

COVID-19 Status v1.01 – User Manual

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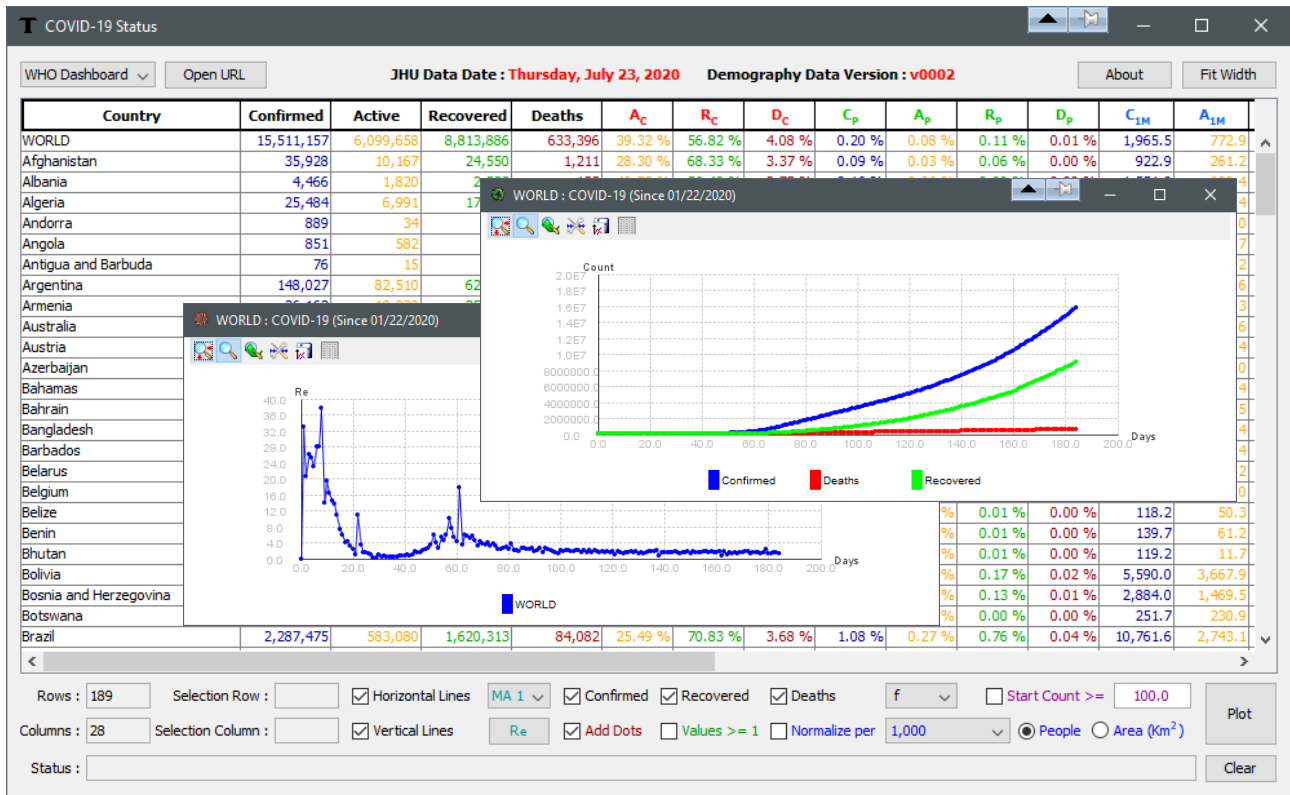


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1. Java

COVID-19 Status application requires **Java** to be installed on your computer. You may visit java.com to check if you have **Java** already installed, or to install **Java** if you don't have it.

2. Installation

Just extract the contents of the *COVID19.zip* file in a location of your choice on your file system. The application is distributed in the form of a standard Java *jar* file and requires no further installation steps.

