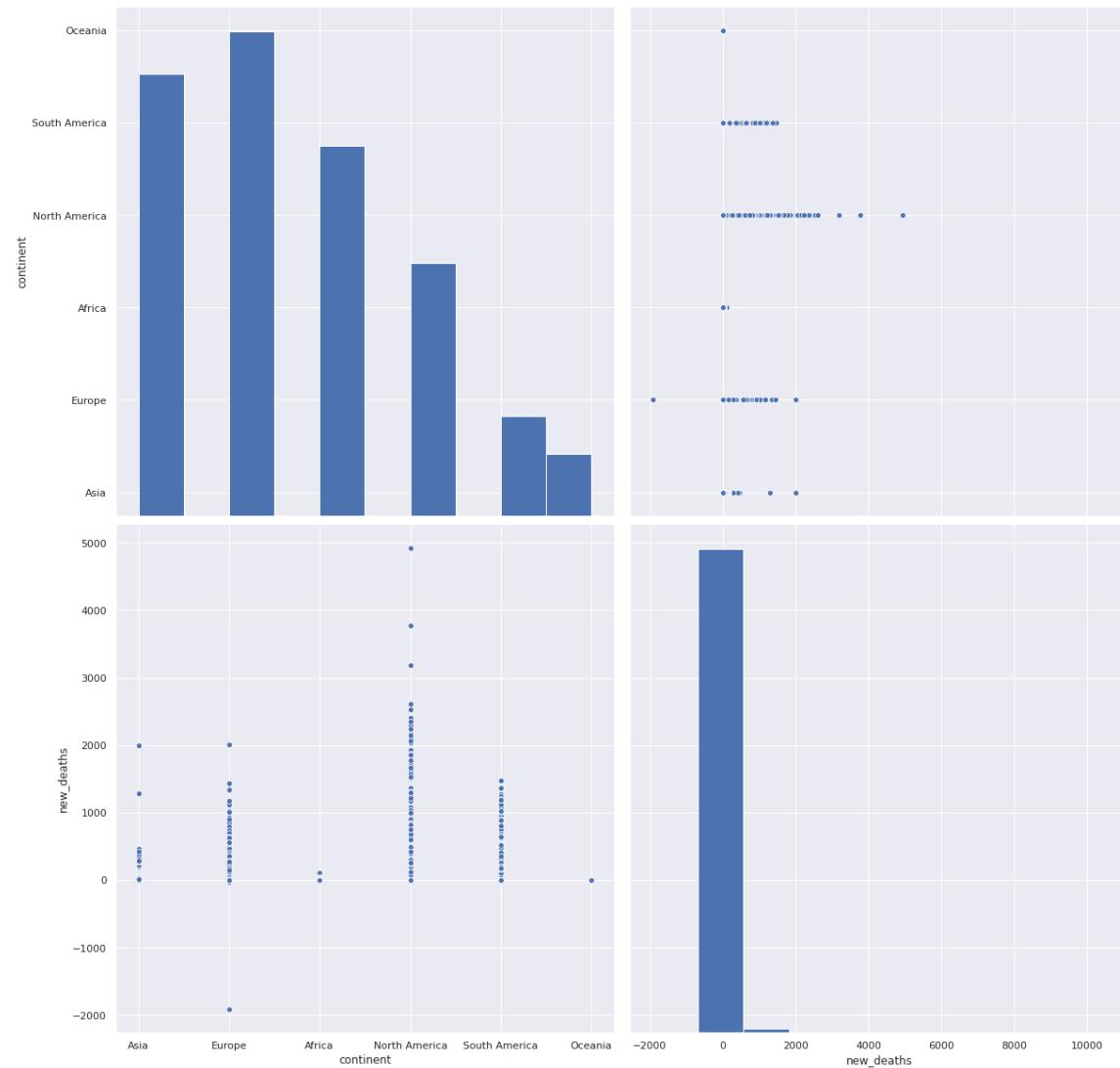


In [43]:

```
sns.pairplot(features, vars=["continent", "new_deaths"], height=8)
```

Out[43]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f913cf28>
```

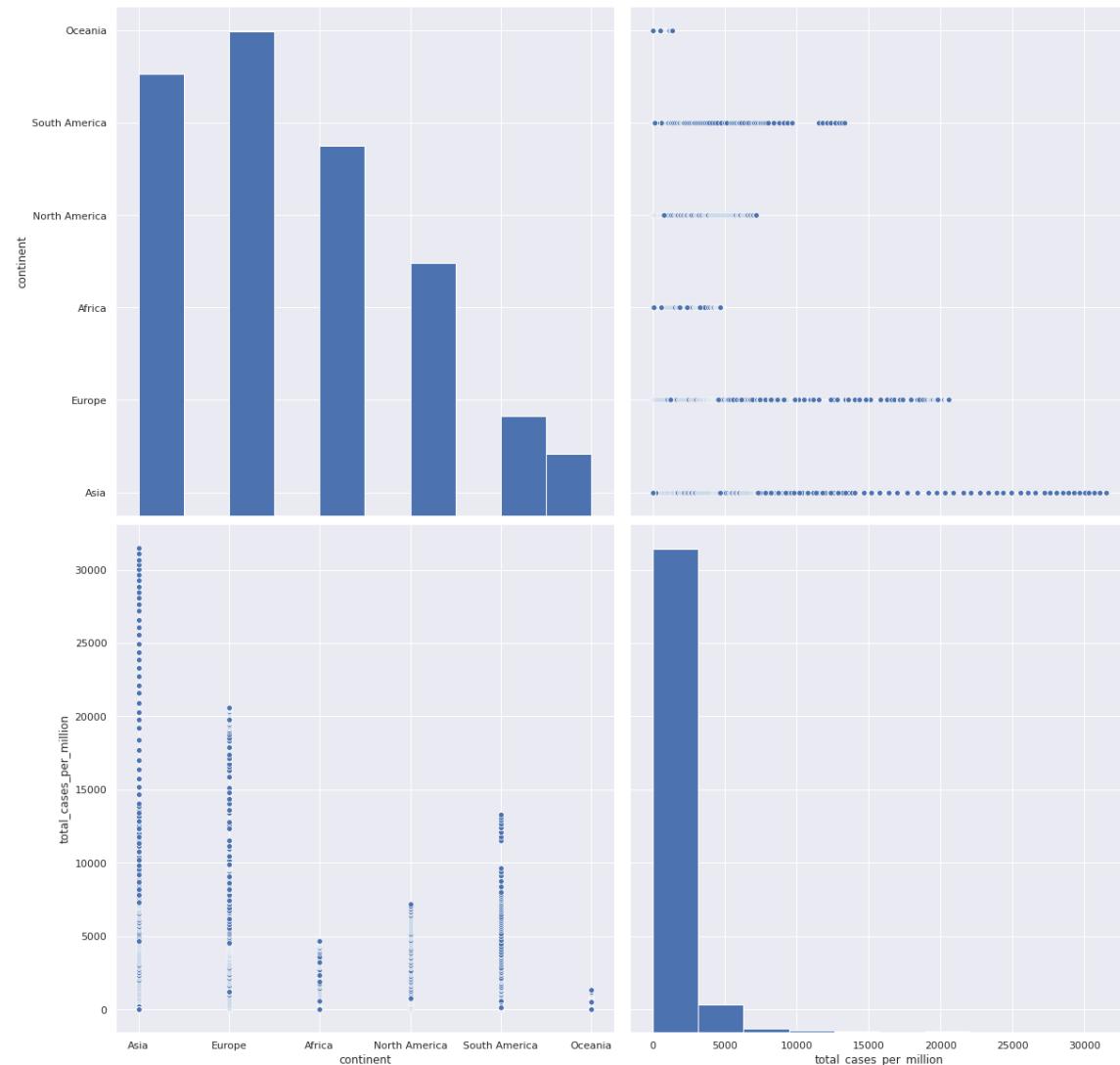


In [44]:

```
sns.pairplot(features, vars=["continent", "total_cases_per_million"], height=8)
```

Out[44]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f91c2c18>
```

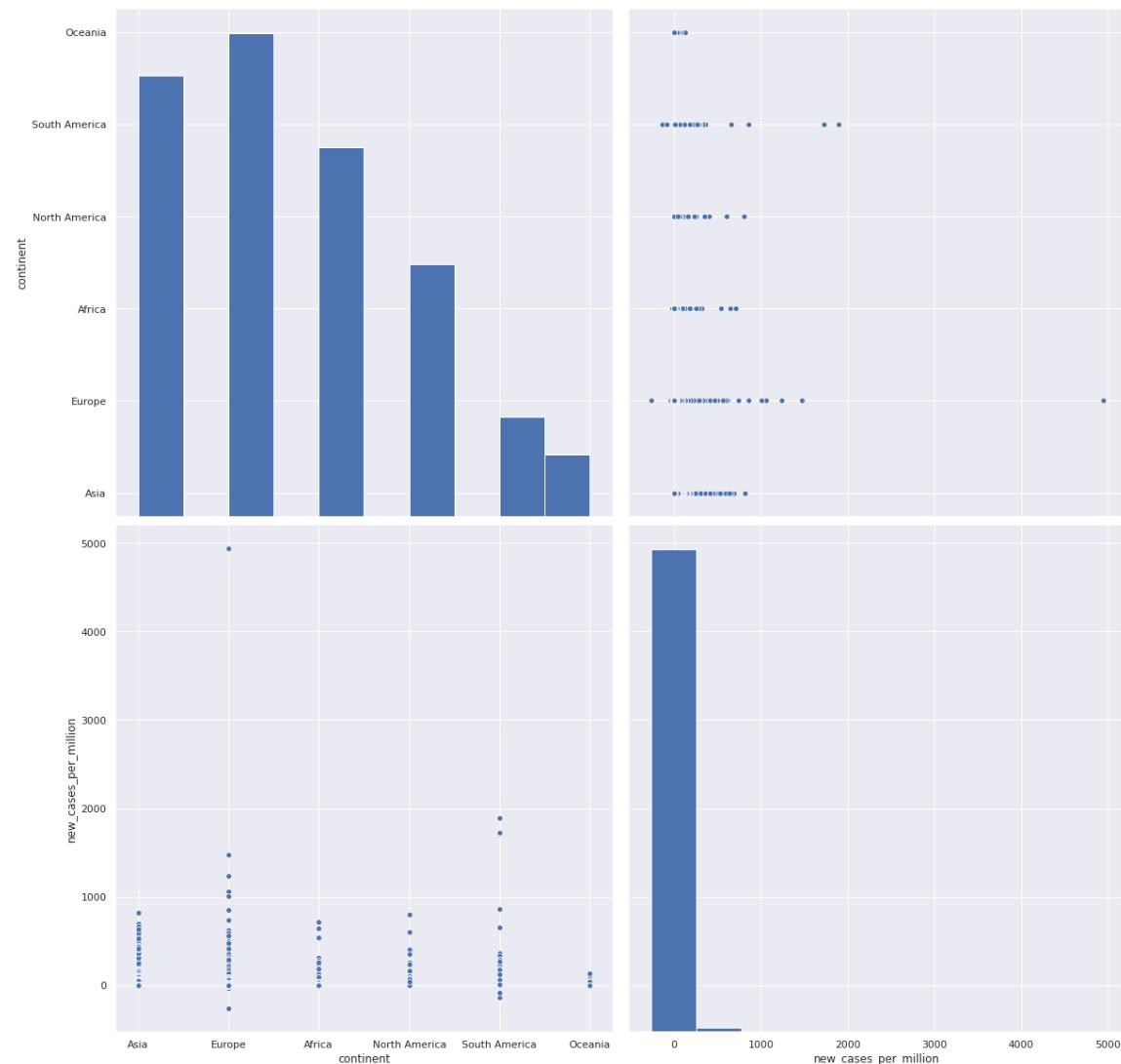


In [45]:

```
sns.pairplot(features, vars=["continent", "new_cases_per_million"], height=8)
```

Out[45]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6fa14b470>
```

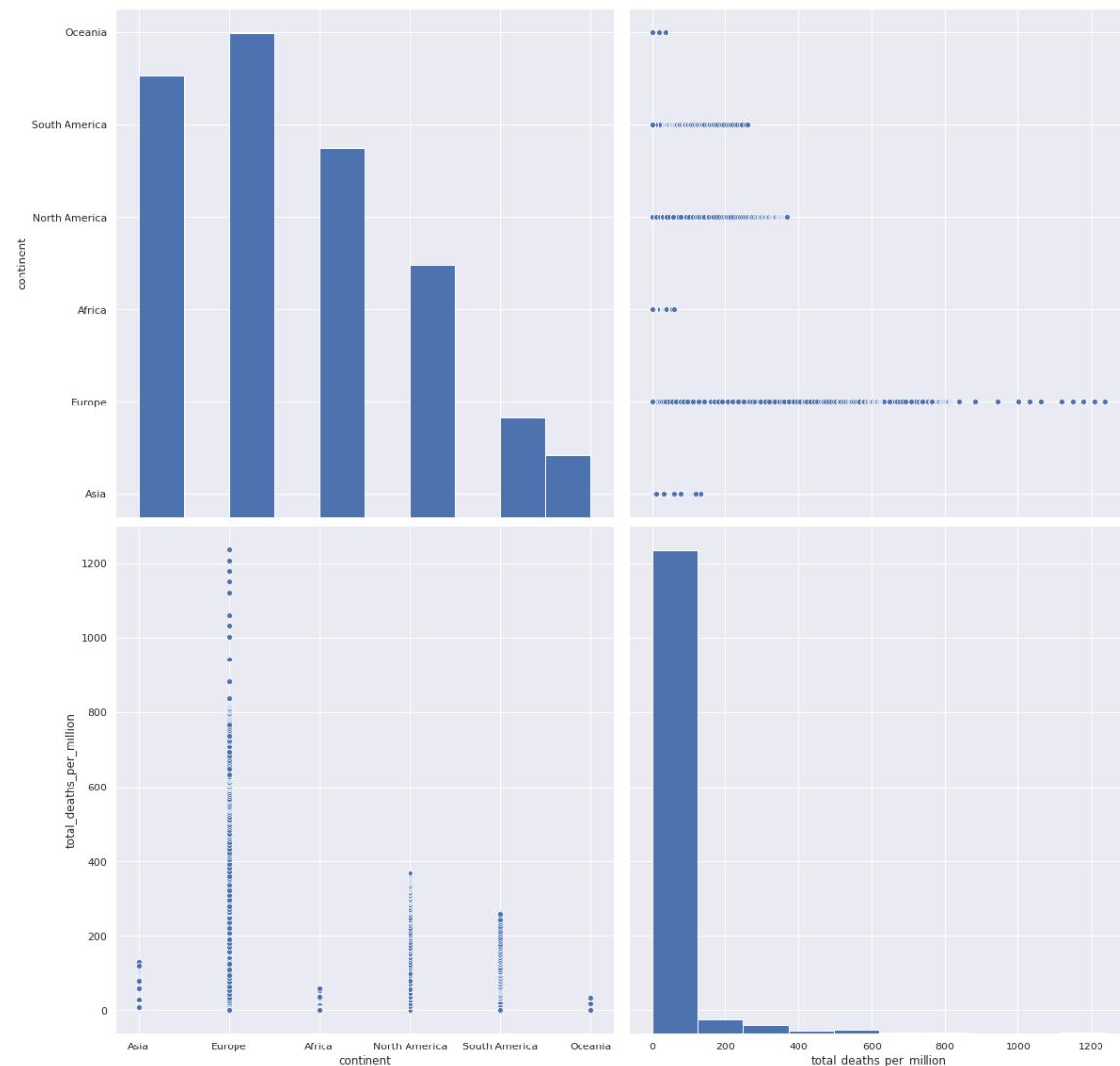


In [46]:

```
sns.pairplot(features, vars=["continent", "total_deaths_per_million"], height=8)
```

Out[46]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f843e5f8>
```

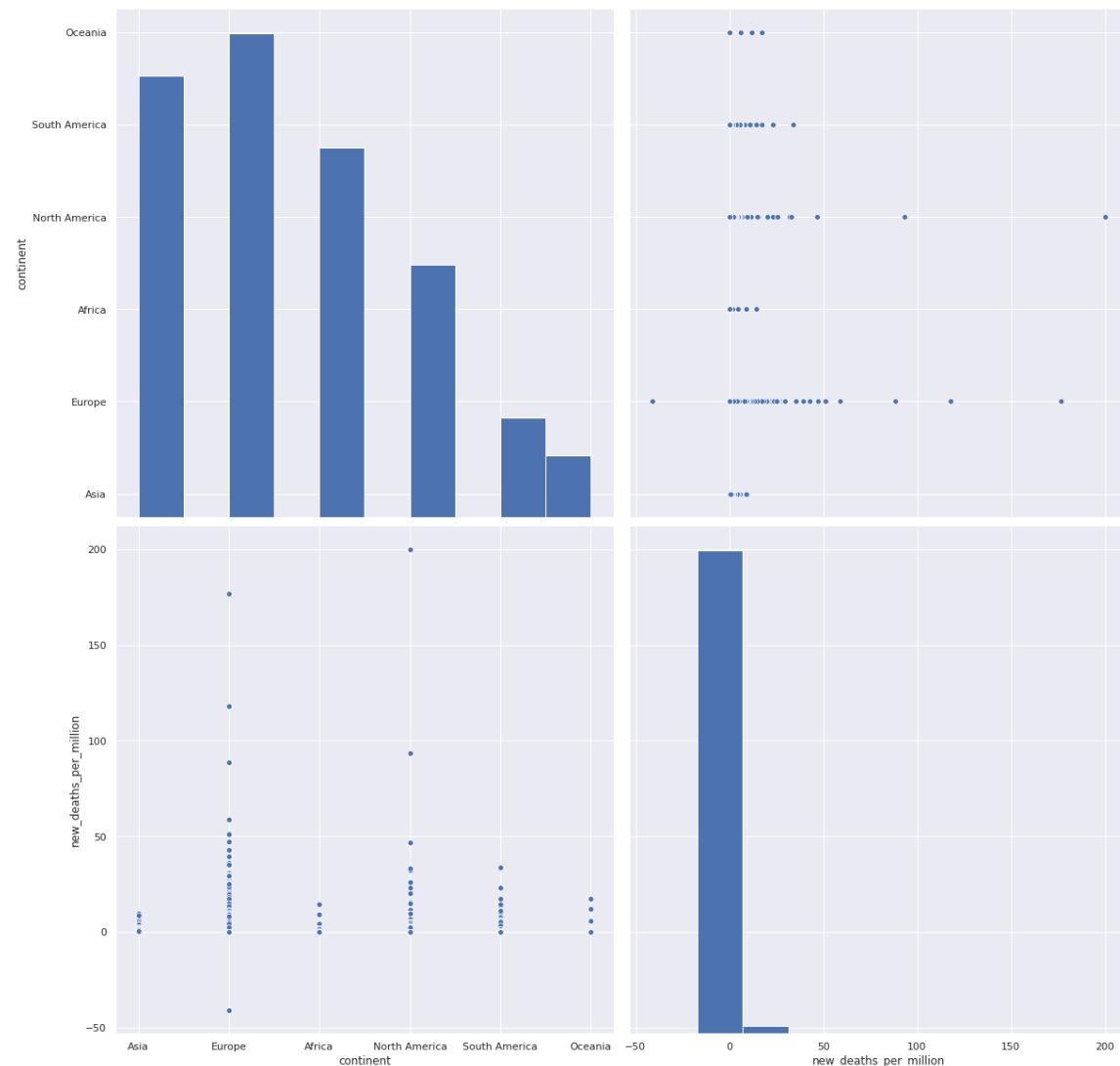


In [47]:

```
sns.pairplot(features, vars=["continent", "new_deaths_per_million"], height=8)
```

Out[47]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f81557f0>
```

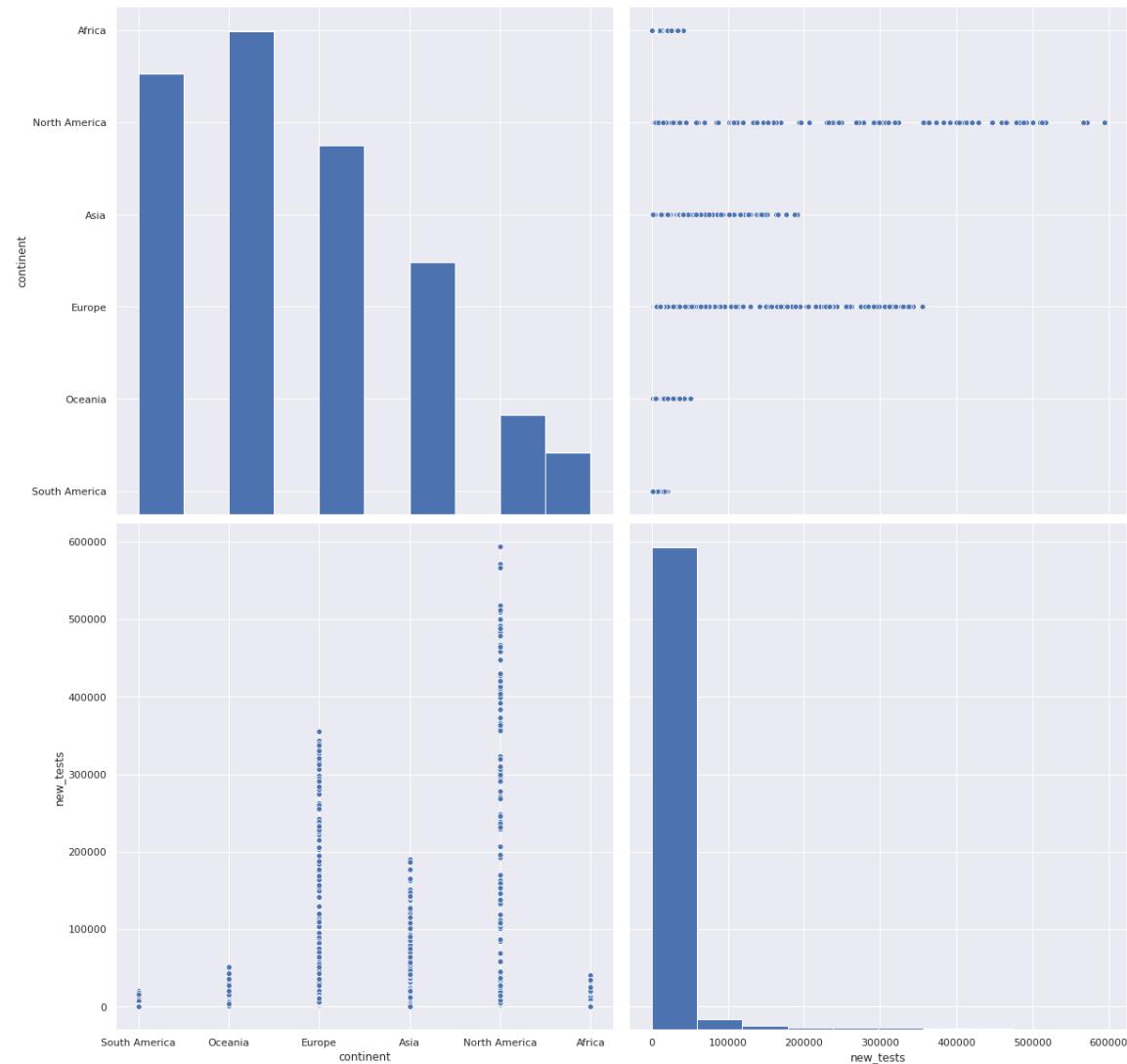


In [48]:

```
sns.pairplot(features, vars=["continent", "new_tests"], height=8)
```

Out[48]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f80946a0>
```

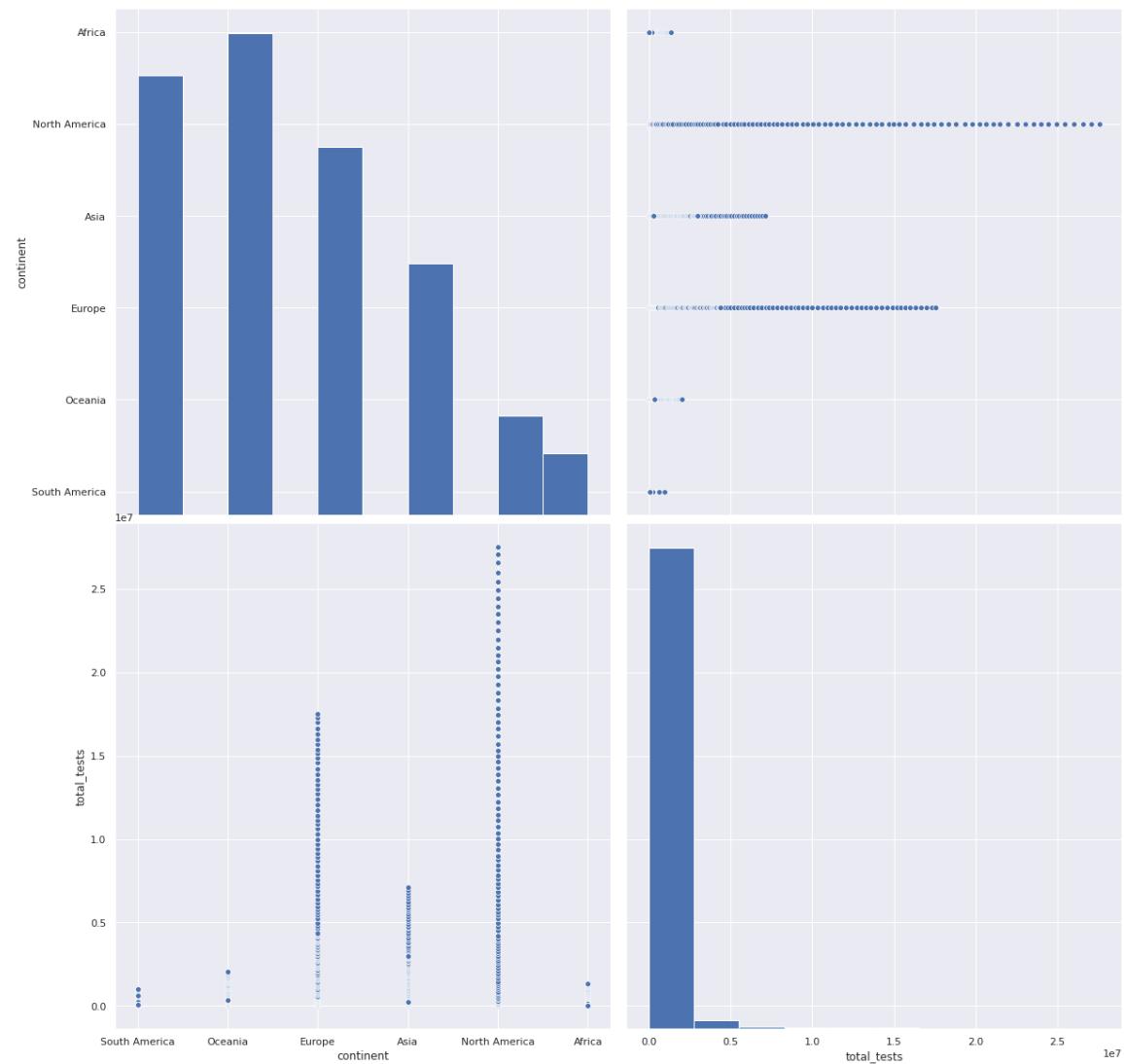


In [49]:

```
sns.pairplot(features, vars=["continent", "total_tests"], height=8)
```

Out[49]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f2d5bf28>
```

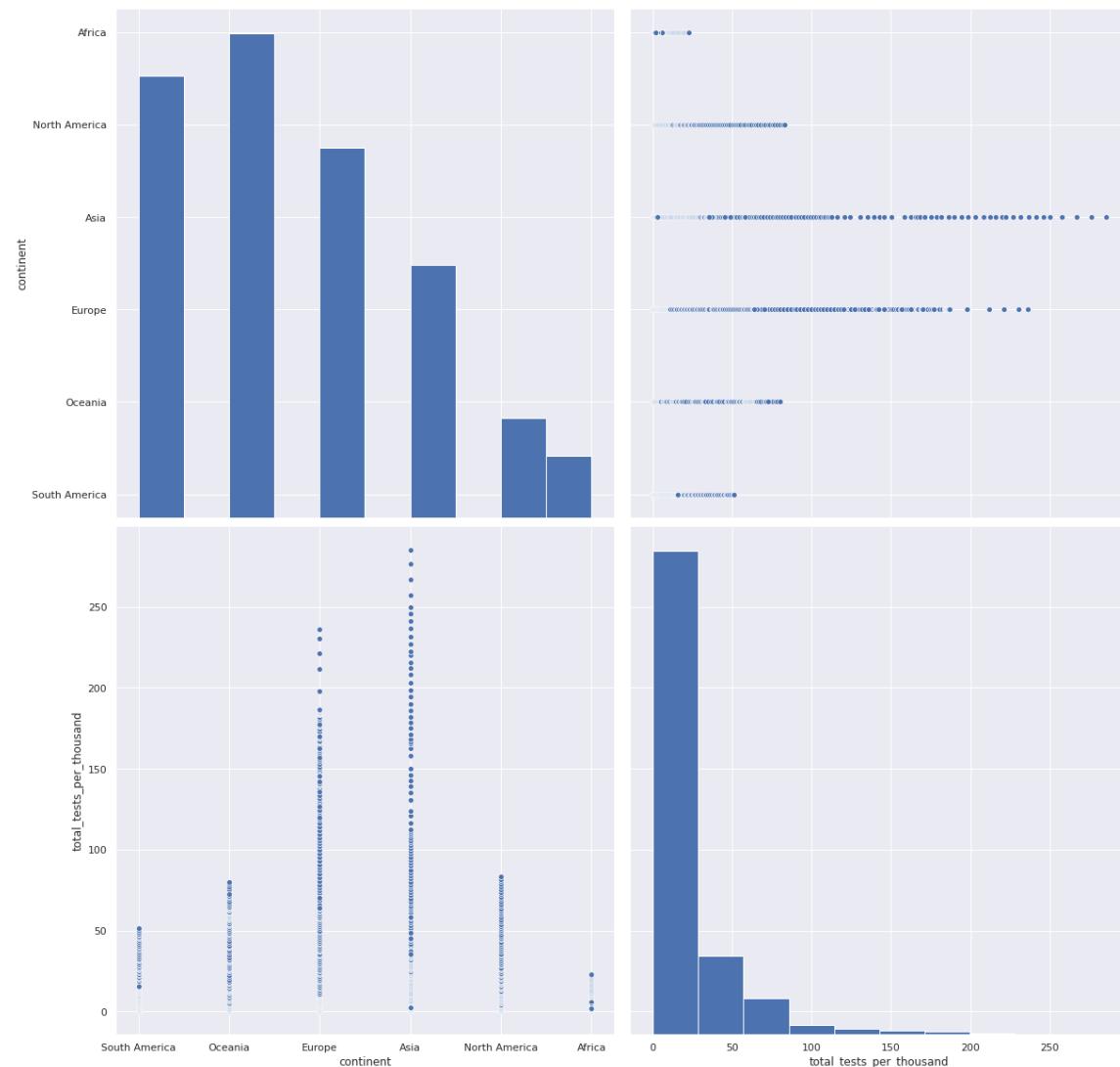


In [50]:

```
sns.pairplot(features, vars=["continent", "total_tests_per_thousand"], height=8)
```

Out[50]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f2cb8160>
```

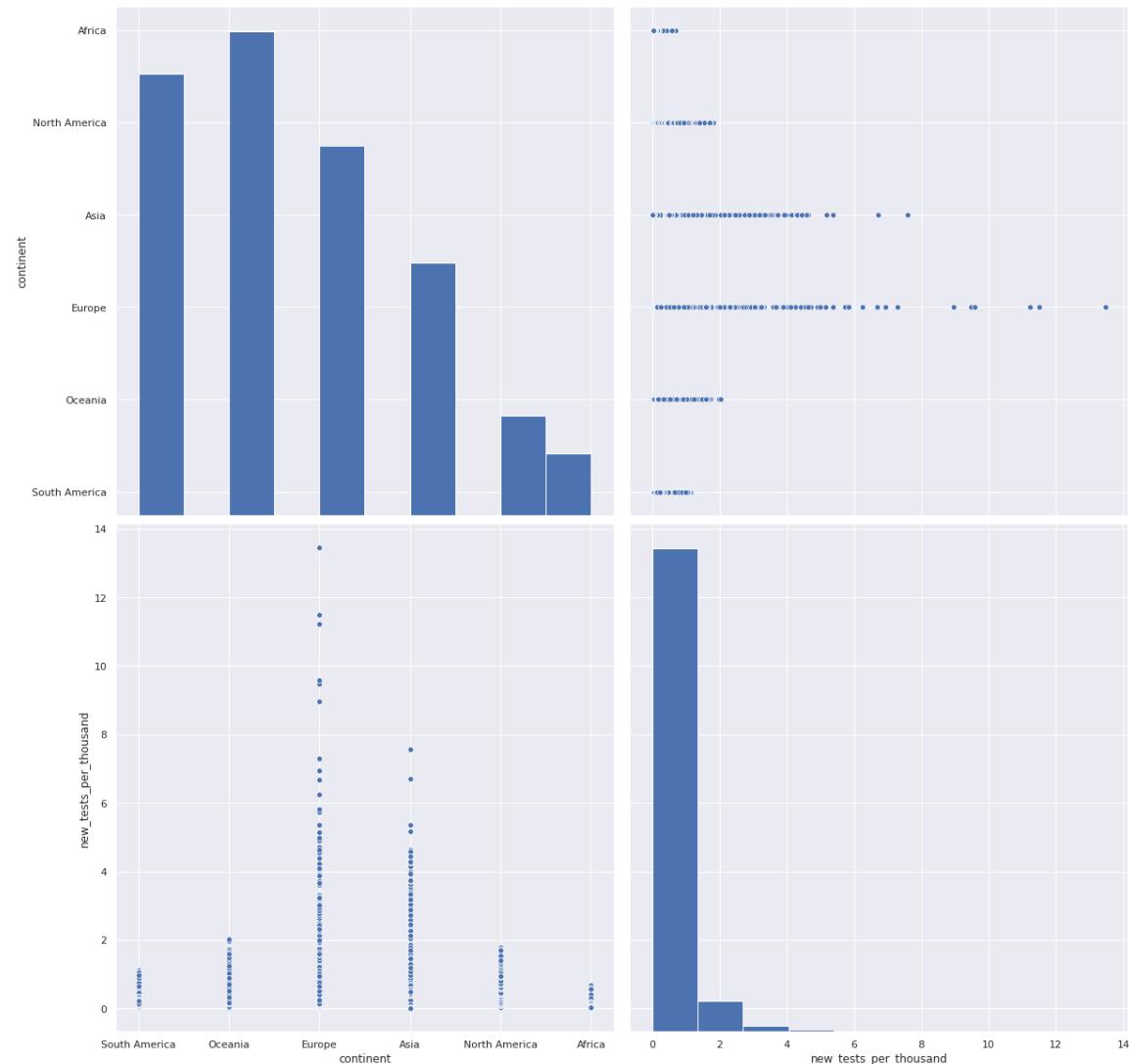


In [51]:

```
sns.pairplot(features, vars=["continent", "new_tests_per_thousand"], height=8)
```

Out[51]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f2a4e400>
```

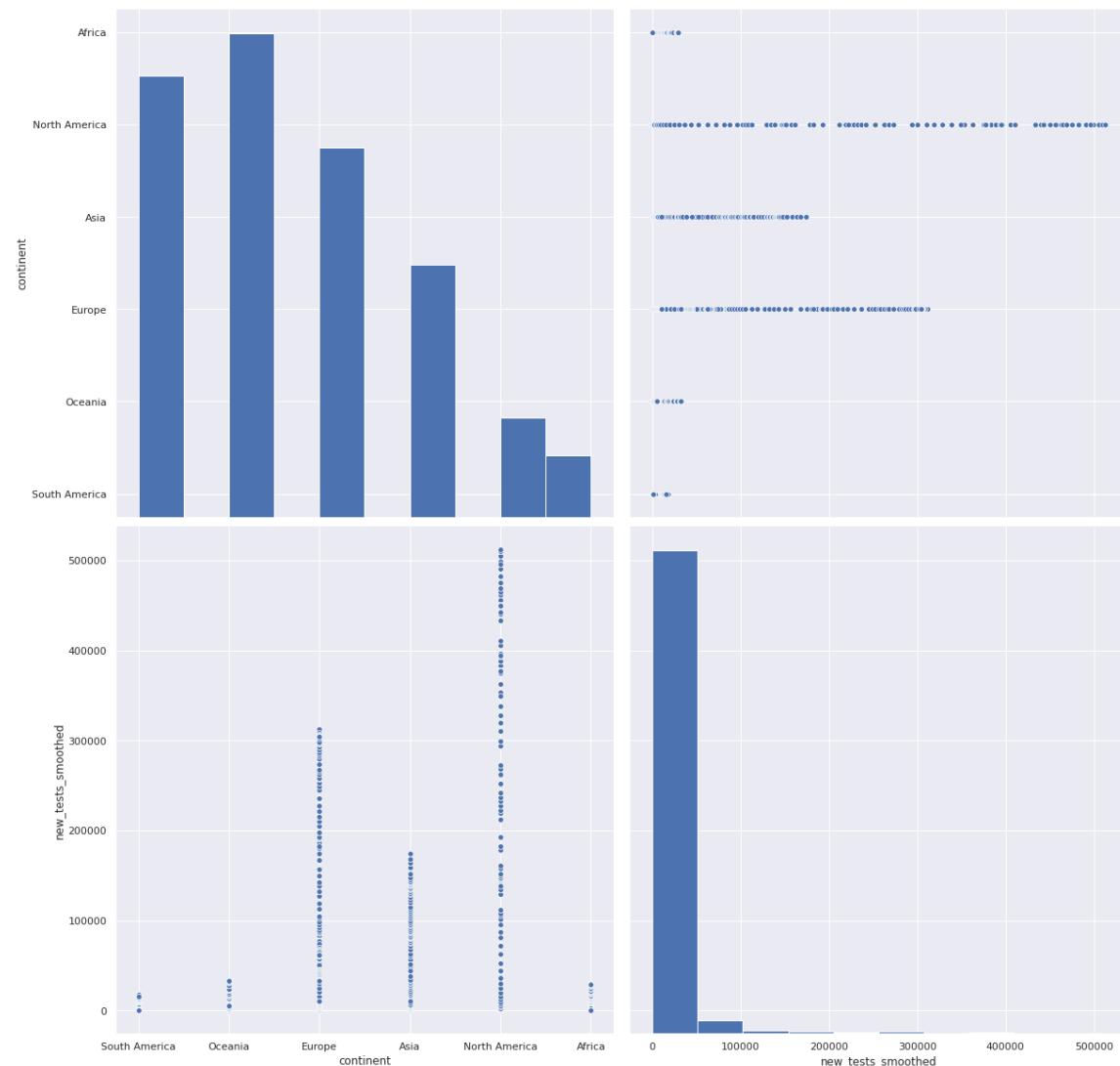


In [52]:

```
sns.pairplot(features, vars=["continent", "new_tests_smoothed"], height=8)
```

Out[52]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f2744d30>
```

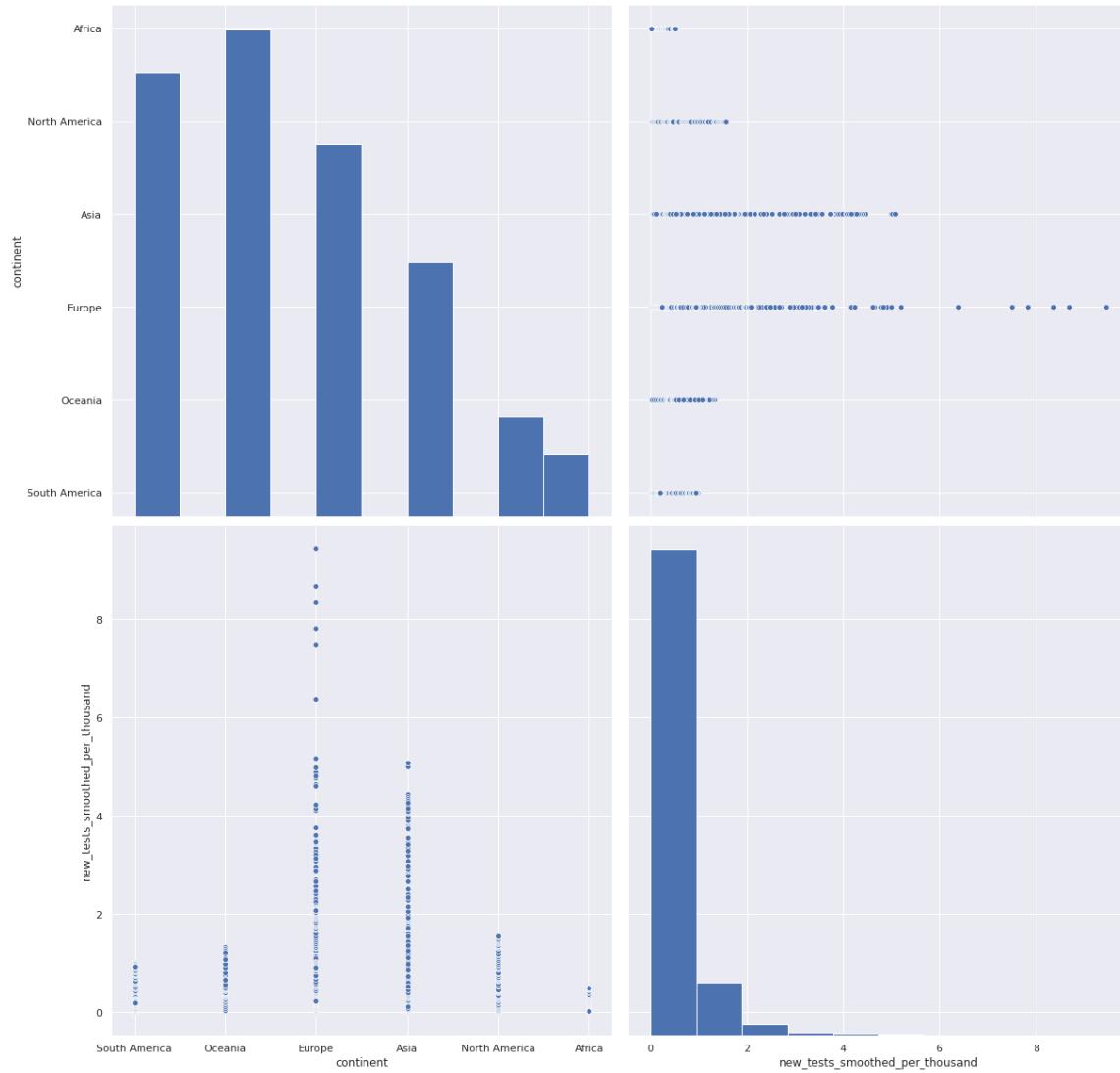


In [53]:

```
sns.pairplot(features, vars=["continent", "new_tests_smoothed_per_thousand"], height=8)
```

Out[53]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f9f6ba58>
```

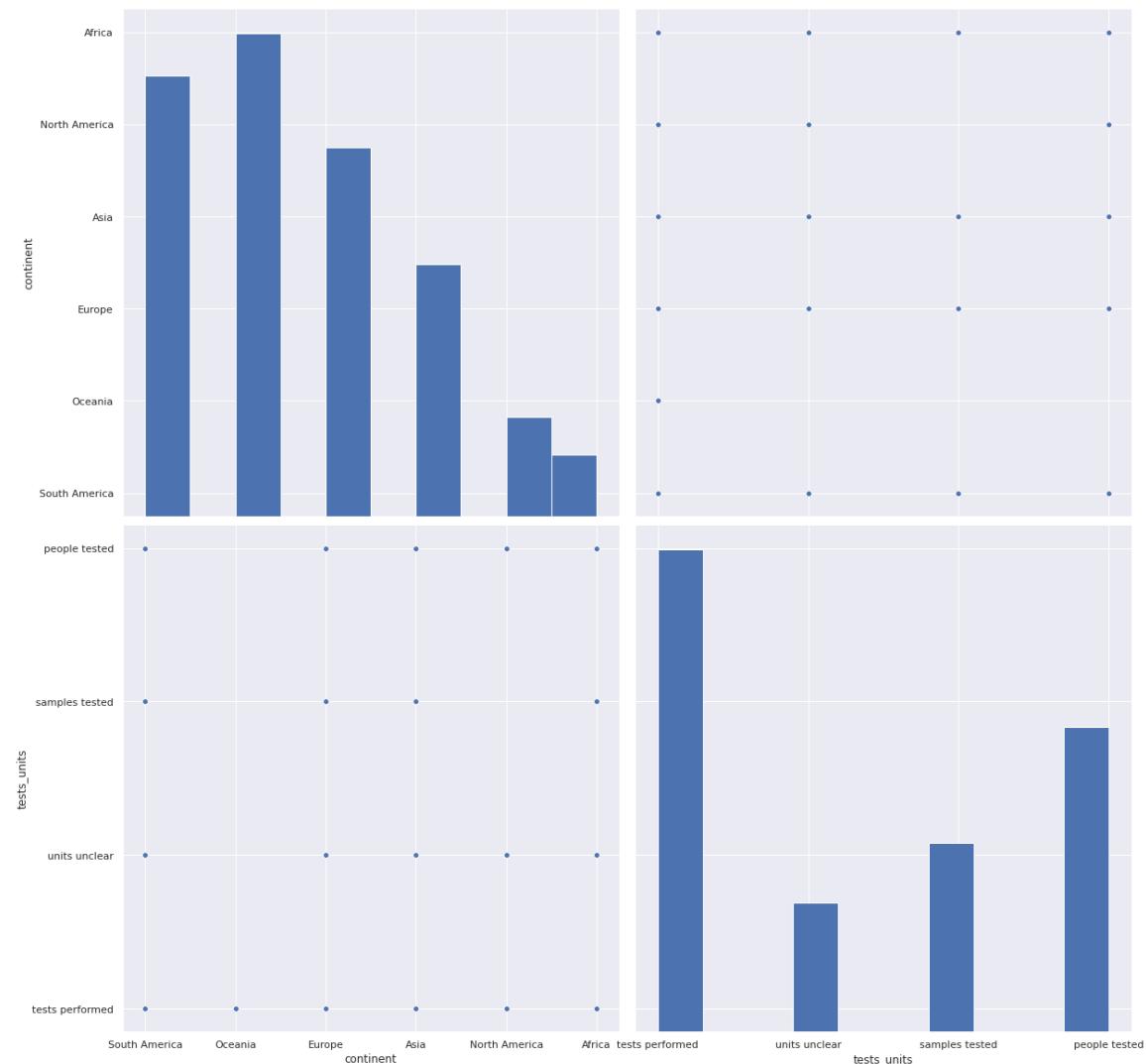


In [54]:

```
sns.pairplot(features, vars=["continent", "tests_units"], height=8)
```

Out[54]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f23c61d0>
```

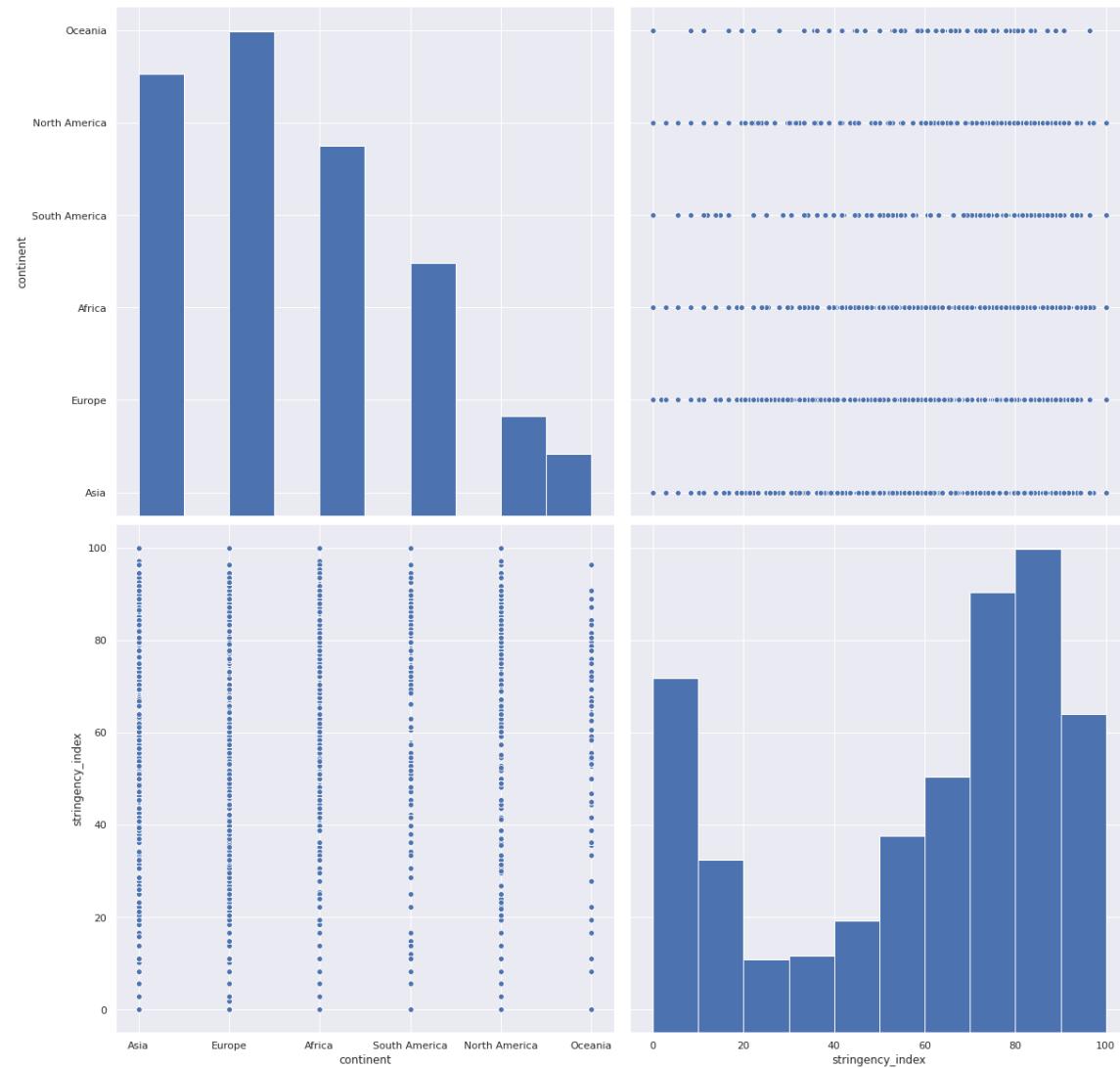


In [55]:

```
sns.pairplot(features, vars=["continent", "stringency_index"], height=8)
```

Out[55]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f259ff98>
```

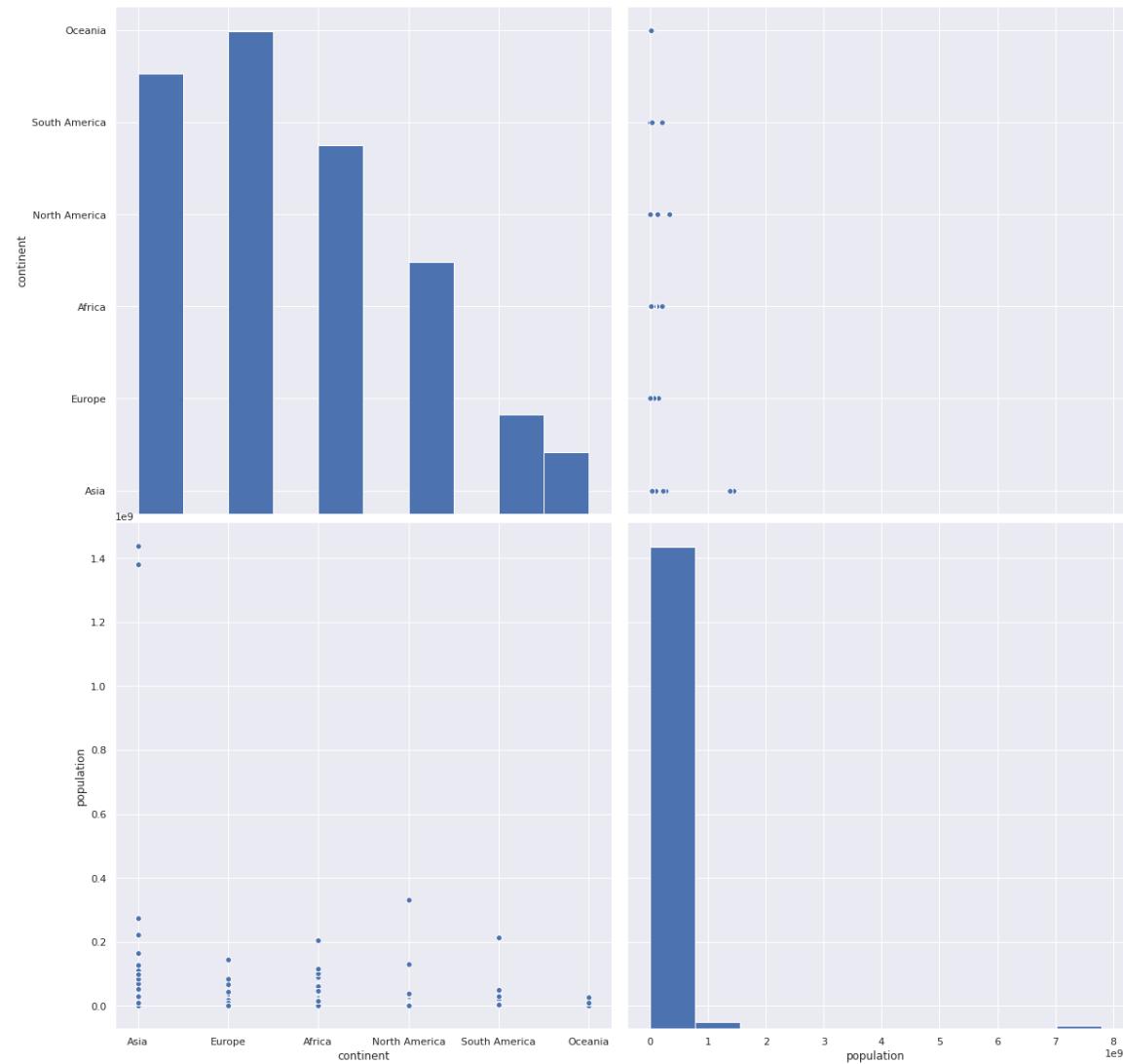


In [56]:

```
sns.pairplot(features, vars=["continent", "population"], height=8)
```

Out[56]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f200acc0>
```

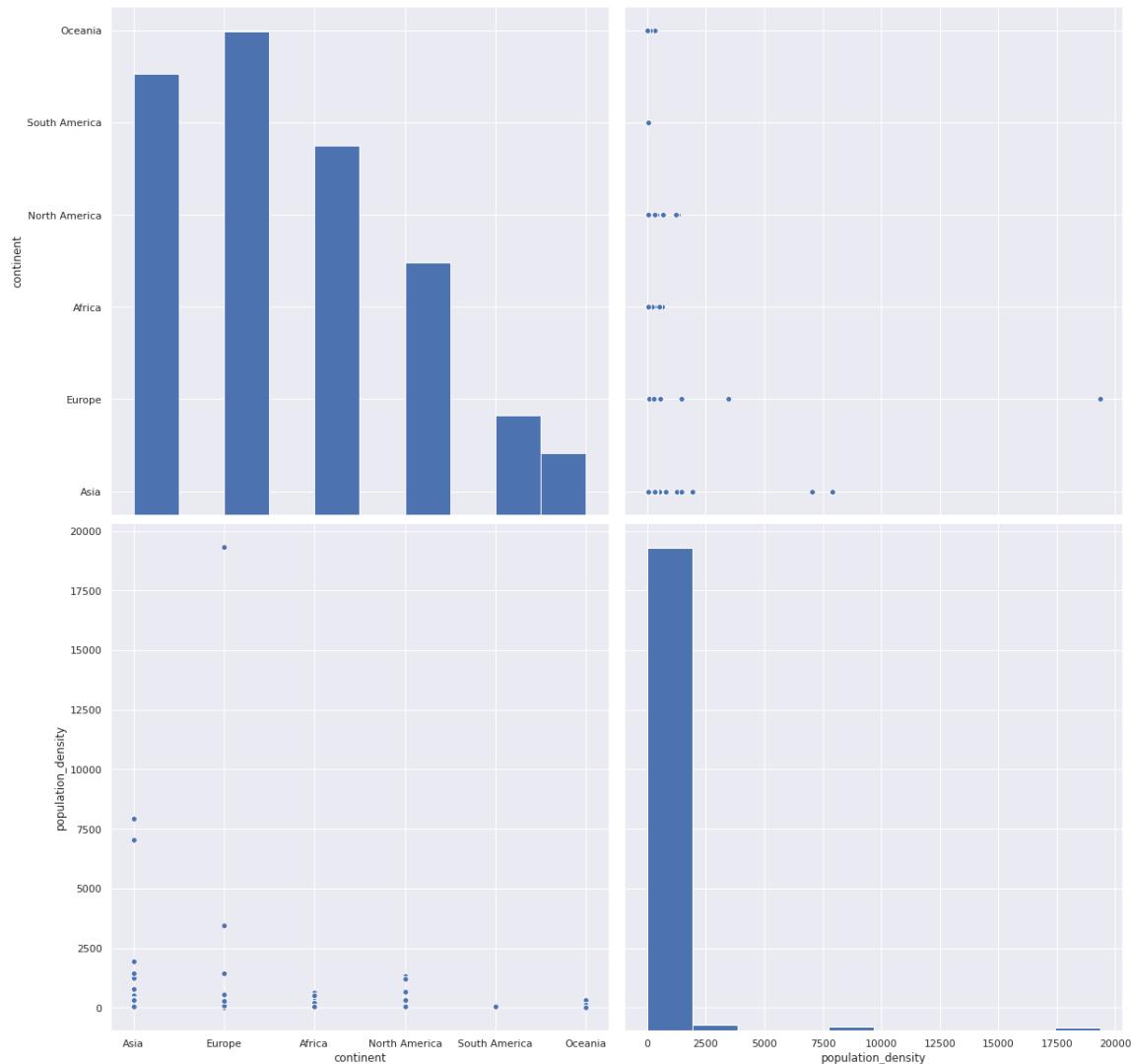


In [57]:

```
sns.pairplot(features, vars=["continent", "population_density"], height=8)
```

Out[57]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f23d1390>
```

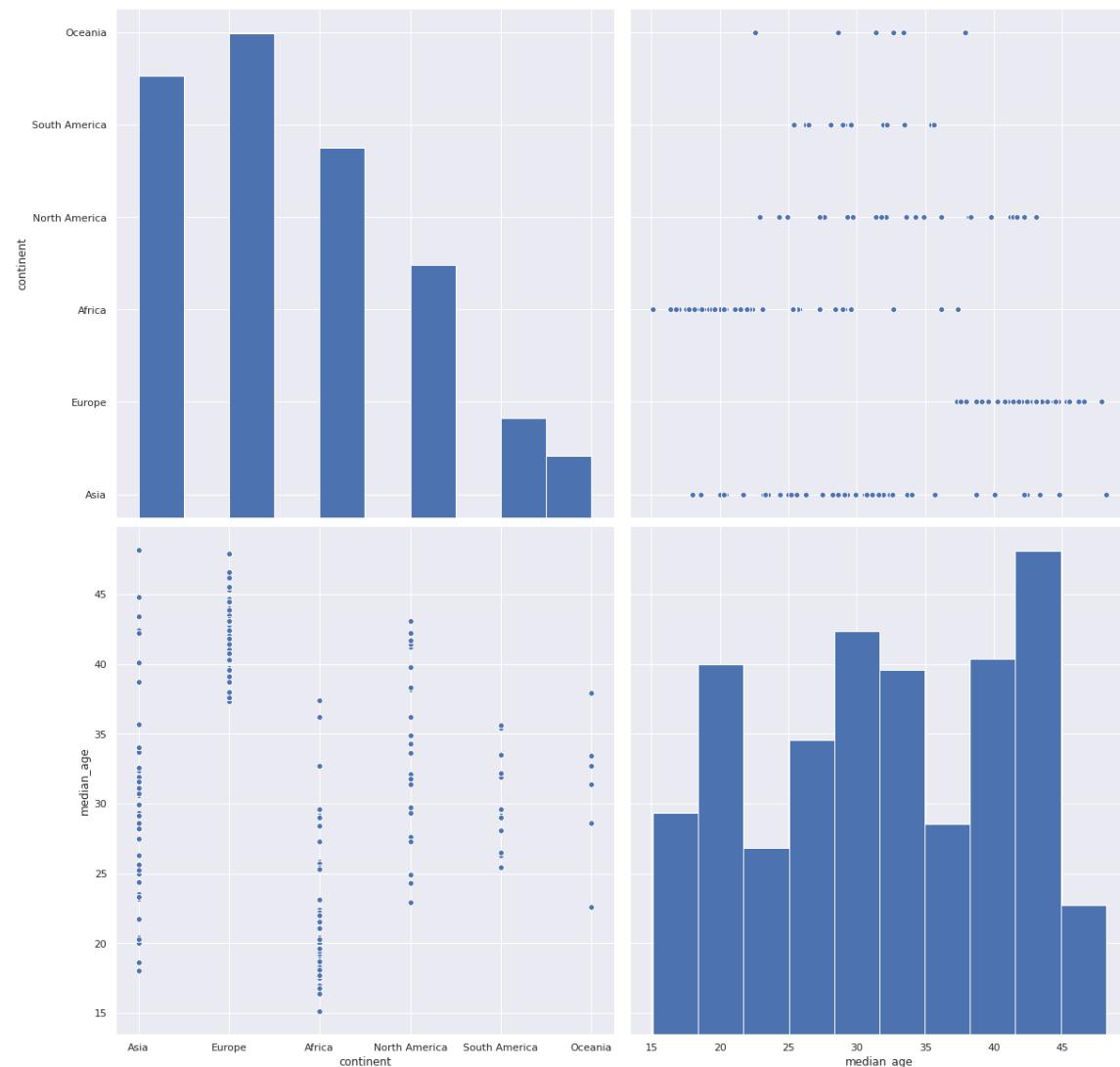


In [58]:

```
sns.pairplot(features, vars=["continent", "median_age"], height=8)
```

Out[58]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f1e1e710>
```

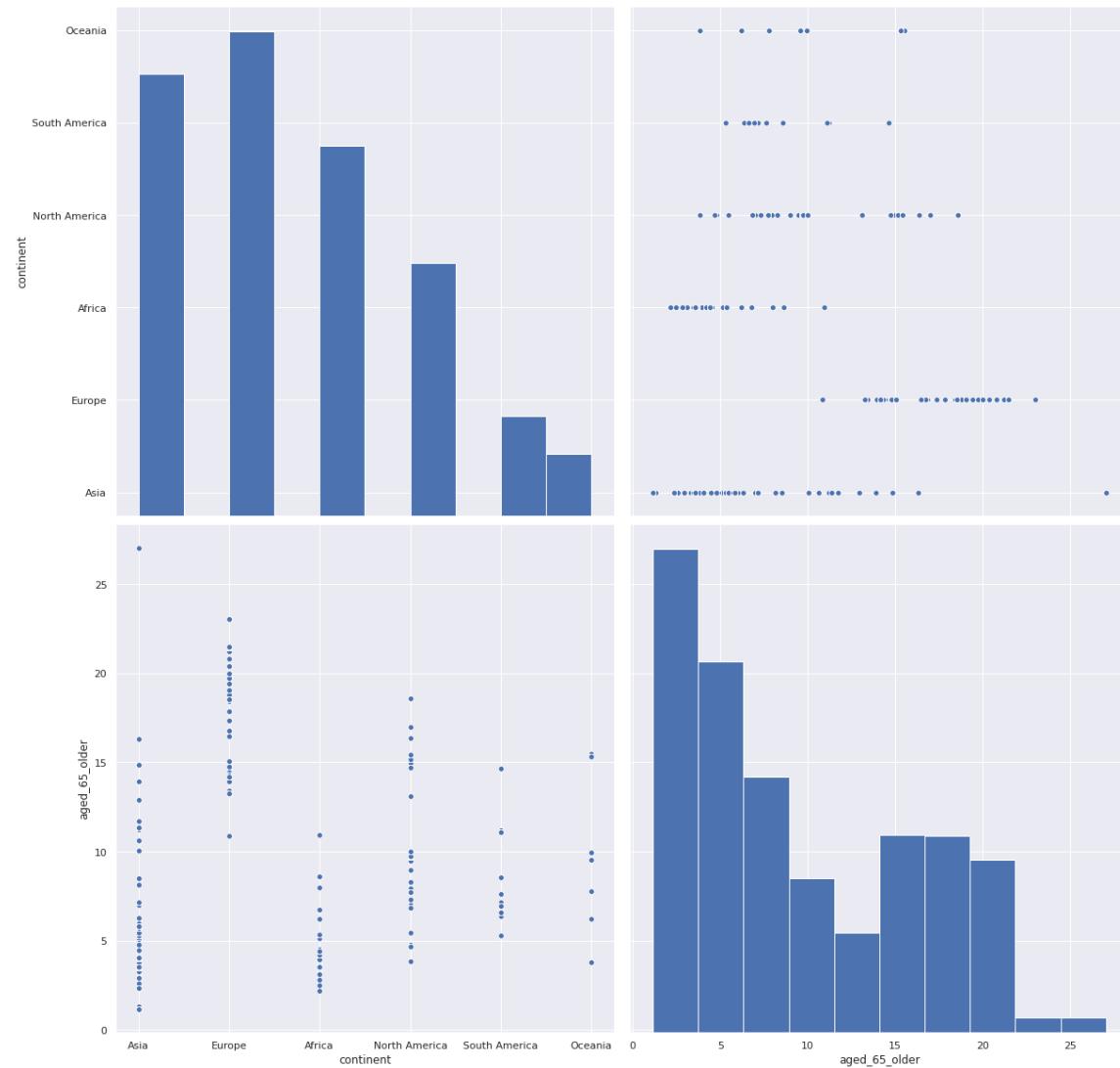


In [59]:

```
sns.pairplot(features, vars=["continent", "aged_65_older"], height=8)
```

Out[59]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f1a28ef0>
```

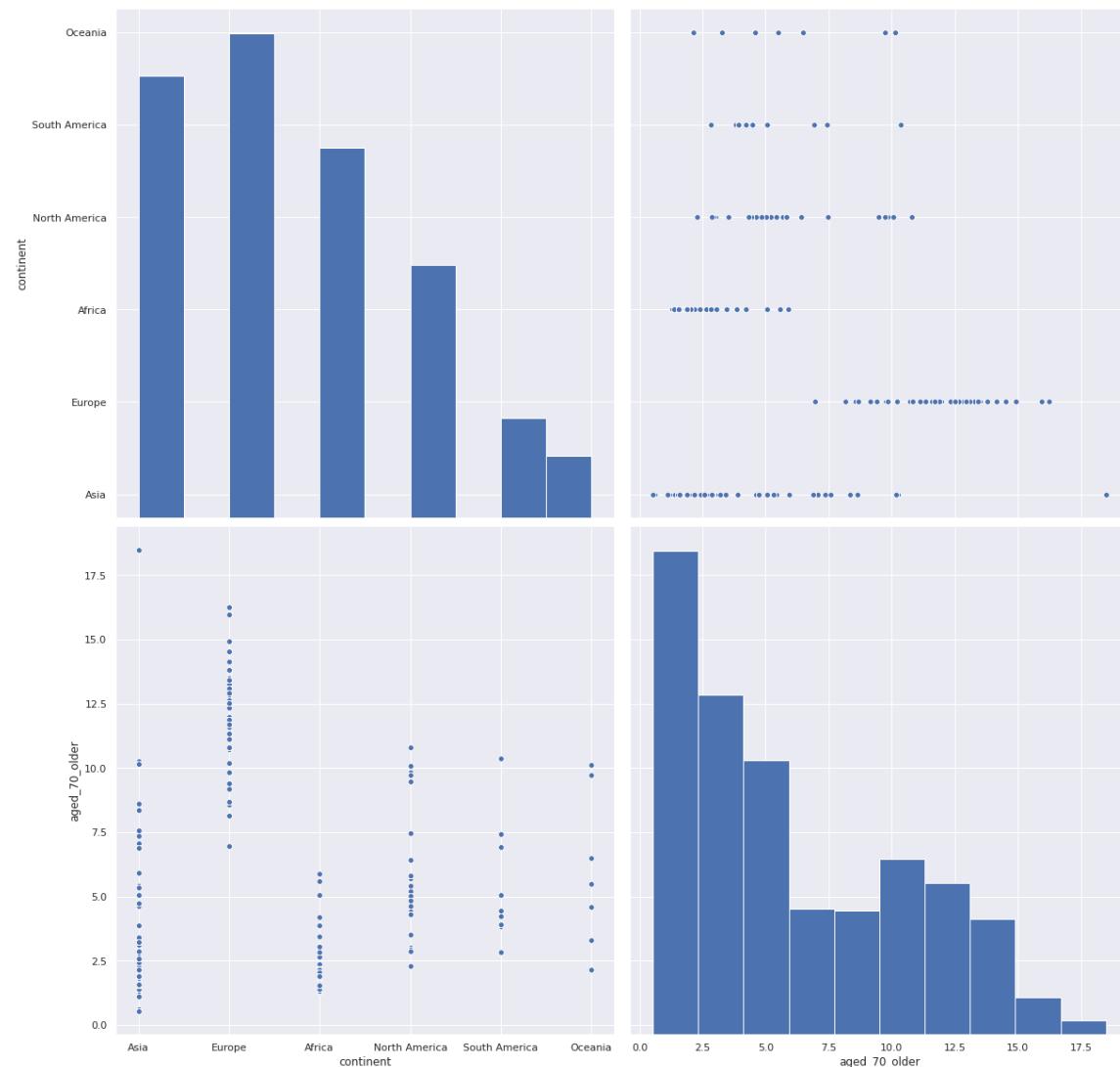


In [60]:

```
sns.pairplot(features, vars=["continent", "aged_70_older"], height=8)
```

Out[60]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f1863d68>
```

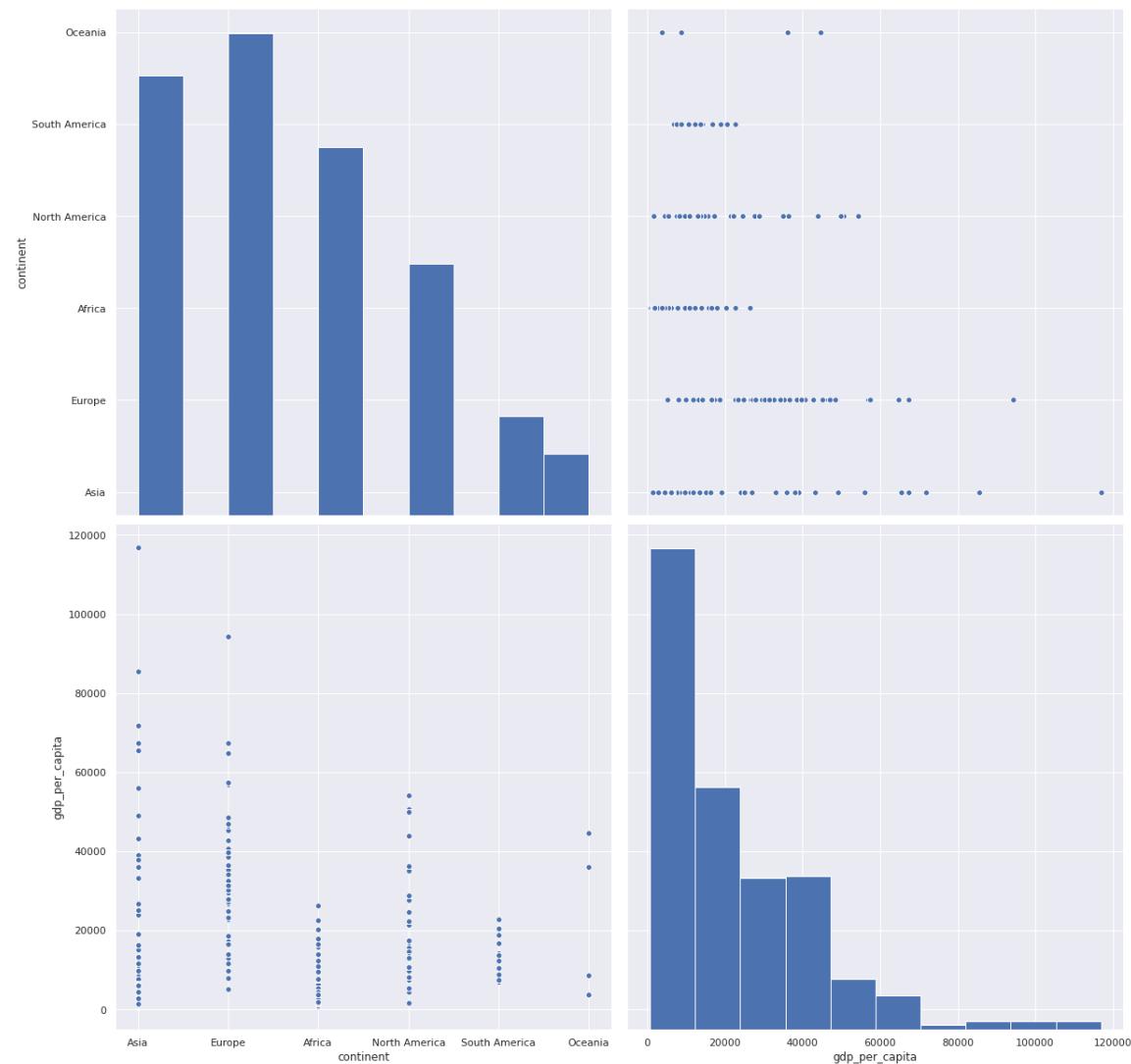


In [61]:

```
sns.pairplot(features, vars=["continent", "gdp_per_capita"], height=8)
```

Out[61]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f17720f0>
```

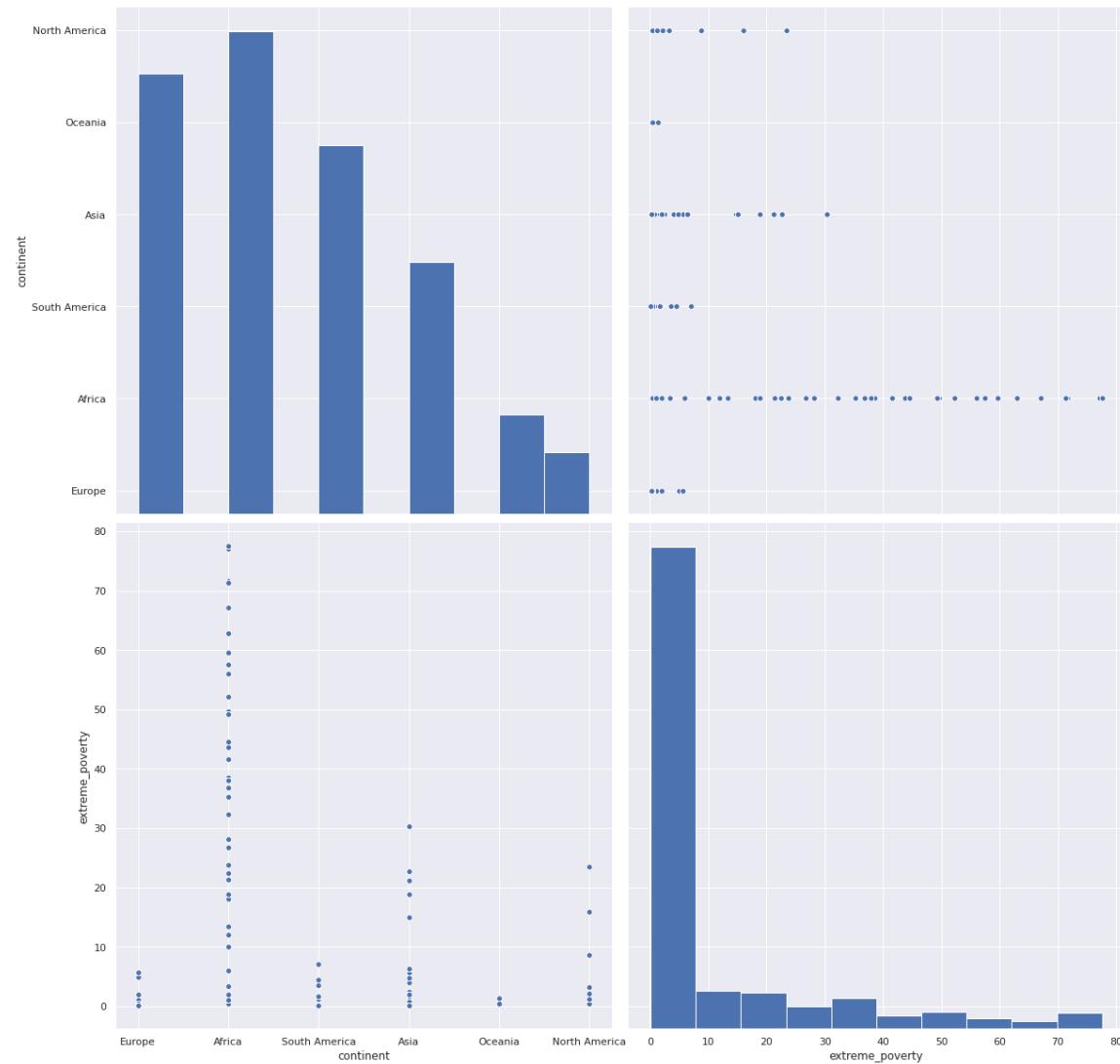


In [62]:

```
sns.pairplot(features, vars=["continent", "extreme_poverty"], height=8)
```

Out[62]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f18c2f98>
```

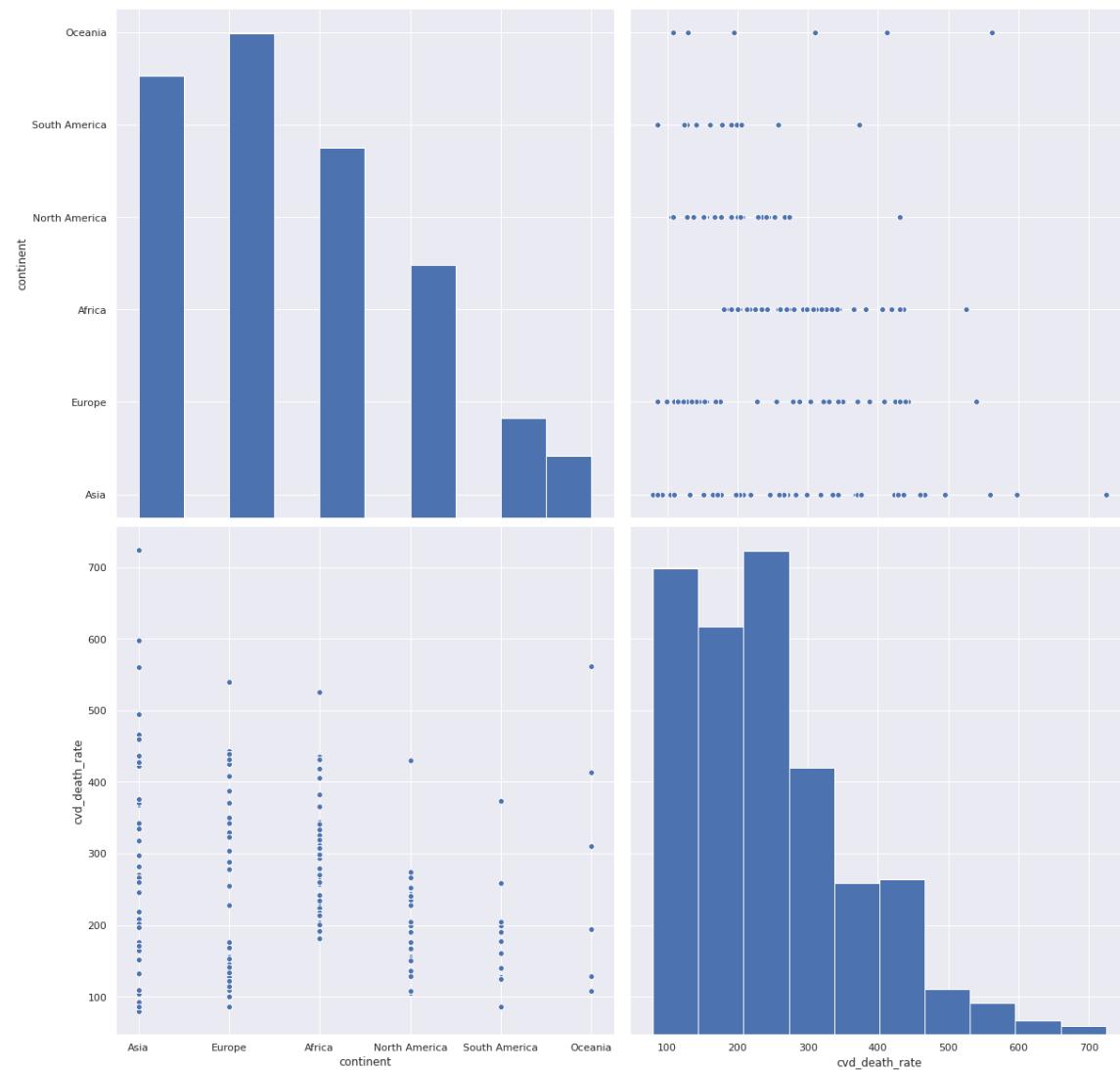


In [63]:

```
sns.pairplot(features, vars=["continent", "cvd_death_rate"], height=8)
```

Out[63]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f222bcc0>
```

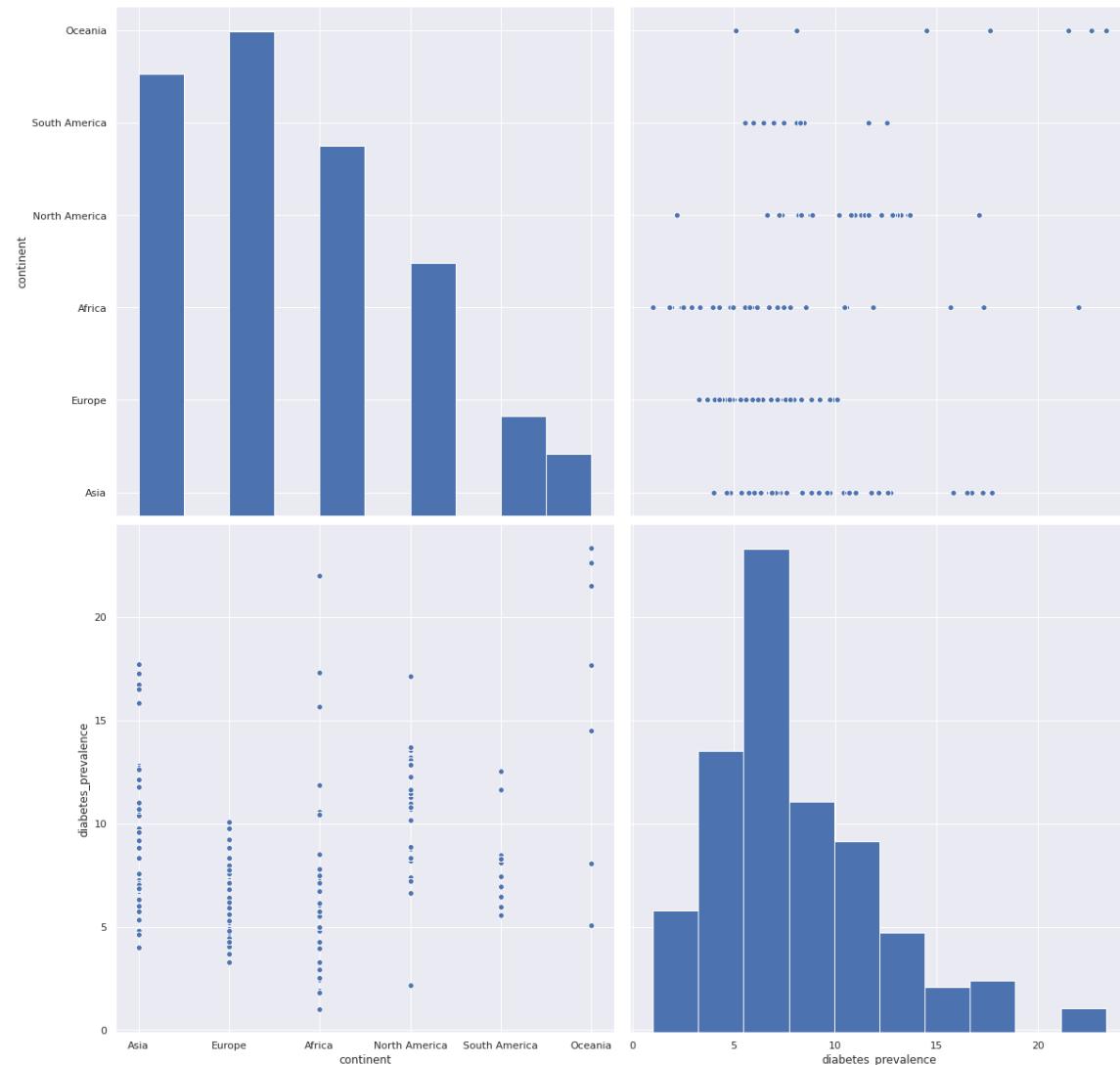


In [64]:

```
sns.pairplot(features, vars=["continent", "diabetes_prevalence"], height=8)
```

Out[64]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f10526d8>
```

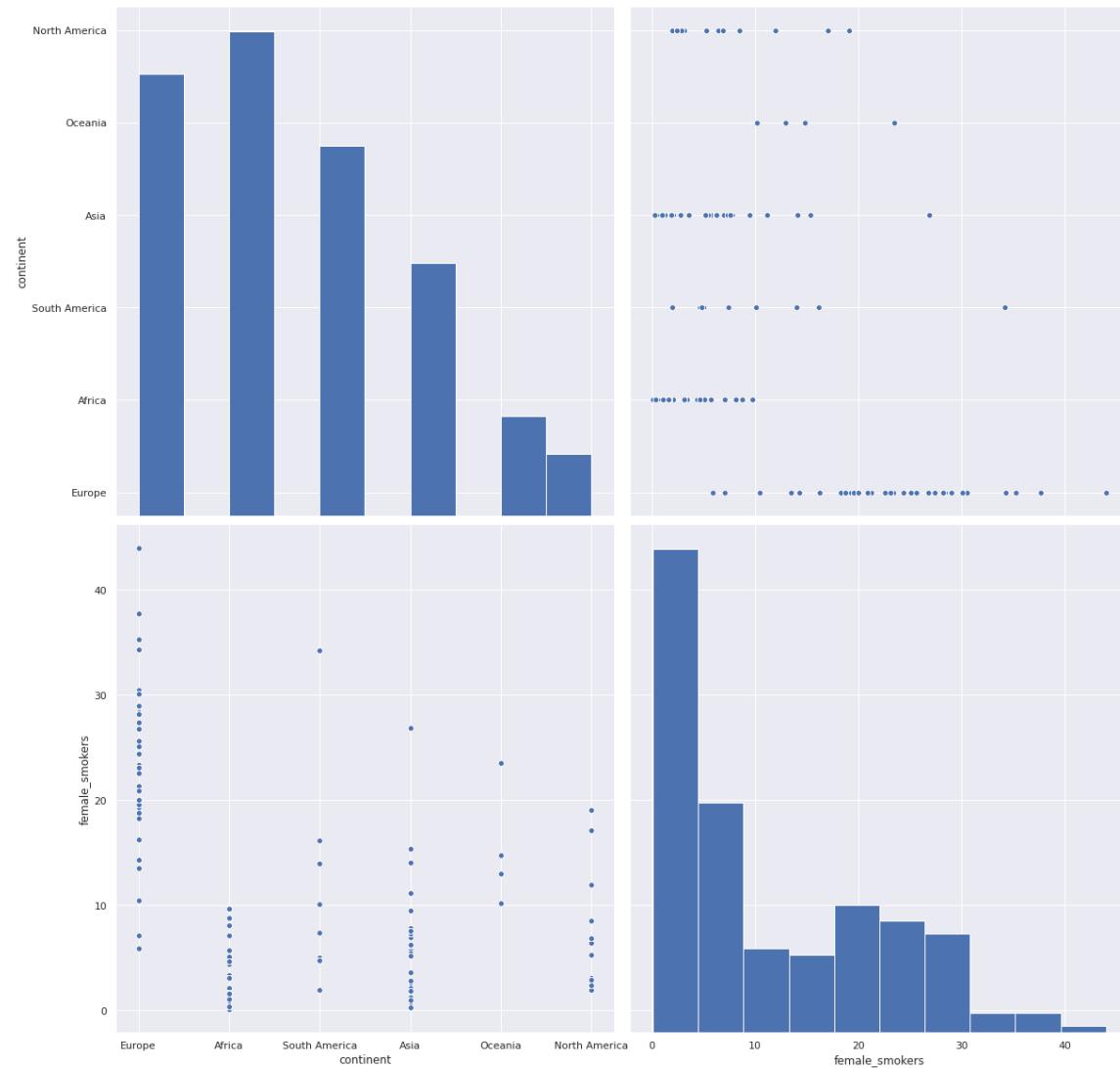


In [65]:

```
sns.pairplot(features, vars=["continent", "female_smokers"], height=8)
```

Out[65]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f0ebb978>
```

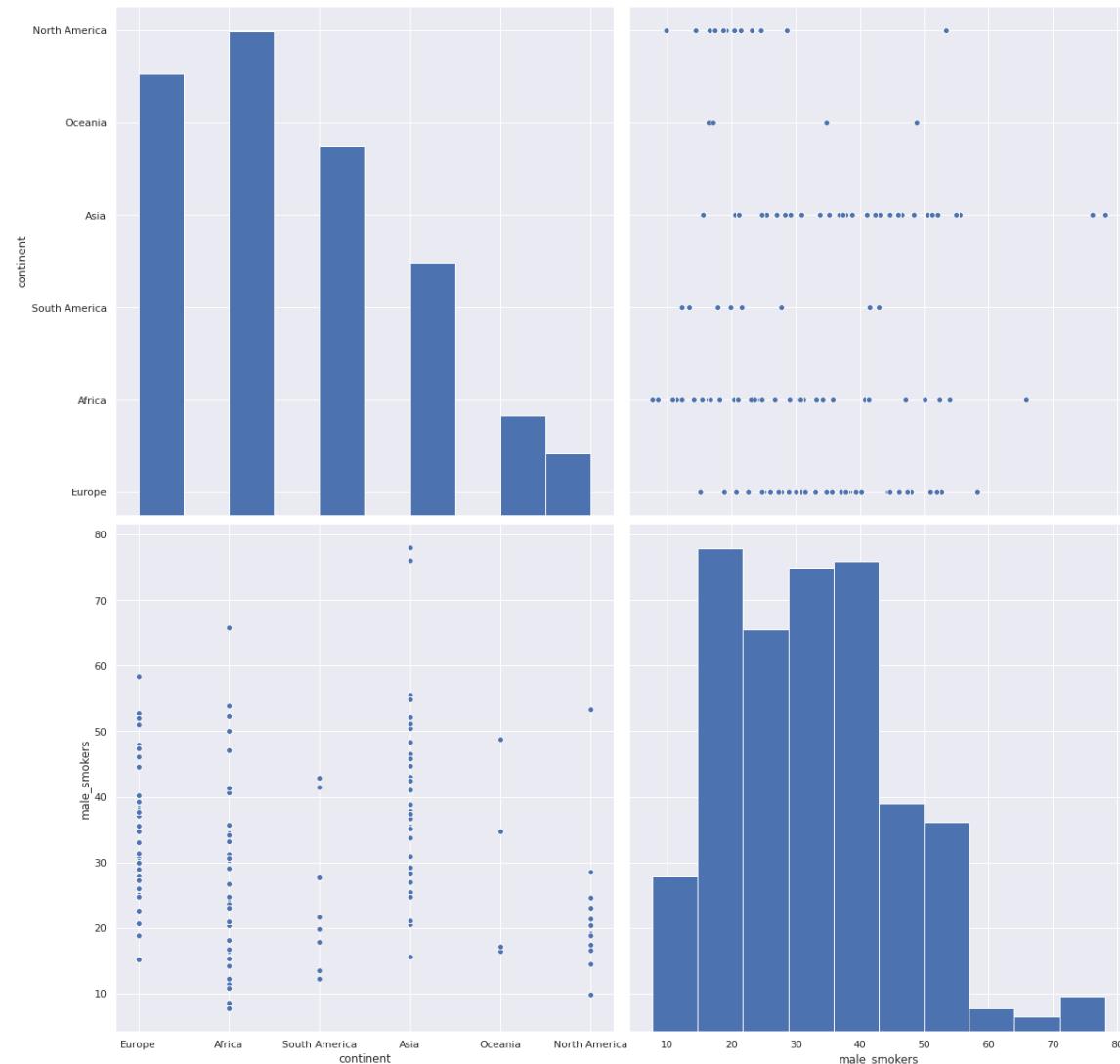


In [66]:

```
sns.pairplot(features, vars=["continent", "male_smokers"], height=8)
```

Out[66]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f0ebbcf8>
```

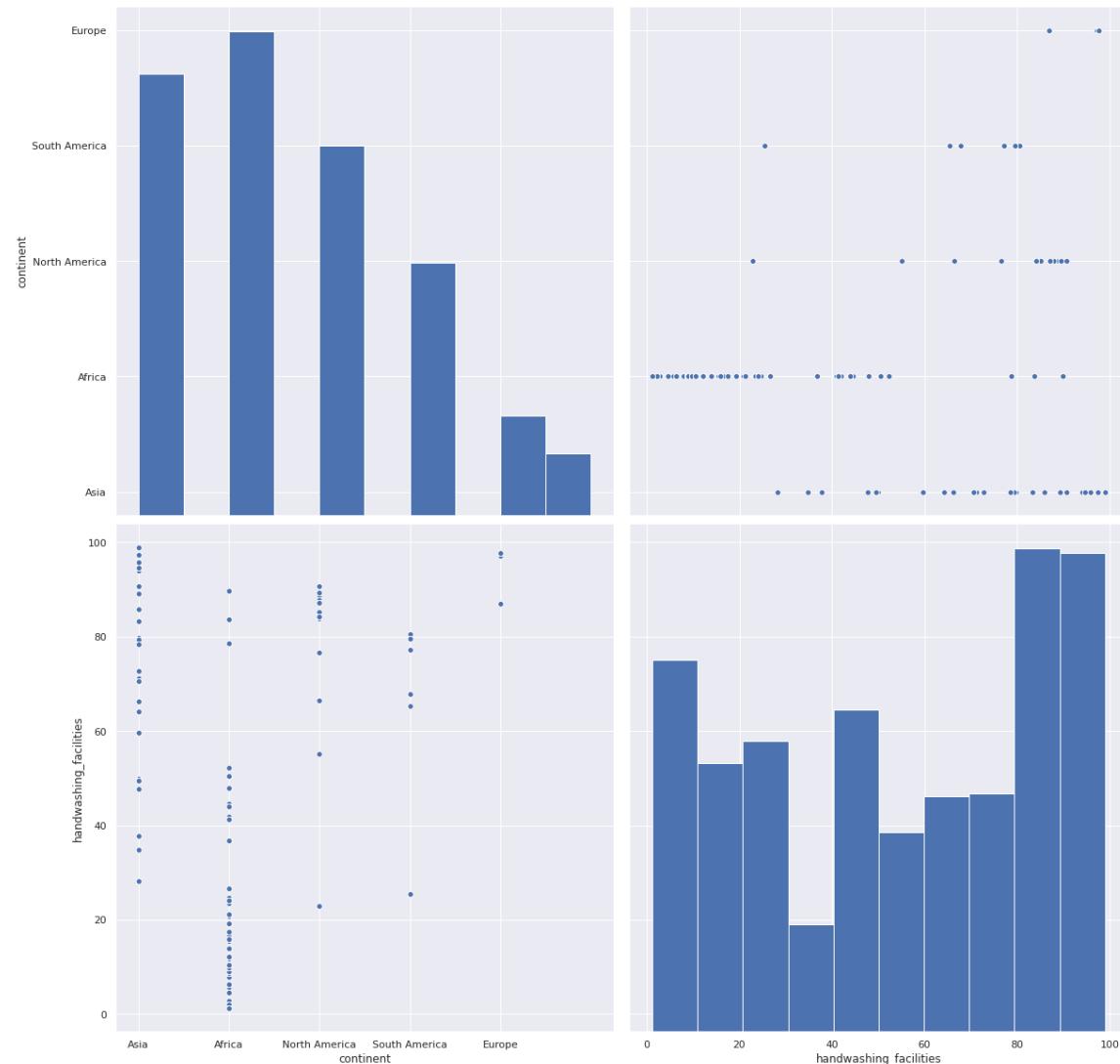


In [67]:

```
sns.pairplot(features, vars=["continent", "handwashing_facilities"], height=8)
```

Out[67]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f0a81128>
```

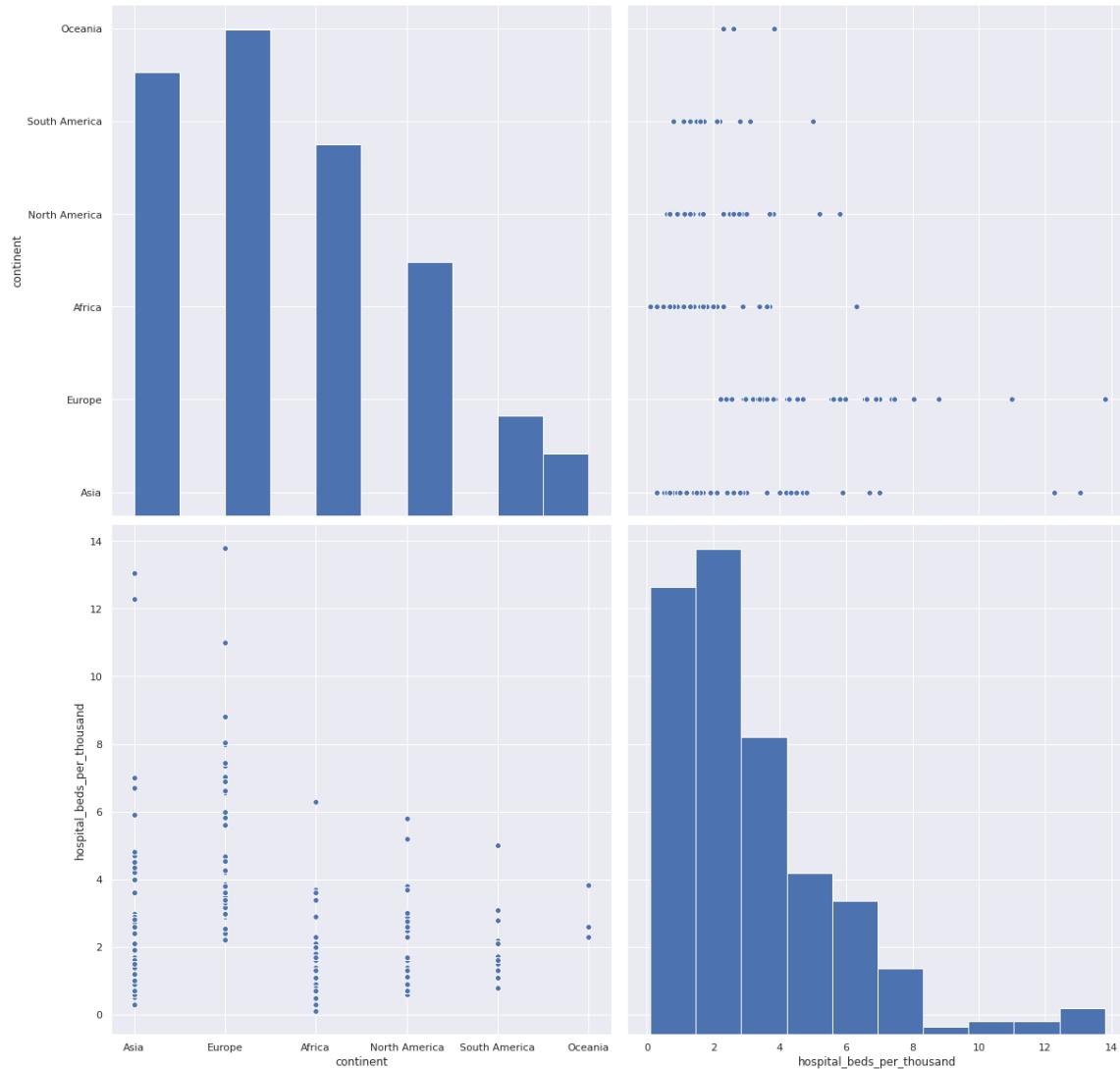


In [68]:

```
sns.pairplot(features, vars=["continent", "hospital_beds_per_thousand"], height=8)
```

Out[68]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f099a8d0>
```

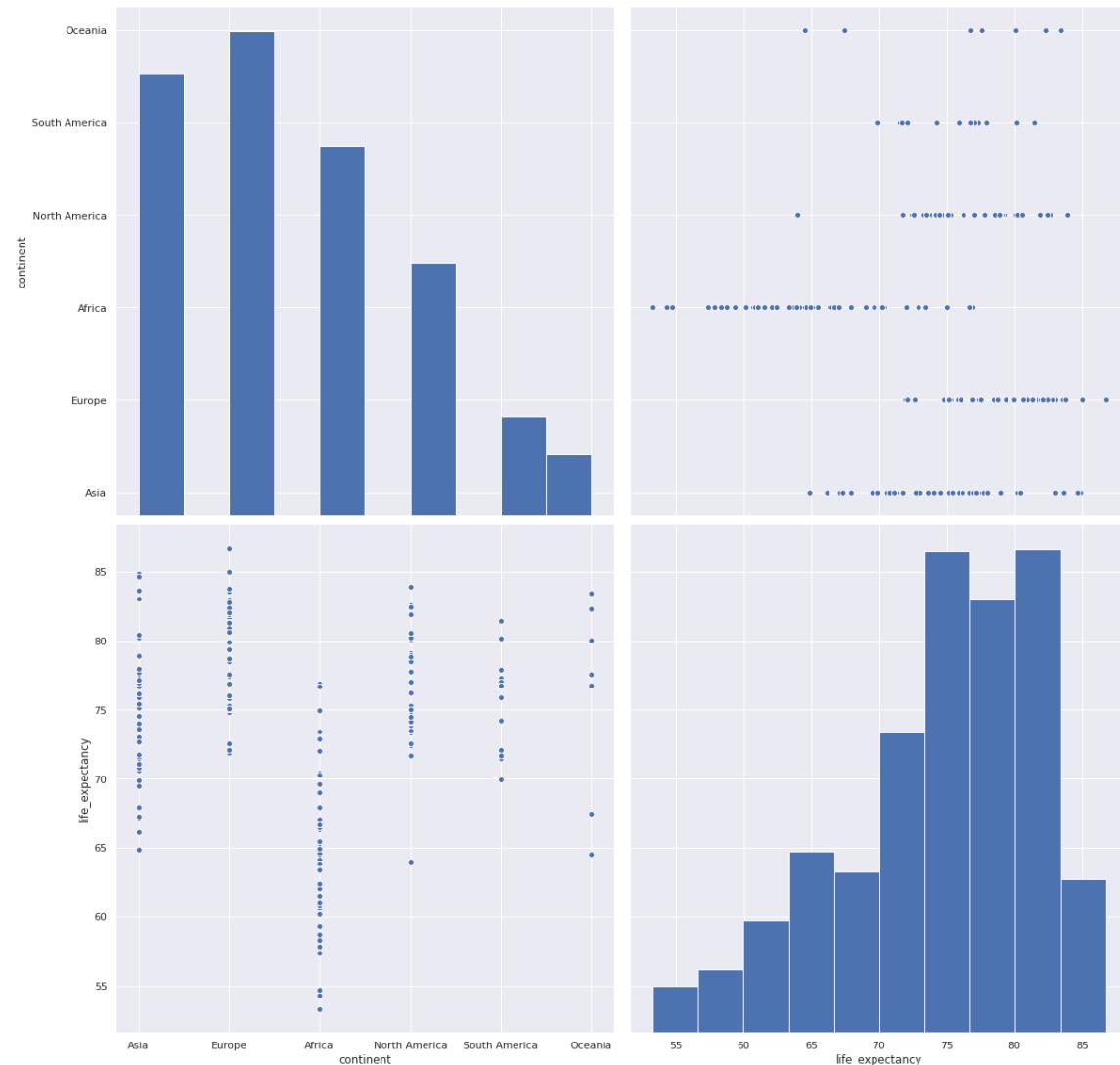


In [69]:

```
sns.pairplot(features, vars=["continent", "life_expectancy"], height=8)
```

Out[69]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f06c5860>
```

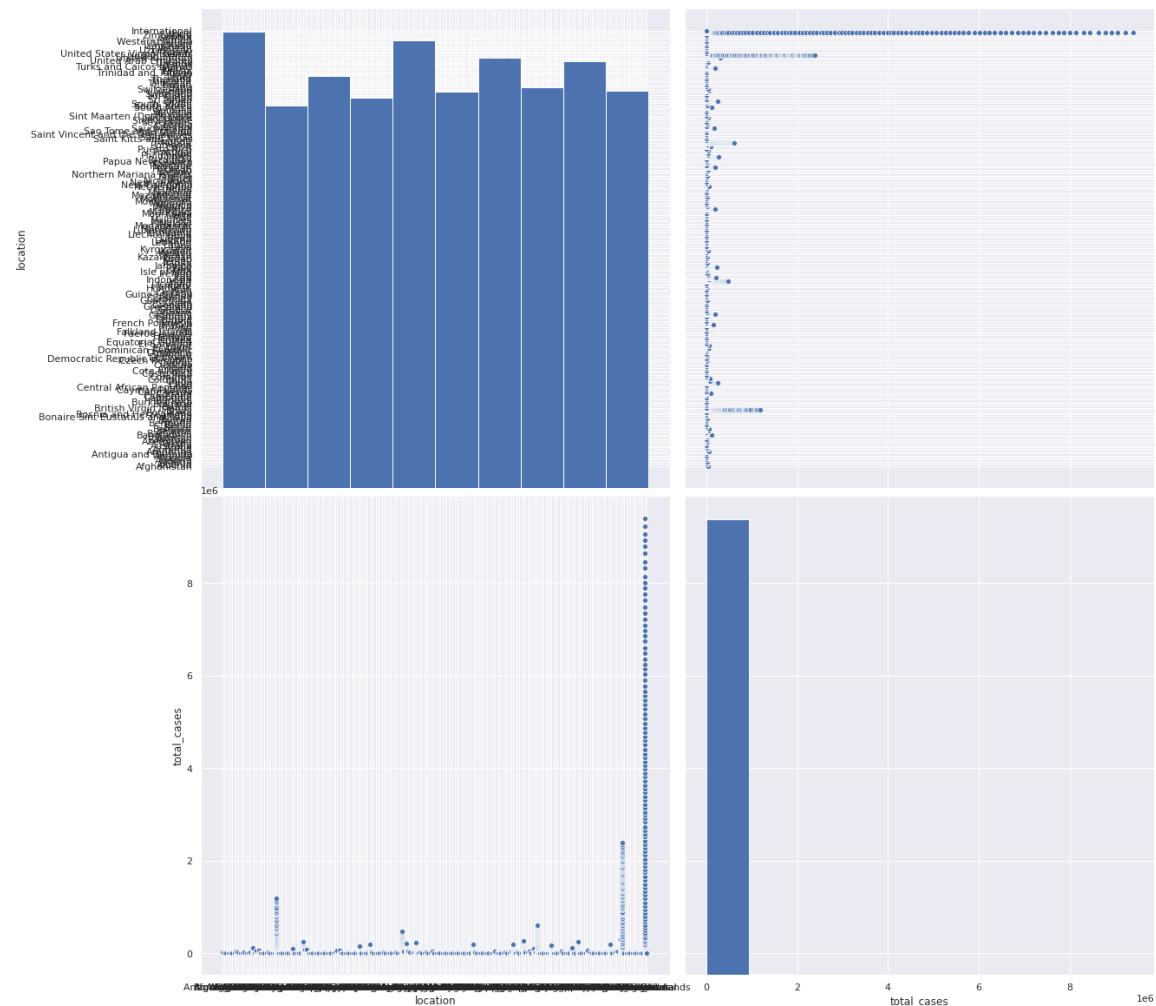


In [70]:

```
sns.pairplot(features, vars=["location", "total_cases"], height=8)
```

Out[70]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6f052edd8>
```

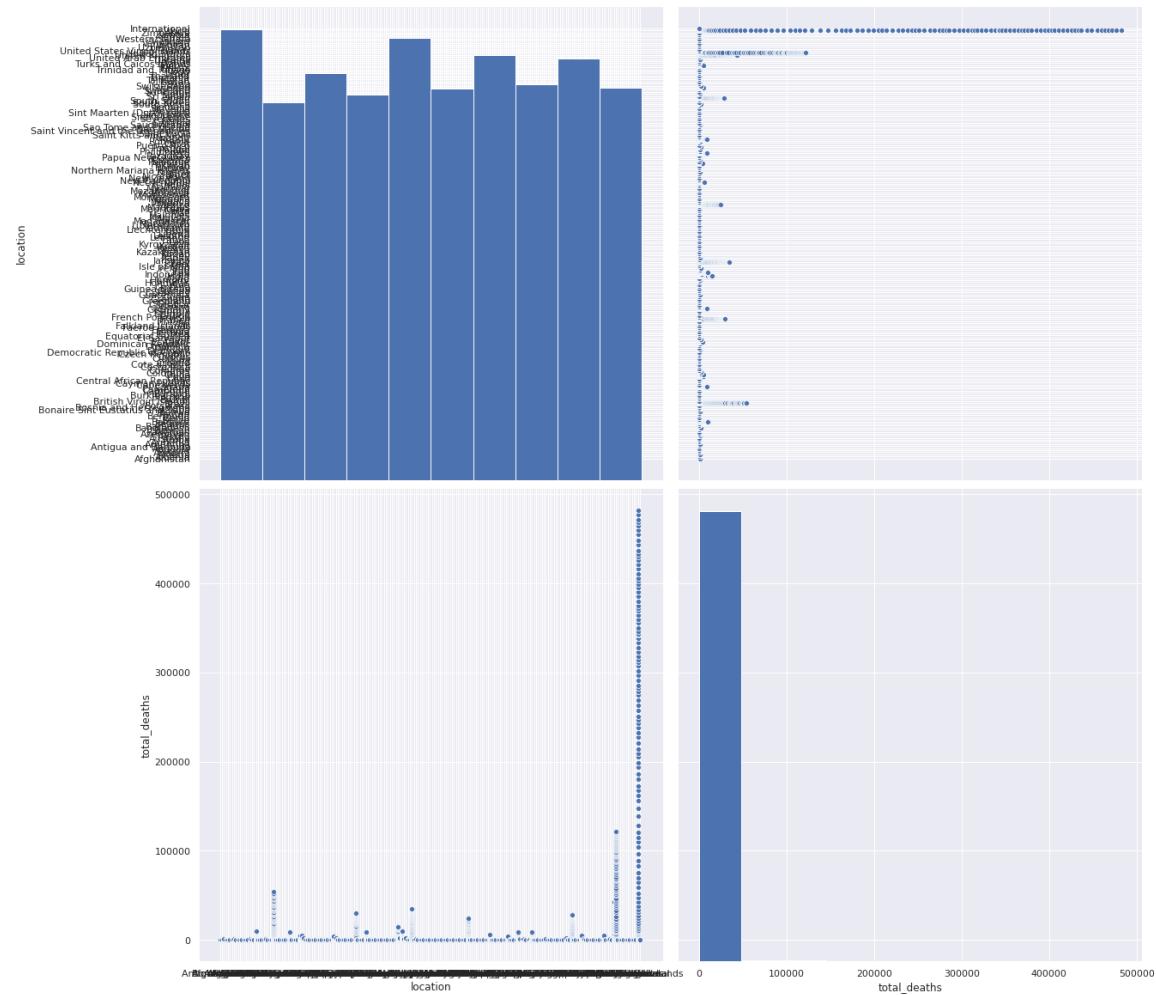


In [71]:

```
sns.pairplot(features, vars=["location", "total_deaths"], height=8)
```

Out[71]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6efbe8208>
```

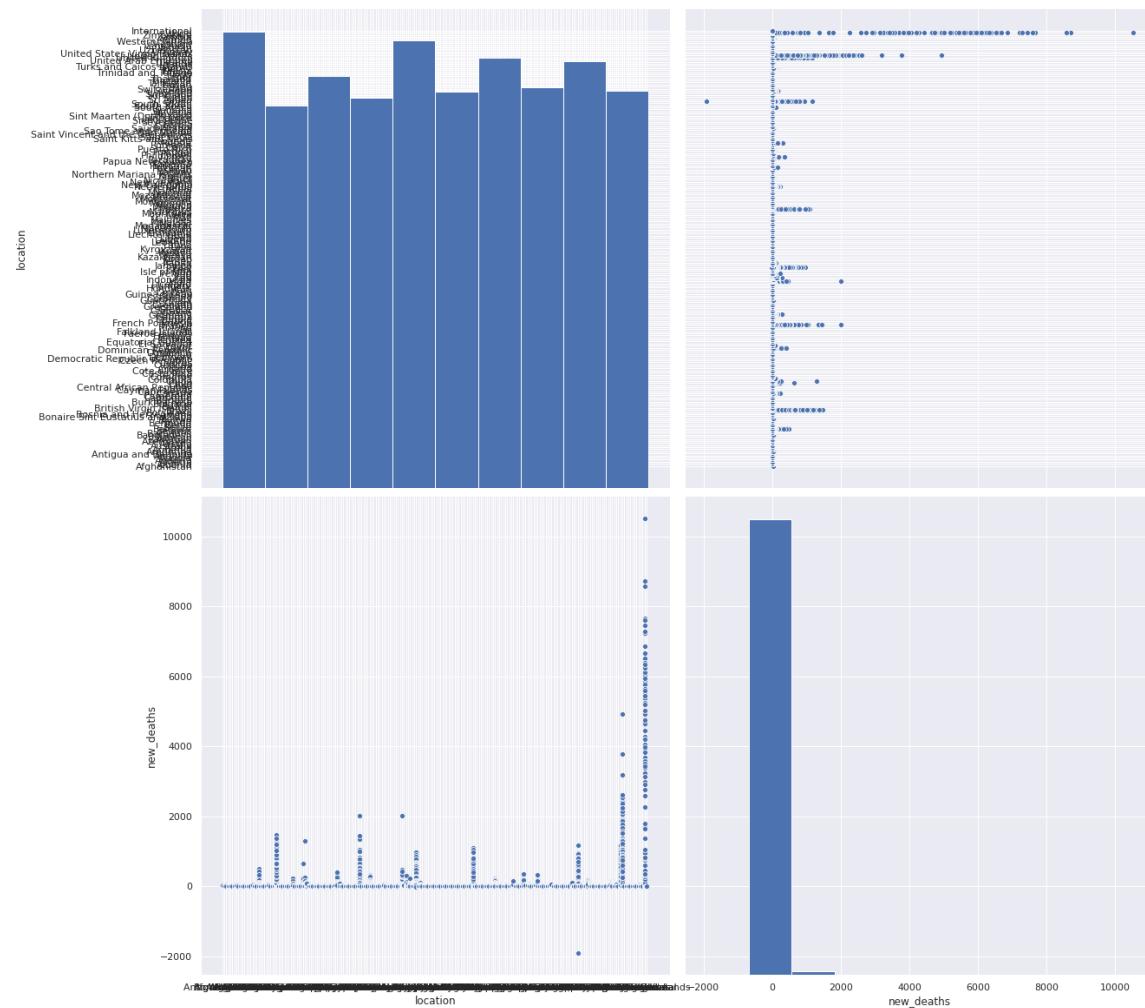


In [72]:

```
sns.pairplot(features, vars=["location", "new_deaths"], height=8)
```

Out[72]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6eec56898>
```

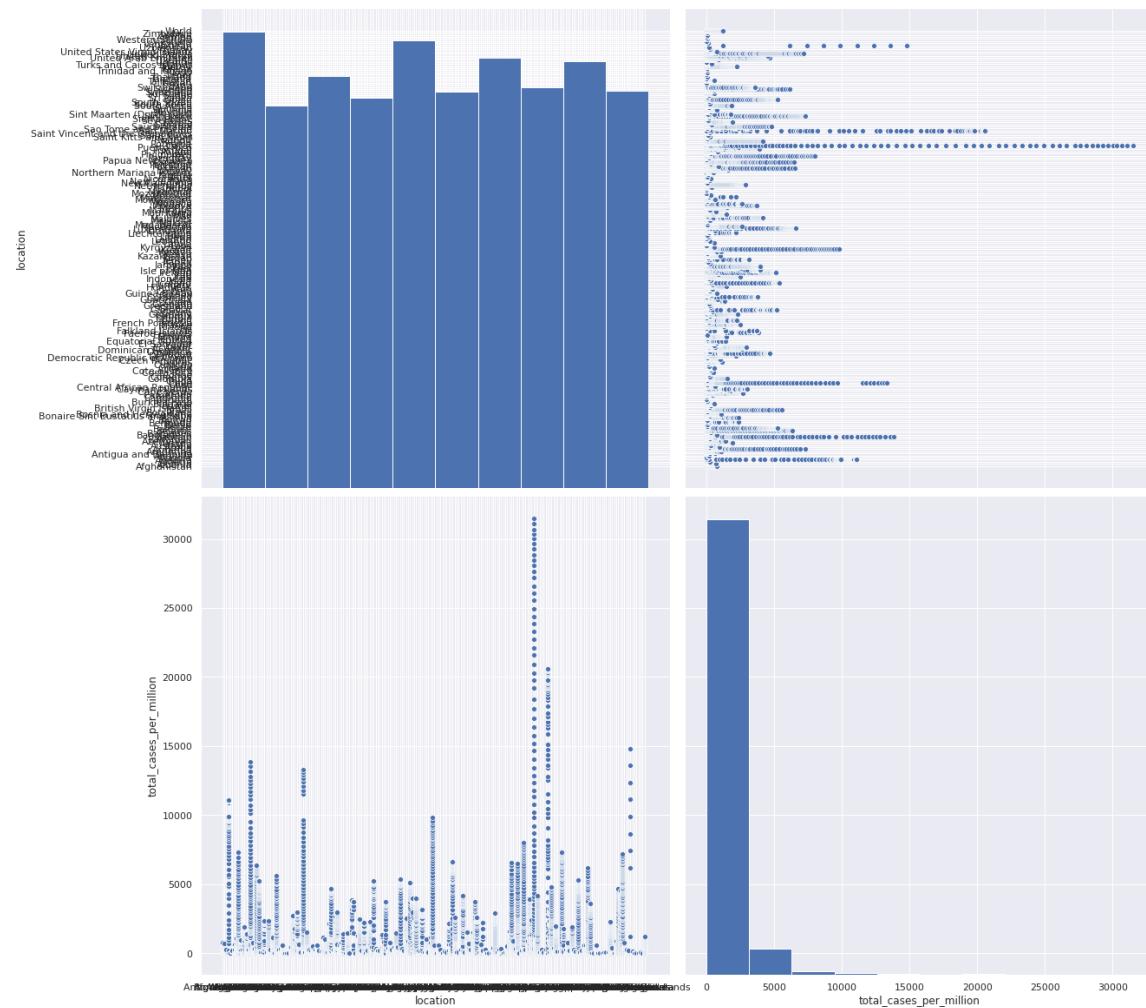


In [73]:

```
sns.pairplot(features, vars=["location", "total_cases_per_million"], height=8)
```

Out[73]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6edcc6e48>
```

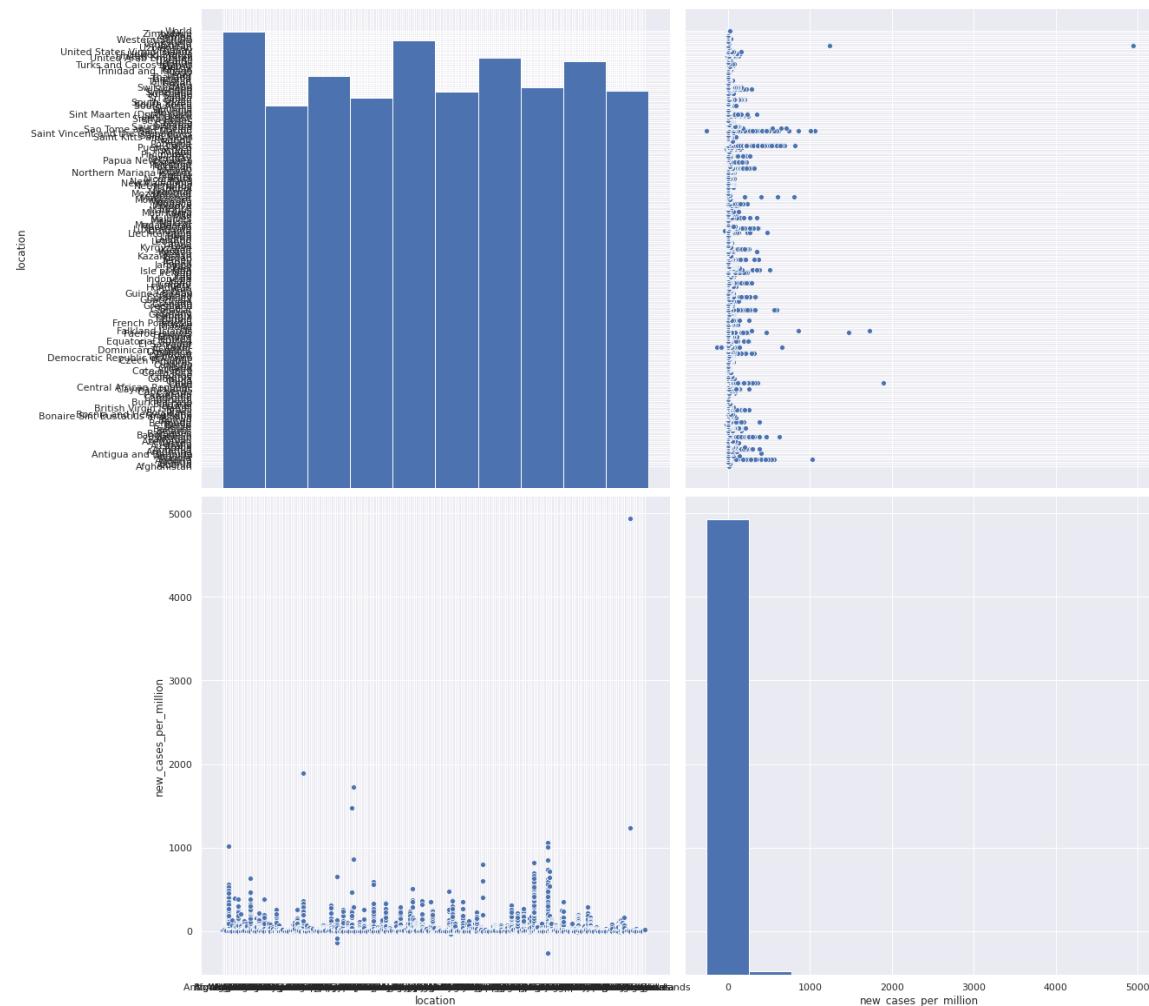


In [74]:

```
sns.pairplot(features, vars=["location", "new_cases_per_million"], height=8)
```

Out[74]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ece16278>
```

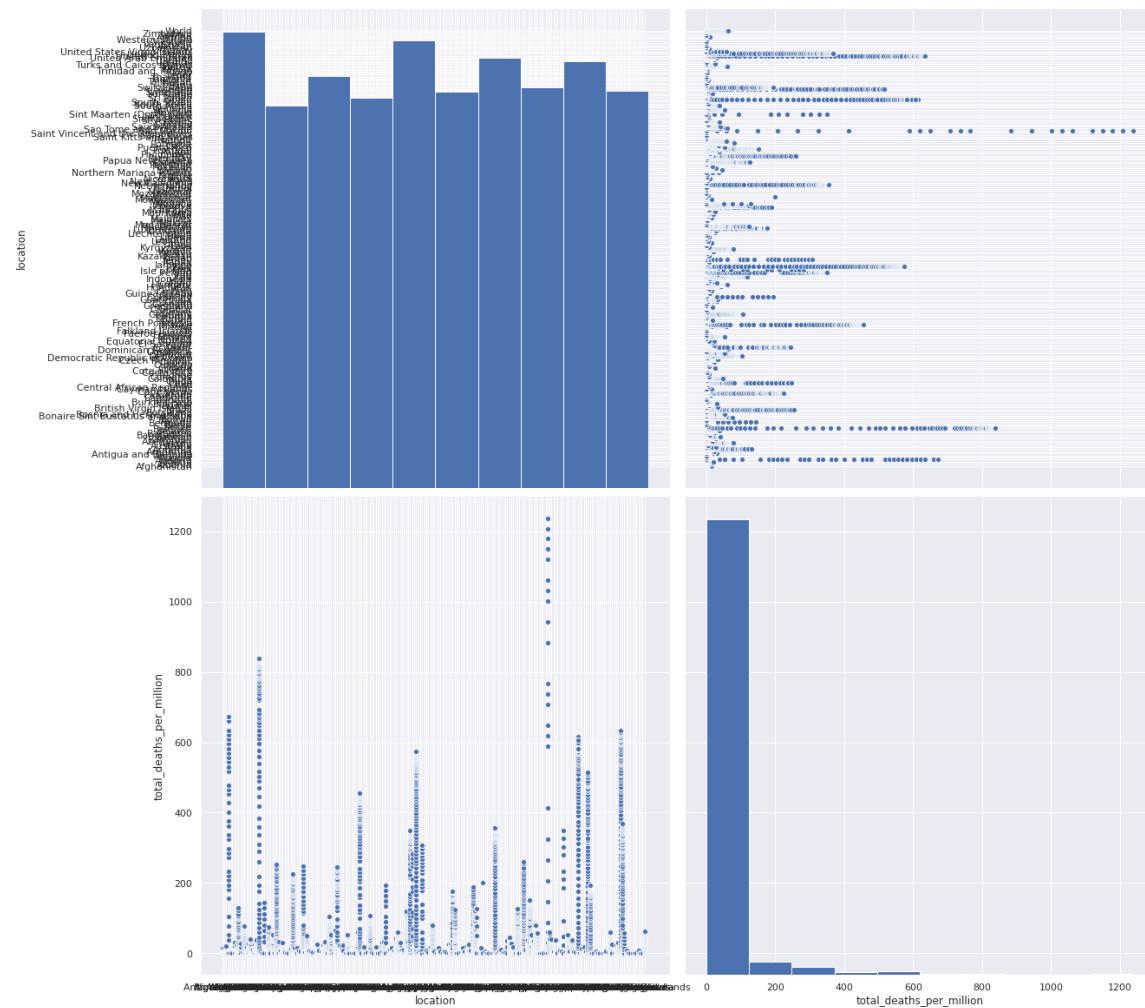


In [75]:

```
sns.pairplot(features, vars=["location", "total_deaths_per_million"], height=8)
```

Out[75]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6eeccb9d30>
```

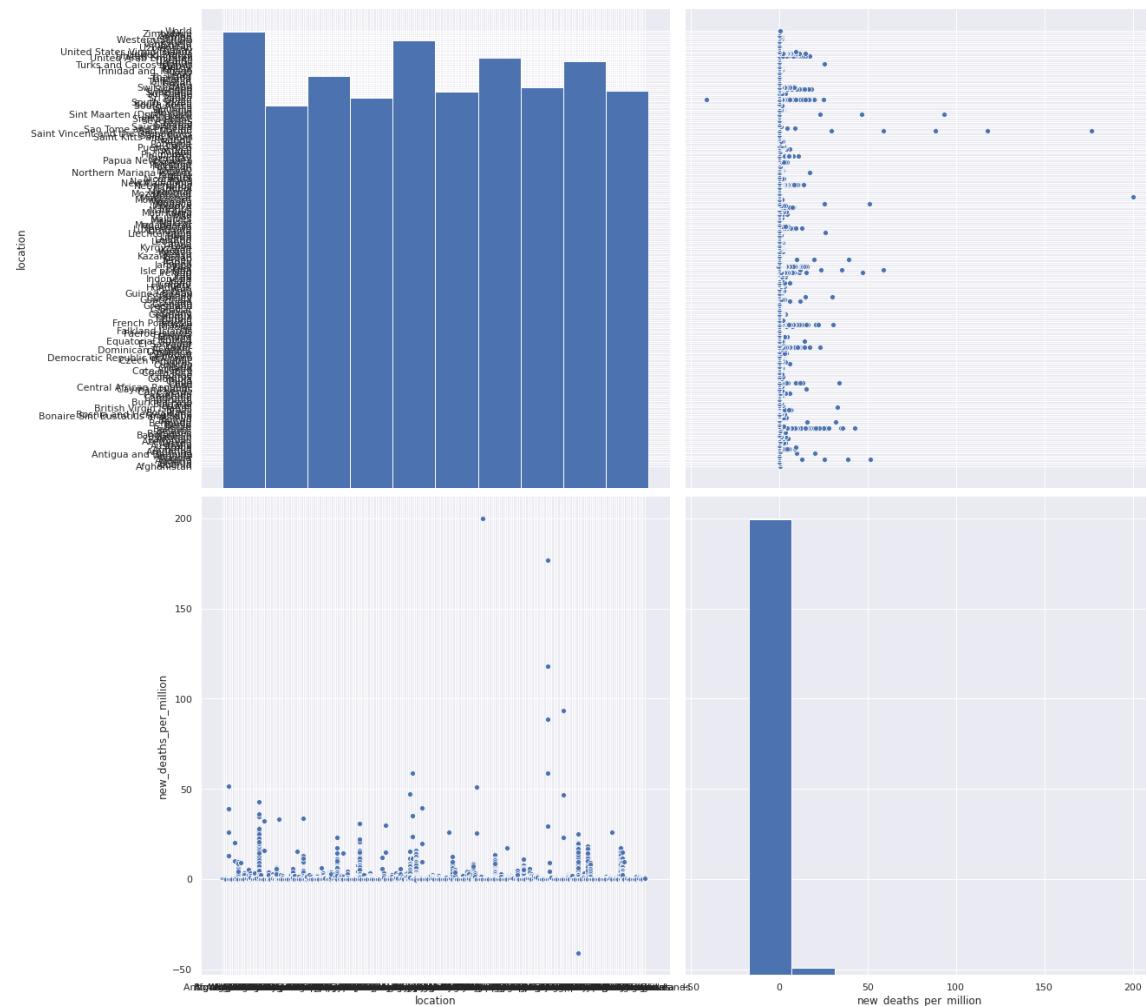


In [76]:

```
sns.pairplot(features, vars=["location", "new_deaths_per_million"], height=8)
```

Out[76]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6eafe46a0>
```

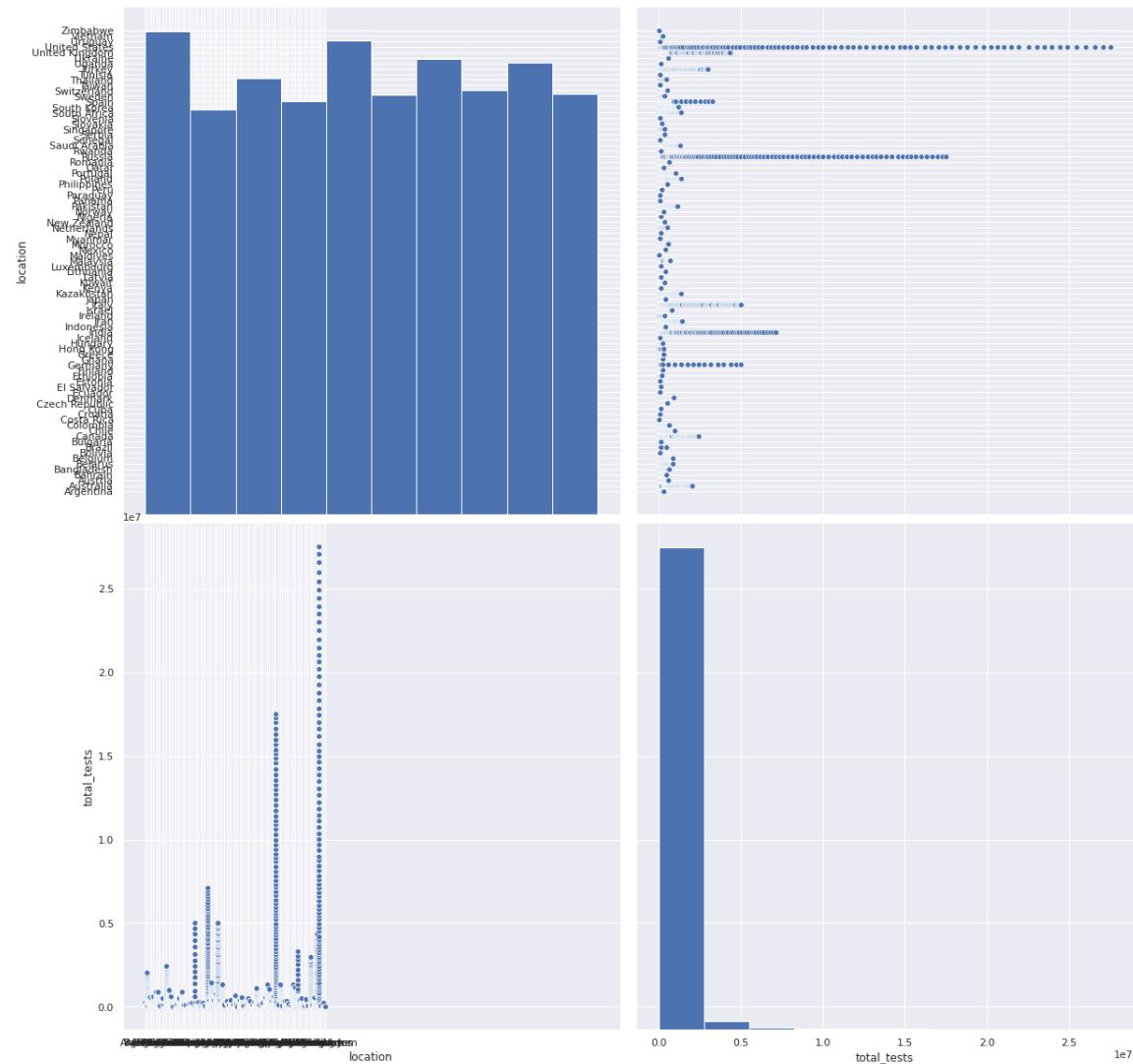


In [77]:

```
sns.pairplot(features, vars=["location", "total_tests"], height=8)
```

Out[77]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ea0465c0>
```

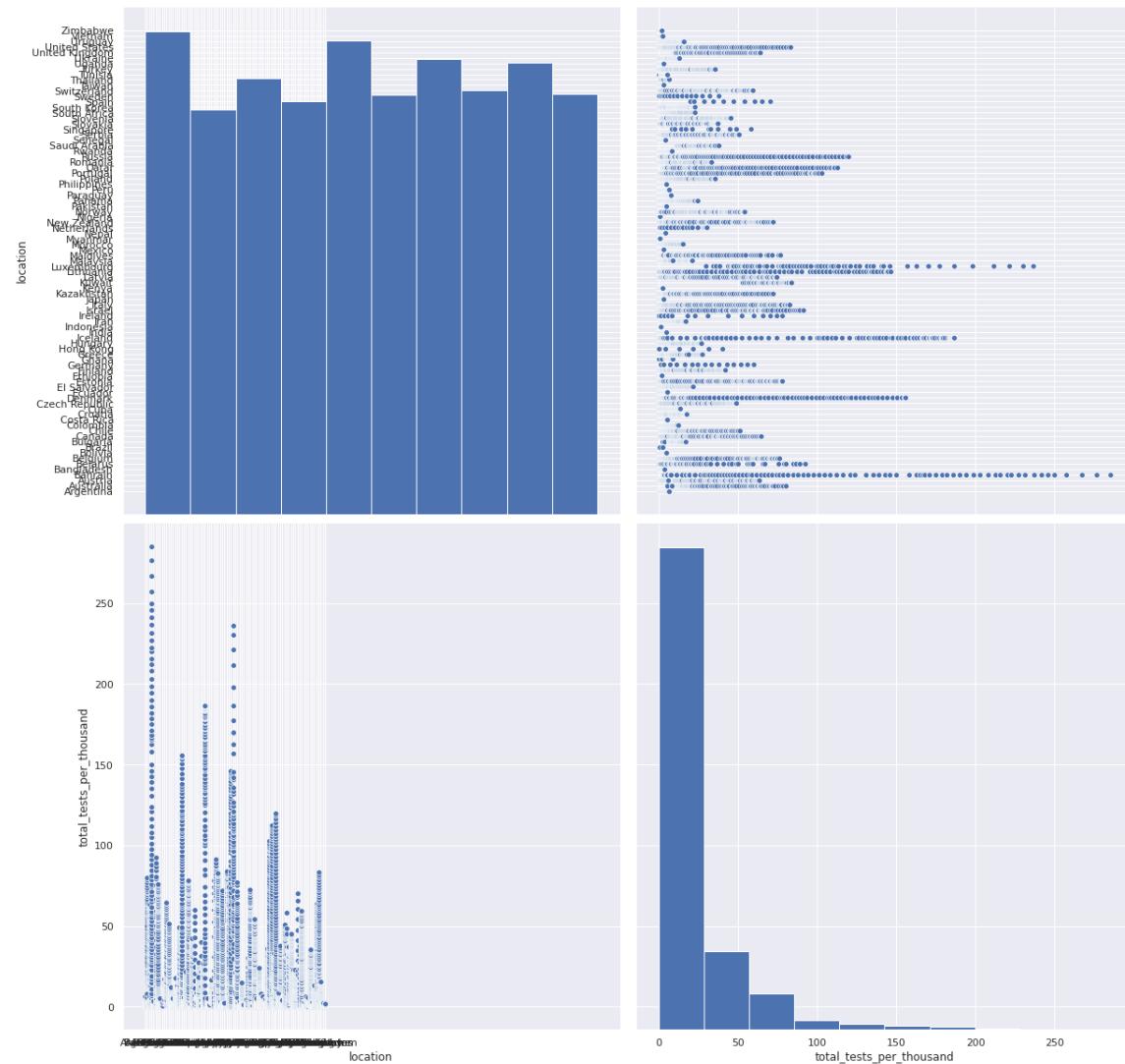


In [78]:

```
sns.pairplot(features, vars=["location", "total_tests_per_thousand"], height=8)
```

Out[78]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e95b45f8>
```

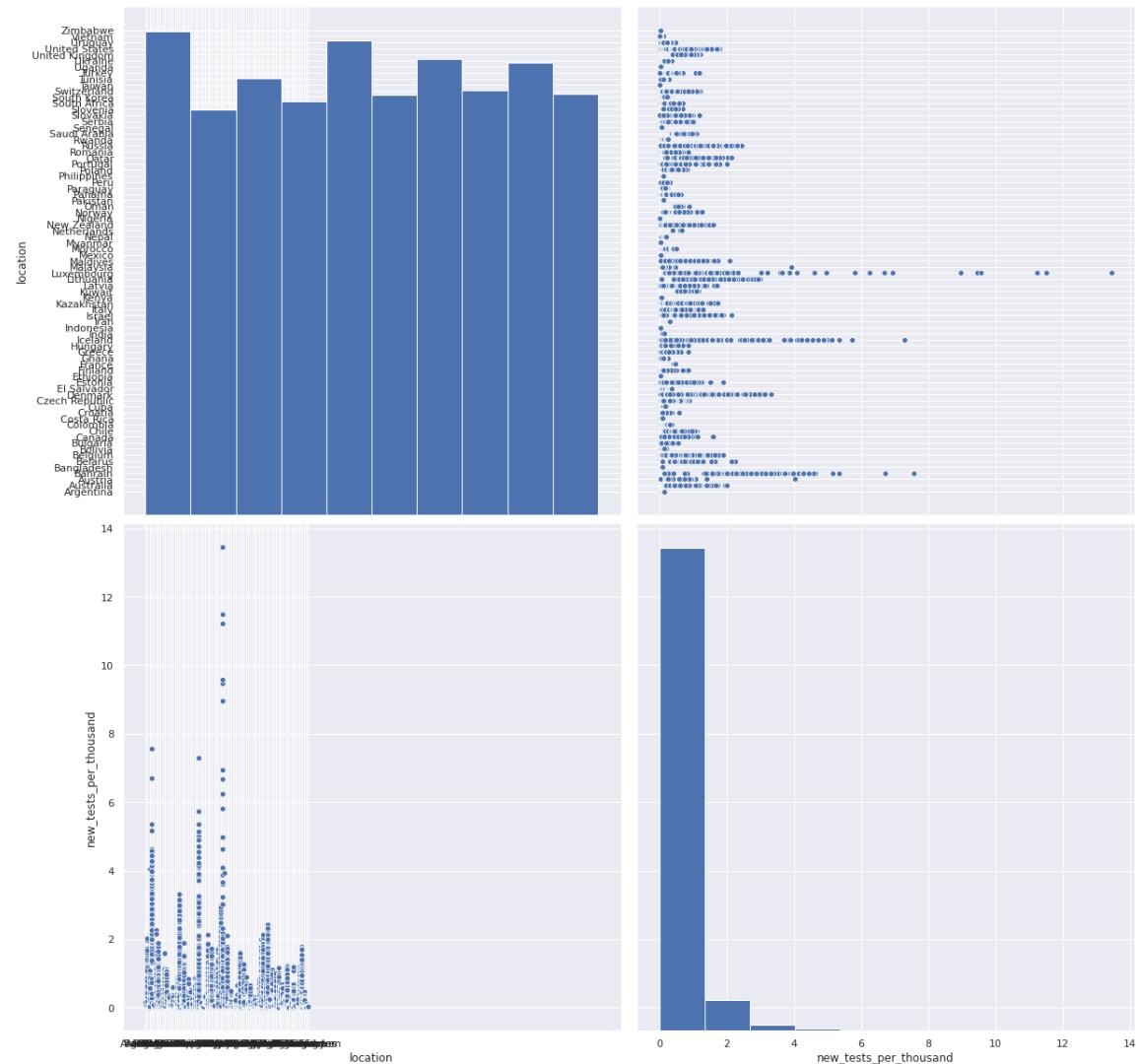


In [79]:

```
sns.pairplot(features, vars=["location", "new_tests_per_thousand"], height=8)
```

Out[79]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e904b828>
```

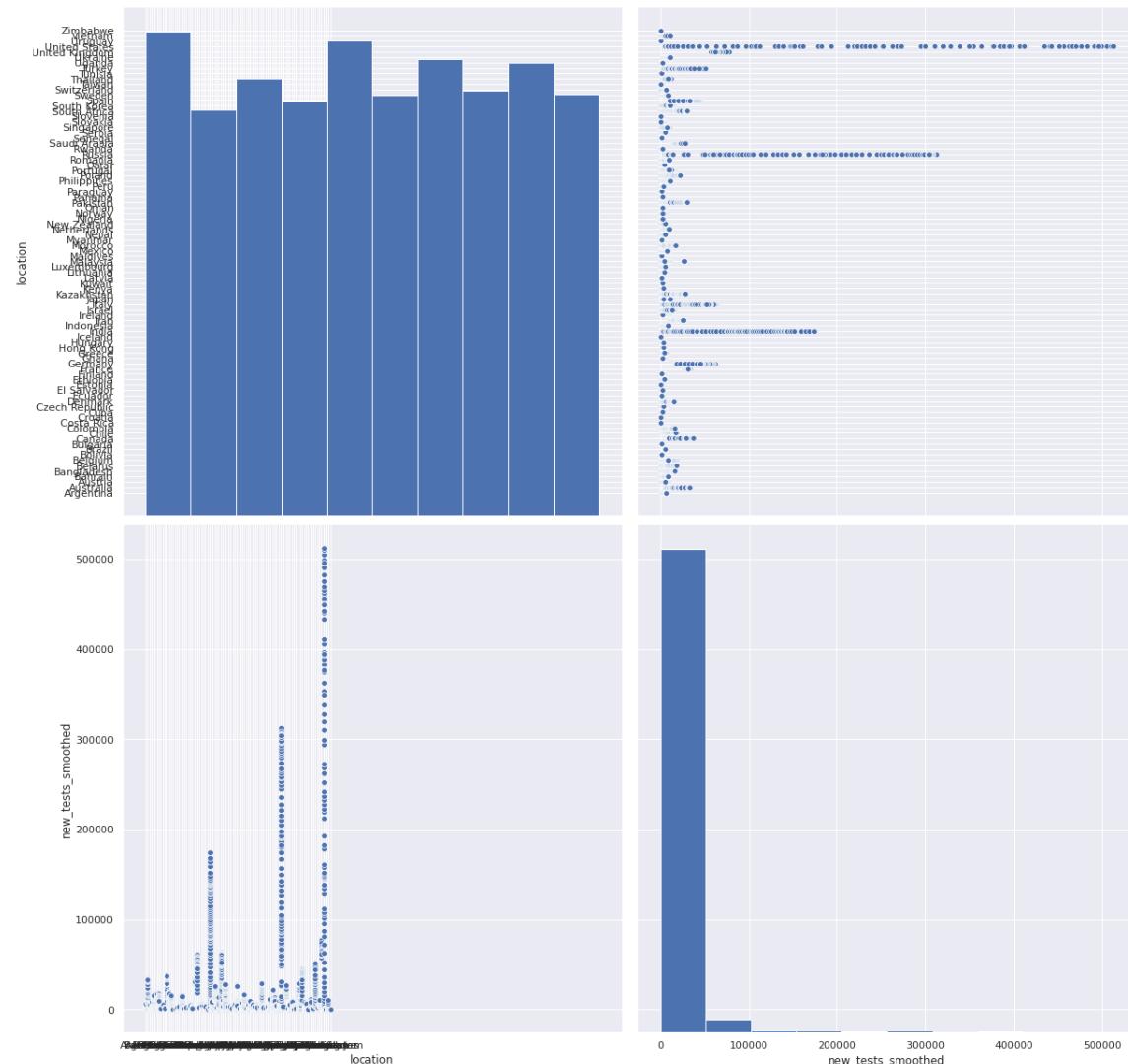


In [80]:

```
sns.pairplot(features, vars=["location", "new_tests_smoothed"], height=8)
```

Out[80]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e904be48>
```

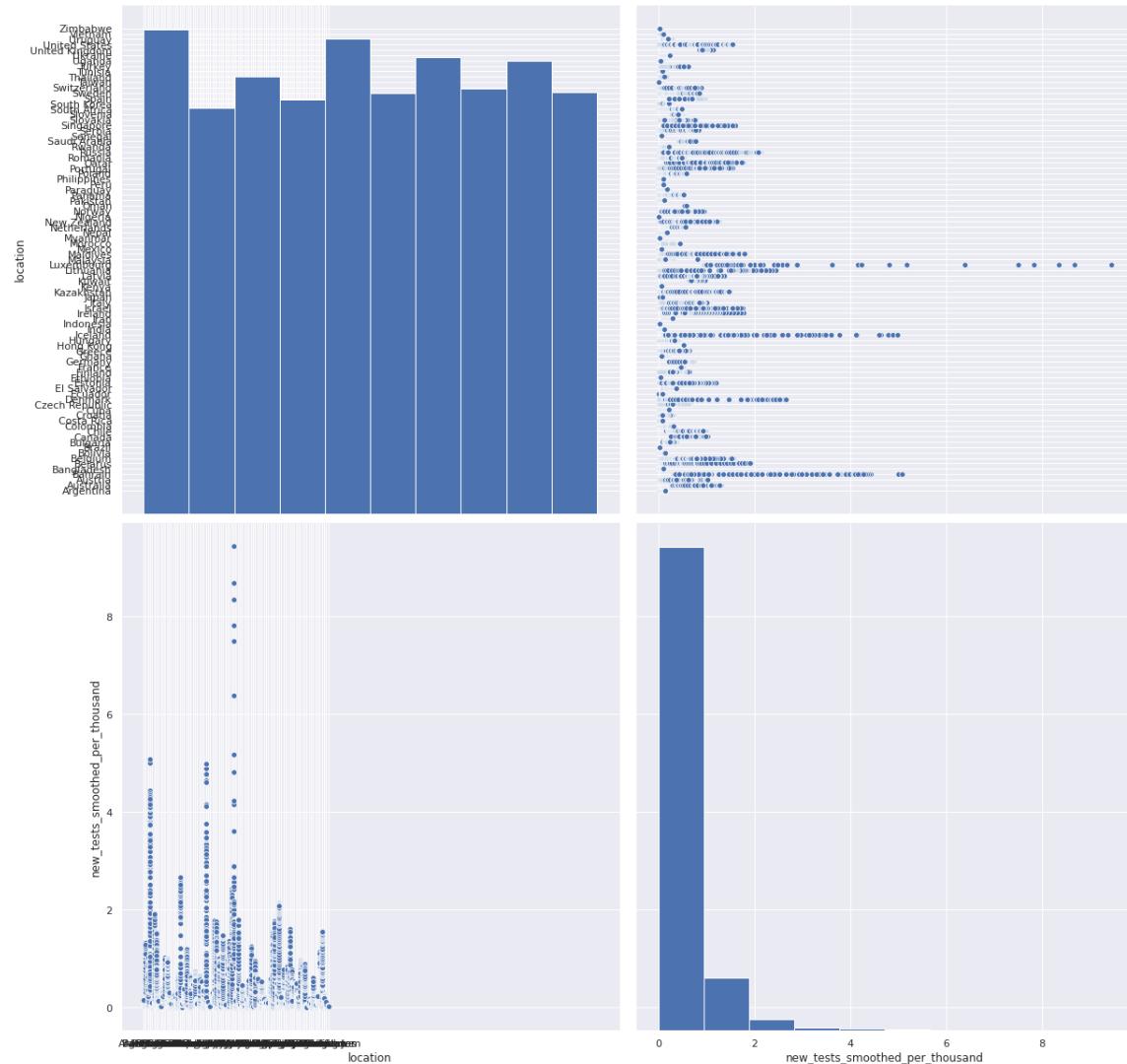


In [81]:

```
sns.pairplot(features, vars=["location", "new_tests_smoothed_per_thousand"], height=8)
```

Out[81]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e8721fd0>
```

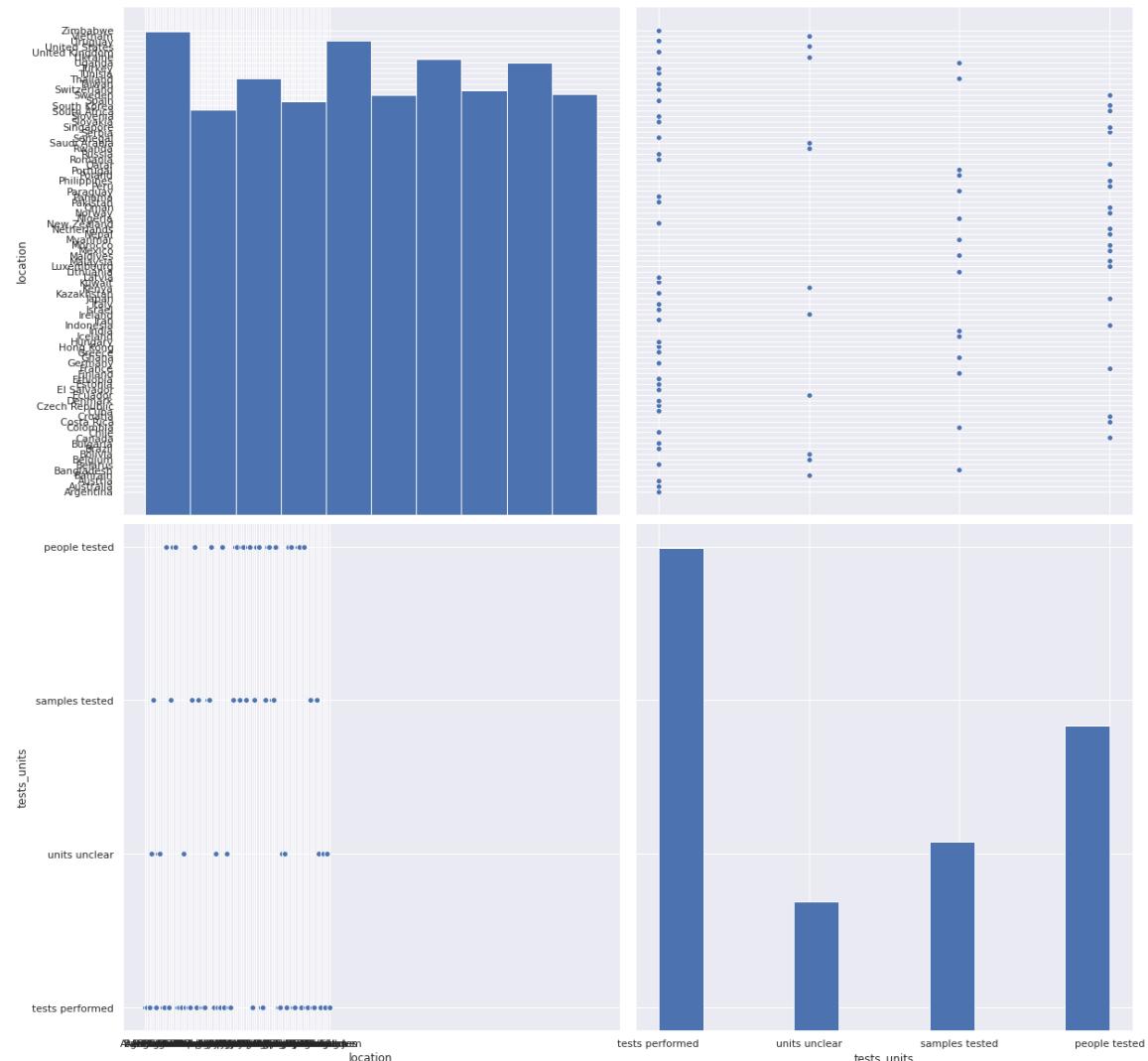


In [82]:

```
sns.pairplot(features, vars=["location", "tests_units"], height=8)
```

Out[82]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e82af860>
```

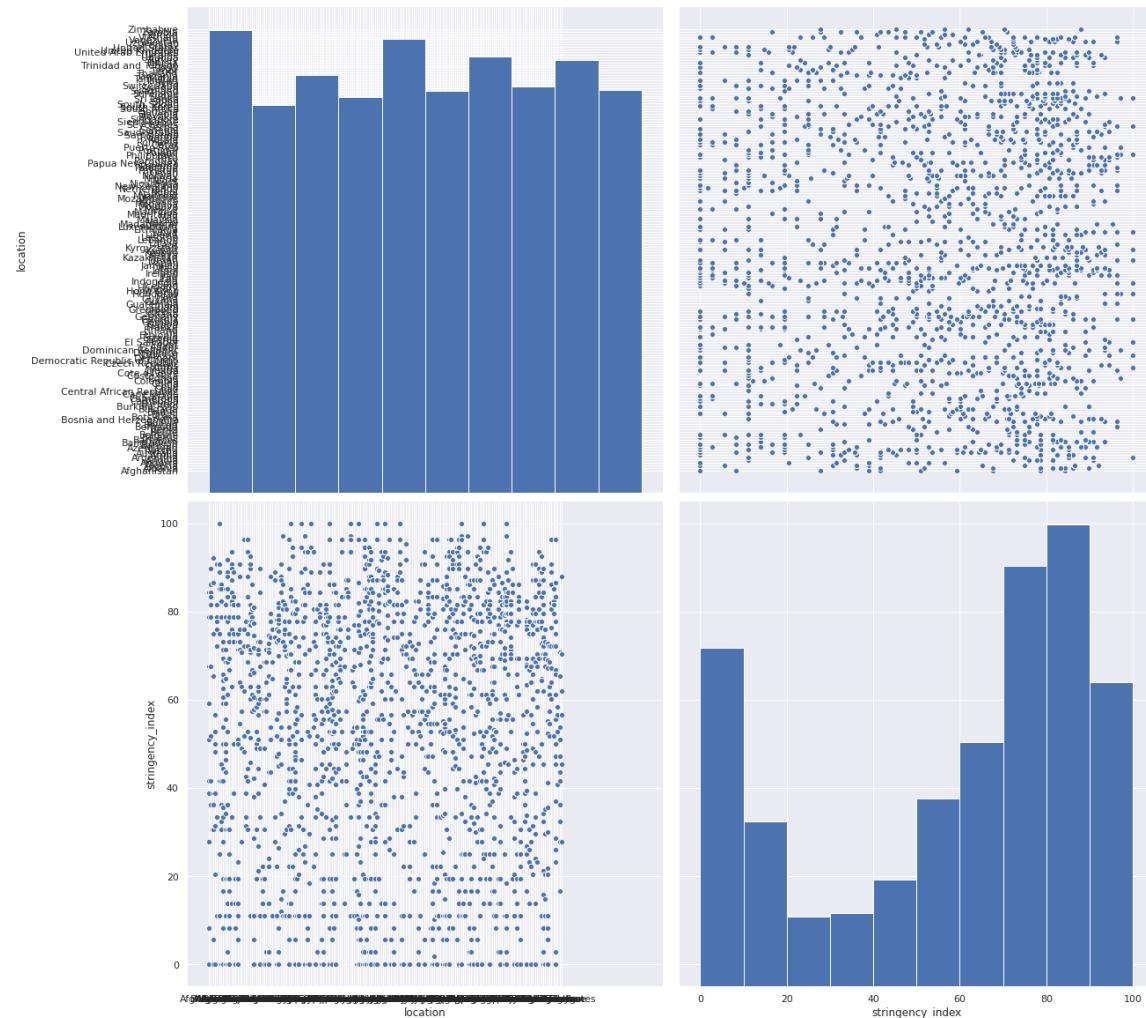


In [83]:

```
sns.pairplot(features, vars=["location", "stringency_index"], height=8)
```

Out[83]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e87b15c0>
```

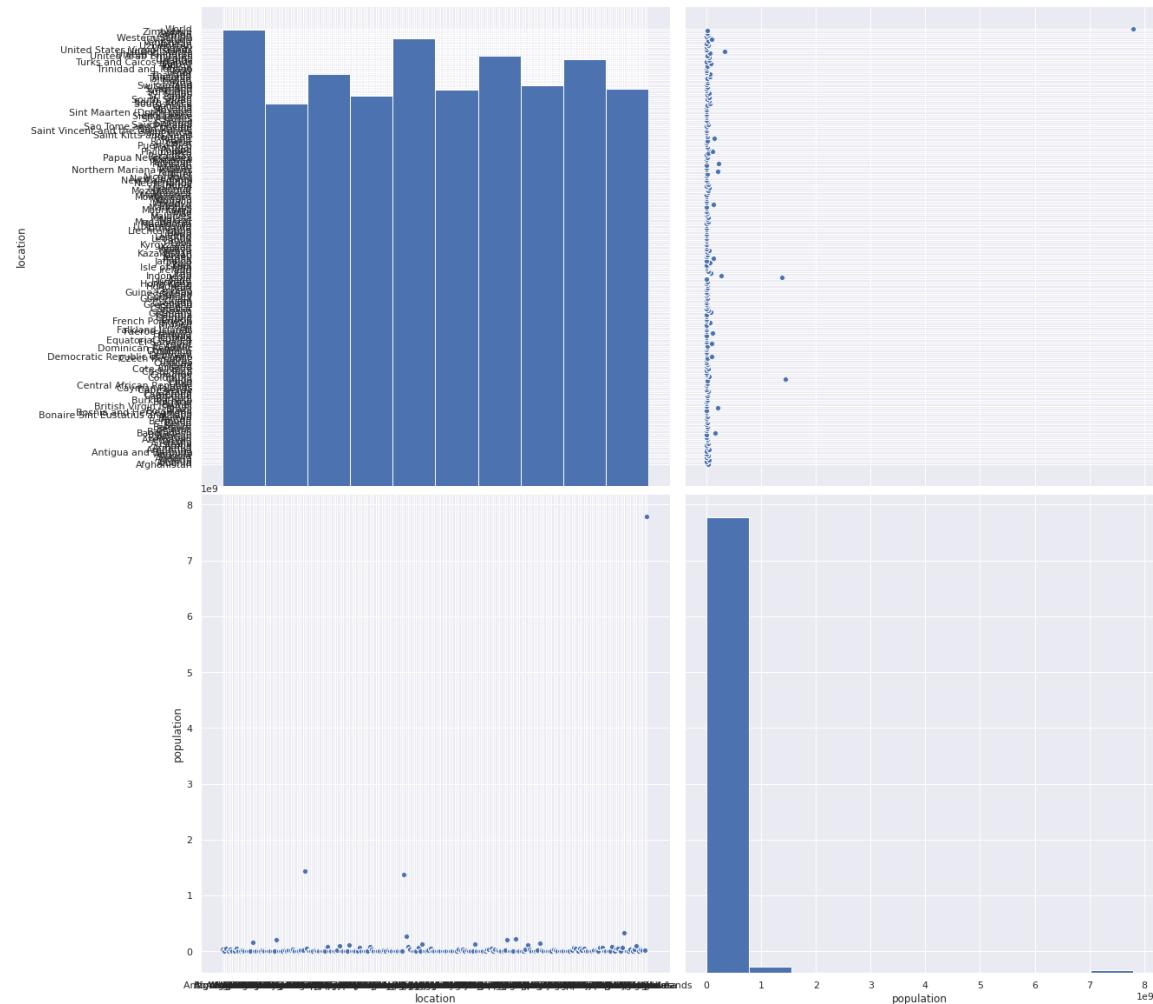


In [84]:

```
sns.pairplot(features, vars=["location", "population"], height=8)
```

Out[84]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e75ee128>
```

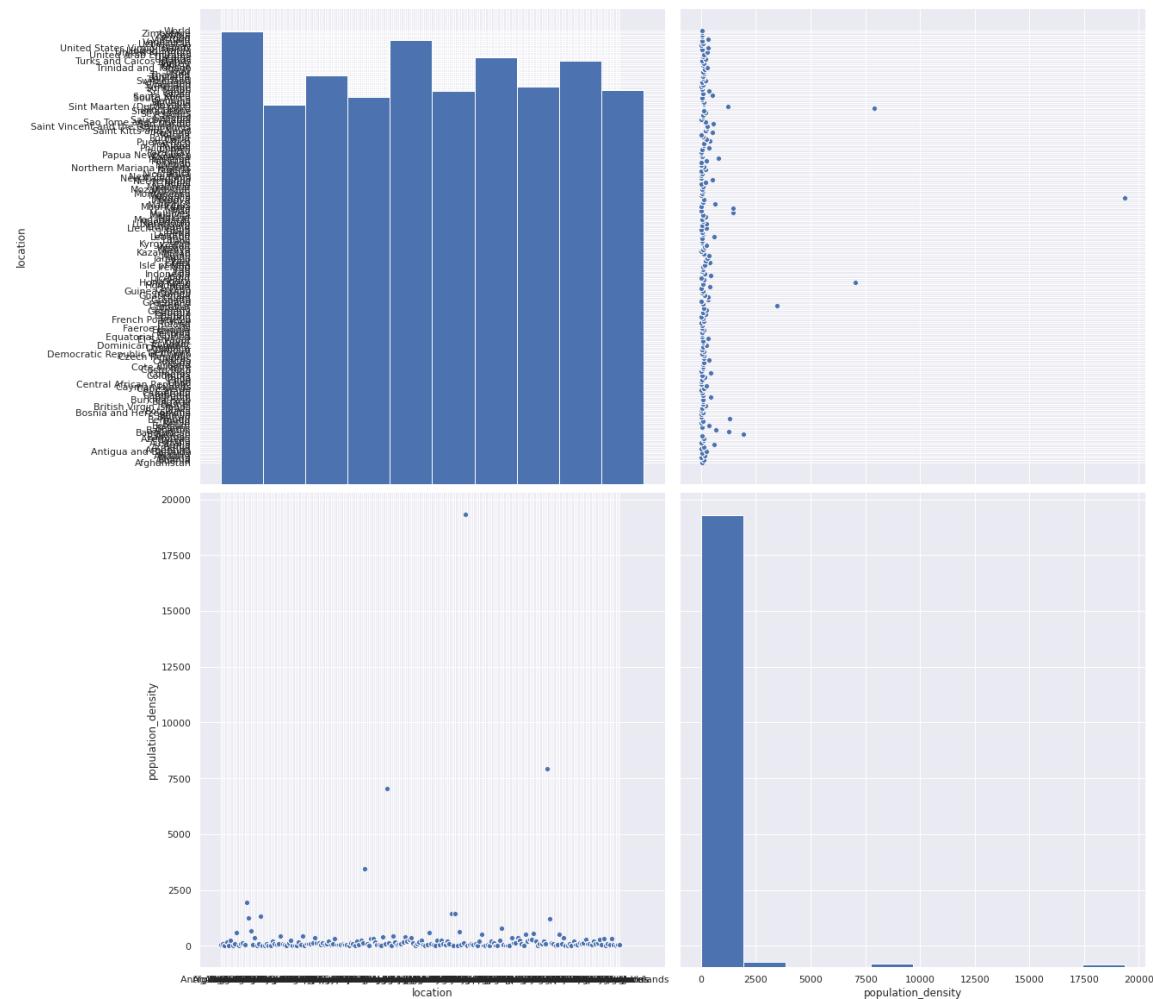


In [85]:

```
sns.pairplot(features, vars=["location", "population_density"], height=8)
```

Out[85]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e667a278>
```

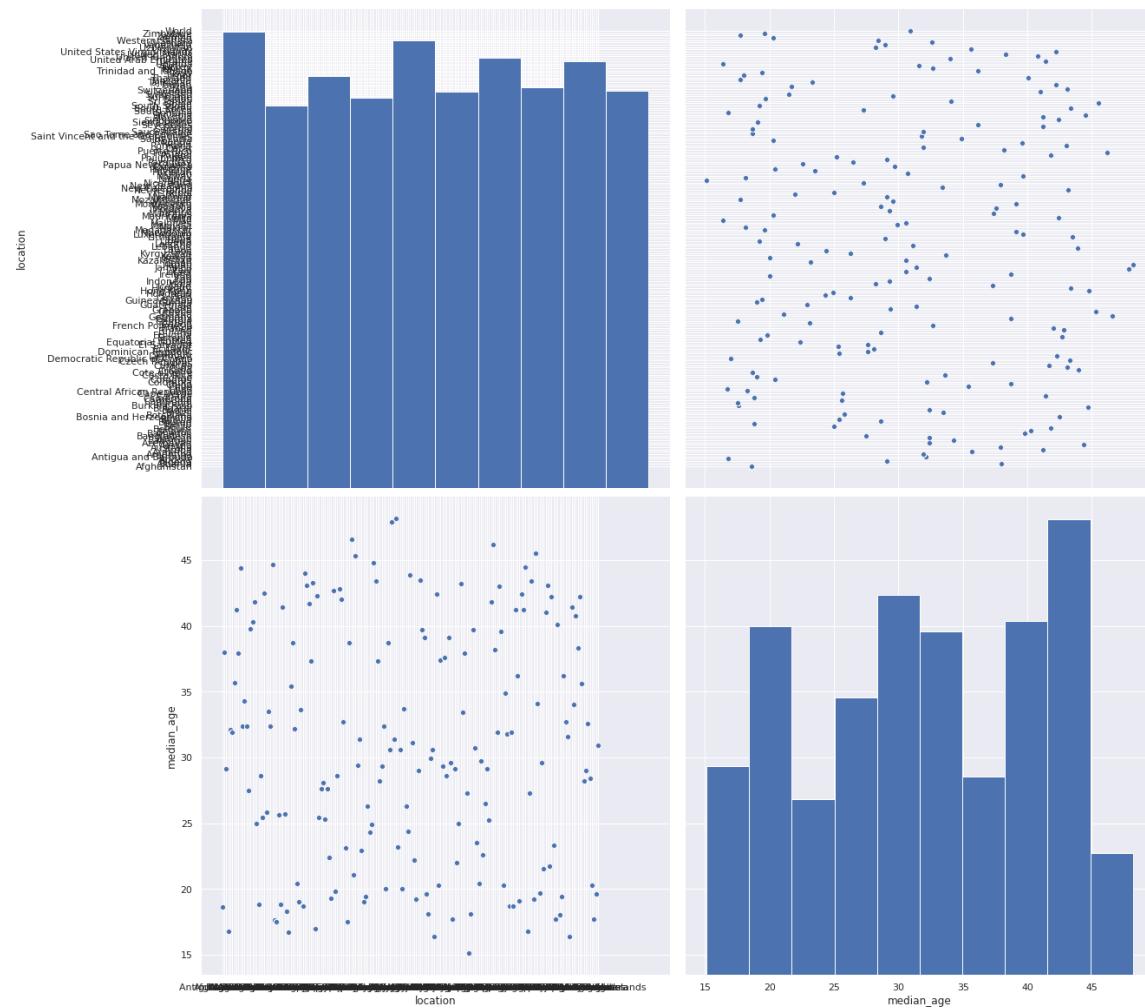


In [86]:

```
sns.pairplot(features, vars=["location", "median_age"], height=8)
```

Out[86]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e5815128>
```

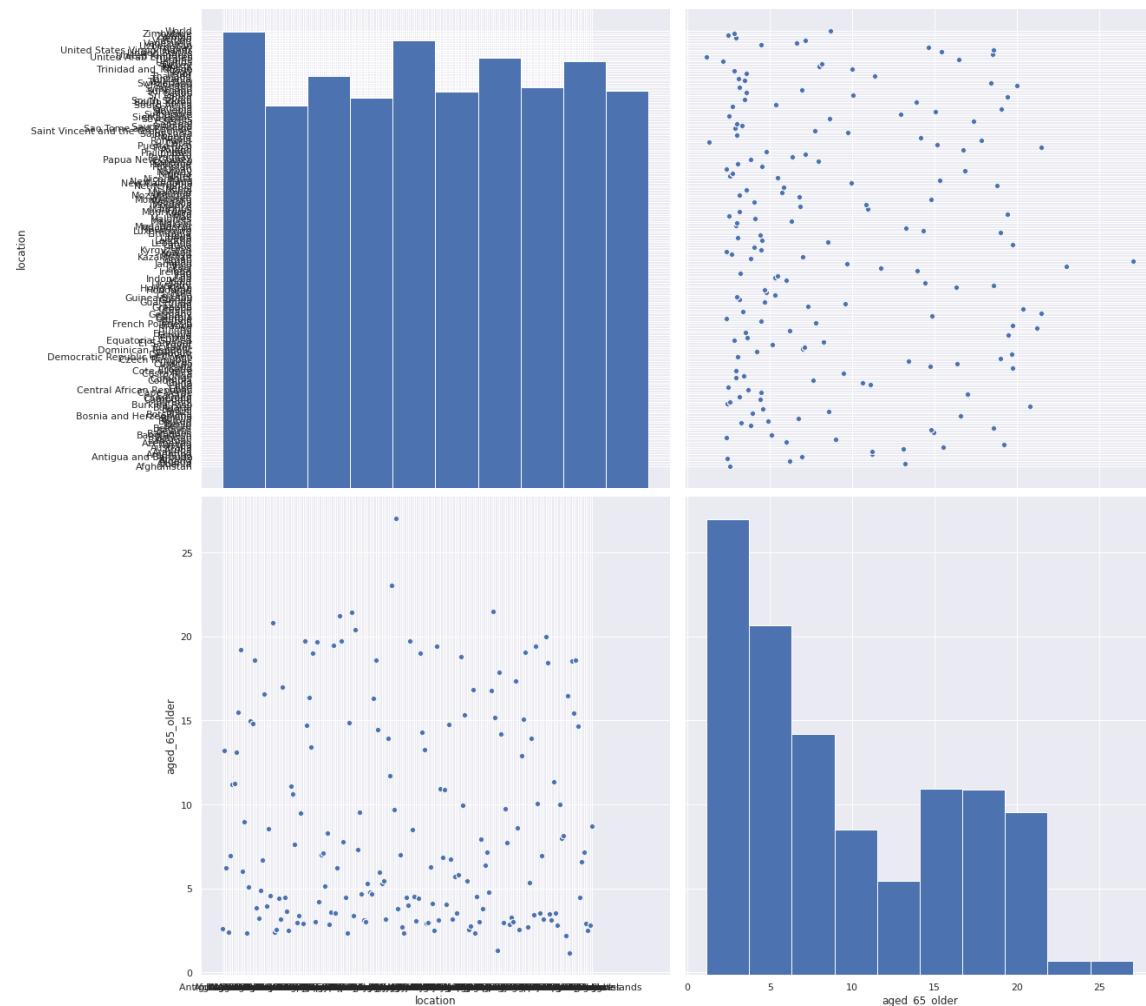


In [87]:

```
sns.pairplot(features, vars=["location", "aged_65_older"], height=8)
```

Out[87]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e494e710>
```

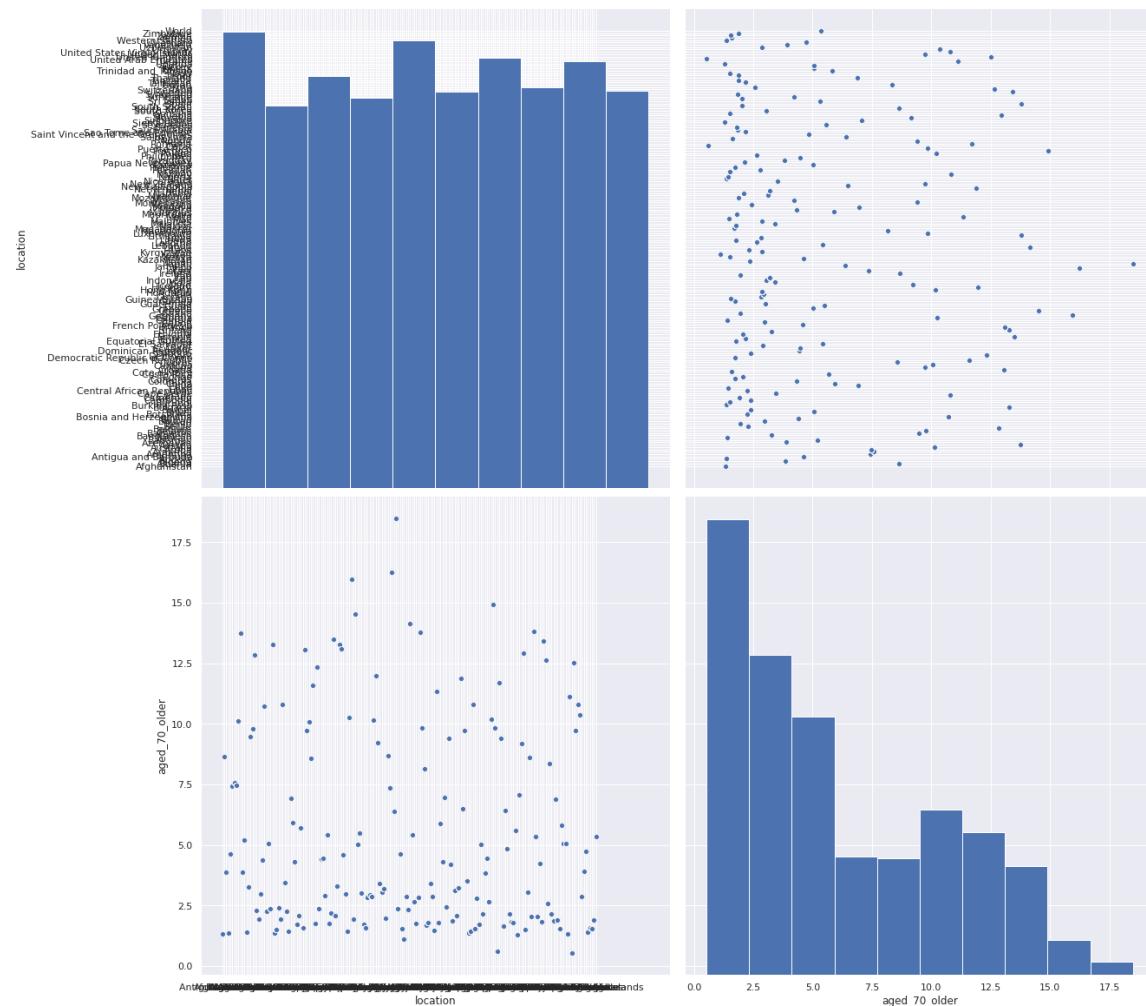


In [88]:

```
sns.pairplot(features, vars=["location", "aged_70_older"], height=8)
```

Out[88]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e3a570f0>
```

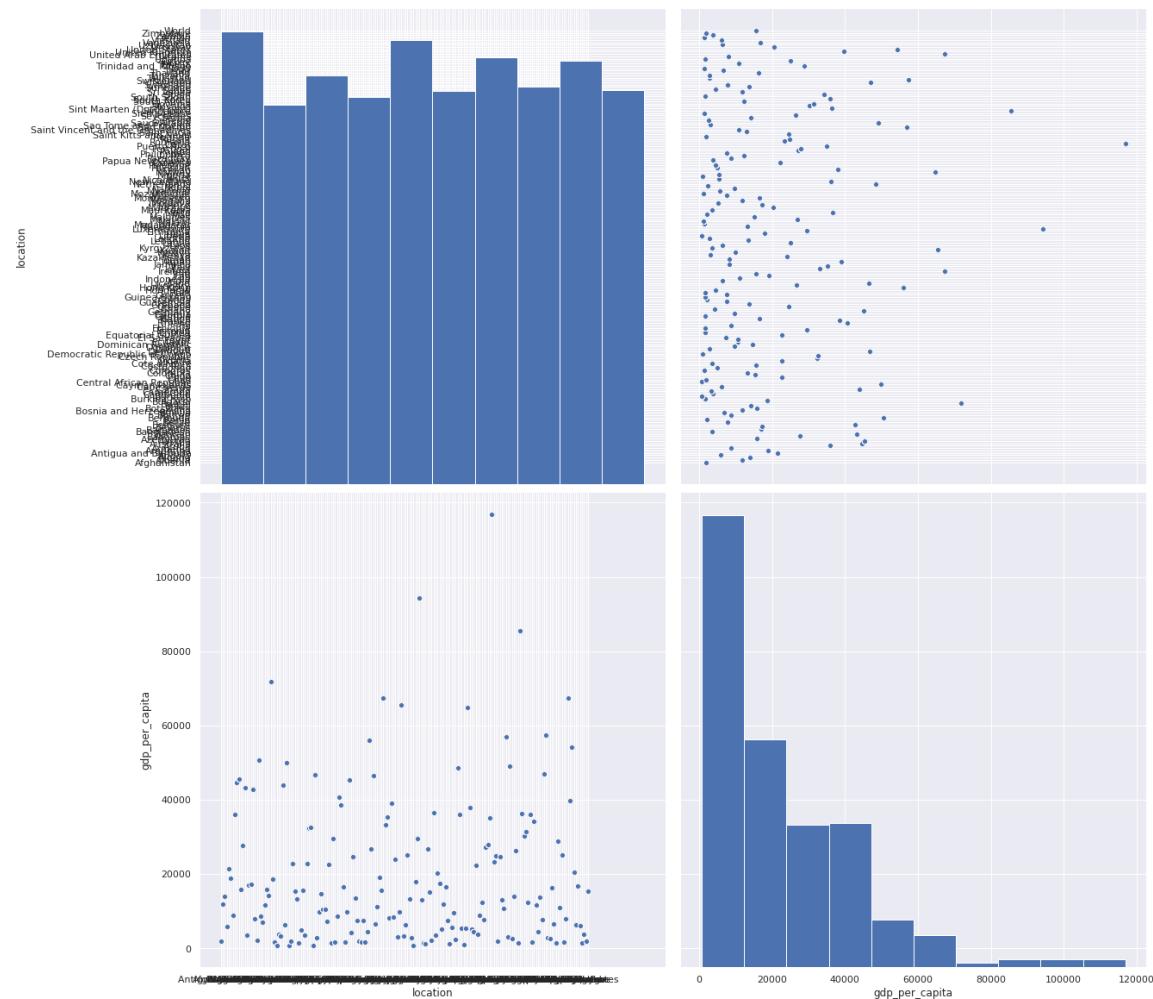


In [89]:

```
sns.pairplot(features, vars=["location", "gdp_per_capita"], height=8)
```

Out[89]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e2c07c18>
```

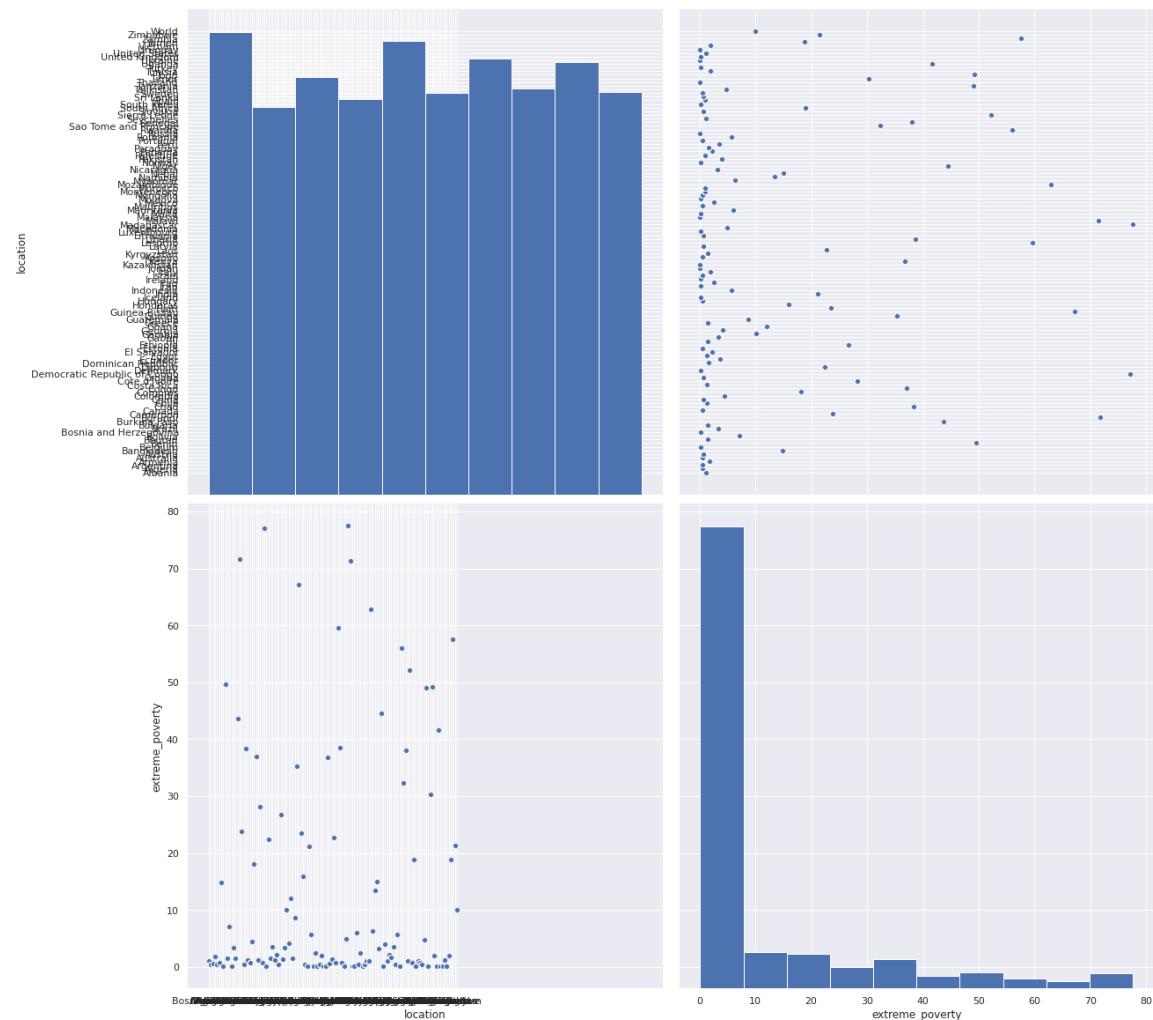


In [90]:

```
sns.pairplot(features, vars=["location", "extreme_poverty"], height=8)
```

Out[90]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e1d97518>
```

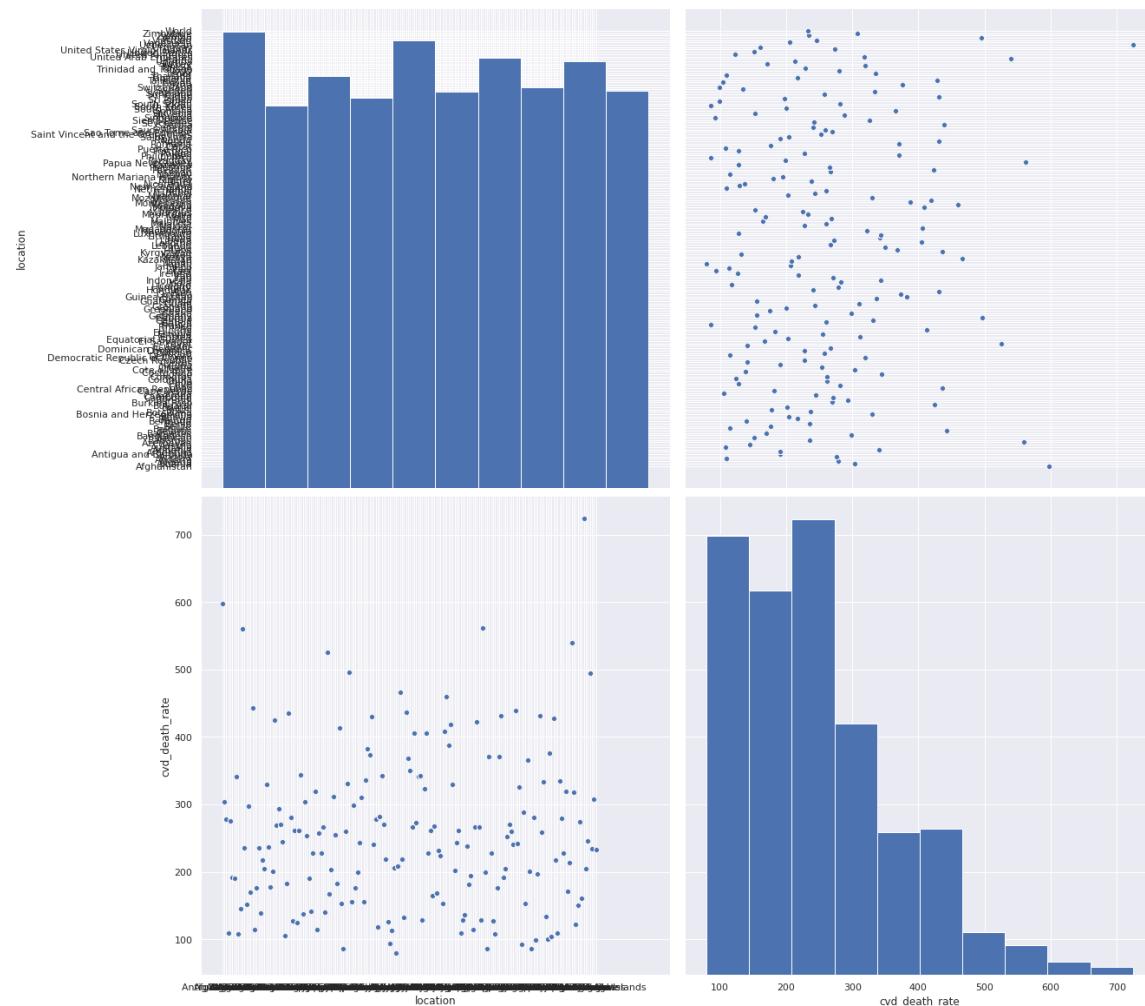


In [91]:

```
sns.pairplot(features, vars=["location", "cvd_death_rate"], height=8)
```

Out[91]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e11b9160>
```

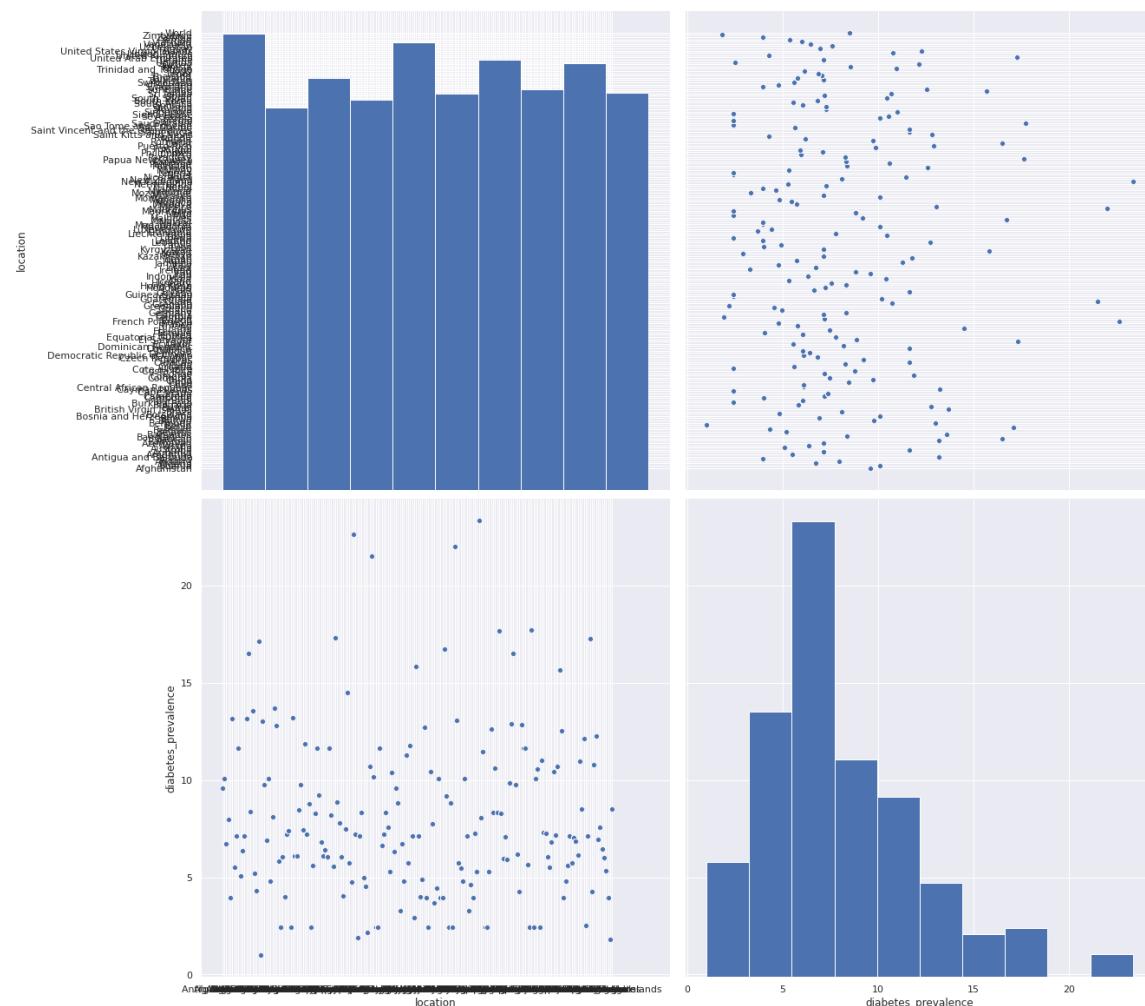


In [92]:

```
sns.pairplot(features, vars=["location", "diabetes_prevalence"], height=8)
```

Out[92]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6e0323978>
```

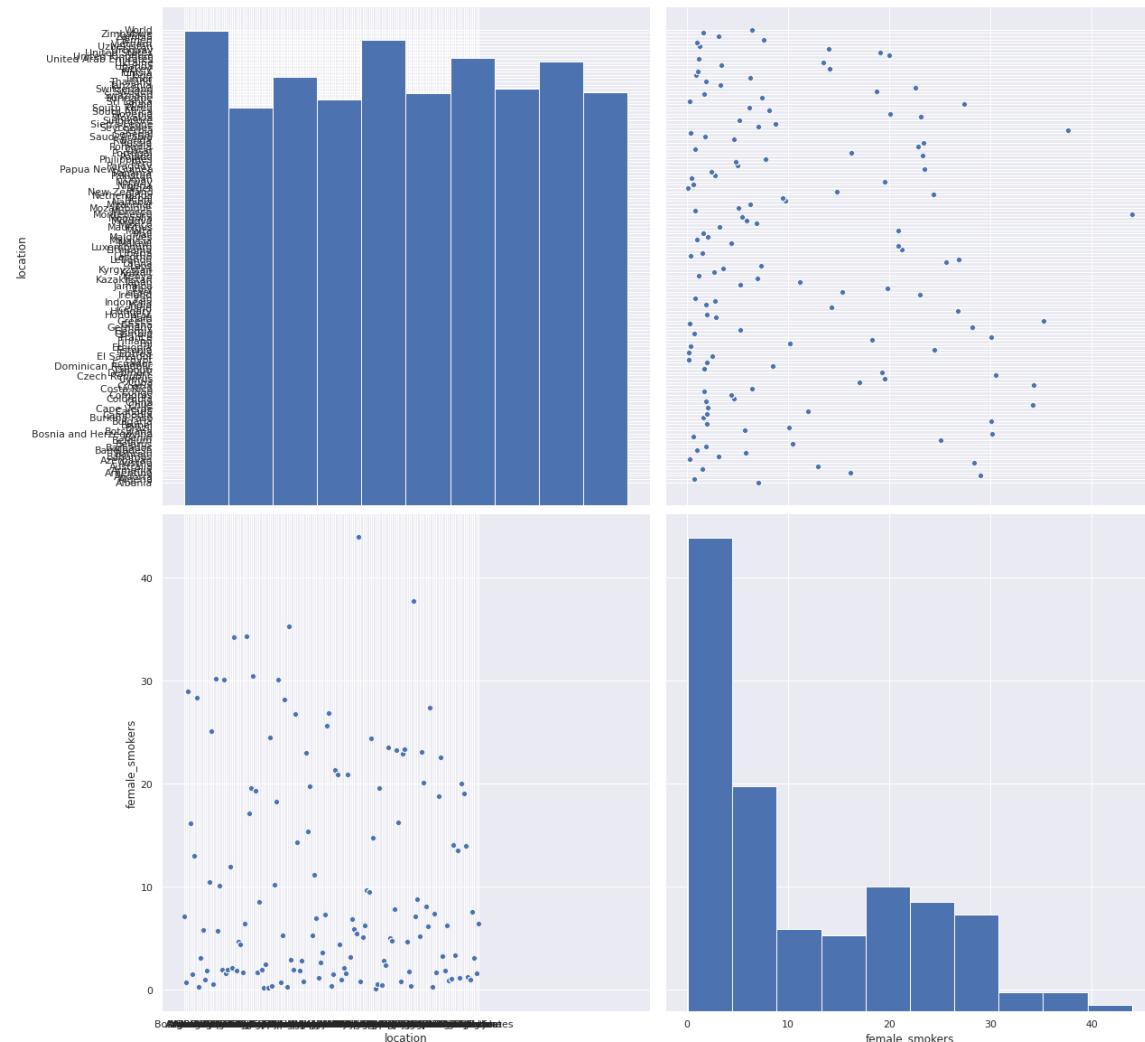


In [93]:

```
sns.pairplot(features, vars=["location", "female_smokers"], height=8)
```

Out[93]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6df533be0>
```

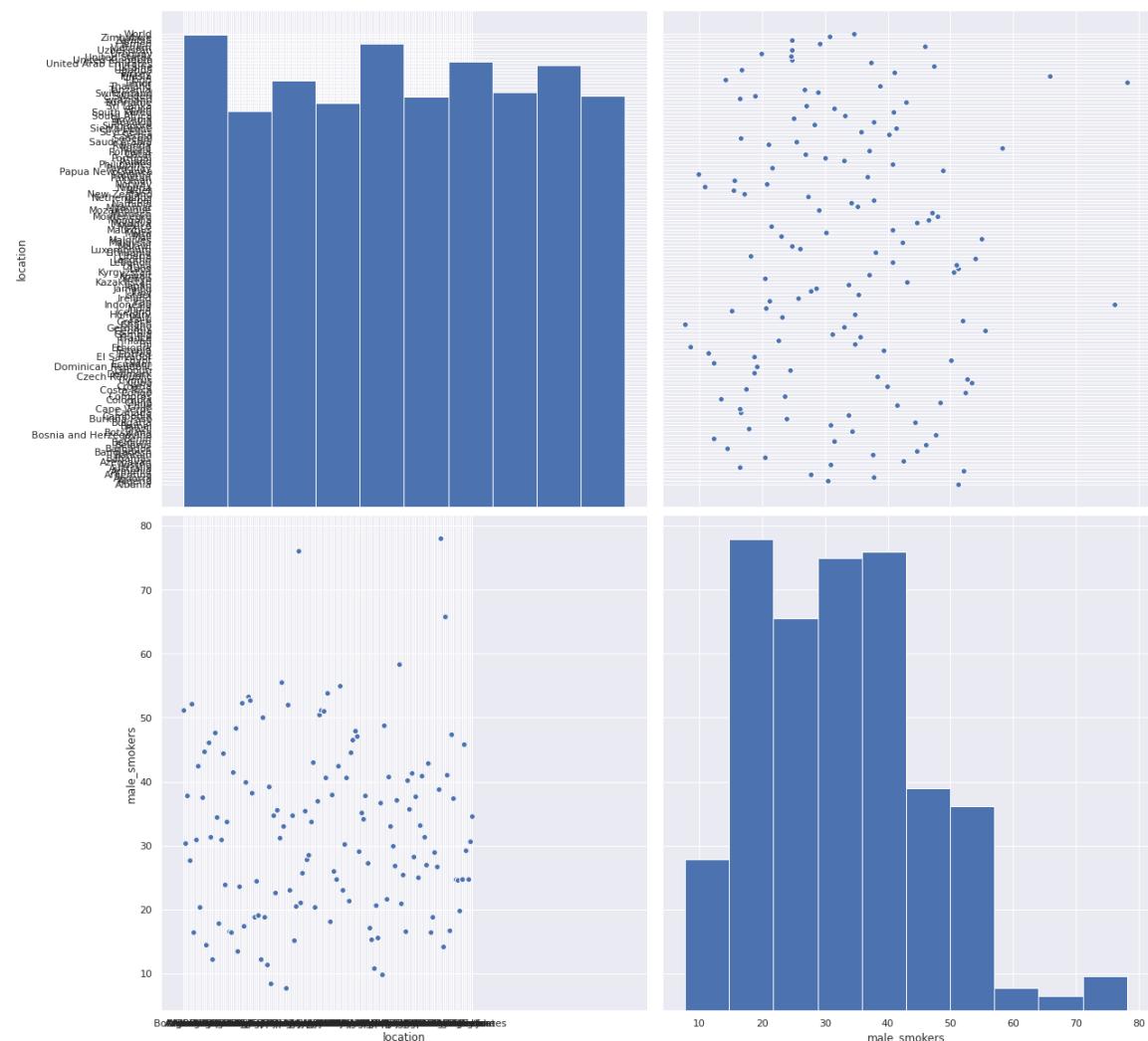


In [94]:

```
sns.pairplot(features, vars=["location", "male_smokers"], height=8)
```

Out[94]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6de84cda0>
```

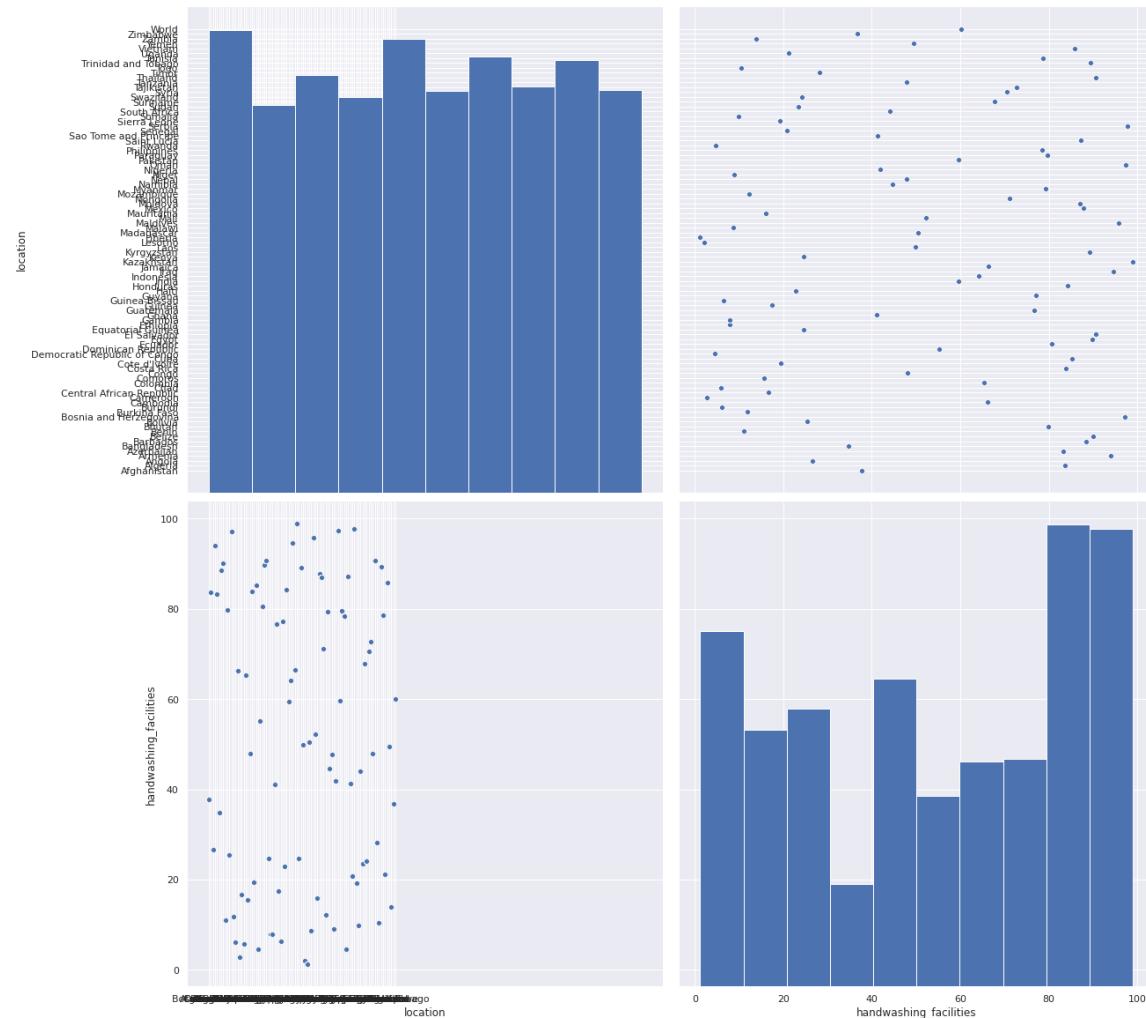


In [95]:

```
sns.pairplot(features, vars=["location", "handwashing_facilities"], height=8)
```

Out[95]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6de1187b8>
```

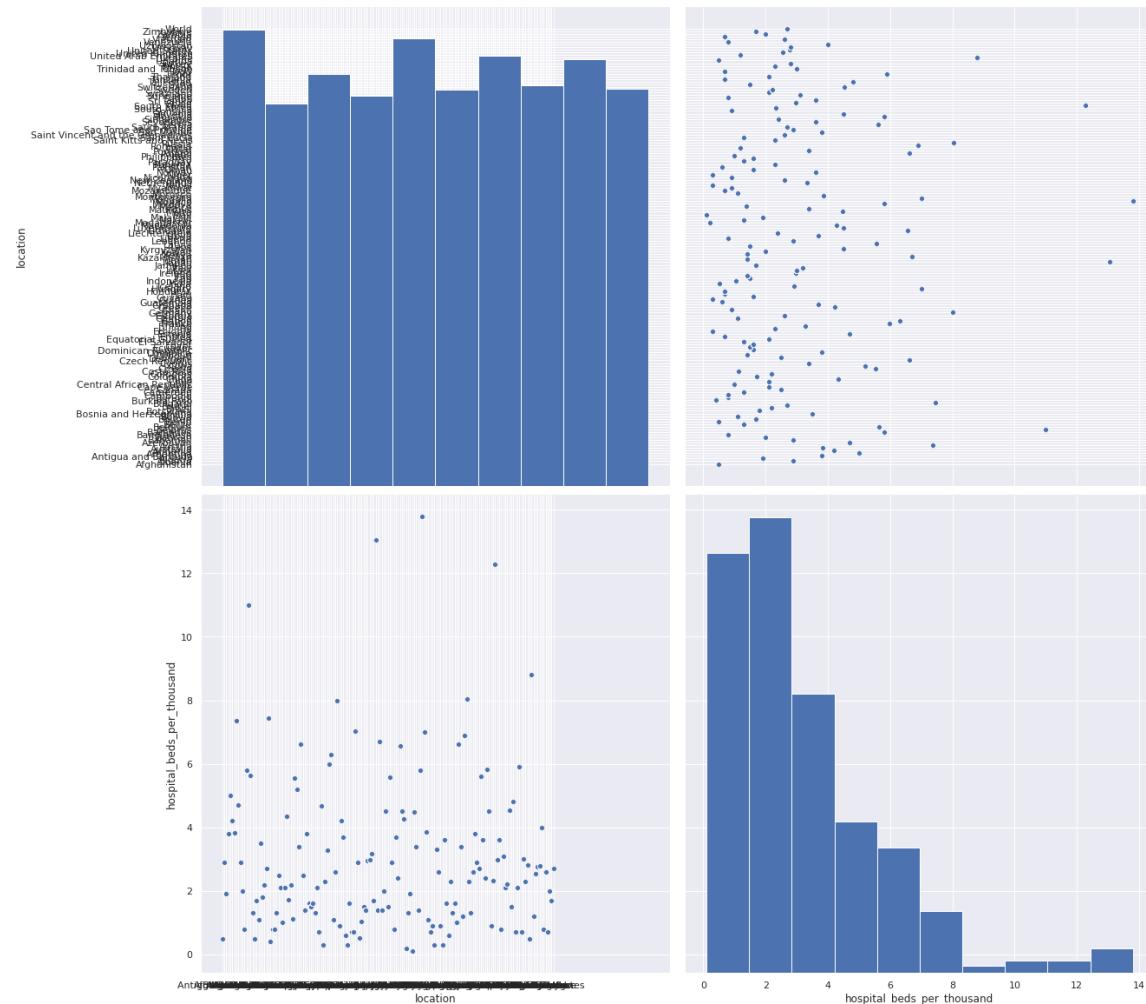


In [96]:

```
sns.pairplot(features, vars=["location", "hospital_beds_per_thousand"], height=8)
```

Out[96]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ddc1f400>
```

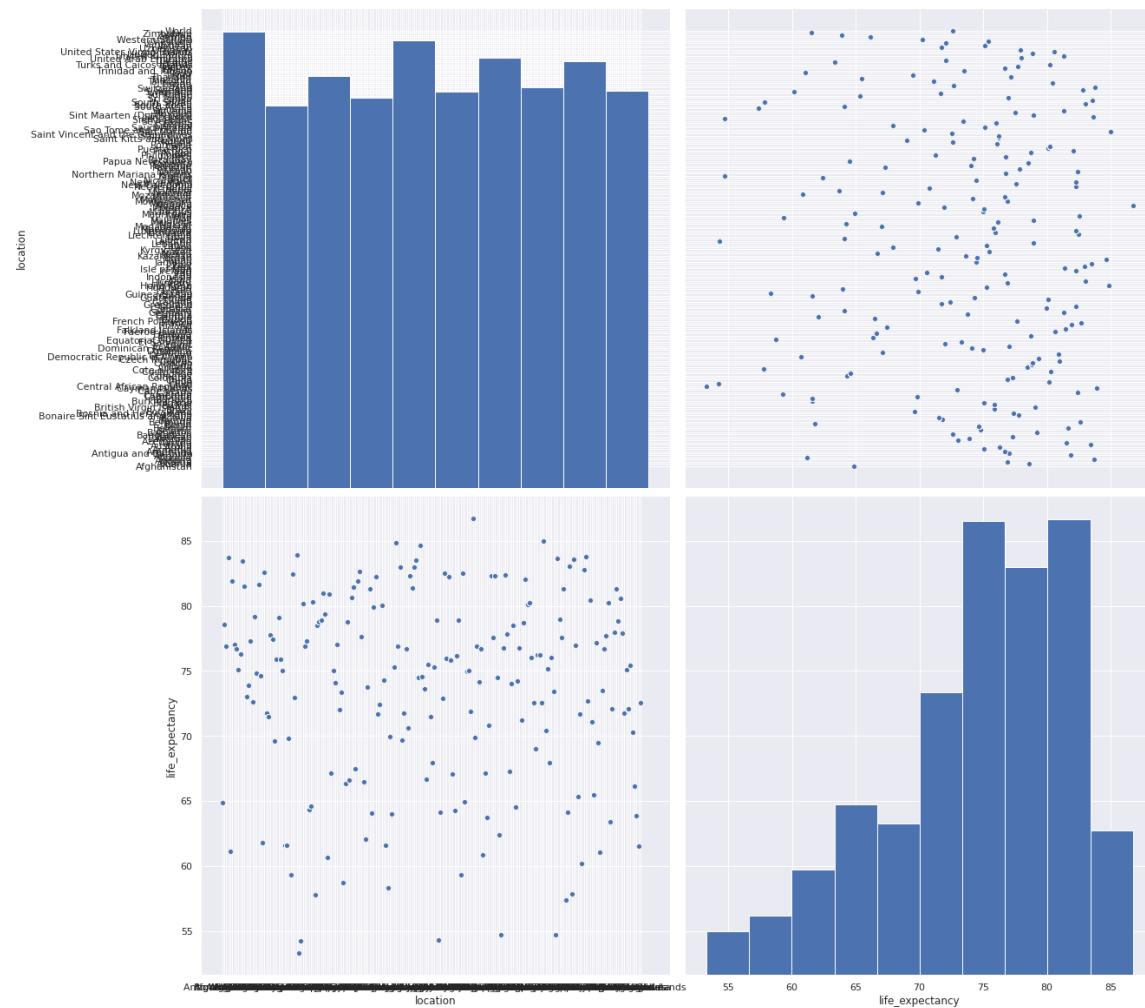


In [97]:

```
sns.pairplot(features, vars=["location", "life_expectancy"], height=8)
```

Out[97]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6dcebd320>
```

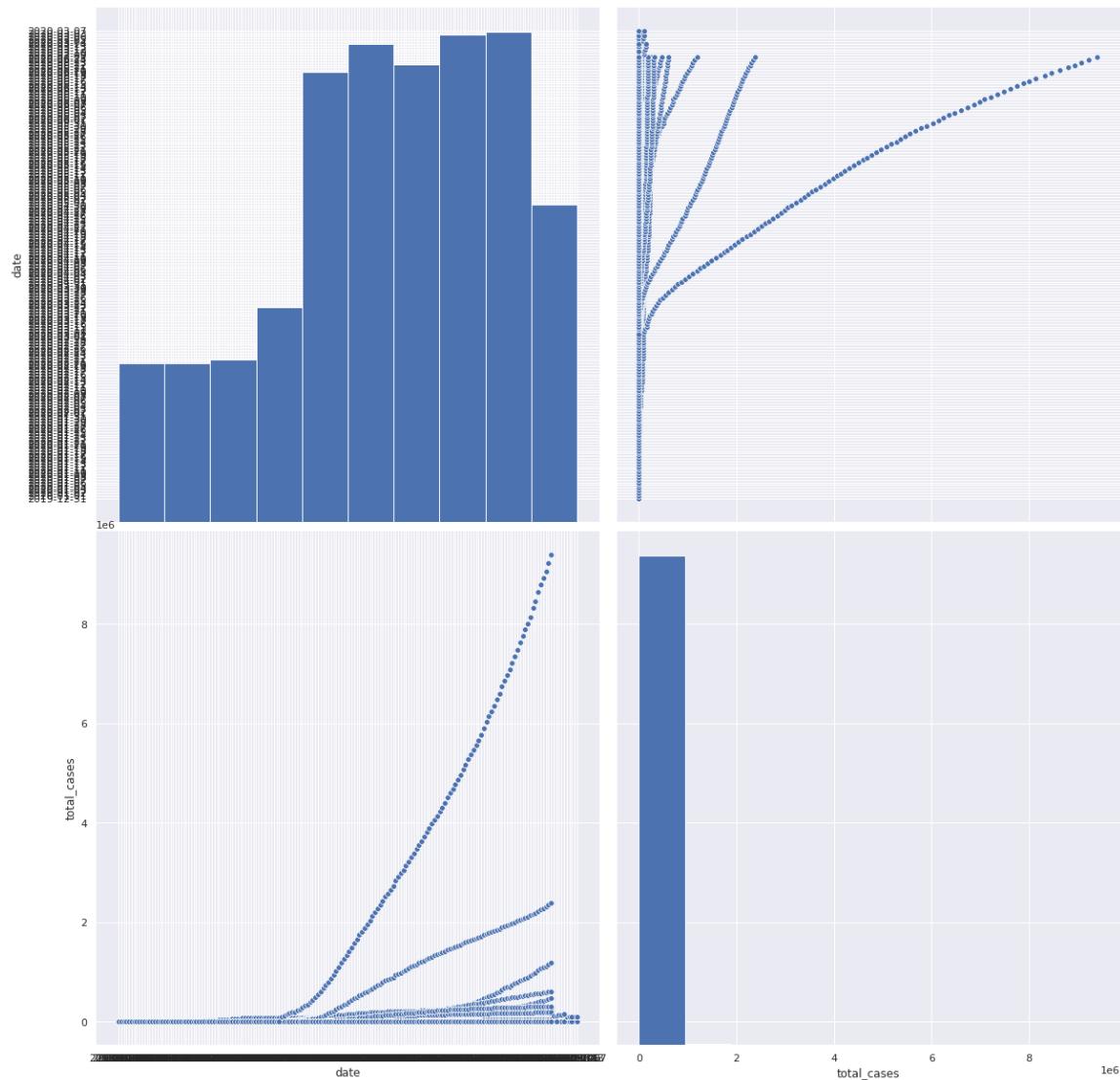


In [98]:

```
sns.pairplot(features, vars=["date", "total_cases"], height=8)
```

Out[98]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6de19cda0>
```

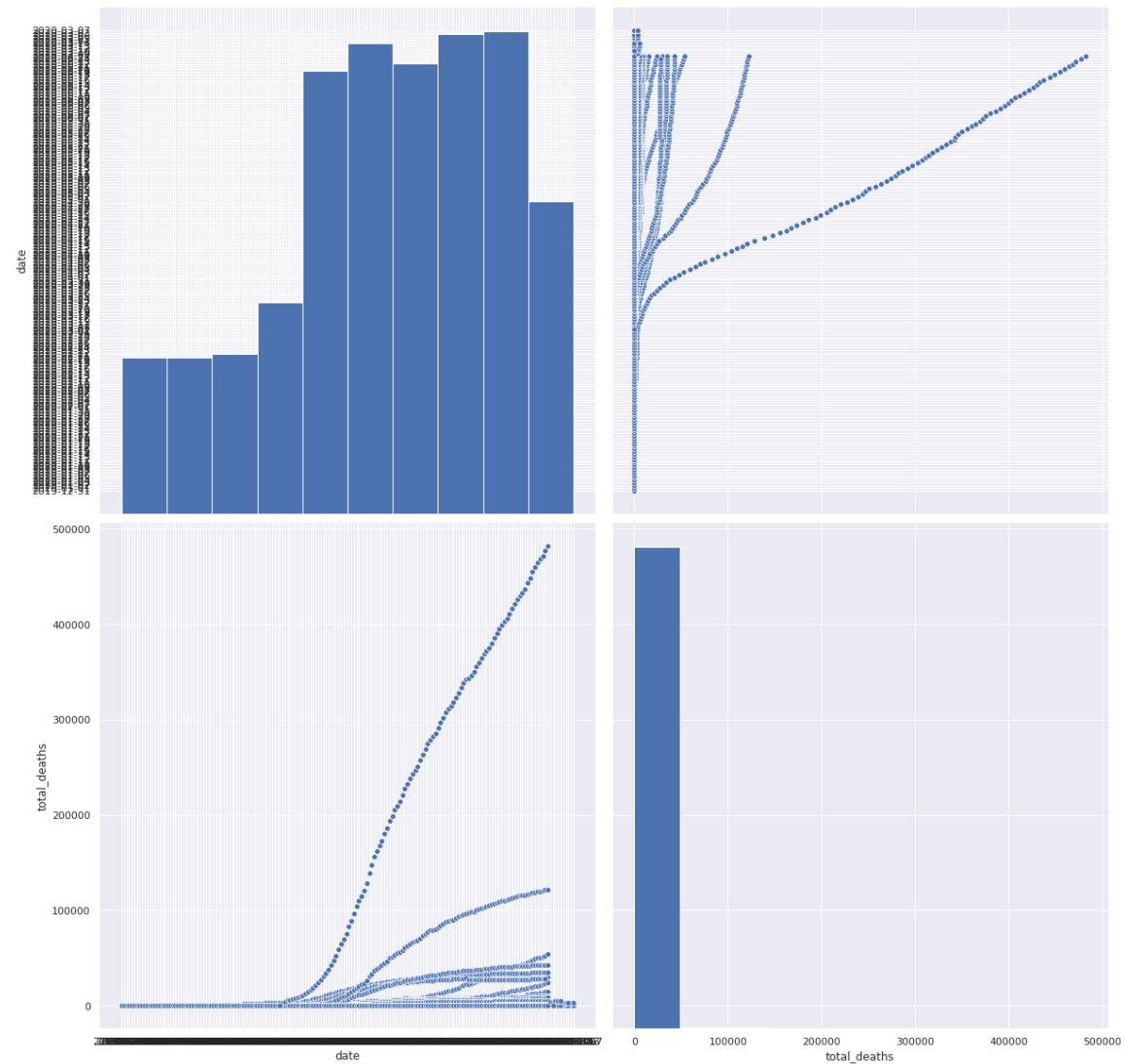


In [99]:

```
sns.pairplot(features, vars=["date", "total_deaths"], height=8)
```

Out[99]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ddc3c898>
```

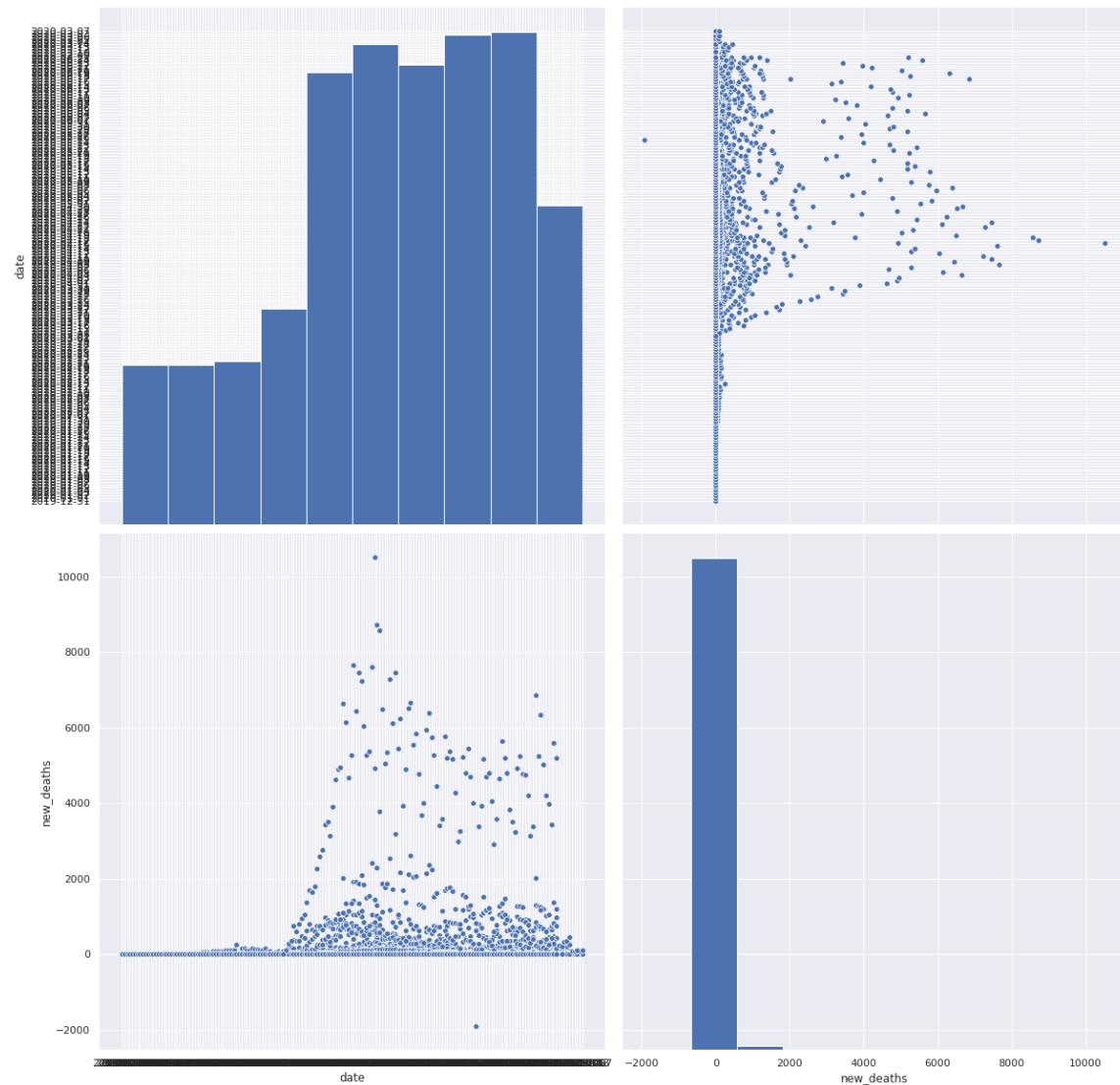


In [100]:

```
sns.pairplot(features, vars=["date", "new_deaths"], height=8)
```

Out[100]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6da9927b8>
```

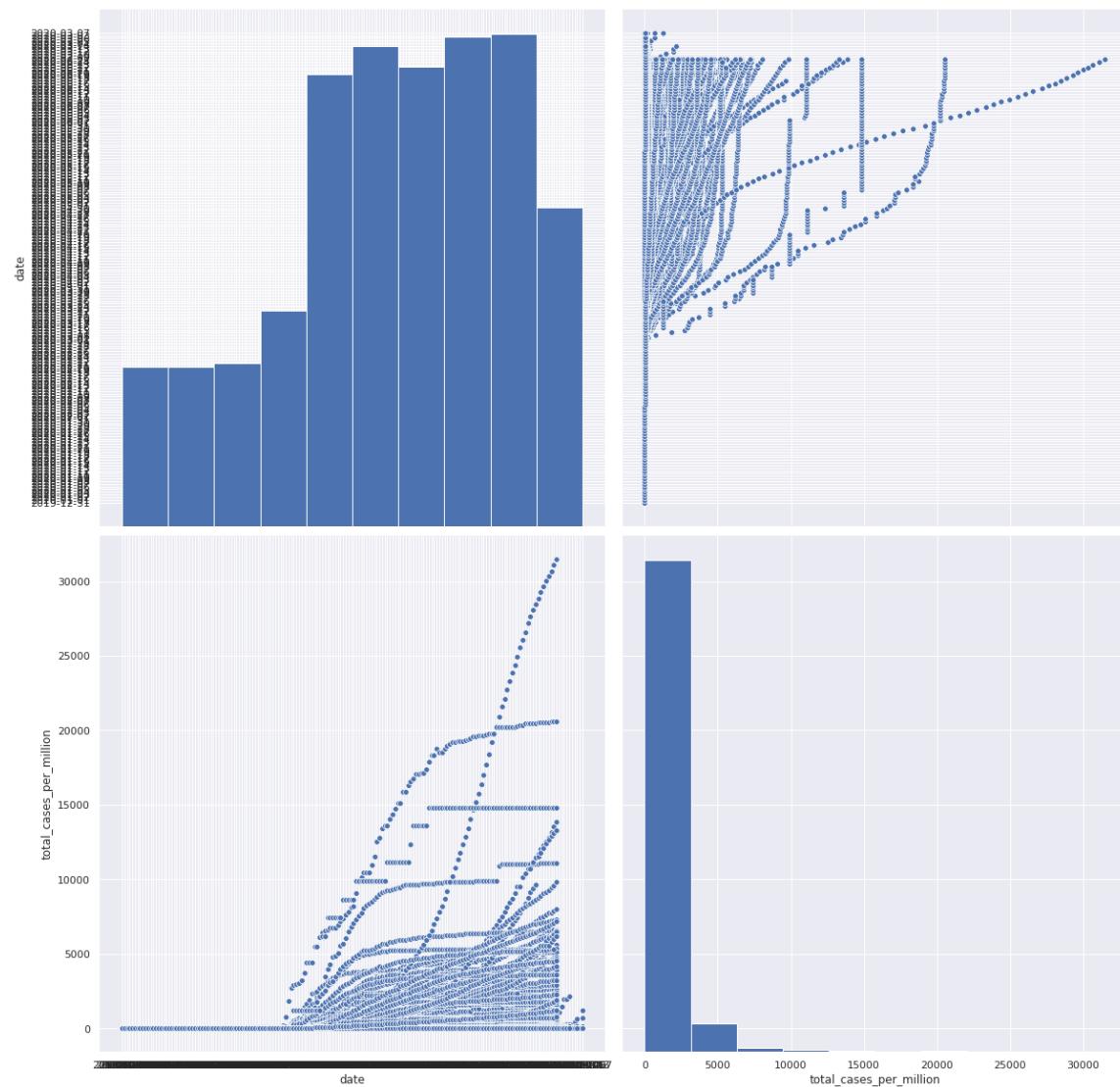


In [101]:

```
sns.pairplot(features, vars=["date", "total_cases_per_million"], height=8)
```

Out[101]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6da137630>
```

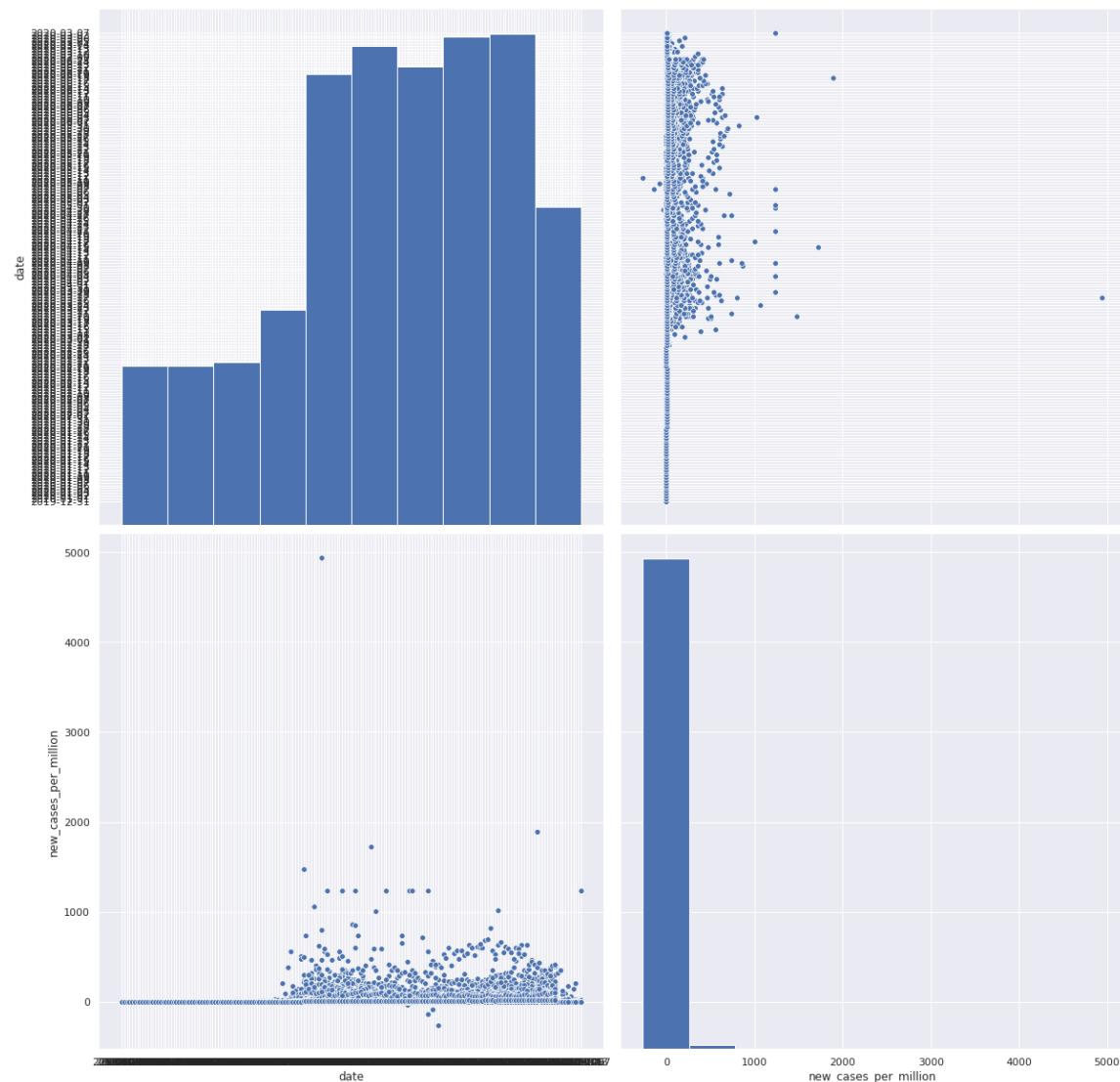


In [102]:

```
sns.pairplot(features, vars=["date", "new_cases_per_million"], height=8)
```

Out[102]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d98fc128>
```

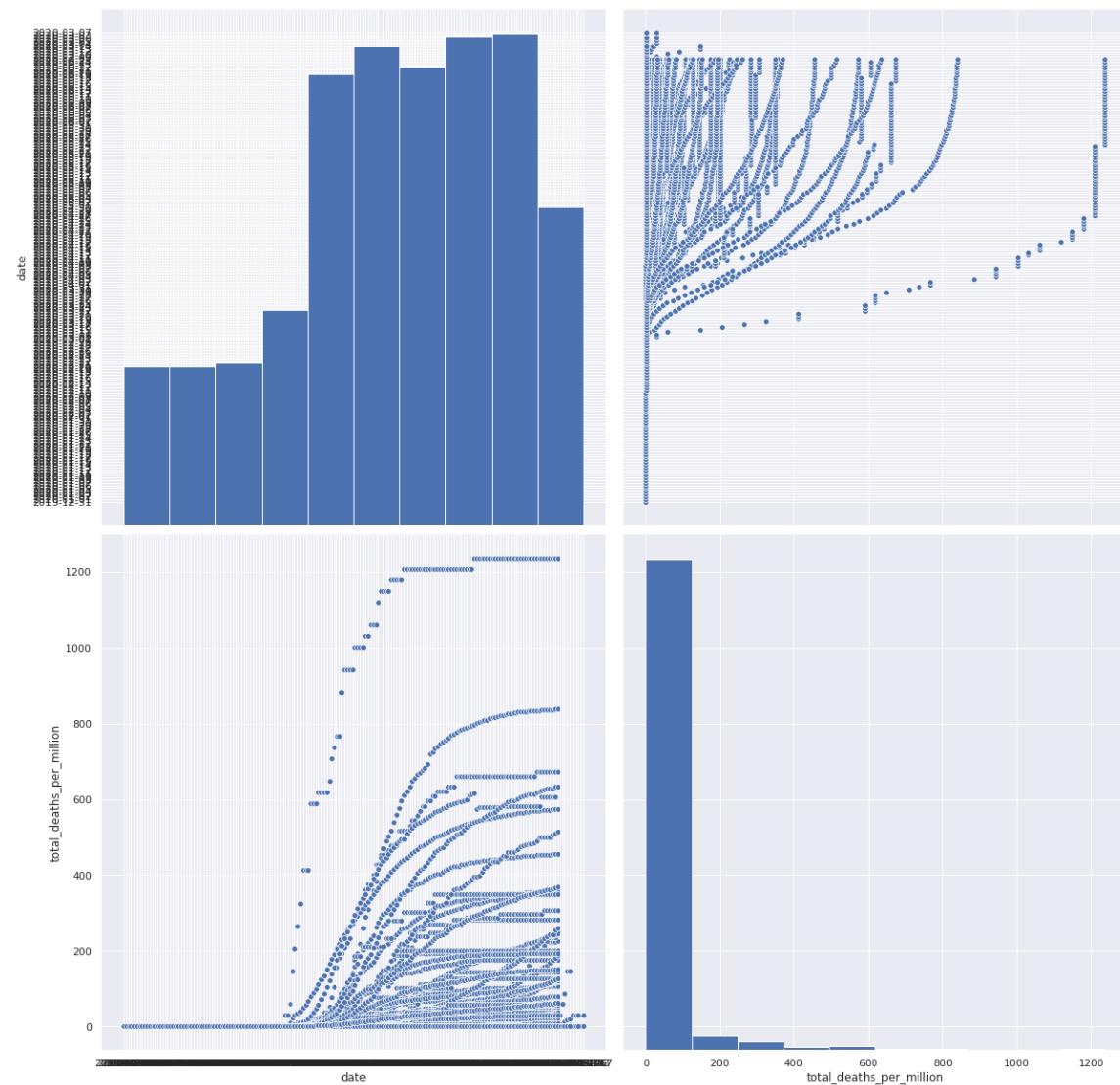


In [103]:

```
sns.pairplot(features, vars=["date", "total_deaths_per_million"], height=8)
```

Out[103]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d90a0208>
```

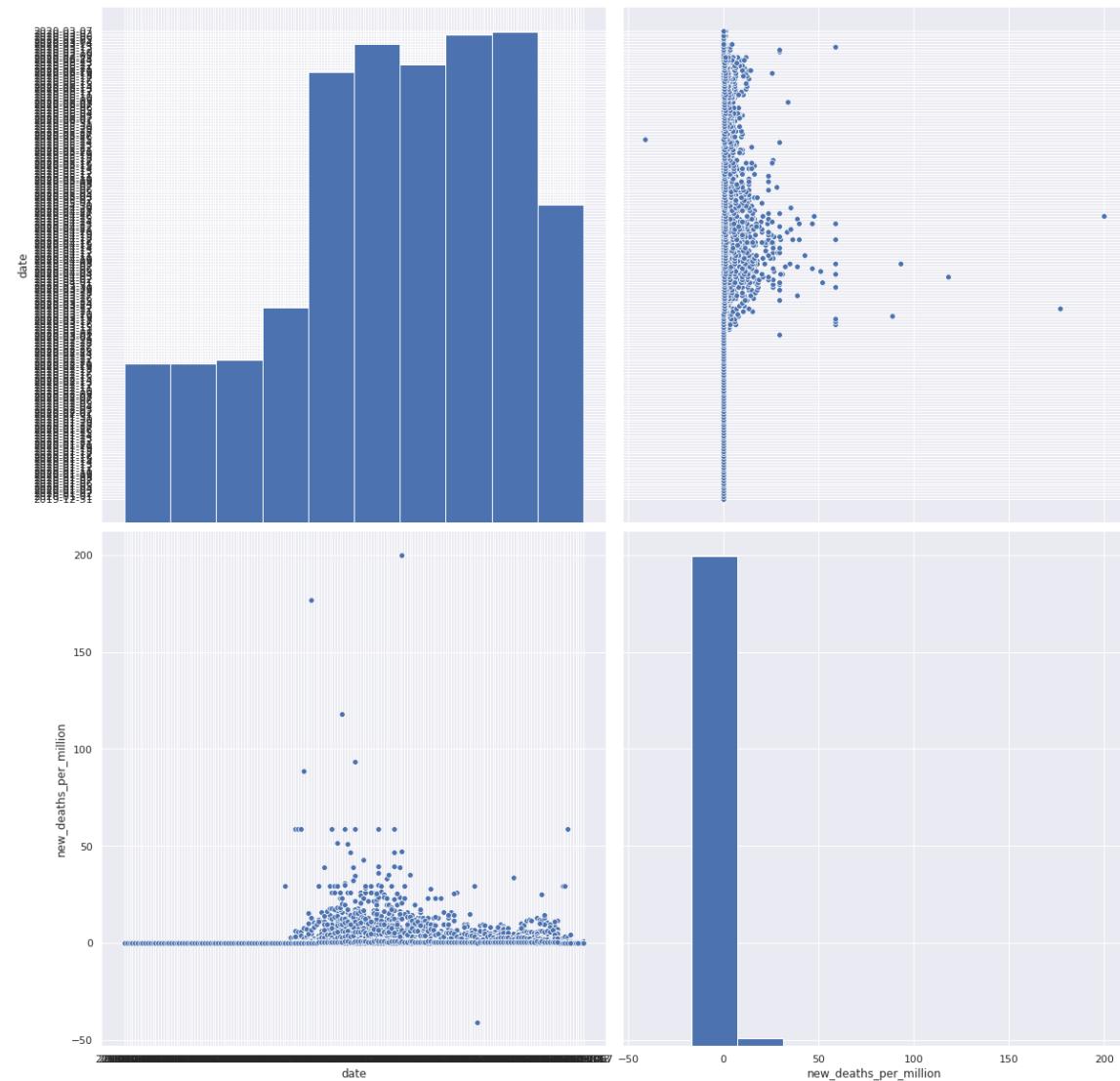


In [104]:

```
sns.pairplot(features, vars=["date", "new_deaths_per_million"], height=8)
```

Out[104]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d885e7b8>
```

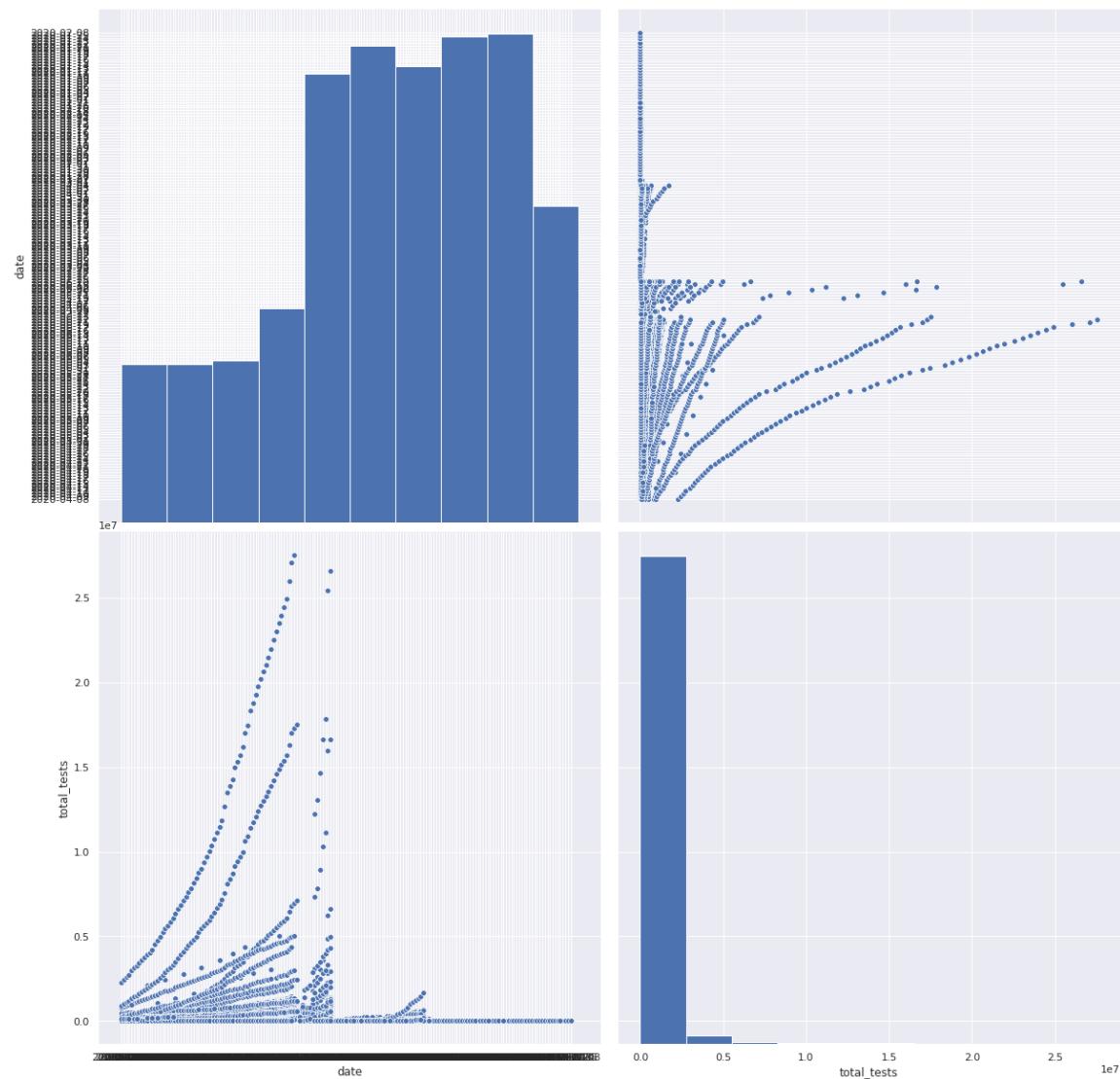


In [105]:

```
sns.pairplot(features, vars=["date", "total_tests"], height=8)
```

Out[105]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d9104780>
```

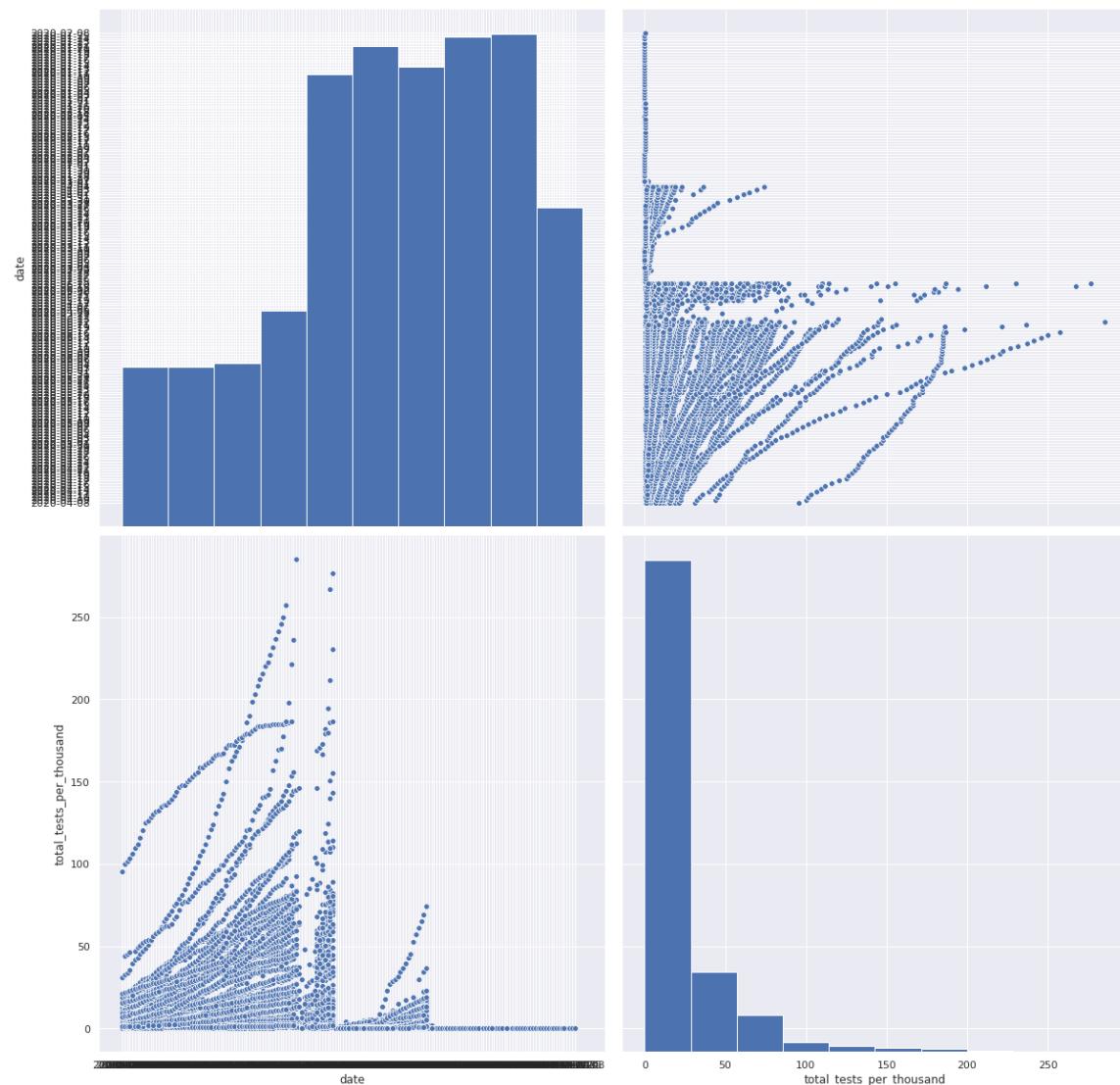


In [106]:

```
sns.pairplot(features, vars=["date", "total_tests_per_thousand"], height=8)
```

Out[106]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d780af60>
```

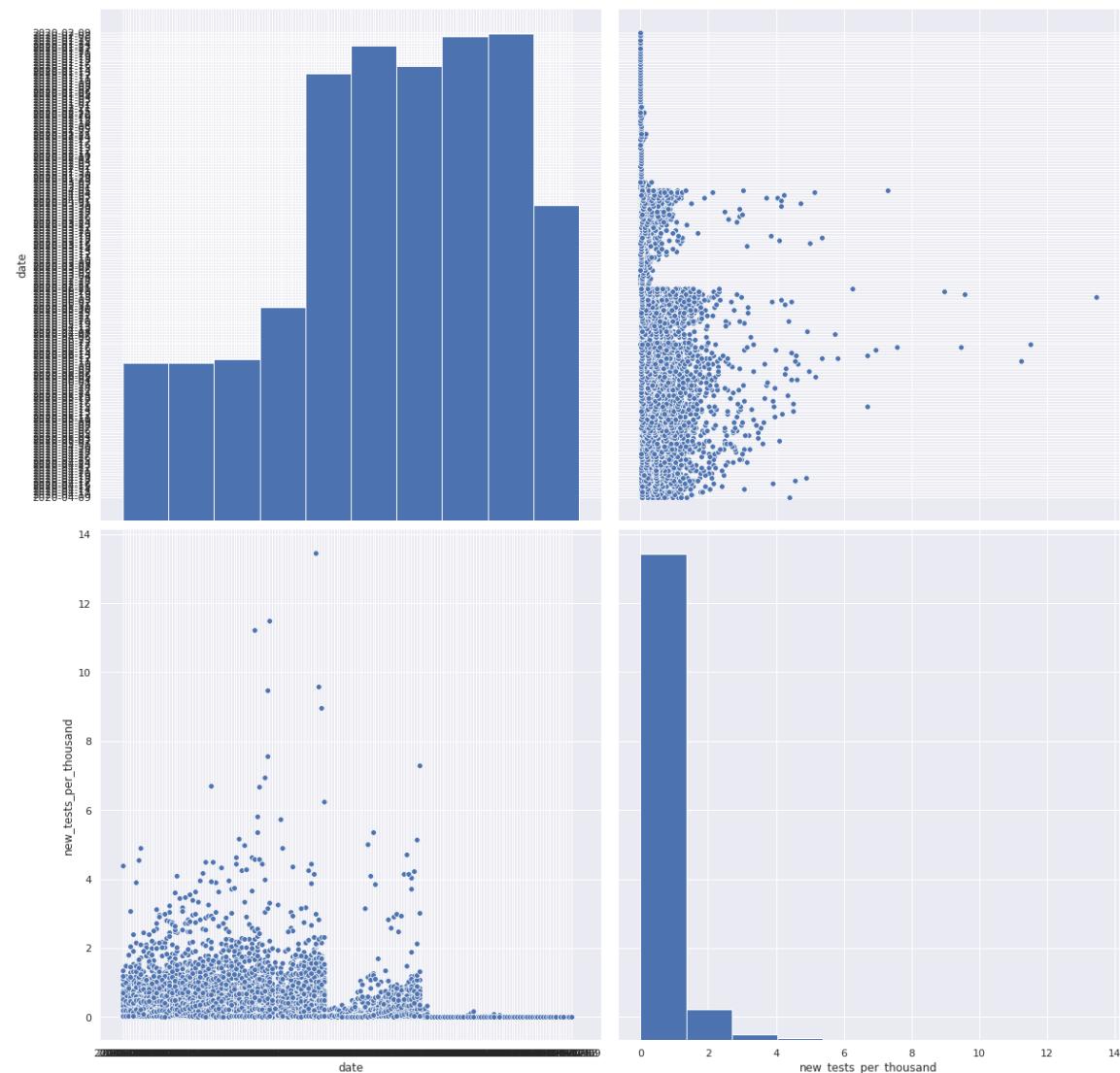


In [107]:

```
sns.pairplot(features, vars=["date", "new_tests_per_thousand"], height=8)
```

Out[107]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d70f8be0>
```

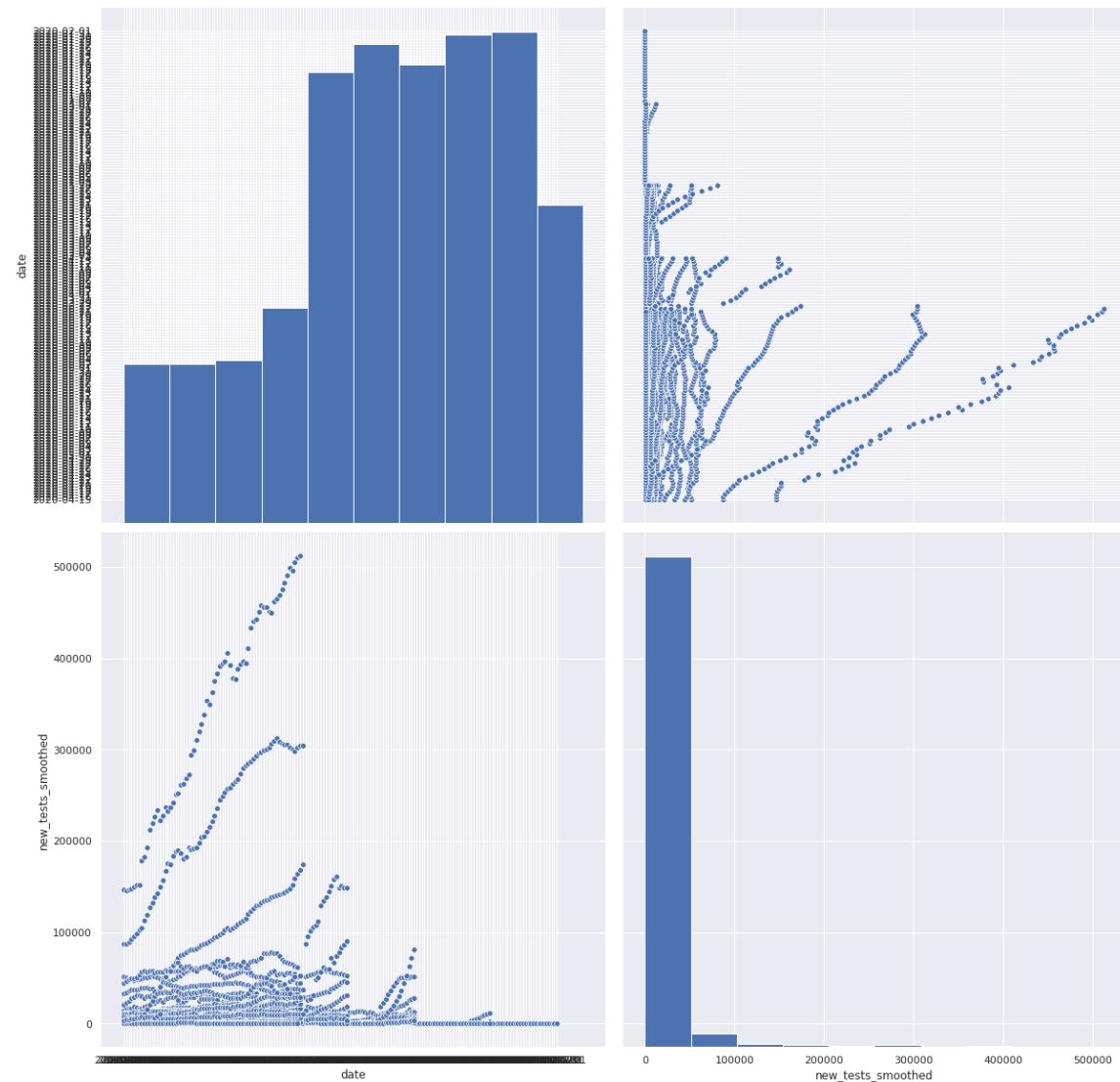


In [108]:

```
sns.pairplot(features, vars=["date", "new_tests_smoothed"], height=8)
```

Out[108]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d683d518>
```

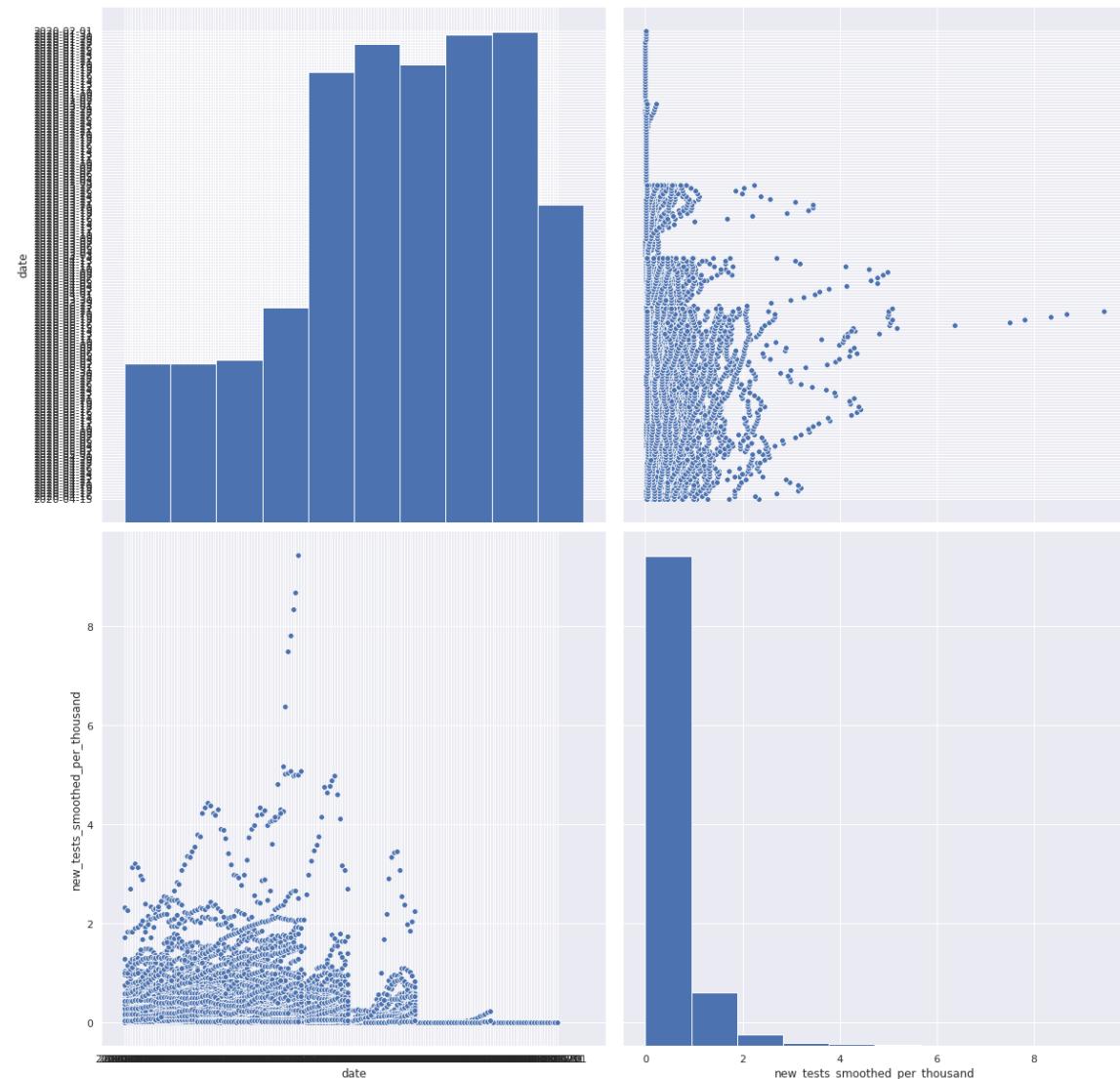


In [109]:

```
sns.pairplot(features, vars=["date", "new_tests_smoothed_per_thousand"], height=8)
```

Out[109]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d6099d30>
```

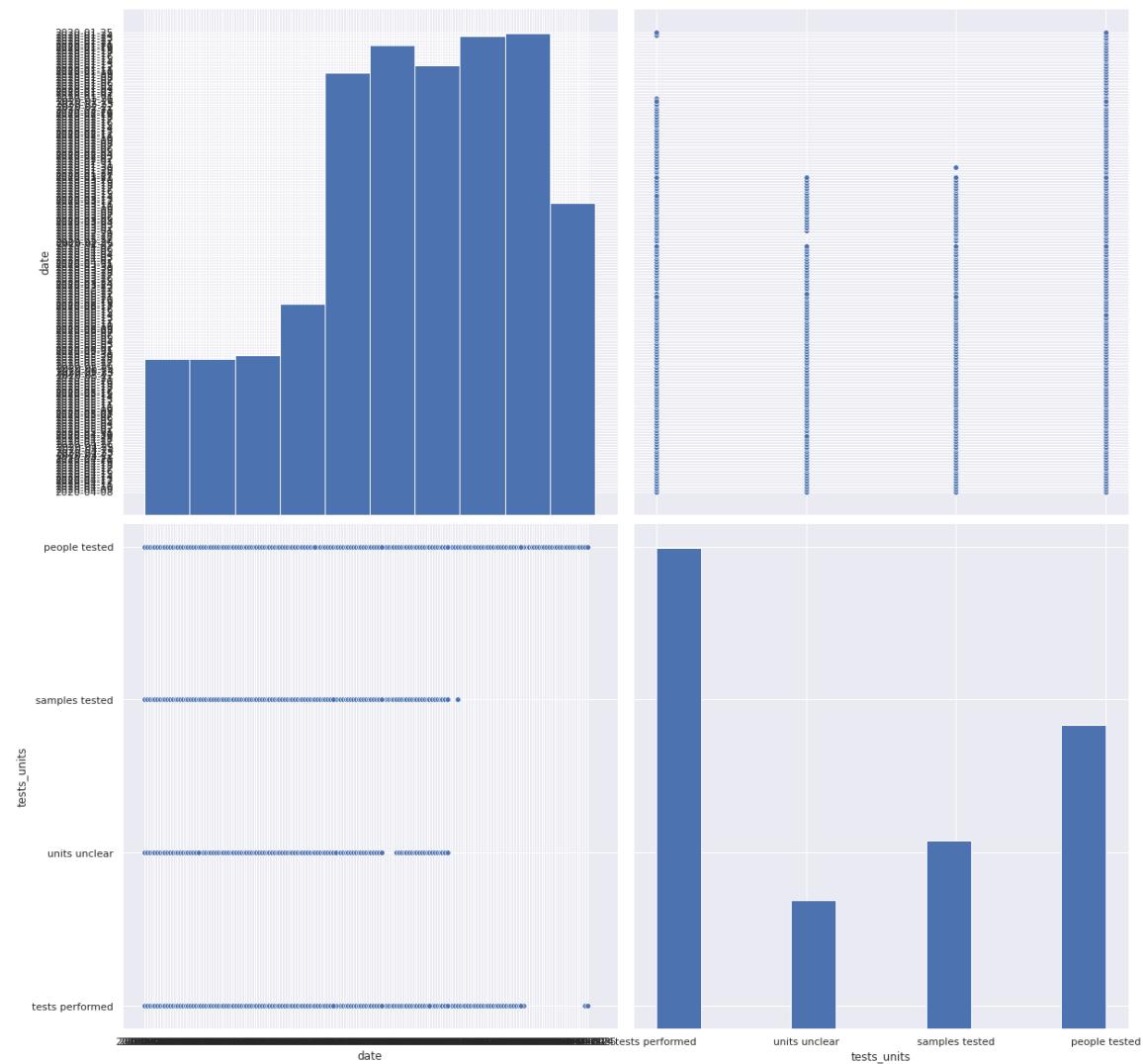


In [110]:

```
sns.pairplot(features, vars=["date", "tests_units"], height=8)
```

Out[110]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d58e24a8>
```

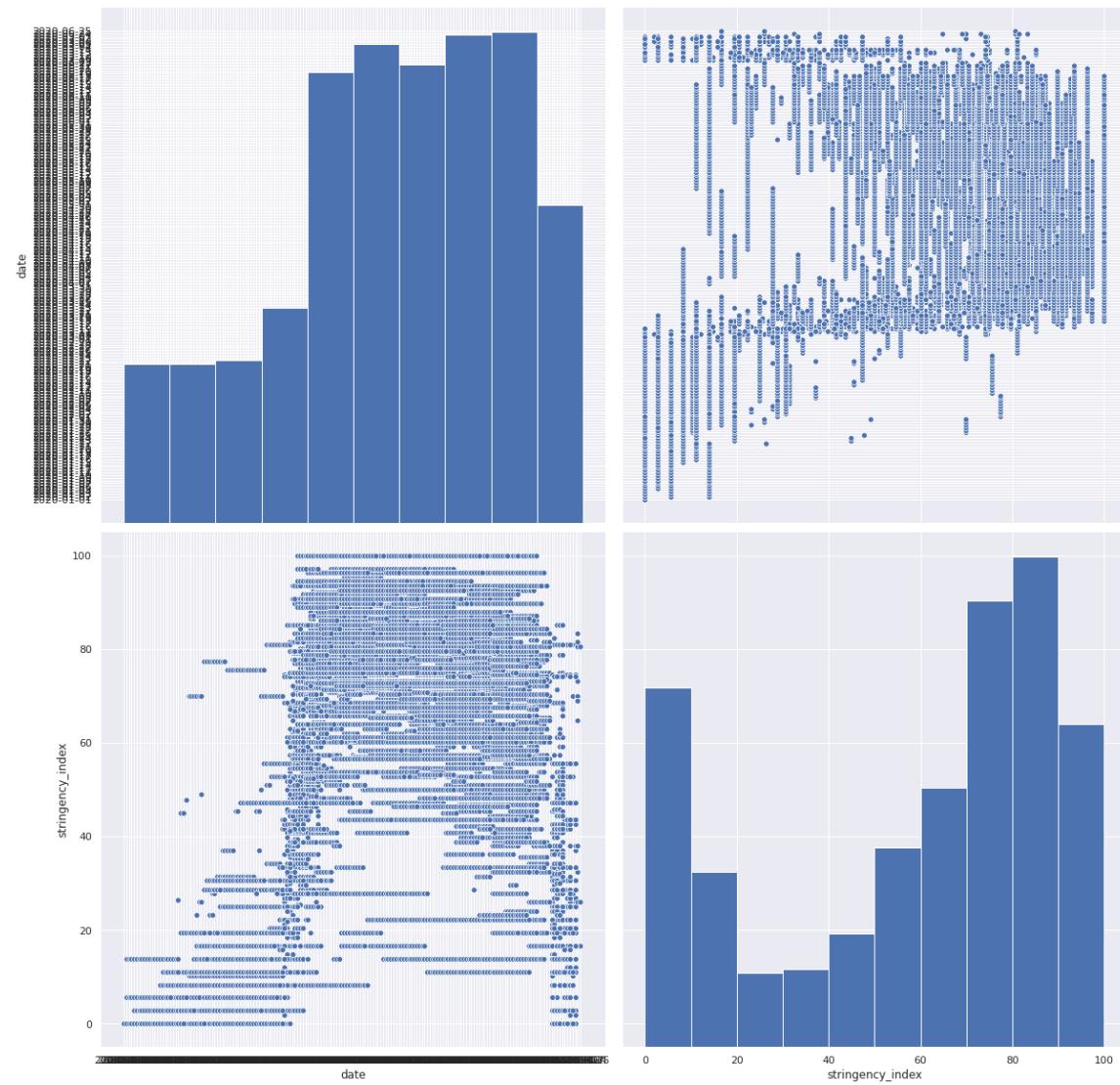


In [111]:

```
sns.pairplot(features, vars=["date", "stringency_index"], height=8)
```

Out[111]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d6051160>
```

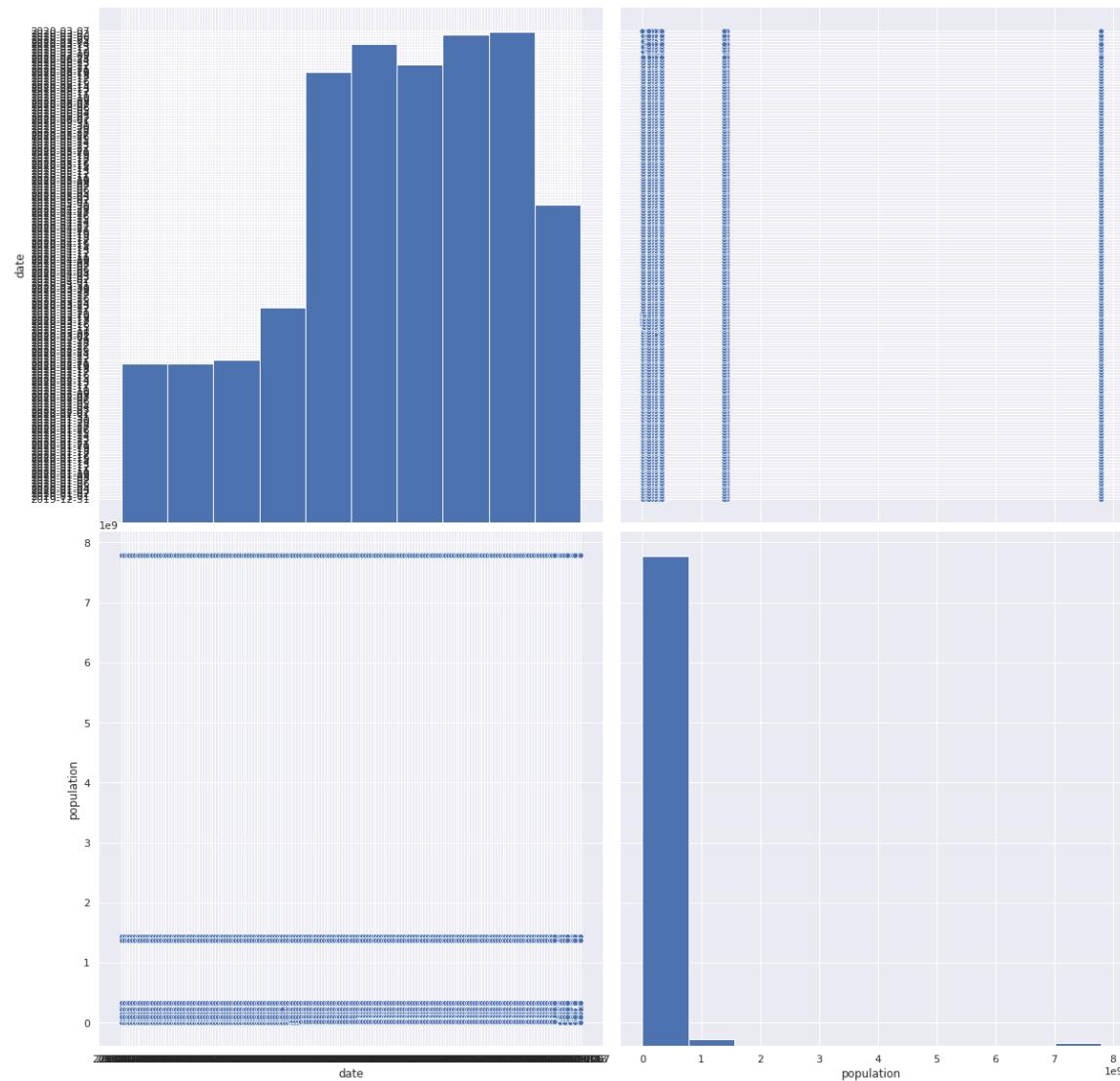


In [112]:

```
sns.pairplot(features, vars=["date", "population"], height=8)
```

Out[112]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d486c630>
```

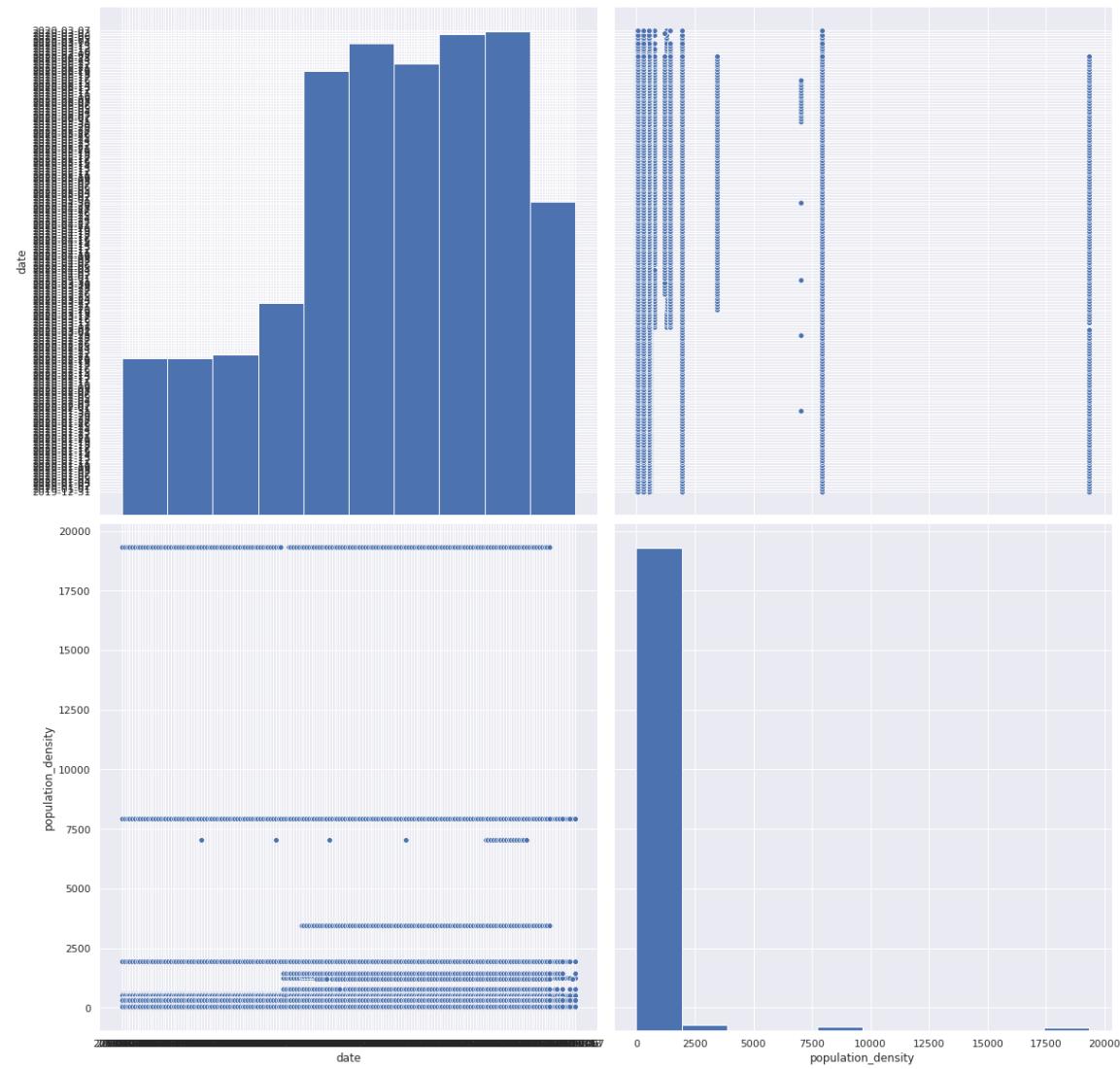


In [113]:

```
sns.pairplot(features, vars=["date", "population_density"], height=8)
```

Out[113]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d403b208>
```

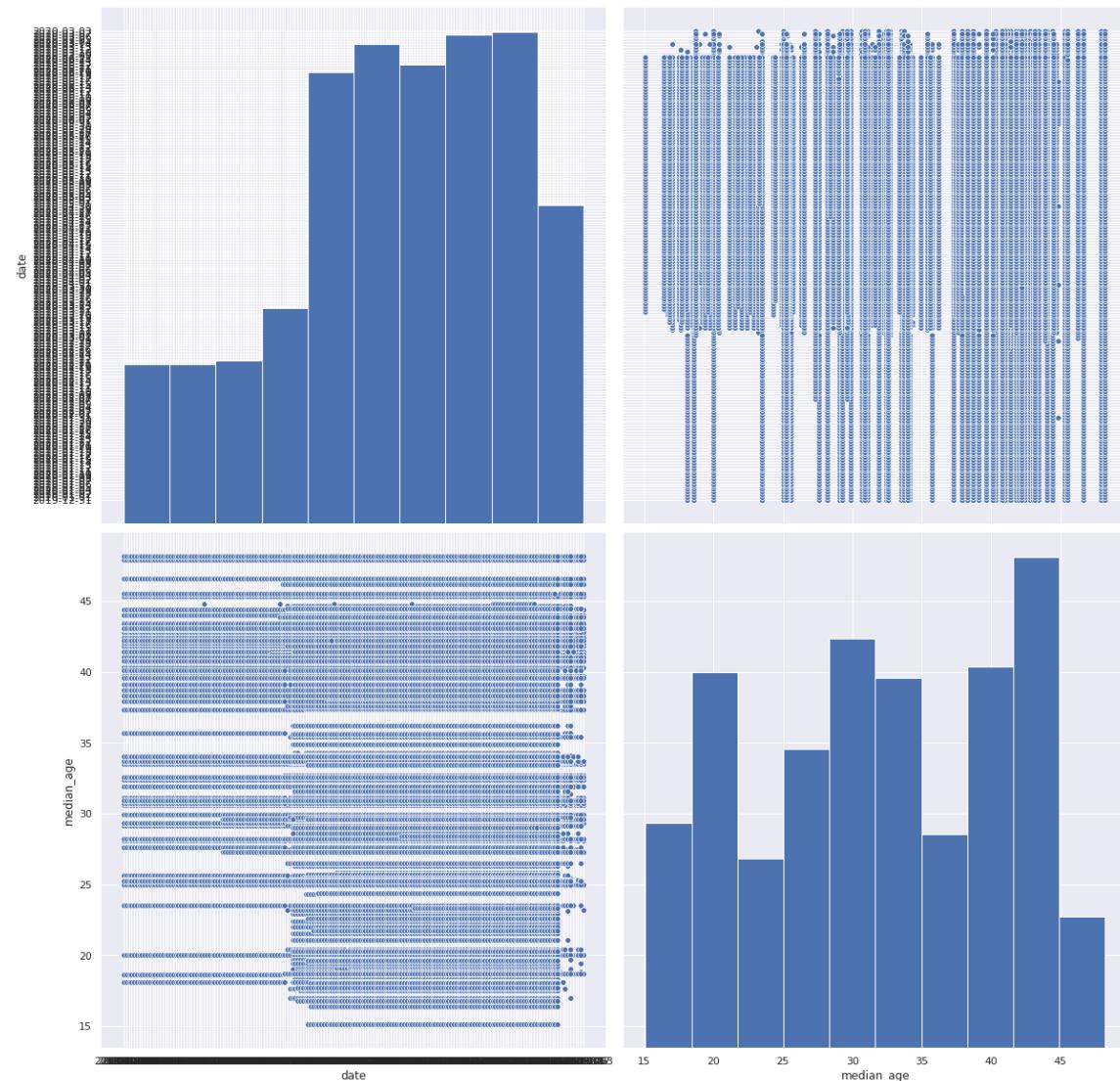


In [114]:

```
sns.pairplot(features, vars=["date", "median_age"], height=8)
```

Out[114]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d3eb2630>
```

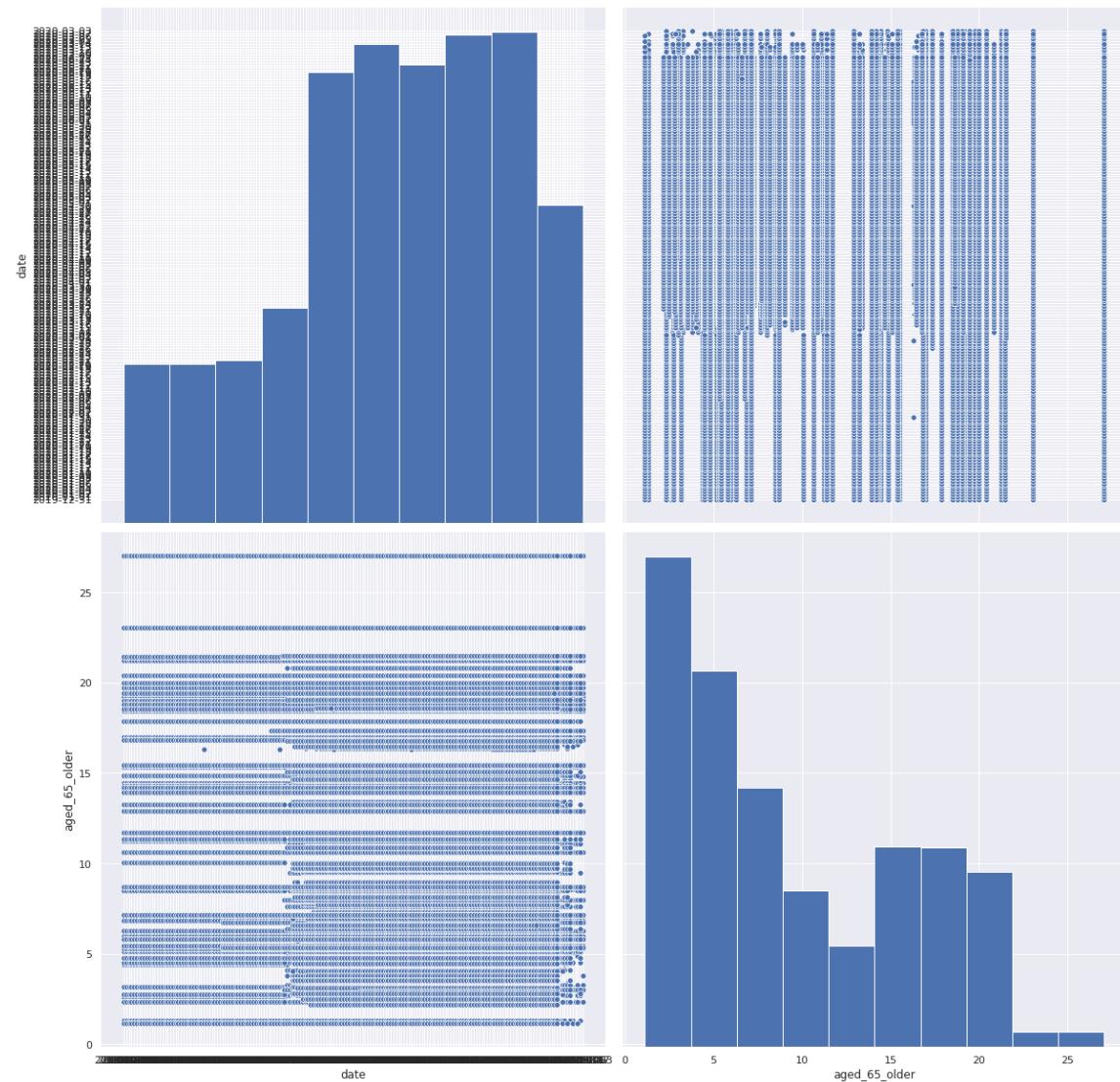


In [115]:

```
sns.pairplot(features, vars=["date", "aged_65_older"], height=8)
```

Out[115]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d2f45be0>
```

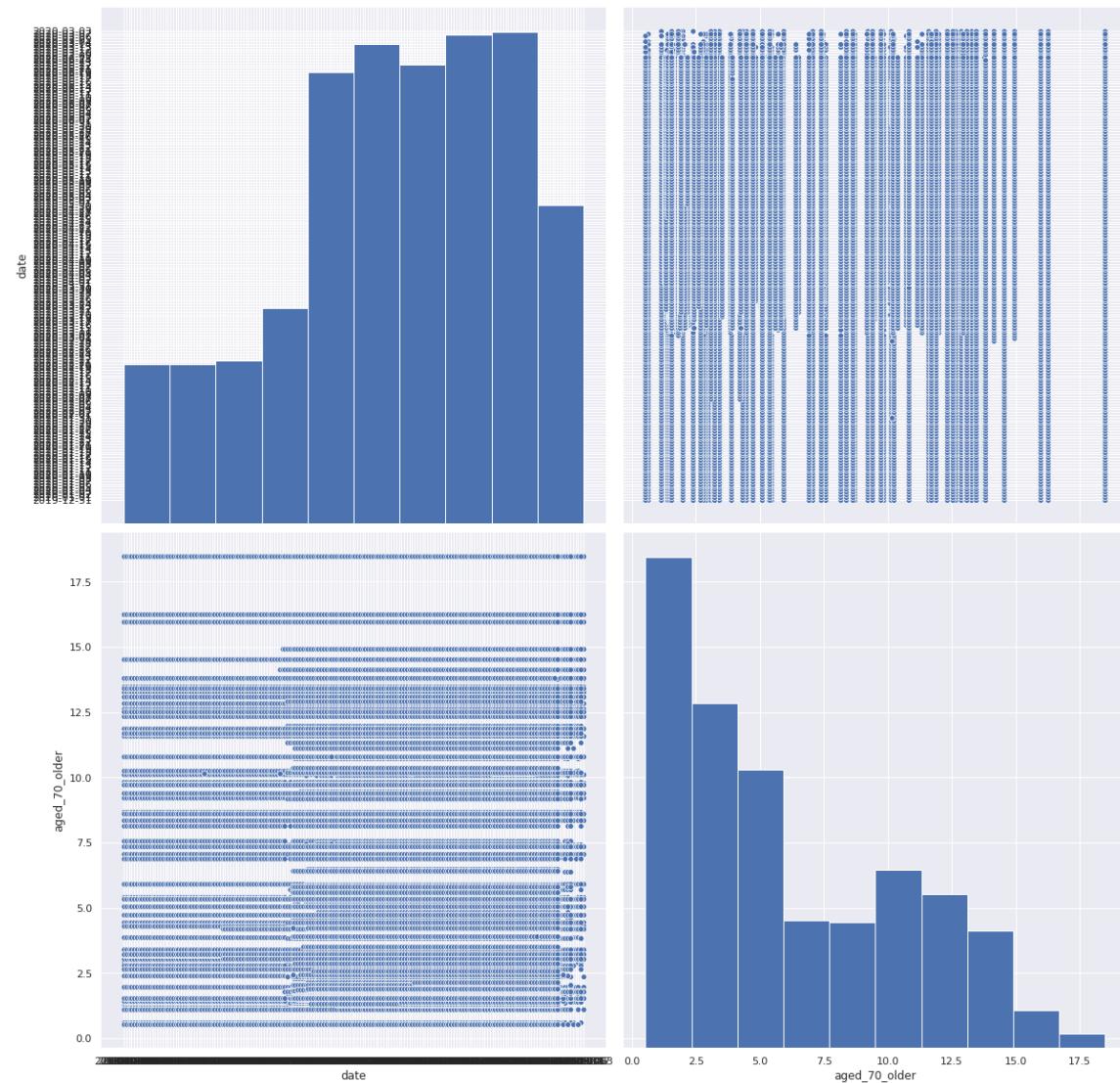


In [116]:

```
sns.pairplot(features, vars=["date", "aged_70_older"], height=8)
```

Out[116]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d27fd940>
```

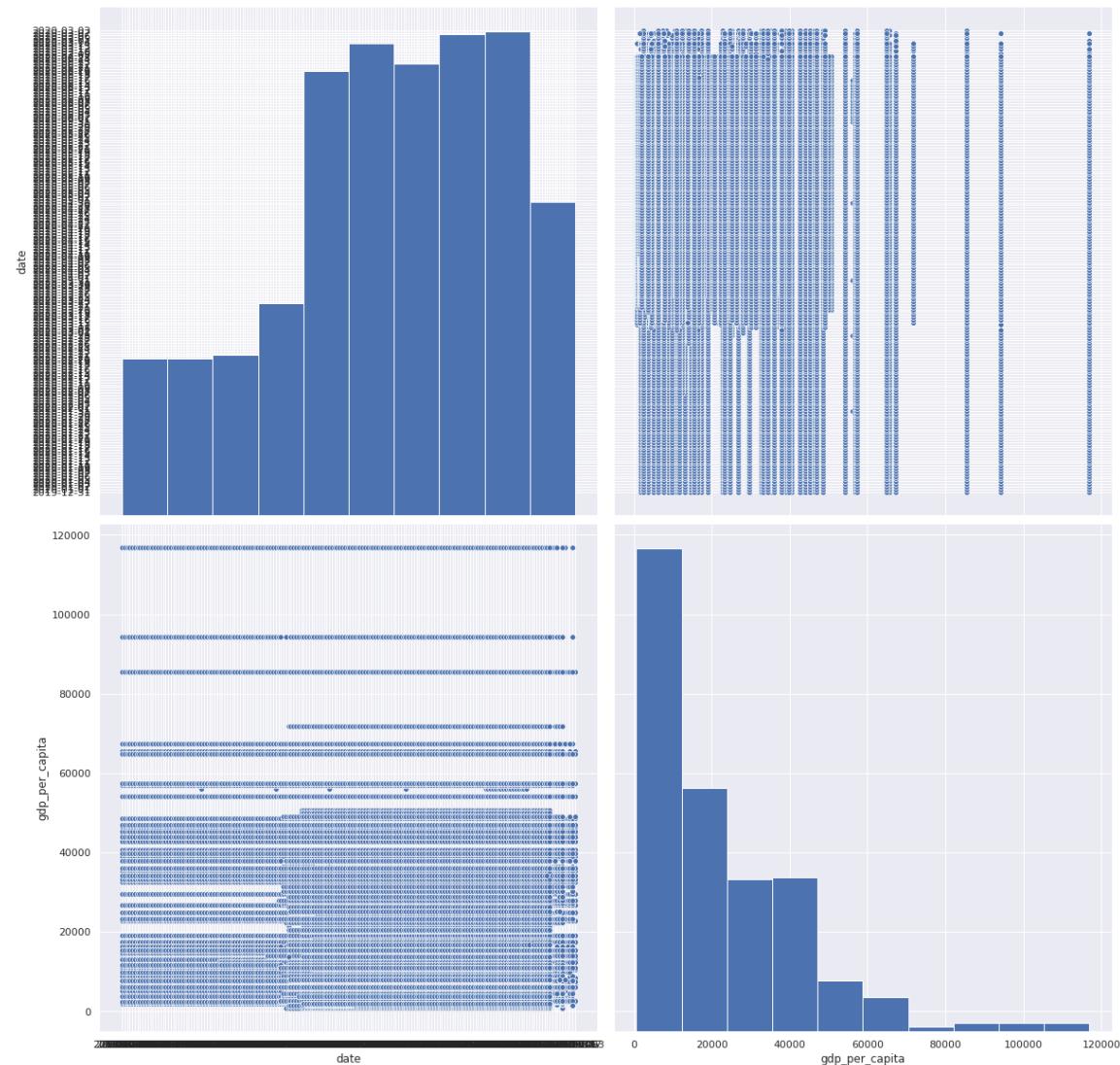


In [117]:

```
sns.pairplot(features, vars=["date", "gdp_per_capita"], height=8)
```

Out[117]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d2866080>
```

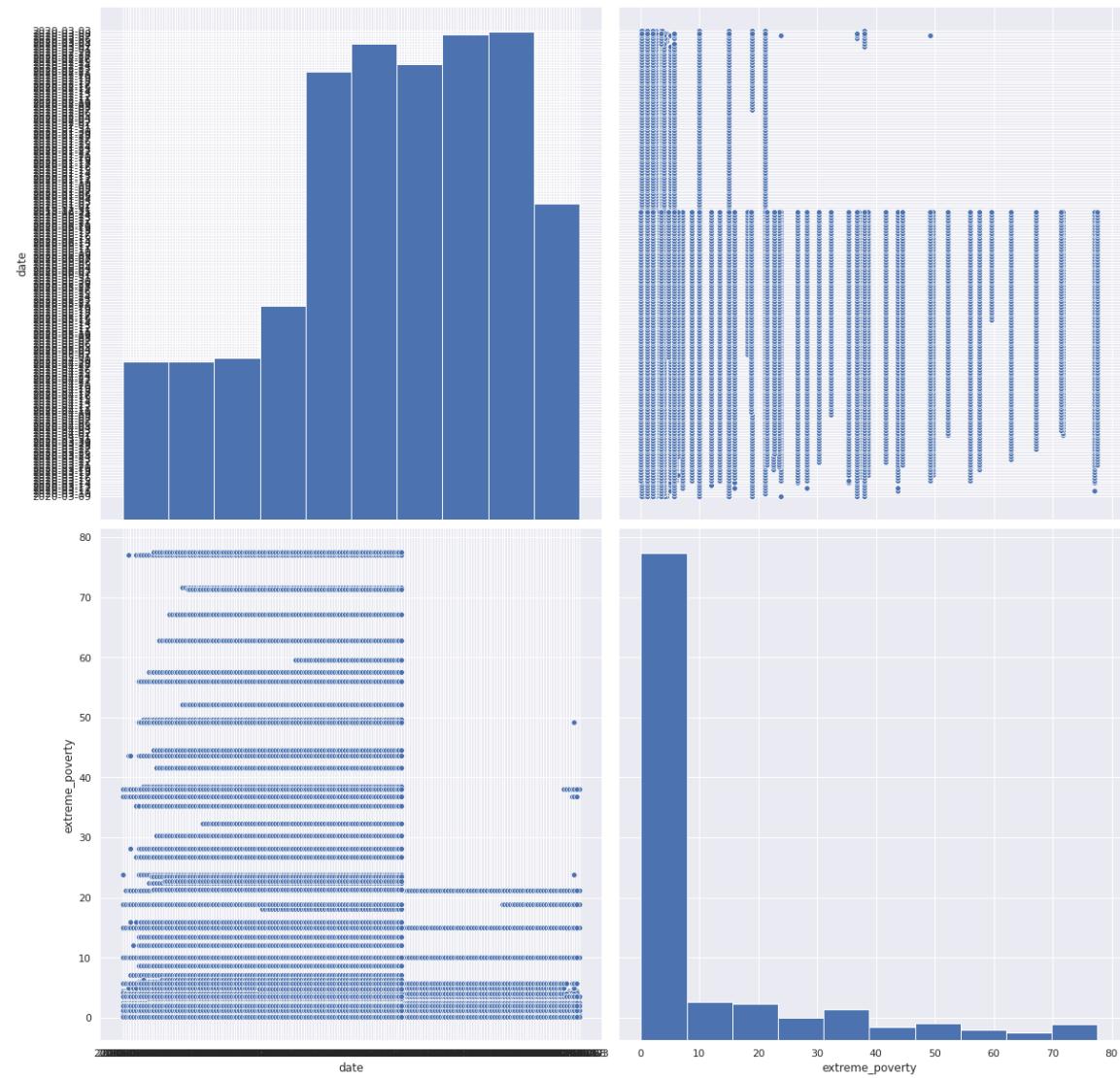


In [118]:

```
sns.pairplot(features, vars=["date", "extreme_poverty"], height=8)
```

Out[118]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d20057f0>
```

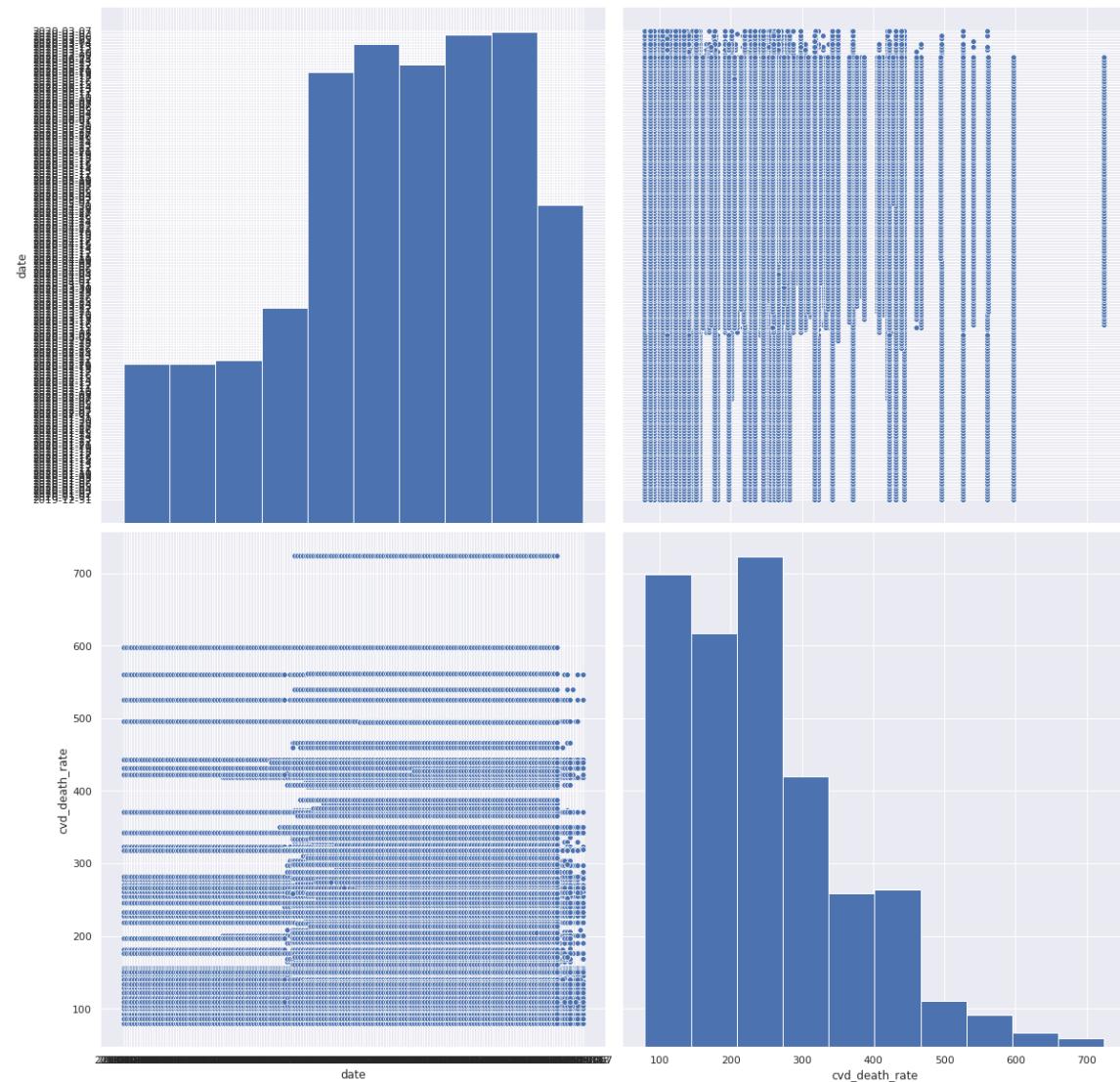


In [119]:

```
sns.pairplot(features, vars=["date", "cvd_death_rate"], height=8)
```

Out[119]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d0e9a160>
```

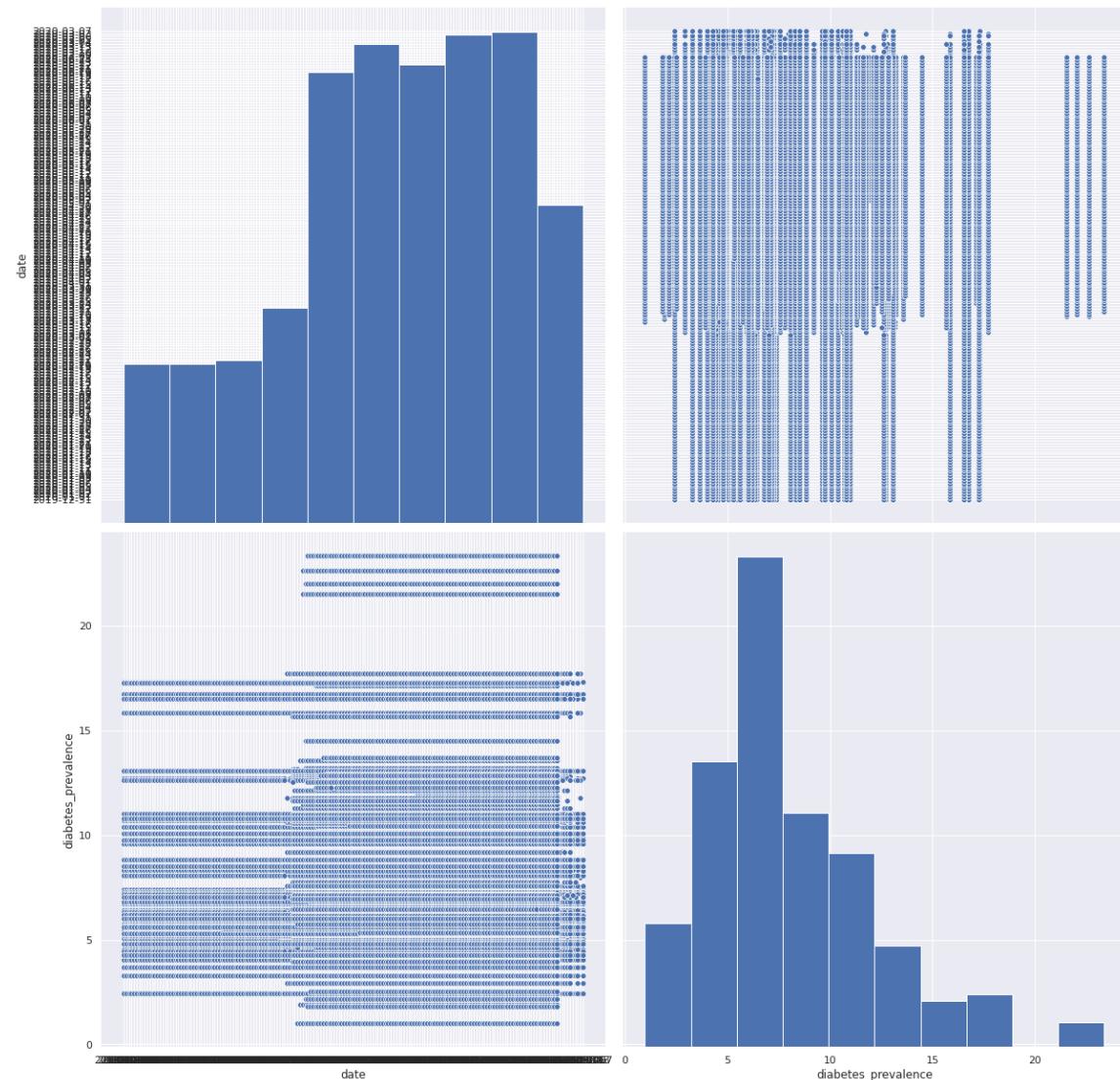


In [120]:

```
sns.pairplot(features, vars=["date", "diabetes_prevalence"], height=8)
```

Out[120]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d06b4dd8>
```

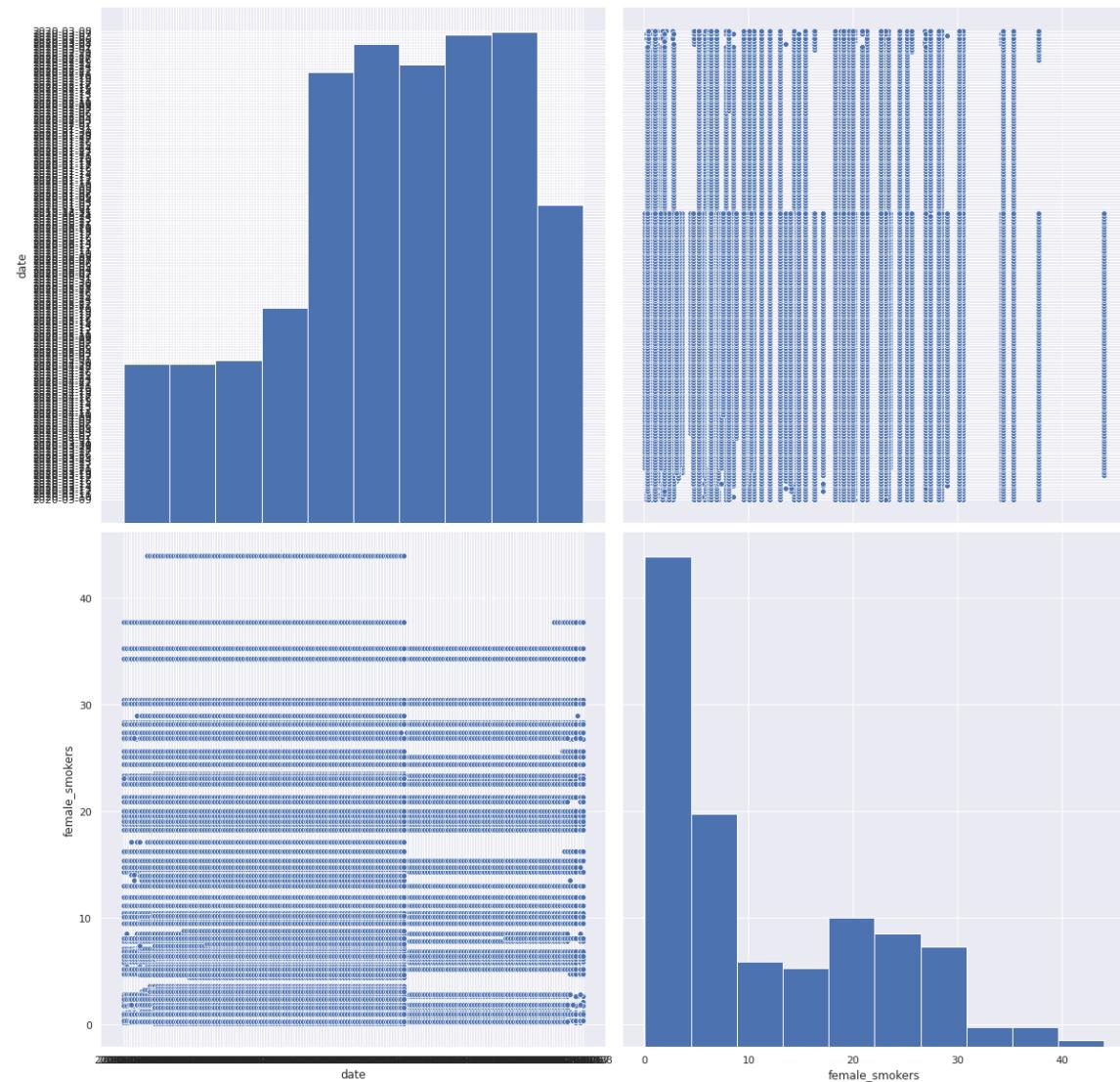


In [121]:

```
sns.pairplot(features, vars=["date", "female_smokers"], height=8)
```

Out[121]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cfef67f0>
```

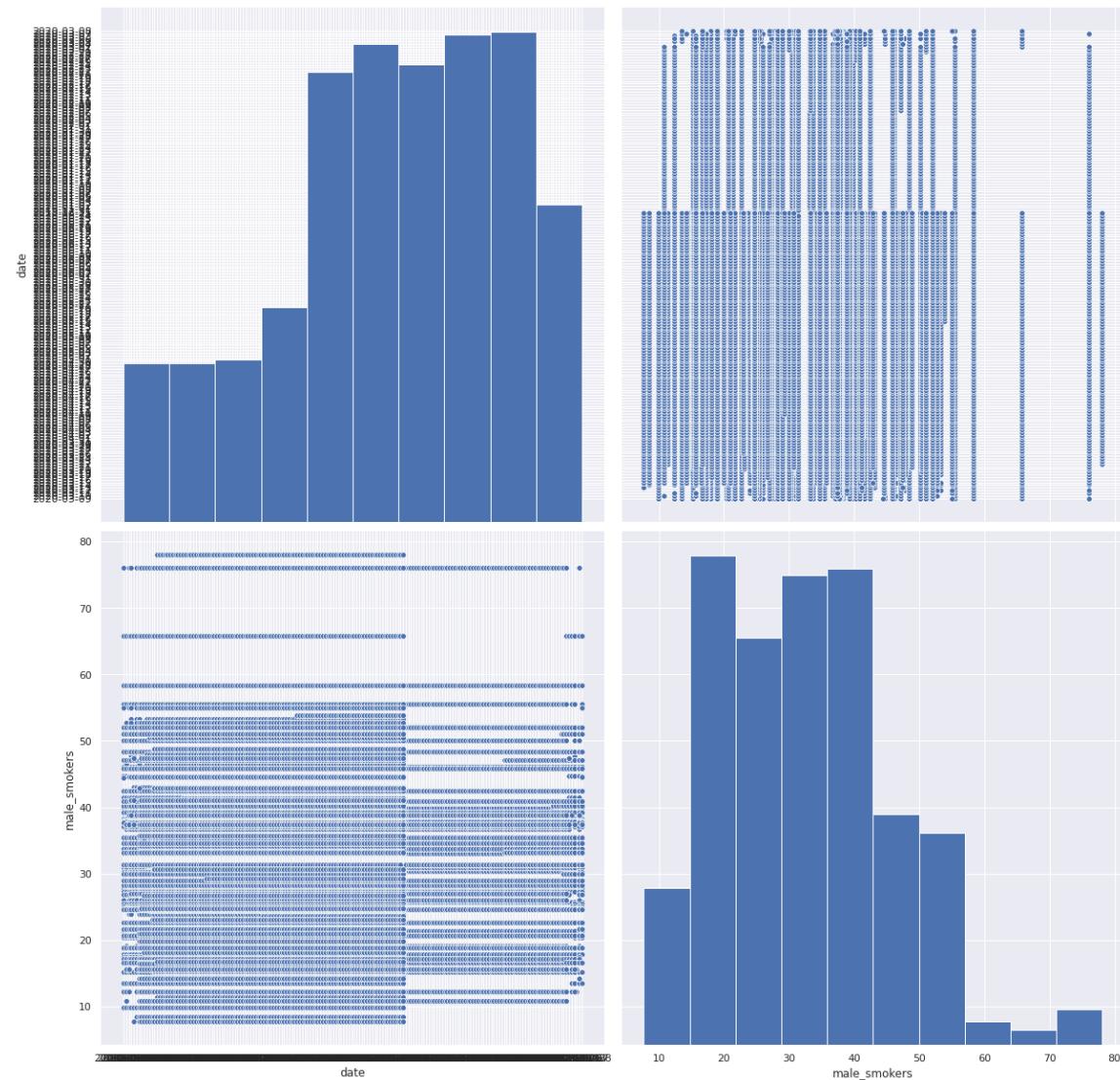


In [122]:

```
sns.pairplot(features, vars=["date", "male_smokers"], height=8)
```

Out[122]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cf61c518>
```

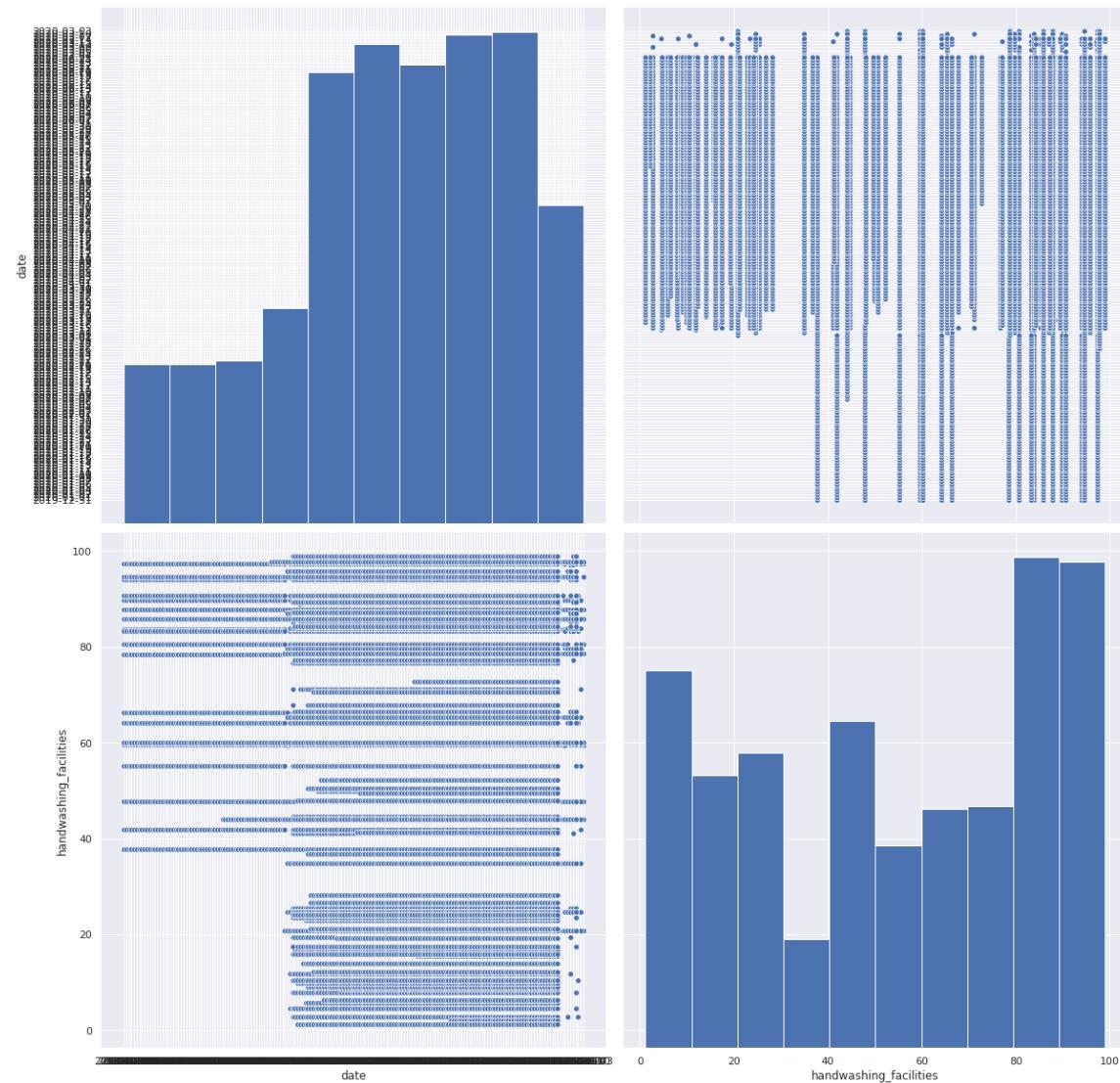


In [123]:

```
sns.pairplot(features, vars=["date", "handwashing_facilities"], height=8)
```

Out[123]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cee4d8d0>
```

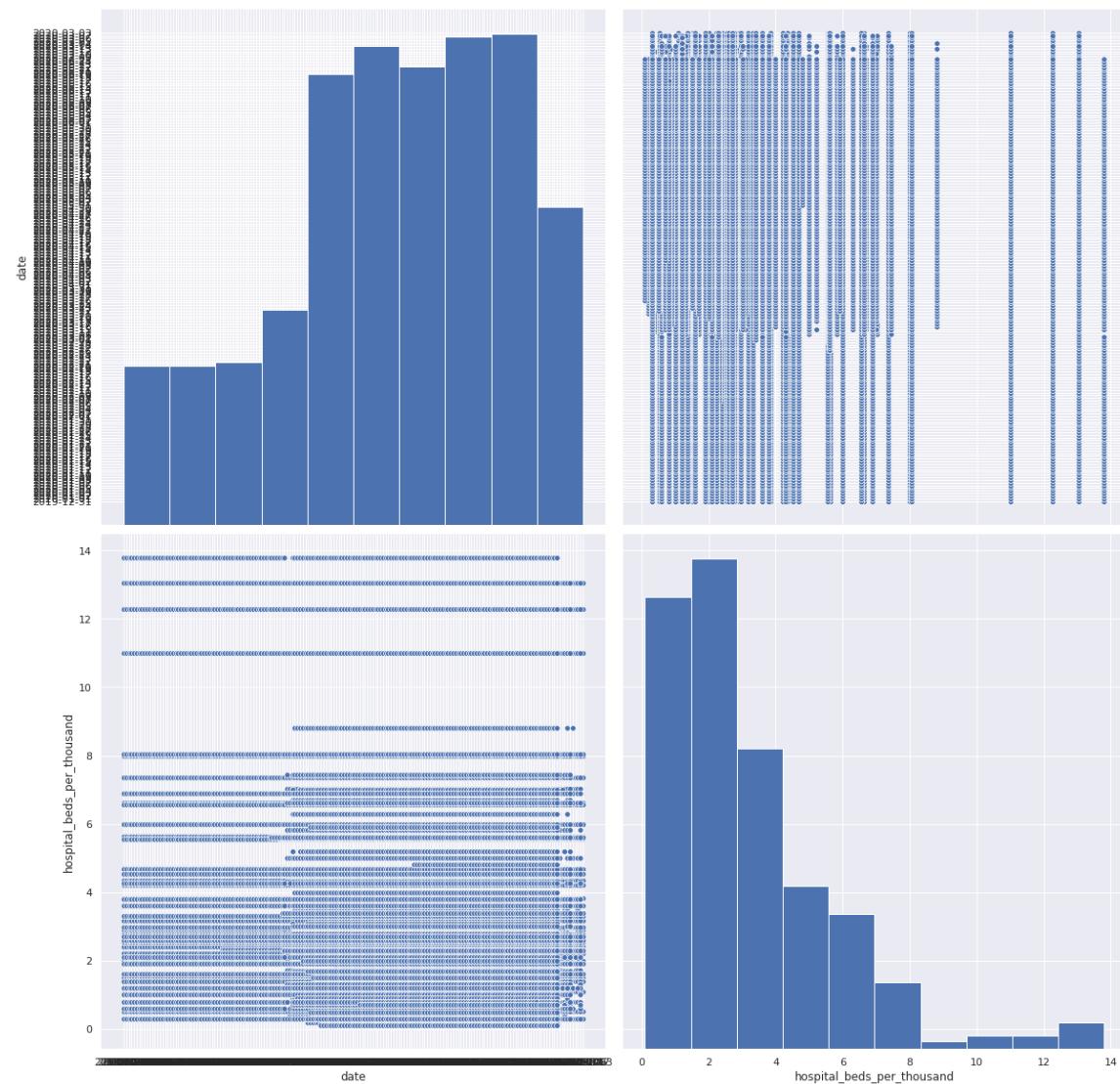


In [124]:

```
sns.pairplot(features, vars=["date", "hospital_beds_per_thousand"], height=8)
```

Out[124]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ce613978>
```

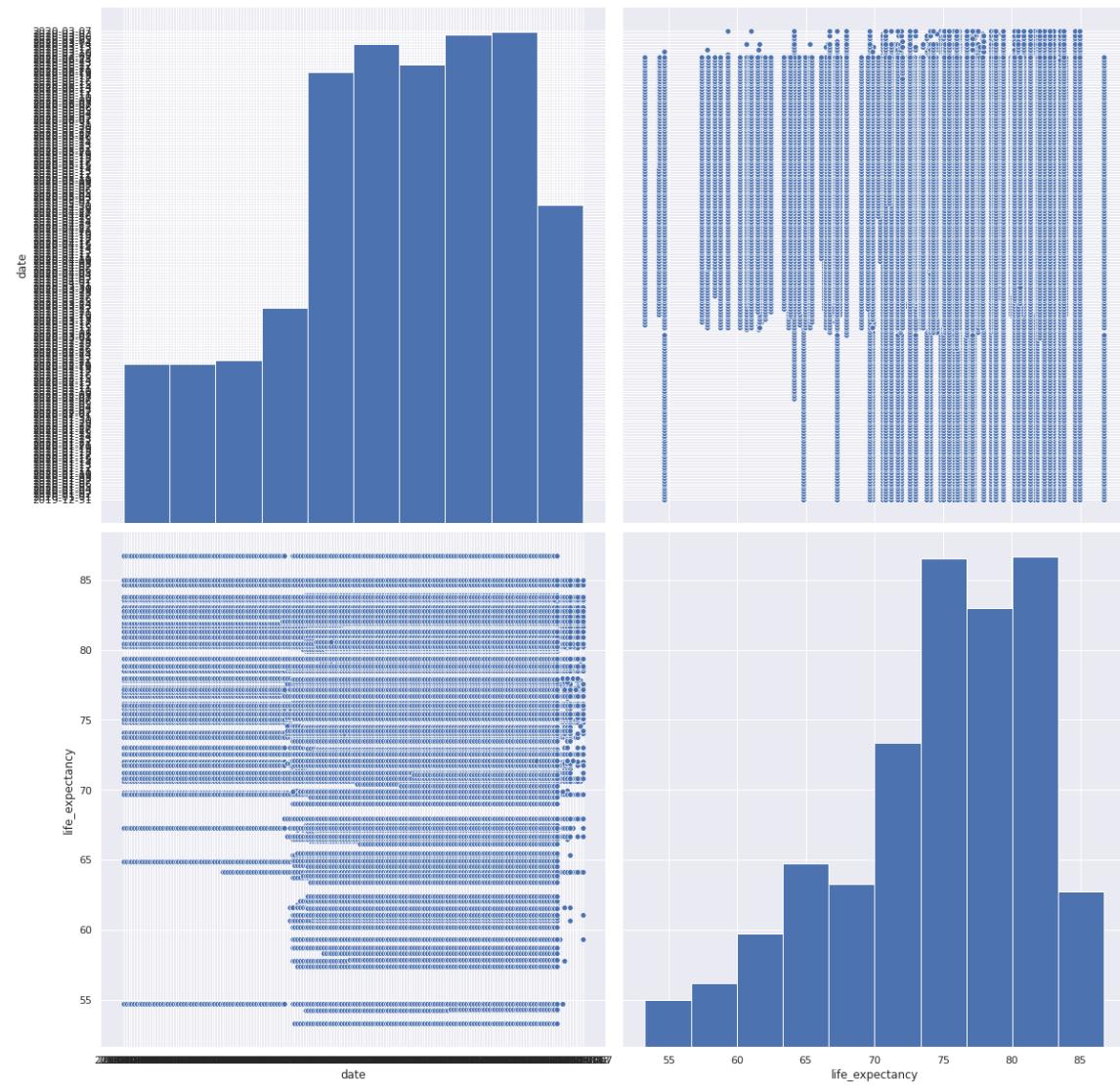


In [125]:

```
sns.pairplot(features, vars=["date", "life_expectancy"], height=8)
```

Out[125]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ce58ccc0>
```

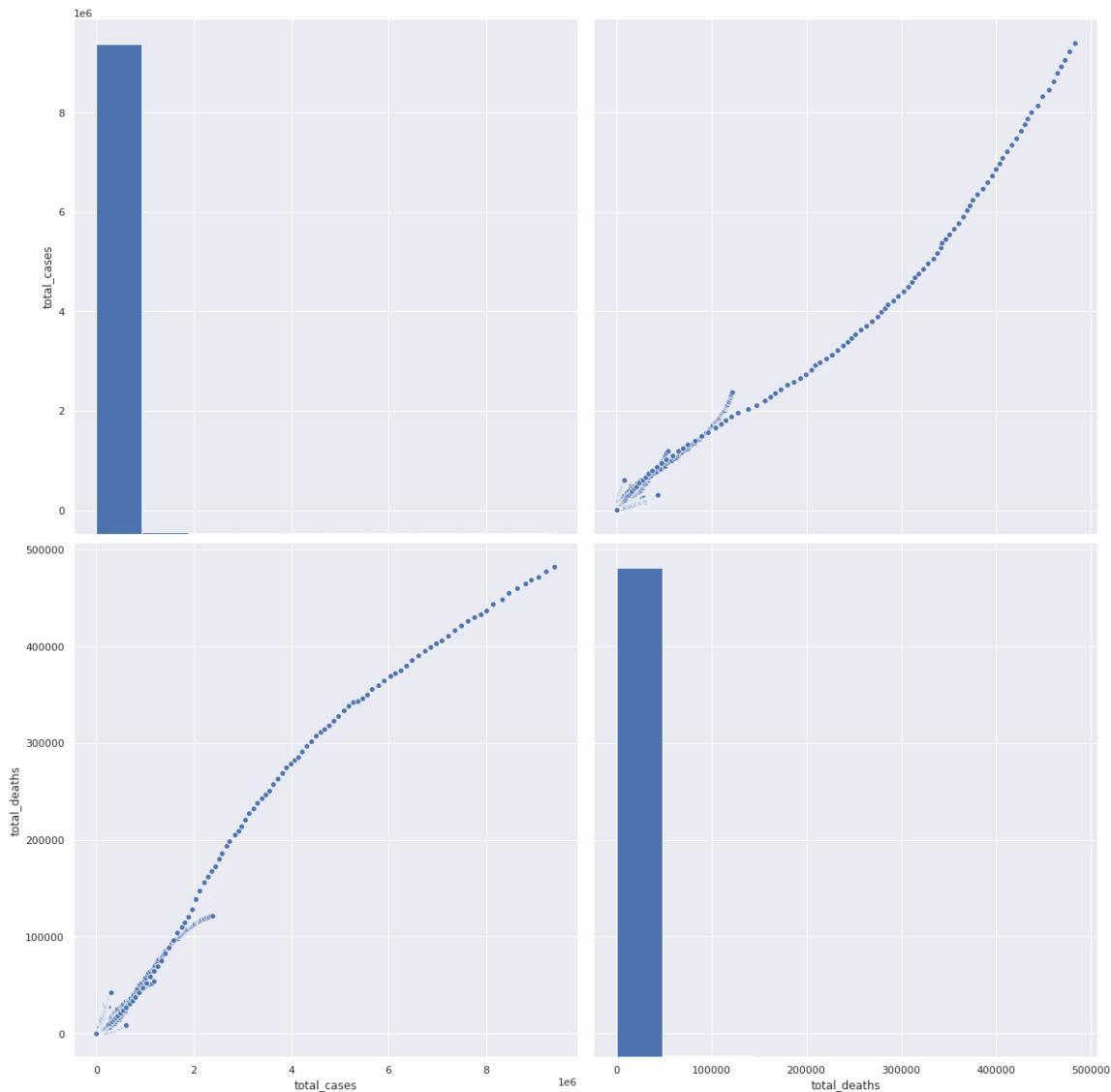


In [126]:

```
sns.pairplot(features, vars=["total_cases", "total_deaths"], height=8)
```

Out[126]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cd56e0f0>
```

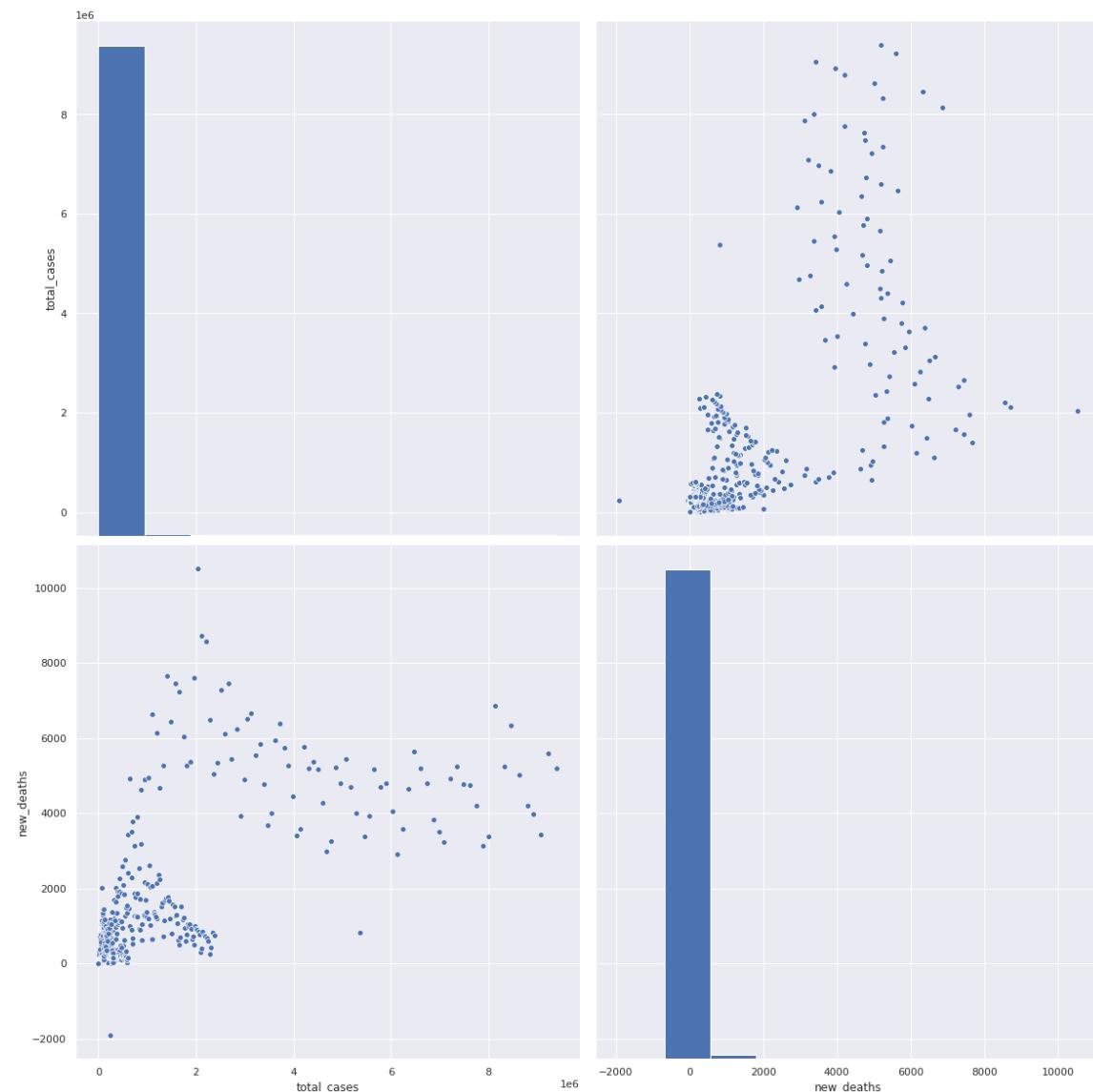


In [127]:

```
sns.pairplot(features, vars=["total_cases", "new_deaths"], height=8)
```

Out[127]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cd352518>
```

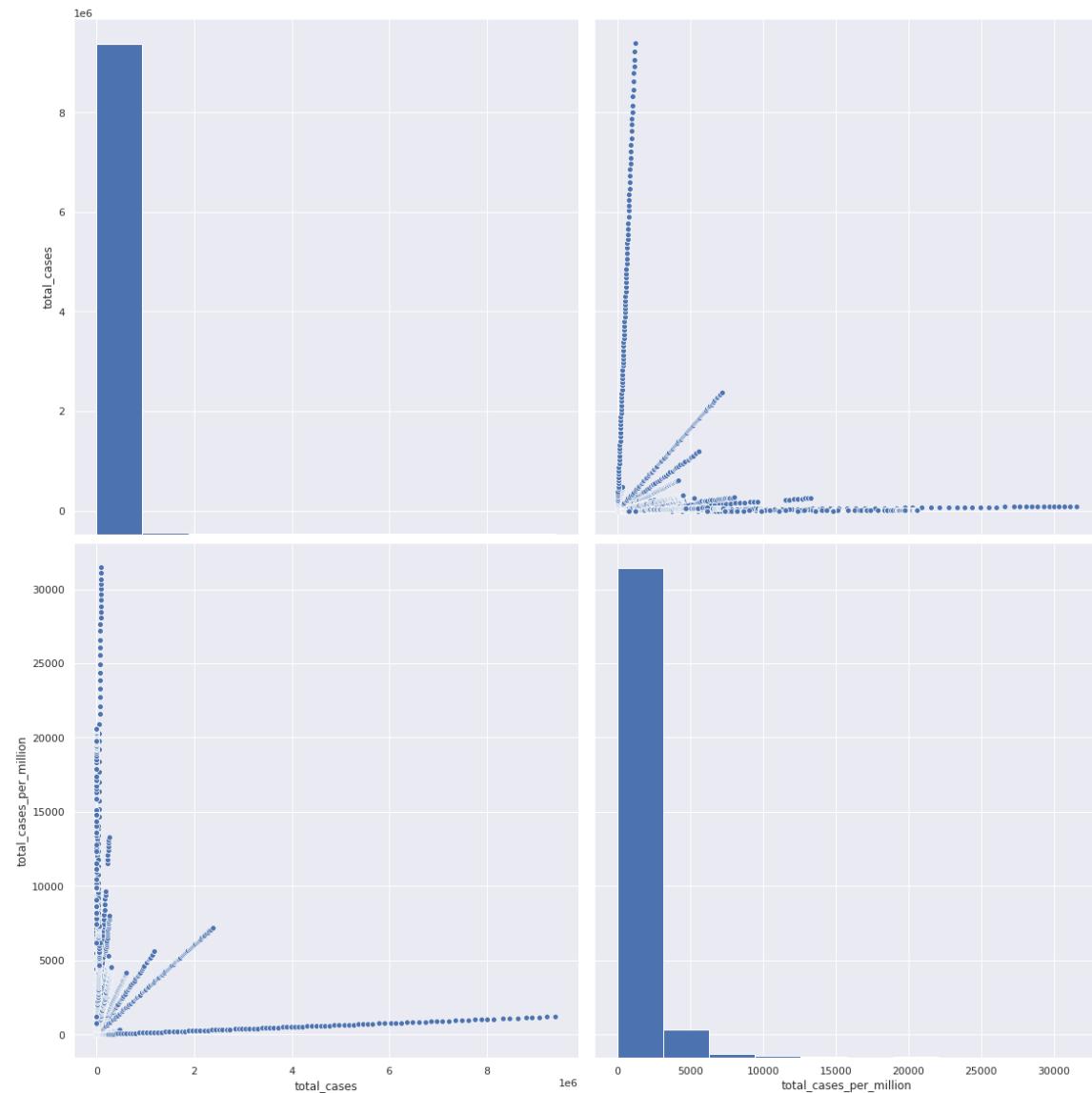


In [128]:

```
sns.pairplot(features, vars=["total_cases", "total_cases_per_million"], height=8)
```

Out[128]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cd157b00>
```

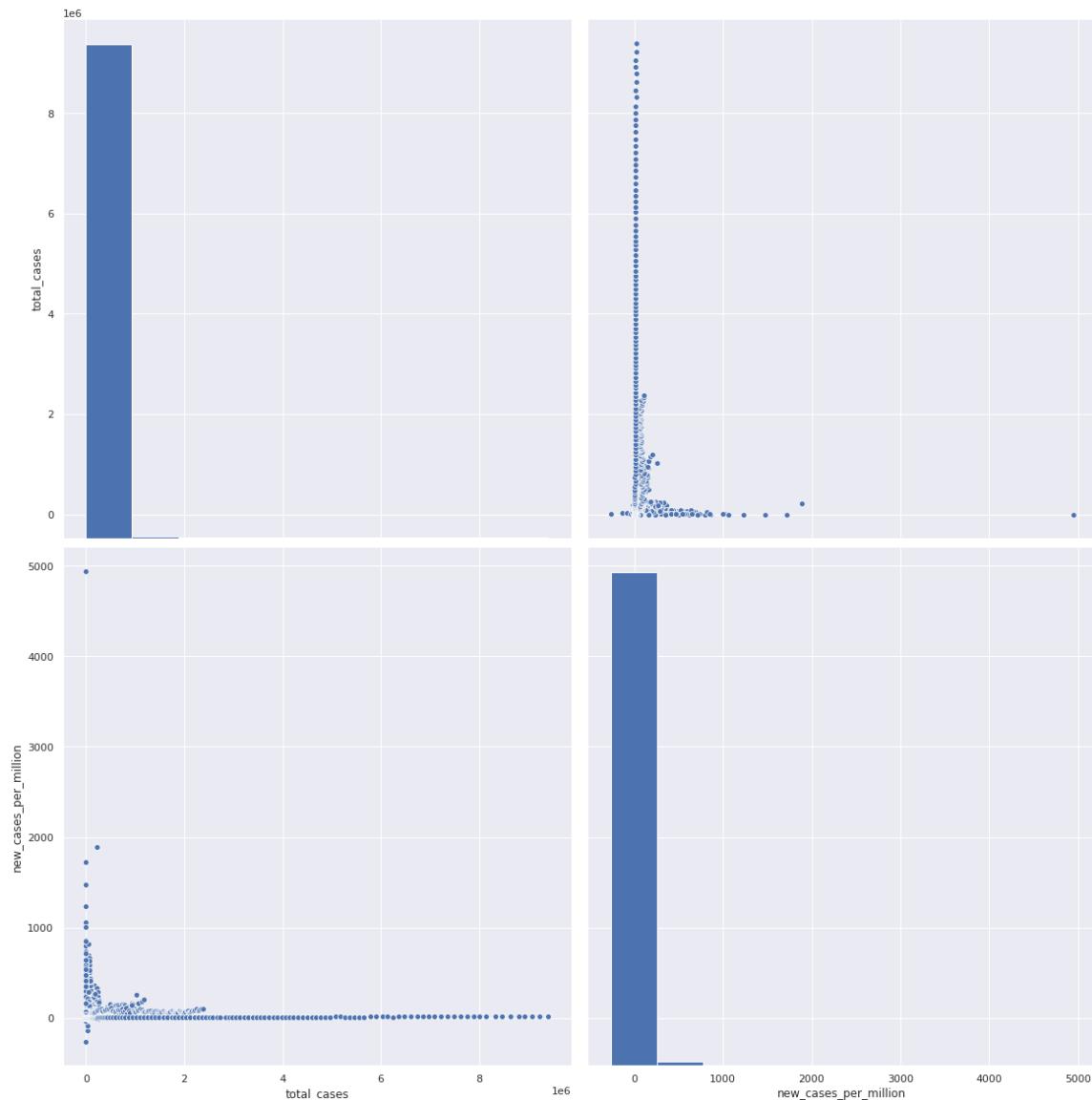


In [129]:

```
sns.pairplot(features, vars=["total_cases", "new_cases_per_million"], height=8)
```

Out[129]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ccf9f198>
```

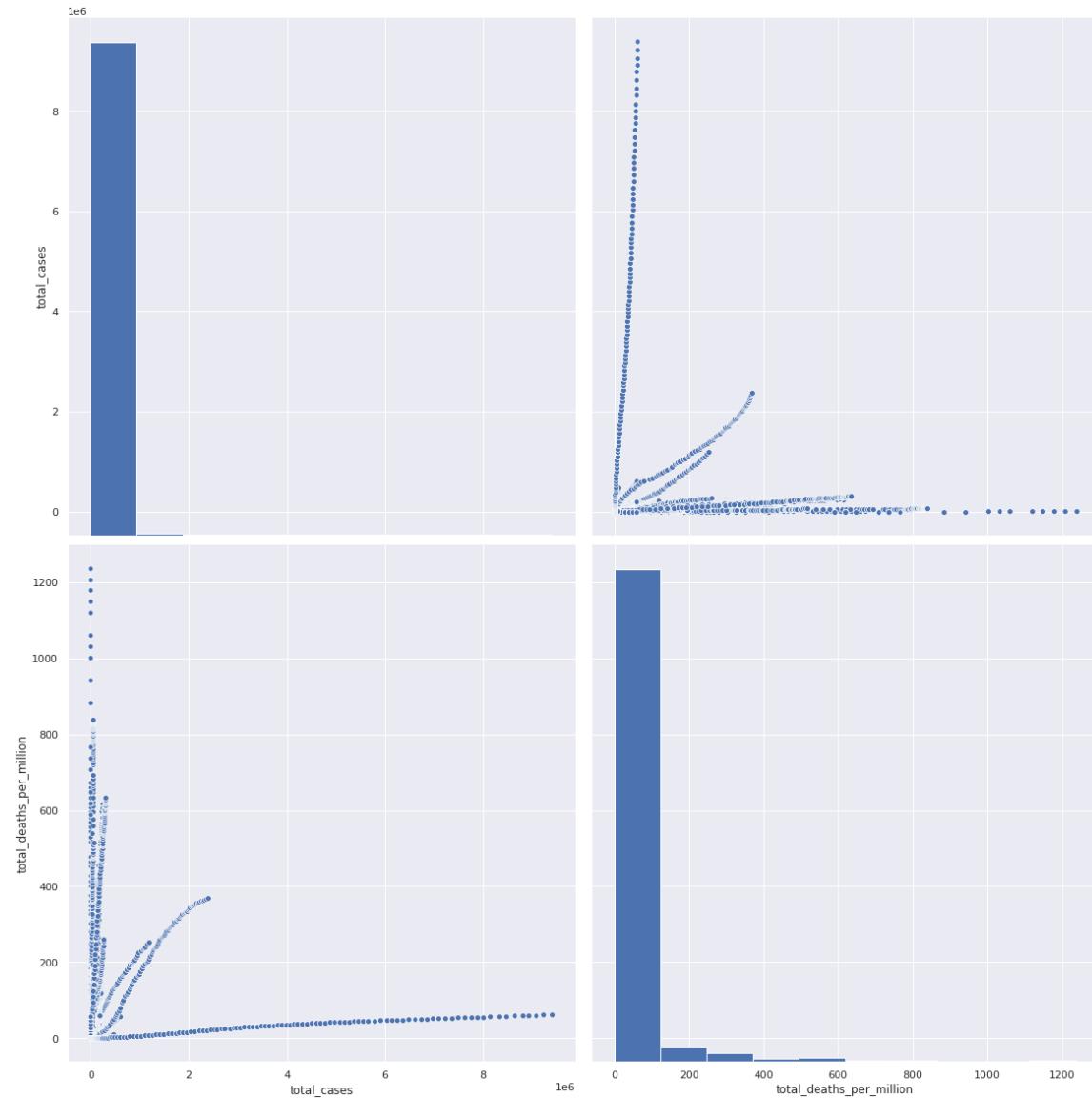


In [130]:

```
sns.pairplot(features, vars=["total_cases", "total_deaths_per_million"], height=8)
```

Out[130]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cccd43978>
```

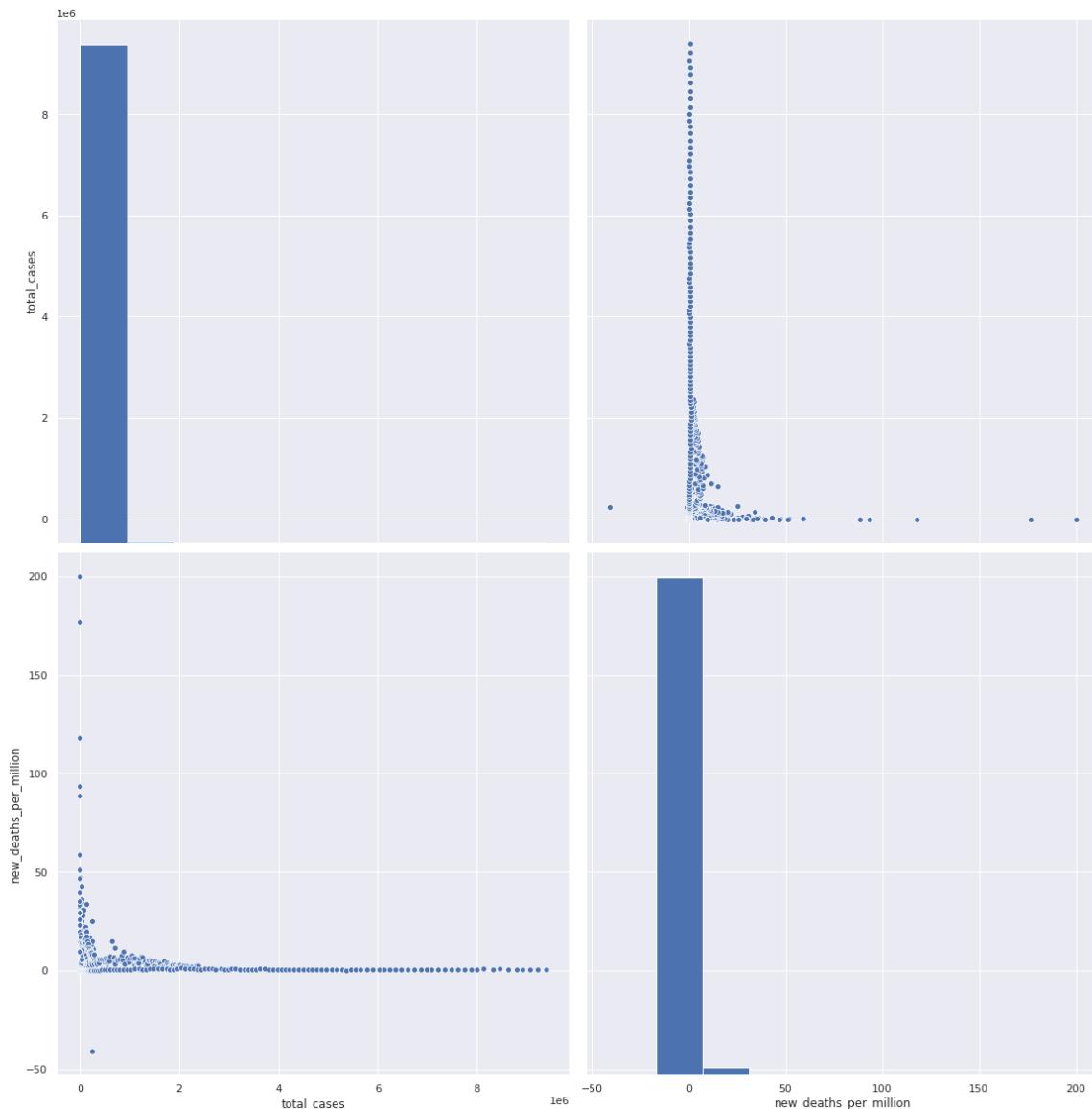


In [131]:

```
sns.pairplot(features, vars=["total_cases", "new_deaths_per_million"], height=8)
```

Out[131]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ccc88f60>
```

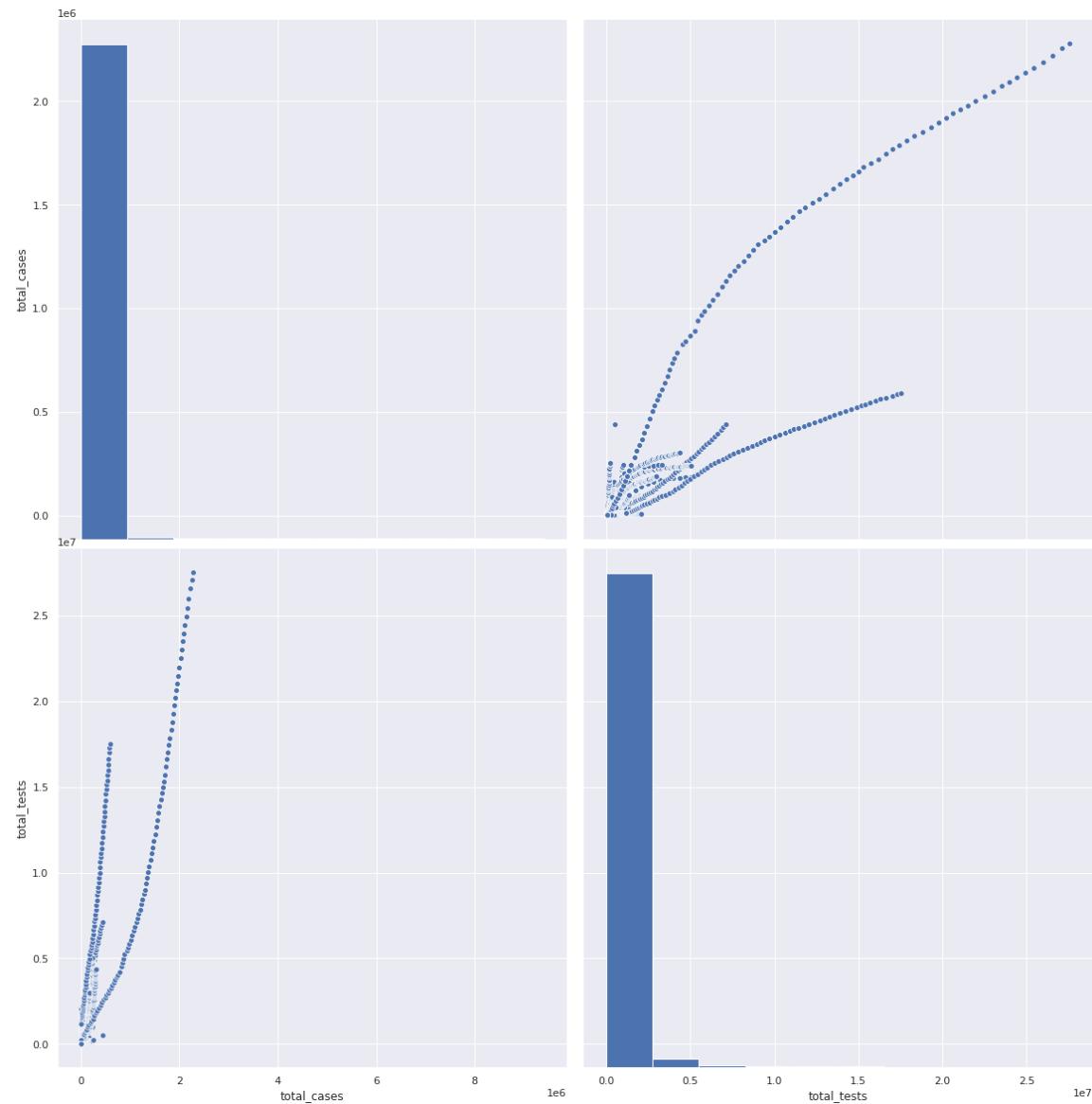


In [132]:

```
sns.pairplot(features, vars=["total_cases", "total_tests"], height=8)
```

Out[132]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc98bfd0>
```

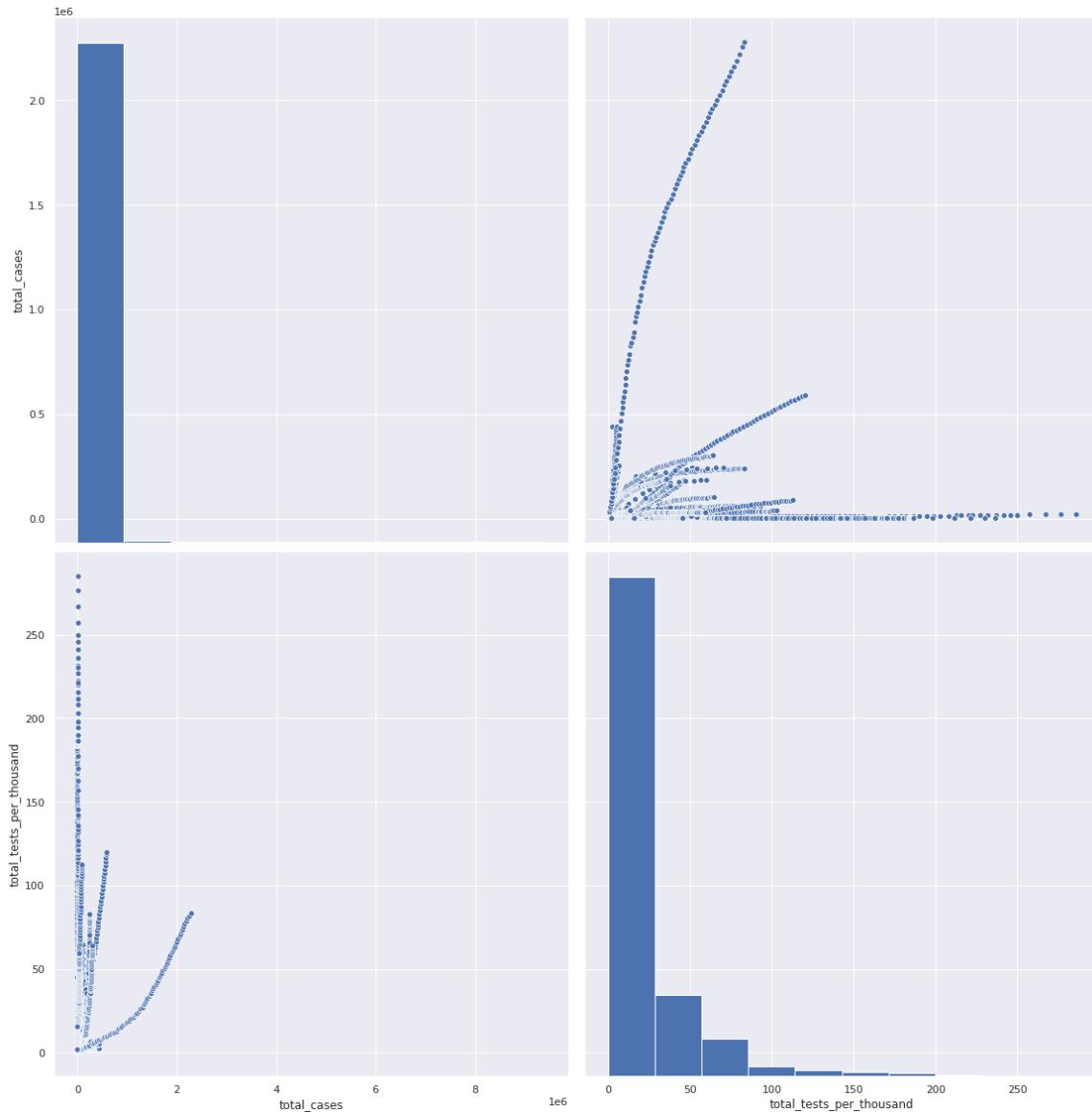


In [133]:

```
sns.pairplot(features, vars=["total_cases", "total_tests_per_thousand"], height=8)
```

Out[133]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc7eab70>
```

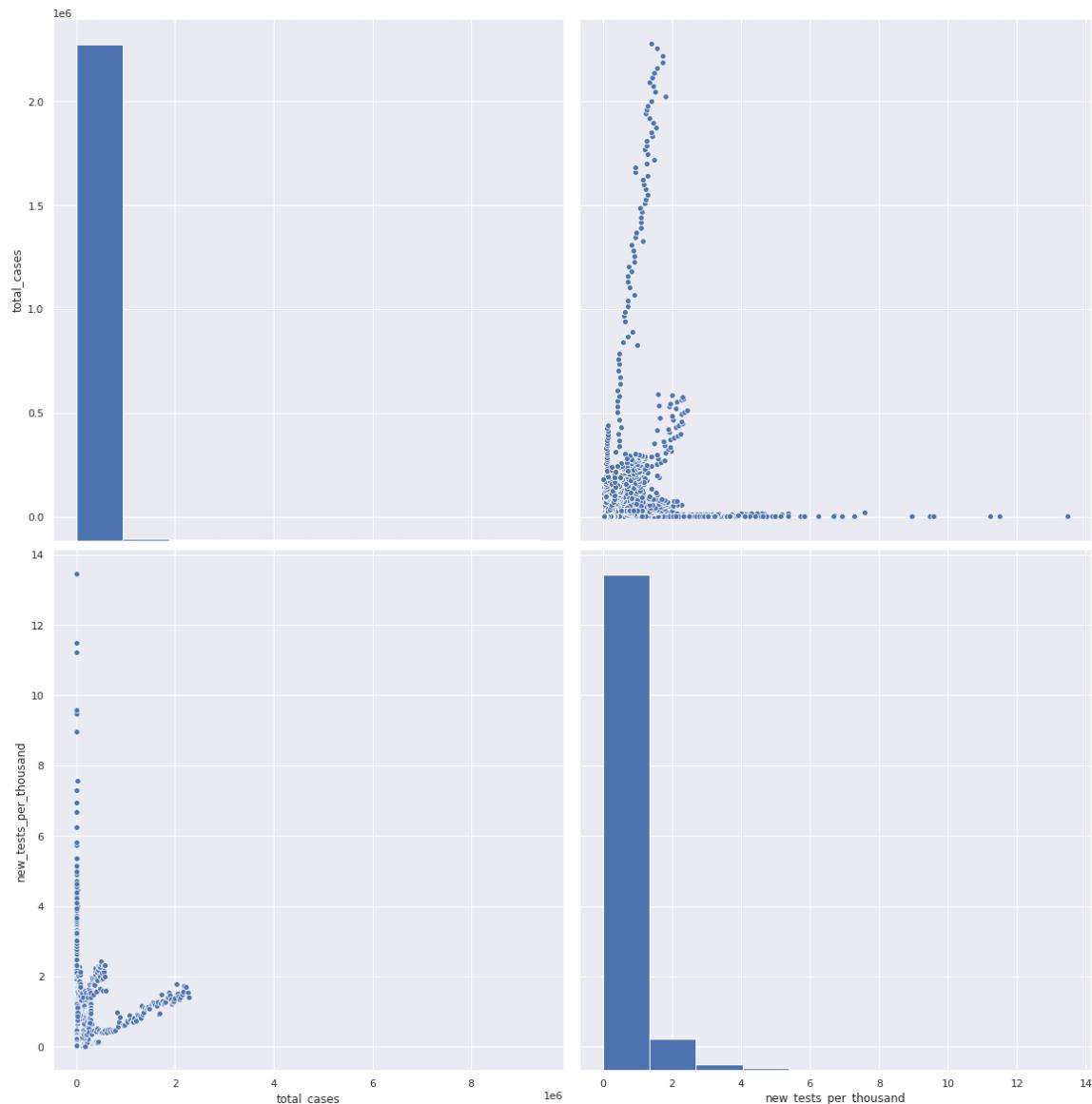


In [134]:

```
sns.pairplot(features, vars=["total_cases", "new_tests_per_thousand"], height=8)
```

Out[134]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc7f00f0>
```

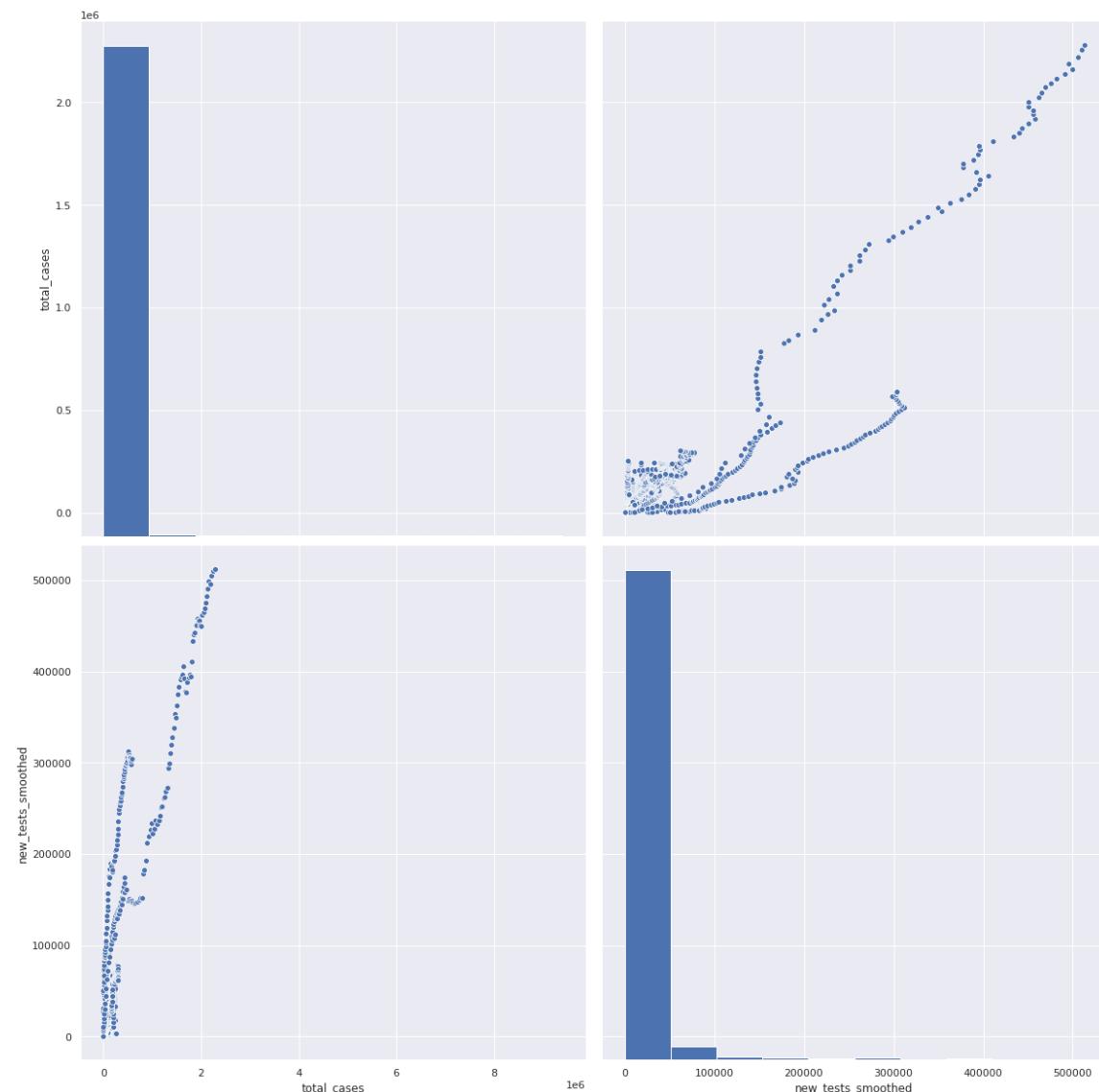


In [135]:

```
sns.pairplot(features, vars=["total_cases", "new_tests_smoothed"], height=8)
```

Out[135]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc38db70>
```

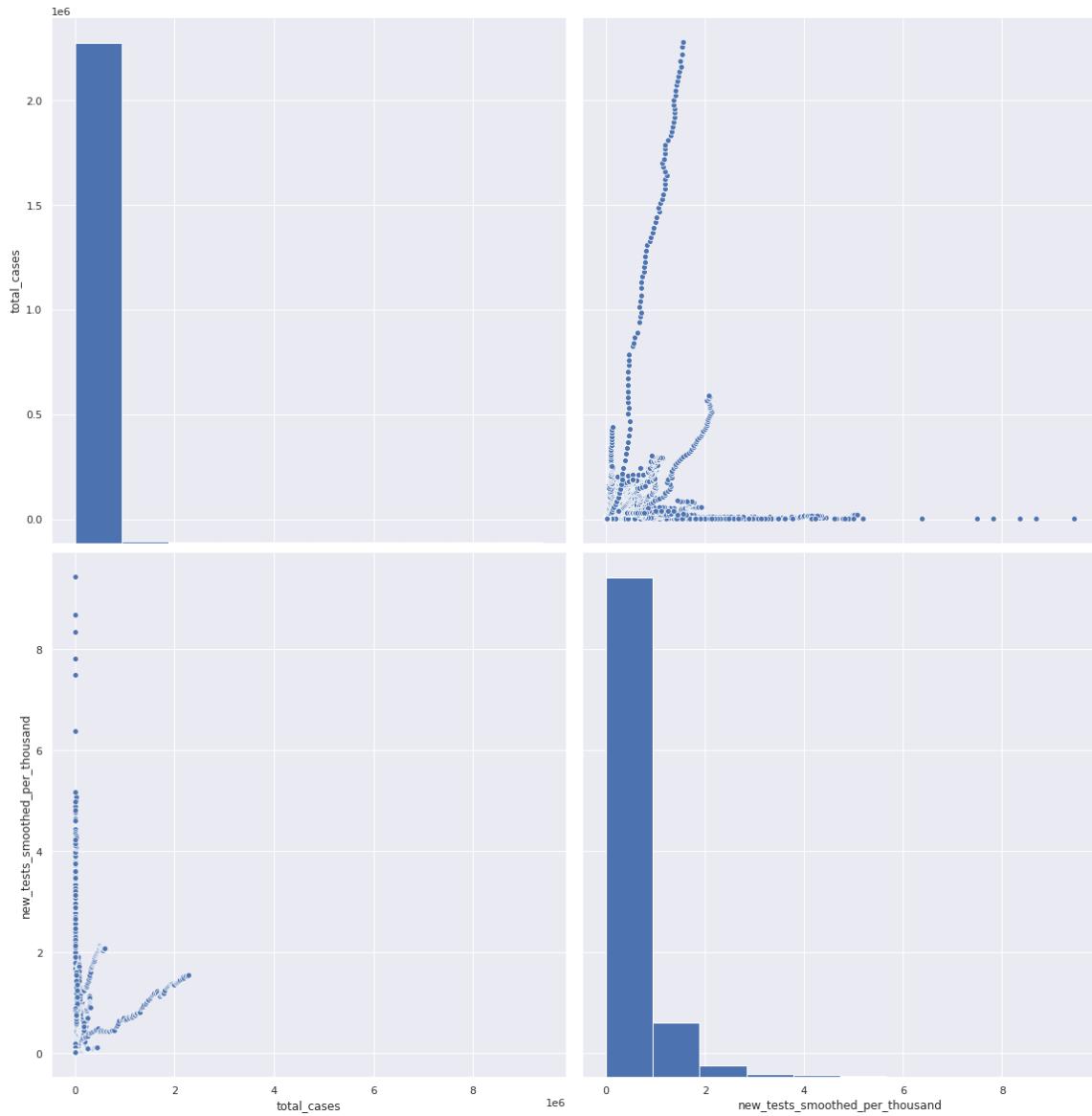


In [136]:

```
sns.pairplot(features, vars=["total_cases", "new_tests_smoothed_per_thousand"], height=8)
```

Out[136]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc3fe6a0>
```

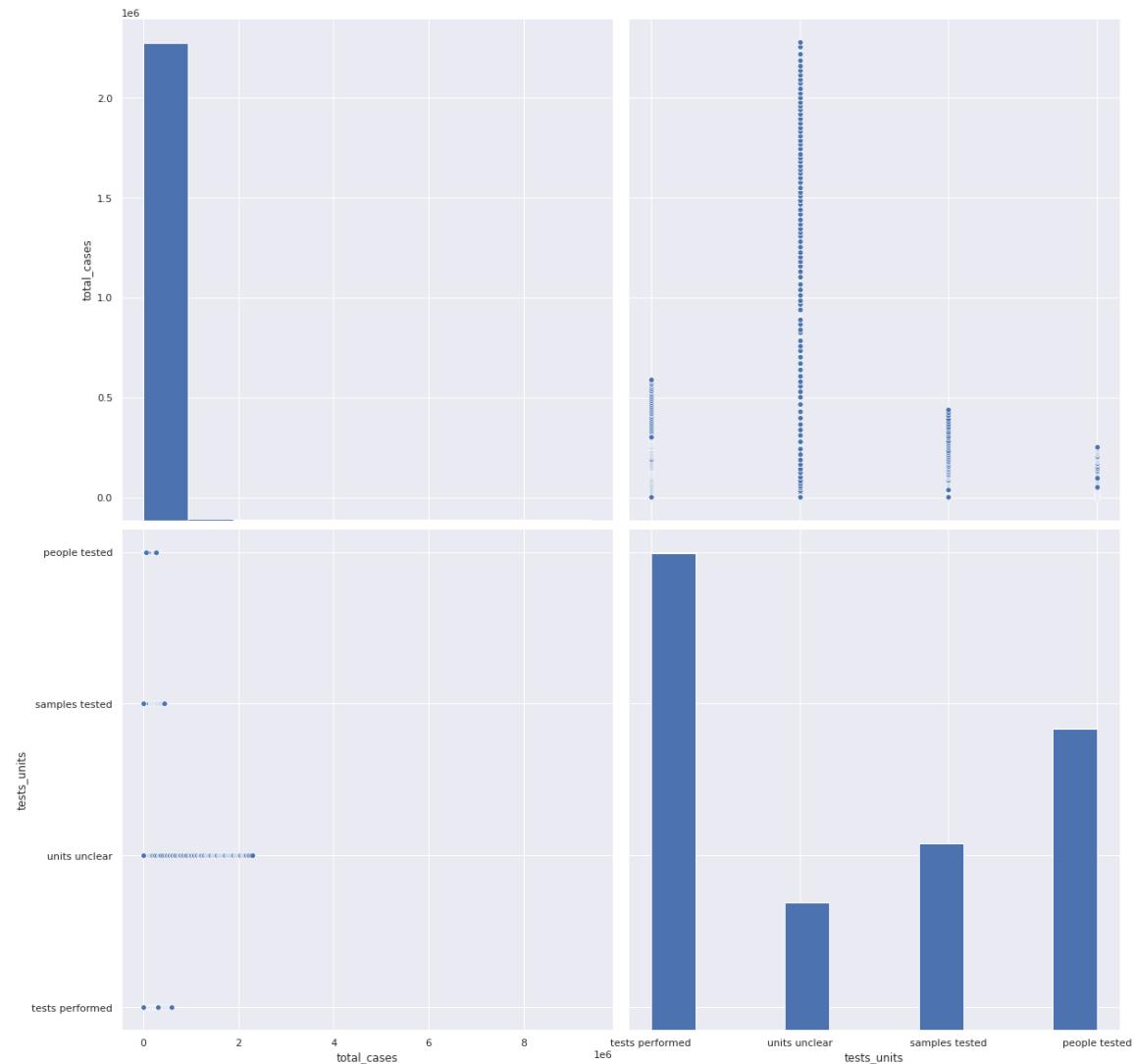


In [137]:

```
sns.pairplot(features, vars=["total_cases", "tests_units"], height=8)
```

Out[137]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc02a320>
```

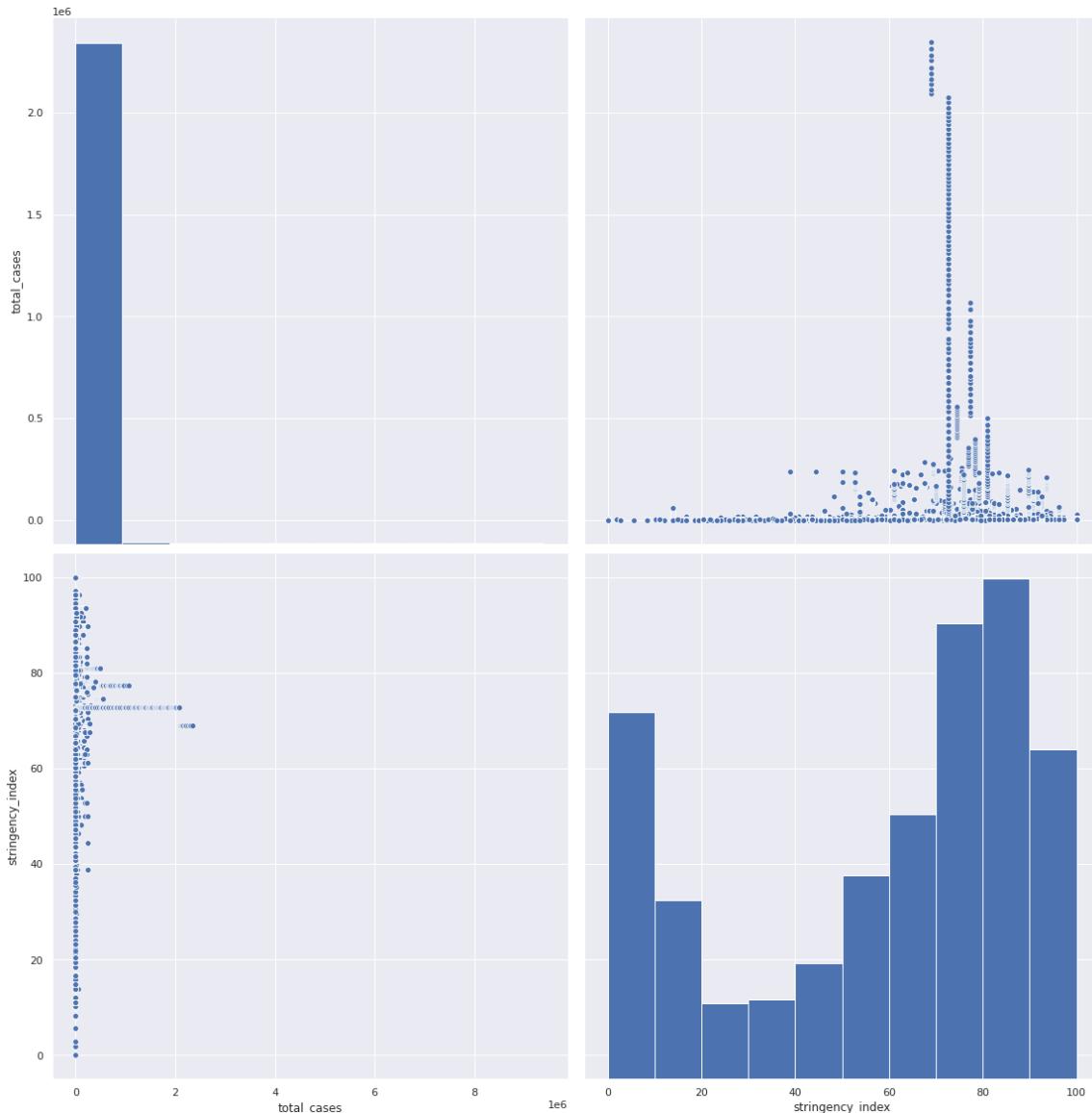


In [138]:

```
sns.pairplot(features, vars=["total_cases", "stringency_index"], height=8)
```

Out[138]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cbe81f98>
```

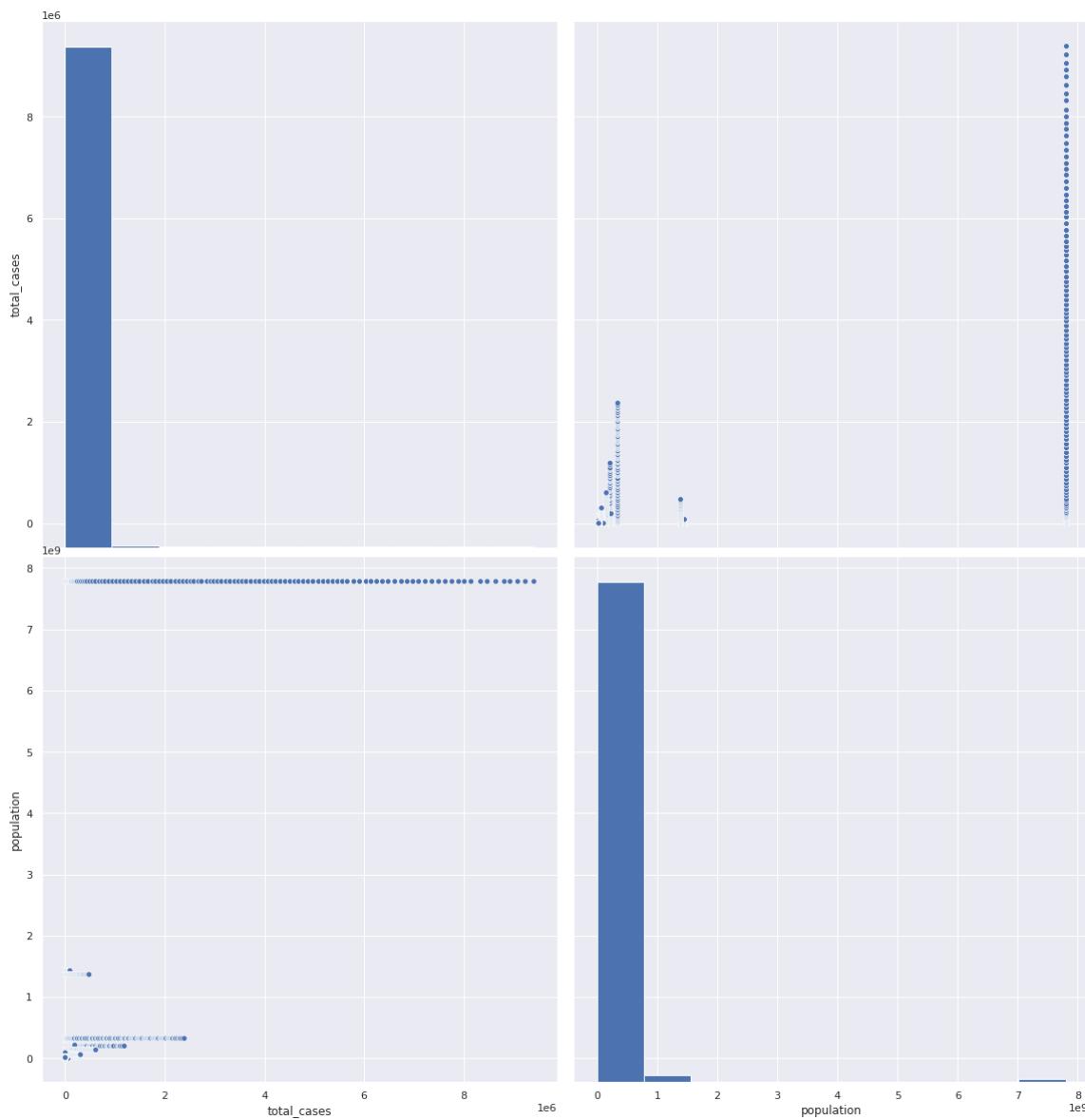


In [139]:

```
sns.pairplot(features, vars=["total_cases", "population"], height=8)
```

Out[139]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cbc0b6d8>
```

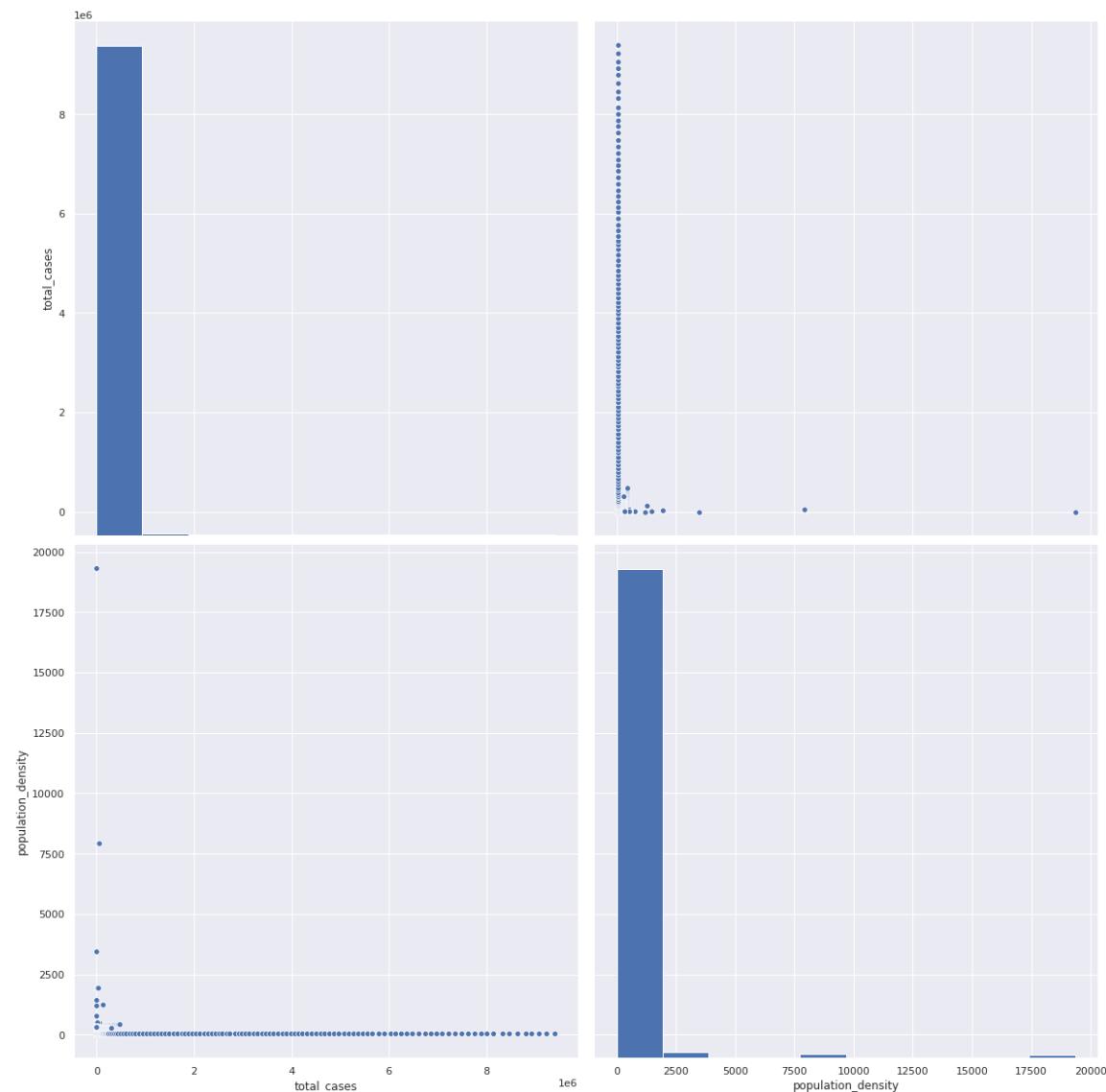


In [140]:

```
sns.pairplot(features, vars=["total_cases", "population_density"], height=8)
```

Out[140]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cc102828>
```

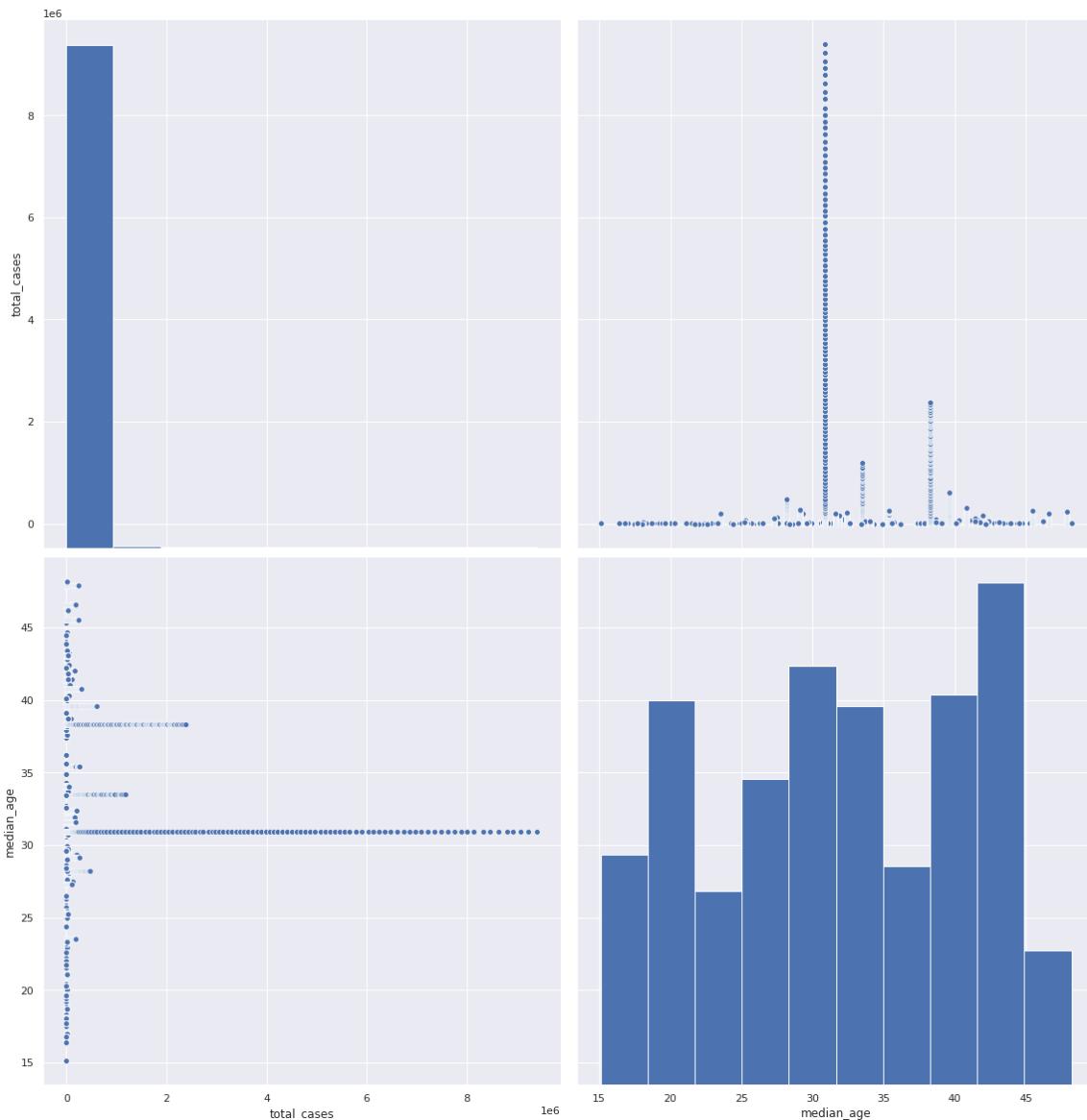


In [141]:

```
sns.pairplot(features, vars=["total_cases", "median_age"], height=8)
```

Out[141]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cb919f60>
```

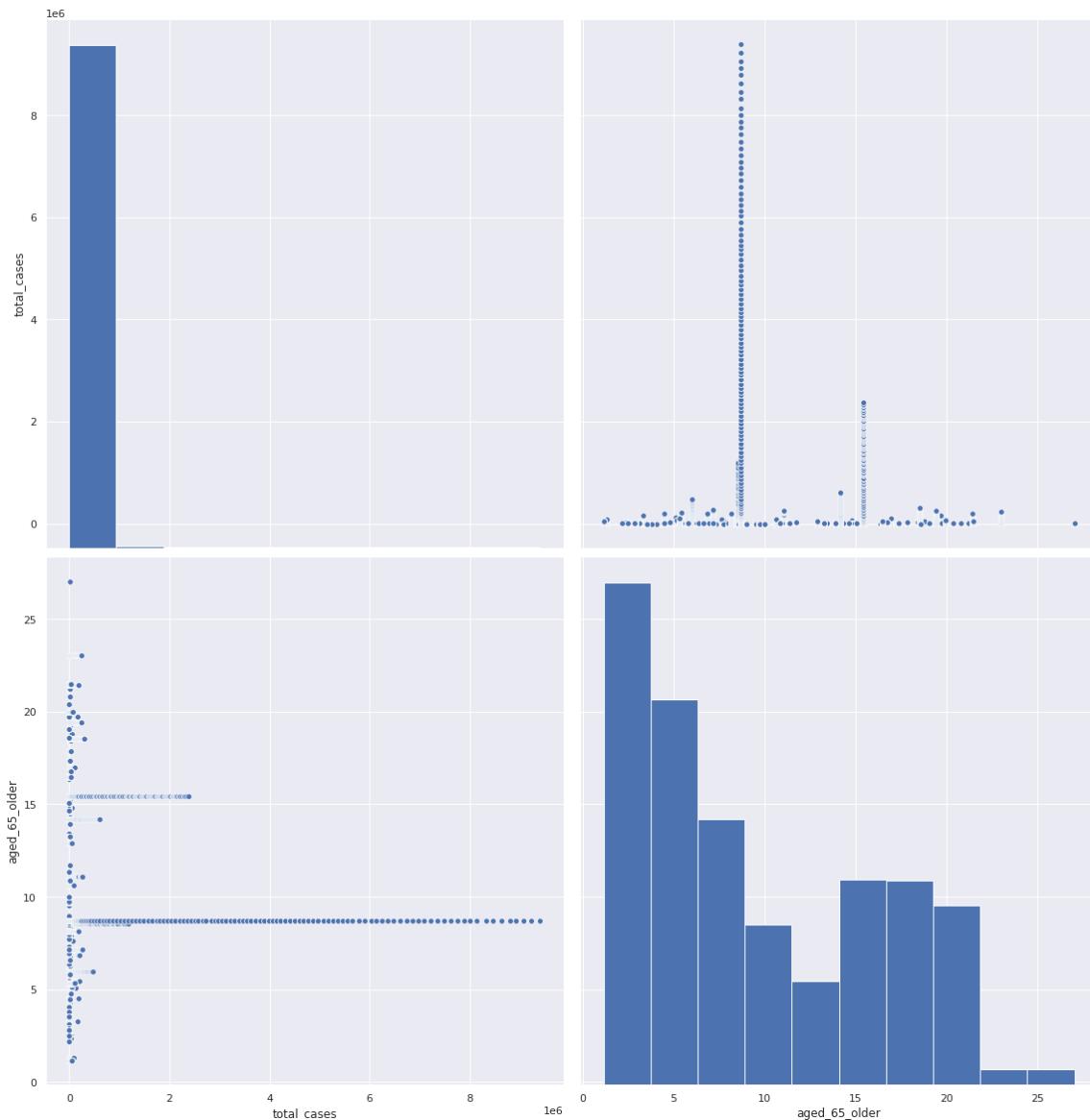


In [142]:

```
sns.pairplot(features, vars=["total_cases", "aged_65_older"], height=8)
```

Out[142]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cb6203c8>
```

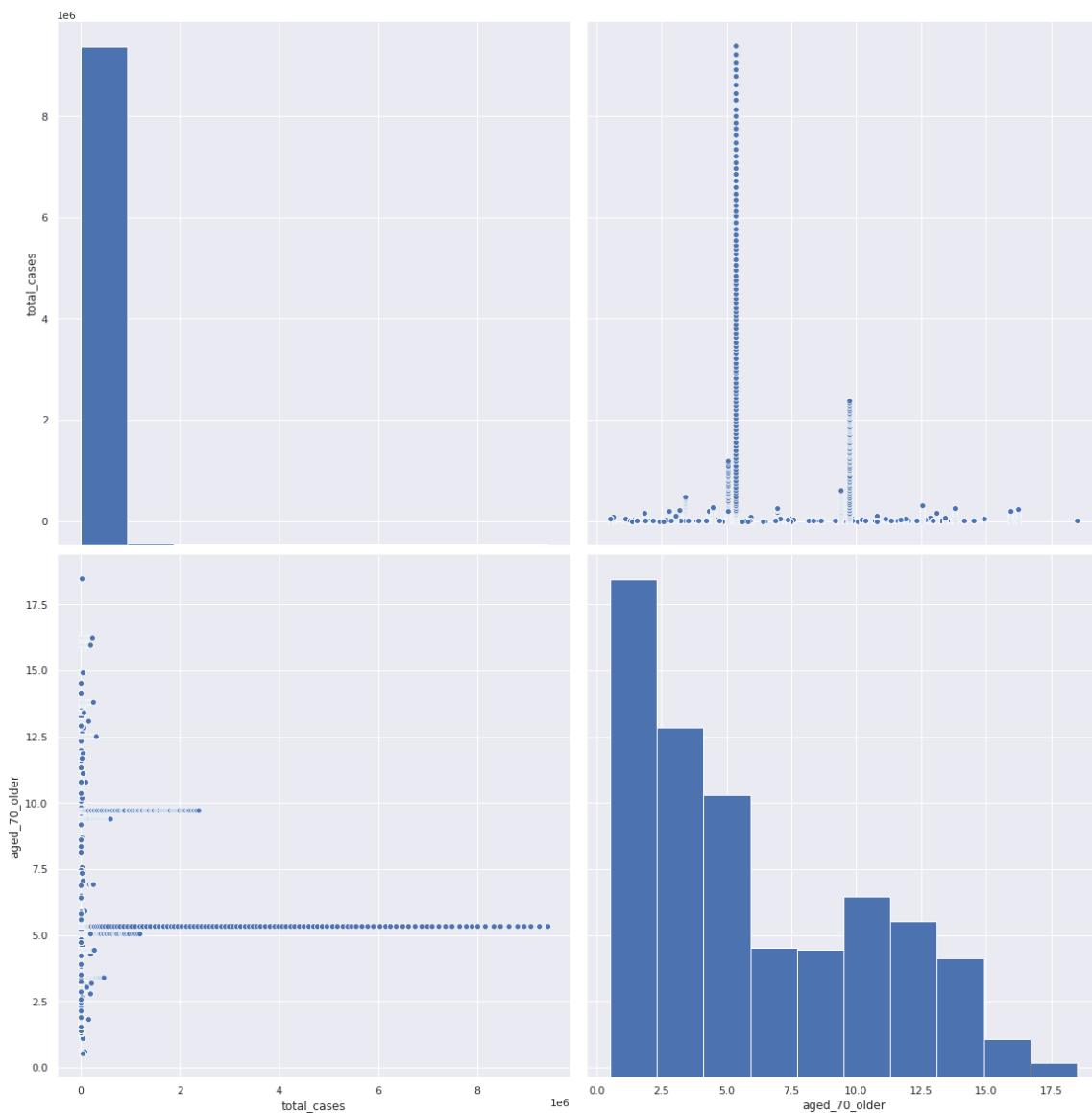


In [143]:

```
sns.pairplot(features, vars=["total_cases", "aged_70_older"], height=8)
```

Out[143]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cb403588>
```

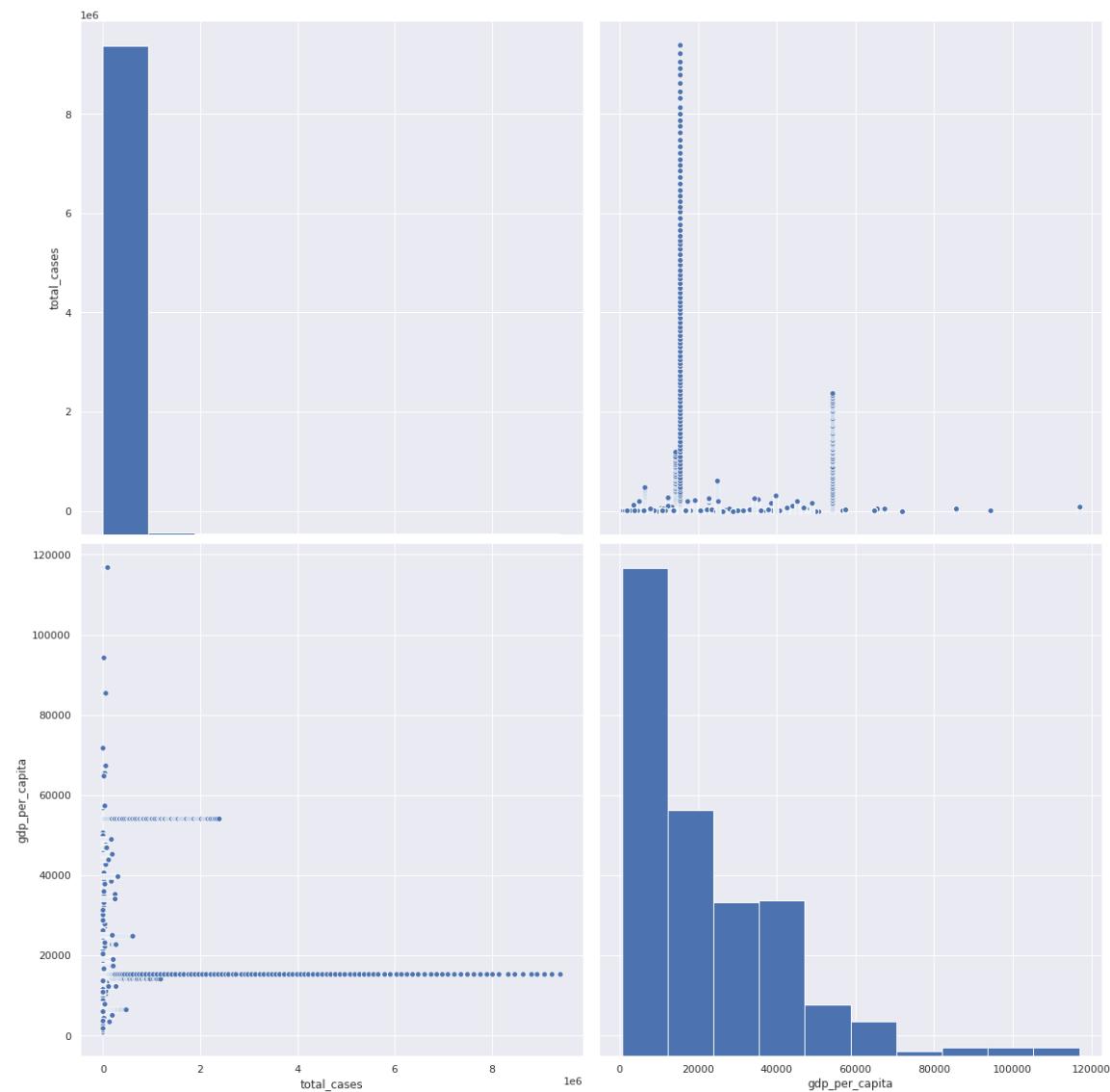


In [144]:

```
sns.pairplot(features, vars=["total_cases", "gdp_per_capita"], height=8)
```

Out[144]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cb263550>
```

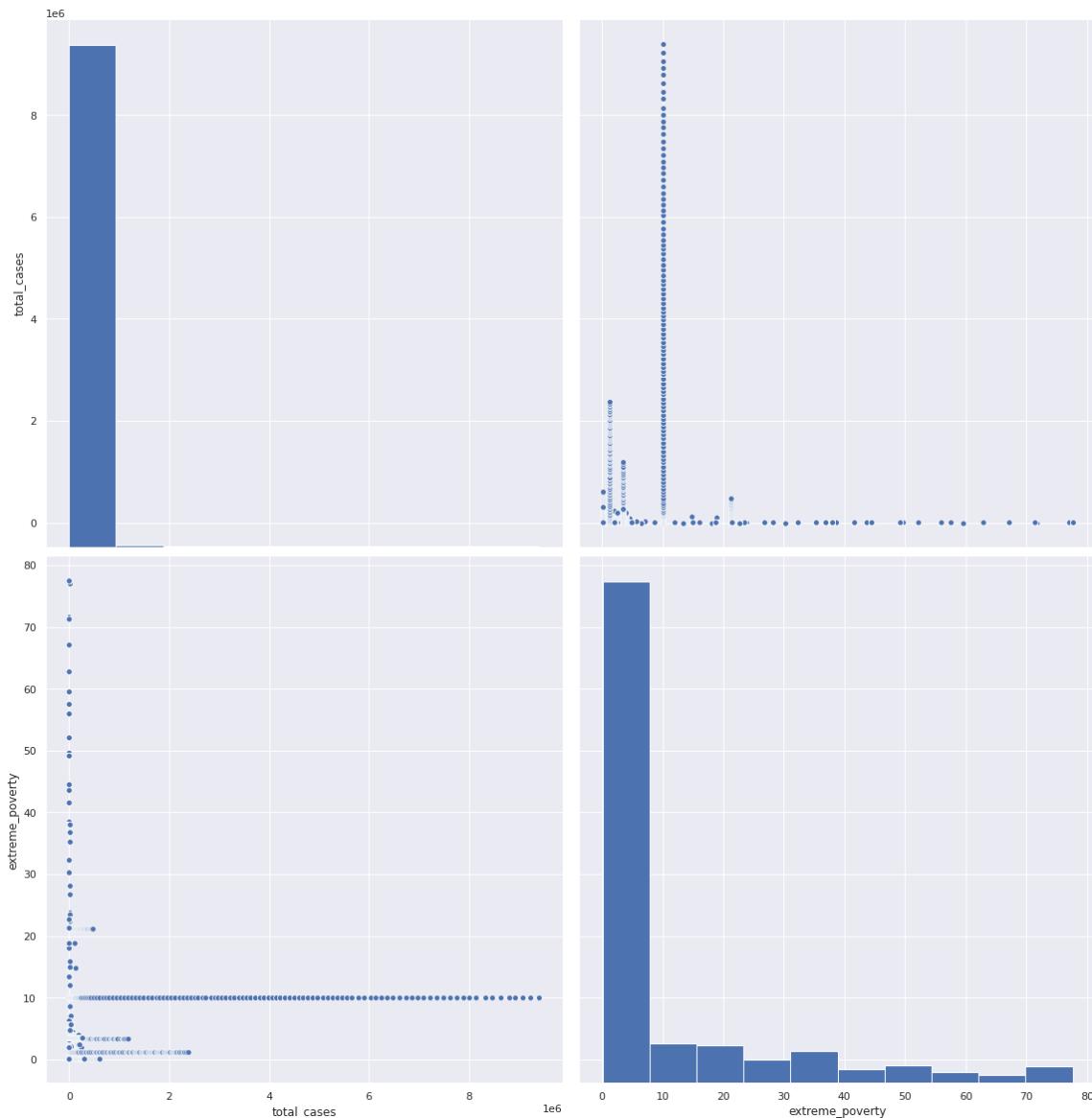


In [145]:

```
sns.pairplot(features, vars=["total_cases", "extreme_poverty"], height=8)
```

Out[145]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cb0829e8>
```

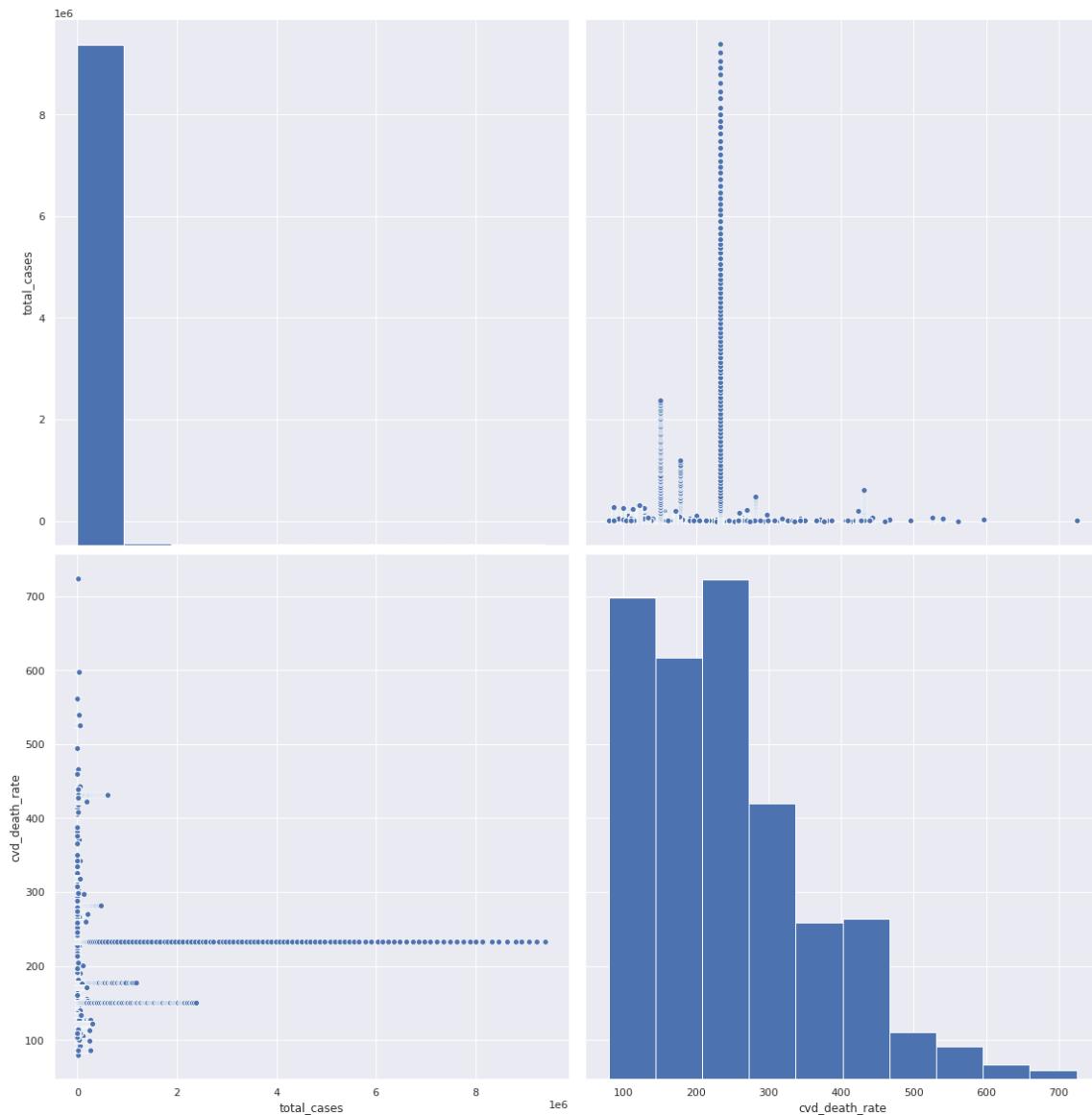


In [146]:

```
sns.pairplot(features, vars=["total_cases", "cvd_death_rate"], height=8)
```

Out[146]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cae78978>
```

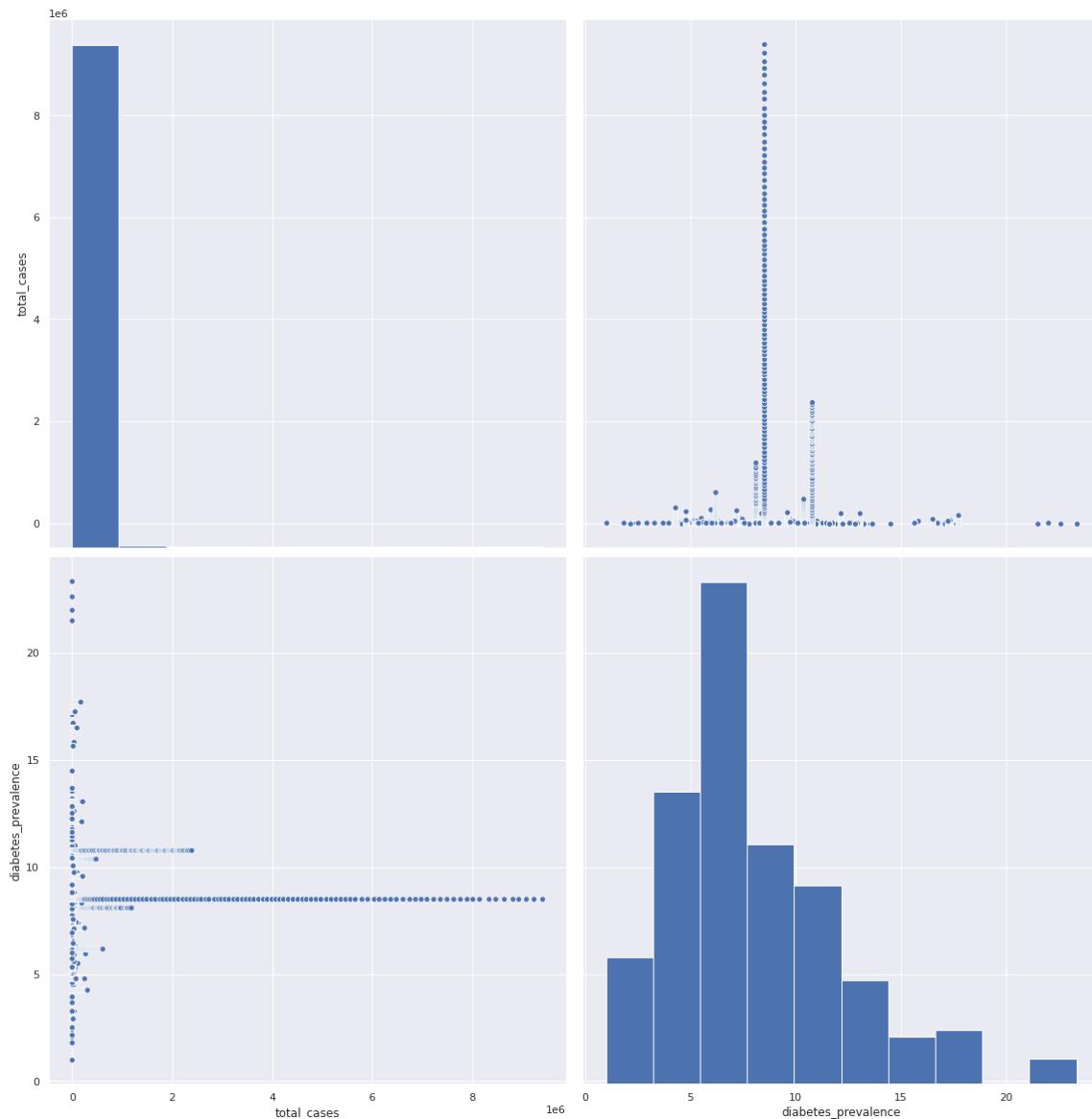


In [147]:

```
sns.pairplot(features, vars=["total_cases", "diabetes_prevalence"], height=8)
```

Out[147]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6d0ffee10>
```

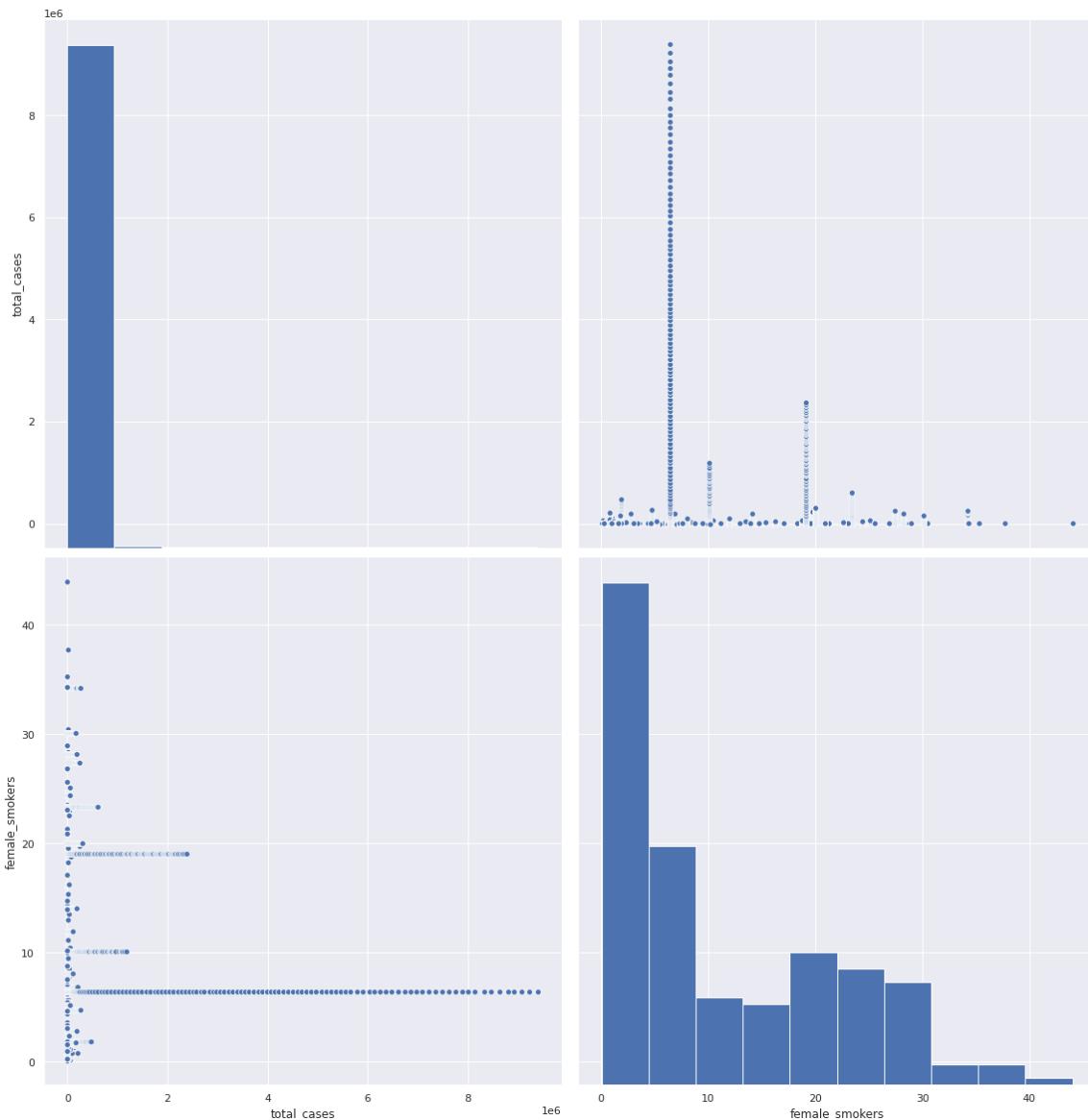


In [148]:

```
sns.pairplot(features, vars=["total_cases", "female_smokers"], height=8)
```

Out[148]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6cab31400>
```

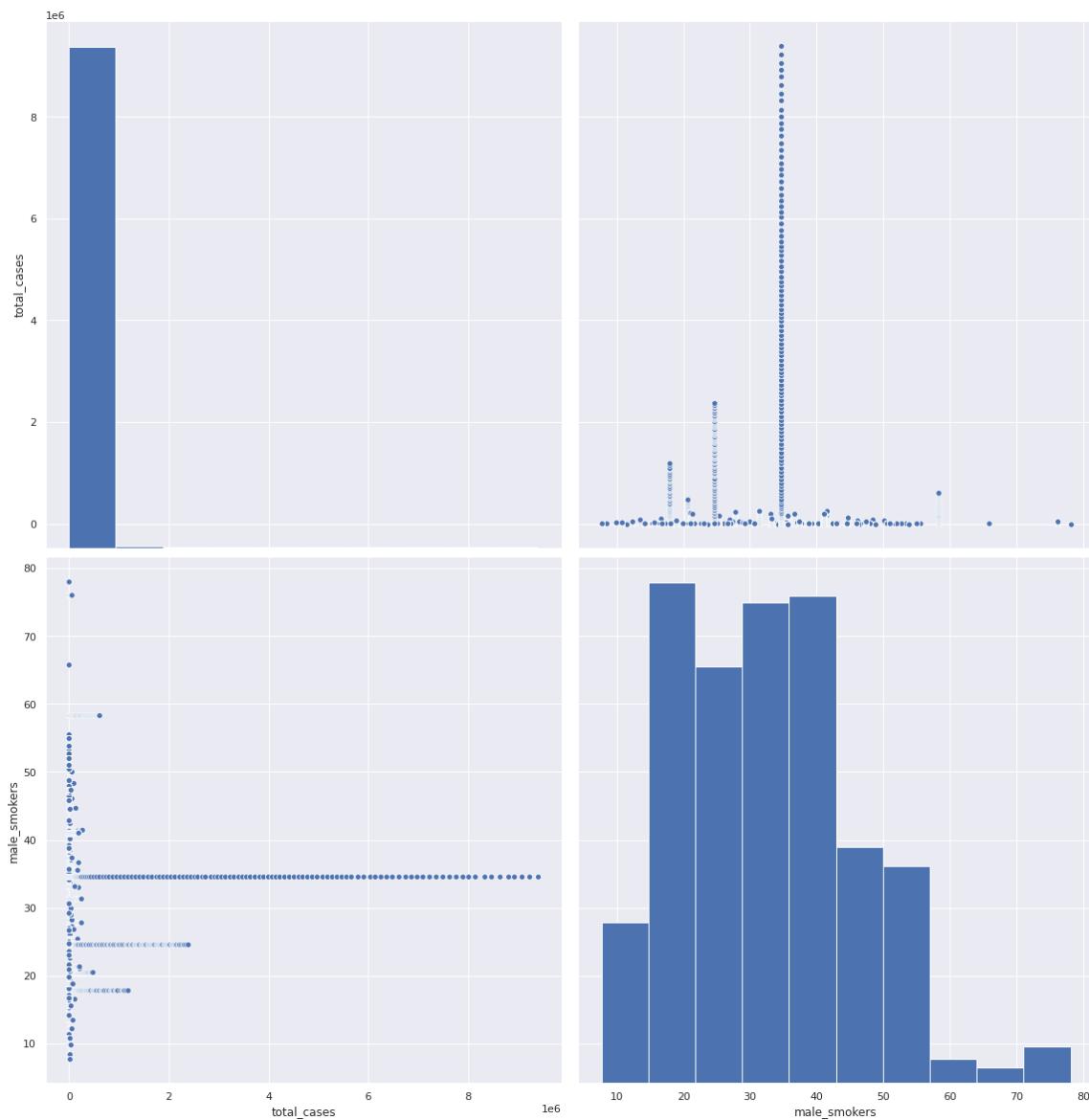


In [149]:

```
sns.pairplot(features, vars=["total_cases", "male_smokers"], height=8)
```

Out[149]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6caad4470>
```

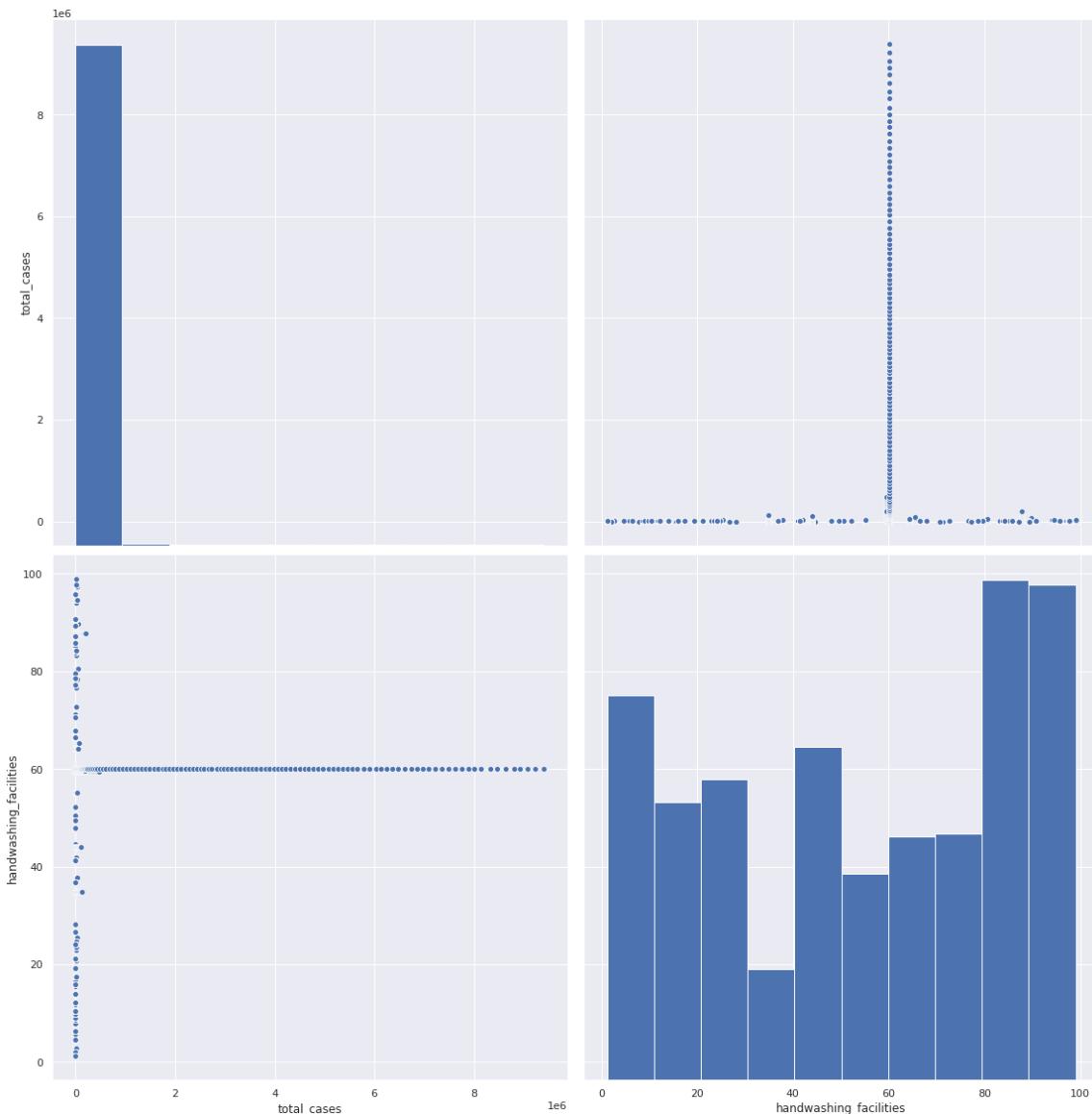


In [150]:

```
sns.pairplot(features, vars=["total_cases", "handwashing_facilities"], height=8)
```

Out[150]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ca6f19e8>
```

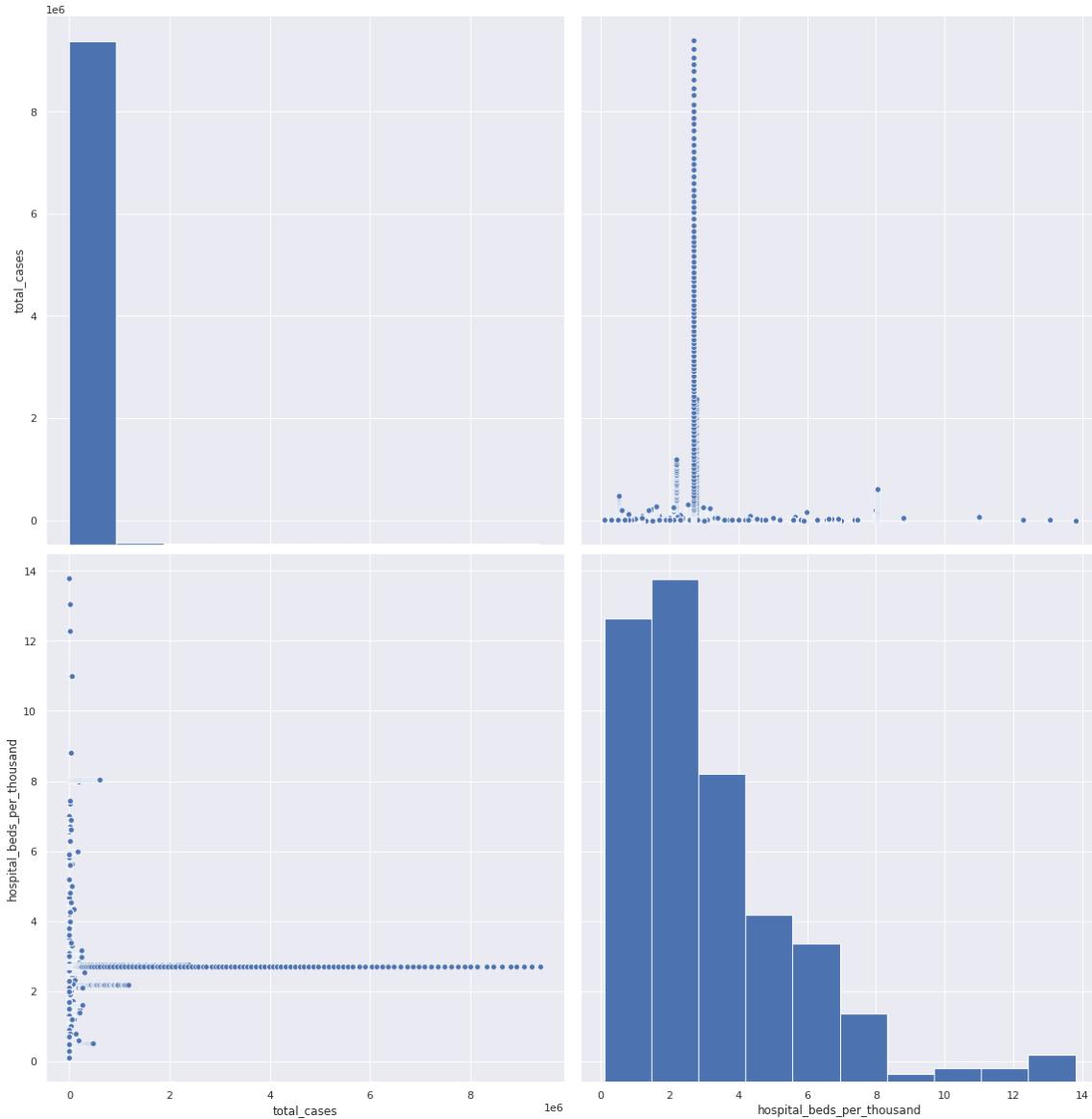


In [151]:

```
sns.pairplot(features, vars=["total_cases", "hospital_beds_per_thousand"], height=8)
```

Out[151]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ca4f0a20>
```

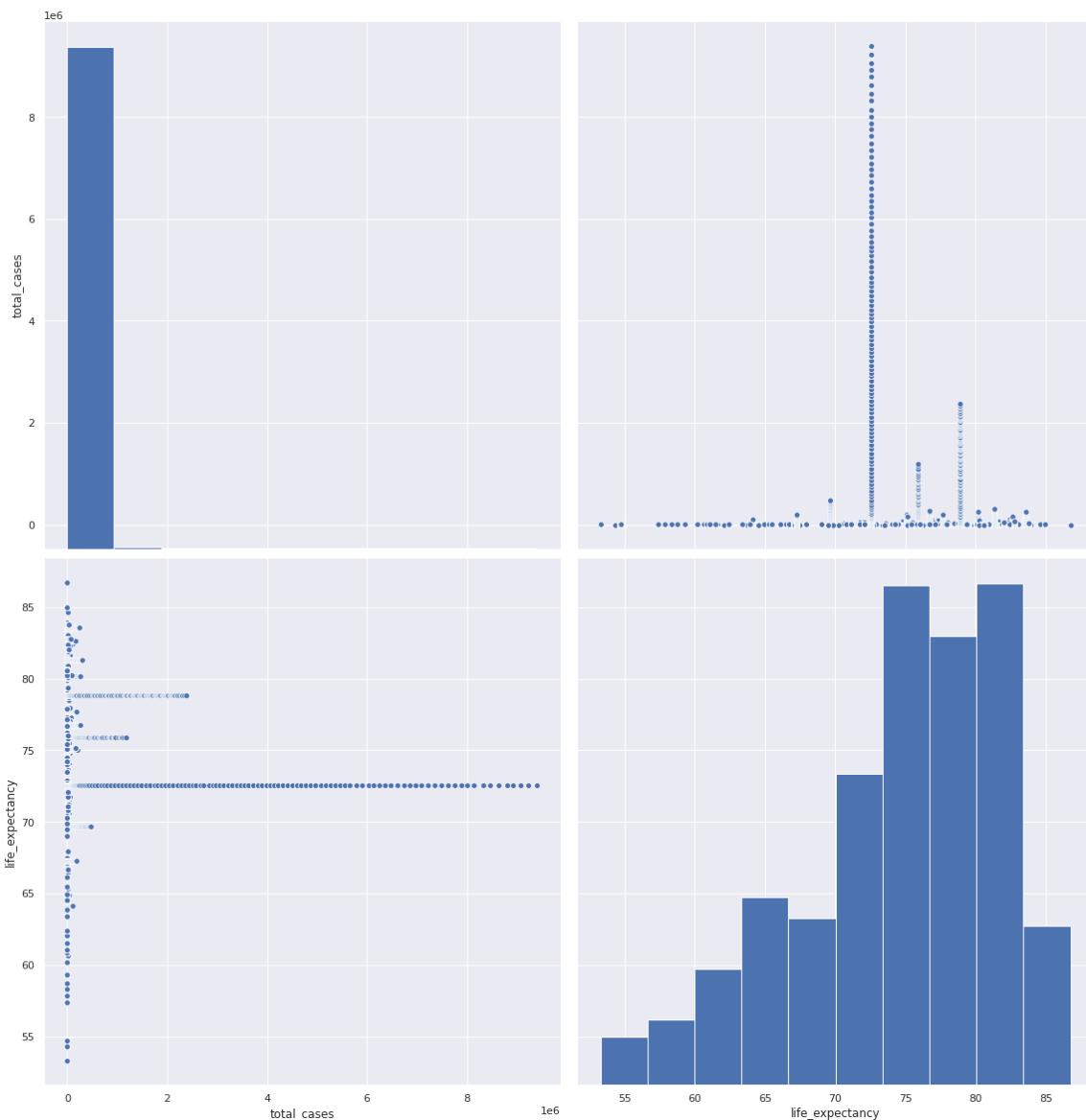


In [152]:

```
sns.pairplot(features, vars=["total_cases", "life_expectancy"], height=8)
```

Out[152]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ca2eb5f8>
```

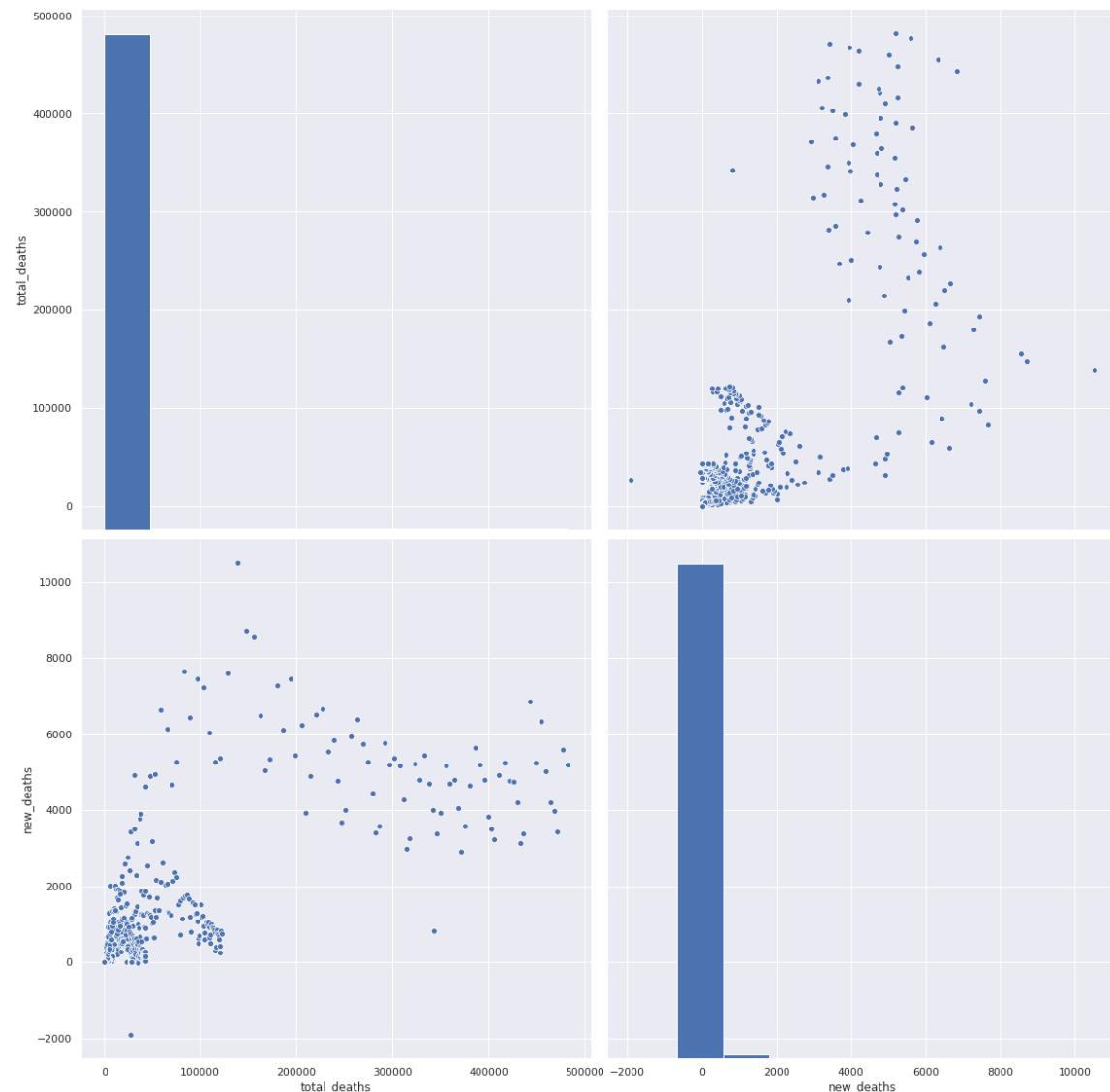


In [153]:

```
sns.pairplot(features, vars=["total_deaths", "new_deaths"], height=8)
```

