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# Welcome To Plus Magazine!



## From rainbows to rogue waves

Dispersion lies at the heart of many dramatic phenomena - explore the maths that explains it!



What is the Abel Prize?

Find out more about one of the highest honours in maths, named after a tragic Norwegian genius.



Maths in a minute: Correlation versus causation

They're not the same thing even though it's sometimes tempting to think they are.



When being wrong is right

What can we learn from the COVID crisis about finding consensus?

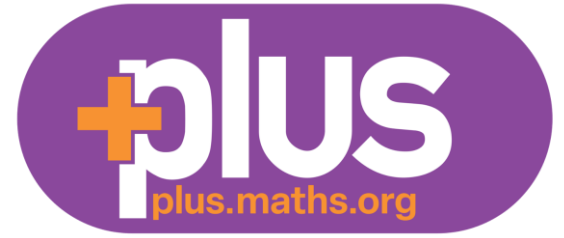


Maths in a minute: Percentage error

Life isn't an exact science so you often need to estimate things. But how do you know how good your estimate is?

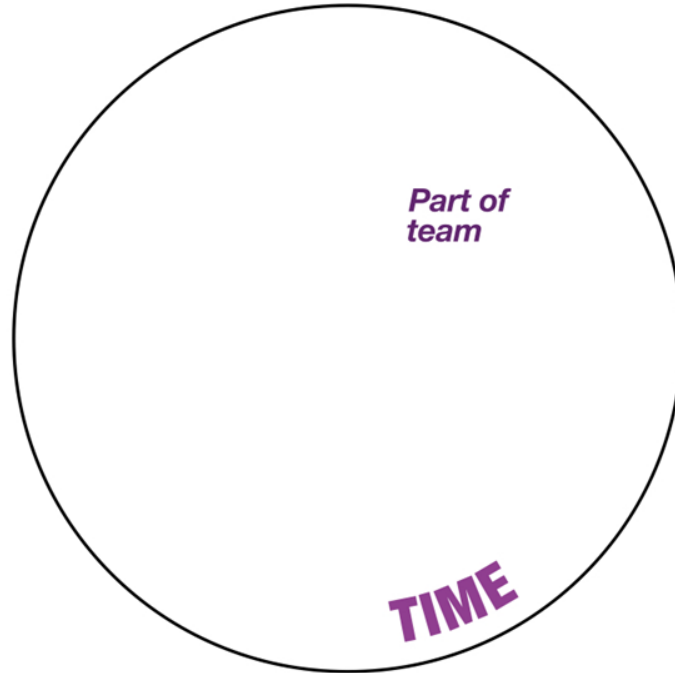


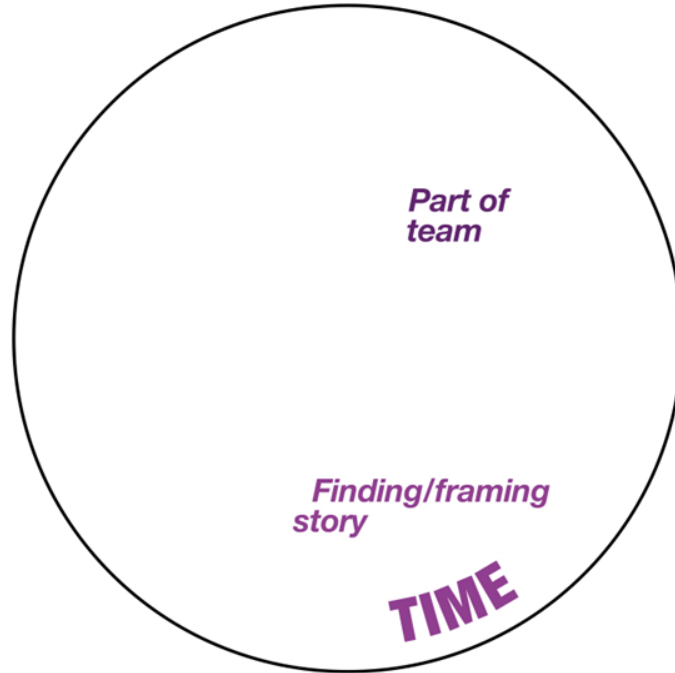
# JUNIPER

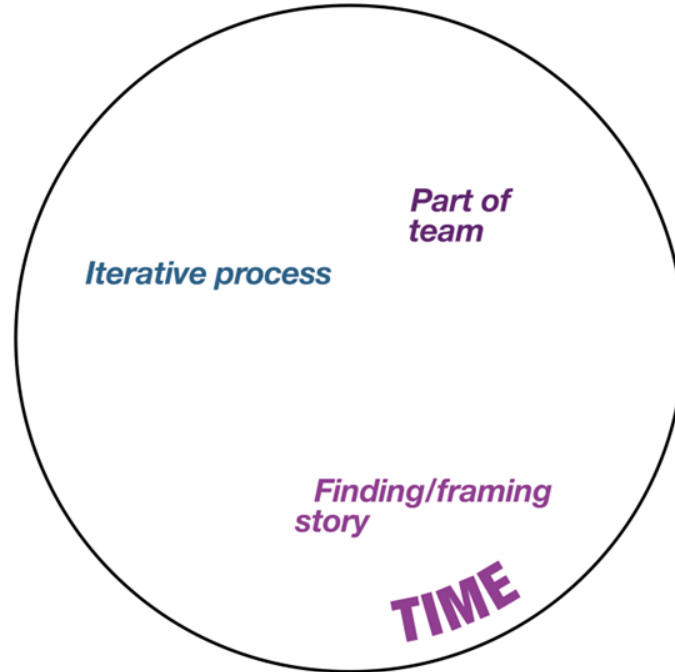


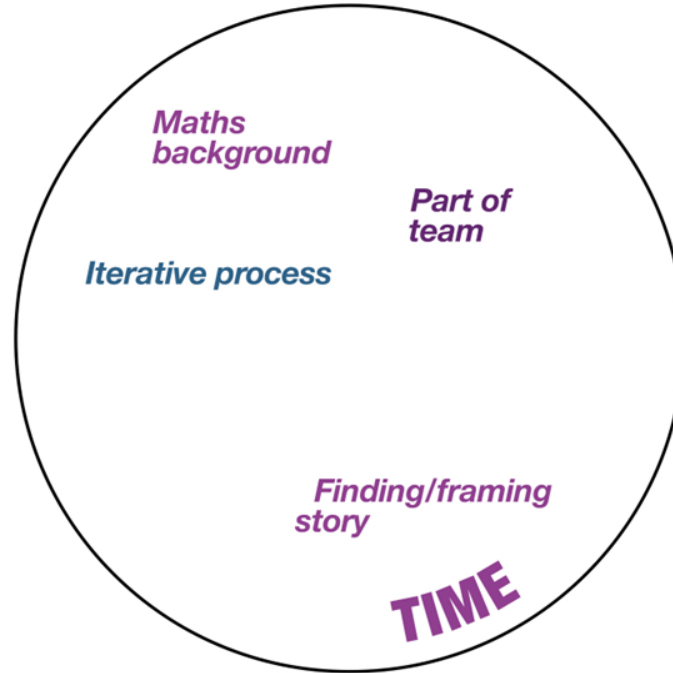
- JUNIPER: **J**oint **U**niversities **P**andemic and **E**pidemiological **R**esearch
- Consortium of modelling groups from seven universities: Bristol, Cambridge, Exeter, Lancaster, LSHTM, Manchester, Oxford, and Warwick
- Formed in the autumn of 2020 to provide quantitative epidemiological advice in response to the evolving pandemic
- Funded by UKRI