3. Running

On most operating systems, you should be able to easily run the application by double clicking on the *Covid19.jar* file. If that does not work (rarely), you may type the following command on a command prompt (terminal) to run the application:

PROMPT> java -jar Covid19.jar

A third way to run the application on Windows operating systems is to double click on the *Run.bat* file, which simply just executes the same command above.

4. Usage

When you run the application, it first displays a small window, with the title *Wait*, at the center of the screen, while it fetches and processes most recent data from the GitHub repository¹ maintained by Johns Hopkins University (JHU), Center for Systems Science and Engineering (CSSE)². Then, it closes the *Wait* window and opens the *main window*. All further functionality is available by point-and-click operations on the main window (which will be introduced later in this document).

5. Data

The application requires and uses two sets of data:

- **COVID Dataset:** This first data set is dynamic, and it is downloaded fresh from JHU GitHub repository each time you run the application. This set contains current number of COVID-19 cases for each country (*confirmed*, *deaths*, *recovered*, and *active*) and **3** time-series data per each country (*confirmed*, *deaths*, and *recovered*, all dating back to January 22, 2020).
- **Demography Dataset:** This second data set is compiled mostly from *Worldometer*³, and missing values are filled in by referring to various other sites like *IndexMundi*⁴ and *Wikipedia*⁵. This set is statically stored as a regular excel file named *Demography.xlsx*. The demography data contains *population*, *median age*, and *land area* values for each country (and also some cruise ships with observed COVID-19 cases).

It is important that the *Demography Dataset* contains all the countries and cruise ships listed in *COVID Dataset*, and the spelling of the names of countries and cruise ships match exactly (otherwise,

¹ <https://github.com/CSSEGISandData/COVID-19>

² <https://systems.jhu.edu/research/public-health/ncov>

³ <https://www.worldometers.info/world-population/population-by-country>

⁴ <https://www.indexmundi.com/factbook/fields/median-age>

⁵ https://en.wikipedia.org/wiki/Main_Page

some functionalities of the application may not perform properly). Upon start, the application checks if any name in **COVID Dataset** is not covered in **Demography Dataset**, and if so, prints a warning message in the status field at the bottom of the main window. If you see a warning, you need to add data for the uncovered country in the **Demography.xlsx** file (or you may check the software website for a new version of the **Demography.xlsx** file that the author might already have distributed), and run the application again.

Once all the data is read in, the application presents both the raw and processed data in a big table inside the main window. The columns of the big table are described in **Table 1**.

6. Effective Reproduction Number (R_e)

R_e is approximated using a simple discrete **SIR** (Susceptible-Infectious-Recovered) *model*⁶.

Let;

$c(t)$ denote the number of (cumulative) **confirmed** cases,

$r(t)$ denote the number of (cumulative) **recovered** cases,

$d(t)$ denote the number of (cumulative) **deaths**,

$S(t)$ denote the number of **susceptible** people in the **SIR** model,

$I(t)$ denote the number of **infected** people in the **SIR** model,

$R(t)$ denote the number of **recovered** people in the **SIR** model,

n denote the time period (number of **days**) over which R_e is approximated,

N denote the **population** (assumed to be constant during the most recent n days), and

R_e^n denote the **effective reproduction number** approximated based on the most recent n days,

Then, the R_e^n values presented by the application are calculated as follows:

$$S(t) = N - c(t)$$

$$I(t) = c(t) - [r(t) + d(t)]$$

$$R(t) = r(t) + d(t)$$

$$S'(t) = S(t) - S(t - n) = N - c(t) - N + c(t - n) = c(t - n) - c(t)$$

$$R'(t) = R(t) - R(t - n) = r(t) + d(t) - [r(t - n) + d(t - n)]$$

$$R_e^n = \frac{-S'(t)}{R'(t)} = \frac{c(t) - c(t - n)}{r(t) + d(t) - r(t - n) - d(t - n)}$$

In rare cases the calculation might yield **exceptional** results: When up-to-date data is not available for a country, JHU database duplicates most recent valid value to fill the missing entries, and in such cases R_e^n might end up to be 0/0 which is reported as -0.0 by the application. Similarly, very high results are capped at 100 in R_e **plots**, and very low negative results are capped at -1 (negative values occur when JHU data has corrections breaking the monotonic cumulative nature of some time series).

