



# **Mathematical Analysis of Covid-19 Positive Case Data Using the Fibonacci Sequence**

Gus Reinhart



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## Research Question:

The purpose of my project is to determine if there are correlations between the Fibonacci Sequence and Covid-19 data of total cases in the United States. Therefore I hope to explore if the Fibonacci Sequence can be used to predict and explain the rate at which Covid-19 has spread. The findings from my project may be significant in understanding how mathematics and nature are intertwined. If mathematics modeling can be of use in understanding infectious disease, perhaps steps can be taken accordingly by policy makers and other stakeholders to better communicate with scientists which would benefit public health and the common good.

## Math Framework:

**Infectious diseases** are disorders that are caused by organisms such as bacteria, viruses, fungi or parasites.

**Epidemiology** is the method used to find the causes and health outcomes of diseases within populations.

**Frequency** refers to the number of health events, but also the relationship of that number to the size of the population.

**Patterns** refer to the health-related events by time, place and person. The breakdown of time may influence the disease occurrence.

**Coronavirus**, Covid-19, is an infectious disease caused by a newly discovered coronavirus (SARS-CoV-2).

**Fibonacci sequence** is a mathematical formula in which each number in the sequence is the sum of the two numbers that precede it. For example the sequence goes: 0, 1, 1, 2, 3, 5, 8, 13, 21, 34 and so on. The mathematical equation describing the Fibonacci sequence is  $x_n + 2 = x_n + 1 + x_n$ .

## Findings:

The rate of growth for the standard deviation of 1, 4, and 7 day averages stayed within 1. What this means is that growth will not be exponential because if the standard deviation is above 1, the growth factor for the number of positive covid cases would be exponential. If the standard deviation was below 1, that would show the data is leveling off. When comparing the covid positive case data to the average distance from the Fibonacci number that corresponds with that day, it was discovered that on average the positive case number per day is closer to the Fibonacci sequence number than to a regular whole number. The average distance between a Fibonacci number and the subsequent number in the Fibonacci sequence is 61.8%. This 61.8% correlates to a 30.8% deviation between two Fibonacci sequence numbers. The covid positive case data, utilizing those same parameters, show a 13% deviation based upon the absolute values.

## Conclusions:

The general purpose of this project was to determine if the Fibonacci Sequence correlates to Covid-19 case numbers in the United States from January 22nd, 2020 through December 31st, 2020. The purpose of this project is to determine if the Fibonacci Sequence will occur in the U.S. Covid-19 case number data because studies have shown that the Fibonacci Sequence occurs over time in case numbers of other infectious diseases.

The first hypothesis was that the average deviation in new positive Covid-19 cases would be higher than 1. However, I reject this hypothesis because based on the graphs after Day 70 all the averages stay within 1 percentage point of the standard line.

The second hypothesis was that the Fibonacci Sequence would occur consistently over time in the Covid-19 total daily case numbers. I loosely accept this hypothesis because although the standard deviation for the Fibonacci sequence number is 31%, the Covid positive case numbers data is 13% which is closer to a Fibonacci number than a regular whole number.