Out[153]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6ca126828>
```

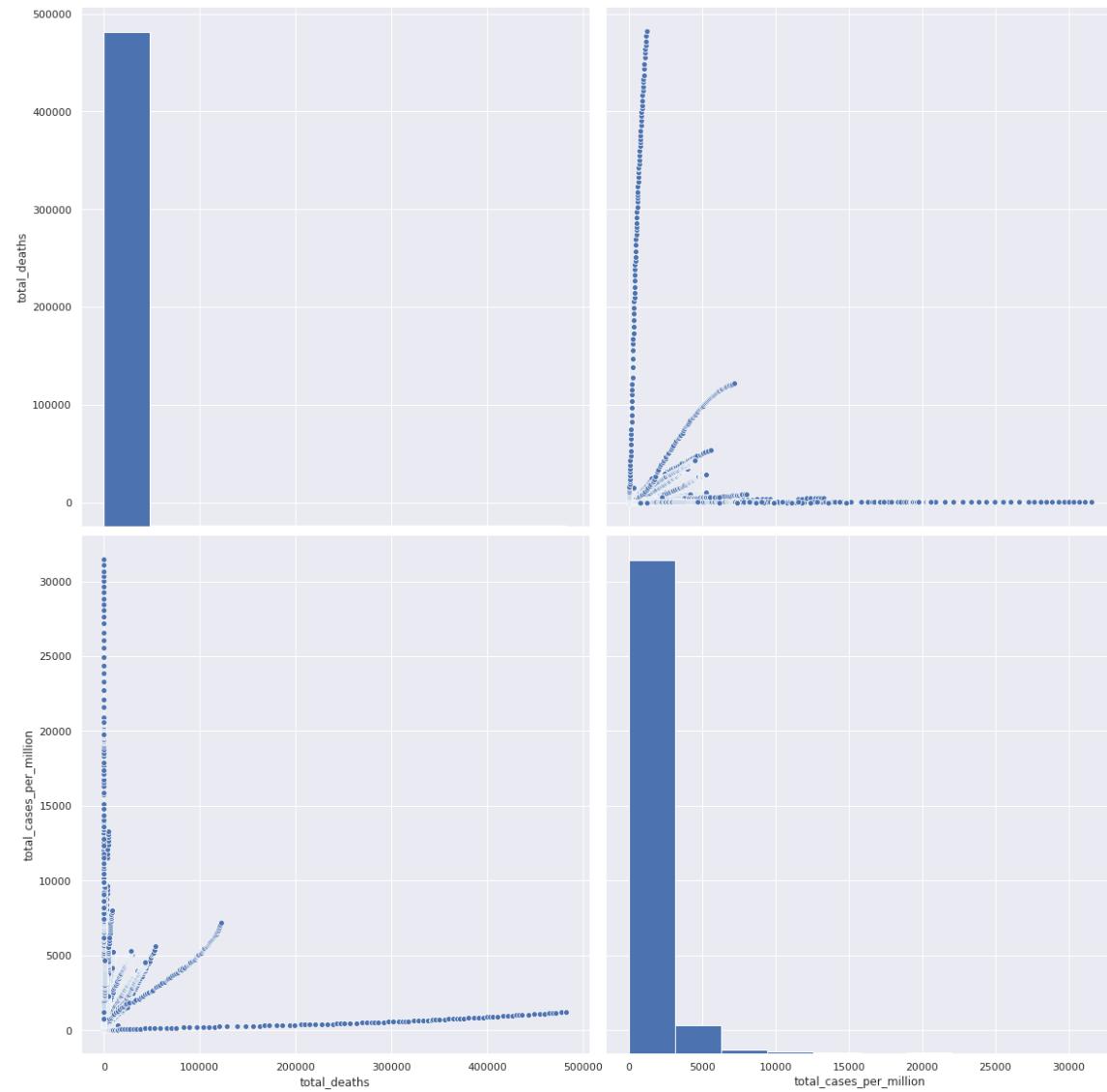


In [154]:

```
sns.pairplot(features, vars=["total_deaths", "total_cases_per_million"], height=8)
```

Out[154]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c9edff60>
```

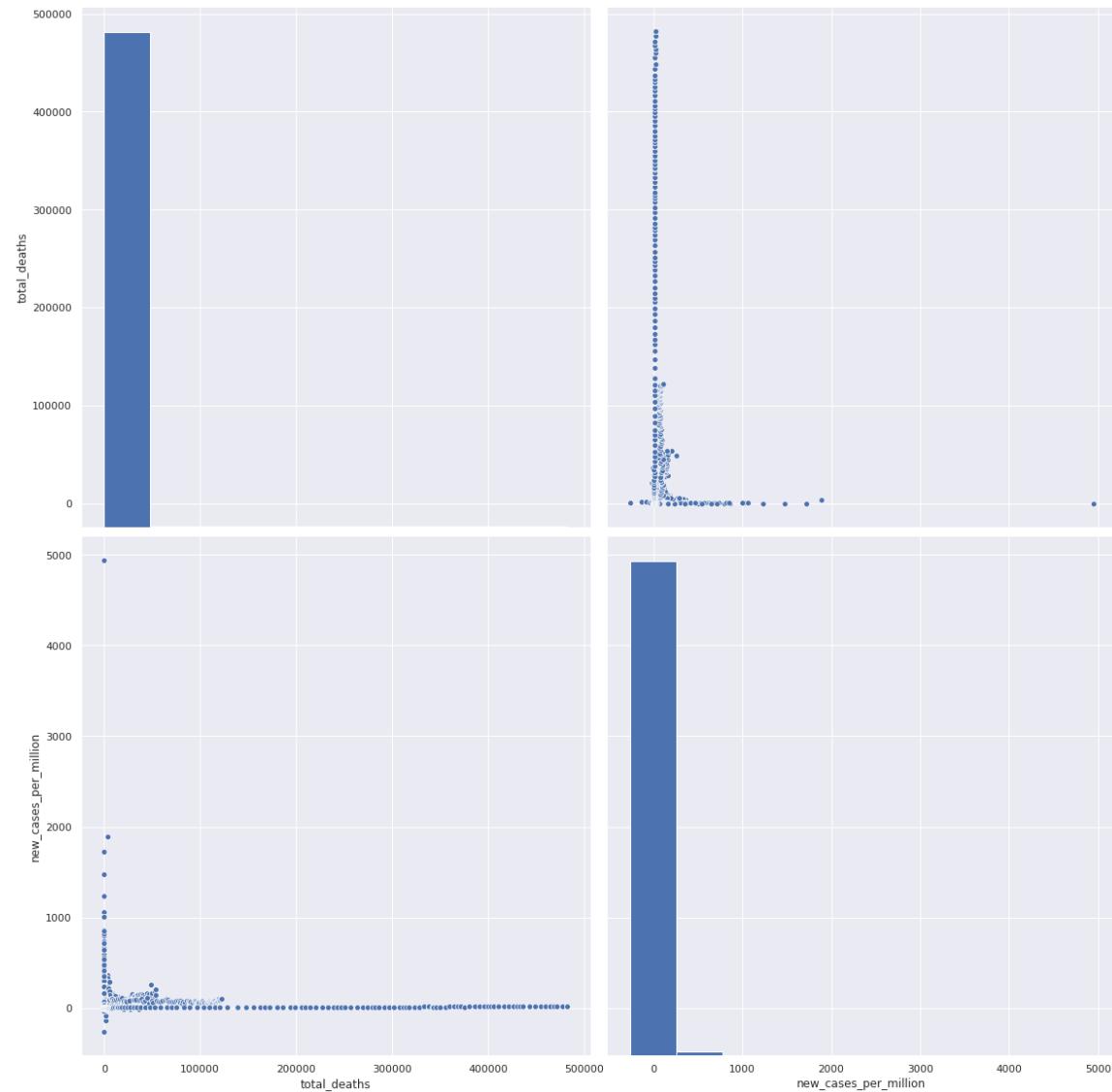


In [155]:

```
sns.pairplot(features, vars=["total_deaths", "new_cases_per_million"], height=8)
```

Out[155]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c9ce1c18>
```

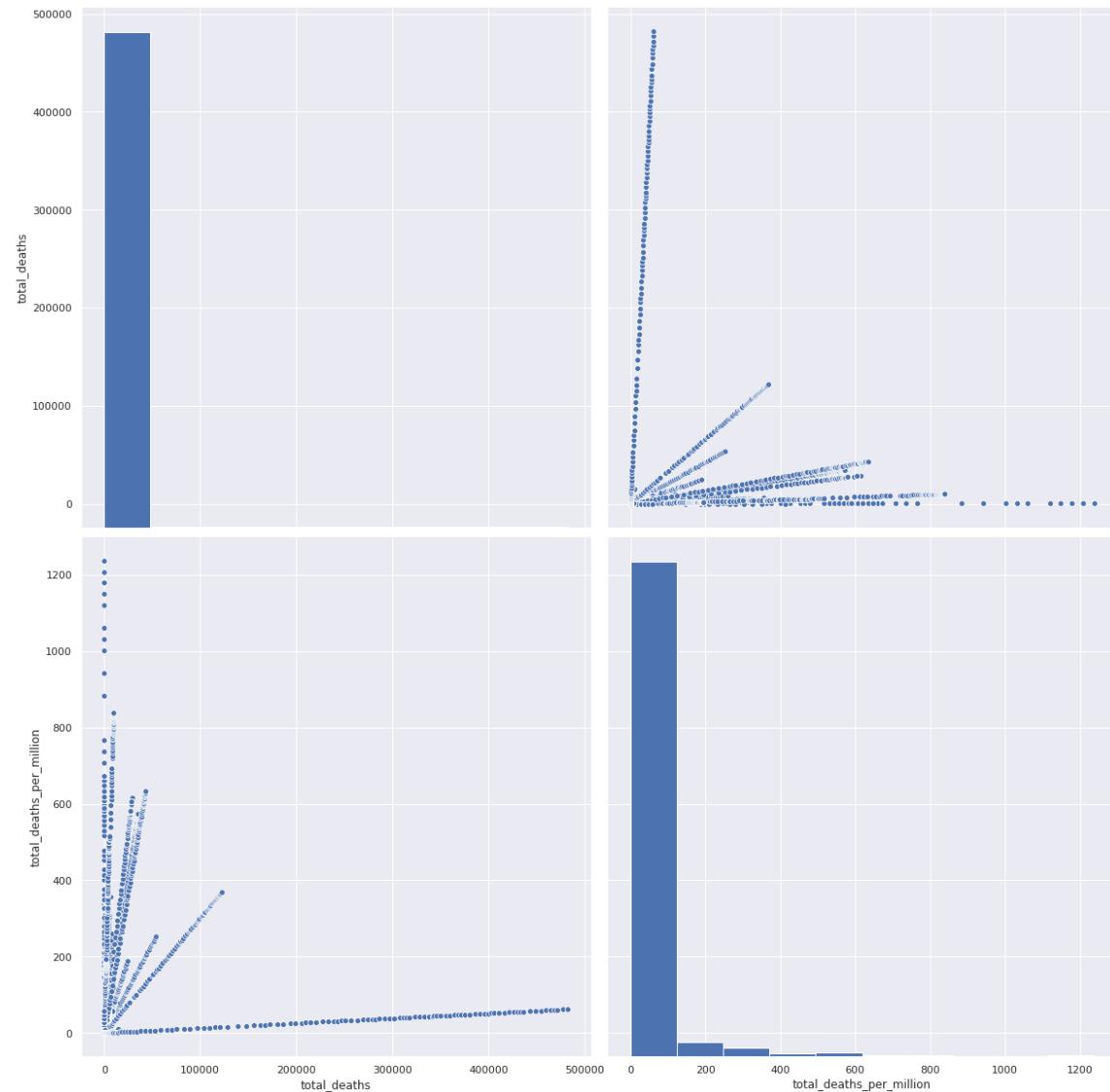


In [156]:

```
sns.pairplot(features, vars=["total_deaths", "total_deaths_per_million"], height=8)
```

Out[156]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c9b29160>
```

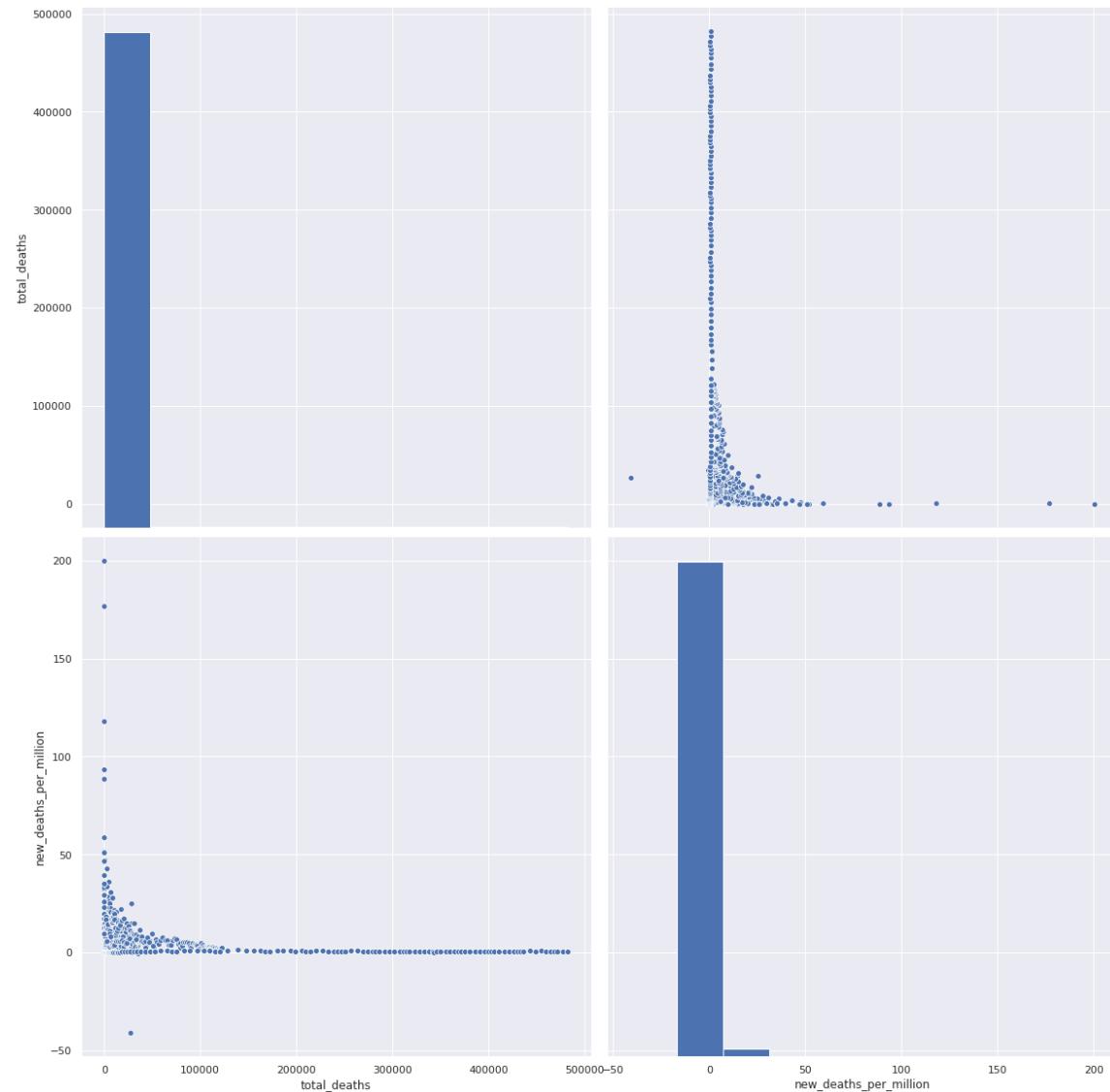


In [157]:

```
sns.pairplot(features, vars=["total_deaths", "new_deaths_per_million"], height=8)
```

Out[157]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c98d9828>
```

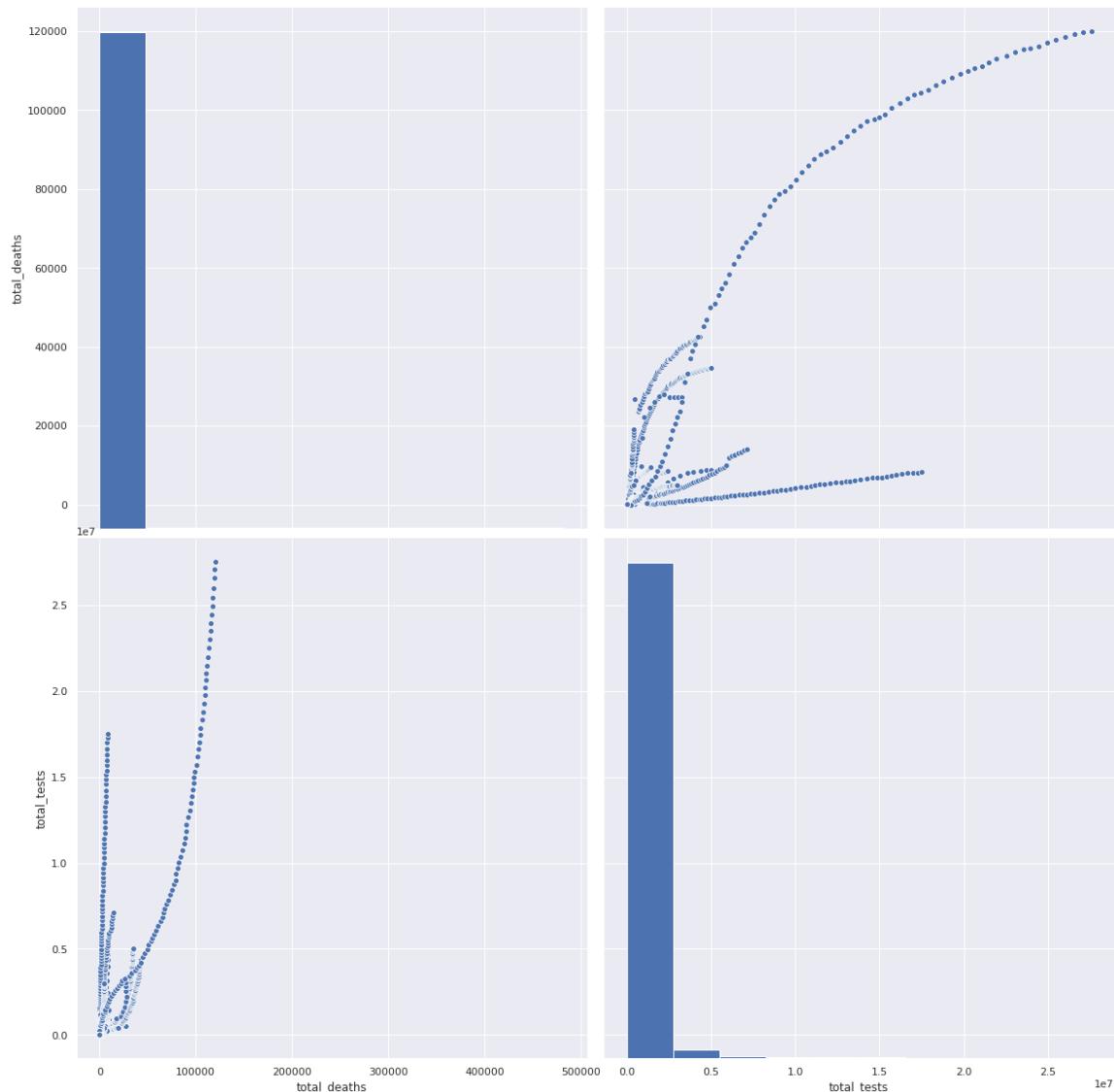


In [158]:

```
sns.pairplot(features, vars=["total_deaths", "total_tests"], height=8)
```

Out[158]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c9833dd8>
```

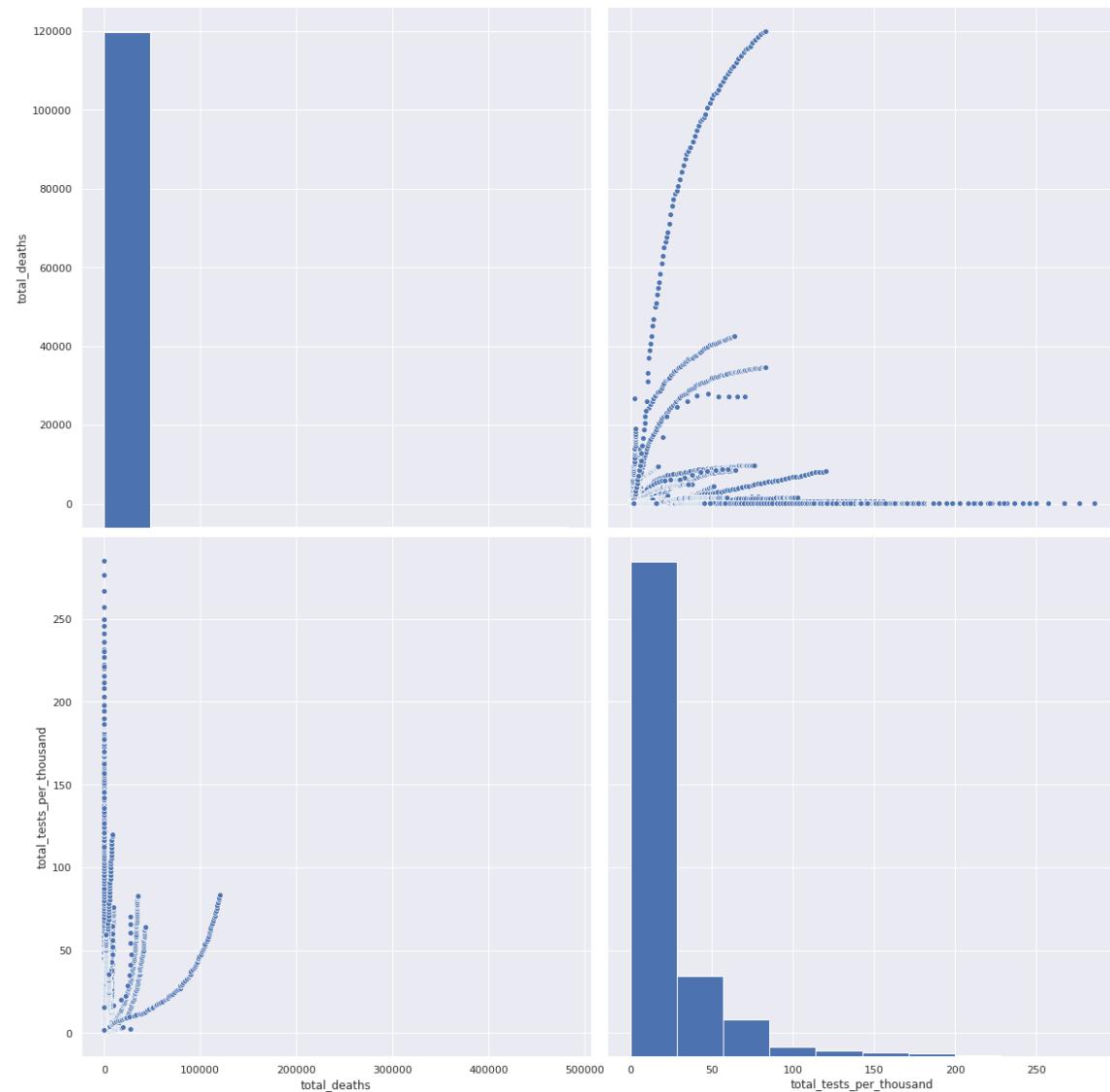


In [159]:

```
sns.pairplot(features, vars=["total_deaths", "total_tests_per_thousand"], height=8)
```

Out[159]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c95b1898>
```

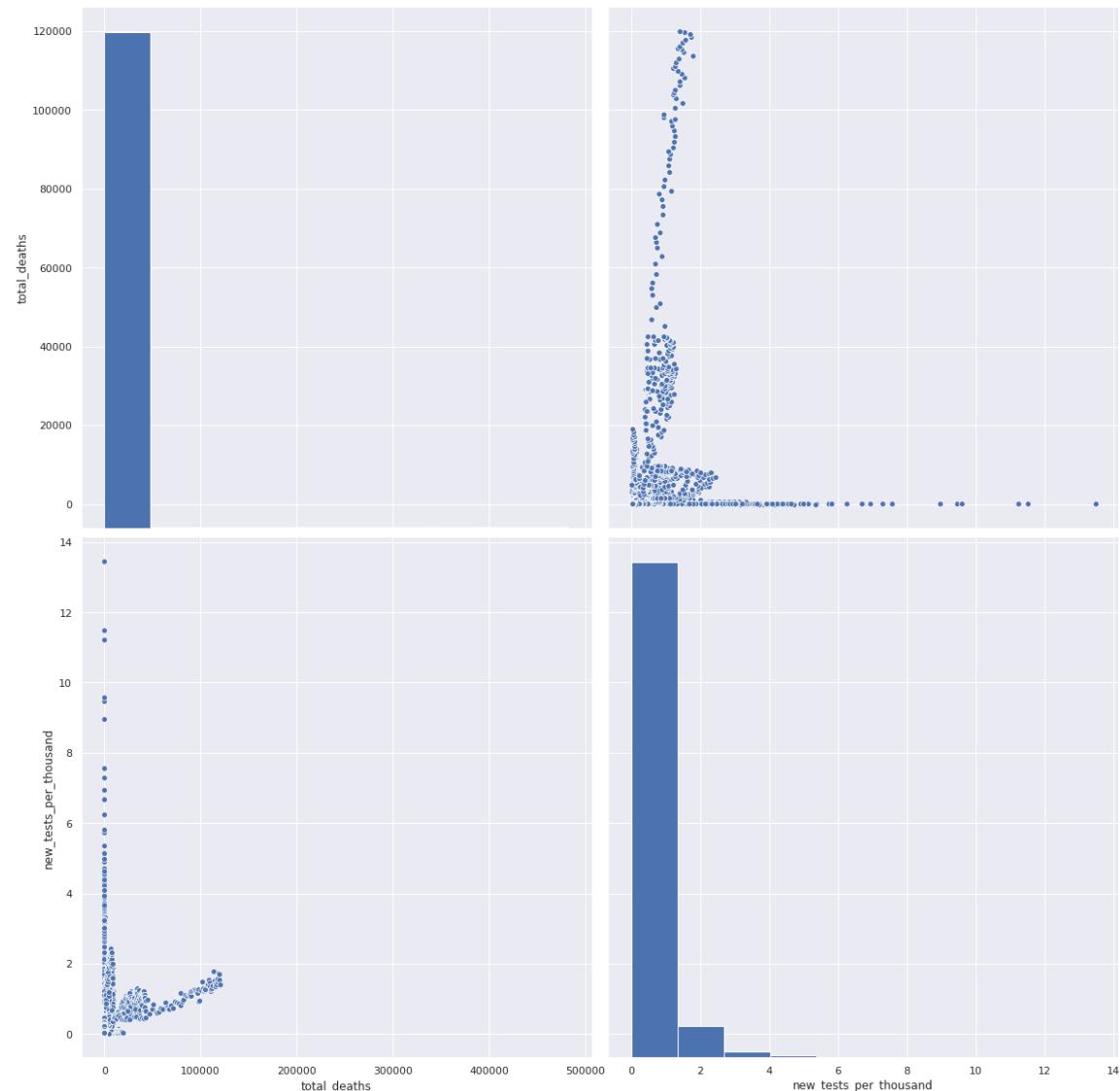


In [160]:

```
sns.pairplot(features, vars=["total_deaths", "new_tests_per_thousand"], height=8)
```

Out[160]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c9437a20>
```

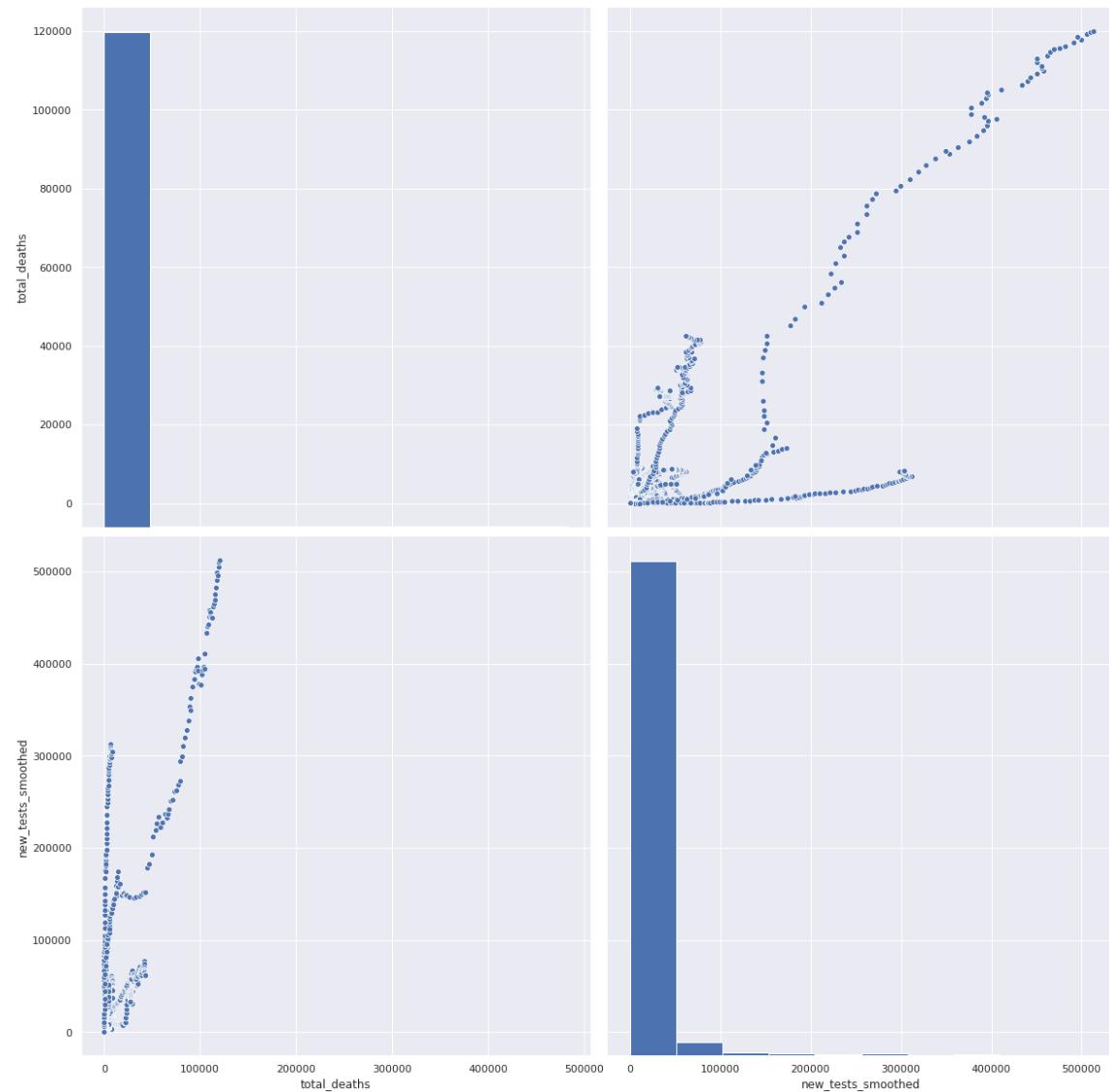


In [161]:

```
sns.pairplot(features, vars=["total_deaths", "new_tests_smoothed"], height=8)
```

Out[161]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c91db390>
```

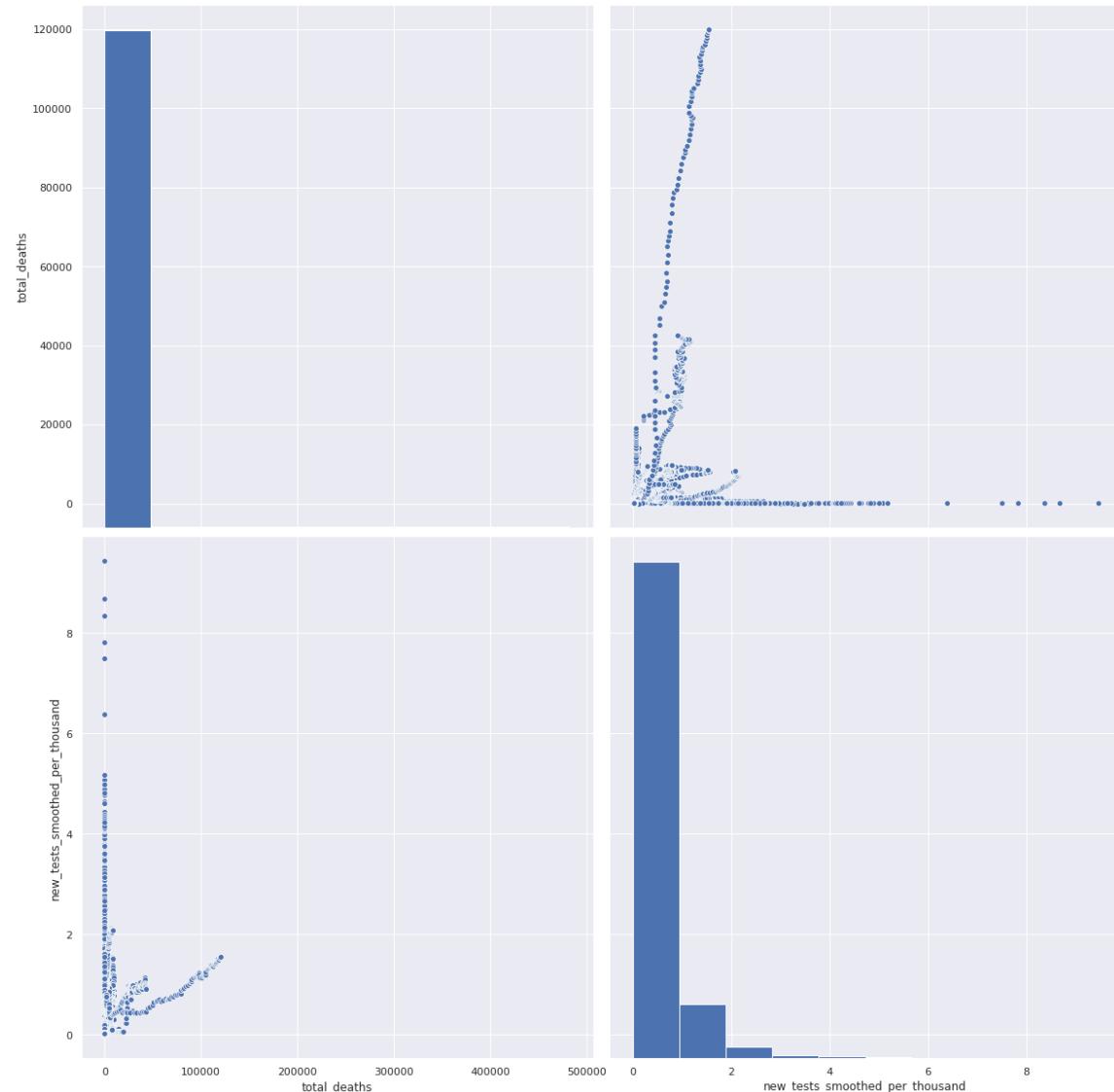


In [162]:

```
sns.pairplot(features, vars=["total_deaths", "new_tests_smoothed_per_thousand"], height=8)
```

Out[162]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c8f1a710>
```

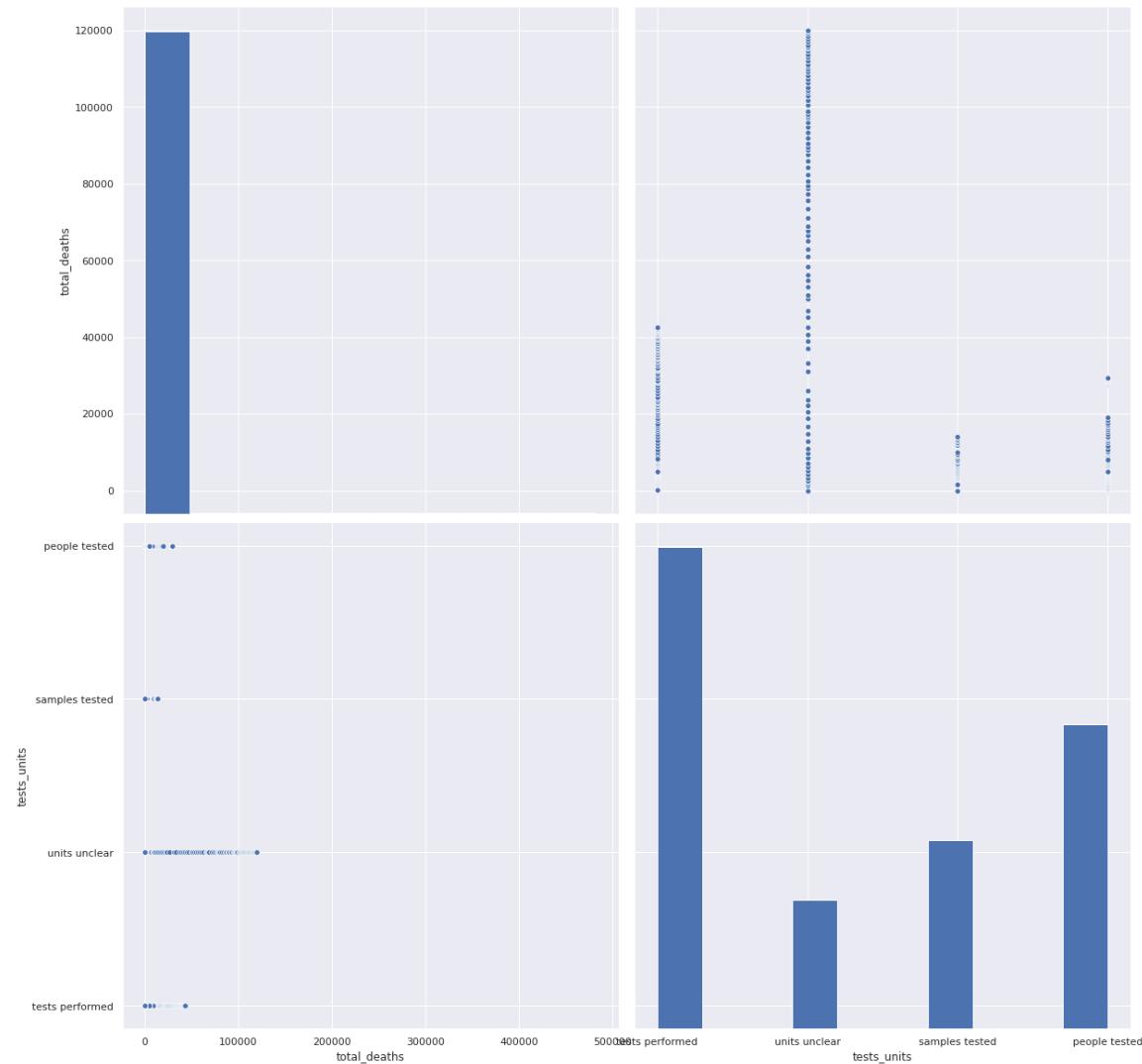


In [163]:

```
sns.pairplot(features, vars=["total_deaths", "tests_units"], height=8)
```

Out[163]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c9733cc0>
```

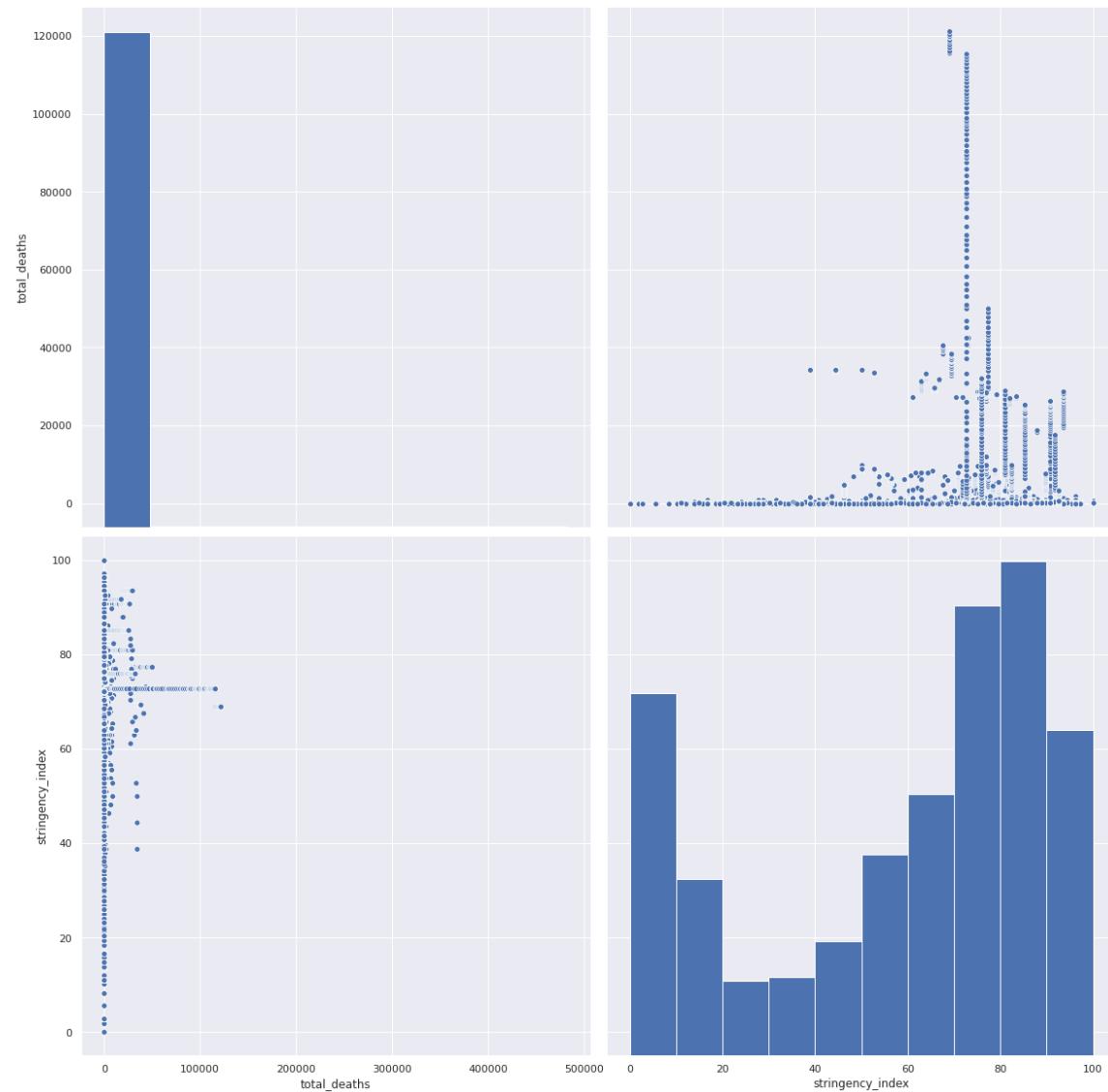


In [164]:

```
sns.pairplot(features, vars=["total_deaths", "stringency_index"], height=8)
```

Out[164]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c8b42cc0>
```

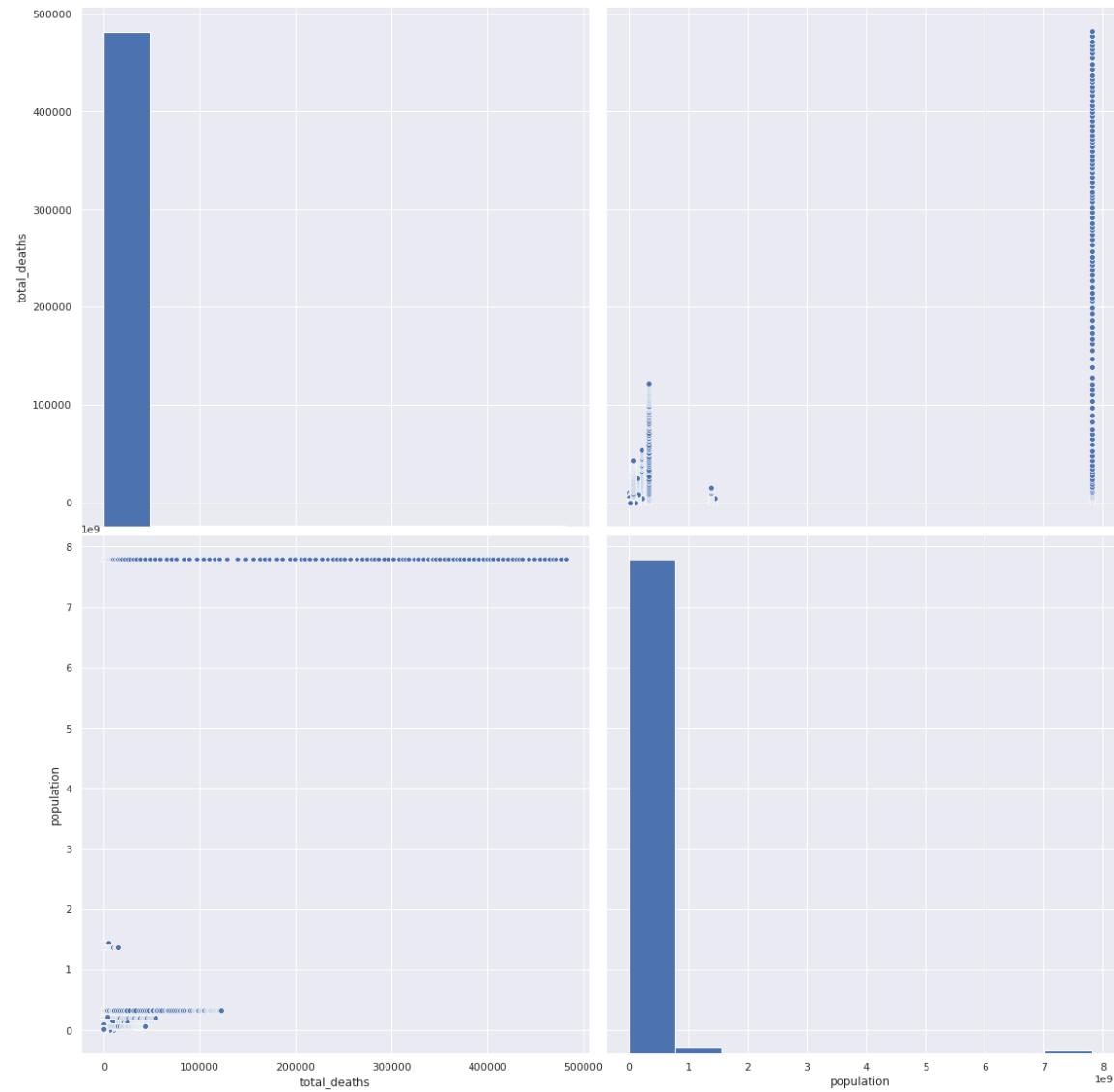


In [165]:

```
sns.pairplot(features, vars=["total_deaths", "population"], height=8)
```

Out[165]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c8e3c668>
```

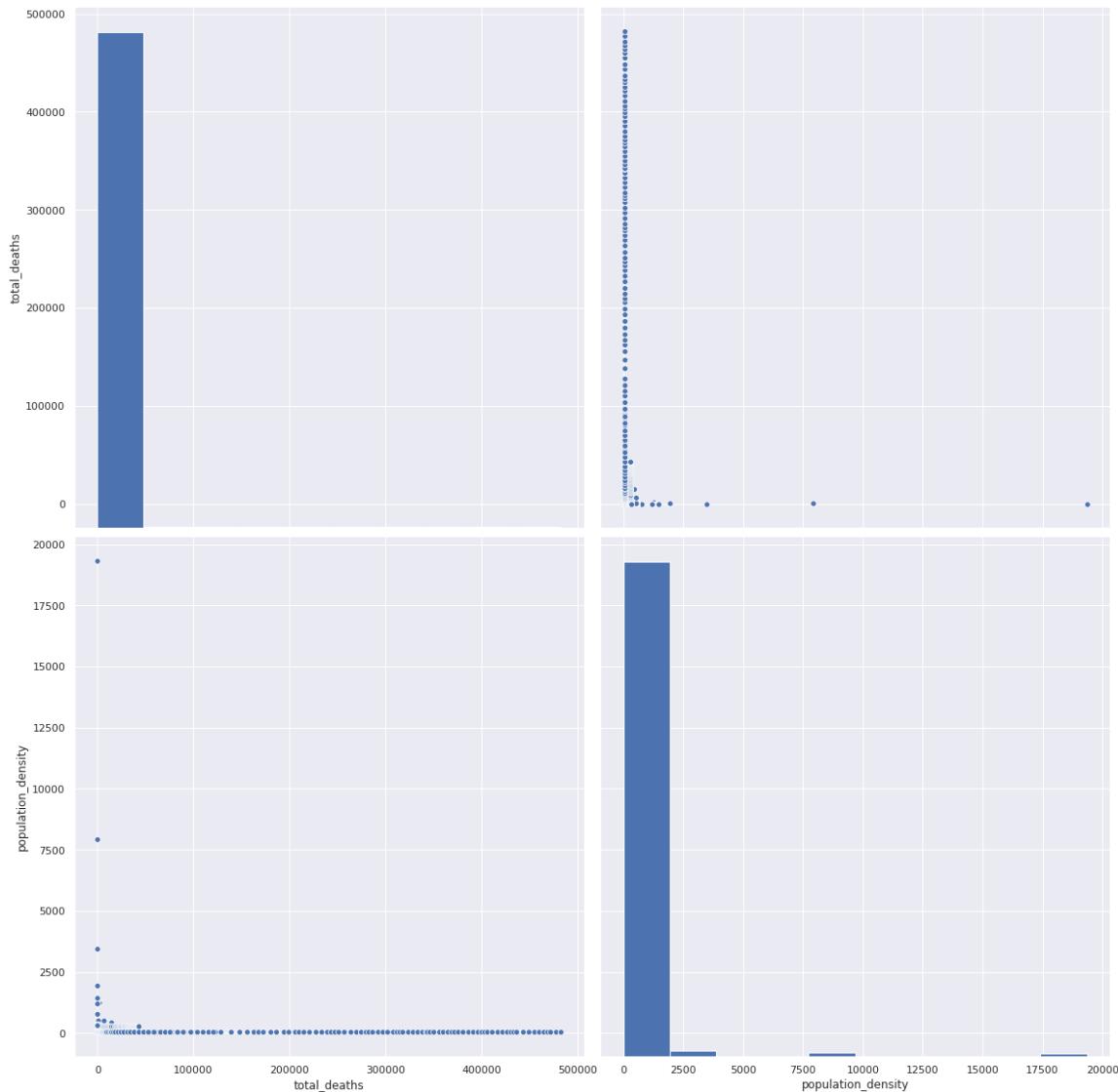


In [166]:

```
sns.pairplot(features, vars=["total_deaths", "population_density"], height=8)
```

Out[166]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c8730be0>
```

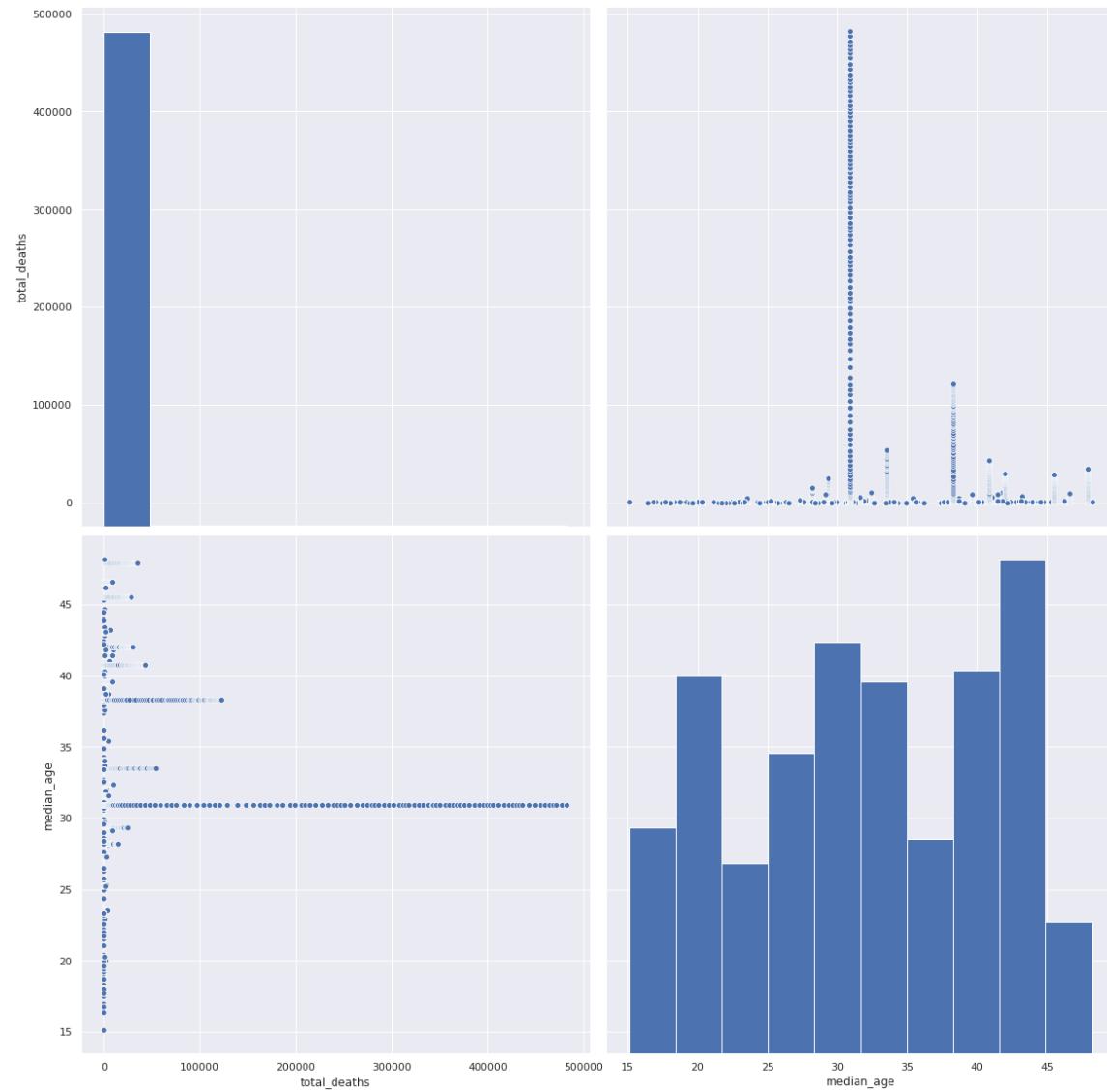


In [167]:

```
sns.pairplot(features, vars=["total_deaths", "median_age"], height=8)
```

Out[167]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c84c4080>
```

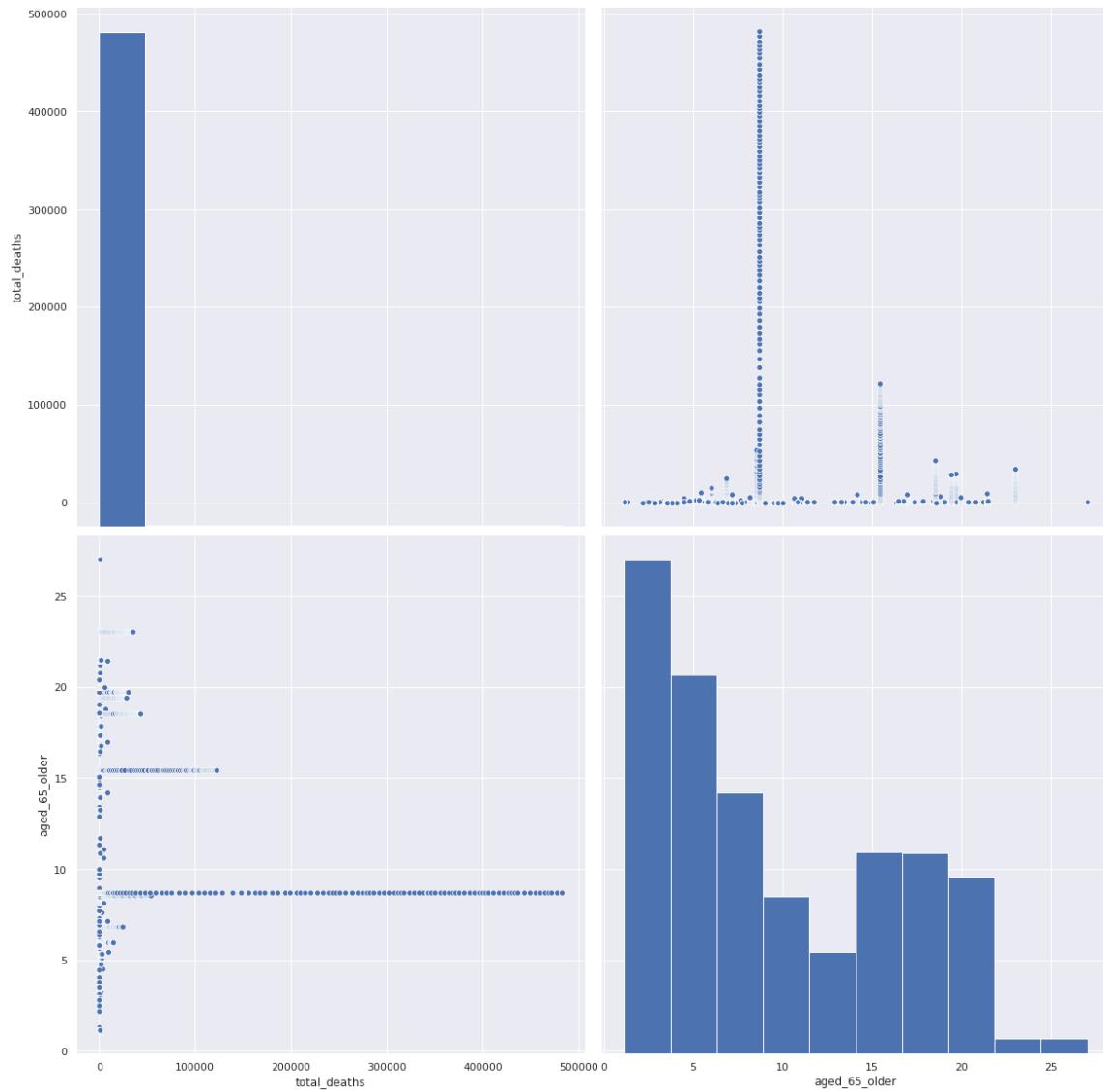


In [168]:

```
sns.pairplot(features, vars=["total_deaths", "aged_65_older"], height=8)
```

Out[168]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c82dff60>
```

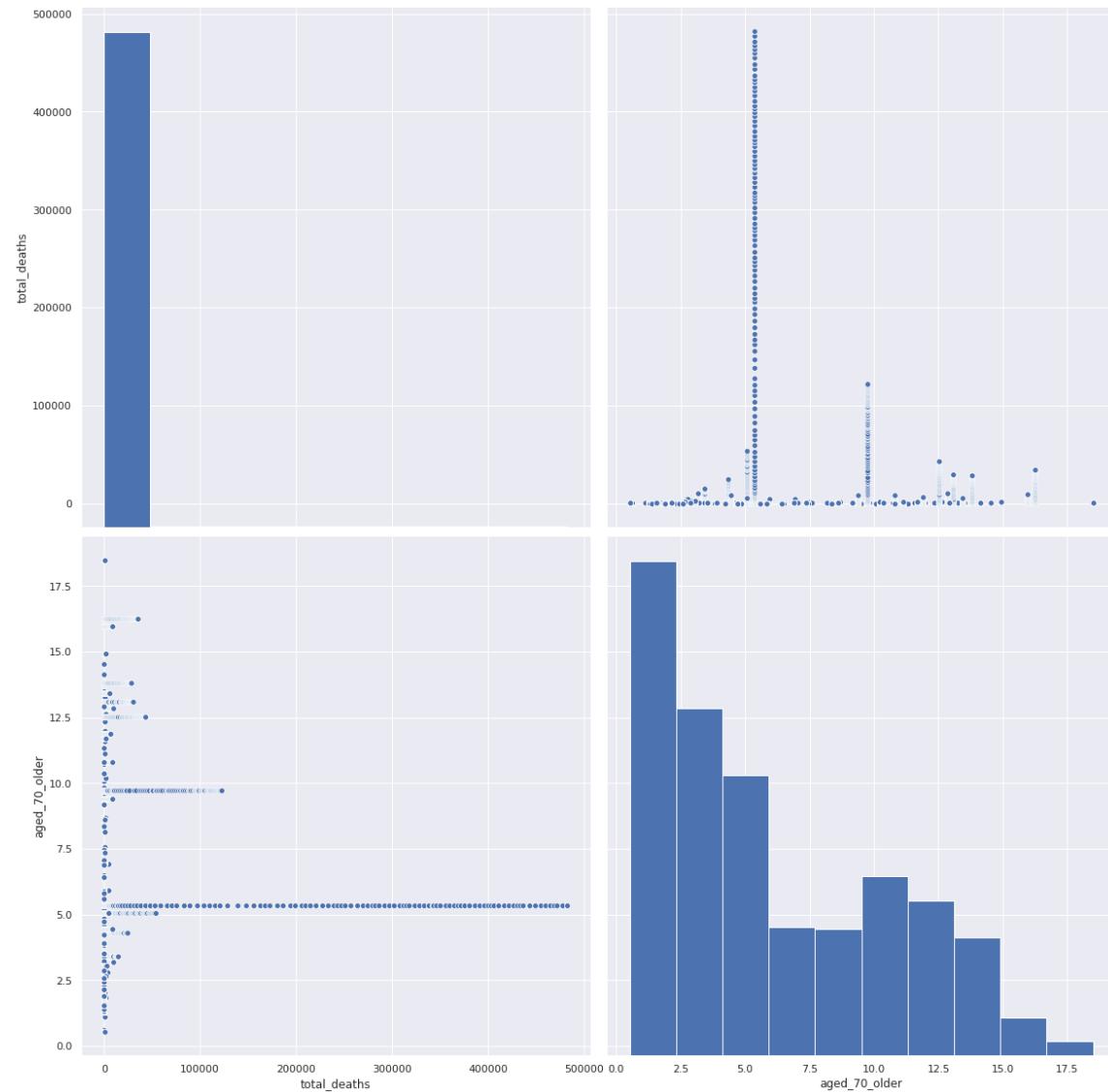


In [169]:

```
sns.pairplot(features, vars=["total_deaths", "aged_70_older"], height=8)
```

Out[169]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c80d0b00>
```

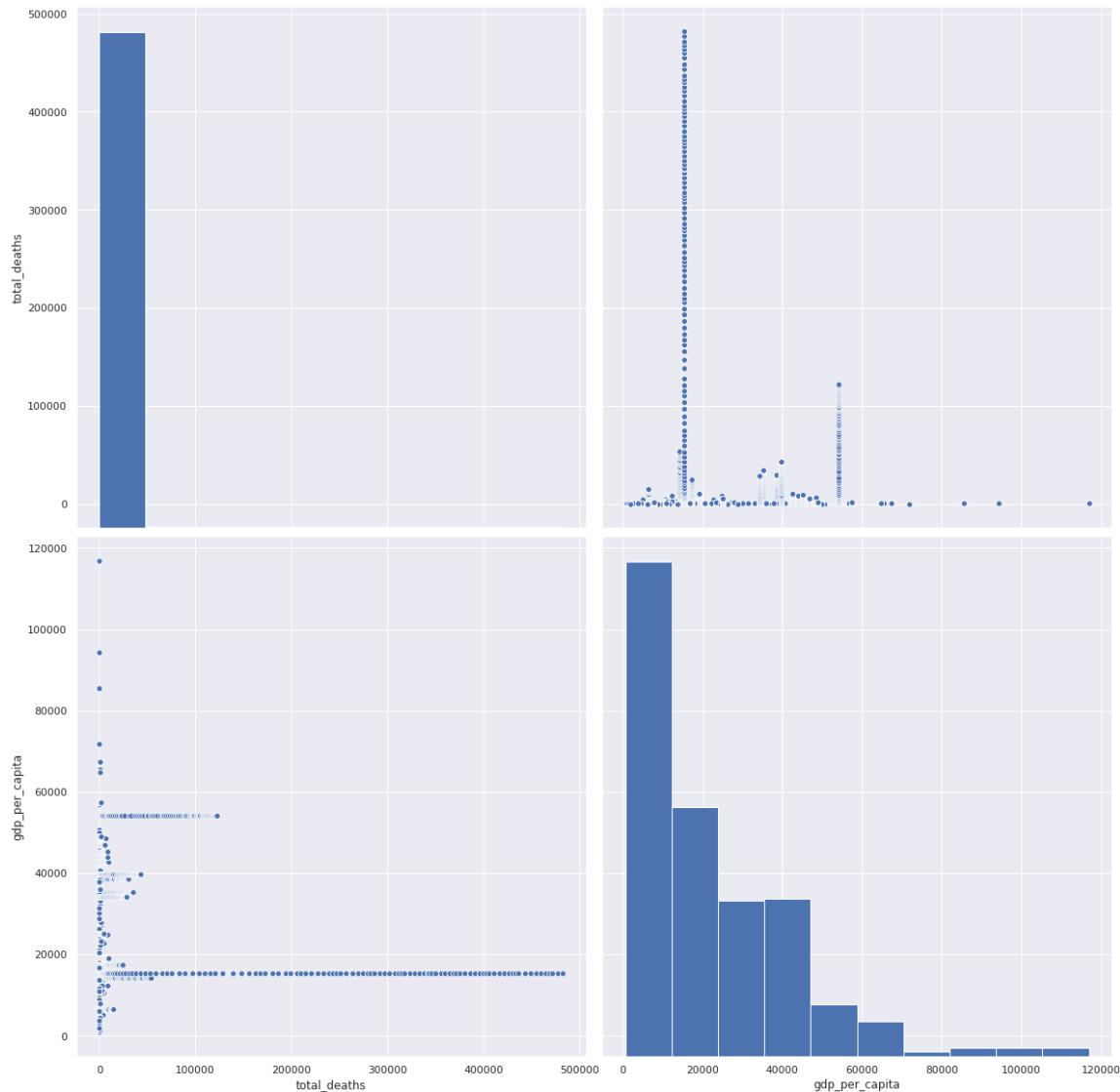


In [170]:

```
sns.pairplot(features, vars=["total_deaths", "gdp_per_capita"], height=8)
```

Out[170]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c823a278>
```

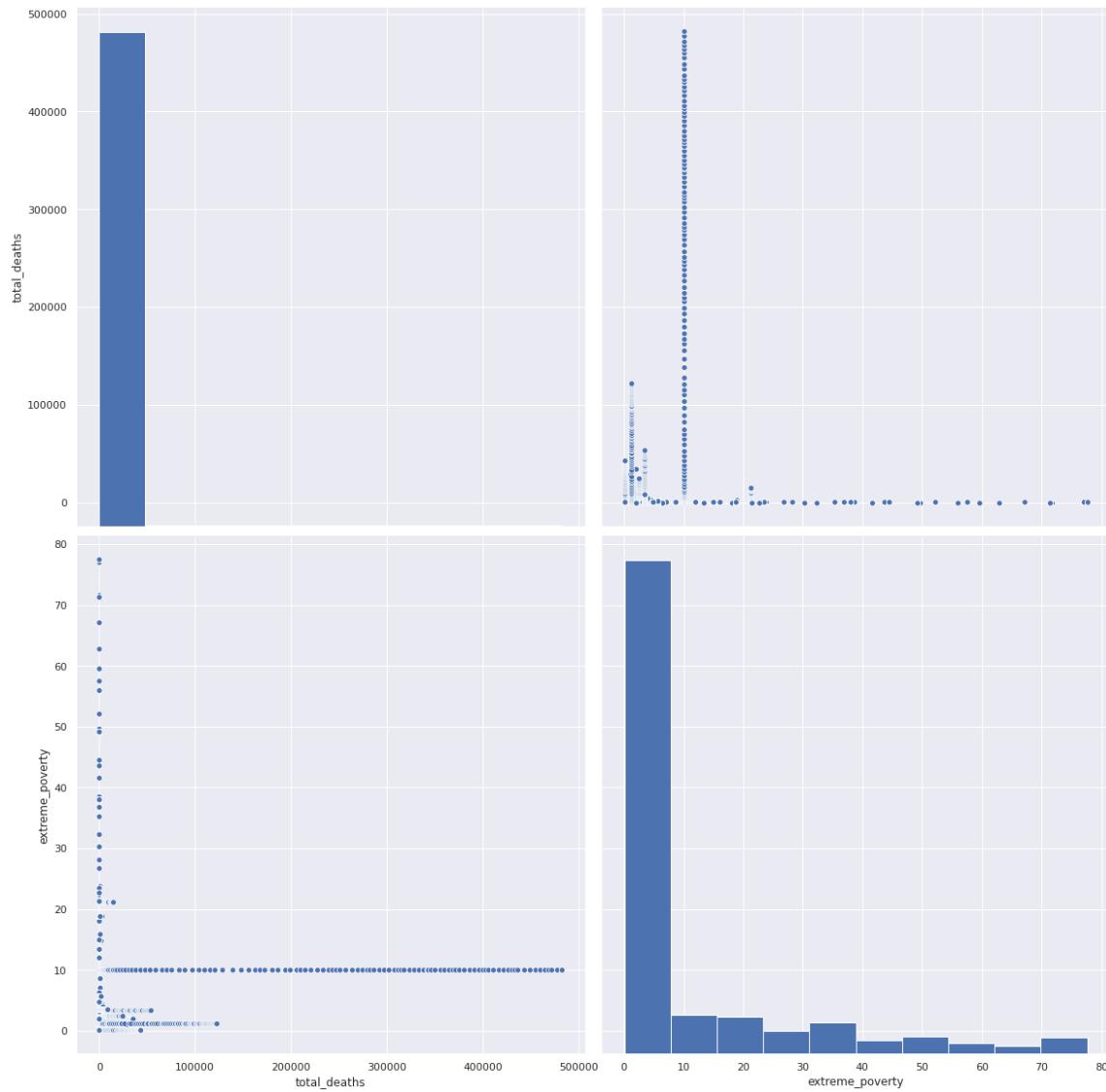


In [171]:

```
sns.pairplot(features, vars=["total_deaths", "extreme_poverty"], height=8)
```

Out[171]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c820ed30>
```

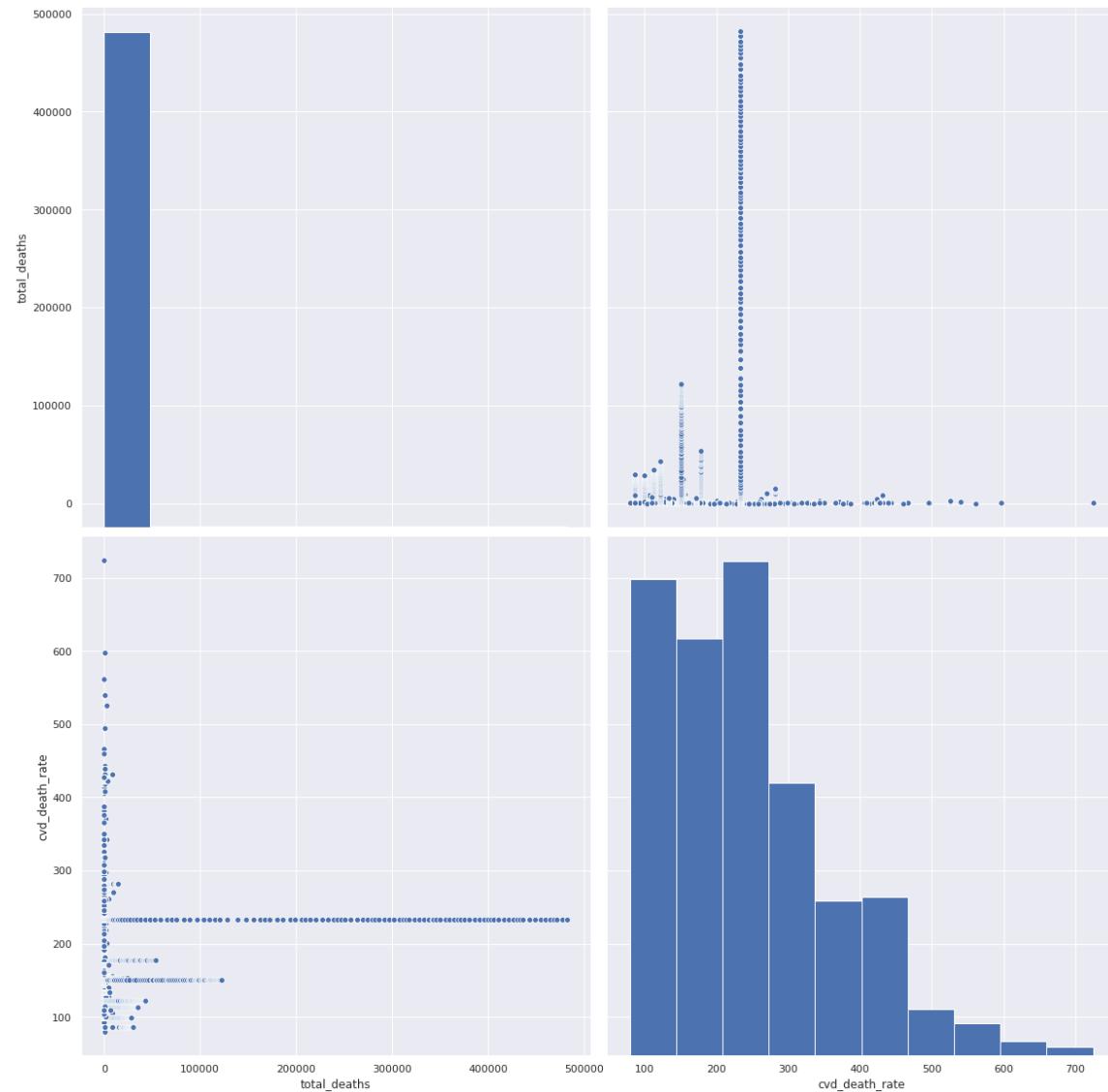


In [172]:

```
sns.pairplot(features, vars=["total_deaths", "cvd_death_rate"], height=8)
```

Out[172]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c7b2add8>
```

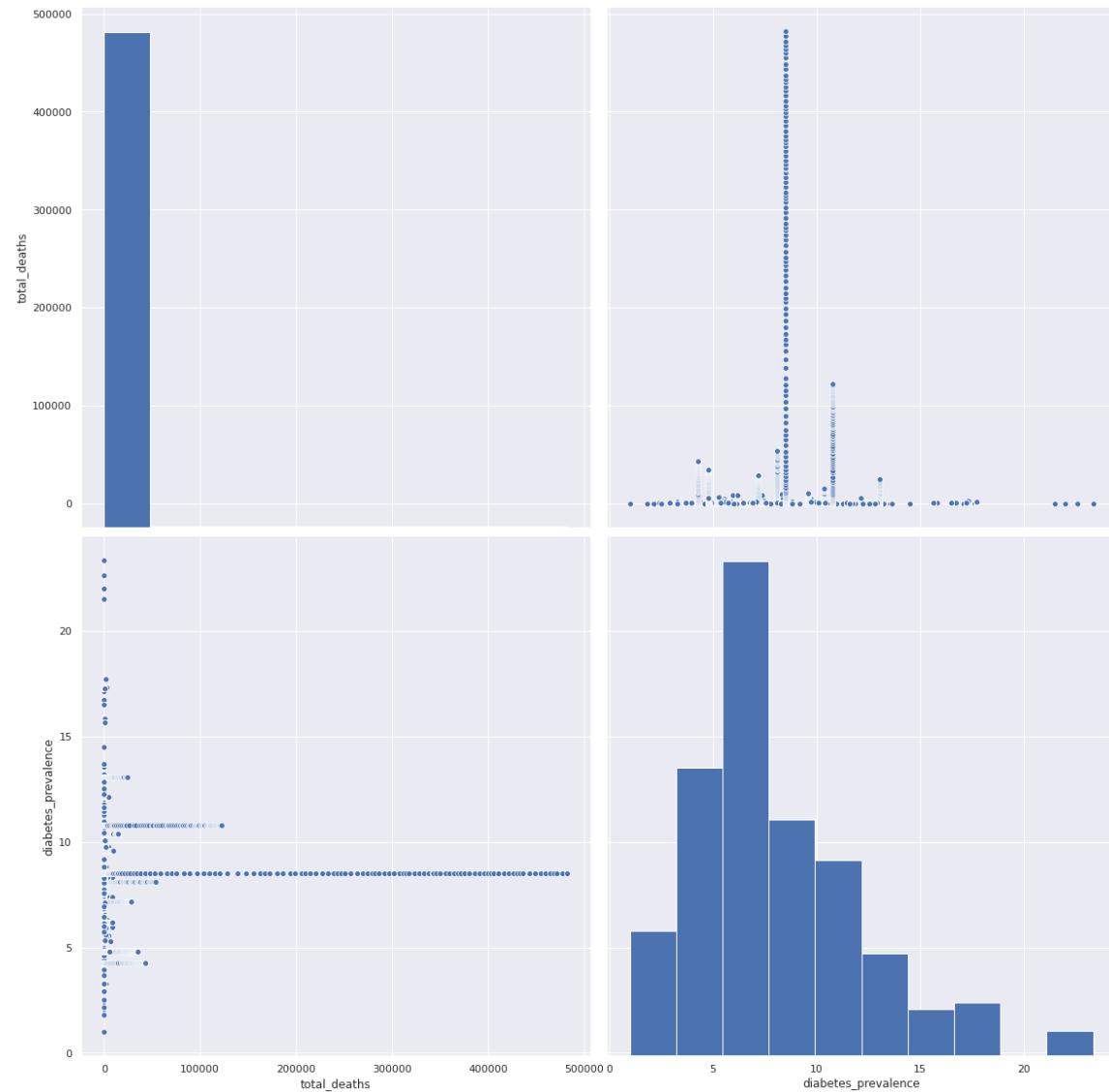


In [173]:

```
sns.pairplot(features, vars=["total_deaths", "diabetes_prevalence"], height=8)
```

Out[173]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c793a780>
```

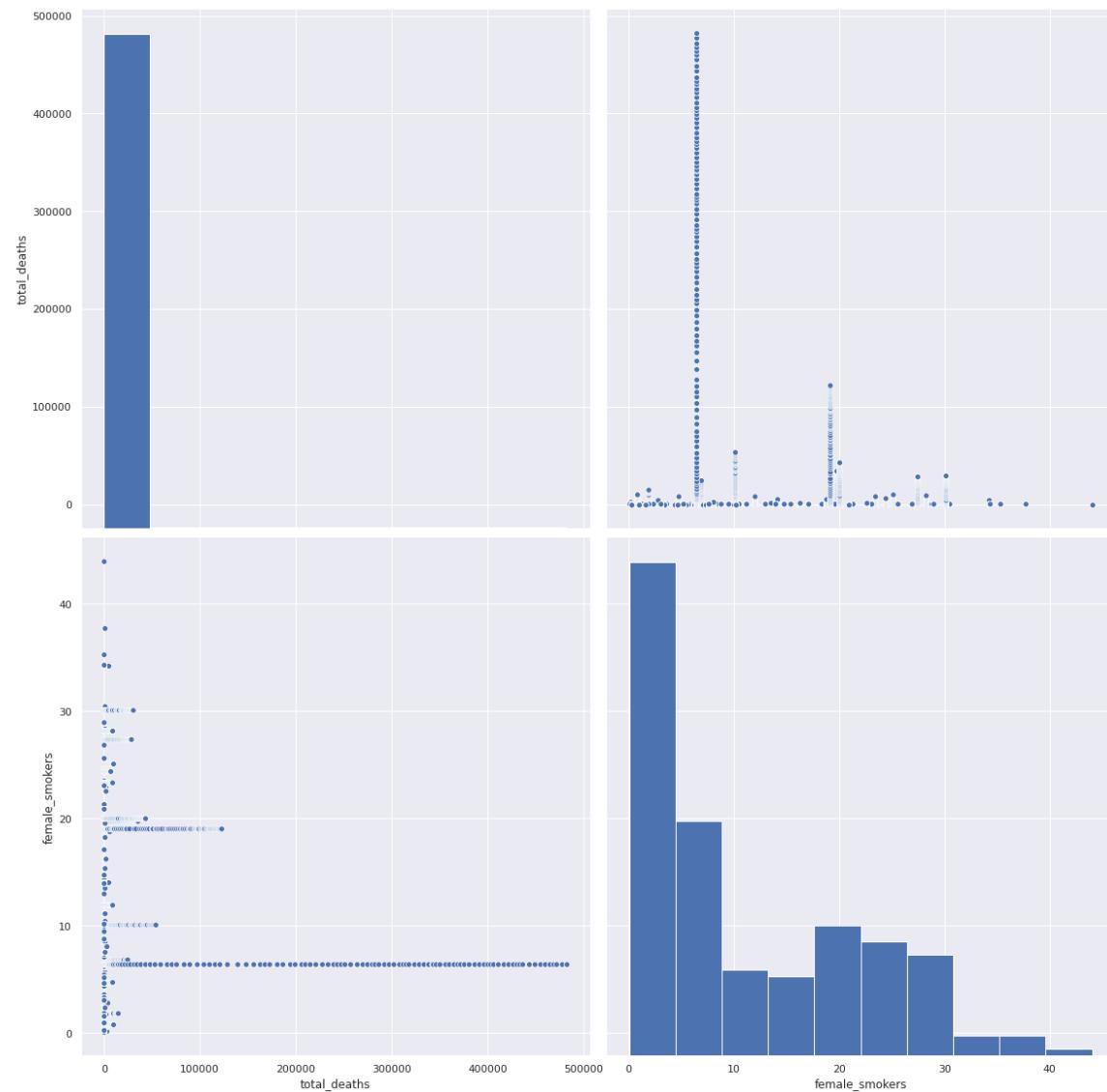


In [174]:

```
sns.pairplot(features, vars=["total_deaths", "female_smokers"], height=8)
```

Out[174]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c83f3940>
```

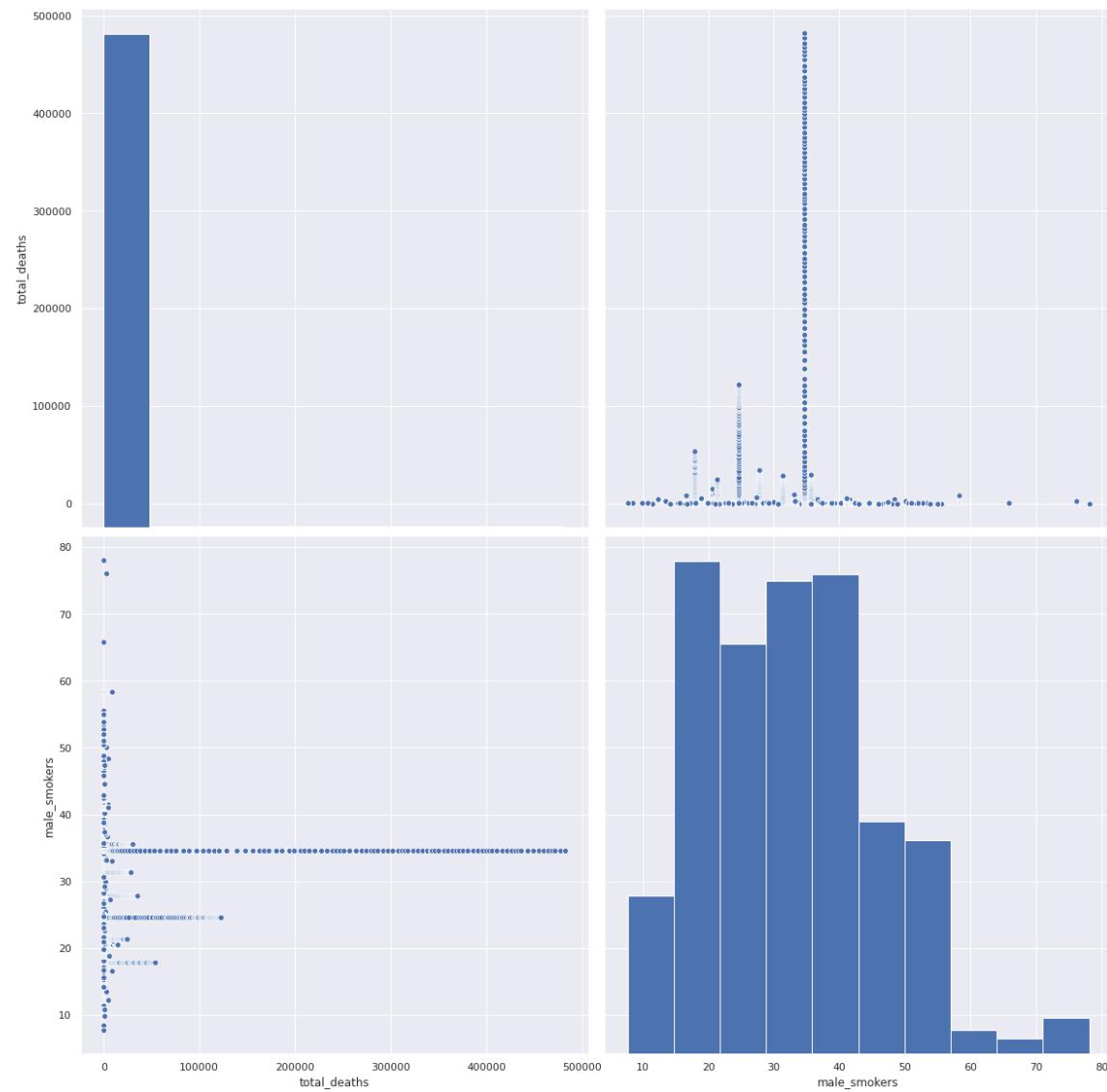


In [175]:

```
sns.pairplot(features, vars=["total_deaths", "male_smokers"], height=8)
```

Out[175]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c7549940>
```

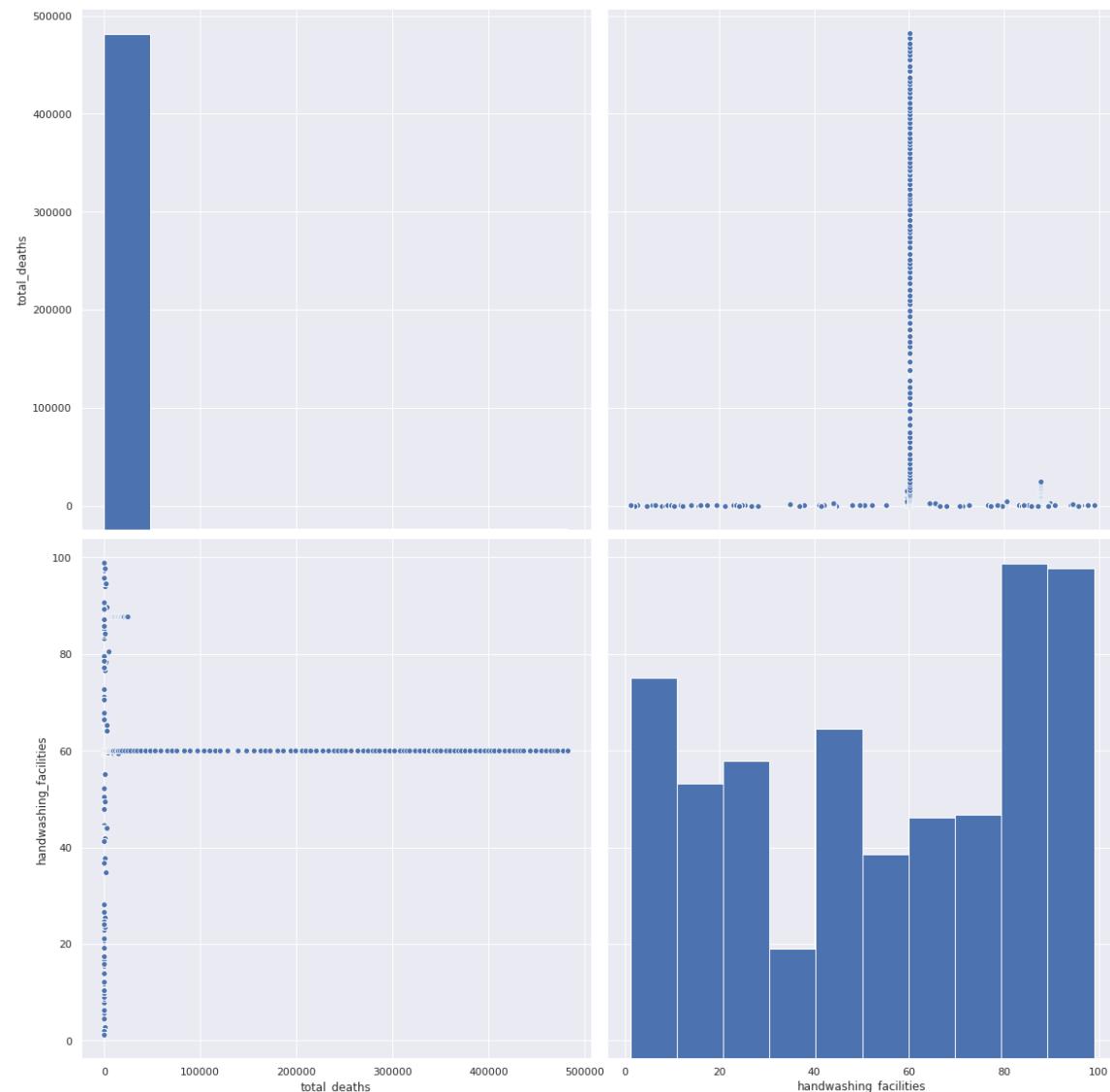


In [176]:

```
sns.pairplot(features, vars=["total_deaths", "handwashing_facilities"], height=8)
```

Out[176]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c73264a8>
```

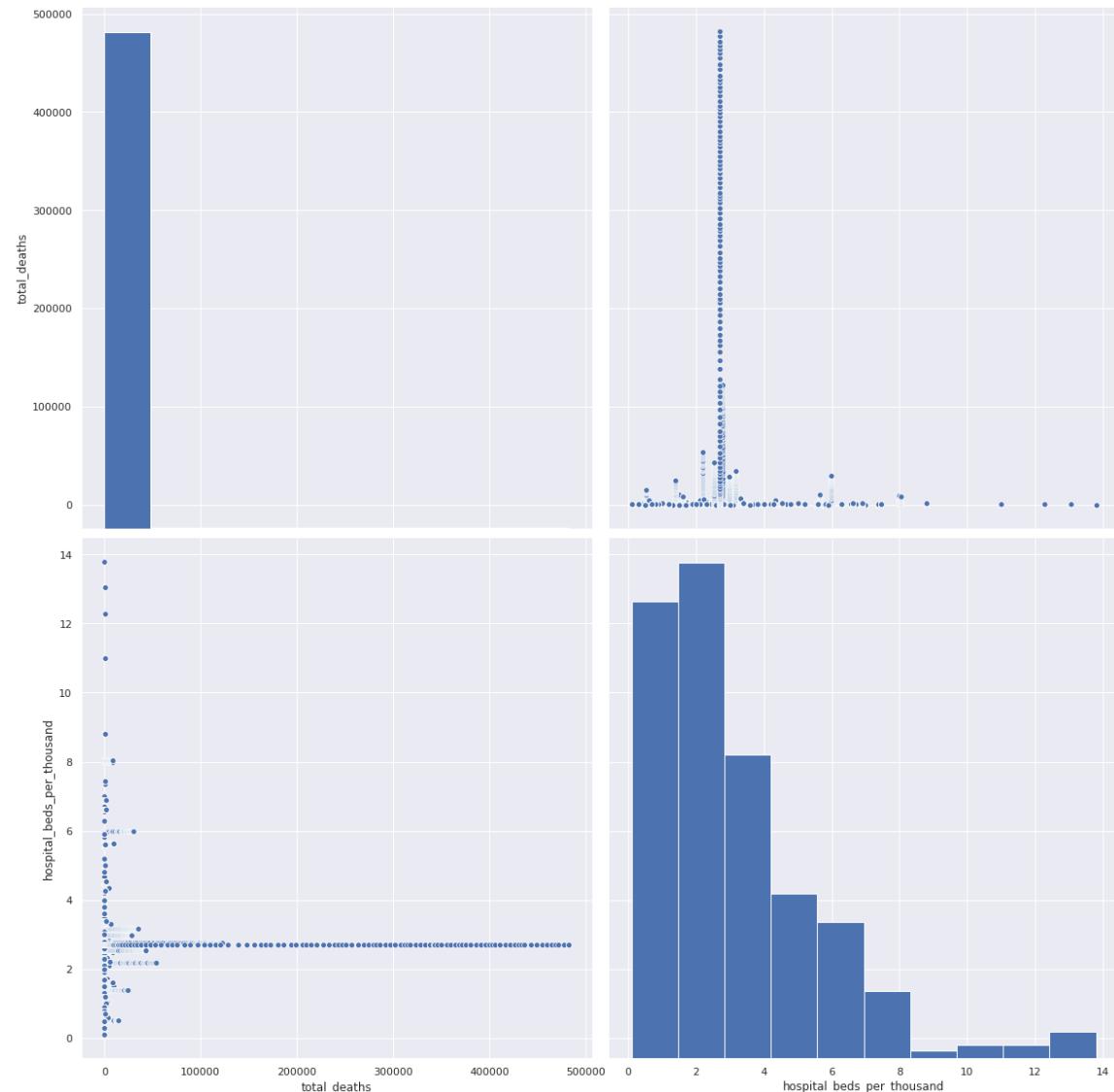


In [177]:

```
sns.pairplot(features, vars=["total_deaths", "hospital_beds_per_thousand"], height=8)
```

Out[177]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c70c9a20>
```

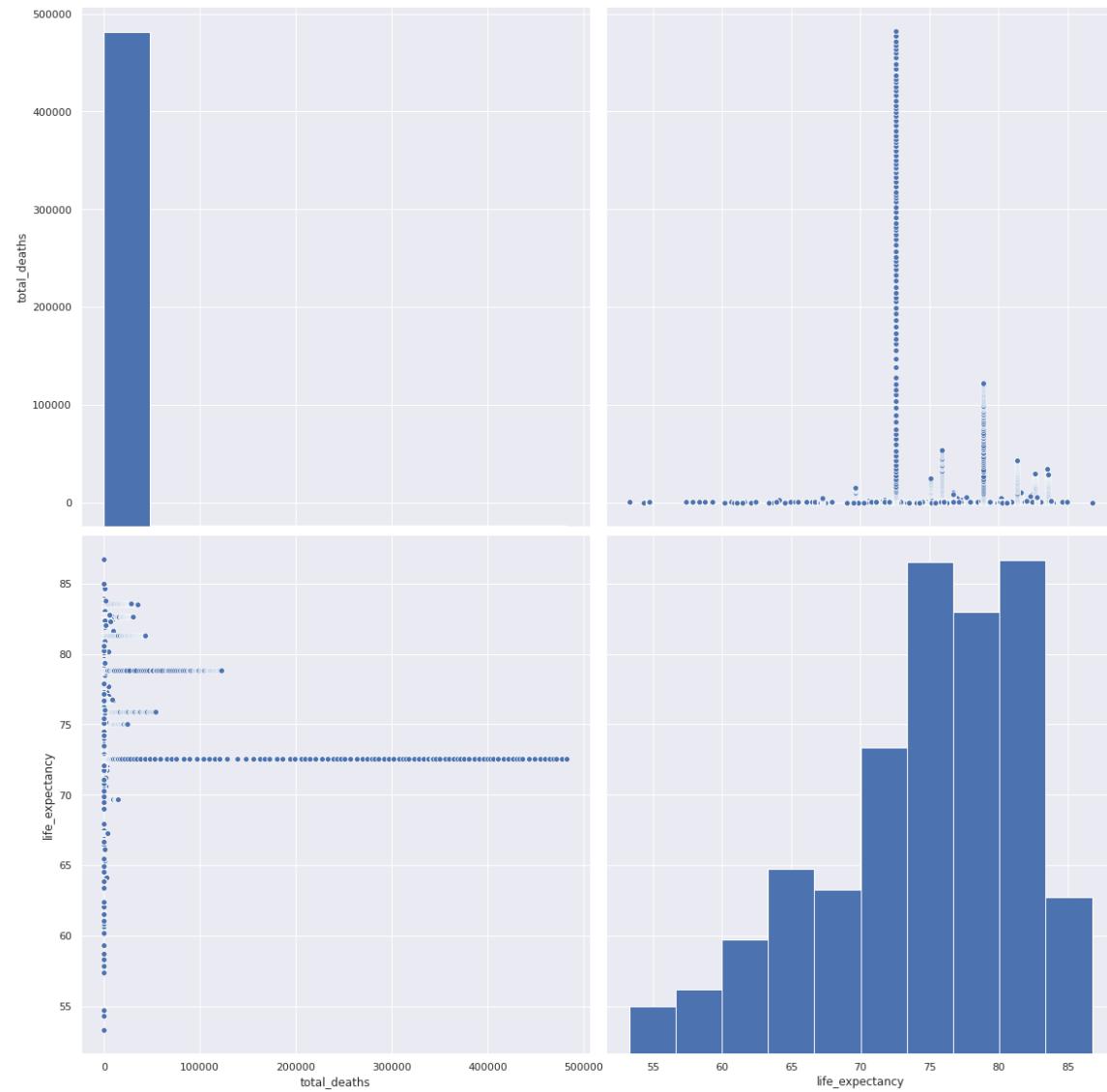


In [178]:

```
sns.pairplot(features, vars=["total_deaths", "life_expectancy"], height=8)
```

Out[178]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c6ec97f0>
```

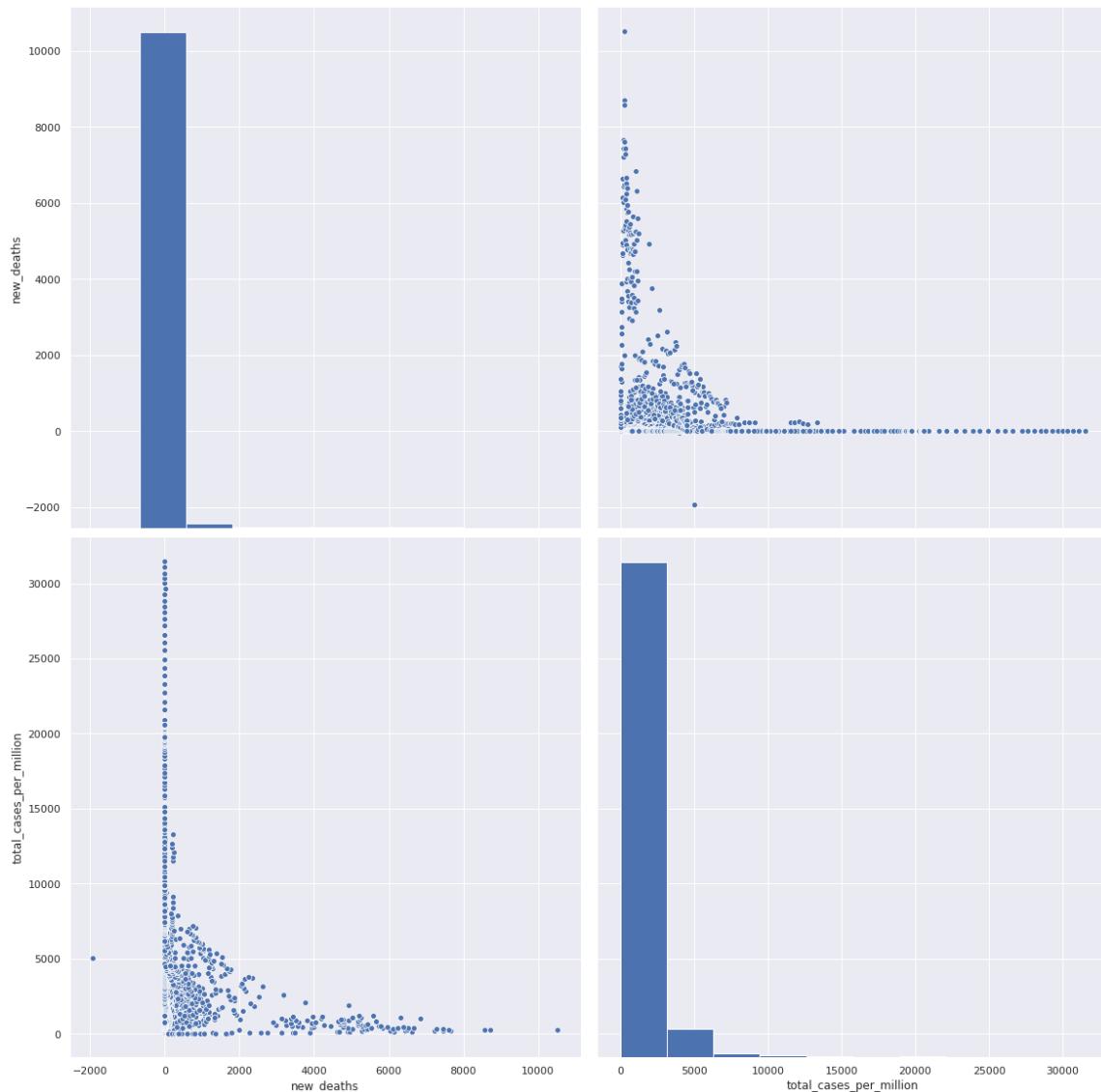


In [179]:

```
sns.pairplot(features, vars=["new_deaths", "total_cases_per_million"], height=8)
```

Out[179]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c6cca550>
```

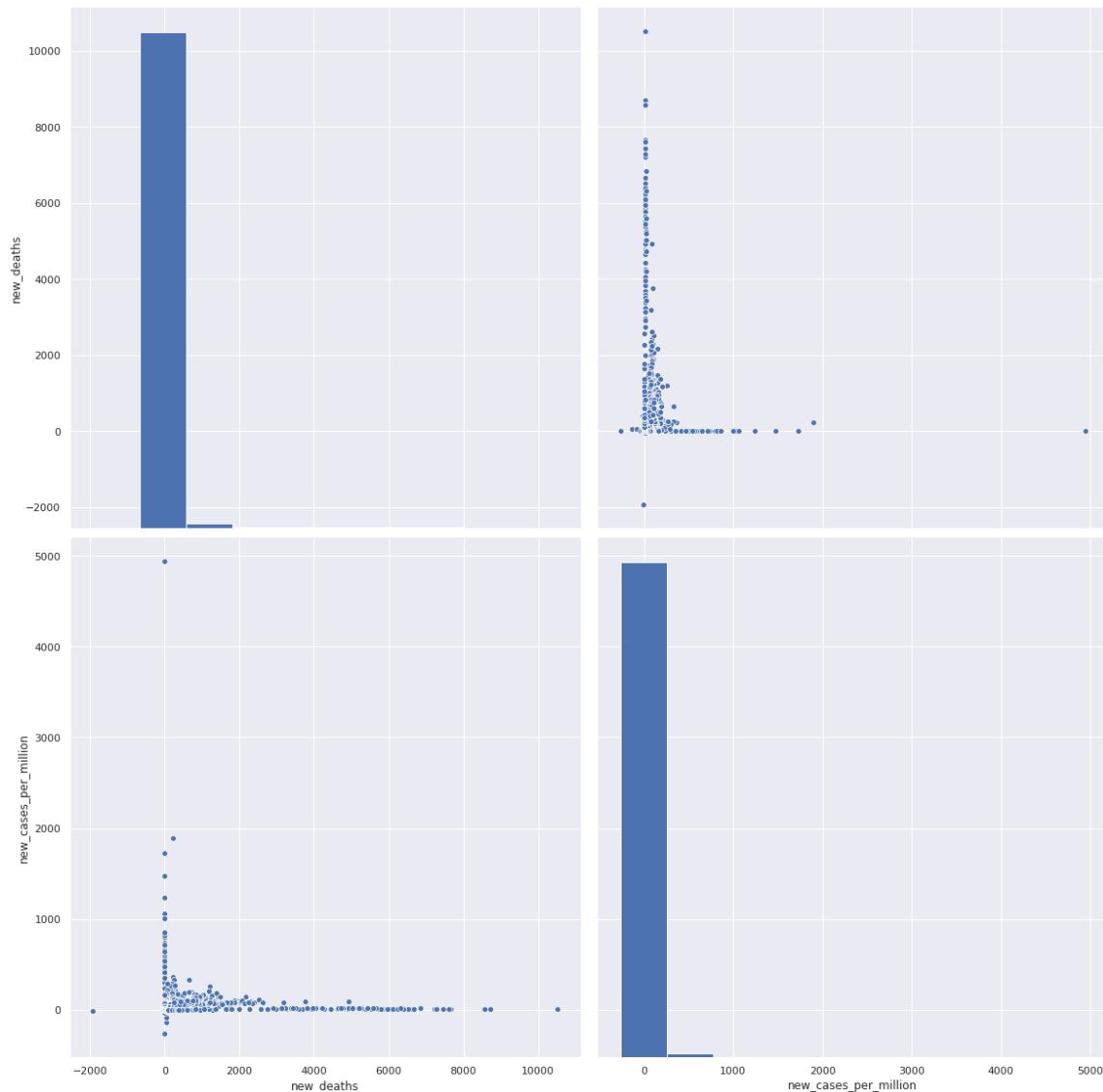


In [180]:

```
sns.pairplot(features, vars=["new_deaths", "new_cases_per_million"], height=8)
```

Out[180]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c6b2e710>
```

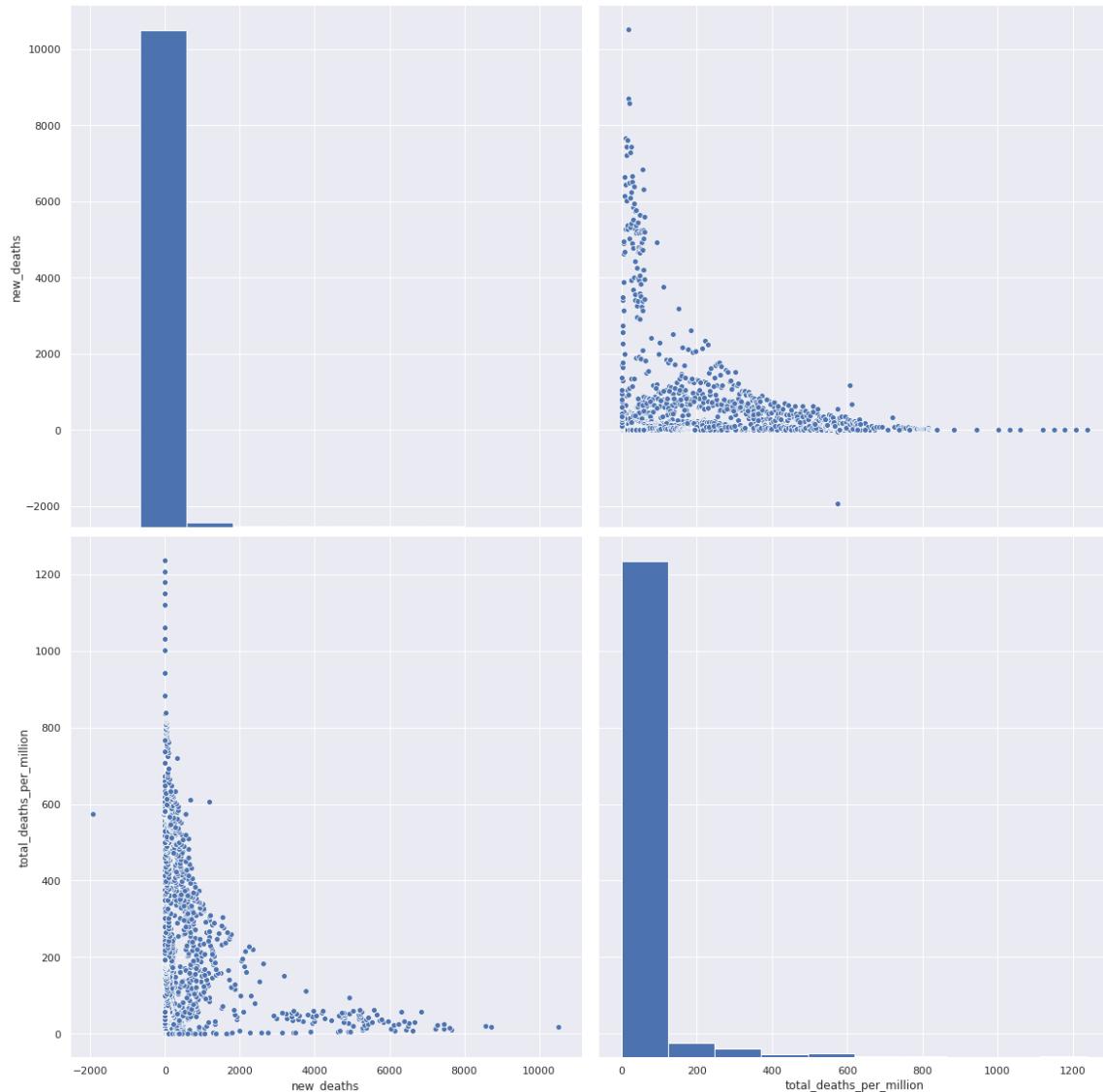


In [181]:

```
sns.pairplot(features, vars=["new_deaths", "total_deaths_per_million"], height=8)
```

Out[181]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c6fe39e8>
```

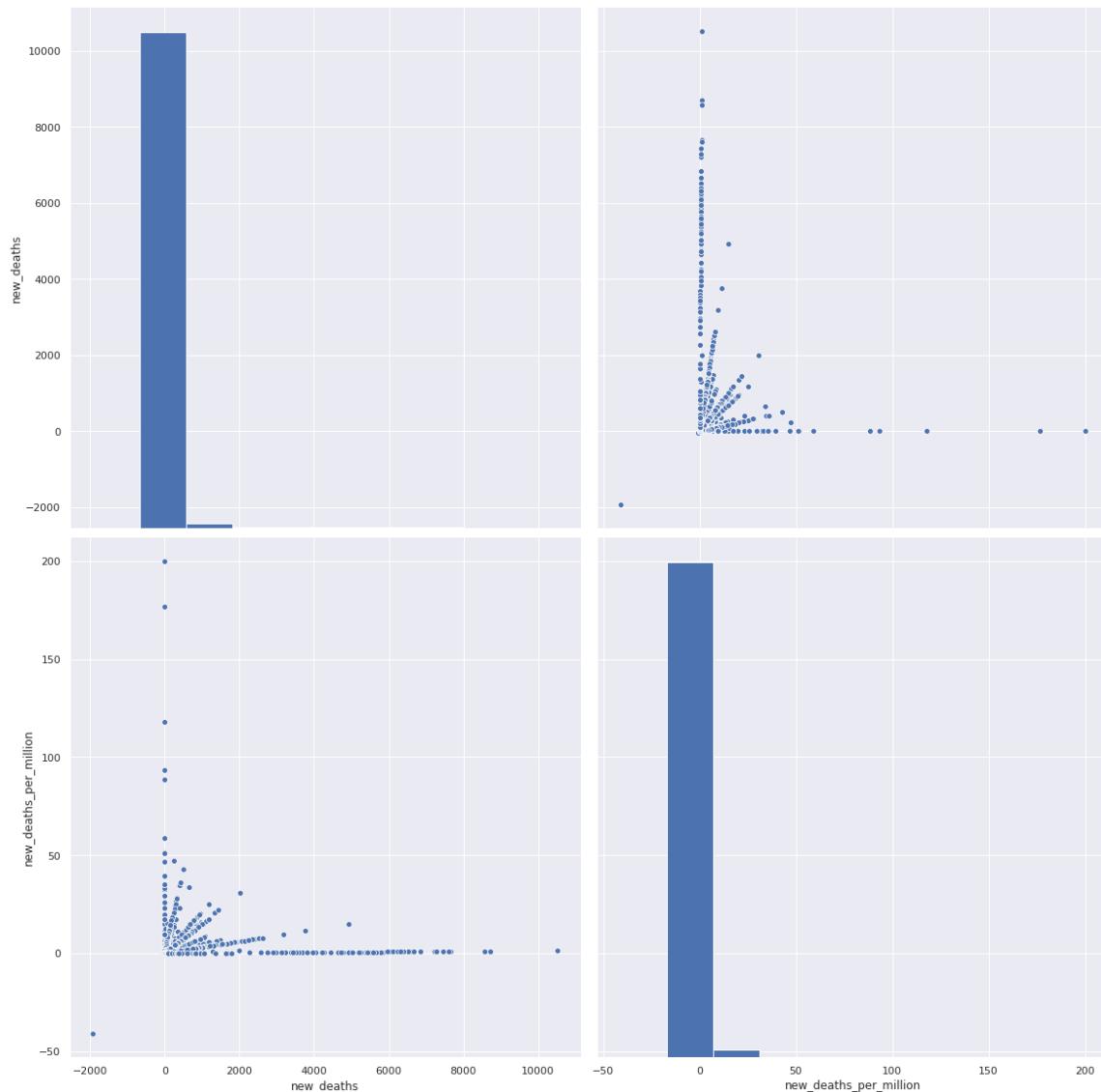


In [182]:

```
sns.pairplot(features, vars=["new_deaths", "new_deaths_per_million"], height=8)
```

Out[182]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c69134e0>
```

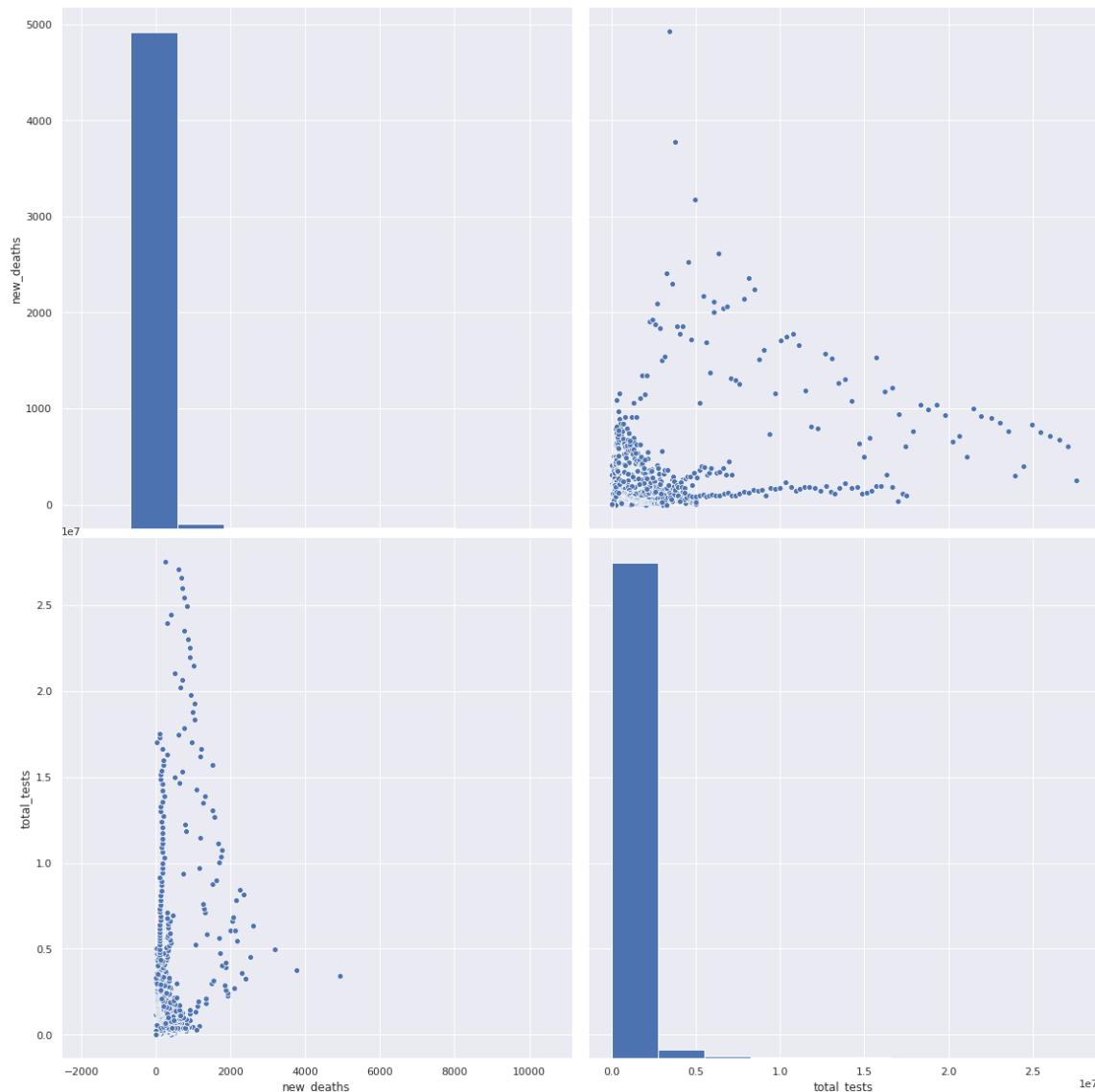


In [183]:

```
sns.pairplot(features, vars=["new_deaths", "total_tests"], height=8)
```

Out[183]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c6640ba8>
```

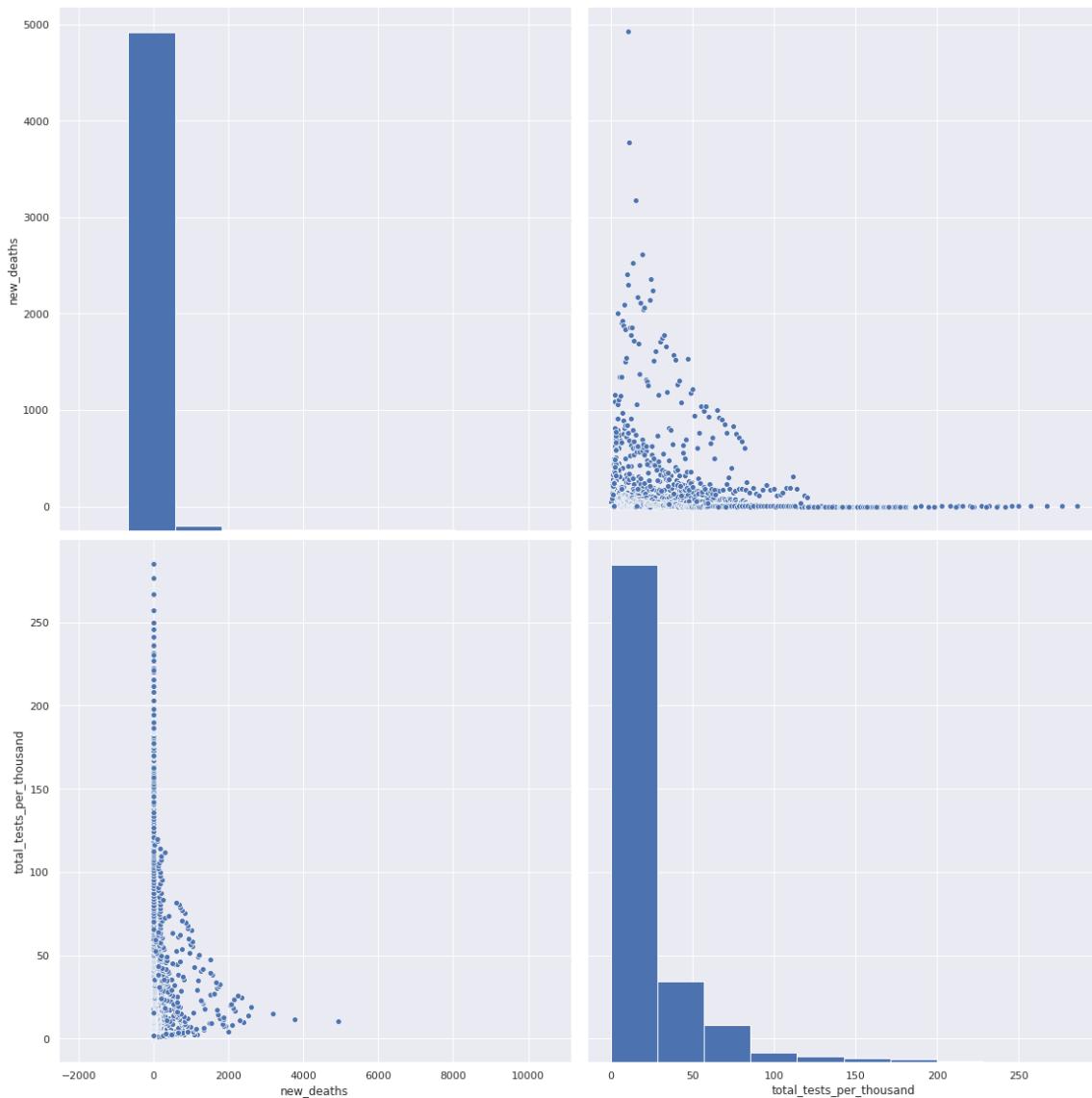


In [184]:

```
sns.pairplot(features, vars=["new_deaths", "total_tests_per_thousand"], height=8)
```

Out[184]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c6a66390>
```

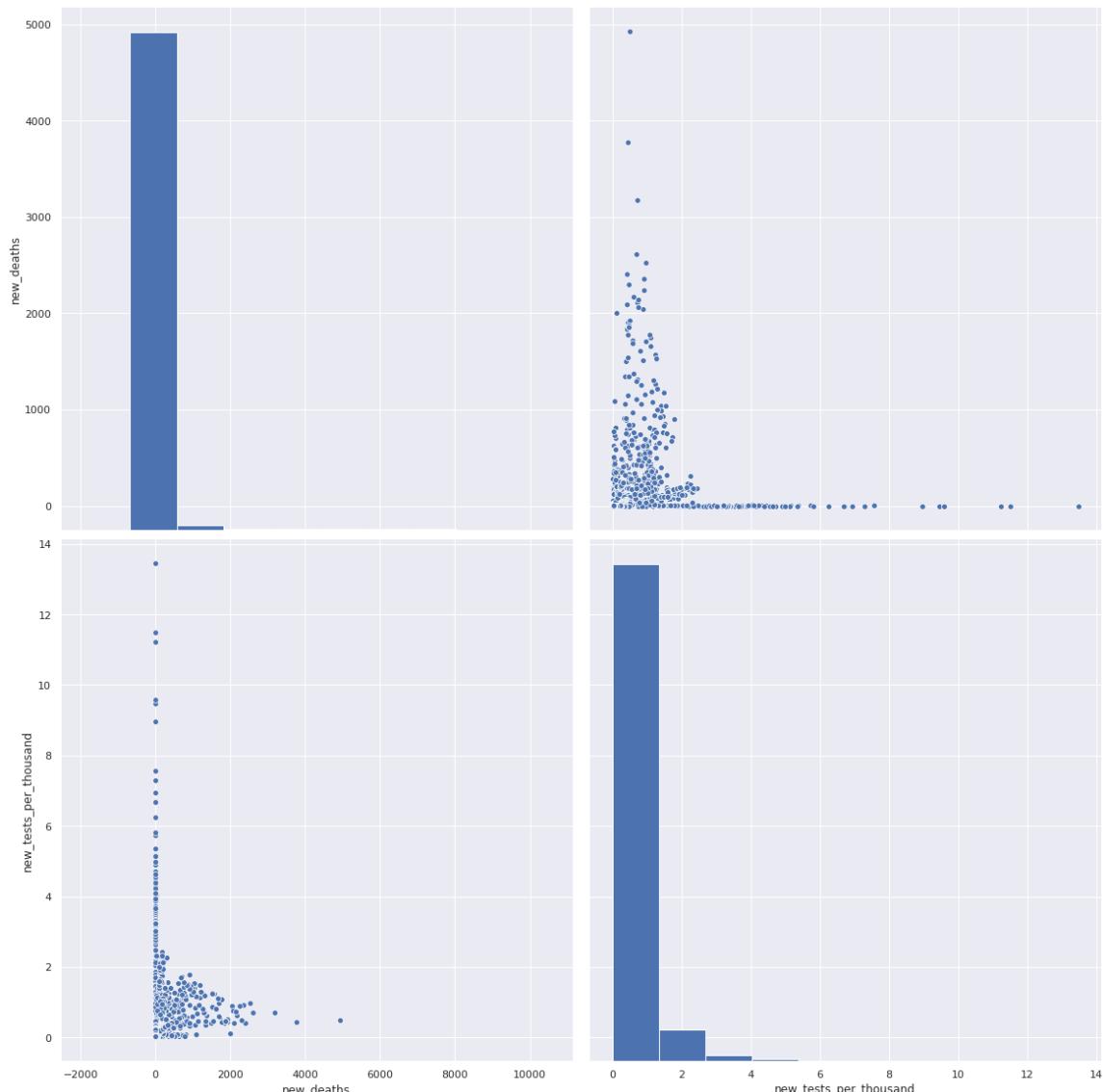


In [185]:

```
sns.pairplot(features, vars=["new_deaths", "new_tests_per_thousand"], height=8)
```

Out[185]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c61d8fd0>
```

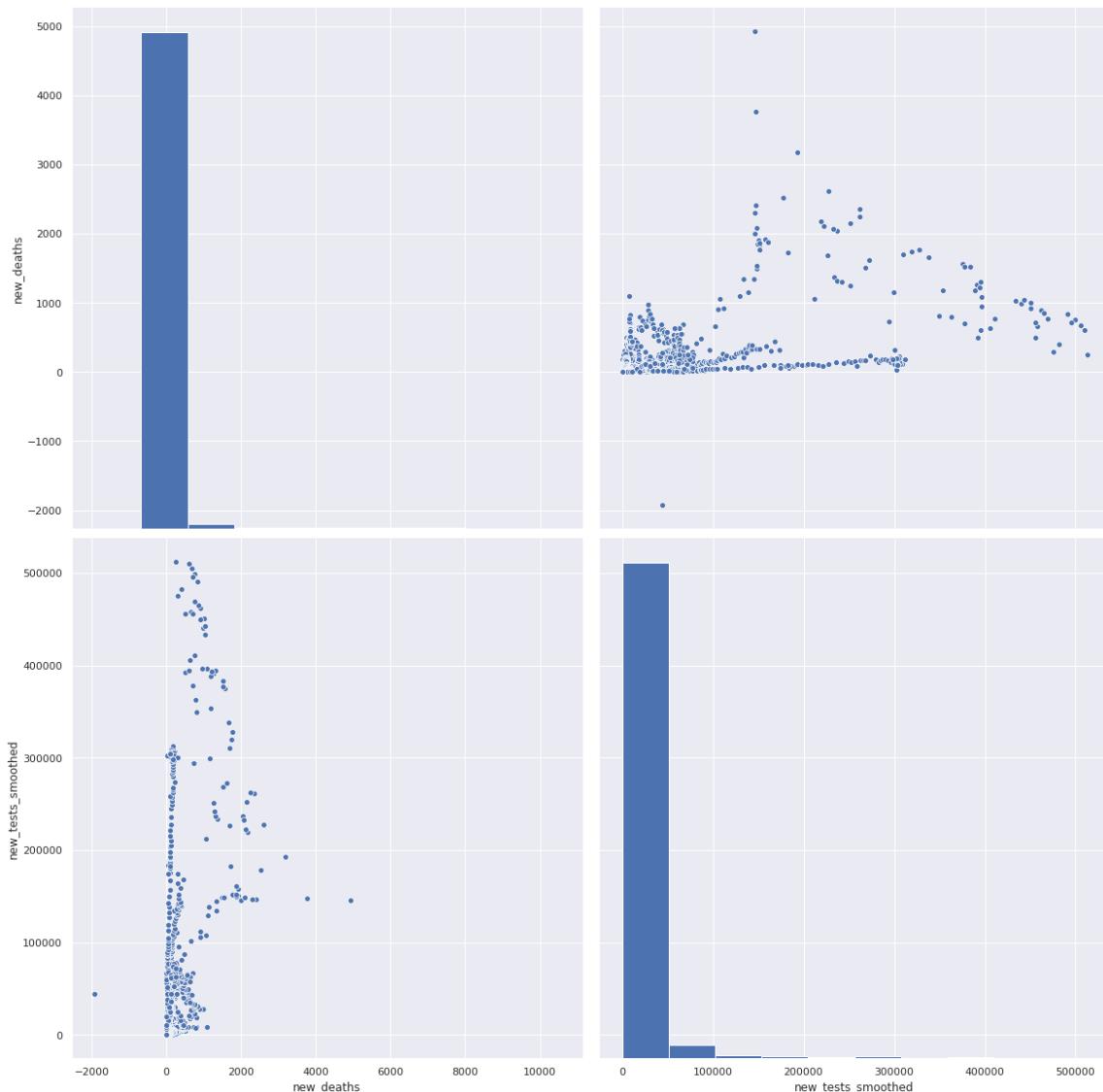


In [186]:

```
sns.pairplot(features, vars=["new_deaths", "new_tests_smoothed"], height=8)
```

Out[186]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c5ed3978>
```

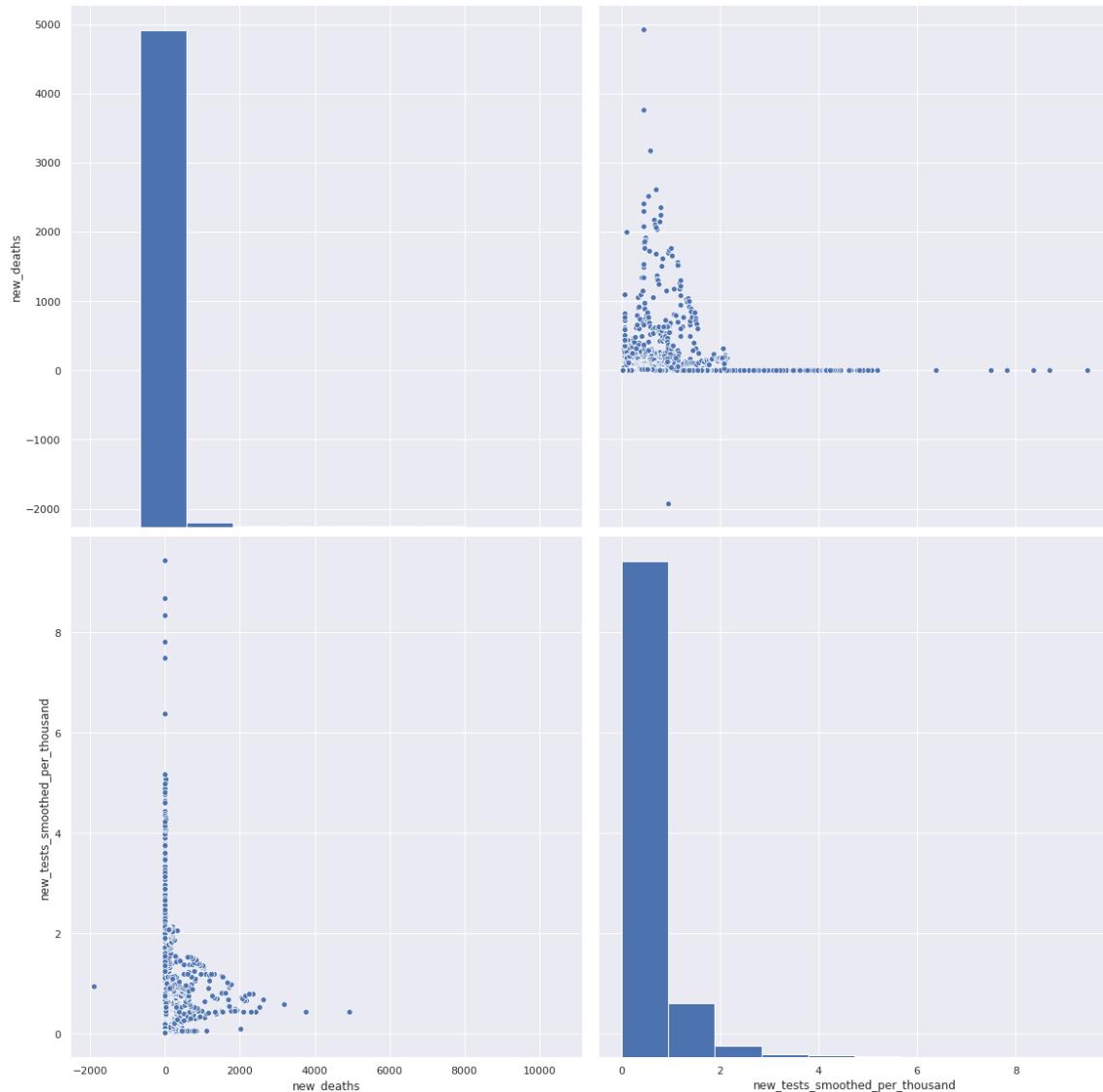


In [187]:

```
sns.pairplot(features, vars=["new_deaths", "new_tests_smoothed_per_thousand"], height=8)
```

Out[187]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c5ef30b8>
```

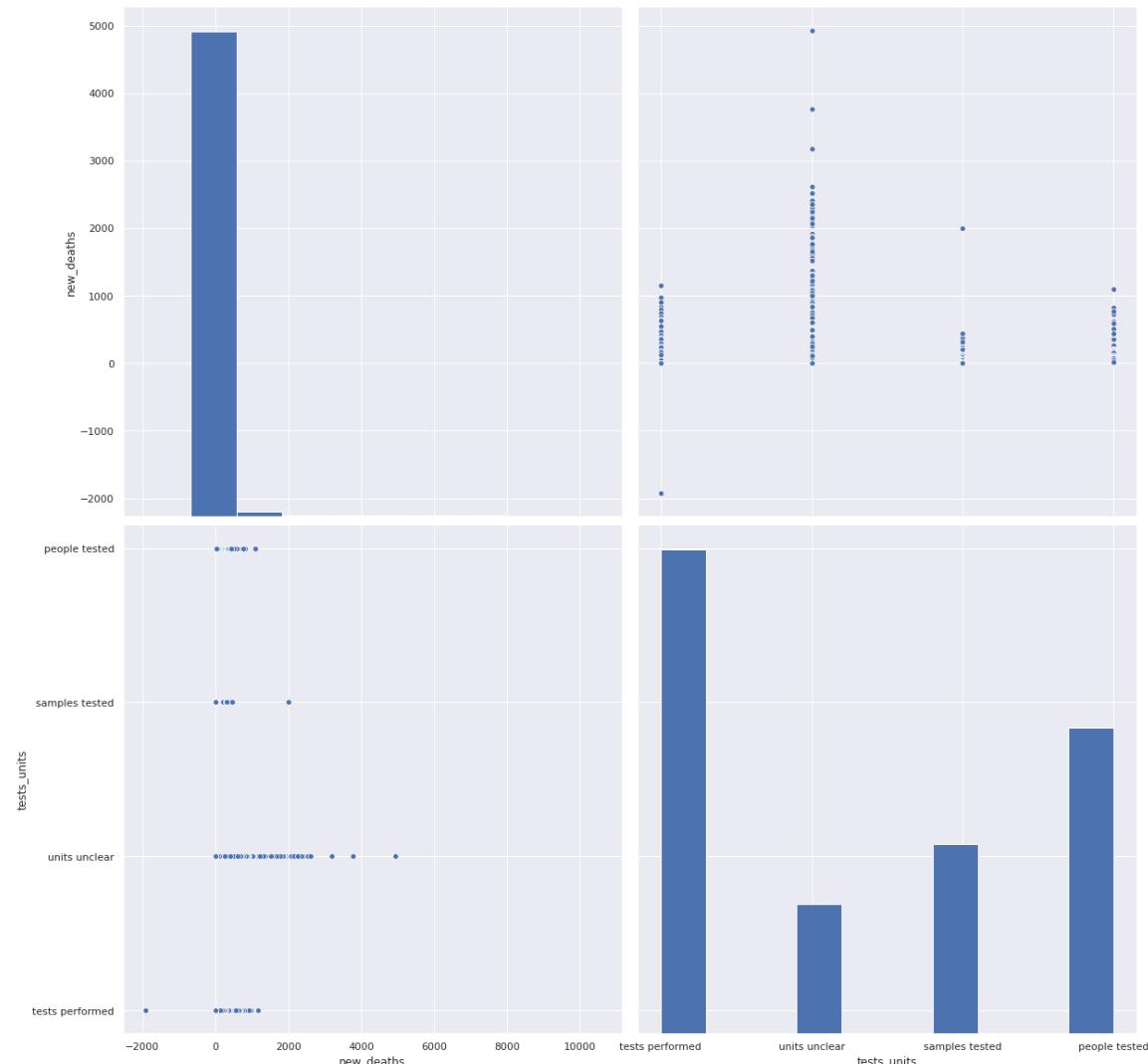


In [188]:

```
sns.pairplot(features, vars=["new_deaths", "tests_units"], height=8)
```

Out[188]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c5ccfcc0>
```

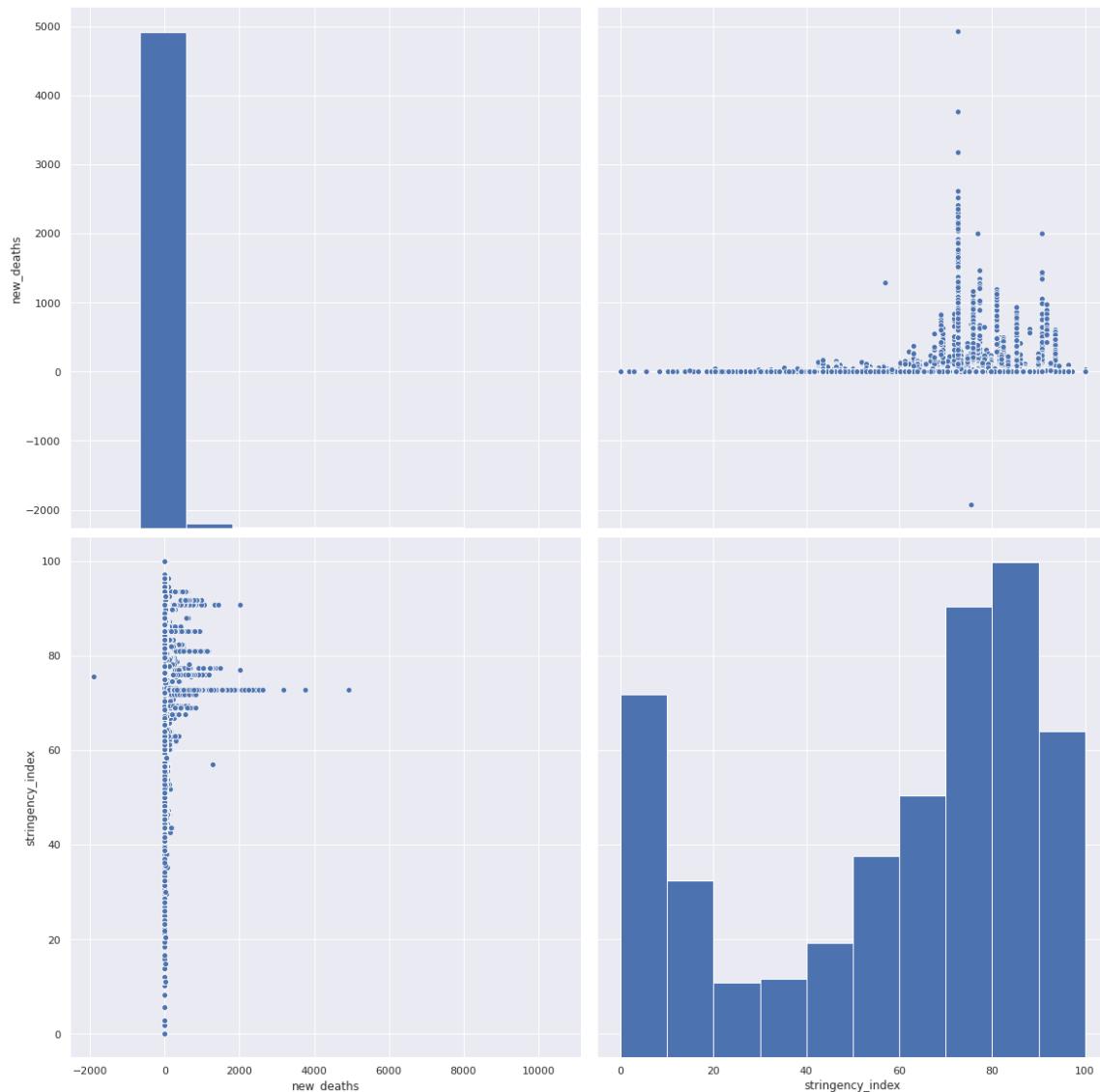


In [189]:

```
sns.pairplot(features, vars=["new_deaths", "stringency_index"], height=8)
```

Out[189]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c5aec30>
```

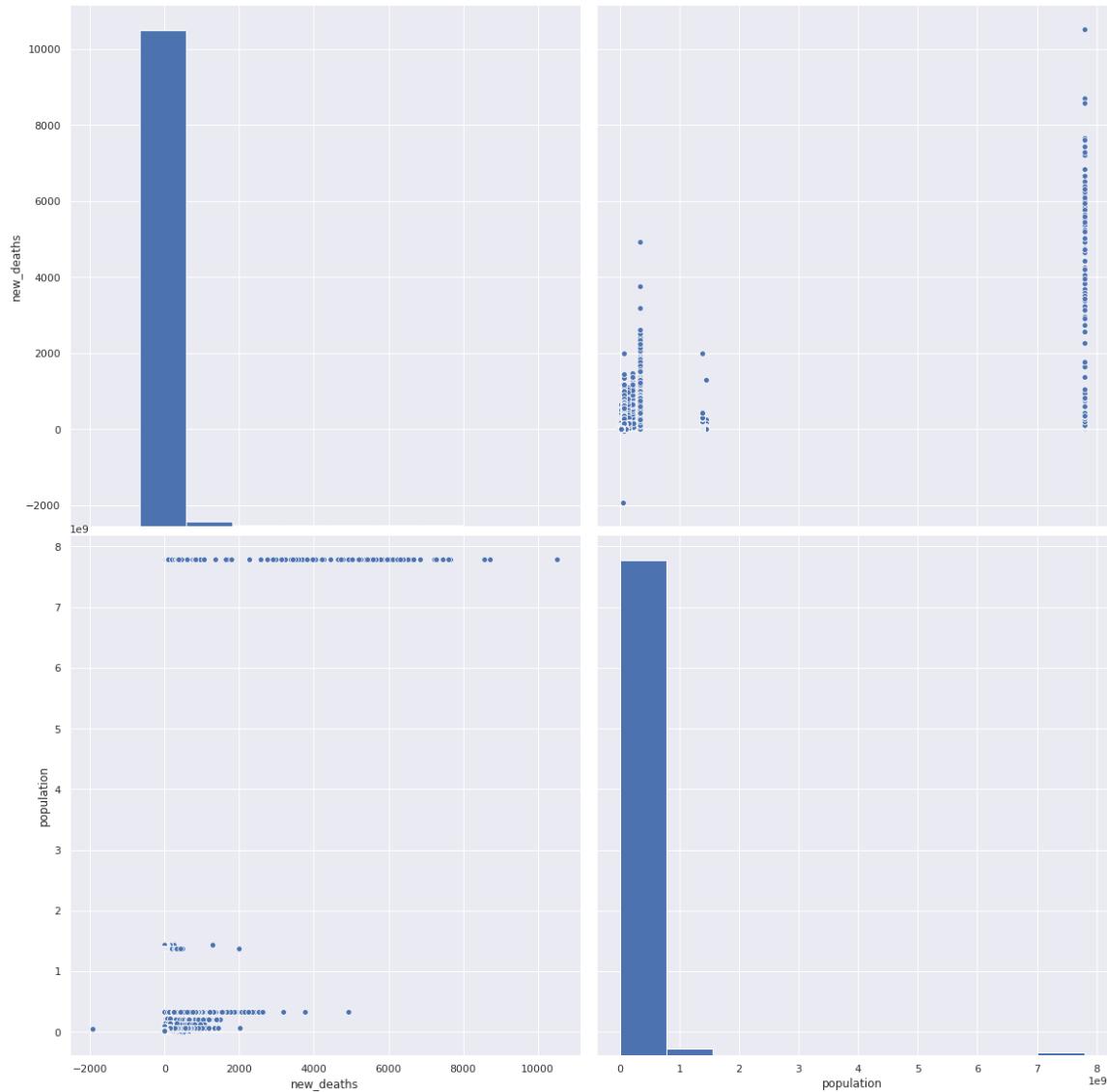


In [190]:

```
sns.pairplot(features, vars=["new_deaths", "population"], height=8)
```

Out[190]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c56e4cf8>
```

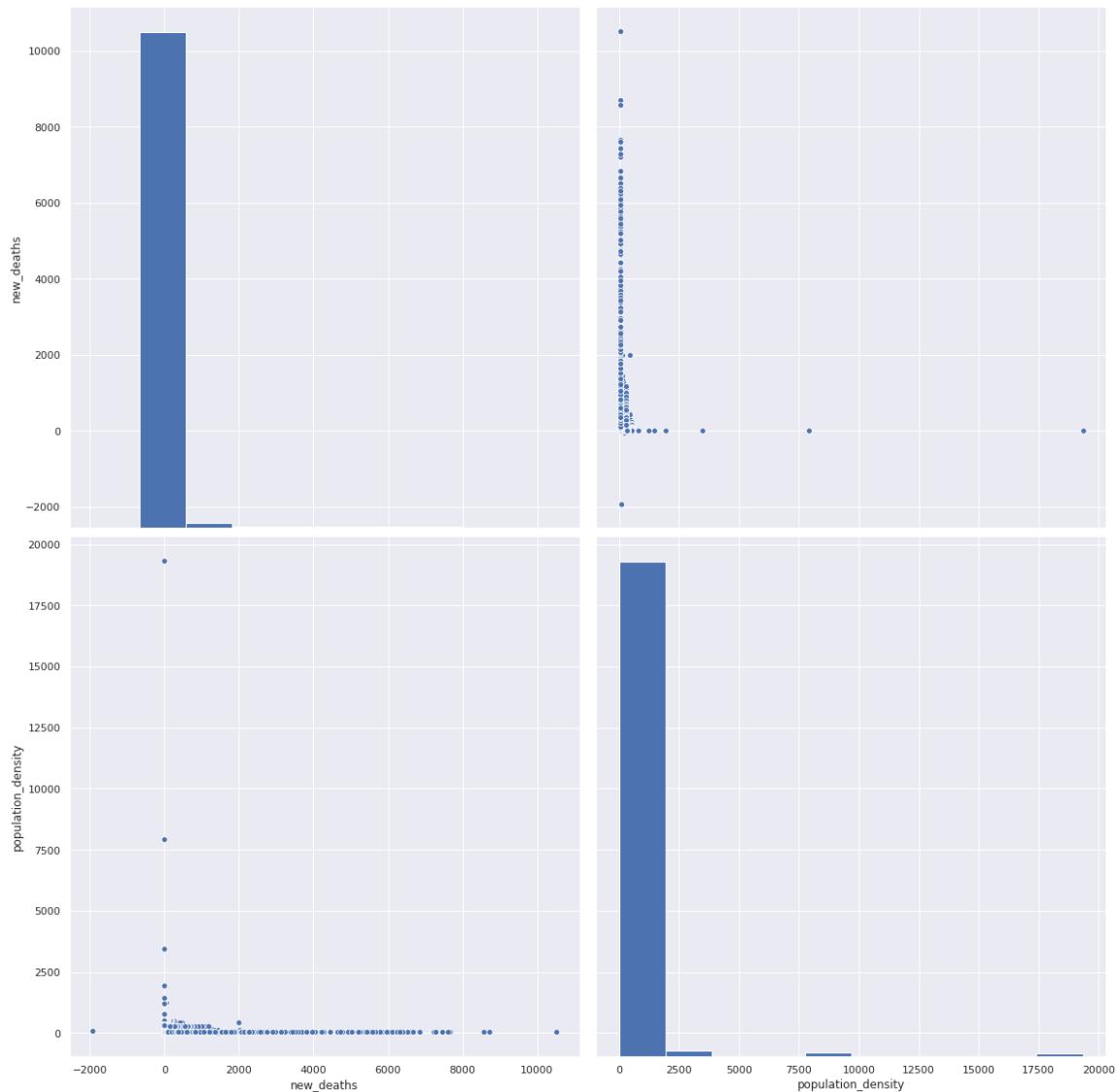


In [191]:

```
sns.pairplot(features, vars=["new_deaths", "population_density"], height=8)
```

Out[191]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c54f1c88>
```

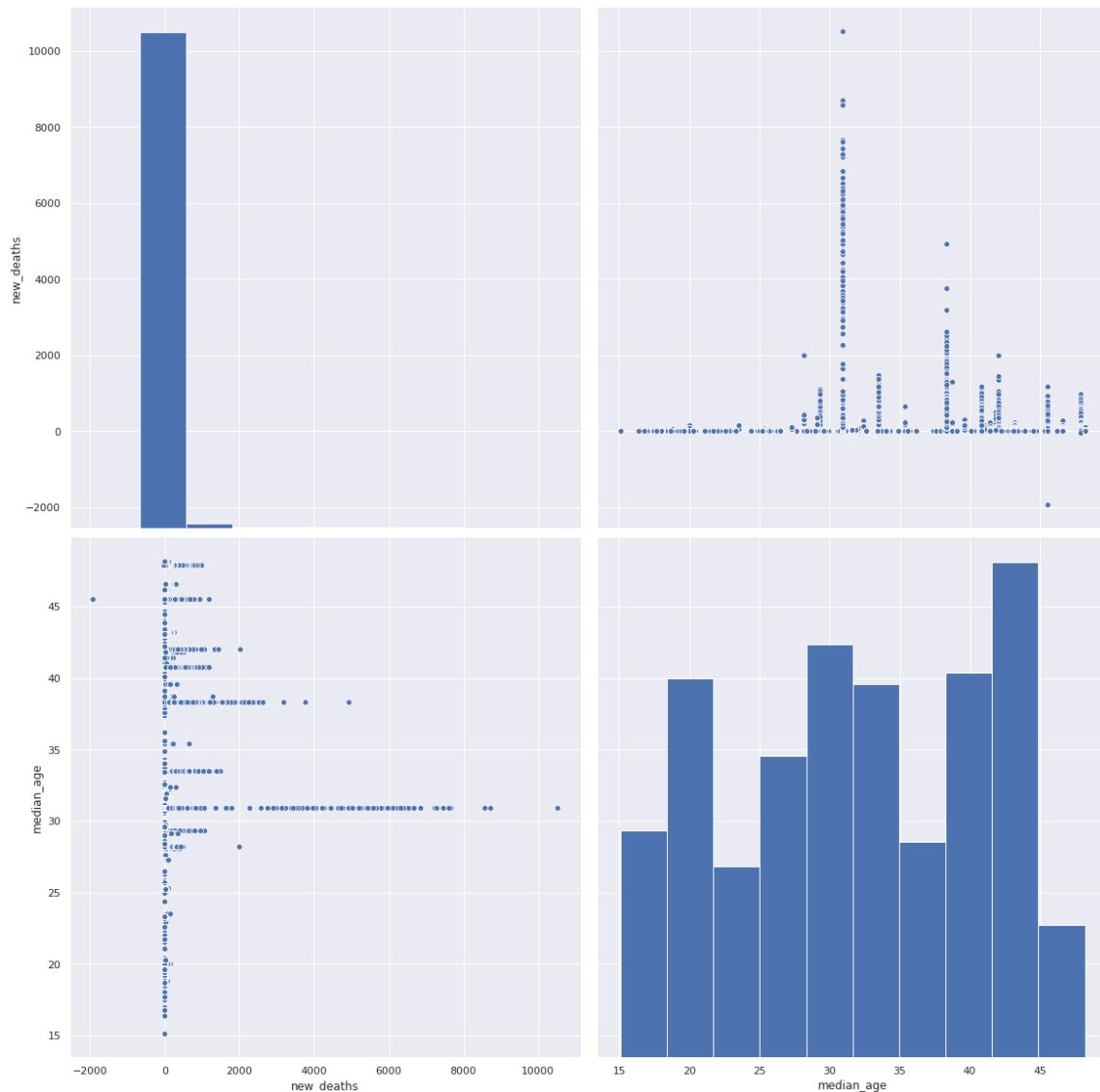


In [192]:

```
sns.pairplot(features, vars=["new_deaths", "median_age"], height=8)
```

Out[192]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c52d7320>
```

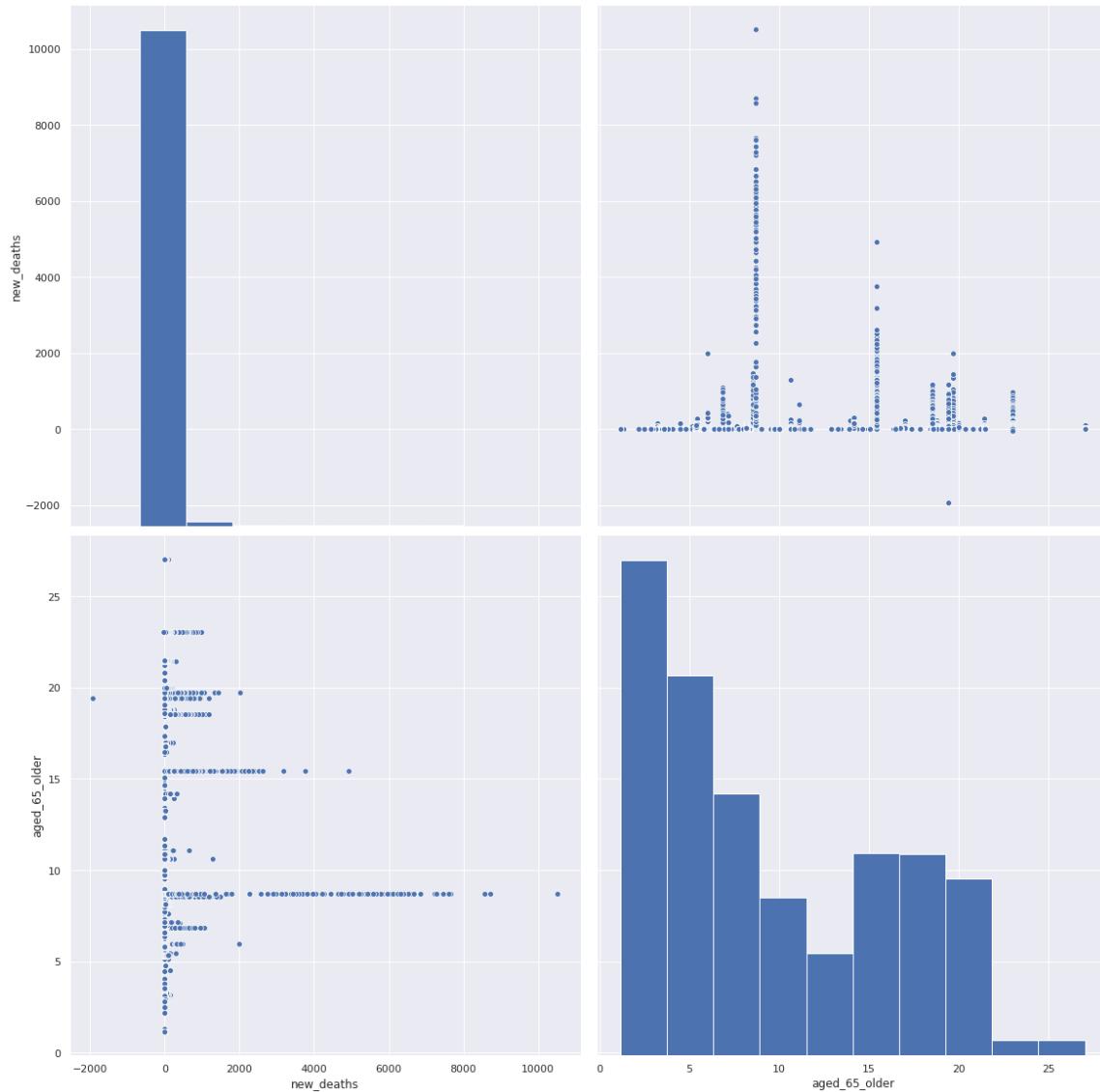


In [193]:

```
sns.pairplot(features, vars=["new_deaths", "aged_65_older"], height=8)
```

Out[193]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c5111b70>
```

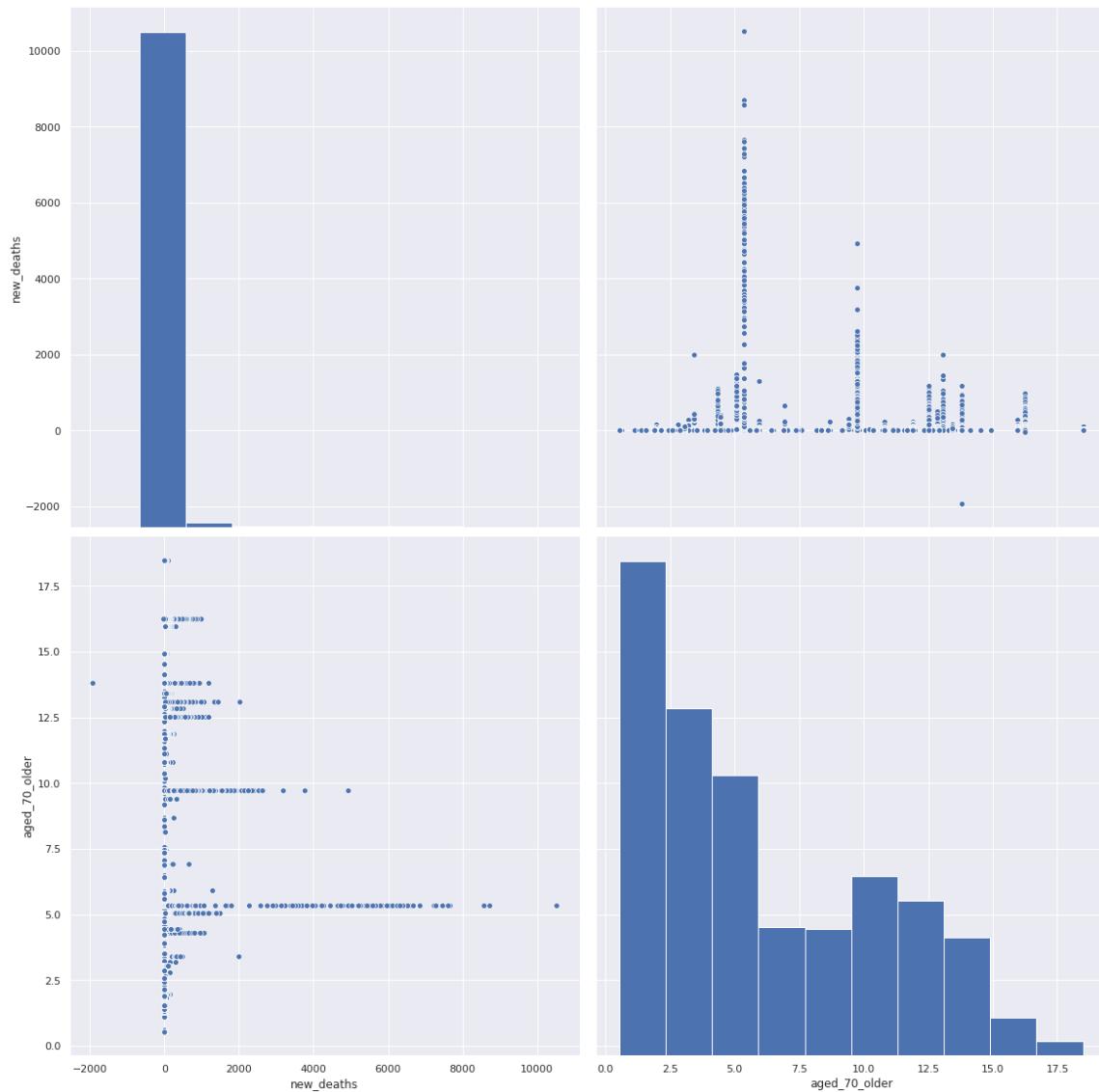


In [194]:

```
sns.pairplot(features, vars=["new_deaths", "aged_70_older"], height=8)
```

Out[194]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c4ea8cf8>
```

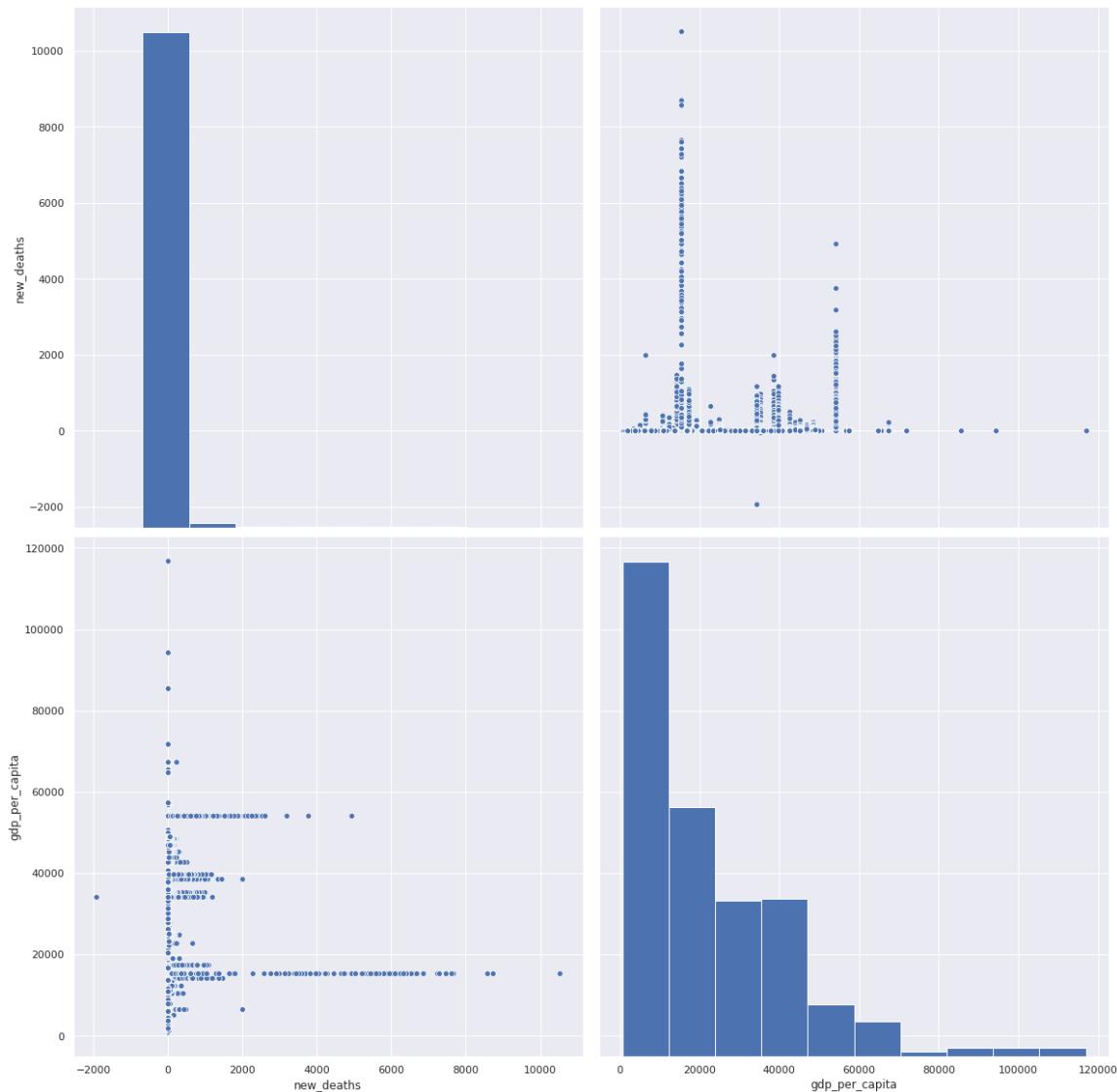


In [195]:

```
sns.pairplot(features, vars=["new_deaths", "gdp_per_capita"], height=8)
```

Out[195]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c4d2fa90>
```

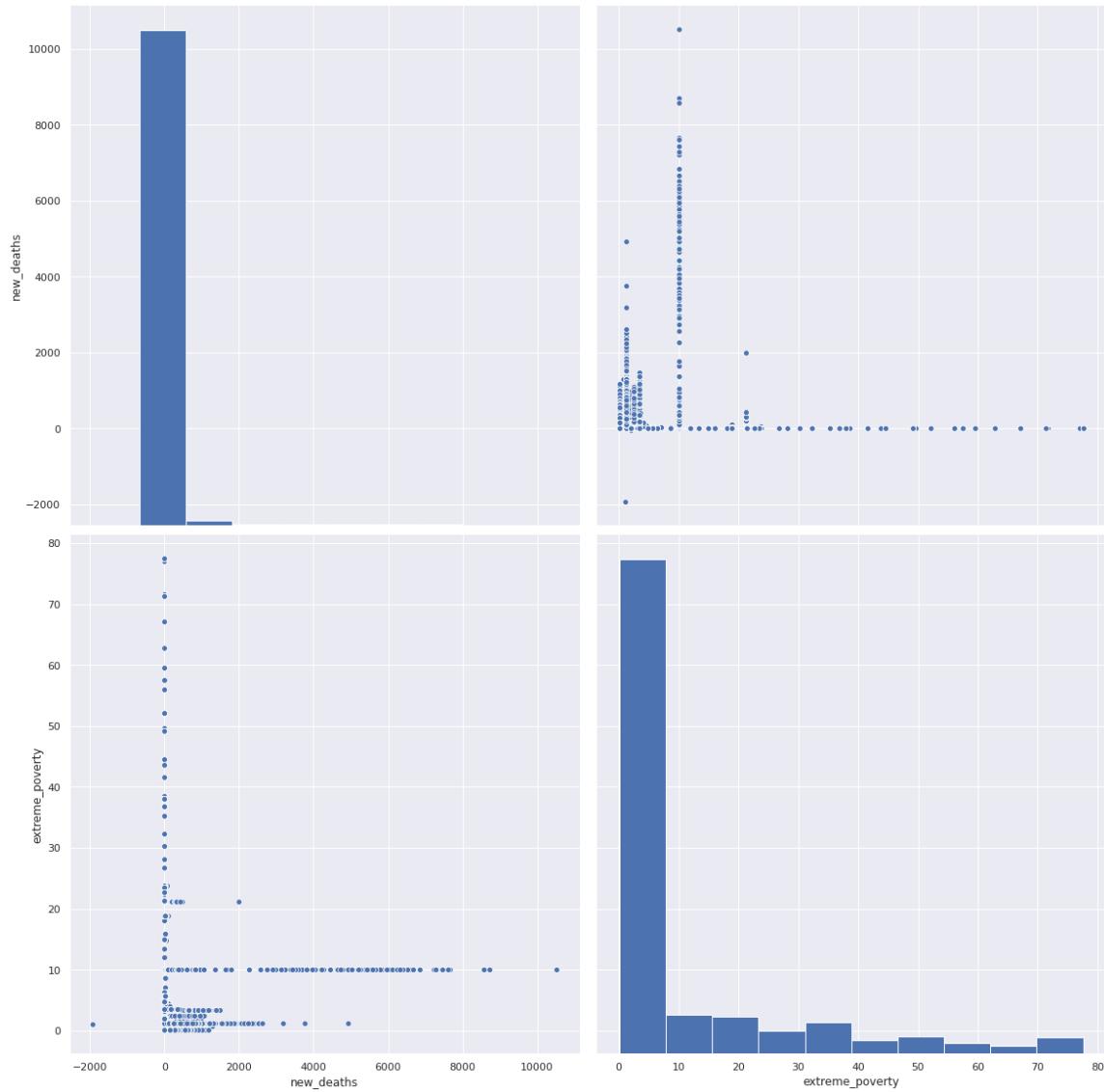


In [196]:

```
sns.pairplot(features, vars=["new_deaths", "extreme_poverty"], height=8)
```

Out[196]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c4b355f8>
```

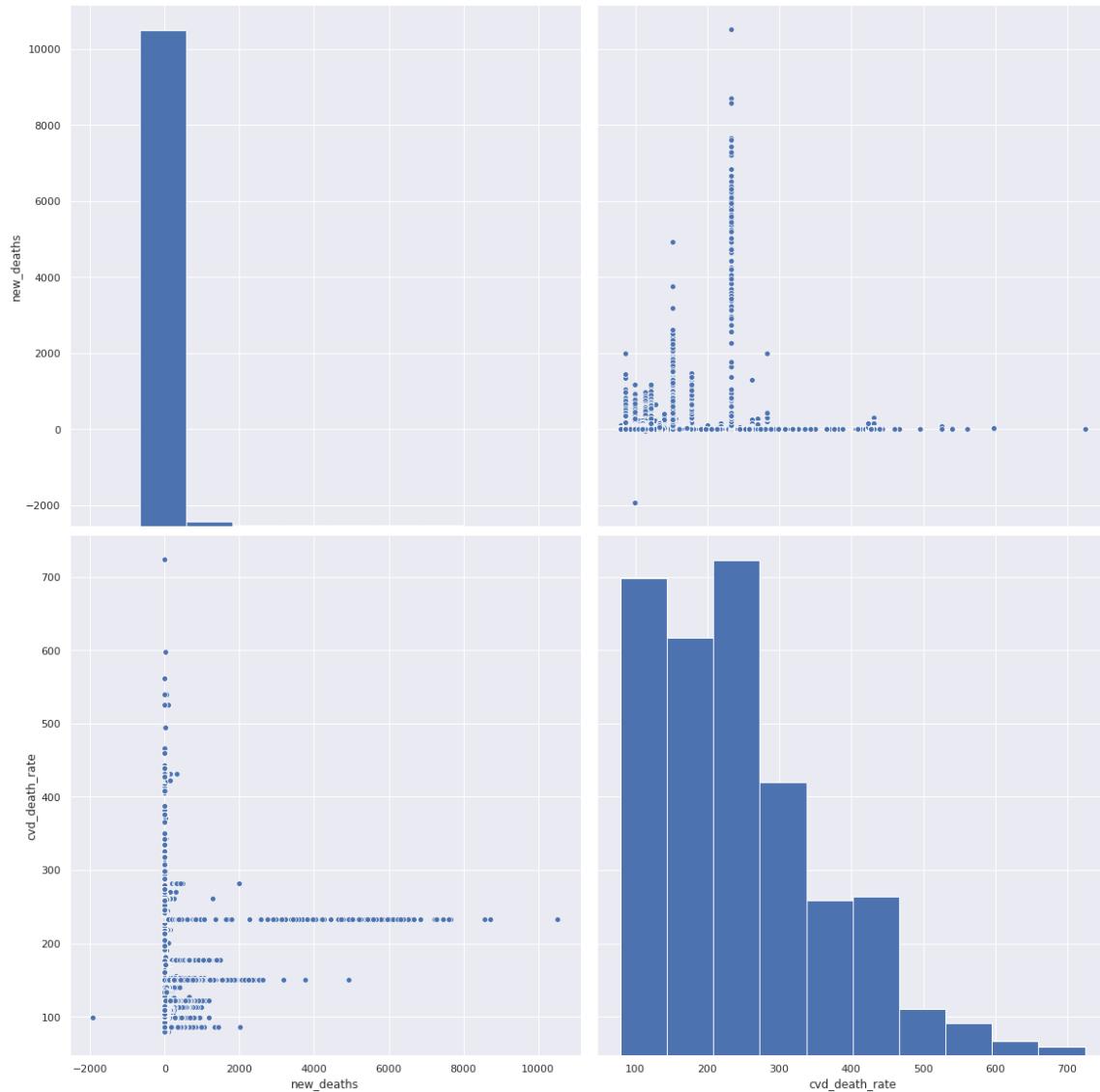


In [197]:

```
sns.pairplot(features, vars=["new_deaths", "cvd_death_rate"], height=8)
```

Out[197]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c48669e8>
```

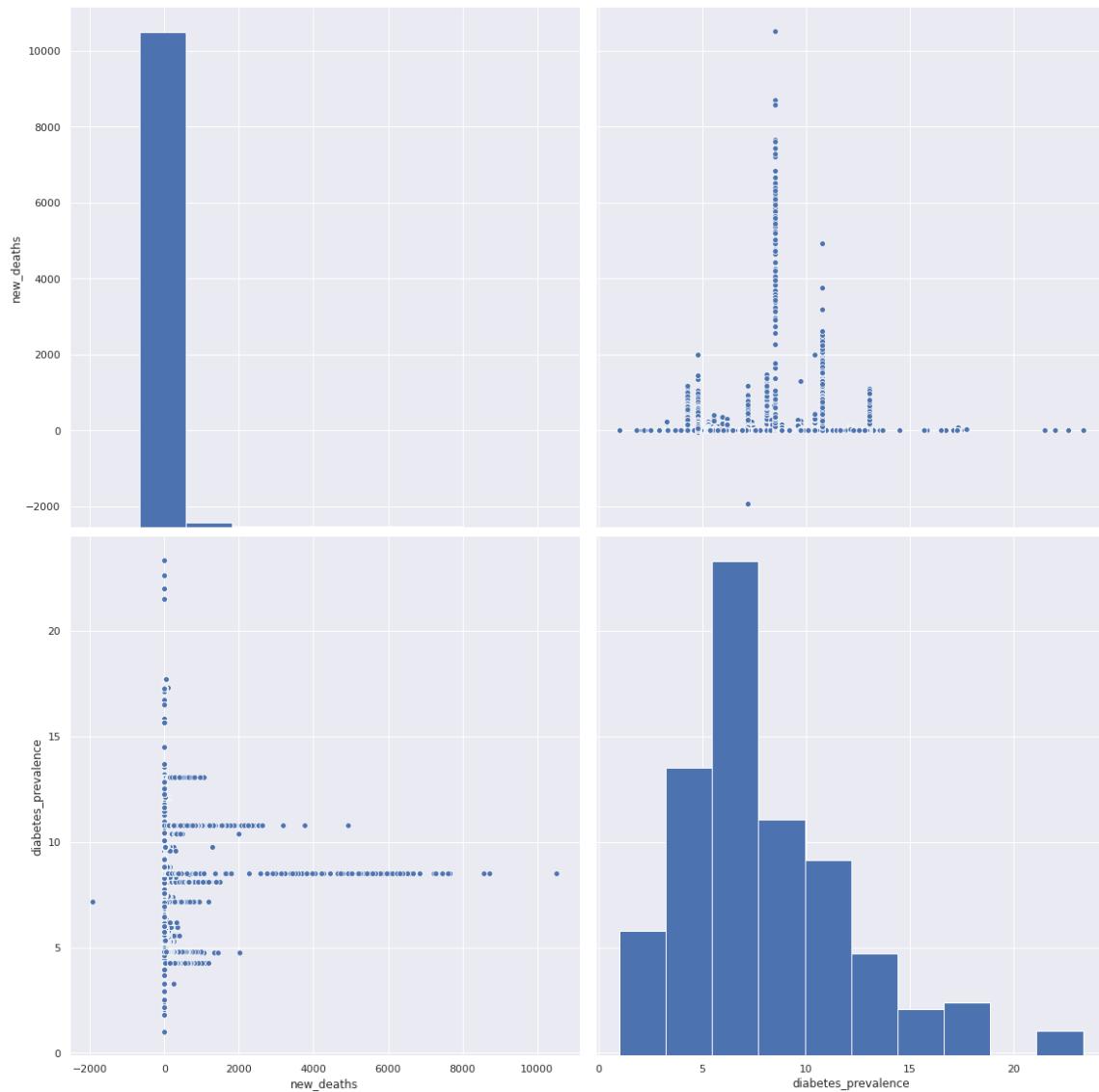


In [198]:

```
sns.pairplot(features, vars=["new_deaths", "diabetes_prevalence"], height=8)
```

Out[198]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c47a1748>
```

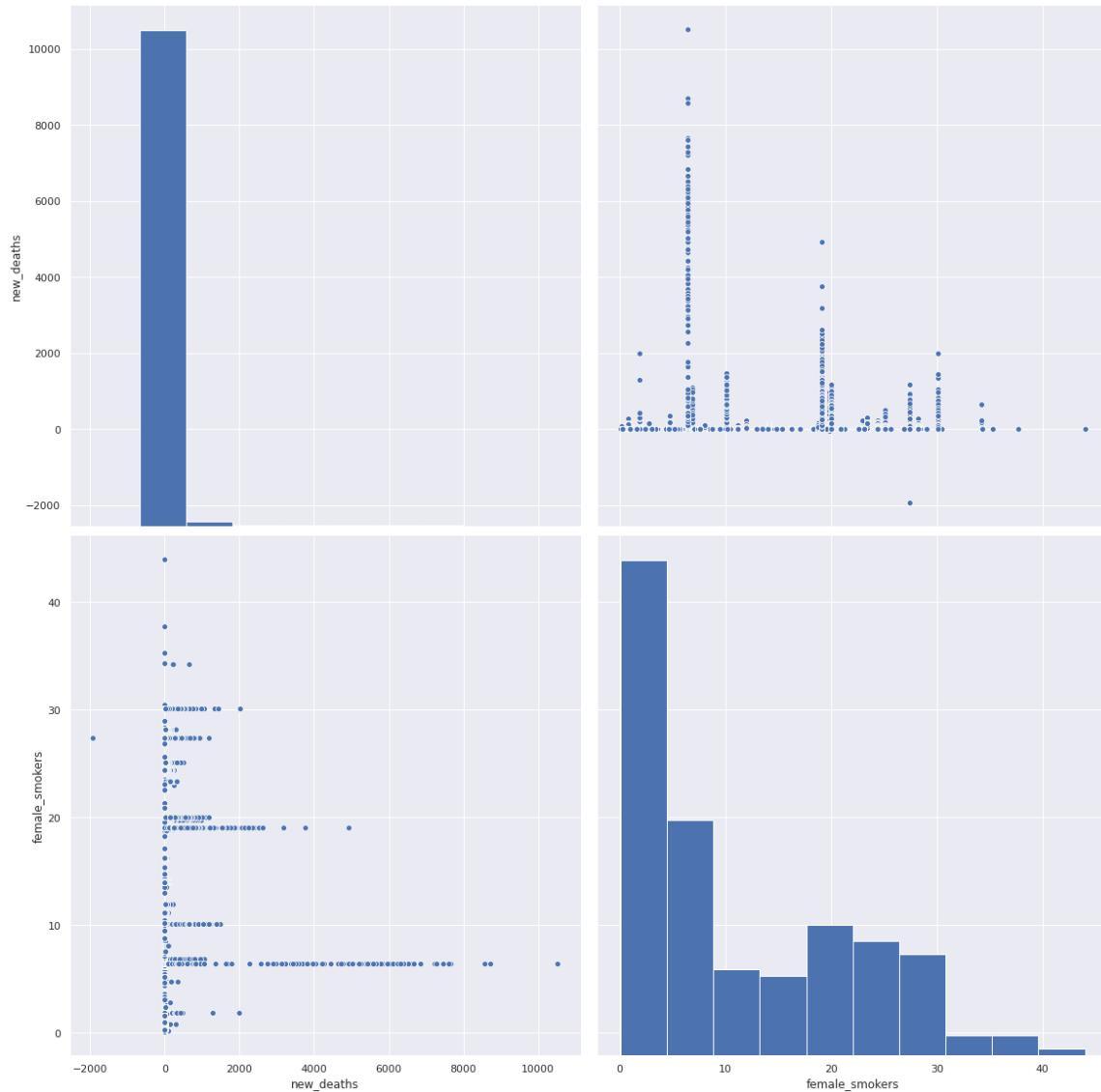


In [199]:

```
sns.pairplot(features, vars=["new_deaths", "female_smokers"], height=8)
```

Out[199]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c5090dd8>
```

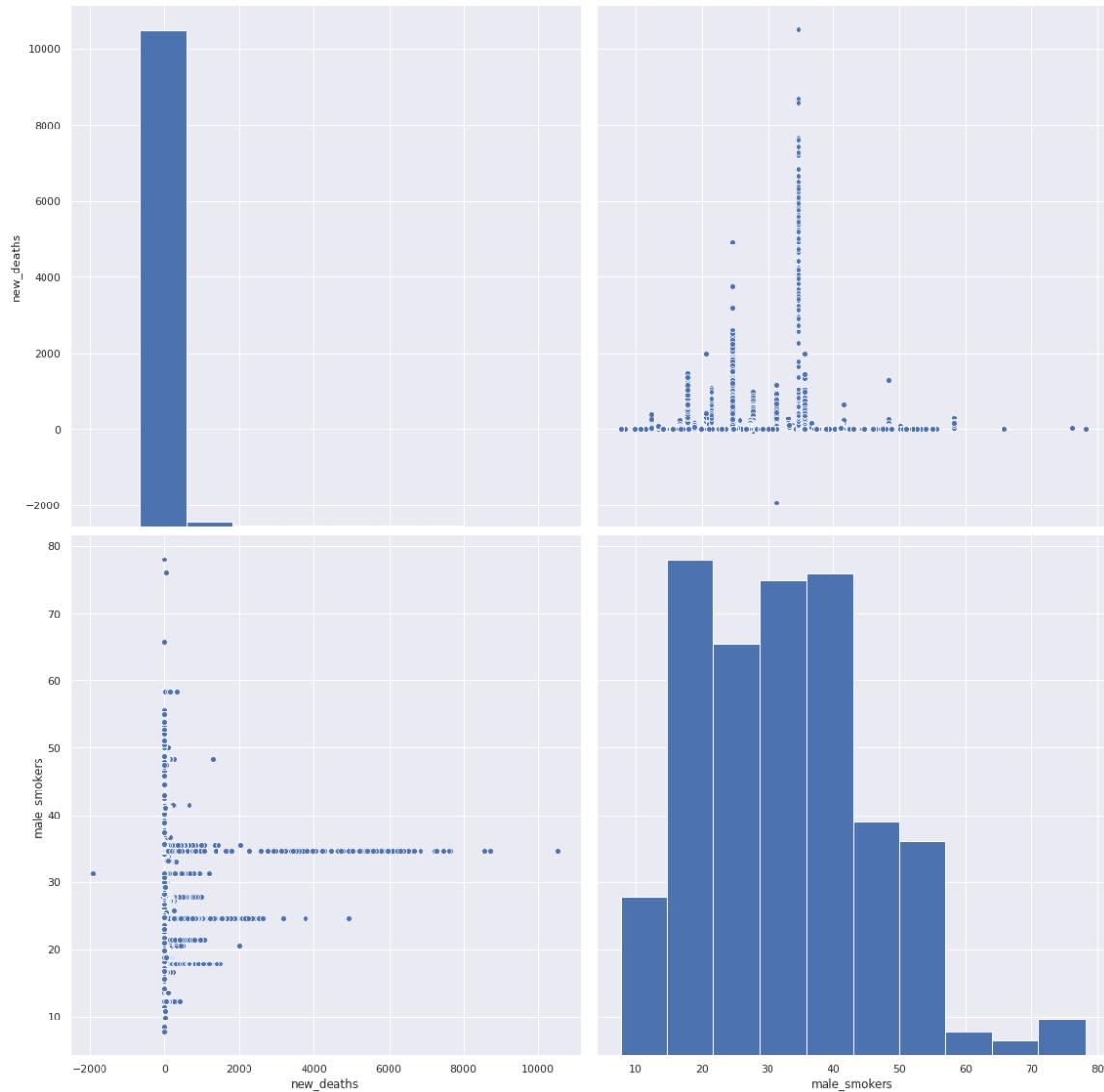


In [200]:

```
sns.pairplot(features, vars=["new_deaths", "male_smokers"], height=8)
```

Out[200]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c43a2ac8>
```

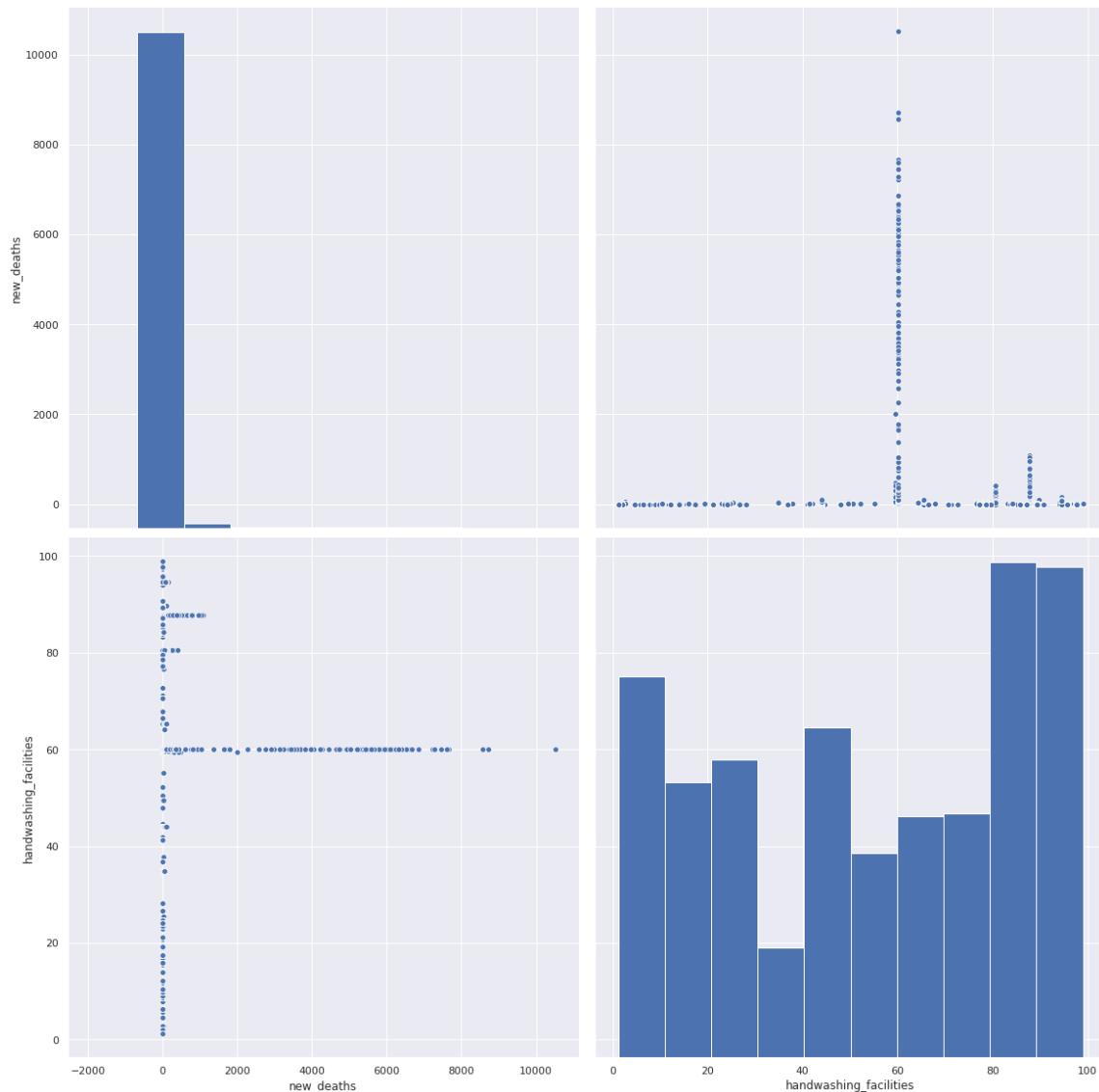


In [201]:

```
sns.pairplot(features, vars=["new_deaths", "handwashing_facilities"], height=8)
```

Out[201]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c405d668>
```

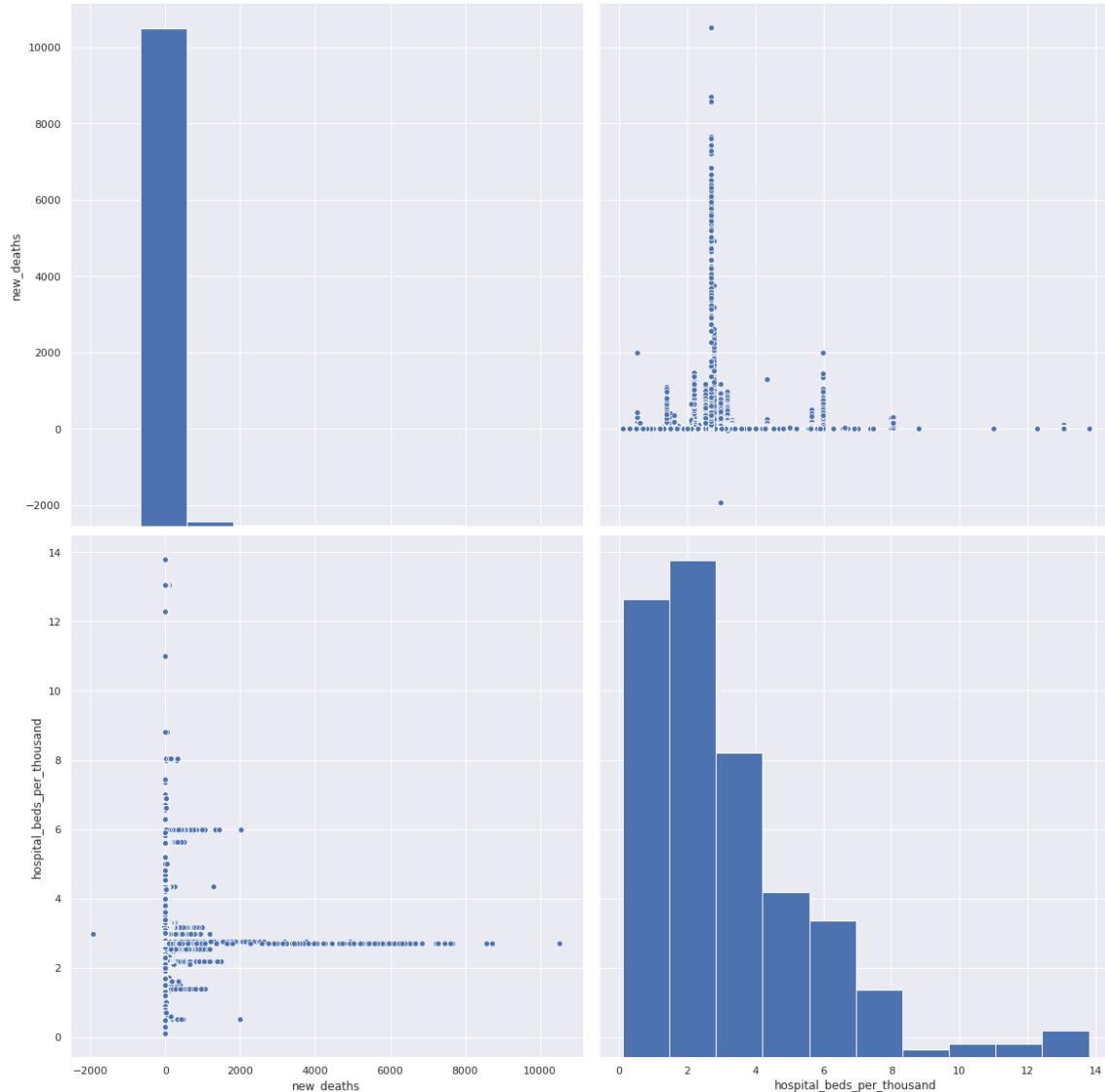


In [202]:

```
sns.pairplot(features, vars=["new_deaths", "hospital_beds_per_thousand"], height=8)
```

Out[202]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c3e5b6a0>
```

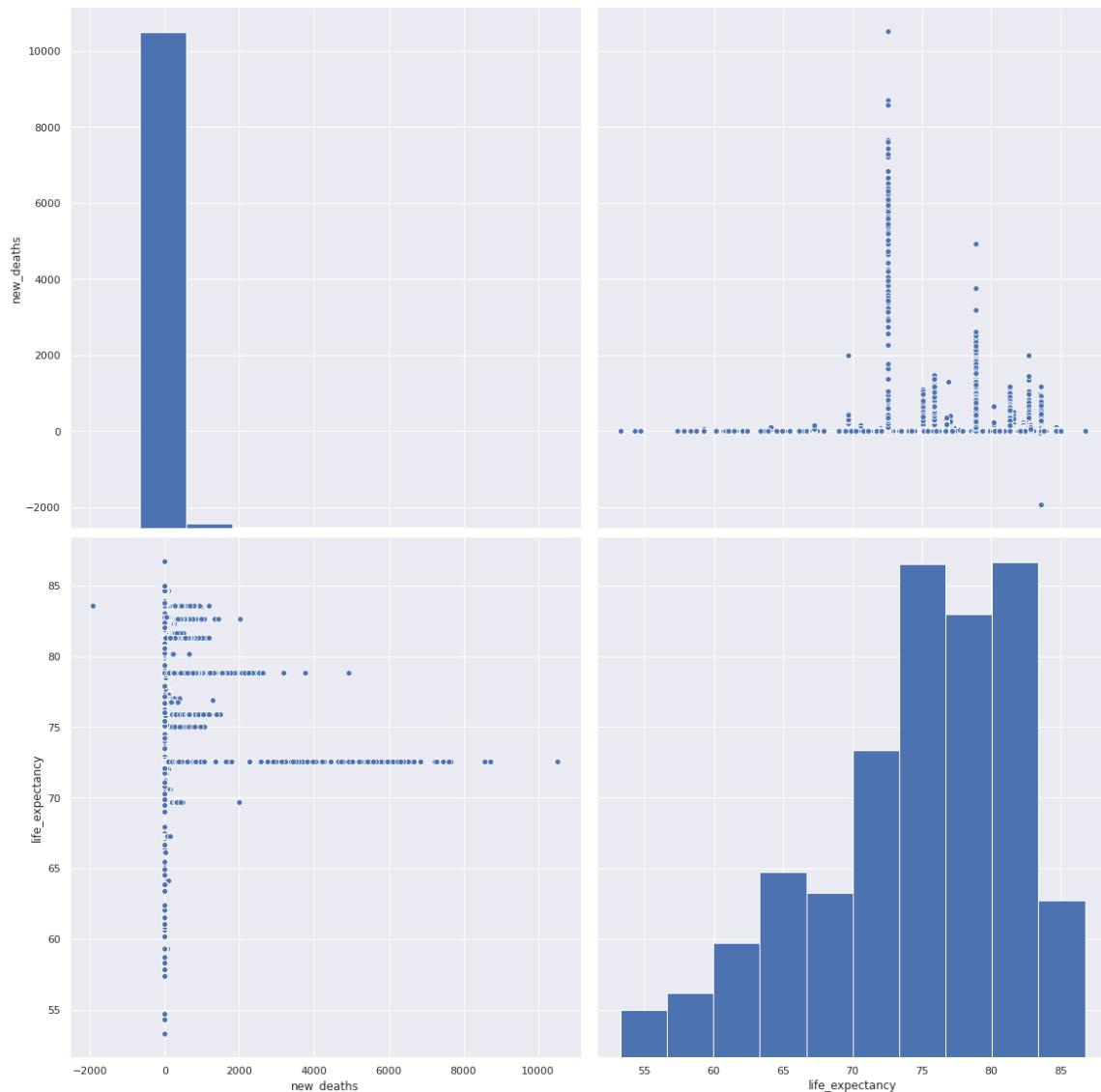


In [203]:

```
sns.pairplot(features, vars=["new_deaths", "life_expectancy"], height=8)
```

Out[203]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c3c468d0>
```

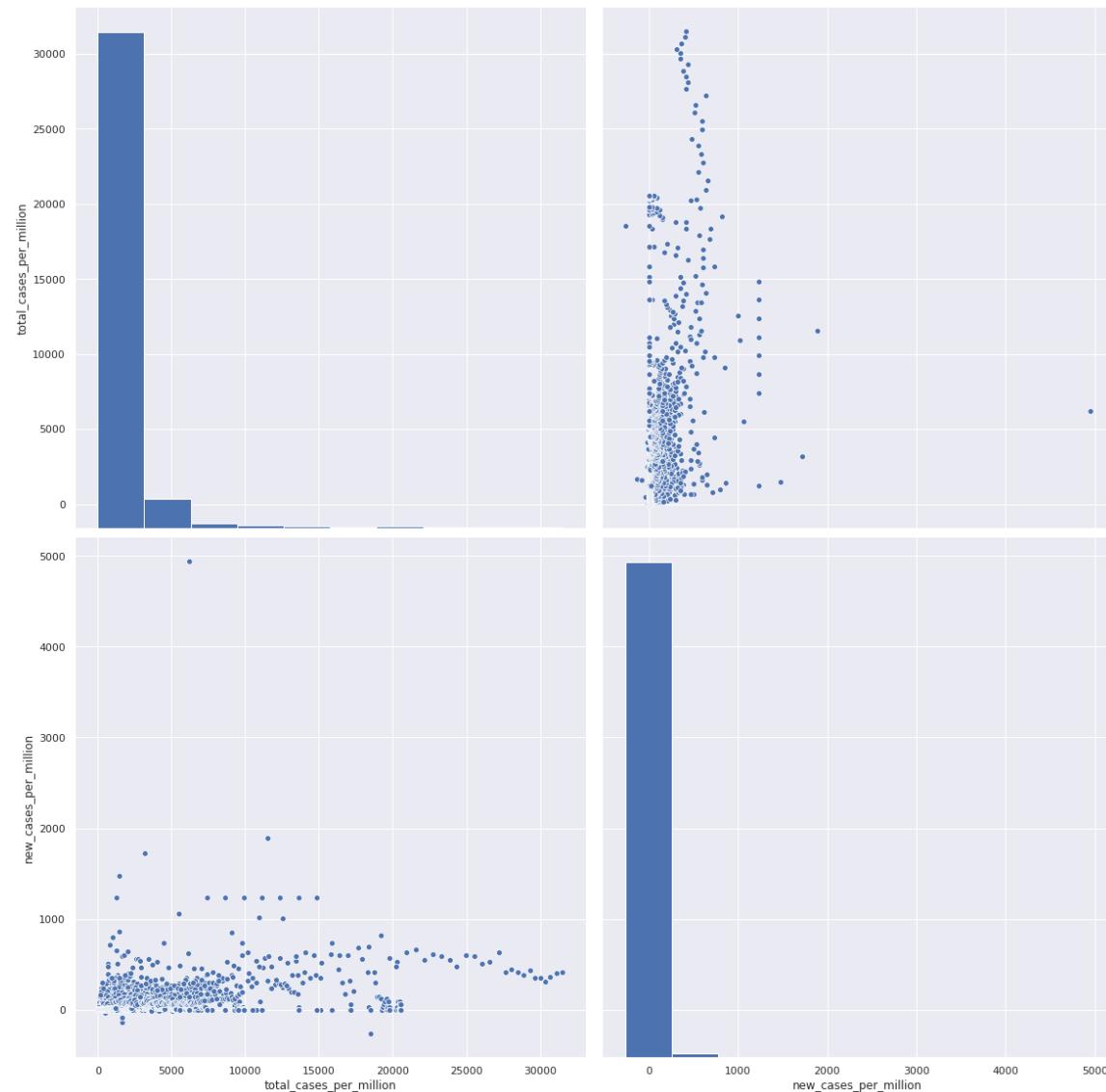


In [204]:

```
sns.pairplot(features, vars=["total_cases_per_million", "new_cases_per_million"], height=8)
```

Out[204]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c3db5828>
```

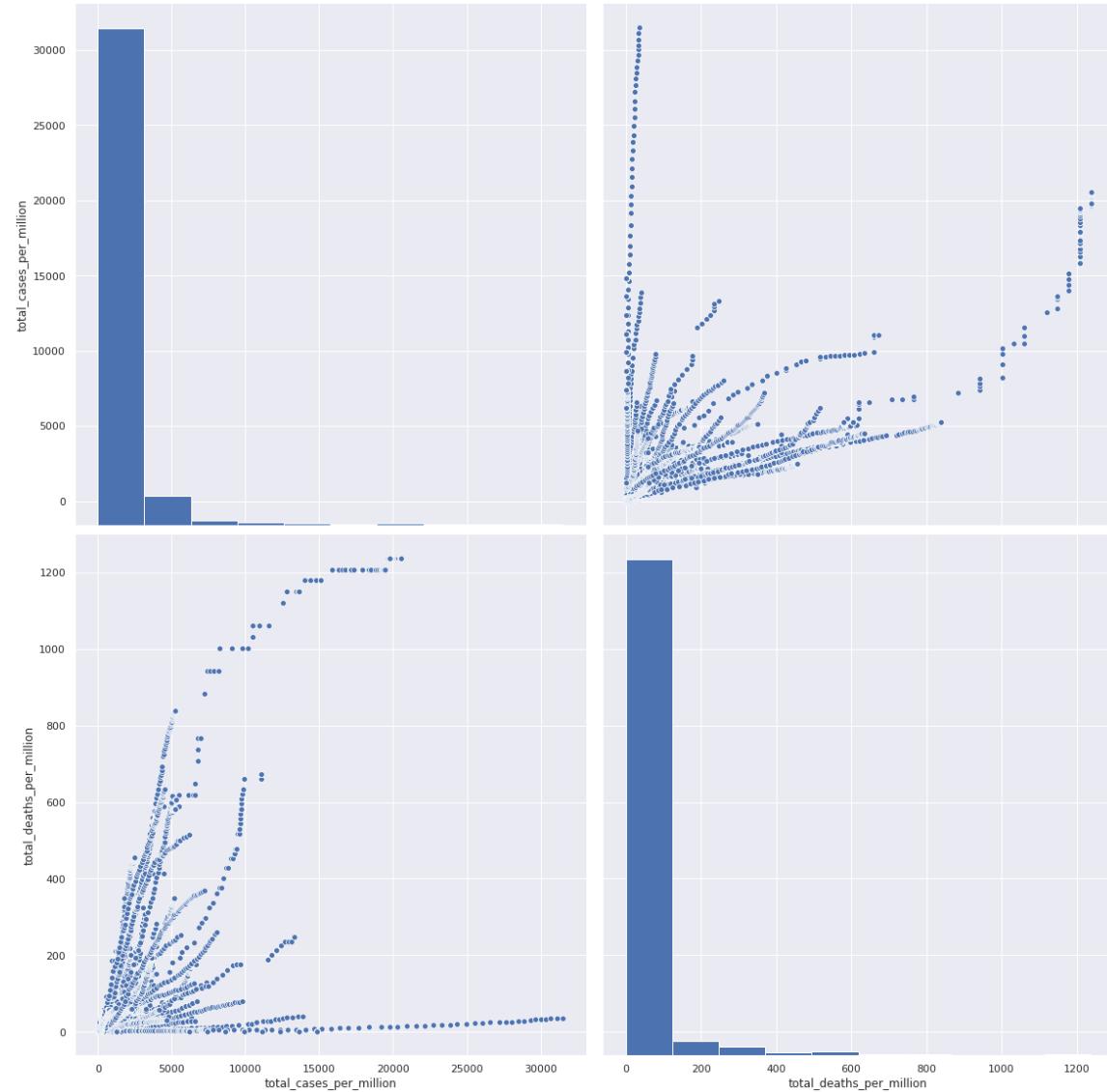


In [205]:

```
sns.pairplot(features, vars=["total_cases_per_million", "total_deaths_per_million"], height=8)
```

Out[205]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c3880c88>
```

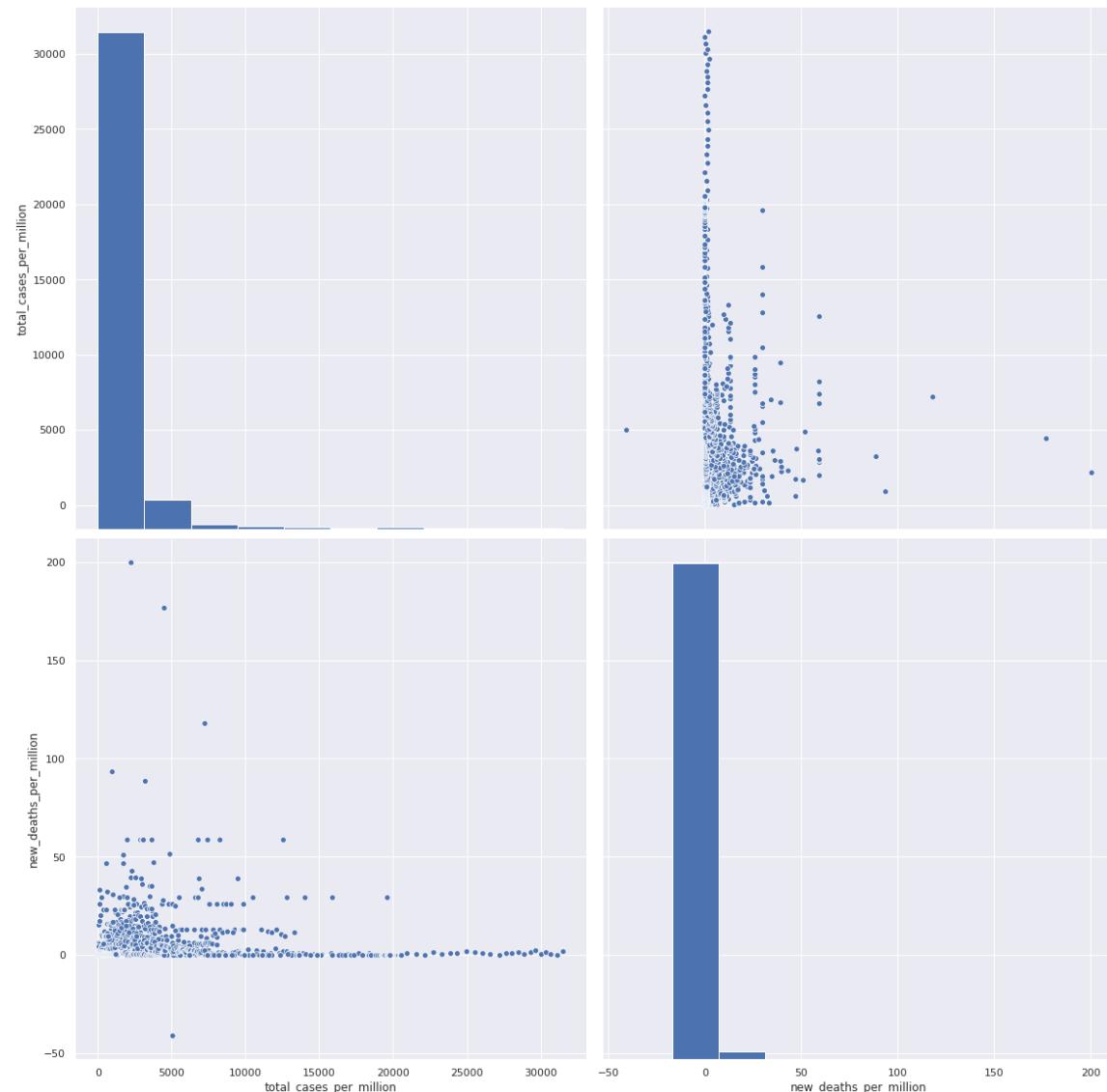


In [206]:

```
sns.pairplot(features, vars=["total_cases_per_million", "new_deaths_per_million"], height=8)
```

Out[206]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c4160b38>
```

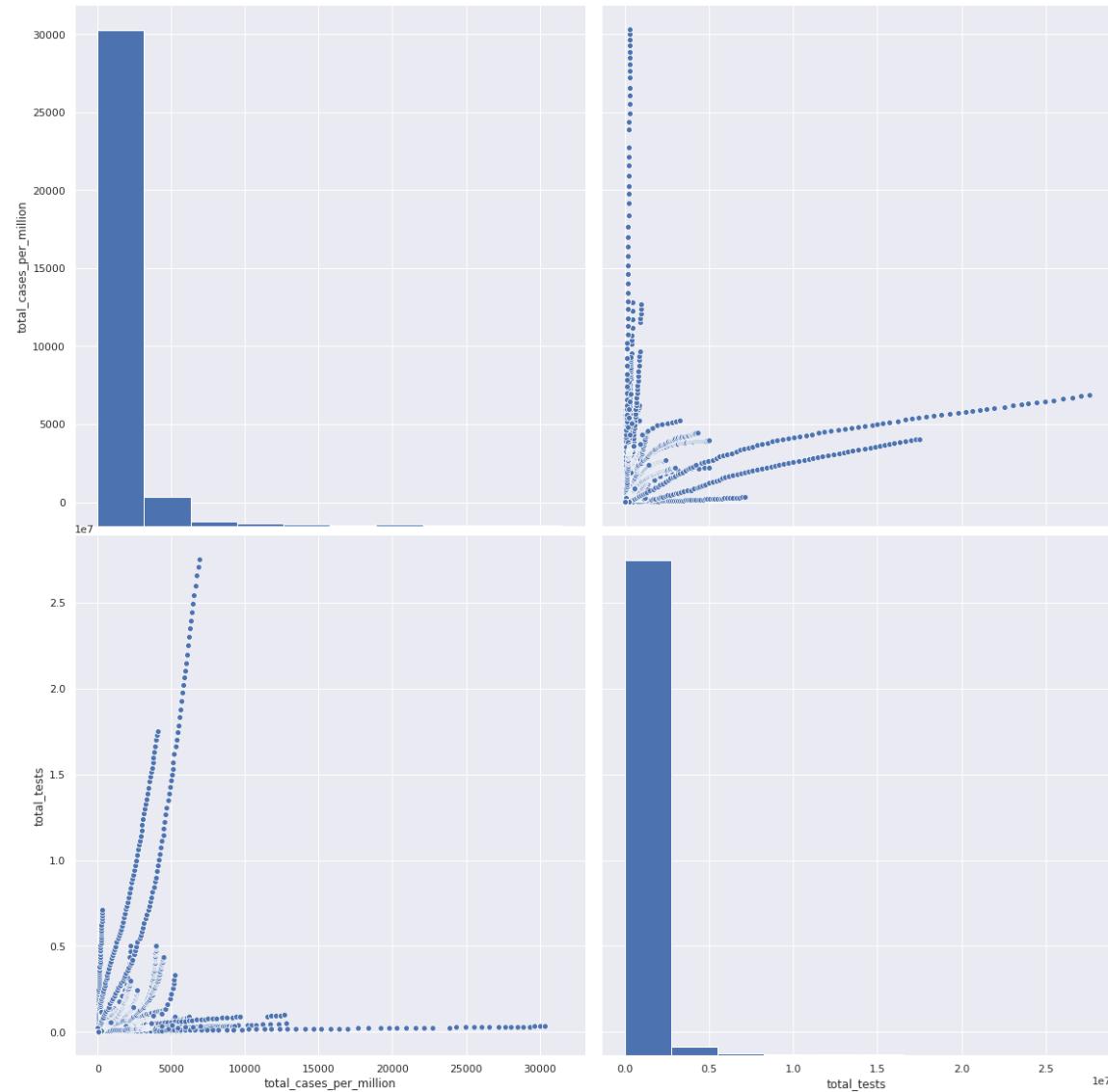


In [207]:

```
sns.pairplot(features, vars=["total_cases_per_million", "total_tests"], height=8)
```