⁶ https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology

Table 1. Description of columns of big table

Column	Description
Country	Name of the <i>country</i>
Confirmed	Number of (cumulative) <i>confirmed</i> Covid-19 cases
Active	Number of <i>active</i> Covid-19 cases
Recovered	Number of (cumulative) <i>recovered</i> Covid-19 cases
Deaths	Number of (cumulative) <i>deaths</i> due to Covid-19
Ac	Ratio of <i>active</i> cases as a percentage of confirmed cases
Rc	Ratio of <i>recovered</i> cases as a percentage of confirmed cases
Dc	Ratio of <i>deaths</i> as a percentage of confirmed cases
Cp	Ratio of <i>confirmed</i> cases as a percentage of the country's population
Ap	Ratio of <i>active</i> cases as a percentage of the country's population
Rp	Ratio of <i>recovered</i> cases as a percentage of the country's population
Dp	Ratio of <i>deaths</i> as a percentage of the country's population
C_{1M}	Number of <i>confirmed</i> cases per 1 million people
A_{1M}	Number of <i>active</i> cases per 1 million people
R_{1M}	Number of <i>recovered</i> cases per 1 million people
D_{1M}	Number of <i>deaths</i> per 1 million people
Re¹	<i>Effective reproduction number</i> based on most recent <i>day</i> 's data
Re⁷	<i>Effective reproduction number</i> based on most recent <i>week</i> 's data
Re¹⁴	<i>Effective reproduction number</i> based on most recent <i>fortnight</i> 's data
rc	<i>Growth rate</i> of <i>confirmed</i> cases based on an exponential growth model
rr	<i>Growth rate</i> of <i>recovered</i> cases based on an exponential growth model
rd	<i>Growth rate</i> of <i>deaths</i> based on an exponential growth model
Ãge	<i>Median age</i> of the country's population
Population	<i>Population</i> of the country
Share	Ratio of country's <i>population</i> as a percentage of the world's total population
Area (Km²)	<i>Land area</i> of the country
Share	Ratio of country's <i>land area</i> as a percentage of the world's total land area
P/Km²	<i>Density</i> (population per square kilometer)

7. Growth Rate (r)

Growth rates for **confirmed** cases, **recovered** cases and **deaths** are also calculated and displayed by the application for each country using an **exponential growth model**⁷. It should be noted that the exponential growth model is not a good mathematical model that could explain the governing dynamics of how those specific time-series evolve in real life. Nevertheless, the presented growth rates of hypothetical geometric growths might provide the users with some extra insight into how fast the progressions have been so far.

The calculation of the growth rate of **confirmed** cases (r_C) is described below. The growth rates for **recovered** cases (r_R) and **deaths** (r_D) are also calculated in the same way.

Let;

c_0 denote the first ever reported **non-zero** value of the (cumulative) confirmed cases⁸,

c_N denote the **recent** value of the (cumulative) confirmed cases, and

n denote the number of **days** passed between c_0 and c_N ,

Then, the growth rate for confirmed cases (r_C) is calculated as follows:

$$c_N = c_0(1 + r_C)^n$$

$$r_C = \sqrt[n]{\frac{c_N}{c_0}} - 1$$

Note that in order to provide fairness among countries, c_0 is always taken as 1 in all calculations. (Initial non-zero case counts might vary from country to country, and different values might affect the calculation result, therefore, it is assumed that all time-series start with 1 as their first non-zero value, and the calculation is basically focused on finding the growth rate that is required to start with the value 1 and reach the current value in exactly n days with a purely geometric growth process.)