# INTRODUCTION

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# FRAMEWORK

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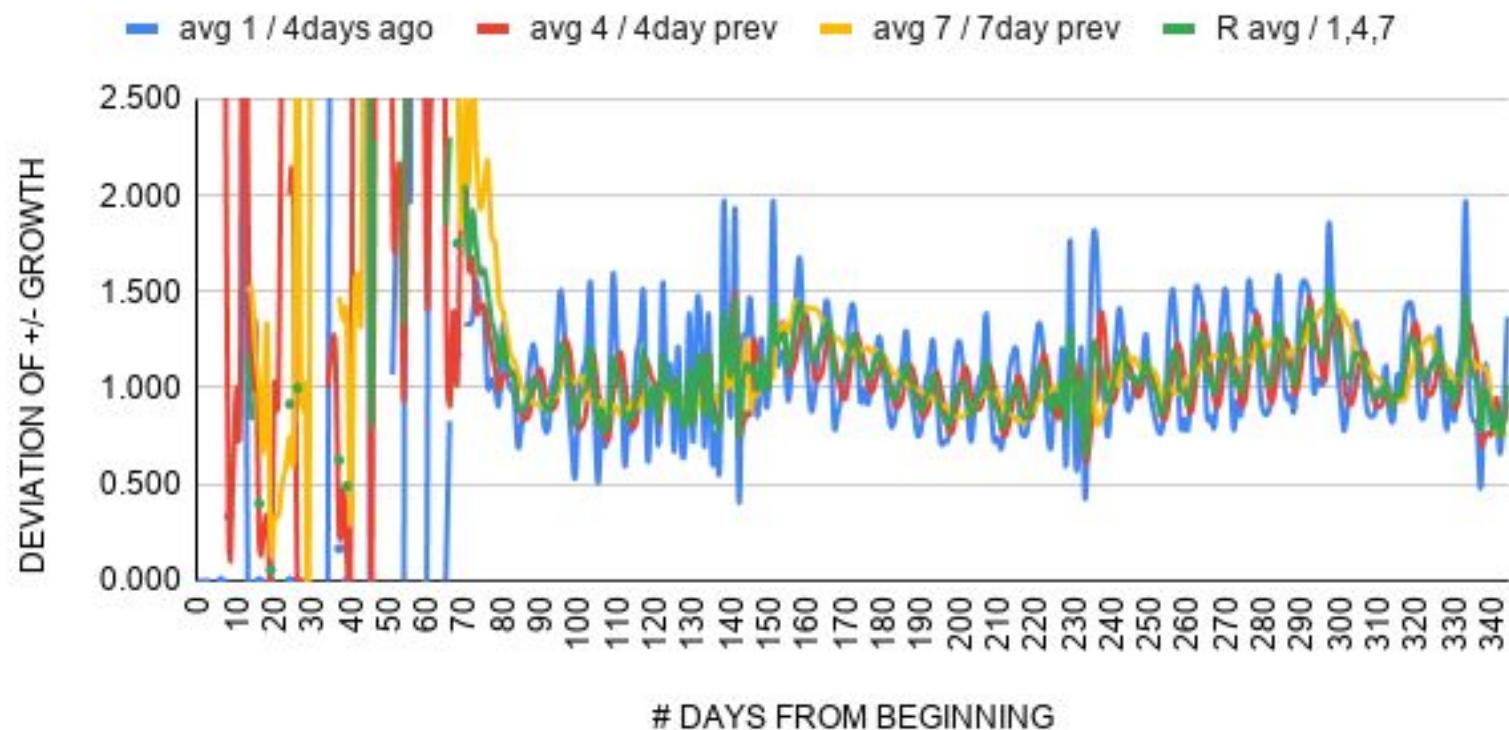
# FORMULAS

1. GROWTH FACTOR = NEW DAILY CASES CURRENT DAY / NEW DAILY CASES PREVIOUS DAY.
2. GROWTH AVERAGE = NEW DAILY CASES CURRENT DAY / NEW DAILY CASES FOUR DAYS PRIOR.
3. GROWTH AVERAGE 4 DAYS = SUM OF NEW DAILY CASES MOST RECENT FOUR DAYS / NEW DAILY CASES FROM DAYS FIVE TO EIGHT PRIOR.
4. GROWTH AVERAGE 7 DAYS = SUM OF NEW DAILY CASES MOST RECENT SEVEN DAYS / NEW DAILY CASES FROM DAYS EIGHT TO 14 PRIOR.
5. CLOSEST TO FIBONACCI = FIND THE CLOSEST FIBONACCI NUMBER RELATED TO NEW DAILY CASES
6. DIFFERENCE IN NEW TO FIBONACCI = CURRENT NEW DAILY CASE - CLOSEST FIBONACCI NUMBER
7. FIBONACCI PERCENT CHANGE = DIFFERENCE IN NEW TO FIBONACCI / CLOSEST TO FIBONACCI
8. ABSOLUTE FIBONACCI CHANGE = ABSOLUTE VALUE OF THE PERCENT CHANGE ASSOCIATED WITH FIBONACCI VALUE CHANGE
9. AVERAGE PERCENT DIFFERENCE FIBONACCI = ((CURRENT FIBONACCI # - PREVIOUS FIBONACCI #) / PREVIOUS FIBONACCI #) / 2
  - a. THIS AVERAGE IS EQUAL TO 30.90 % BASED ON FIBONACCI SEQUENCE #. THIS NUMBER IS A GIVEN.
10. AVERAGE ABSOLUTE FIBONACCI CHANGE = (SUM OF ALL ABSOLUTE FIBONACCI CHANGED) / TOTAL NUMBER OF OCCURANCES