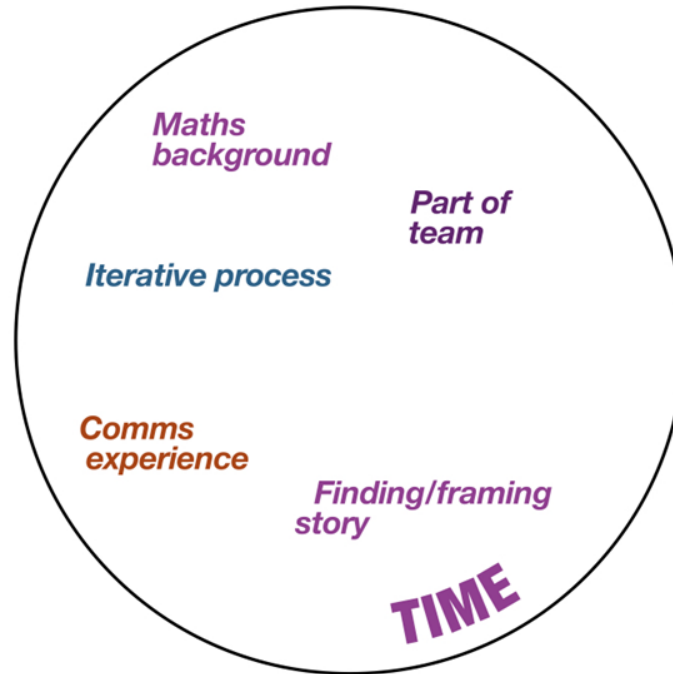


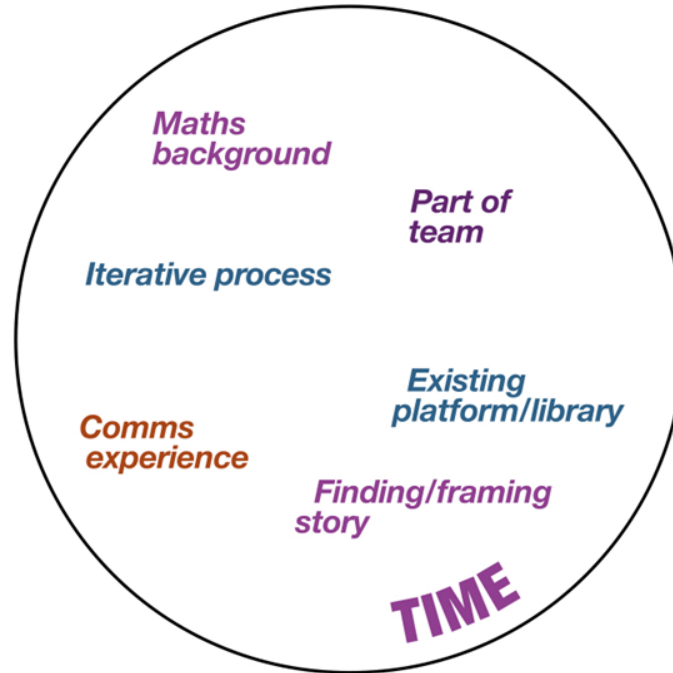


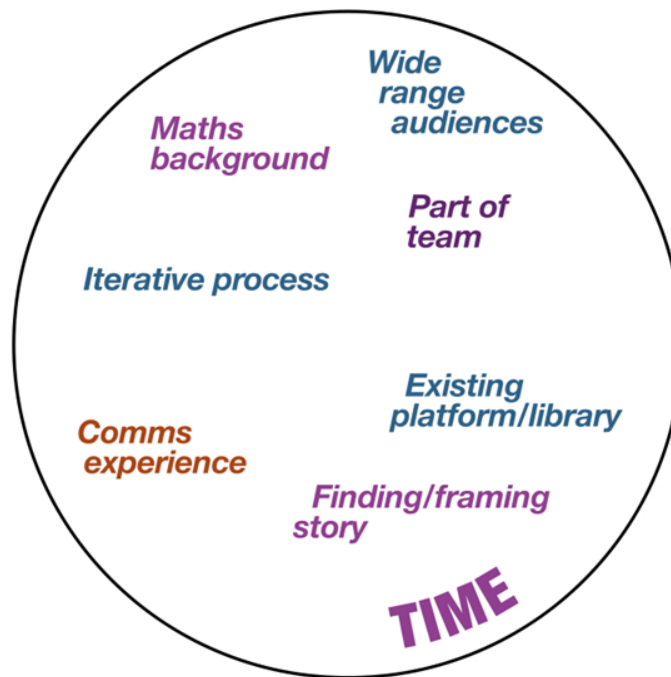














## Maths in

Two things many of us will have heard about recently (the first concept of herd immunity and a new concept of "nought").

### The basic reproduction number

Given an infectious disease, such as COVID-19, the *number* of the disease: the average number of new infections that go on to infect, given that everyone is susceptible to the disease. For COVID-19 this is currently around 1.5. For seasonal strains of flu, it lies between 1 and 2, and for measles it's a whopping 12 to 18.

You can see how a large enough  $R_0$  can lead to exponential growth. For example, if  $R_0$  is equal to 2 then the following growth of new infections:

- 1st generation: 2 new infections
- 2nd generation: 4 new infections
- 3rd generation: 8 new infections
- 4th generation: 16 new infections.

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## Careful with you

Rachel Thomas and Maria Pollock

It's been a very strange year for everyone around the world. A year for a brief respite and to see our families and friends, followed by a relaxation of the COVID restrictions for Christmas, and then a return to normal, even if just for a few days.

But what impact might this brief relaxation of the restrictions have? The question Ellen Brooks Pollock and Leon Danon, epidemiologists at Bristol and the University of Exeter, considered as part of their work feeds its results into the [Scientific Advisory Group](#).