8. Features

Features/functionalities of the application are marked and numbered in **Figure 1**, and they are explained below:

Feature 1: At the center of the main window is the big table that displays all raw and processed data from **COVID** and **Demography** data sets. You may resize the window to see more of the table or use vertical and horizontal scroll bars around the table for the same purpose. The **columns** of the table can be **resized** and also **reordered** (by dragging with the mouse). The column headers can be clicked for **sorting** the table in increasing or decreasing order. One or more rows of the table can be clicked/selected for plotting the time-series data associated with those countries (plotting is explained later).

Feature 2: Links to some important online COVID-19 dashboards and data sources are collected here. You may choose one from the checkbox and click the **Open URL** button. If this feature of Java is supported on your system, your browser will be opened, and the selected URL will be loaded.

⁷ https://en.wikipedia.org/wiki/Exponential_growth

⁸ Also referred to as **patient zero**, or **index case**

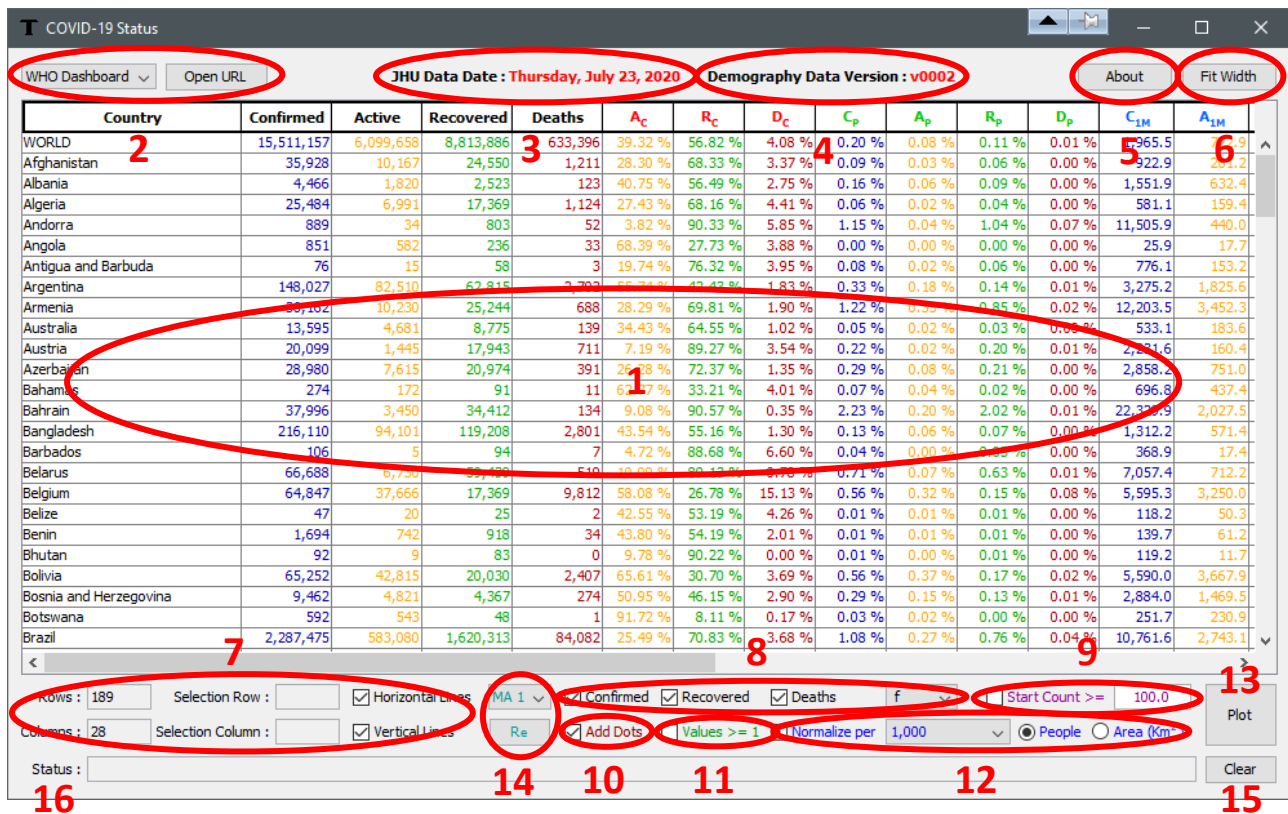


Figure 1. Main window – features/functionality

Feature 3: The date of the *COVID Dataset* fetched from the JHU GitHub repository is printed at the top of the table.