Out[207]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c3415cf8>
```

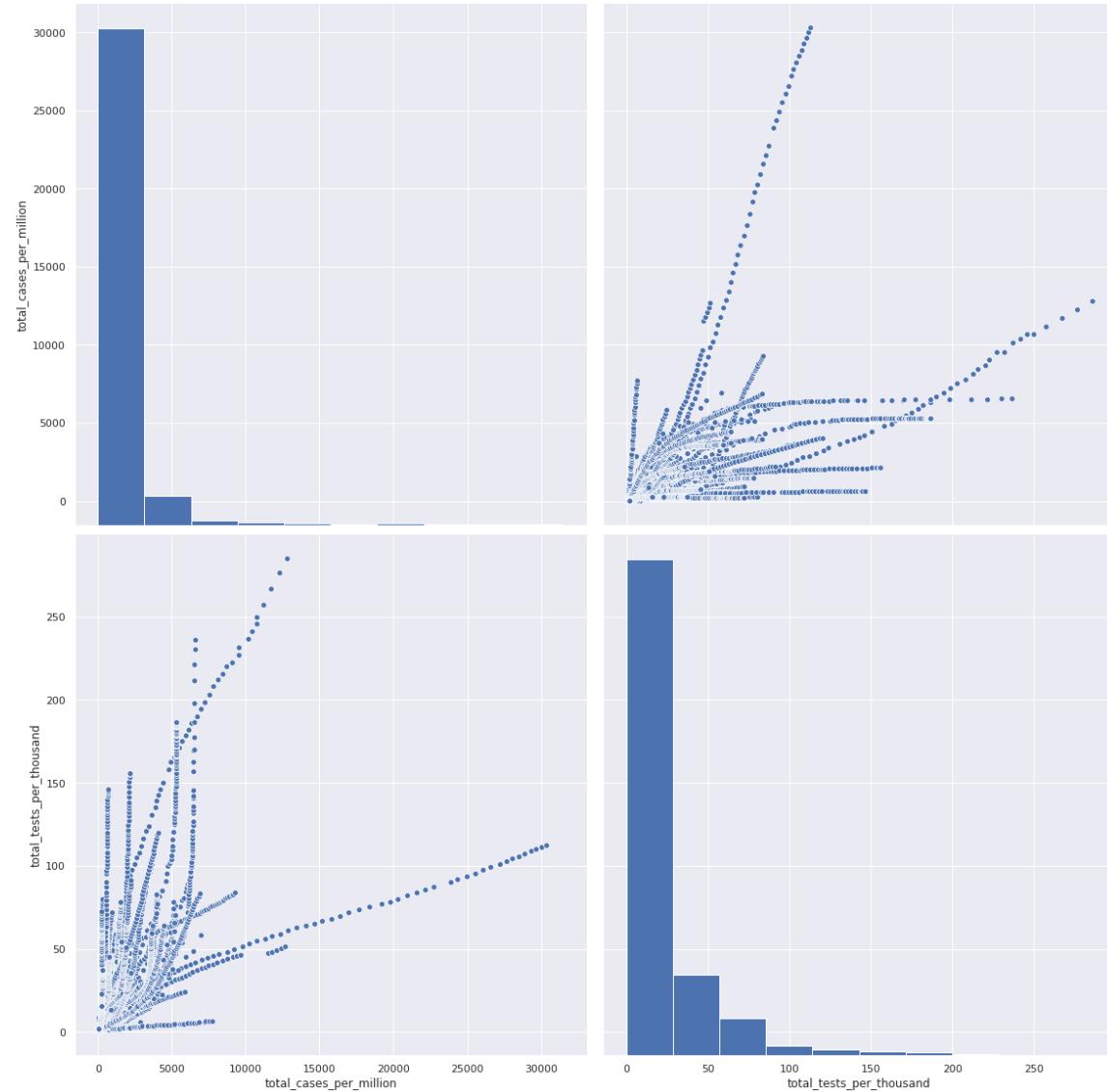


In [208]:

```
sns.pairplot(features, vars=["total_cases_per_million", "total_tests_per_thousan  
d"], height=8)
```

Out[208]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c77dccc0>
```

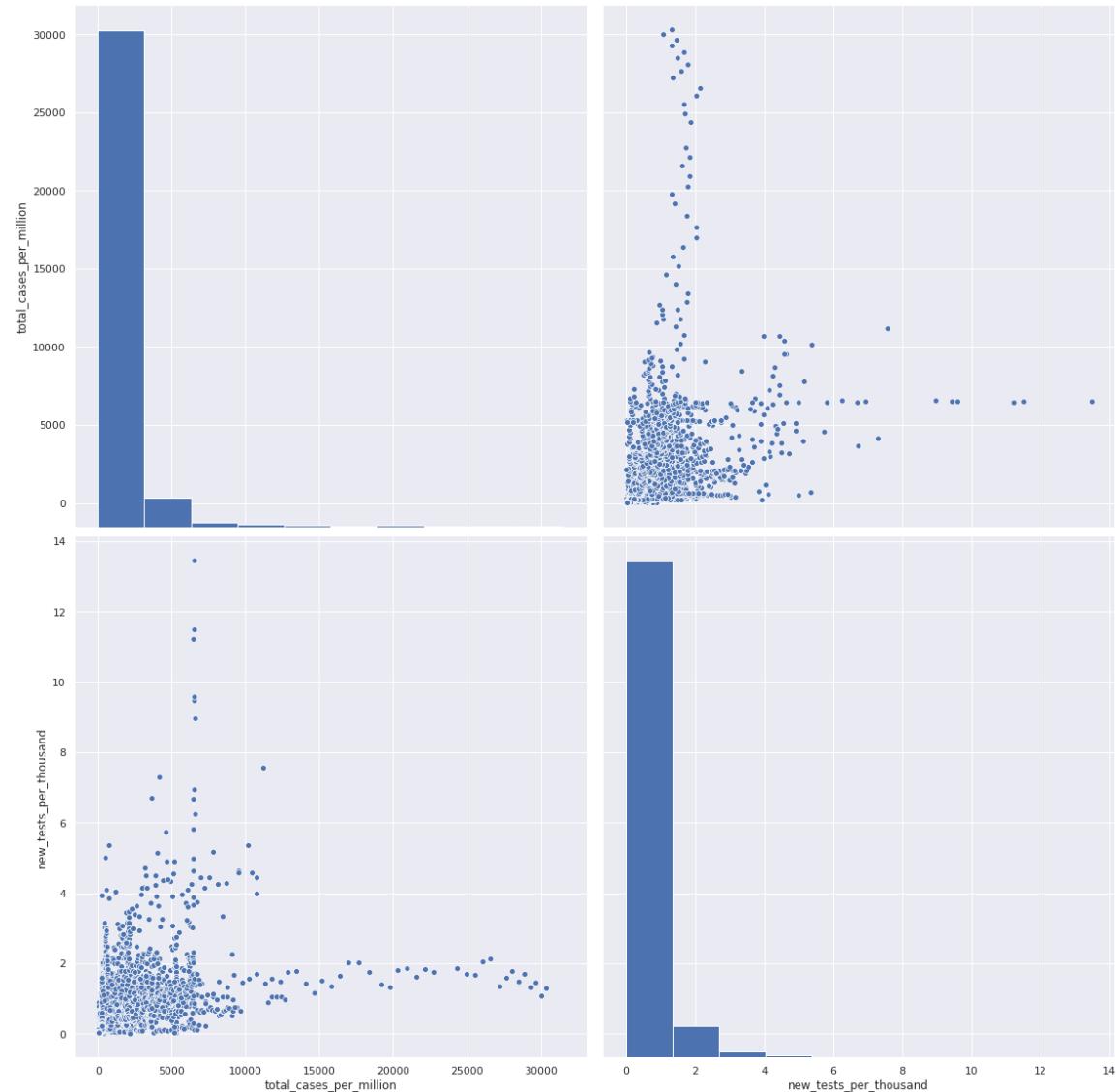


In [209]:

```
sns.pairplot(features, vars=["total_cases_per_million", "new_tests_per_thousand"], height=8)
```

Out[209]:

```
<seaborn.axisgrid.PairGrid at 0x7fc6c308cb70>
```

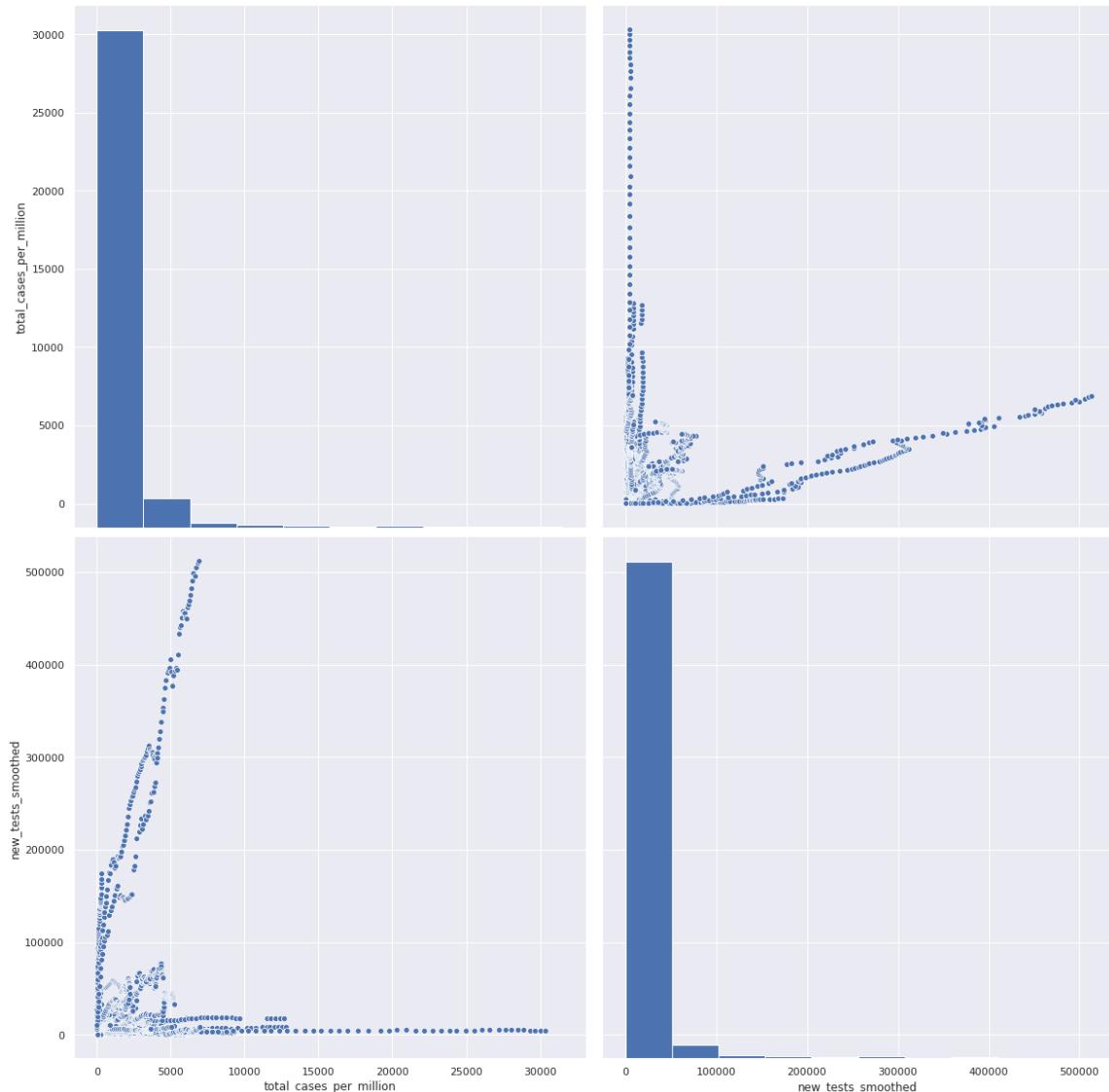


In [4]:

```
sns.pairplot(features, vars=["total_cases_per_million", "new_tests_smoothed"], height=8)
```

Out[4]:

```
<seaborn.axisgrid.PairGrid at 0x7f64a86bcc50>
```

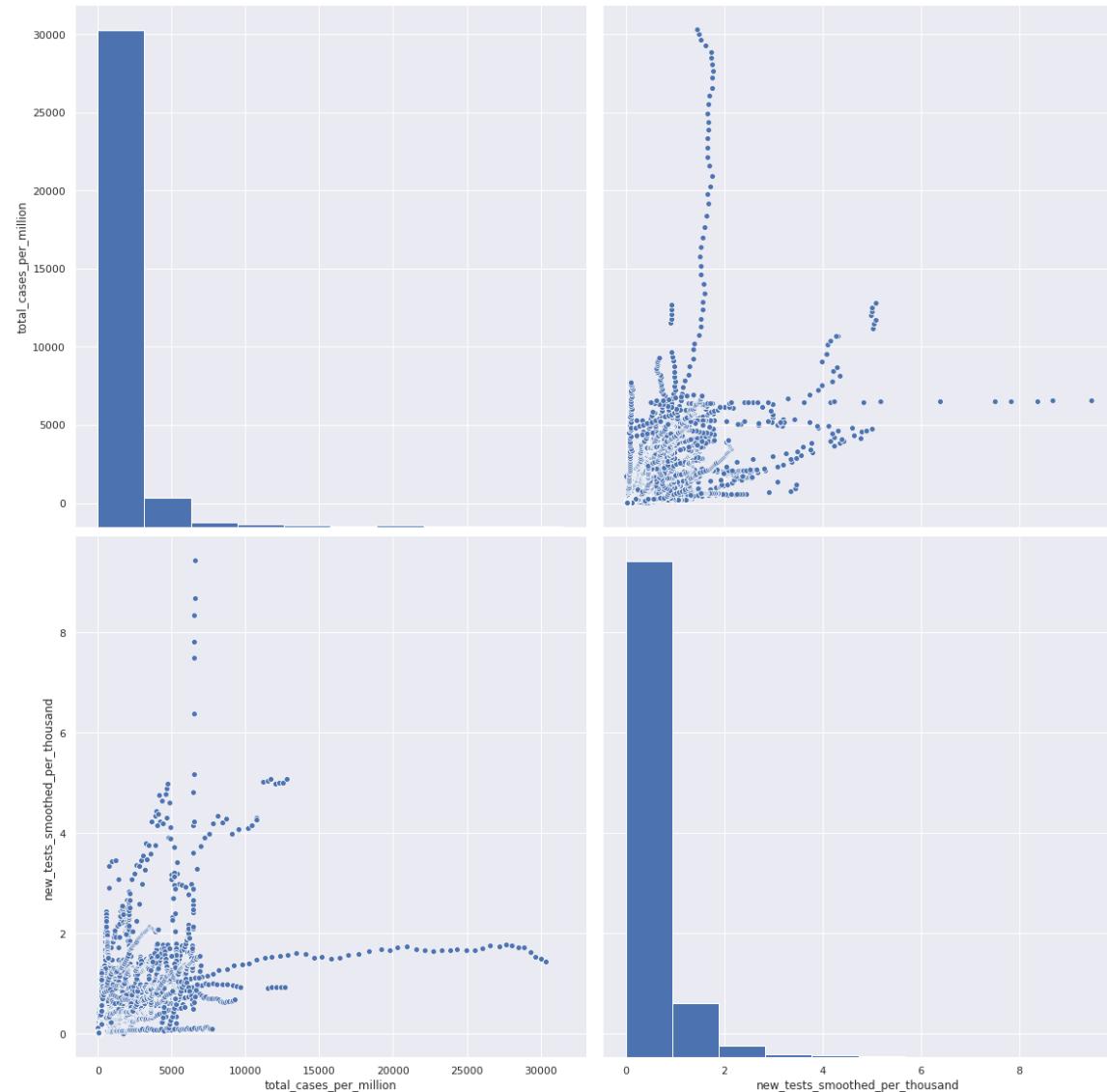


In [5]:

```
sns.pairplot(features, vars=["total_cases_per_million", "new_tests_smoothed_per_thousand"], height=8)
```

Out[5]:

```
<seaborn.axisgrid.PairGrid at 0x7f645d9d18d0>
```

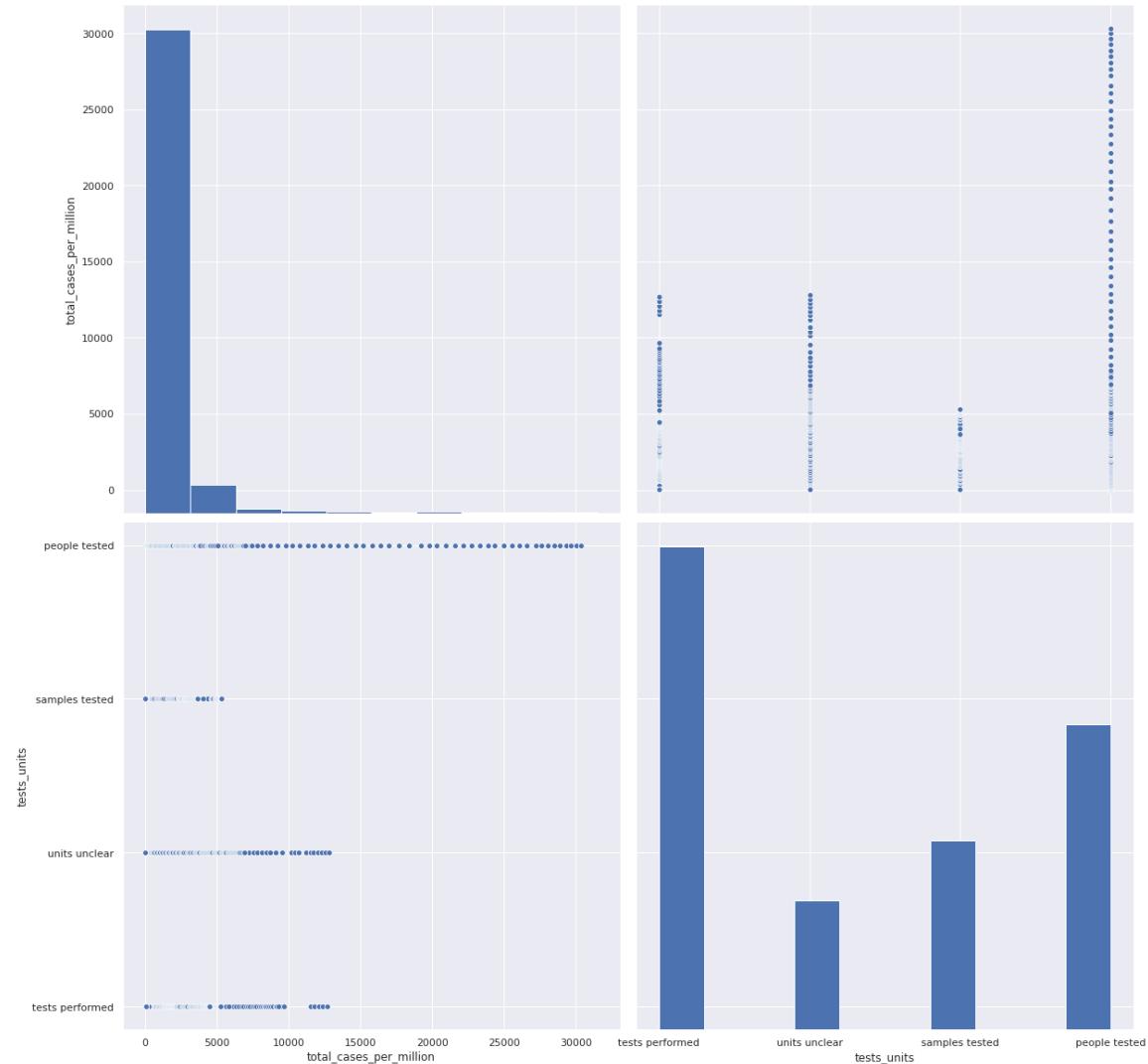


In [6]:

```
sns.pairplot(features, vars=["total_cases_per_million", "tests_units"], height=8)
```

Out[6]:

```
<seaborn.axisgrid.PairGrid at 0x7f645c5f0e10>
```

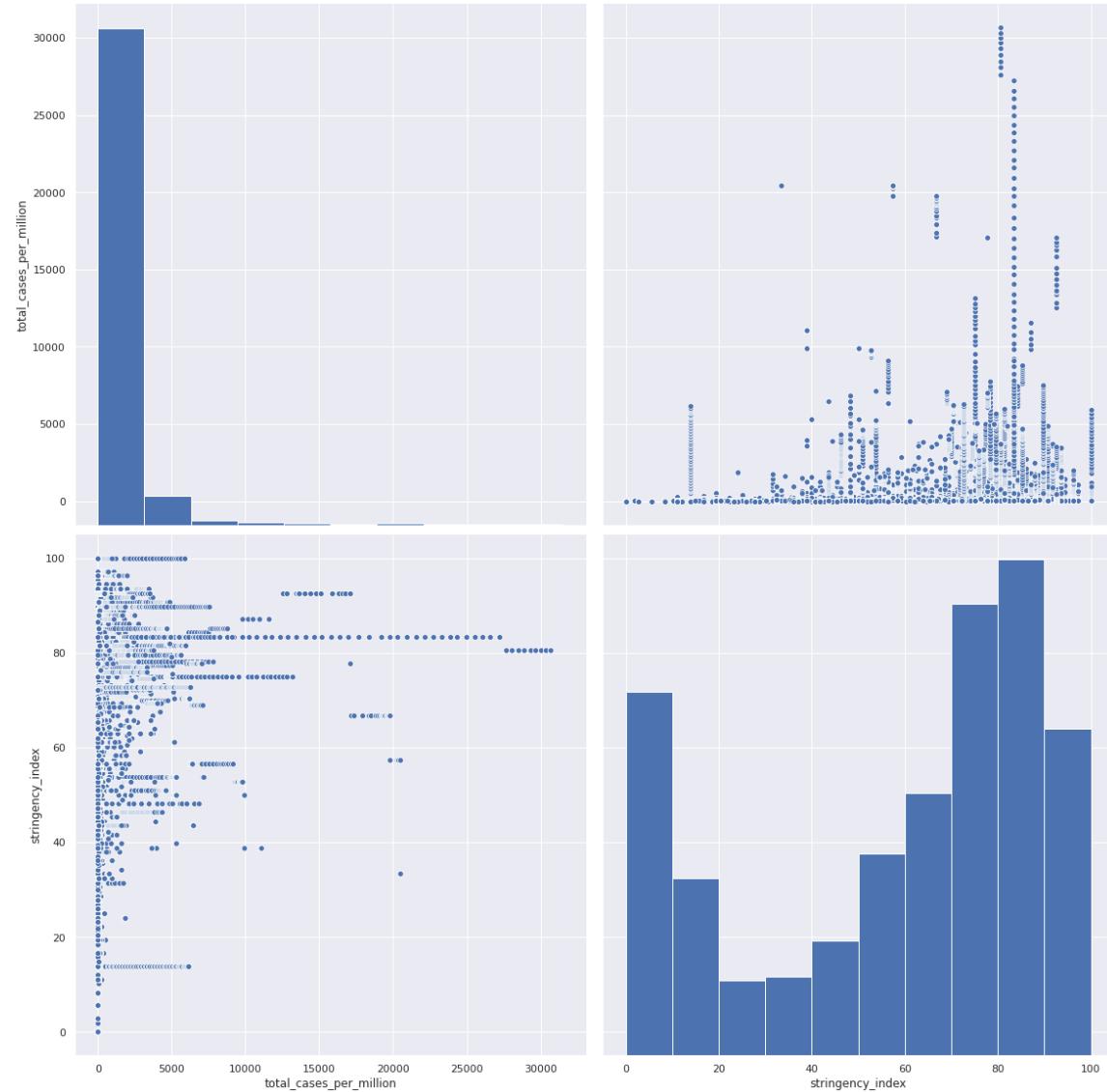


In [7]:

```
sns.pairplot(features, vars=["total_cases_per_million", "stringency_index"], height=8)
```

Out[7]:

```
<seaborn.axisgrid.PairGrid at 0x7f645c4b08d0>
```

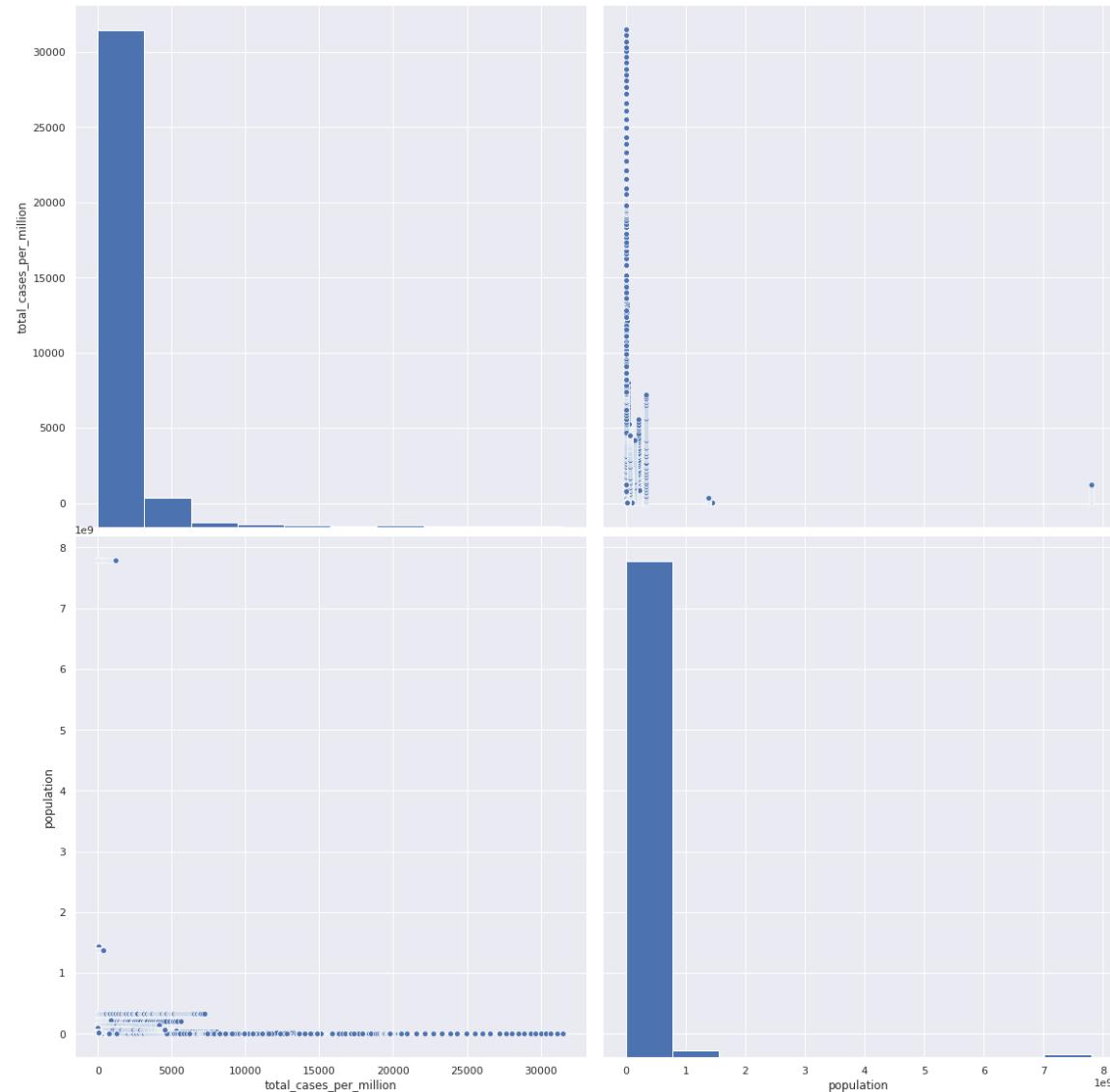


In [8]:

```
sns.pairplot(features, vars=["total_cases_per_million", "population"], height=8)
```

Out[8]:

```
<seaborn.axisgrid.PairGrid at 0x7f645c263470>
```

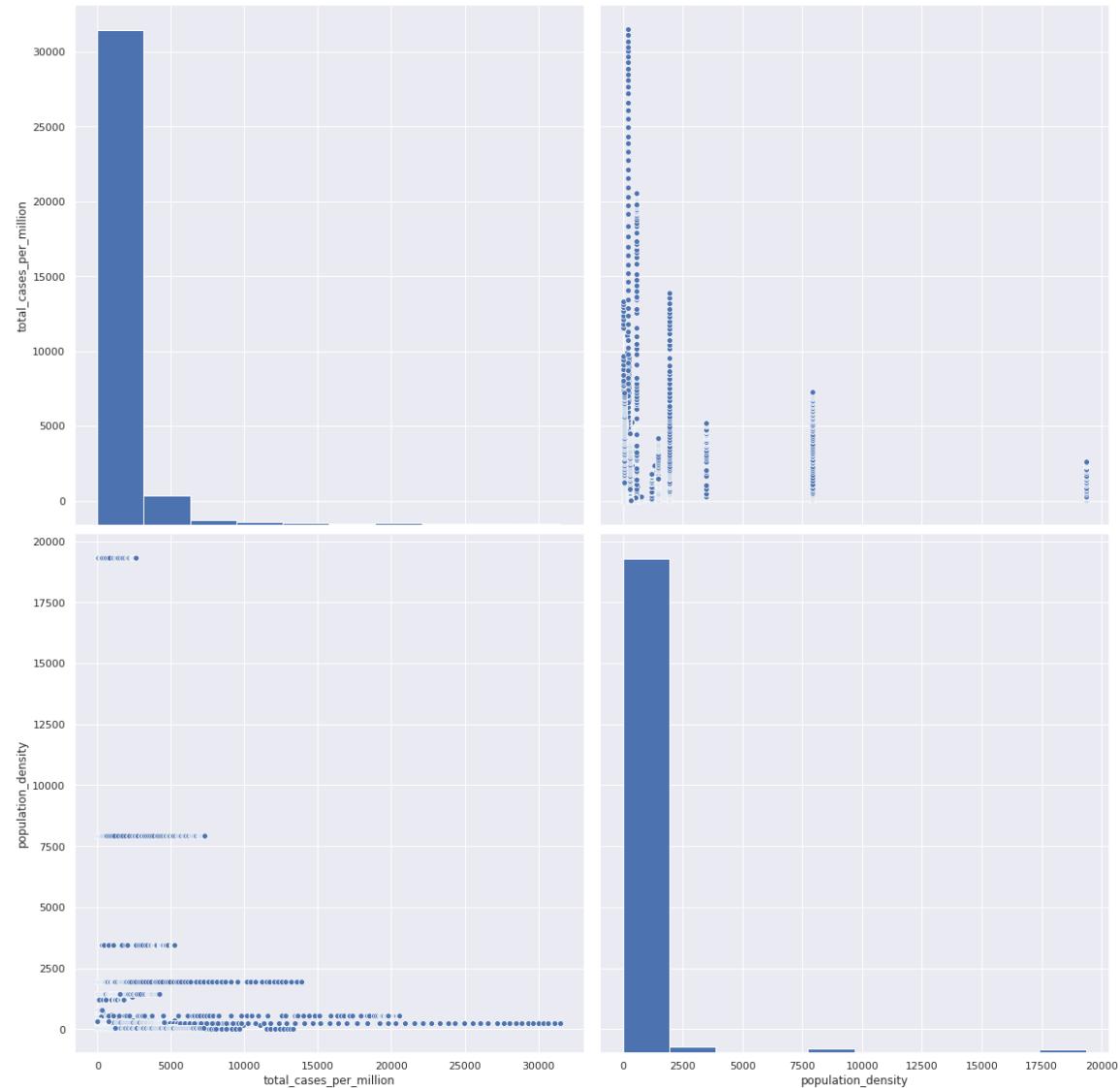


In [9]:

```
sns.pairplot(features, vars=["total_cases_per_million", "population_density"], height=8)
```

Out[9]:

```
<seaborn.axisgrid.PairGrid at 0x7f645775e080>
```

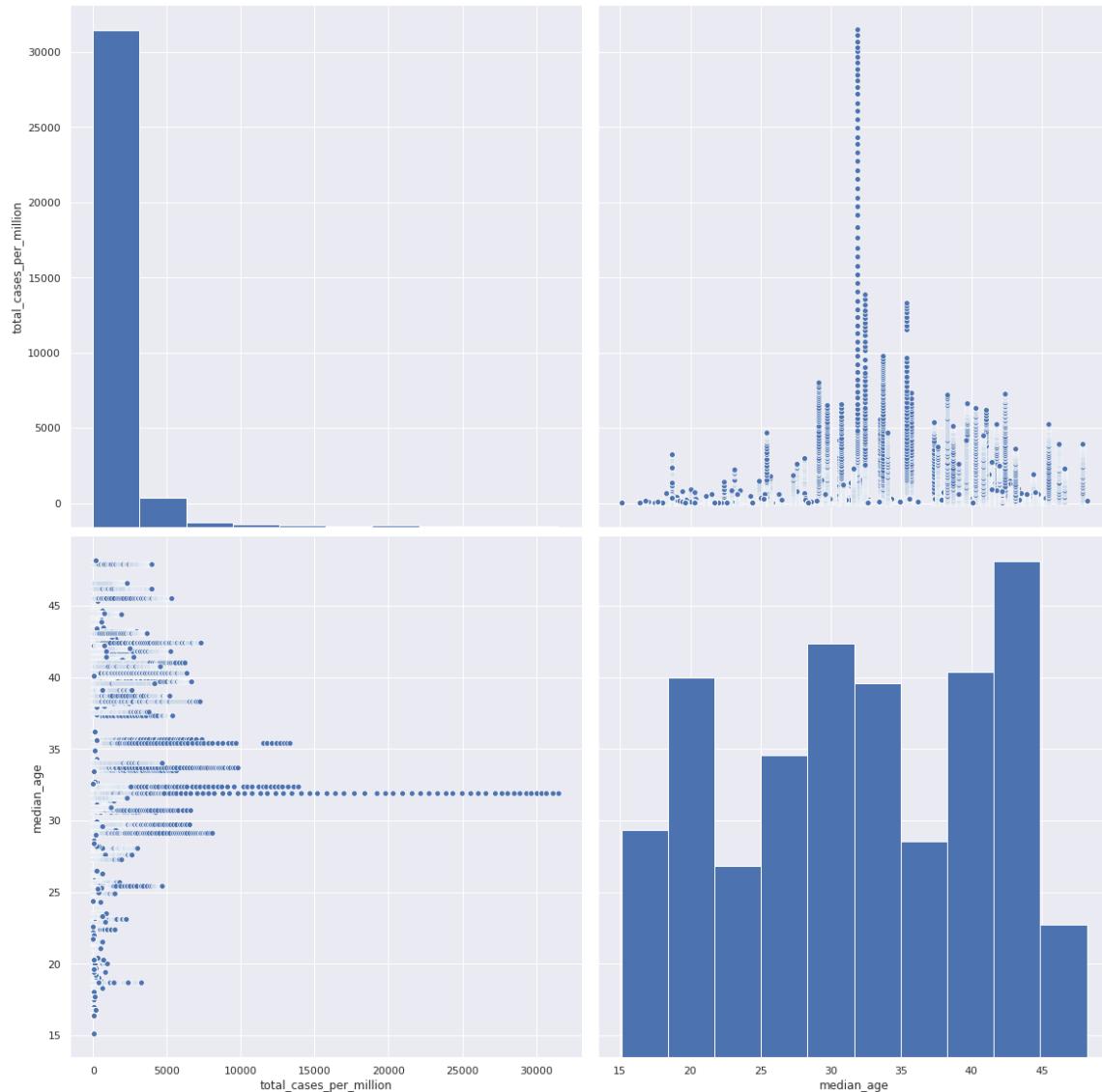


In [10]:

```
sns.pairplot(features, vars=["total_cases_per_million", "median_age"], height=8)
```

Out[10]:

```
<seaborn.axisgrid.PairGrid at 0x7f64575ba4a8>
```

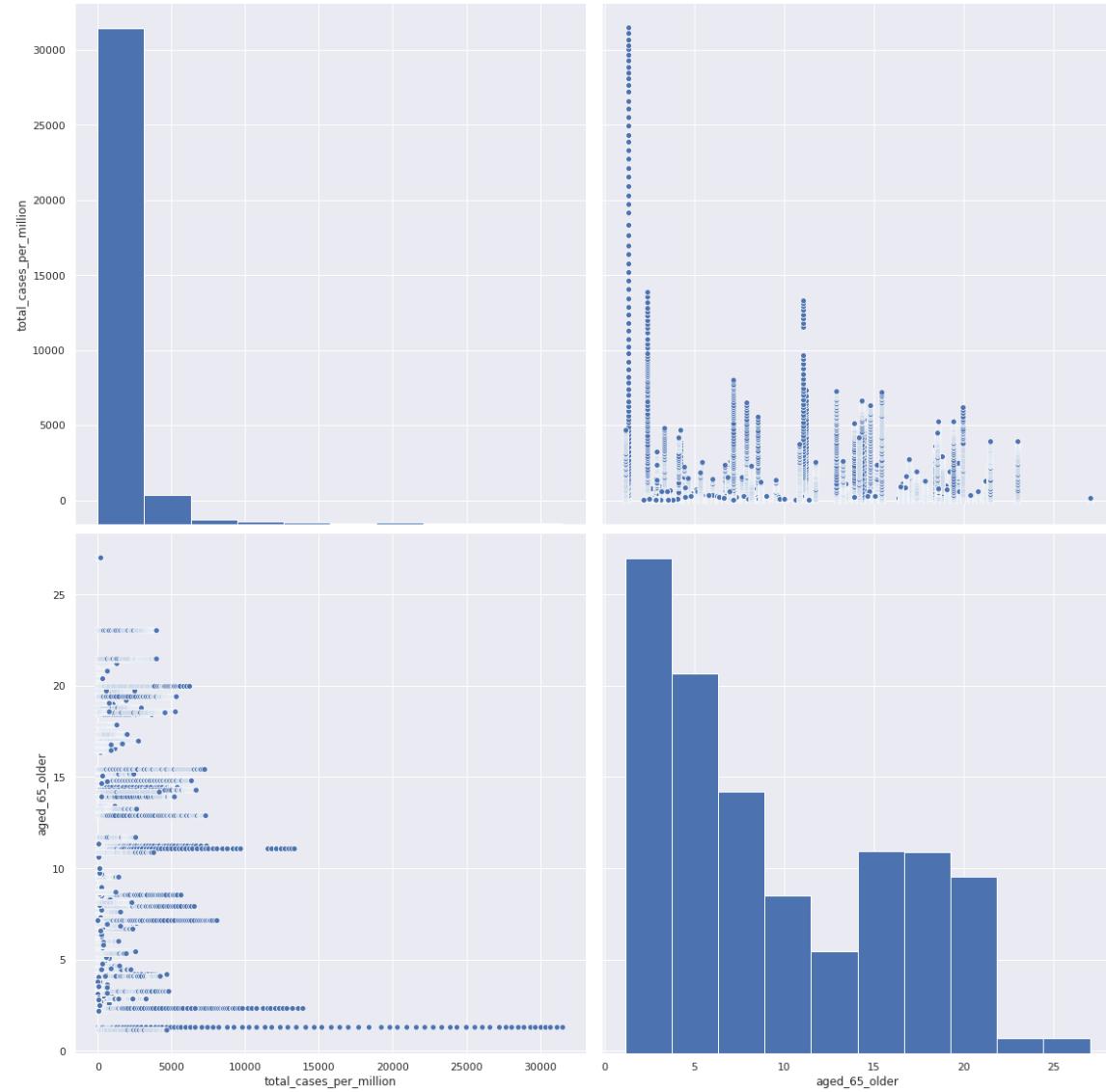


In [11]:

```
sns.pairplot(features, vars=["total_cases_per_million", "aged_65_older"], height=8)
```

Out[11]:

```
<seaborn.axisgrid.PairGrid at 0x7f645734c780>
```

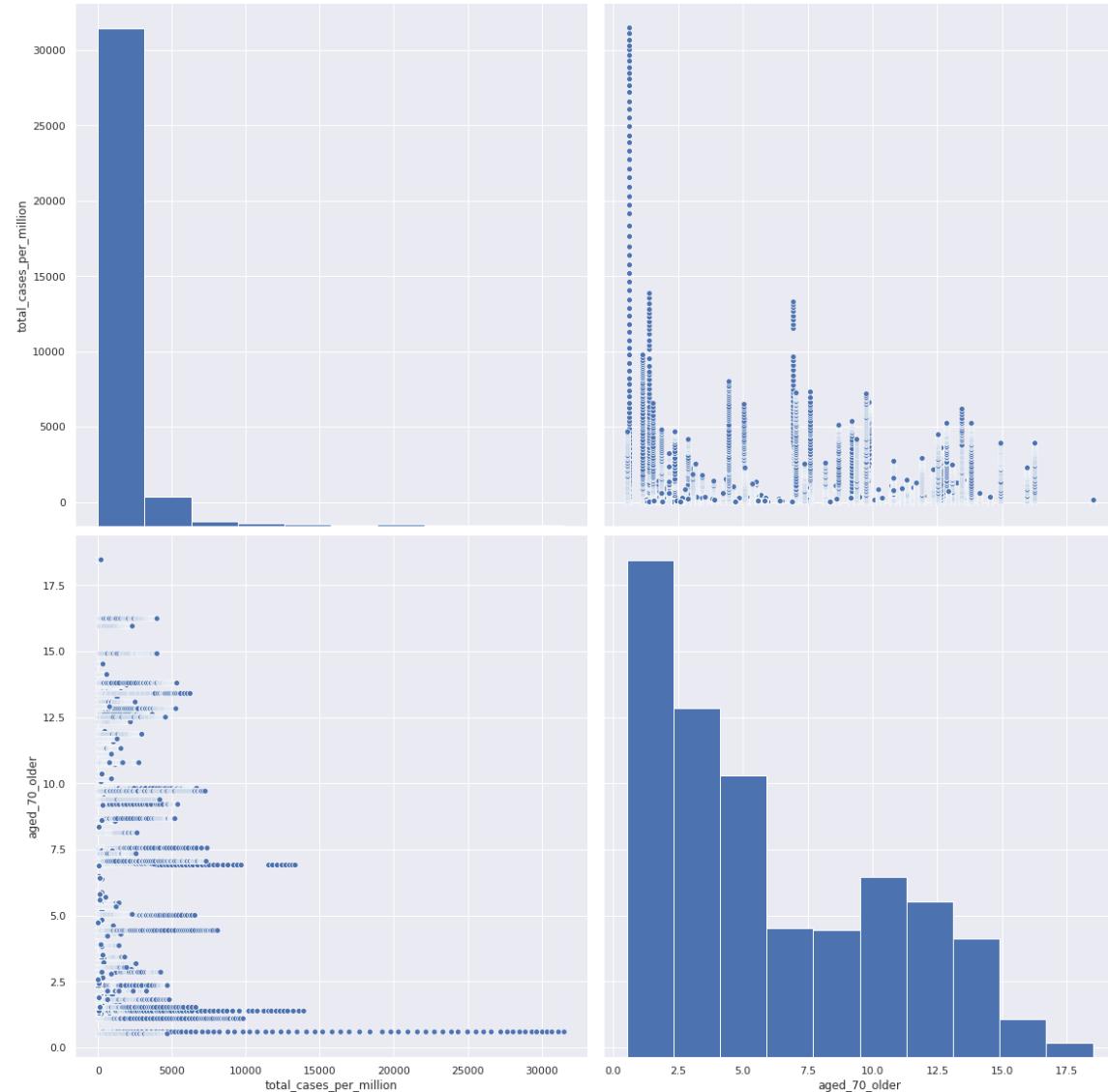


In [12]:

```
sns.pairplot(features, vars=["total_cases_per_million", "aged_70_older"], height=8)
```

Out[12]:

```
<seaborn.axisgrid.PairGrid at 0x7f64571b64e0>
```

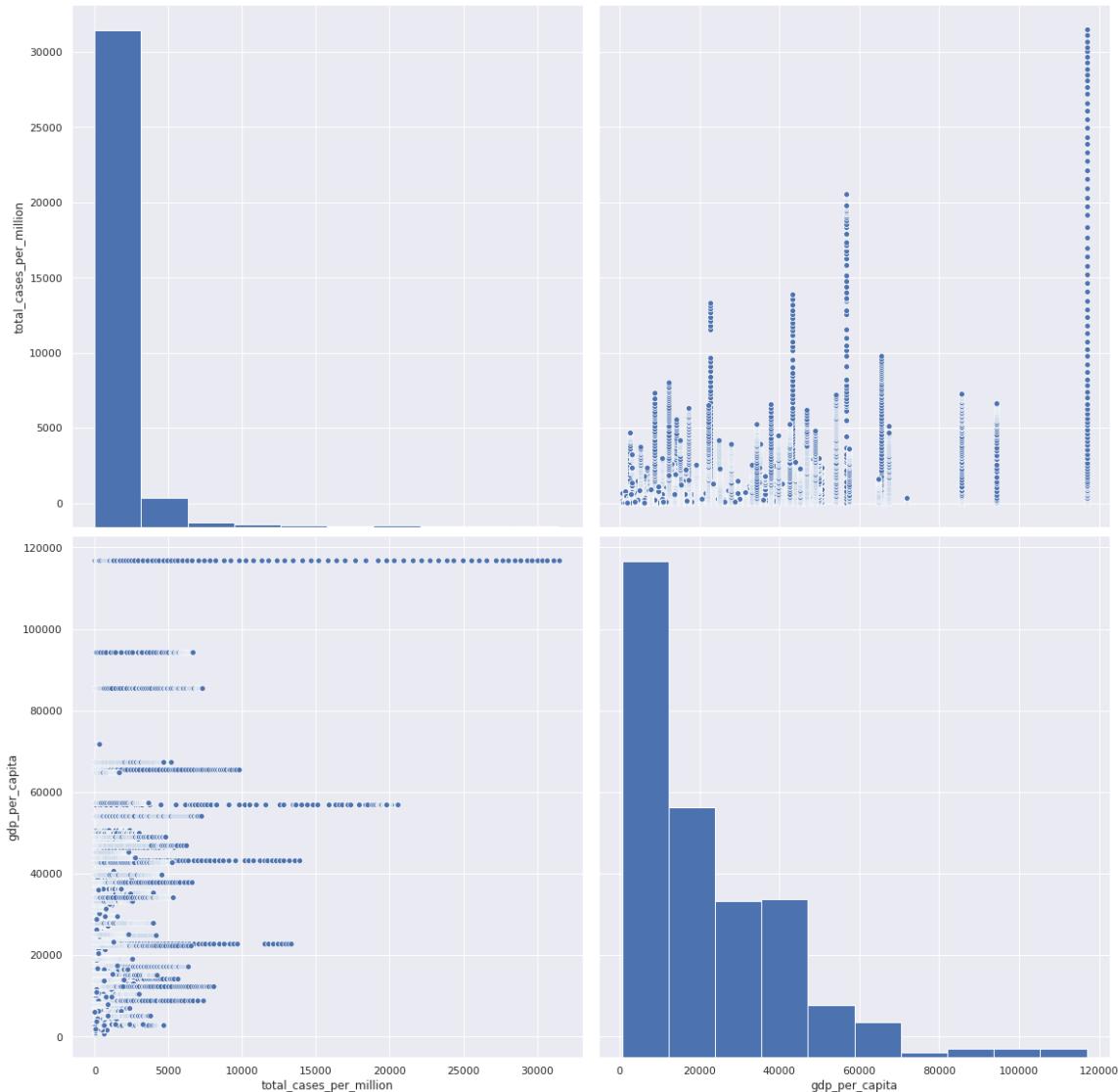


In [13]:

```
sns.pairplot(features, vars=["total_cases_per_million", "gdp_per_capita"], height=8)
```

Out[13]:

```
<seaborn.axisgrid.PairGrid at 0x7f6456f7b4e0>
```

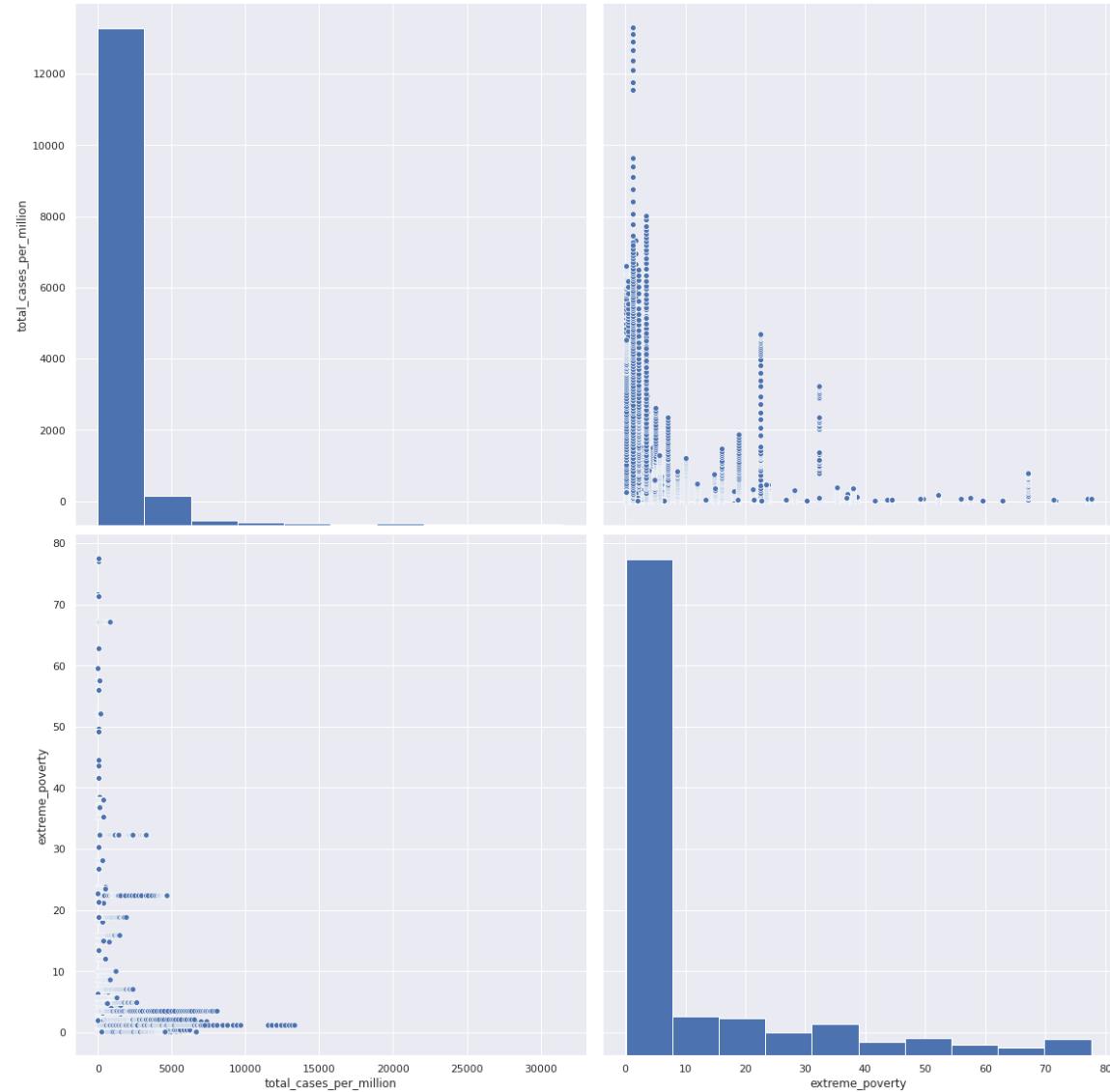


In [14]:

```
sns.pairplot(features, vars=["total_cases_per_million", "extreme_poverty"], height=8)
```

Out[14]:

```
<seaborn.axisgrid.PairGrid at 0x7f6456d246a0>
```

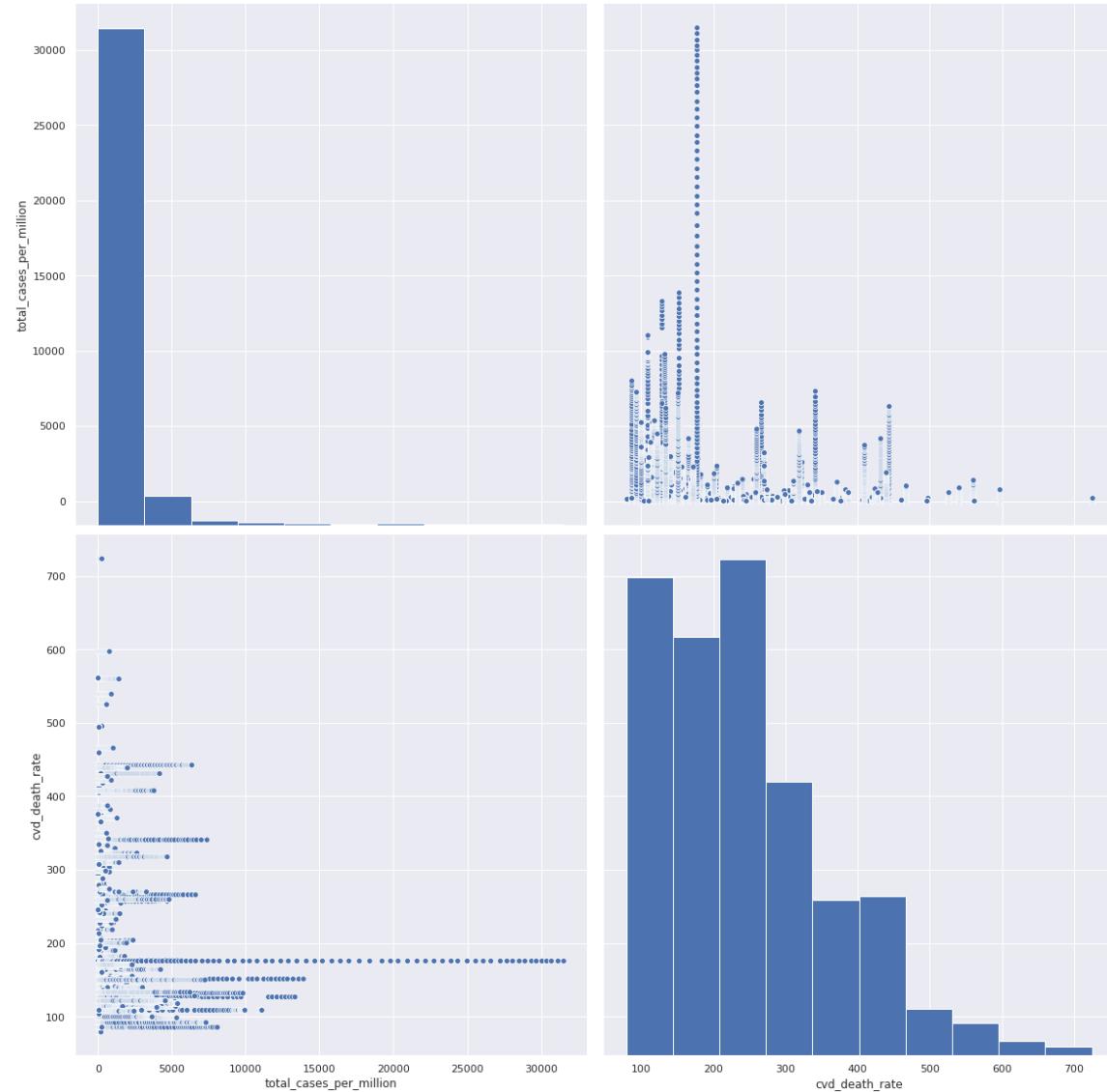


In [15]:

```
sns.pairplot(features, vars=["total_cases_per_million", "cvd_death_rate"], height=8)
```

Out[15]:

```
<seaborn.axisgrid.PairGrid at 0x7f6456e4f6d8>
```

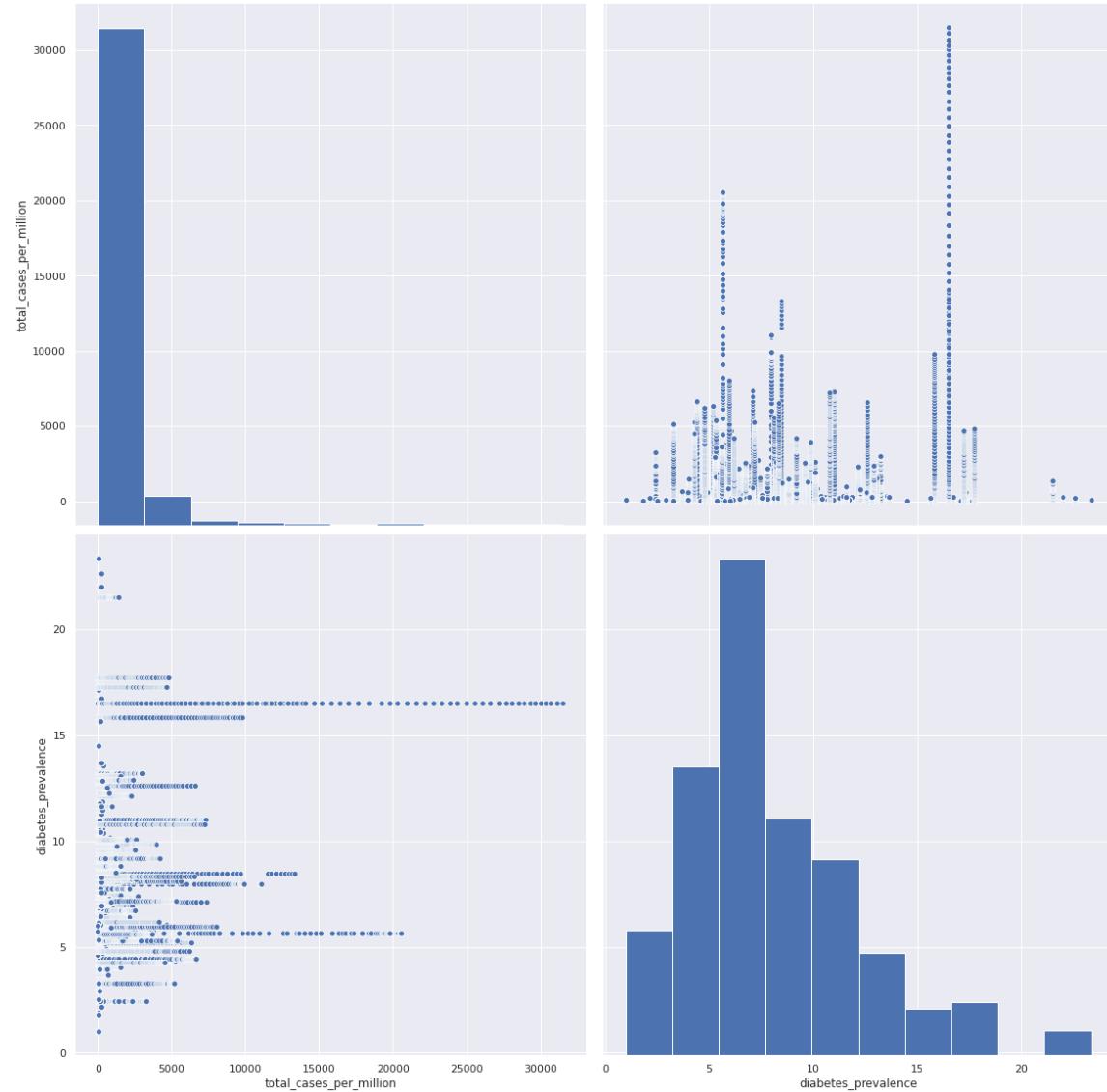


In [16]:

```
sns.pairplot(features, vars=["total_cases_per_million", "diabetes_prevalence"], height=8)
```

Out[16]:

```
<seaborn.axisgrid.PairGrid at 0x7f64569c1320>
```

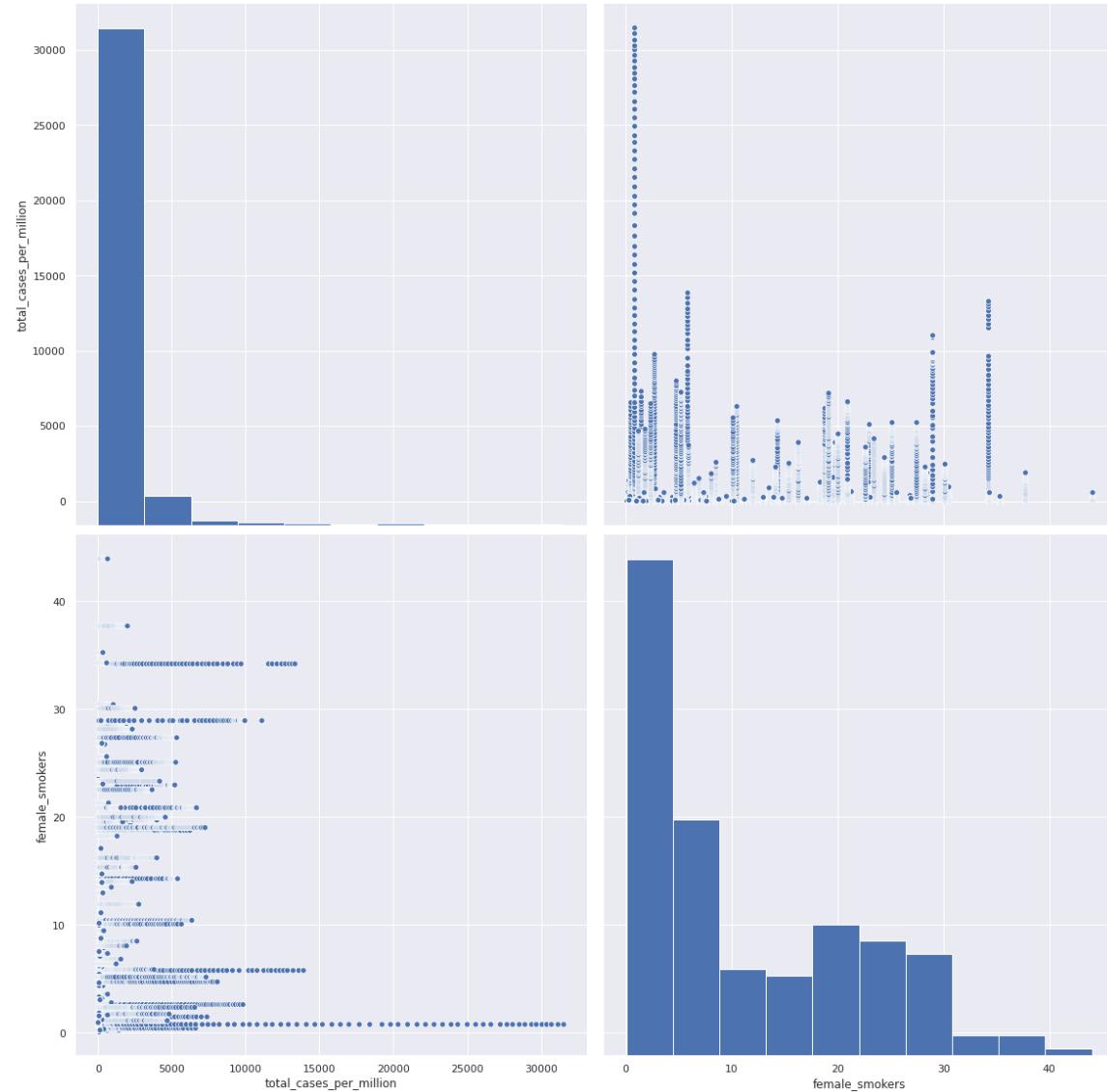


In [17]:

```
sns.pairplot(features, vars=["total_cases_per_million", "female_smokers"], height=8)
```

Out[17]:

```
<seaborn.axisgrid.PairGrid at 0x7f6456734588>
```

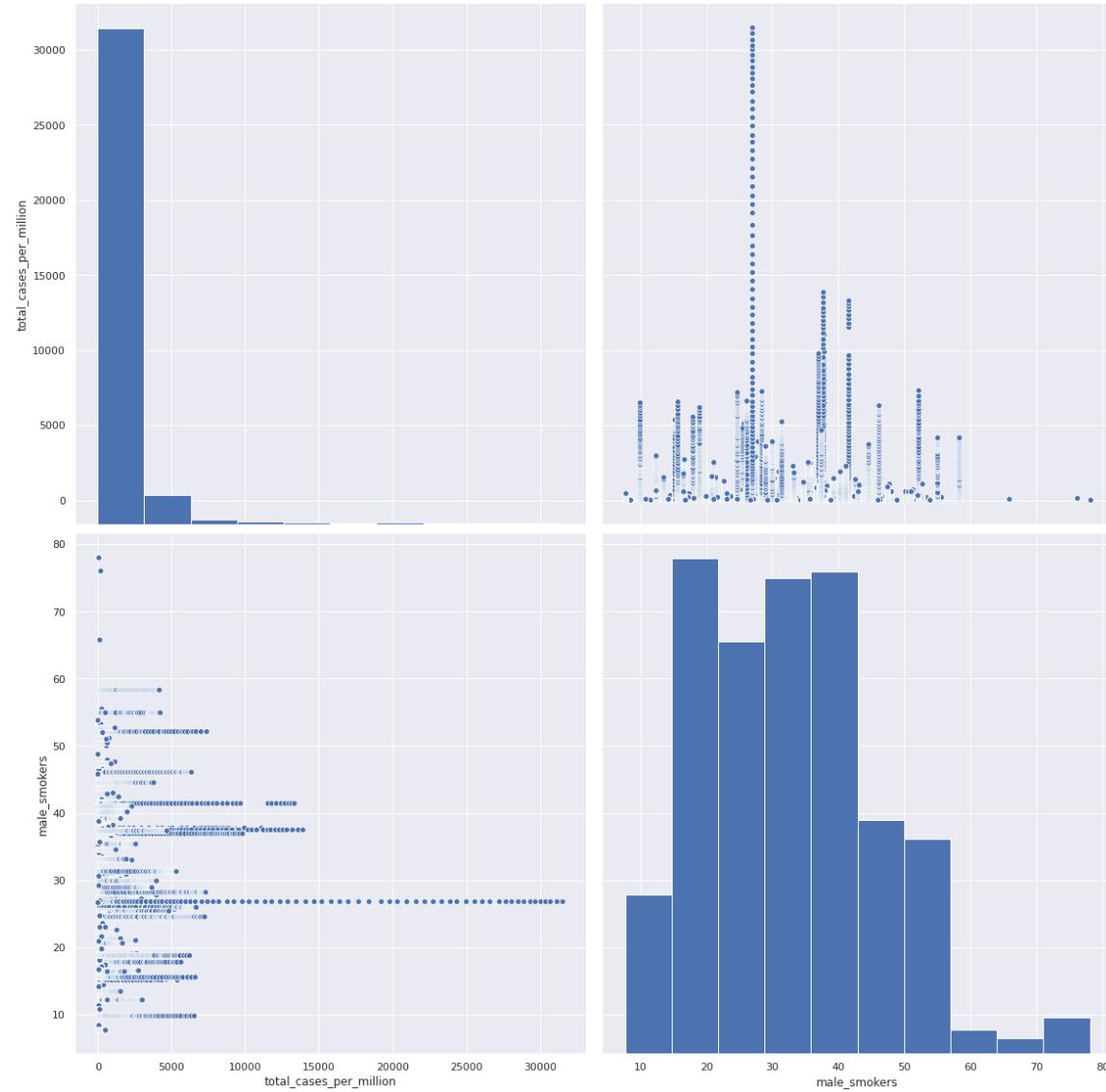


In [18]:

```
sns.pairplot(features, vars=["total_cases_per_million", "male_smokers"], height=8)
```

Out[18]:

```
<seaborn.axisgrid.PairGrid at 0x7f6456522048>
```

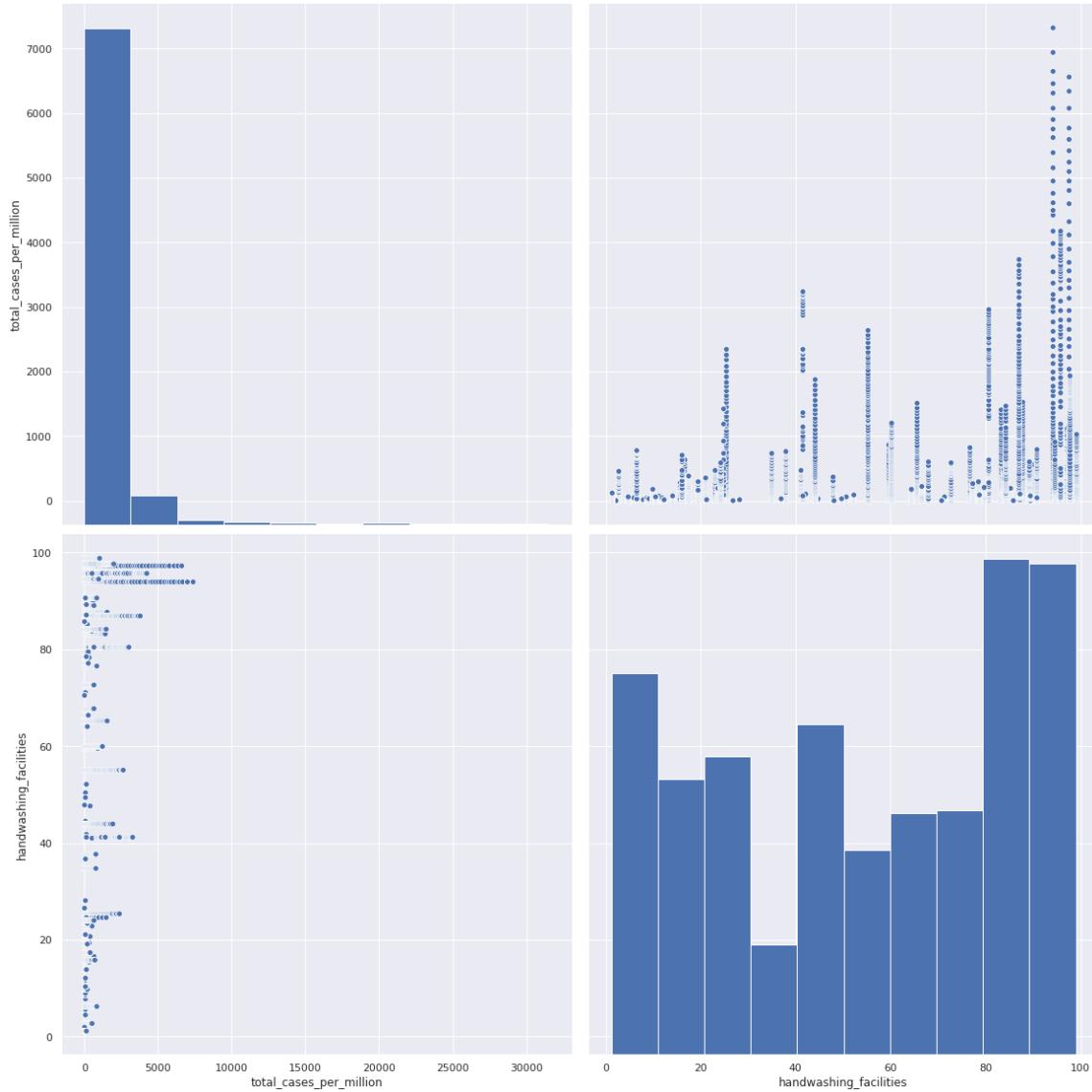


In [19]:

```
sns.pairplot(features, vars=["total_cases_per_million", "handwashing_facilities"], height=8)
```

Out[19]:

```
<seaborn.axisgrid.PairGrid at 0x7f645643b2b0>
```

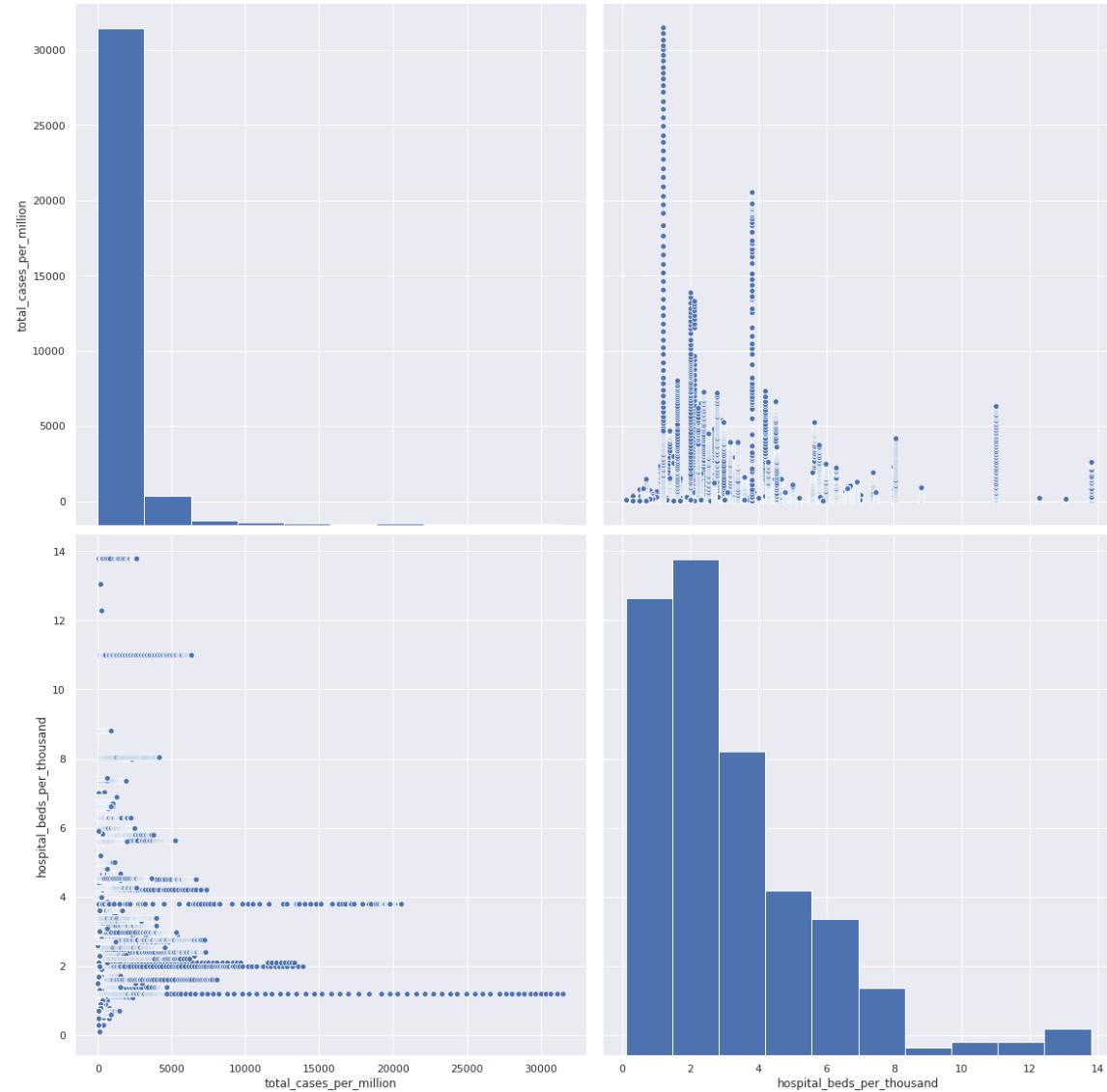


In [20]:

```
sns.pairplot(features, vars=["total_cases_per_million", "hospital_beds_per_thous  
and"], height=8)
```

Out[20]:

```
<seaborn.axisgrid.PairGrid at 0x7f64561330f0>
```

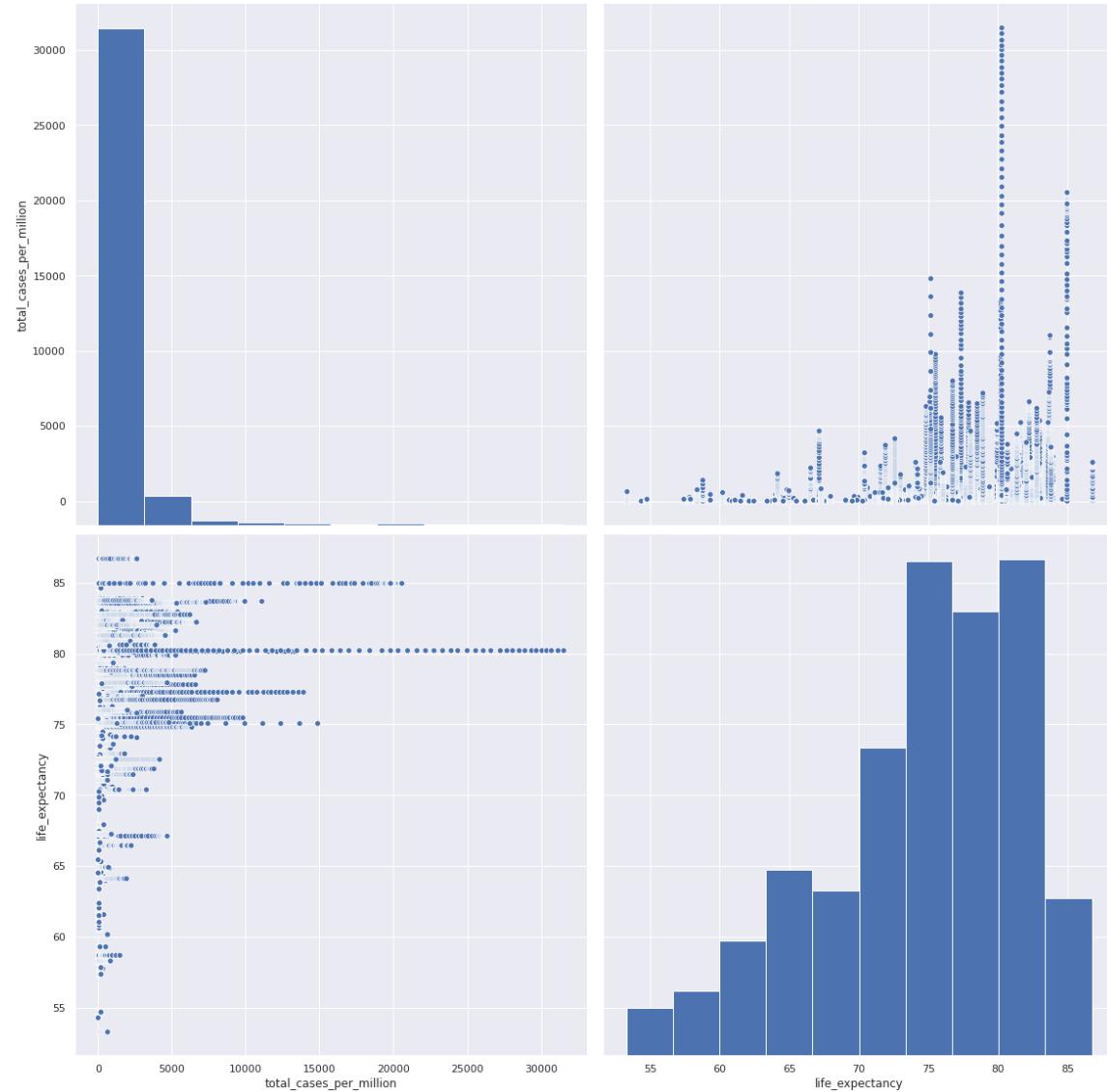


In [21]:

```
sns.pairplot(features, vars=["total_cases_per_million", "life_expectancy"], height=8)
```

Out[21]:

```
<seaborn.axisgrid.PairGrid at 0x7f64567182b0>
```

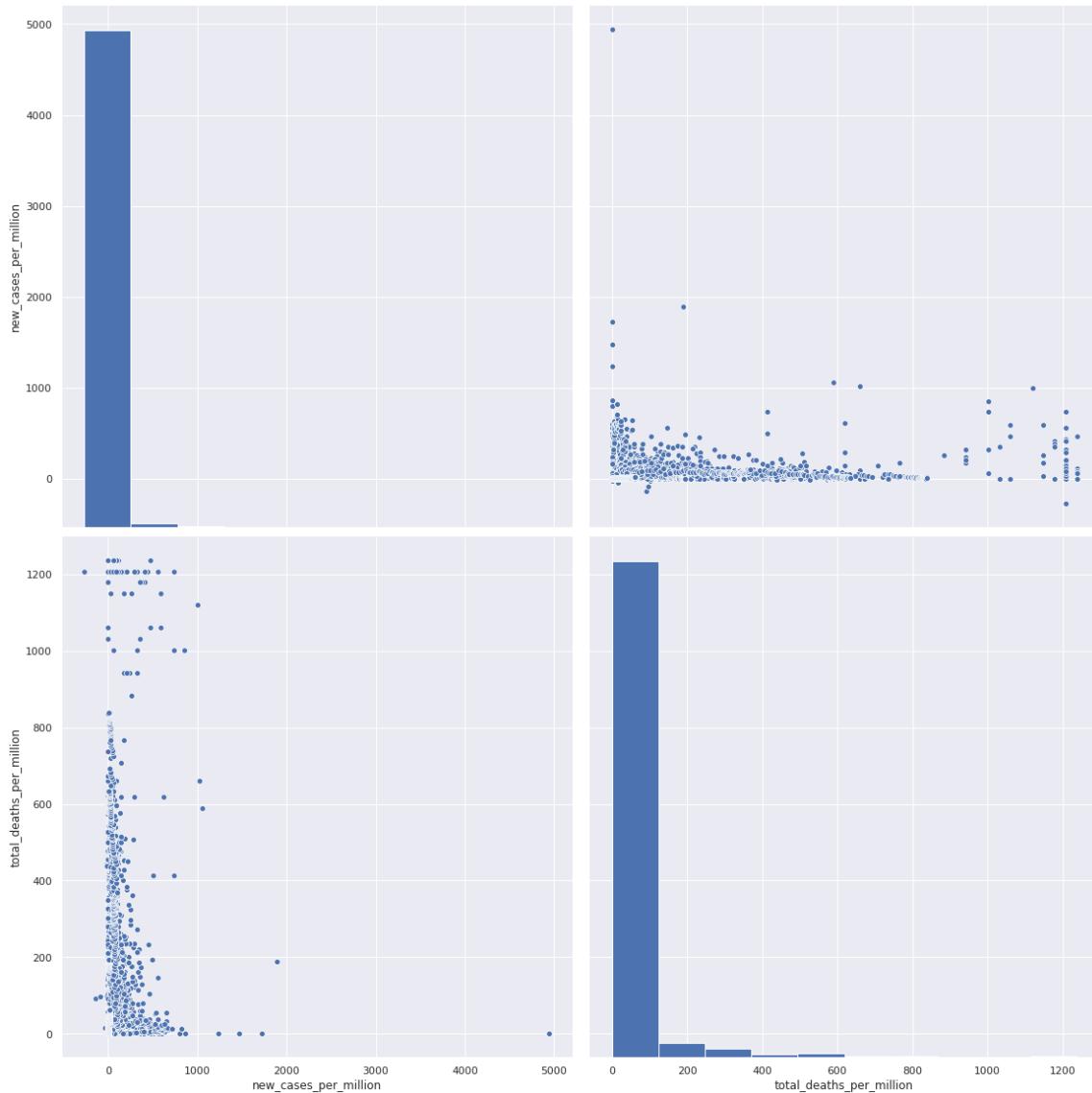


In [22]:

```
sns.pairplot(features, vars=["new_cases_per_million", "total_deaths_per_million"], height=8)
```

Out[22]:

```
<seaborn.axisgrid.PairGrid at 0x7f6455d4c828>
```

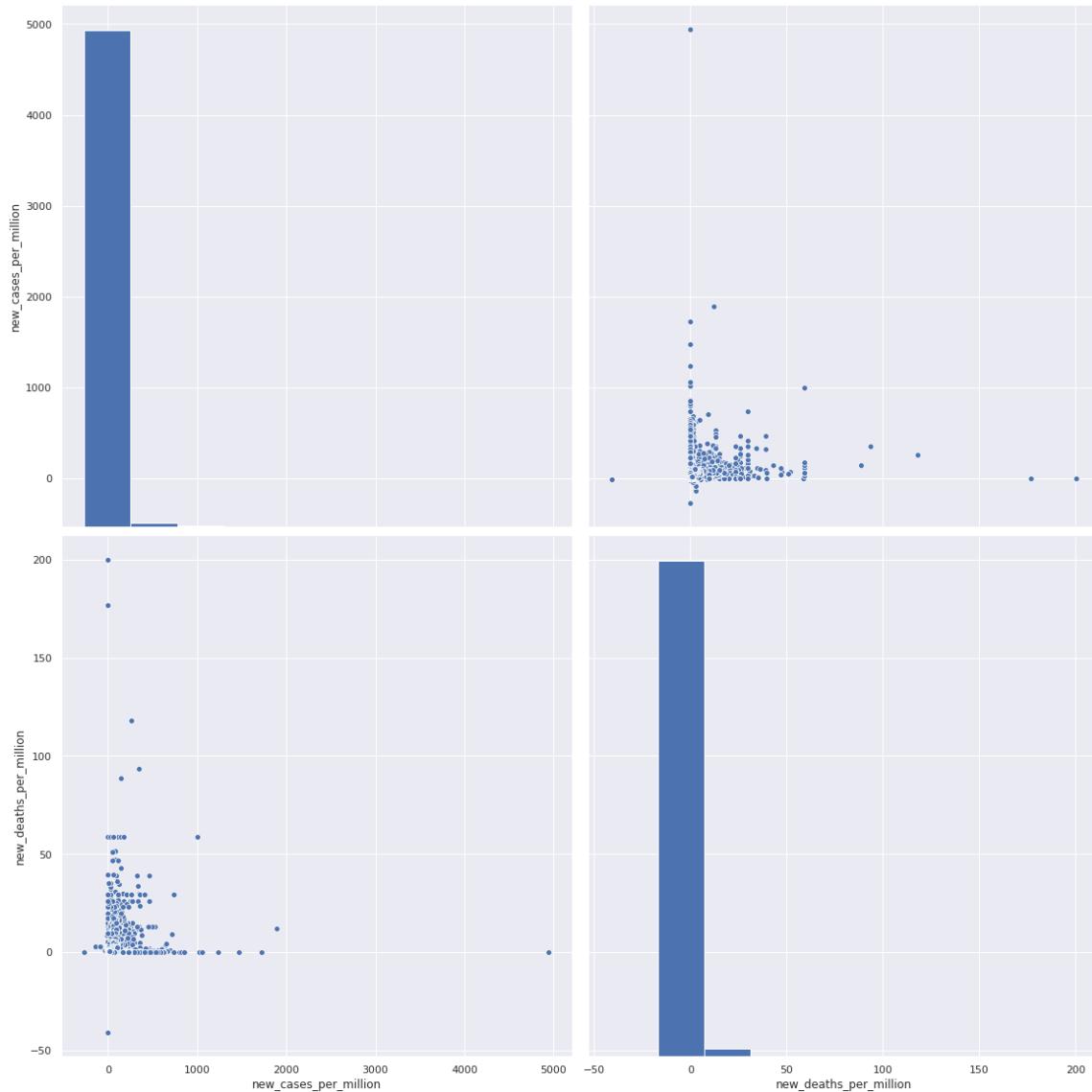


In [23]:

```
sns.pairplot(features, vars=["new_cases_per_million", "new_deaths_per_million"], height=8)
```

Out[23]:

```
<seaborn.axisgrid.PairGrid at 0x7f6455cdd6a0>
```

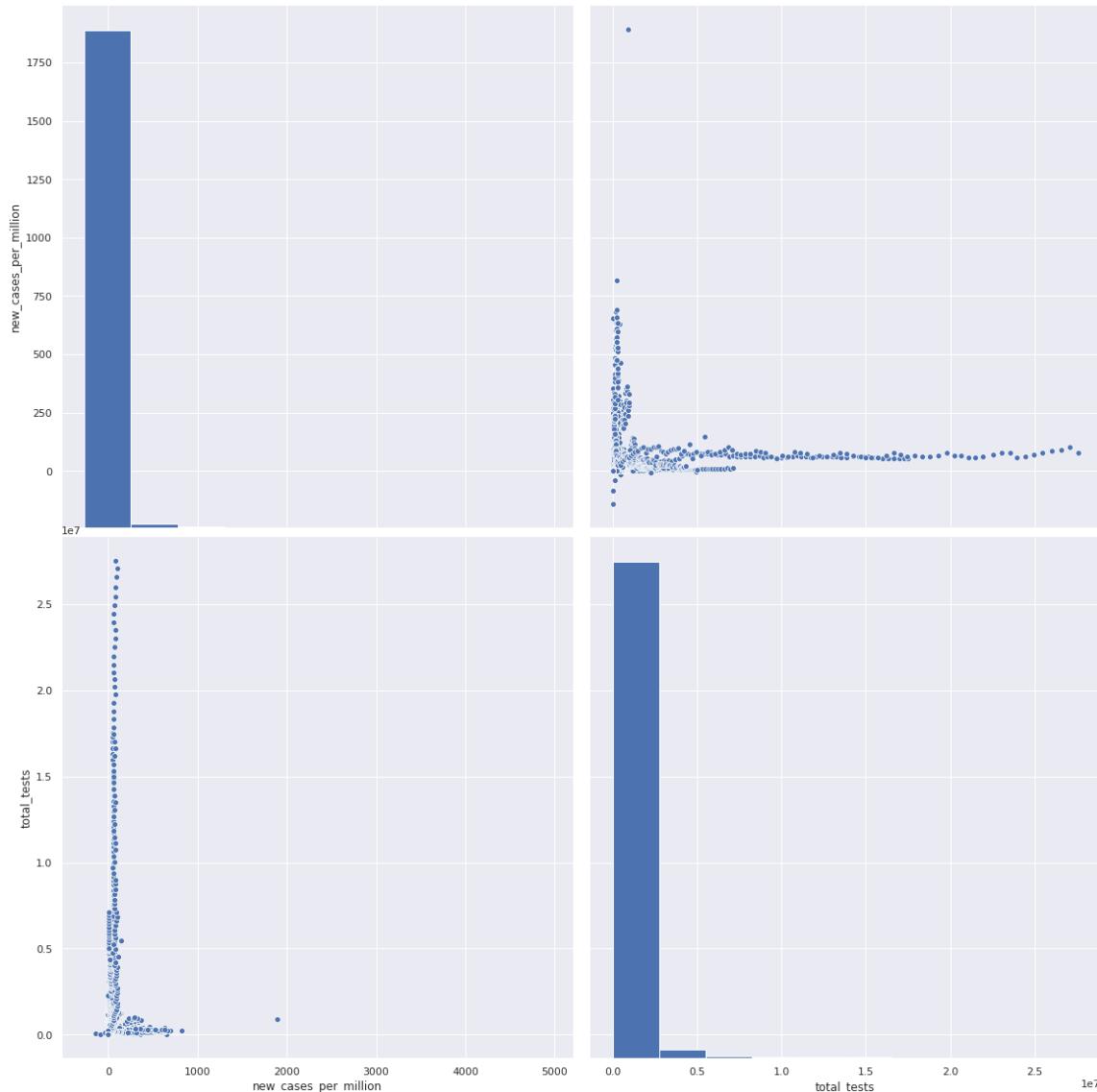


In [24]:

```
sns.pairplot(features, vars=["new_cases_per_million", "total_tests"], height=8)
```

Out[24]:

```
<seaborn.axisgrid.PairGrid at 0x7f6455938860>
```

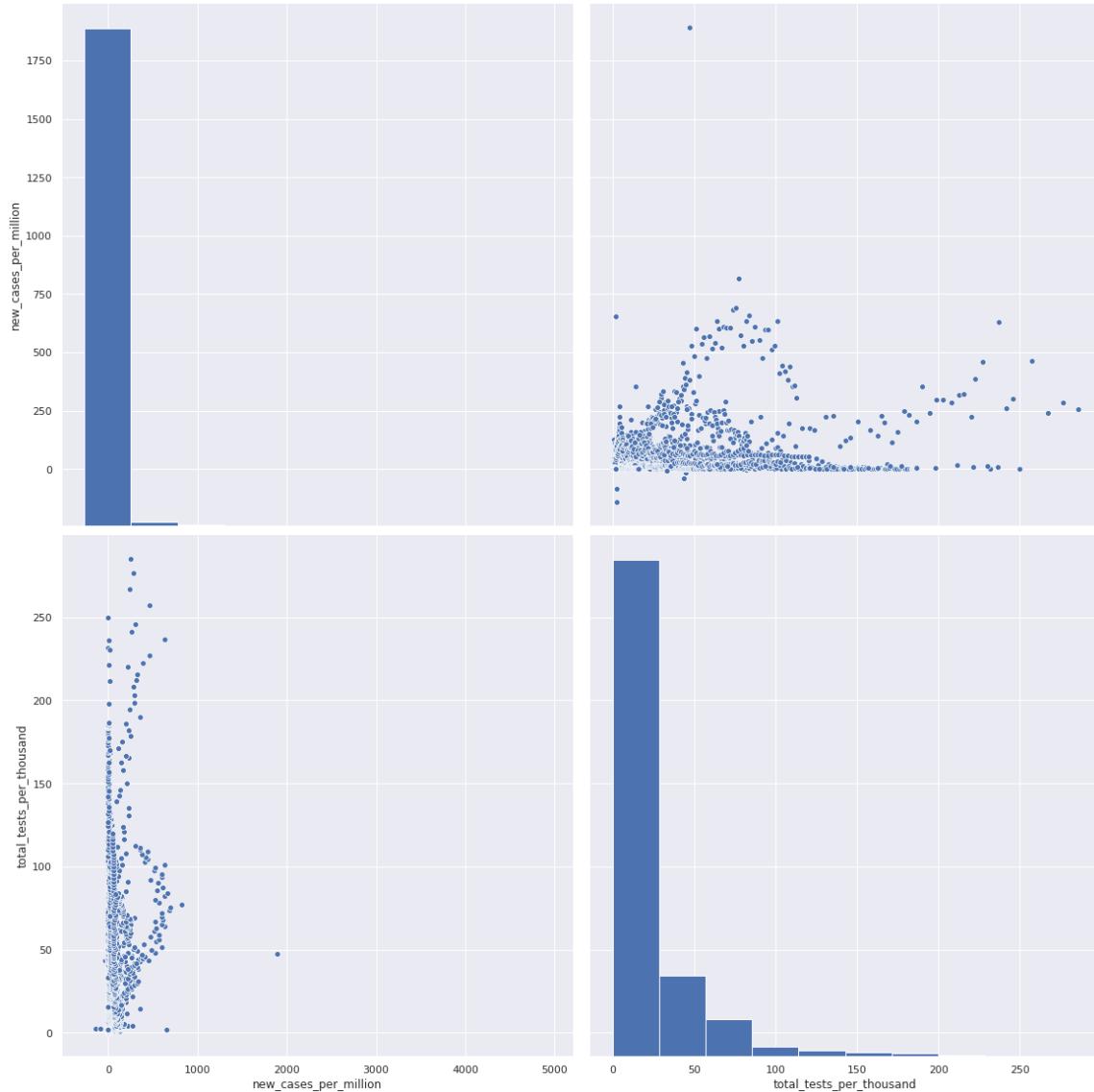


In [25]:

```
sns.pairplot(features, vars=["new_cases_per_million", "total_tests_per_thousand"], height=8)
```

Out[25]:

```
<seaborn.axisgrid.PairGrid at 0x7f6455f13518>
```

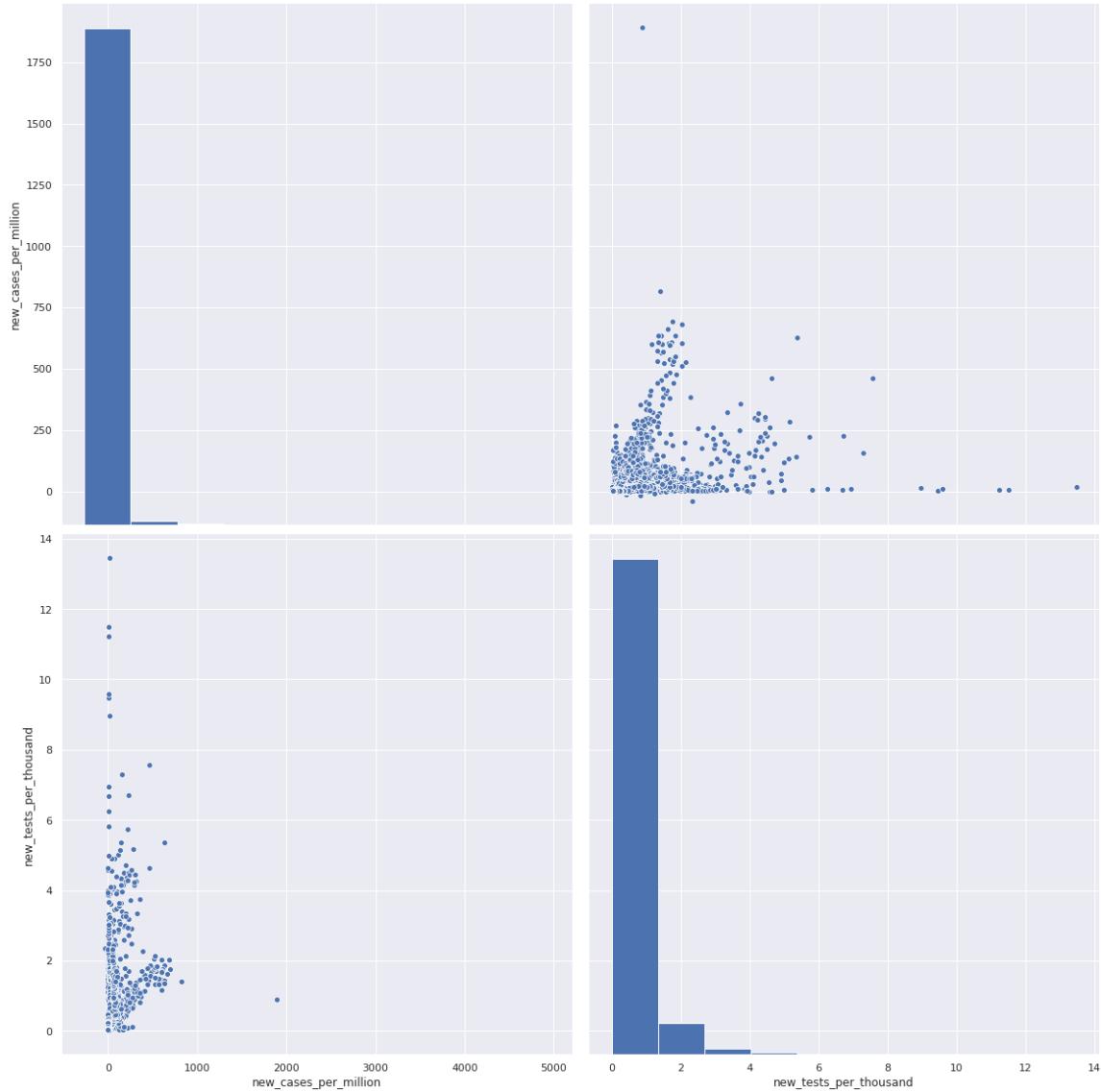


In [26]:

```
sns.pairplot(features, vars=["new_cases_per_million", "new_tests_per_thousand"], height=8)
```

Out[26]:

```
<seaborn.axisgrid.PairGrid at 0x7f645551b940>
```

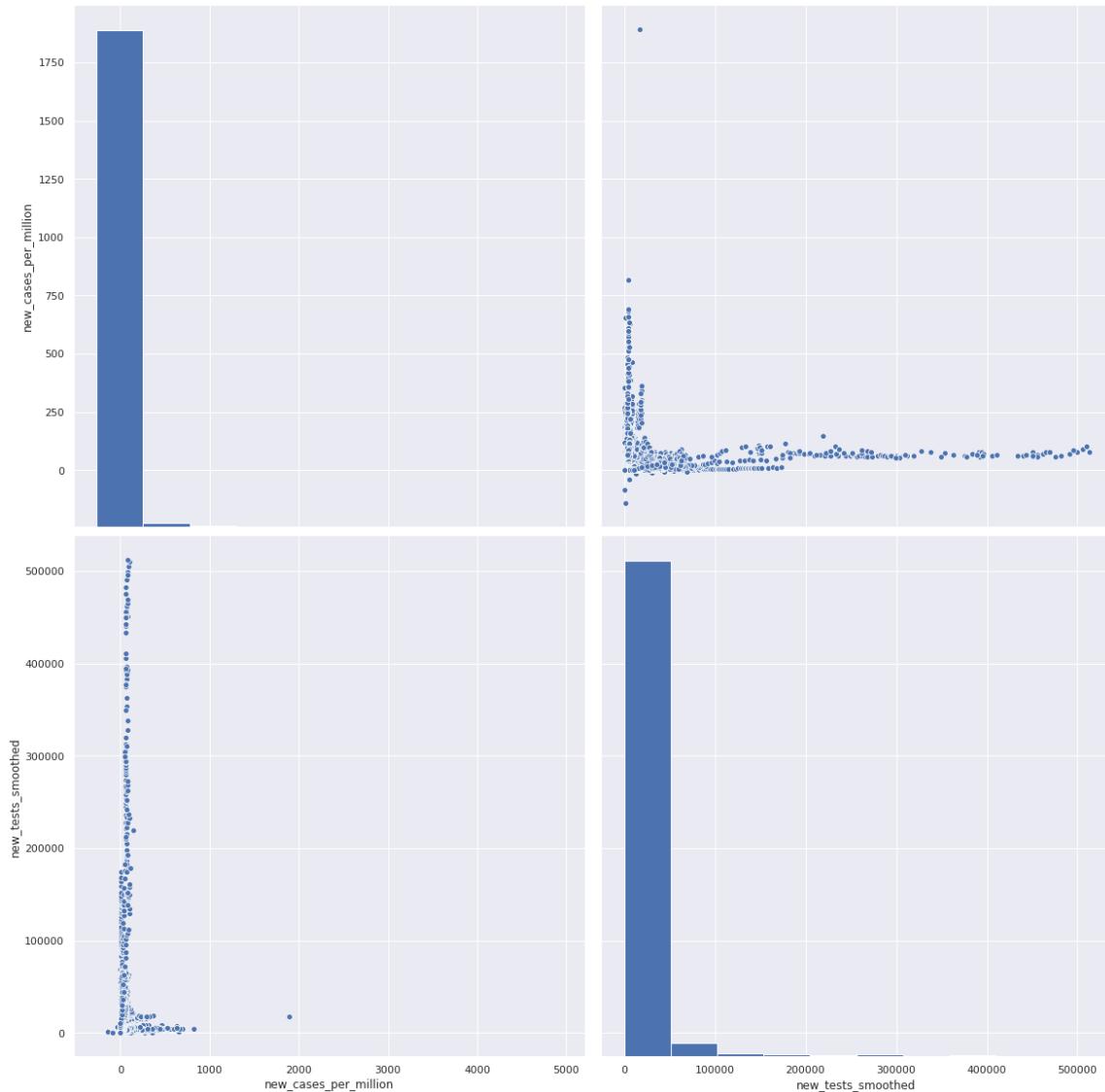


In [27]:

```
sns.pairplot(features, vars=["new_cases_per_million", "new_tests_smoothed"], height=8)
```

Out[27]:

```
<seaborn.axisgrid.PairGrid at 0x7f64552c7208>
```

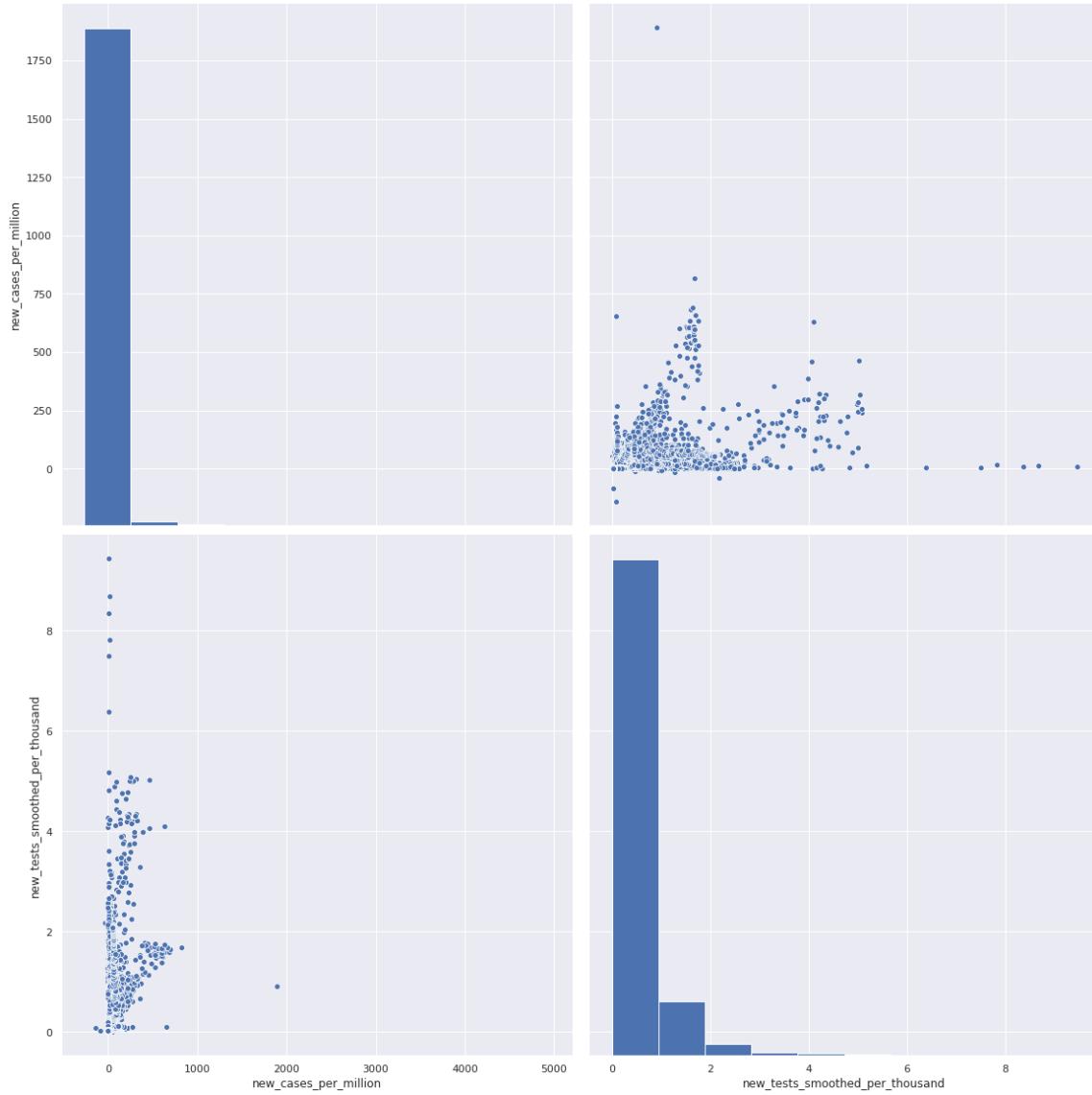


In [28]:

```
sns.pairplot(features, vars=["new_cases_per_million", "new_tests_smoothed_per_thousand"], height=8)
```

Out[28]:

```
<seaborn.axisgrid.PairGrid at 0x7f64550e4b00>
```

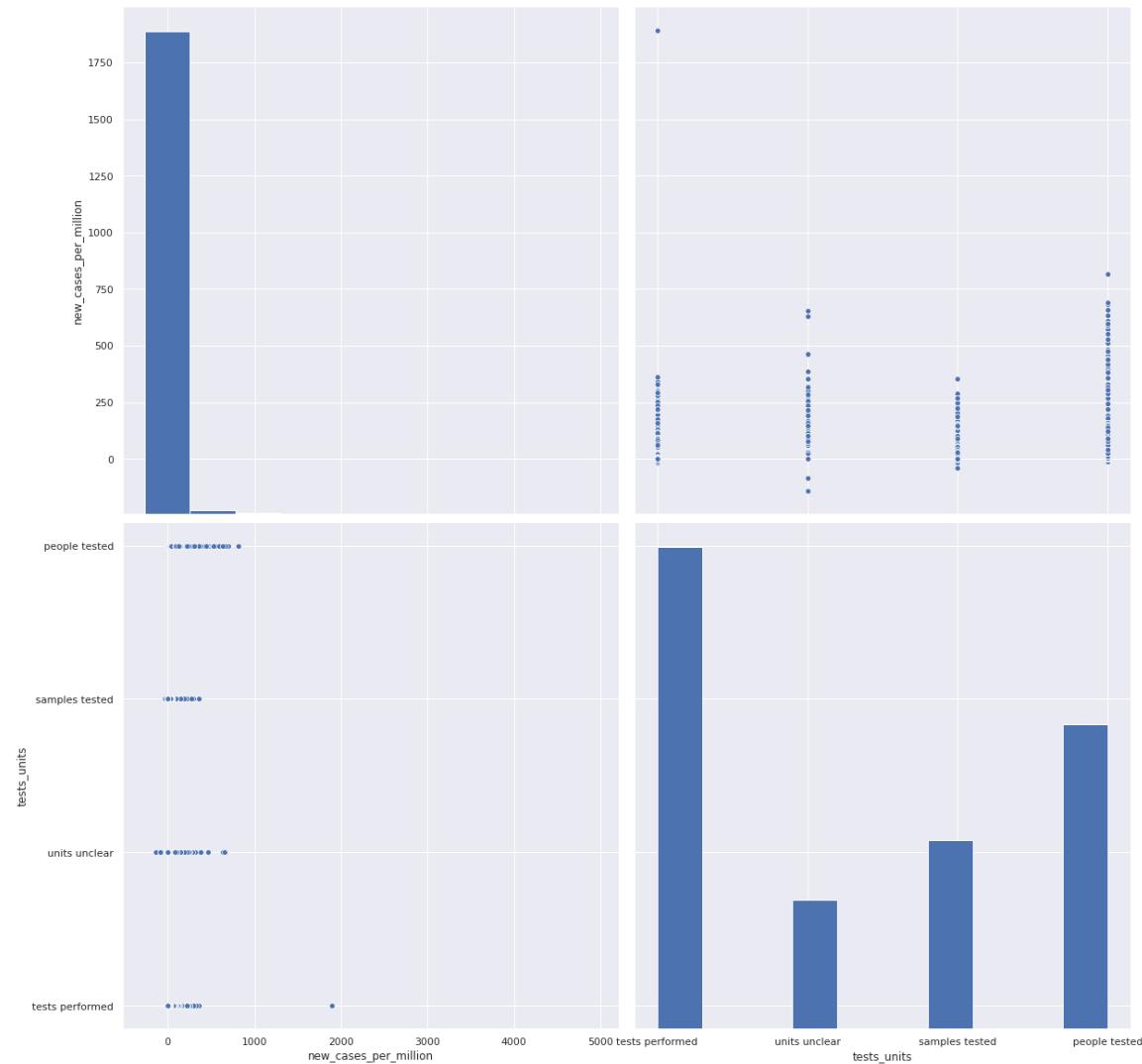


In [29]:

```
sns.pairplot(features, vars=["new_cases_per_million", "tests_units"], height=8)
```

Out[29]:

```
<seaborn.axisgrid.PairGrid at 0x7f6455061f60>
```

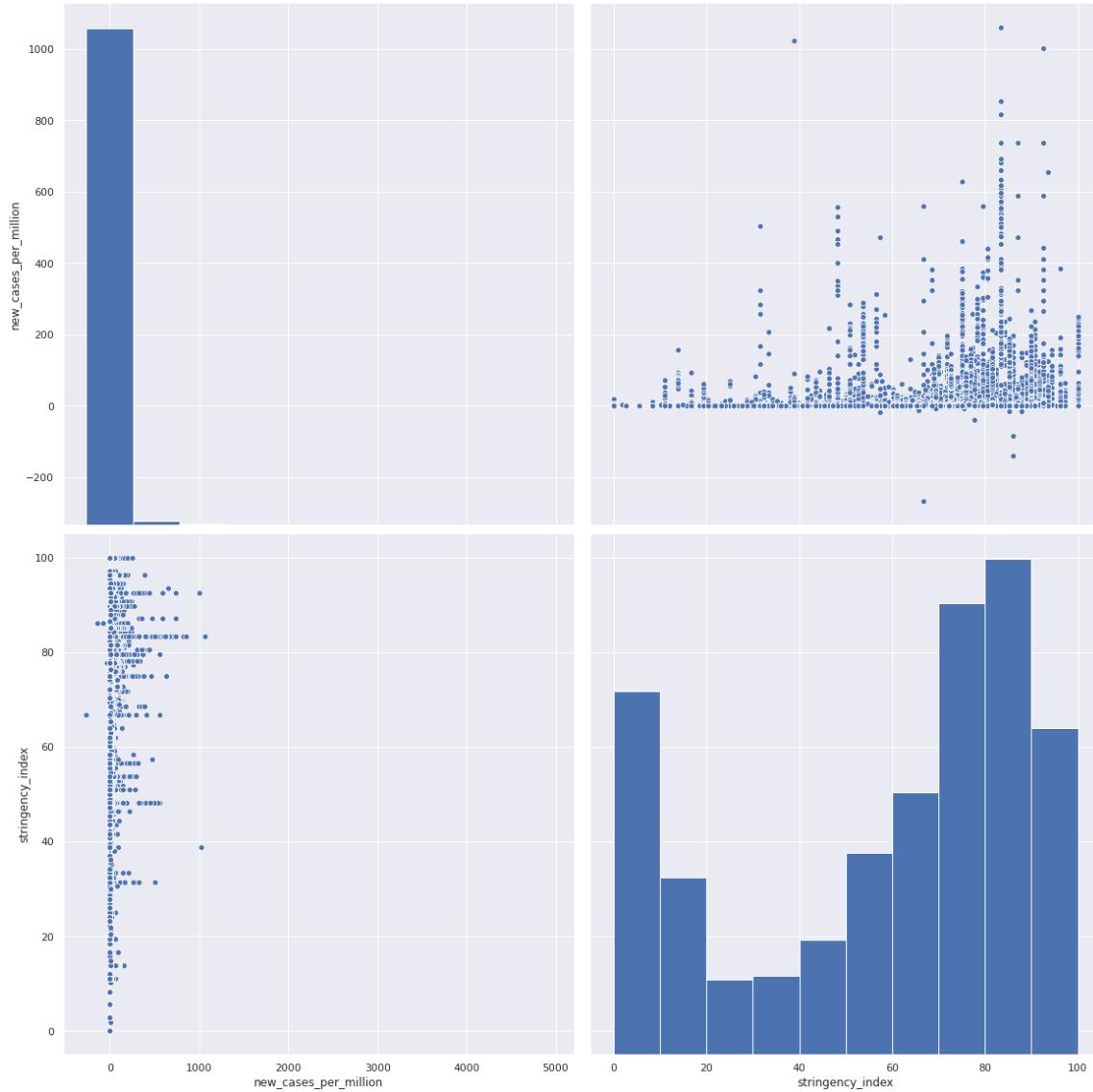


In [30]:

```
sns.pairplot(features, vars=["new_cases_per_million", "stringency_index"], height=8)
```

Out[30]:

```
<seaborn.axisgrid.PairGrid at 0x7f6454d24da0>
```

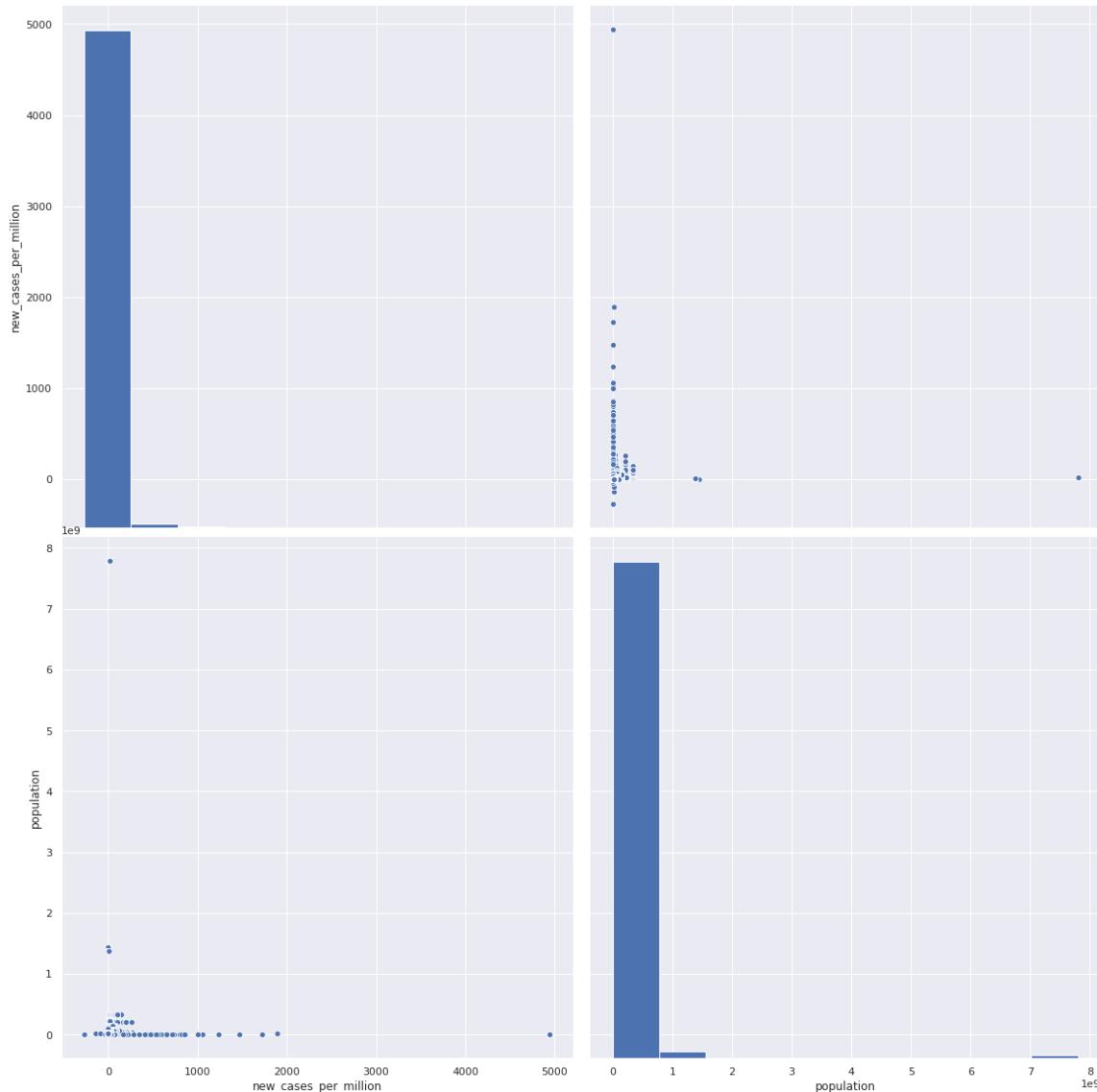


In [31]:

```
sns.pairplot(features, vars=["new_cases_per_million", "population"], height=8)
```

Out[31]:

```
<seaborn.axisgrid.PairGrid at 0x7f6454e2de48>
```

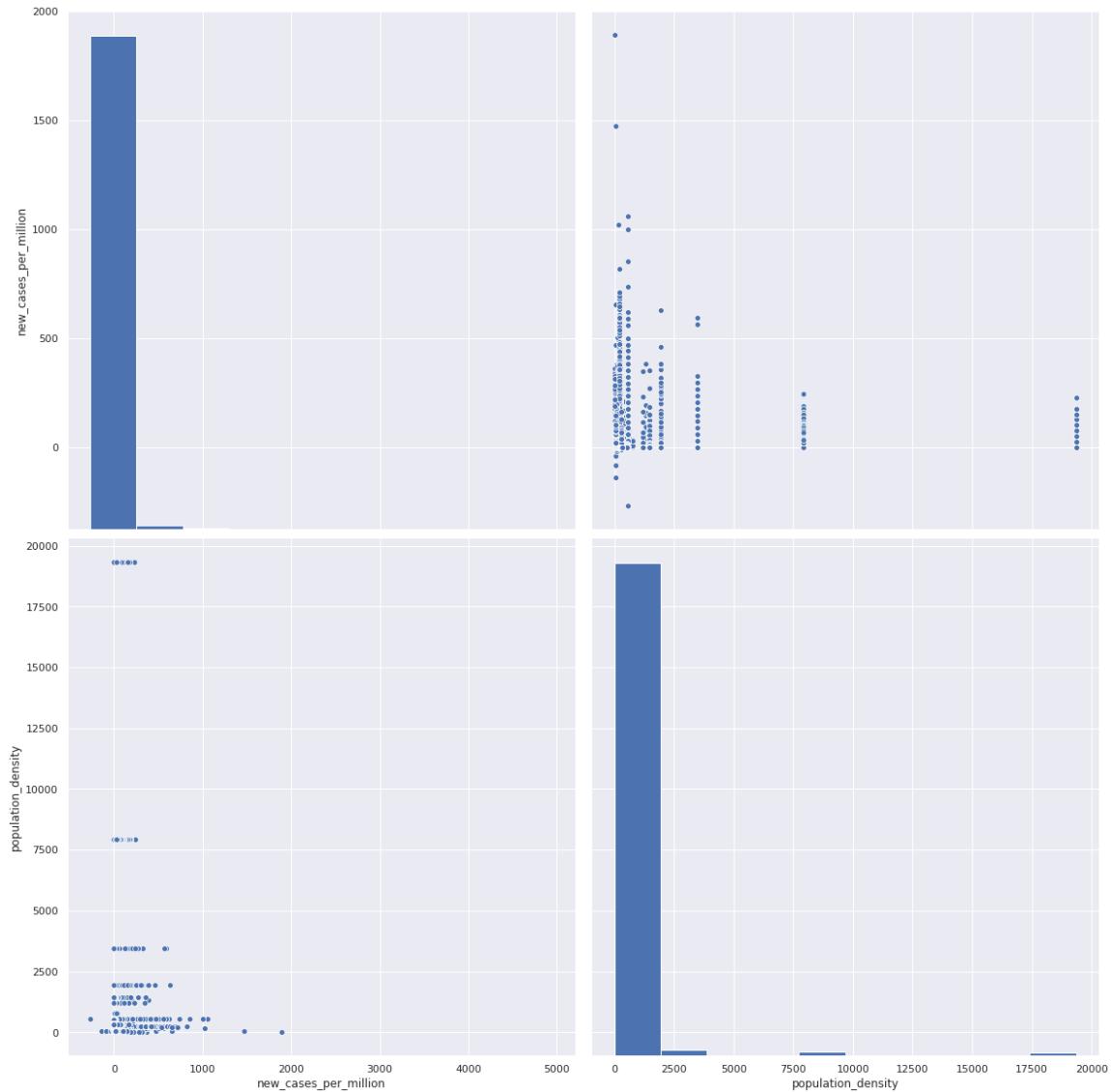


In [32]:

```
sns.pairplot(features, vars=["new_cases_per_million", "population_density"], height=8)
```

Out[32]:

```
<seaborn.axisgrid.PairGrid at 0x7f64552dc0f0>
```

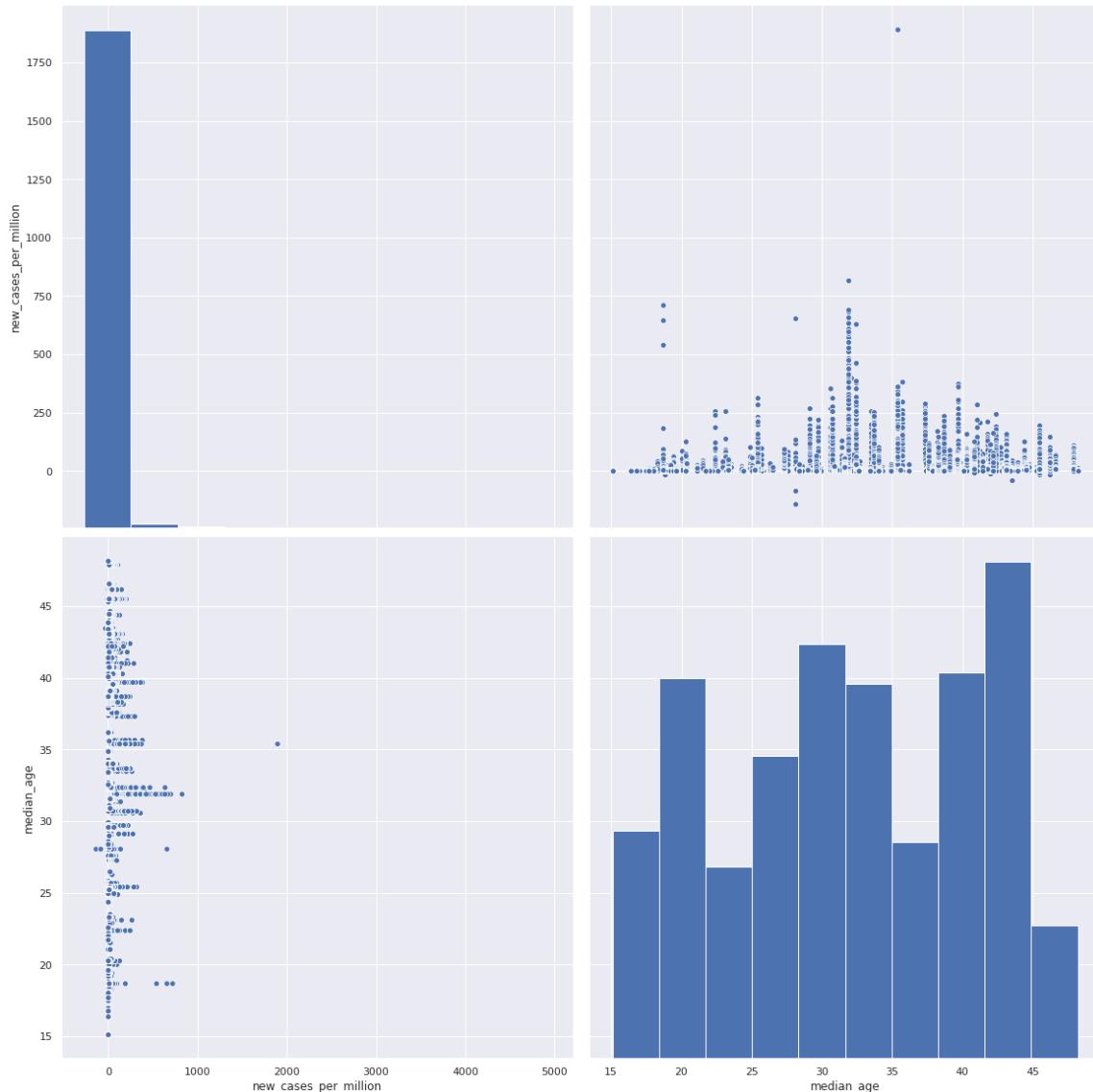


In [33]:

```
sns.pairplot(features, vars=["new_cases_per_million", "median_age"], height=8)
```

Out[33]:

```
<seaborn.axisgrid.PairGrid at 0x7f64546de1d0>
```

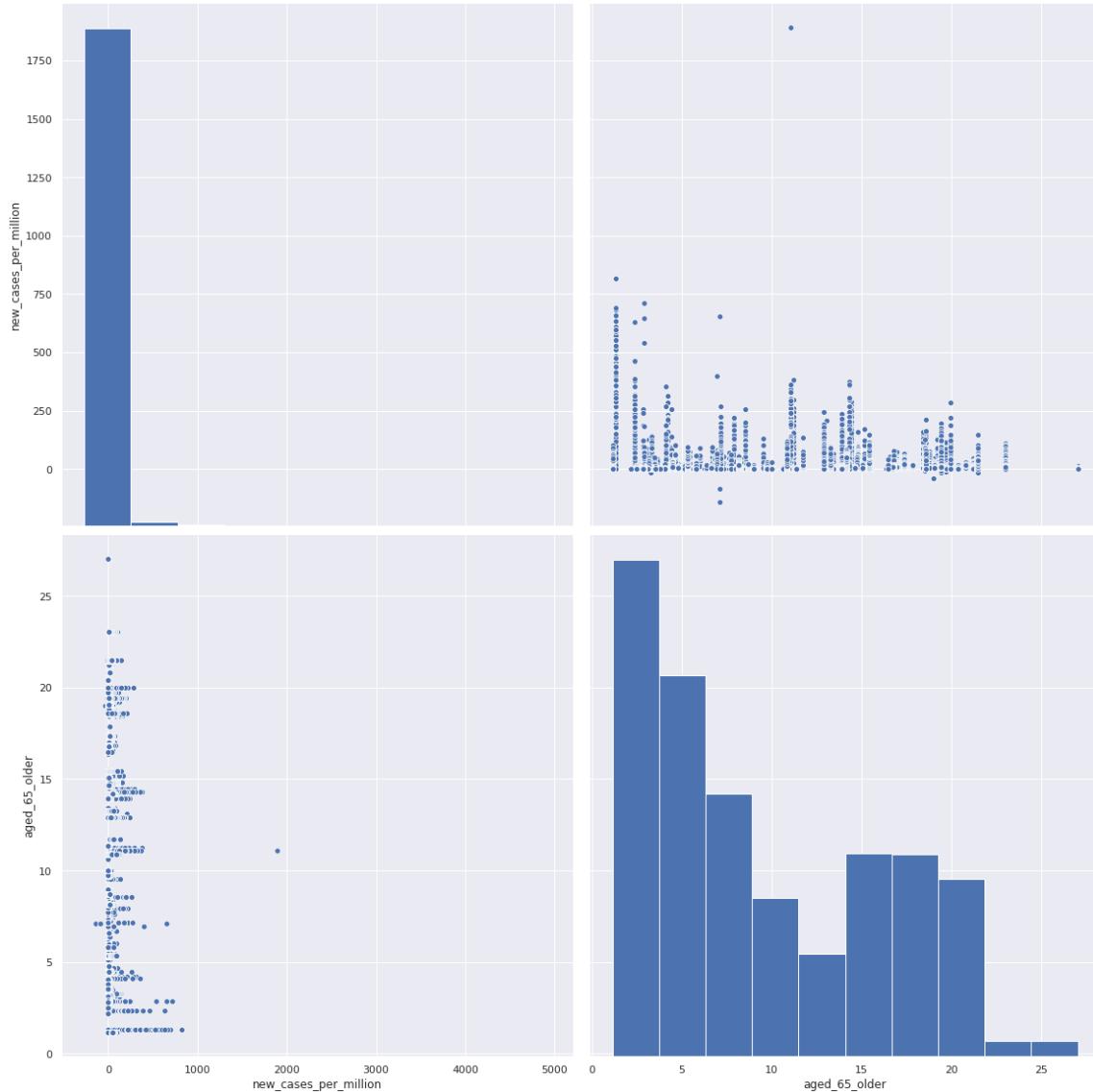


In [34]:

```
sns.pairplot(features, vars=["new_cases_per_million", "aged_65_older"], height=8)
```

Out[34]:

```
<seaborn.axisgrid.PairGrid at 0x7f64544ed048>
```

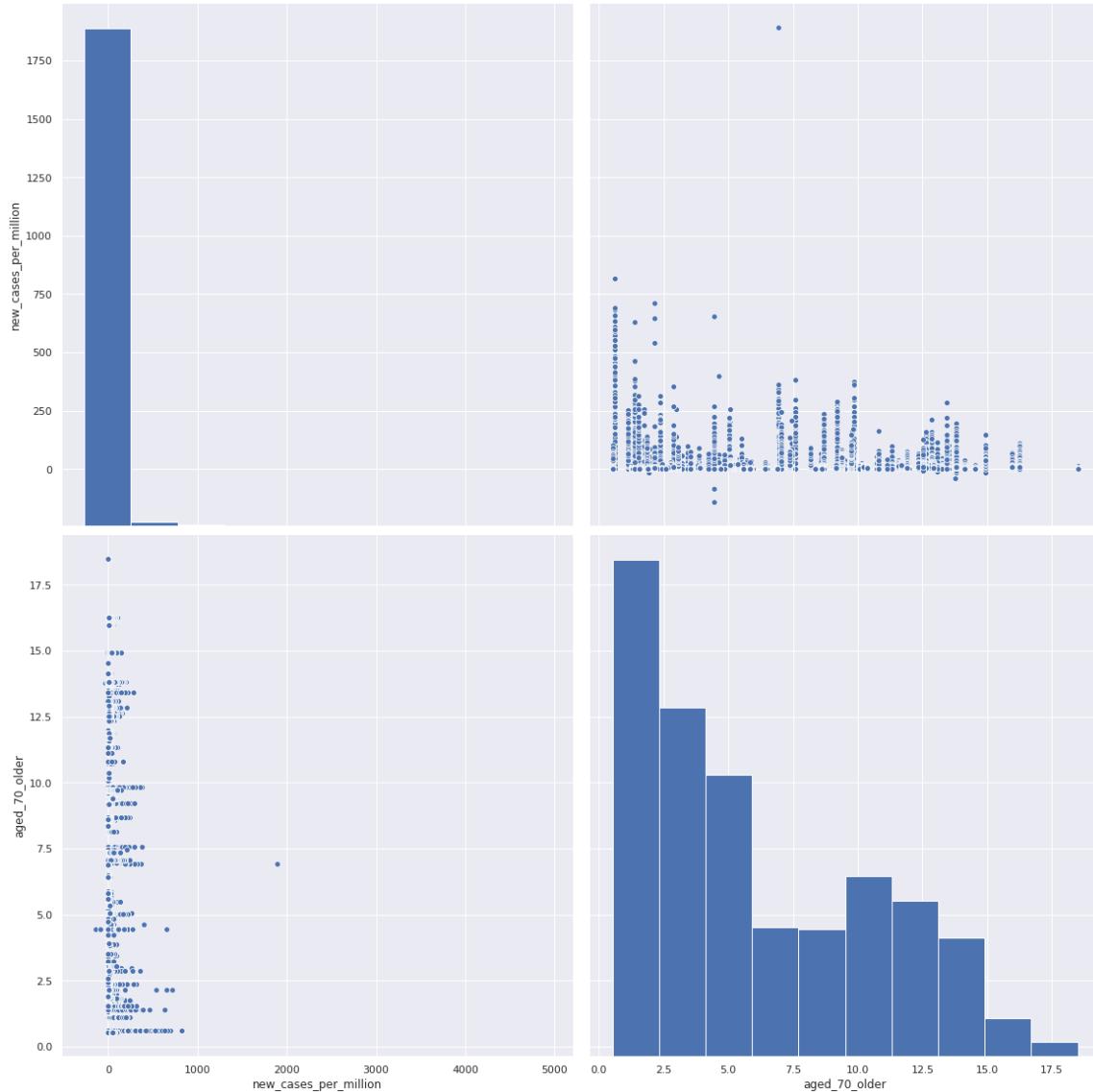


In [35]:

```
sns.pairplot(features, vars=["new_cases_per_million", "aged_70_older"], height=8)
```

Out[35]:

```
<seaborn.axisgrid.PairGrid at 0x7f645435ec50>
```

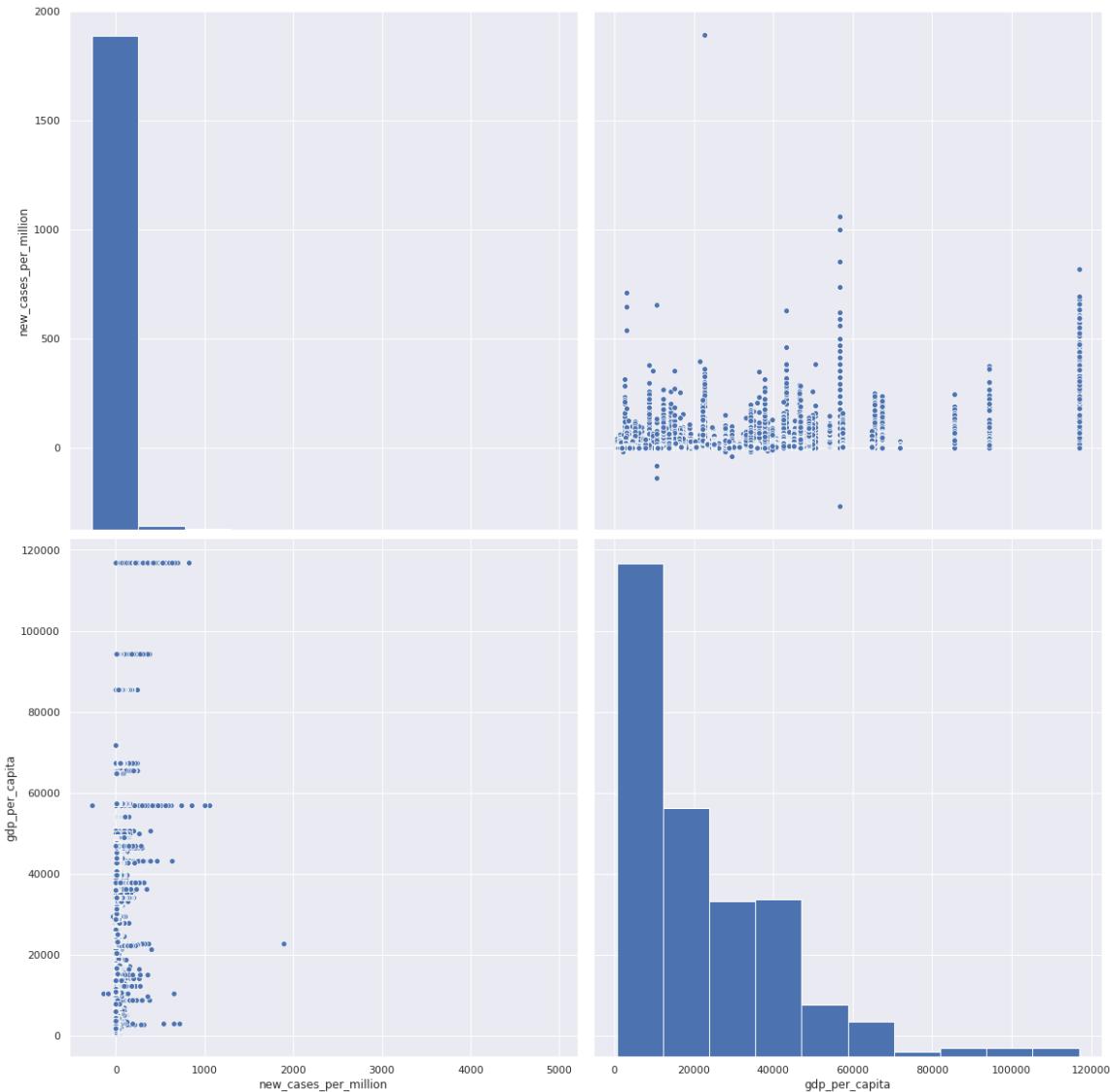


In [36]:

```
sns.pairplot(features, vars=["new_cases_per_million", "gdp_per_capita"], height=8)
```

Out[36]:

```
<seaborn.axisgrid.PairGrid at 0x7f6454090ef0>
```

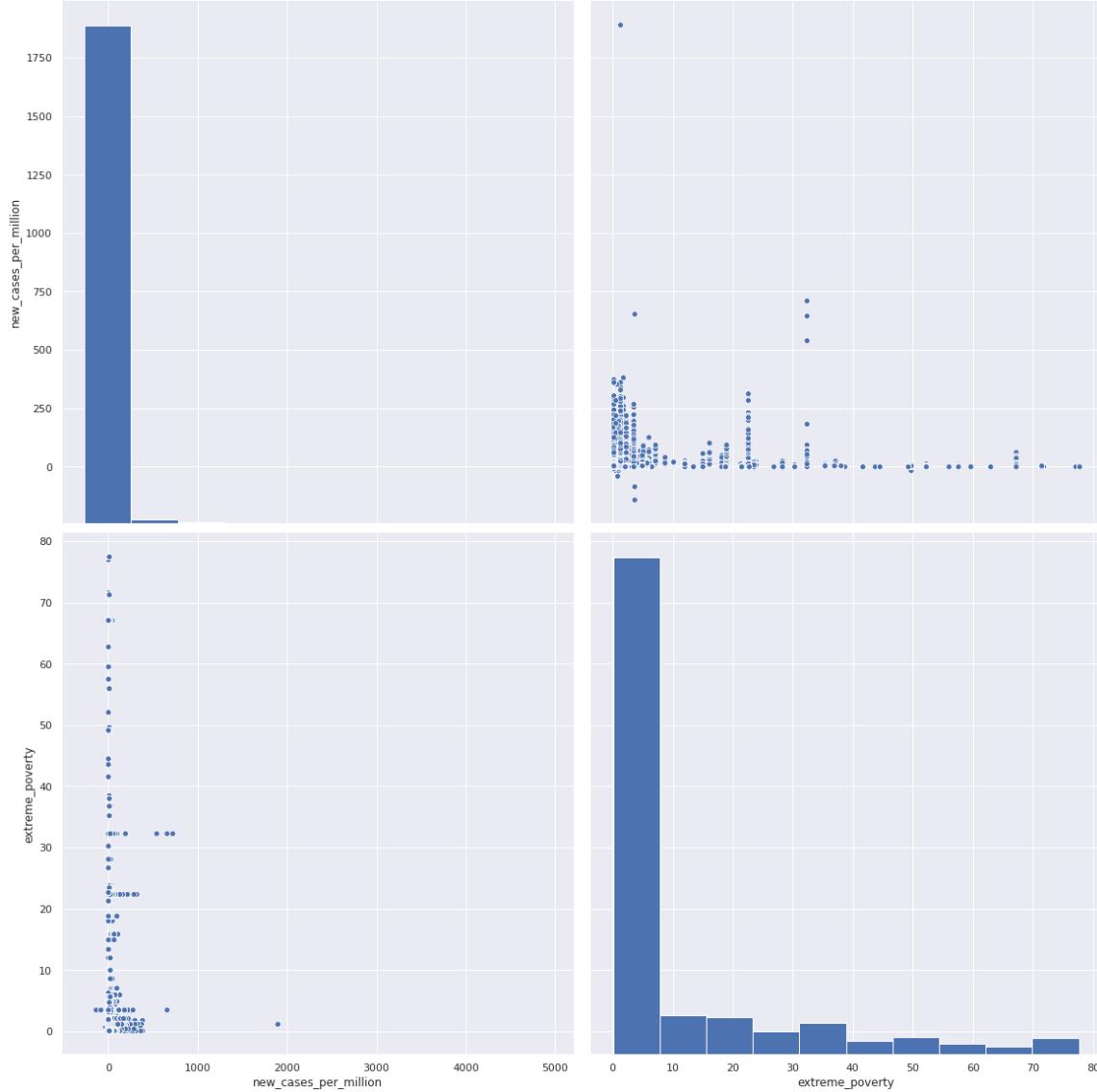


In [37]:

```
sns.pairplot(features, vars=["new_cases_per_million", "extreme_poverty"], height=8)
```

Out[37]:

```
<seaborn.axisgrid.PairGrid at 0x7f6453ec8908>
```

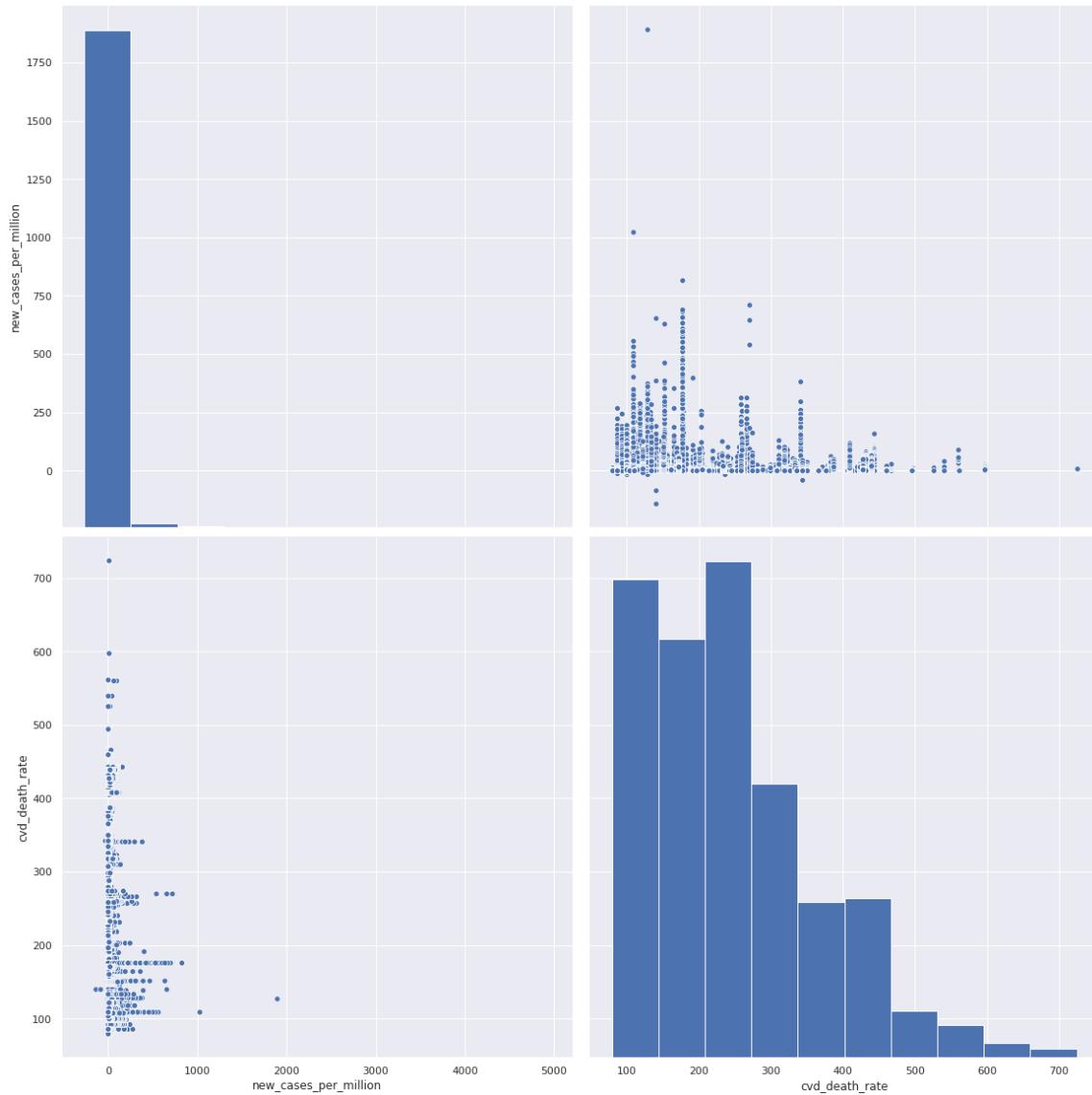


In [38]:

```
sns.pairplot(features, vars=["new_cases_per_million", "cvd_death_rate"], height=8)
```

Out[38]:

```
<seaborn.axisgrid.PairGrid at 0x7f6453ce9080>
```

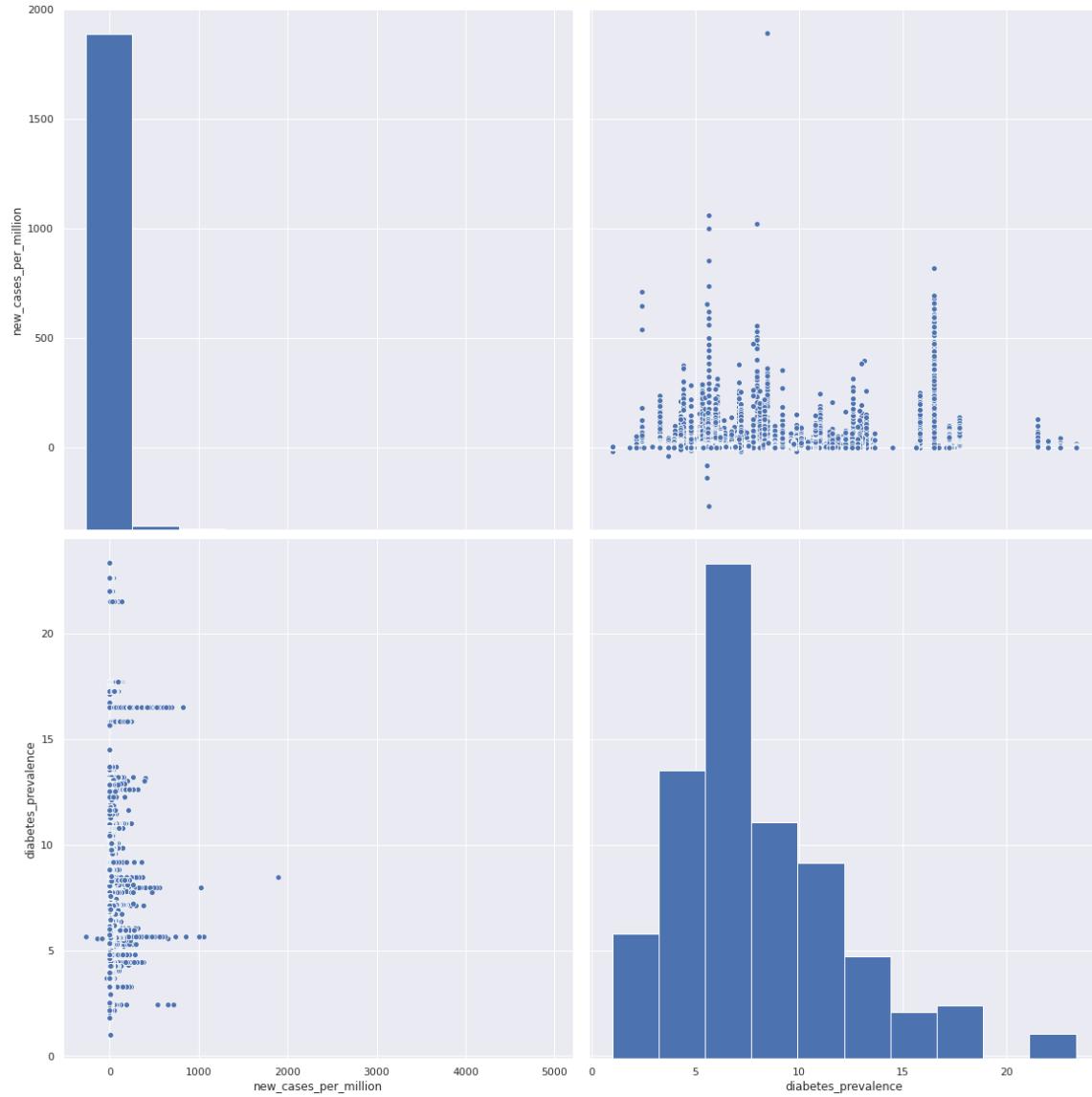


In [39]:

```
sns.pairplot(features, vars=["new_cases_per_million", "diabetes_prevalence"], height=8)
```

Out[39]:

```
<seaborn.axisgrid.PairGrid at 0x7f6453a953c8>
```

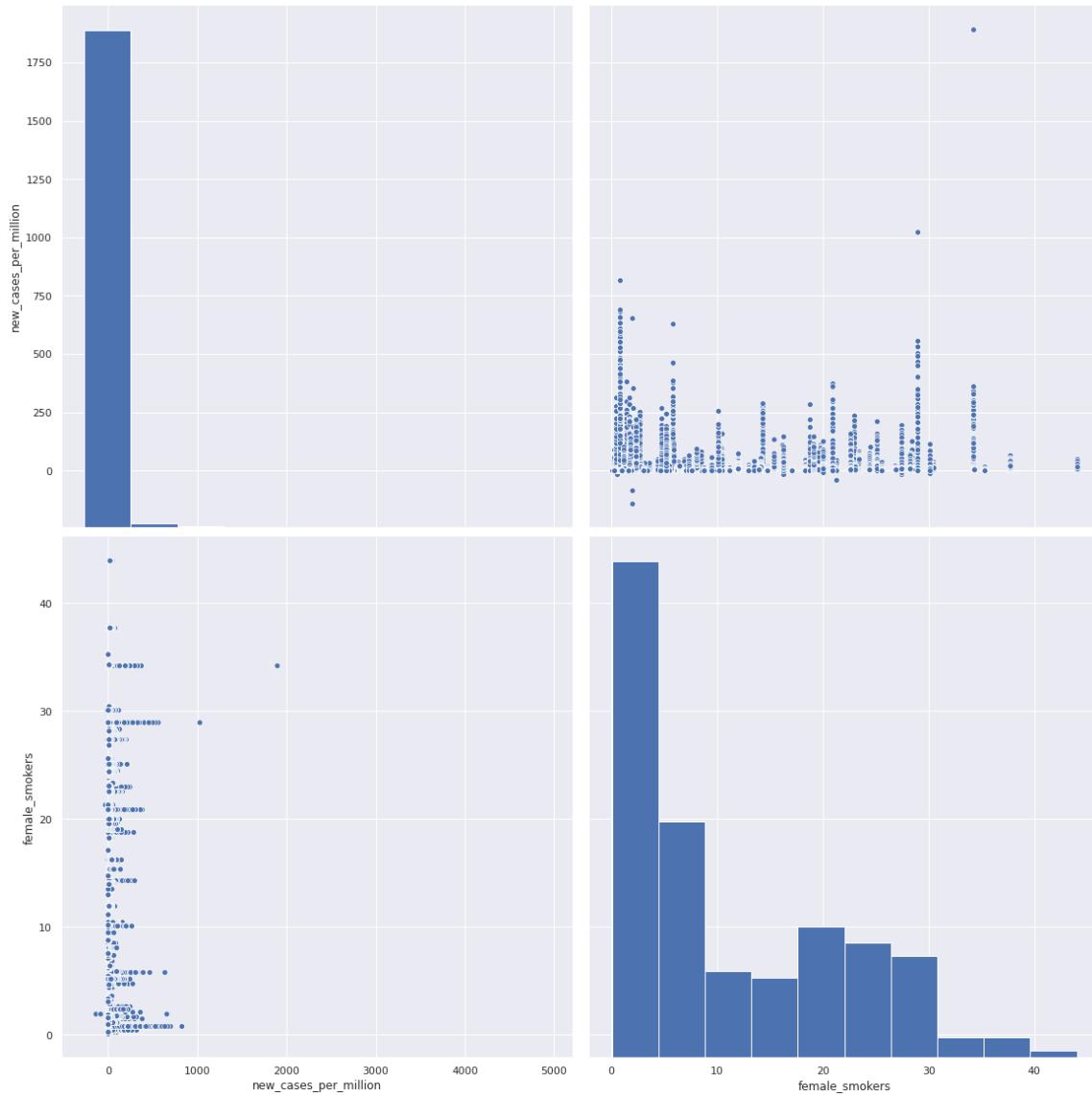


In [40]:

```
sns.pairplot(features, vars=["new_cases_per_million", "female_smokers"], height=8)
```

Out[40]:

```
<seaborn.axisgrid.PairGrid at 0x7f645478d7f0>
```

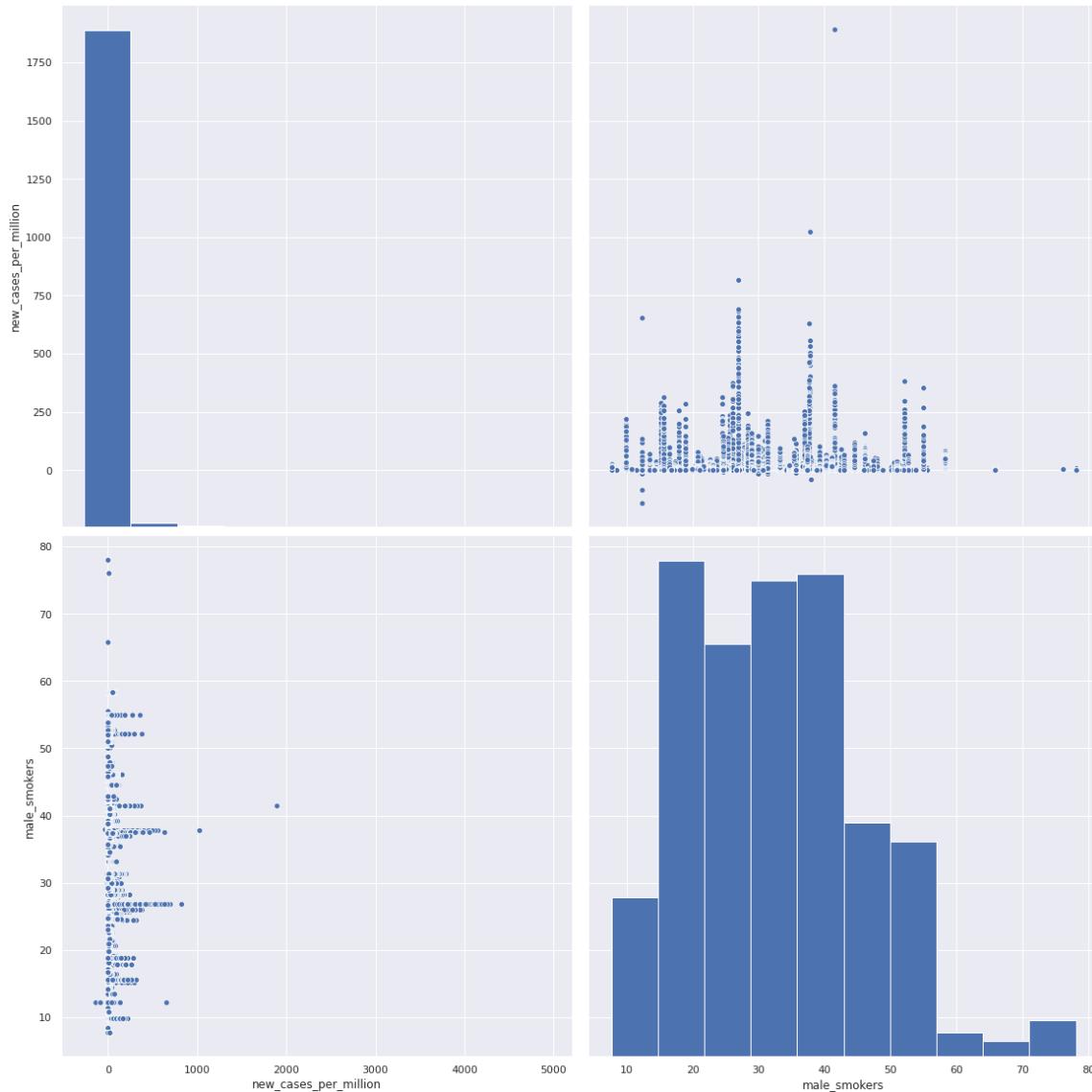


In [41]:

```
sns.pairplot(features, vars=["new_cases_per_million", "male_smokers"], height=8)
```

Out[41]:

```
<seaborn.axisgrid.PairGrid at 0x7f645370fa90>
```

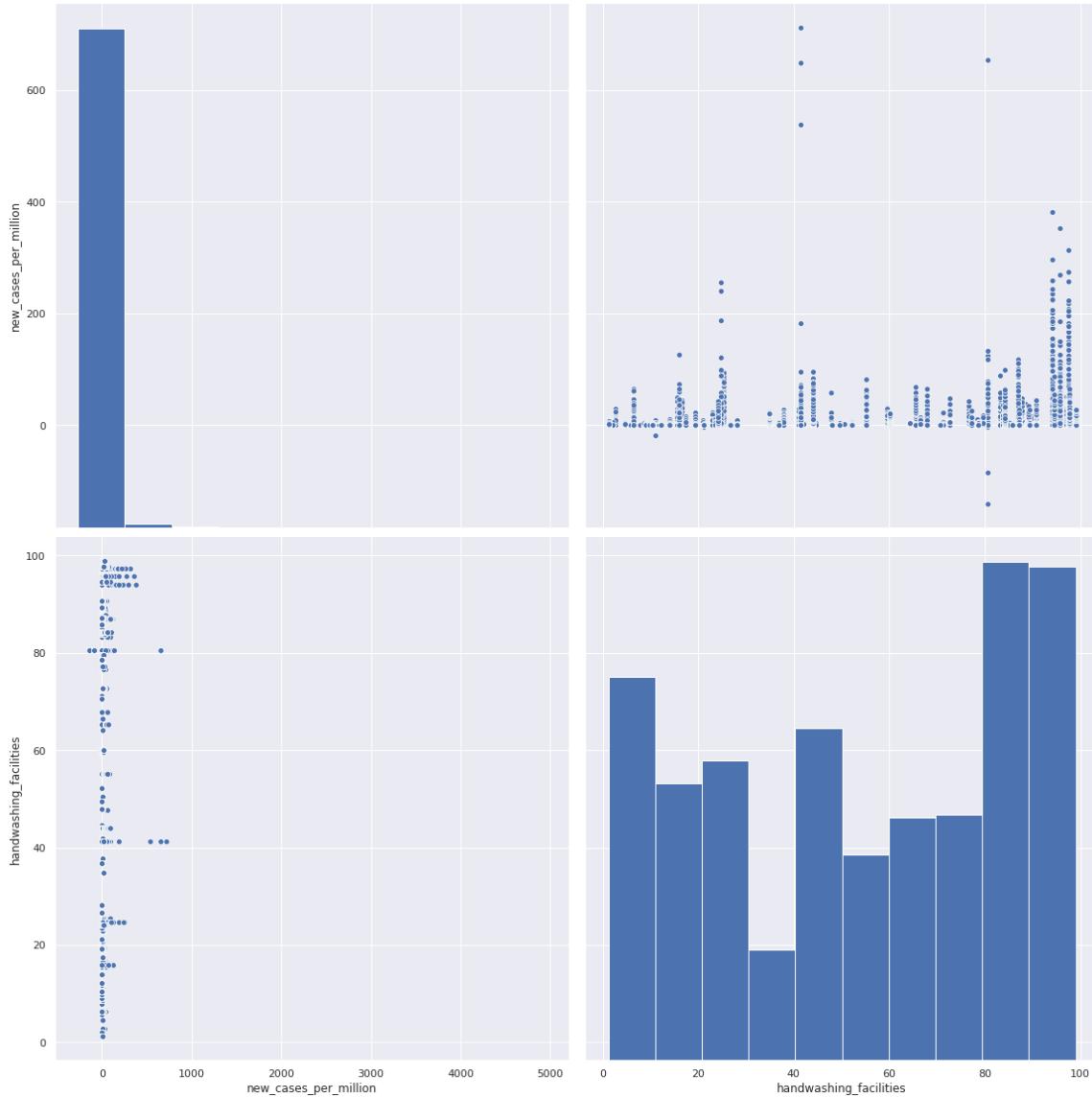


In [42]:

```
sns.pairplot(features, vars=["new_cases_per_million", "handwashing_facilities"], height=8)
```

Out[42]:

```
<seaborn.axisgrid.PairGrid at 0x7f64536c3080>
```

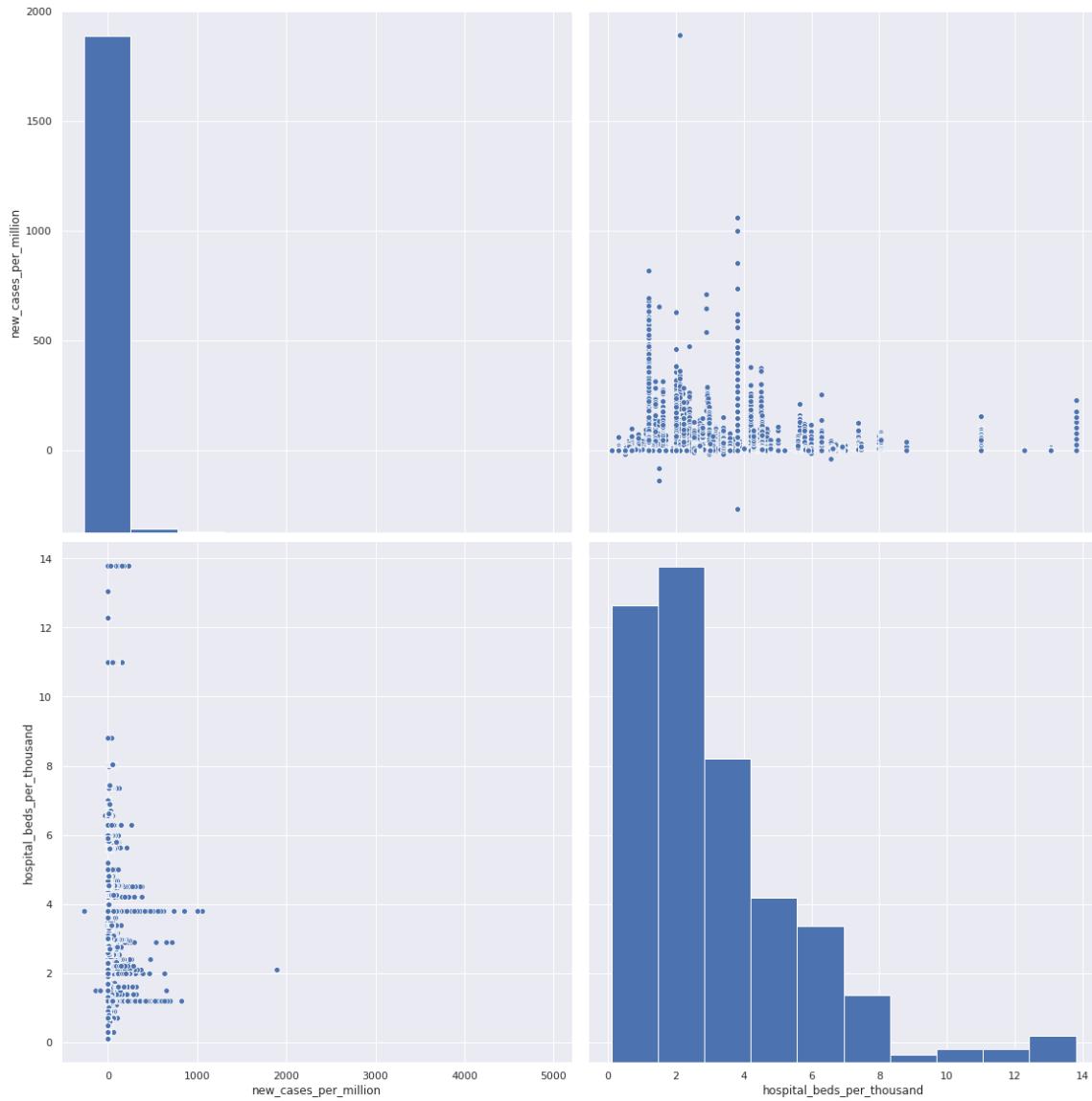


In [43]:

```
sns.pairplot(features, vars=["new_cases_per_million", "hospital_beds_per_thousan  
d"], height=8)
```

Out[43]:

```
<seaborn.axisgrid.PairGrid at 0x7f64532e2e80>
```

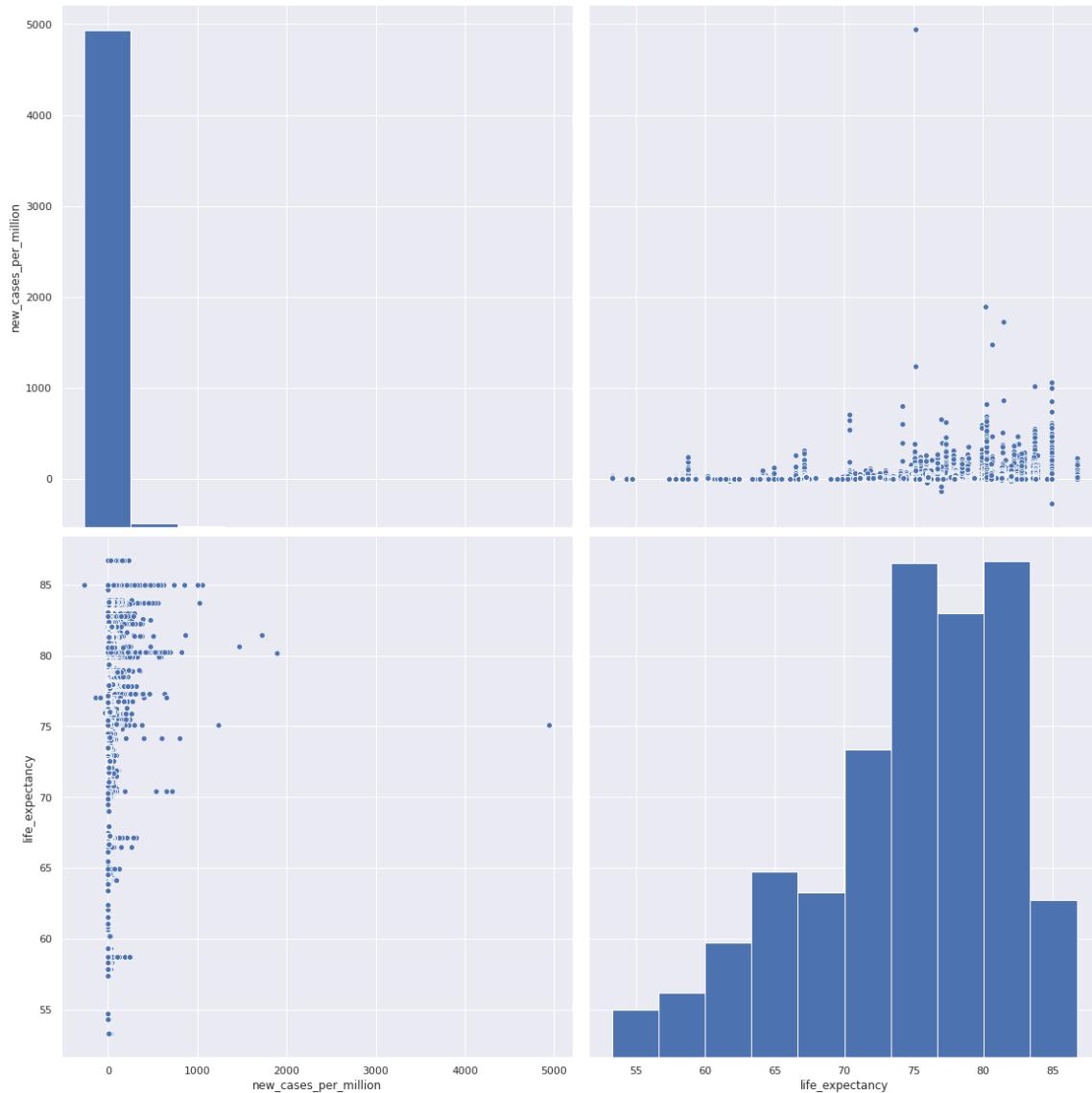


In [44]:

```
sns.pairplot(features, vars=["new_cases_per_million", "life_expectancy"], height=8)
```

Out[44]:

```
<seaborn.axisgrid.PairGrid at 0x7f64530cd780>
```

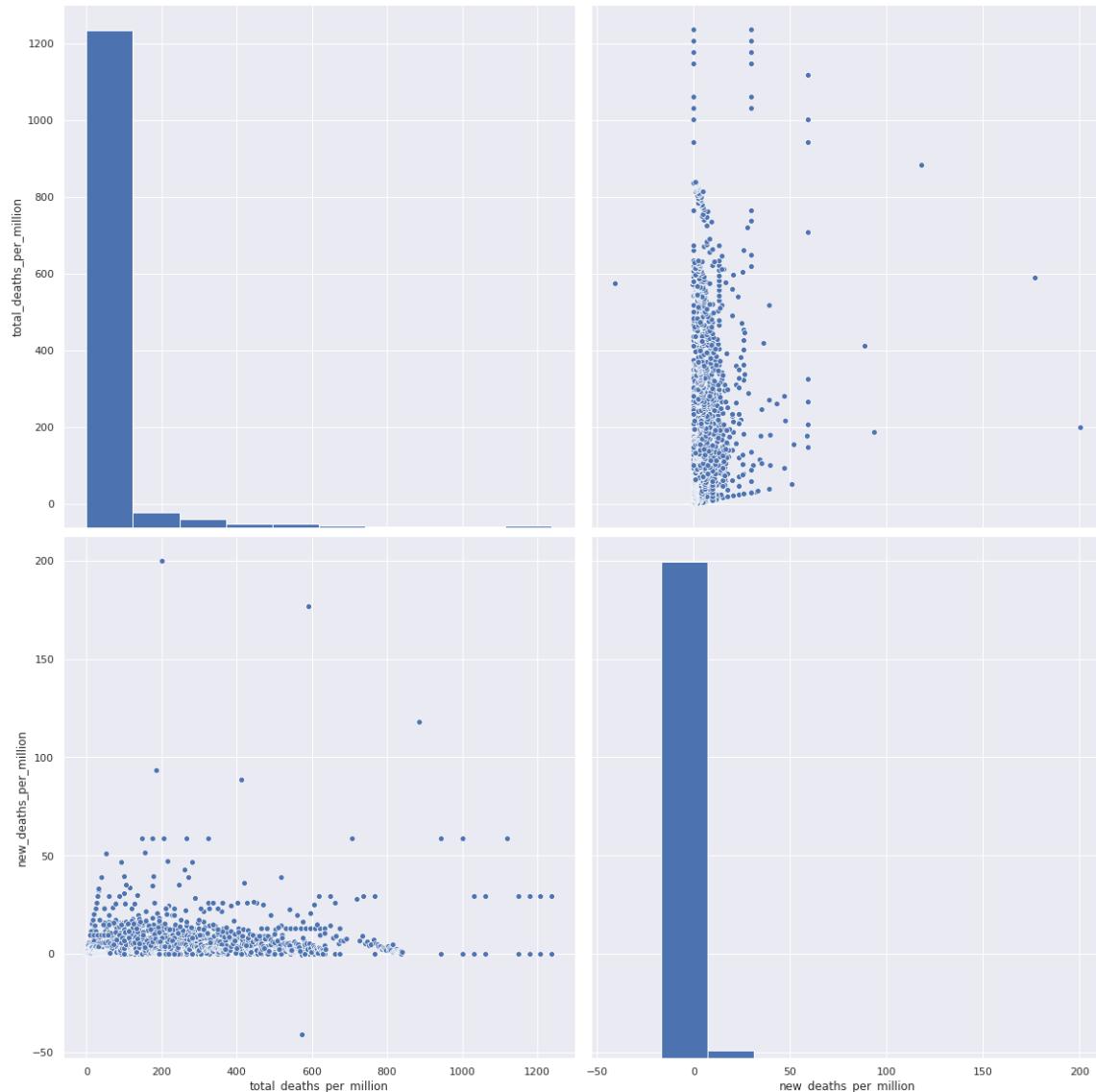


In [45]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "new_deaths_per_million"], height=8)
```

Out[45]:

```
<seaborn.axisgrid.PairGrid at 0x7f6453039b00>
```

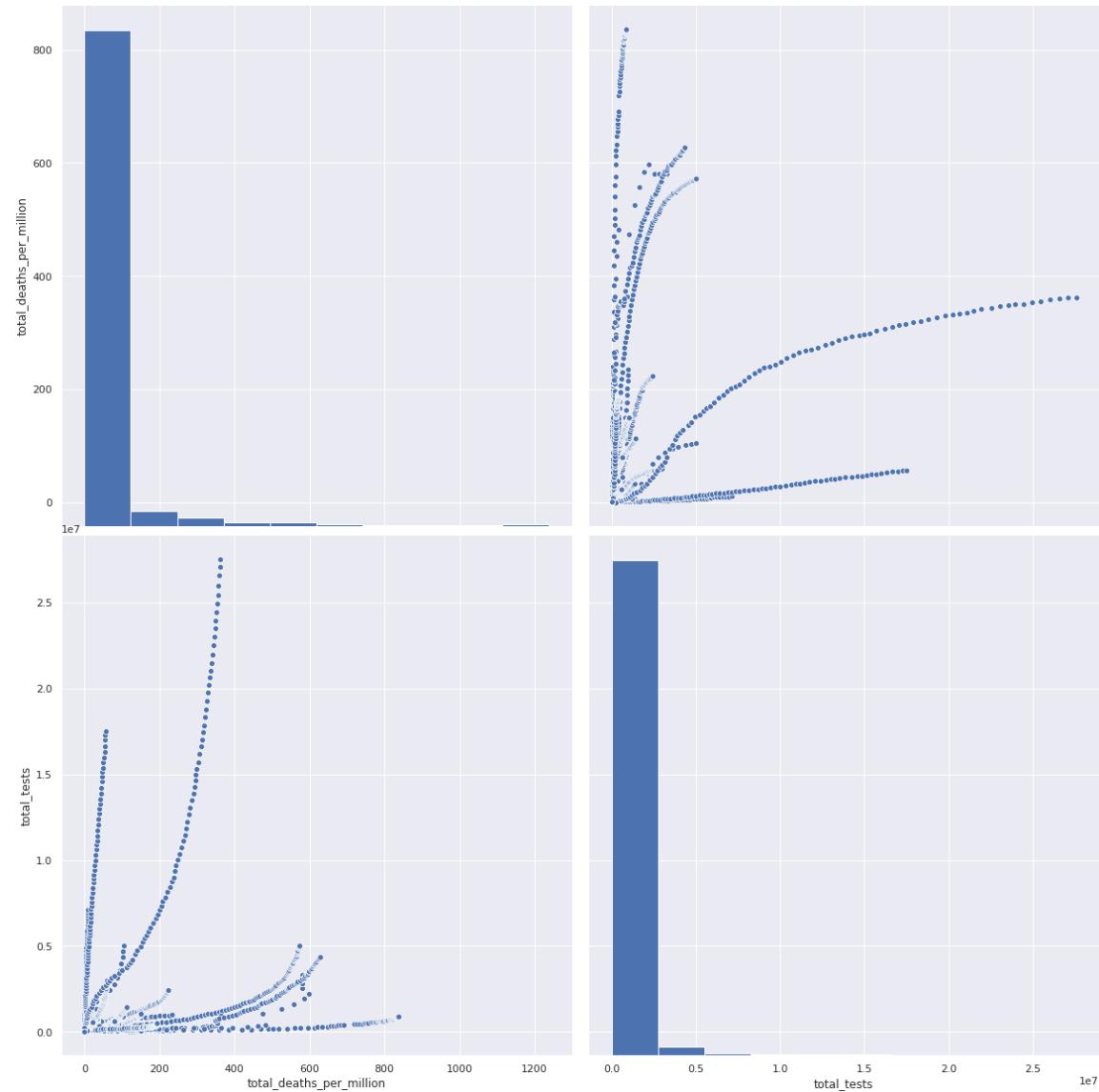


In [46]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "total_tests"], height=8)
```

Out[46]:

```
<seaborn.axisgrid.PairGrid at 0x7f6452cd3208>
```

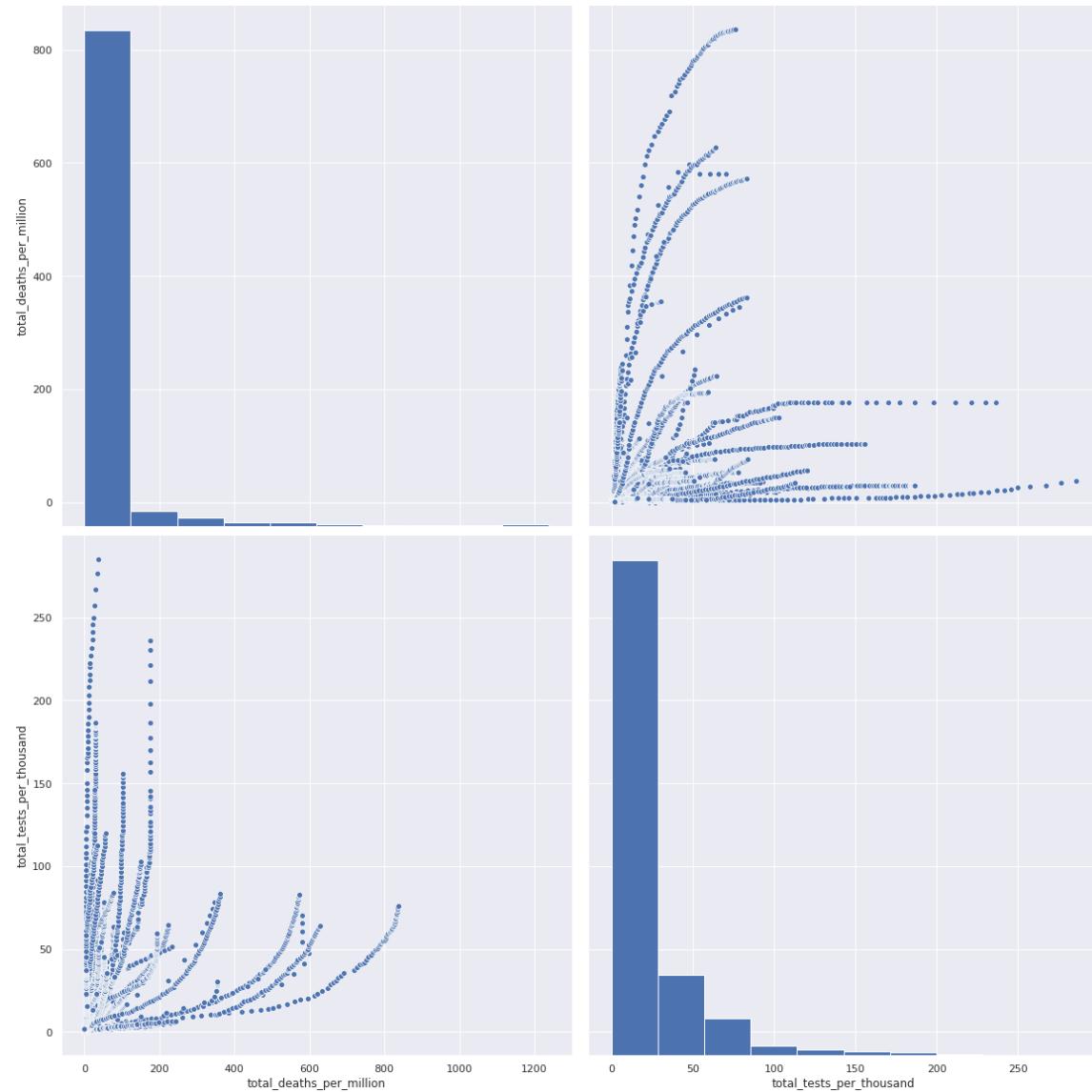


In [47]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "total_tests_per_thousa  
nd"], height=8)
```

Out[47]:

```
<seaborn.axisgrid.PairGrid at 0x7f6452b08e80>
```

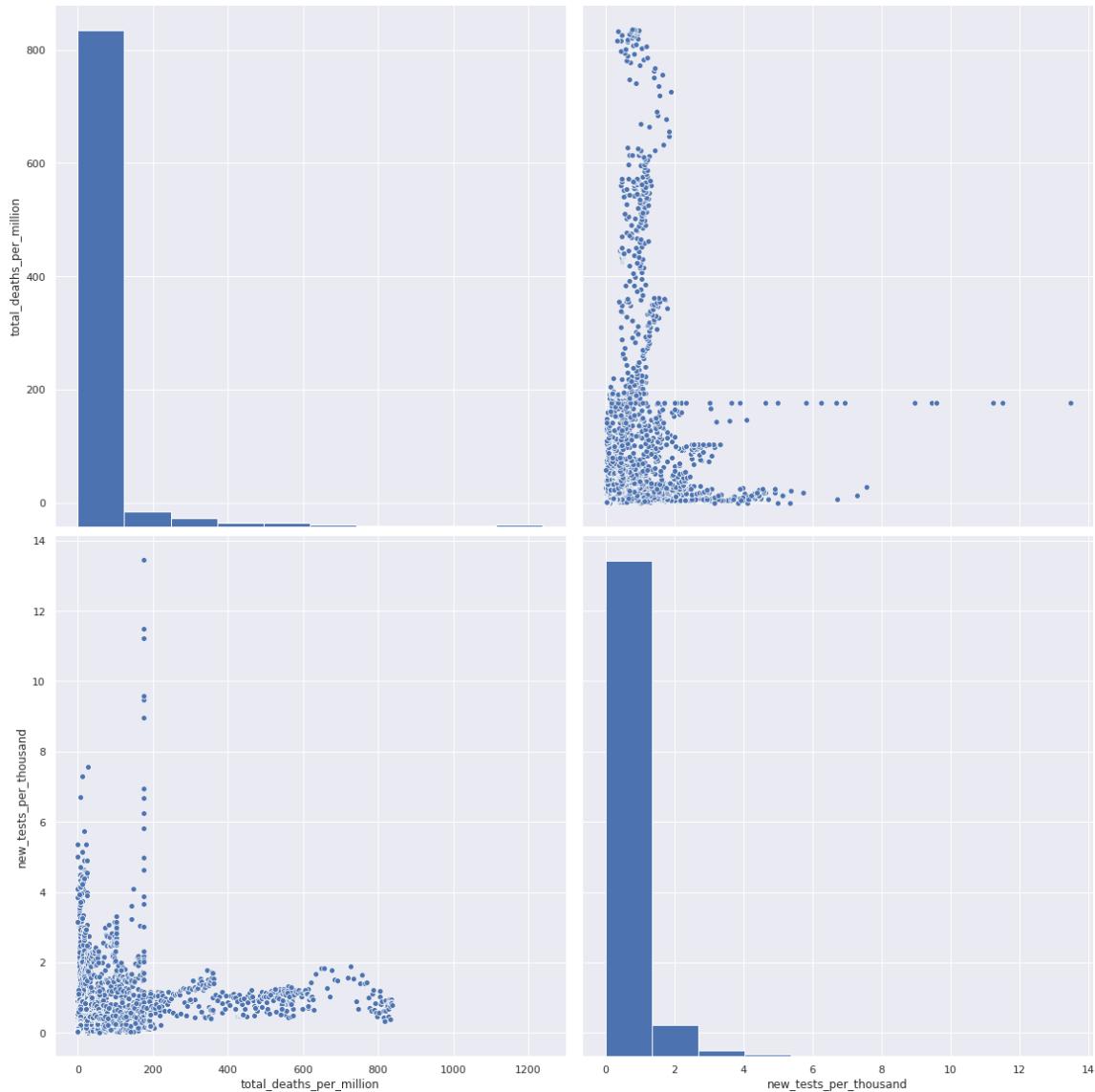


In [48]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "new_tests_per_thousan  
d"], height=8)
```

Out[48]:

```
<seaborn.axisgrid.PairGrid at 0x7f64528f71d0>
```

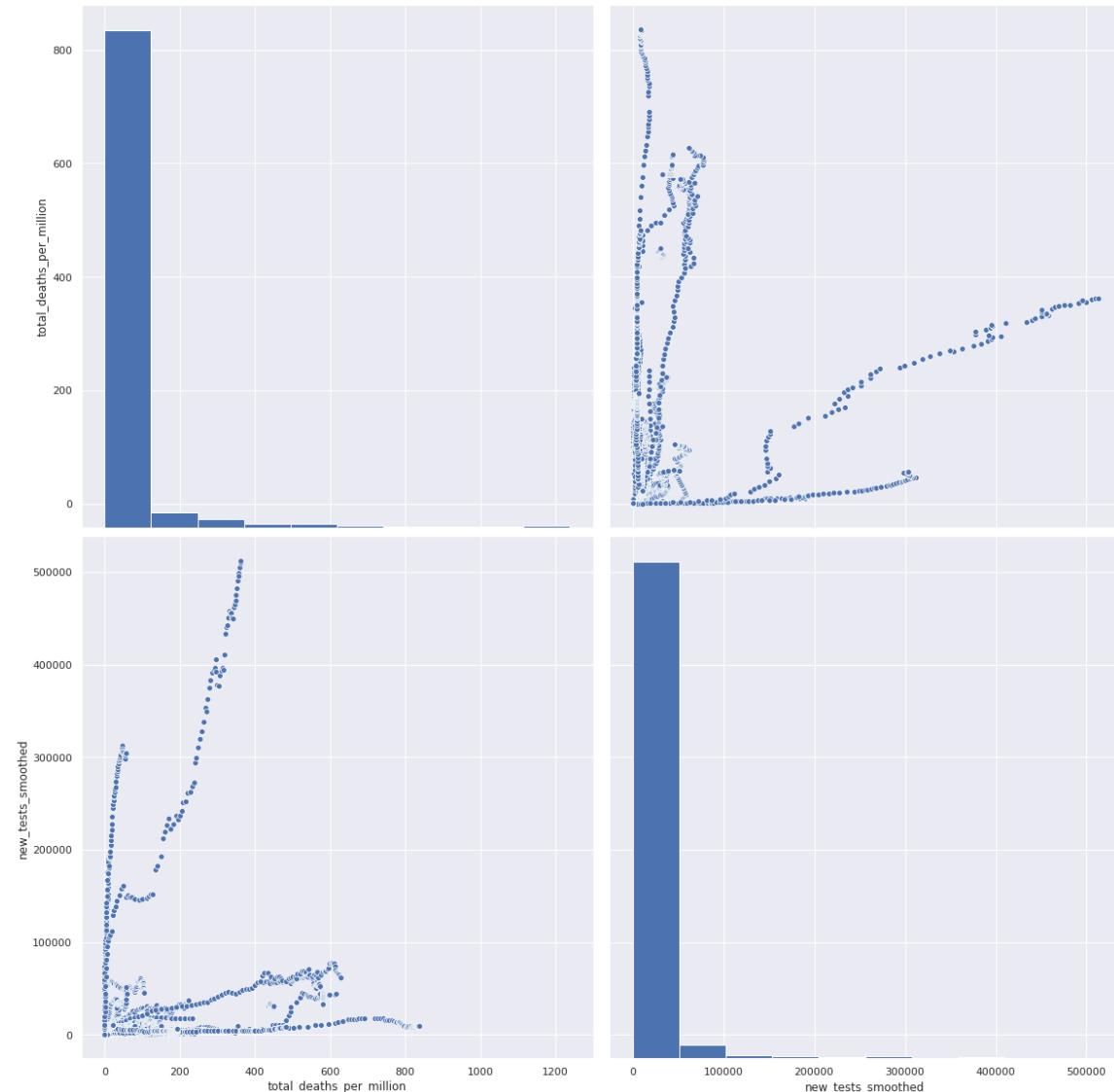


In [49]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "new_tests_smoothed"], height=8)
```

Out[49]:

```
<seaborn.axisgrid.PairGrid at 0x7f64527e1358>
```

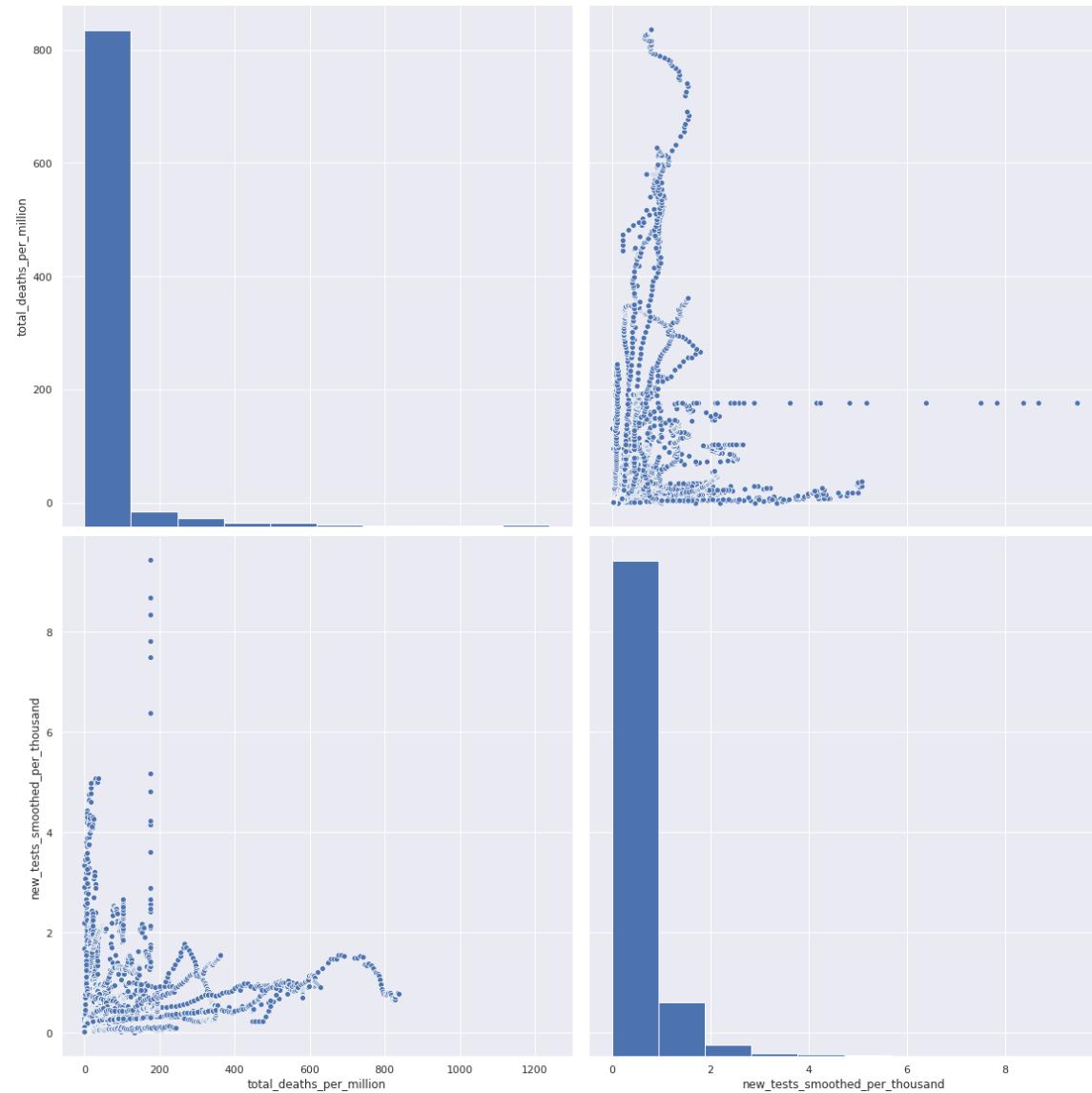


In [50]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "new_tests_smoothed_per_thousand"], height=8)
```

Out[50]:

```
<seaborn.axisgrid.PairGrid at 0x7f64537b79e8>
```

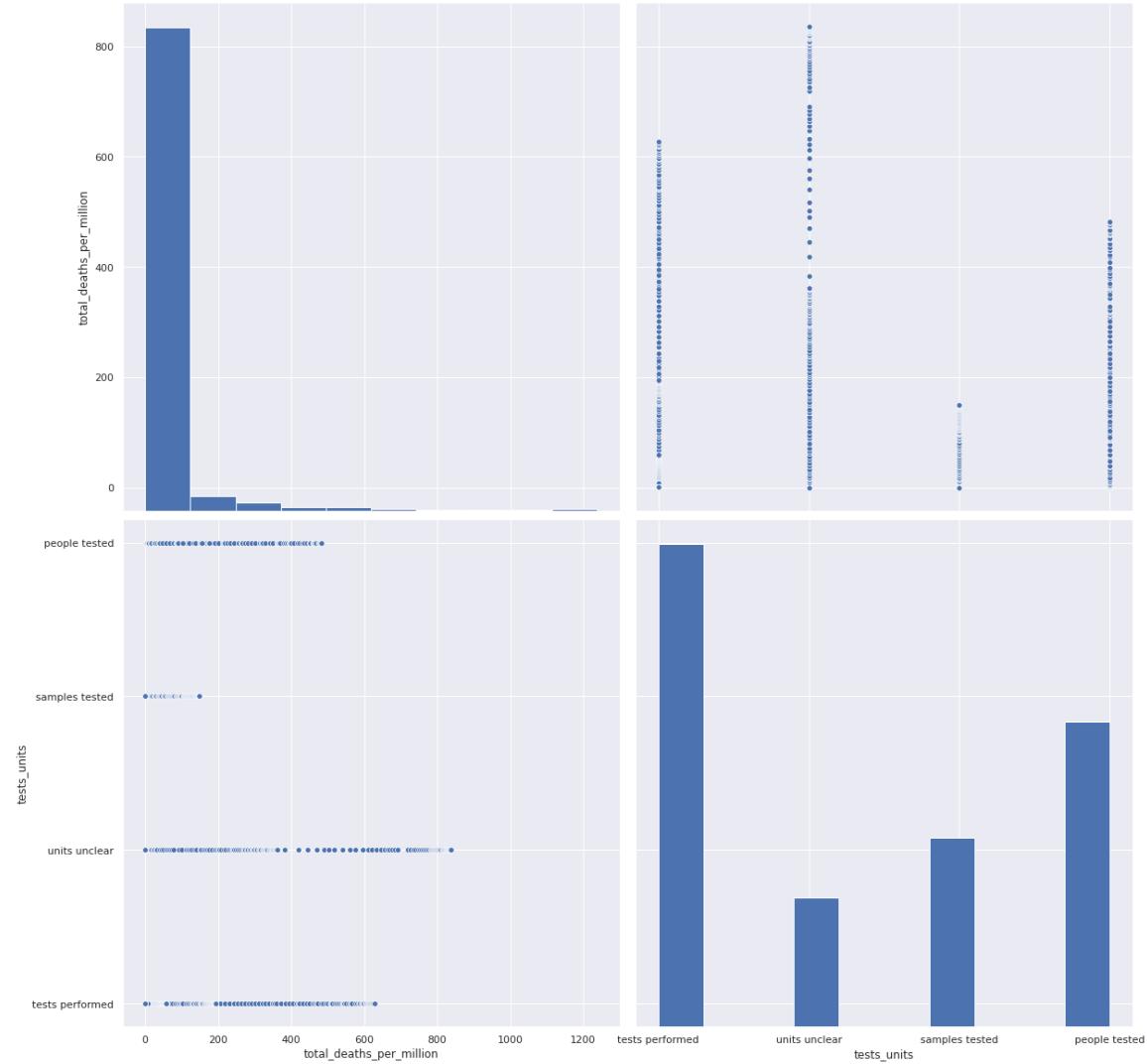


In [51]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "tests_units"], height=8)
```

Out[51]:

```
<seaborn.axisgrid.PairGrid at 0x7f6452318ac8>
```

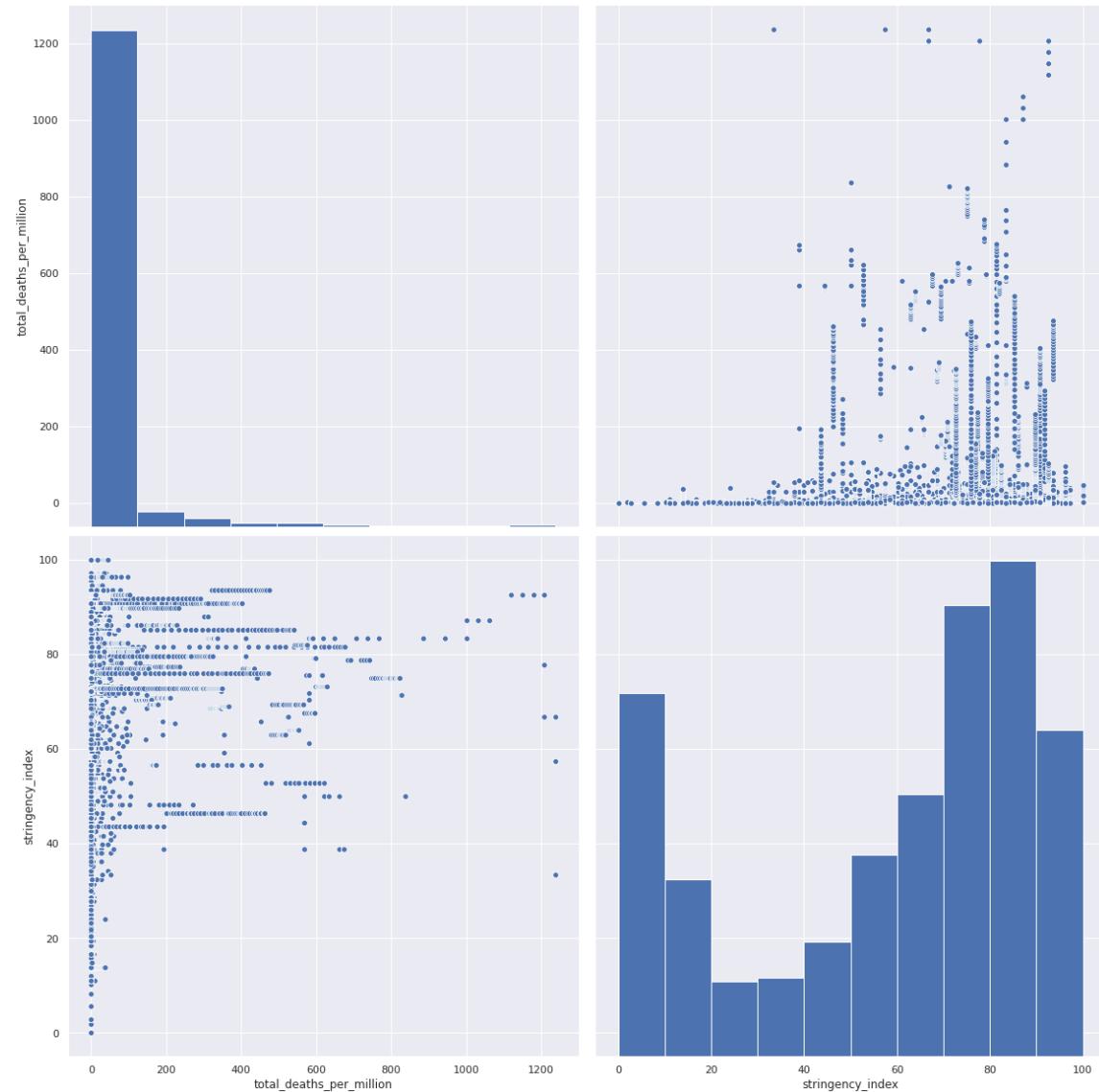


In [52]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "stringency_index"], height=8)
```

Out[52]:

```
<seaborn.axisgrid.PairGrid at 0x7f6452120f60>
```

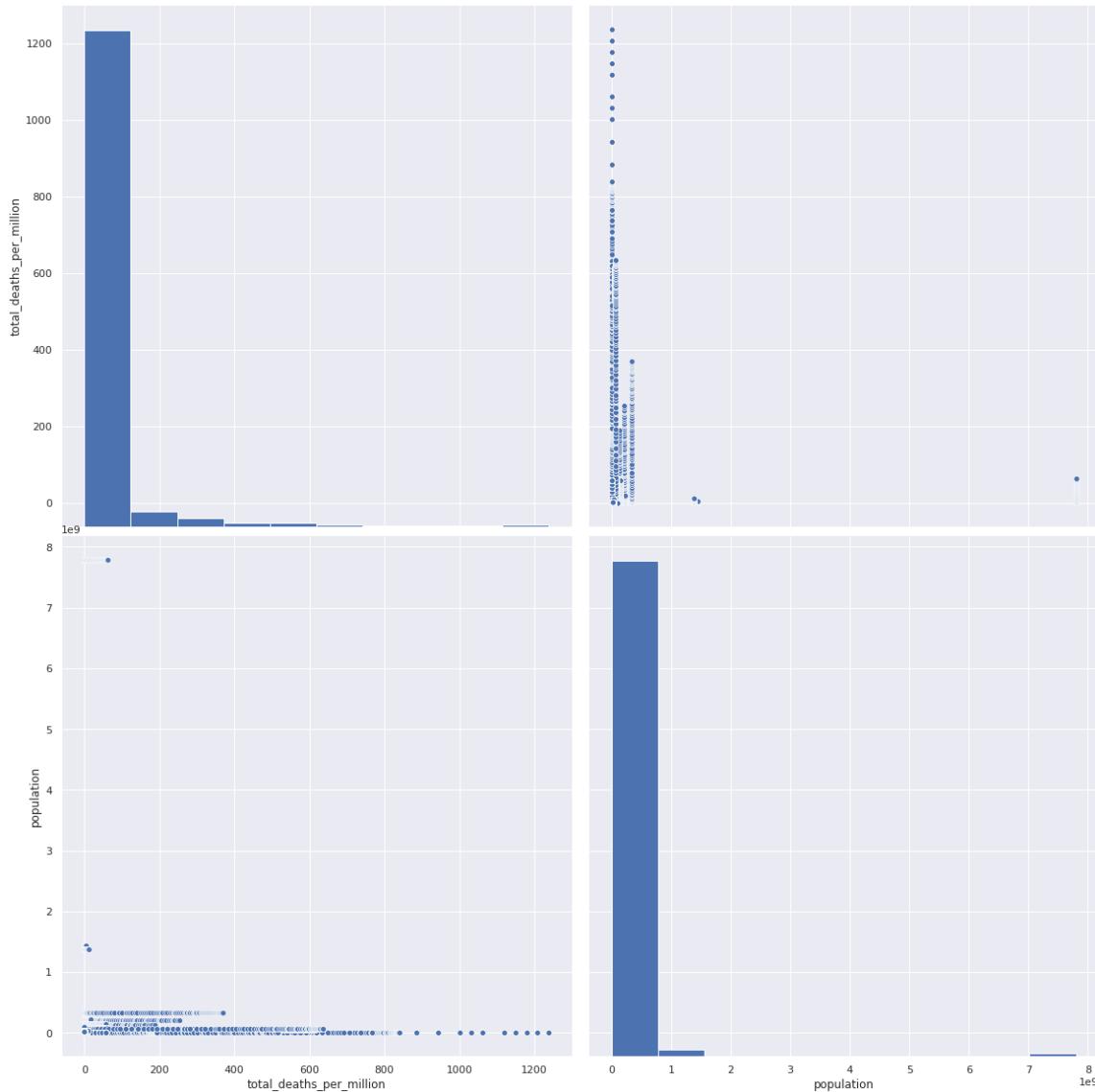


In [53]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "population"], height=8)
```

Out[53]:

```
<seaborn.axisgrid.PairGrid at 0x7f6451f323c8>
```

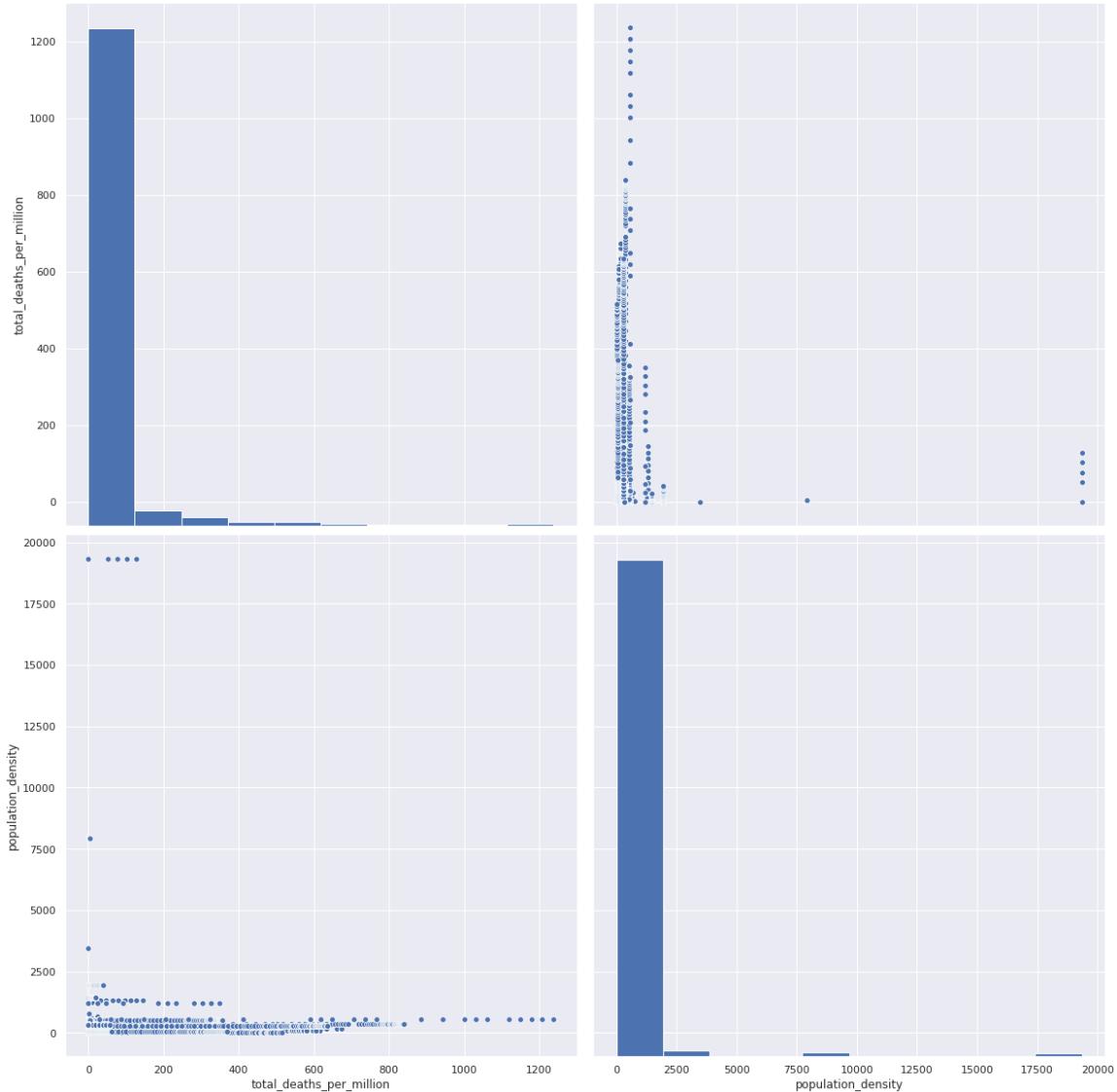


In [54]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "population_density"],  
height=8)
```

Out[54]:

```
<seaborn.axisgrid.PairGrid at 0x7f6451f04438>
```

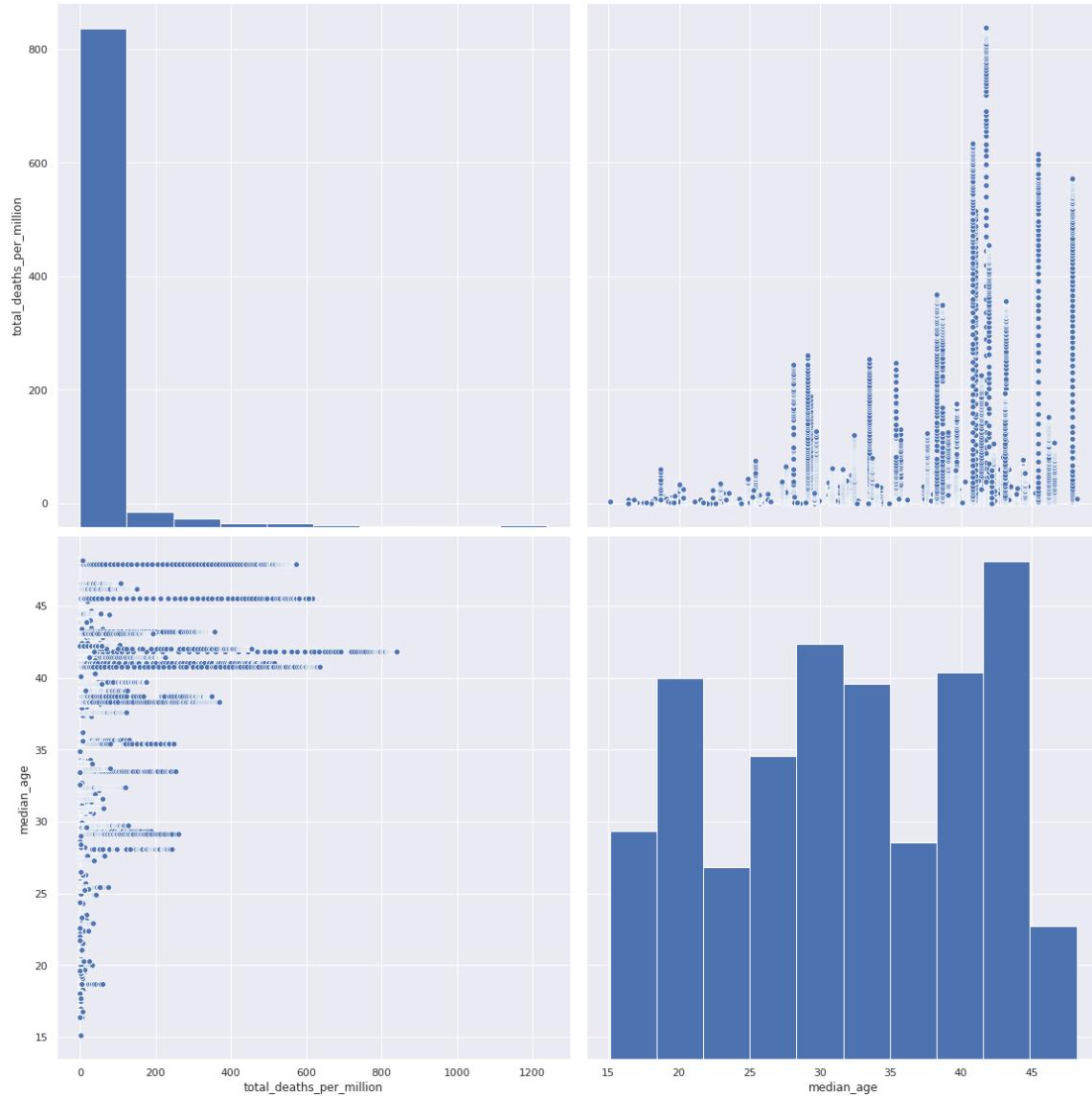


In [55]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "median_age"], height=8)
```

Out[55]:

```
<seaborn.axisgrid.PairGrid at 0x7f6451af4898>
```

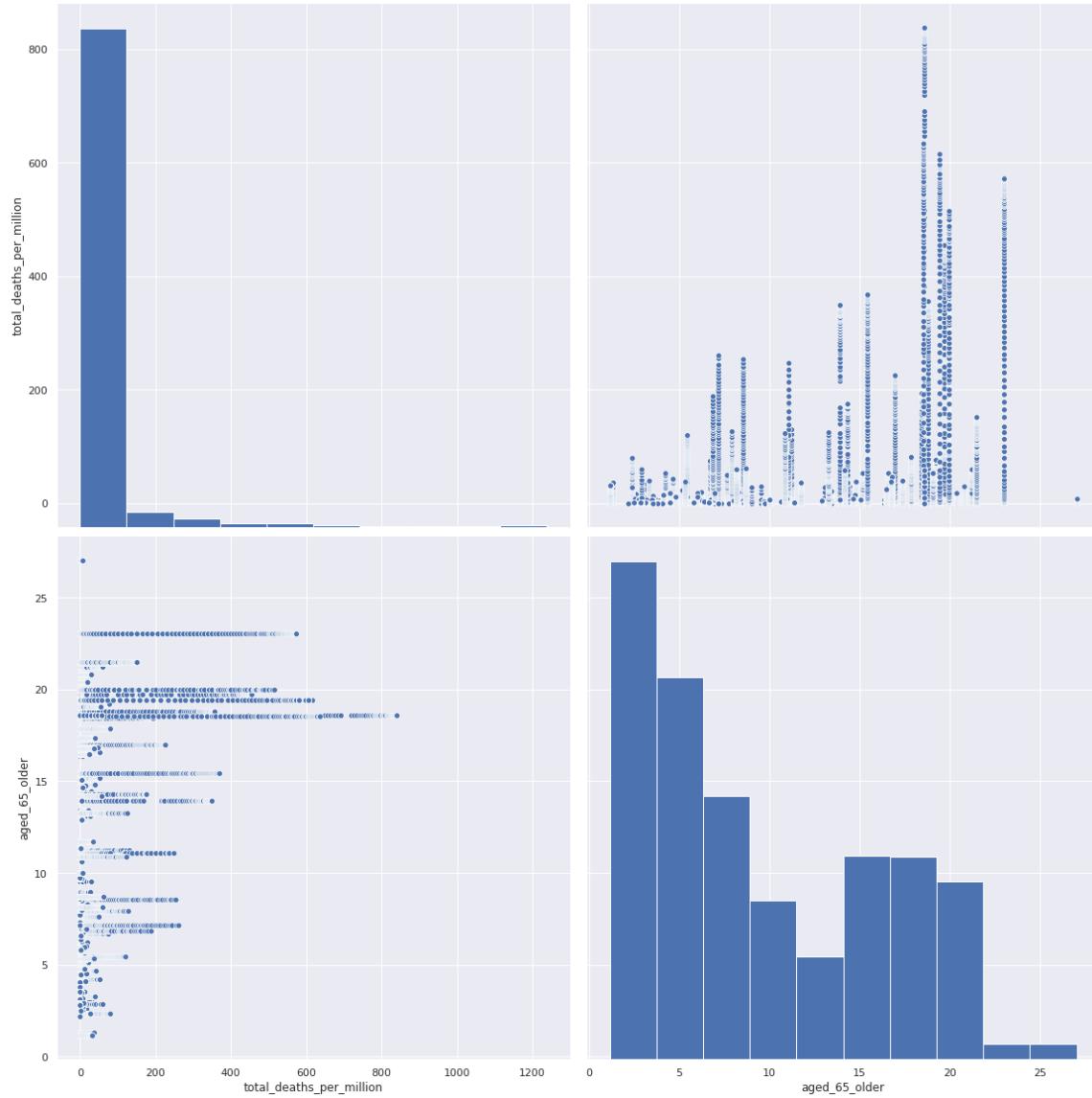


In [56]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "aged_65_older"], height=8)
```