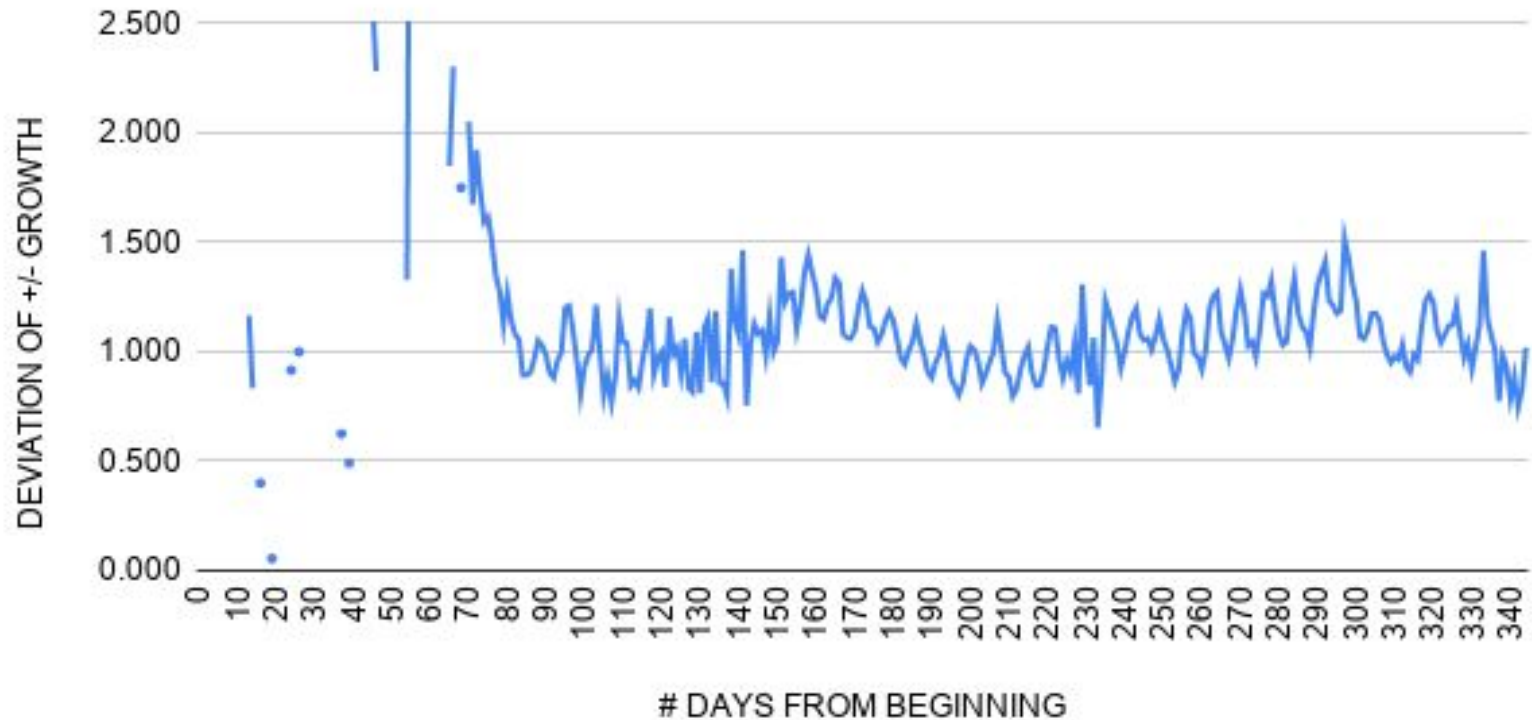
# FINDINGS

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# AGGERGATE DEVIATION OF CURRENT, 4 DAYS, 7 DAYS, AND COMBINED AVERAGE