Feature 4: The version of the *Demography Dataset* (*Demography.xlsx* file) is printed at the top of the table.

Feature 5: The *About* button opens up a small window at the center of the screen with the author and version information for the application and the *Demography Dataset*.

Feature 6: The *Fit Width* button tries to set the width of the window such that all columns of the table are visible. Note that you can always resize the window yourselves.

Feature 7: The total number of rows and columns of the table are statically printed on the left (The number of rows depends on *COVID Dataset* and may change from day to day, the number of columns is always the same). When a single cell is clicked inside the table, the row and column number of the selection is printed at the center. And you may toggle horizontal and vertical cell boundaries of the table by the checkboxes on the right.

Features 8 to 13 are used to generate *time-series plots*. In order to generate a plot, you need to first select one or more rows (countries) from the table. Then you adjust some plotting parameters using Features 8 to 12, and then click the *Plot* button (Feature 13) to open up a new graphical window with the plot.

Feature 8: There are 3 time series per each country (*confirmed*, *recovered* and *deaths*) in the *COVID Dataset*. Here, you may choose which ones you want plotted. Also, to the right of the checkboxes, there is a combo box which allows you to choose whether you want the original data (counts), or a discrete-time derivative of the data (up to order 3). Briefly; *f* is the original data in *count*, *f'* is the

velocity in *count/day*, f'' is the acceleration in *count/day*², and f''' is the jerk/jolt in *count/day*³.

There are **4 optional operations** you may apply on raw data before it gets plotted. These operations are described below in the same order that they are (optionally) applied on the data:

- The raw counts can be *normalized* by the *population* or the *land area* of their respective countries. In this case, the new unit of measurement will be *count/x people* or *count/x km²* where x is a parameter that can be set by the user.
- Starting from the leftmost entries (past dates), the selected time series can be *shifted left*, dropping all entries that are below a user specified value, say n . This is useful, for example, in cases where you are interested in comparing the time-series data for a few countries only after the $n = 100^{\text{th}}$ case of COVID is observed in each of them (so the leftmost entries of all time-series until the 100th case will be dropped, and all time-series will start at around 100th case). When a time-series is shifted left, the entries that become empty at the far-right side (recent dates) are filled by replicating the last (most recent date) data. Another consideration for this operation is that, if all of the entries in a time-series are completely above or completely below n , that time series will not be modified by this operation.
- The selected time series can be discrete-time *differentiated* up to order 3.
- All entries in a time series that are below 1.0 can be set to 1.0 making all entries positive and *greater than or equal to 1.0*. This may be useful in cases where *logarithmic plots* need to be generated.

With the optional operations in mind, we continue with the remaining features:

Feature 9: This is the second optional operation described above. You may check the box and set n here to filter time series before plotting.

Feature 10: The generated plots will be in the form of line plots. If this box is checked, explicit dot markers will be added to the plots making discrete nature of the plots more visible.

Feature 11: This is the fourth optional operation described above.

Feature 12: This is the first optional operation described above, where you can set x and normalize time series by either *population* or by *land area*.

Feature 13: Once you are done choosing the countries, time series, and optional operations, you click the *Plot* button, and a new window with your choice of the plot will open up.

Feature 14: *Effective reproduction numbers* for the selected countries can be plotted as a *function of time* by clicking on the R_e button. The generated plots will contain the R_e^1 values calculated for each day for each selected country. Optionally, it is also possible to smooth the generated plots by applying a *simple moving average* operator (with the *length* parameter between 2 and 7 that is chosen using the combo box above the R_e button). It is important to note that the effective reproduction number plots will also observe the Features 10 and 11 described above.