Out[56]:

```
<seaborn.axisgrid.PairGrid at 0x7f64518f4198>
```

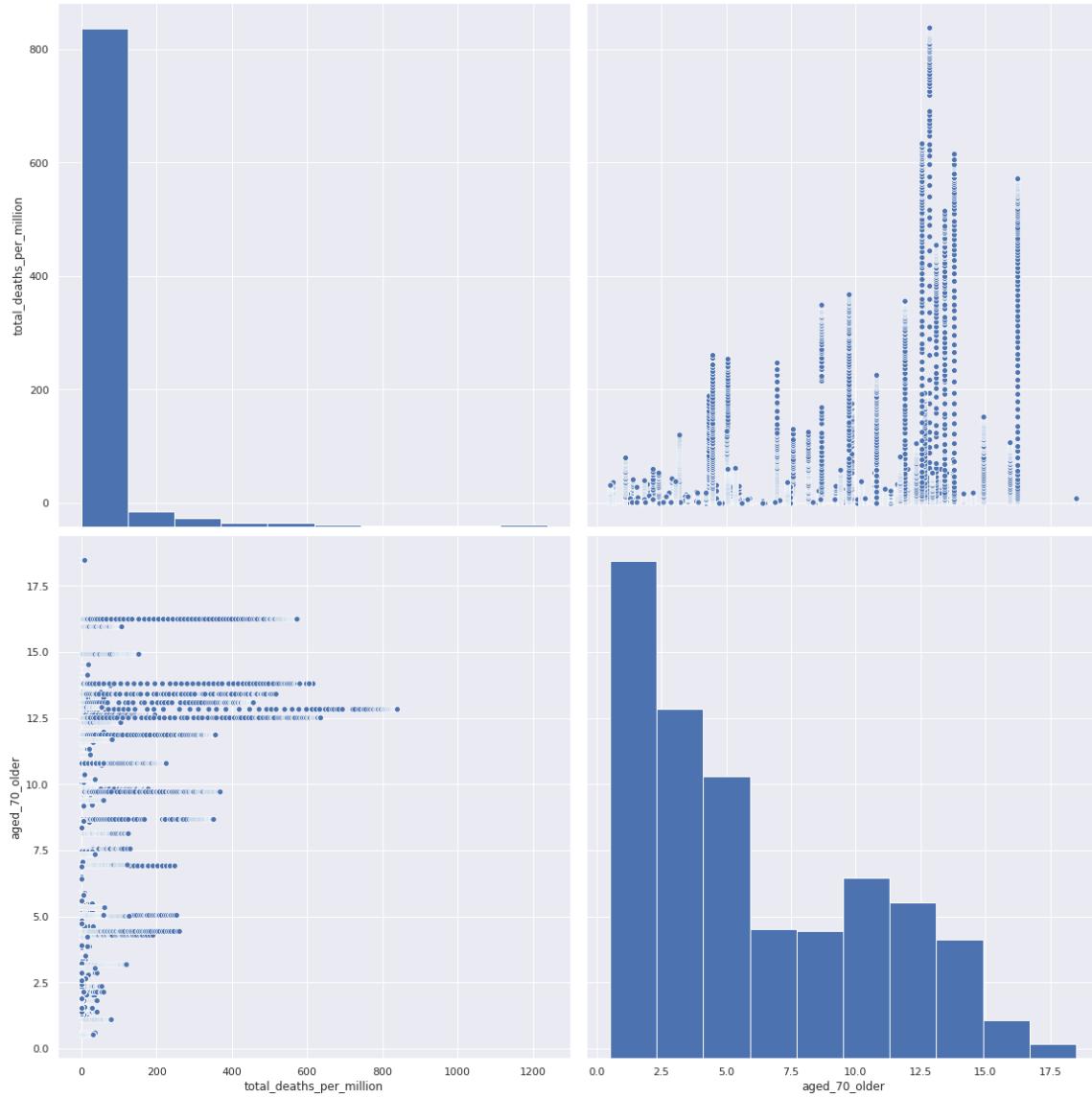


In [57]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "aged_70_older"], height=8)
```

Out[57]:

```
<seaborn.axisgrid.PairGrid at 0x7f64517113c8>
```

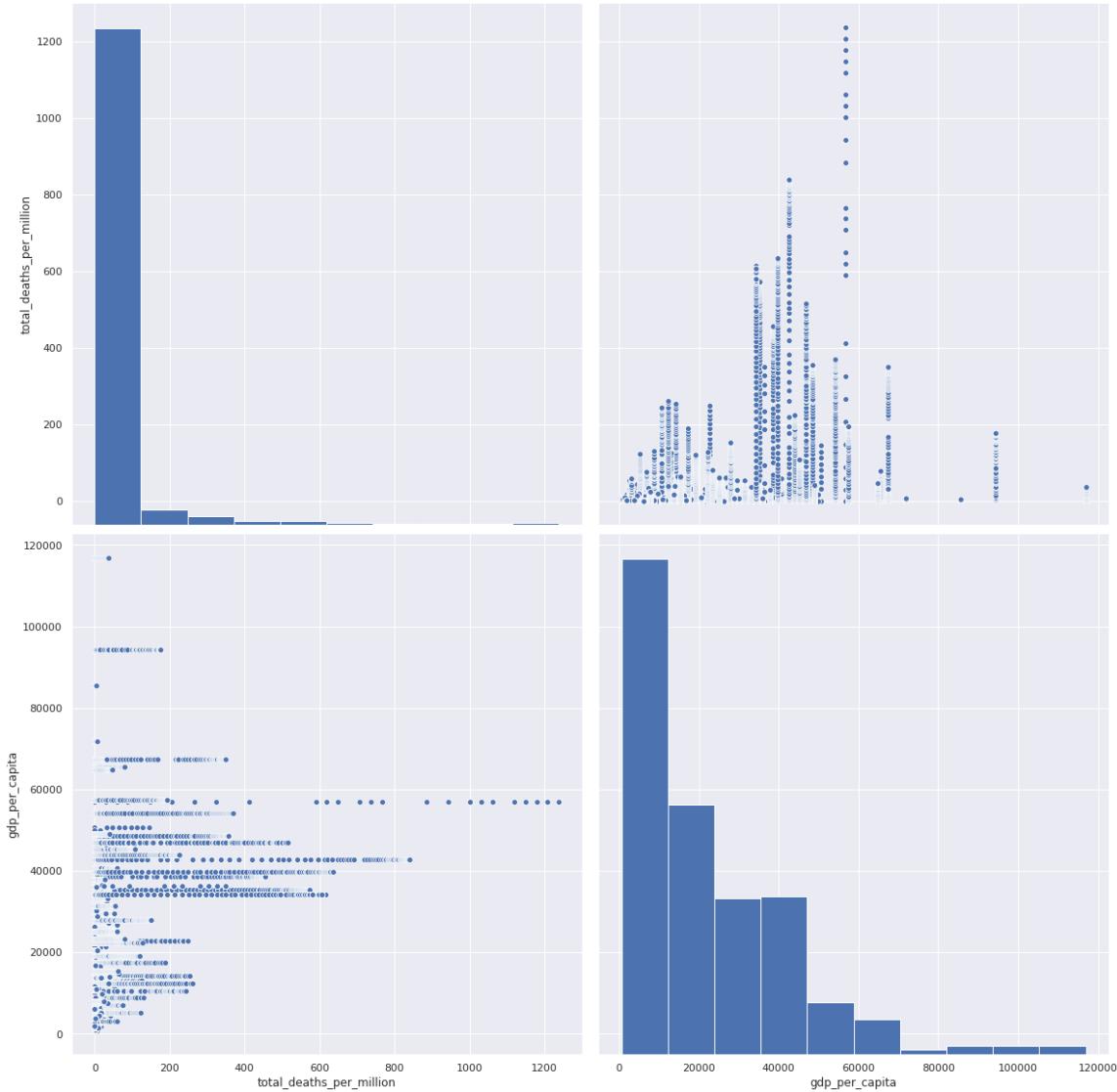


In [58]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "gdp_per_capita"], height=8)
```

Out[58]:

```
<seaborn.axisgrid.PairGrid at 0x7f64518d6940>
```

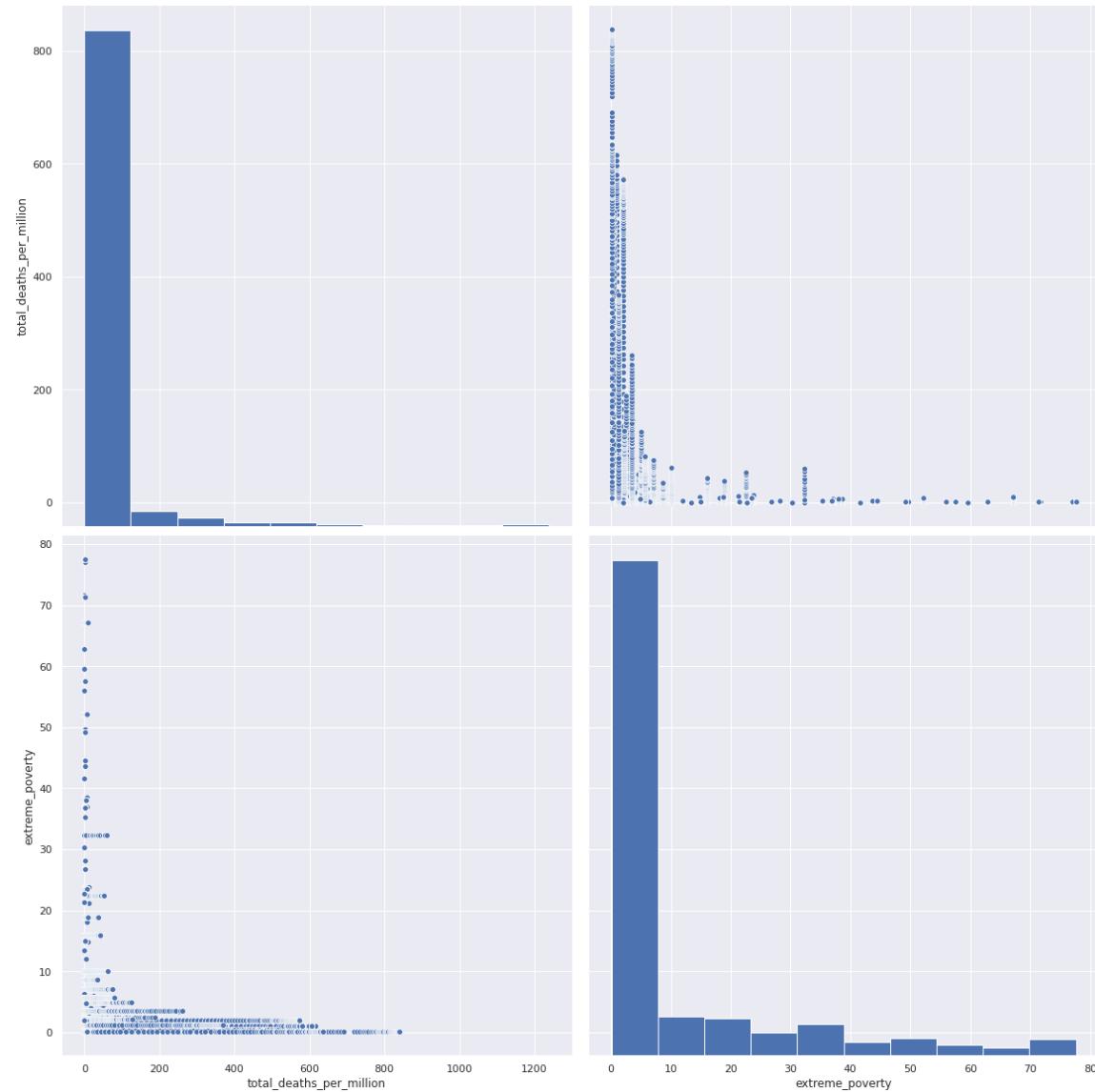


In [59]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "extreme_poverty"], height=8)
```

Out[59]:

```
<seaborn.axisgrid.PairGrid at 0x7f64512bff28>
```

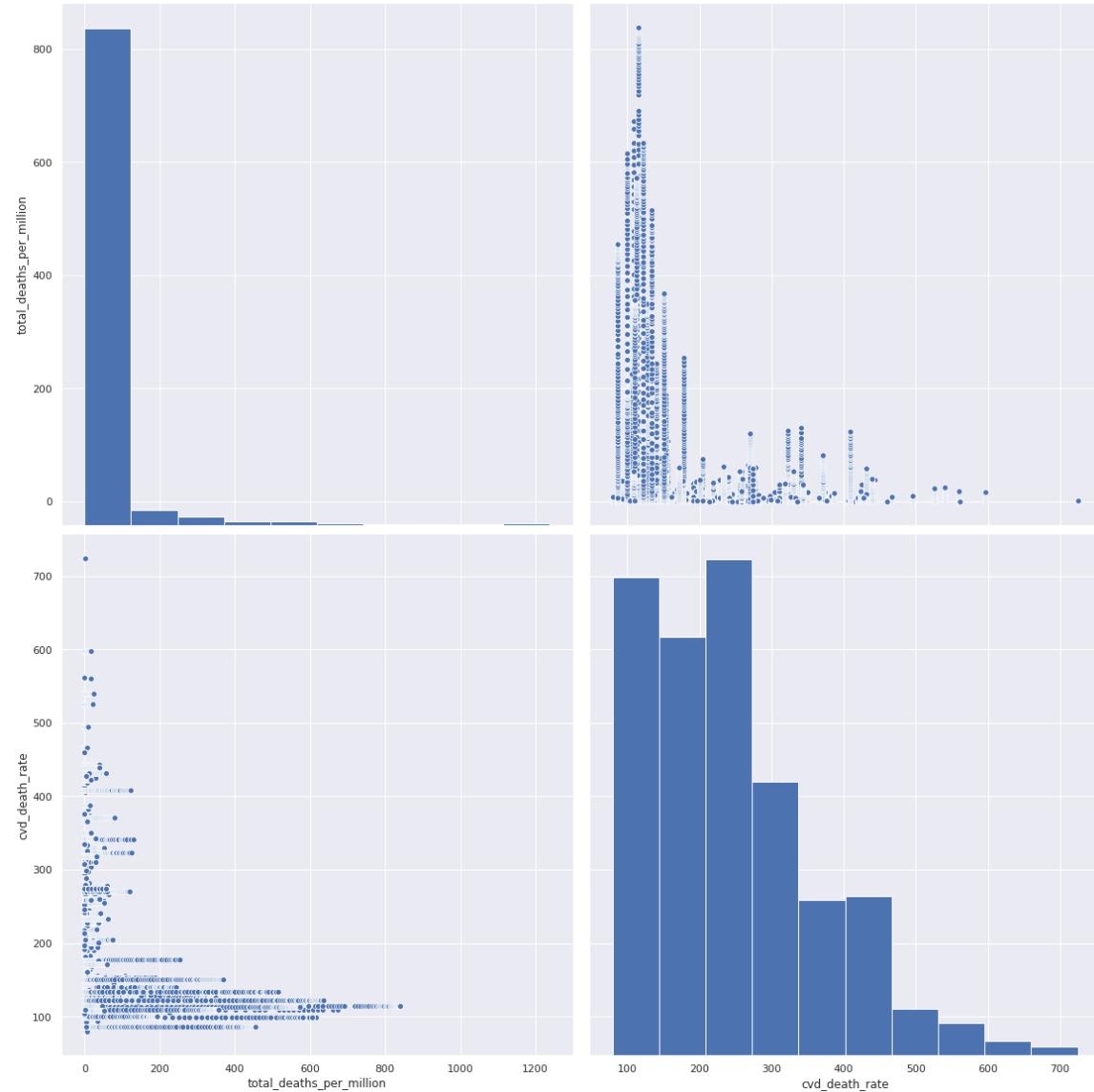


In [60]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "cvd_death_rate"], height=8)
```

Out[60]:

```
<seaborn.axisgrid.PairGrid at 0x7f64510f4470>
```

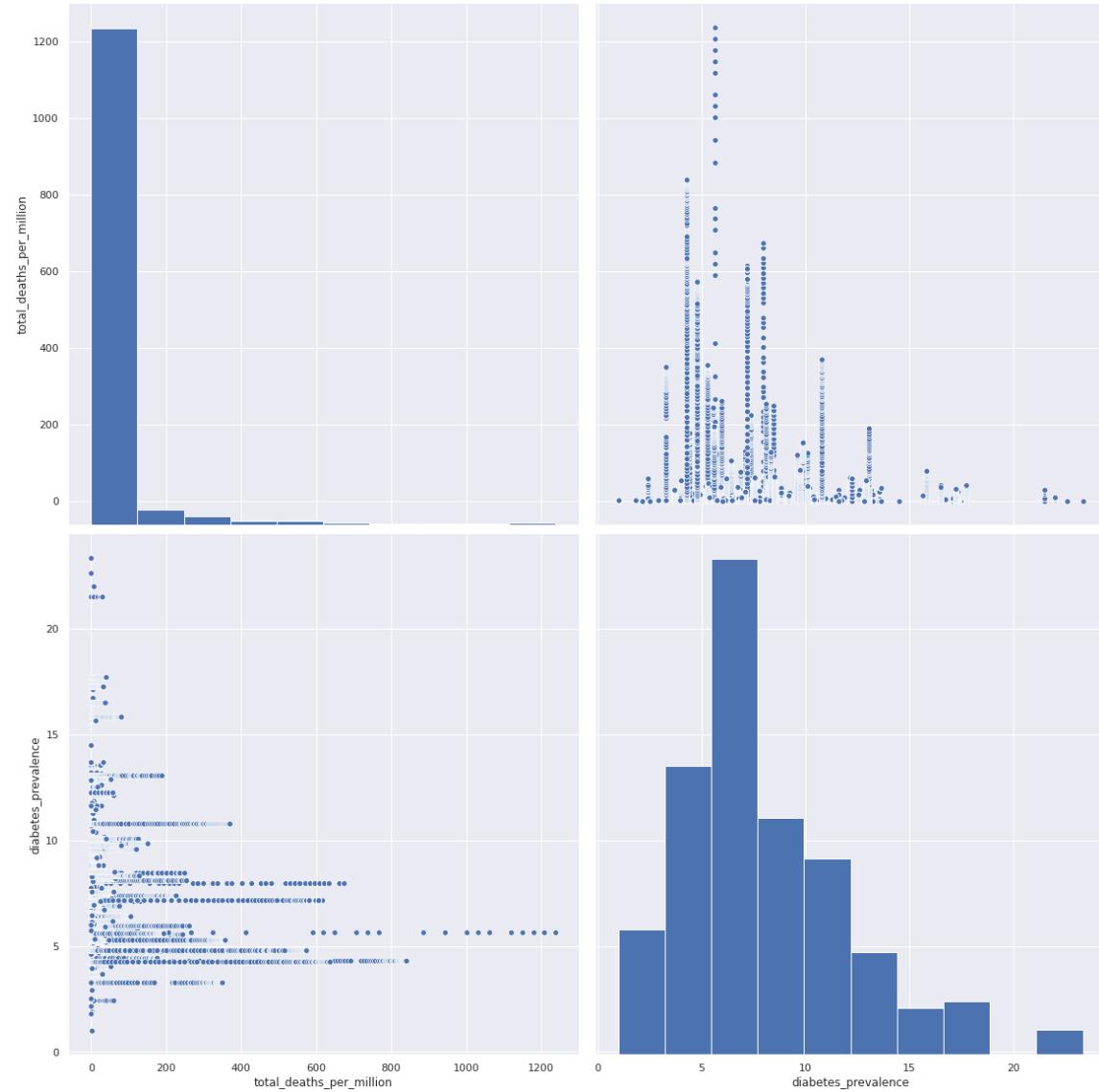


In [61]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "diabetes_prevalence"], height=8)
```

Out[61]:

```
<seaborn.axisgrid.PairGrid at 0x7f6450ffc3c8>
```

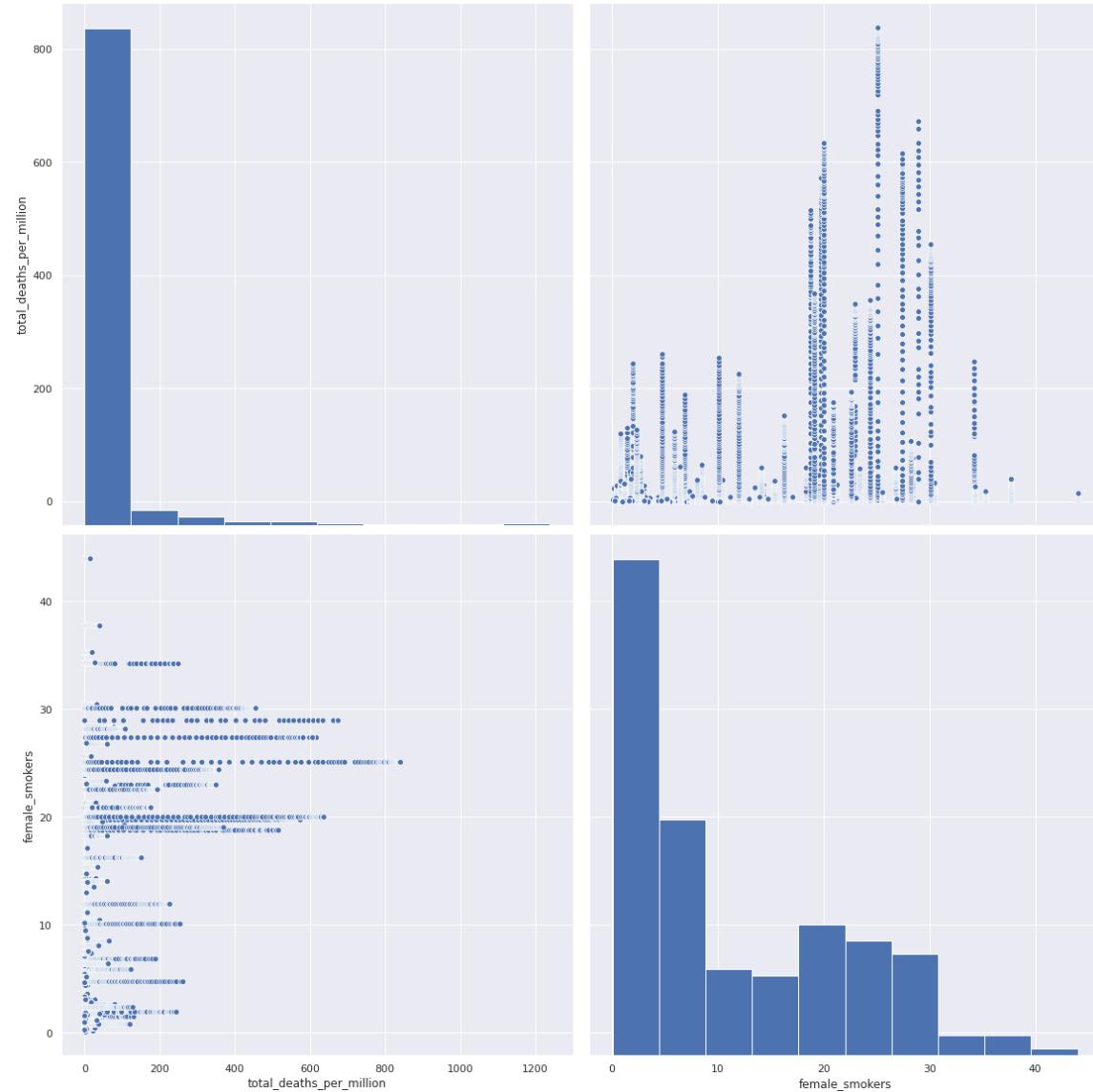


In [62]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "female_smokers"], height=8)
```

Out[62]:

```
<seaborn.axisgrid.PairGrid at 0x7f6454524240>
```

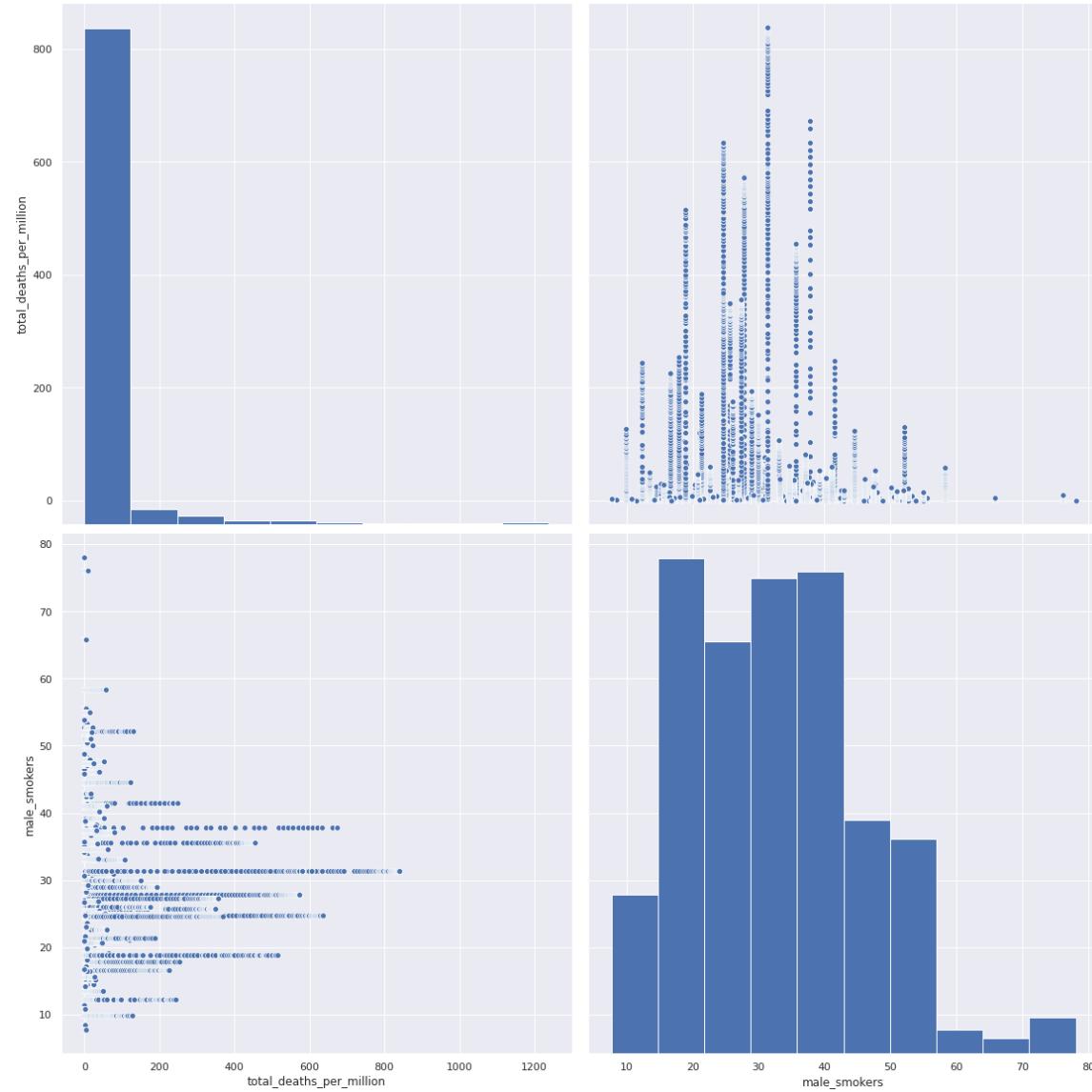


In [63]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "male_smokers"], height=8)
```

Out[63]:

```
<seaborn.axisgrid.PairGrid at 0x7f6450ade780>
```

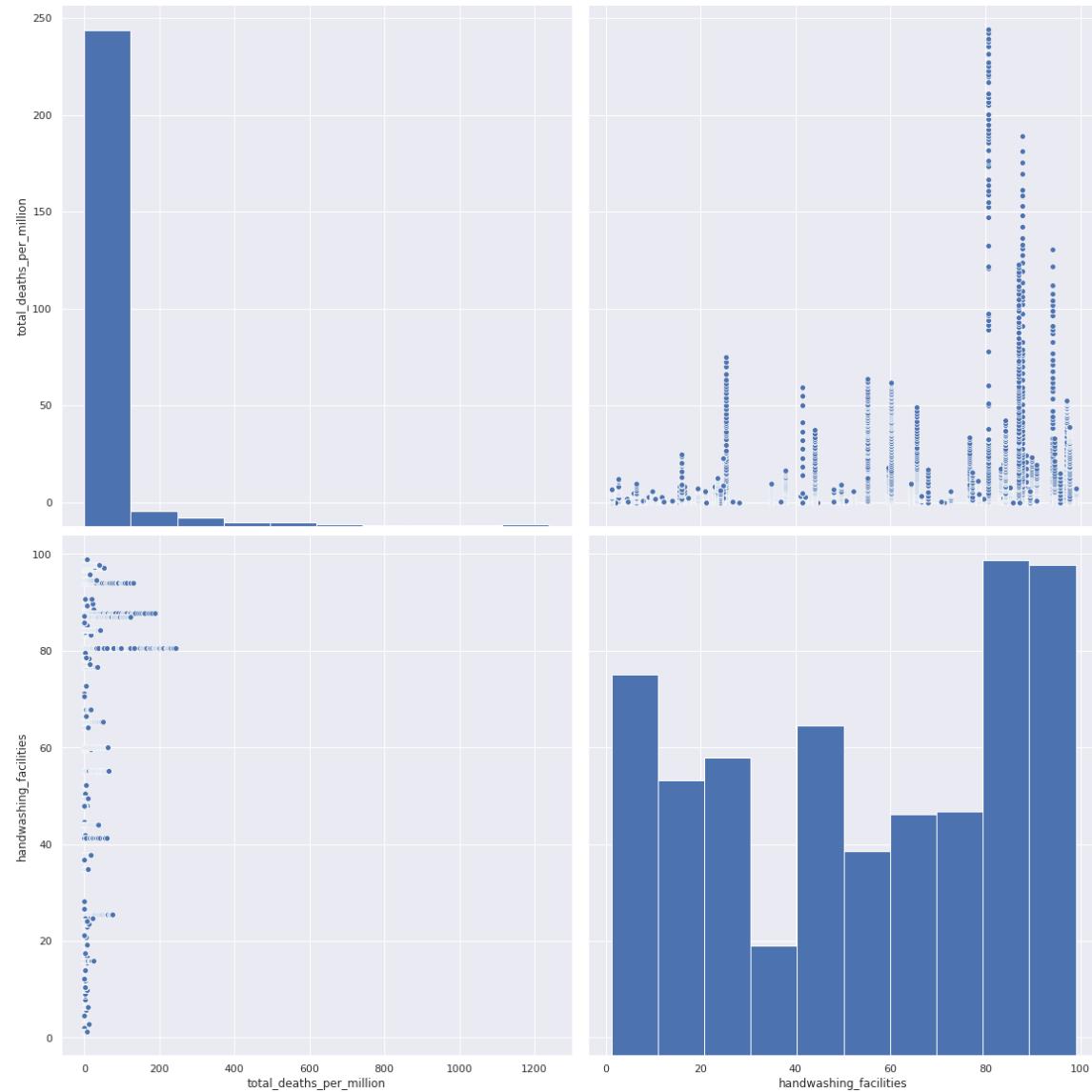


In [64]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "handwashing_facilities"], height=8)
```

Out[64]:

```
<seaborn.axisgrid.PairGrid at 0x7f64508f04e0>
```

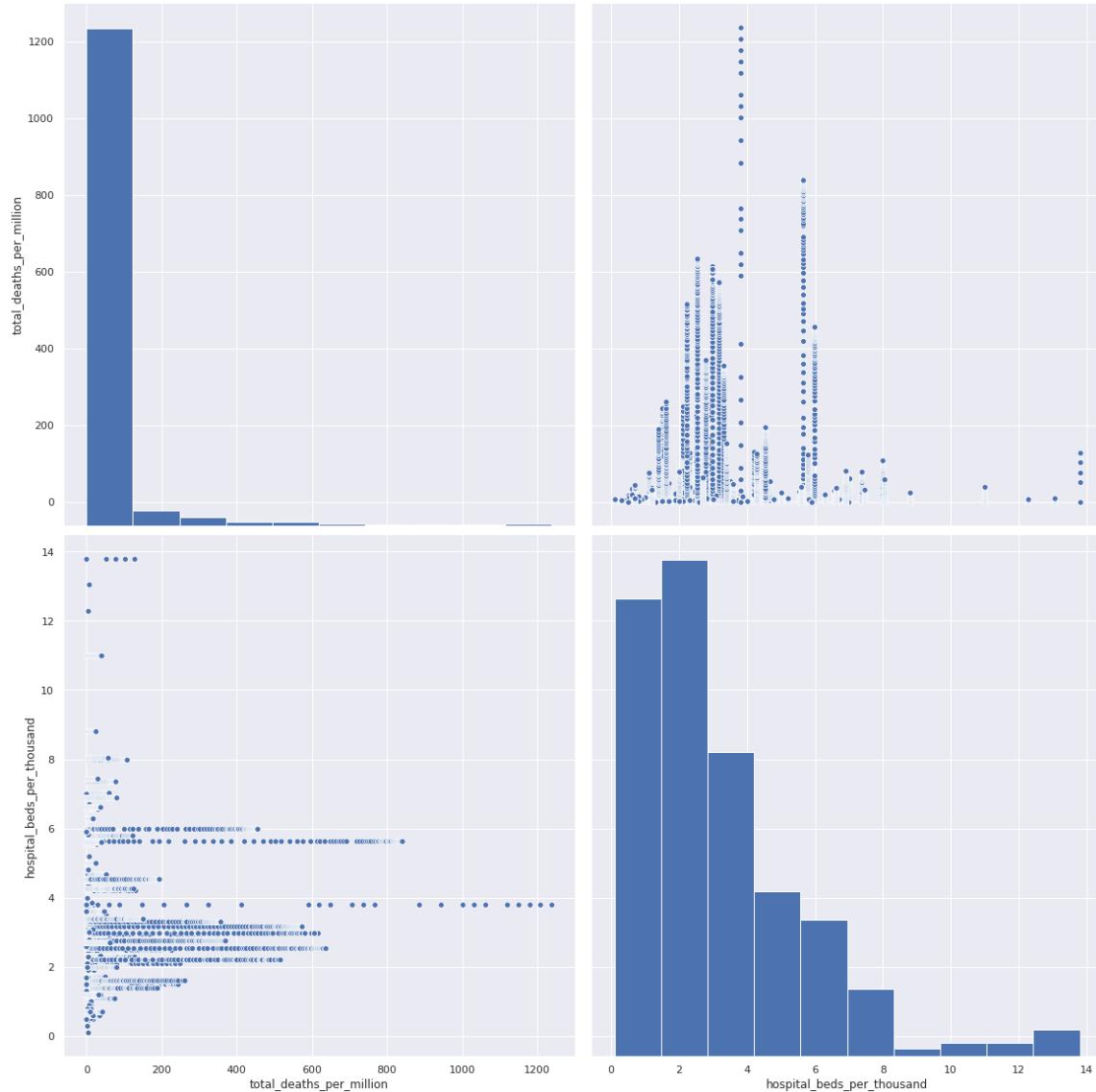


In [65]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "hospital_beds_per_thou  
sand"], height=8)
```

Out[65]:

```
<seaborn.axisgrid.PairGrid at 0x7f64506cbc18>
```

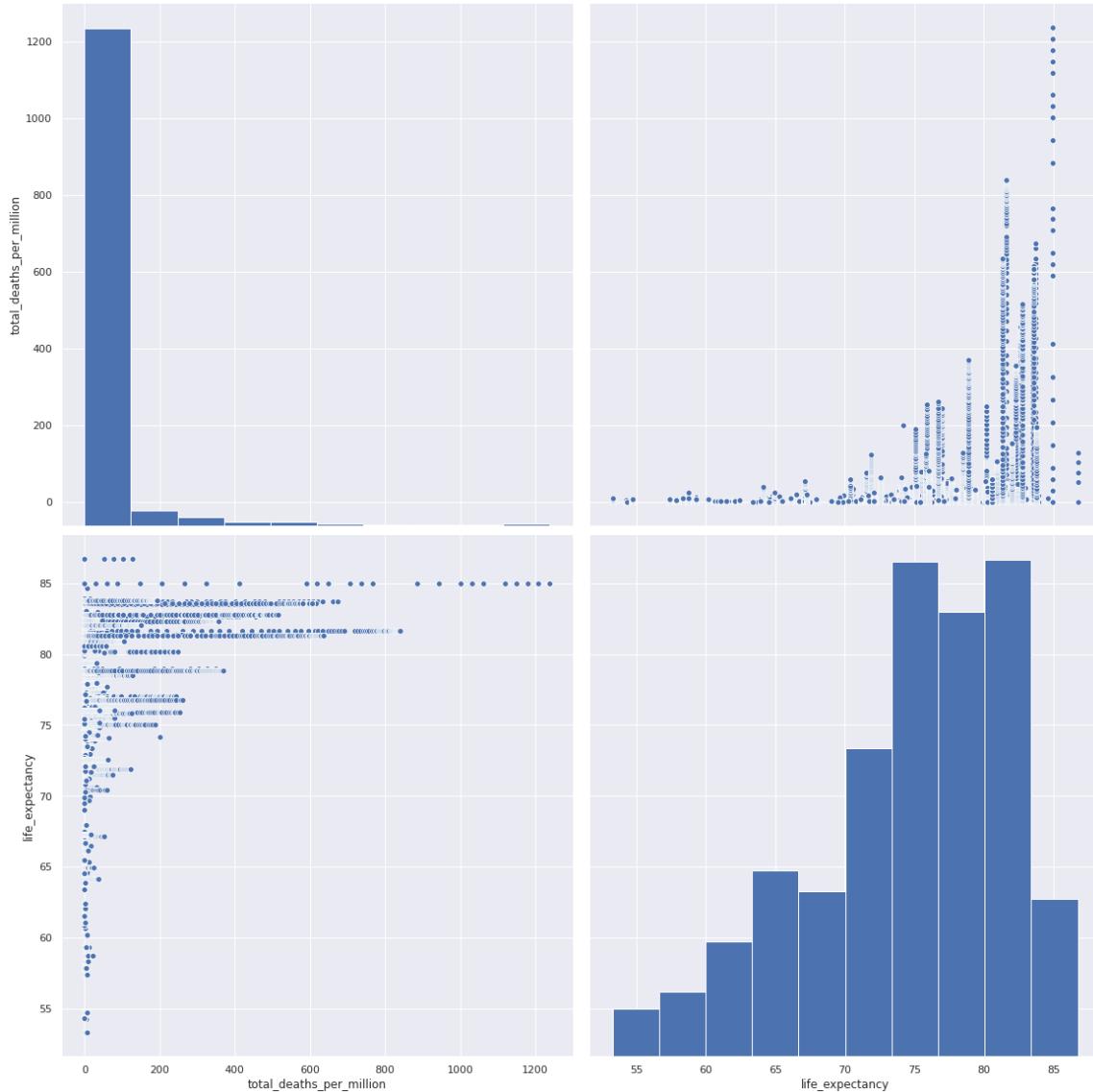


In [66]:

```
sns.pairplot(features, vars=["total_deaths_per_million", "life_expectancy"], height=8)
```

Out[66]:

```
<seaborn.axisgrid.PairGrid at 0x7f64504eb7b8>
```

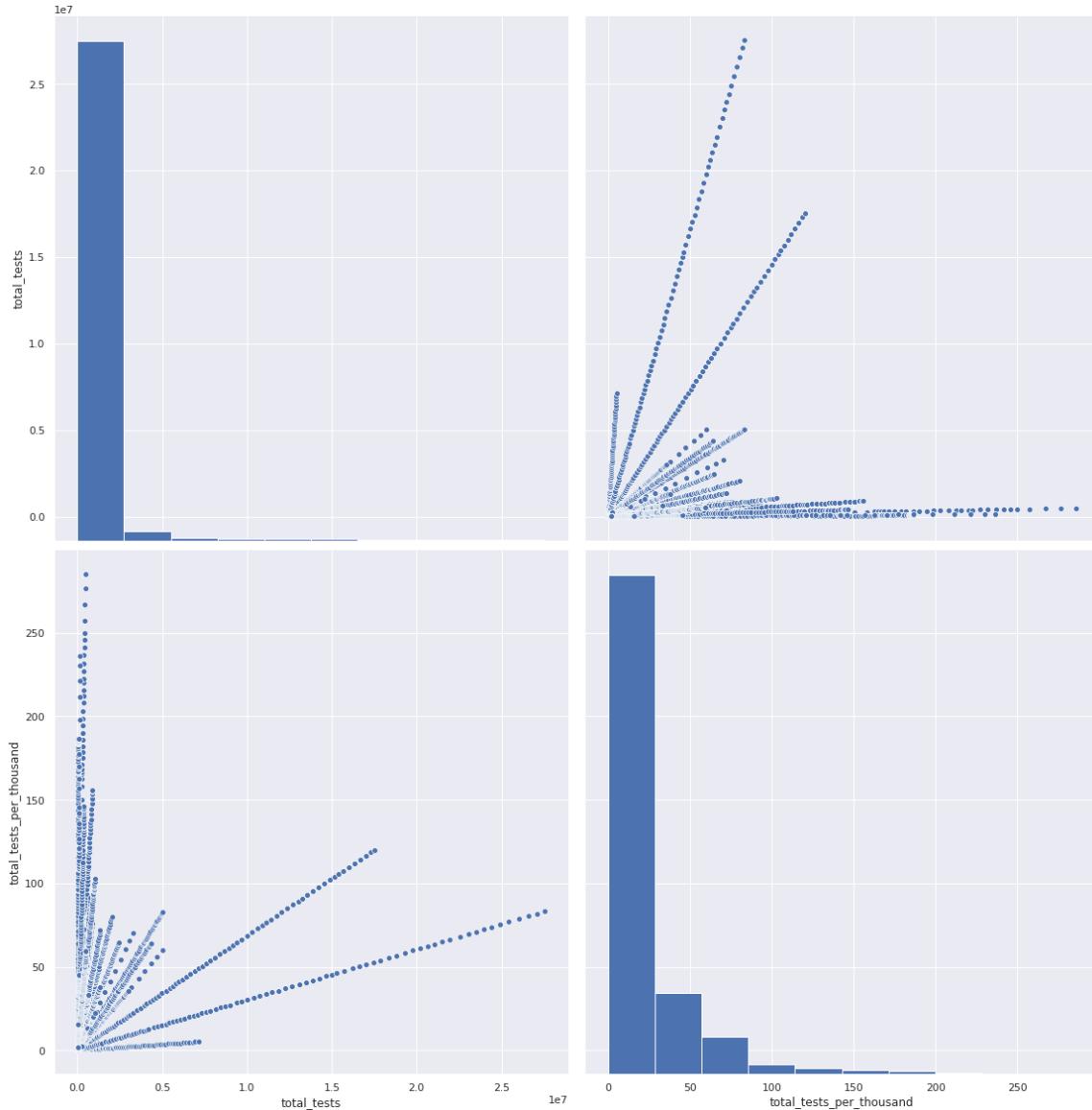


In [67]:

```
sns.pairplot(features, vars=["total_tests", "total_tests_per_thousand"], height=8)
```

Out[67]:

```
<seaborn.axisgrid.PairGrid at 0x7f64503370b8>
```

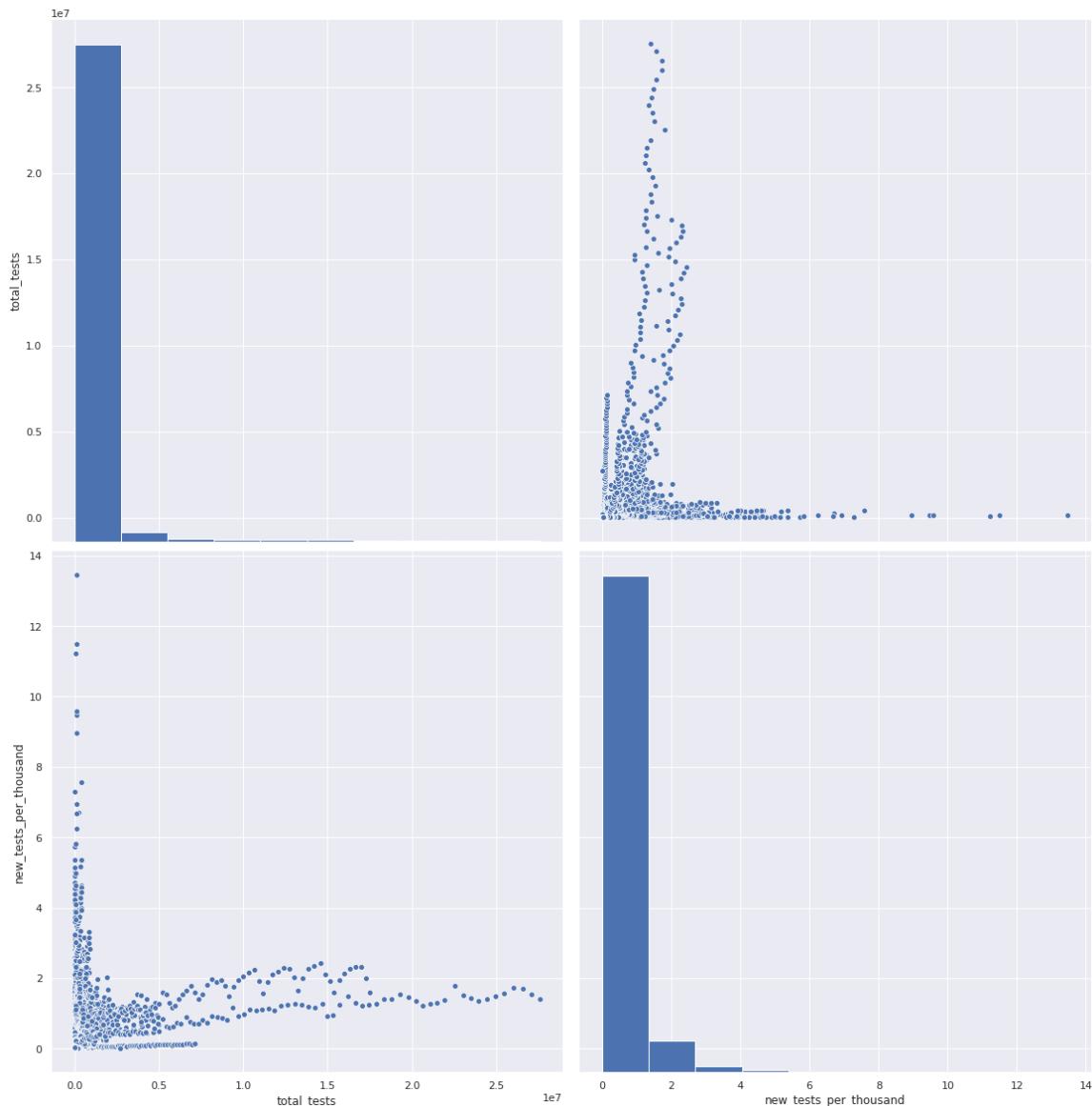


In [68]:

```
sns.pairplot(features, vars=["total_tests", "new_tests_per_thousand"], height=8)
```

Out[68]:

```
<seaborn.axisgrid.PairGrid at 0x7f64500e5b70>
```

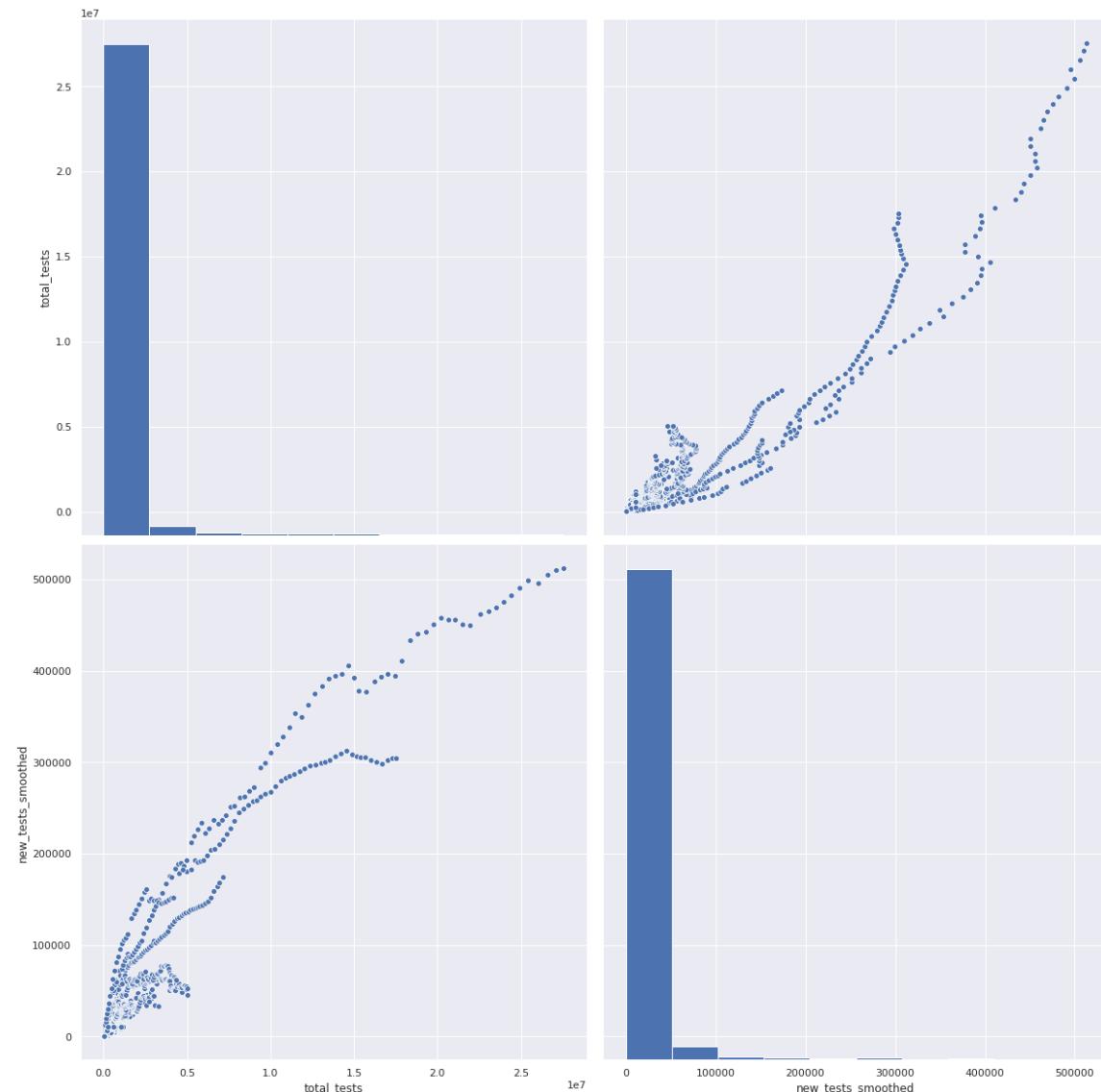


In [69]:

```
sns.pairplot(features, vars=["total_tests", "new_tests_smoothed"], height=8)
```

Out[69]:

```
<seaborn.axisgrid.PairGrid at 0x7f6450125cf8>
```

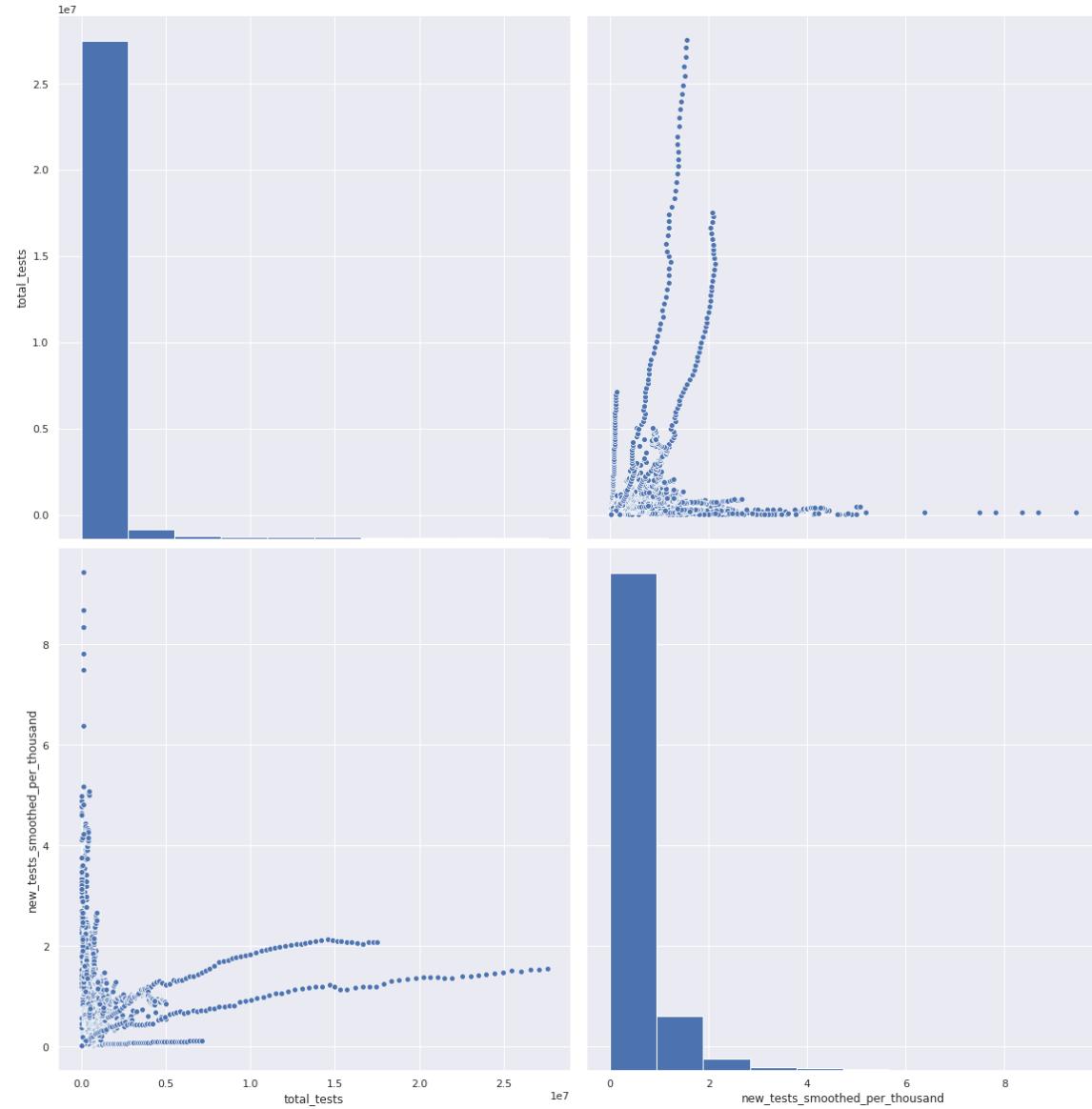


In [70]:

```
sns.pairplot(features, vars=["total_tests", "new_tests_smoothed_per_thousand"], height=8)
```

Out[70]:

```
<seaborn.axisgrid.PairGrid at 0x7f644fc80f98>
```

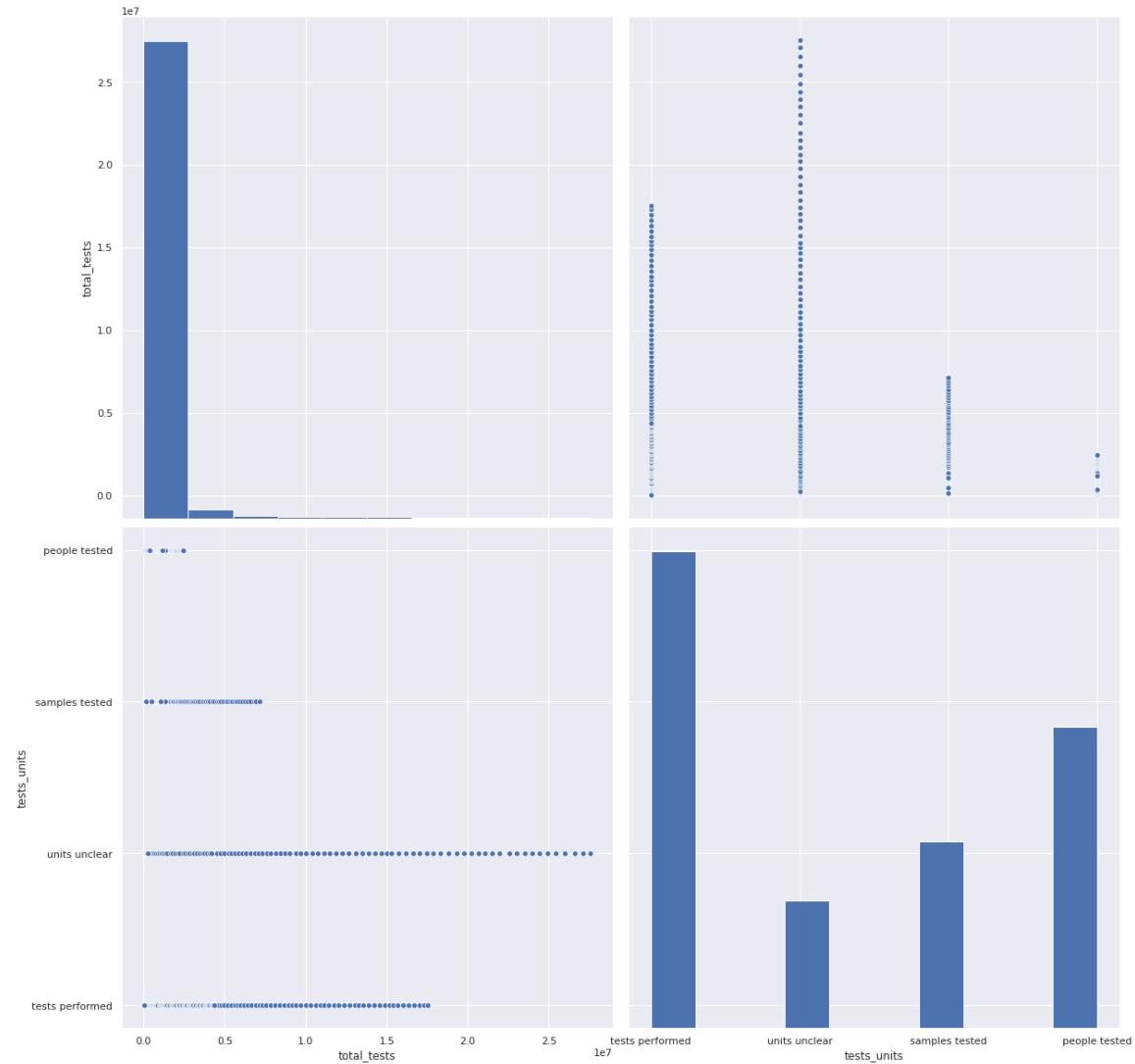


In [71]:

```
sns.pairplot(features, vars=["total_tests", "tests_units"], height=8)
```

Out[71]:

```
<seaborn.axisgrid.PairGrid at 0x7f644fb69ef0>
```

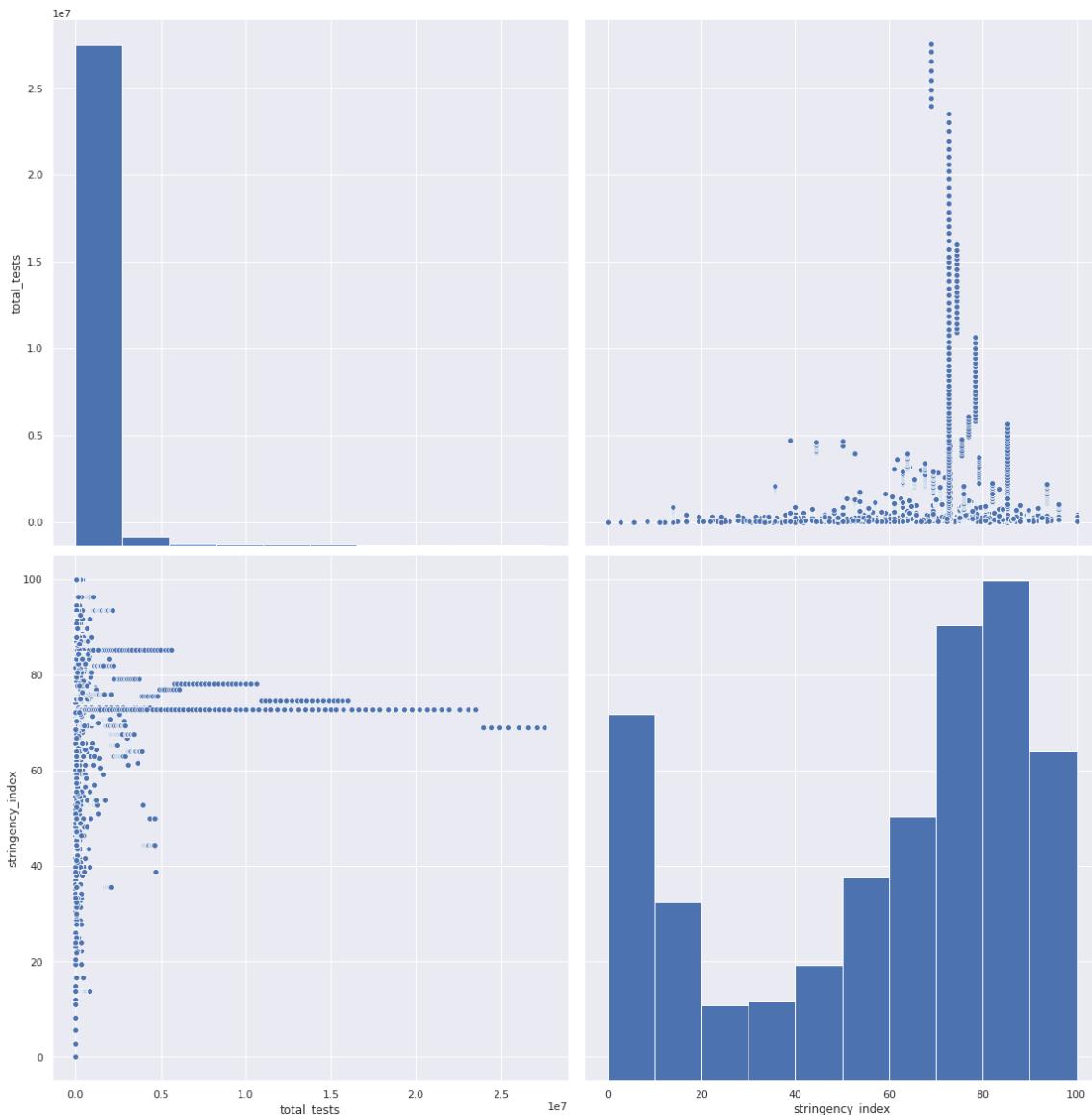


In [72]:

```
sns.pairplot(features, vars=["total_tests", "stringency_index"], height=8)
```

Out[72]:

```
<seaborn.axisgrid.PairGrid at 0x7f644f9376d8>
```

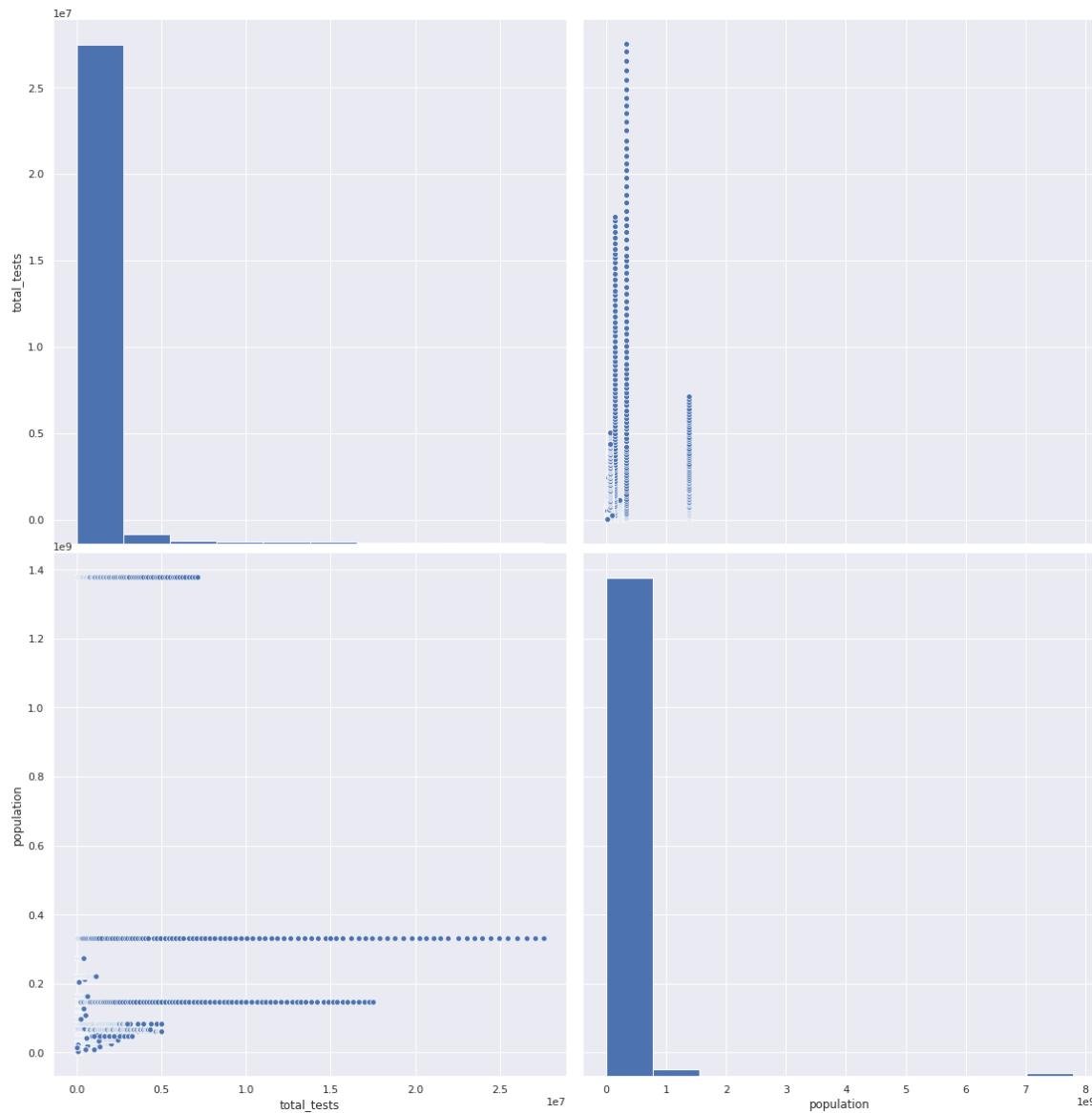


In [73]:

```
sns.pairplot(features, vars=["total_tests", "population"], height=8)
```

Out[73]:

```
<seaborn.axisgrid.PairGrid at 0x7f644f6c4cc0>
```

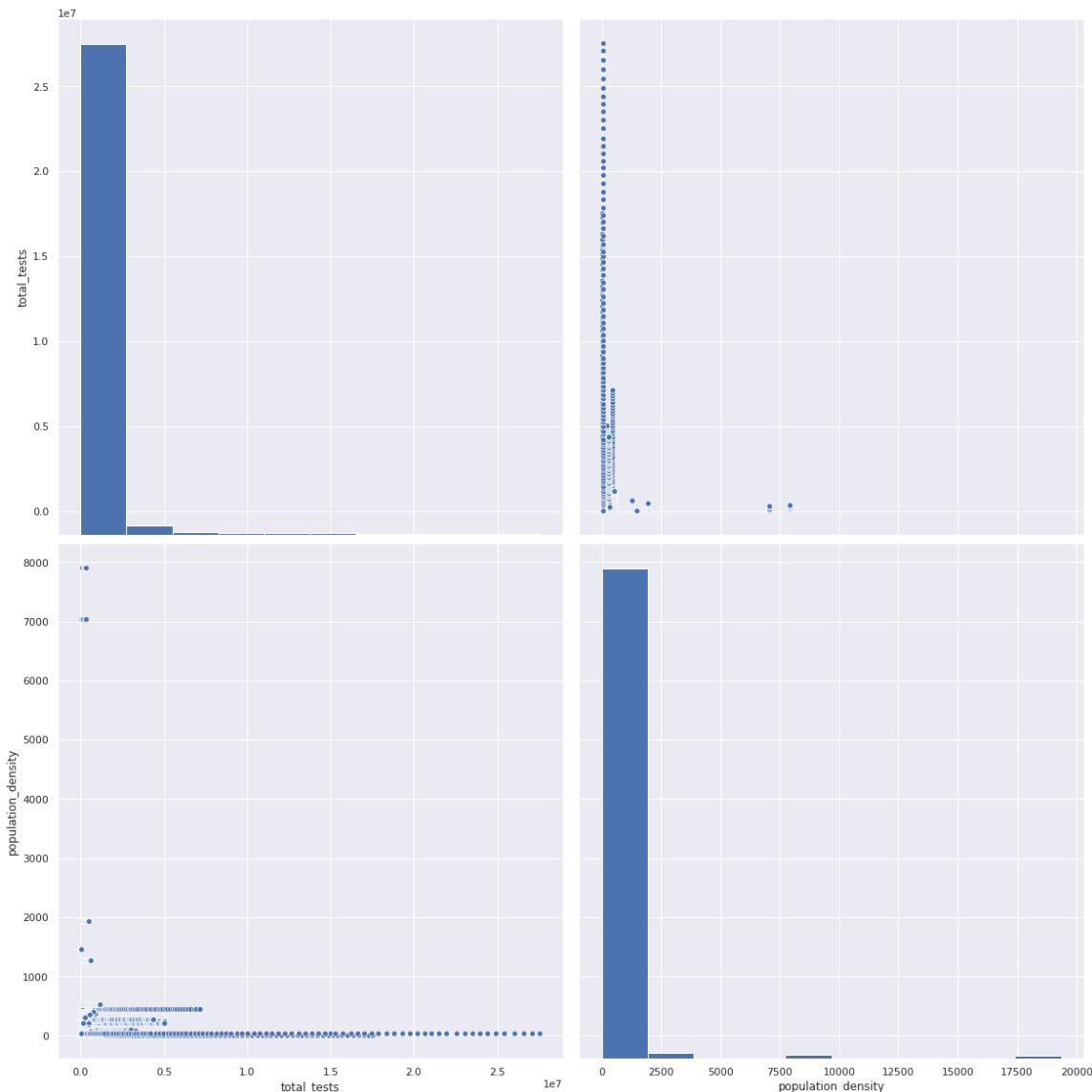


In [74]:

```
sns.pairplot(features, vars=["total_tests", "population_density"], height=8)
```

Out[74]:

```
<seaborn.axisgrid.PairGrid at 0x7f644f5c9438>
```

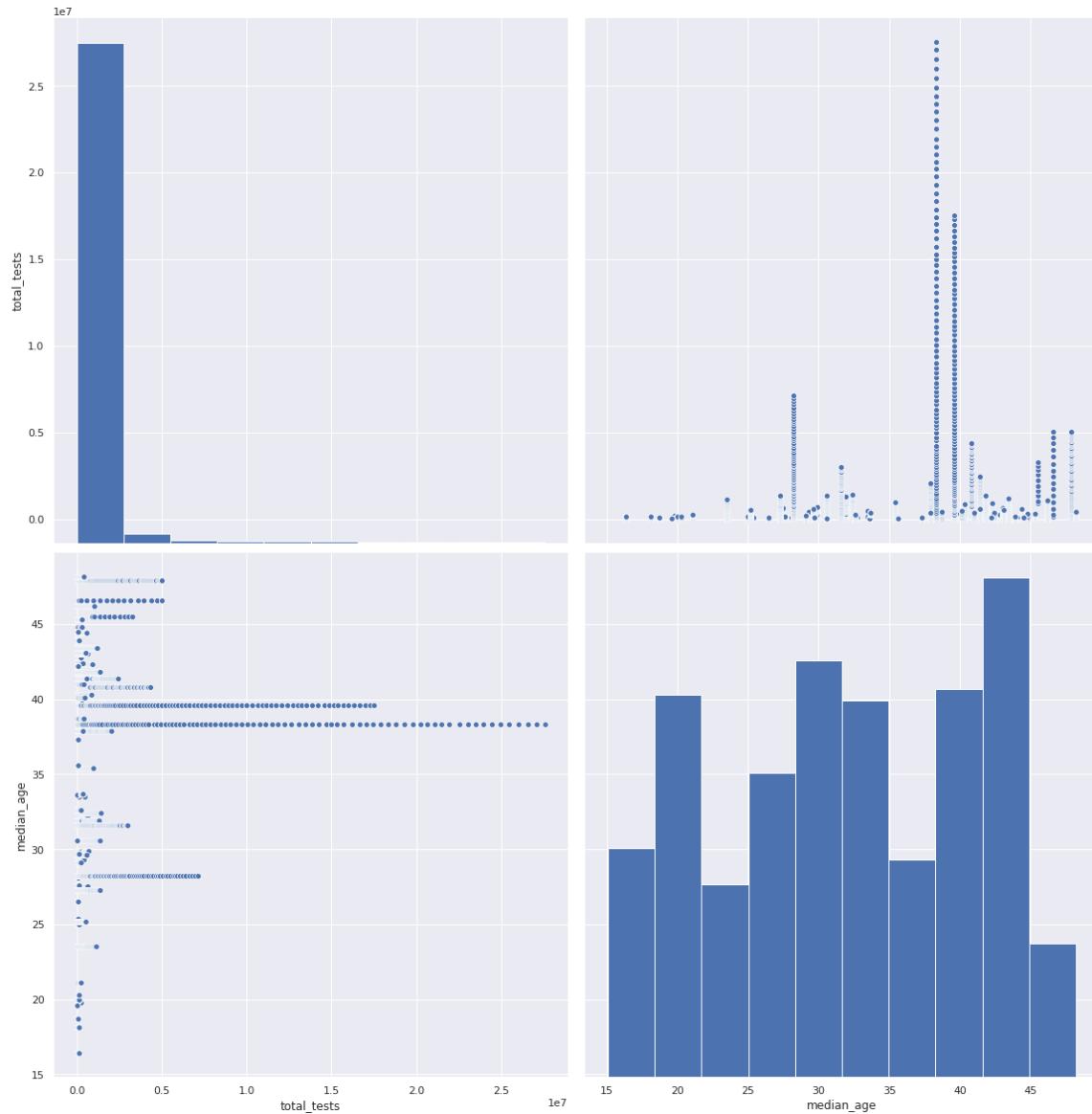


In [75]:

```
sns.pairplot(features, vars=["total_tests", "median_age"], height=8)
```

Out[75]:

```
<seaborn.axisgrid.PairGrid at 0x7f644f2c52e8>
```

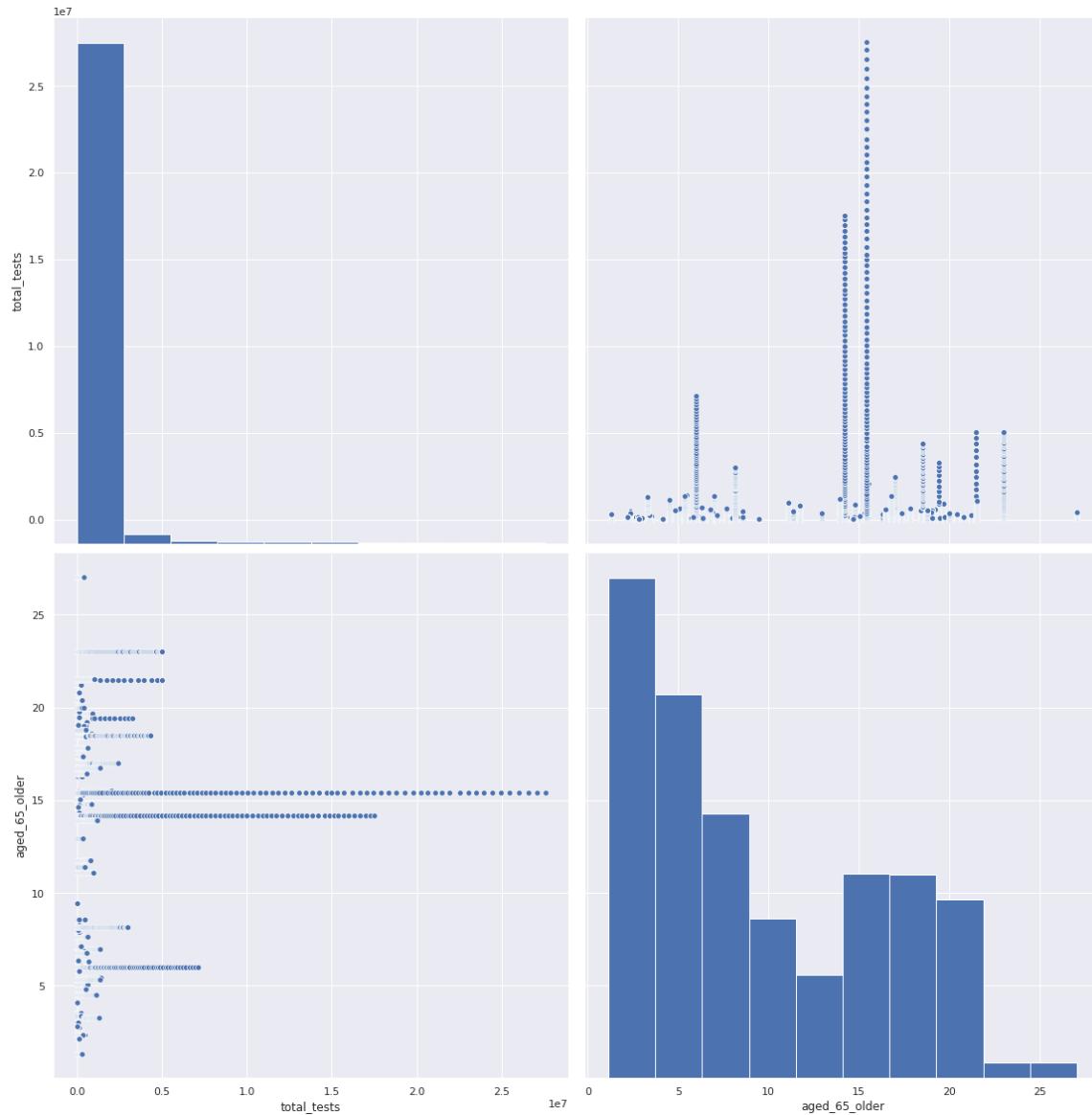


In [76]:

```
sns.pairplot(features, vars=["total_tests", "aged_65_older"], height=8)
```

Out[76]:

```
<seaborn.axisgrid.PairGrid at 0x7f644f39b710>
```

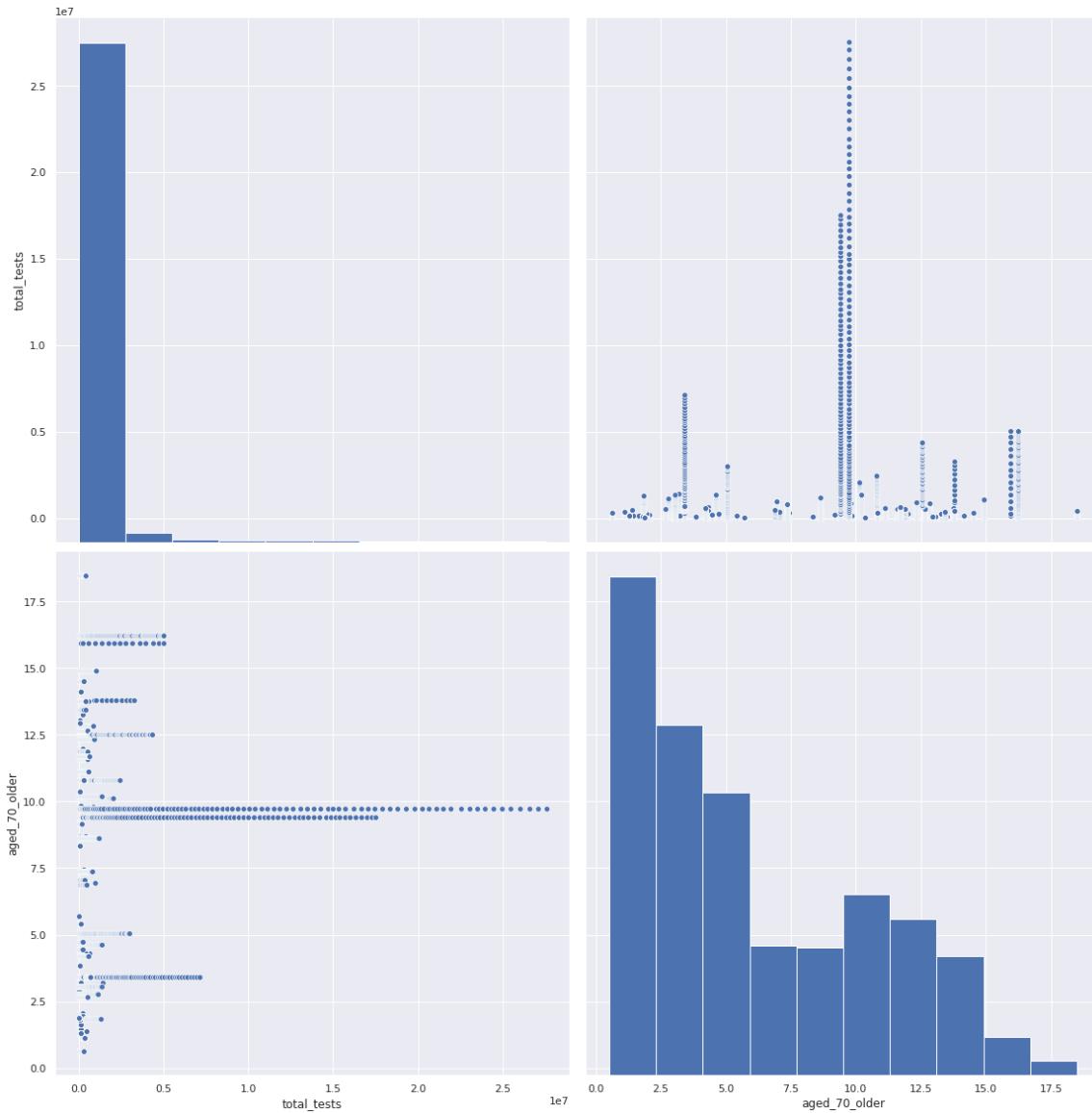


In [77]:

```
sns.pairplot(features, vars=["total_tests", "aged_70_older"], height=8)
```

Out[77]:

```
<seaborn.axisgrid.PairGrid at 0x7f644f02d358>
```

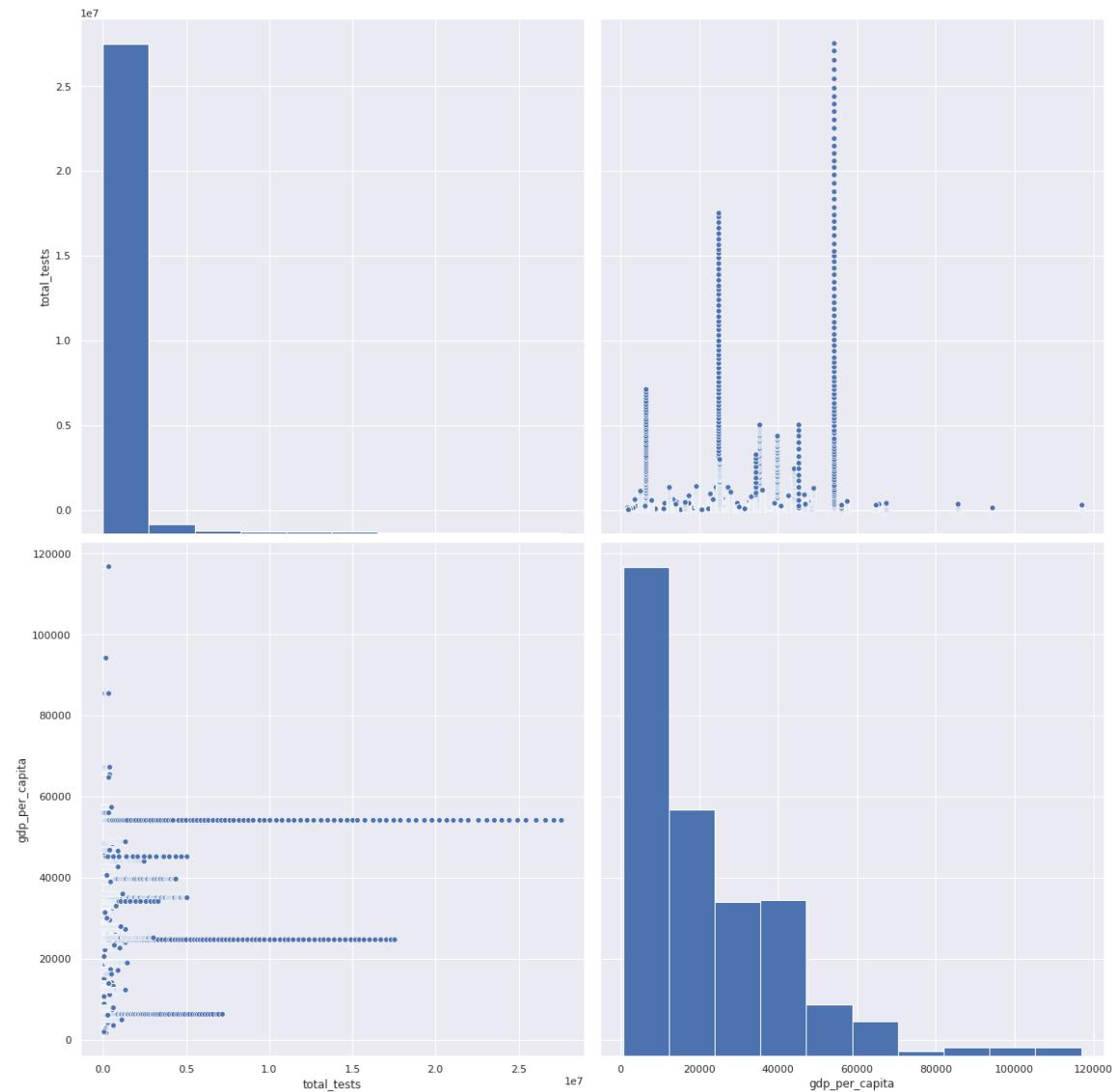


In [78]:

```
sns.pairplot(features, vars=["total_tests", "gdp_per_capita"], height=8)
```

Out[78]:

```
<seaborn.axisgrid.PairGrid at 0x7f644eda48d0>
```

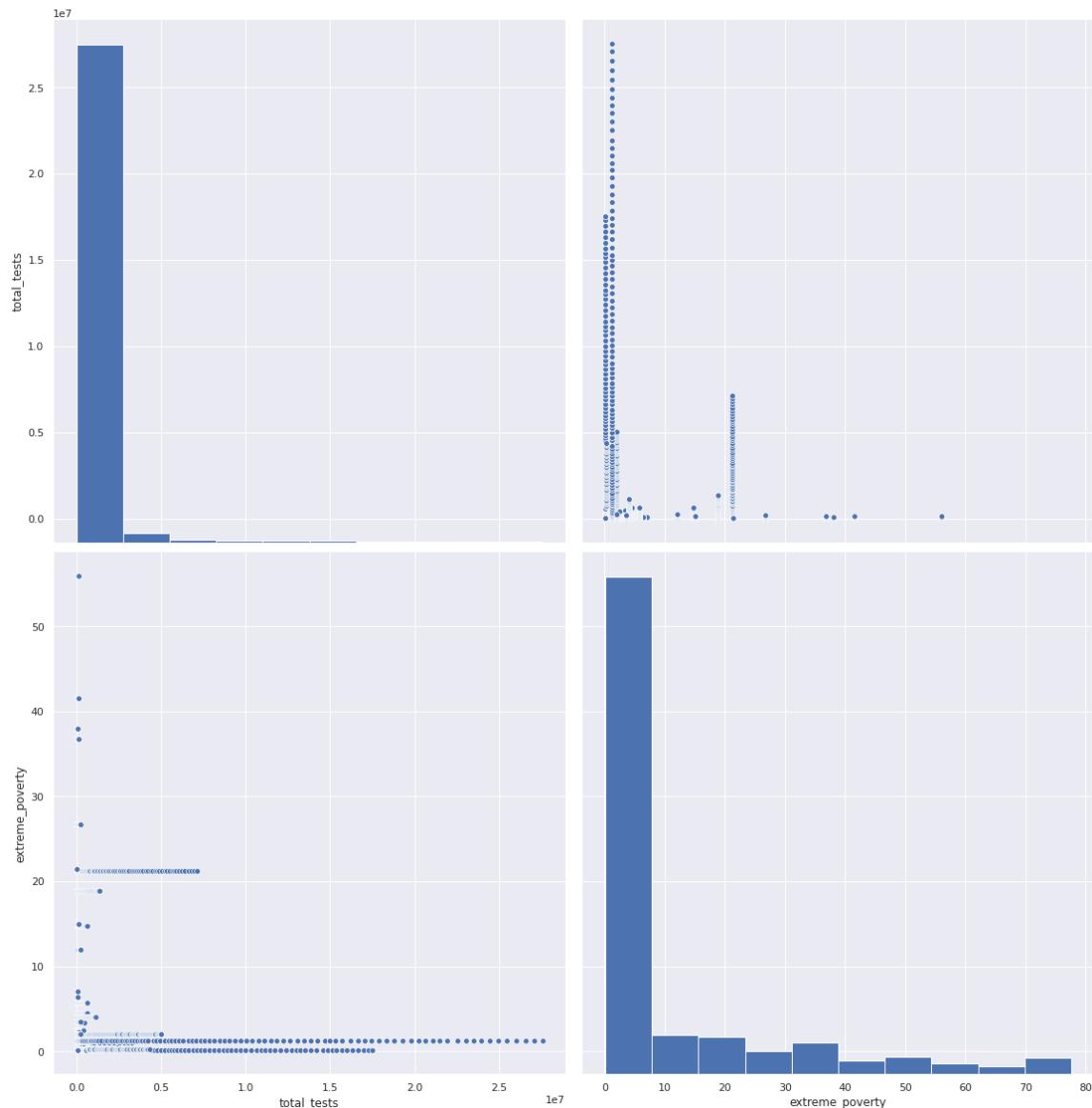


In [79]:

```
sns.pairplot(features, vars=["total_tests", "extreme_poverty"], height=8)
```

Out[79]:

```
<seaborn.axisgrid.PairGrid at 0x7f644eac8a58>
```

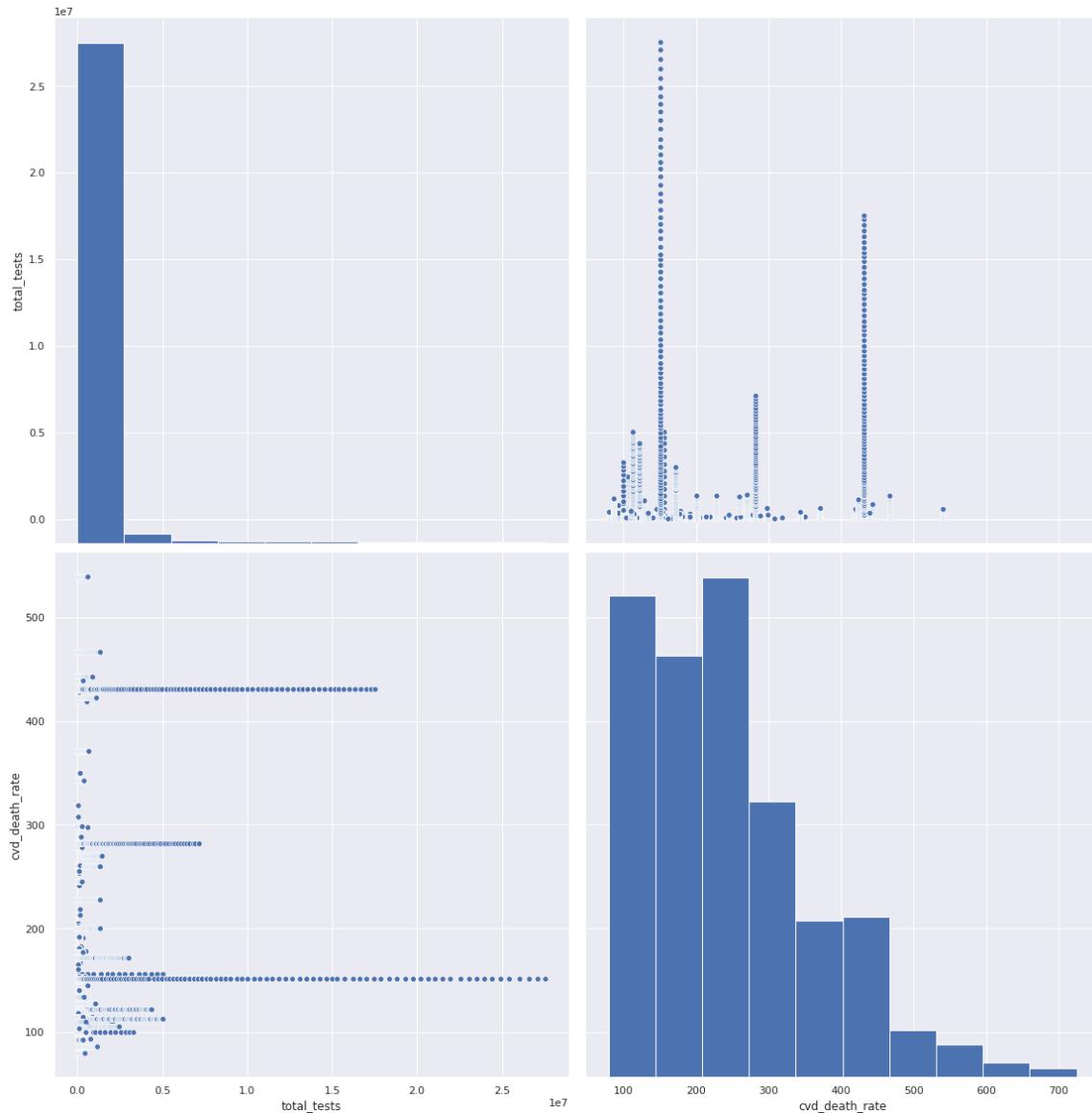


In [80]:

```
sns.pairplot(features, vars=["total_tests", "cvd_death_rate"], height=8)
```

Out[80]:

```
<seaborn.axisgrid.PairGrid at 0x7f644e8c5dd8>
```

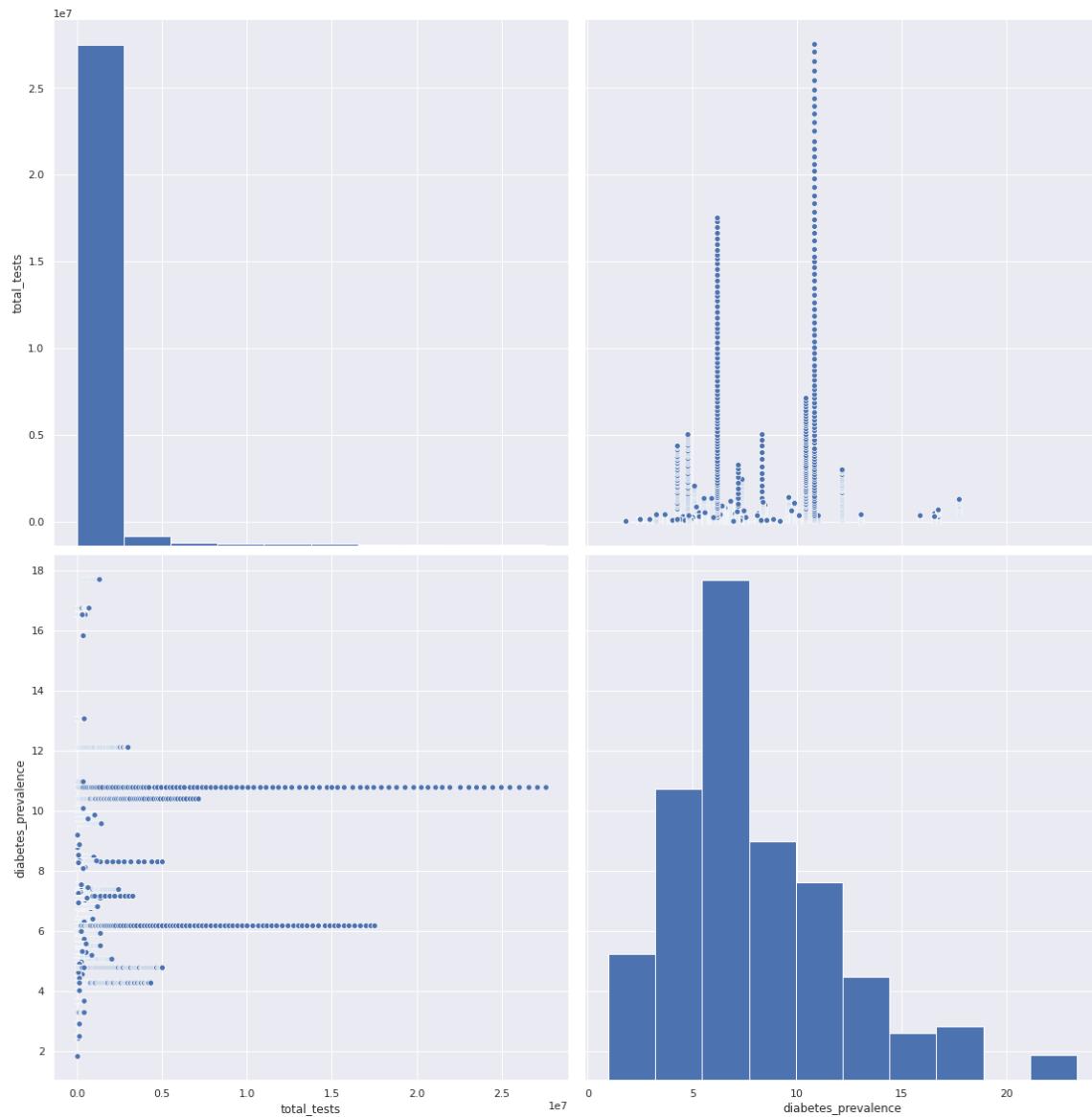


In [81]:

```
sns.pairplot(features, vars=["total_tests", "diabetes_prevalence"], height=8)
```

Out[81]:

```
<seaborn.axisgrid.PairGrid at 0x7f644e879ac8>
```

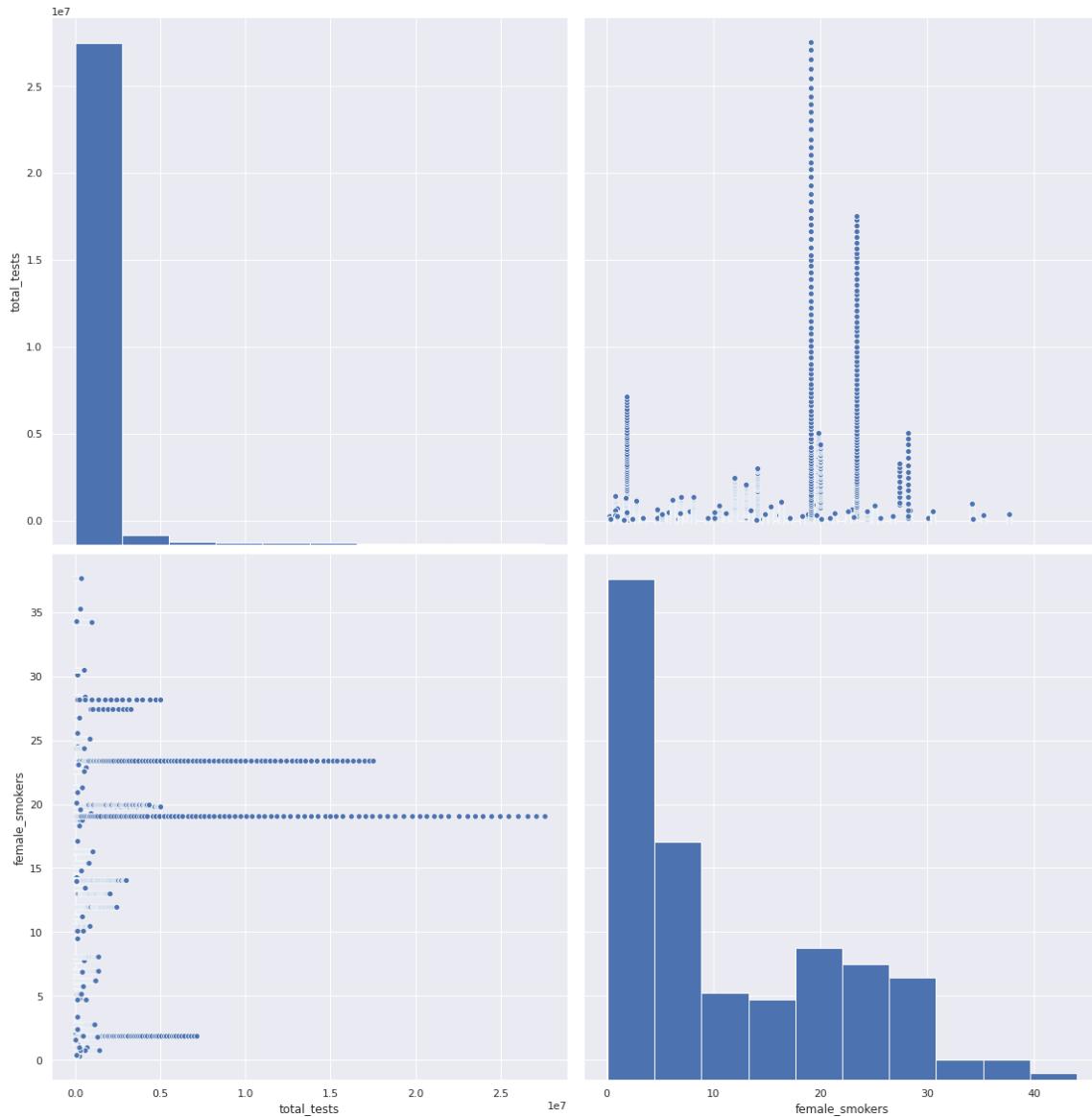


In [82]:

```
sns.pairplot(features, vars=["total_tests", "female_smokers"], height=8)
```

Out[82]:

```
<seaborn.axisgrid.PairGrid at 0x7f644e629d68>
```

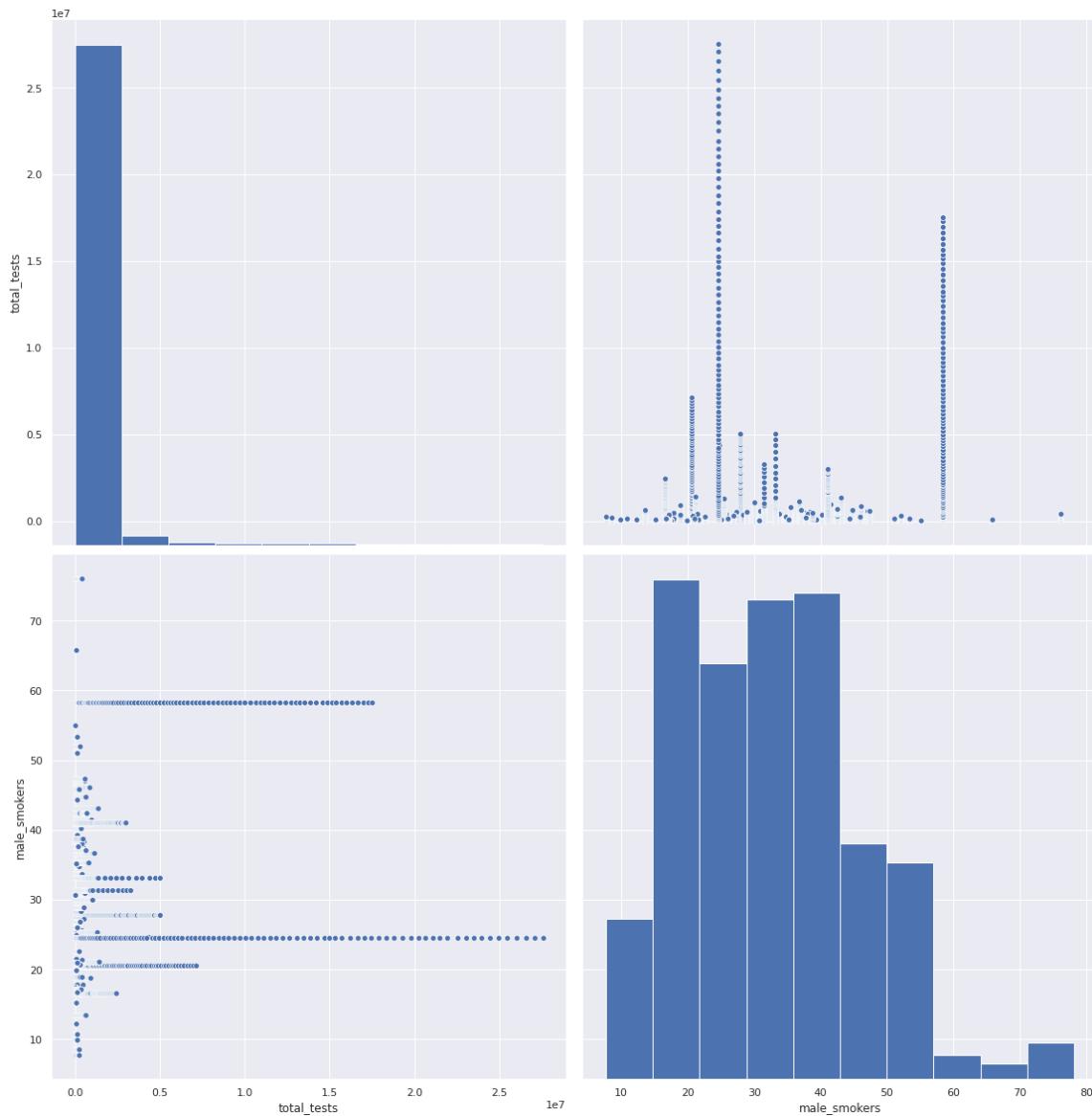


In [83]:

```
sns.pairplot(features, vars=["total_tests", "male_smokers"], height=8)
```

Out[83]:

```
<seaborn.axisgrid.PairGrid at 0x7f644e30fd30>
```

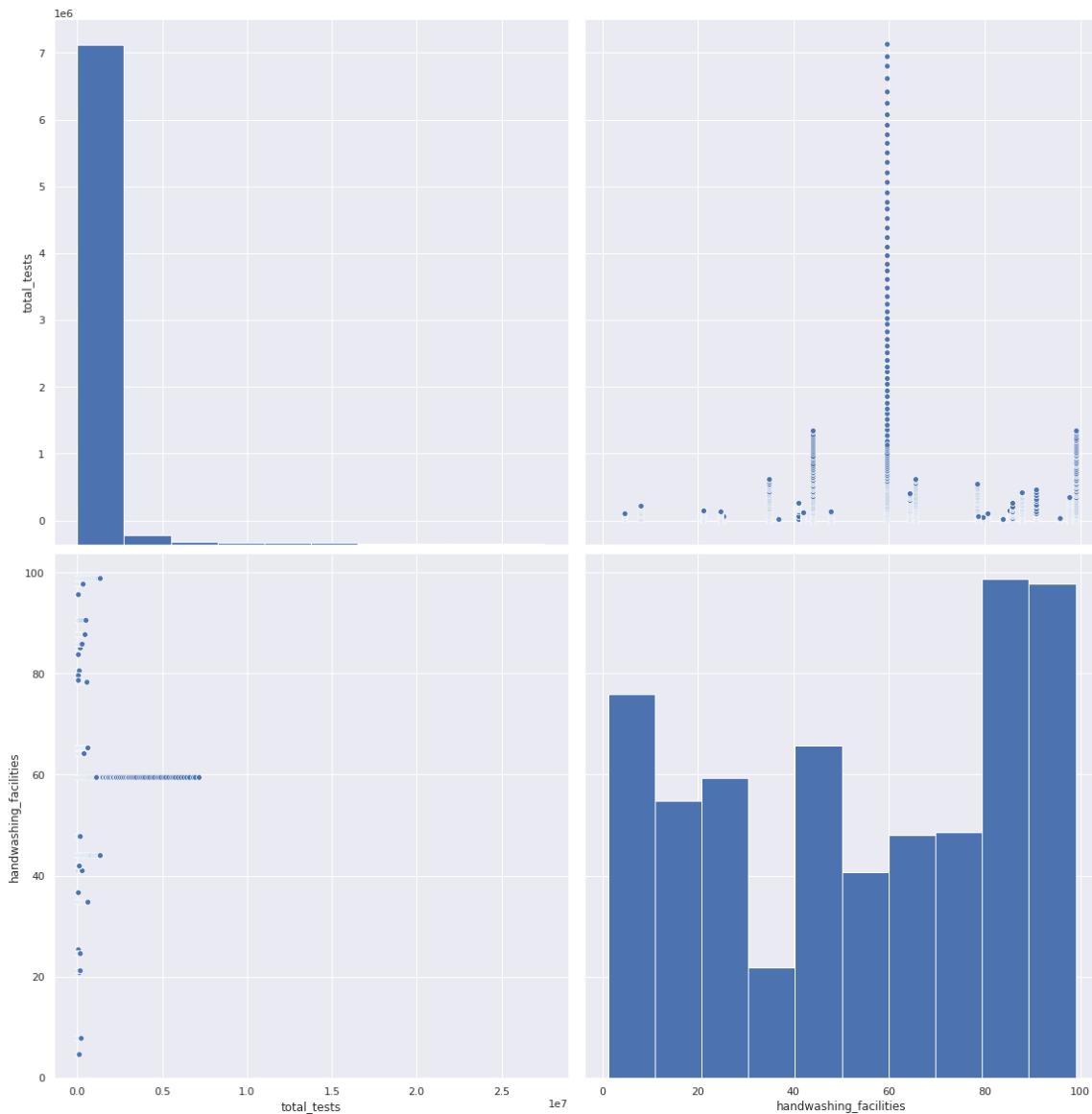


In [84]:

```
sns.pairplot(features, vars=["total_tests", "handwashing_facilities"], height=8)
```

Out[84]:

```
<seaborn.axisgrid.PairGrid at 0x7f644e792470>
```

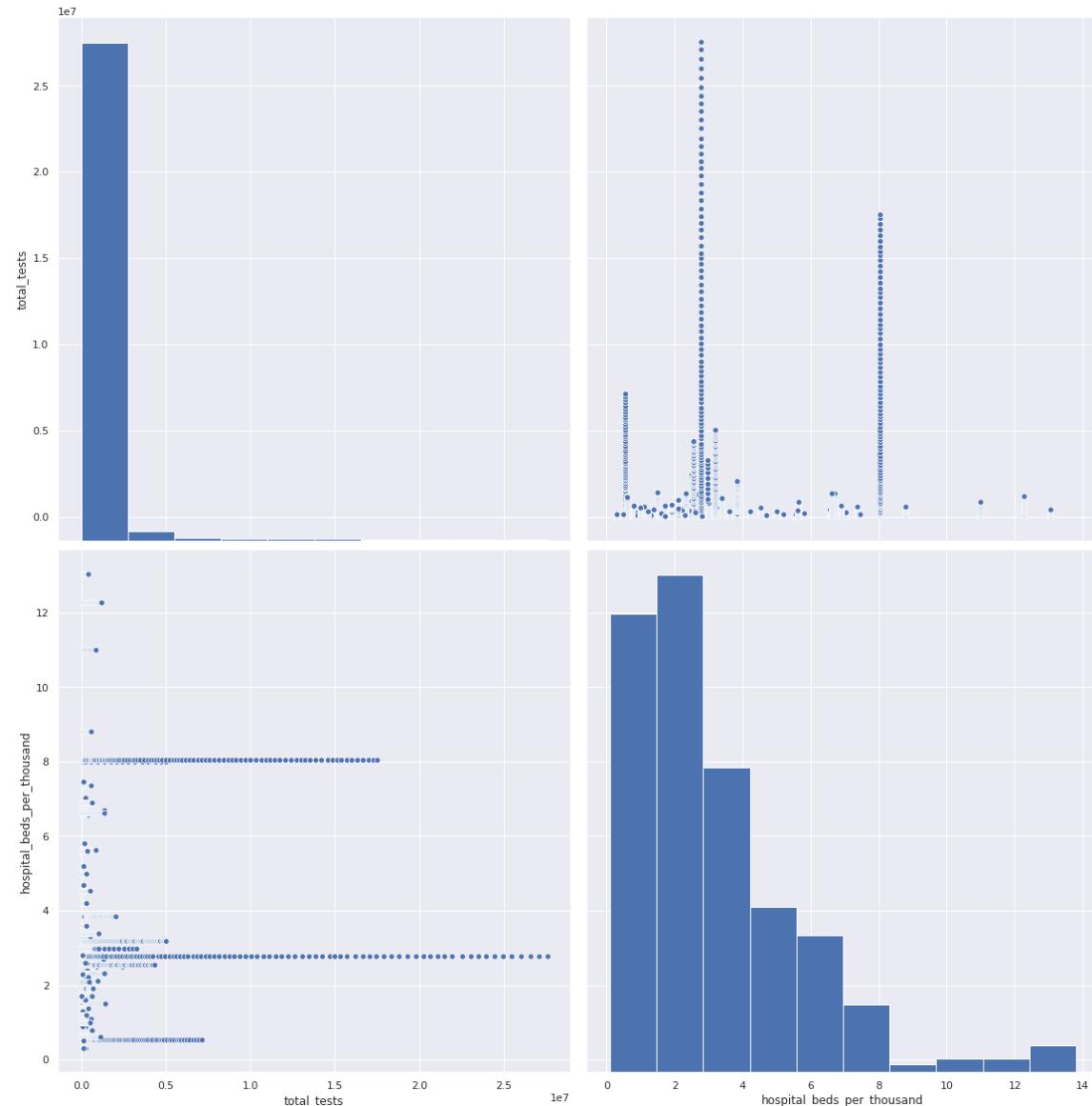


In [85]:

```
sns.pairplot(features, vars=["total_tests", "hospital_beds_per_thousand"], height=8)
```

Out[85]:

```
<seaborn.axisgrid.PairGrid at 0x7f644dec0b8>
```

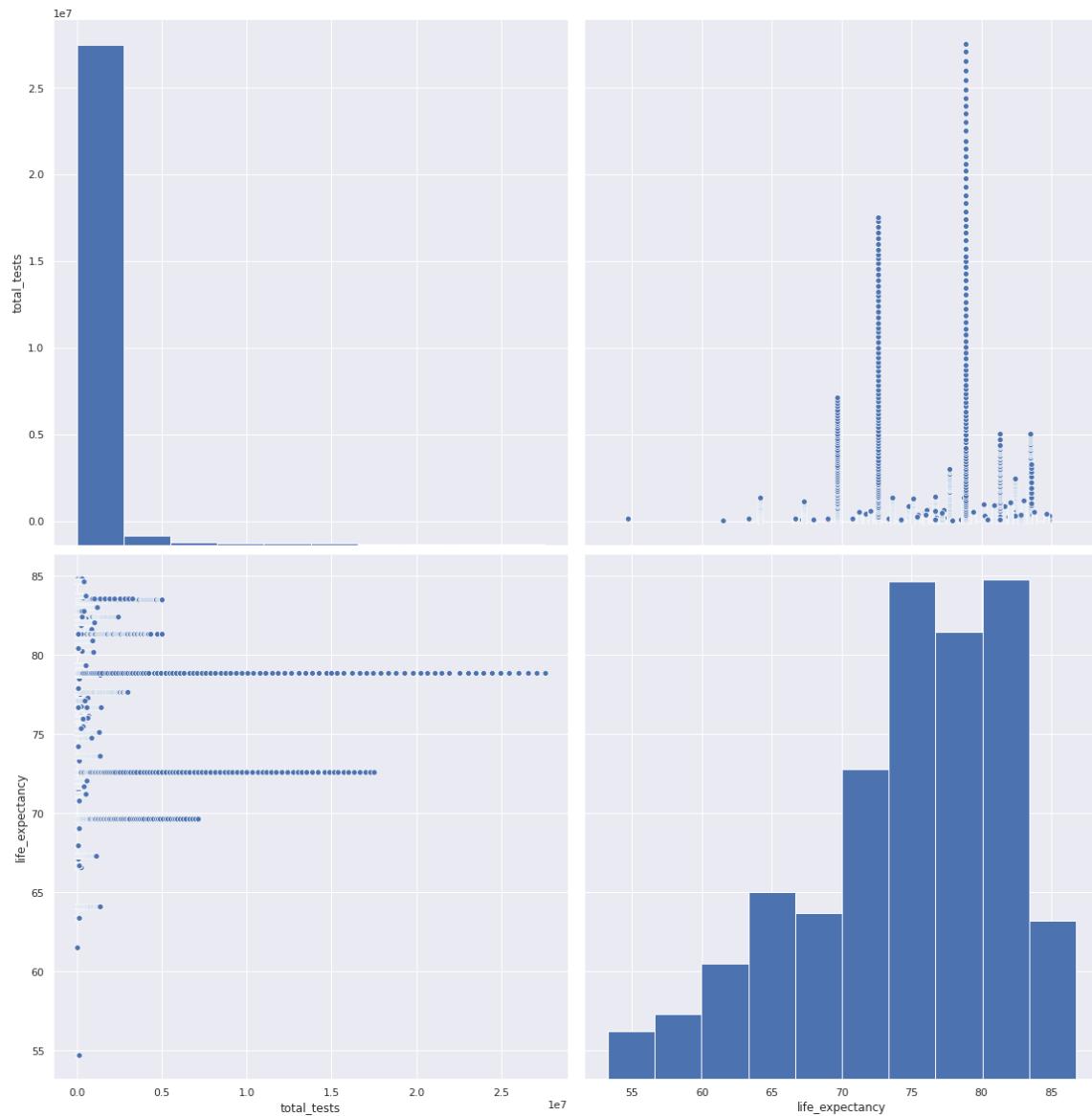


In [86]:

```
sns.pairplot(features, vars=["total_tests", "life_expectancy"], height=8)
```

Out[86]:

```
<seaborn.axisgrid.PairGrid at 0x7f644dd239e8>
```

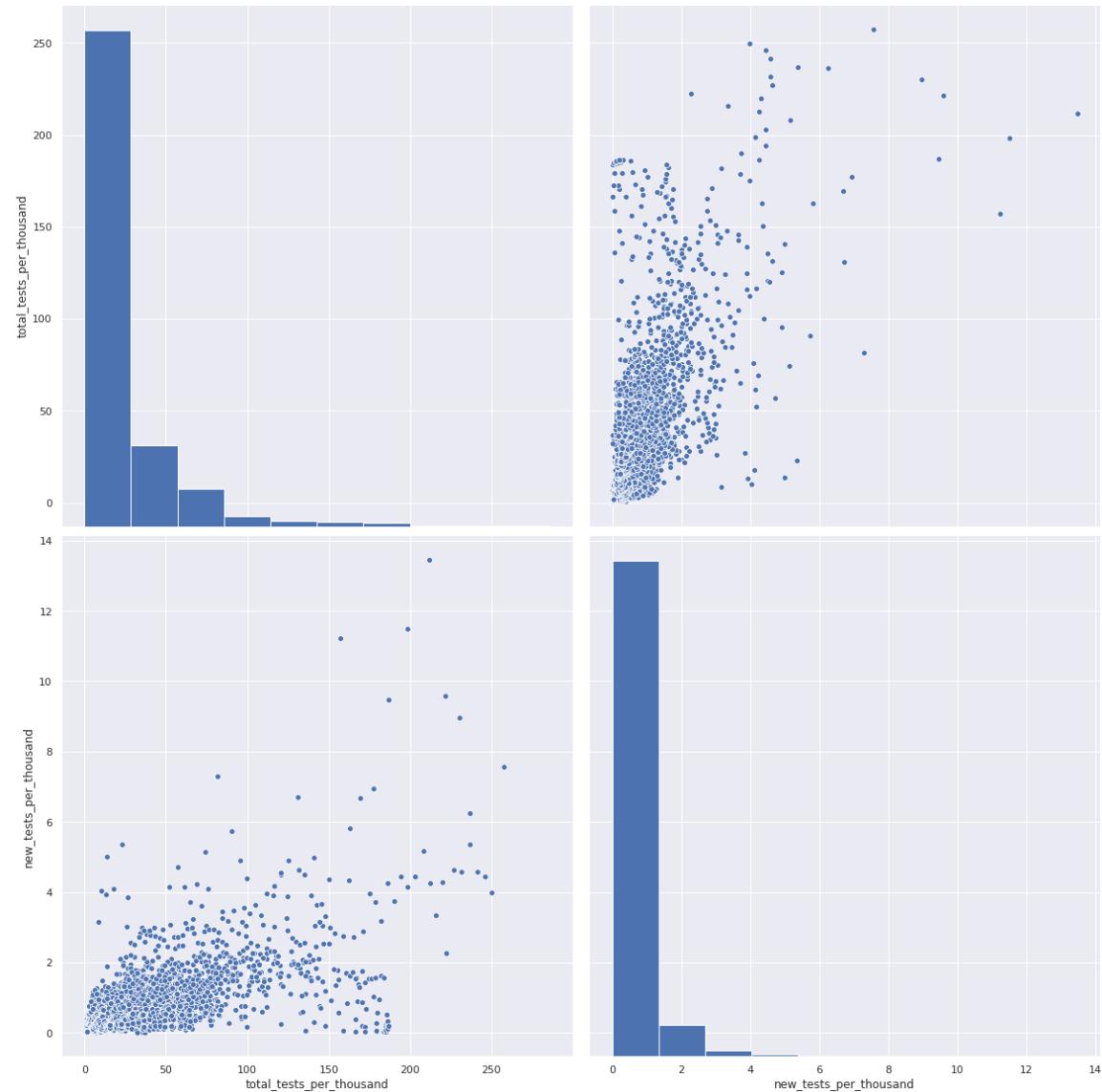


In [87]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "new_tests_per_thousan  
d"], height=8)
```

Out[87]:

```
<seaborn.axisgrid.PairGrid at 0x7f644db74128>
```

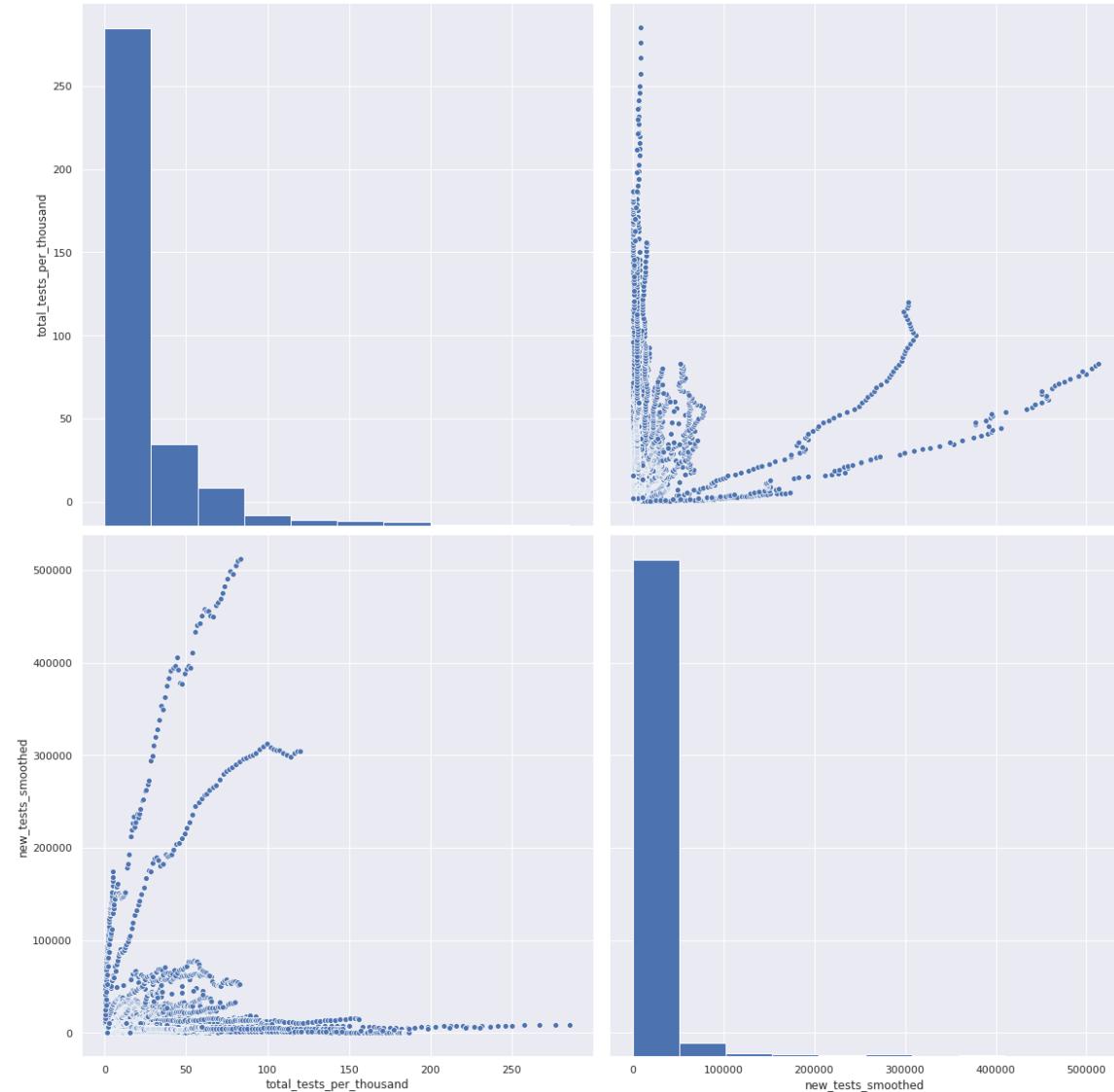


In [88]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "new_tests_smoothed"], height=8)
```

Out[88]:

```
<seaborn.axisgrid.PairGrid at 0x7f644d8ca550>
```

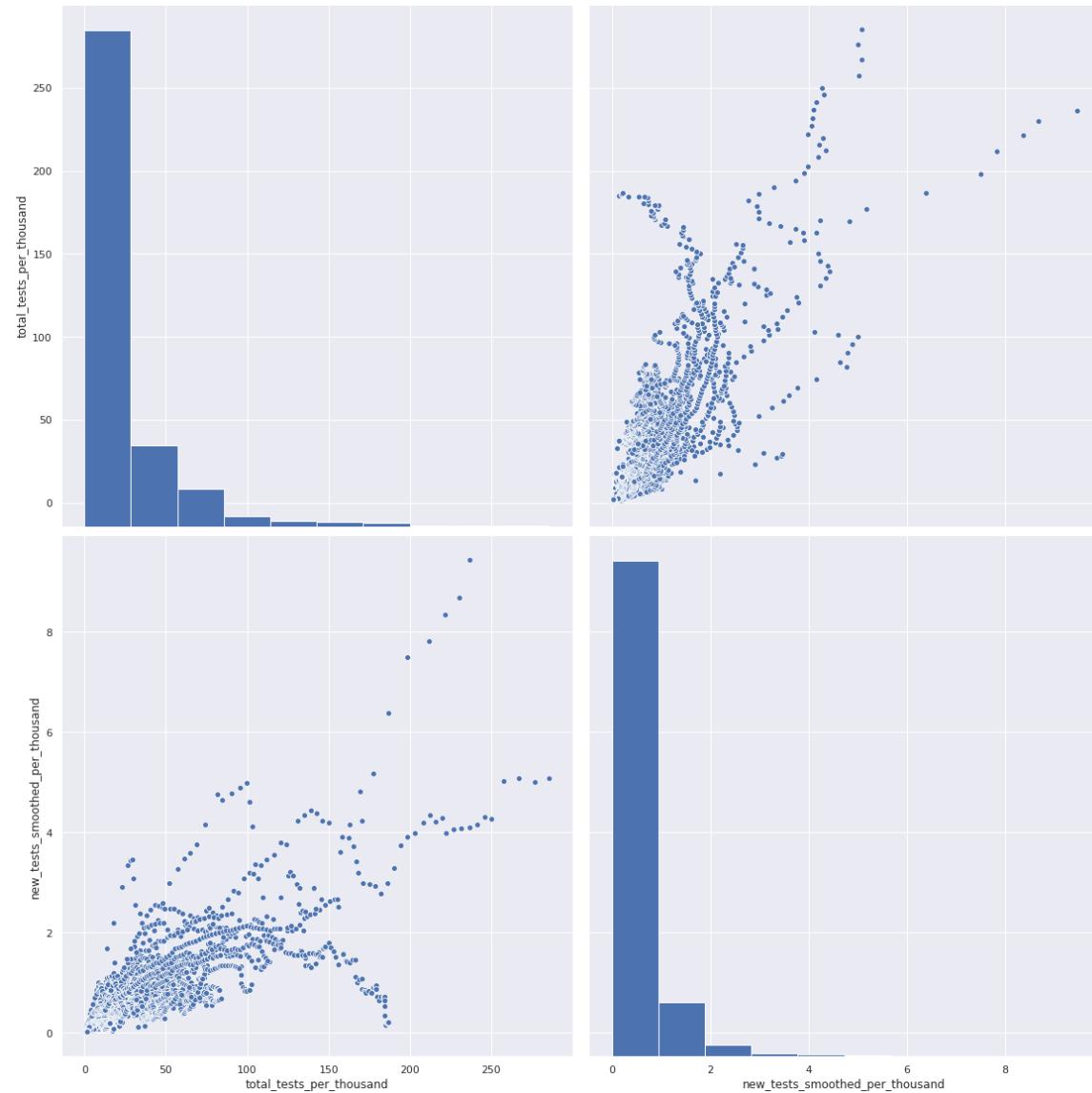


In [89]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "new_tests_smoothed_per_thousand"], height=8)
```

Out[89]:

```
<seaborn.axisgrid.PairGrid at 0x7f644d6d0c18>
```

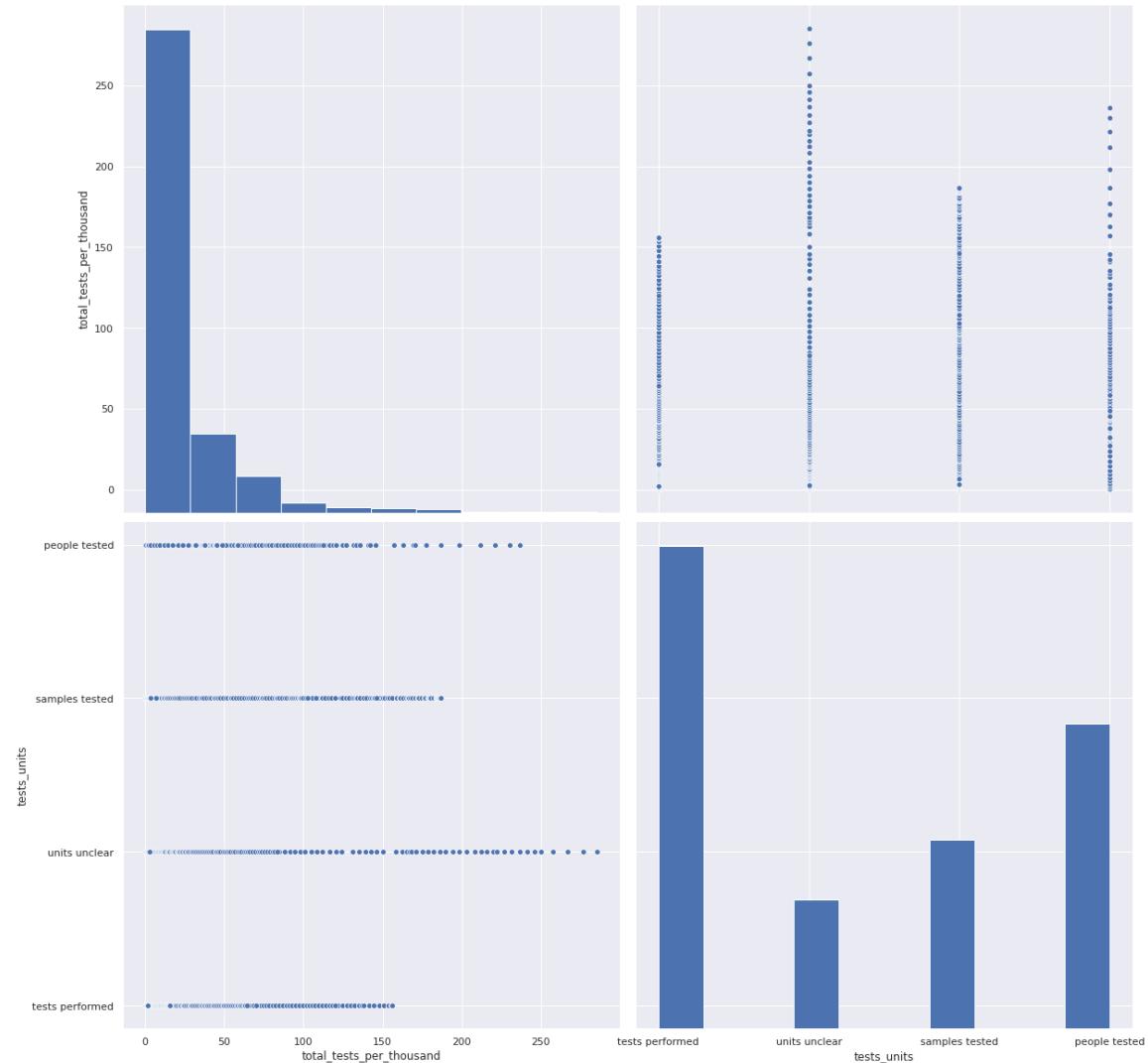


In [90]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "tests_units"], height=8)
```

Out[90]:

```
<seaborn.axisgrid.PairGrid at 0x7f644d4c5cc0>
```

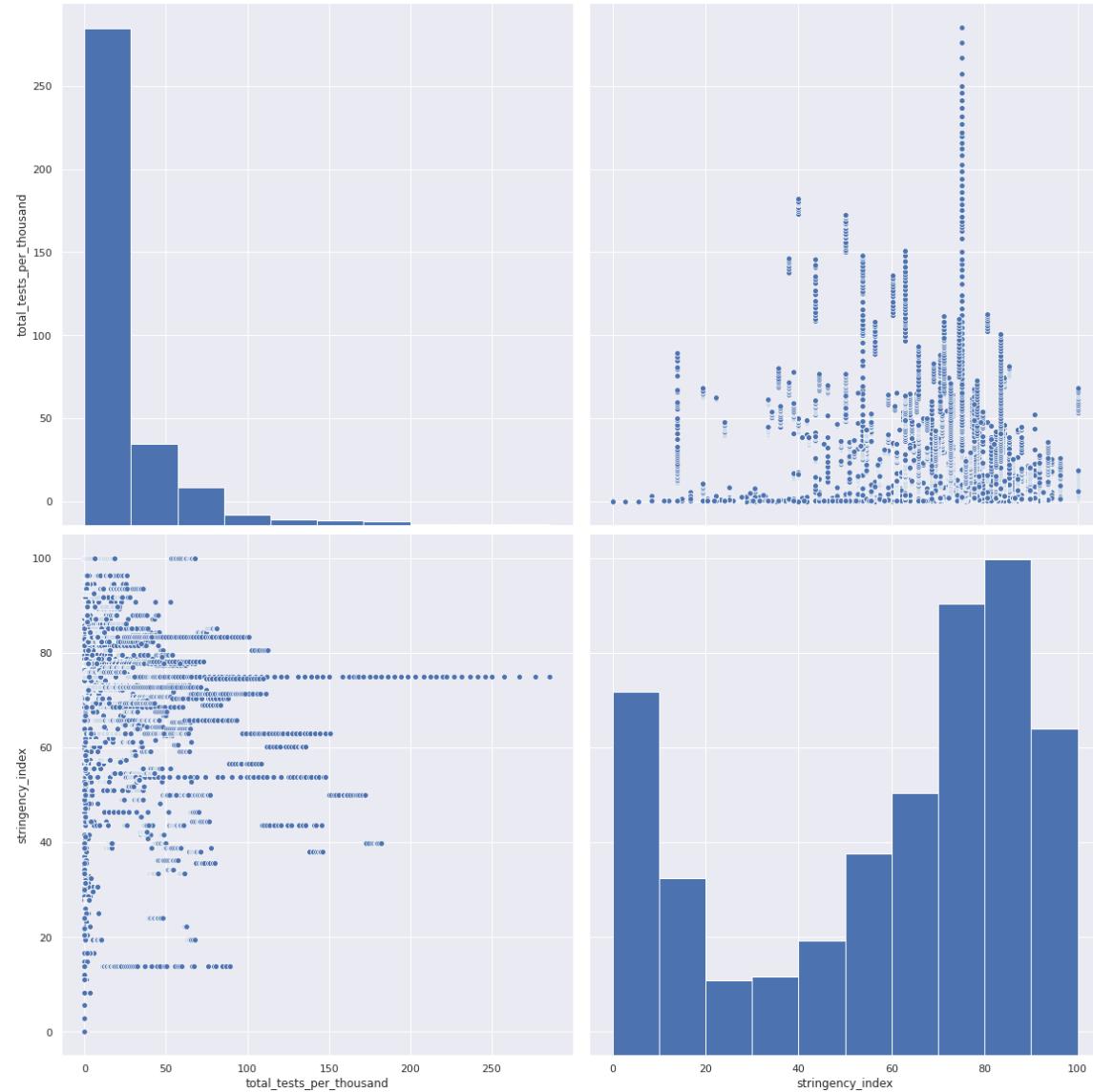


In [91]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "stringency_index"], height=8)
```

Out[91]:

```
<seaborn.axisgrid.PairGrid at 0x7f644d5149e8>
```

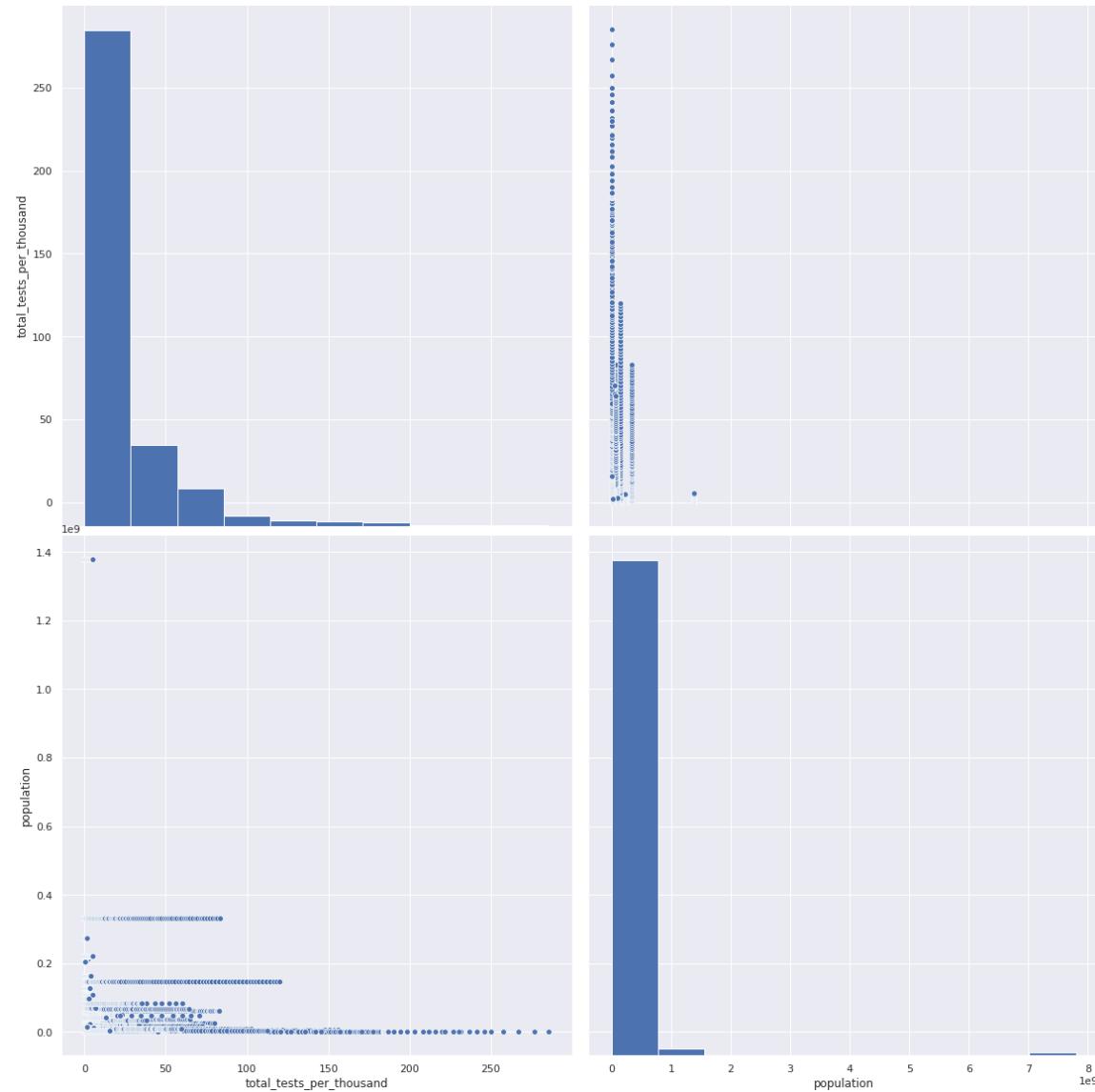


In [92]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "population"], height=8)
```

Out[92]:

```
<seaborn.axisgrid.PairGrid at 0x7f644d111e10>
```

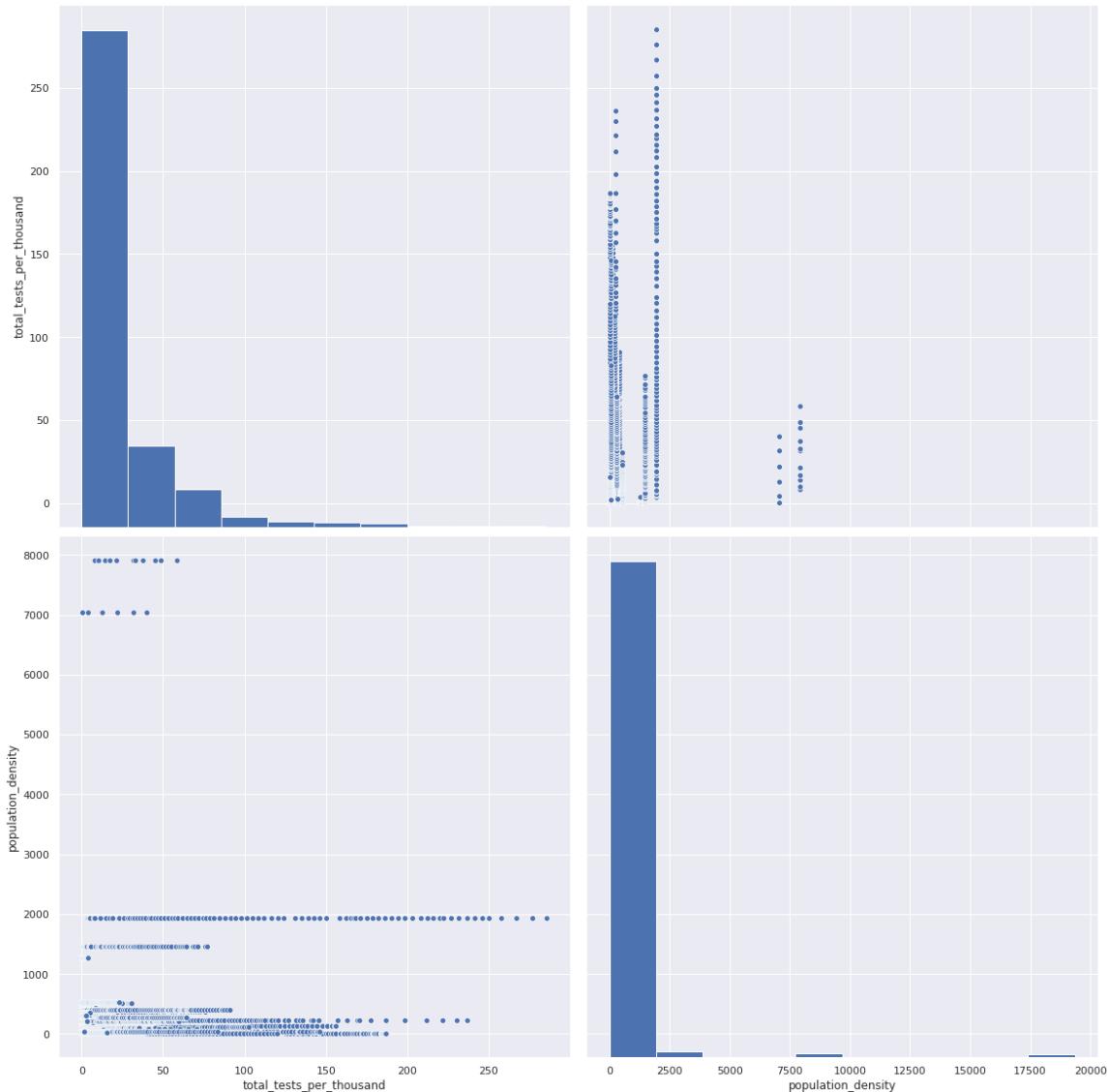


In [93]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "population_density"],  
height=8)
```

Out[93]:

```
<seaborn.axisgrid.PairGrid at 0x7f644cf1e470>
```

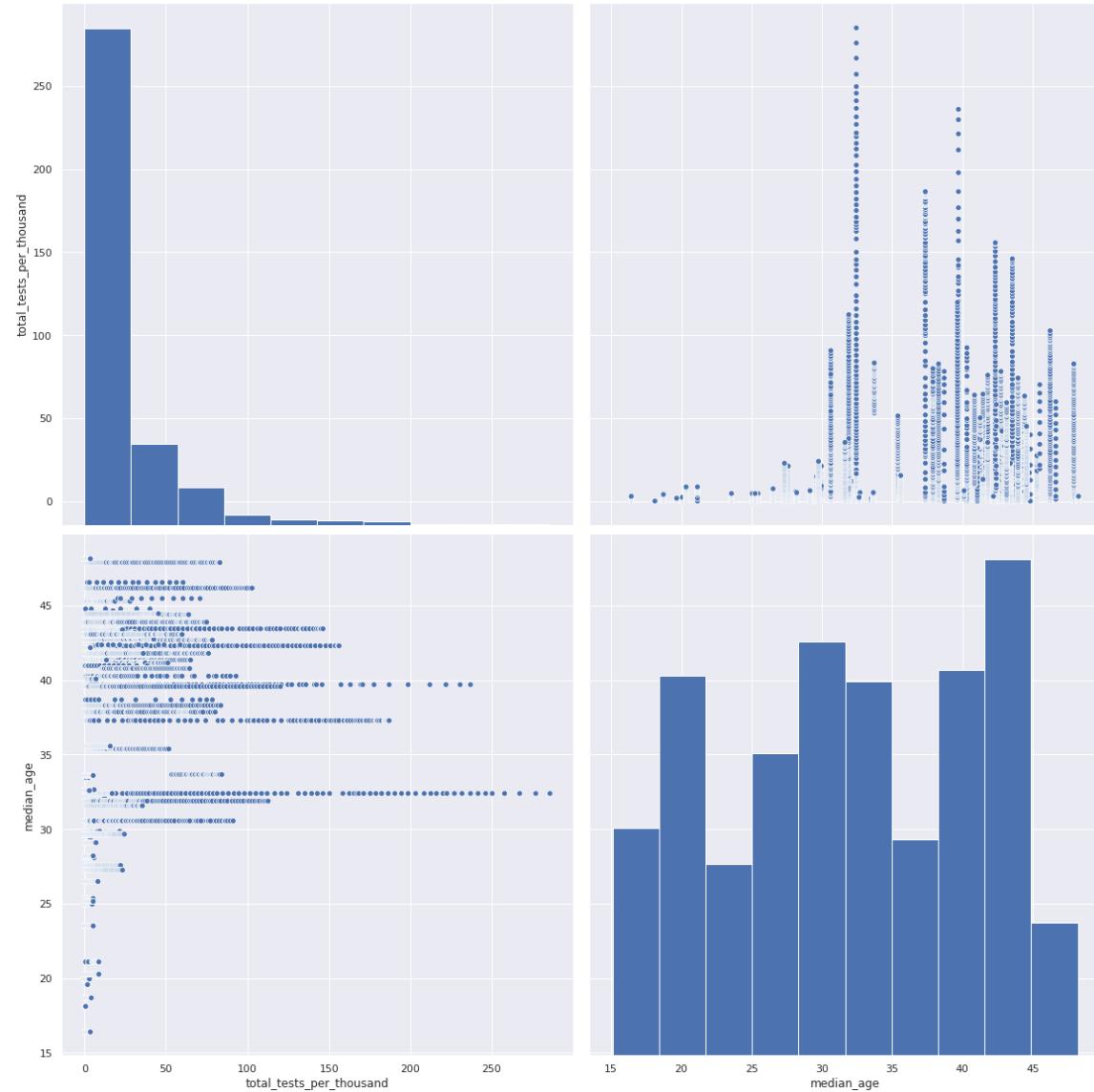


In [94]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "median_age"], height=8)
```

Out[94]:

```
<seaborn.axisgrid.PairGrid at 0x7f644ed3ad30>
```

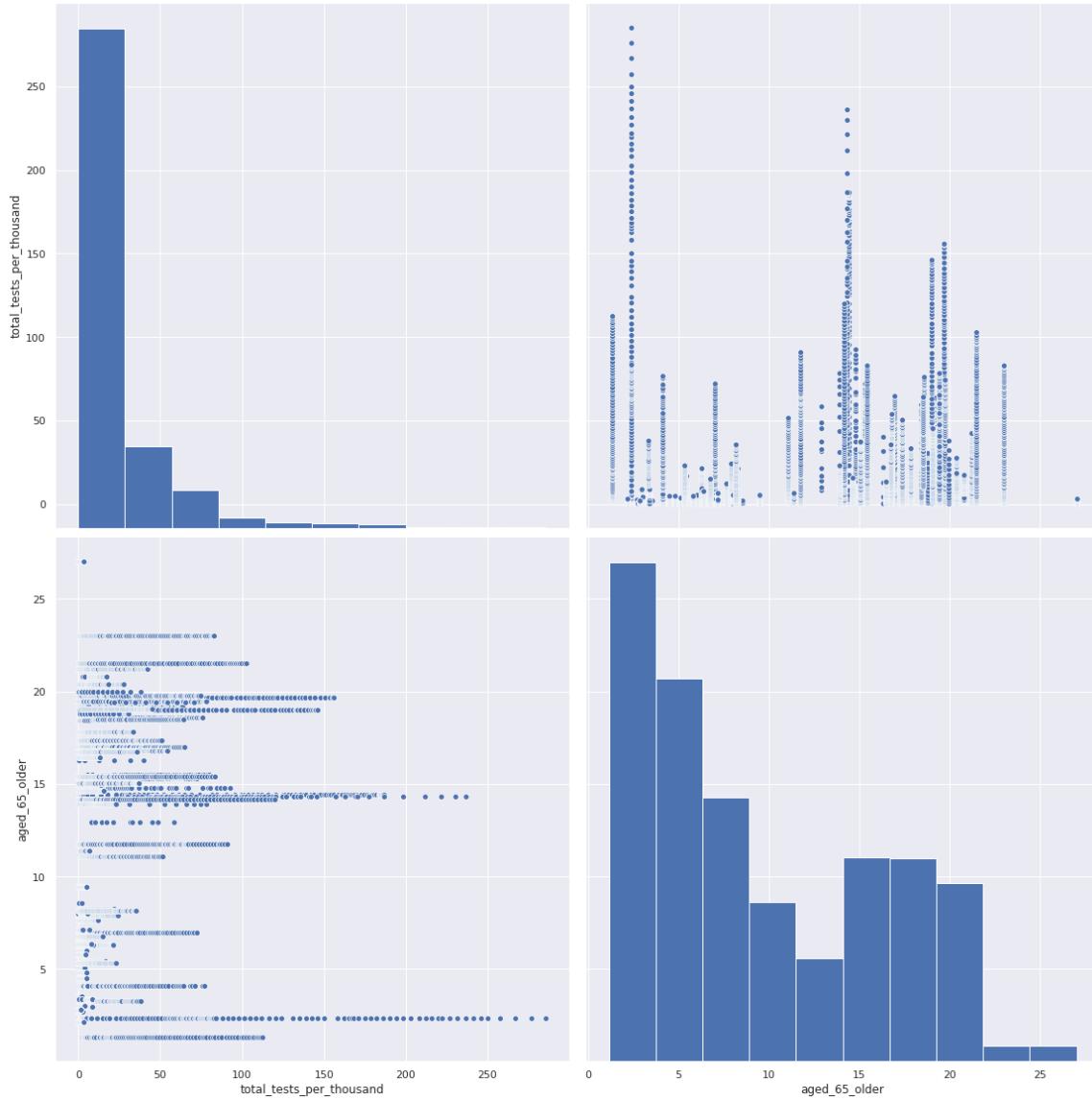


In [95]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "aged_65_older"], height=8)
```

Out[95]:

```
<seaborn.axisgrid.PairGrid at 0x7f644cb520b8>
```

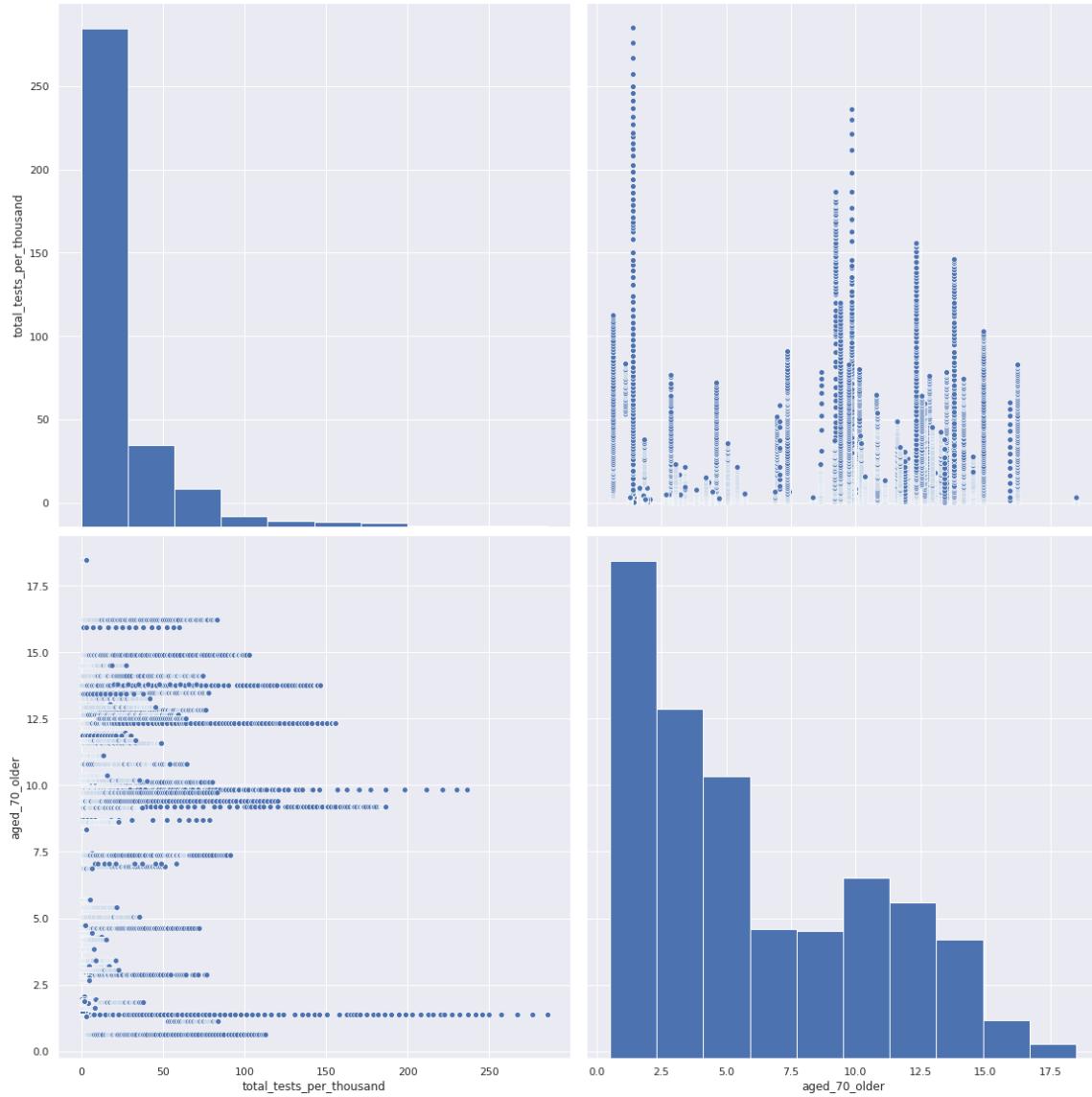


In [96]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "aged_70_older"], height=8)
```

Out[96]:

```
<seaborn.axisgrid.PairGrid at 0x7f644ca01978>
```

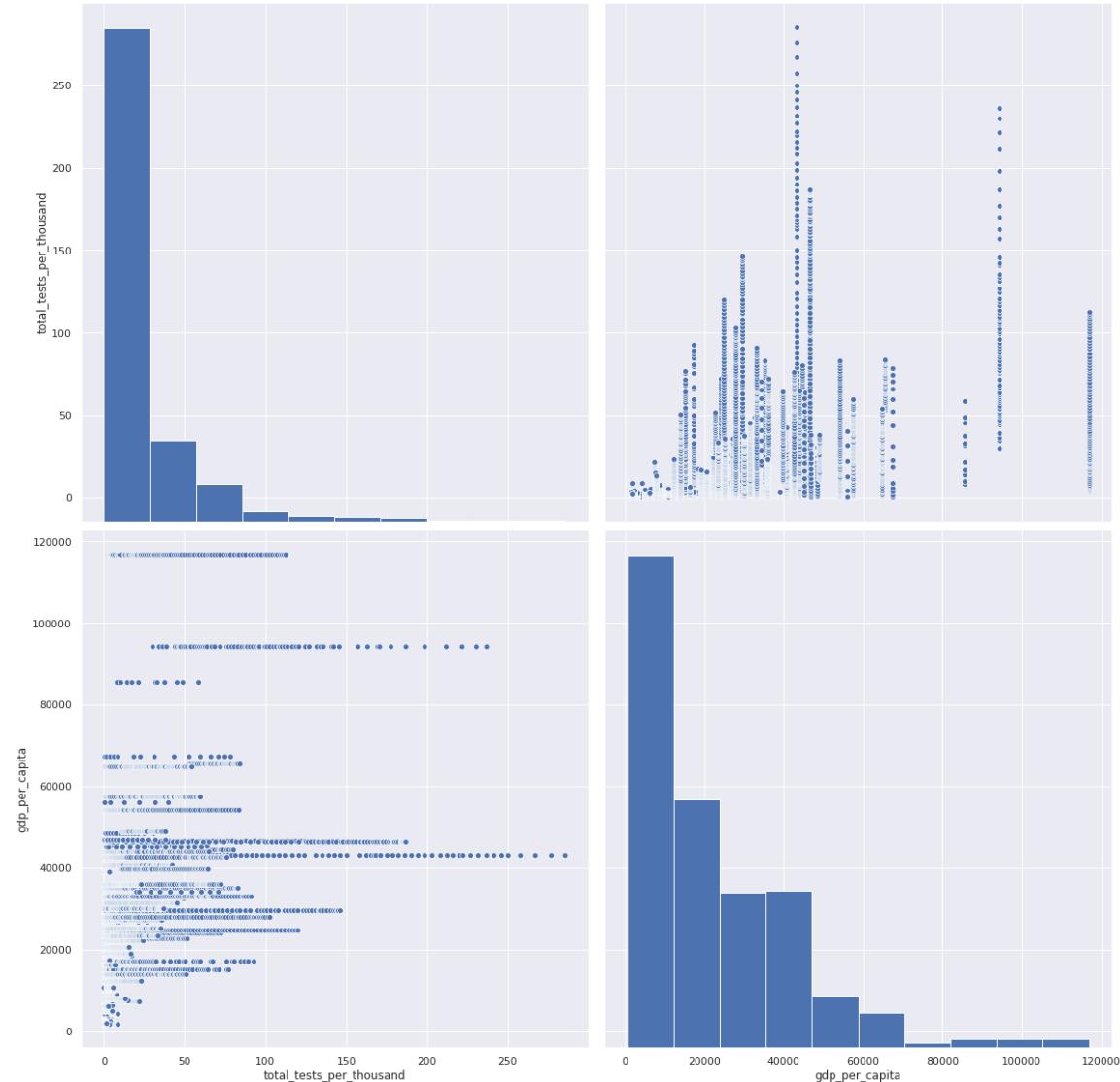


In [97]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "gdp_per_capita"], height=8)
```

Out[97]:

```
<seaborn.axisgrid.PairGrid at 0x7f644c96e908>
```

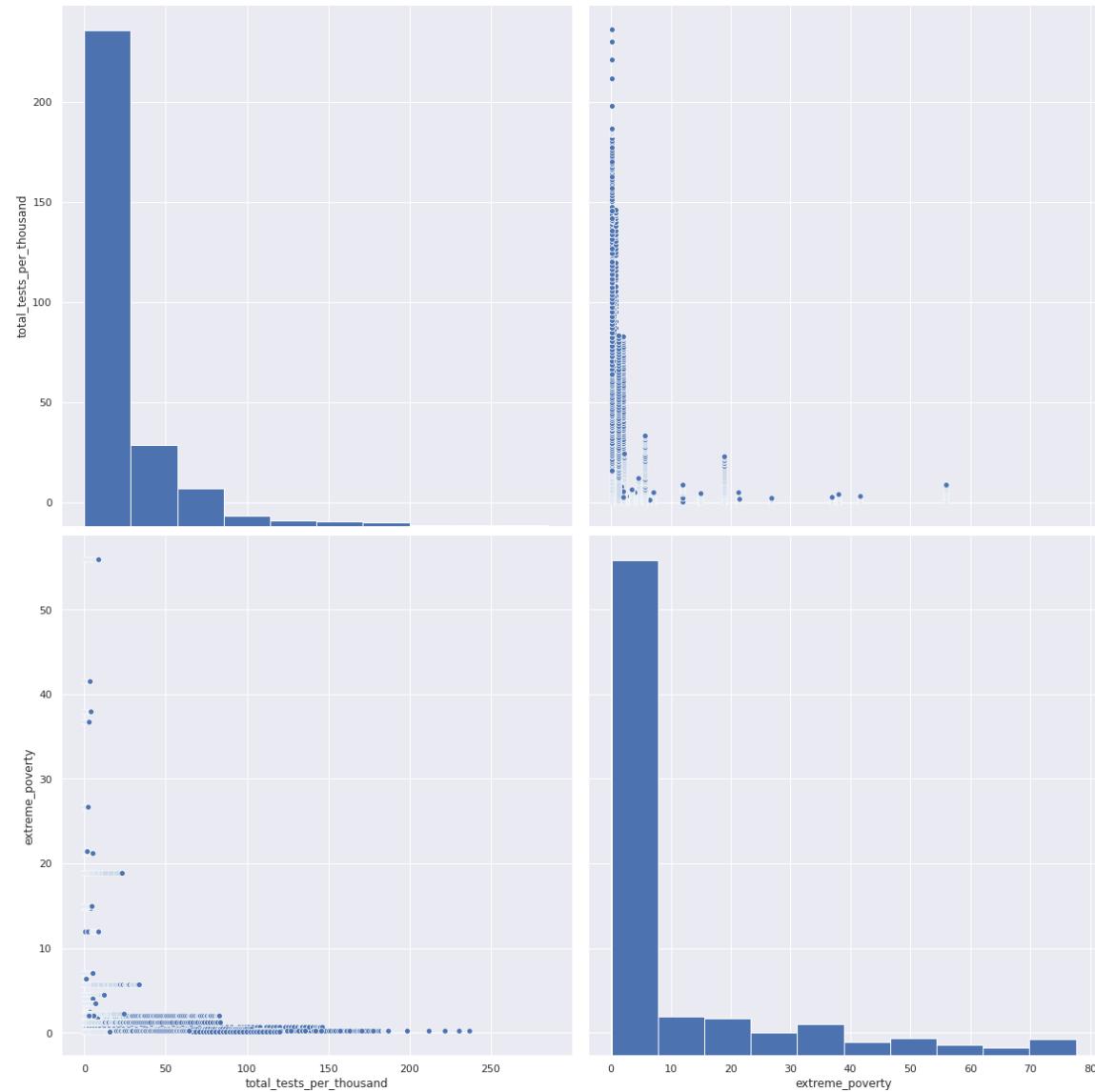


In [98]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "extreme_poverty"], height=8)
```

Out[98]:

```
<seaborn.axisgrid.PairGrid at 0x7f644c511898>
```

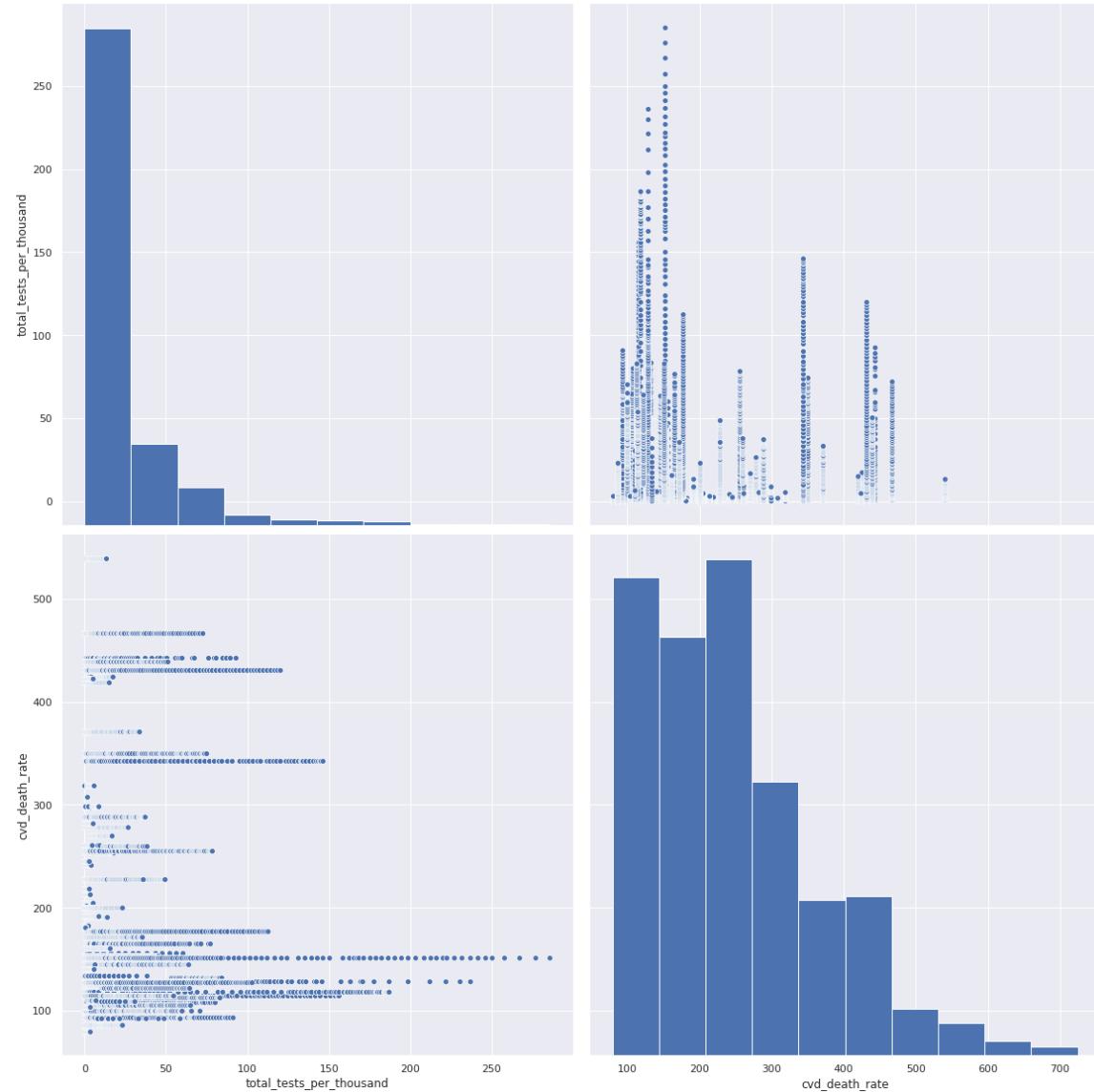


In [99]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "cvd_death_rate"], height=8)
```

Out[99]:

```
<seaborn.axisgrid.PairGrid at 0x7f644c3606a0>
```

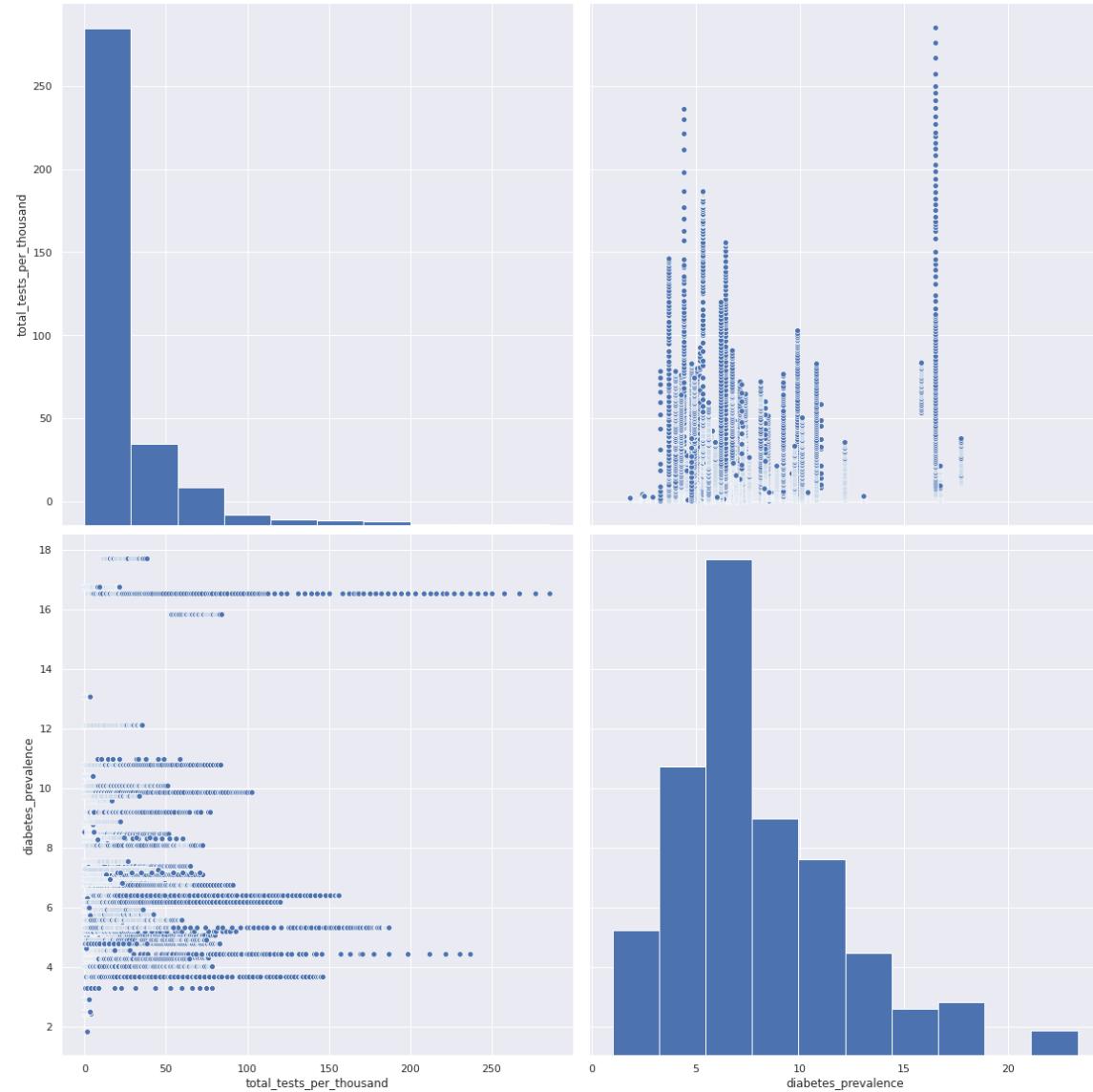


In [100]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "diabetes_prevalence"],  
height=8)
```

Out[100]:

```
<seaborn.axisgrid.PairGrid at 0x7f644c222780>
```

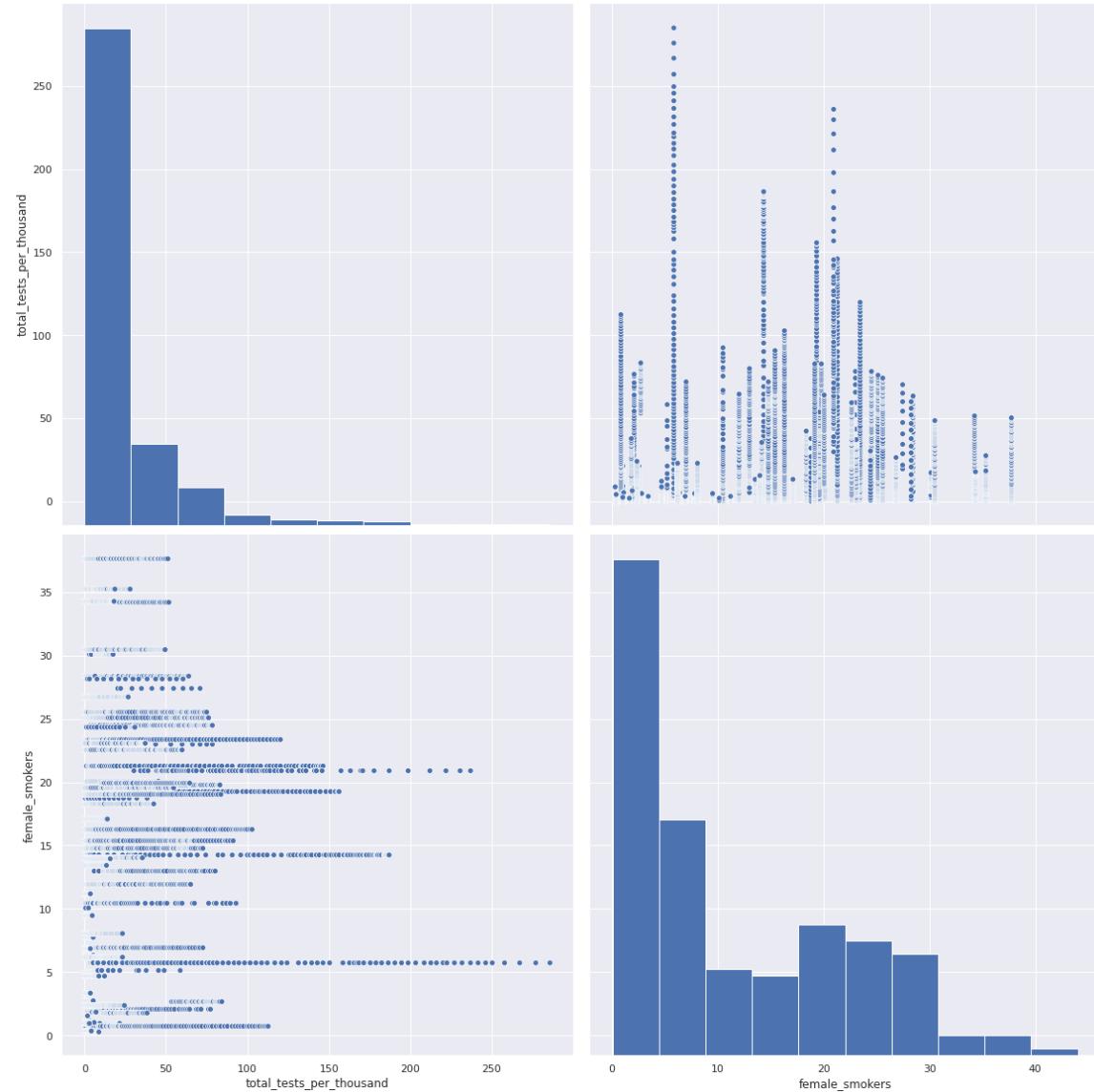


In [101]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "female_smokers"], height=8)
```

Out[101]:

```
<seaborn.axisgrid.PairGrid at 0x7f644bf69080>
```

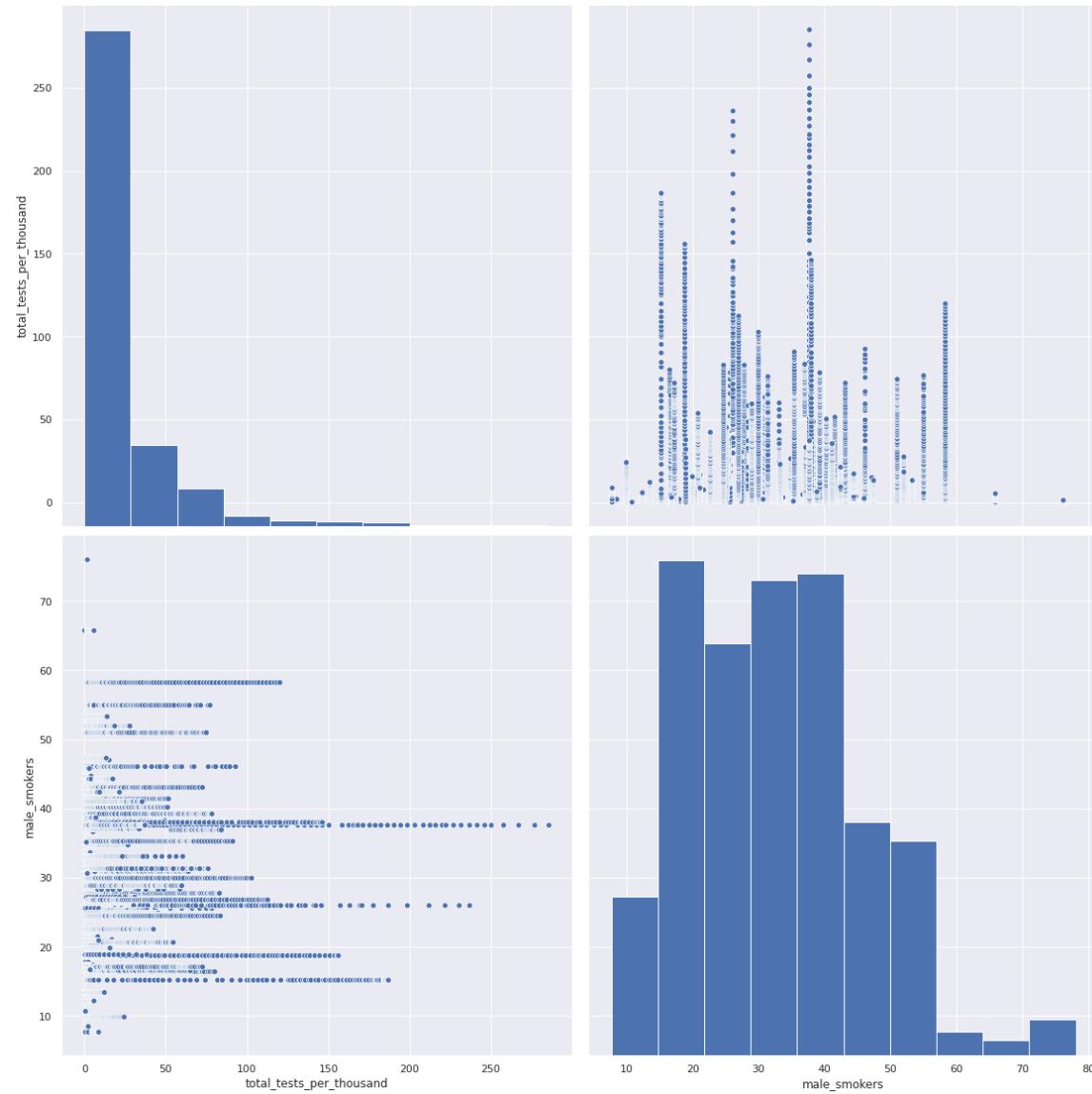


In [102]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "male_smokers"], height=8)
```

Out[102]:

```
<seaborn.axisgrid.PairGrid at 0x7f644bd3f630>
```

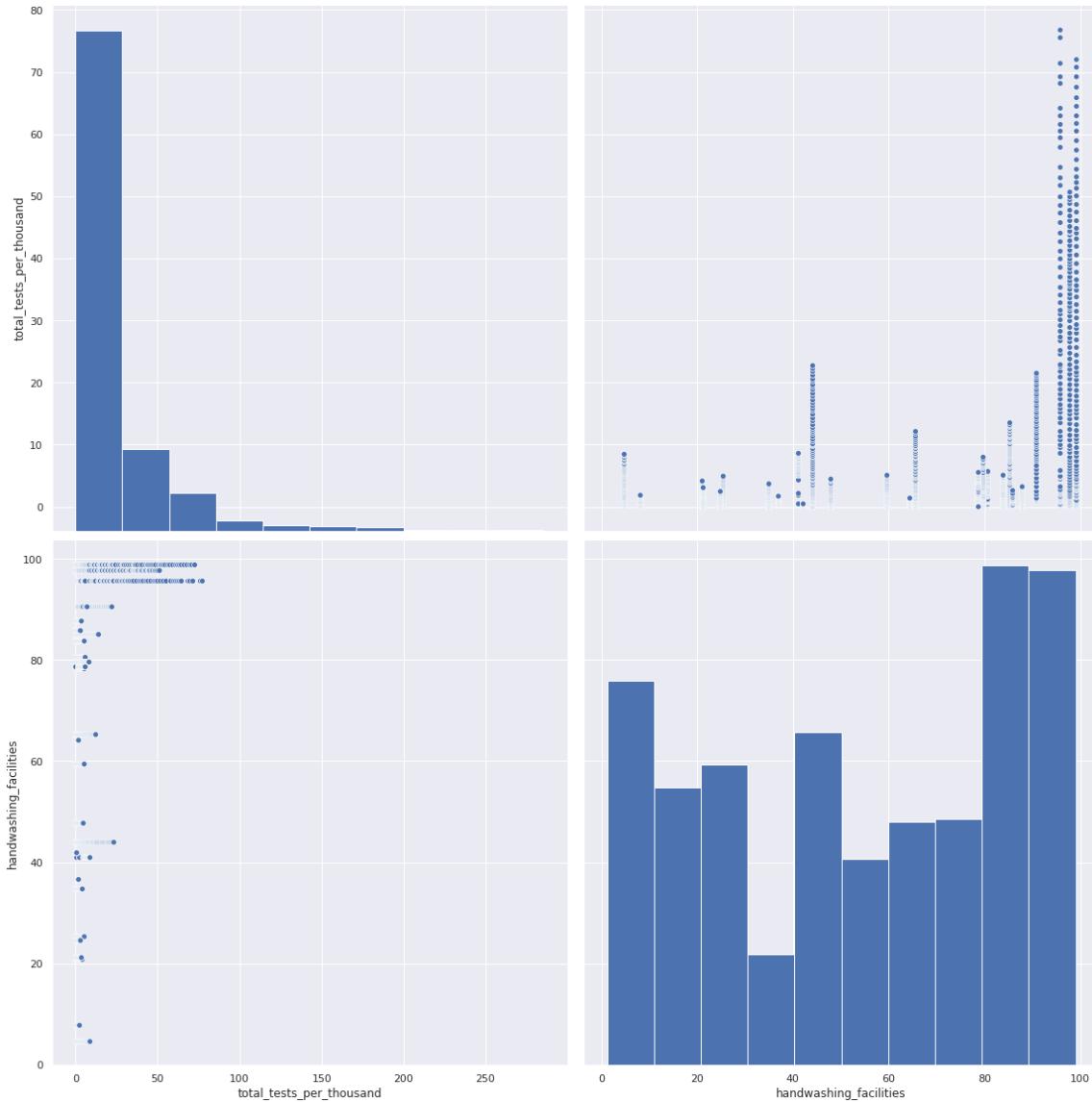


In [103]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "handwashing_facilities"], height=8)
```

Out[103]:

```
<seaborn.axisgrid.PairGrid at 0x7f644be78240>
```

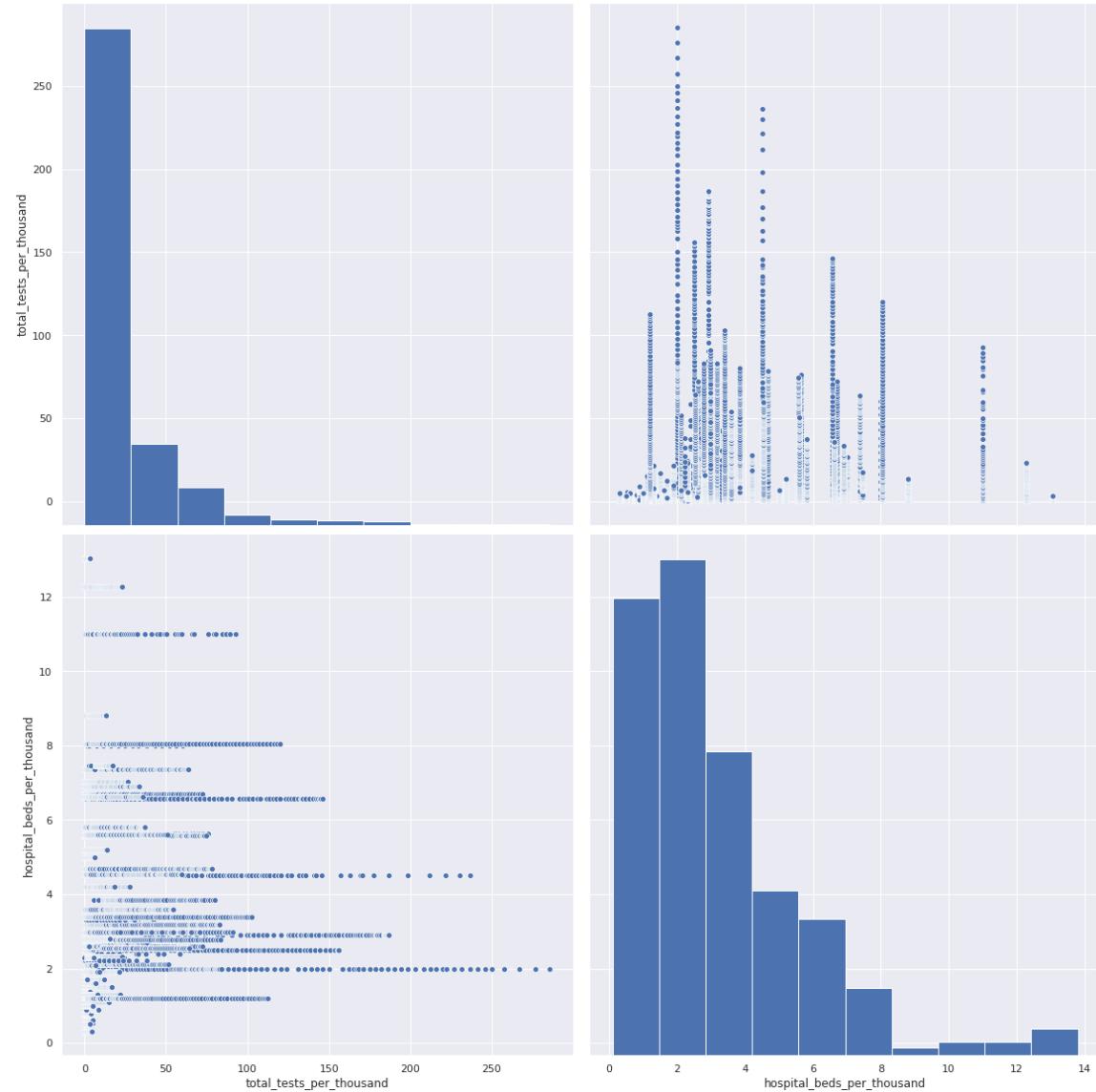


In [104]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "hospital_beds_per_thou  
sand"], height=8)
```

Out[104]:

```
<seaborn.axisgrid.PairGrid at 0x7f644b902438>
```

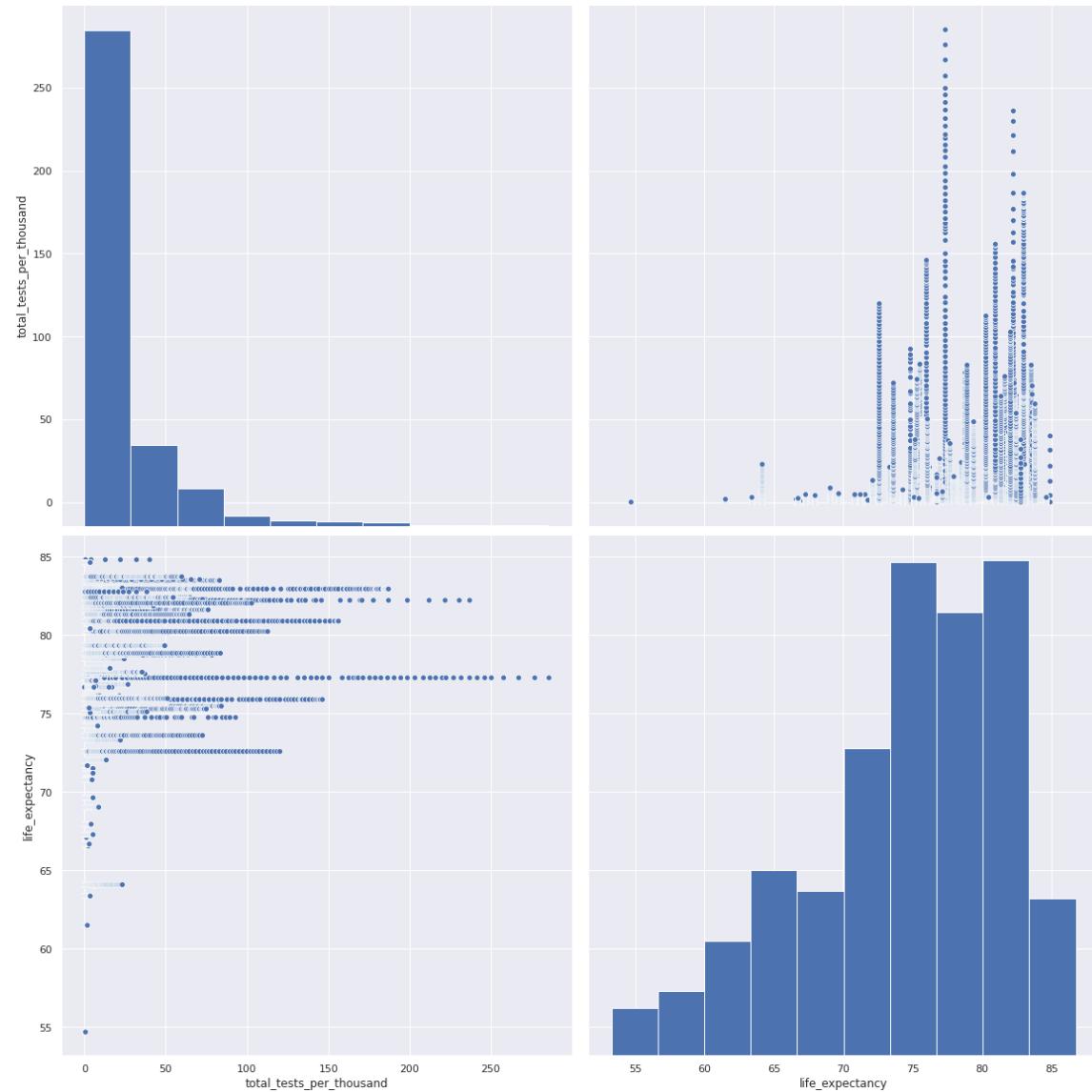


In [105]:

```
sns.pairplot(features, vars=["total_tests_per_thousand", "life_expectancy"], height=8)
```

Out[105]:

```
<seaborn.axisgrid.PairGrid at 0x7f644b7681d0>
```

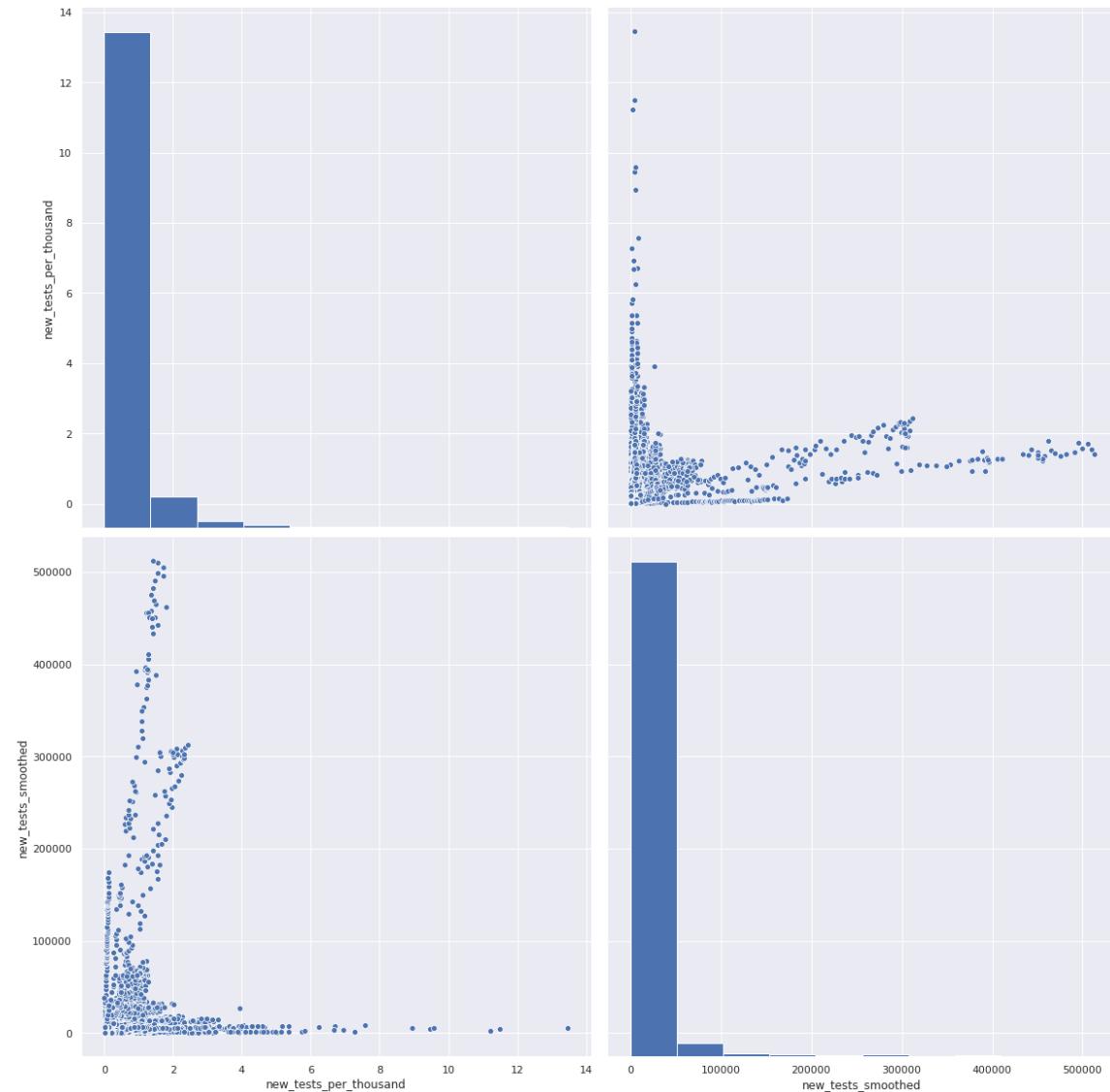


In [106]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "new_tests_smoothed"], height=8)
```

Out[106]:

```
<seaborn.axisgrid.PairGrid at 0x7f644b57a898>
```

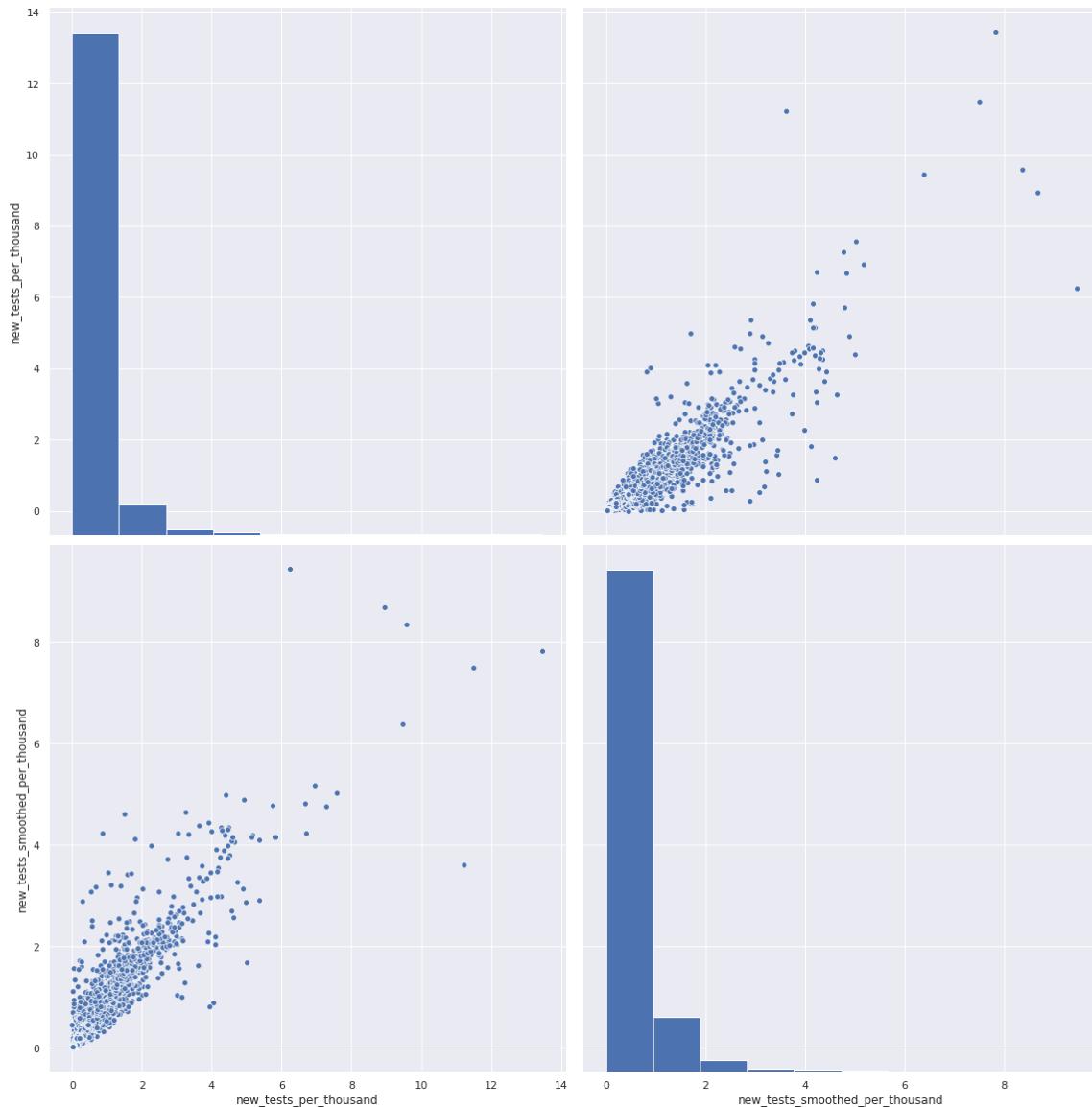


In [107]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "new_tests_smoothed_per_thousand"], height=8)
```

Out[107]:

```
<seaborn.axisgrid.PairGrid at 0x7f644b378668>
```

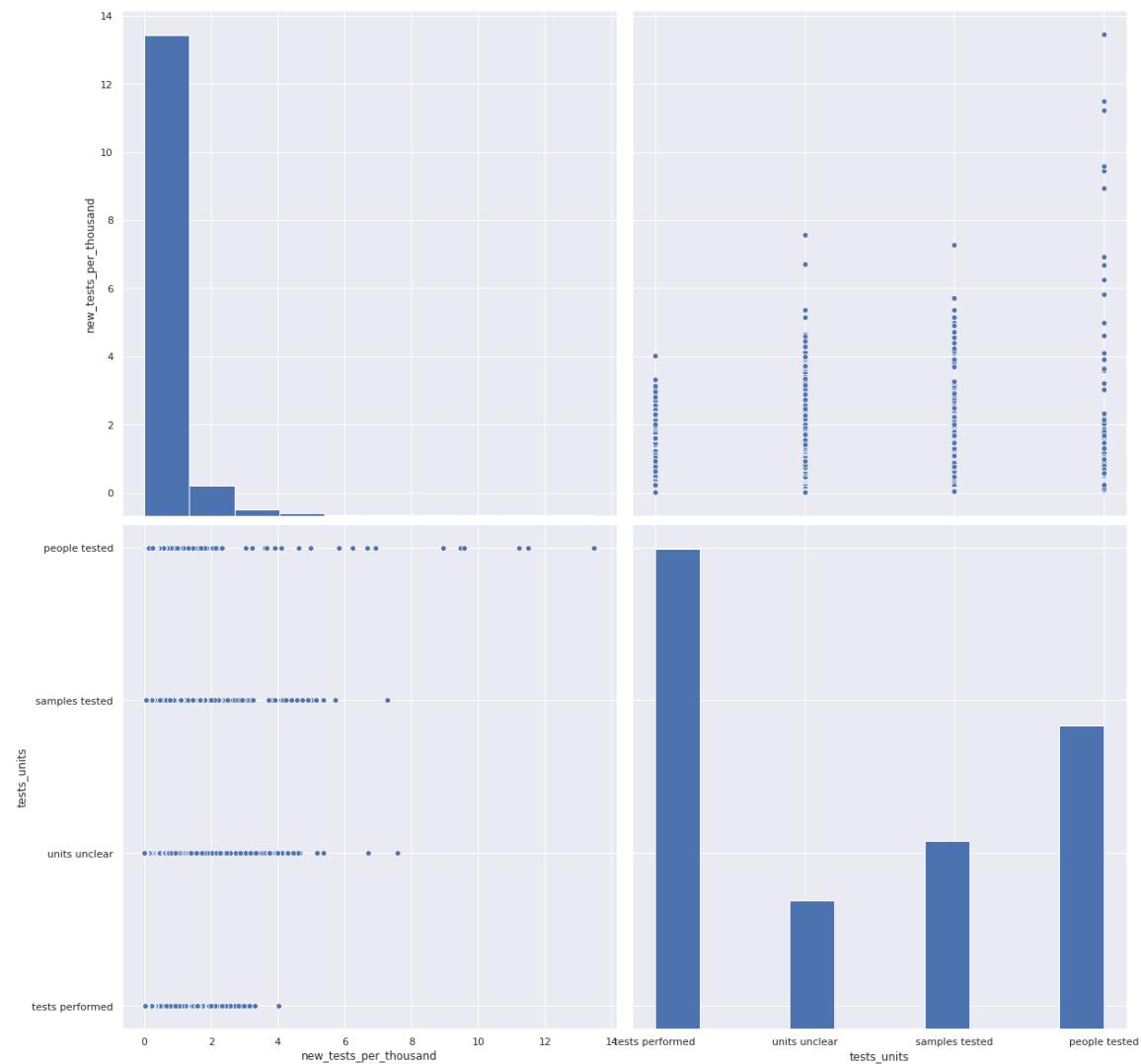


In [108]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "tests_units"], height=8)
```

Out[108]:

```
<seaborn.axisgrid.PairGrid at 0x7f644b269208>
```

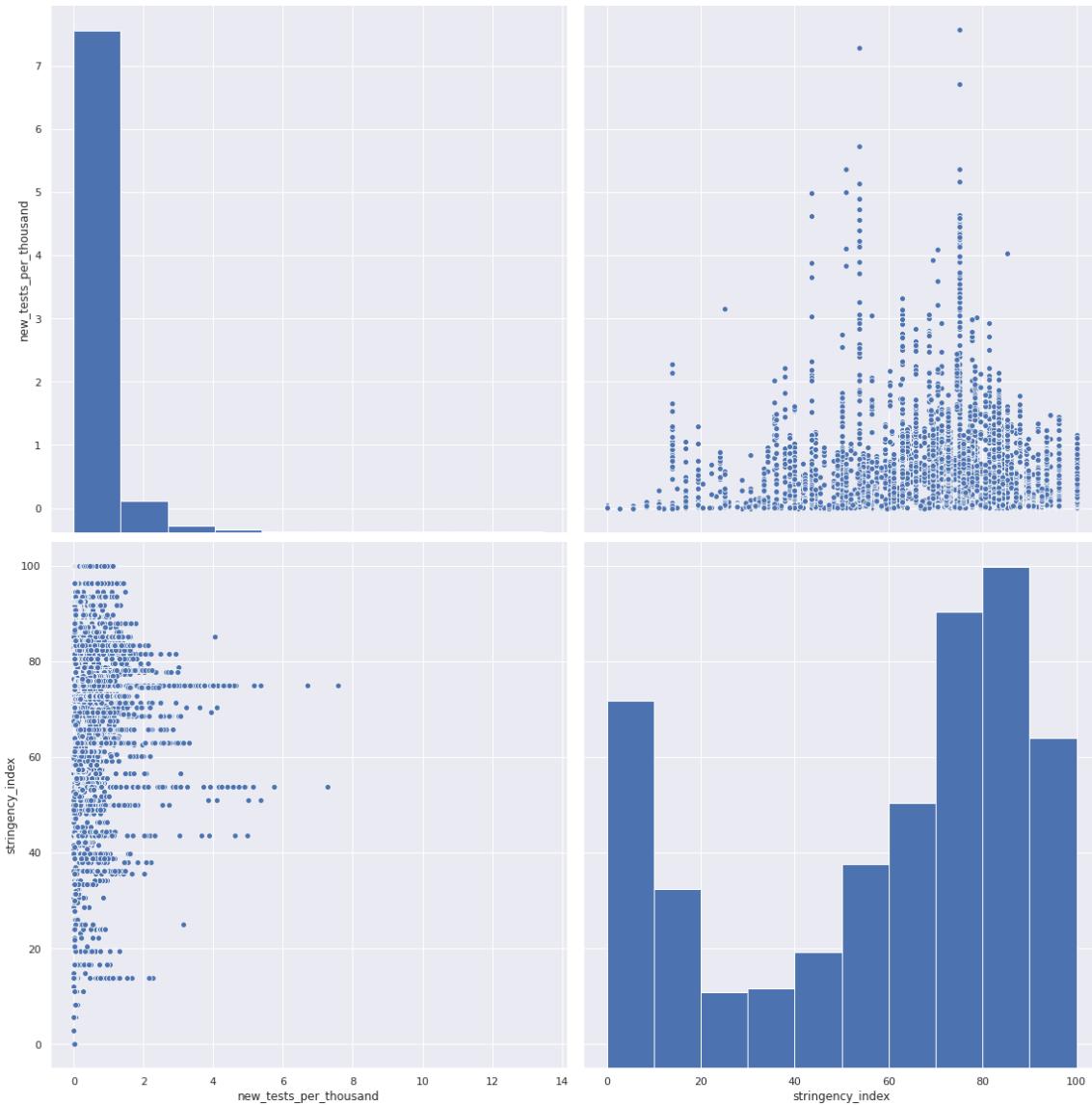


In [109]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "stringency_index"], height=8)
```

Out[109]:

```
<seaborn.axisgrid.PairGrid at 0x7f644af6f4e0>
```

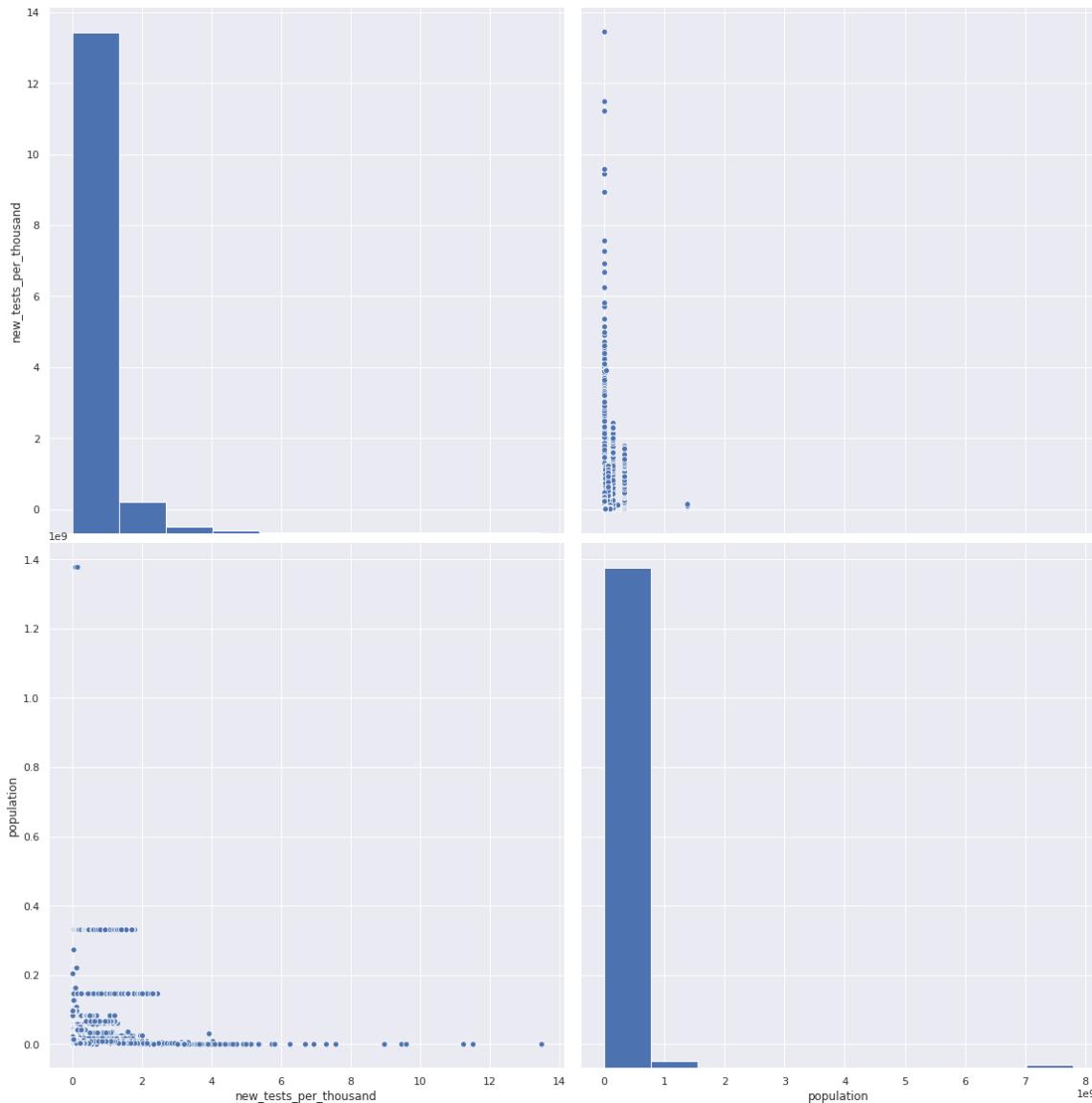


In [110]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "population"], height=8)
```