Their work showed that, if everyone pushes these restrictions, then that the epidemic will grow exponentially at a much slower rate. If those who have decided to form Christmas bubbles choose not to form Christmas bubbles, the virus is

### Fulfilling your $R$ potential

We are all now familiar with the  $R$  number – the average number of new infections for gauging the current state of the epidemic (you

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## On the mathematical frontline: Francesca Scarabel

Submitted by Rachel on



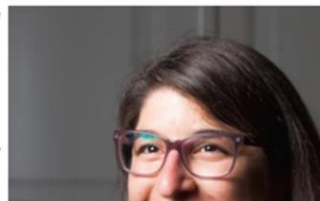
Maths on the Move

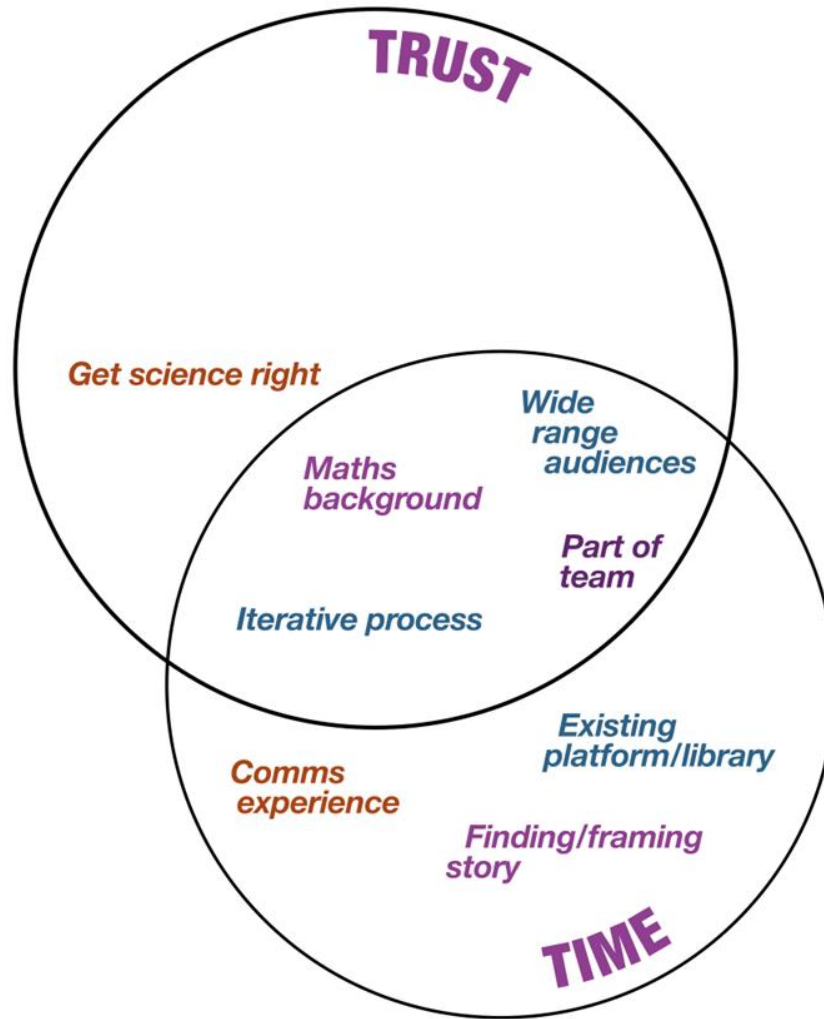
### On the mathematical frontline: Francesca Scarabel