Feature 15: When you click on the *Clear* button, your selected rows (countries) on the table, if any, will be unselected (the table will be cleared of any selections), the *Selection Row* and *Selection Column* fields of Feature 7 will be cleared, and also any text in *Status* field (Feature 15) will be cleared.

Feature 16: The long text field at the bottom of the window is used to display warnings and results of user operations. It is useful to keep an eye on the status field during your work with the application. Especially if you see a warning in the status field immediately after running the application, you may need to update *Demography Dataset* for the application to continue to function properly.

9. Plots

A sample plot is shown in **Figure 2**.

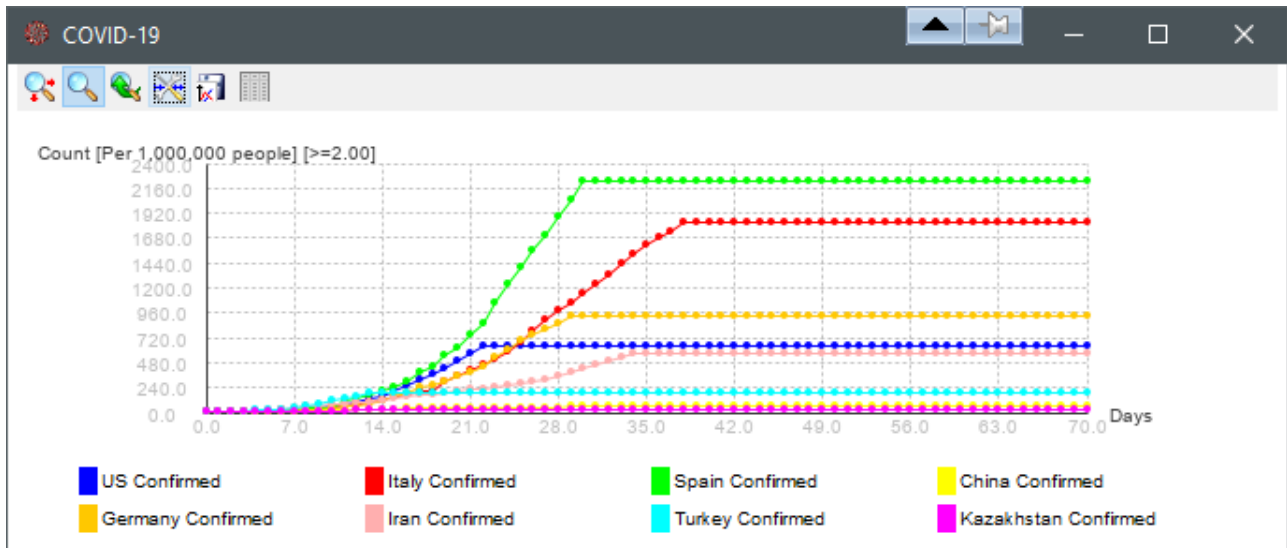


Figure 2. Sample plot

In the given example, the user chose *confirmed* time series for 8 countries, normalized them per 1 million people, and chose to start each time series when at least 2 cases (per 1 million people) have been observed.

The plots are generated using *JMathPlot*⁹ library. Each plot opens up in an individual window of its own. You may individually work on each plot window, or close a plot window without affecting any other plot windows. Plot windows can be resized. Main features of plots are marked in **Figure 3**, and explained below (for more information on capabilities of plots, you may refer to *JMathPlot*'s own documentation).

Feature 1: Each plot window will have a random virus icon (out of 5 different icons).

Feature 2: (Center axes) You may click on this button first, and then drag the plot around (reposition) inside the window.

Feature 3: (Zoom) You may click on this button first, and then draw a rectangle on the plot. The selected rectangular region of the plot will be zoomed in.

Feature 4: (Reset zoom & axes) Resets any repositioning and zooming applied on the plot.