Out[110]:

```
<seaborn.axisgrid.PairGrid at 0x7f644ad0aef0>
```

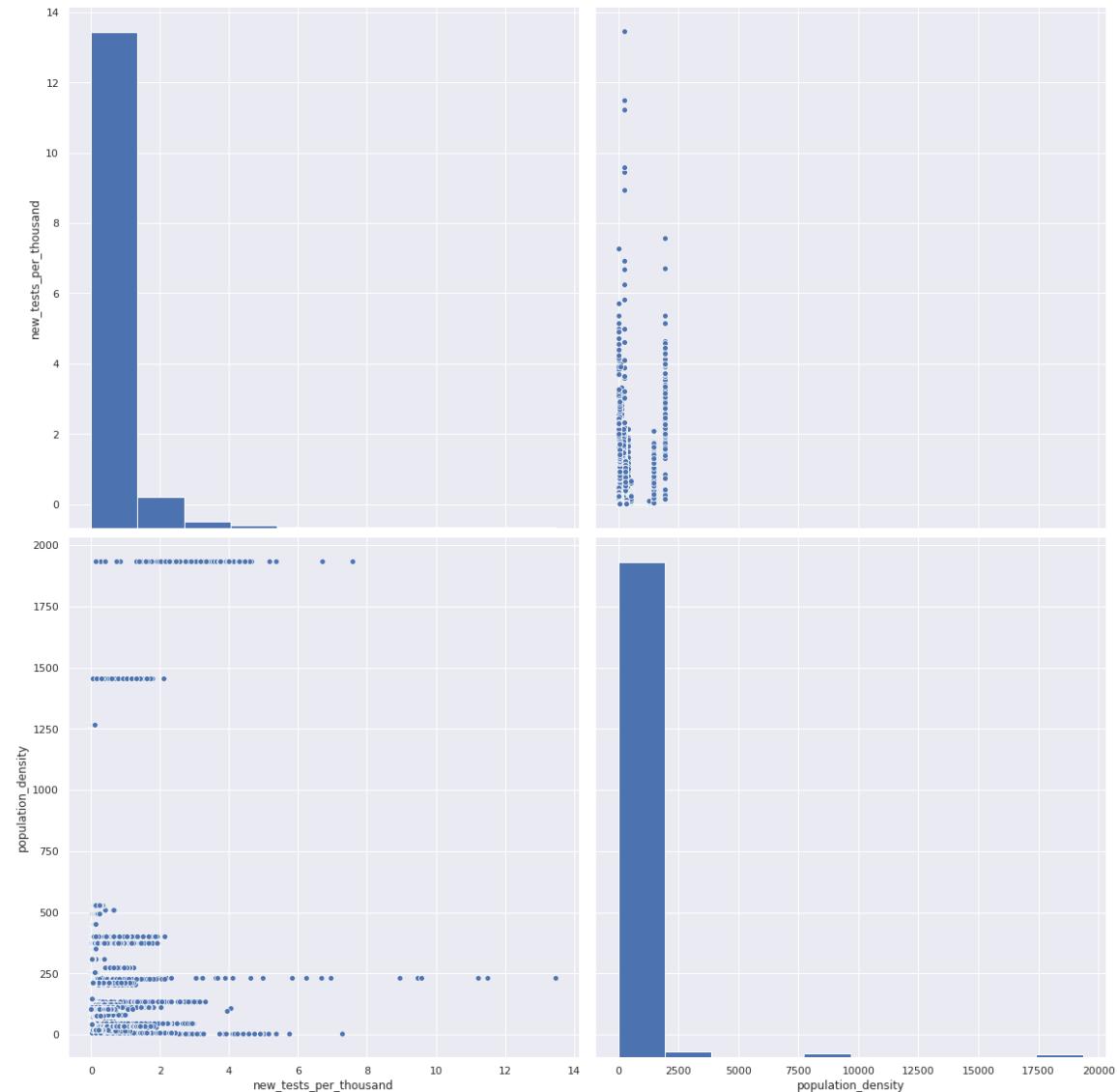


In [111]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "population_density"], height=8)
```

Out[111]:

```
<seaborn.axisgrid.PairGrid at 0x7f644ac21710>
```

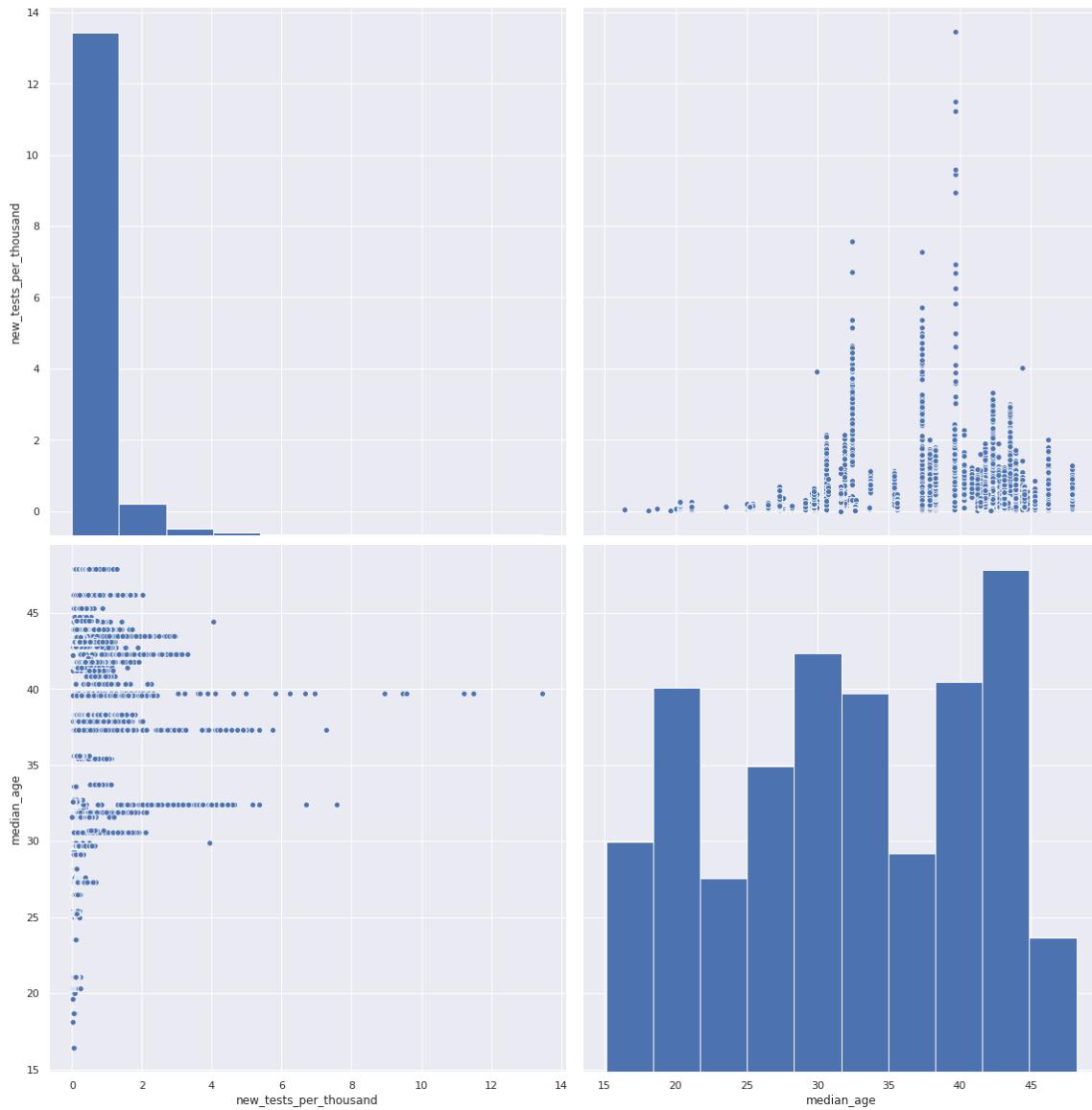


In [112]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "median_age"], height=8)
```

Out[112]:

```
<seaborn.axisgrid.PairGrid at 0x7f644a9279b0>
```

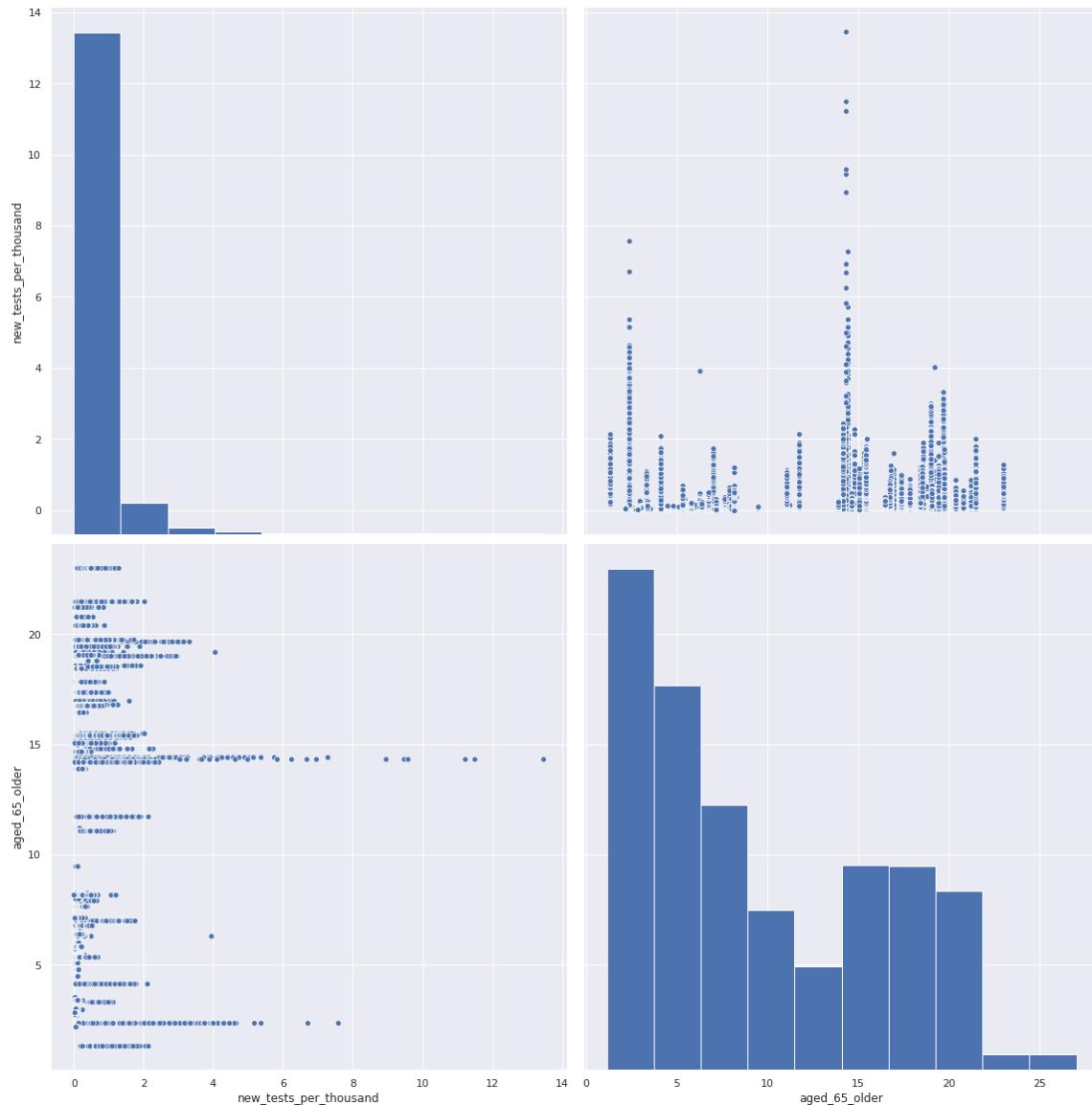


In [113]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "aged_65_older"], height=8)
```

Out[113]:

```
<seaborn.axisgrid.PairGrid at 0x7f644a6ec710>
```

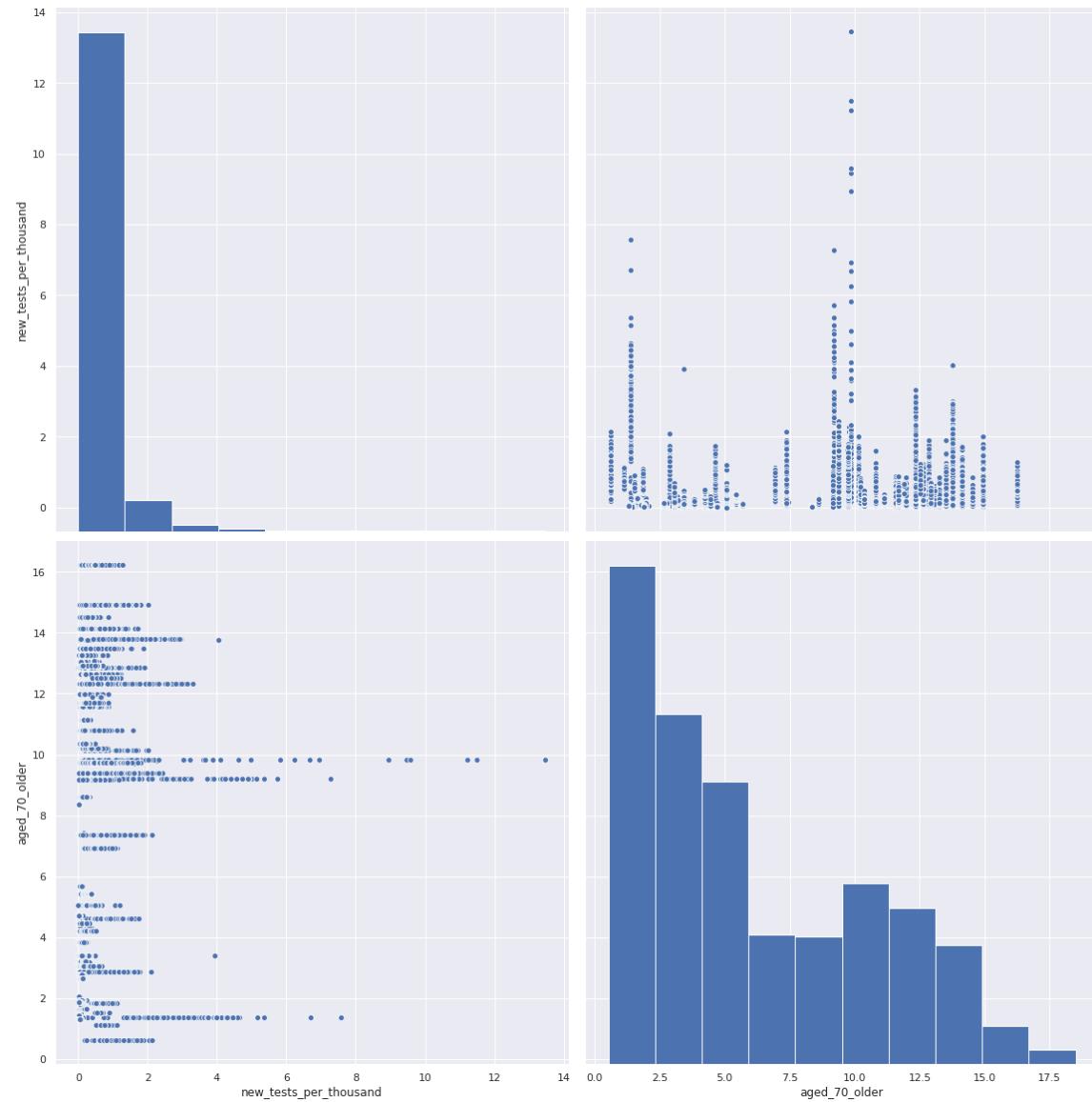


In [114]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "aged_70_older"], height=8)
```

Out[114]:

```
<seaborn.axisgrid.PairGrid at 0x7f644a5e4dd8>
```

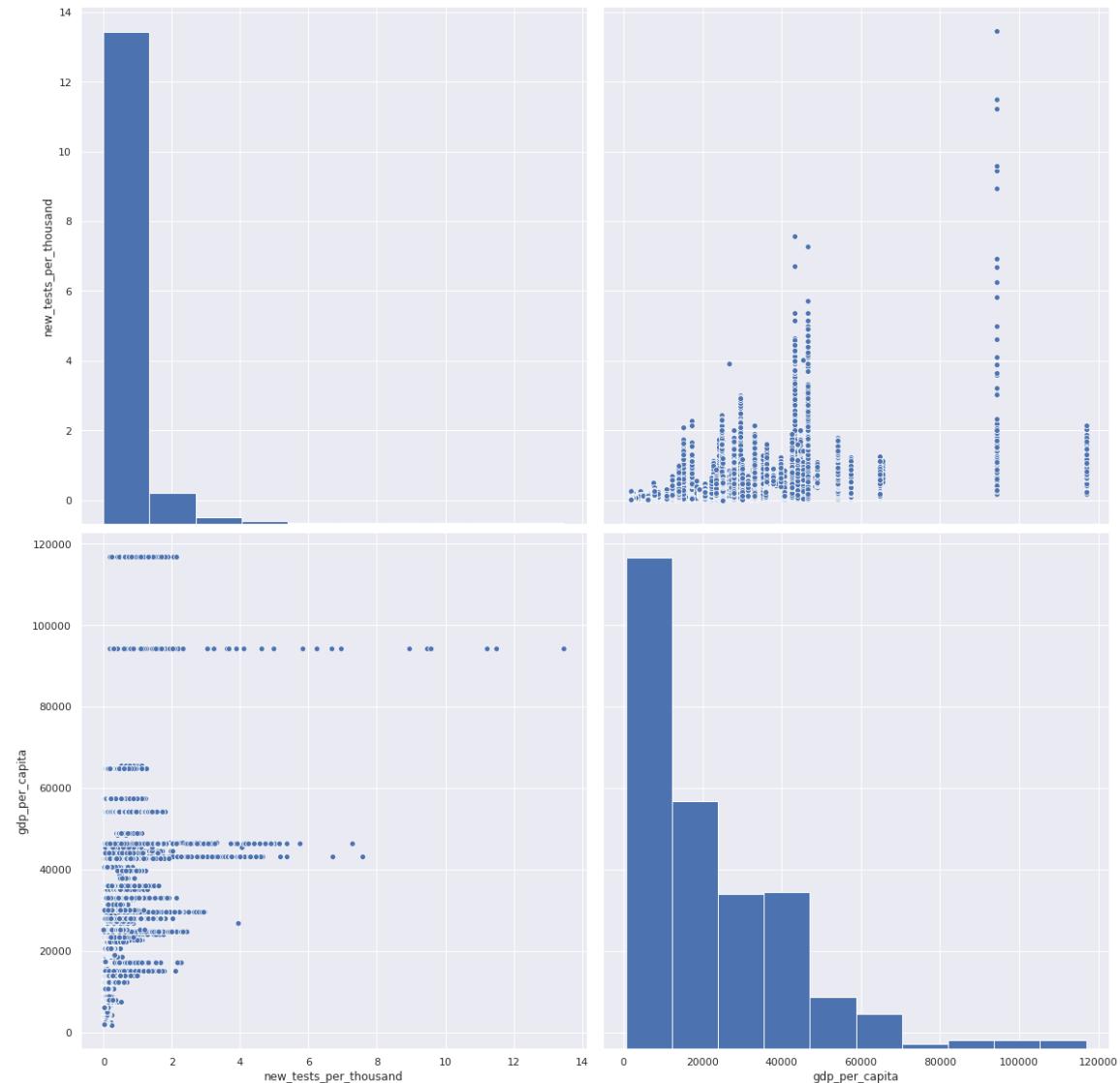


In [115]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "gdp_per_capita"], height=8)
```

Out[115]:

```
<seaborn.axisgrid.PairGrid at 0x7f644c9d0630>
```

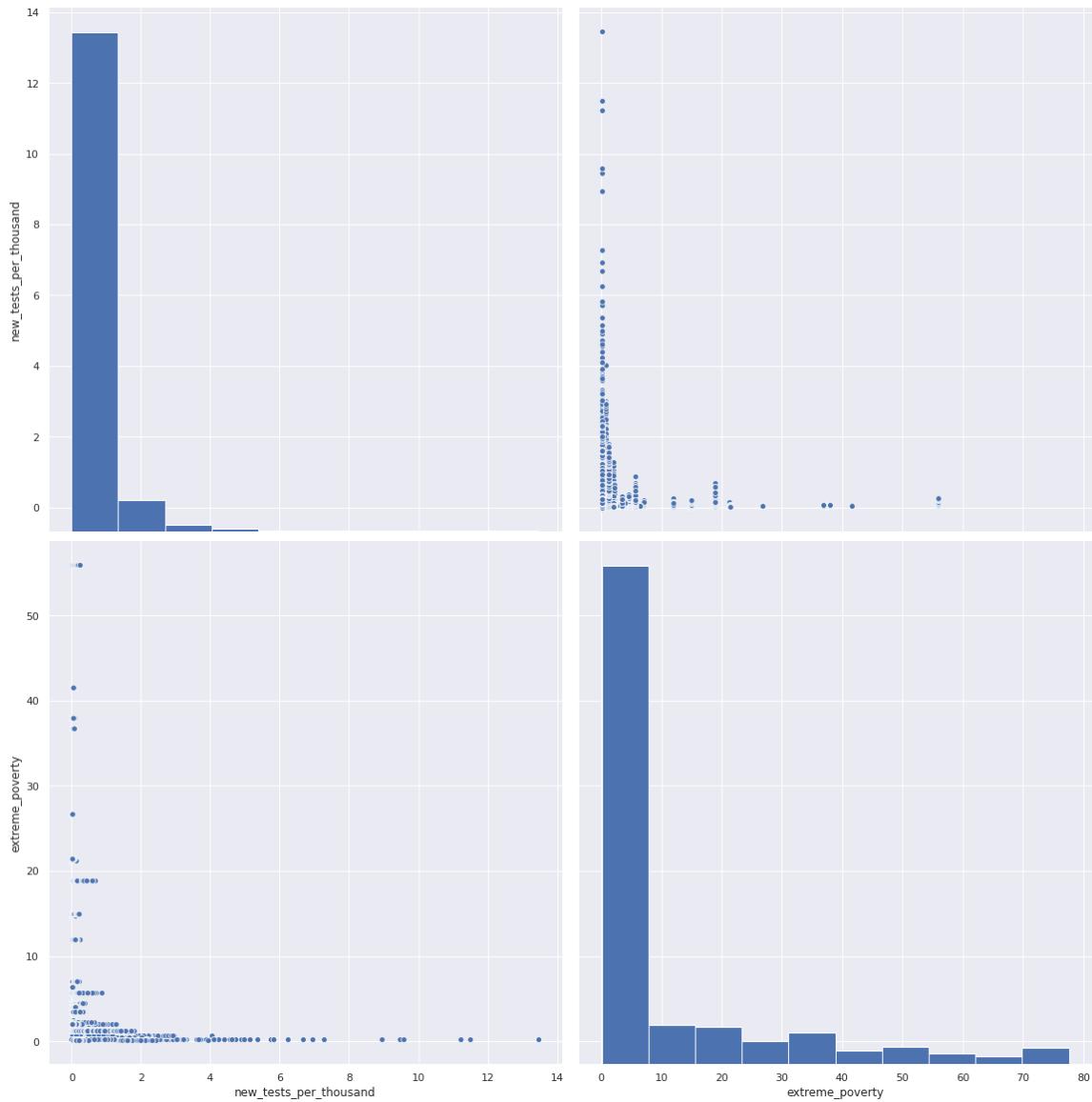


In [116]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "extreme_poverty"], height=8)
```

Out[116]:

```
<seaborn.axisgrid.PairGrid at 0x7f644a0828d0>
```

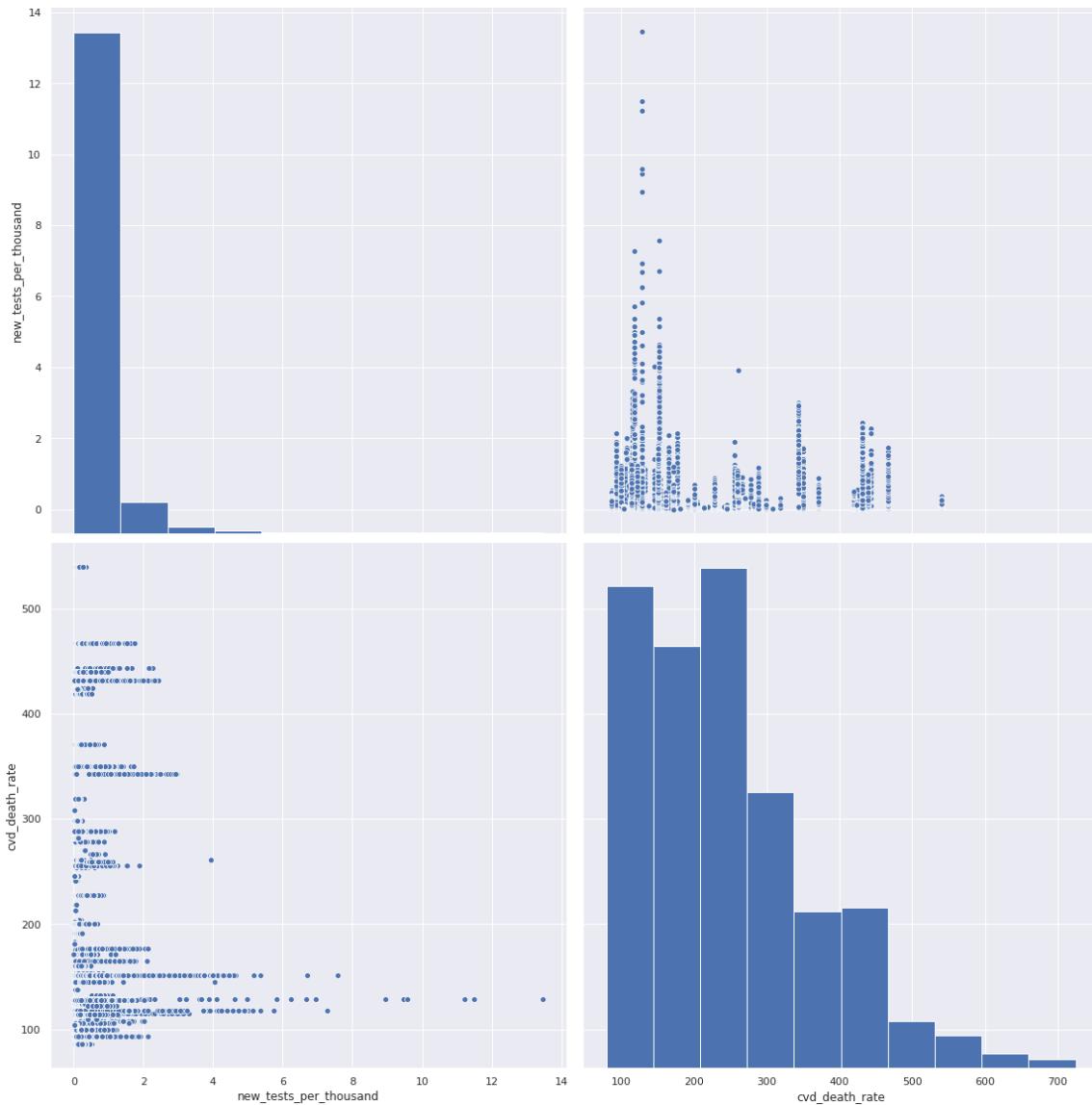


In [117]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "cvd_death_rate"], height=8)
```

Out[117]:

```
<seaborn.axisgrid.PairGrid at 0x7f6449ed8438>
```

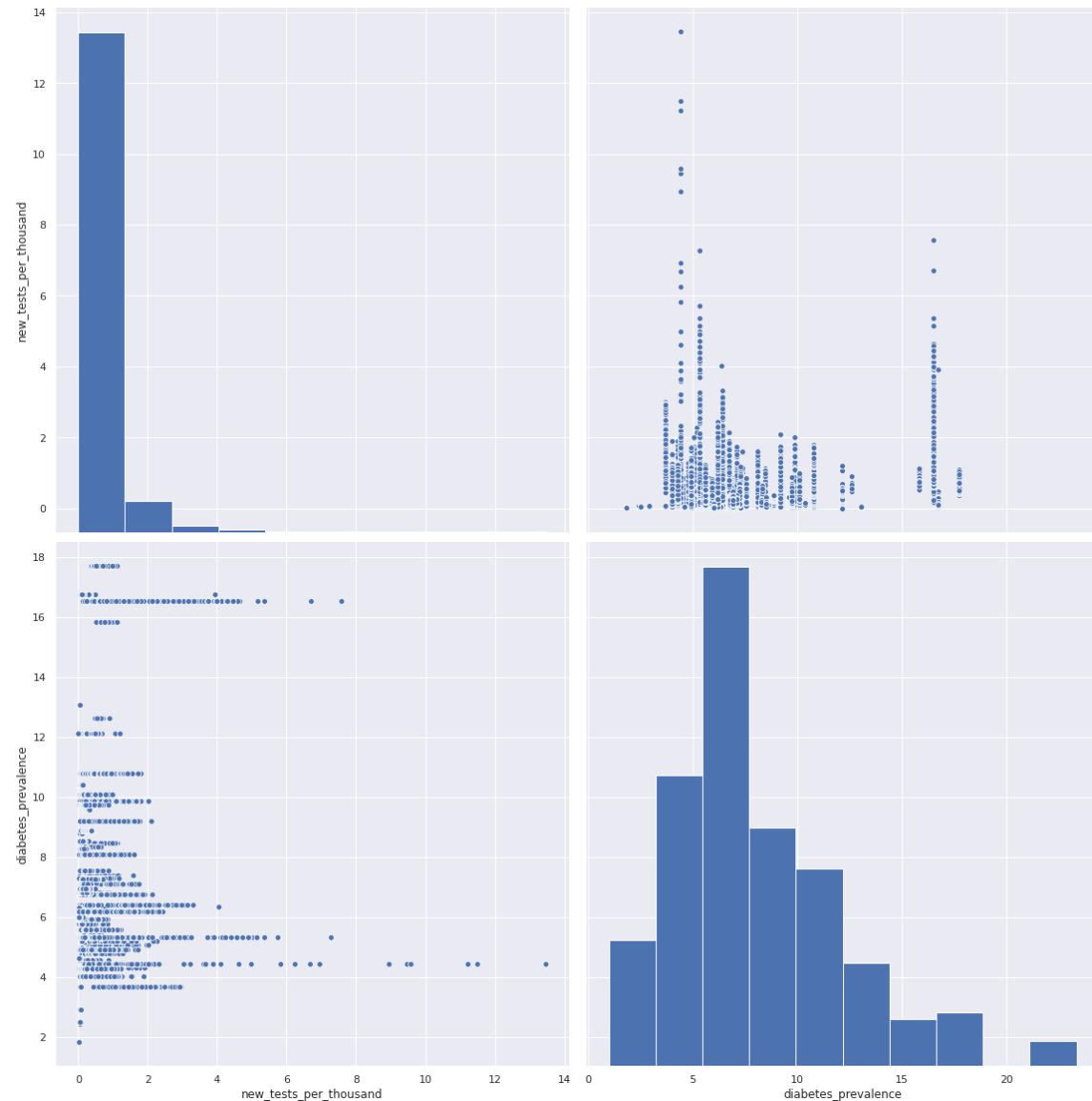


In [118]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "diabetes_prevalence"], height=8)
```

Out[118]:

```
<seaborn.axisgrid.PairGrid at 0x7f6449dad3c8>
```

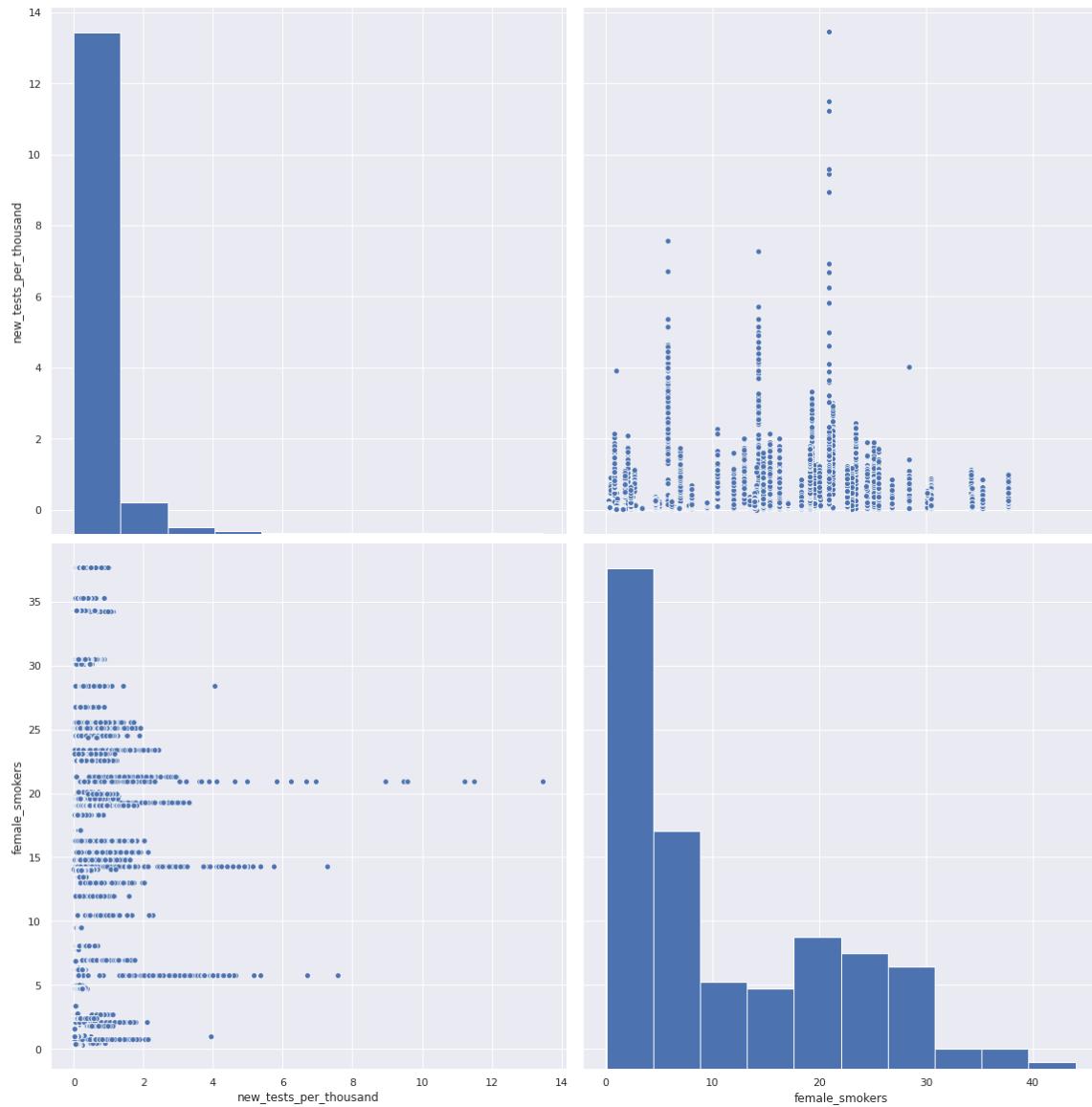


In [119]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "female_smokers"], height=8)
```

Out[119]:

```
<seaborn.axisgrid.PairGrid at 0x7f644a00fc18>
```

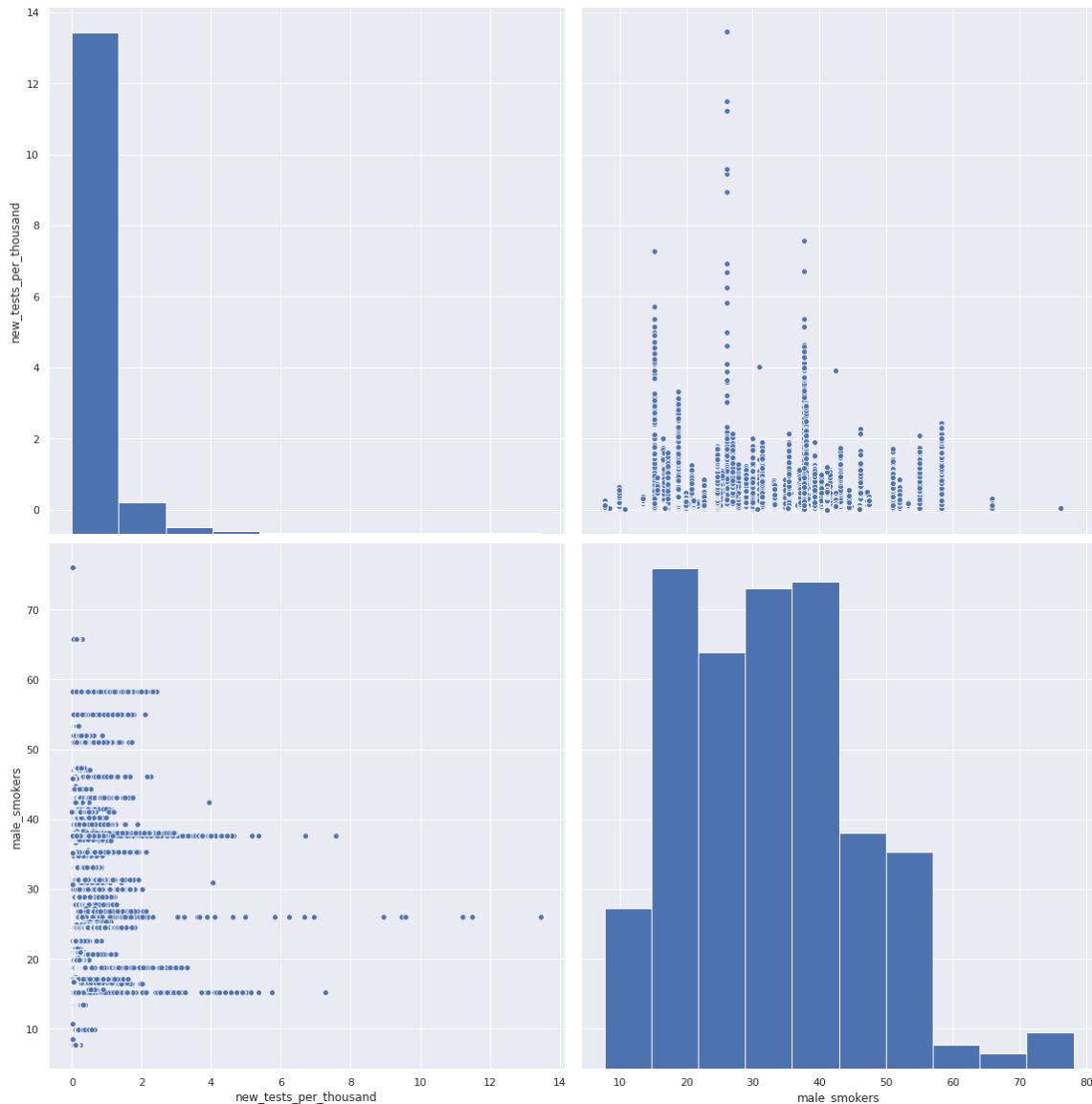


In [120]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "male_smokers"], height=8)
```

Out[120]:

```
<seaborn.axisgrid.PairGrid at 0x7f64498a0978>
```

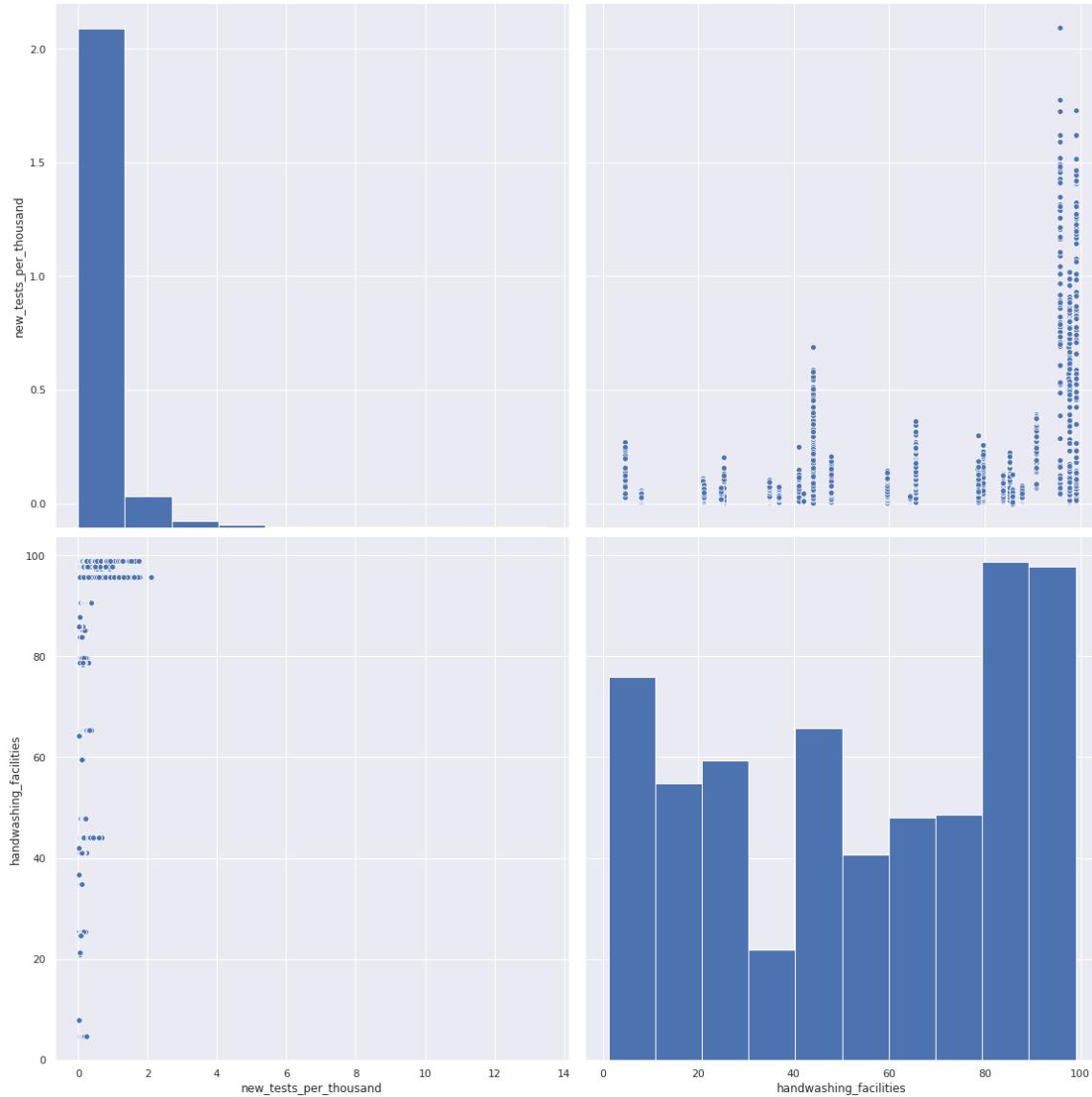


In [121]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "handwashing_facilities"], height=8)
```

Out[121]:

```
<seaborn.axisgrid.PairGrid at 0x7f6449847cf8>
```

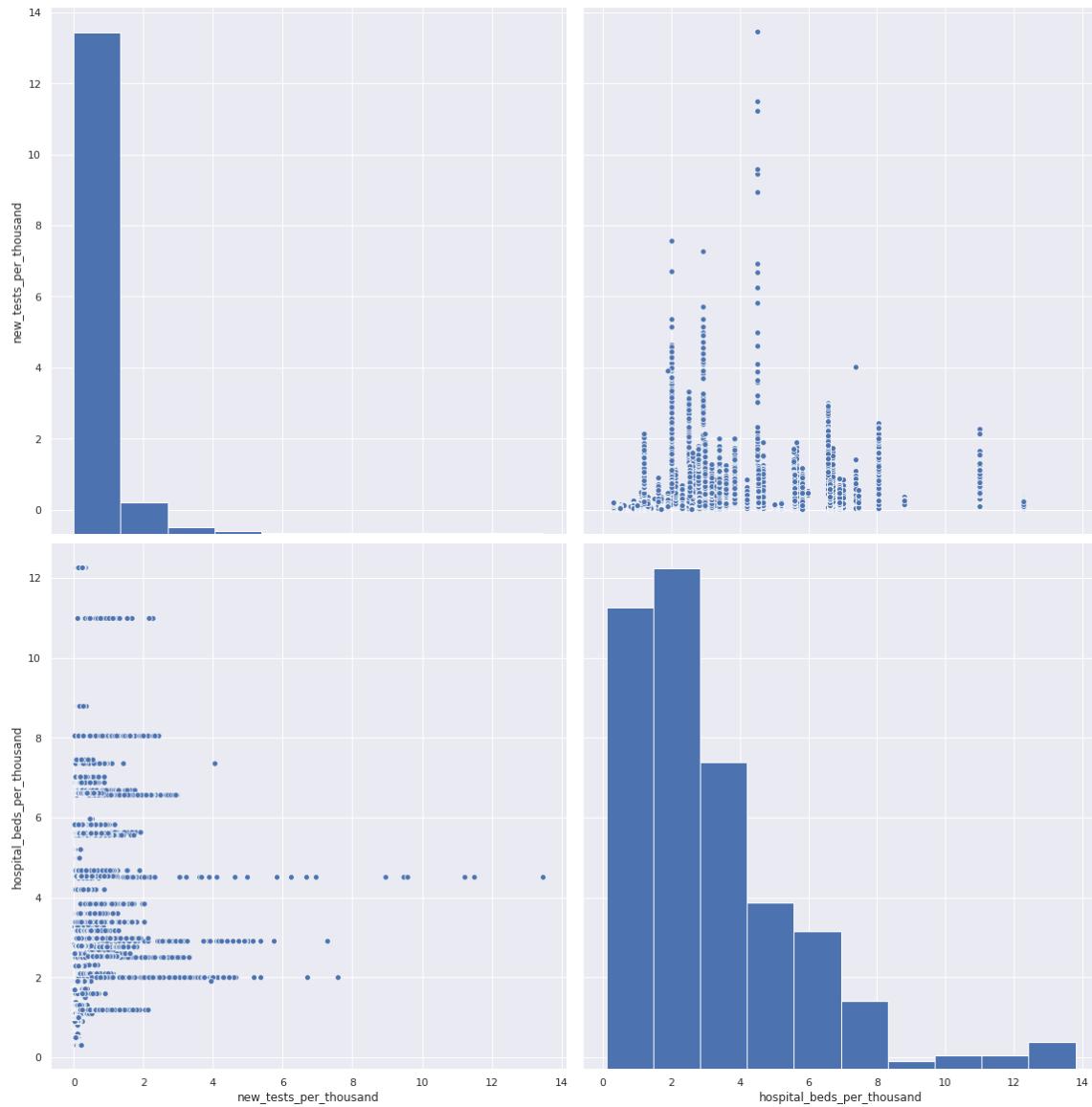


In [122]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "hospital_beds_per_thousa  
nd"], height=8)
```

Out[122]:

```
<seaborn.axisgrid.PairGrid at 0x7f64494e0a58>
```

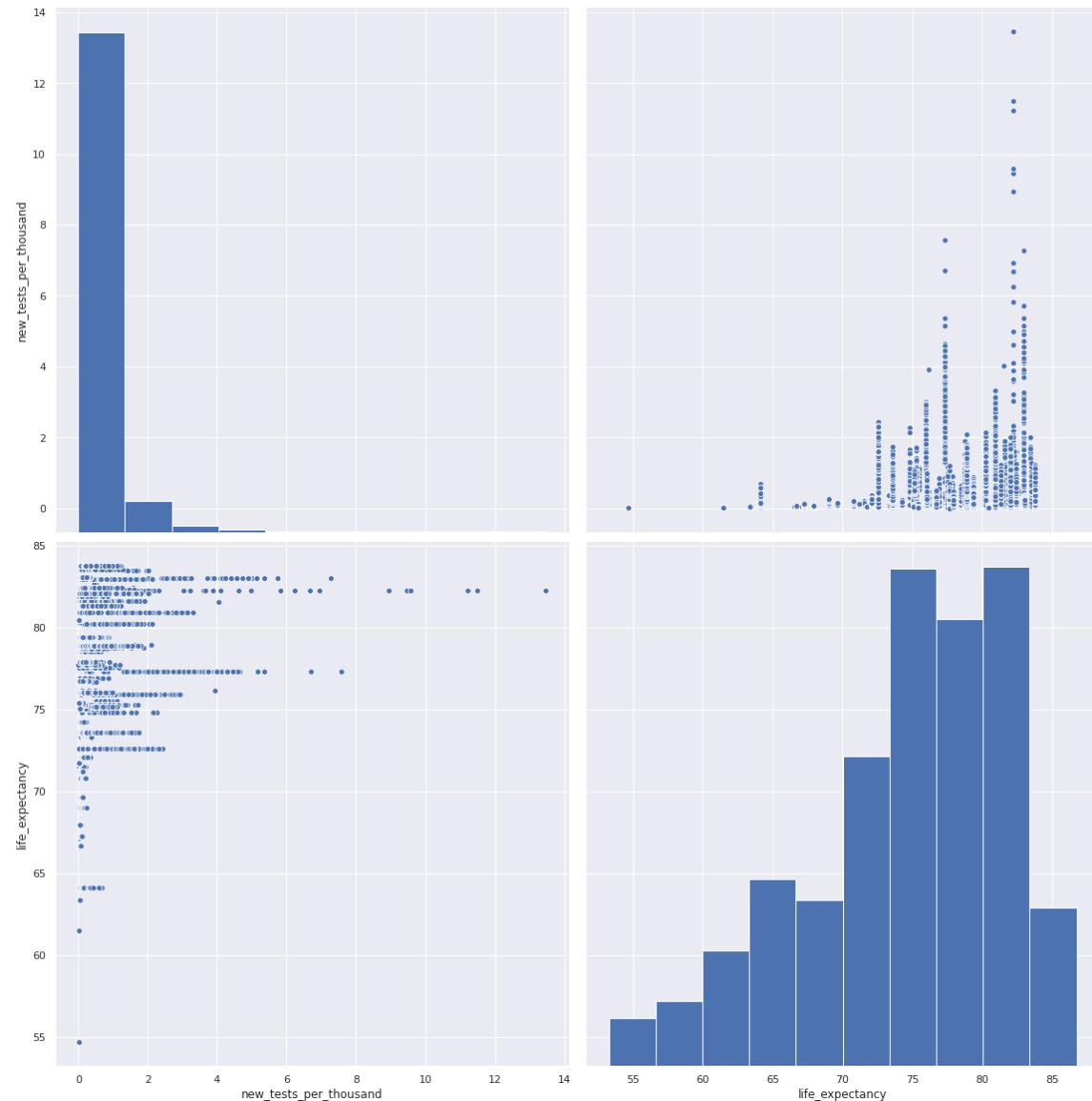


In [123]:

```
sns.pairplot(features, vars=["new_tests_per_thousand", "life_expectancy"], height=8)
```

Out[123]:

```
<seaborn.axisgrid.PairGrid at 0x7f6449271898>
```

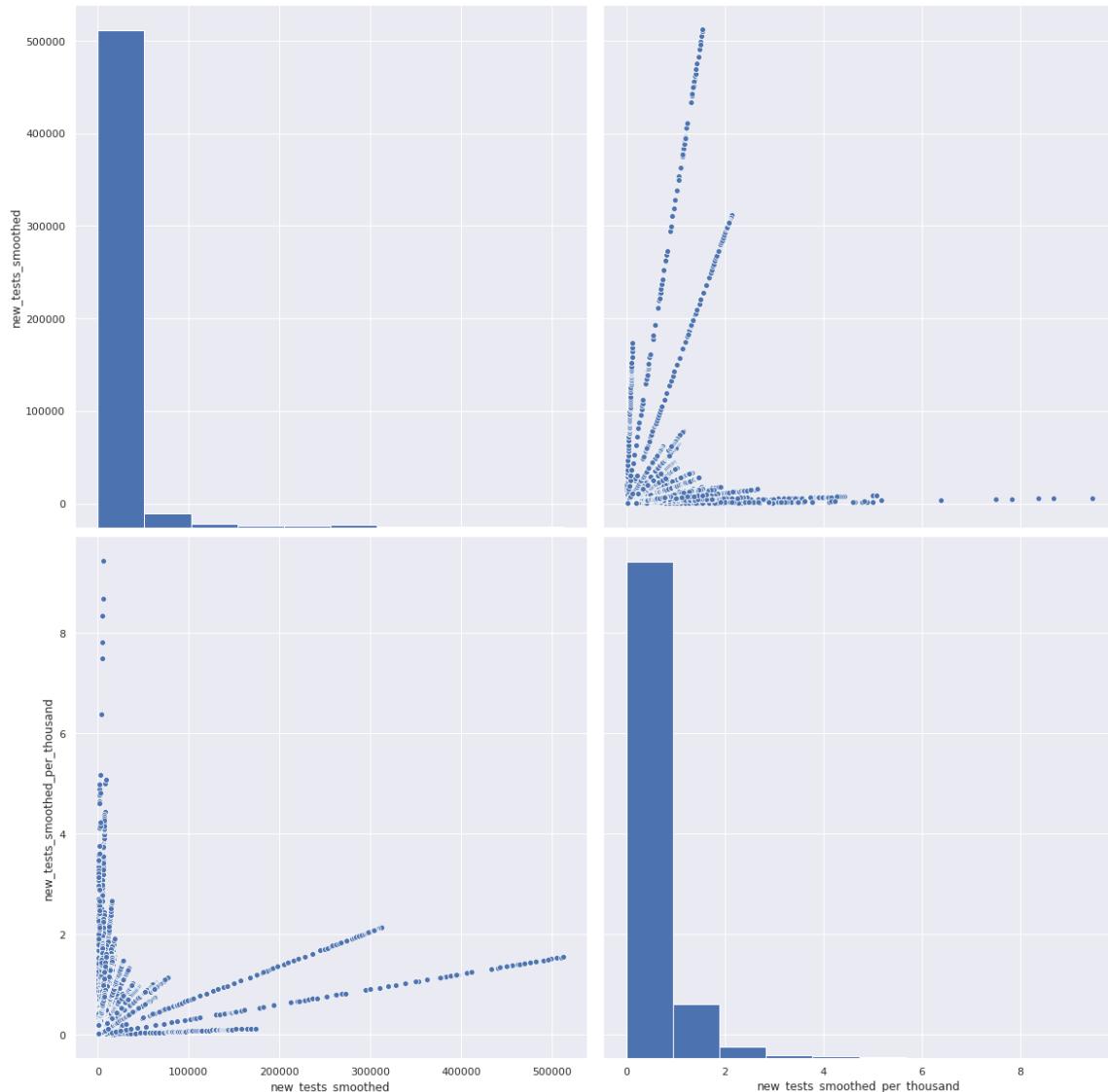


In [124]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "new_tests_smoothed_per_thous  
and"], height=8)
```

Out[124]:

```
<seaborn.axisgrid.PairGrid at 0x7f6449557438>
```

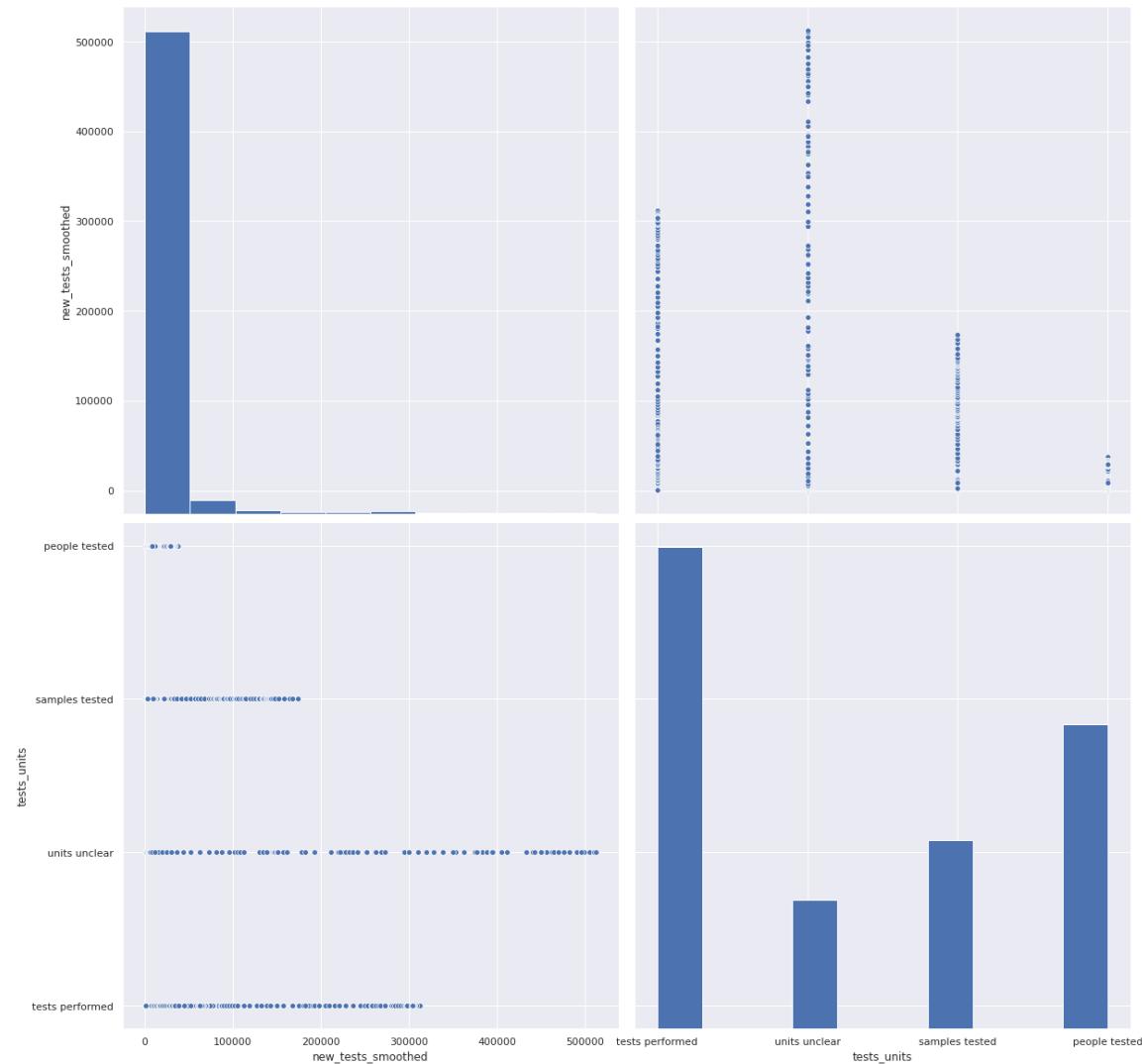


In [125]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "tests_units"], height=8)
```

Out[125]:

```
<seaborn.axisgrid.PairGrid at 0x7f6449153048>
```

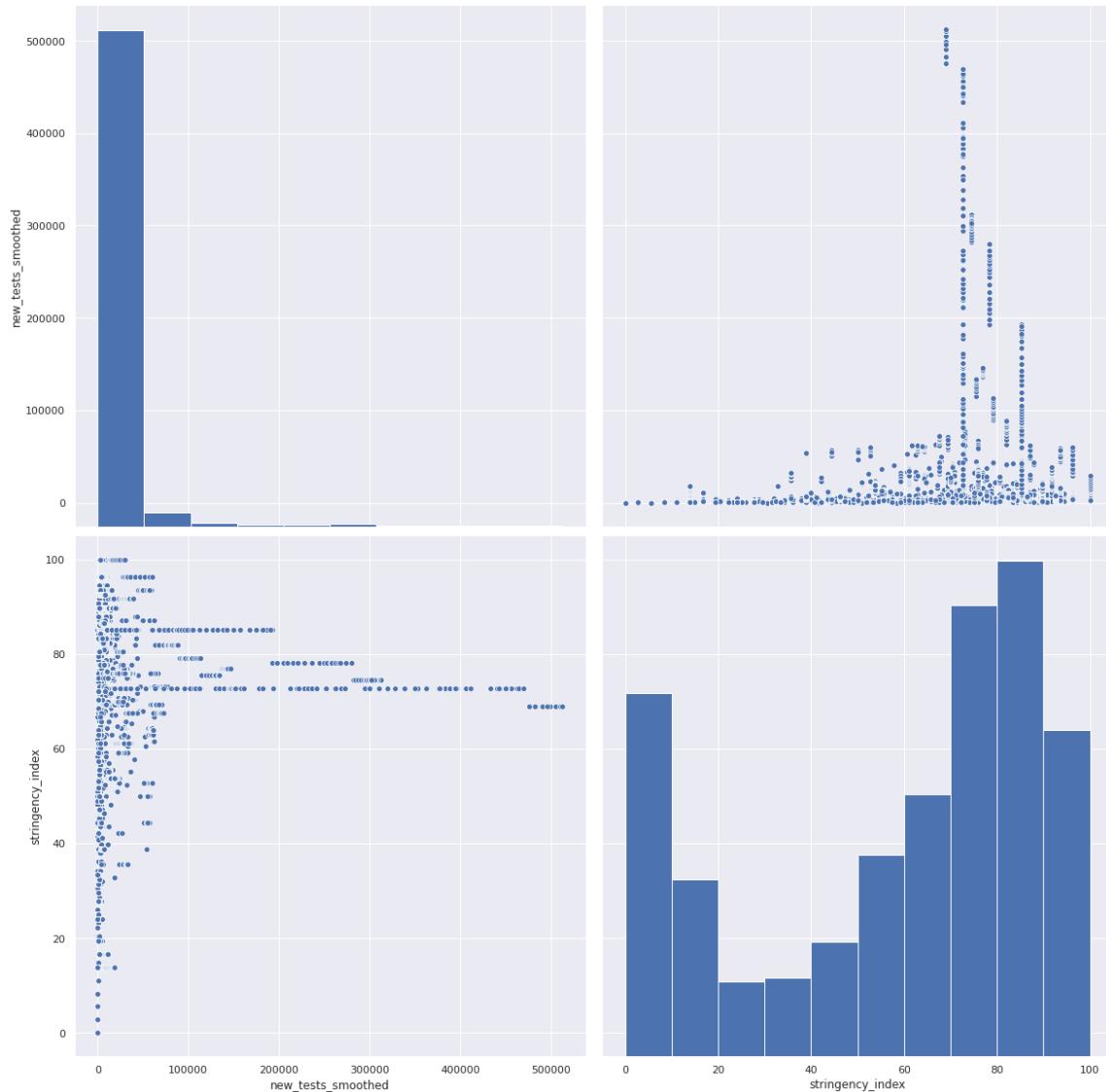


In [126]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "stringency_index"], height=8)
```

Out[126]:

```
<seaborn.axisgrid.PairGrid at 0x7f6448cb6ac8>
```

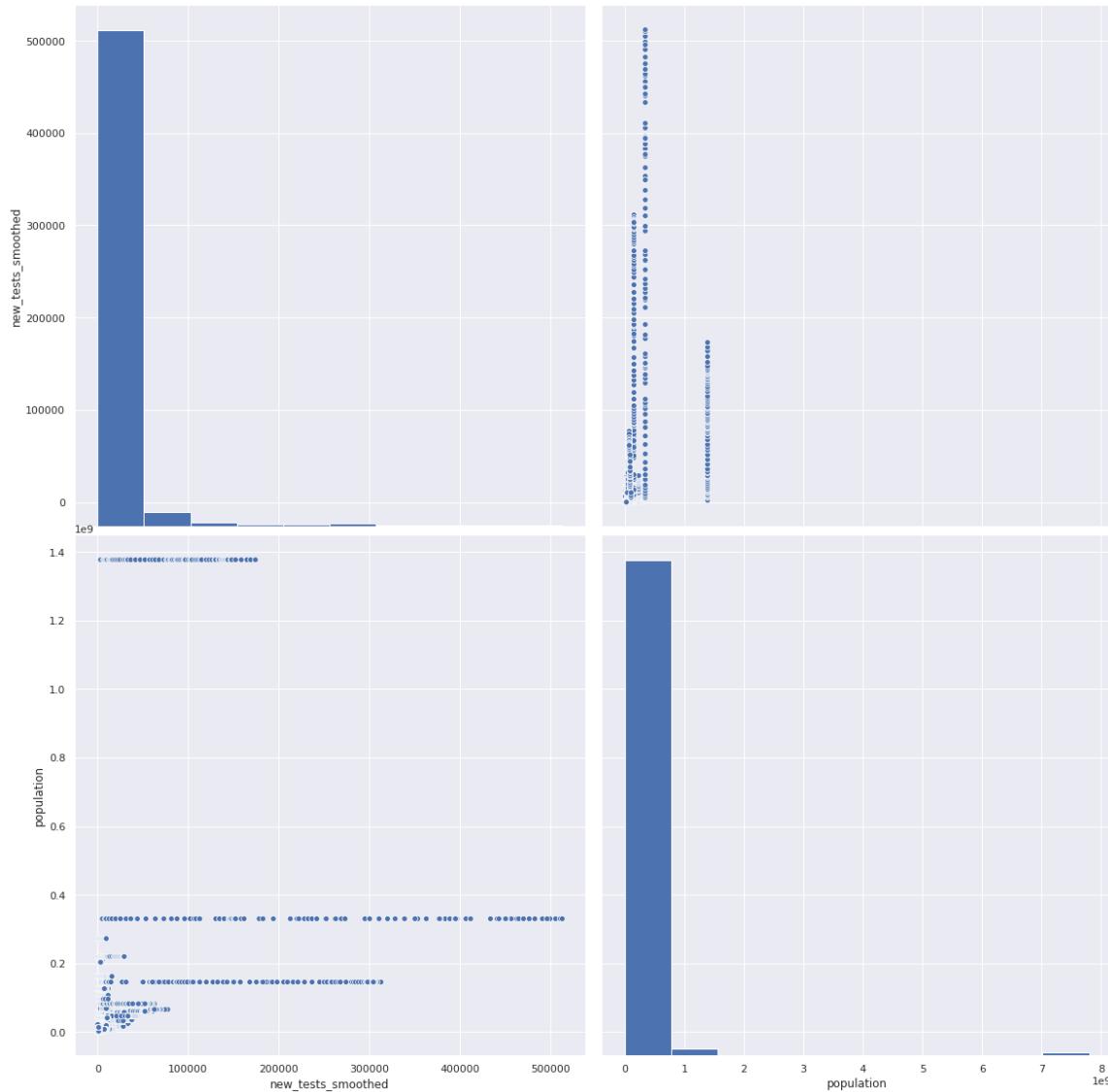


In [127]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "population"], height=8)
```

Out[127]:

```
<seaborn.axisgrid.PairGrid at 0x7f6448a56a20>
```

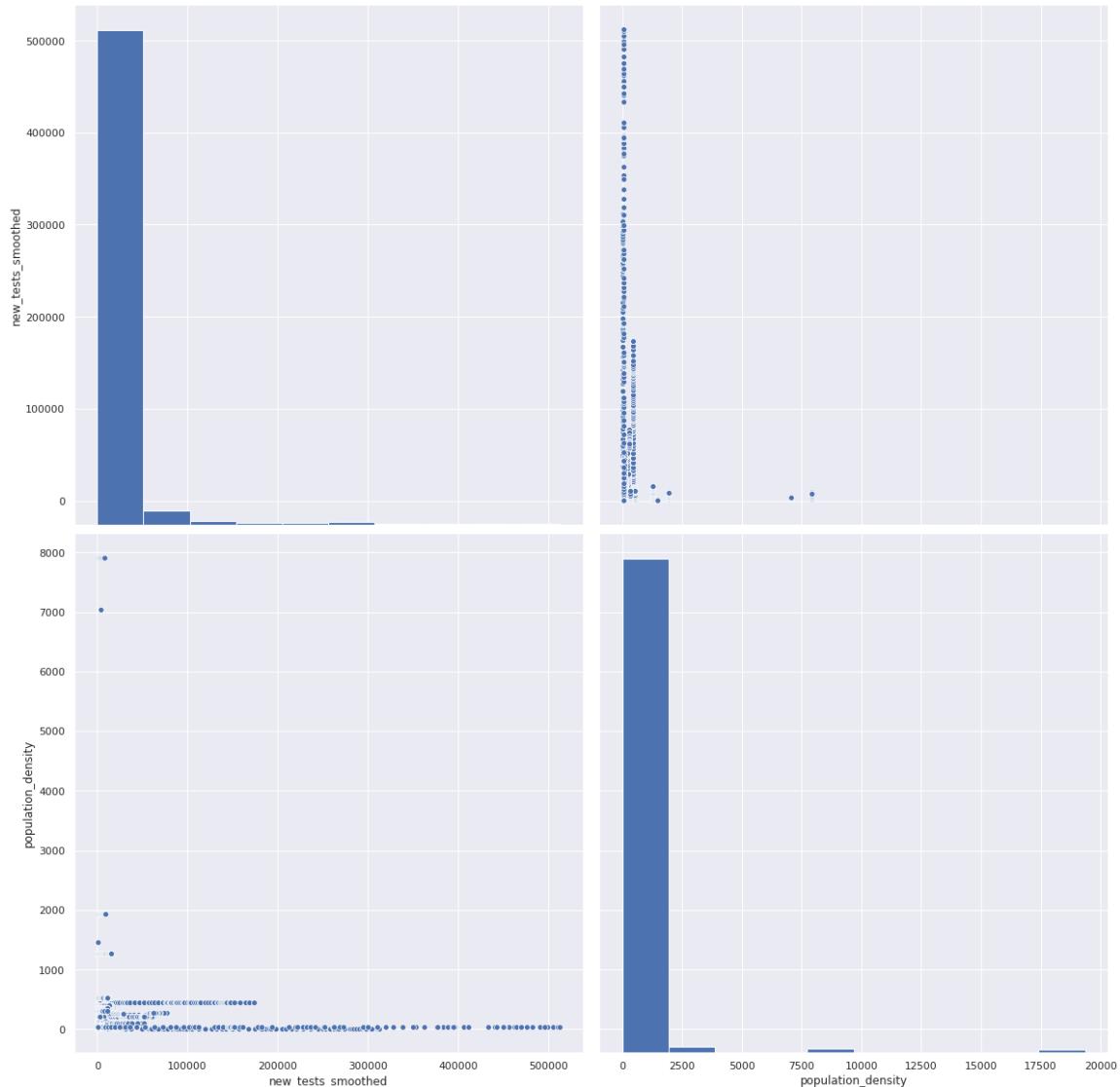


In [128]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "population_density"], height=8)
```

Out[128]:

```
<seaborn.axisgrid.PairGrid at 0x7f644885a4a8>
```

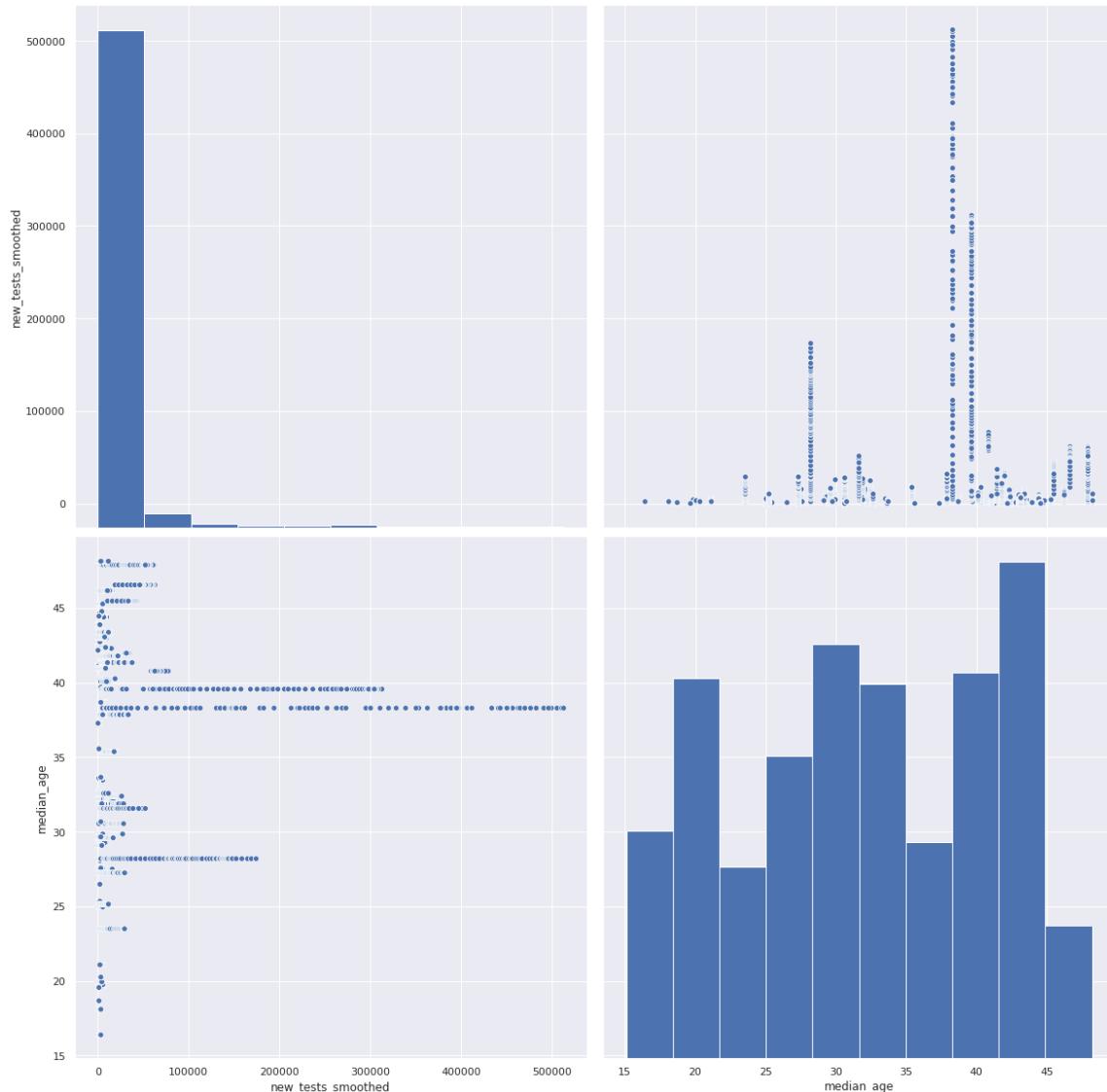


In [129]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "median_age"], height=8)
```

Out[129]:

```
<seaborn.axisgrid.PairGrid at 0x7f644864bc18>
```

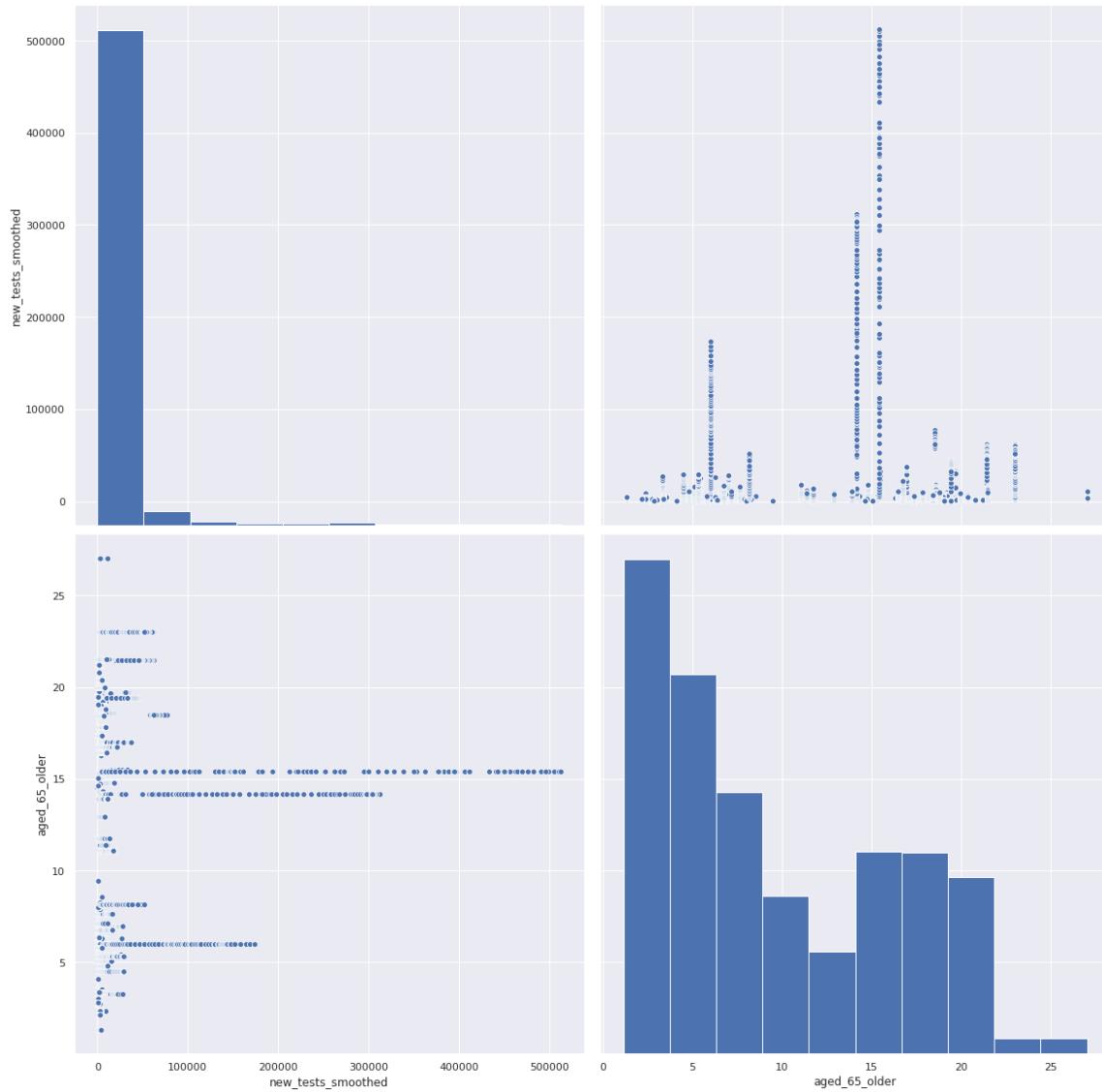


In [130]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "aged_65_older"], height=8)
```

Out[130]:

```
<seaborn.axisgrid.PairGrid at 0x7f64484b0a58>
```

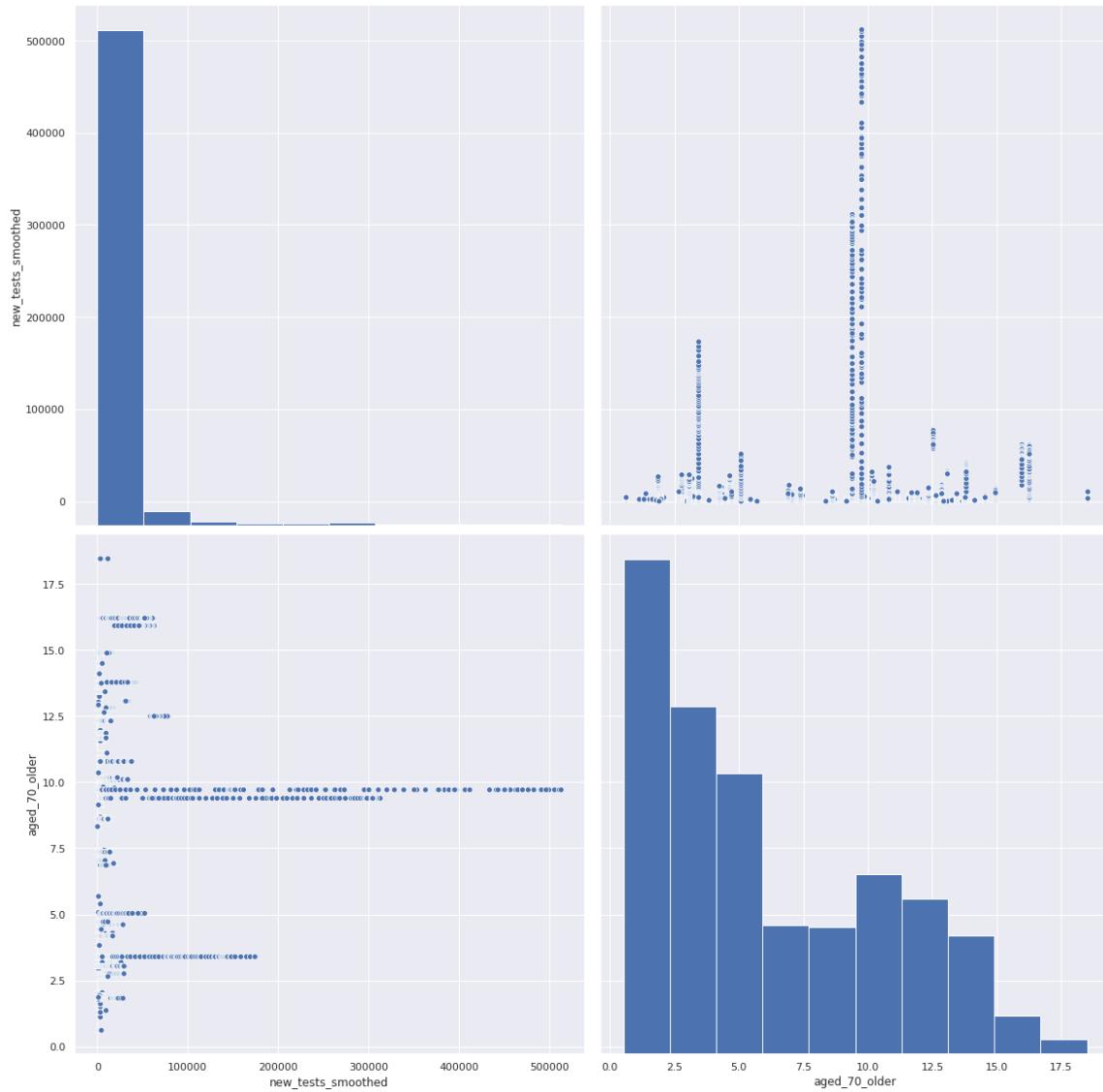


In [131]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "aged_70_older"], height=8)
```

Out[131]:

```
<seaborn.axisgrid.PairGrid at 0x7f64488530f0>
```

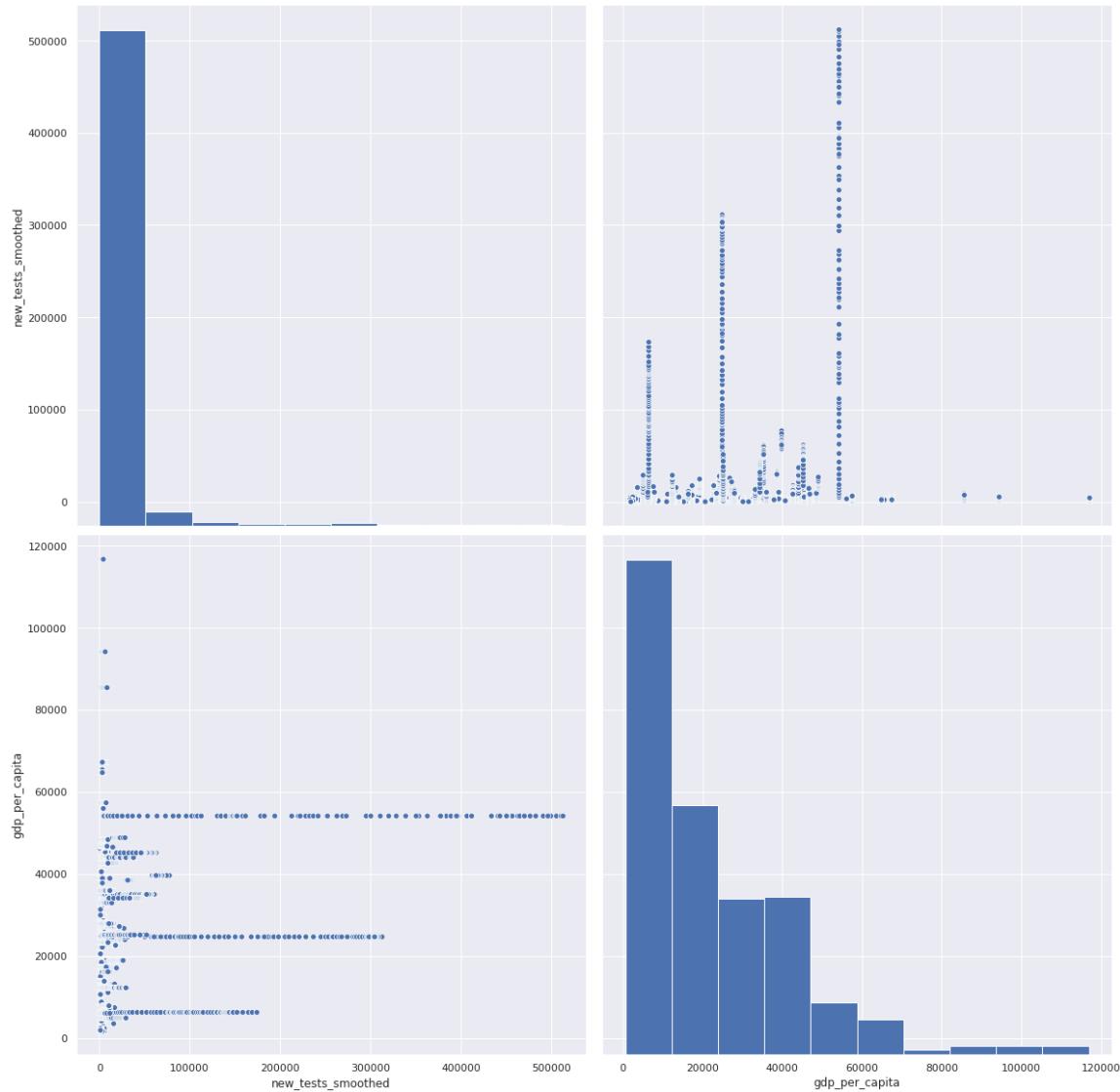


In [132]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "gdp_per_capita"], height=8)
```

Out[132]:

```
<seaborn.axisgrid.PairGrid at 0x7f6448050e80>
```

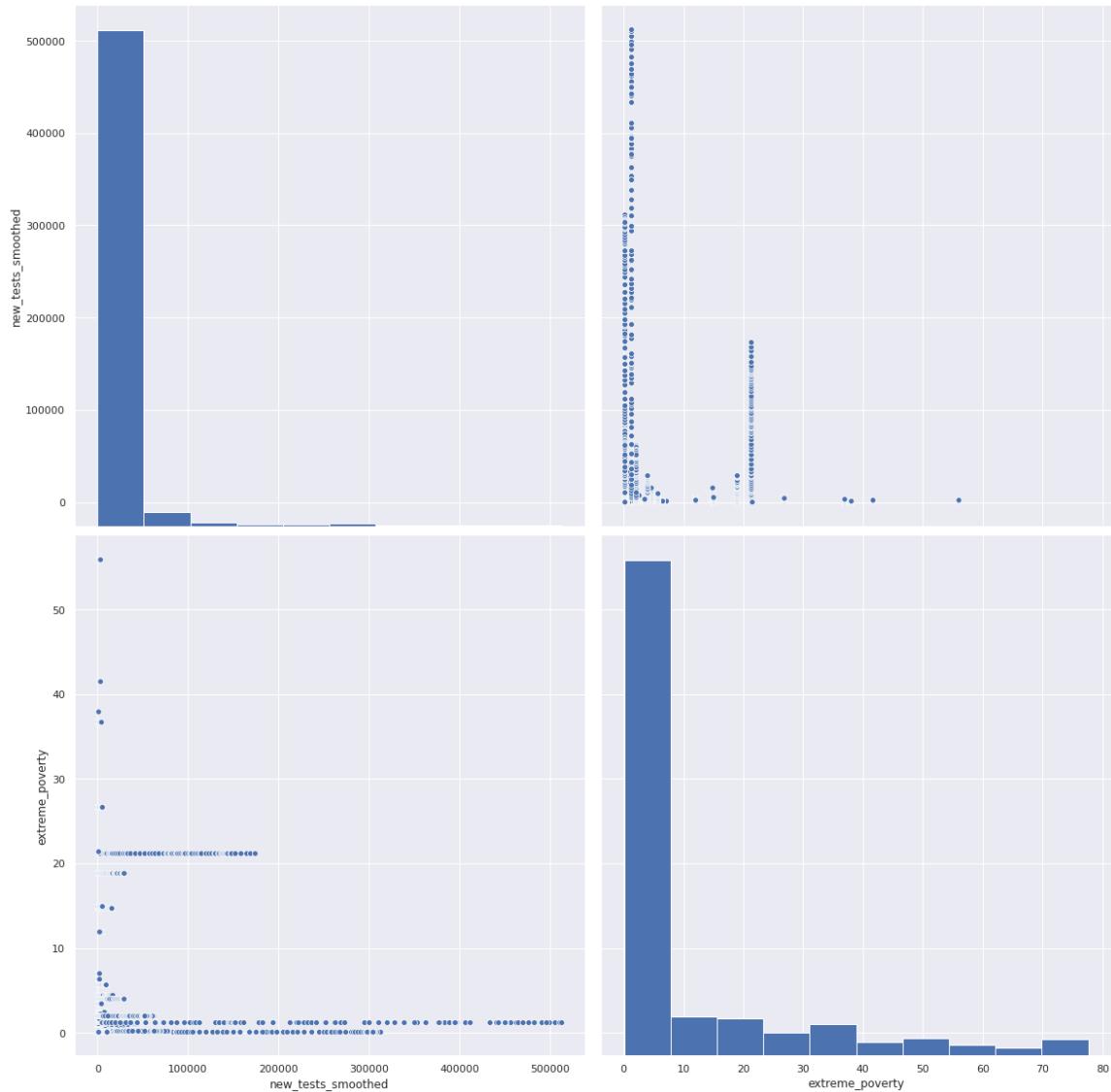


In [133]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "extreme_poverty"], height=8)
```

Out[133]:

```
<seaborn.axisgrid.PairGrid at 0x7f6448056208>
```

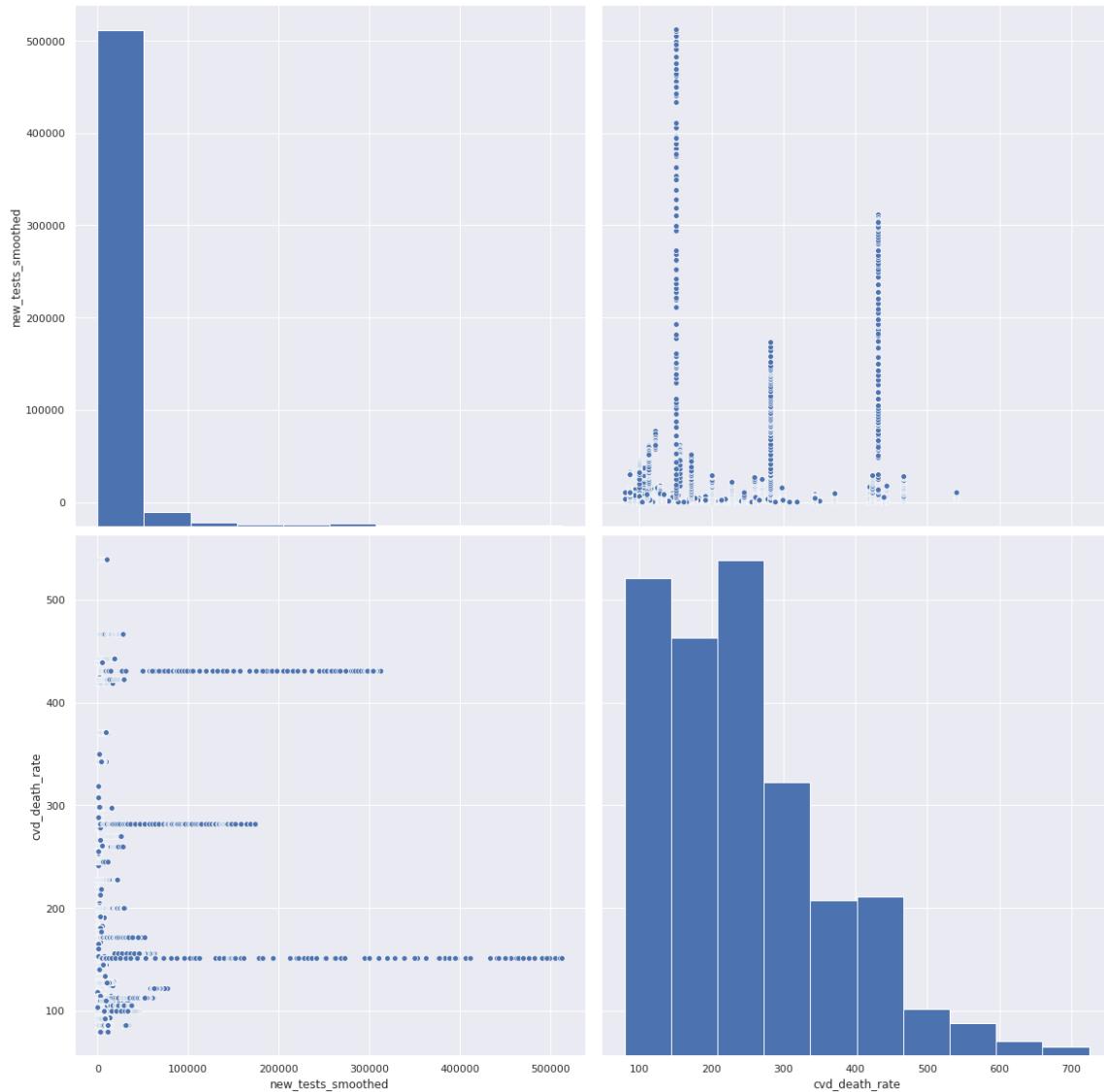


In [134]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "cvd_death_rate"], height=8)
```

Out[134]:

```
<seaborn.axisgrid.PairGrid at 0x7f6447c73358>
```

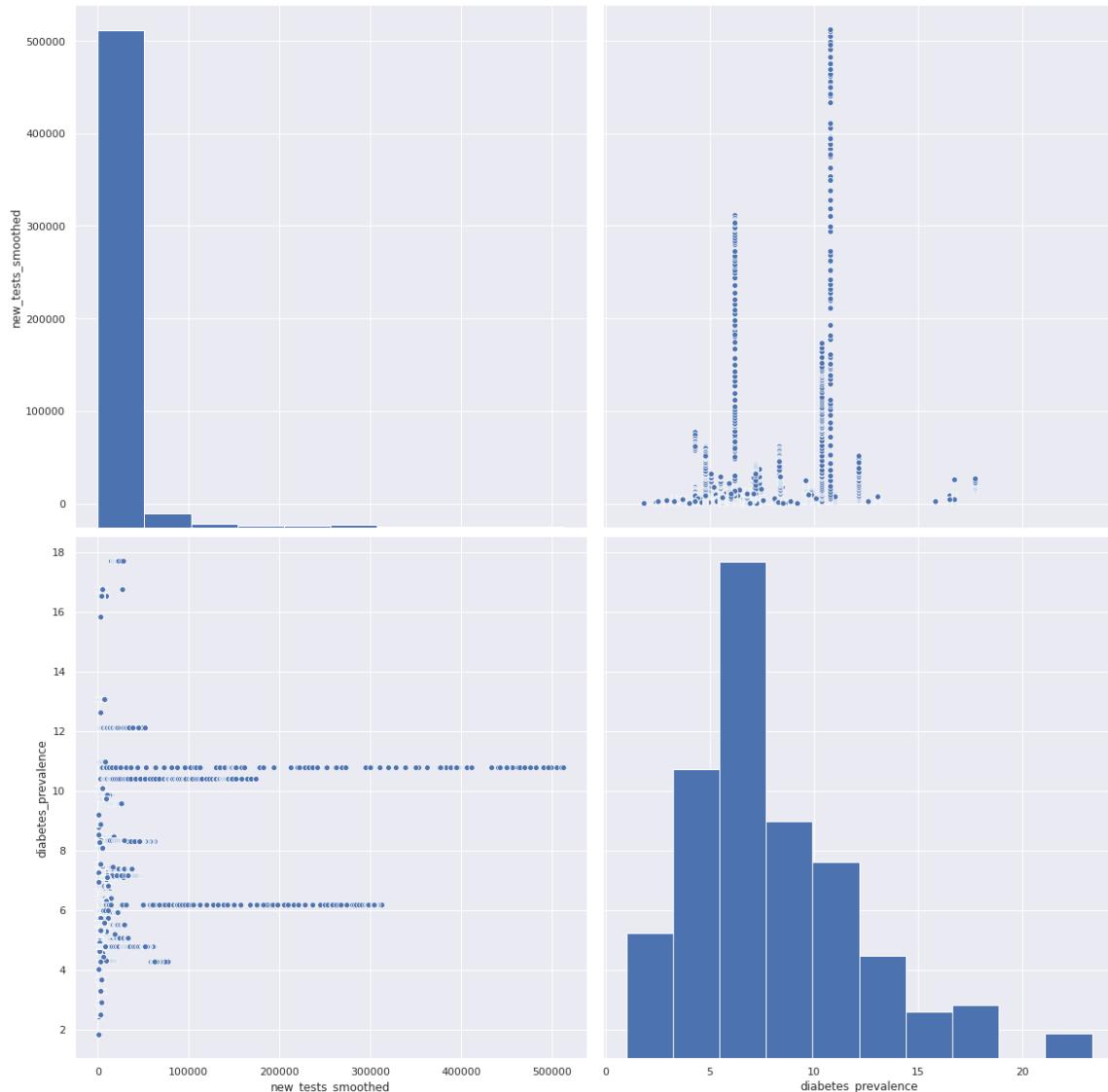


In [135]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "diabetes_prevalence"], height=8)
```

Out[135]:

```
<seaborn.axisgrid.PairGrid at 0x7f6447a70550>
```

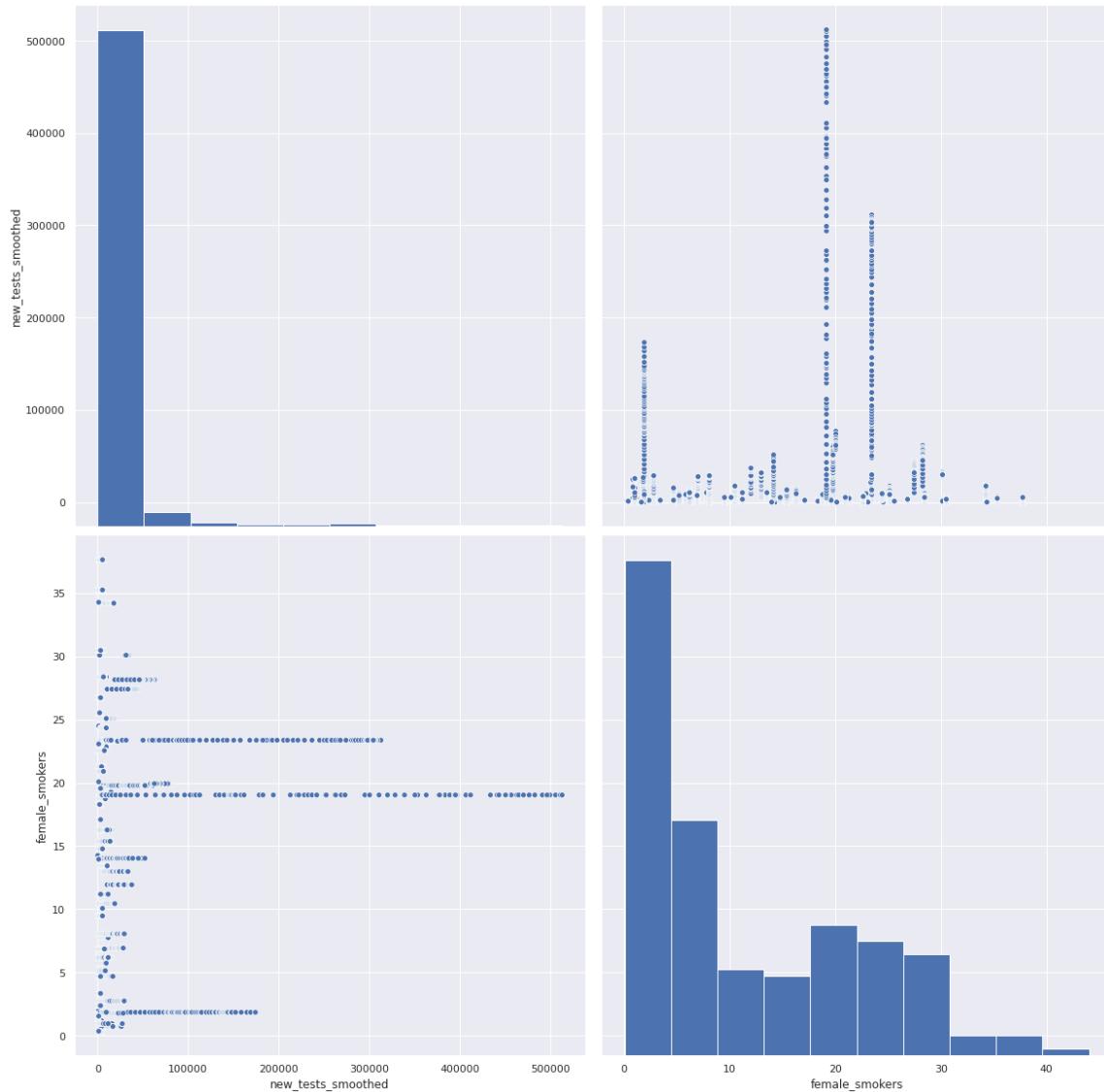


In [136]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "female_smokers"], height=8)
```

Out[136]:

```
<seaborn.axisgrid.PairGrid at 0x7f6447adae48>
```

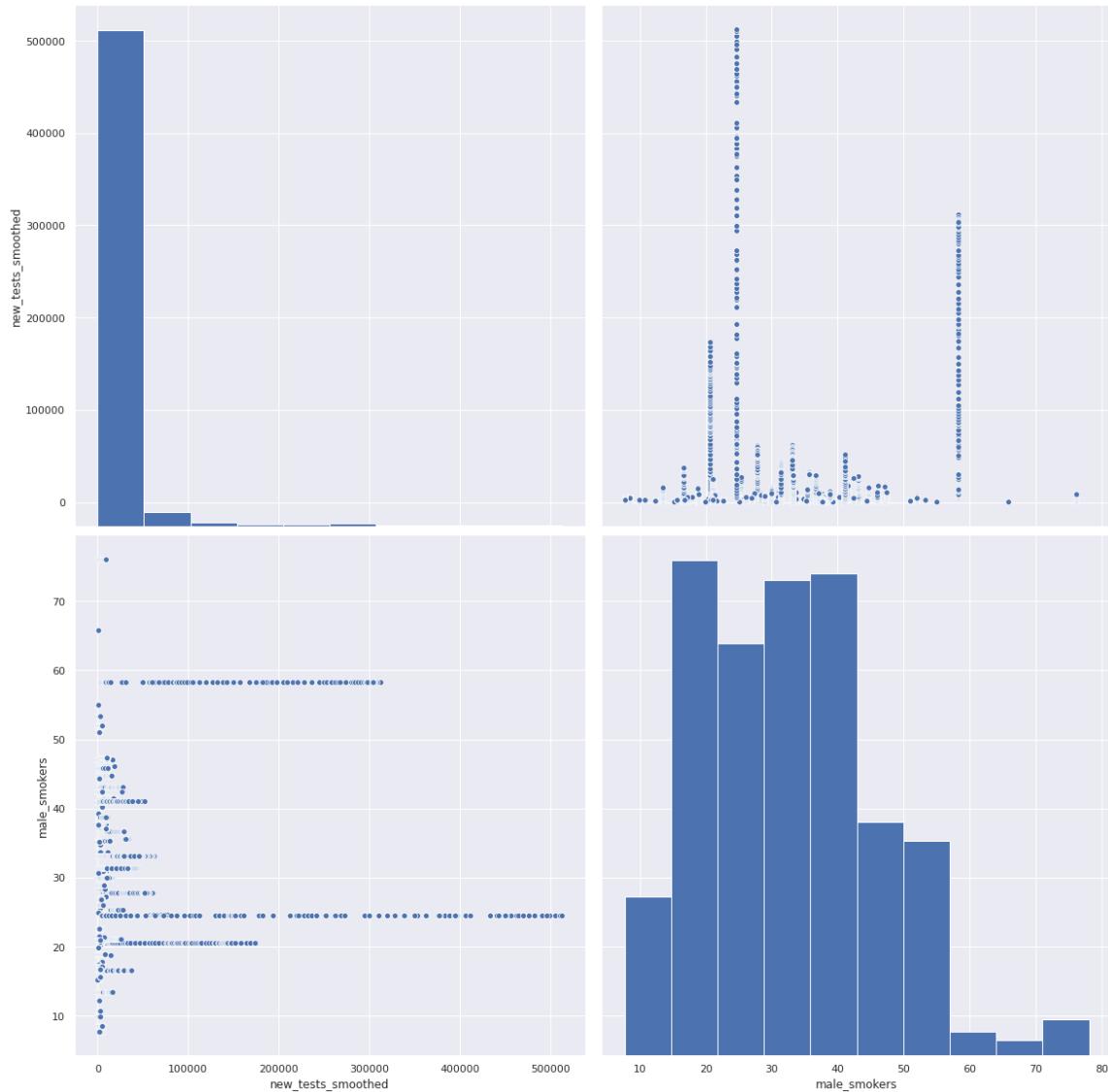


In [137]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "male_smokers"], height=8)
```

Out[137]:

```
<seaborn.axisgrid.PairGrid at 0x7f6447643a20>
```

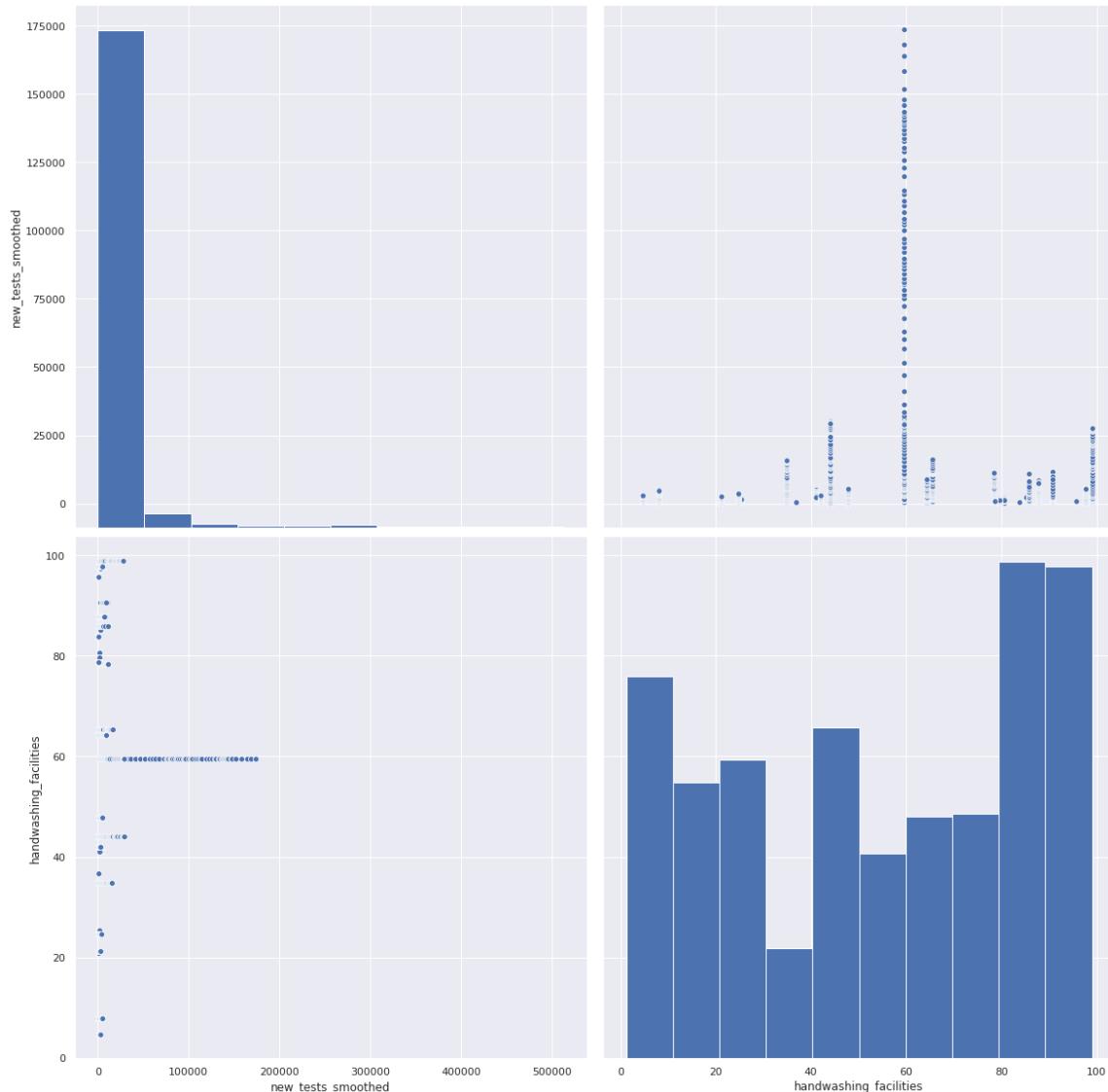


In [138]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "handwashing_facilities"], height=8)
```

Out[138]:

```
<seaborn.axisgrid.PairGrid at 0x7f6448122e10>
```

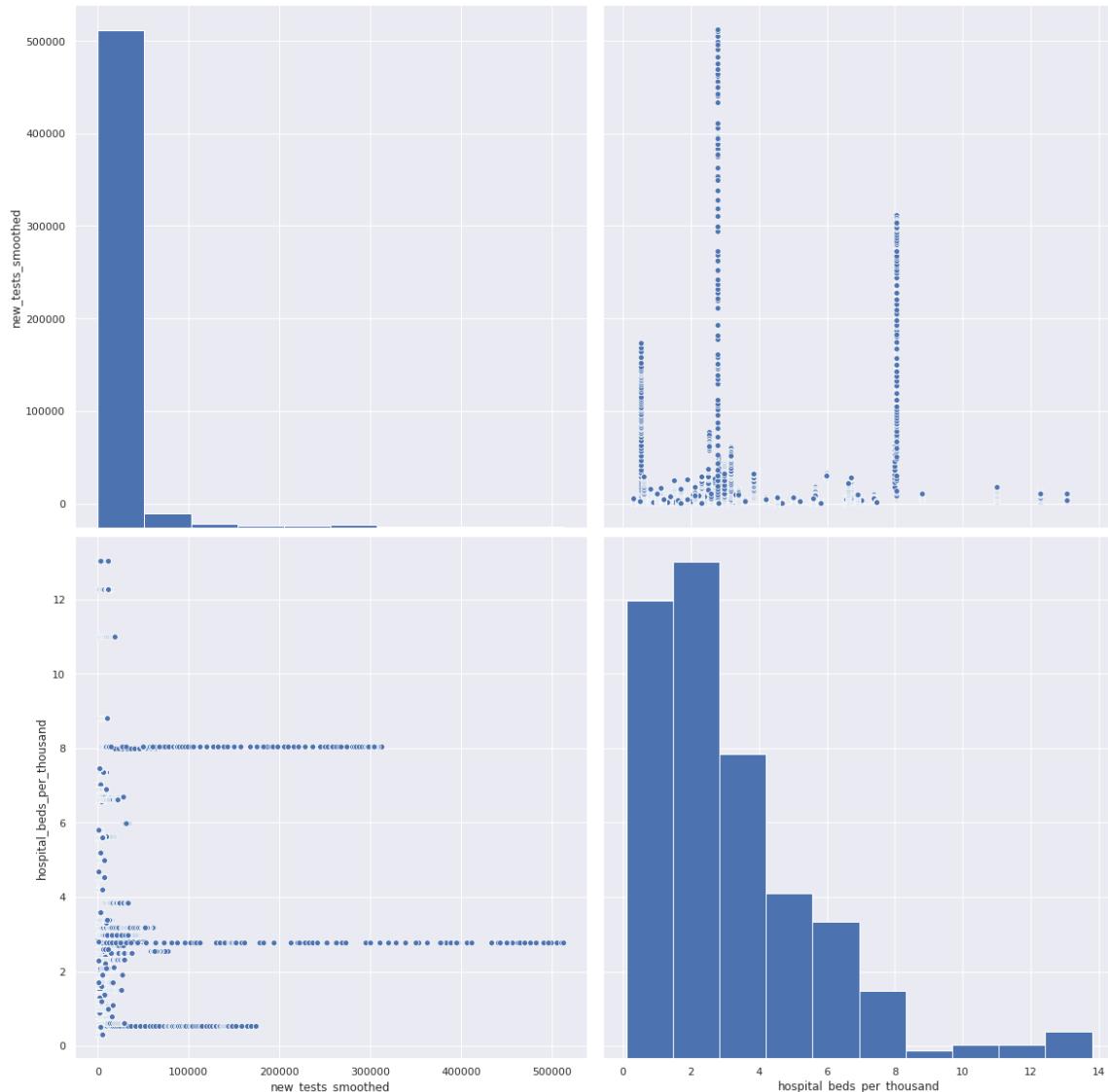


In [139]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "hospital_beds_per_thousand"], height=8)
```

Out[139]:

```
<seaborn.axisgrid.PairGrid at 0x7f64472b0f98>
```

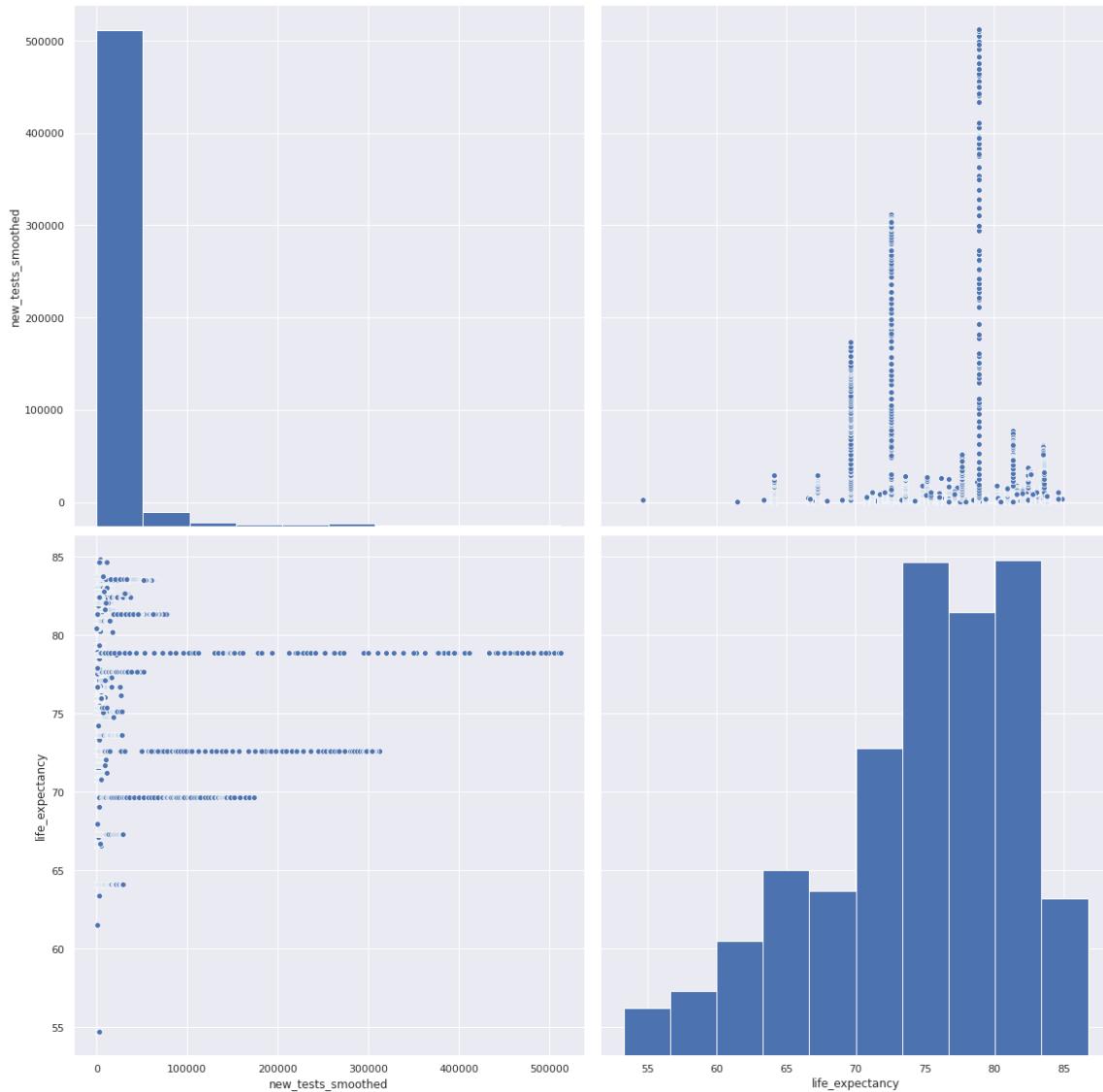


In [140]:

```
sns.pairplot(features, vars=["new_tests_smoothed", "life_expectancy"], height=8)
```

Out[140]:

```
<seaborn.axisgrid.PairGrid at 0x7f644a307748>
```

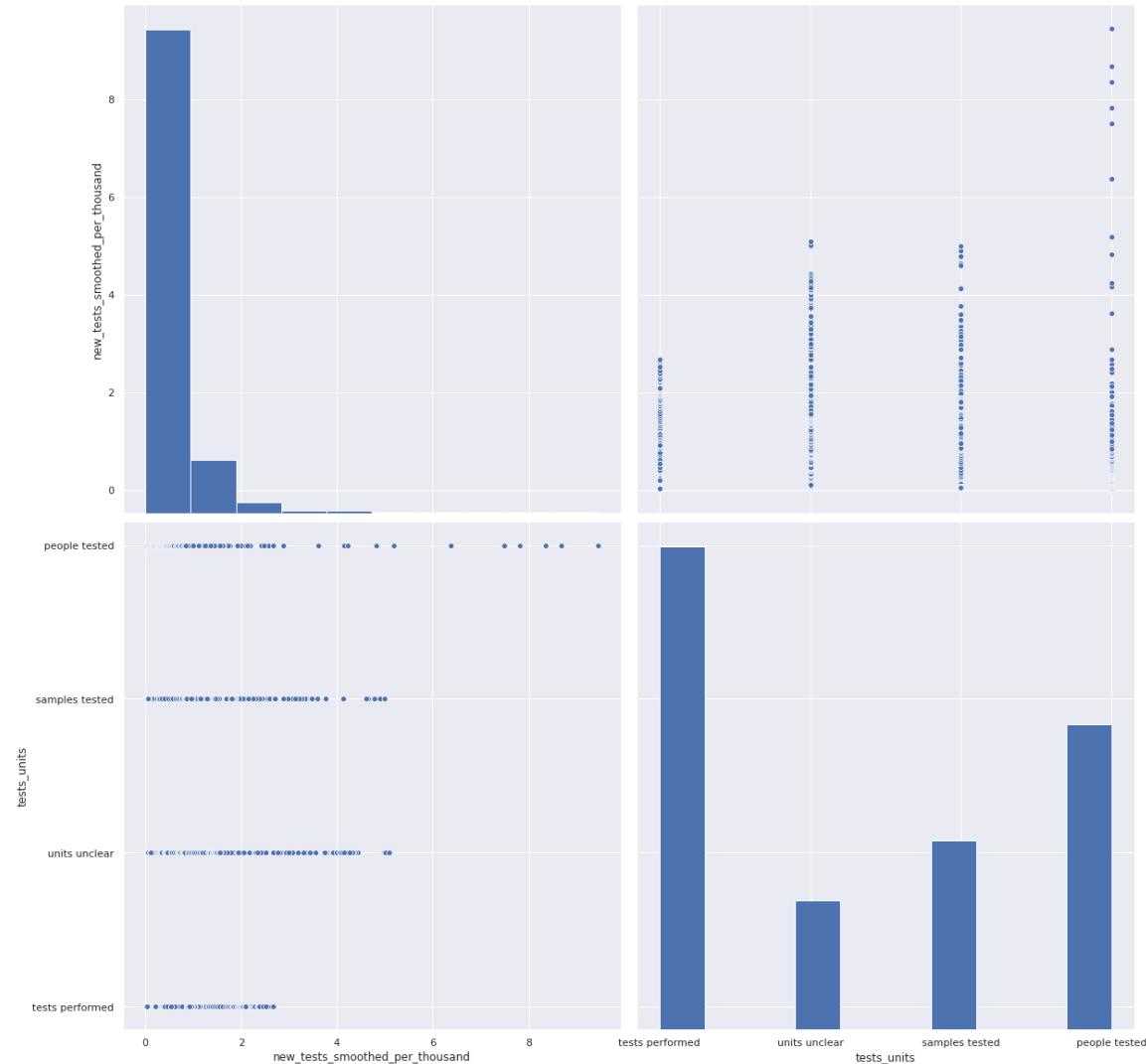


In [141]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "tests_units"], height=8)
```

Out[141]:

```
<seaborn.axisgrid.PairGrid at 0x7f6446ea4d68>
```

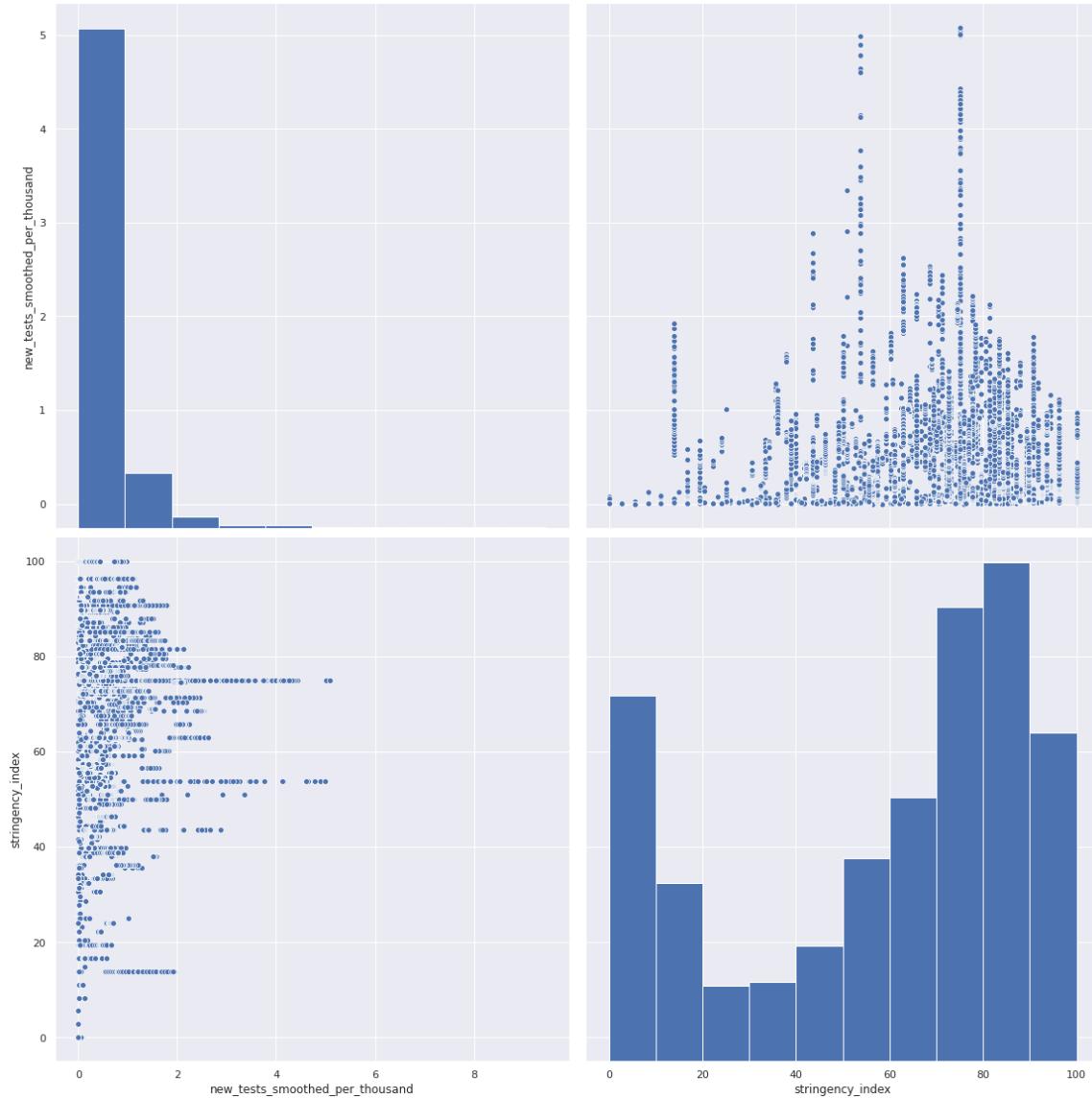


In [142]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "stringency_index"], height=8)
```

Out[142]:

```
<seaborn.axisgrid.PairGrid at 0x7f6446ca0f98>
```

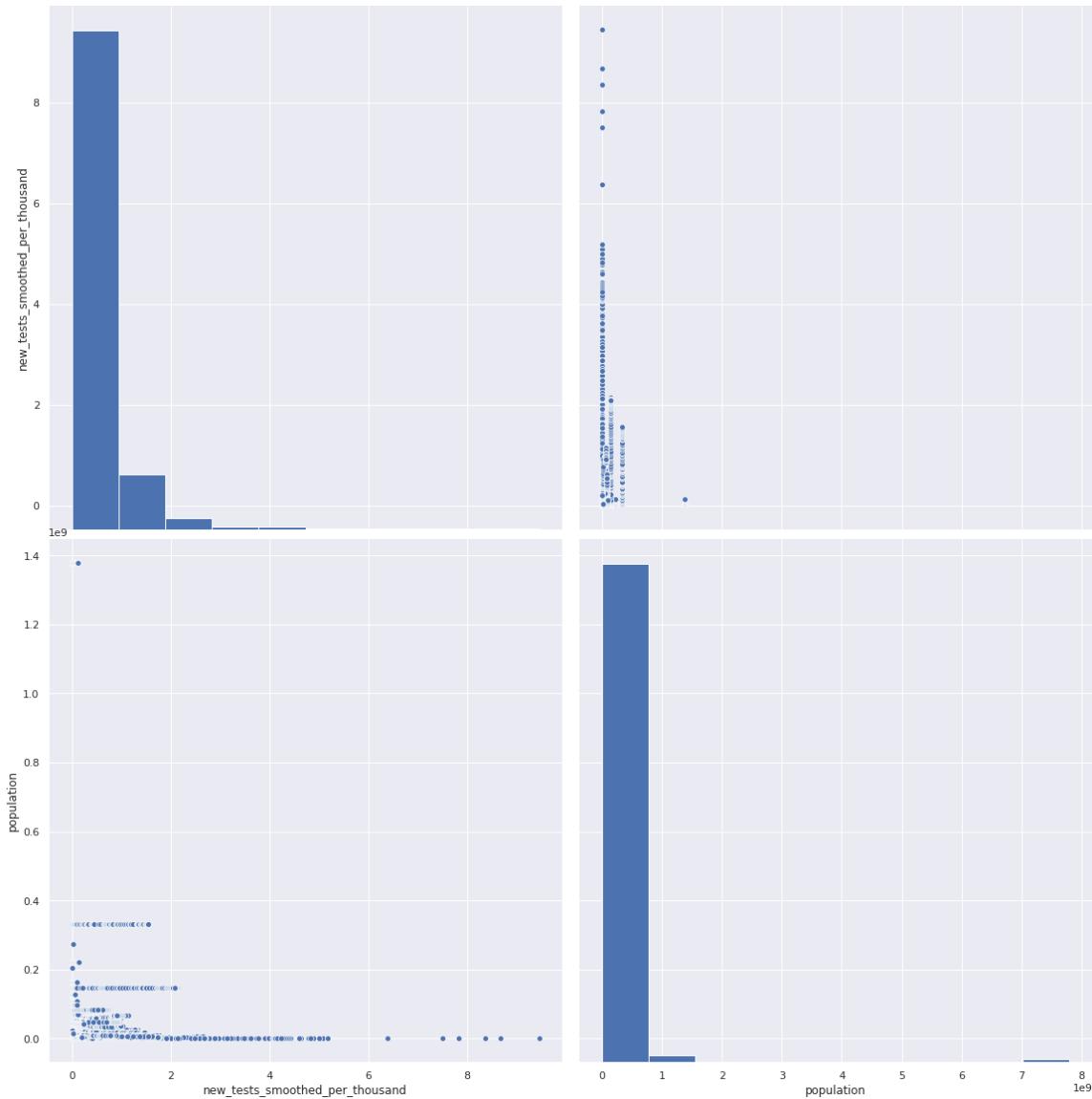


In [143]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "population"], height=8)
```

Out[143]:

```
<seaborn.axisgrid.PairGrid at 0x7f6446a86780>
```

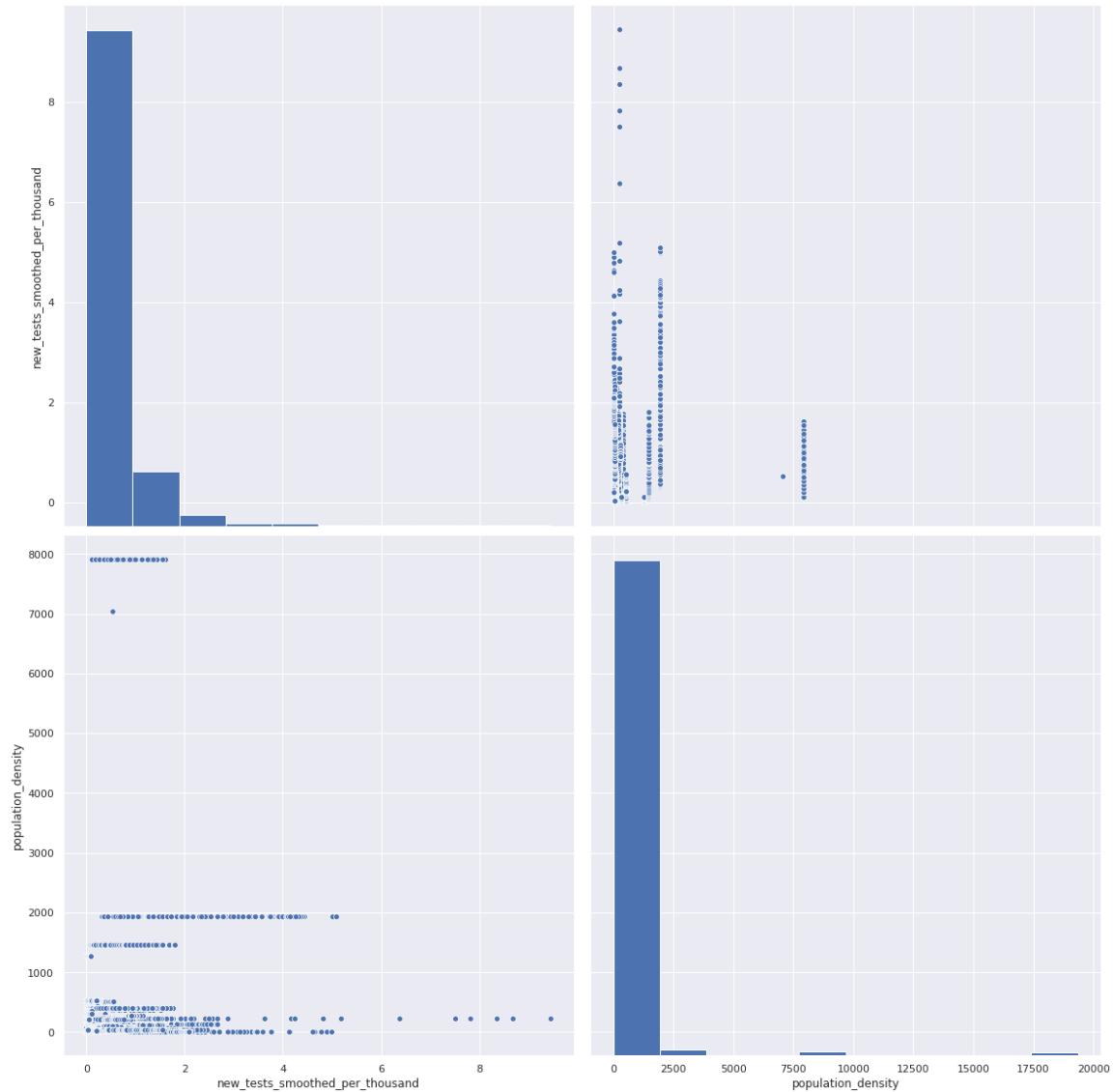


In [144]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "population_density"], height=8)
```

Out[144]:

```
<seaborn.axisgrid.PairGrid at 0x7f6446892160>
```

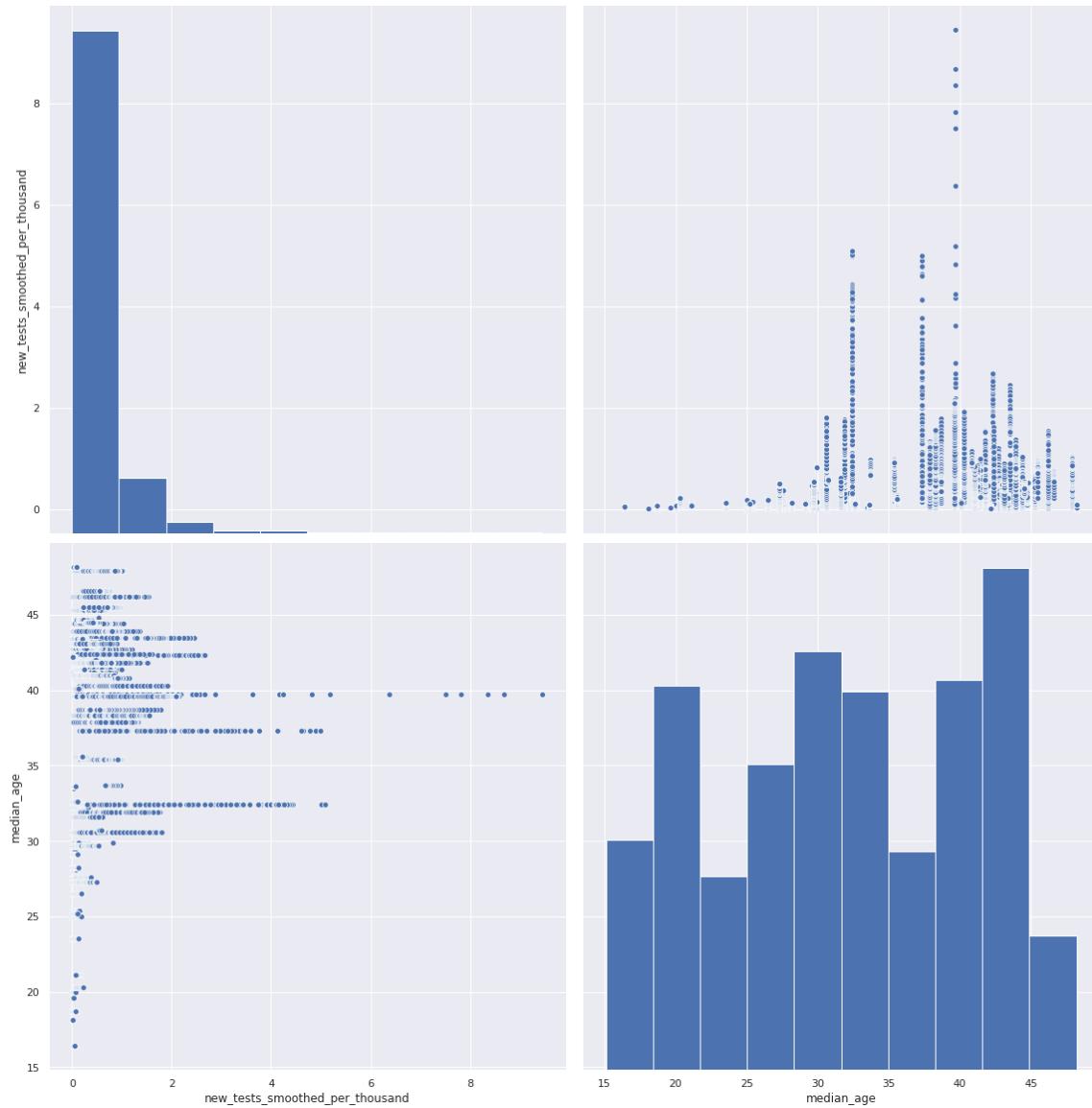


In [4]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "median_age"], height=8)
```

Out[4]:

```
<seaborn.axisgrid.PairGrid at 0x7f105402e6a0>
```

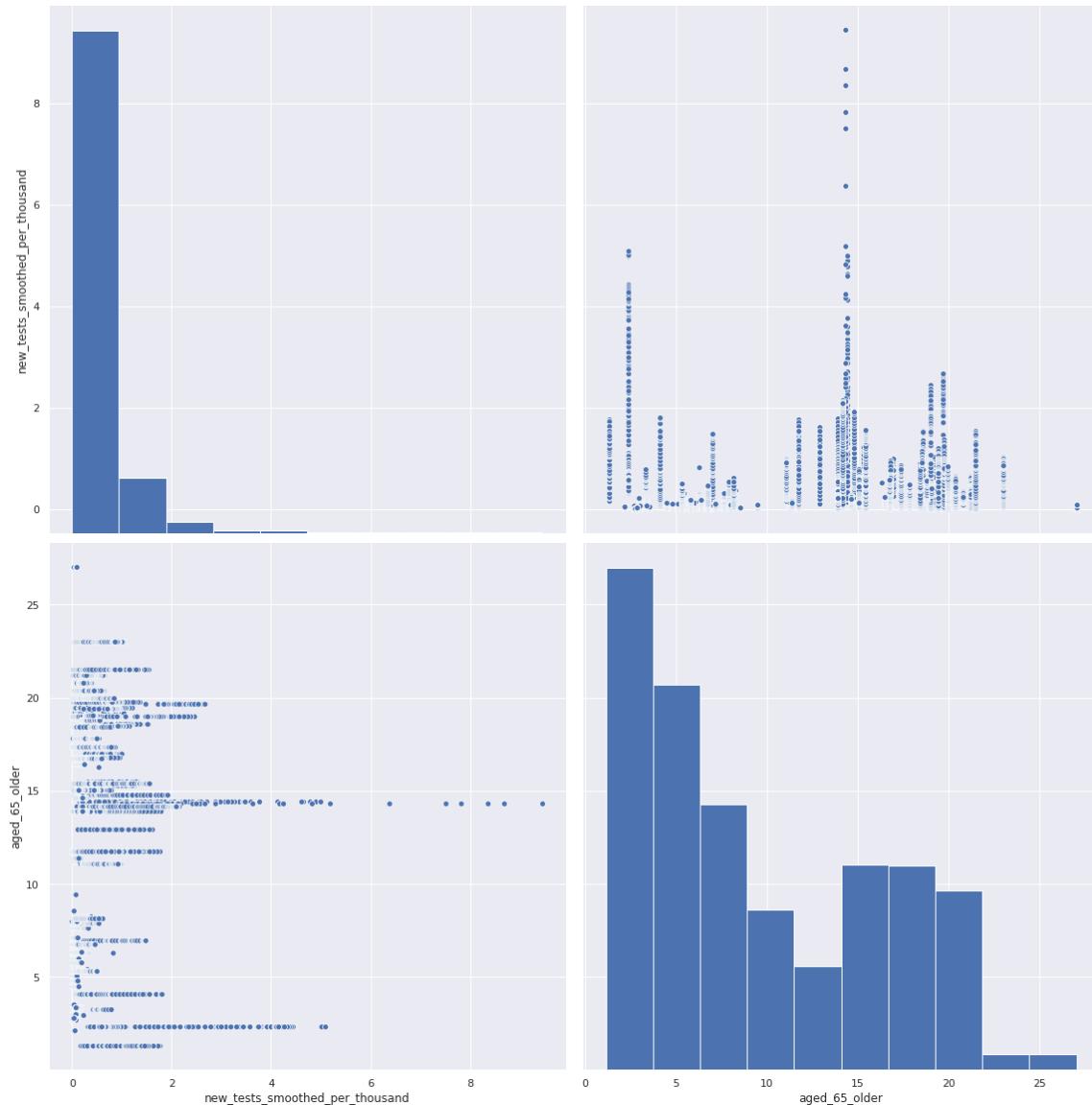


In [5]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "aged_65_older"], height=8)
```

Out[5]:

```
<seaborn.axisgrid.PairGrid at 0x7f1009144208>
```

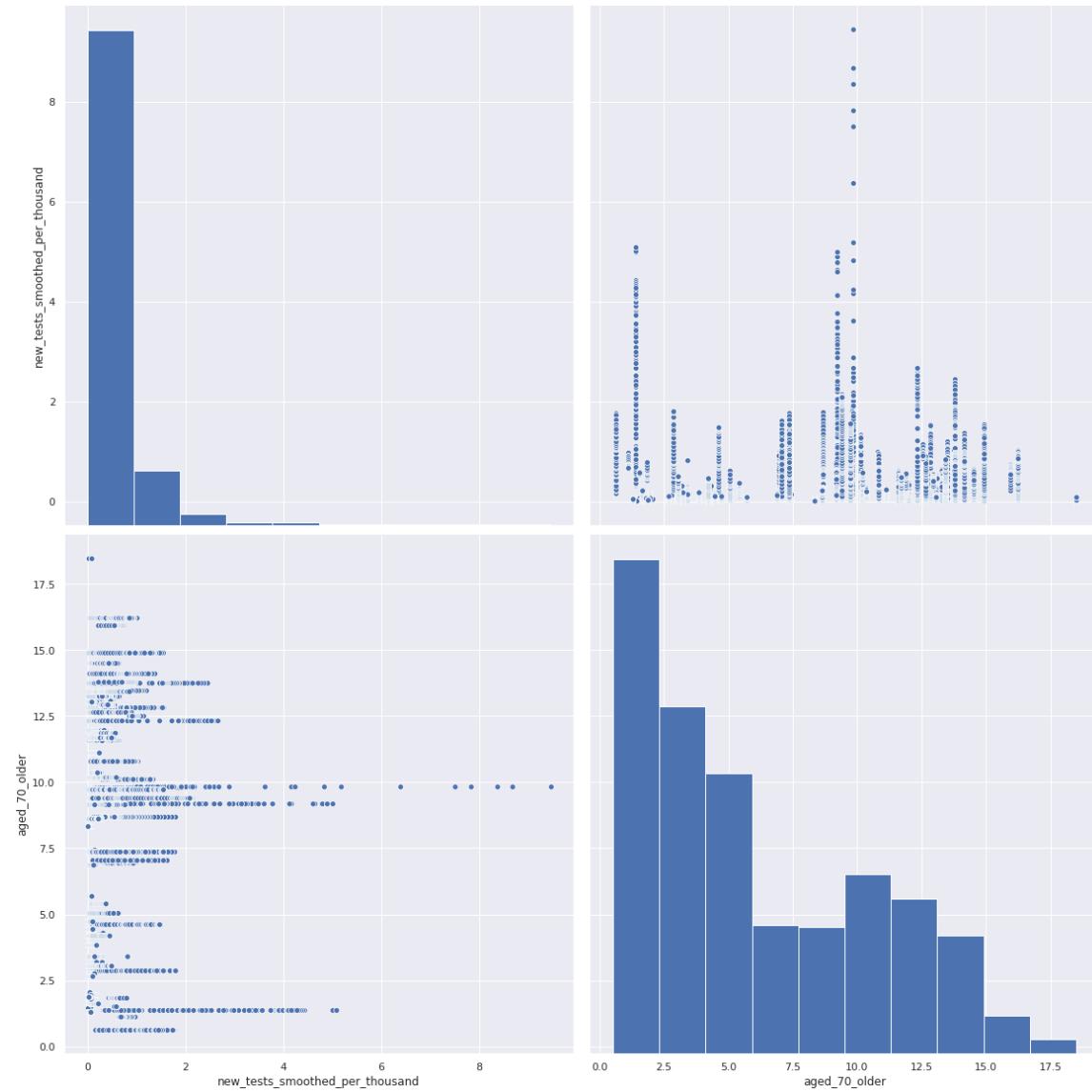


In [6]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "aged_70_older"], height=8)
```

Out[6]:

```
<seaborn.axisgrid.PairGrid at 0x7f100805ae48>
```

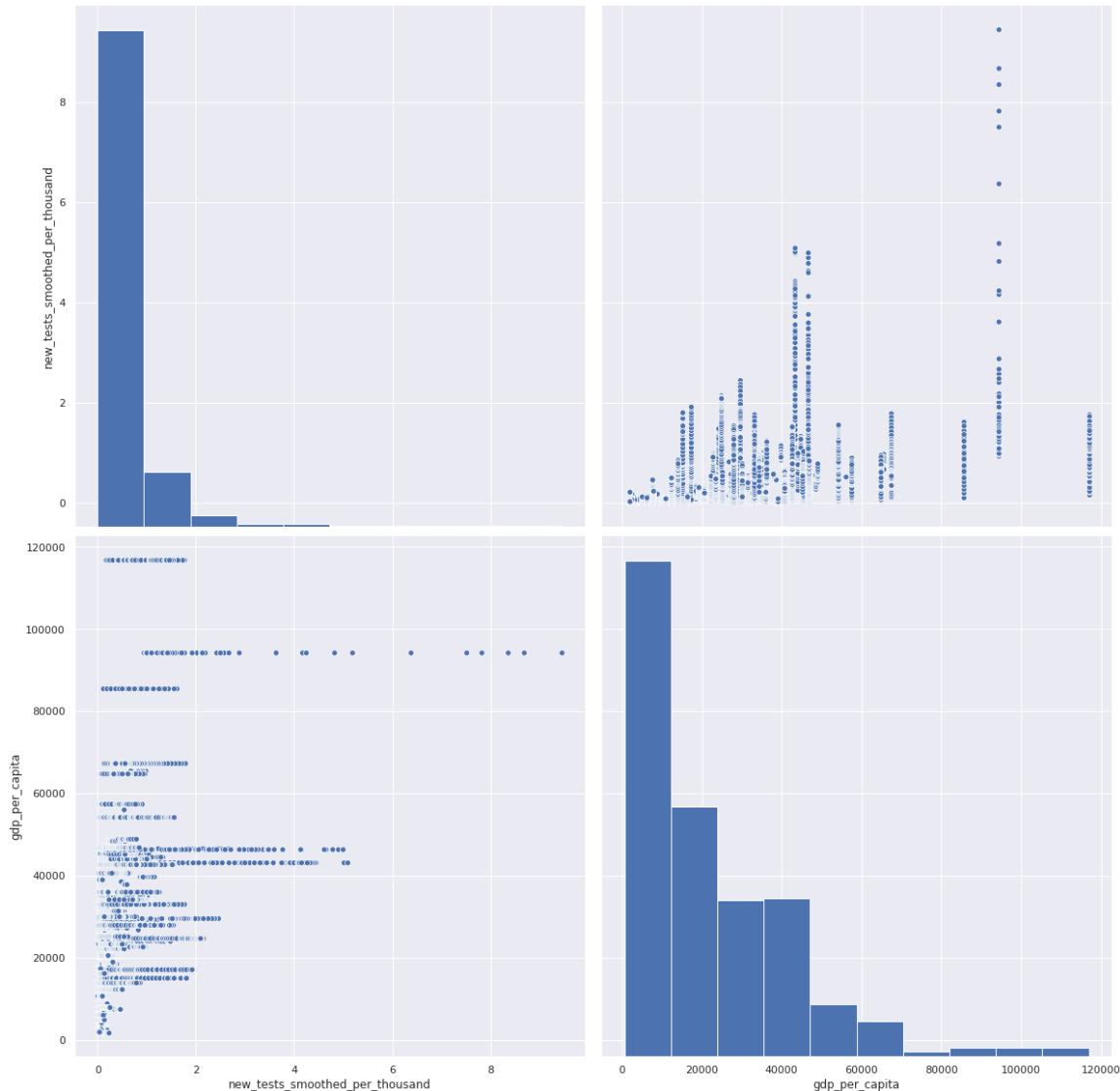


In [7]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "gdp_per_capita"], height=8)
```

Out[7]:

```
<seaborn.axisgrid.PairGrid at 0x7f1002ebf128>
```

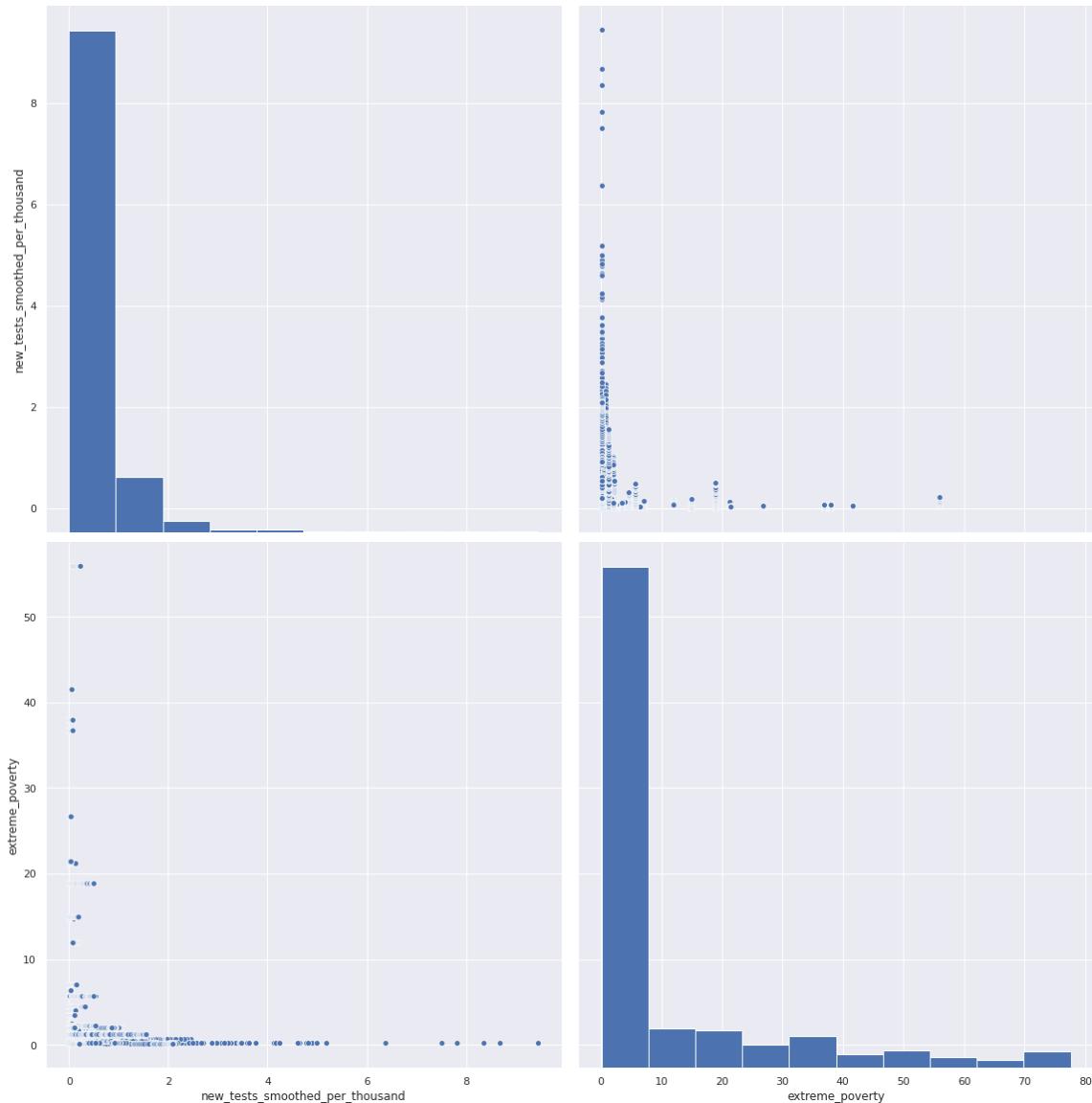


In [8]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "extreme_poverty"], height=8)
```

Out[8]:

```
<seaborn.axisgrid.PairGrid at 0x7f10080dabe0>
```

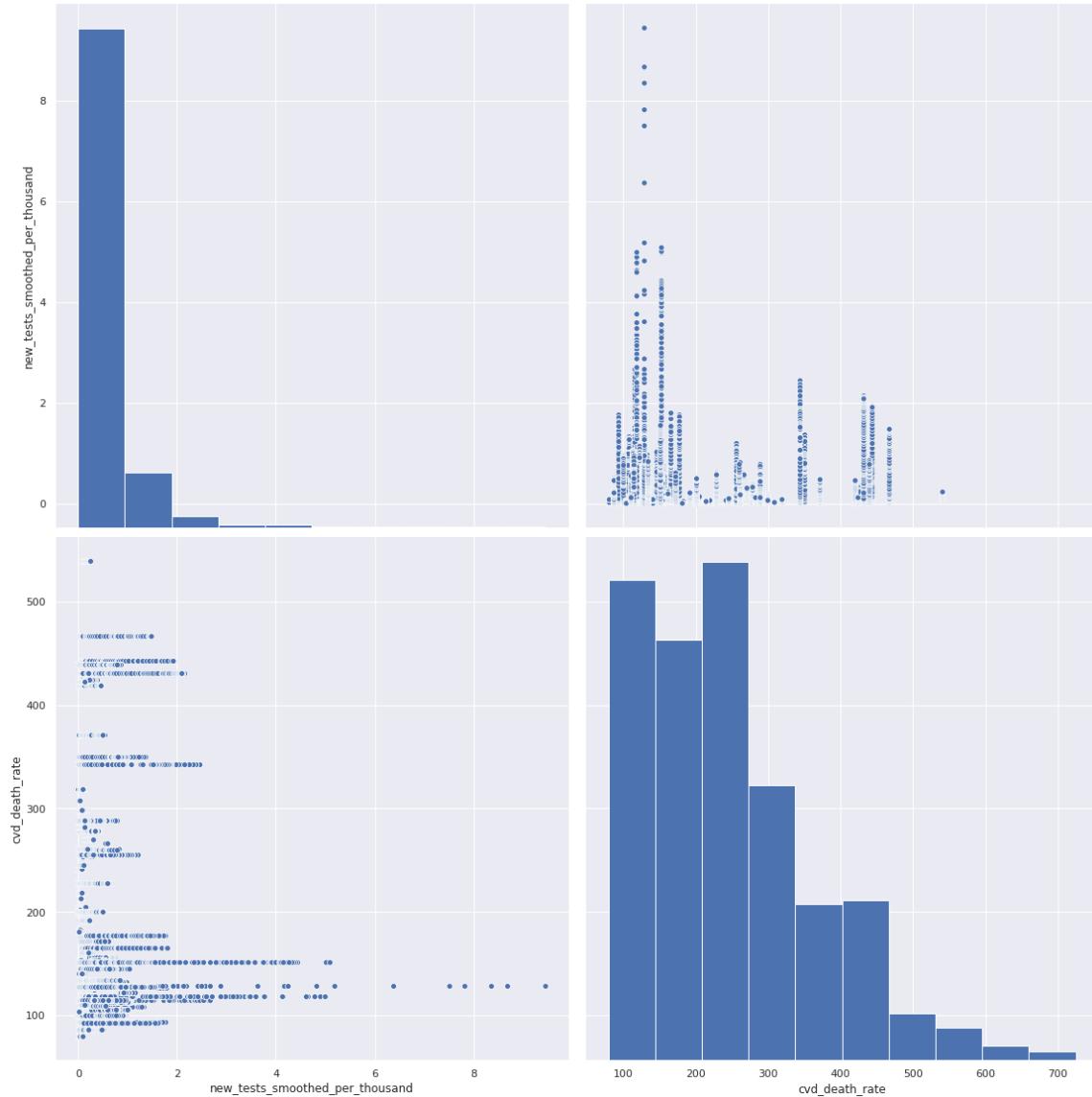


In [9]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "cvd_death_rate"], height=8)
```

Out[9]:

```
<seaborn.axisgrid.PairGrid at 0x7f10029c0550>
```

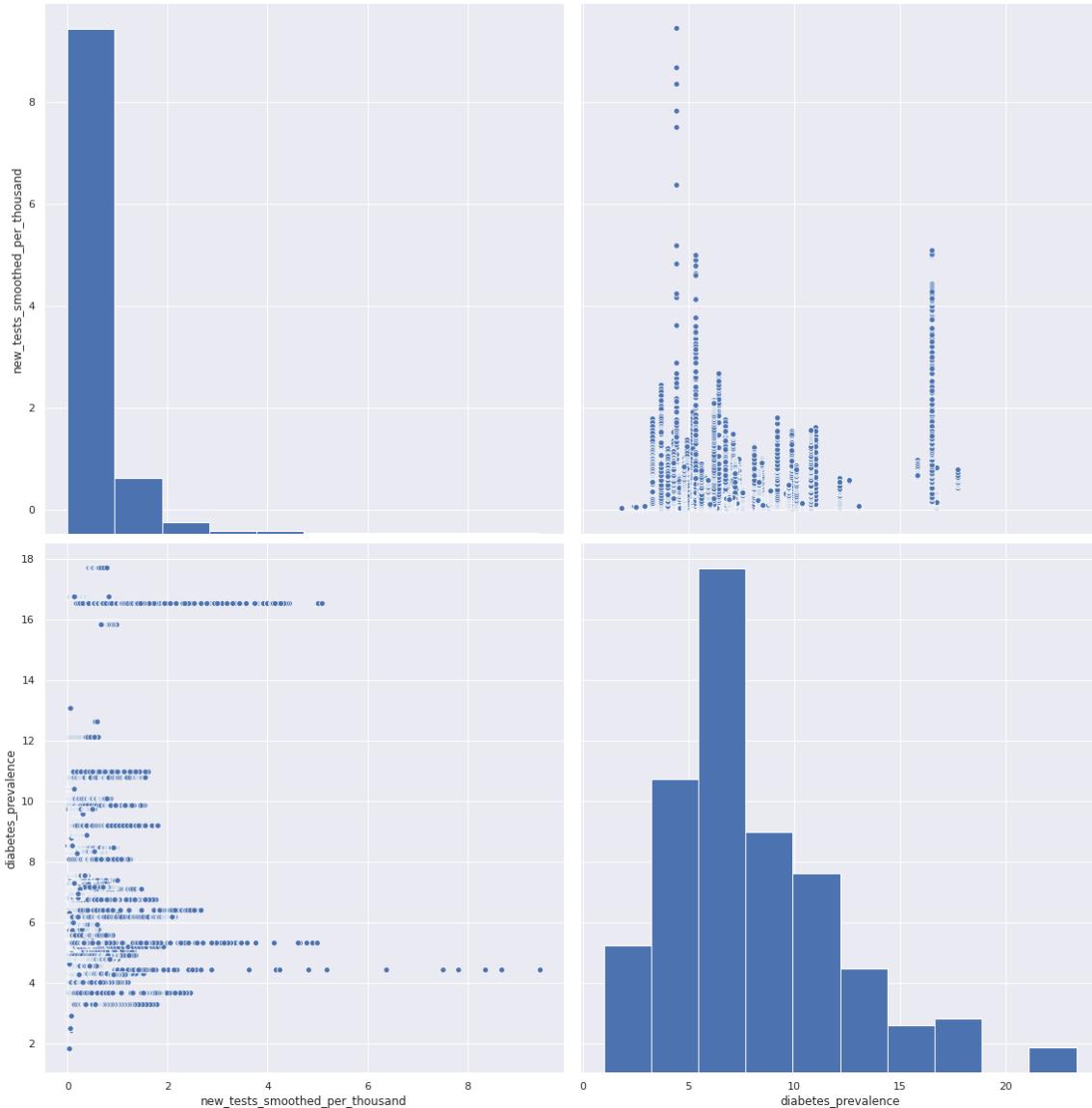


In [10]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "diabetes_prevalence"], height=8)
```

Out[10]:

```
<seaborn.axisgrid.PairGrid at 0x7f10027dab00>
```

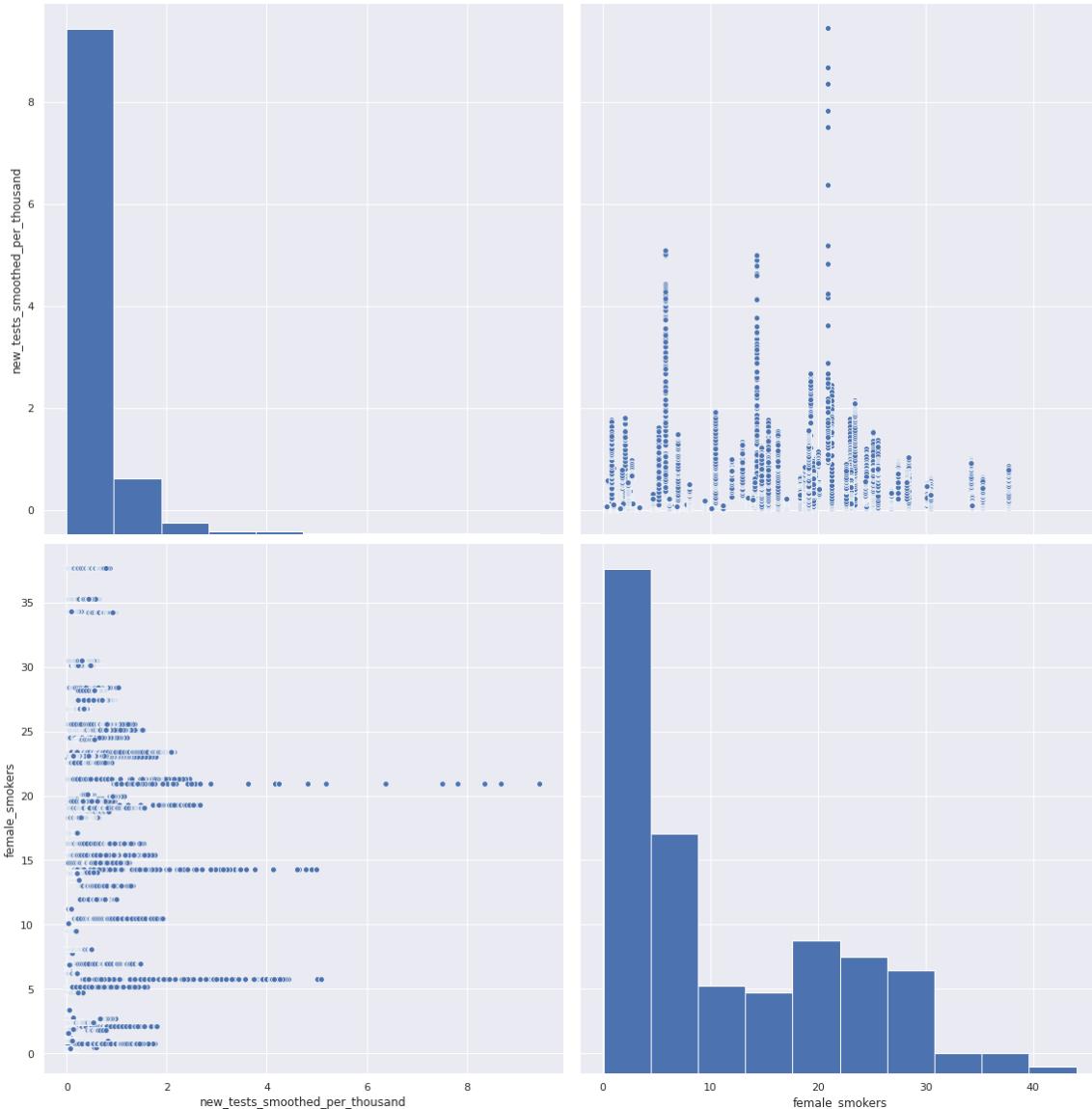


In [11]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "female_smokers"], height=8)
```

Out[11]:

```
<seaborn.axisgrid.PairGrid at 0x7f100264e2e8>
```

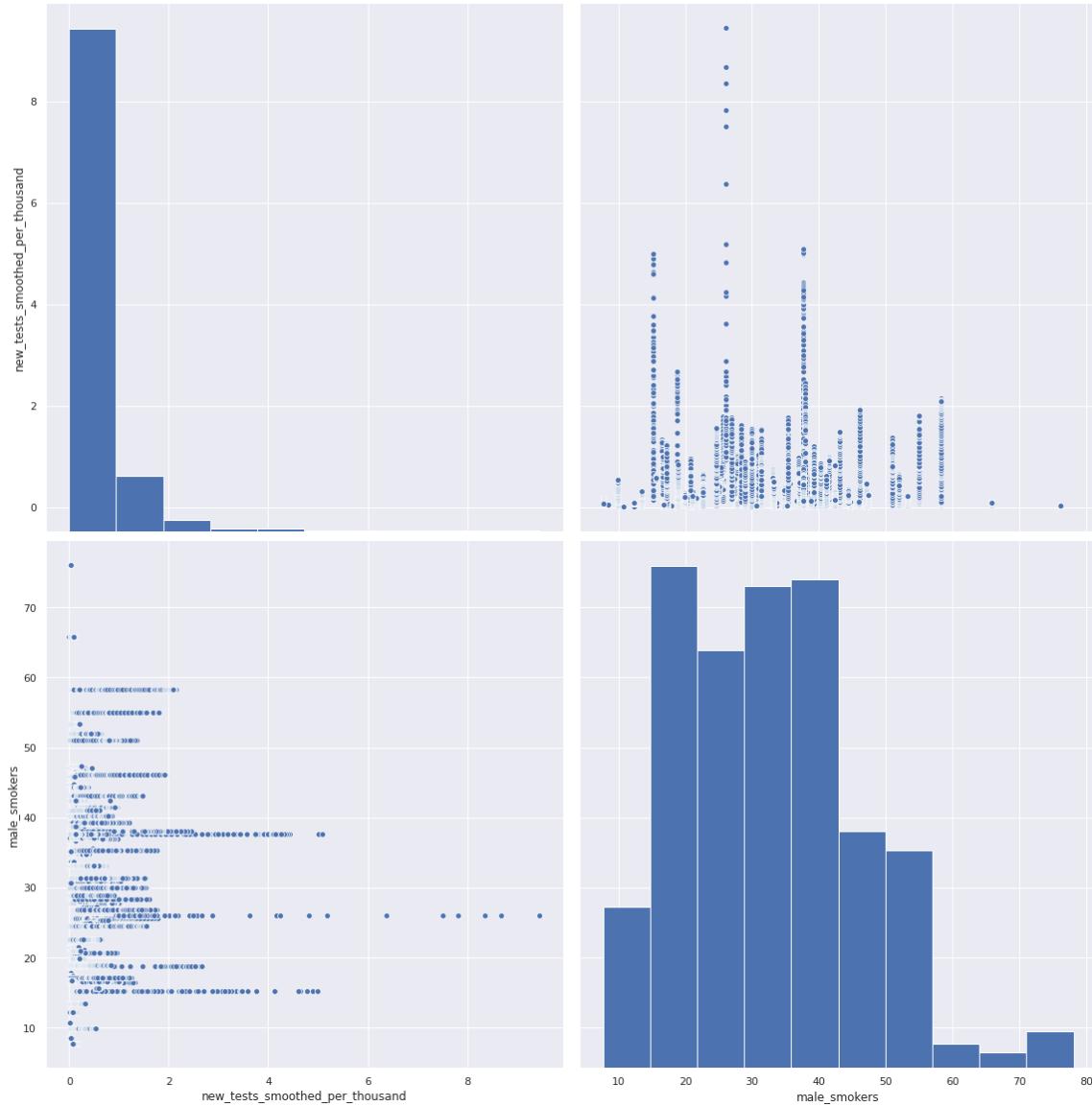


In [12]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "male_smokers"], height=8)
```

Out[12]:

```
<seaborn.axisgrid.PairGrid at 0x7f1002bd85c0>
```

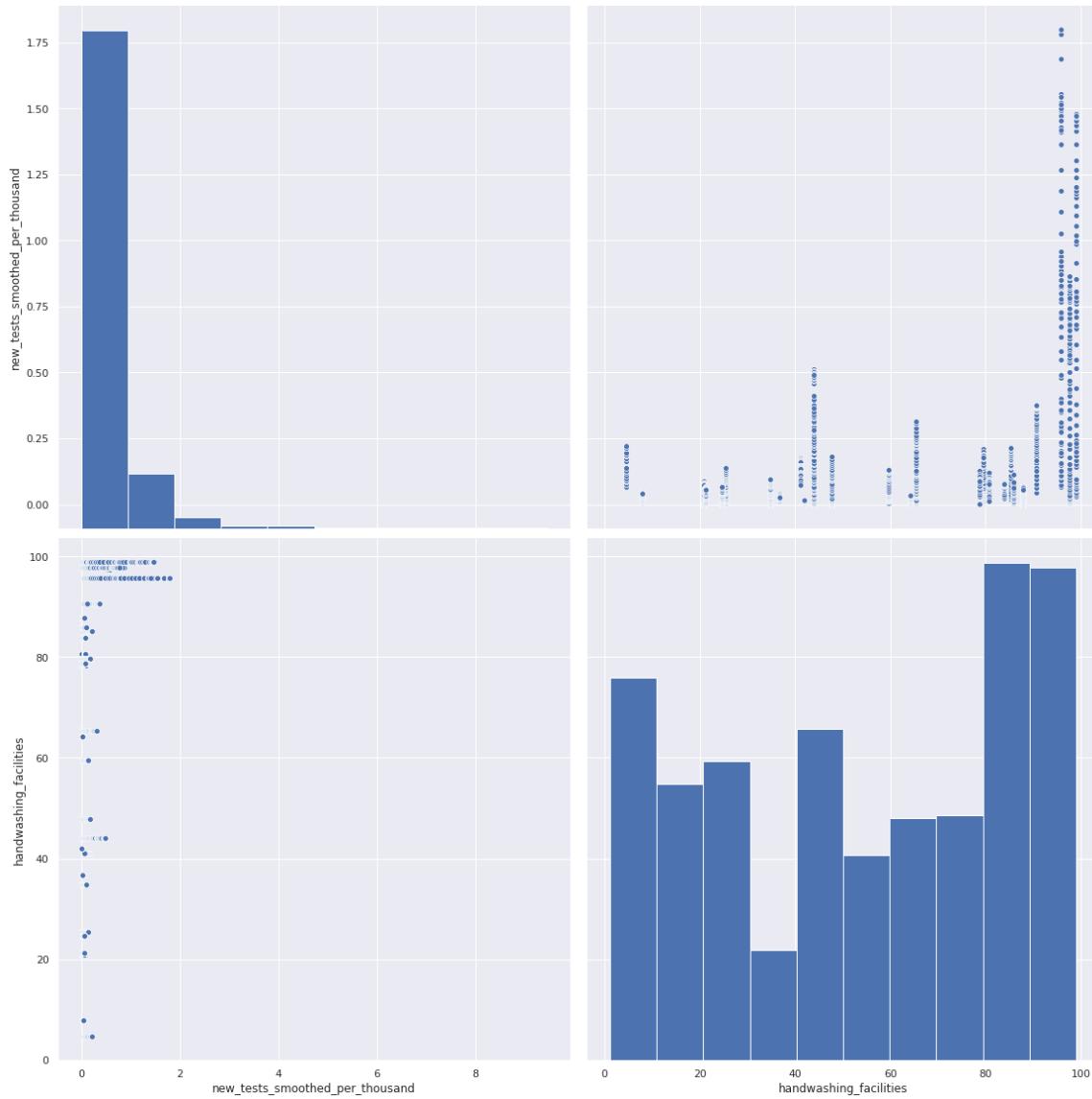


In [13]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "handwashing_facilities"], height=8)
```

Out[13]:

```
<seaborn.axisgrid.PairGrid at 0x7f1002229b70>
```

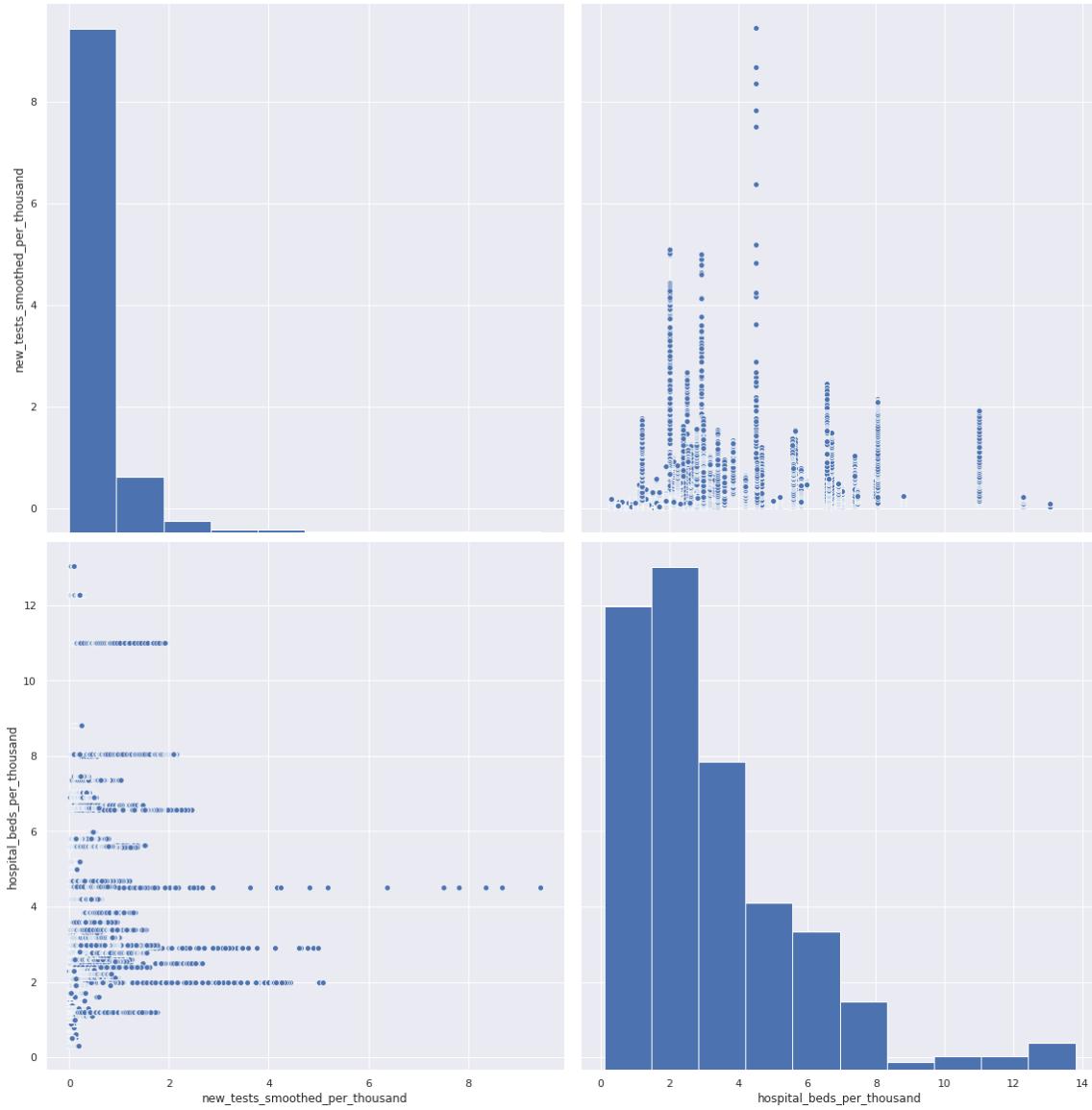


In [14]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "hospital_beds_per_thousand"], height=8)
```

Out[14]:

```
<seaborn.axisgrid.PairGrid at 0x7f10022292e8>
```

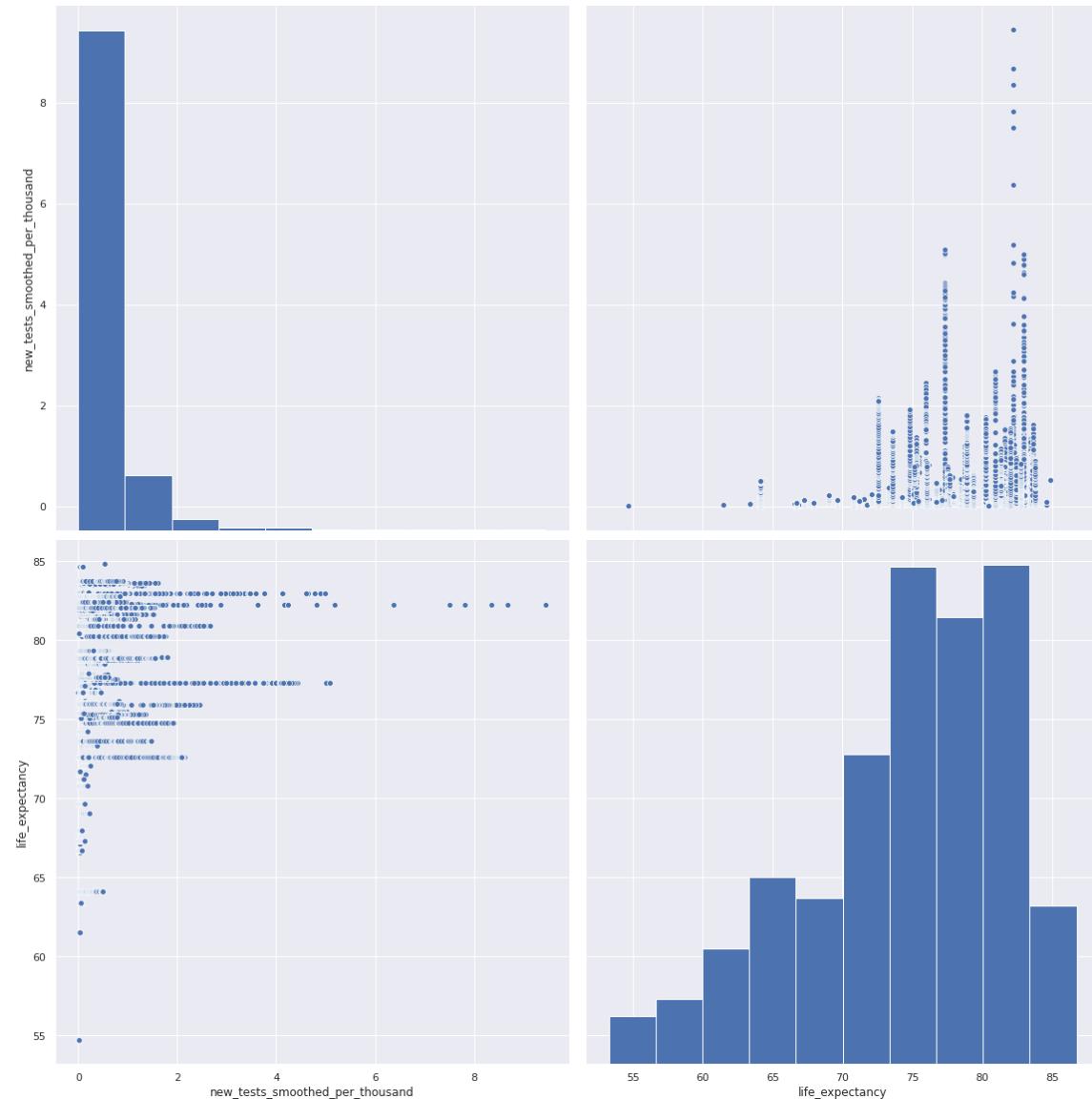


In [15]:

```
sns.pairplot(features, vars=["new_tests_smoothed_per_thousand", "life_expectancy"], height=8)
```

Out[15]:

```
<seaborn.axisgrid.PairGrid at 0x7f1001ecc780>
```

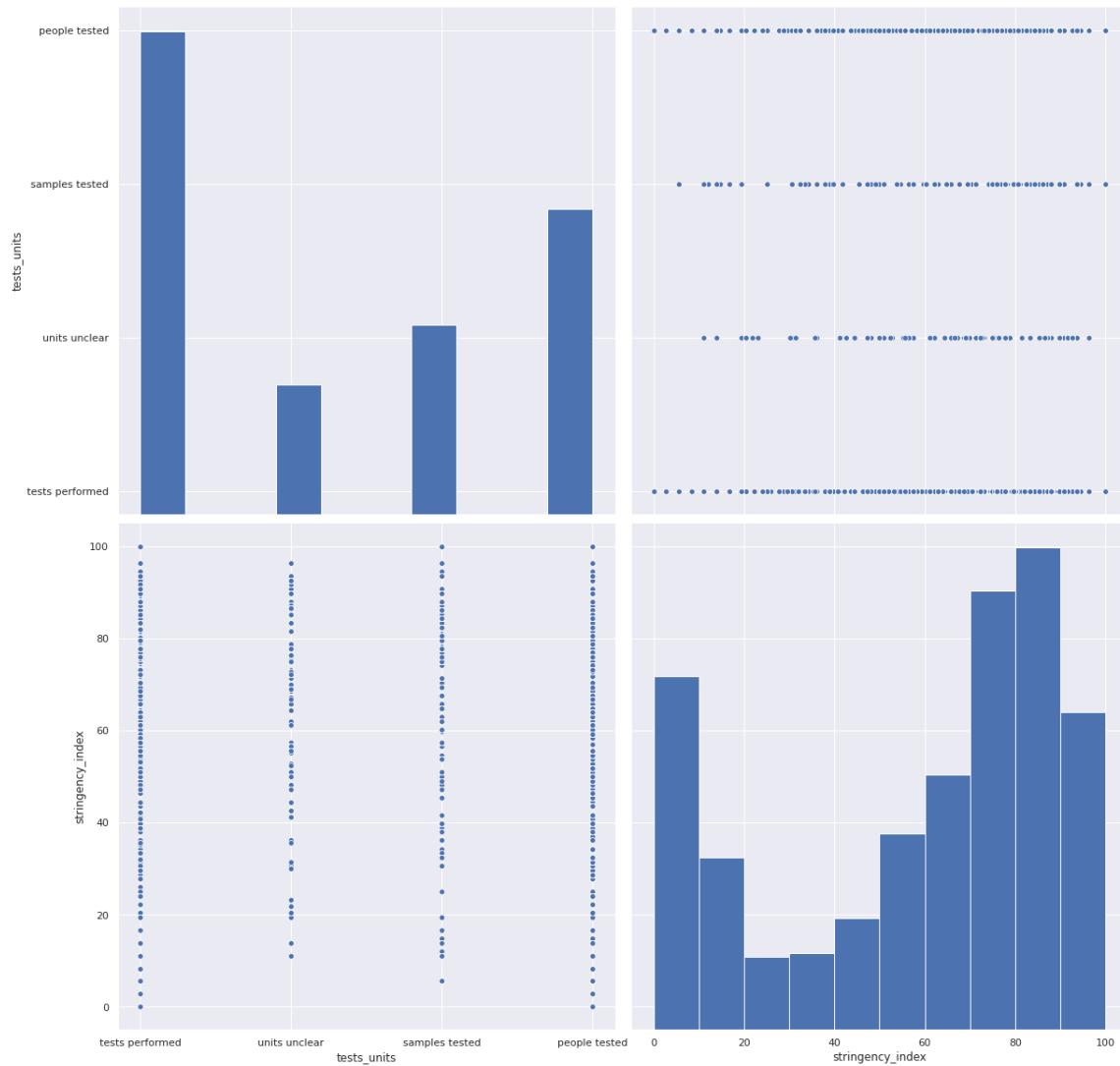


In [16]:

```
sns.pairplot(features, vars=["tests_units", "stringency_index"], height=8)
```

Out[16]:

```
<seaborn.axisgrid.PairGrid at 0x7f1001c25400>
```

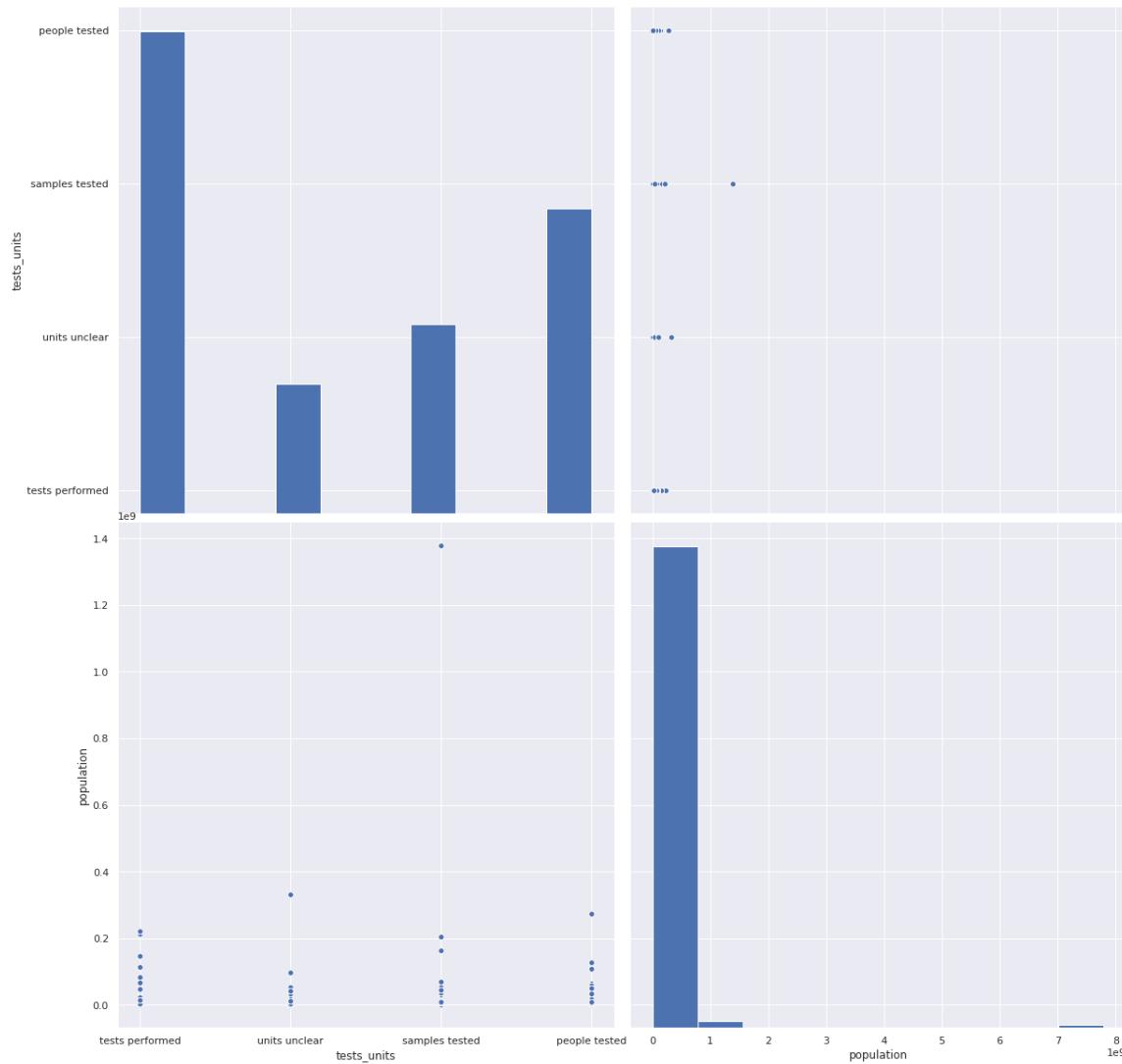


In [17]:

```
sns.pairplot(features, vars=["tests_units", "population"], height=8)
```

Out[17]:

```
<seaborn.axisgrid.PairGrid at 0x7f1001a00f60>
```

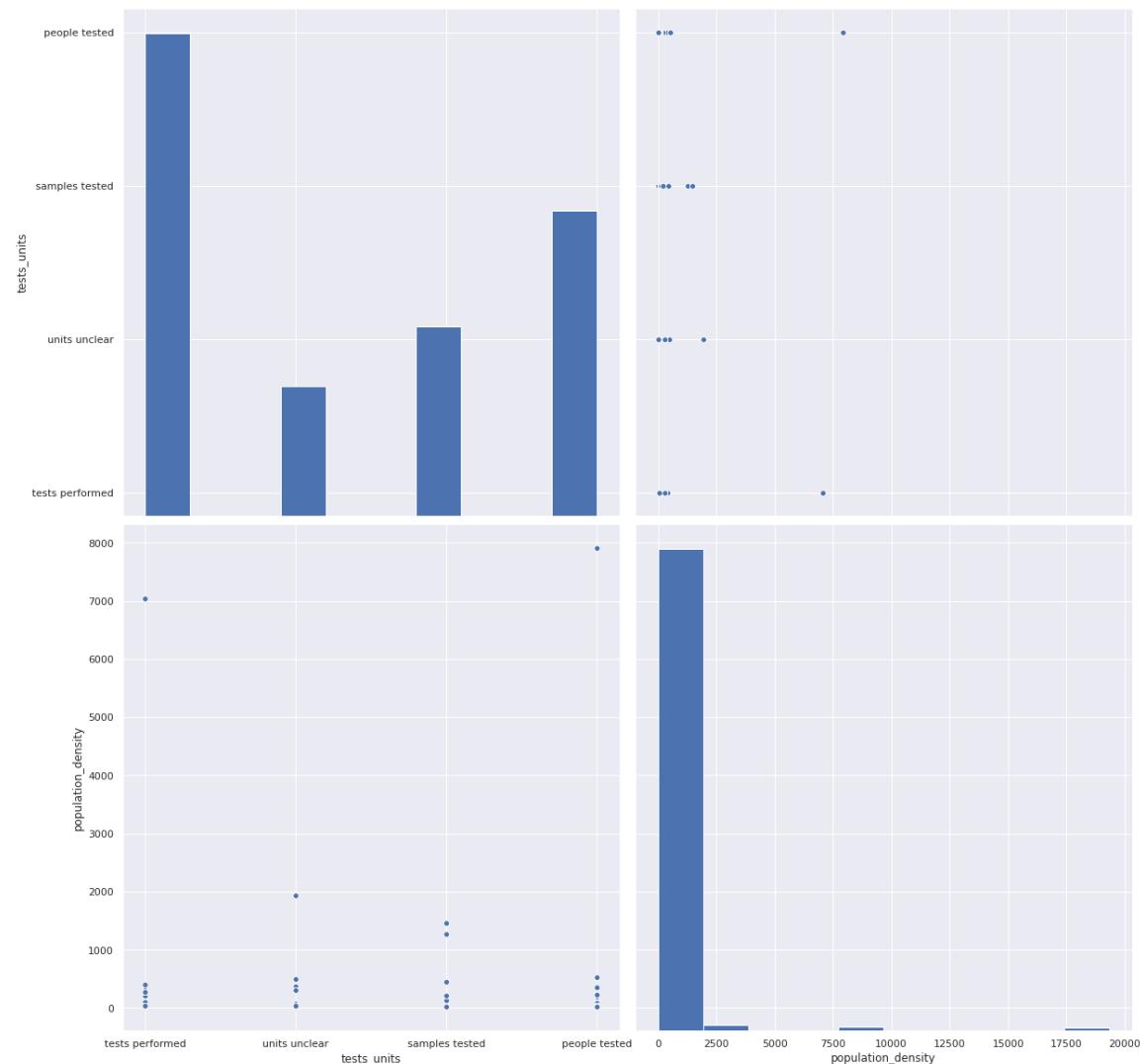


In [18]:

```
sns.pairplot(features, vars=["tests_units", "population_density"], height=8)
```

Out[18]:

```
<seaborn.axisgrid.PairGrid at 0x7f100197dda0>
```

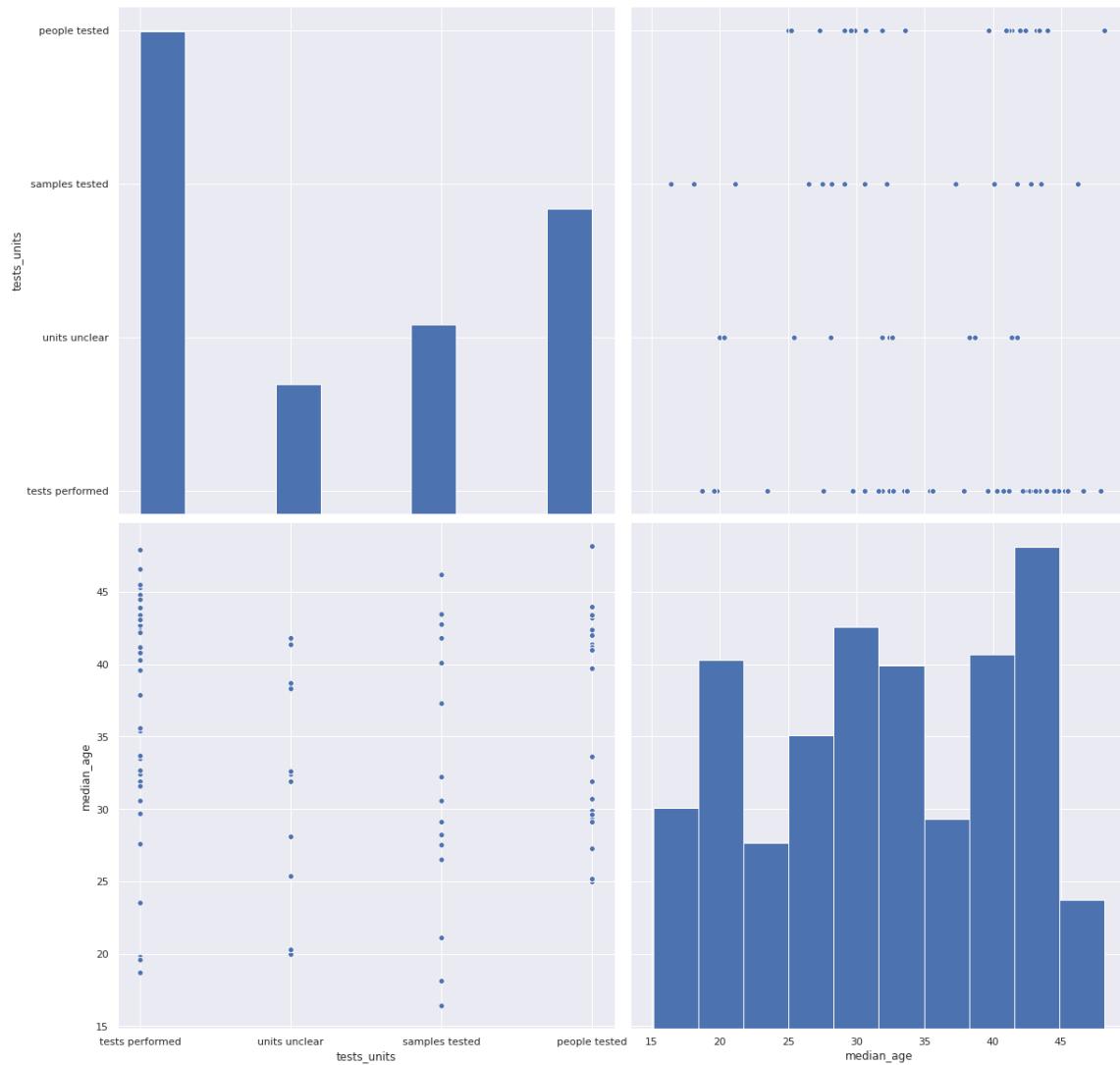


In [19]:

```
sns.pairplot(features, vars=["tests_units", "median_age"], height=8)
```

Out[19]:

```
<seaborn.axisgrid.PairGrid at 0x7f10016fd588>
```

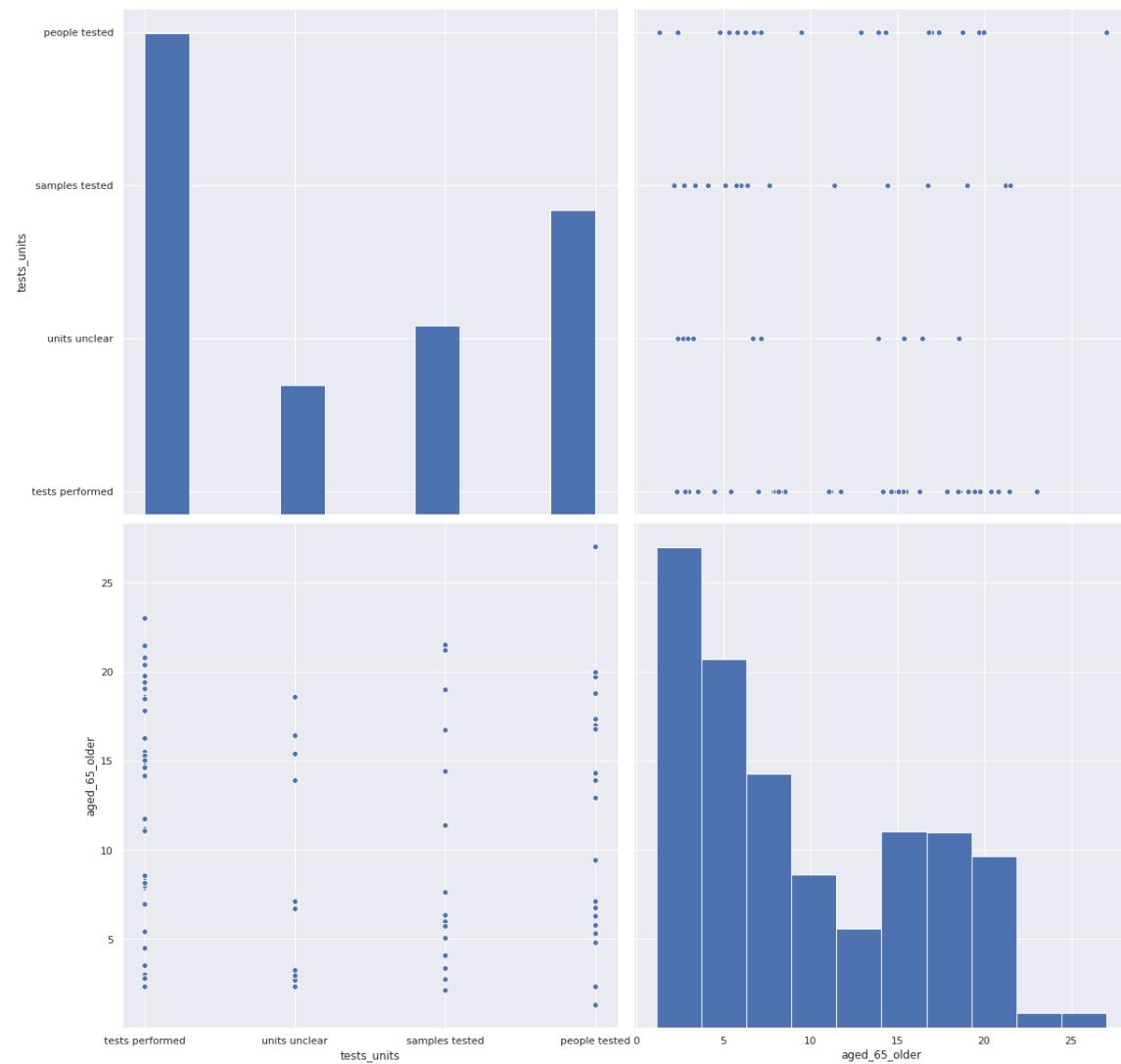


In [20]:

```
sns.pairplot(features, vars=["tests_units", "aged_65_older"], height=8)
```

Out[20]:

```
<seaborn.axisgrid.PairGrid at 0x7f1001464860>
```

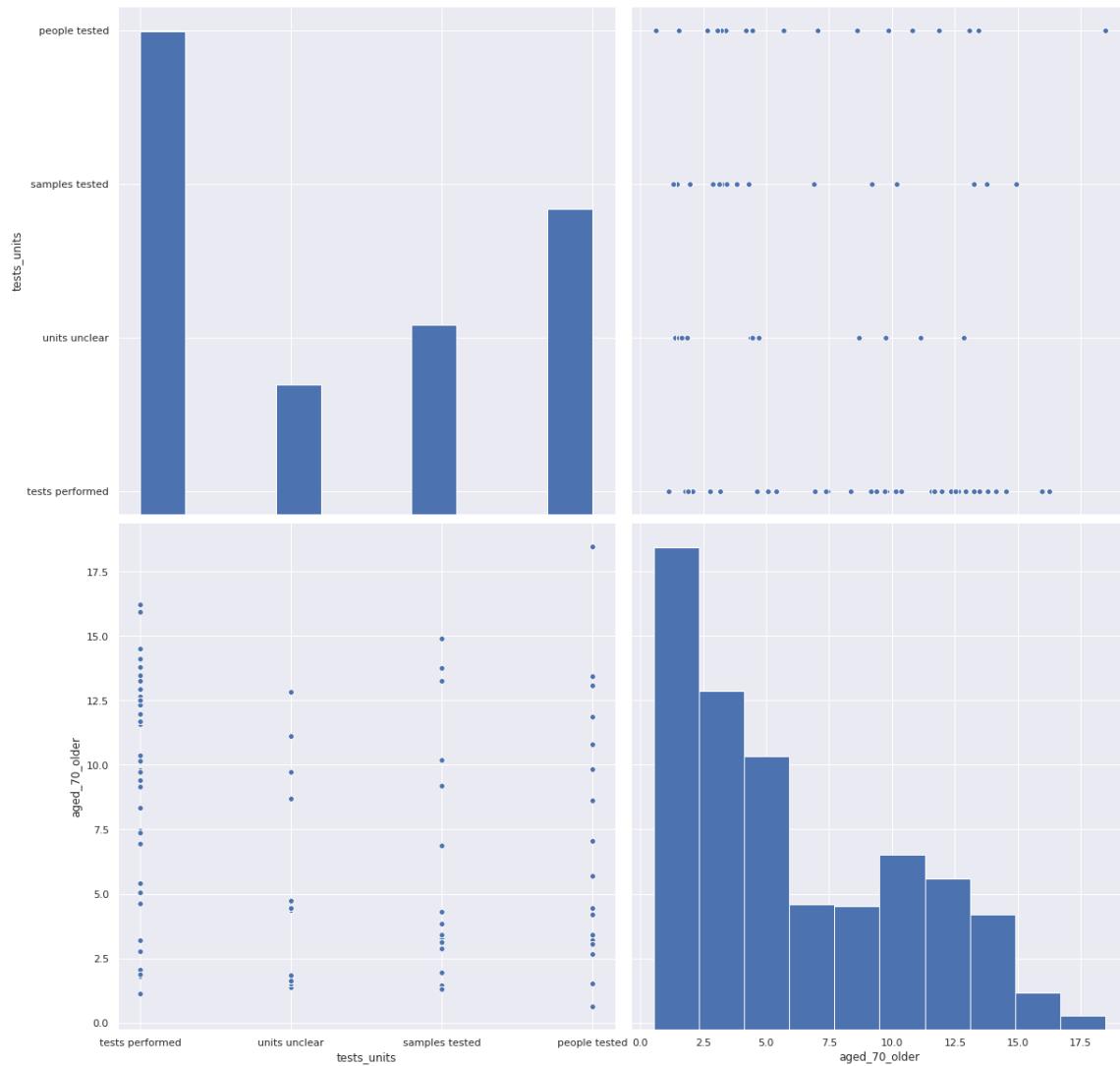


In [21]:

```
sns.pairplot(features, vars=["tests_units", "aged_70_older"], height=8)
```

Out[21]:

```
<seaborn.axisgrid.PairGrid at 0x7f1001d3b278>
```

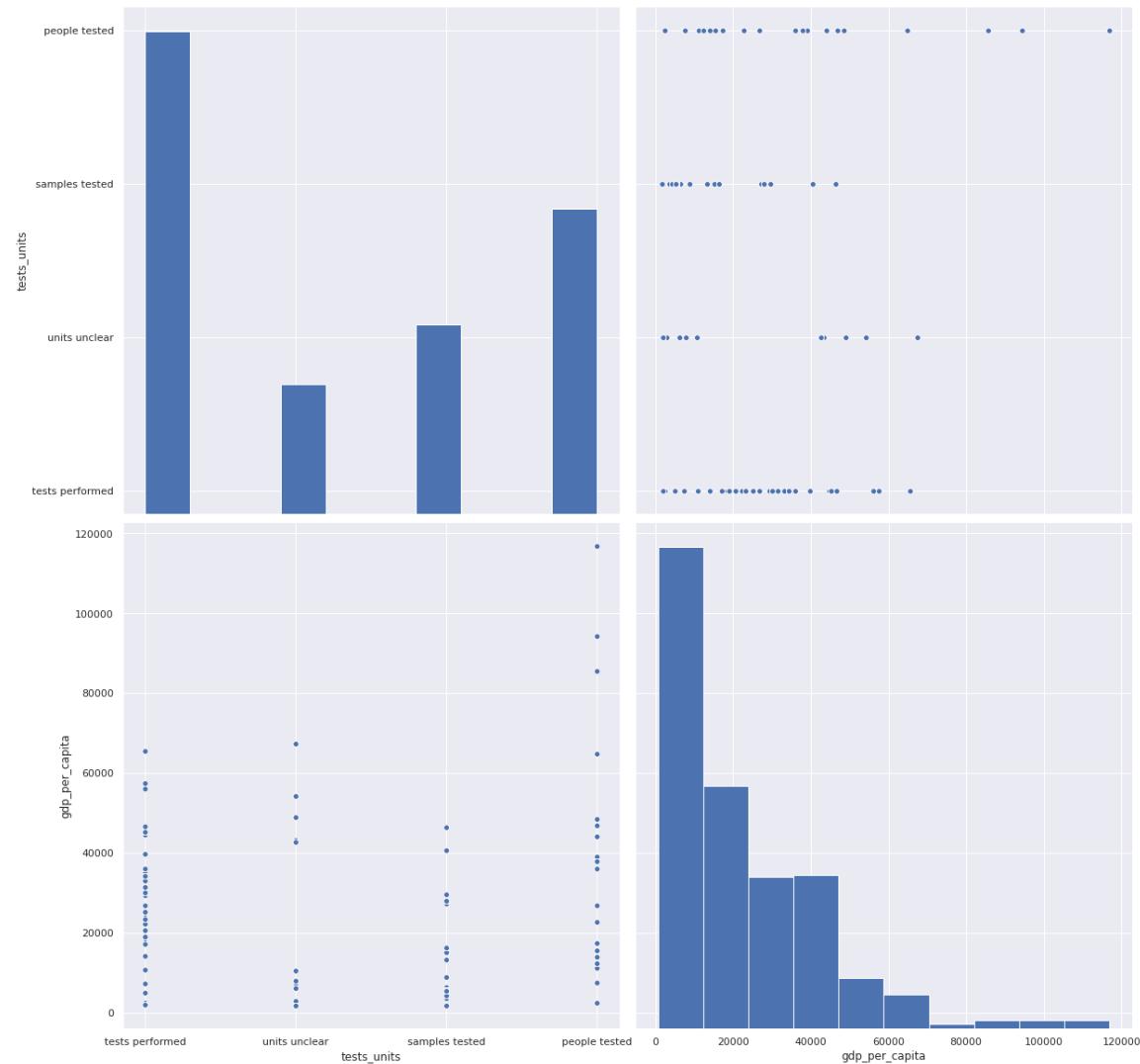


In [22]:

```
sns.pairplot(features, vars=["tests_units", "gdp_per_capita"], height=8)
```

Out[22]:

```
<seaborn.axisgrid.PairGrid at 0x7f10010410b8>
```

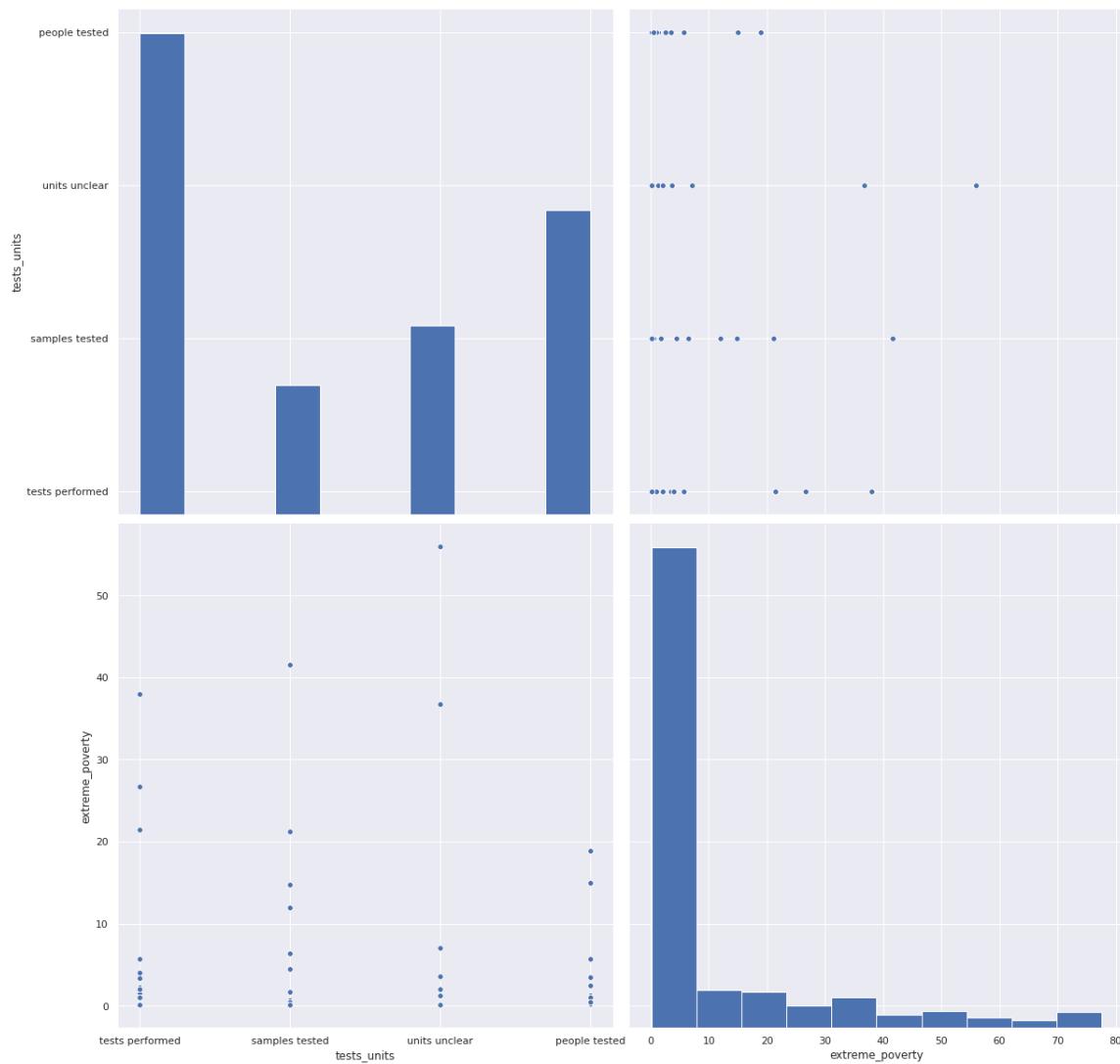


In [23]:

```
sns.pairplot(features, vars=["tests_units", "extreme_poverty"], height=8)
```

Out[23]:

```
<seaborn.axisgrid.PairGrid at 0x7f1000e91ac8>
```

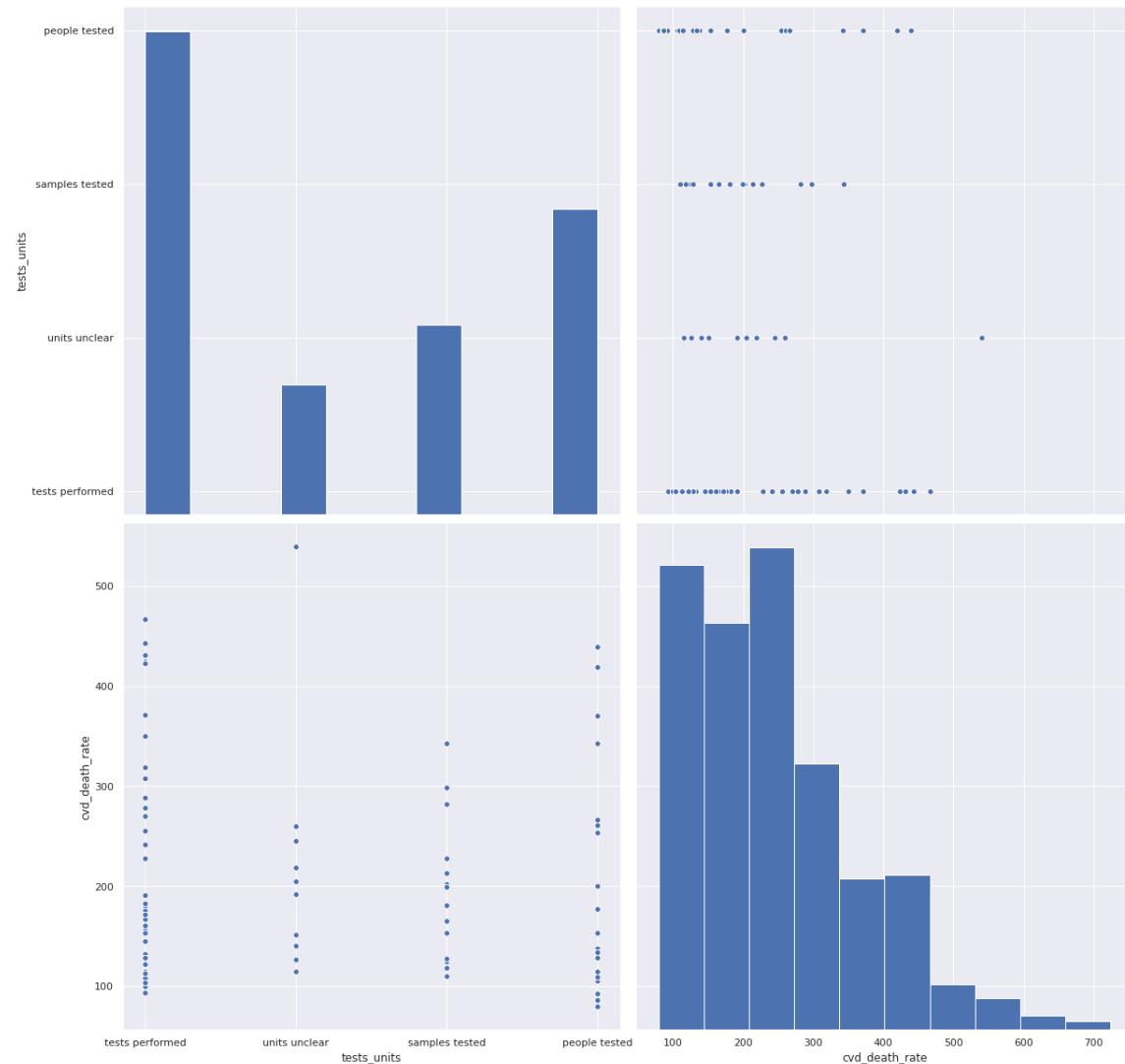


In [24]:

```
sns.pairplot(features, vars=["tests_units", "cvd_death_rate"], height=8)
```

Out[24]:

```
<seaborn.axisgrid.PairGrid at 0x7f1000cfce48>
```

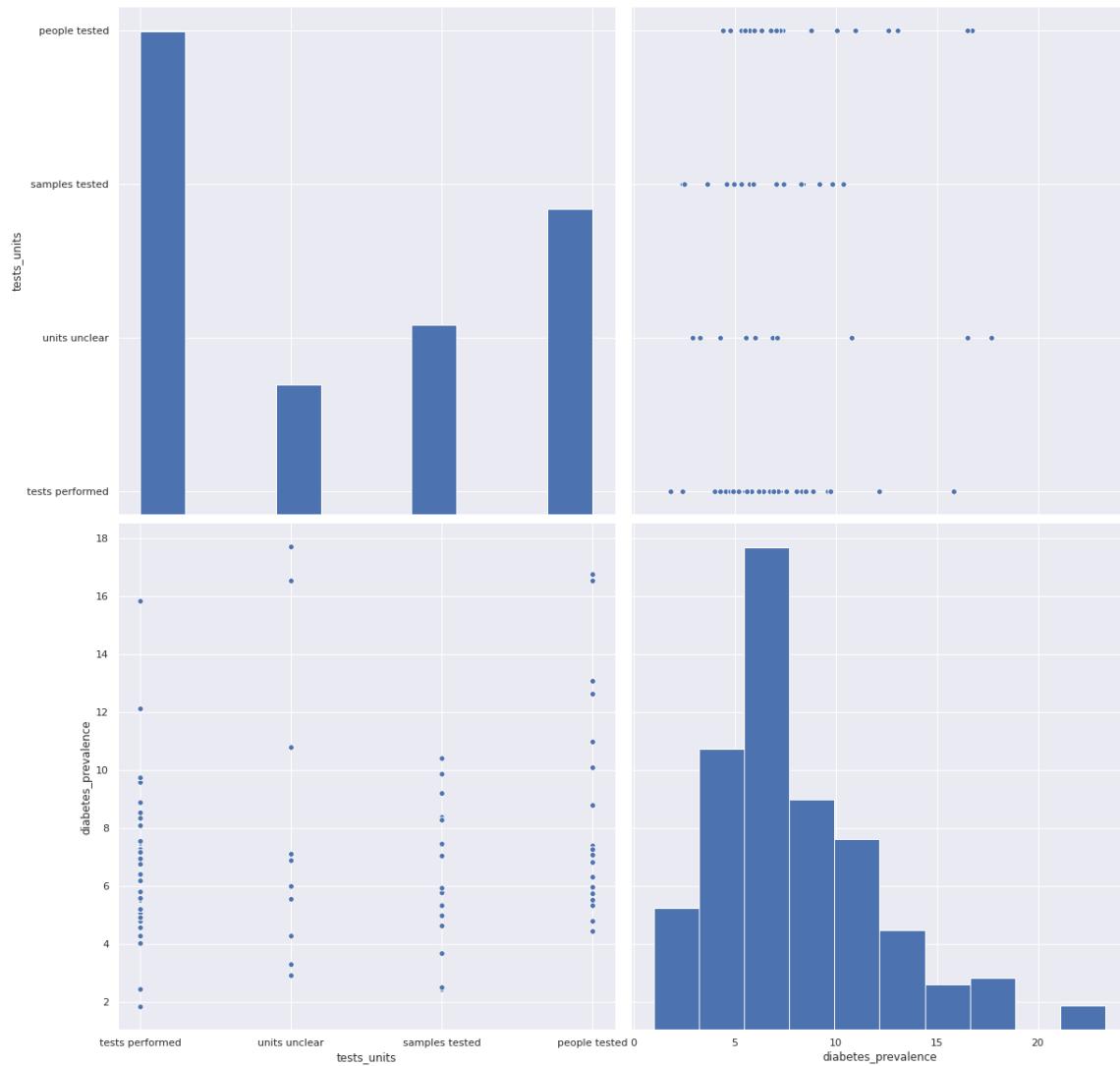


In [25]:

```
sns.pairplot(features, vars=["tests_units", "diabetes_prevalence"], height=8)
```

Out[25]:

```
<seaborn.axisgrid.PairGrid at 0x7f1000c976d8>
```

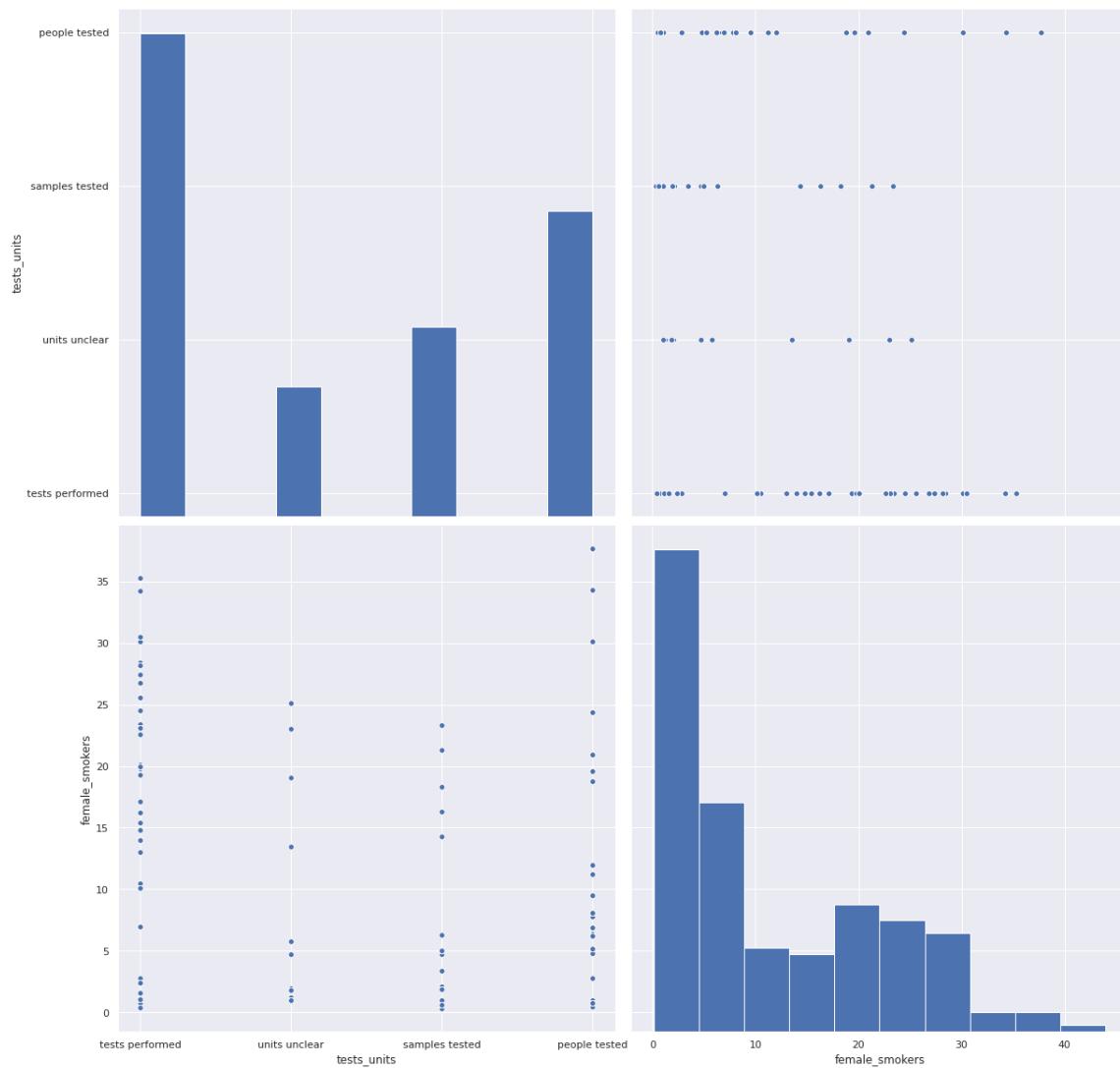


In [26]:

```
sns.pairplot(features, vars=["tests_units", "female_smokers"], height=8)
```

Out[26]:

```
<seaborn.axisgrid.PairGrid at 0x7f1000880c50>
```

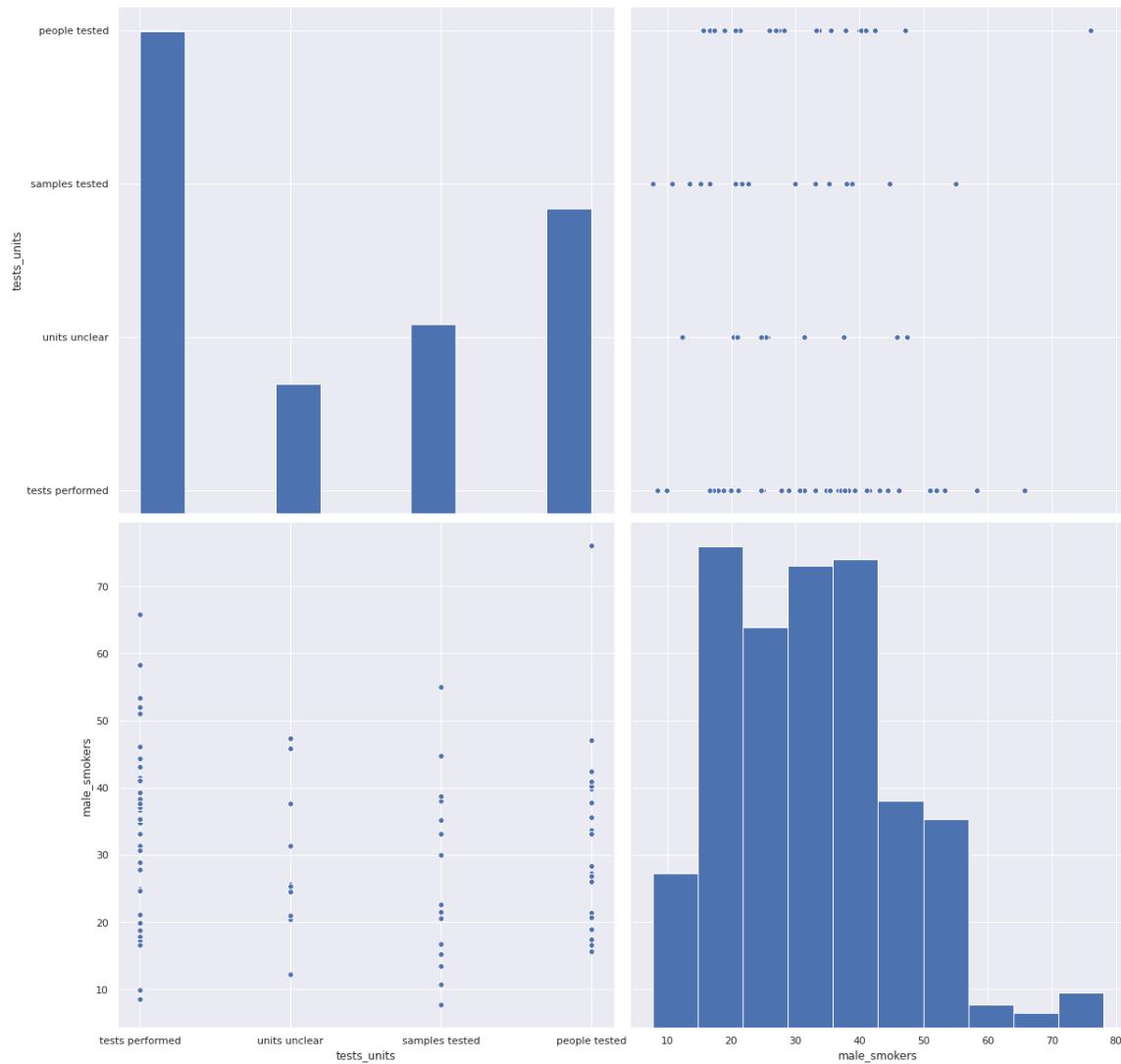


In [27]:

```
sns.pairplot(features, vars=["tests_units", "male_smokers"], height=8)
```

Out[27]:

```
<seaborn.axisgrid.PairGrid at 0x7f10017e1b38>
```

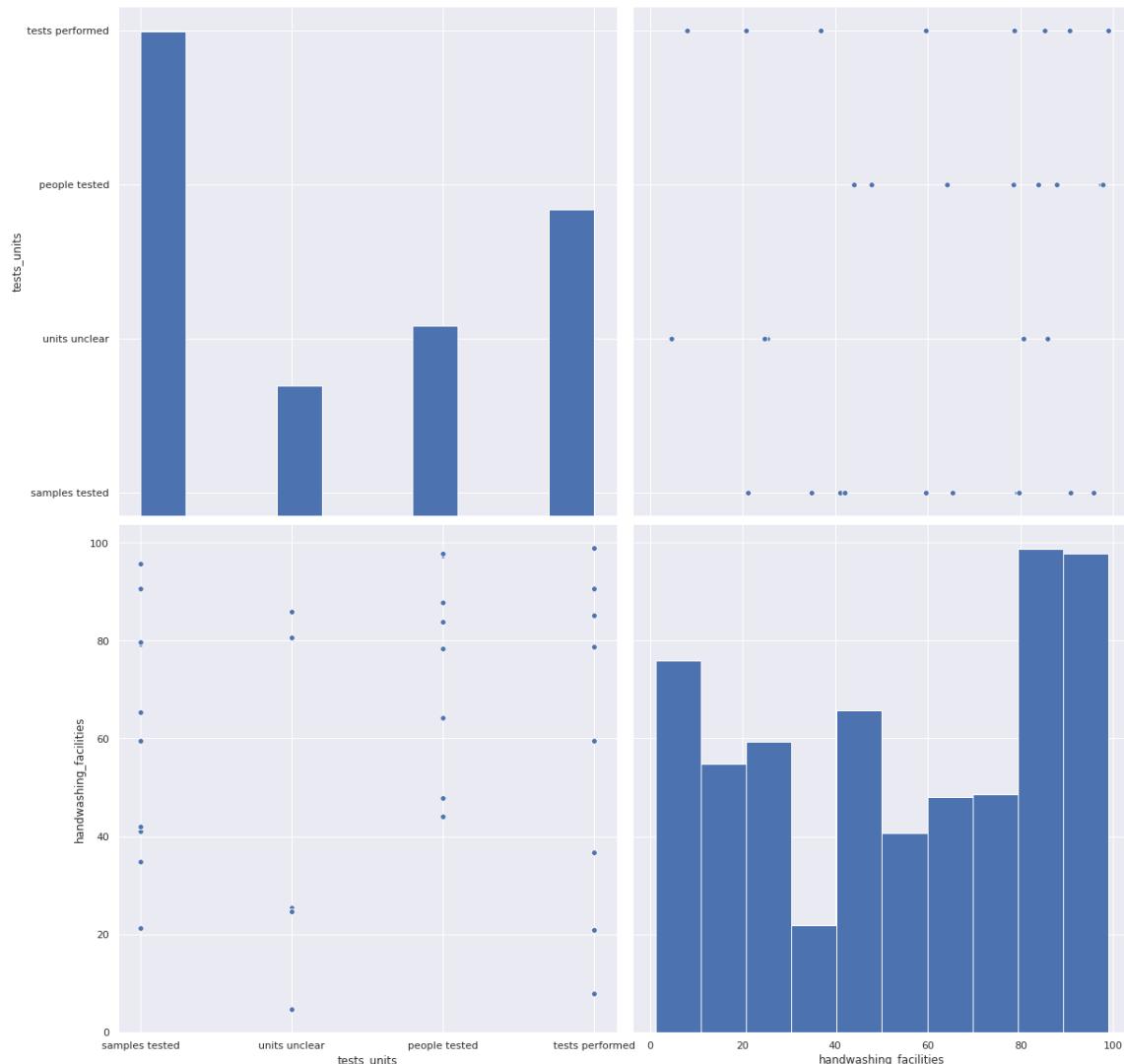


In [28]:

```
sns.pairplot(features, vars=["tests_units", "handwashing_facilities"], height=8)
```

Out[28]:

```
<seaborn.axisgrid.PairGrid at 0x7f1000524ef0>
```

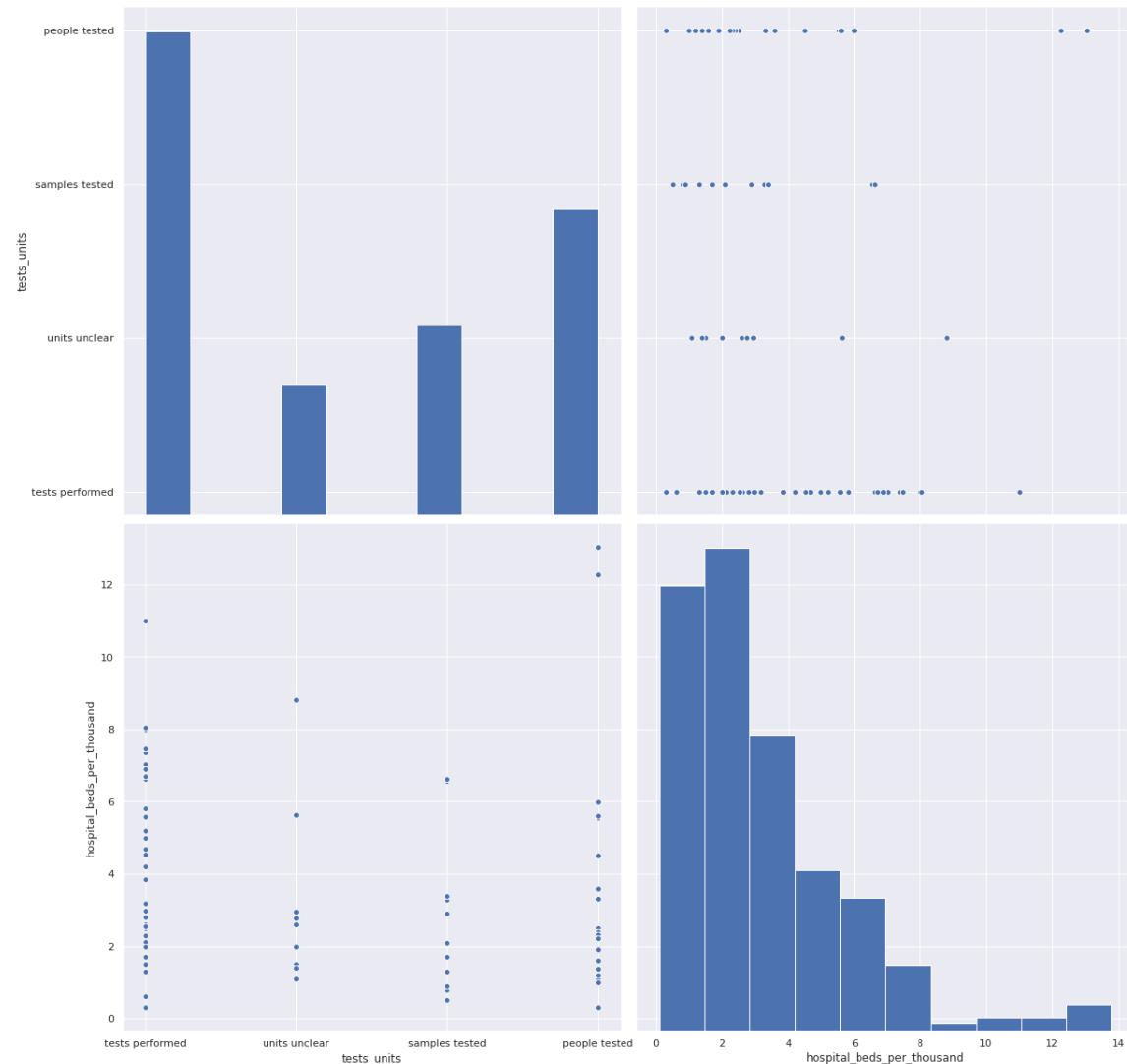


In [29]:

```
sns.pairplot(features, vars=["tests_units", "hospital_beds_per_thousand"], height=8)
```

Out[29]:

```
<seaborn.axisgrid.PairGrid at 0x7f10003182b0>
```

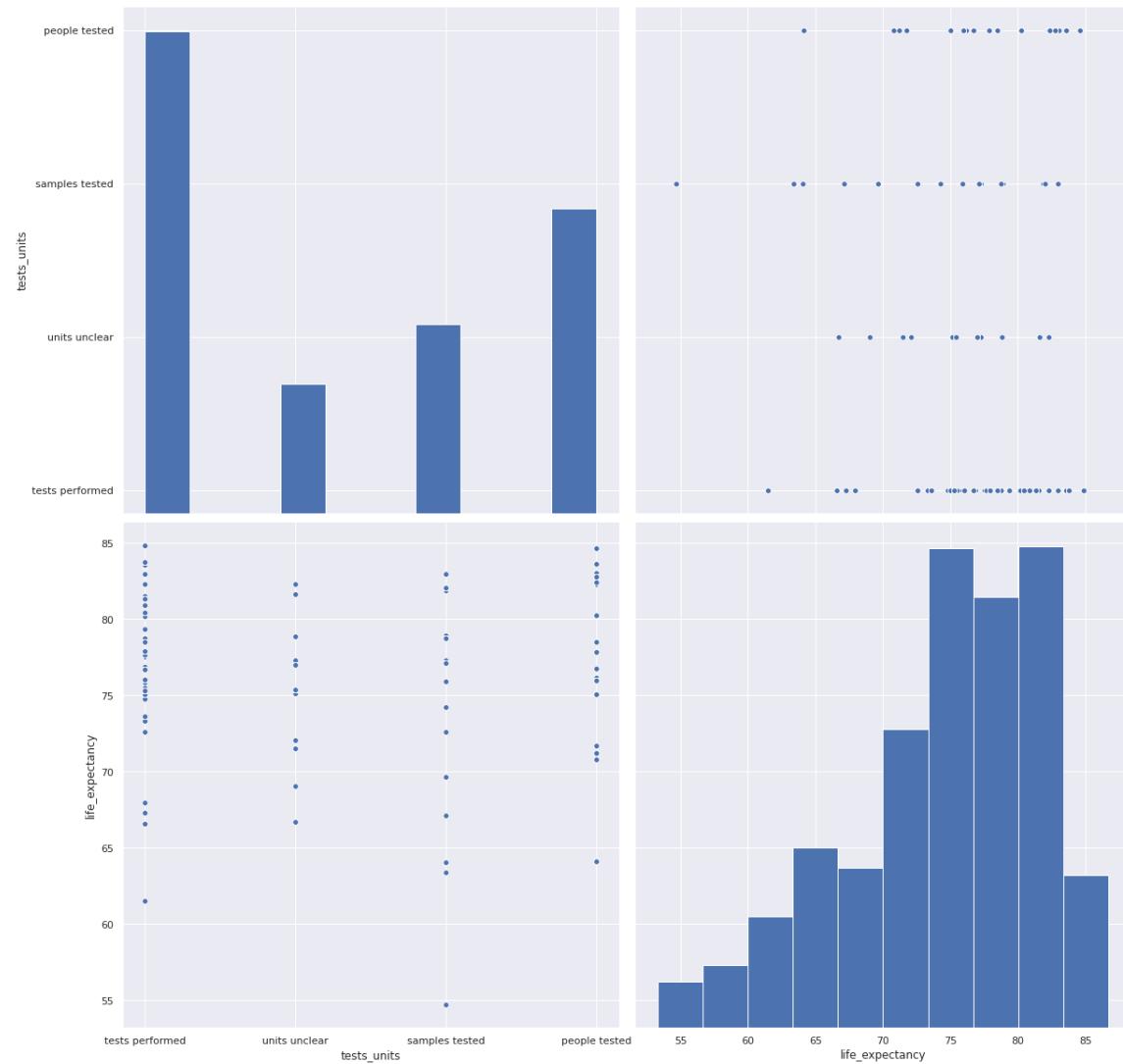


In [30]:

```
sns.pairplot(features, vars=["tests_units", "life_expectancy"], height=8)
```

Out[30]:

```
<seaborn.axisgrid.PairGrid at 0x7f1000130e10>
```

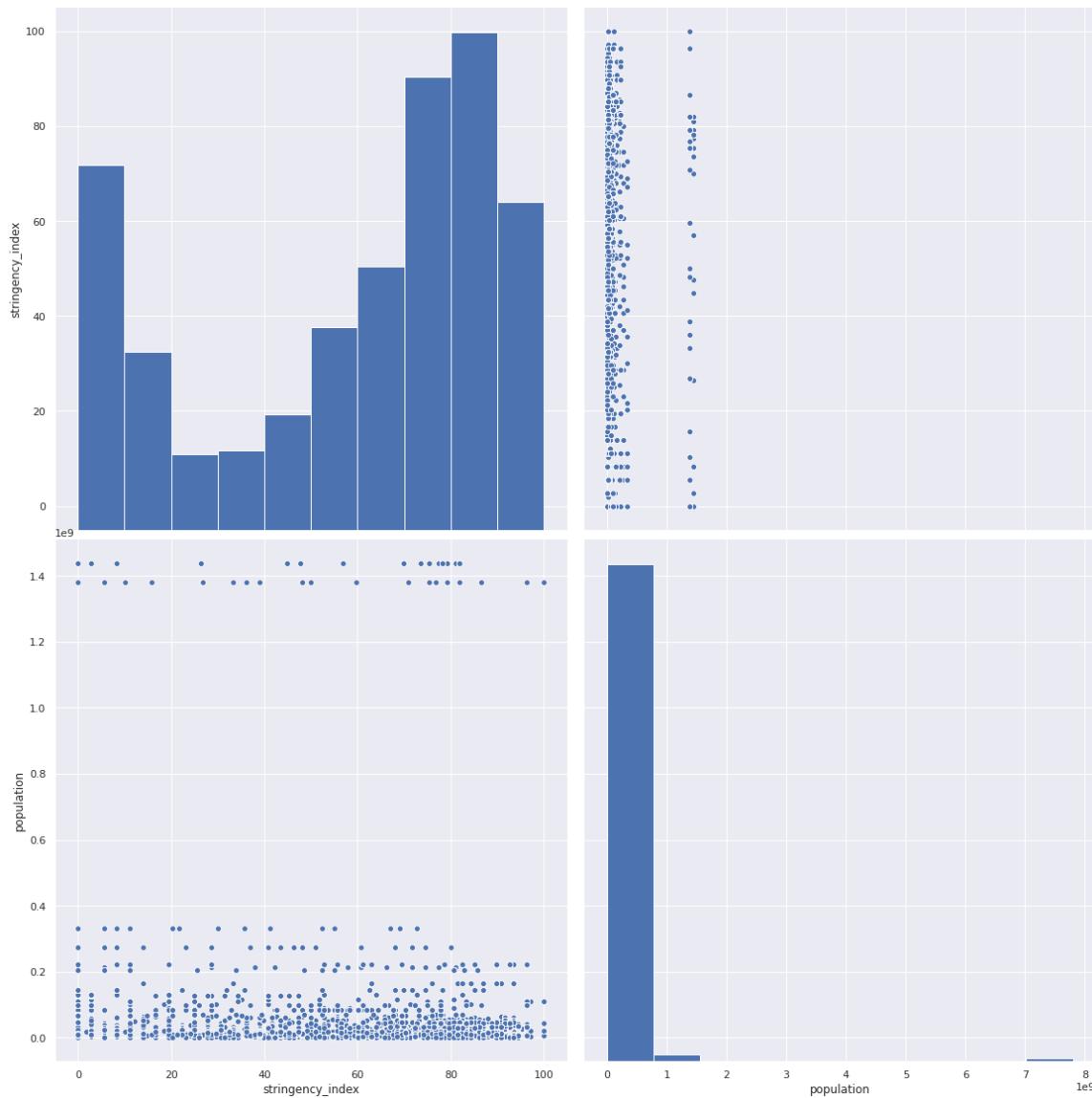


In [31]:

```
sns.pairplot(features, vars=["stringency_index", "population"], height=8)
```

Out[31]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fffffb4e48>
```

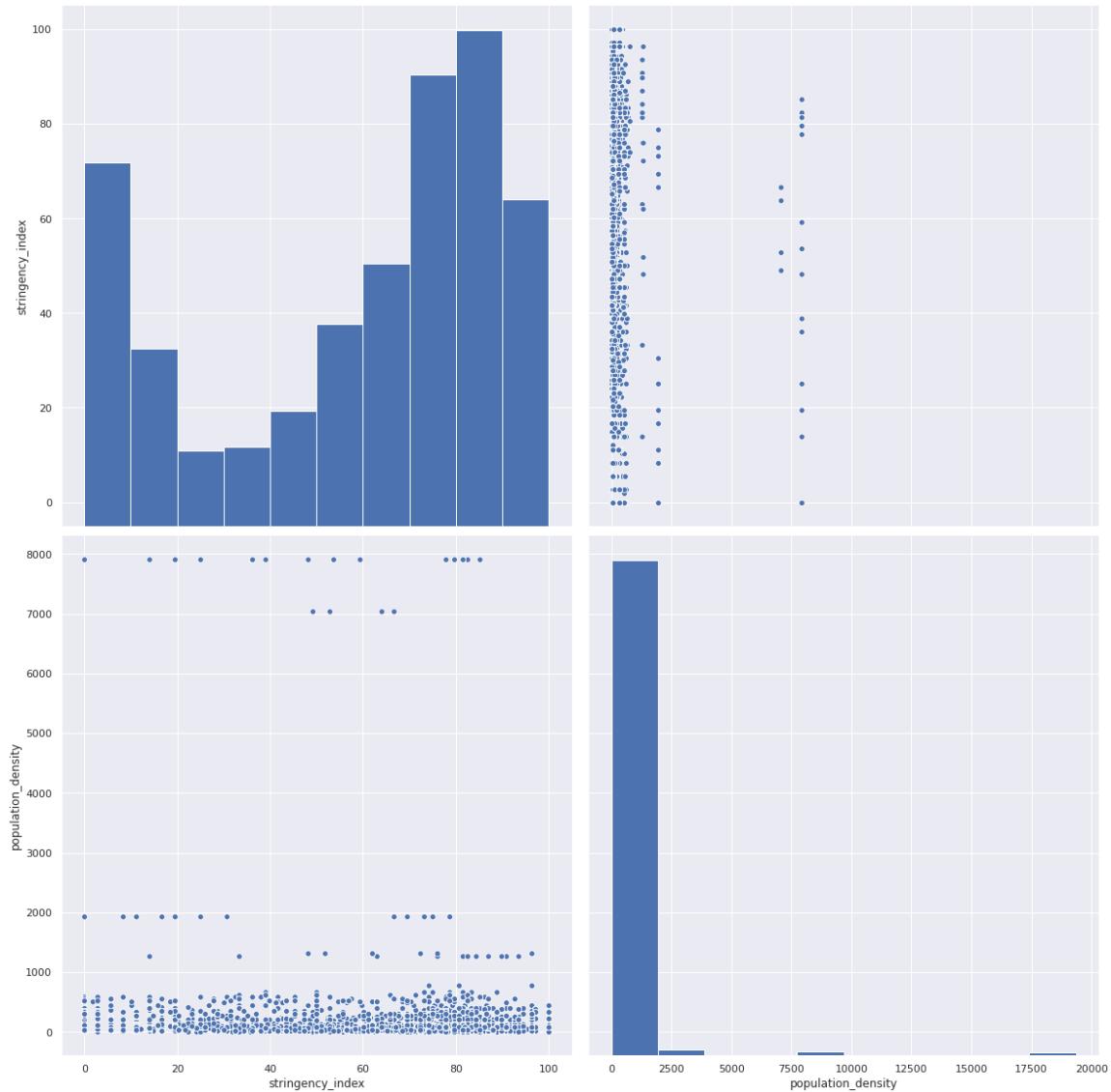


In [32]:

```
sns.pairplot(features, vars=["stringency_index", "population_density"], height=8)
```

Out[32]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffffd25cf8>
```

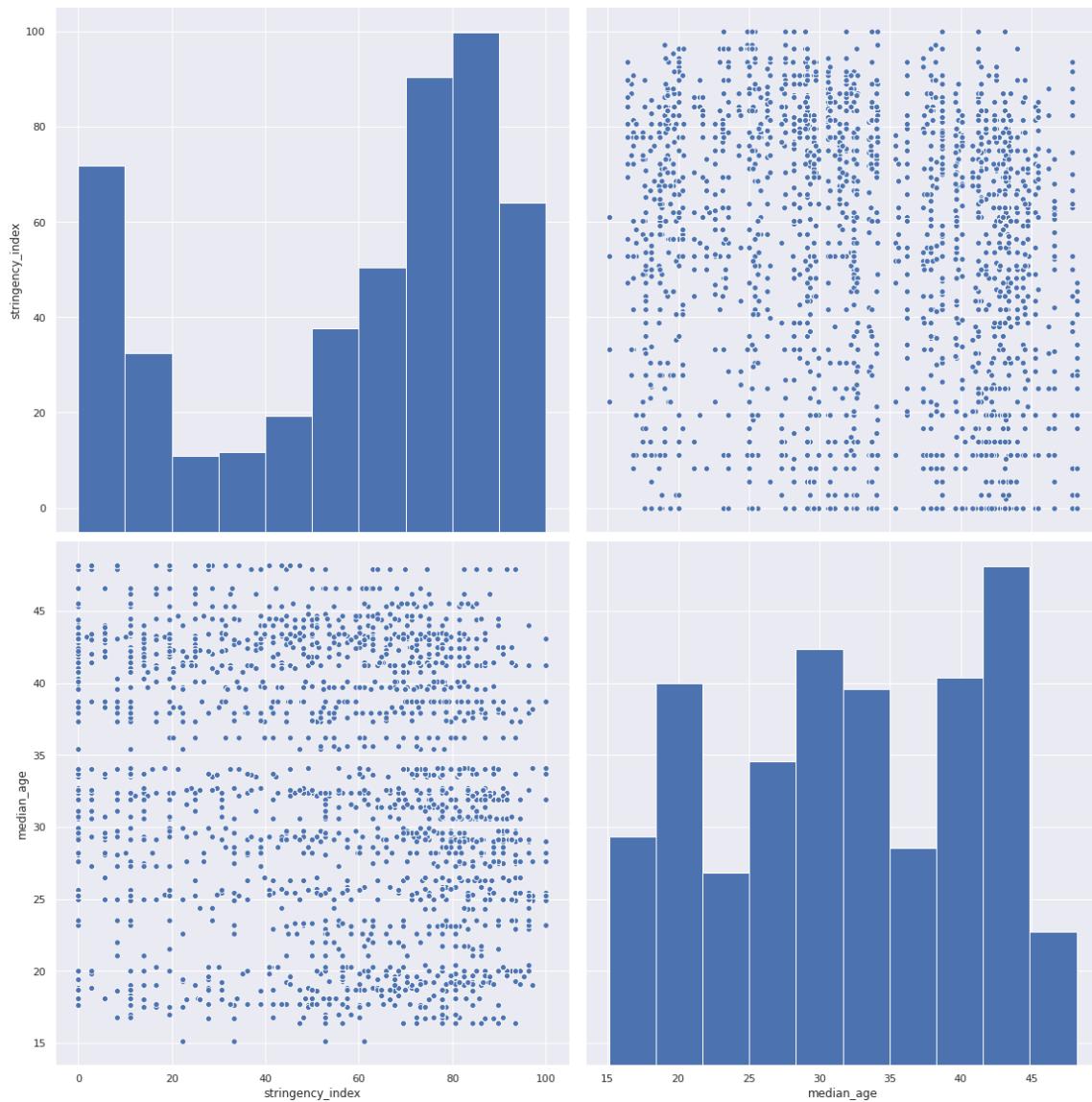


In [33]:

```
sns.pairplot(features, vars=["stringency_index", "median_age"], height=8)
```

Out[33]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fffc7c2e8>
```

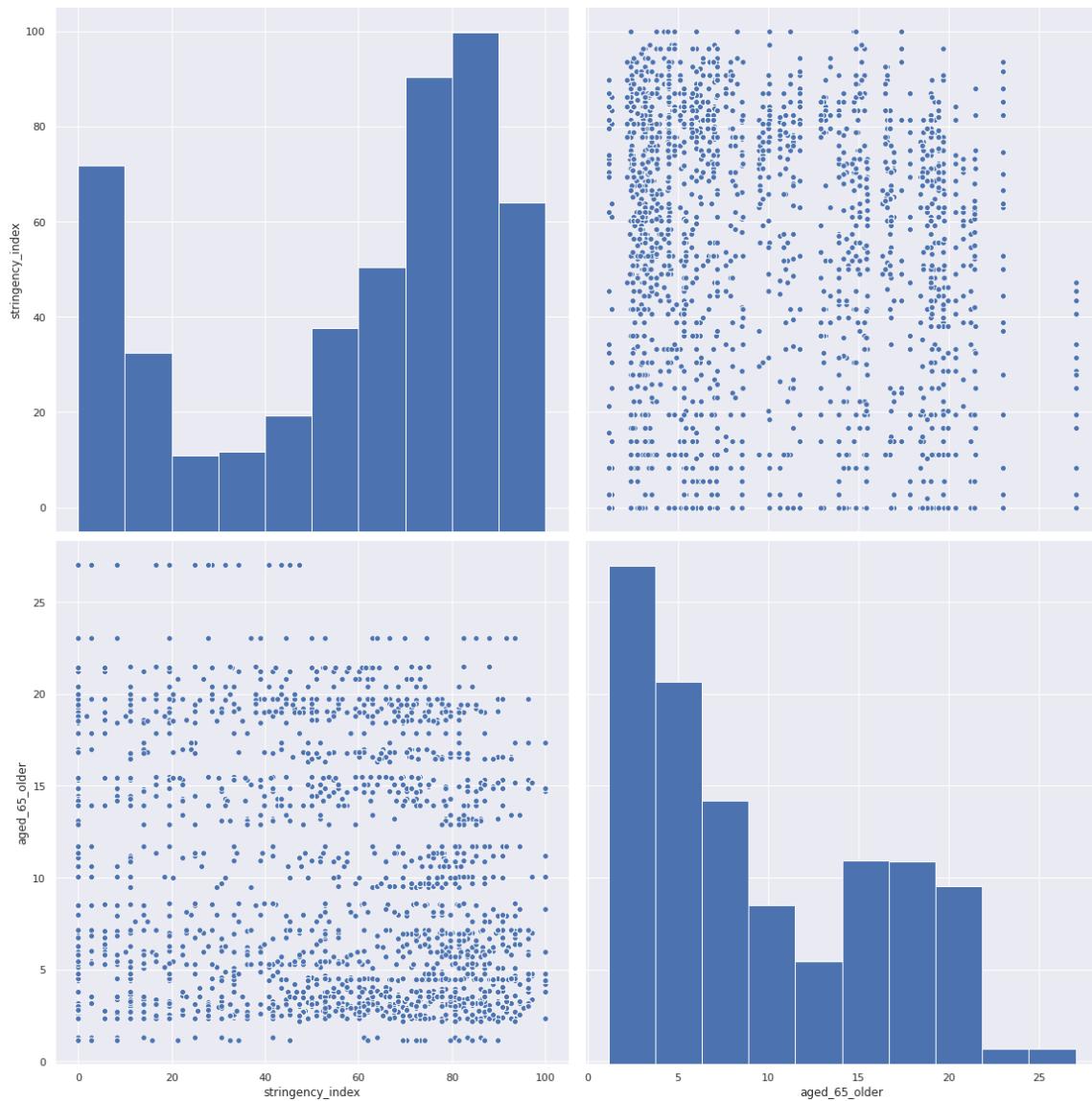


In [34]:

```
sns.pairplot(features, vars=["stringency_index", "aged_65_older"], height=8)
```

Out[34]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff9313c8>
```

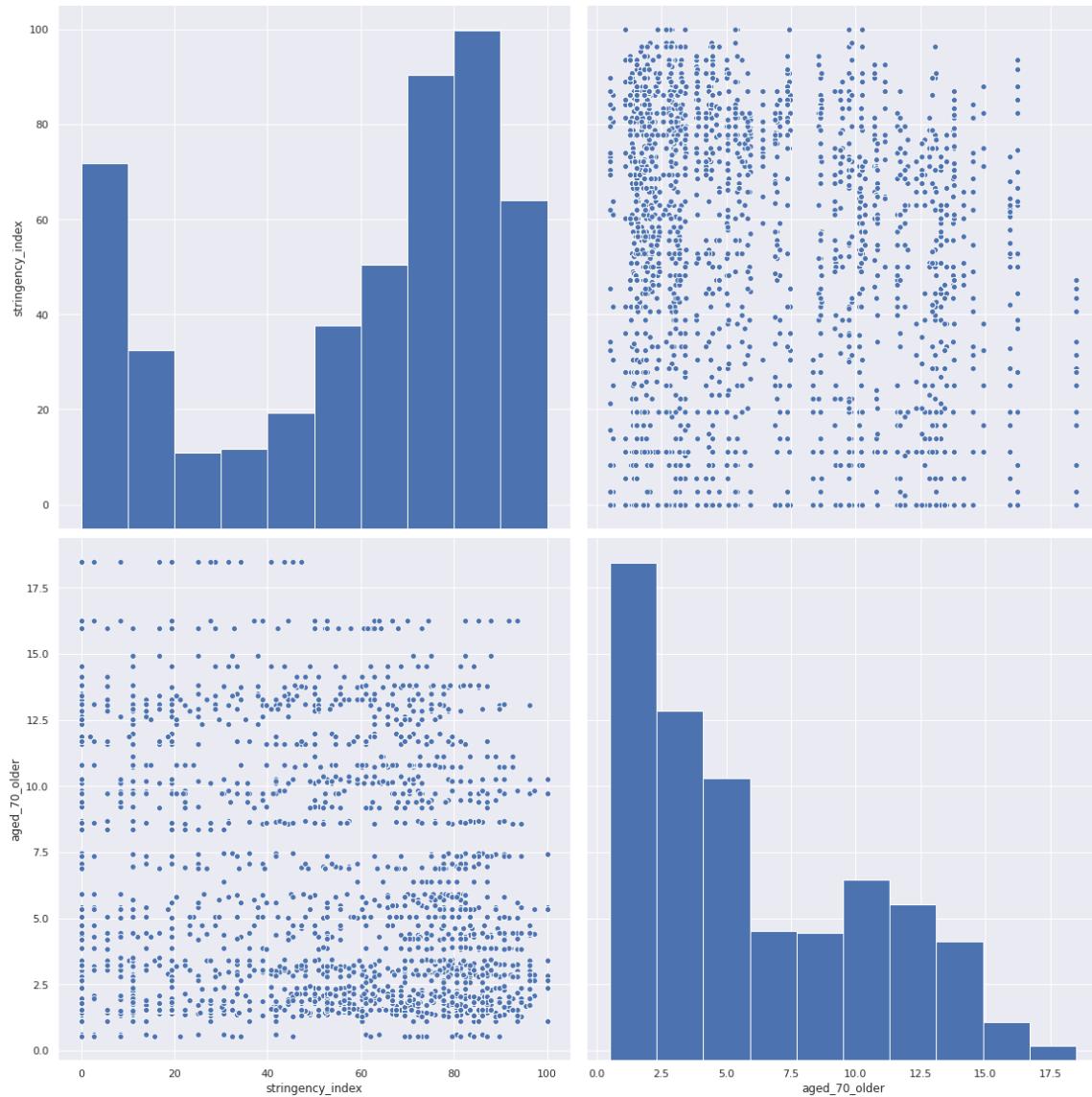


In [35]:

```
sns.pairplot(features, vars=["stringency_index", "aged_70_older"], height=8)
```

Out[35]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff81f198>
```

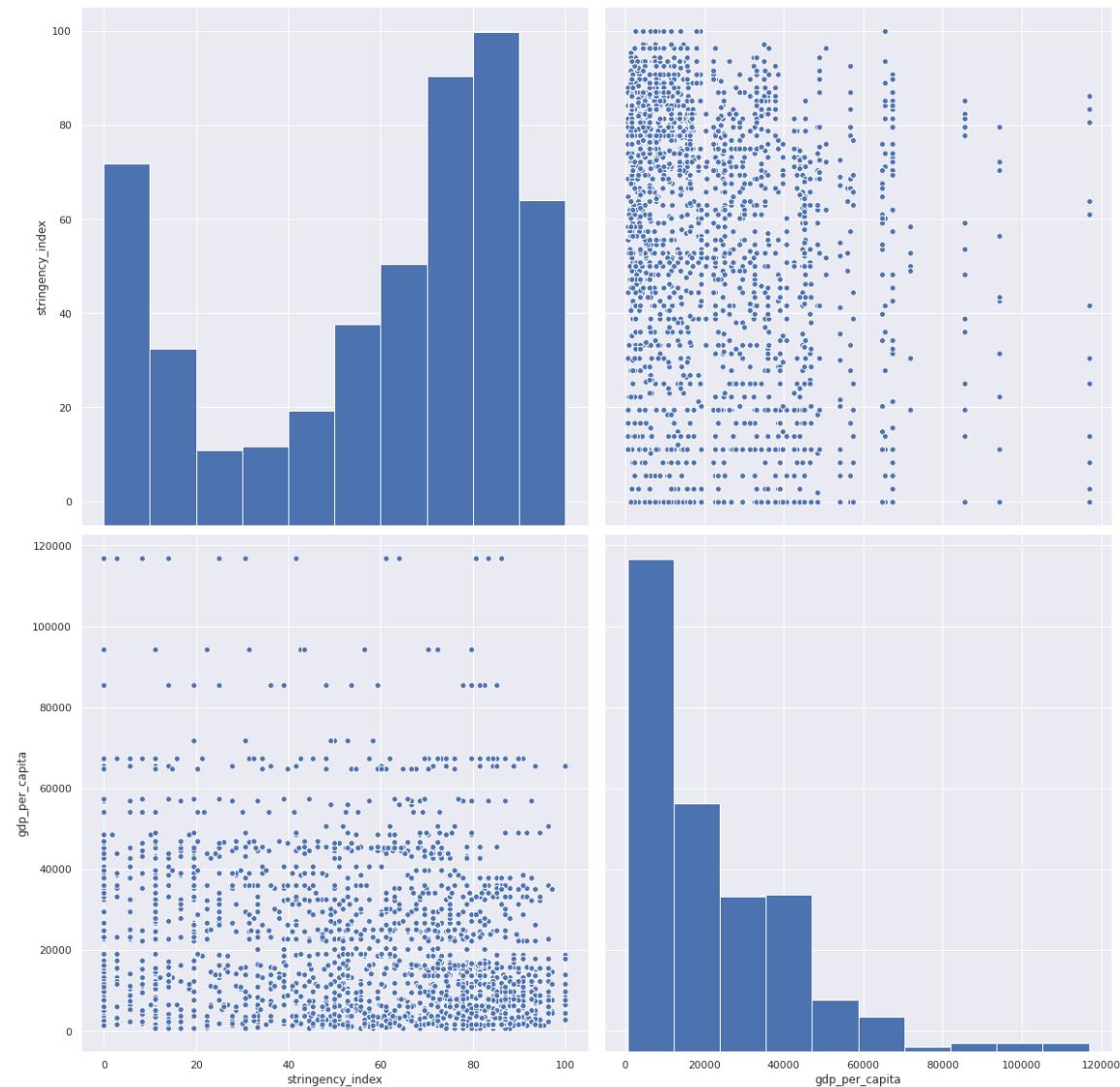


In [36]:

```
sns.pairplot(features, vars=["stringency_index", "gdp_per_capita"], height=8)
```

Out[36]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff59c438>
```

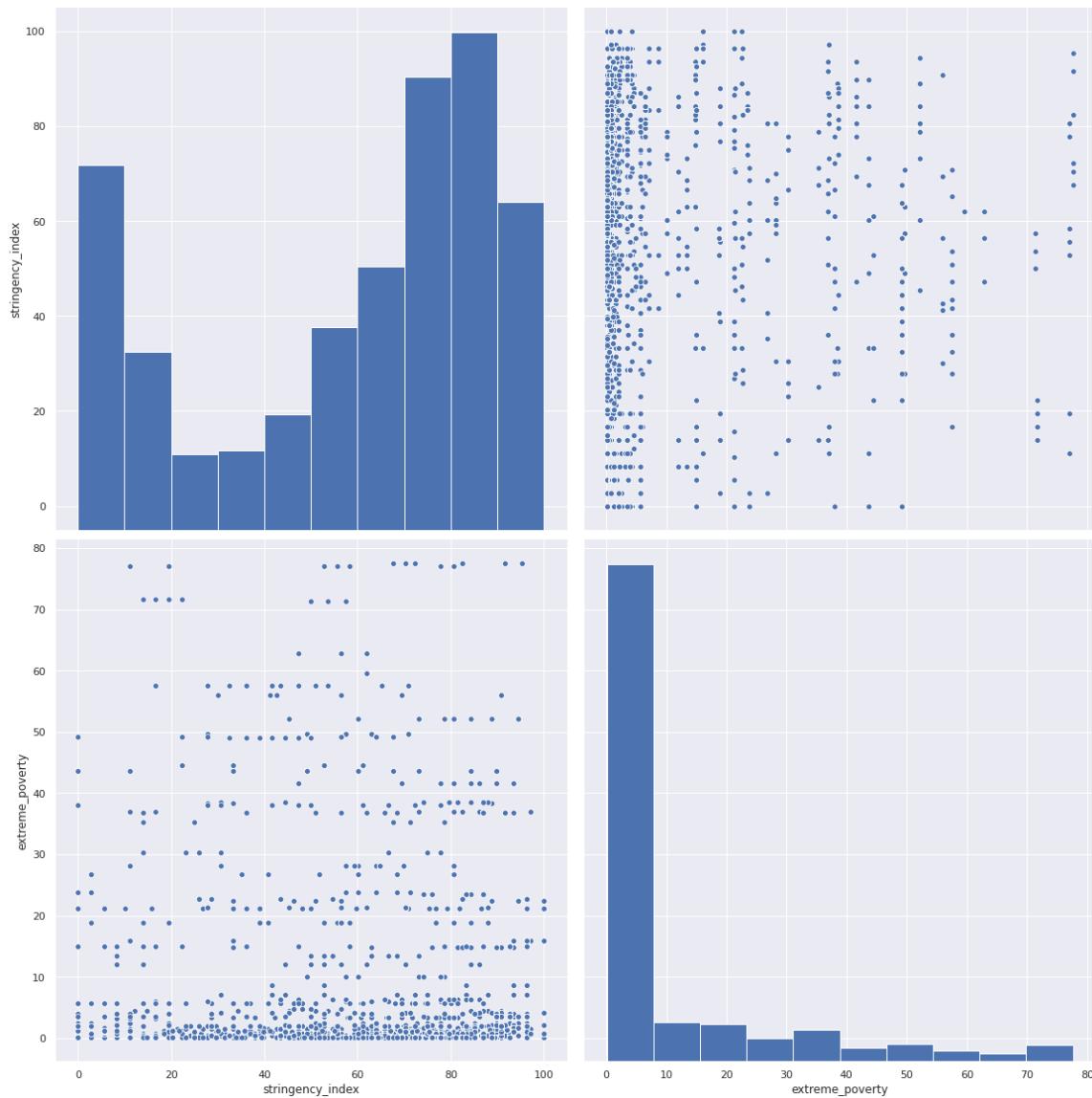


In [37]:

```
sns.pairplot(features, vars=["stringency_index", "extreme_poverty"], height=8)
```

Out[37]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff32a780>
```

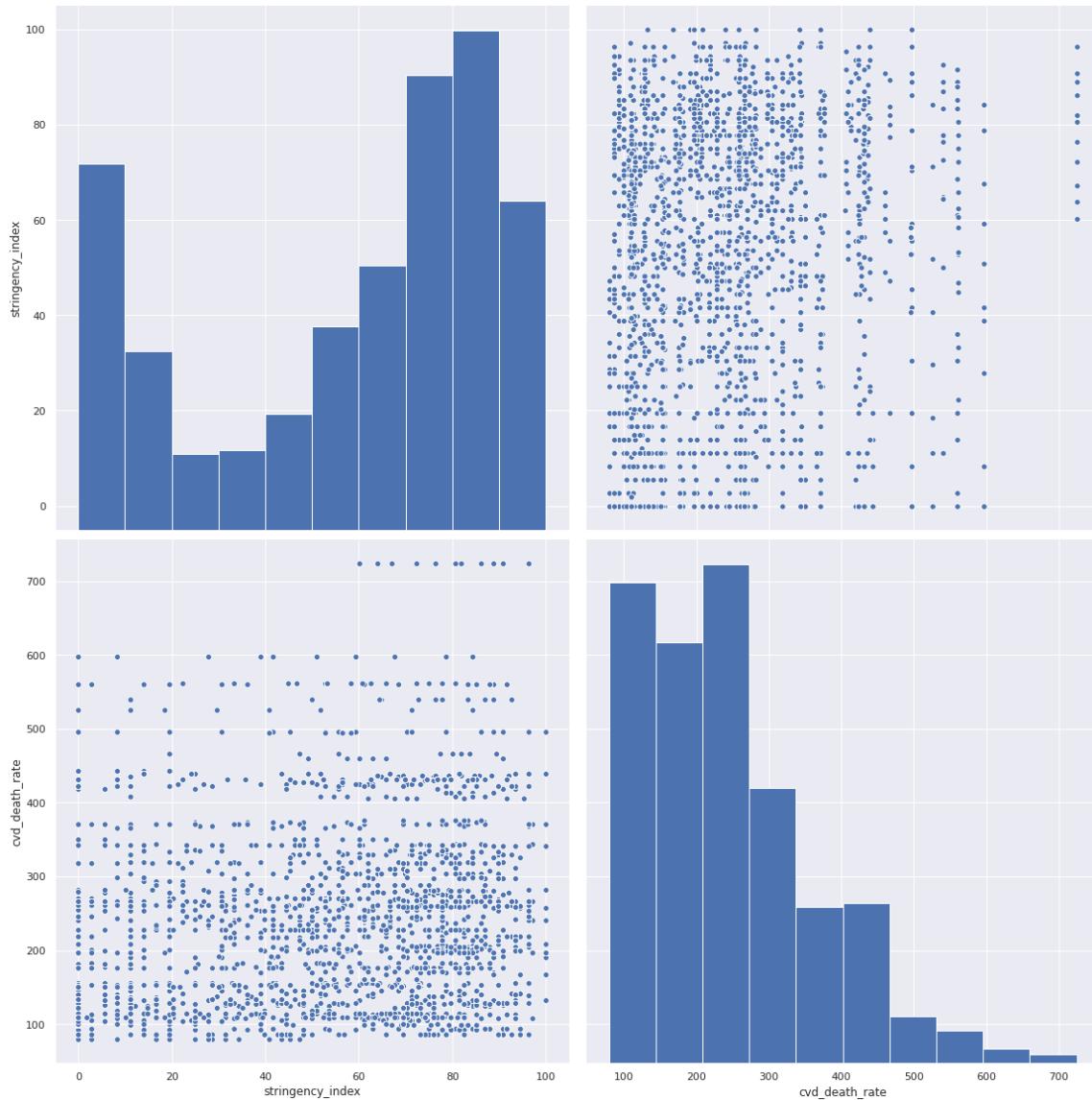


In [38]:

```
sns.pairplot(features, vars=["stringency_index", "cvd_death_rate"], height=8)
```

Out[38]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff13dc50>
```

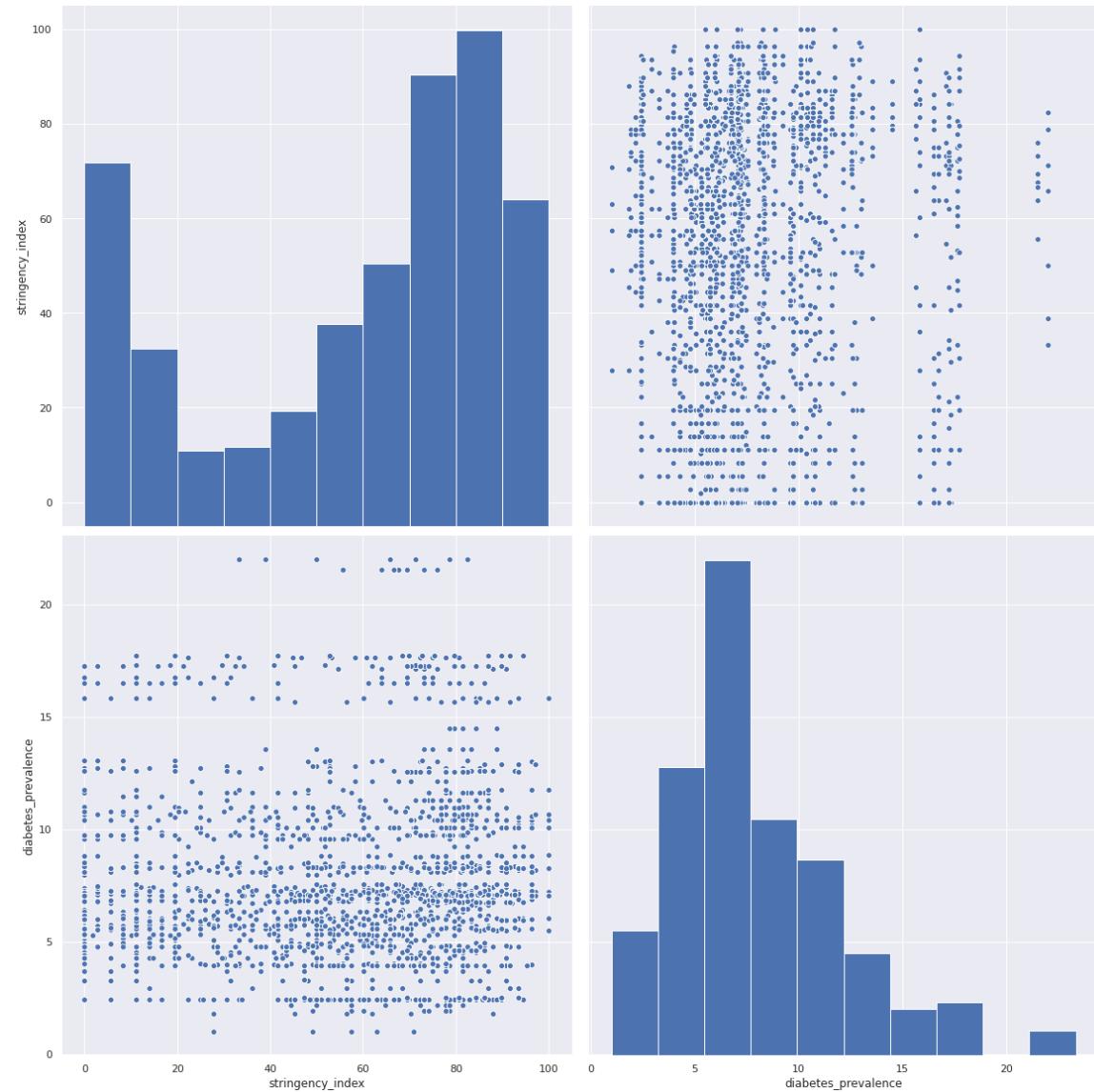


In [39]:

```
sns.pairplot(features, vars=["stringency_index", "diabetes_prevalence"], height=8)
```

Out[39]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffef42390>
```

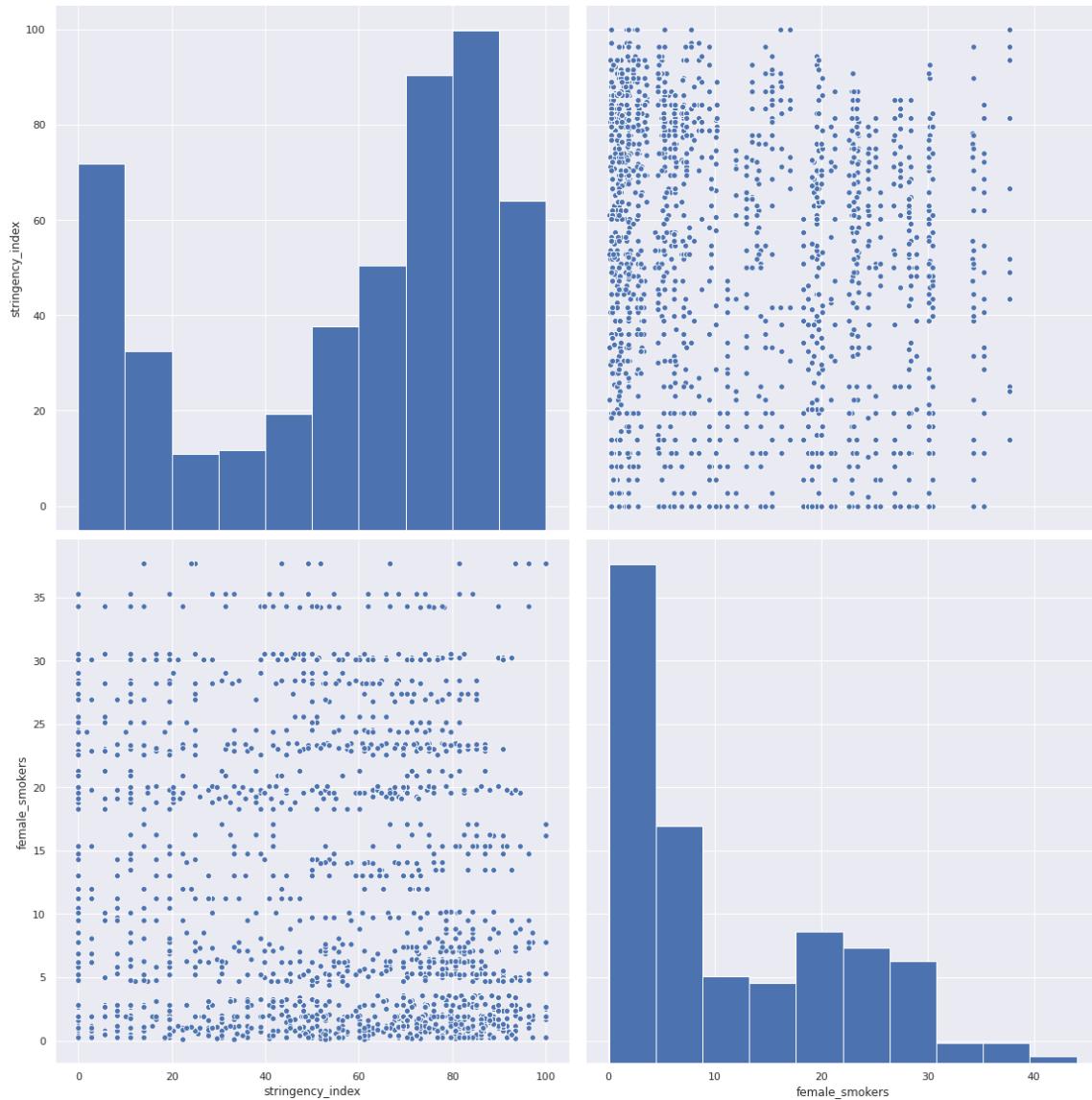


In [40]:

```
sns.pairplot(features, vars=["stringency_index", "female_smokers"], height=8)
```

Out[40]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffed3dcf8>
```

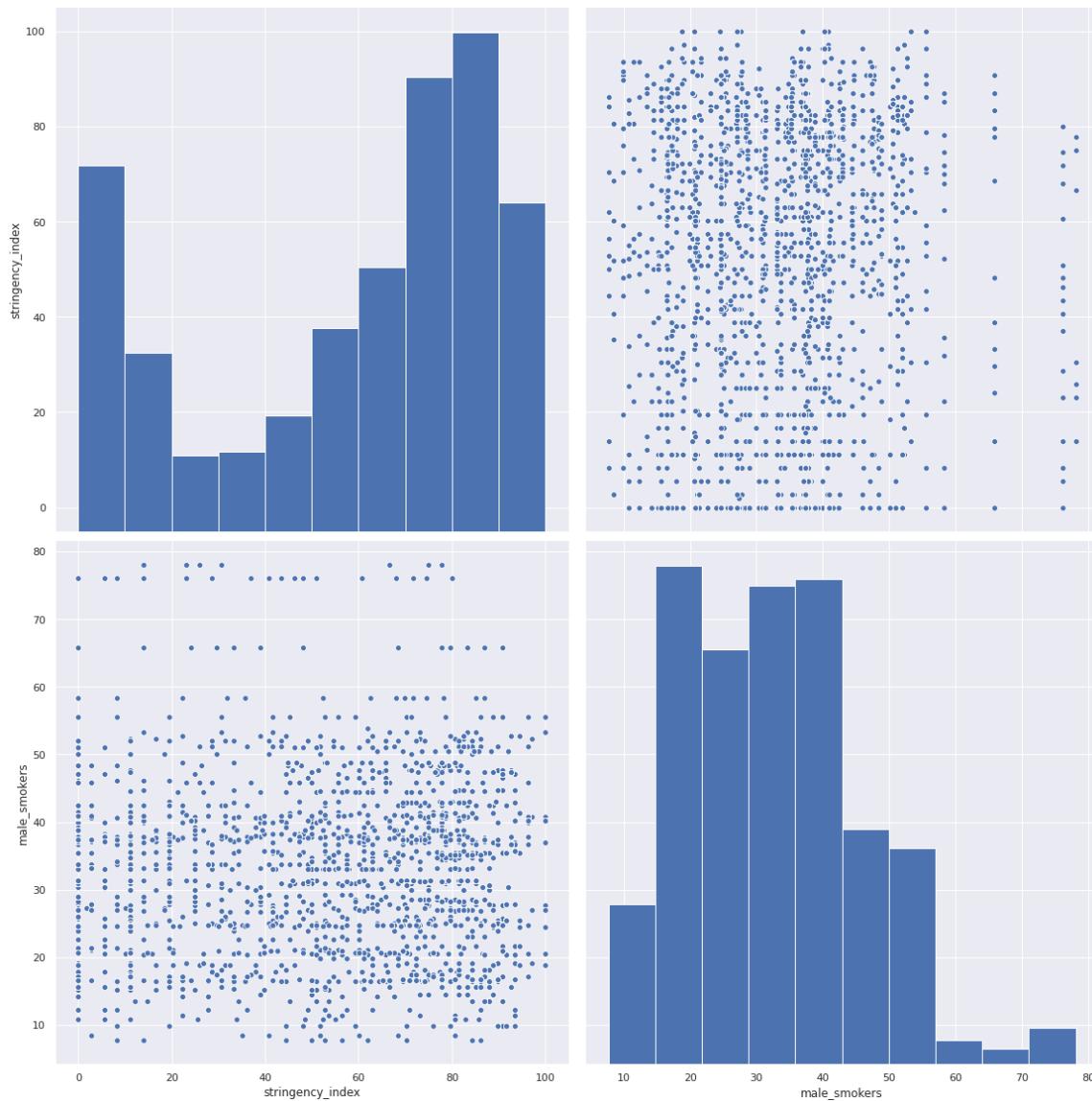


In [41]:

```
sns.pairplot(features, vars=["stringency_index", "male_smokers"], height=8)
```

Out[41]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff479dd8>
```

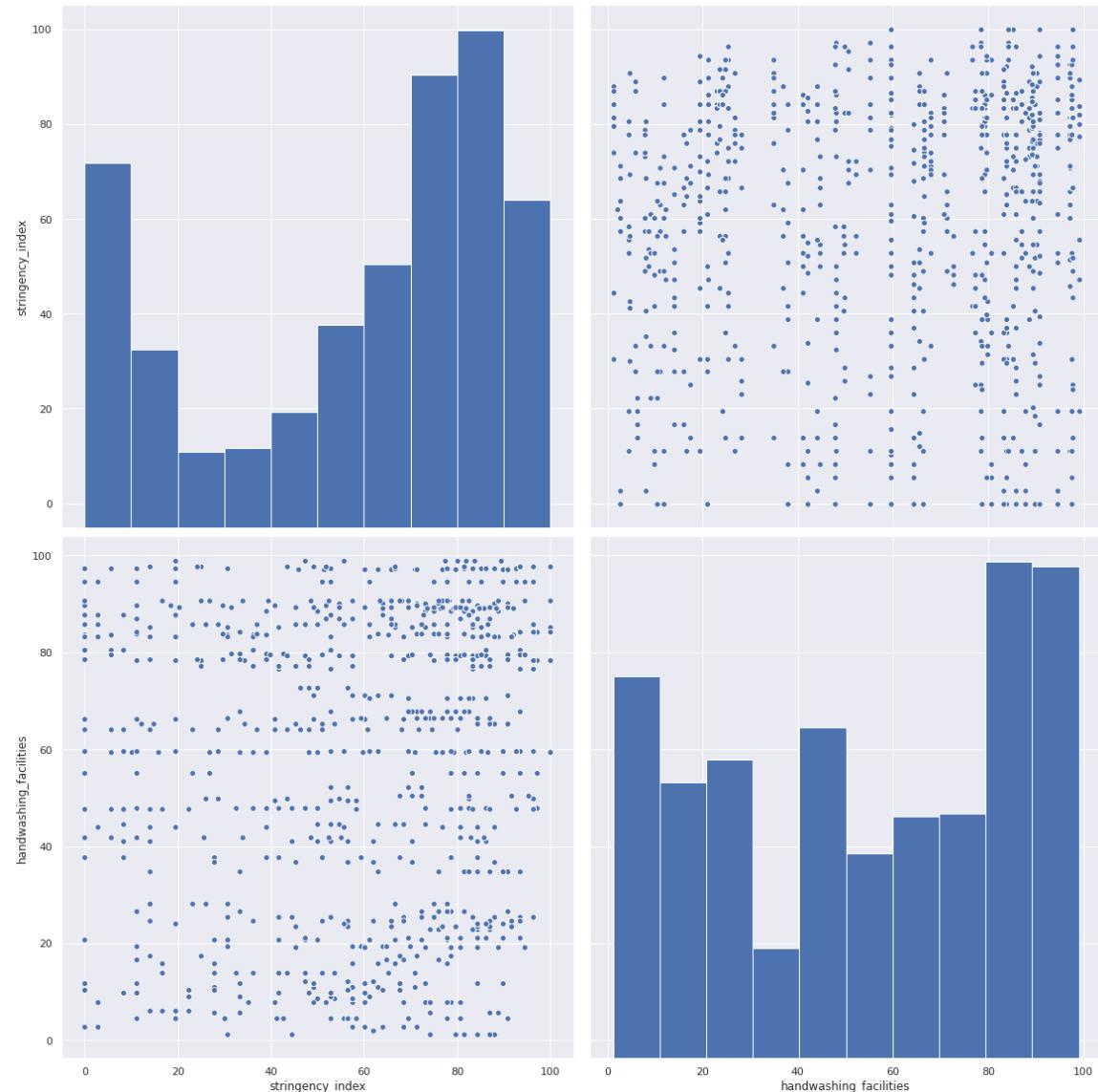


In [42]:

```
sns.pairplot(features, vars=["stringency_index", "handwashing_facilities"], height=8)
```

Out[42]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffe92cf28>
```

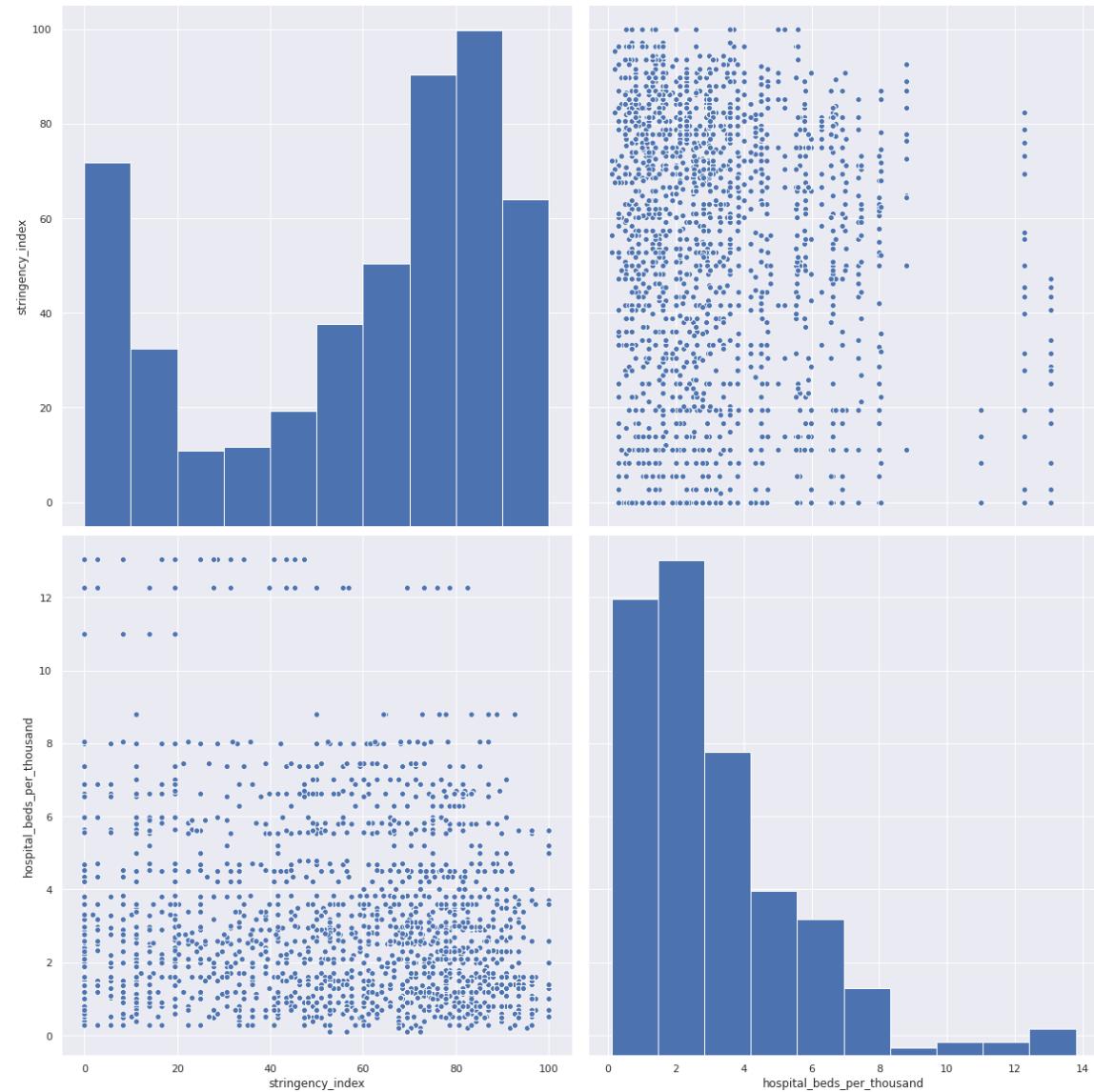


In [43]:

```
sns.pairplot(features, vars=["stringency_index", "hospital_beds_per_thousand"], height=8)
```

Out[43]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fff8ea8d0>
```

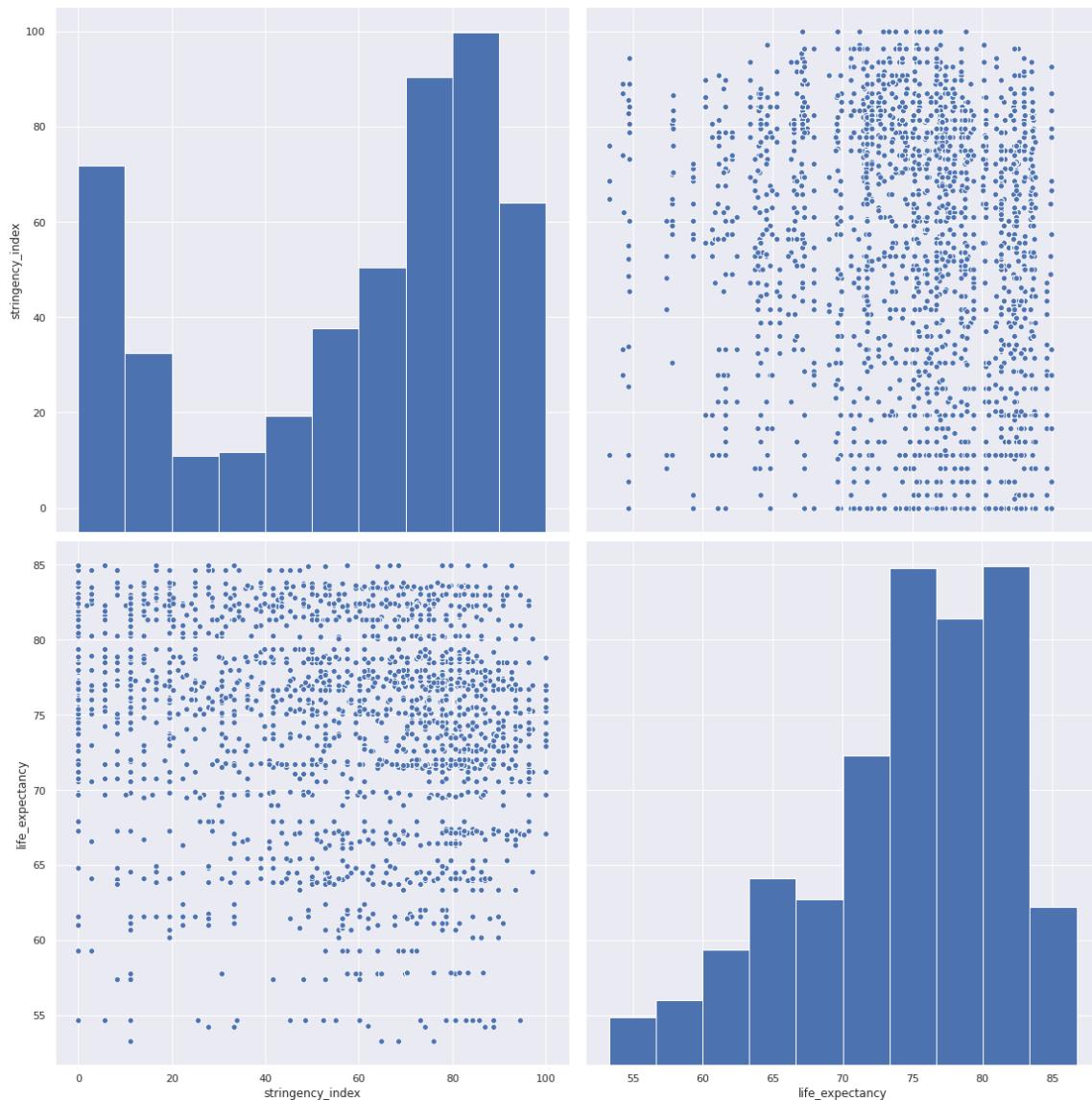


In [44]:

```
sns.pairplot(features, vars=["stringency_index", "life_expectancy"], height=8)
```

Out[44]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffe5f8668>
```

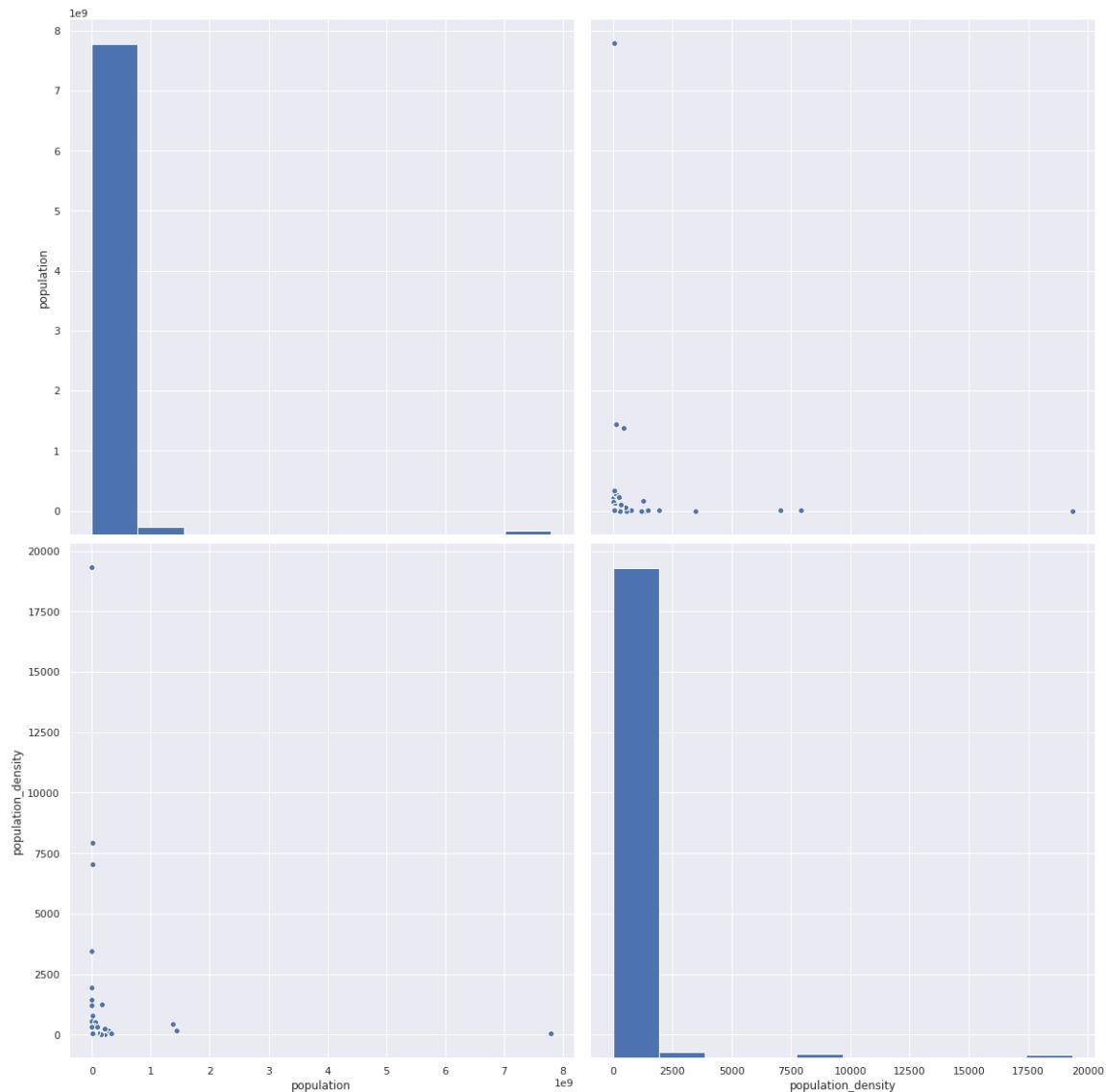


In [45]:

```
sns.pairplot(features, vars=["population", "population_density"], height=8)
```

Out[45]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffe372a58>
```

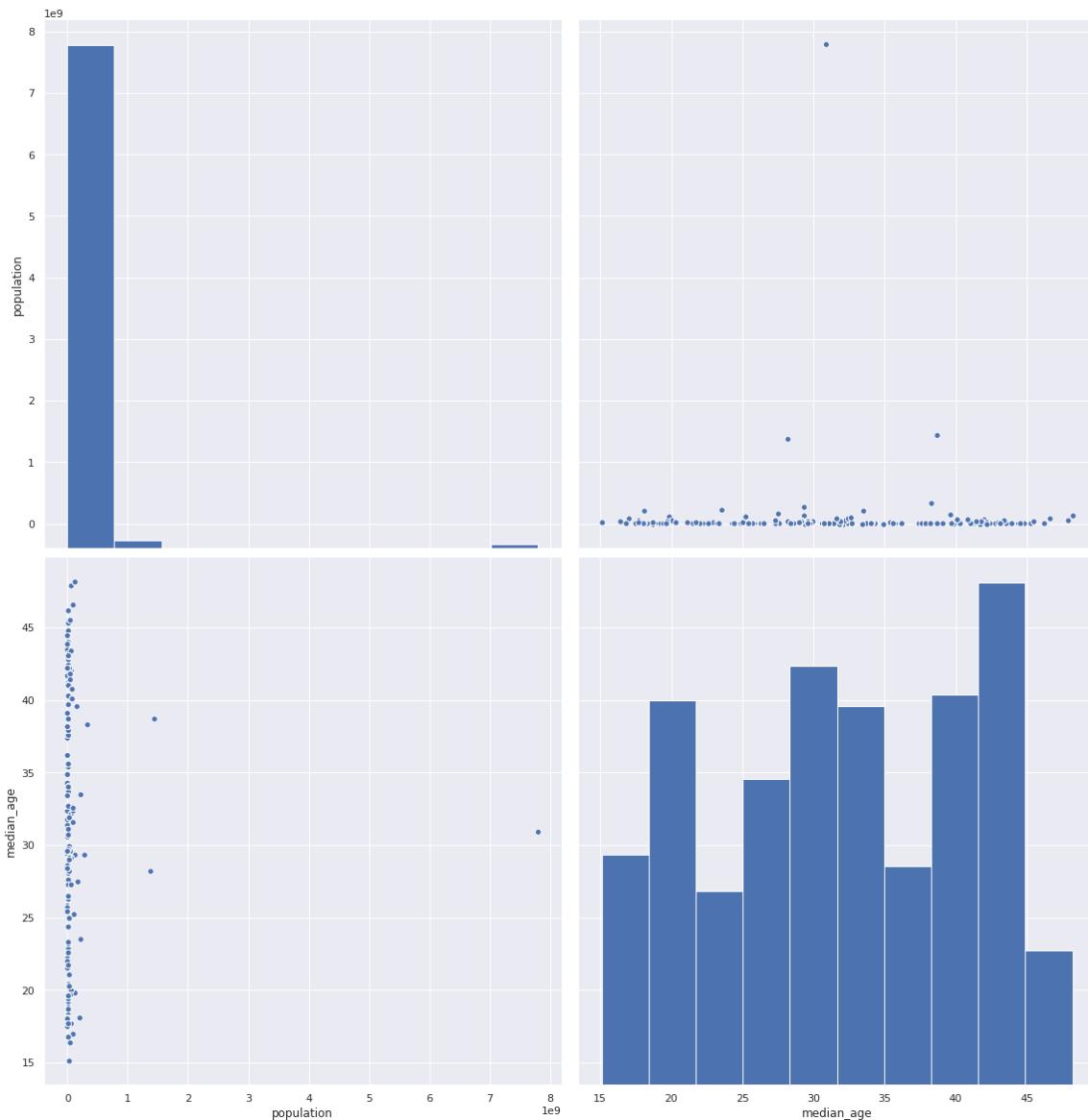


In [46]:

```
sns.pairplot(features, vars=["population", "median_age"], height=8)
```

Out[46]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffe372c88>
```

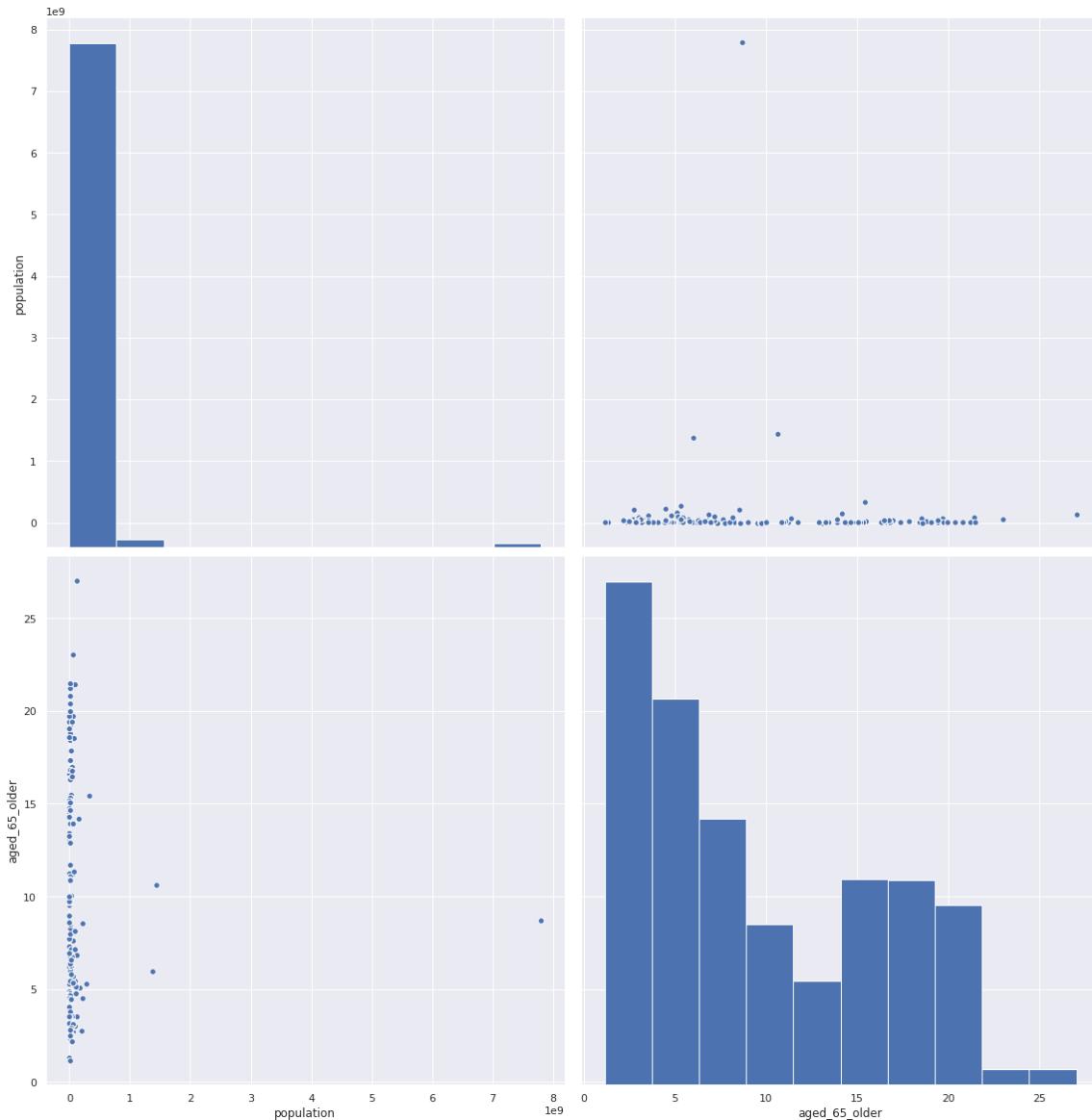


In [47]:

```
sns.pairplot(features, vars=["population", "aged_65_older"], height=8)
```

Out[47]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffdf233c8>
```

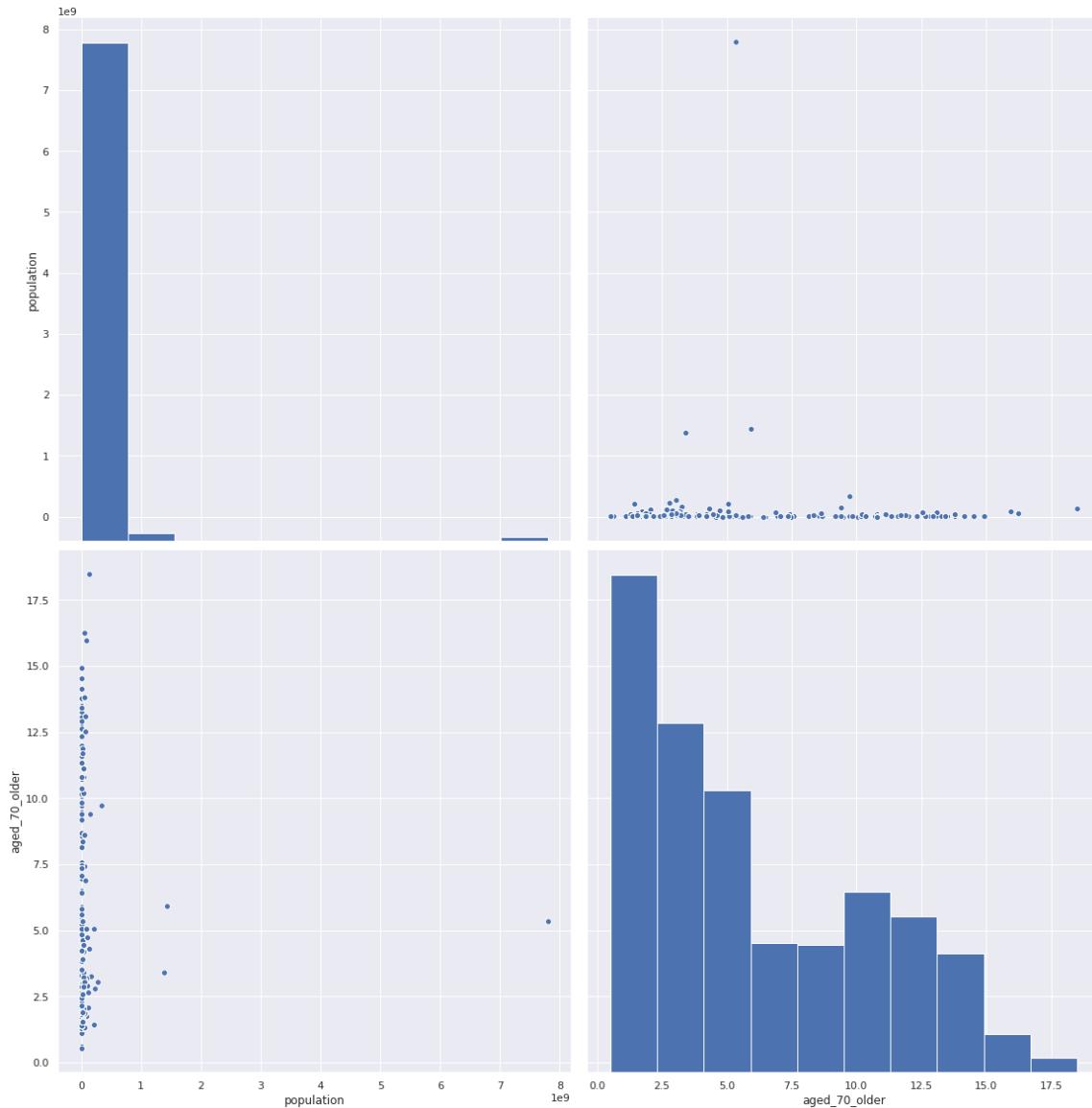


In [48]:

```
sns.pairplot(features, vars=["population", "aged_70_older"], height=8)
```

Out[48]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fffdcf0fd0>
```

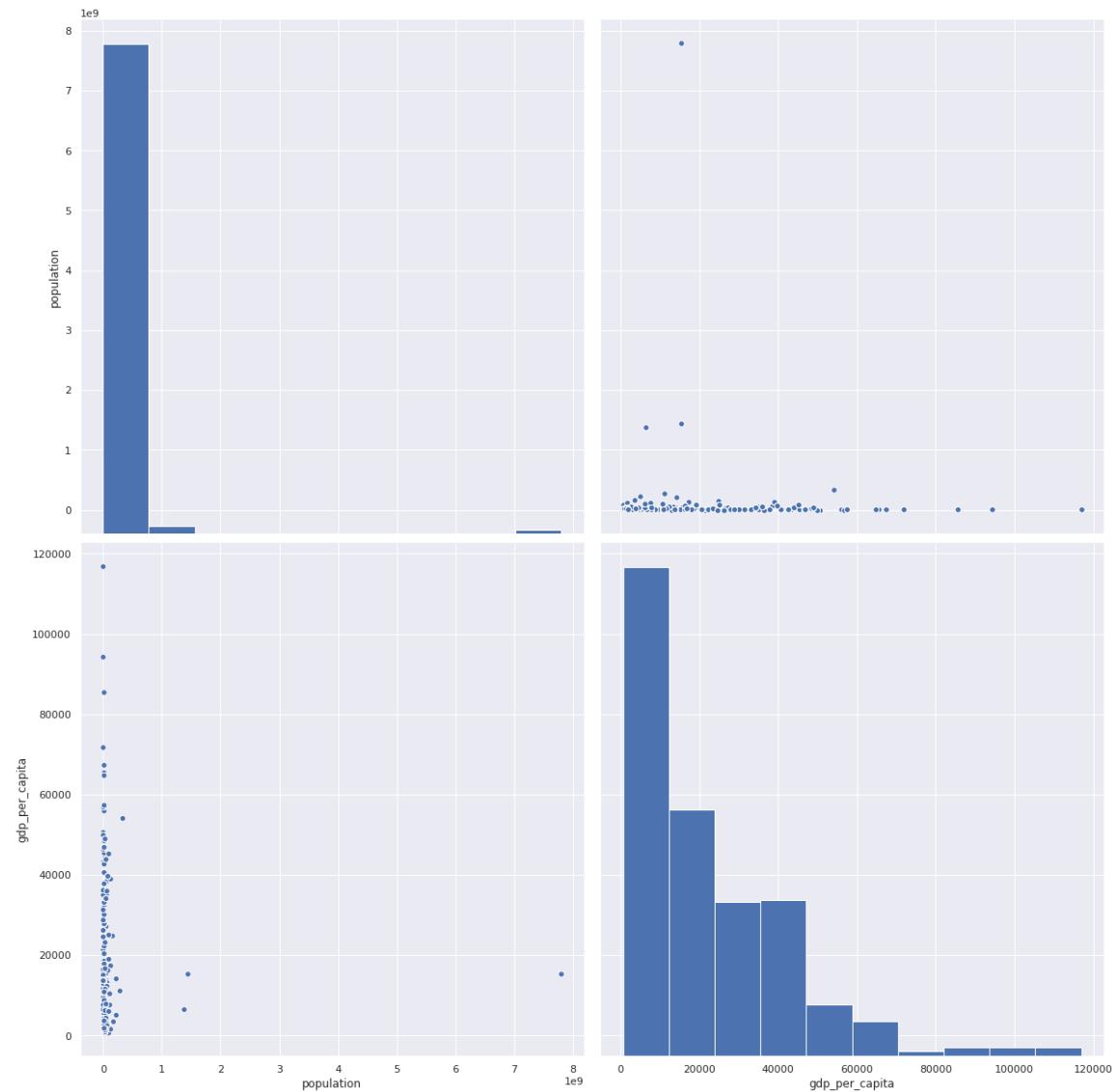


In [49]:

```
sns.pairplot(features, vars=["population", "gdp_per_capita"], height=8)
```

Out[49]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffda9cef0>
```

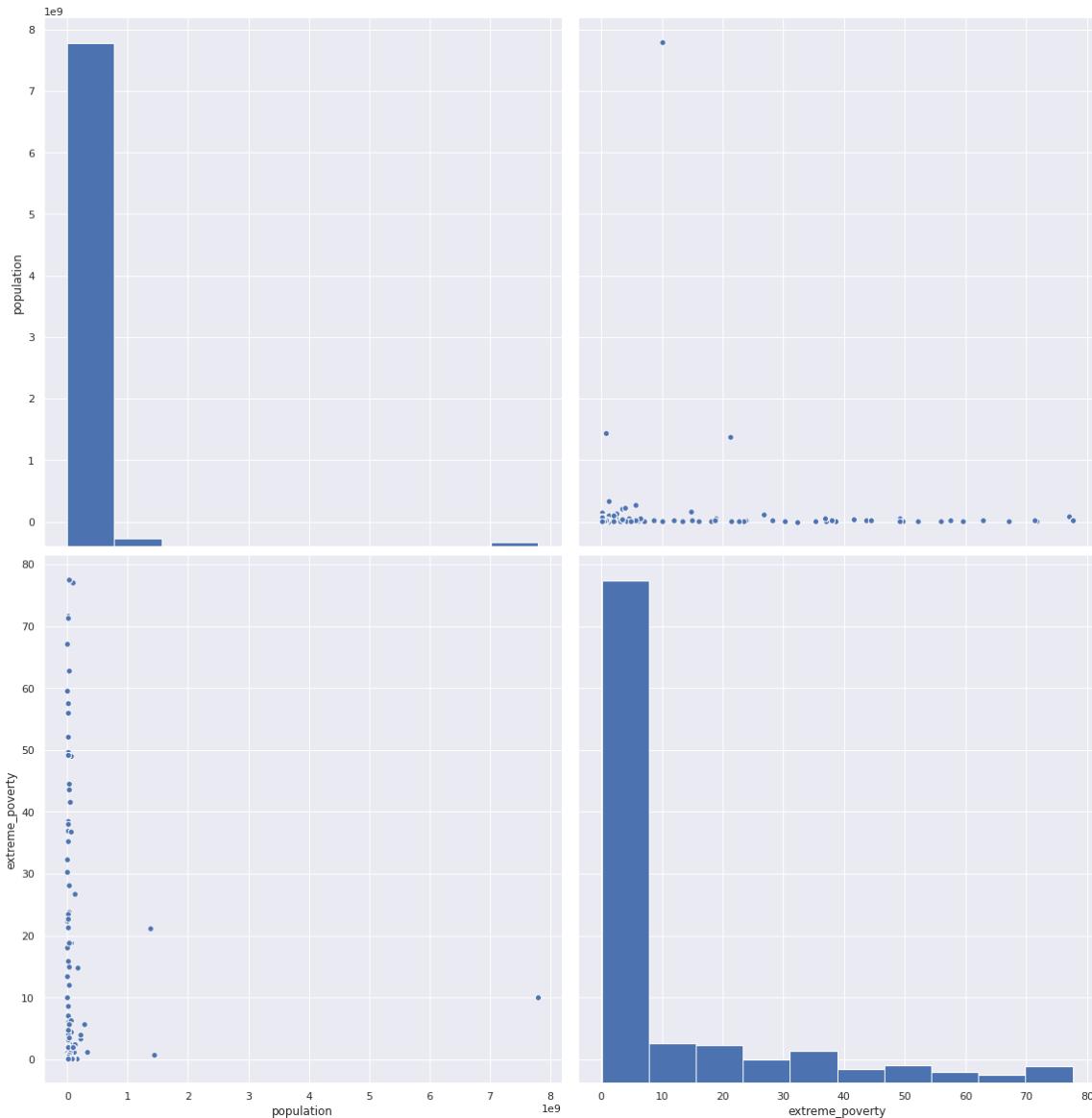


In [50]:

```
sns.pairplot(features, vars=["population", "extreme_poverty"], height=8)
```

Out[50]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffd88eef0>
```

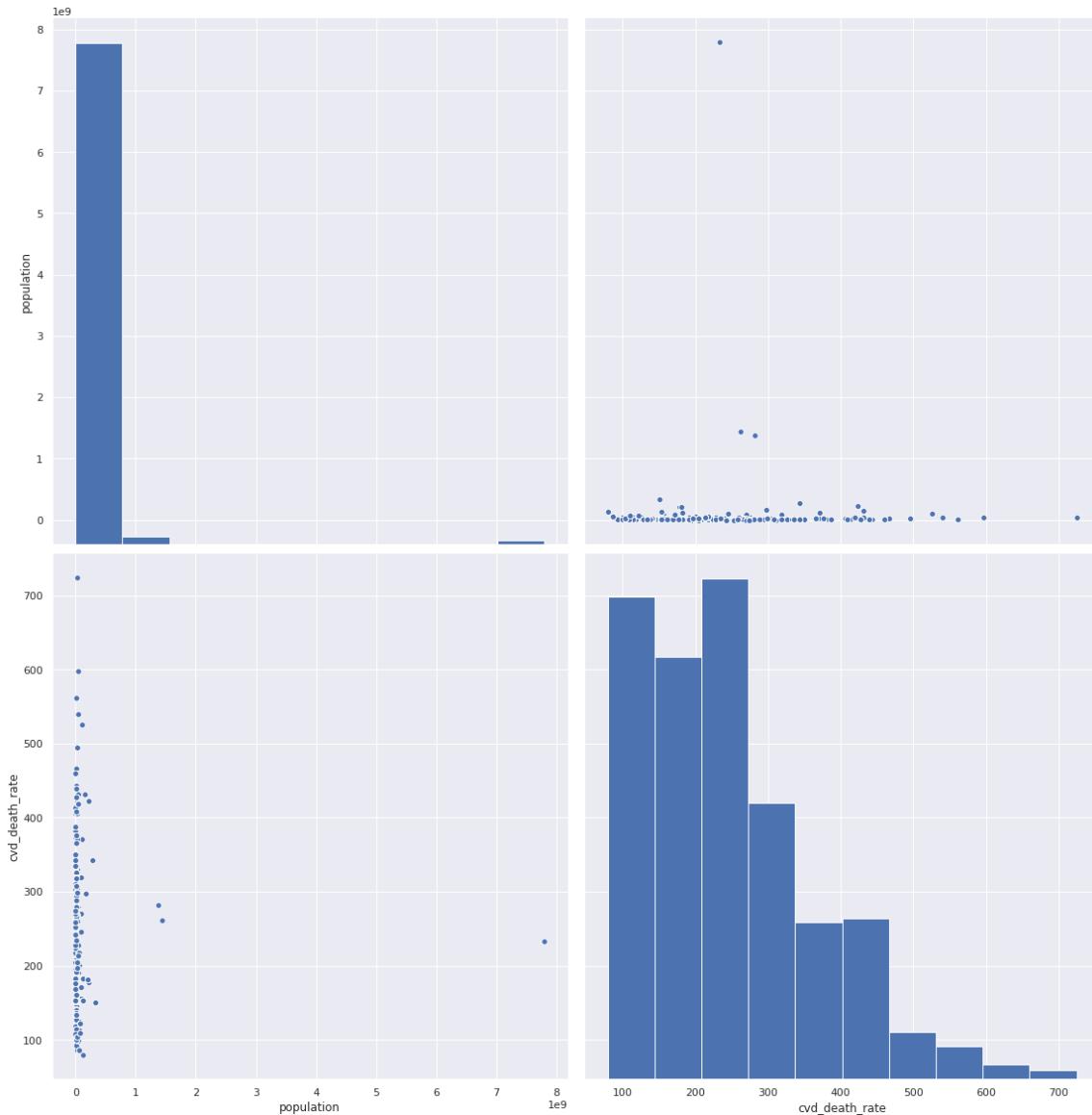


In [51]:

```
sns.pairplot(features, vars=["population", "cvd_death_rate"], height=8)
```

Out[51]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffd683da0>
```

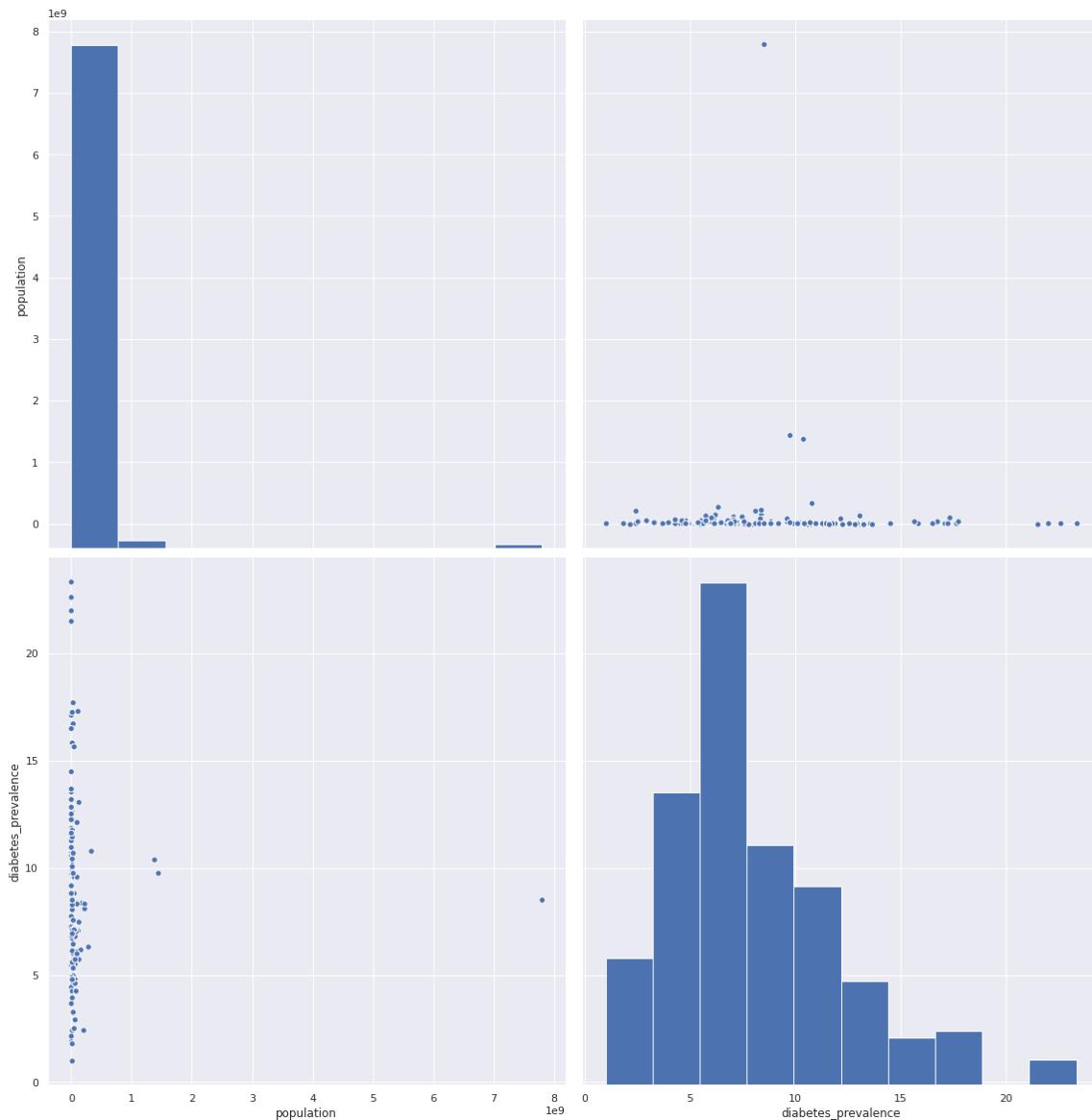


In [52]:

```
sns.pairplot(features, vars=["population", "diabetes_prevalence"], height=8)
```

Out[52]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffd41f400>
```

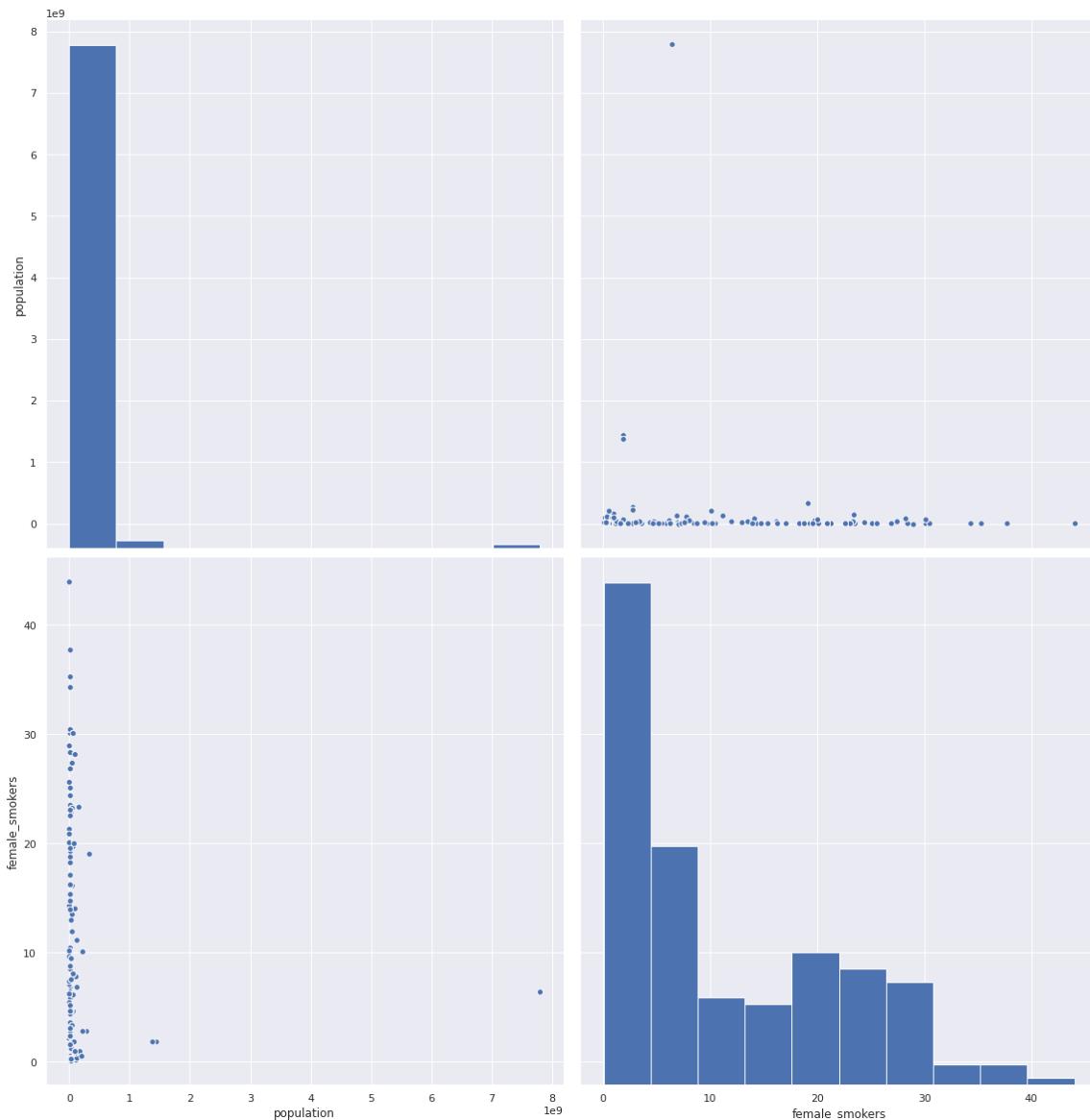


In [53]:

```
sns.pairplot(features, vars=["population", "female_smokers"], height=8)
```

Out[53]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffd49b470>
```

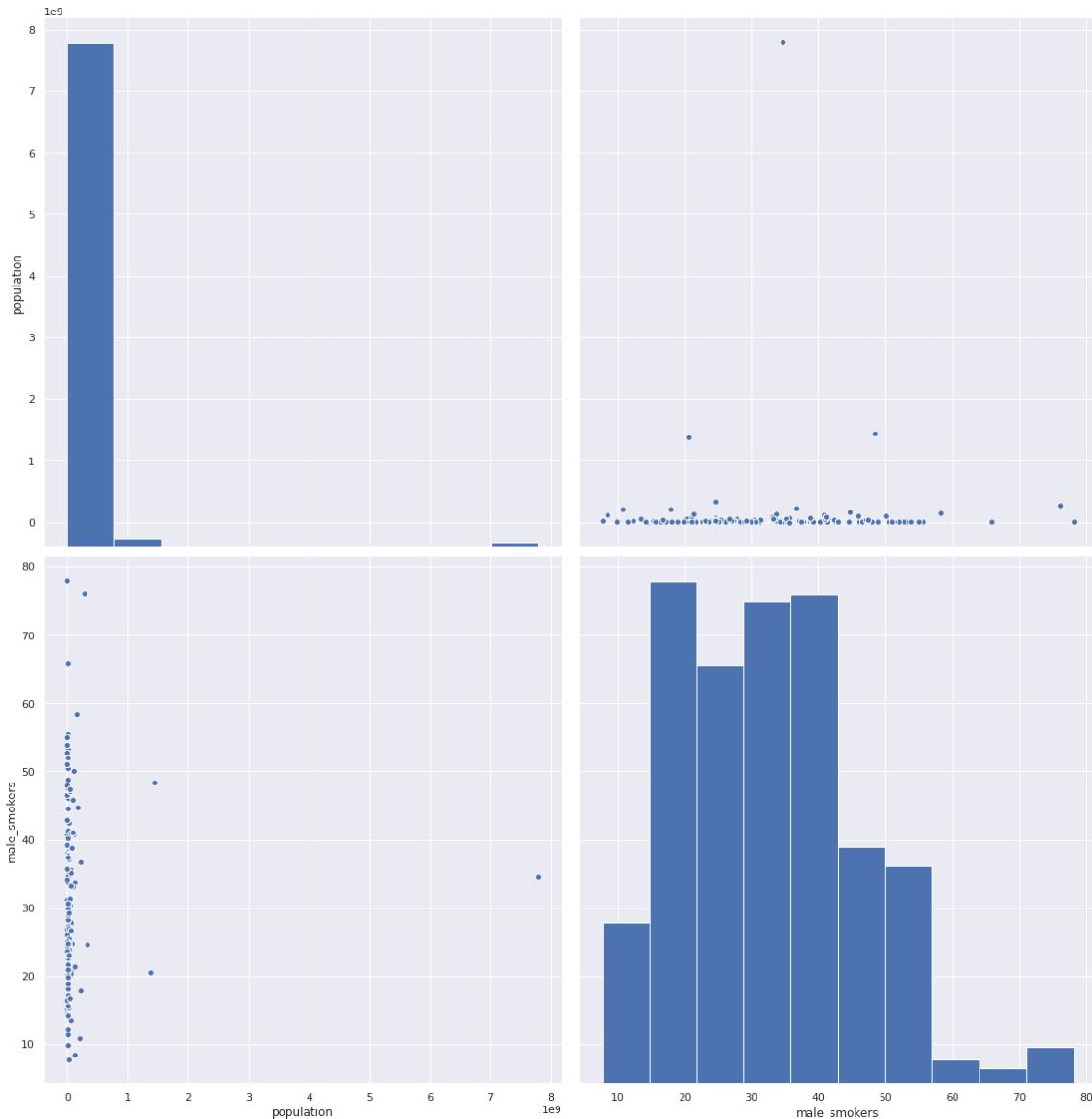


In [54]:

```
sns.pairplot(features, vars=["population", "male_smokers"], height=8)
```

Out[54]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffd0aee48>
```

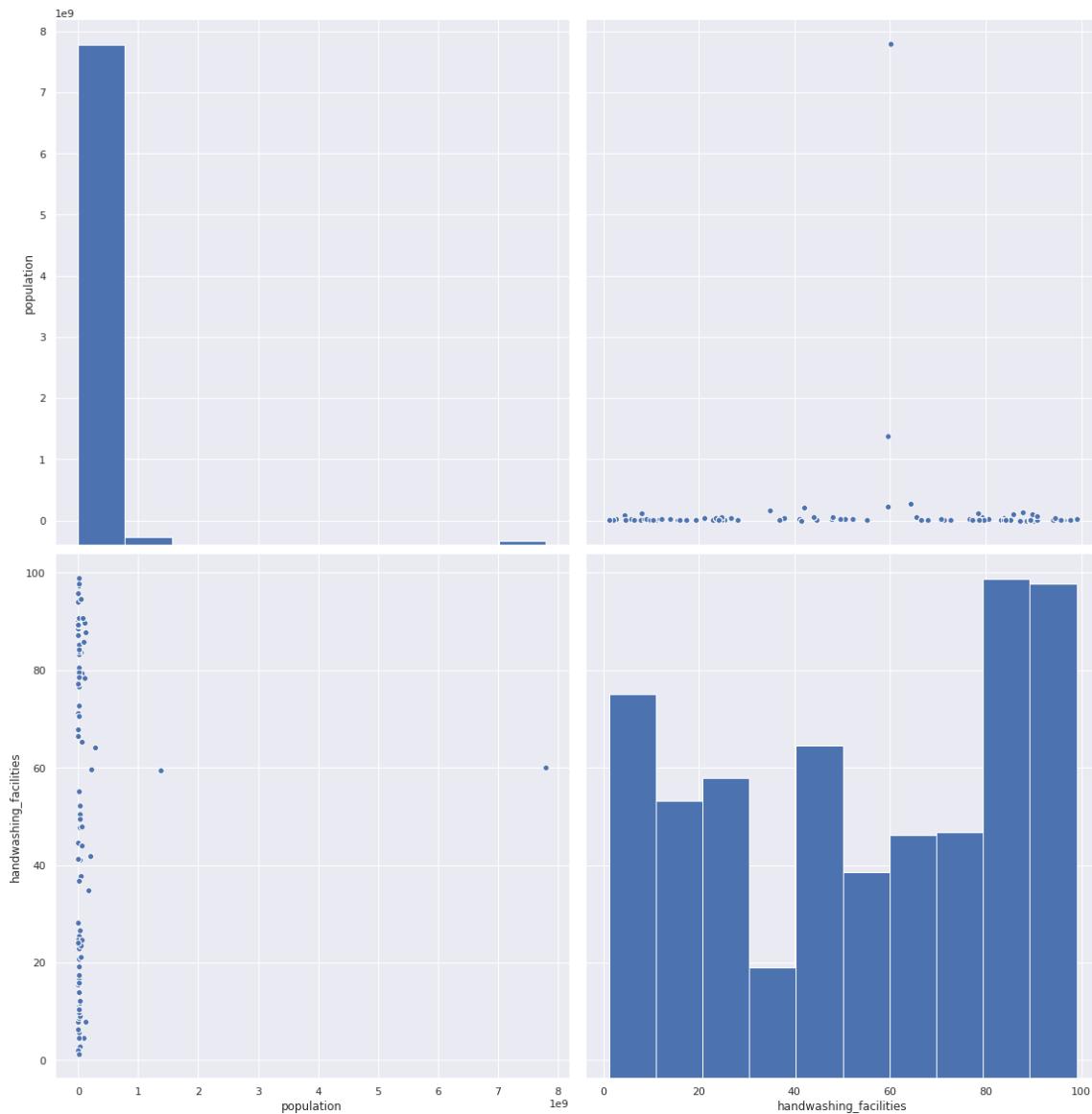


In [55]:

```
sns.pairplot(features, vars=["population", "handwashing_facilities"], height=8)
```

Out[55]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffce28828>
```

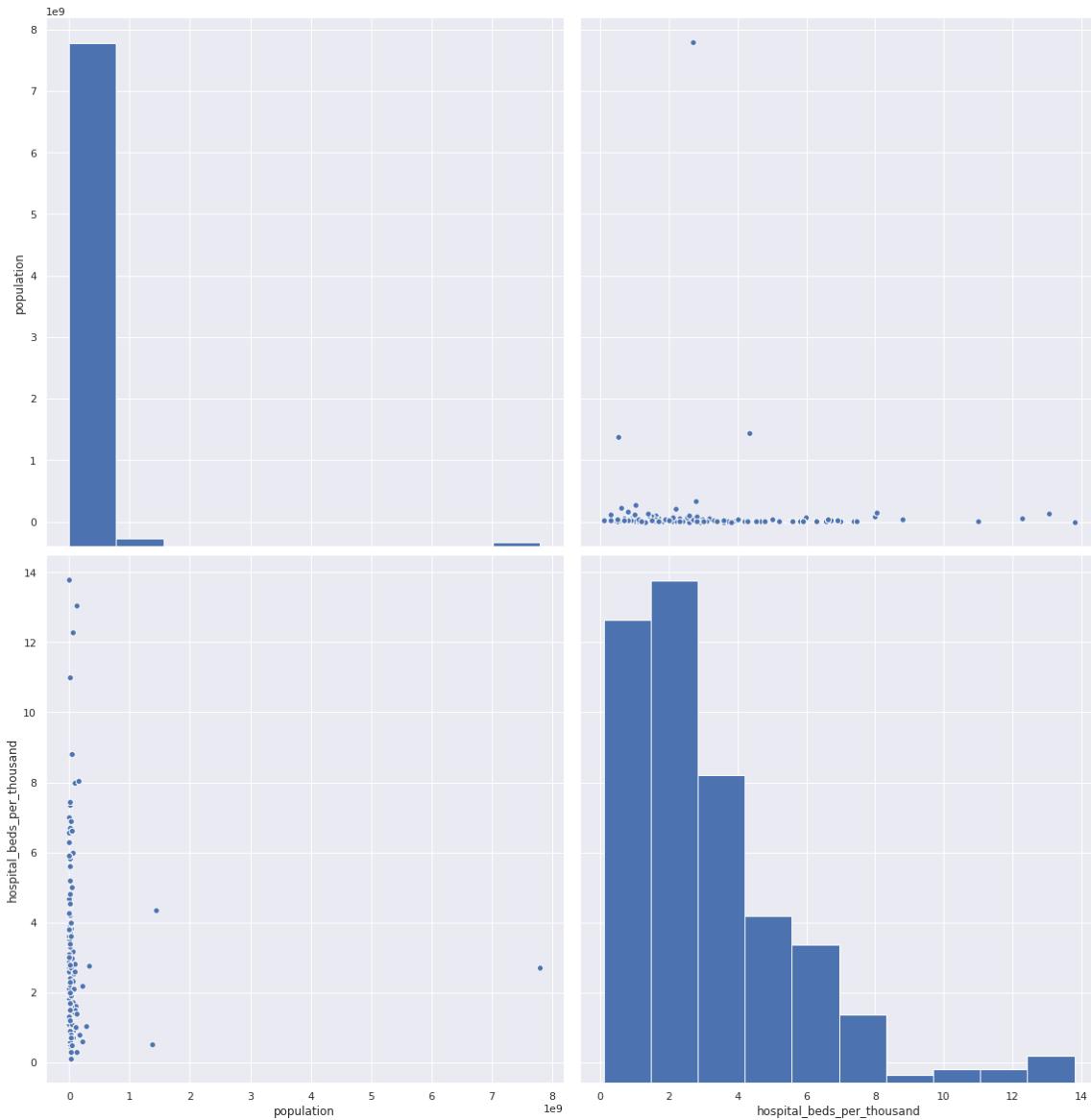


In [56]:

```
sns.pairplot(features, vars=["population", "hospital_beds_per_thousand"], height=8)
```

Out[56]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffcd43860>
```

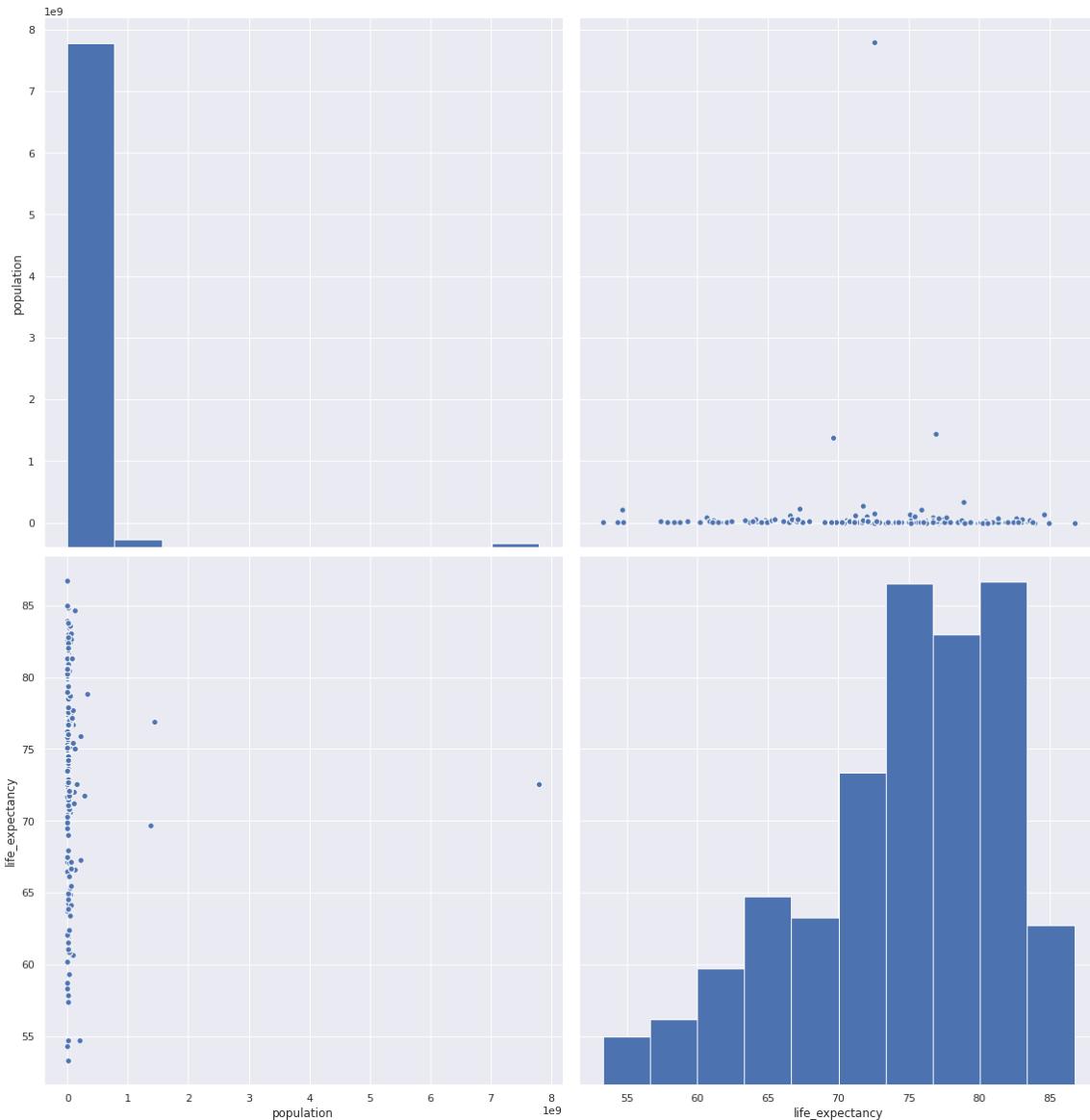


In [57]:

```
sns.pairplot(features, vars=["population", "life_expectancy"], height=8)
```

Out[57]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffca29668>
```

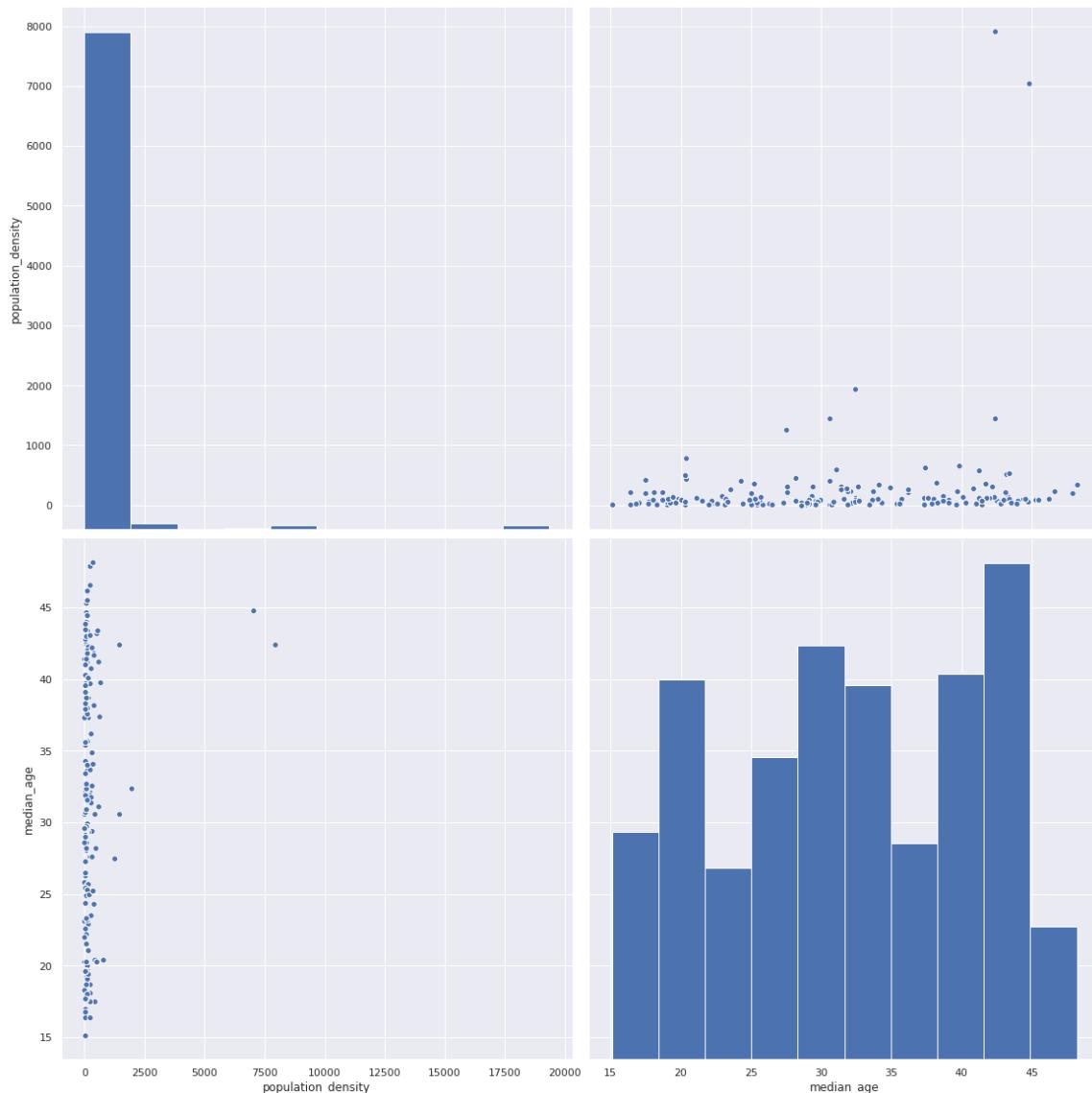


In [58]:

```
sns.pairplot(features, vars=["population_density", "median_age"], height=8)
```

Out[58]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffc7986d8>
```

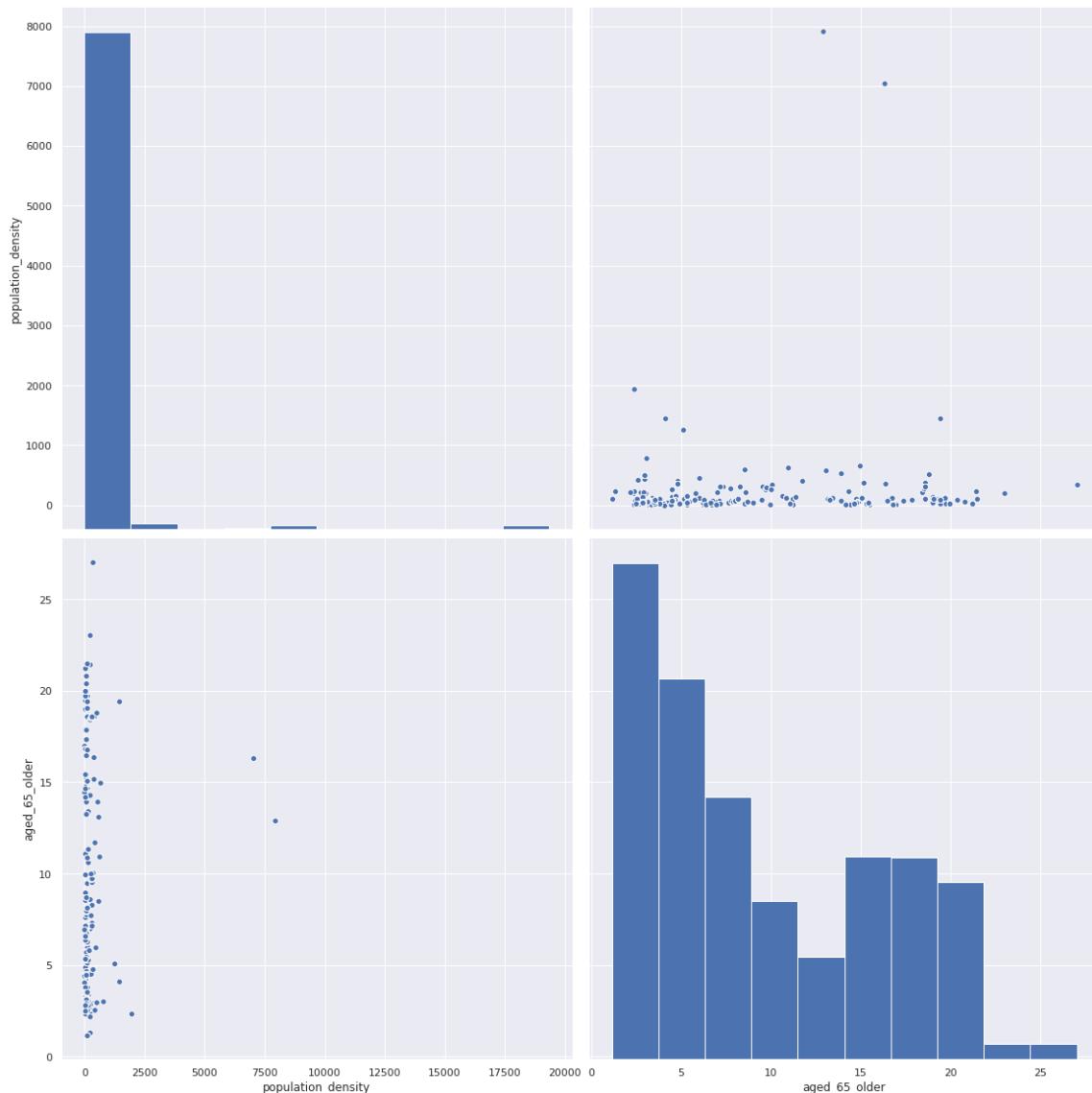


In [59]:

```
sns.pairplot(features, vars=["population_density", "aged_65_older"], height=8)
```

Out[59]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffc5a4ac8>
```

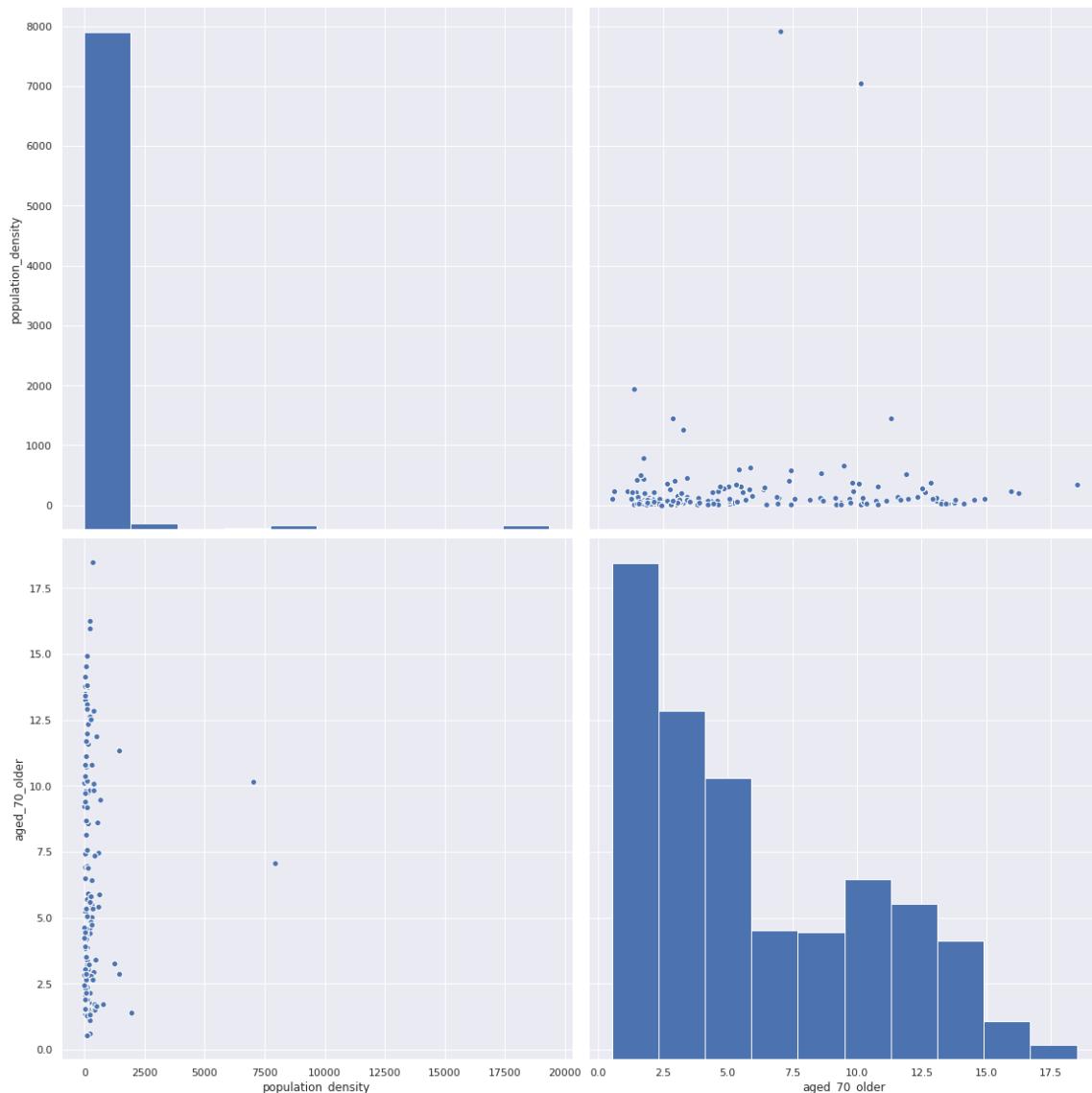


In [60]:

```
sns.pairplot(features, vars=["population_density", "aged_70_older"], height=8)
```

Out[60]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffc7e3710>
```

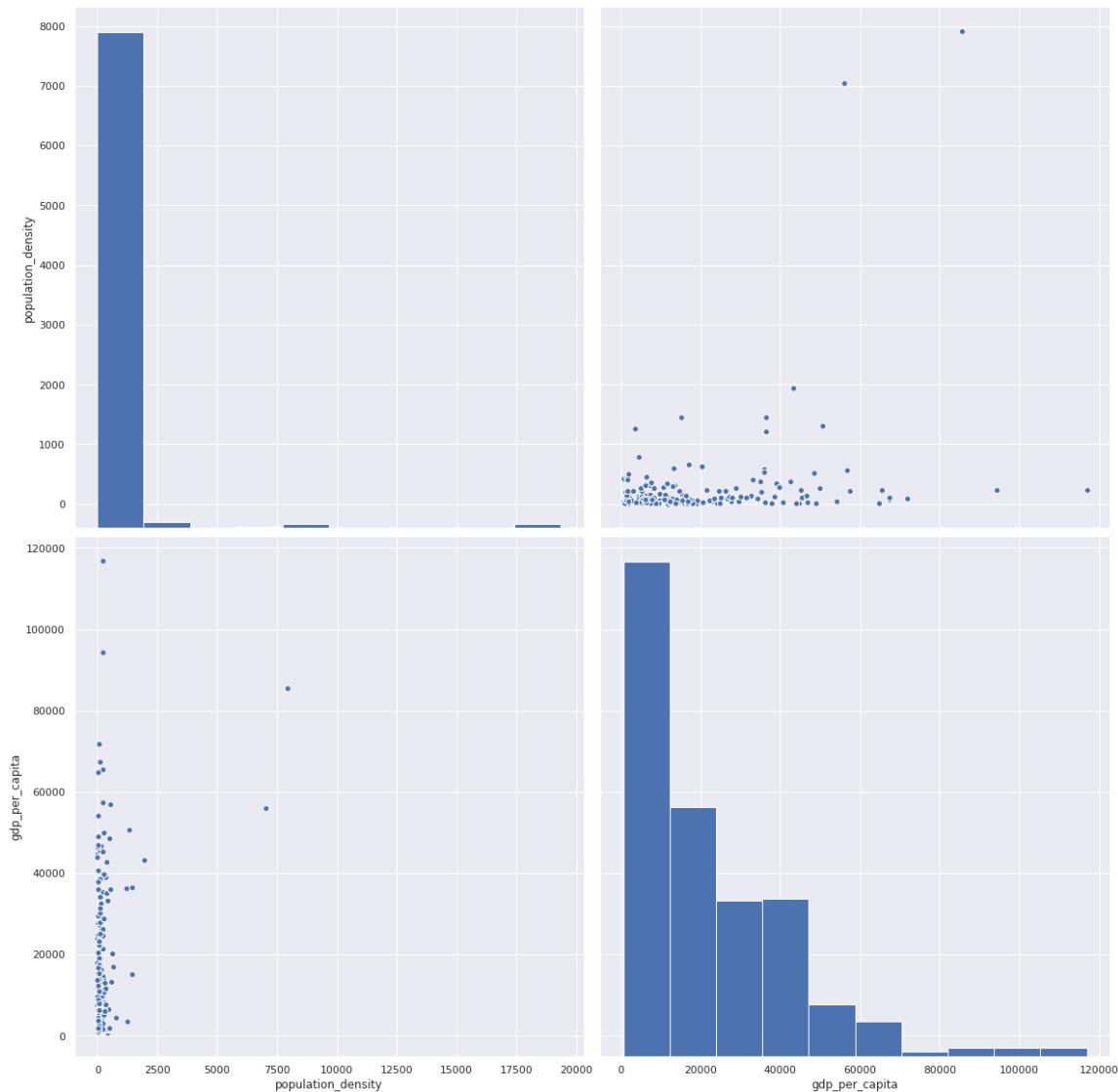


In [61]:

```
sns.pairplot(features, vars=["population_density", "gdp_per_capita"], height=8)
```

Out[61]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffclaa82b0>
```

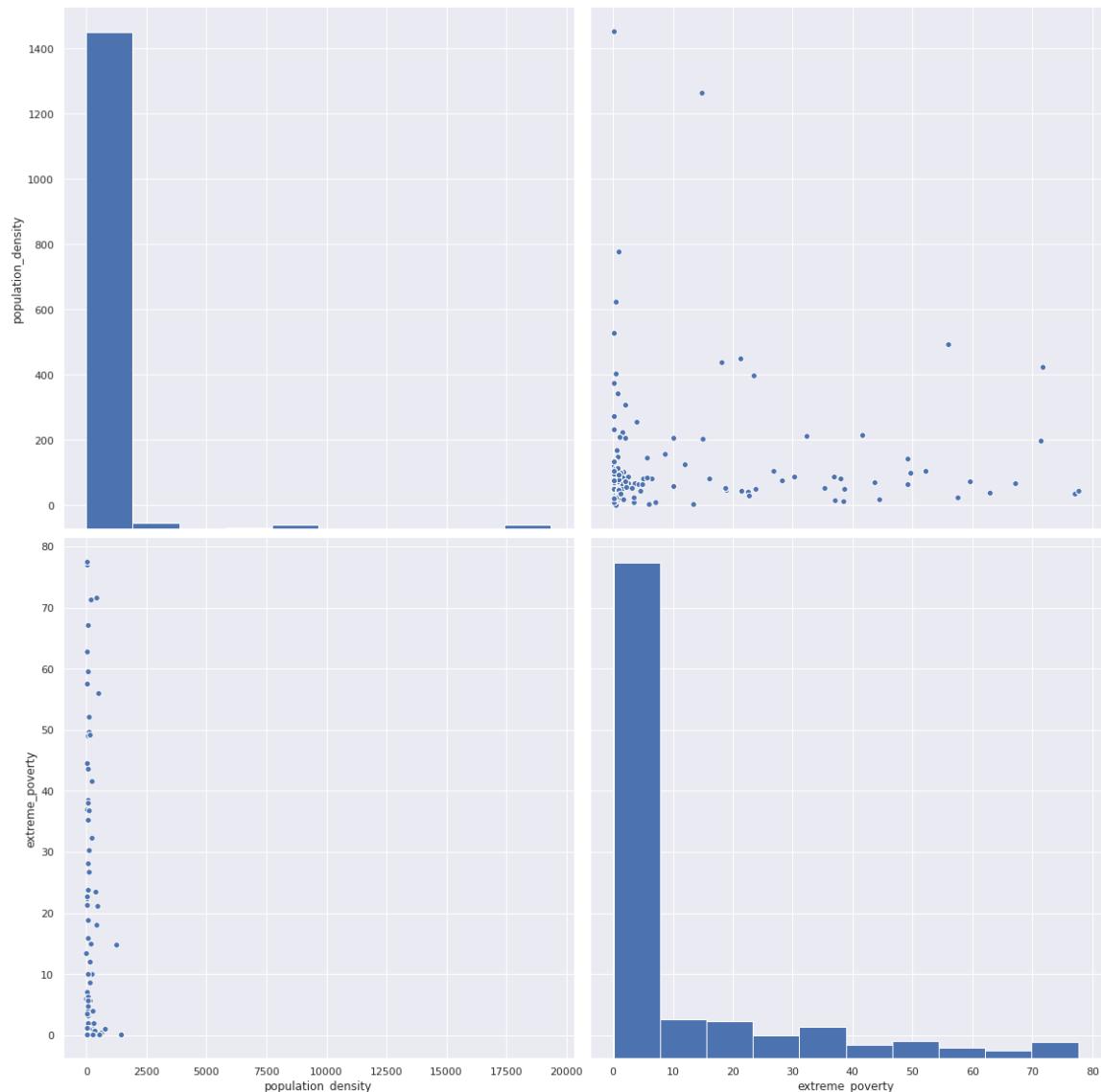


In [62]:

```
sns.pairplot(features, vars=["population_density", "extreme_poverty"], height=8)
```

Out[62]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fffc0b20f0>
```

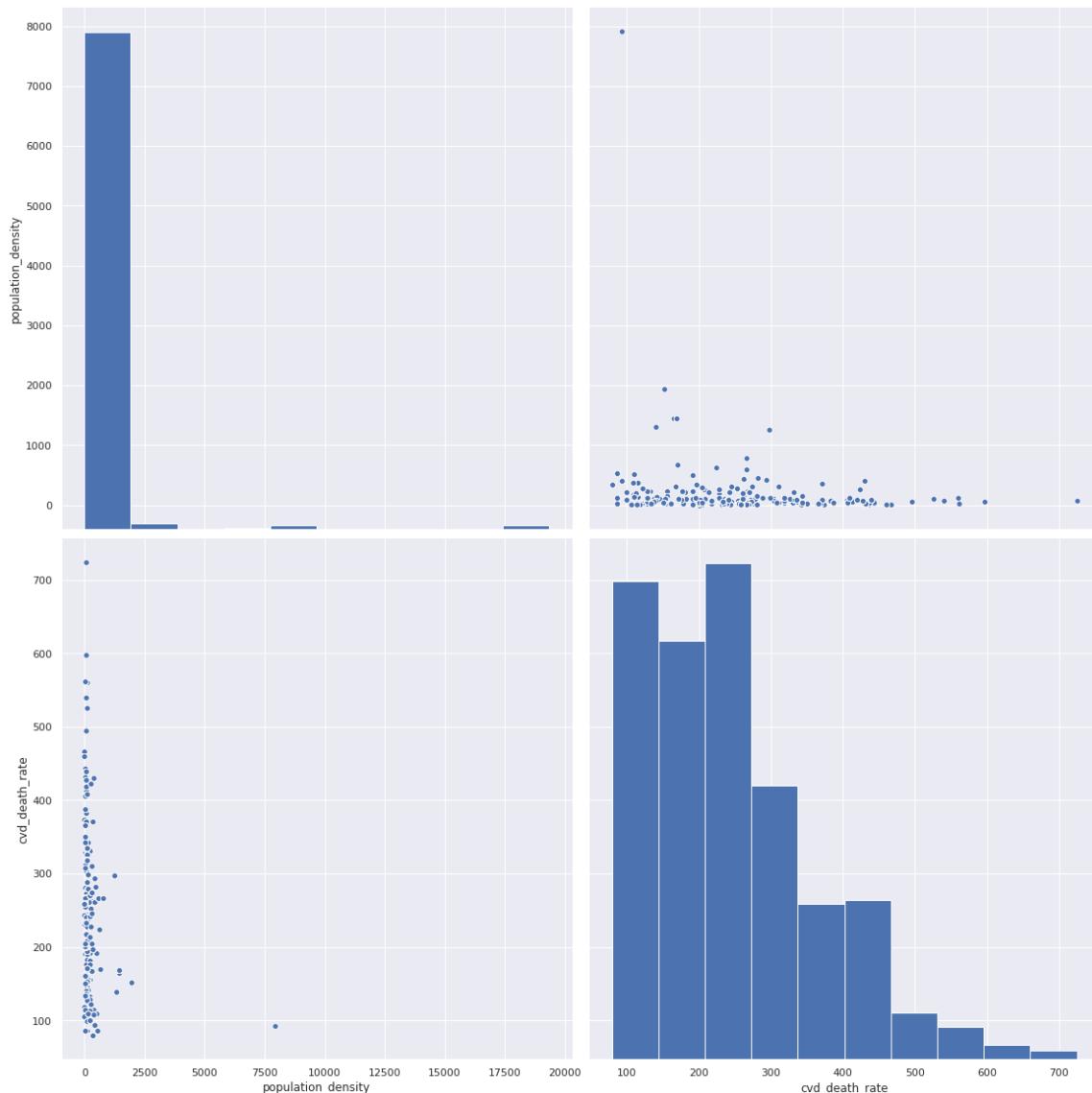


In [63]:

```
sns.pairplot(features, vars=["population_density", "cvd_death_rate"], height=8)
```

Out[63]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffbe02438>
```

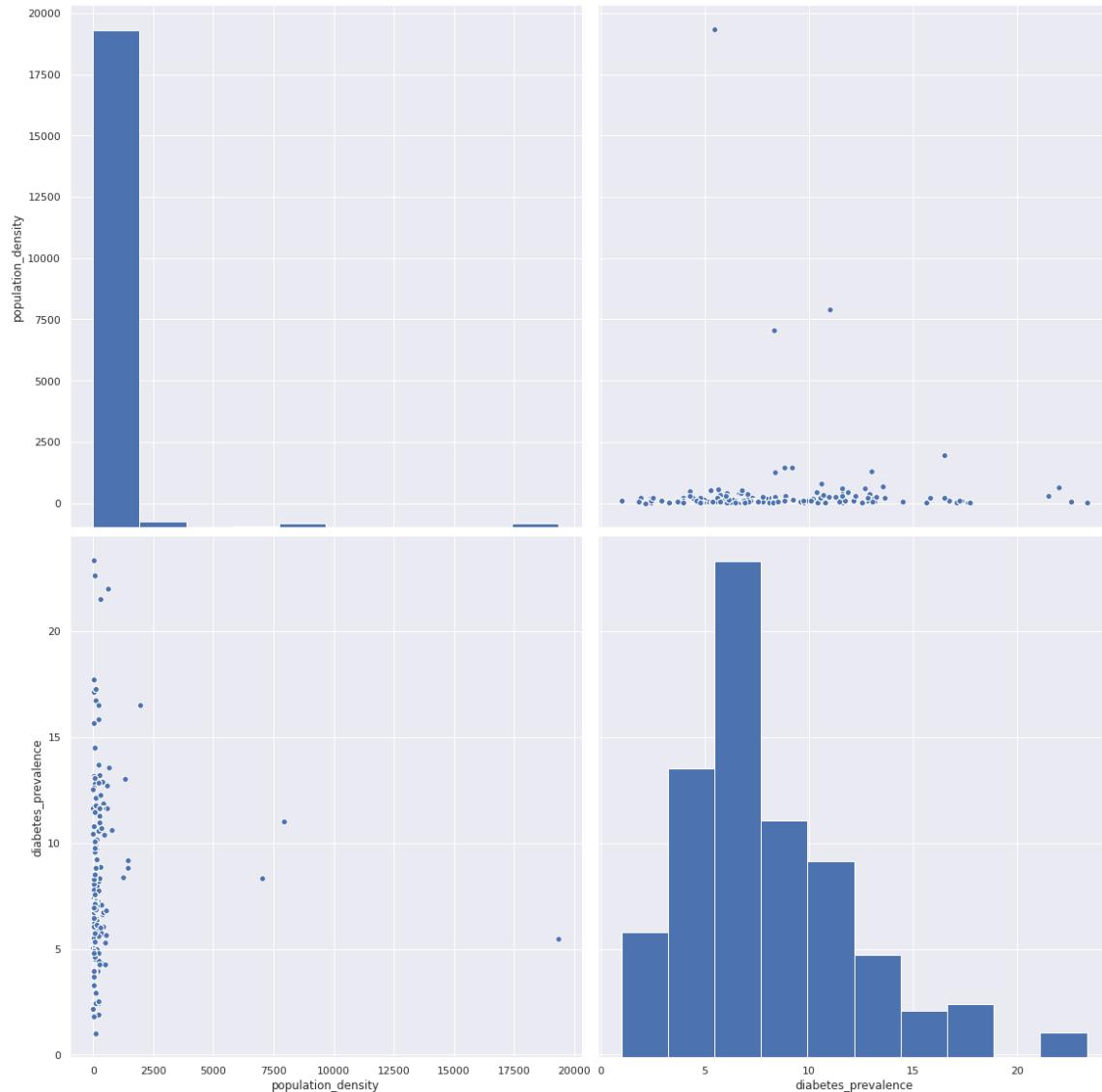


In [64]:

```
sns.pairplot(features, vars=["population_density", "diabetes_prevalence"], height=8)
```

Out[64]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffbac74e0>
```

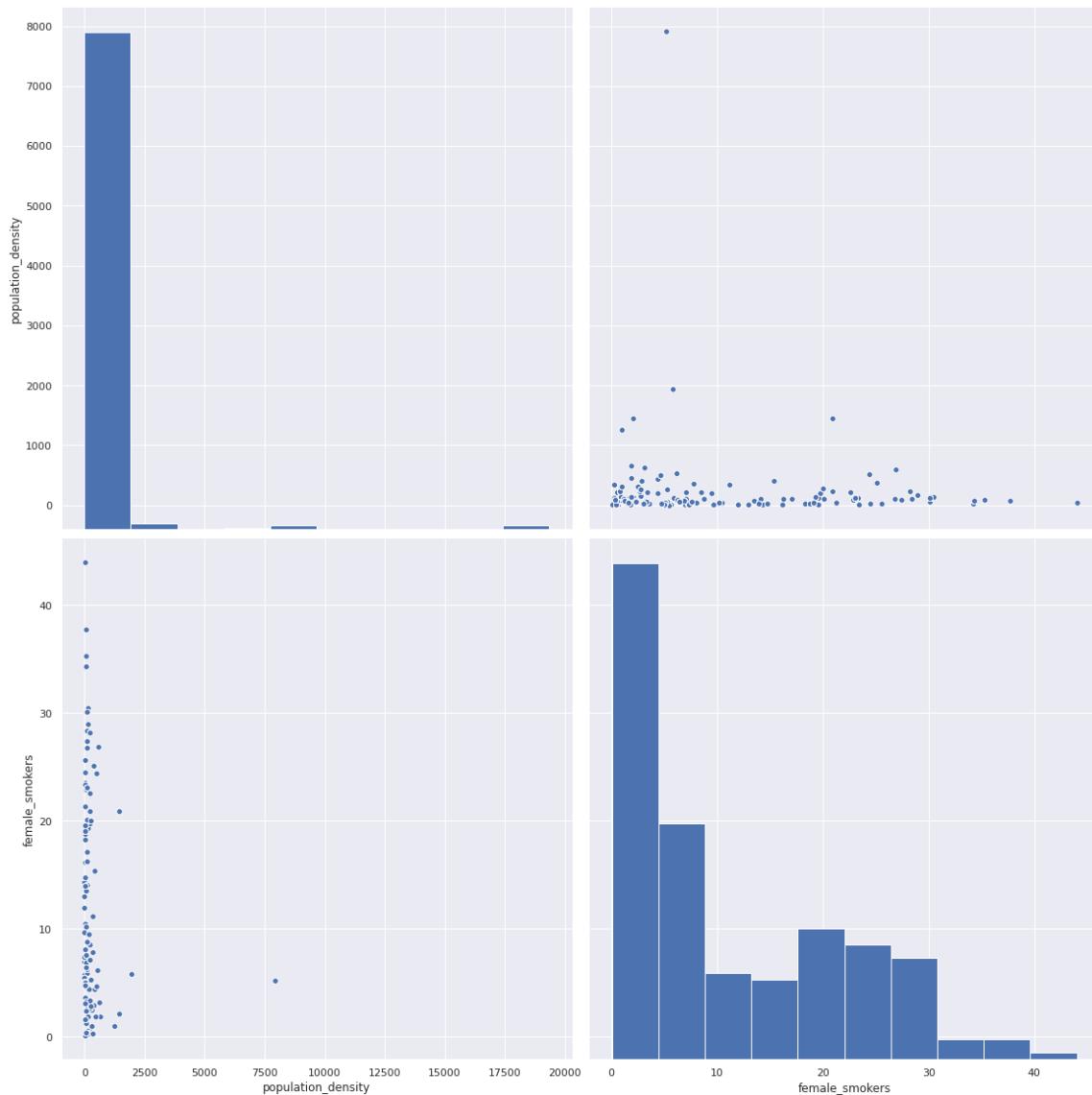


In [65]:

```
sns.pairplot(features, vars=["population_density", "female_smokers"], height=8)
```

Out[65]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffd0a5908>
```

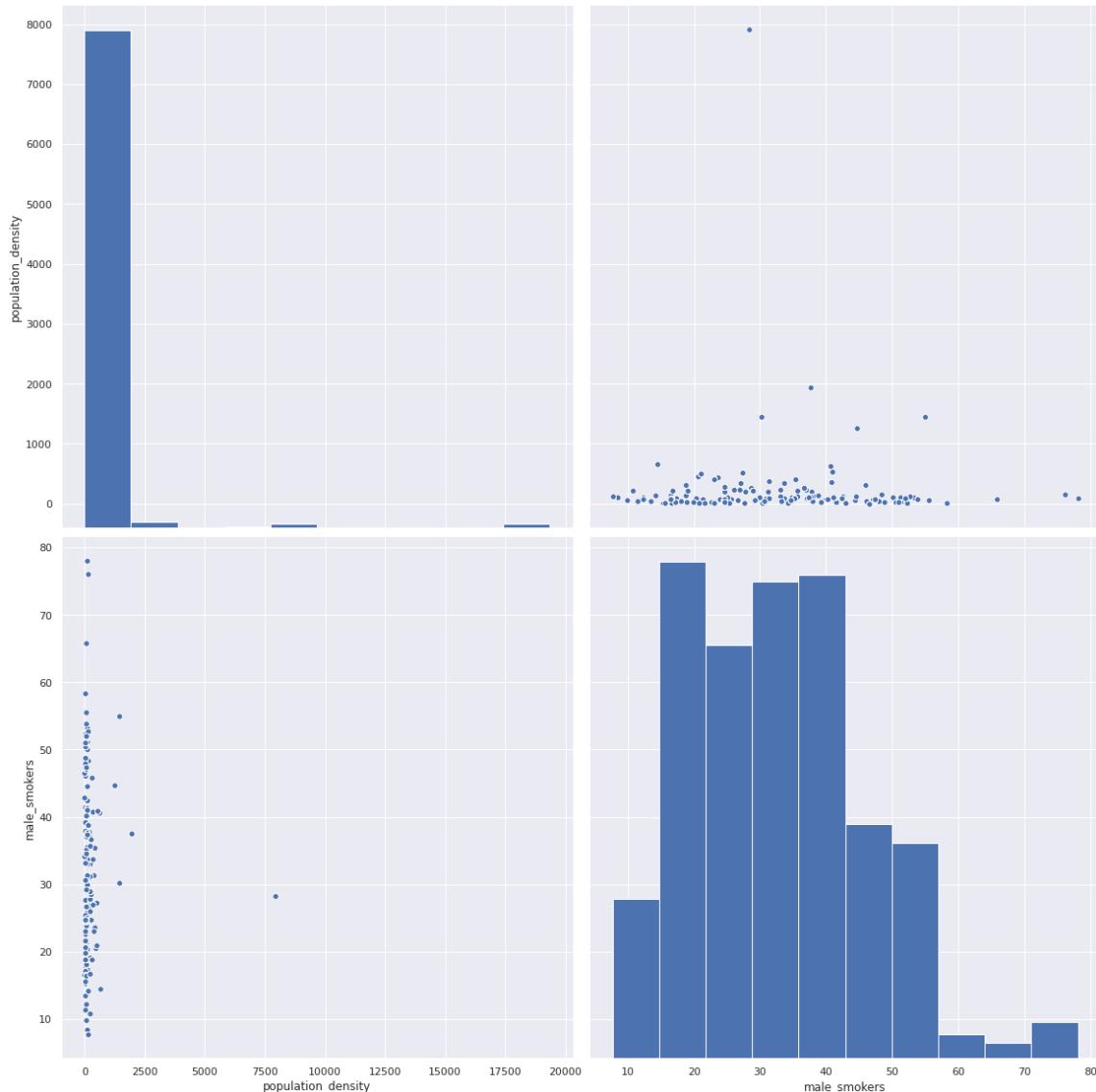


In [66]:

```
sns.pairplot(features, vars=["population_density", "male_smokers"], height=8)
```

Out[66]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffb7aa908>
```

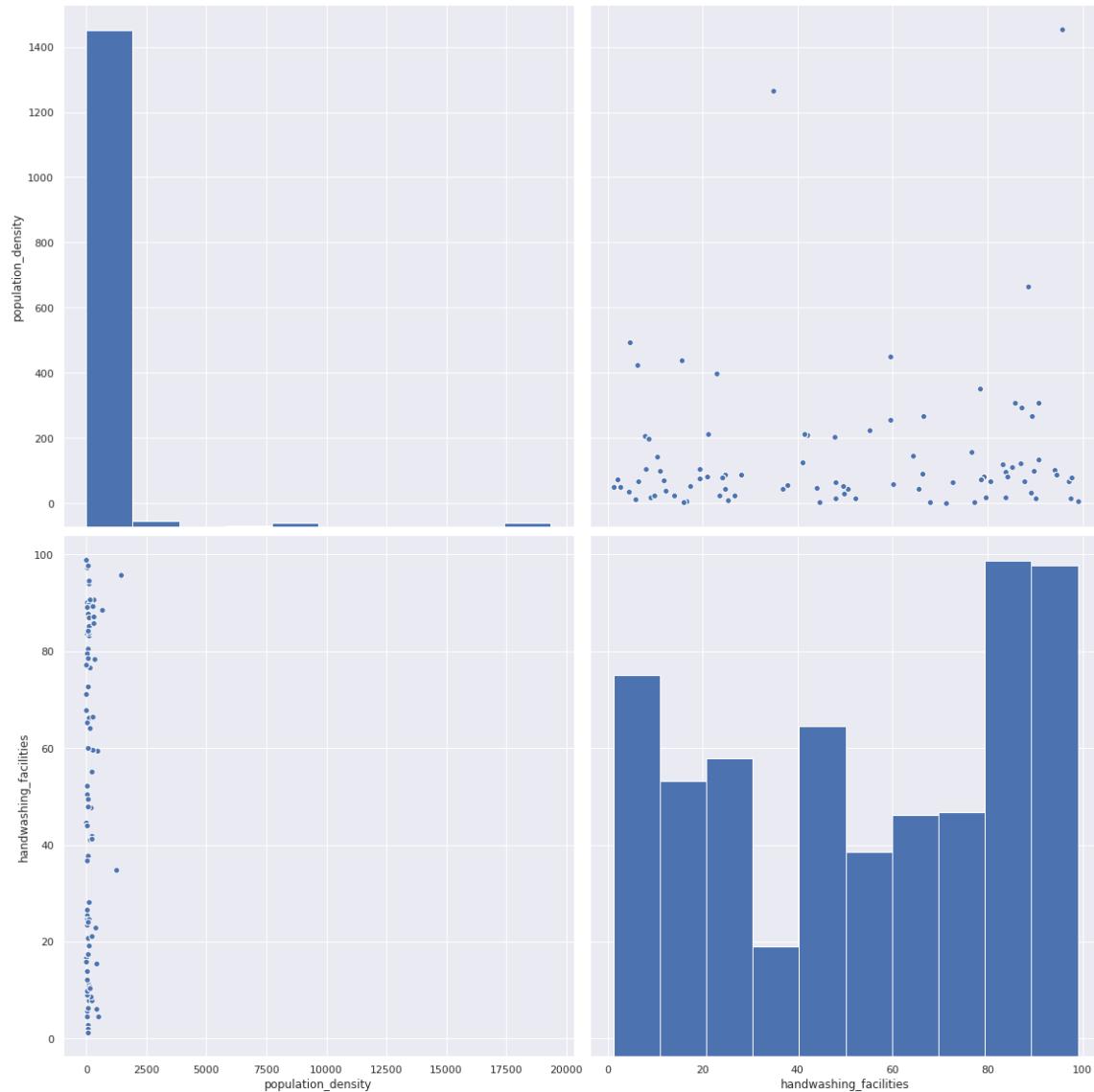


In [67]:

```
sns.pairplot(features, vars=["population_density", "handwashing_facilities"], height=8)
```

Out[67]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffb4d7668>
```

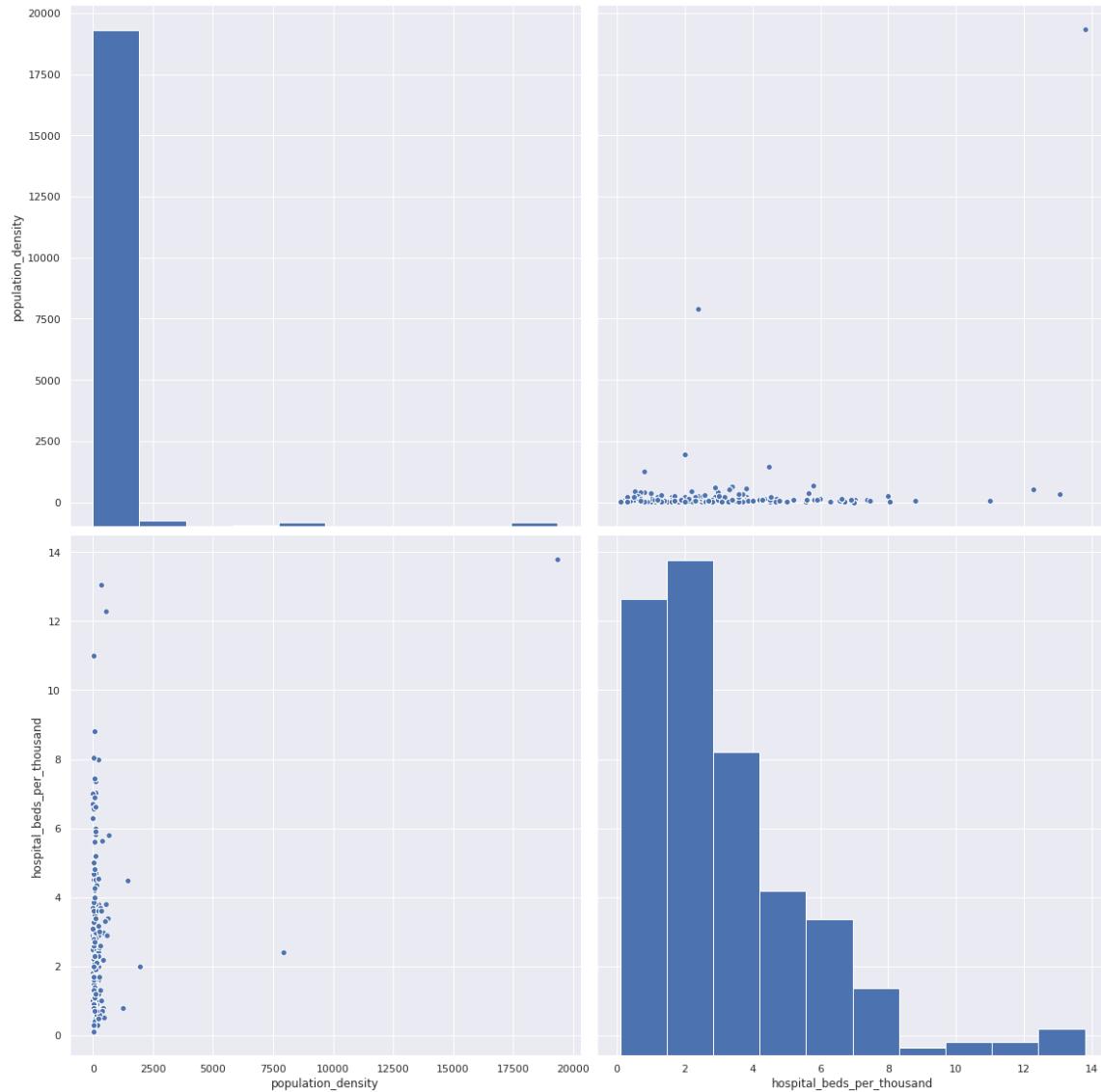


In [68]:

```
sns.pairplot(features, vars=["population_density", "hospital_beds_per_thousand"], height=8)
```

Out[68]:

```
<seaborn.axisgrid.PairGrid at 0x7f0fffc01f780>
```

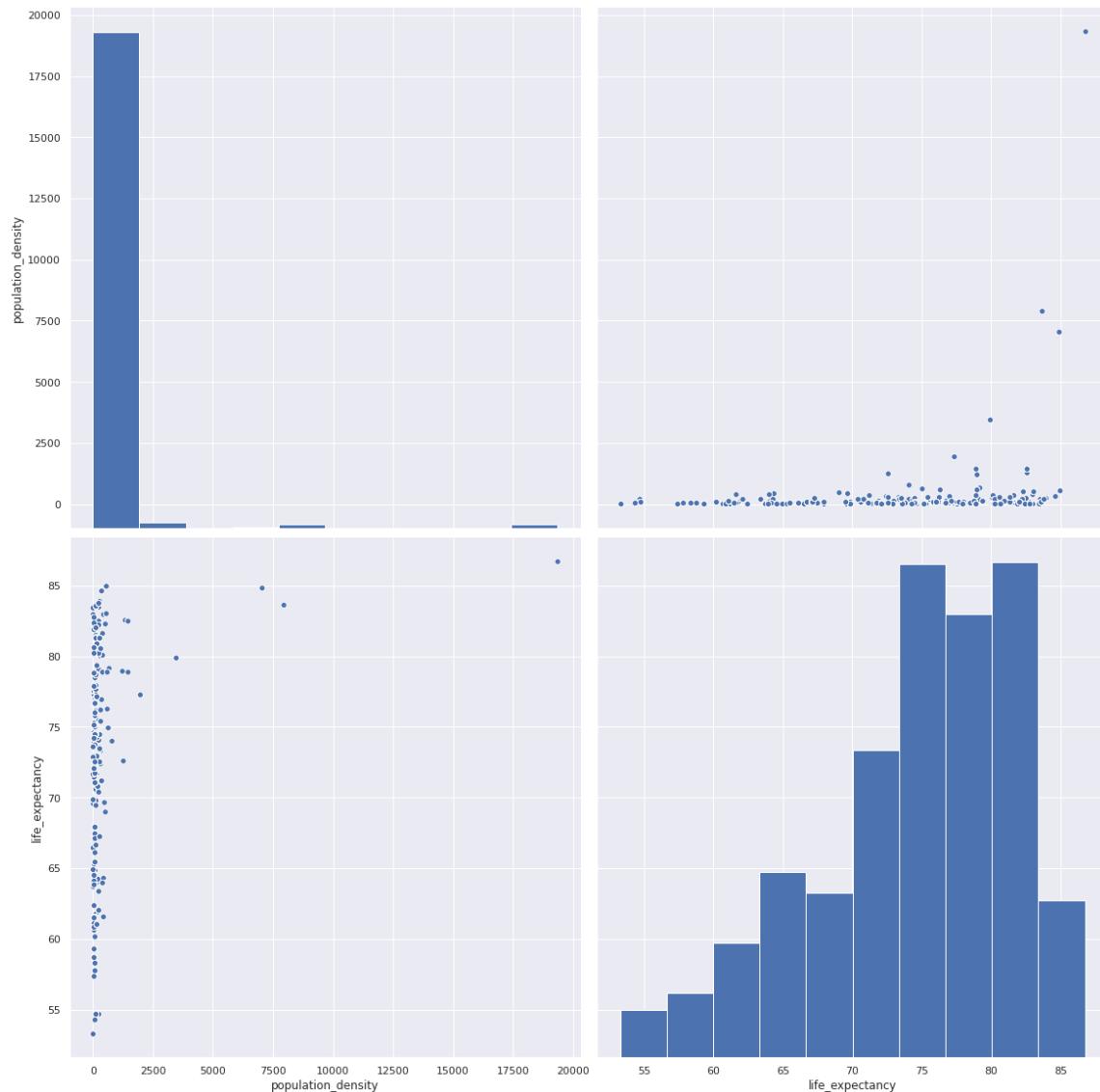


In [69]:

```
sns.pairplot(features, vars=["population_density", "life_expectancy"], height=8)
```

Out[69]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffb09b080>
```

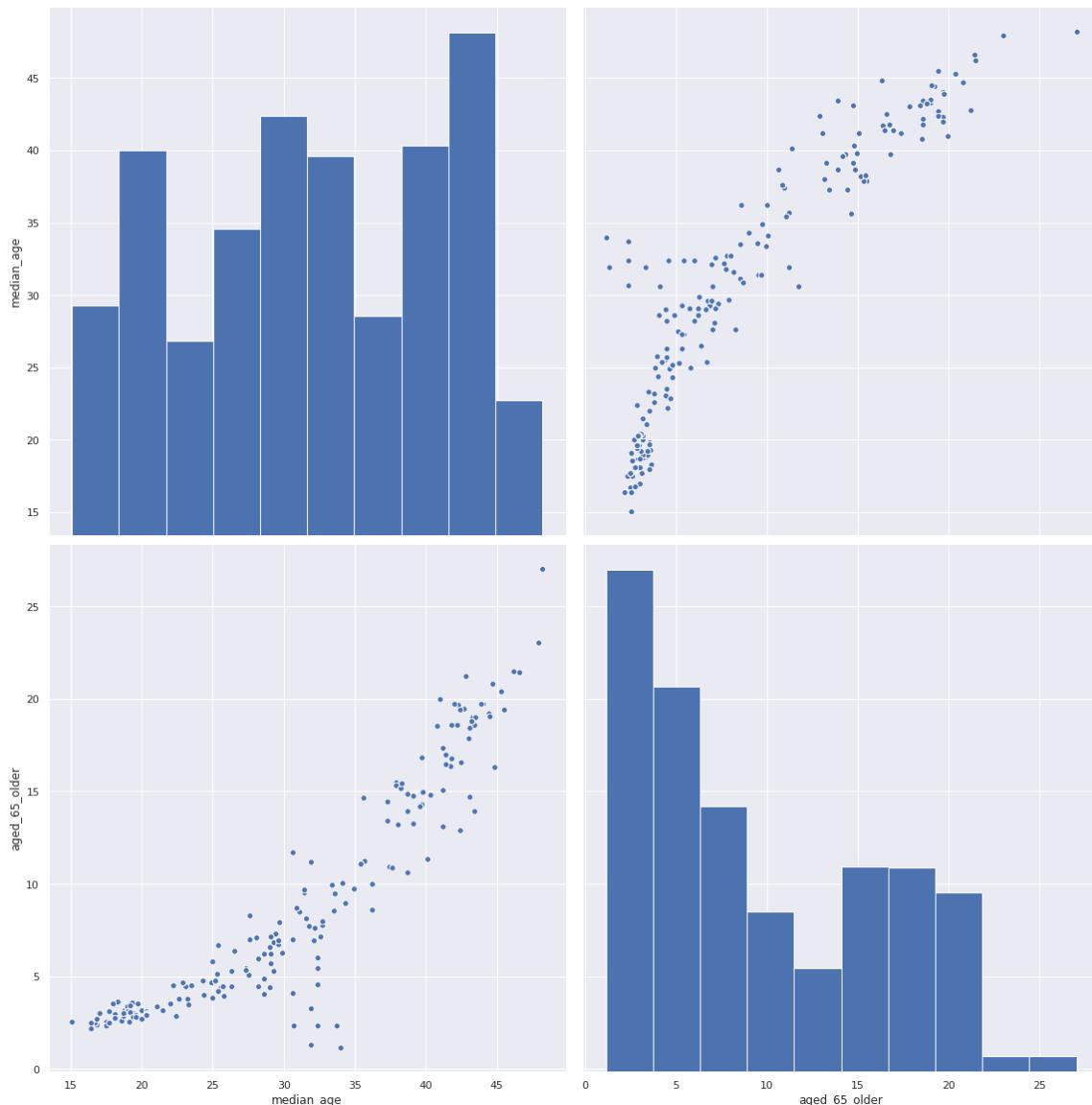


In [70]:

```
sns.pairplot(features, vars=["median_age", "aged_65_older"], height=8)
```

Out[70]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffae4b4e0>
```

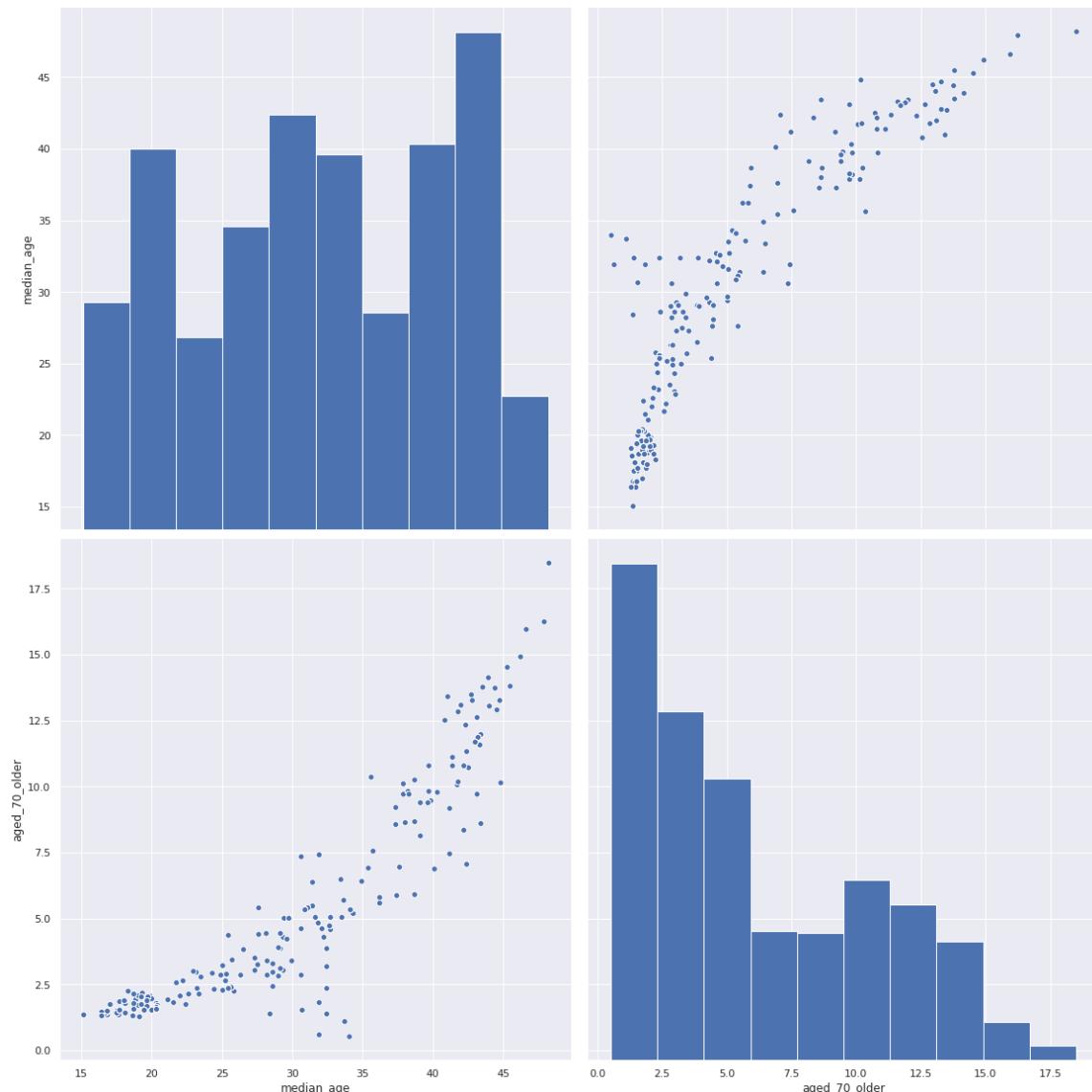


In [71]:

```
sns.pairplot(features, vars=["median_age", "aged_70_older"], height=8)
```

Out[71]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffadafa90>
```

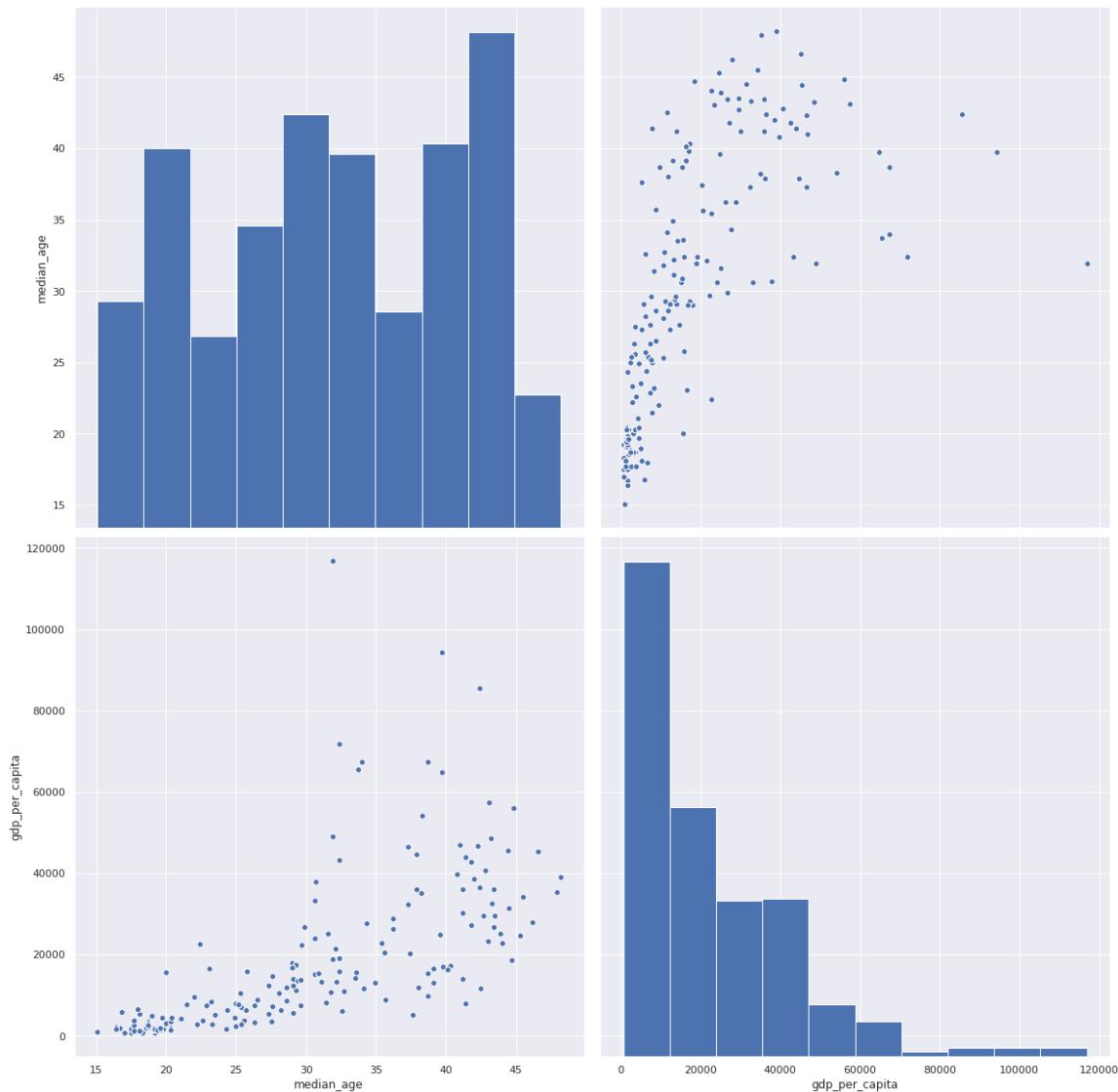


In [72]:

```
sns.pairplot(features, vars=["median_age", "gdp_per_capita"], height=8)
```

Out[72]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffaee3438>
```

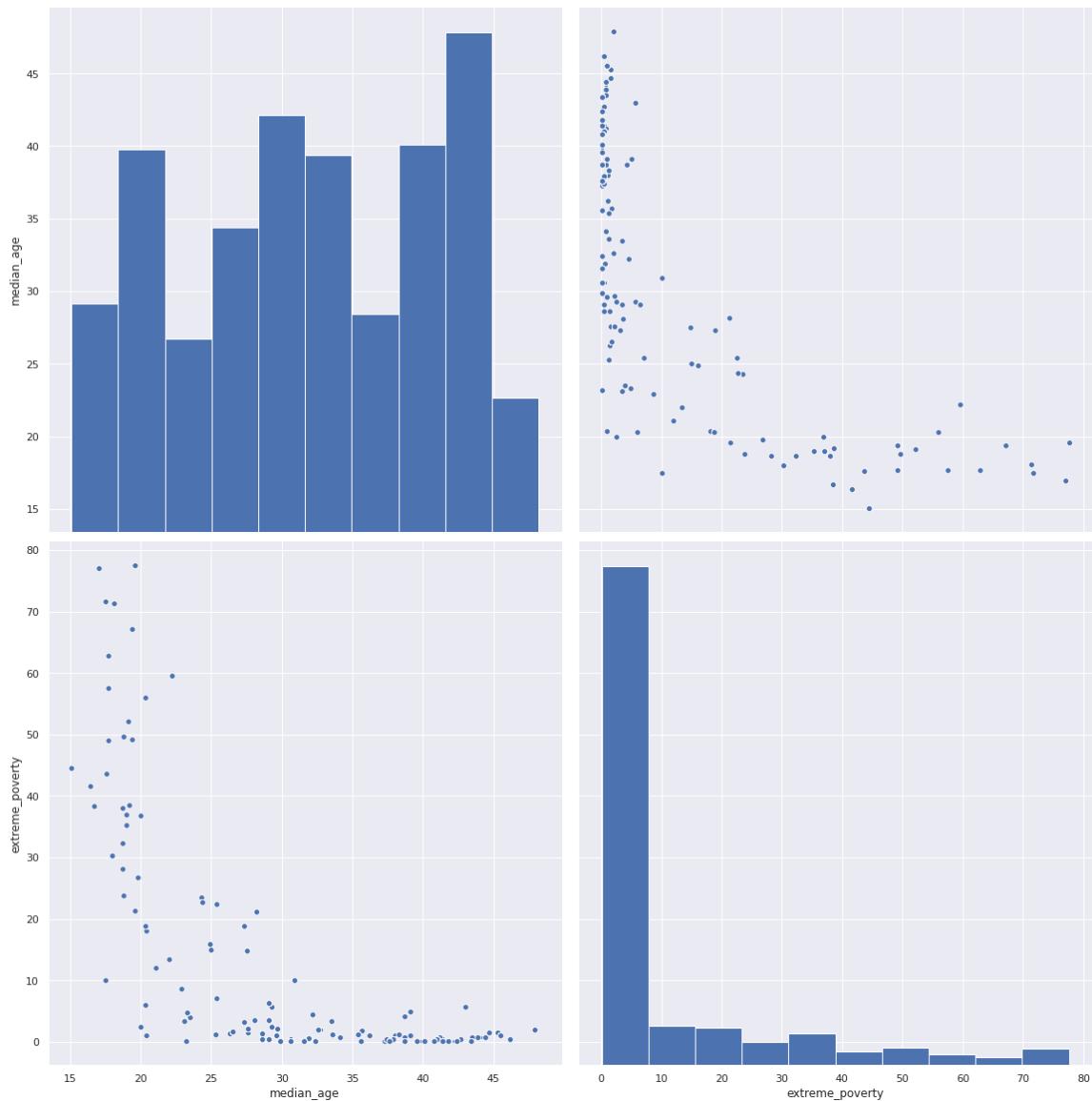


In [73]:

```
sns.pairplot(features, vars=["median_age", "extreme_poverty"], height=8)
```

Out[73]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffa8604e0>
```

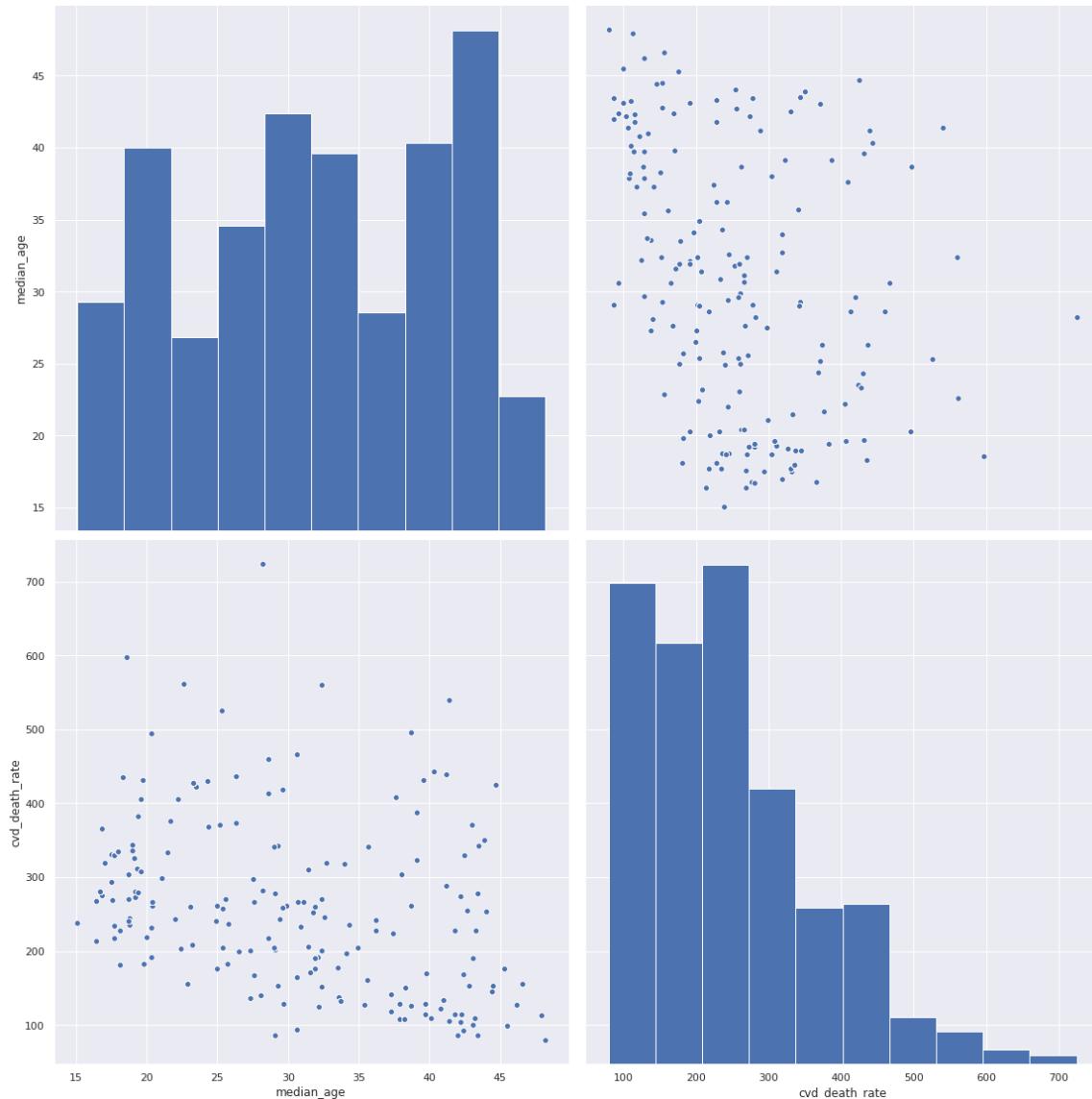


In [74]:

```
sns.pairplot(features, vars=["median_age", "cvd_death_rate"], height=8)
```

Out[74]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffa66c438>
```

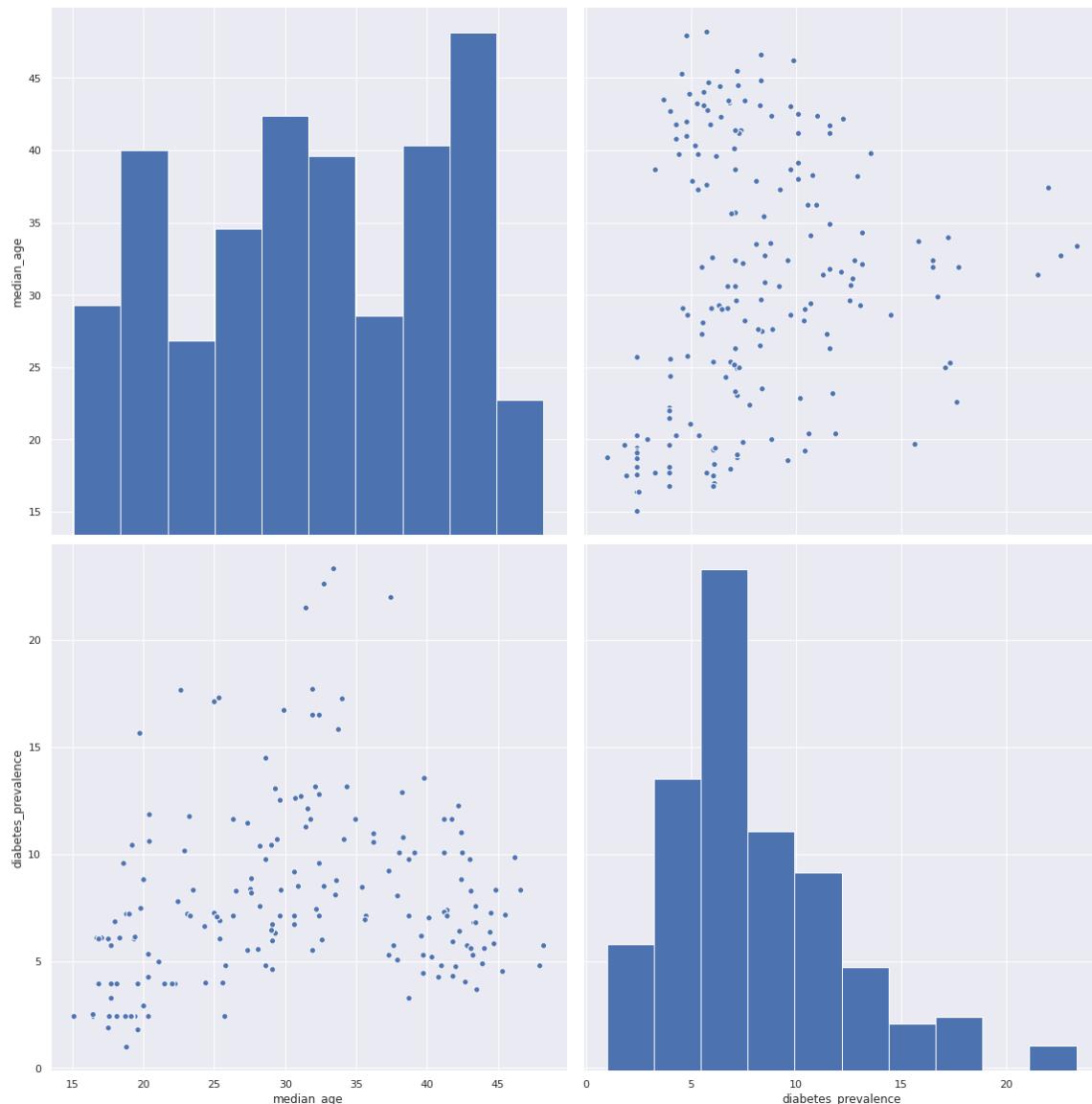


In [75]:

```
sns.pairplot(features, vars=["median_age", "diabetes_prevalence"], height=8)
```

Out[75]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffa474d30>
```

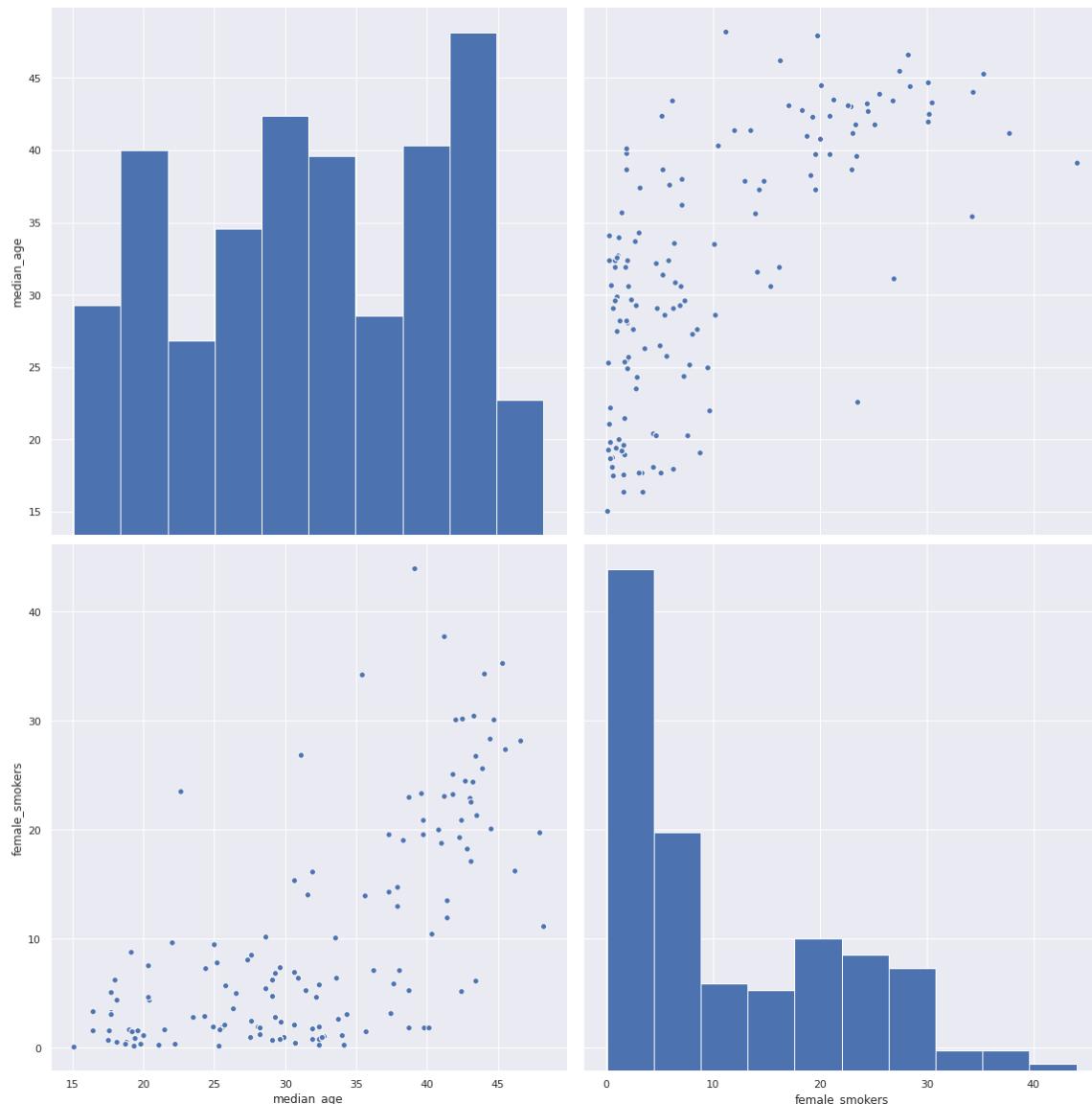


In [76]:

```
sns.pairplot(features, vars=["median_age", "female_smokers"], height=8)
```

Out[76]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffa277cf8>
```

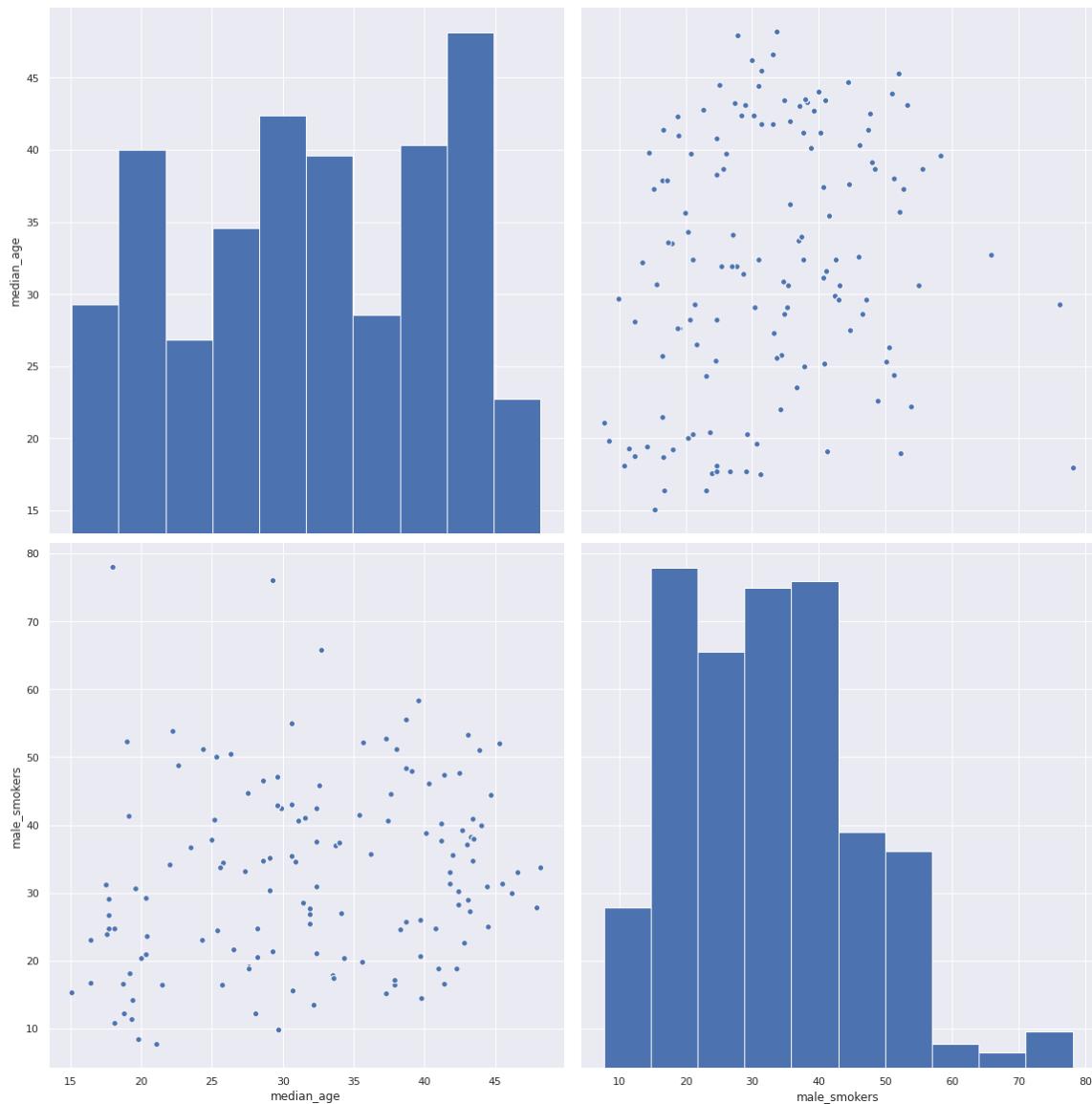


In [77]:

```
sns.pairplot(features, vars=["median_age", "male_smokers"], height=8)
```

Out[77]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffa0756d8>
```

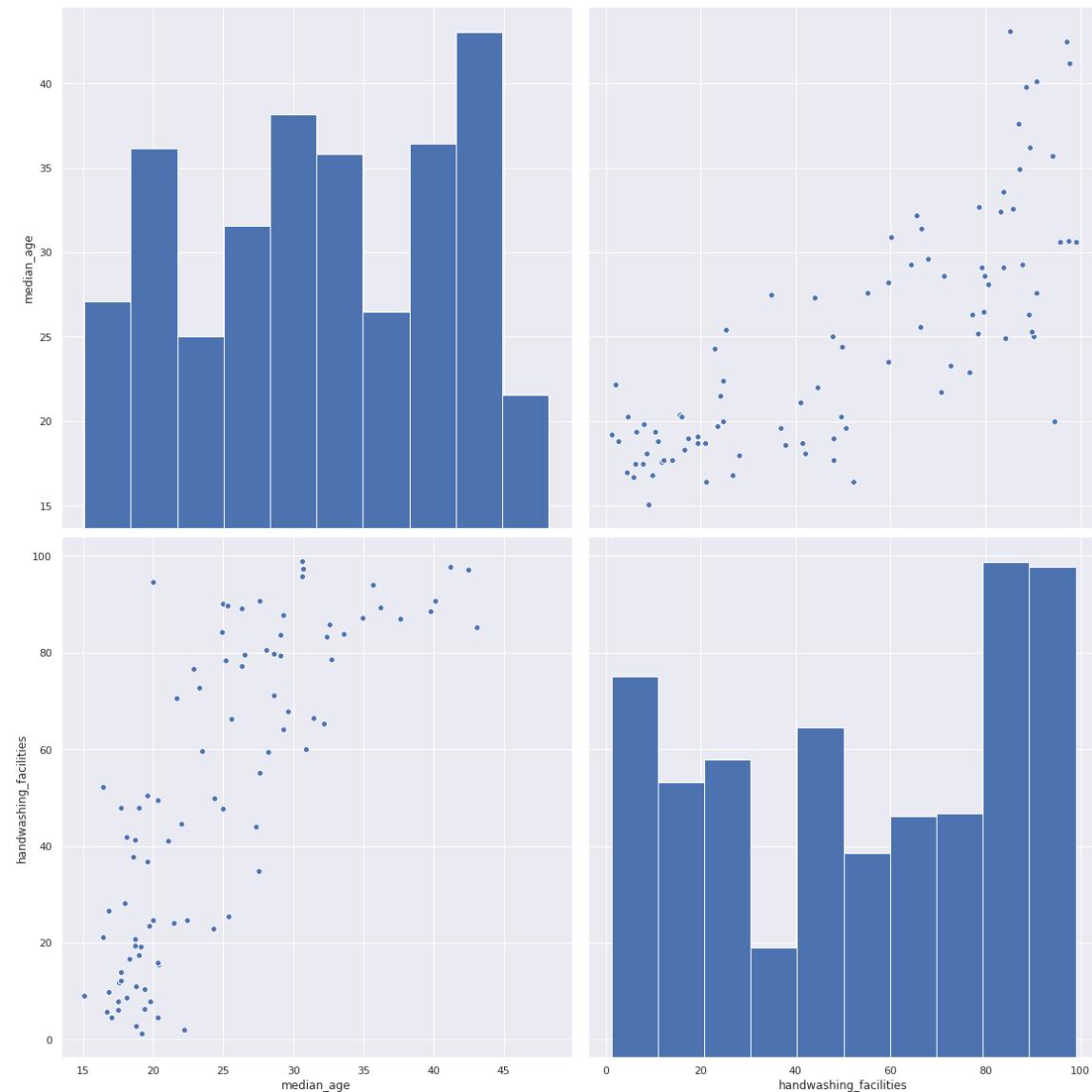


In [78]:

```
sns.pairplot(features, vars=["median_age", "handwashing_facilities"], height=8)
```

Out[78]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff9e79b00>
```