# COMBINED AGGERAGE DEVIATION FOR 1 DAY, 4 DAYS, AND 7 DAYS

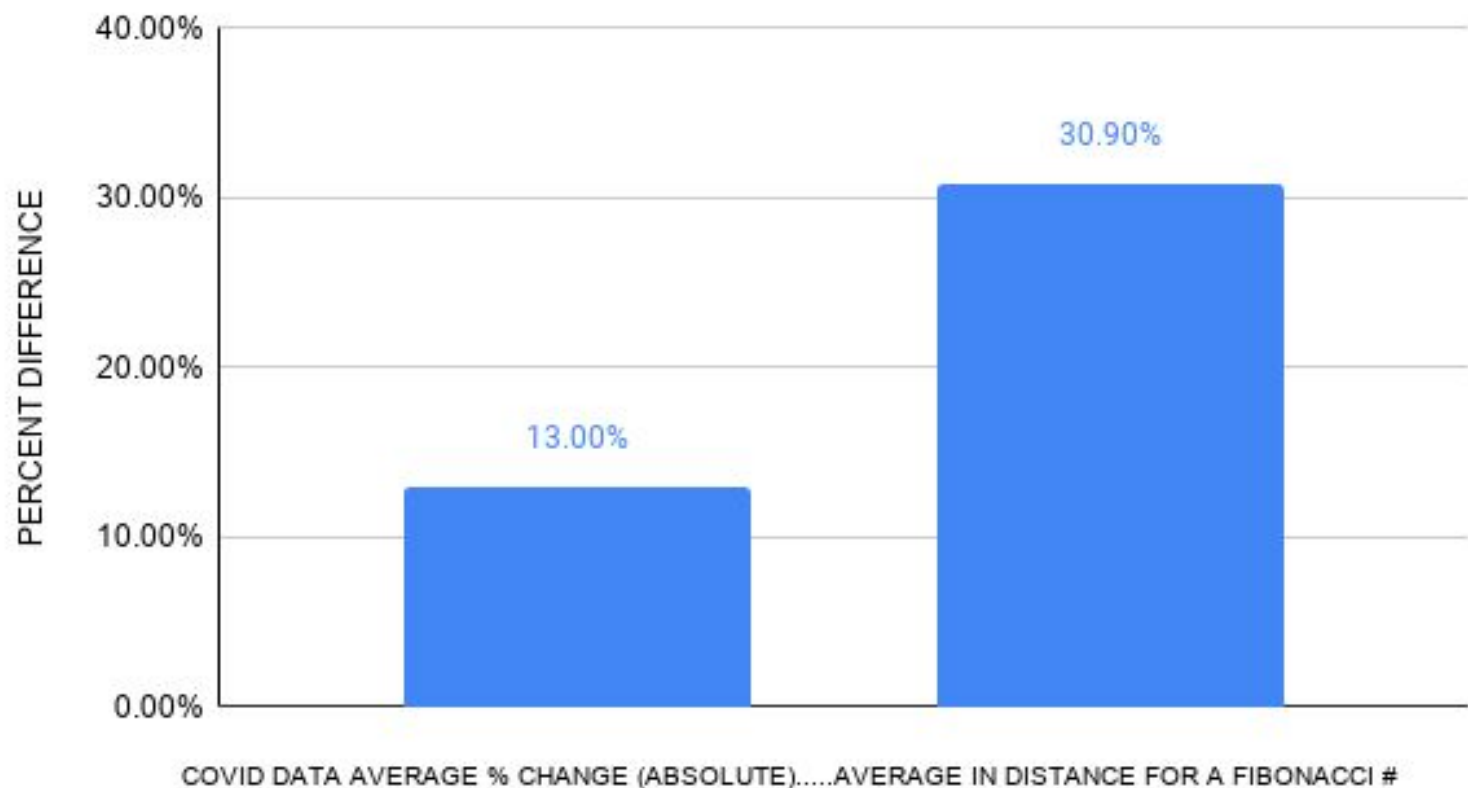




## % CHANGE MONTHLY IN VALUE



## COMPARING COVID DATA AND FIBONACCI # AVERAGES



# CONCLUSIONS

The general purpose of this project was to determine if the Fibonacci Sequence correlates to Covid-19 case numbers in the United States from January 22nd, 2020 through December 31st, 2020. The purpose of this project is to determine if the Fibonacci Sequence will occur in the U.S. Covid-19 case number data because studies have shown that the Fibonacci Sequence occurs over time in case numbers of other infectious diseases.

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# REAL WORLD CONNECTIONS

Mathematical modeling plays an important role in helping to predict, assess, and control potential outbreaks of disease. To help scientists better understand disease factors like ecological, social, economic and demographic factors around the world need to be analyzed and studied. Scientists are getting better at fighting epidemics using mathematics. If scientists are better able to predict the spread of disease early in the spread, measures can then be taken to slow or stop the spread before vast numbers of people are infected. Knowing how the Fibonacci sequence correlates with Covid-19 positive case data as a world-wide pandemic, scientists may be able to study the patterns and predict future outbreak patterns. This project connects to the real world in that the way infectious disease spreads may not occur all that randomly. There are patterns in nature that can be observed, explained, and studied formally.

# NEXT STEPS

One next step in this project is to input positive Covid case data by day for the year 2021. Another possible next step would be to pick another country's positive covid day-by-day data and test to see if the Fibonacci sequence numbers correlate in a comparable way as the United State's positive case data does. A third example of a next step would be to discuss the similarities and differences between the way the Fibonacci numbers correlate to positive Covid case numbers as reported by various countries around the globe.

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