Feature 5: (Set scales) When you click on this button, a new window will open up, allowing you to set the *title*, *scale* (linear or logarithmic) and the *bounds* (minimum and maximum) for both *x* and *y* axes of the plot.

⁹ <https://sites.google.com/site/mulabsltd/products/jmathplot>

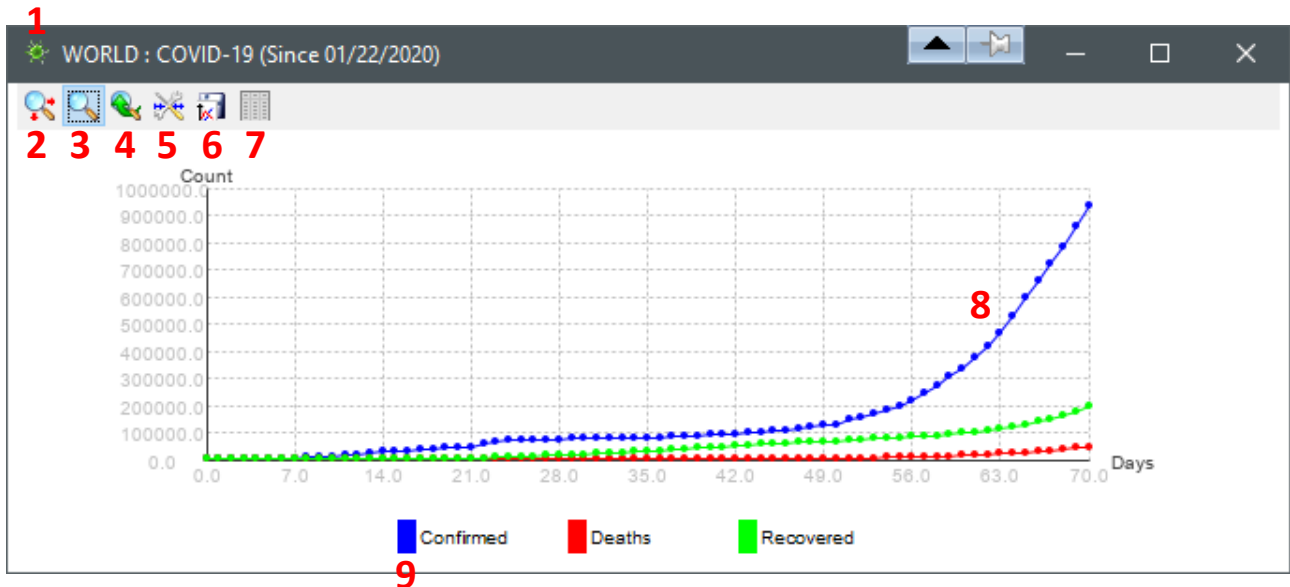


Figure 3. Plots – features/functionalities

Feature 6: (*Save graphics*) Allows you to save the plot as an image file in PNG format.

Feature 7: (*Get datas*) This button brings up a new window that will allow all time-series data displayed in the plot to be set visible/invisible, copied to clipboard, and/or saved as a text file.

Feature 8: You may click on a time series, and both that time series and the corresponding label at the bottom of the plot will be highlighted in black color. You may click again to turn highlighting off.

Feature 9: You may click on a label at the bottom of the plot, and both that label and the corresponding time series will be highlighted in black color. You may click again to turn highlighting off.

10. Contact

Website of the application: <http://selimtemizer.com/software/covid19>

Contact information of the author, **Selim Temizer**, can be located on his website: selimtemizer.com

The author of the software initially developed the application for personal use to gain insight into COVID-19 data that is made publicly available by JHU CSSE, and then shared it freely with the hope that it would be useful in the fight against COVID-19. The author is a computer scientist, and he has absolutely no background in medicine. Although no promises are given, the author is willing to maintain the software (fixing bugs, adding features, etc.) as time and conditions permit.

11. License and Disclaimer

COVID-19 Status (COVID-19)

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