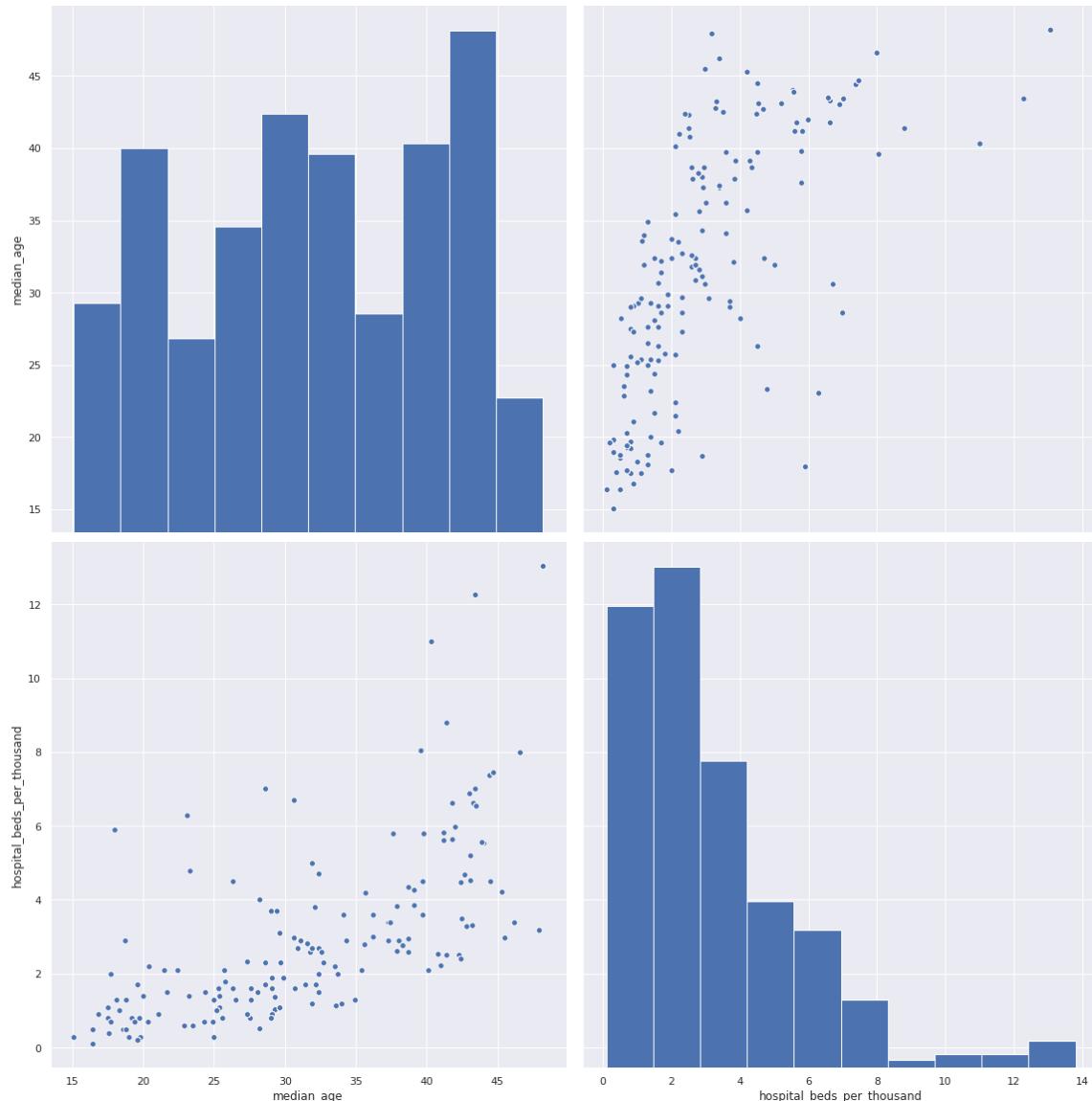


In [79]:

```
sns.pairplot(features, vars=["median_age", "hospital_beds_per_thousand"], height=8)
```

Out[79]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff9c5bef0>
```

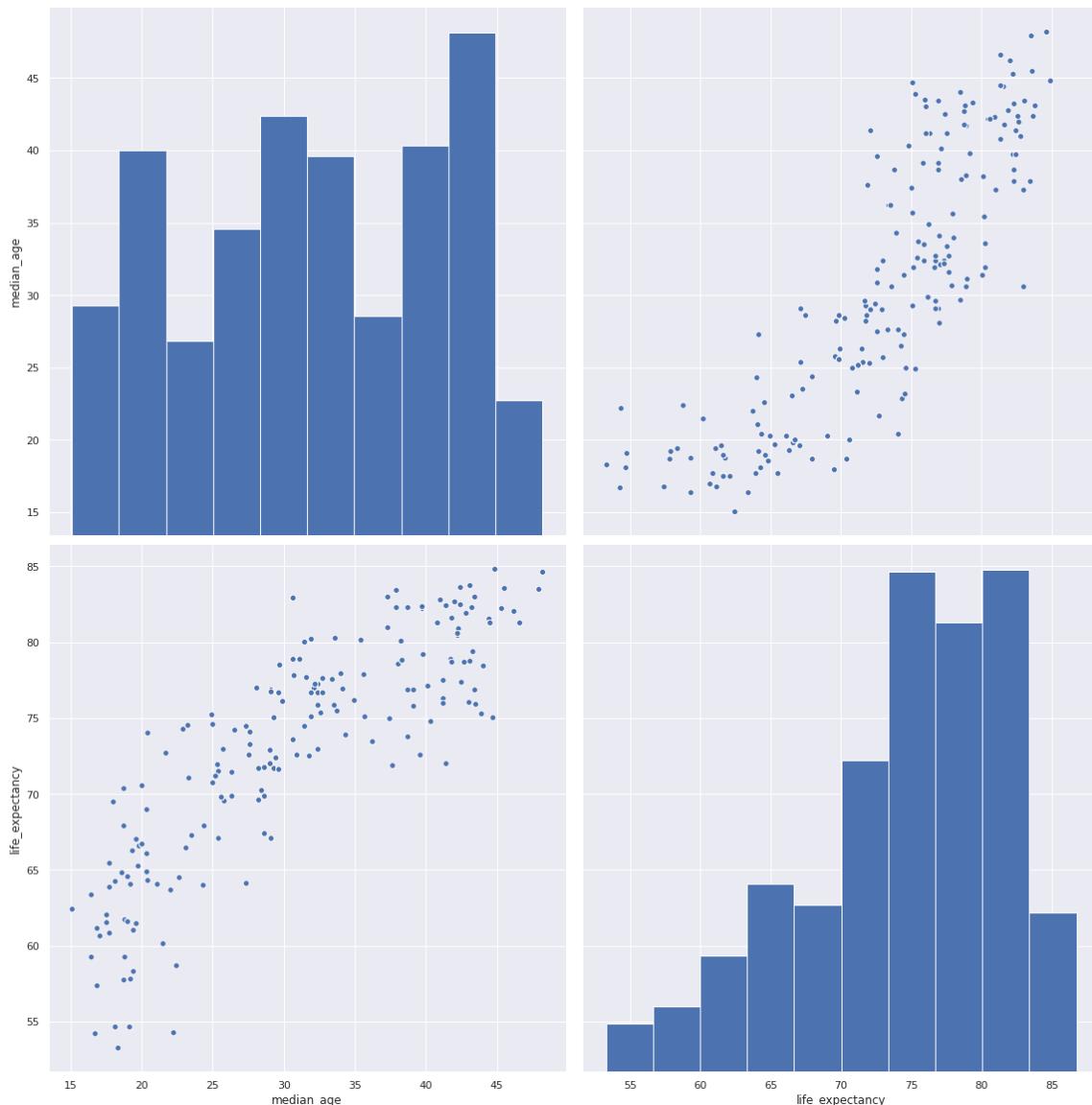


In [80]:

```
sns.pairplot(features, vars=["median_age", "life_expectancy"], height=8)
```

Out[80]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ffb4e8a90>
```

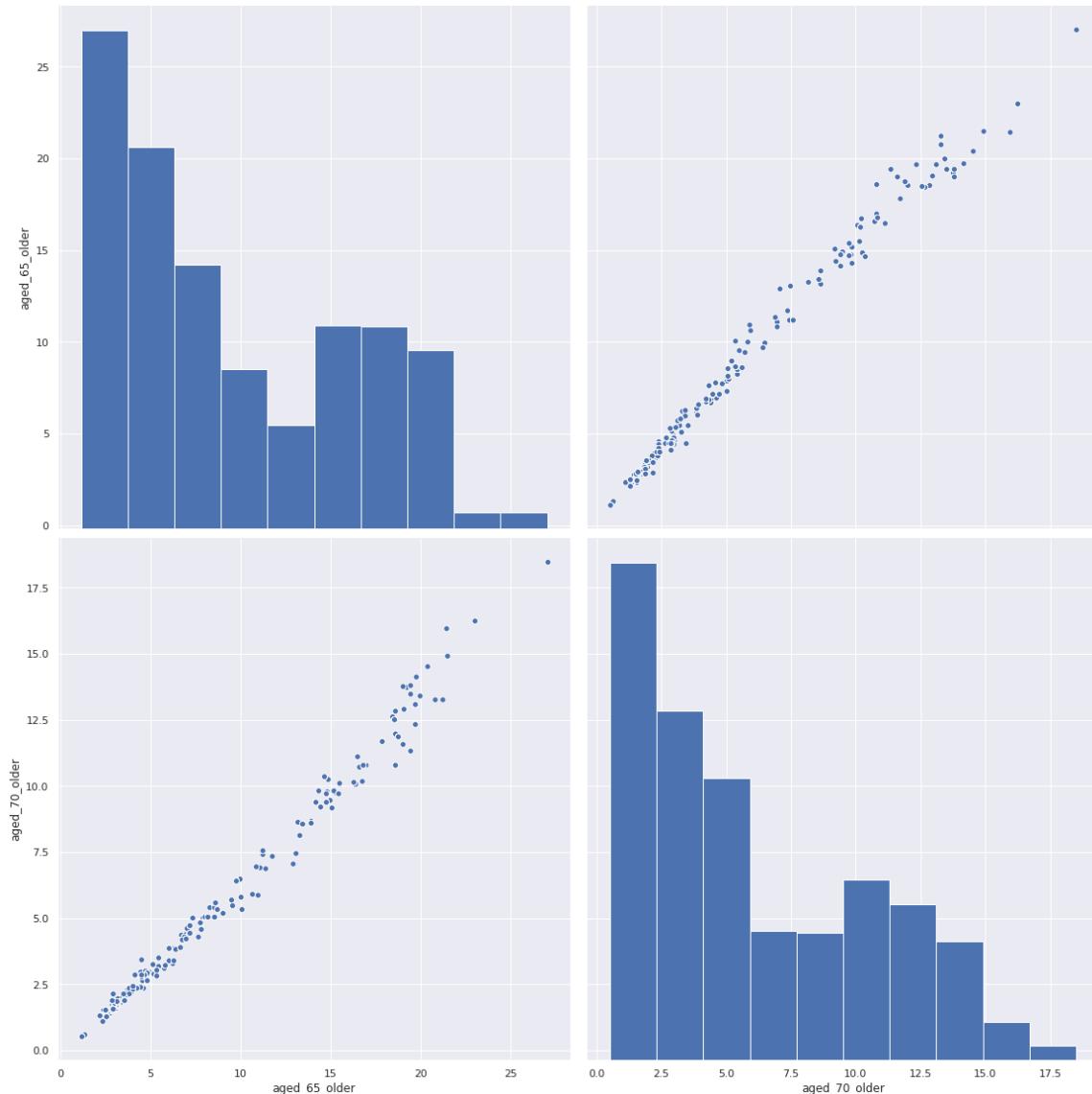


In [81]:

```
sns.pairplot(features, vars=["aged_65_older", "aged_70_older"], height=8)
```

Out[81]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff9870e80>
```

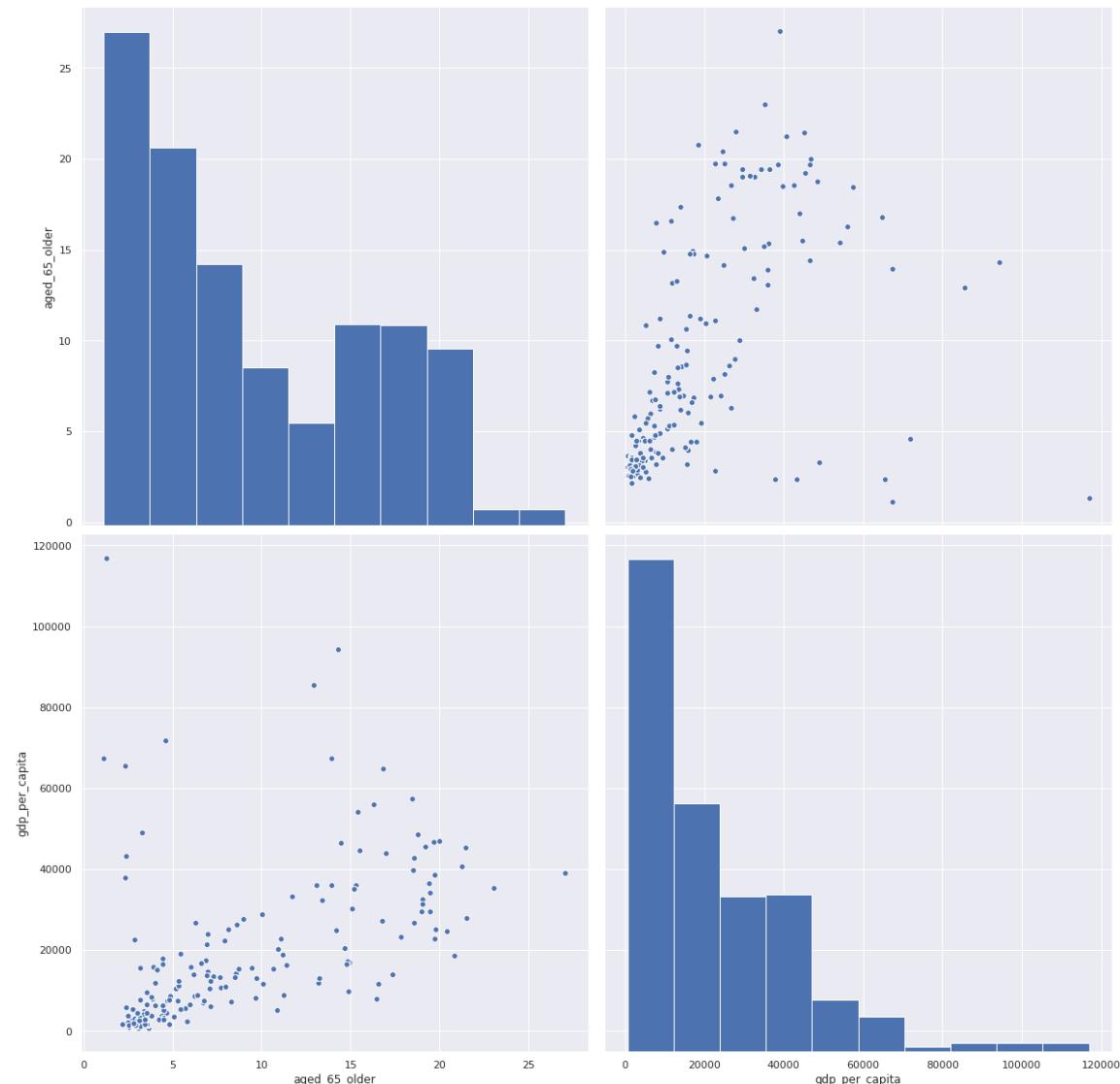


In [82]:

```
sns.pairplot(features, vars=["aged_65_older", "gdp_per_capita"], height=8)
```

Out[82]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff99b7860>
```

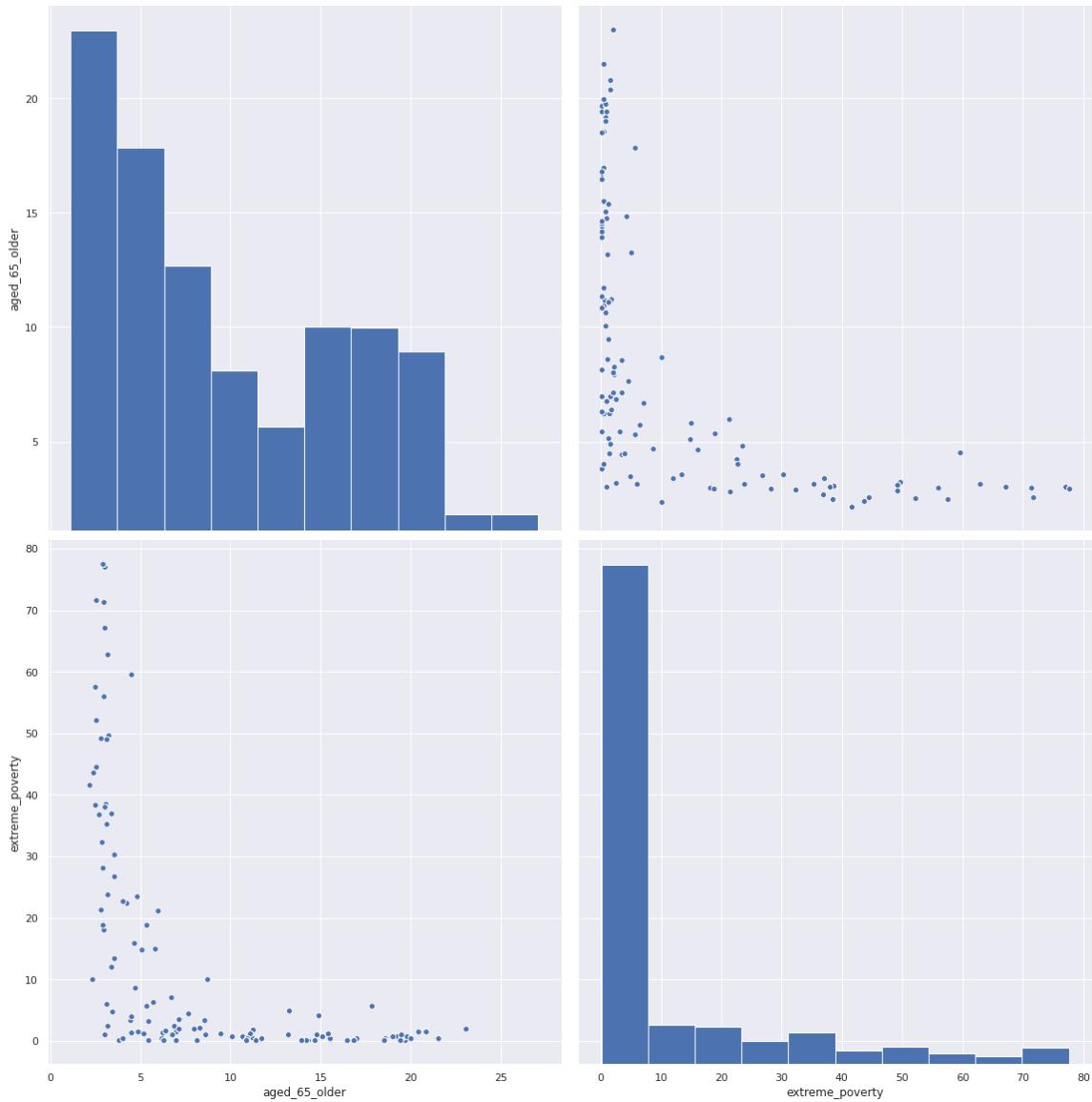


In [83]:

```
sns.pairplot(features, vars=["aged_65_older", "extreme_poverty"], height=8)
```

Out[83]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff947c2e8>
```

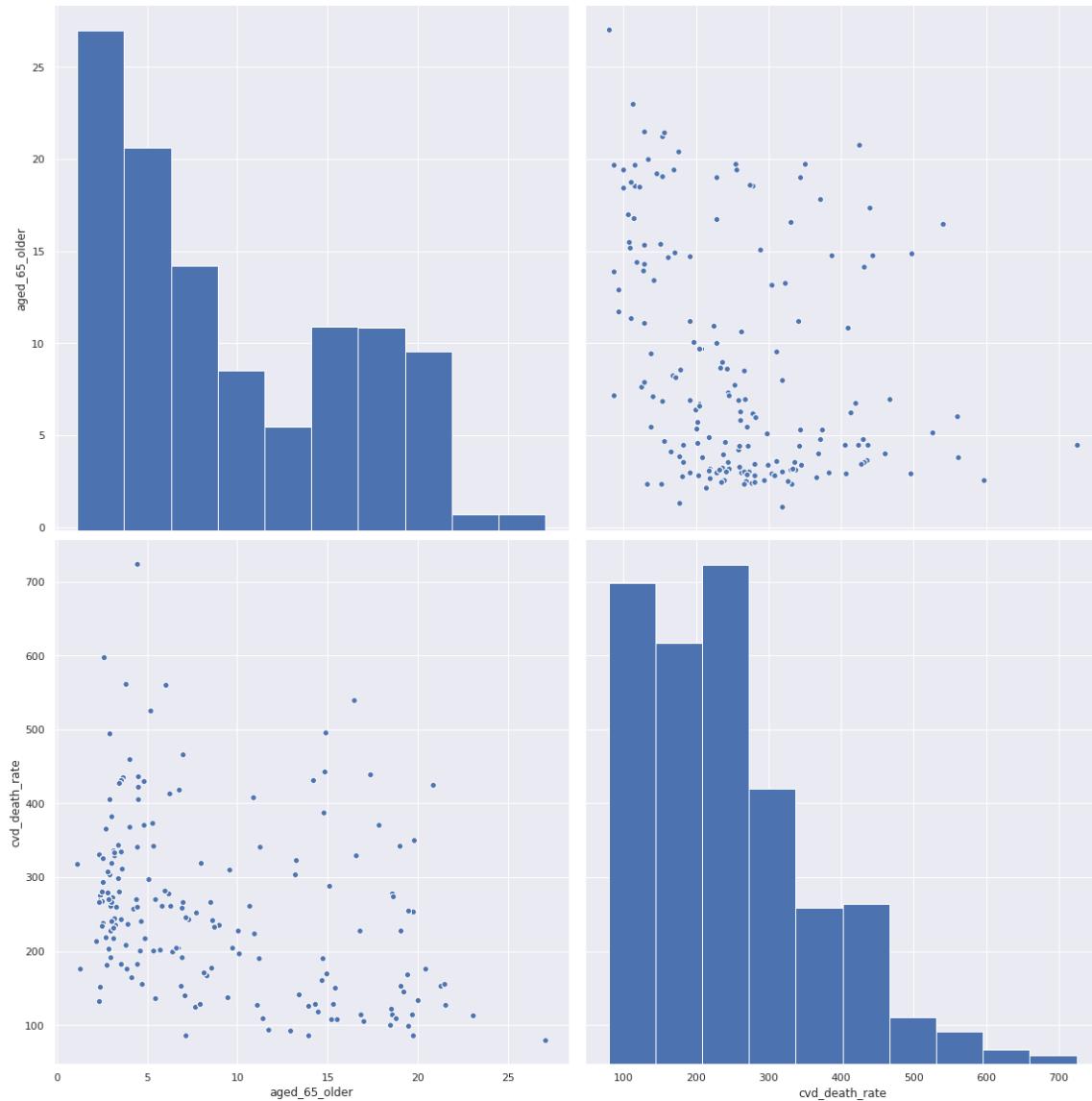


In [84]:

```
sns.pairplot(features, vars=["aged_65_older", "cvd_death_rate"], height=8)
```

Out[84]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff9217a20>
```

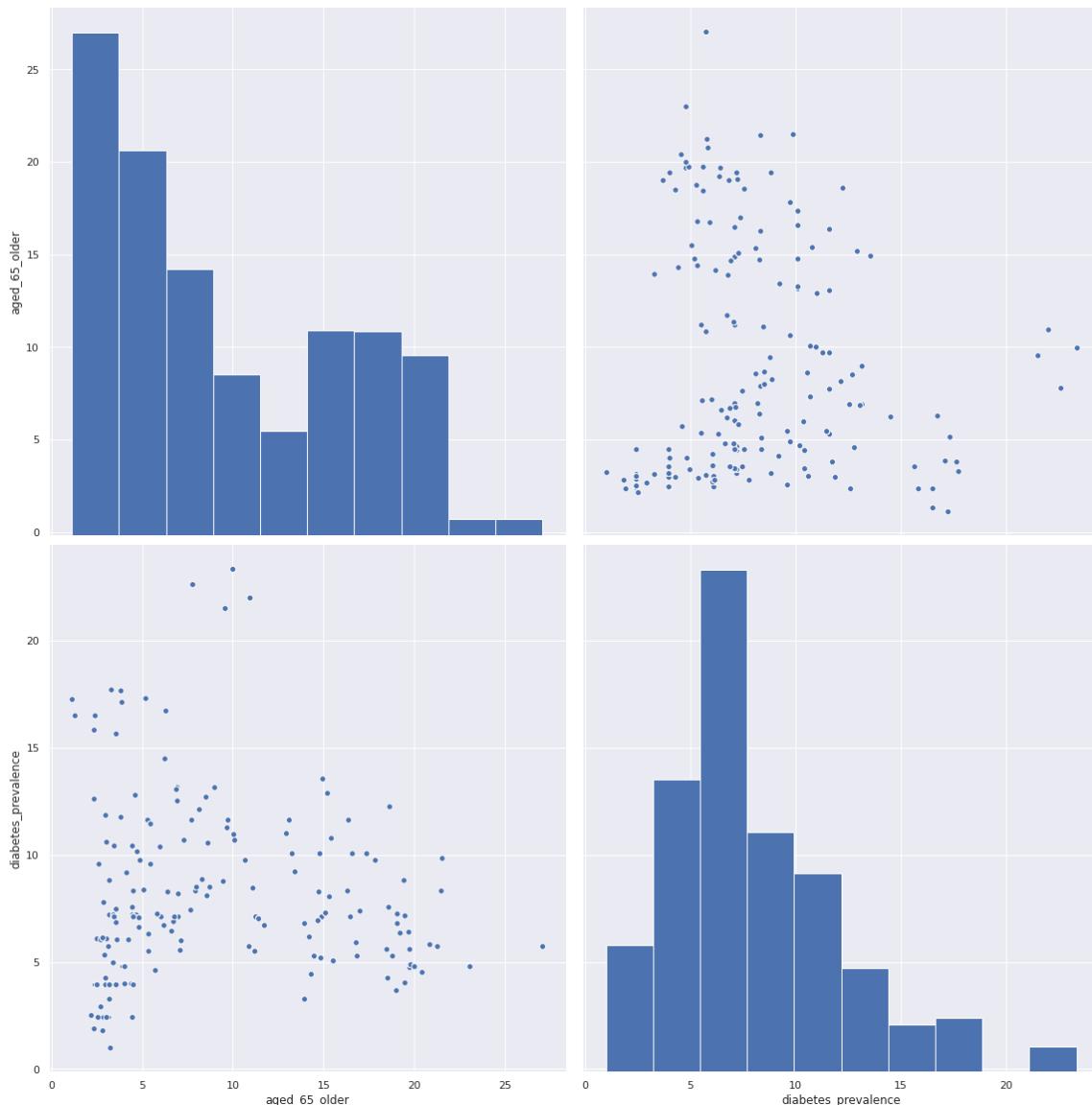


In [85]:

```
sns.pairplot(features, vars=["aged_65_older", "diabetes_prevalence"], height=8)
```

Out[85]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff90127b8>
```

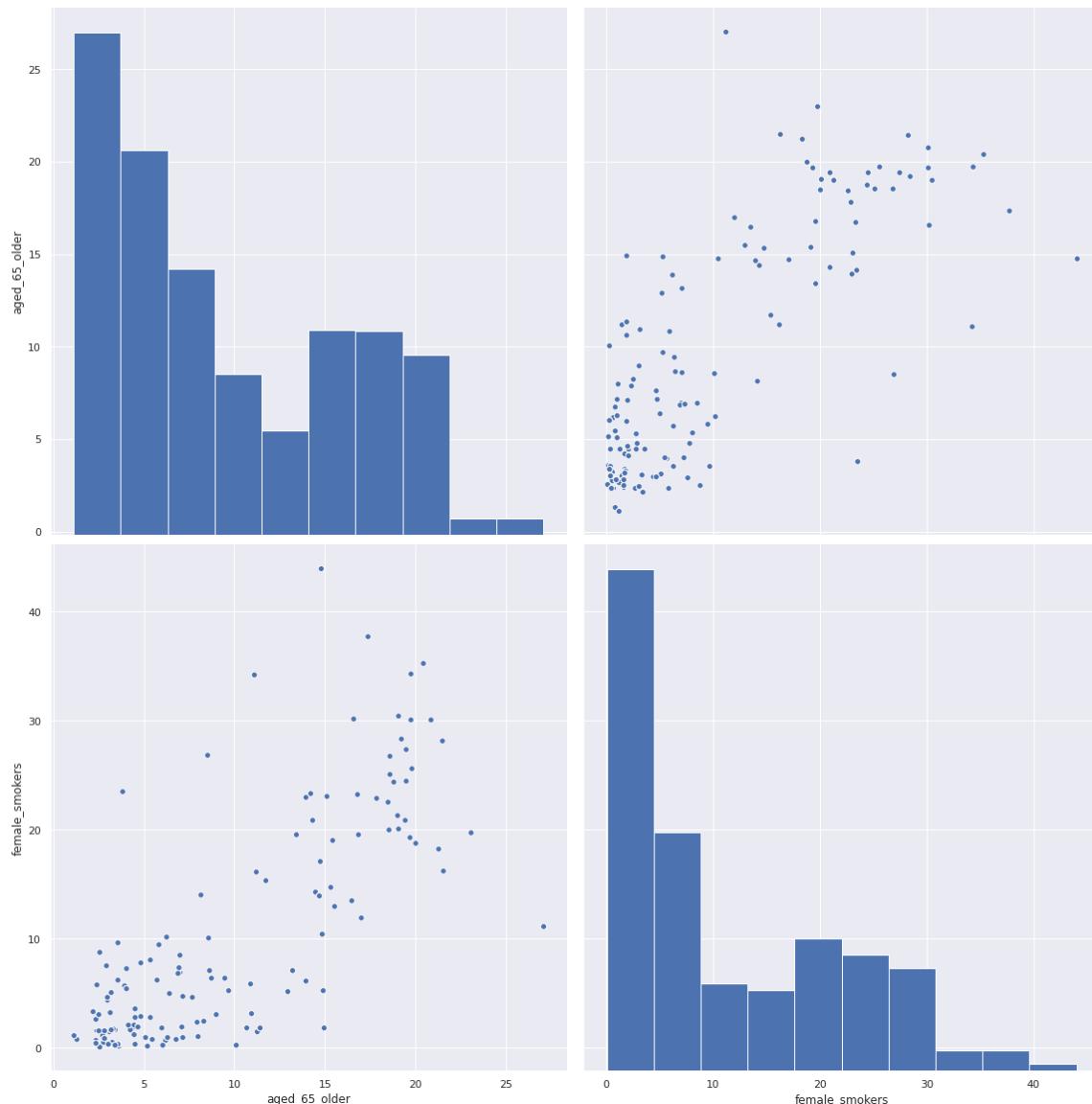


In [86]:

```
sns.pairplot(features, vars=["aged_65_older", "female_smokers"], height=8)
```

Out[86]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff8e74f98>
```

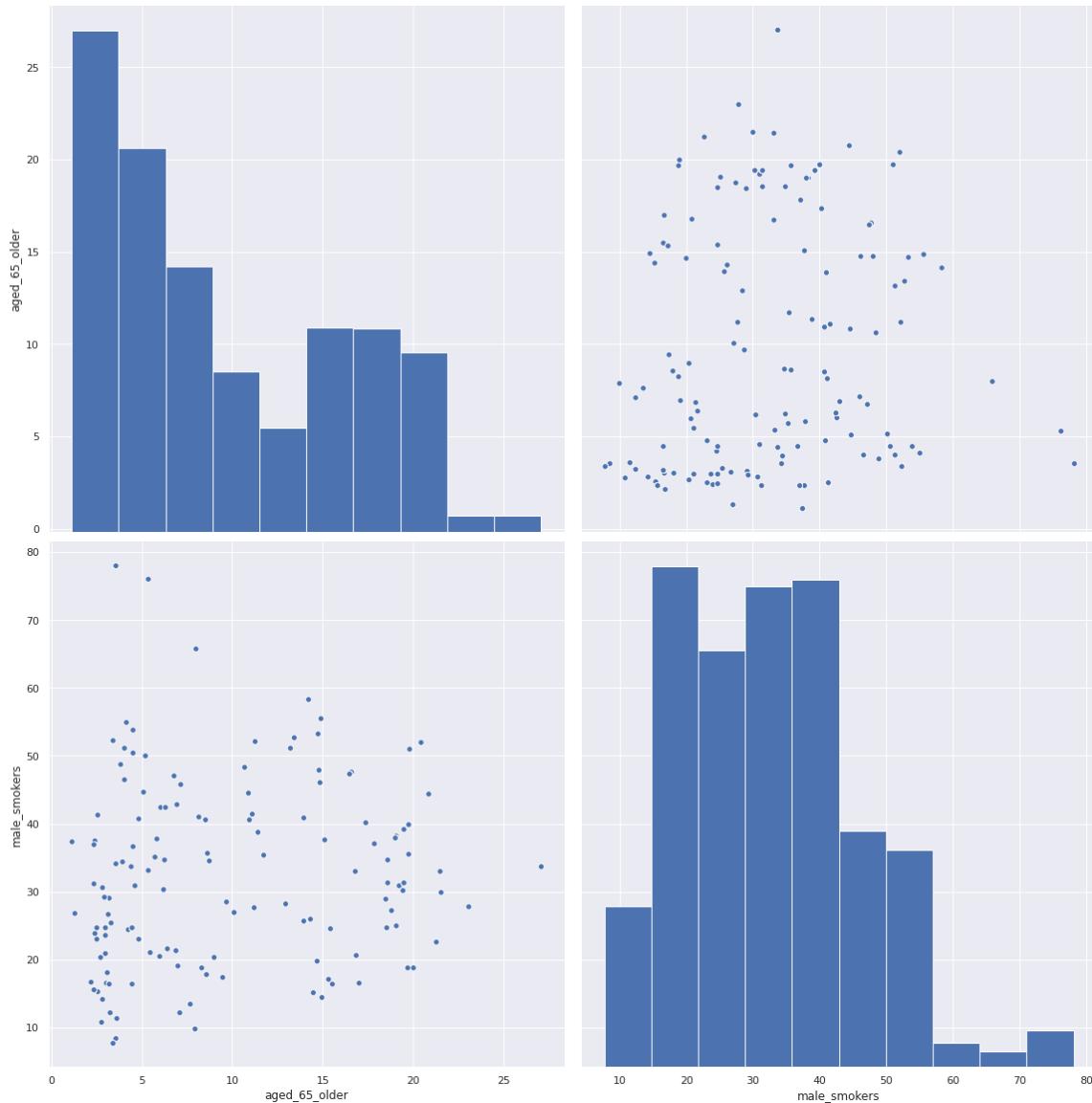


In [87]:

```
sns.pairplot(features, vars=["aged_65_older", "male_smokers"], height=8)
```

Out[87]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff8c6bd68>
```

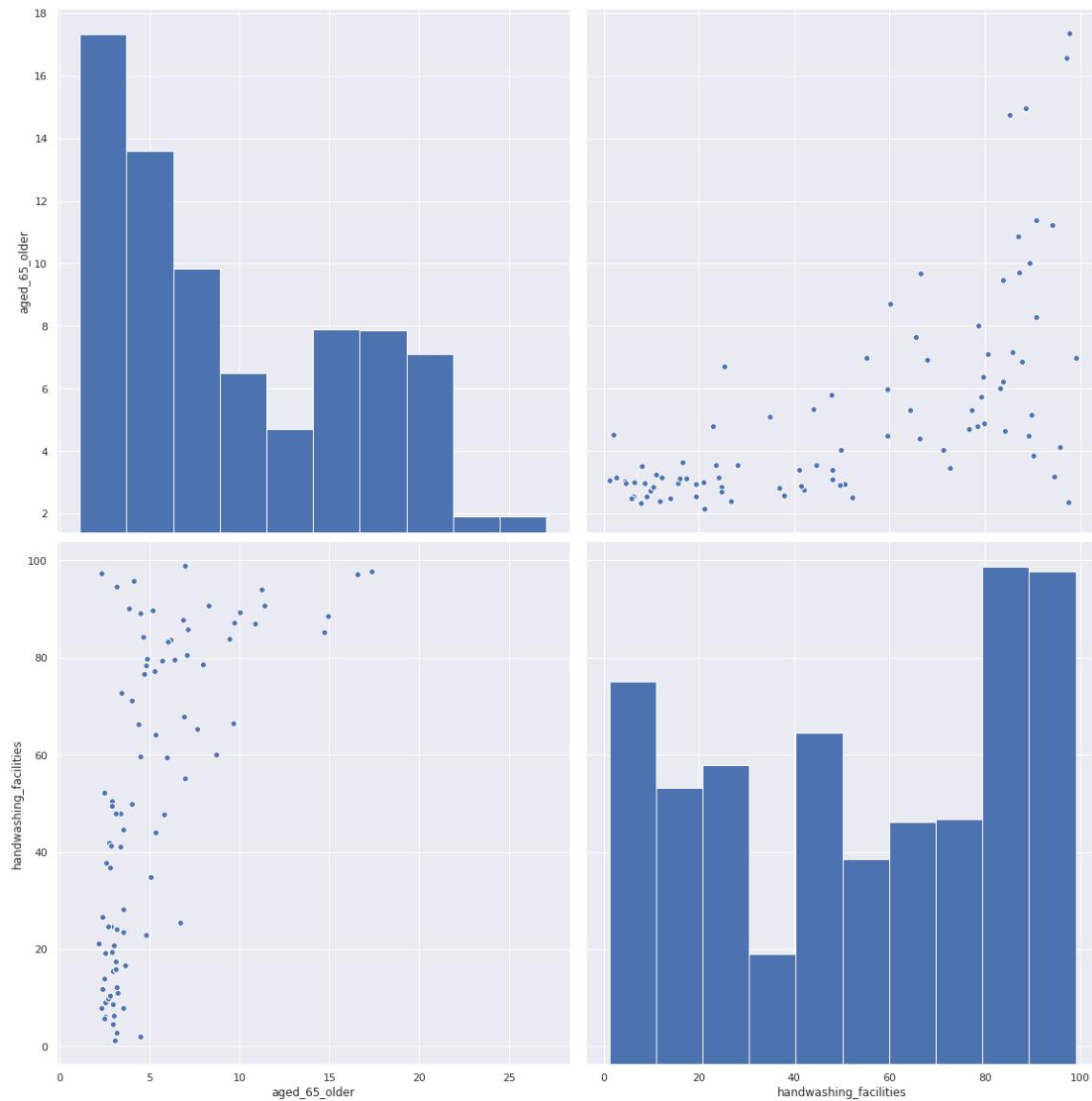


In [88]:

```
sns.pairplot(features, vars=["aged_65_older", "handwashing_facilities"], height=8)
```

Out[88]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff8a54550>
```

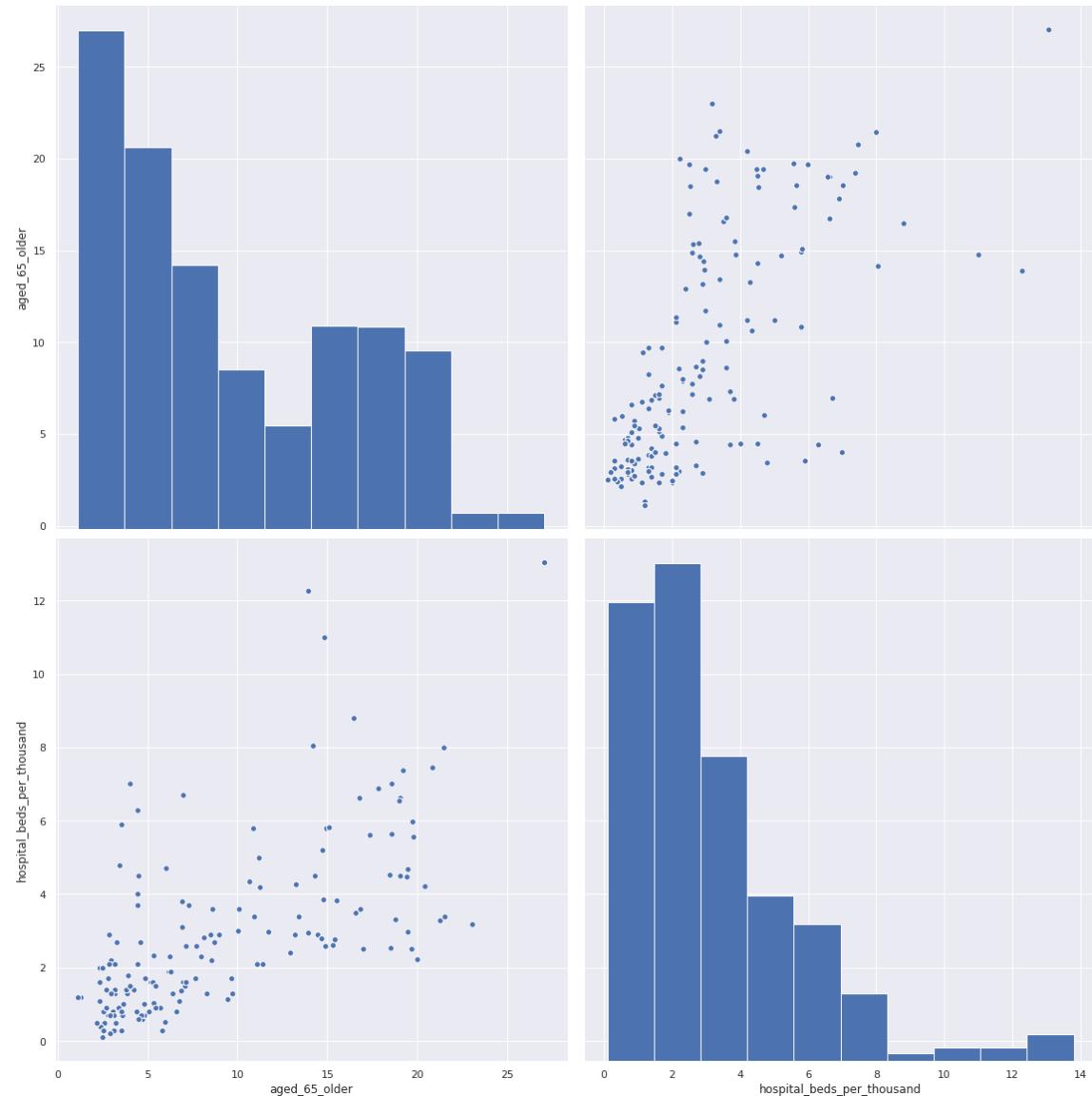


In [89]:

```
sns.pairplot(features, vars=["aged_65_older", "hospital_beds_per_thousand"], height=8)
```

Out[89]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff88722e8>
```

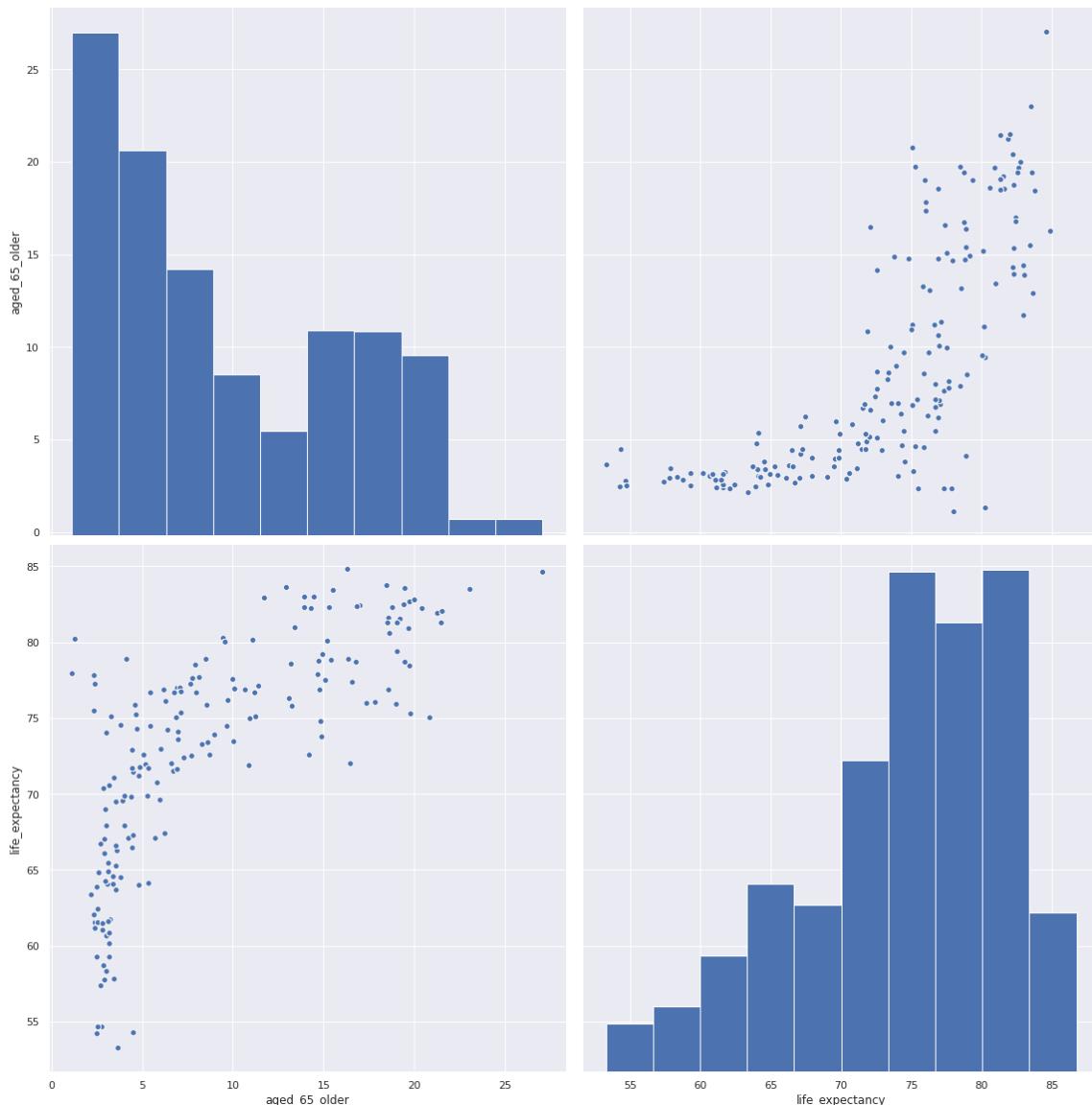


In [90]:

```
sns.pairplot(features, vars=["aged_65_older", "life_expectancy"], height=8)
```

Out[90]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff8a64ba8>
```

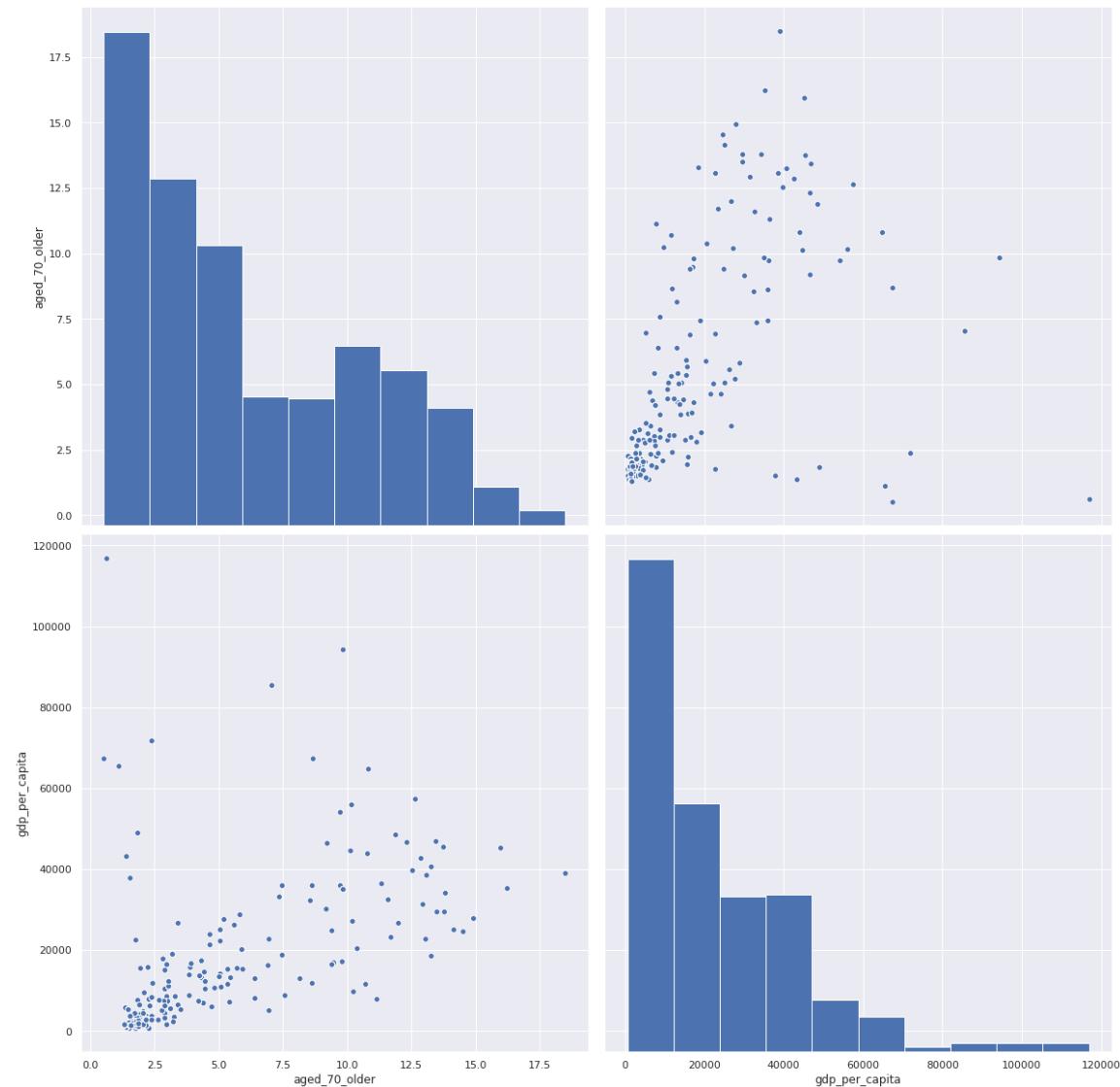


In [91]:

```
sns.pairplot(features, vars=["aged_70_older", "gdp_per_capita"], height=8)
```

Out[91]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff8409b00>
```

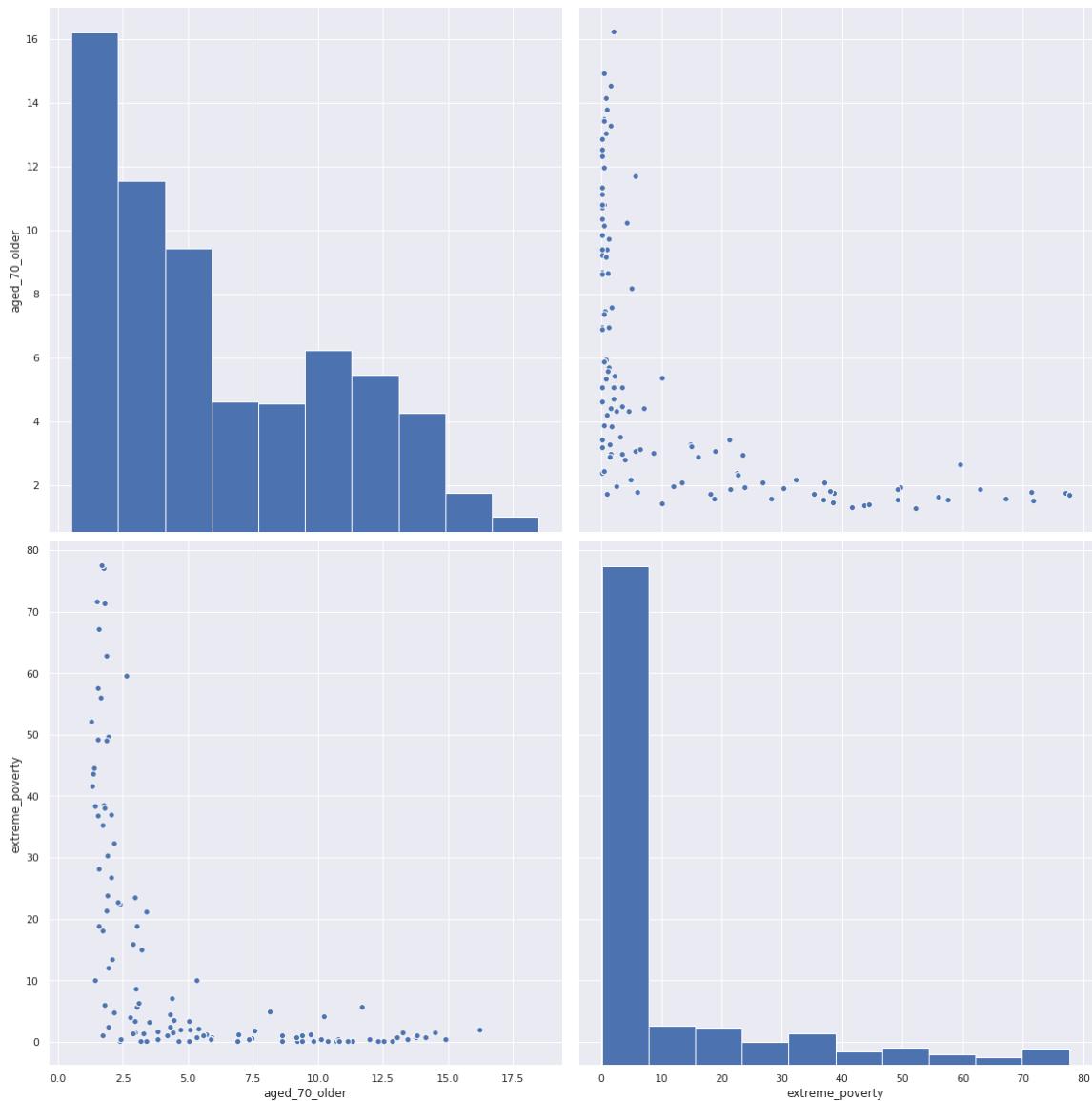


In [92]:

```
sns.pairplot(features, vars=["aged_70_older", "extreme_poverty"], height=8)
```

Out[92]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff8215b70>
```

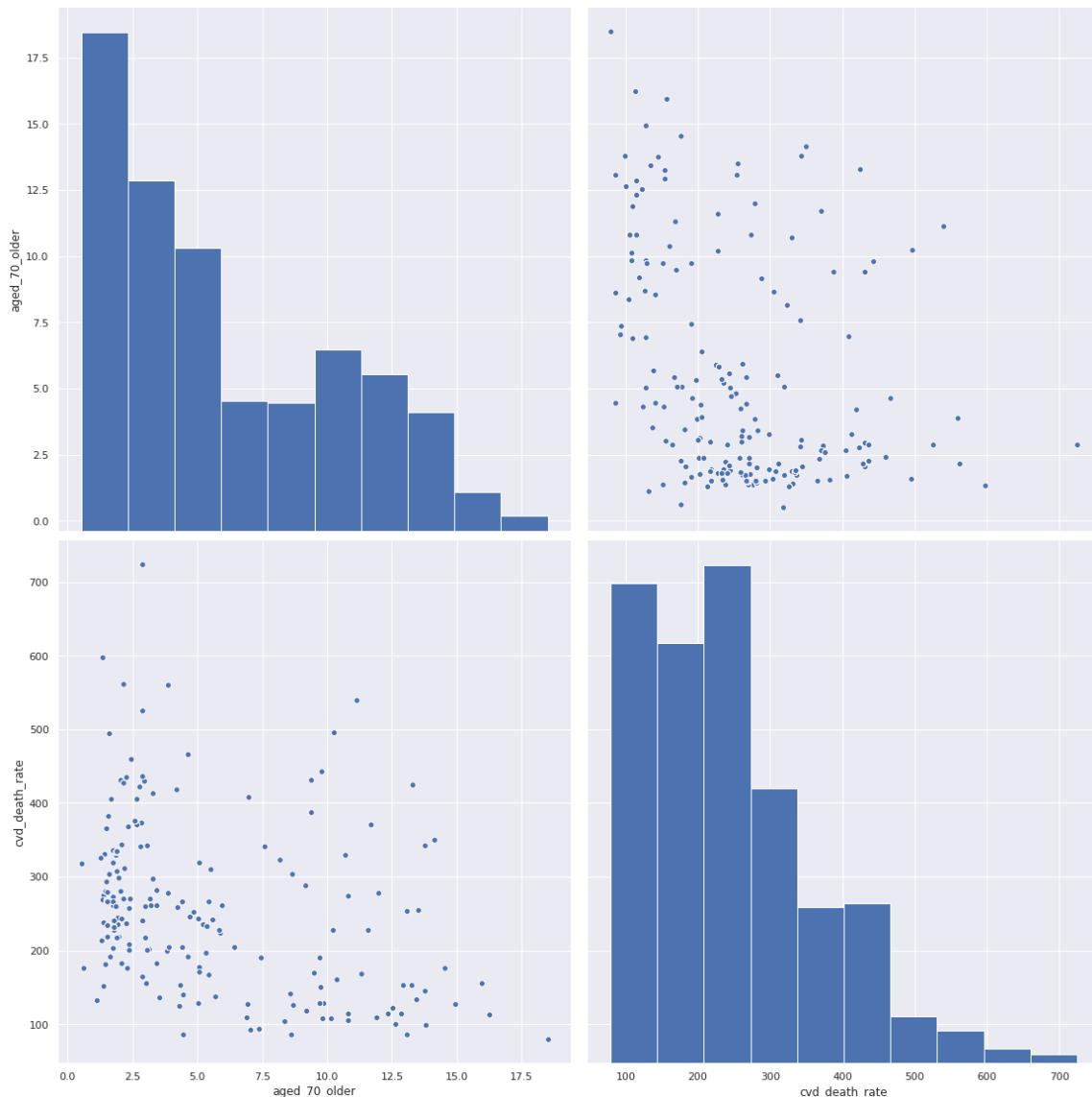


In [93]:

```
sns.pairplot(features, vars=["aged_70_older", "cvd_death_rate"], height=8)
```

Out[93]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff810bbe0>
```

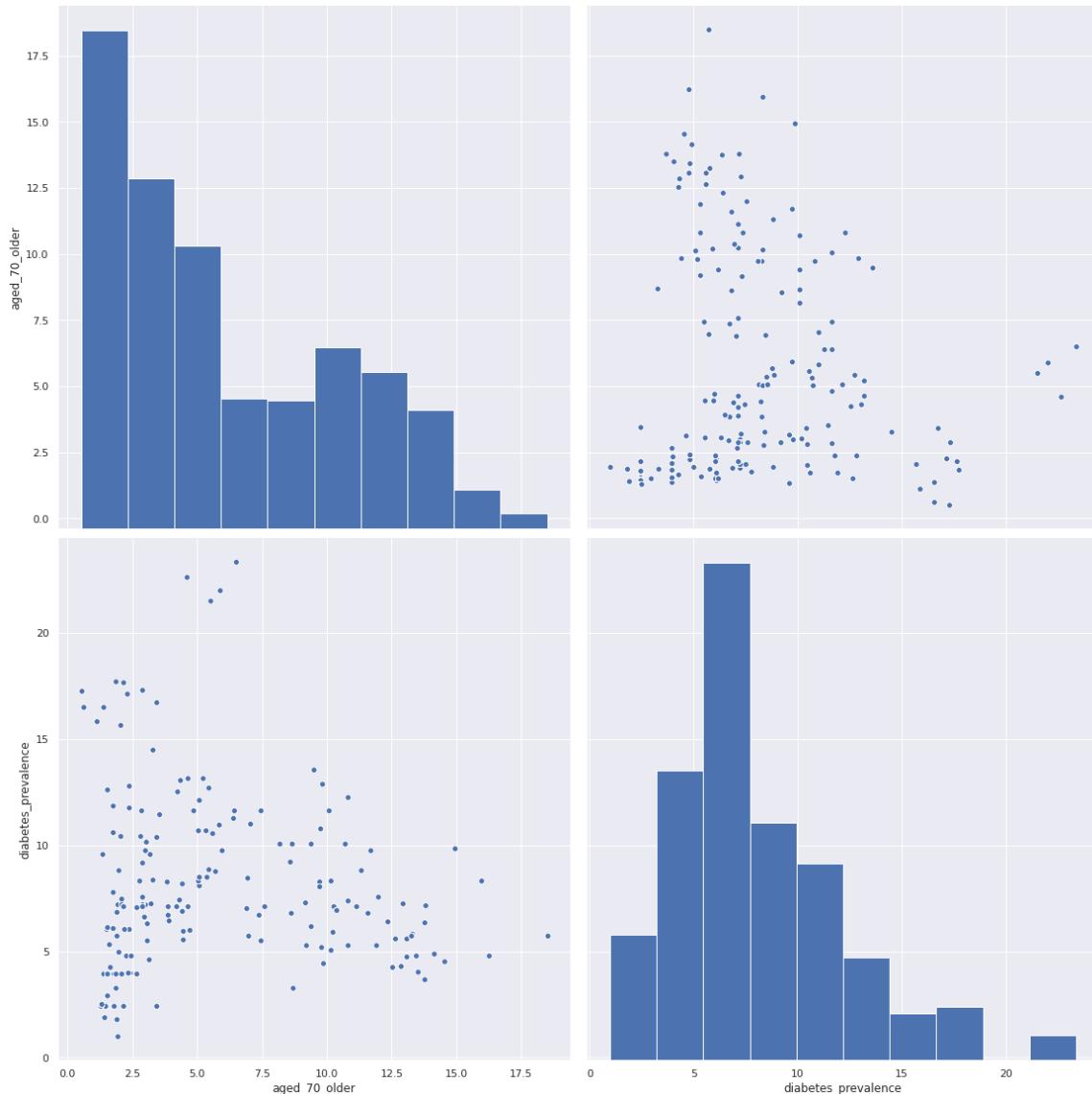


In [94]:

```
sns.pairplot(features, vars=["aged_70_older", "diabetes_prevalence"], height=8)
```

Out[94]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff7dc3da0>
```

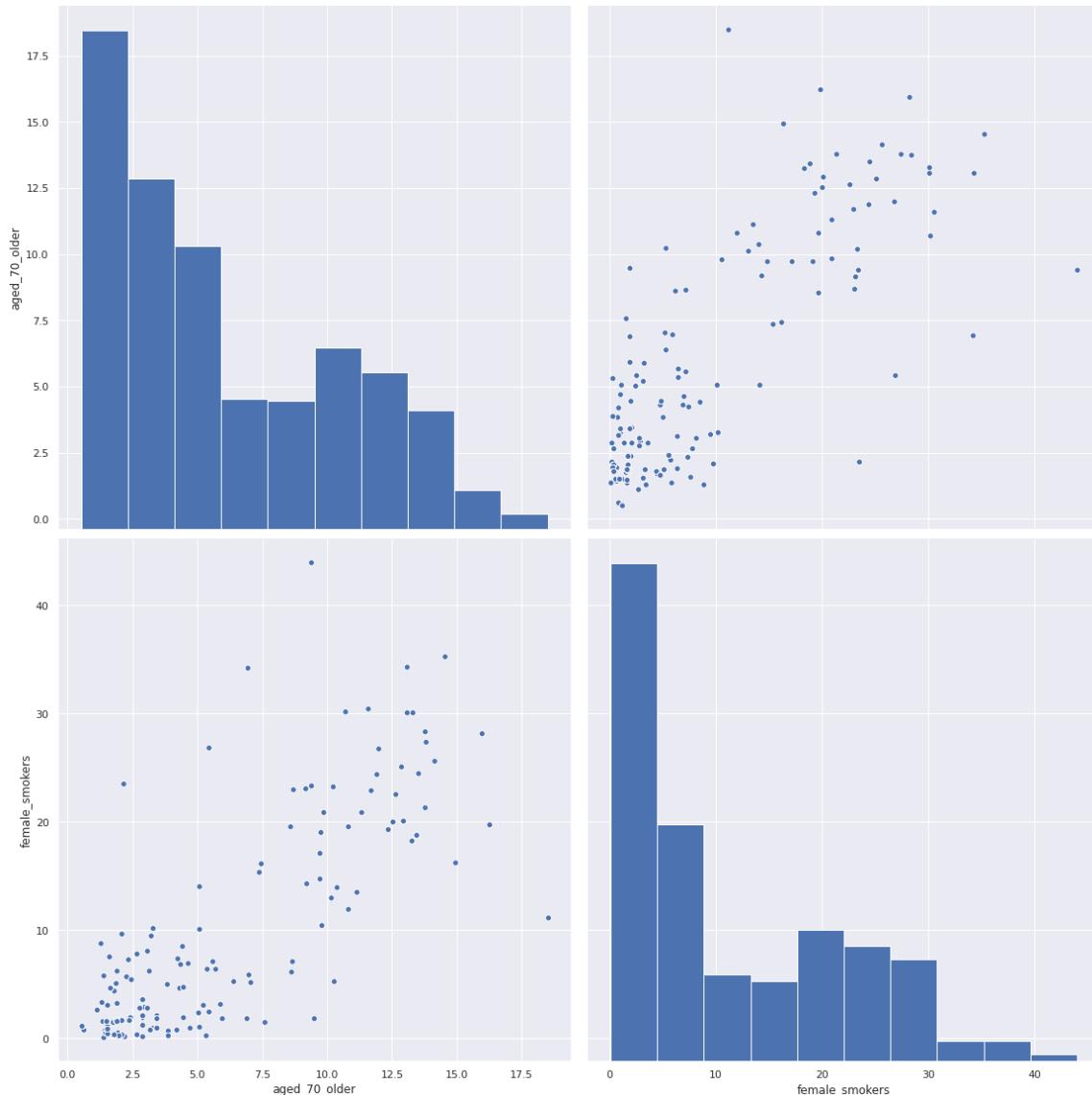


In [95]:

```
sns.pairplot(features, vars=["aged_70_older", "female_smokers"], height=8)
```

Out[95]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff7d2f550>
```

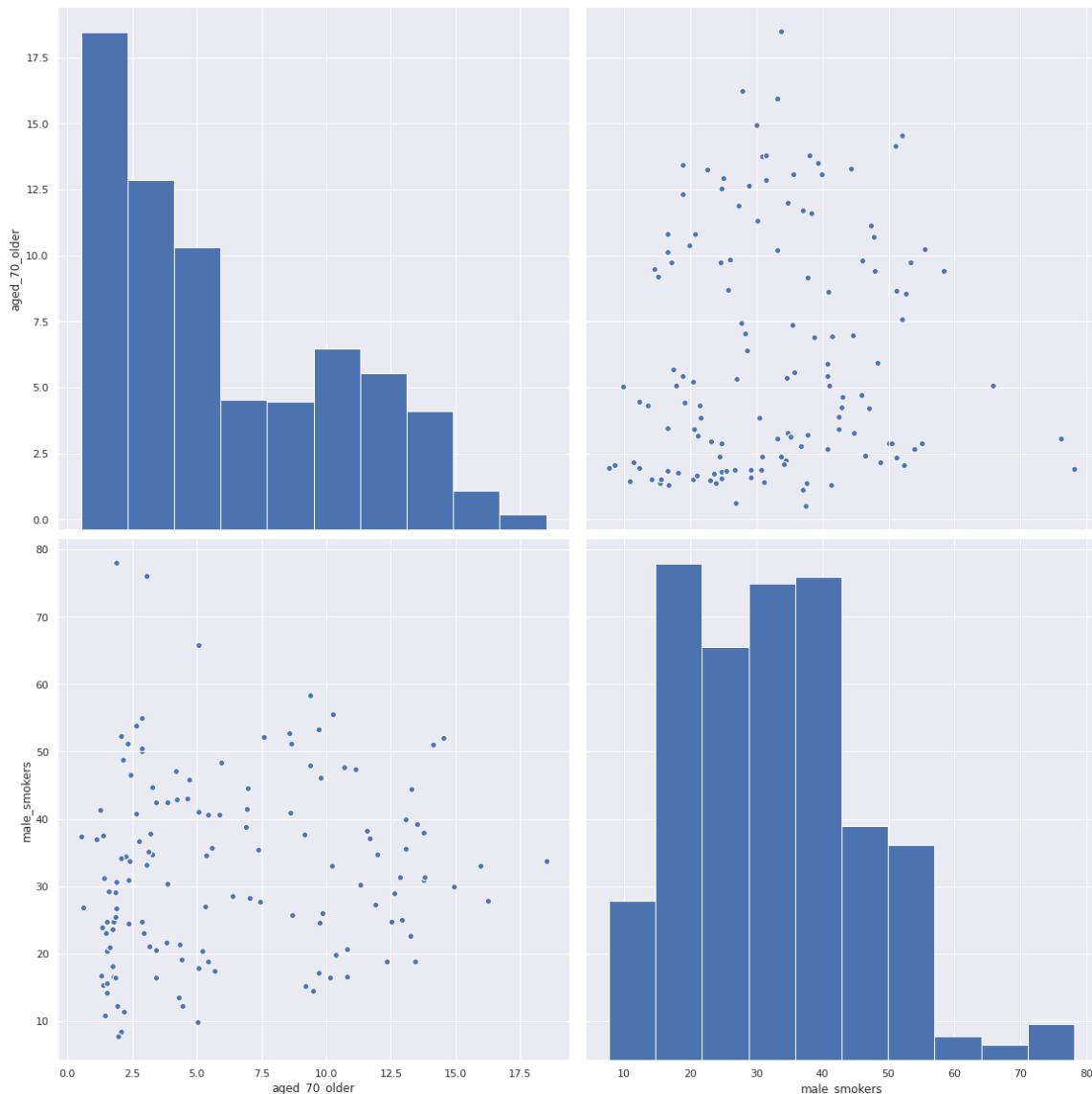


In [96]:

```
sns.pairplot(features, vars=["aged_70_older", "male_smokers"], height=8)
```

Out[96]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff7a0d5c0>
```

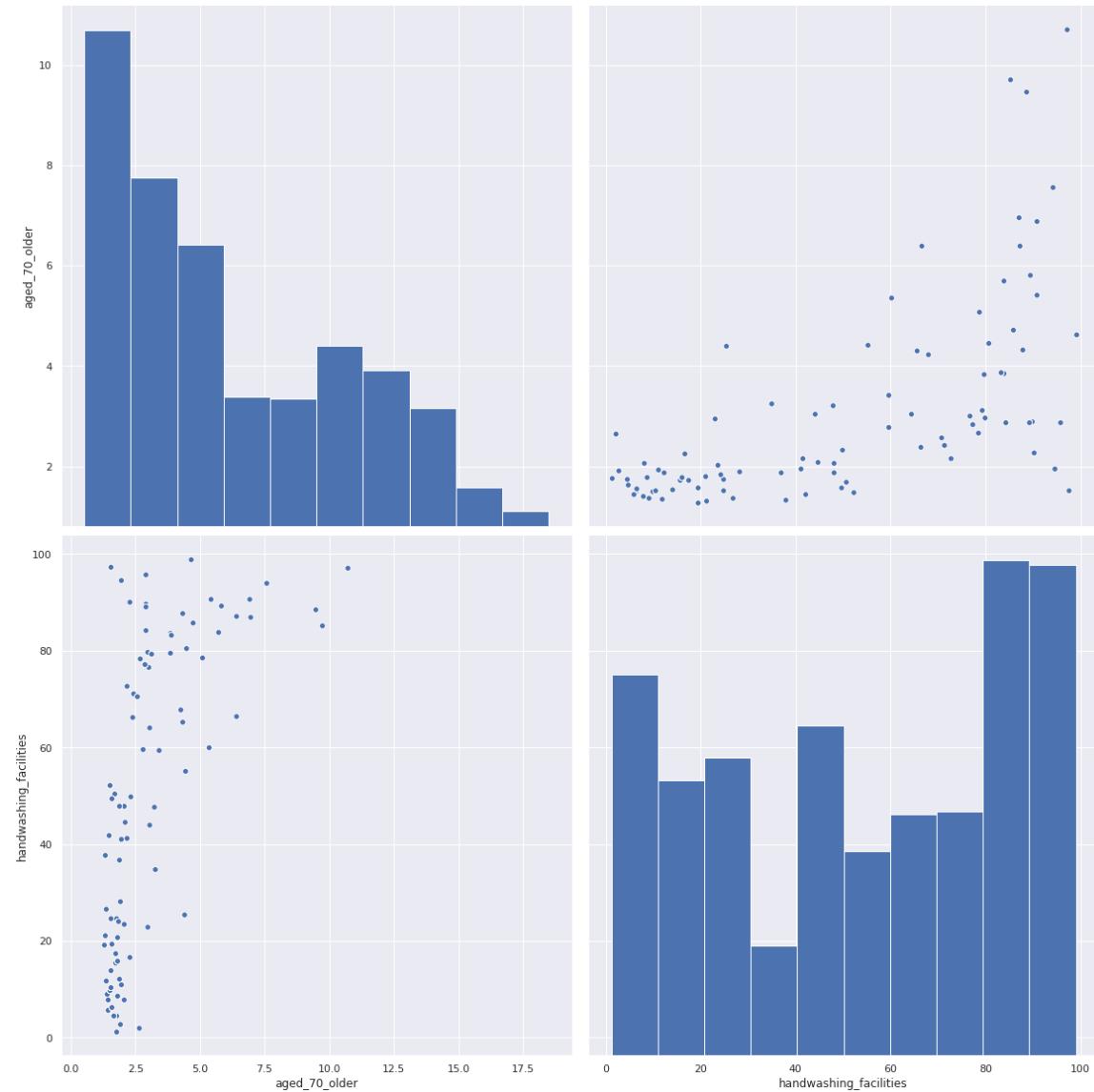


In [97]:

```
sns.pairplot(features, vars=["aged_70_older", "handwashing_facilities"], height=8)
```

Out[97]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff791d048>
```

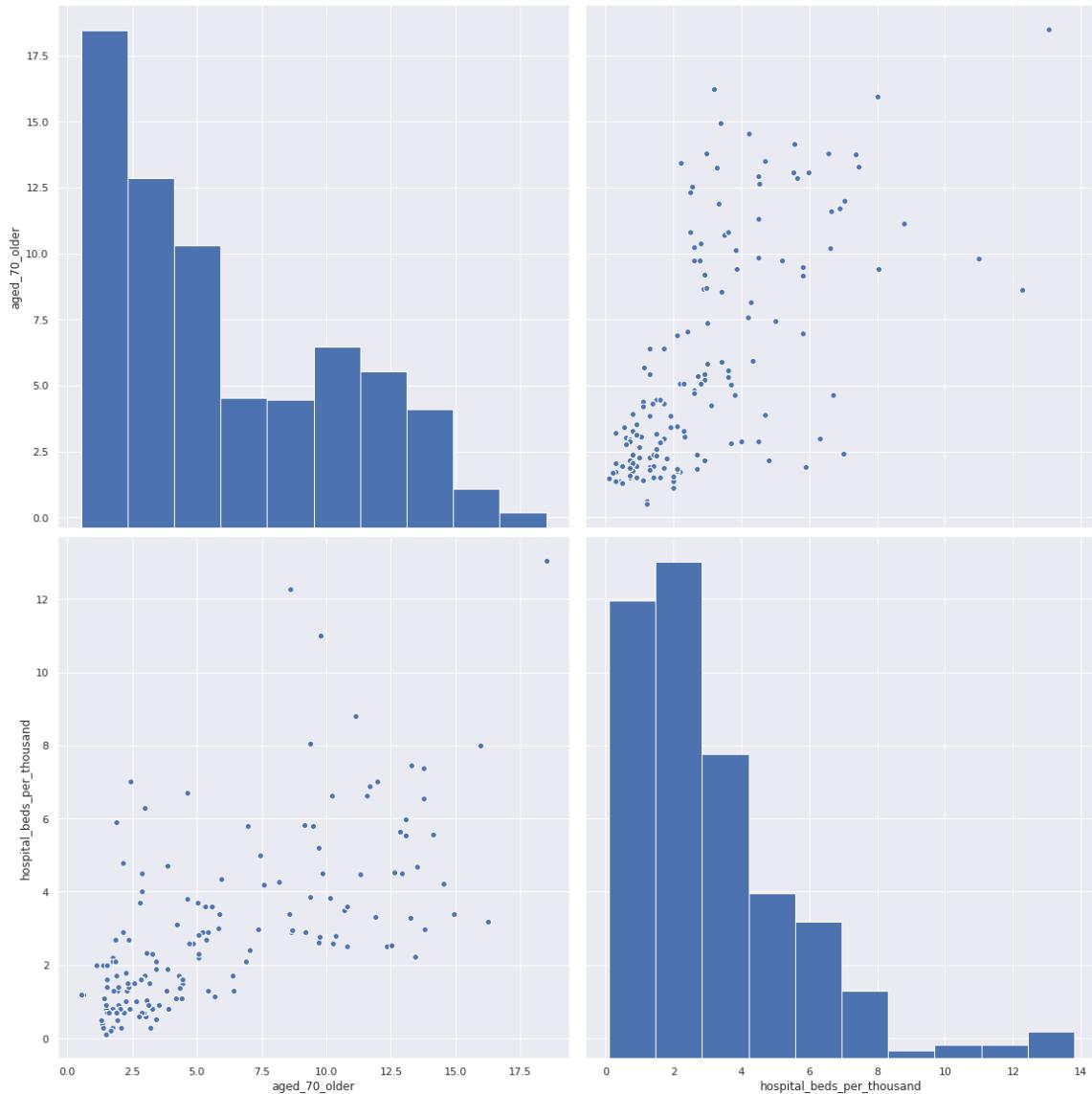


In [98]:

```
sns.pairplot(features, vars=["aged_70_older", "hospital_beds_per_thousand"], height=8)
```

Out[98]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff9951710>
```

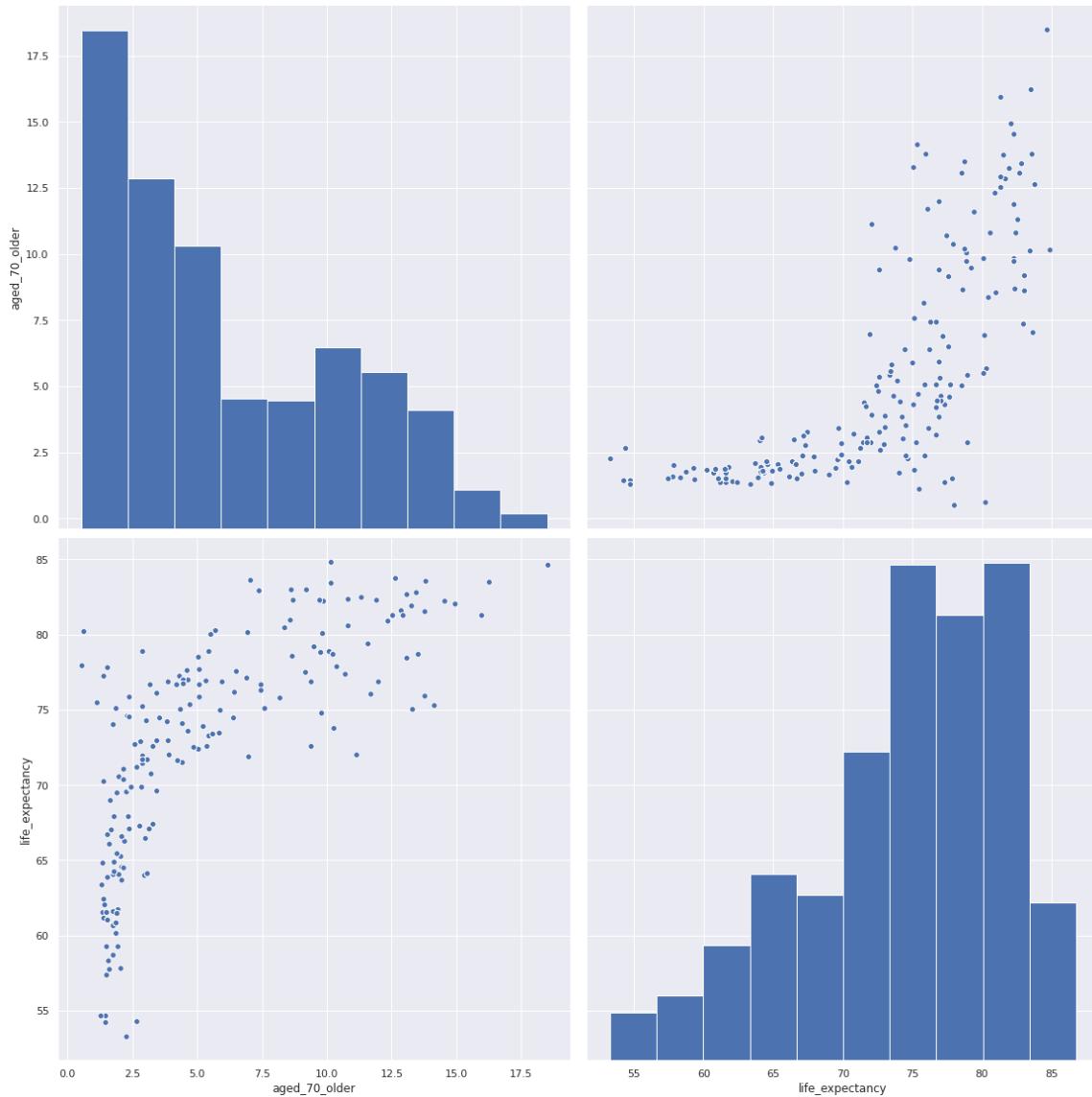


In [99]:

```
sns.pairplot(features, vars=["aged_70_older", "life_expectancy"], height=8)
```

Out[99]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff7408780>
```

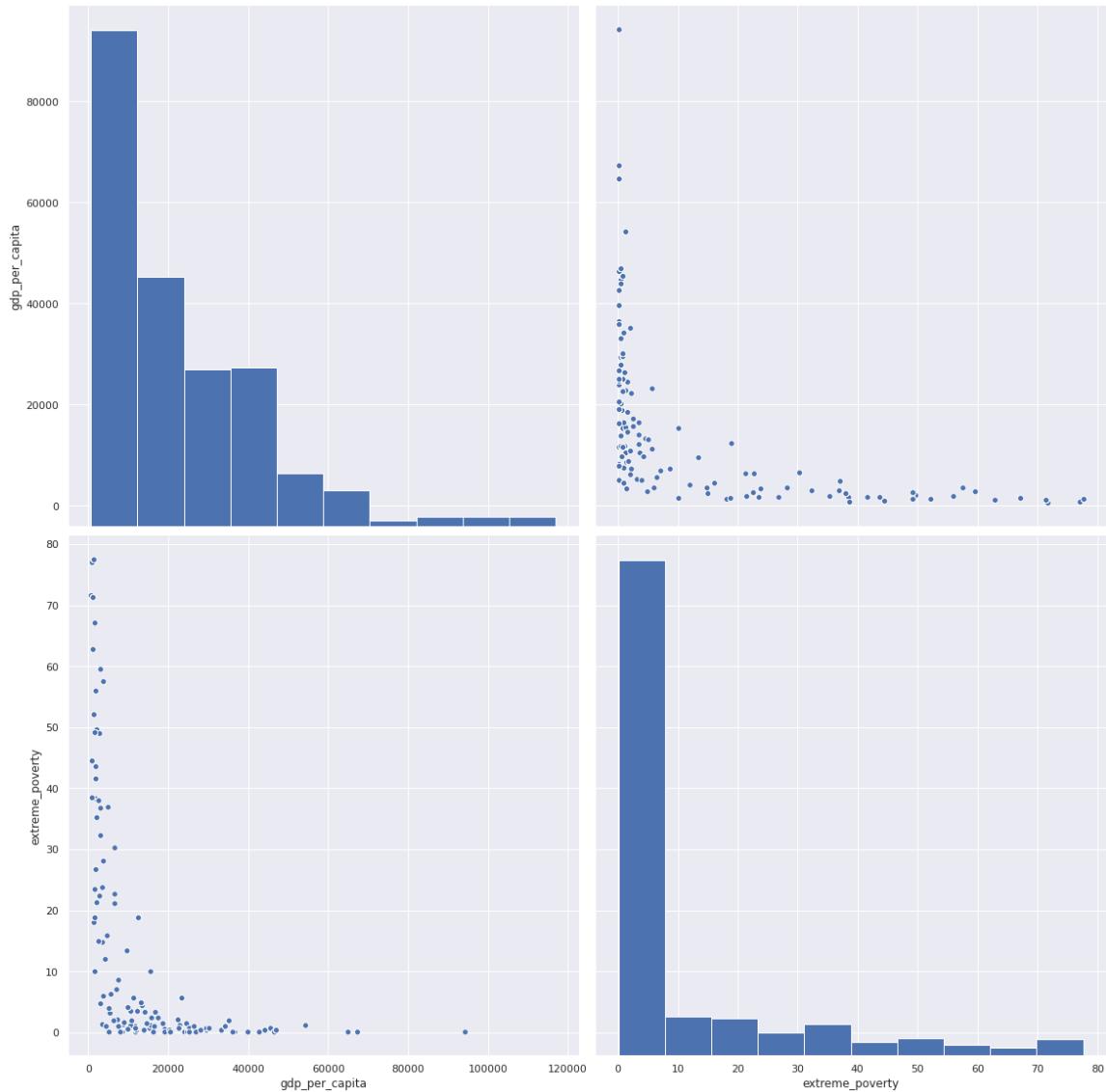


In [100]:

```
sns.pairplot(features, vars=["gdp_per_capita", "extreme_poverty"], height=8)
```

Out[100]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff71fab00>
```

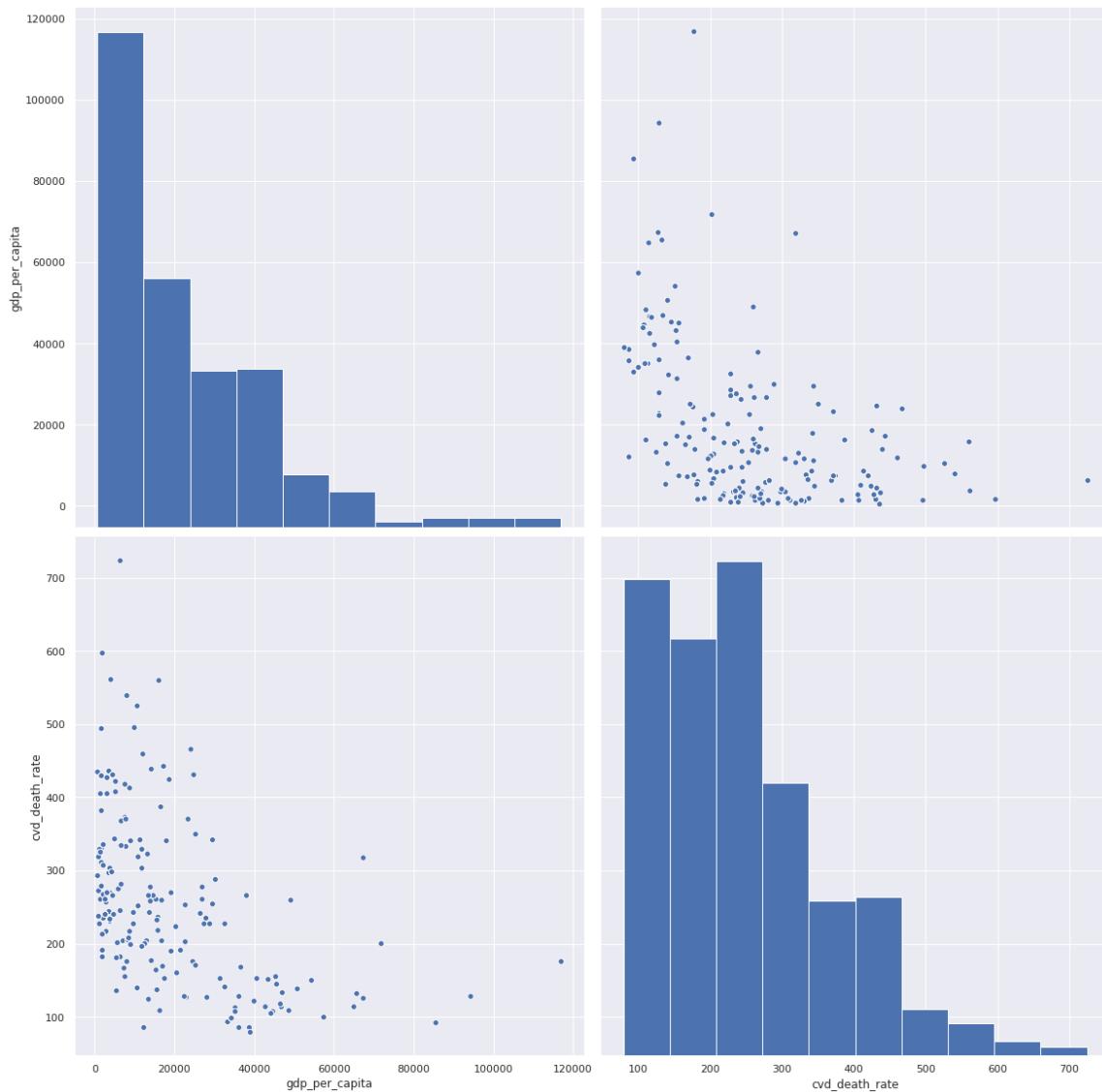


In [101]:

```
sns.pairplot(features, vars=["gdp_per_capita", "cvd_death_rate"], height=8)
```

Out[101]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff6f8b0b8>
```

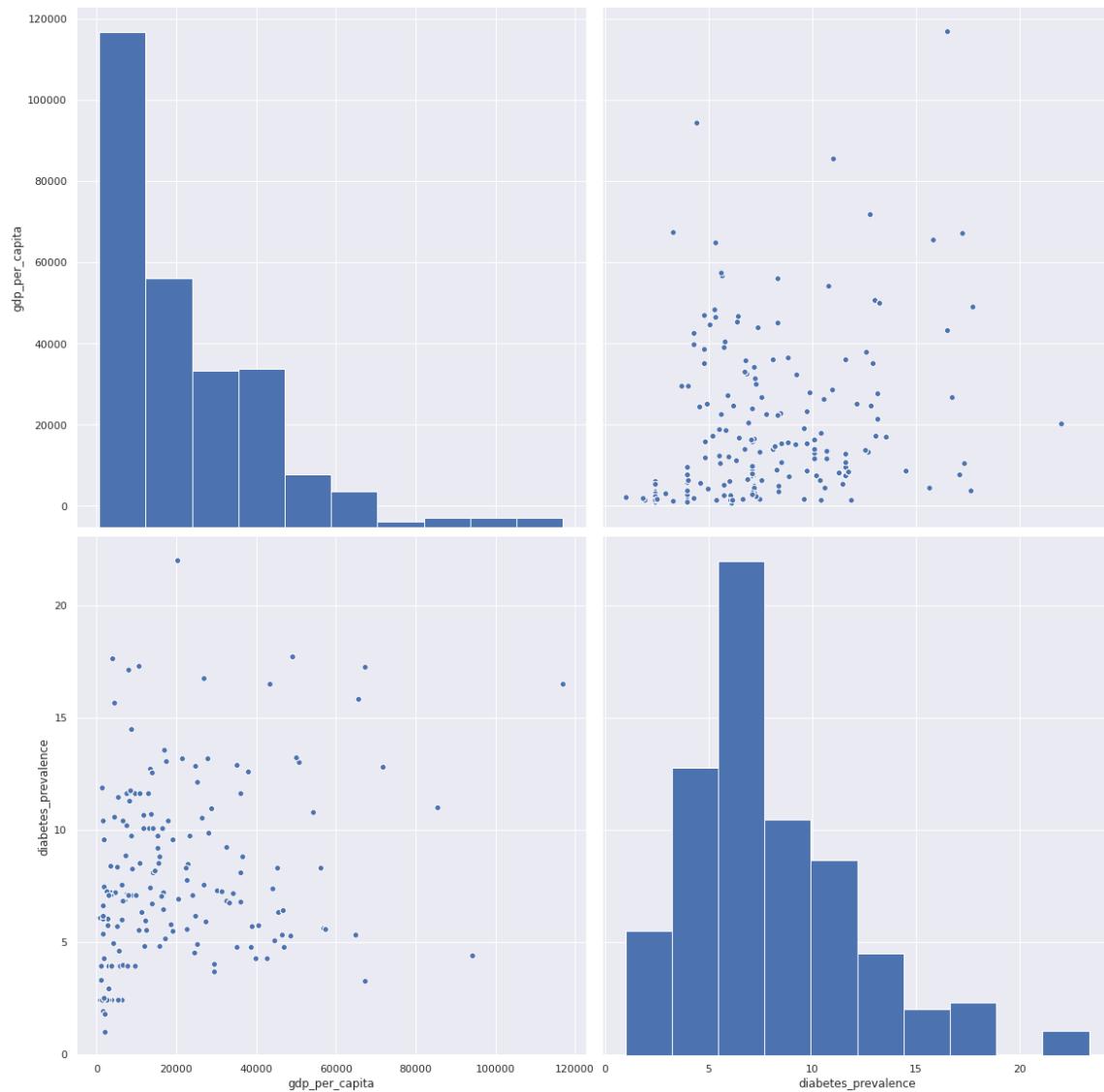


In [102]:

```
sns.pairplot(features, vars=["gdp_per_capita", "diabetes_prevalence"], height=8)
```

Out[102]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff6dd84a8>
```

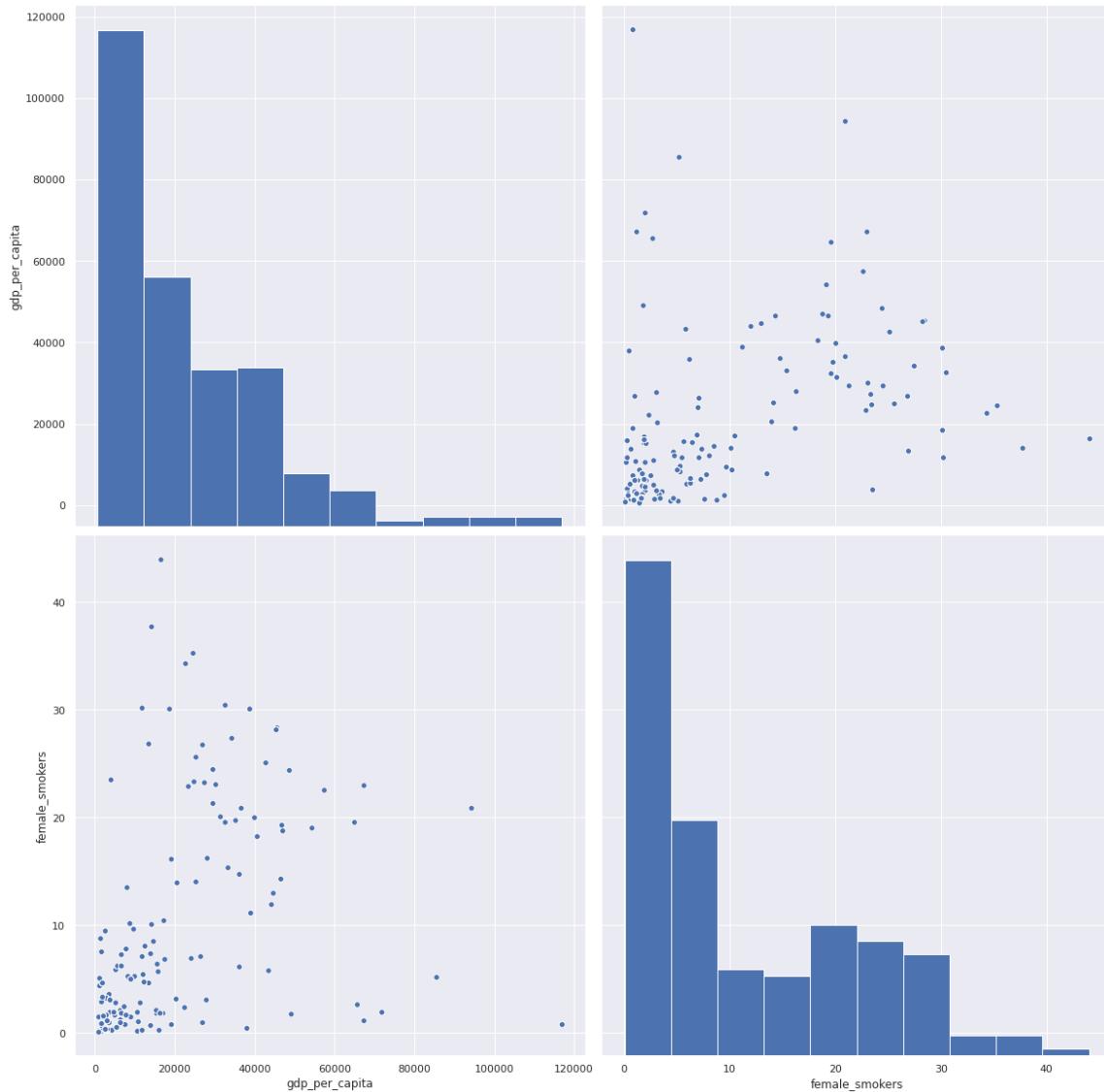


In [103]:

```
sns.pairplot(features, vars=["gdp_per_capita", "female_smokers"], height=8)
```

Out[103]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff6be9be0>
```

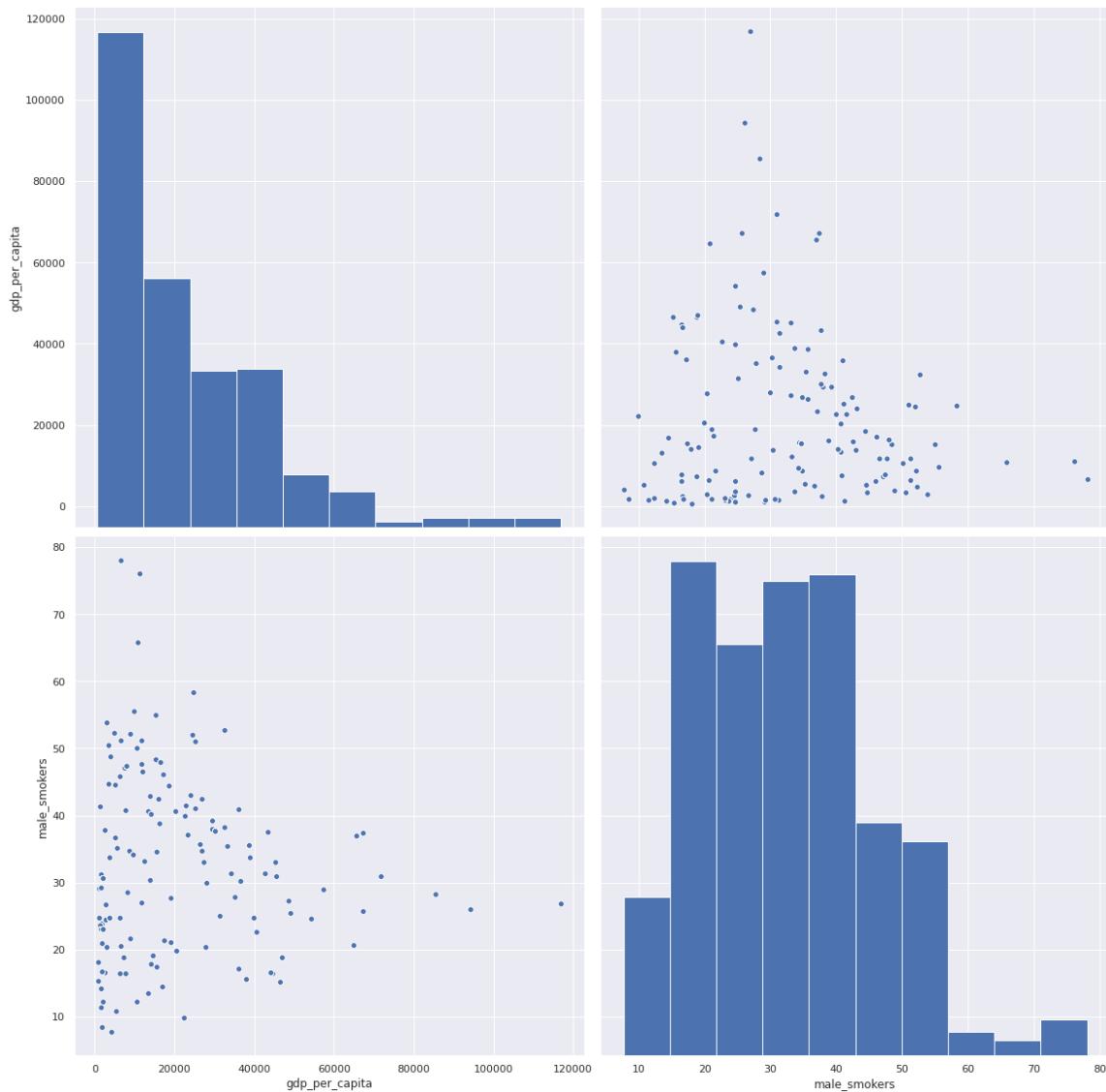


In [104]:

```
sns.pairplot(features, vars=["gdp_per_capita", "male_smokers"], height=8)
```

Out[104]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff69d8208>
```

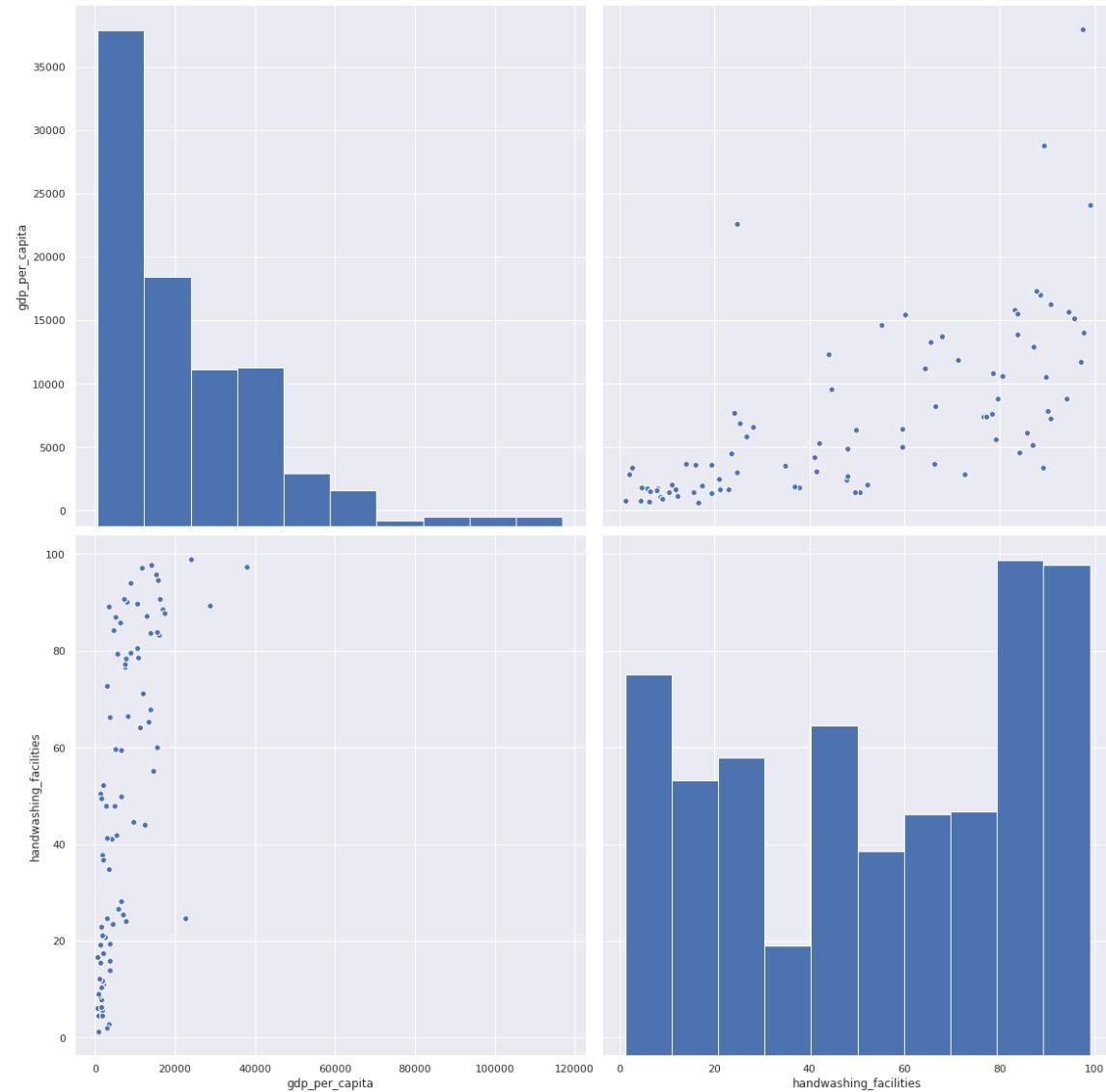


In [105]:

```
sns.pairplot(features, vars=["gdp_per_capita", "handwashing_facilities"], height=8)
```

Out[105]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff6833048>
```

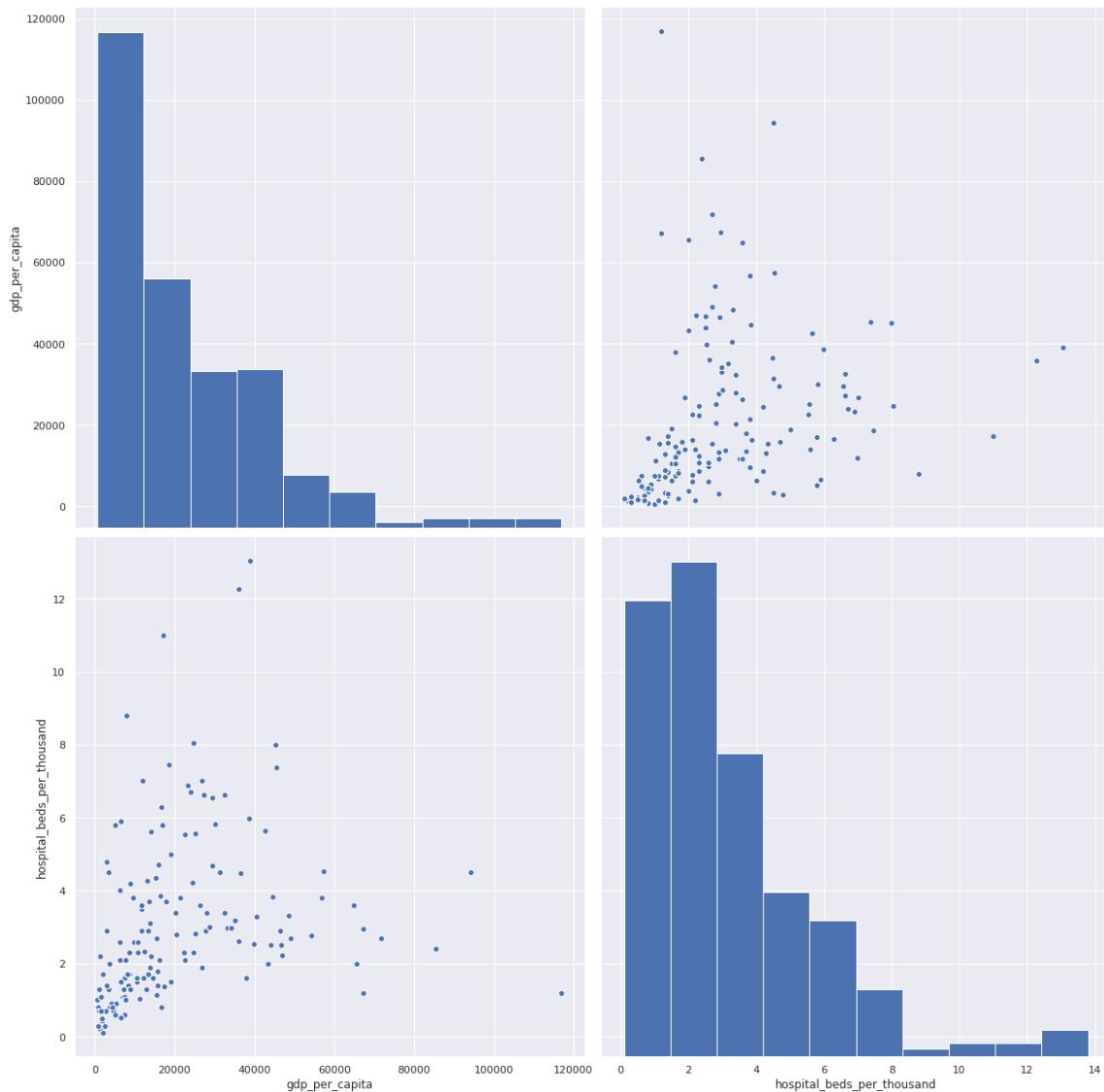


In [106]:

```
sns.pairplot(features, vars=["gdp_per_capita", "hospital_beds_per_thousand"], height=8)
```

Out[106]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff67cd0b8>
```

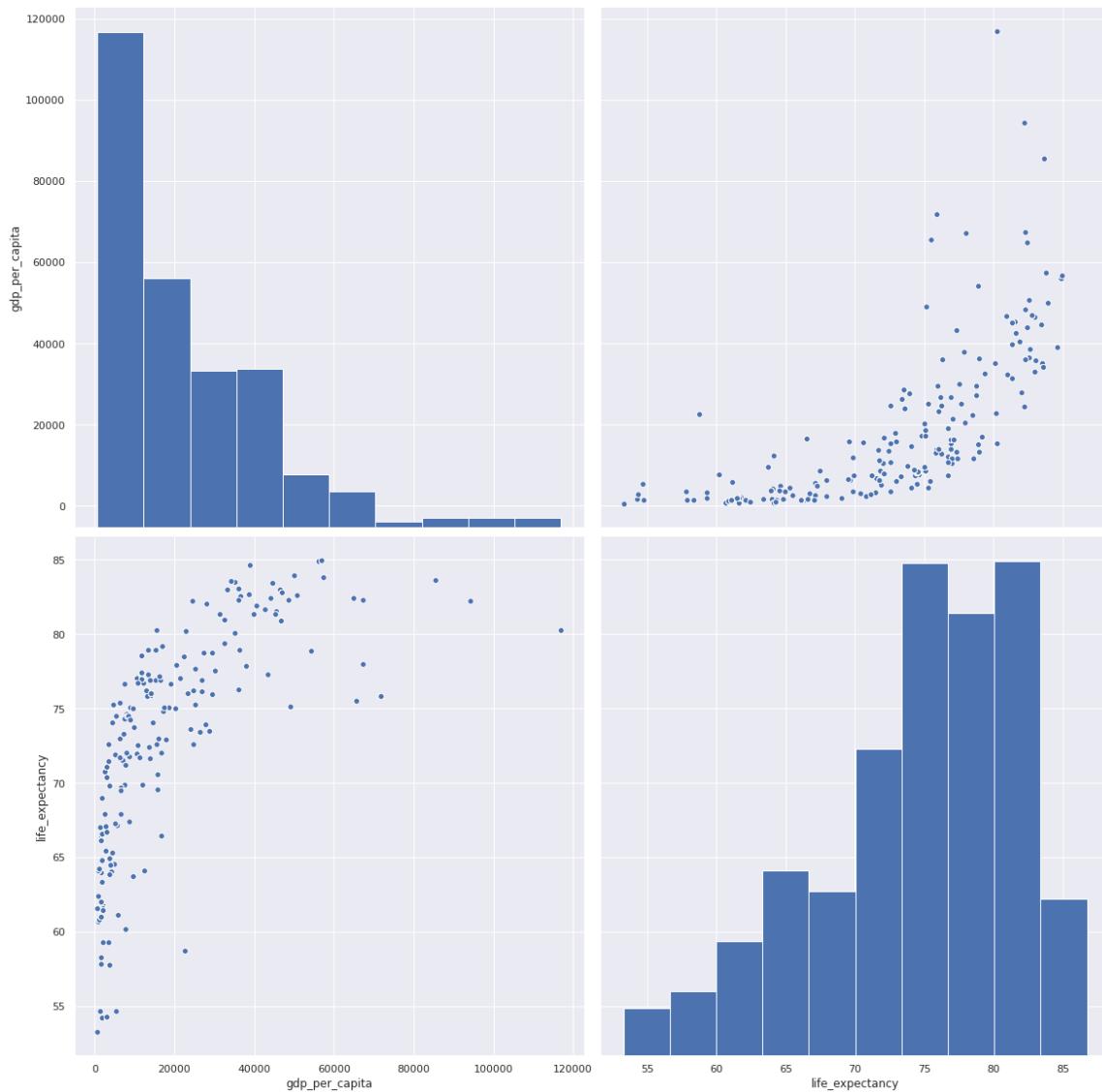


In [107]:

```
sns.pairplot(features, vars=["gdp_per_capita", "life_expectancy"], height=8)
```

Out[107]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff639fa58>
```

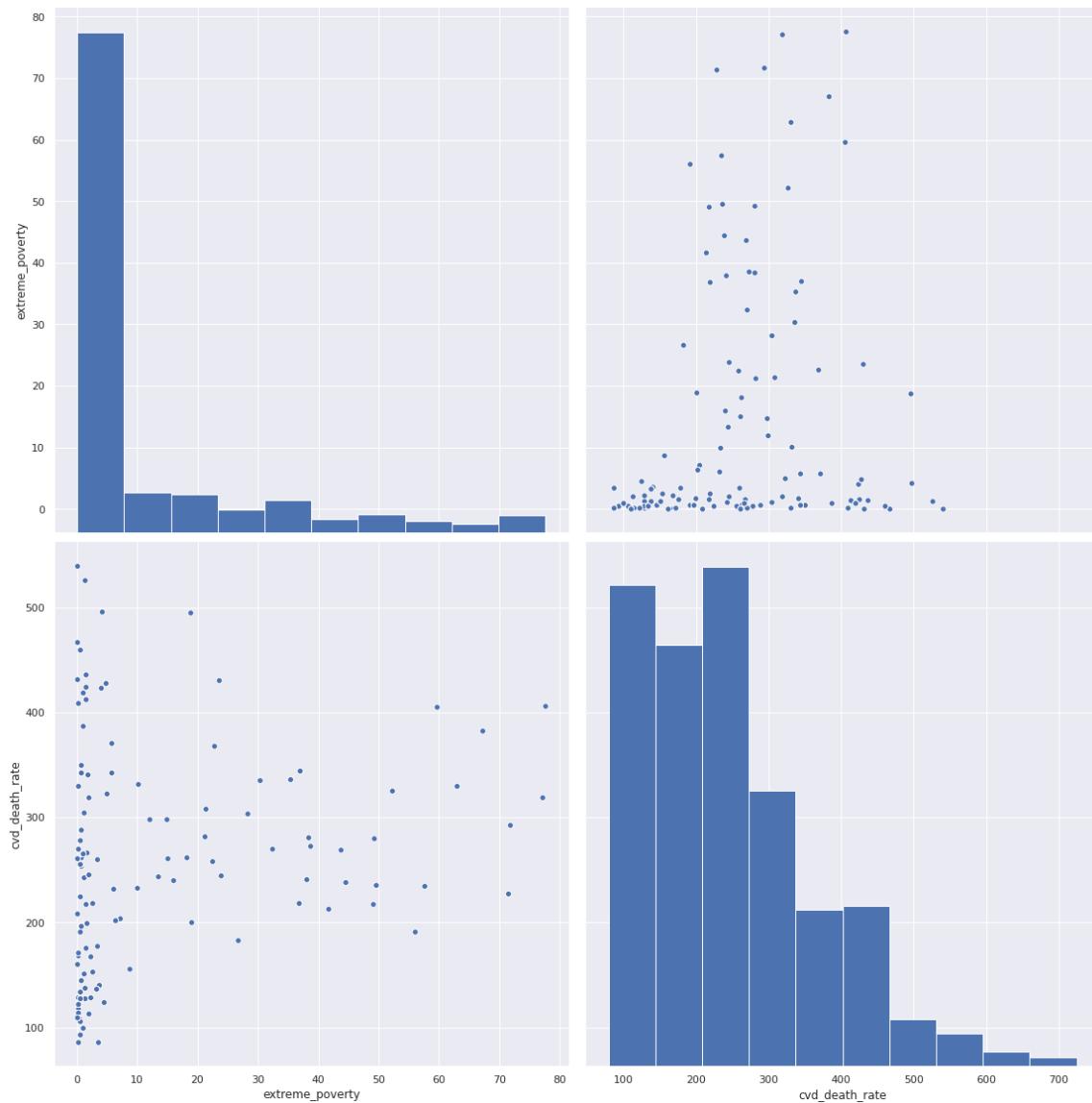


In [108]:

```
sns.pairplot(features, vars=["extreme_poverty", "cvd_death_rate"], height=8)
```

Out[108]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff6214748>
```

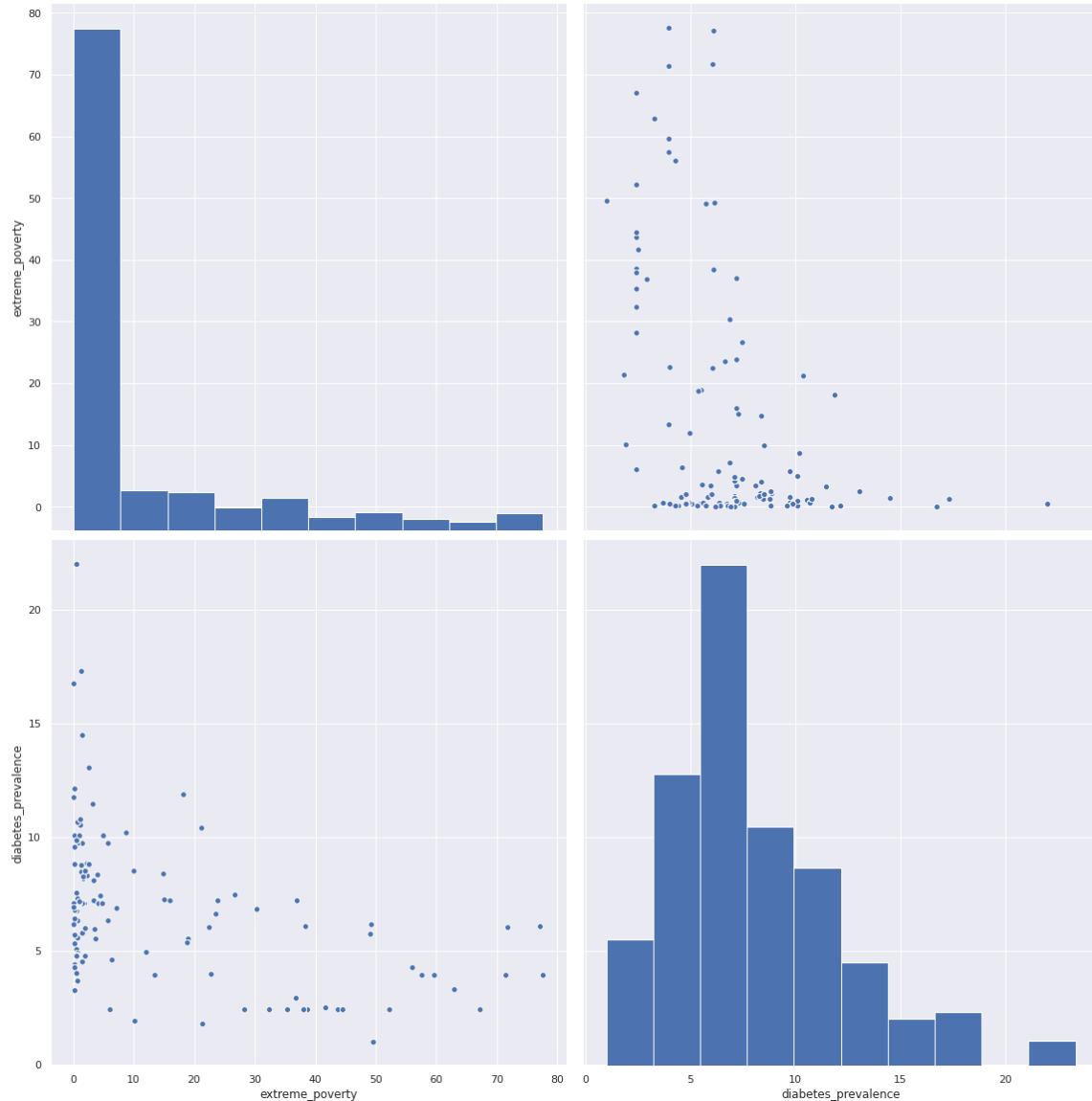


In [109]:

```
sns.pairplot(features, vars=["extreme_poverty", "diabetes_prevalence"], height=8)
```

Out[109]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff5f40898>
```

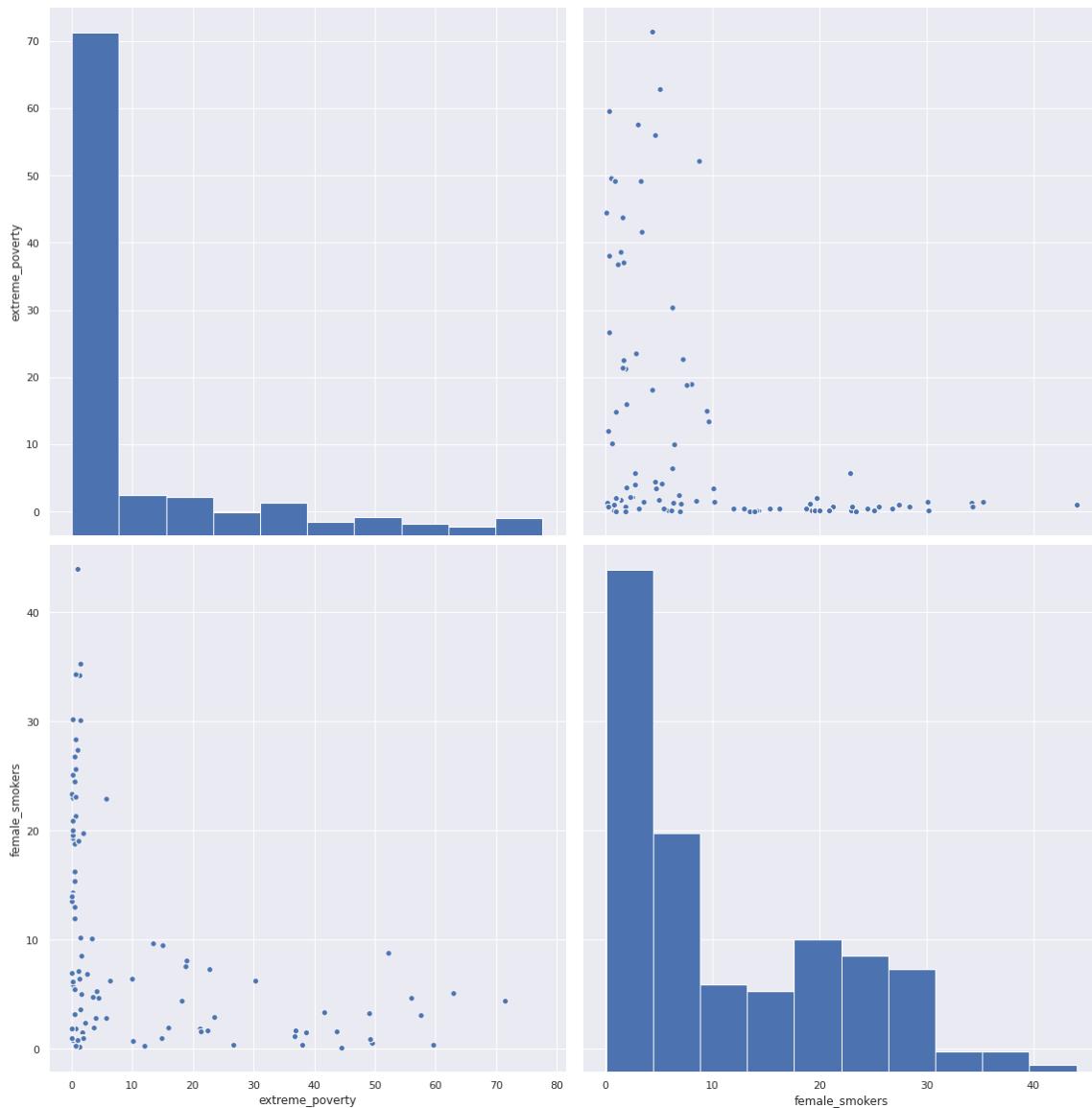


In [110]:

```
sns.pairplot(features, vars=["extreme_poverty", "female_smokers"], height=8)
```

Out[110]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff5ea5668>
```

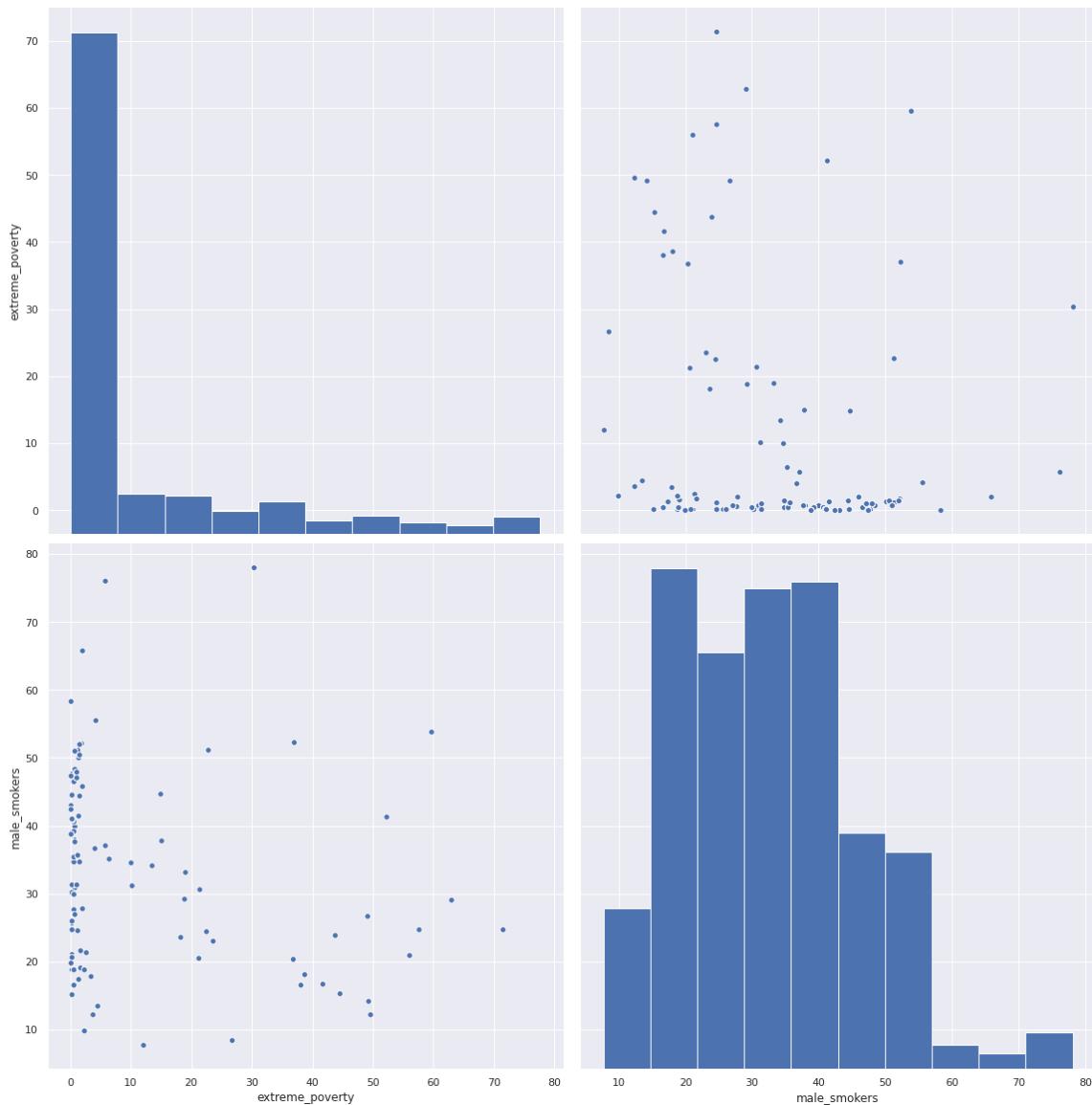


In [111]:

```
sns.pairplot(features, vars=["extreme_poverty", "male_smokers"], height=8)
```

Out[111]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff619f7b8>
```

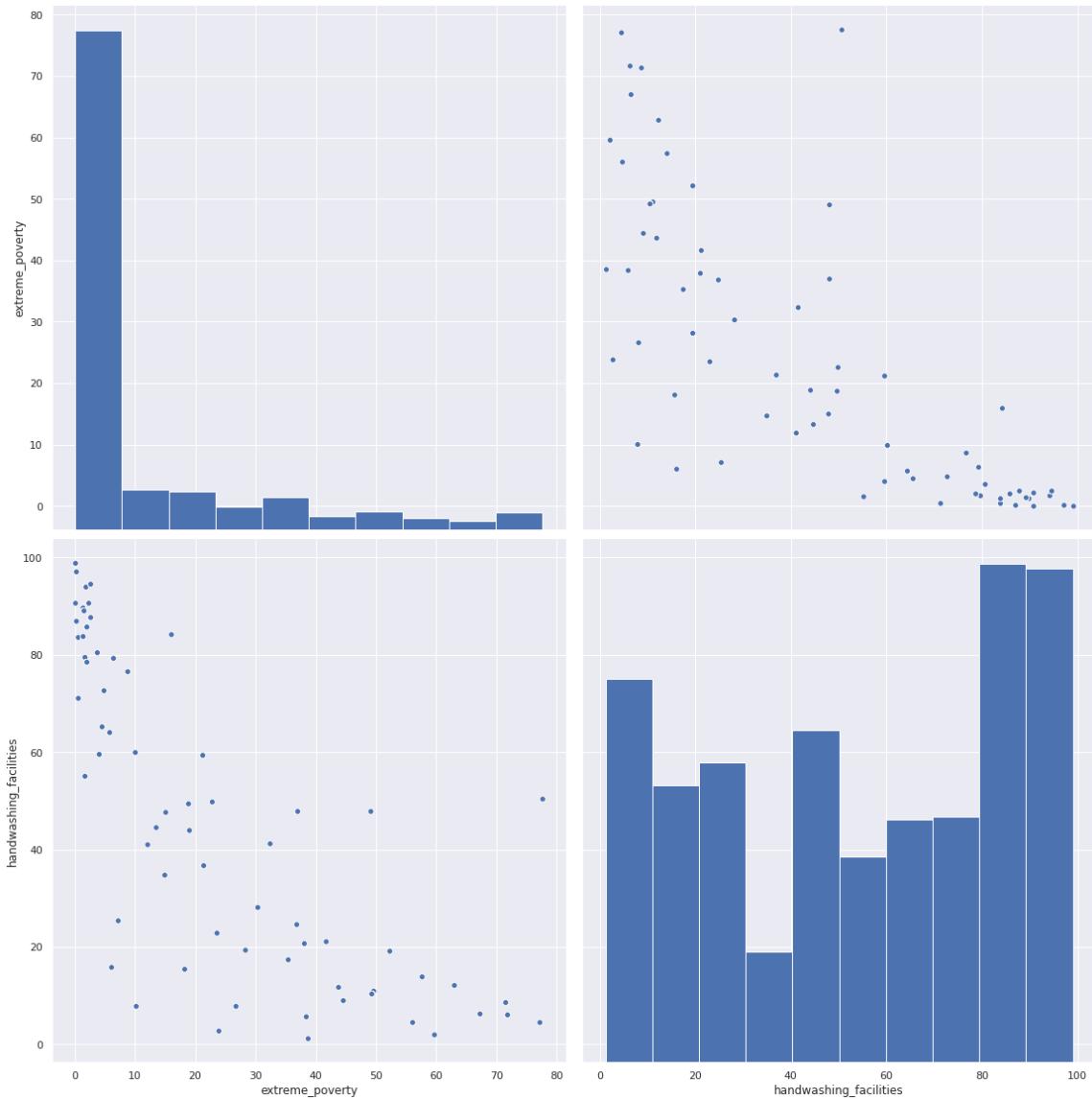


In [112]:

```
sns.pairplot(features, vars=["extreme_poverty", "handwashing_facilities"], height=8)
```

Out[112]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff59437b8>
```

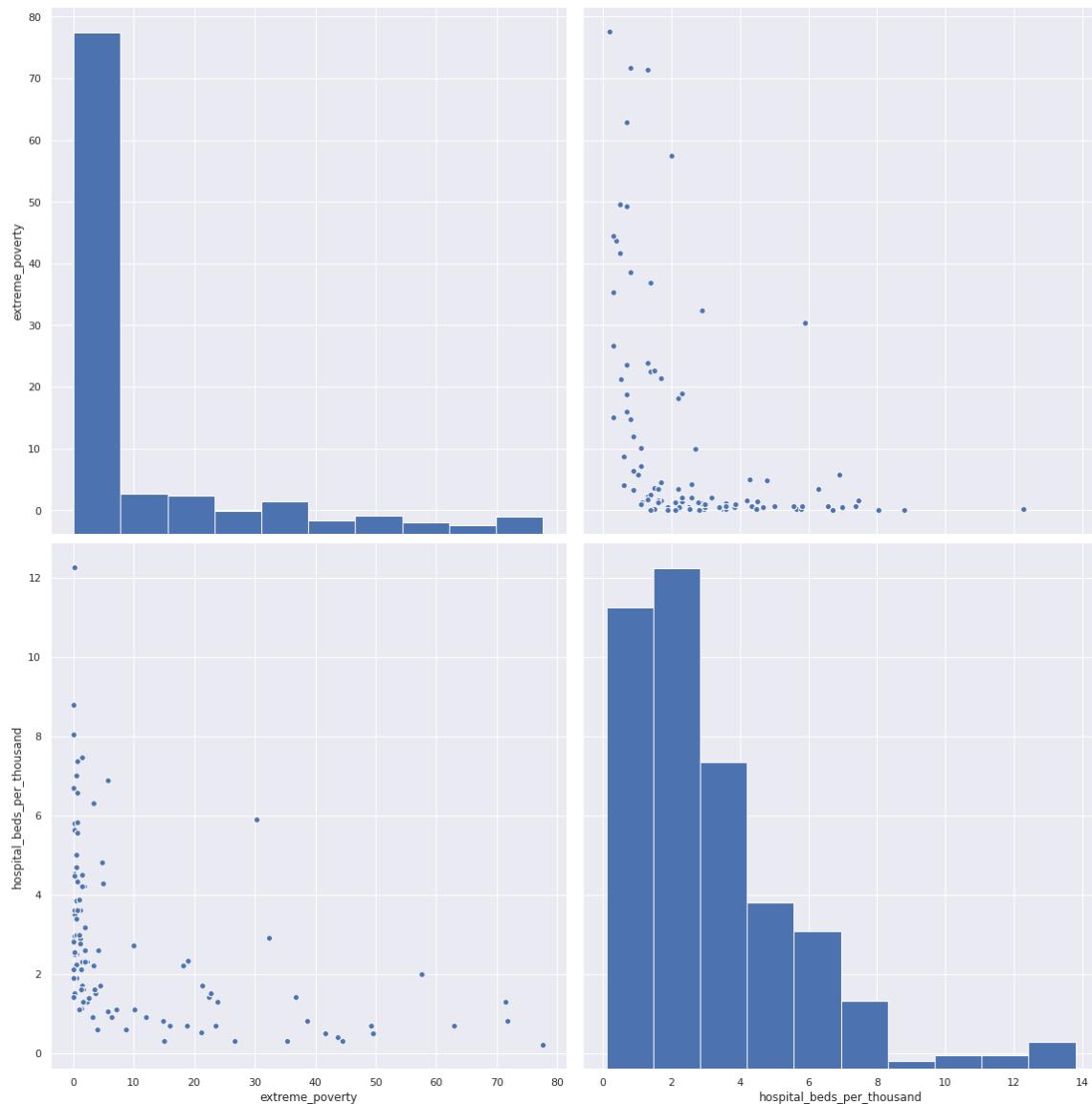


In [113]:

```
sns.pairplot(features, vars=["extreme_poverty", "hospital_beds_per_thousand"], height=8)
```

Out[113]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff60721d0>
```

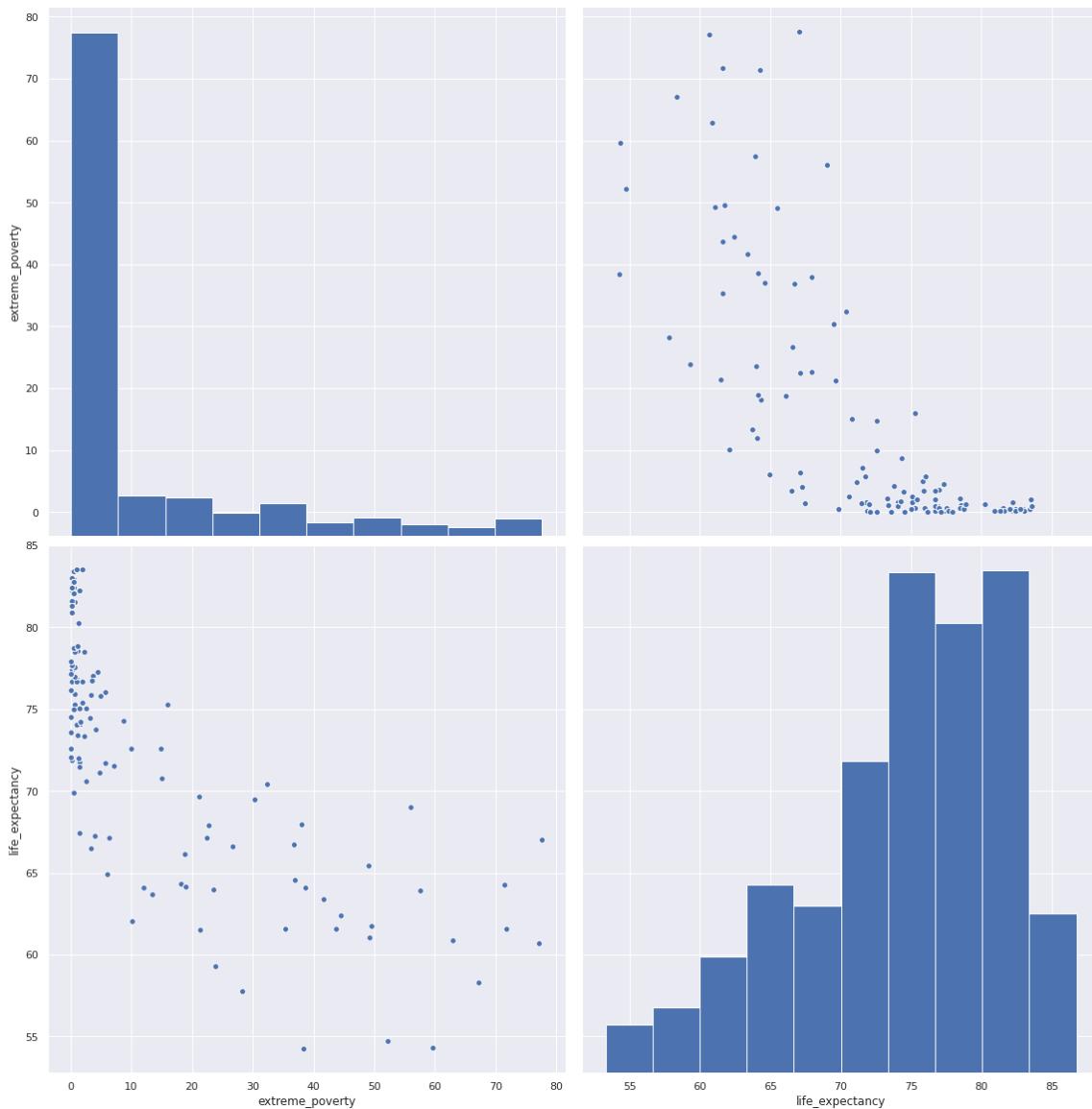


In [114]:

```
sns.pairplot(features, vars=["extreme_poverty", "life_expectancy"], height=8)
```

Out[114]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff5806be0>
```

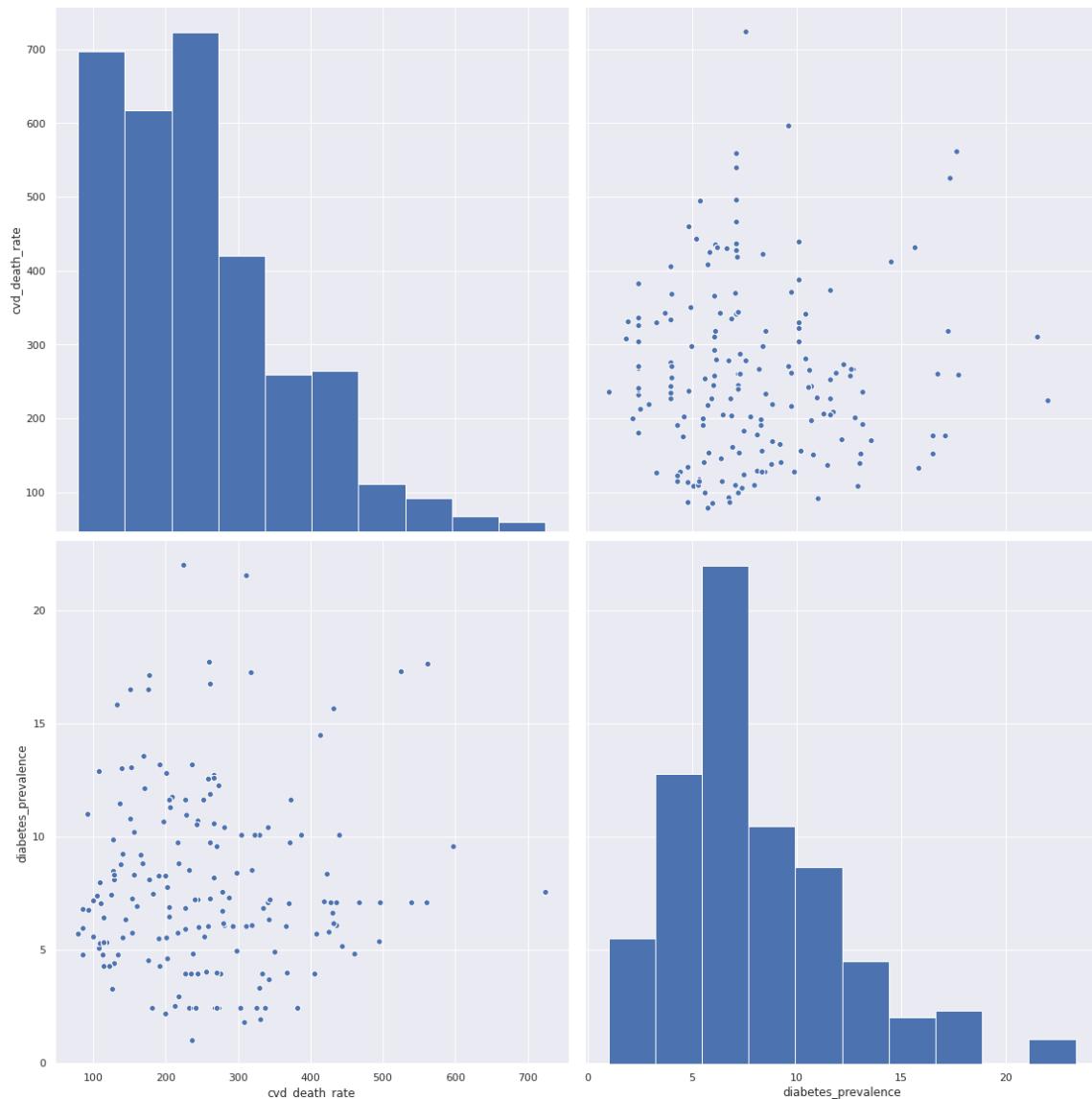


In [115]:

```
sns.pairplot(features, vars=["cvd_death_rate", "diabetes_prevalence"], height=8)
```

Out[115]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff5375e48>
```

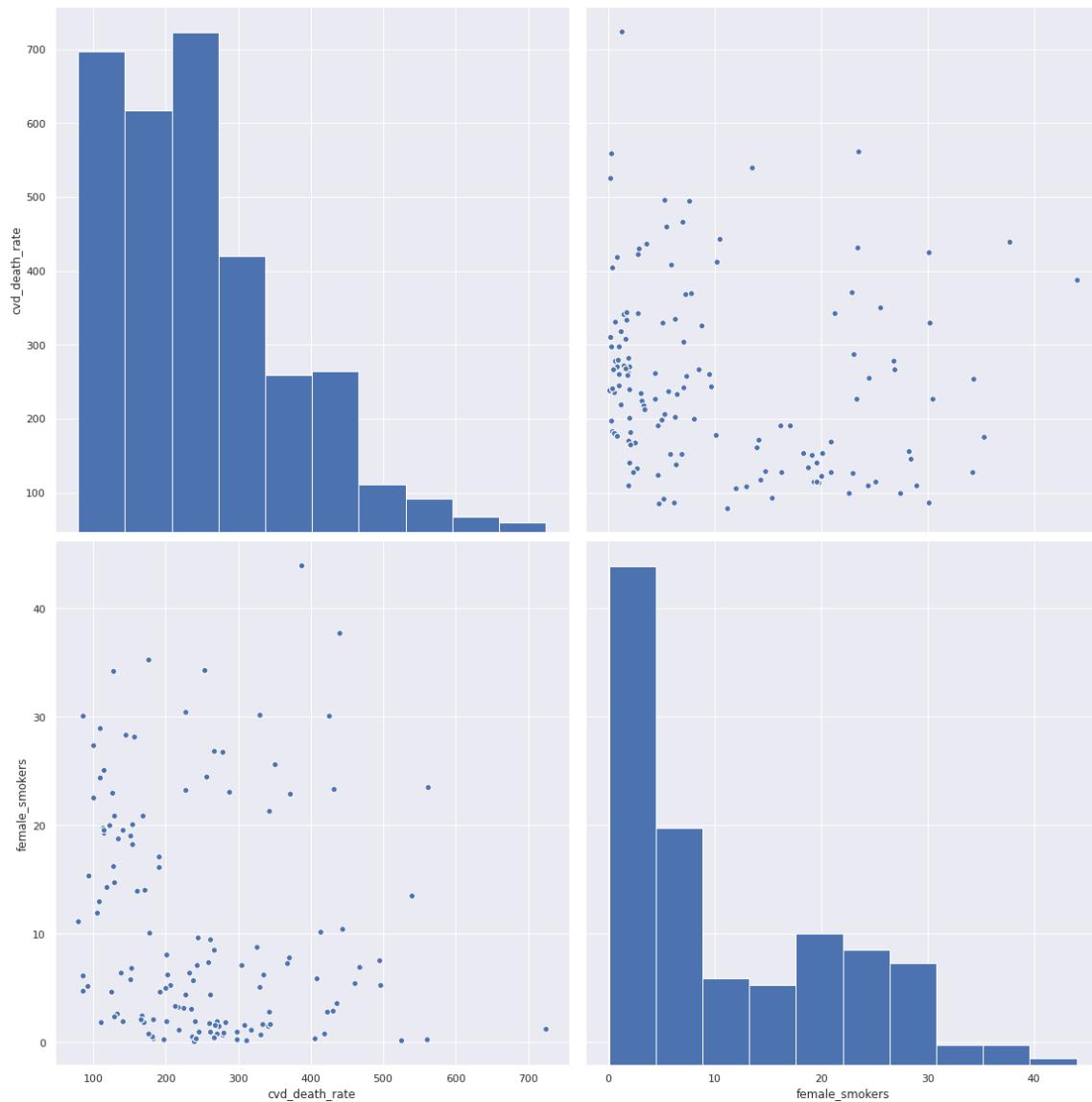


In [116]:

```
sns.pairplot(features, vars=["cvd_death_rate", "female_smokers"], height=8)
```

Out[116]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff50c4278>
```

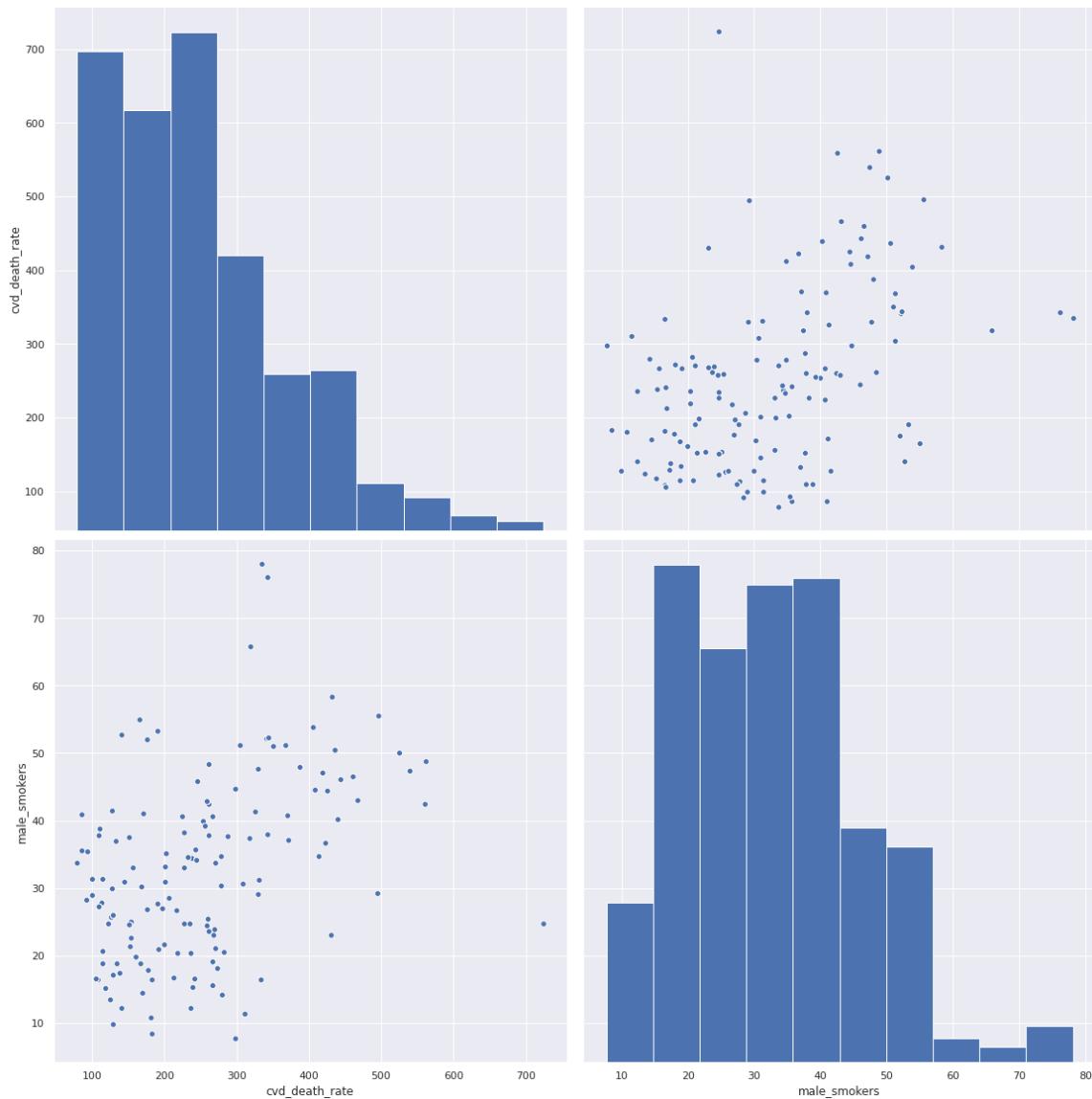


In [117]:

```
sns.pairplot(features, vars=["cvd_death_rate", "male_smokers"], height=8)
```

Out[117]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff4f37358>
```

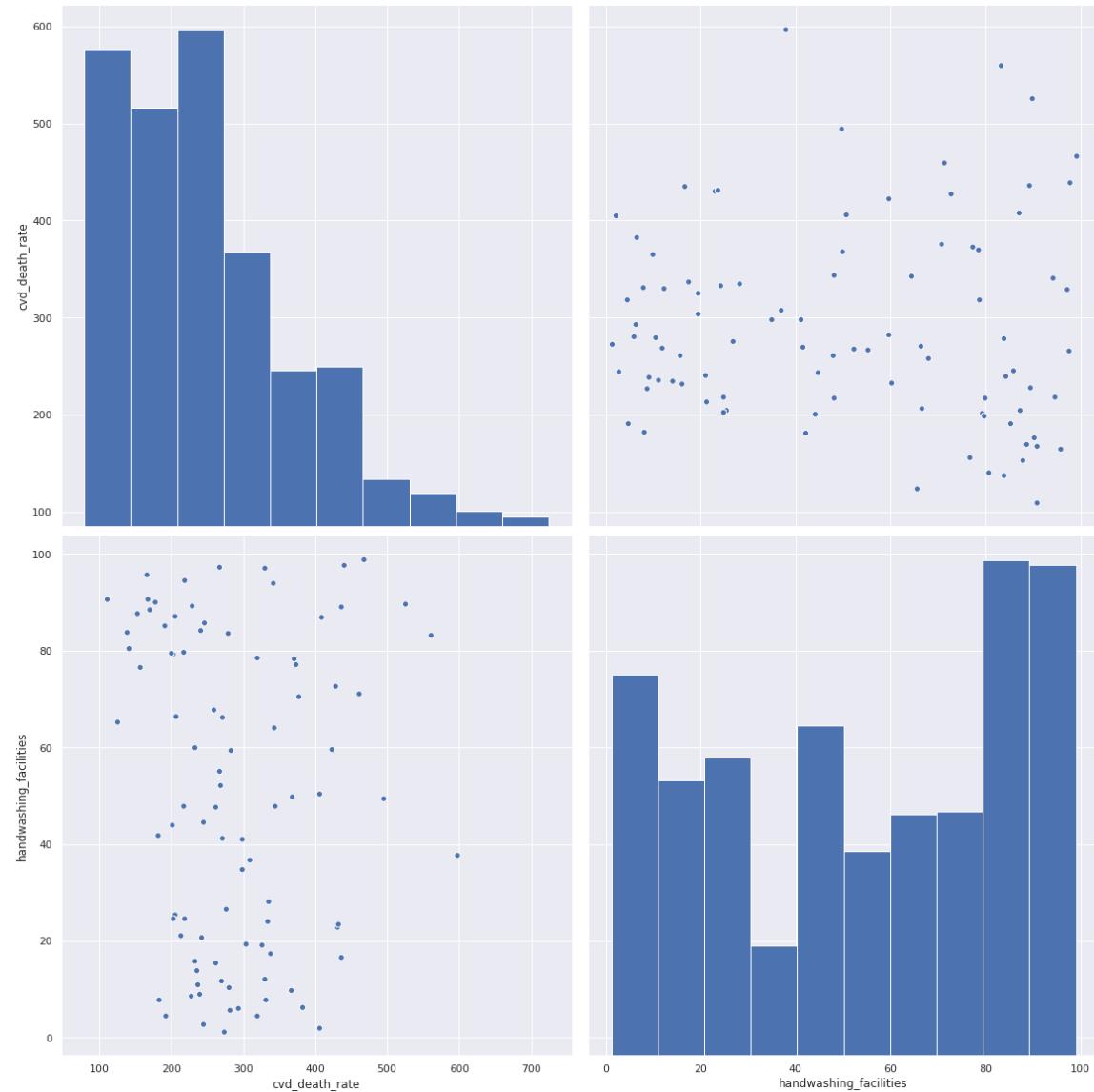


In [118]:

```
sns.pairplot(features, vars=["cvd_death_rate", "handwashing_facilities"], height=8)
```

Out[118]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff4cc6eb8>
```

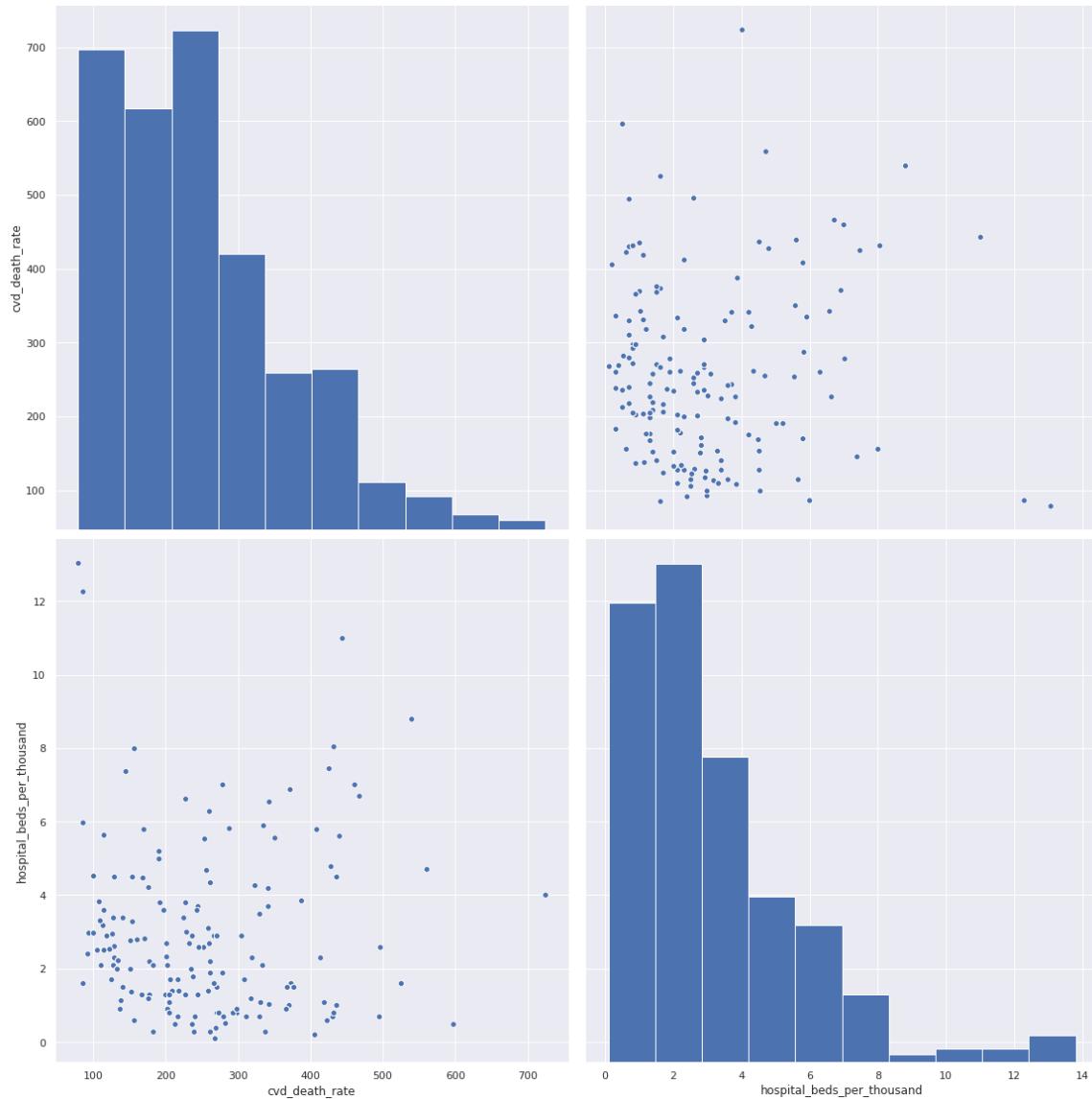


In [119]:

```
sns.pairplot(features, vars=["cvd_death_rate", "hospital_beds_per_thousand"], height=8)
```

Out[119]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff74235f8>
```

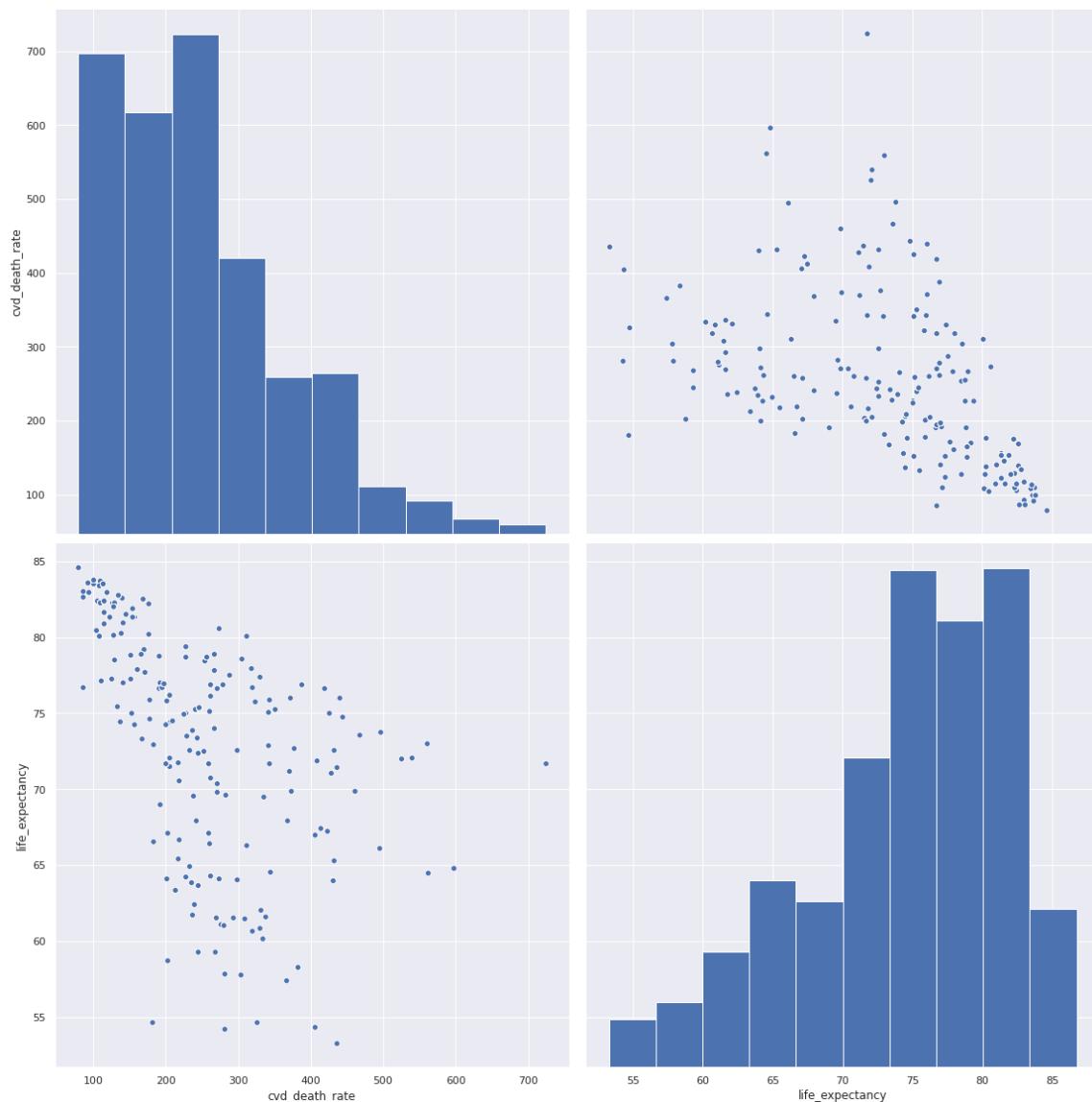


In [120]:

```
sns.pairplot(features, vars=["cvd_death_rate", "life_expectancy"], height=8)
```

Out[120]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff491c710>
```

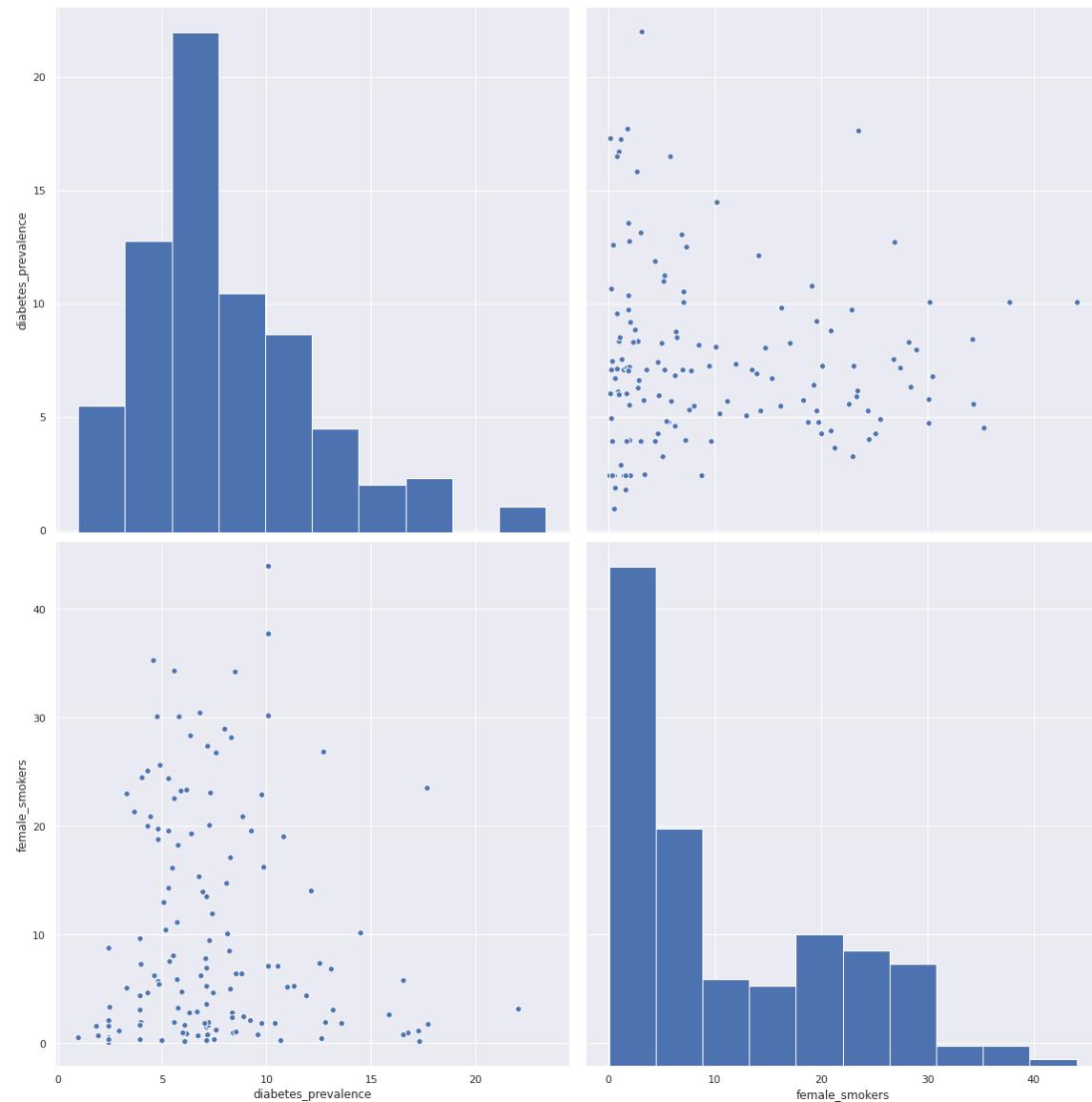


In [121]:

```
sns.pairplot(features, vars=["diabetes_prevalence", "female_smokers"], height=8)
```

Out[121]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff471ce48>
```

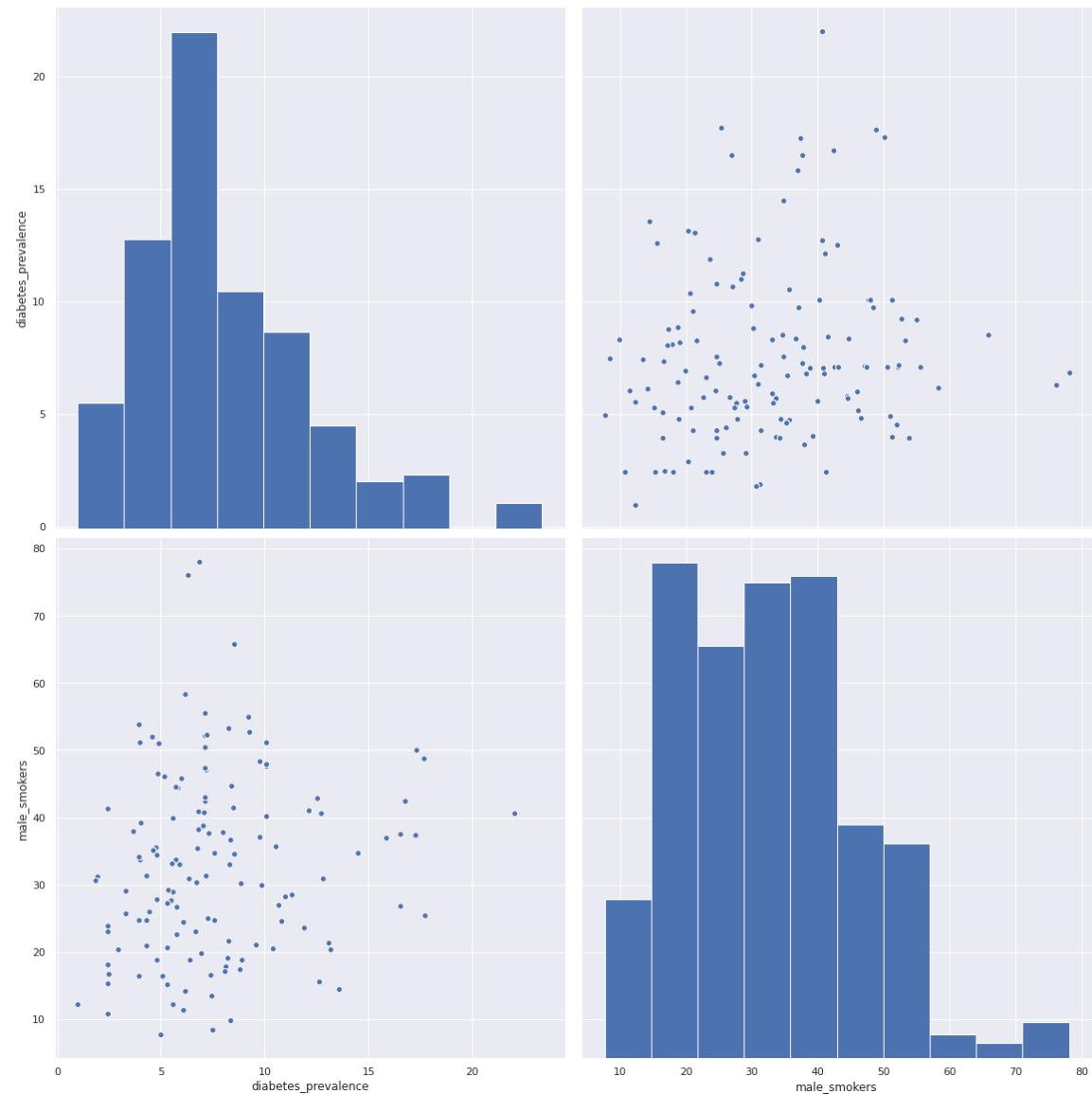


In [122]:

```
sns.pairplot(features, vars=["diabetes_prevalence", "male_smokers"], height=8)
```

Out[122]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff450a198>
```

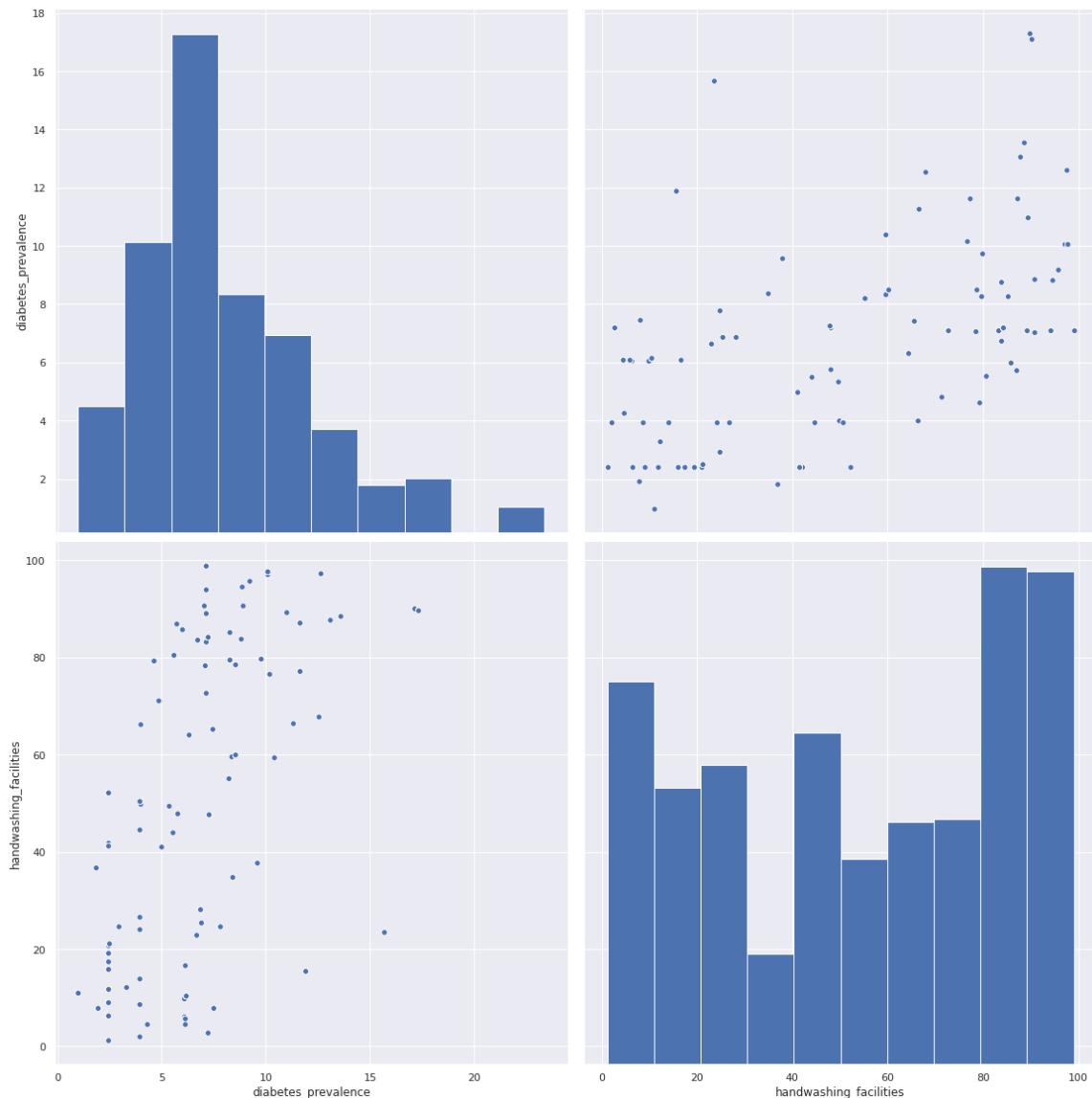


In [123]:

```
sns.pairplot(features, vars=["diabetes_prevalence", "handwashing_facilities"], height=8)
```

Out[123]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff437c2b0>
```

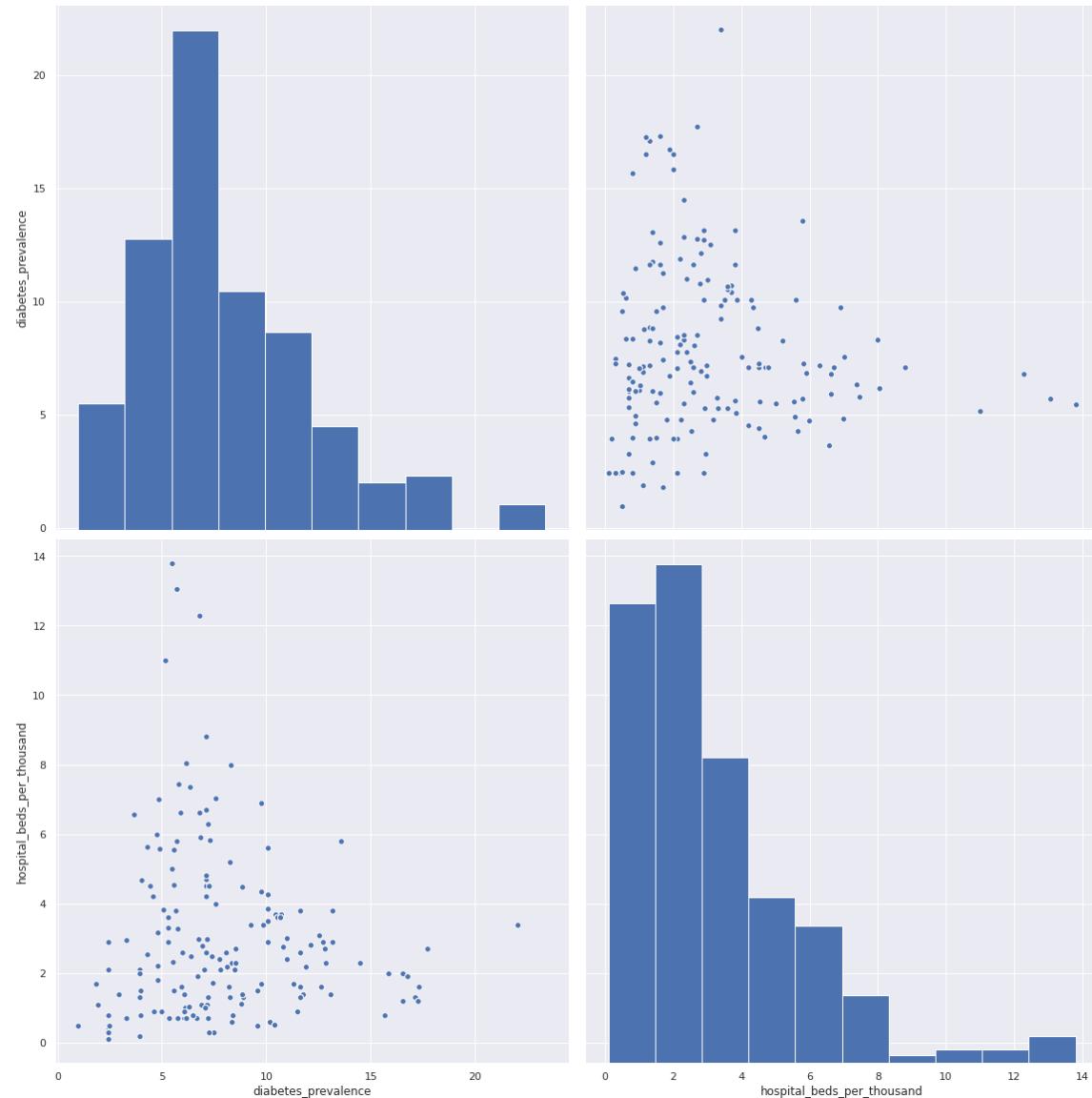


In [124]:

```
sns.pairplot(features, vars=["diabetes_prevalence", "hospital_beds_per_thousand"], height=8)
```

Out[124]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff430e748>
```

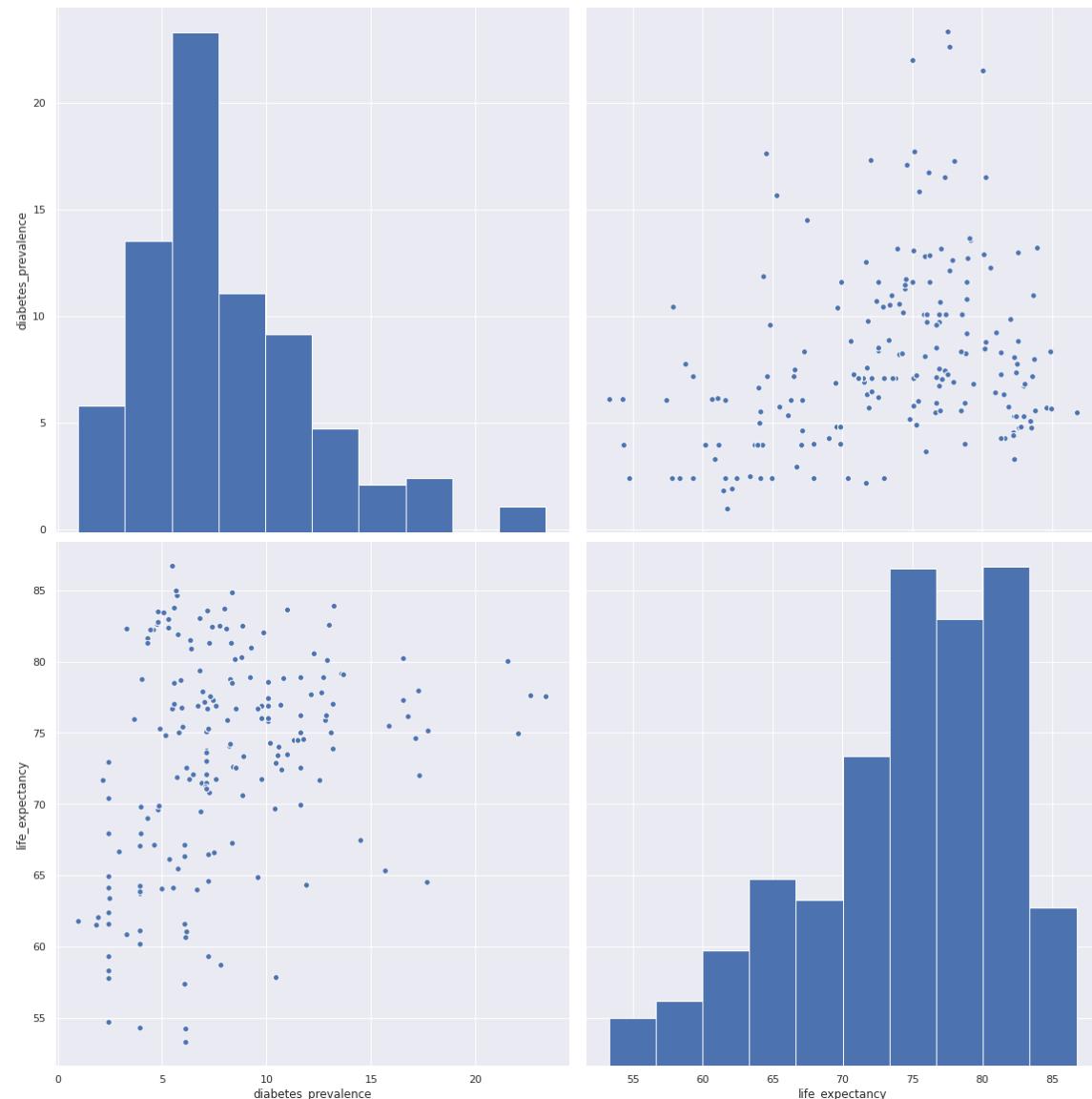


In [125]:

```
sns.pairplot(features, vars=["diabetes_prevalence", "life_expectancy"], height=8)
```

Out[125]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff3f134a8>
```

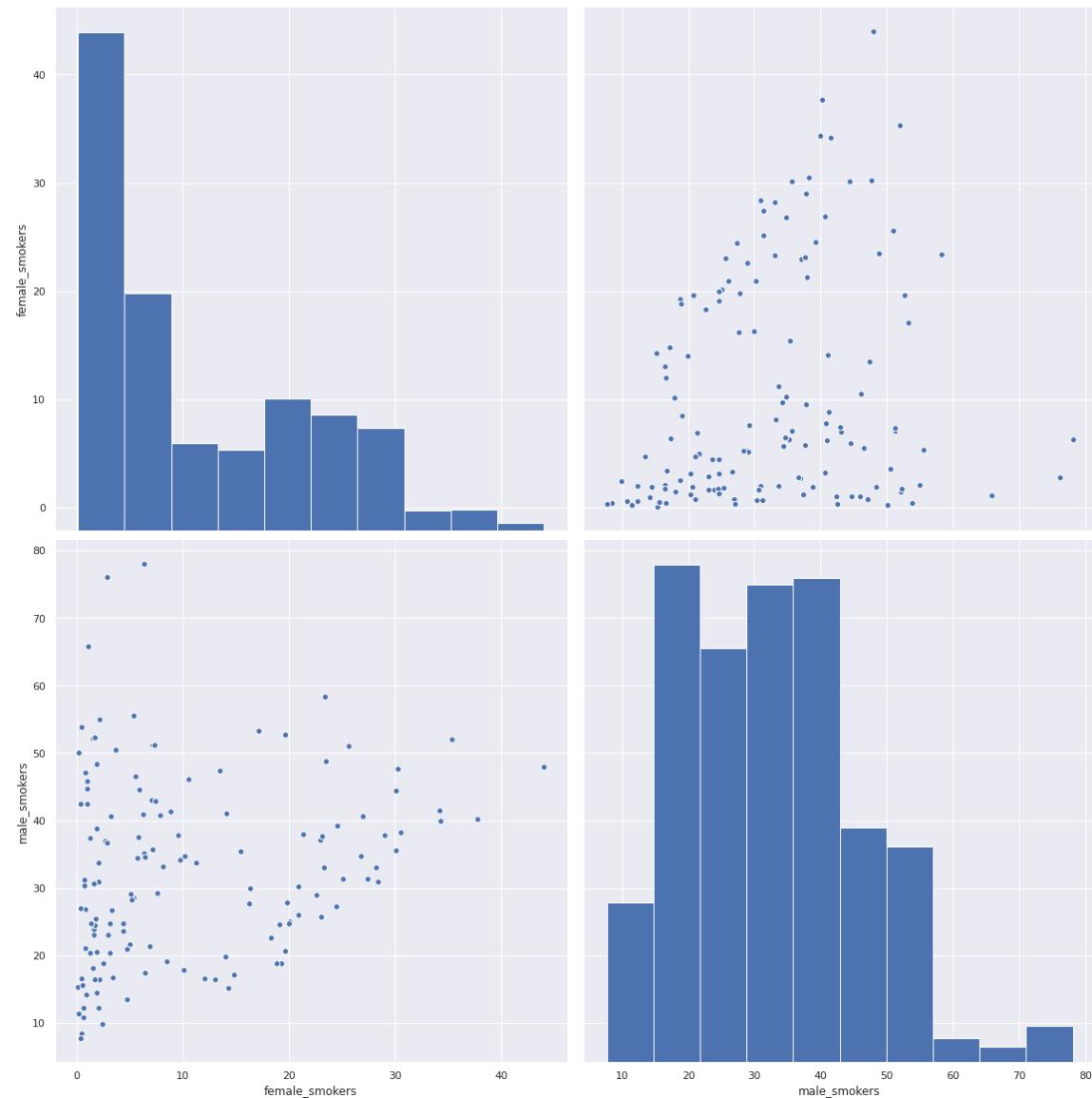


In [126]:

```
sns.pairplot(features, vars=["female_smokers", "male_smokers"], height=8)
```

Out[126]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff3e62978>
```

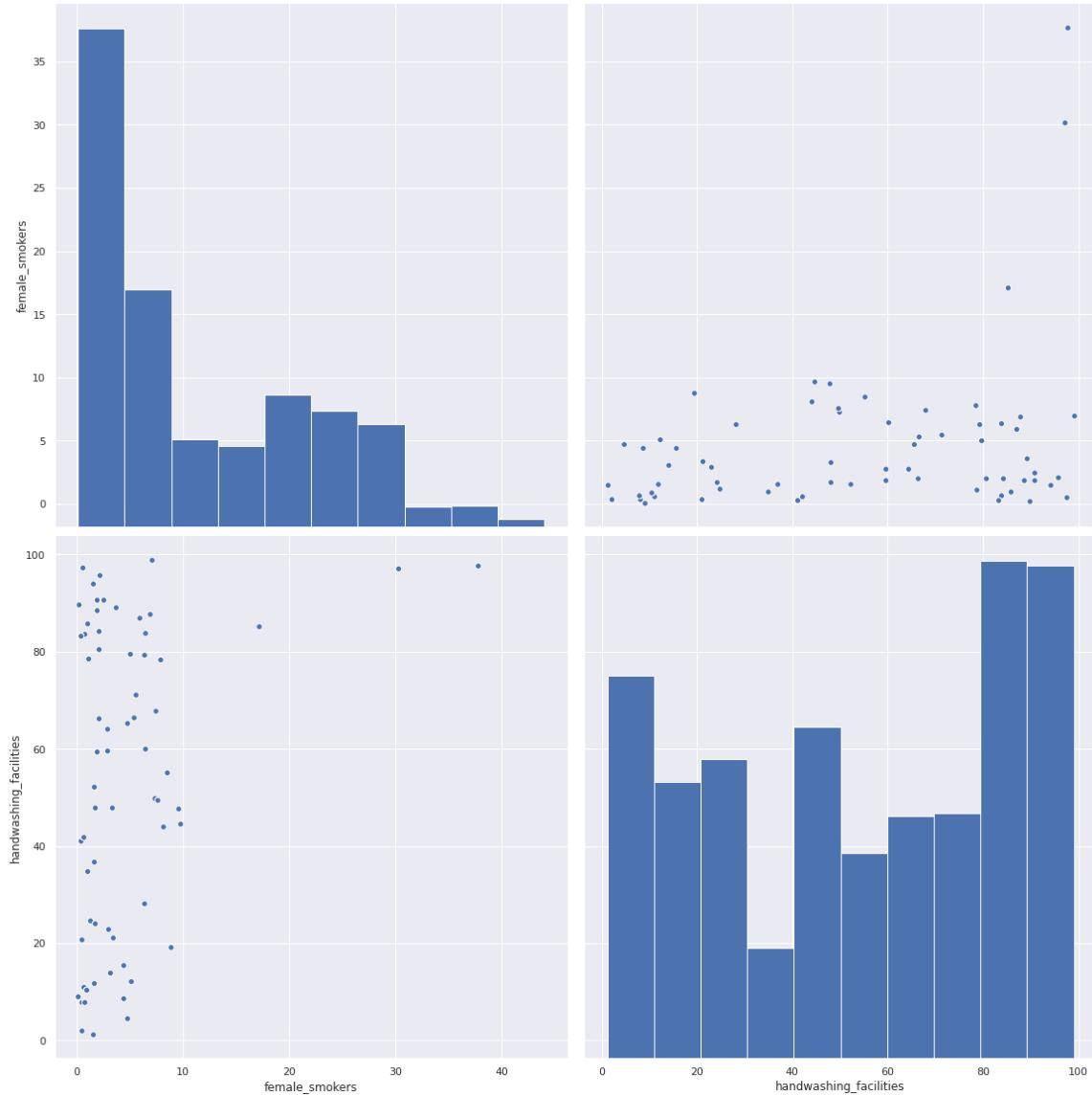


In [127]:

```
sns.pairplot(features, vars=["female_smokers", "handwashing_facilities"], height=8)
```

Out[127]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff3b0c208>
```

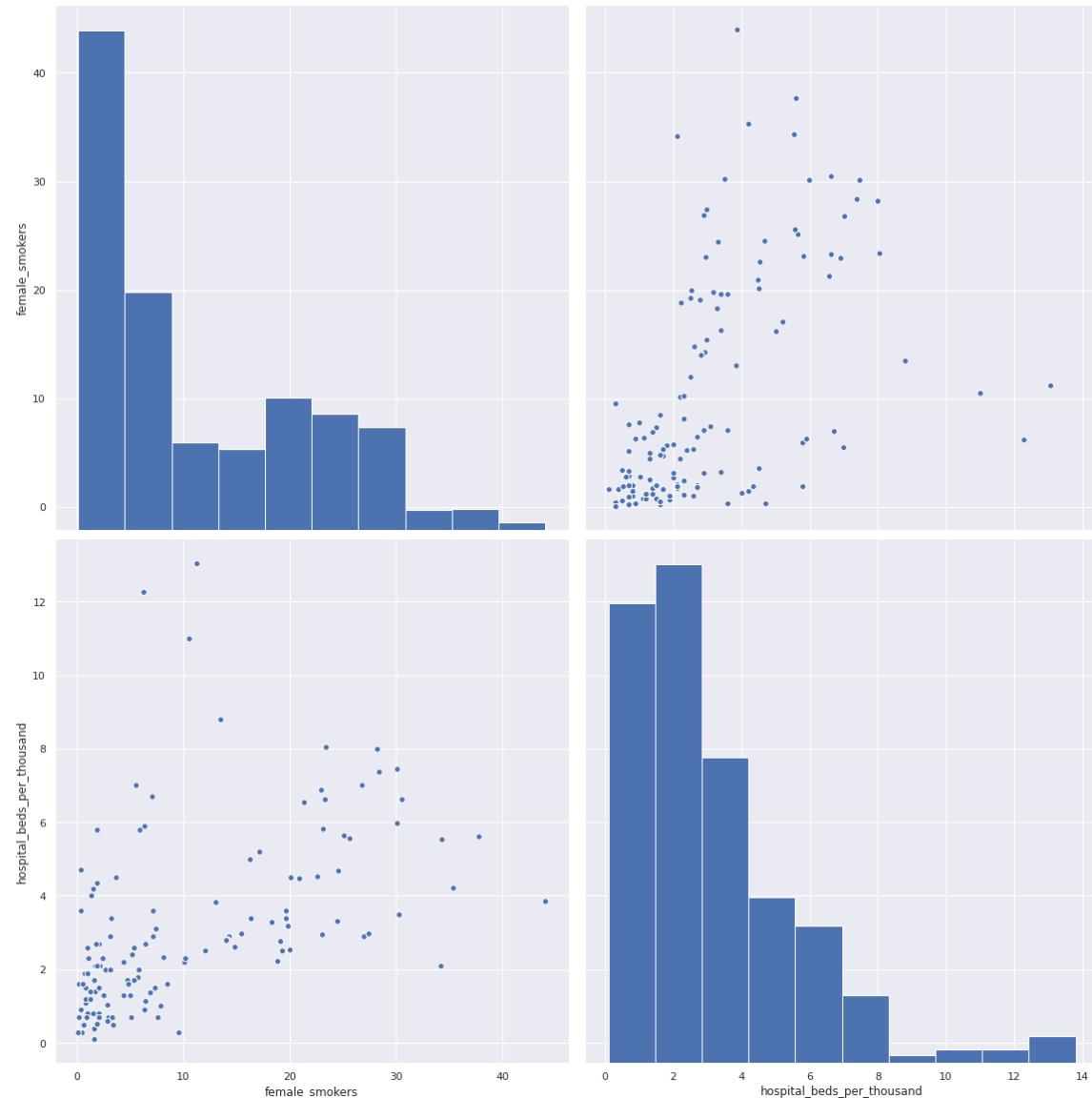


In [128]:

```
sns.pairplot(features, vars=["female_smokers", "hospital_beds_per_thousand"], height=8)
```

Out[128]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff3e06278>
```

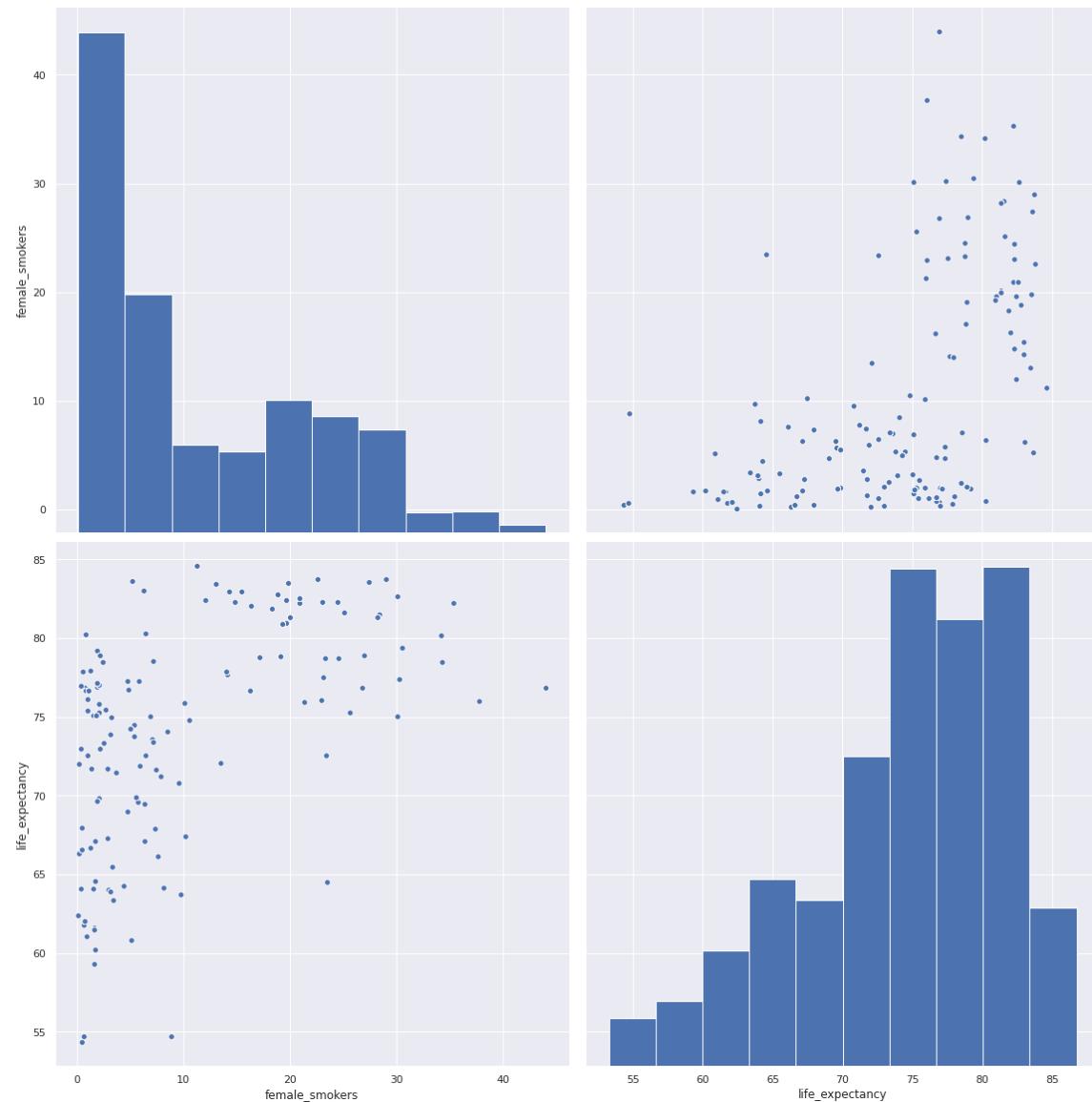


In [129]:

```
sns.pairplot(features, vars=["female_smokers", "life_expectancy"], height=8)
```

Out[129]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff3b89f60>
```

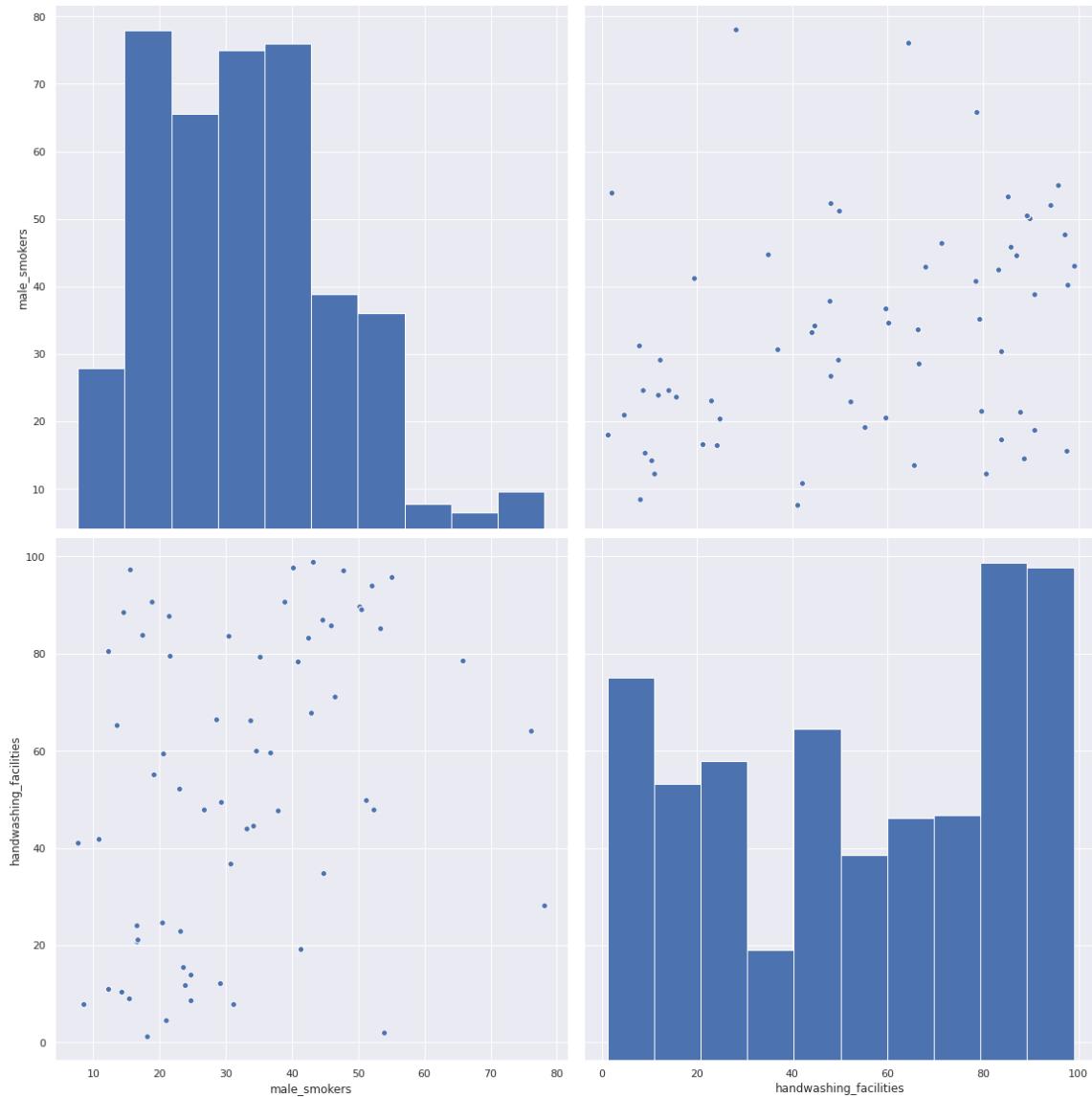


In [130]:

```
sns.pairplot(features, vars=["male_smokers", "handwashing_facilities"], height=8)
```

Out[130]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff354db00>
```

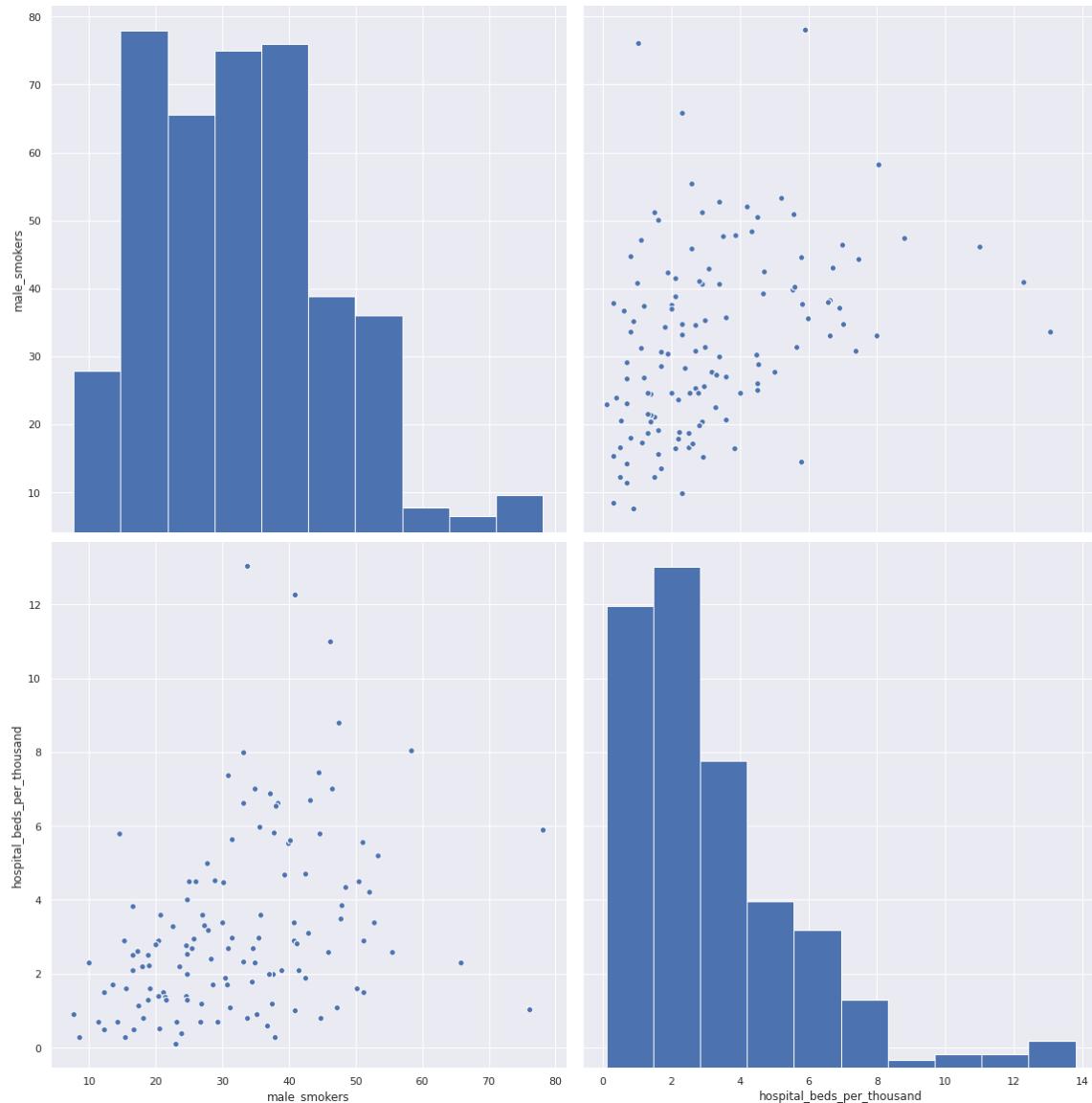


In [131]:

```
sns.pairplot(features, vars=["male_smokers", "hospital_beds_per_thousand"], height=8)
```

Out[131]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff3307710>
```

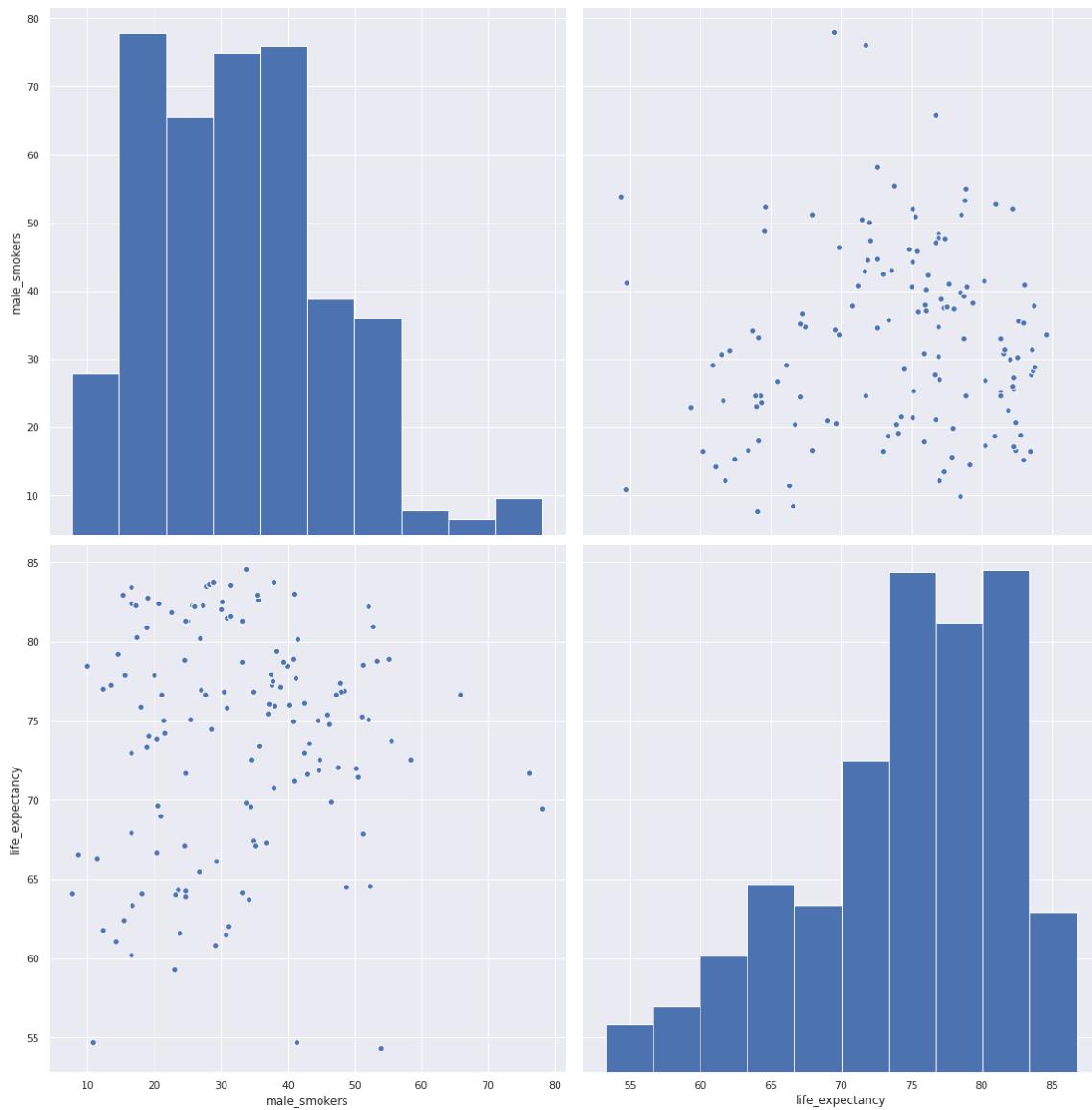


In [132]:

```
sns.pairplot(features, vars=["male_smokers", "life_expectancy"], height=8)
```

Out[132]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff31144e0>
```

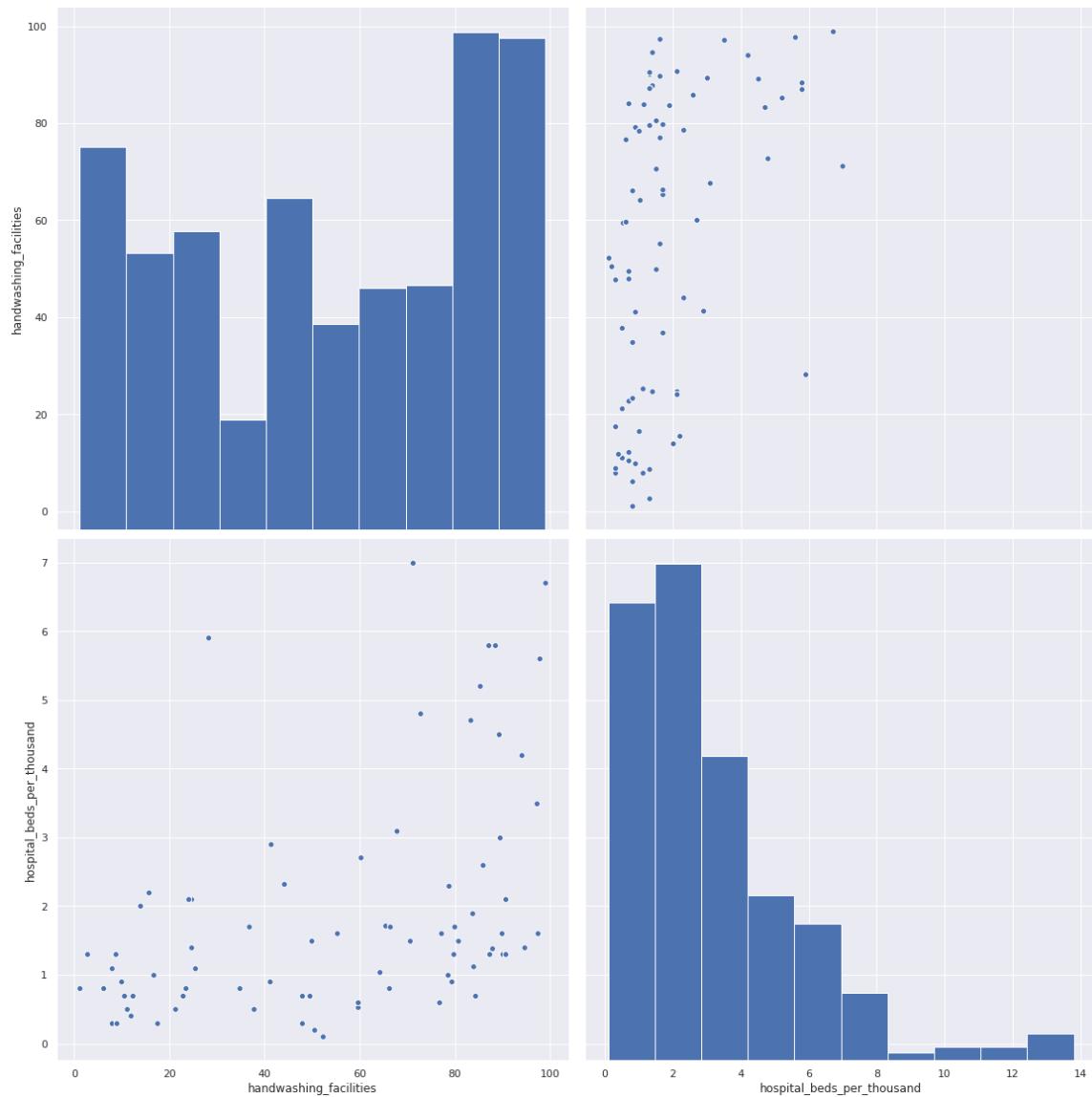


In [133]:

```
sns.pairplot(features, vars=["handwashing_facilities", "hospital_beds_per_thousa  
nd"], height=8)
```

Out[133]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff2f150b8>
```



In [134]:

```
sns.pairplot(features, vars=["handwashing_facilities", "life_expectancy"], height=8)
```

Out[134]:

```
<seaborn.axisgrid.PairGrid at 0x7f0ff2d0e320>
```