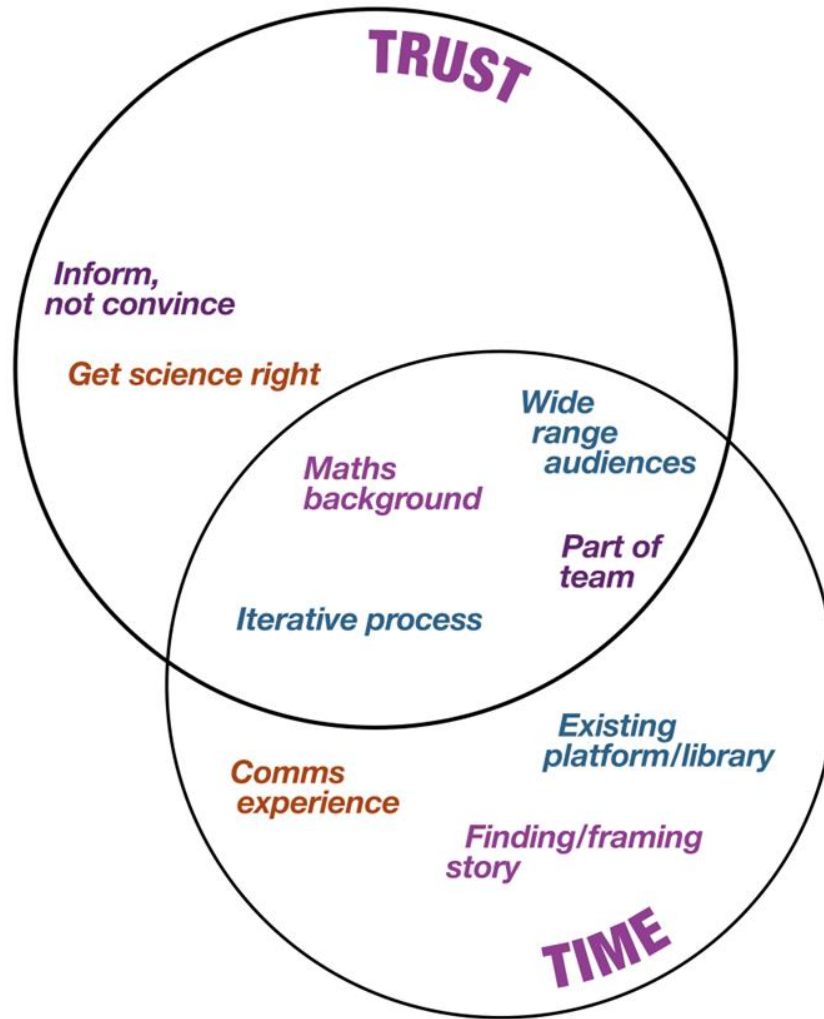


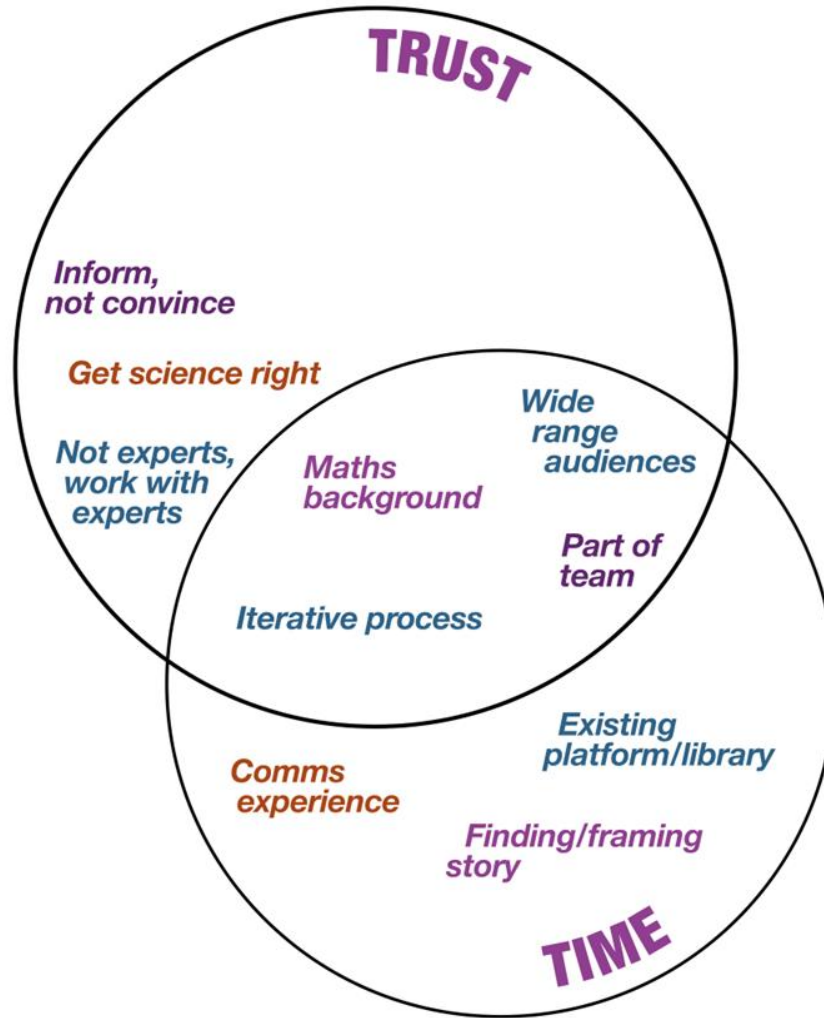
Over the last two years we've done a lot of [reporting](#) on the COVID-19 pandemic and the role mathematics has played in understanding the disease and informing how we've all responded.

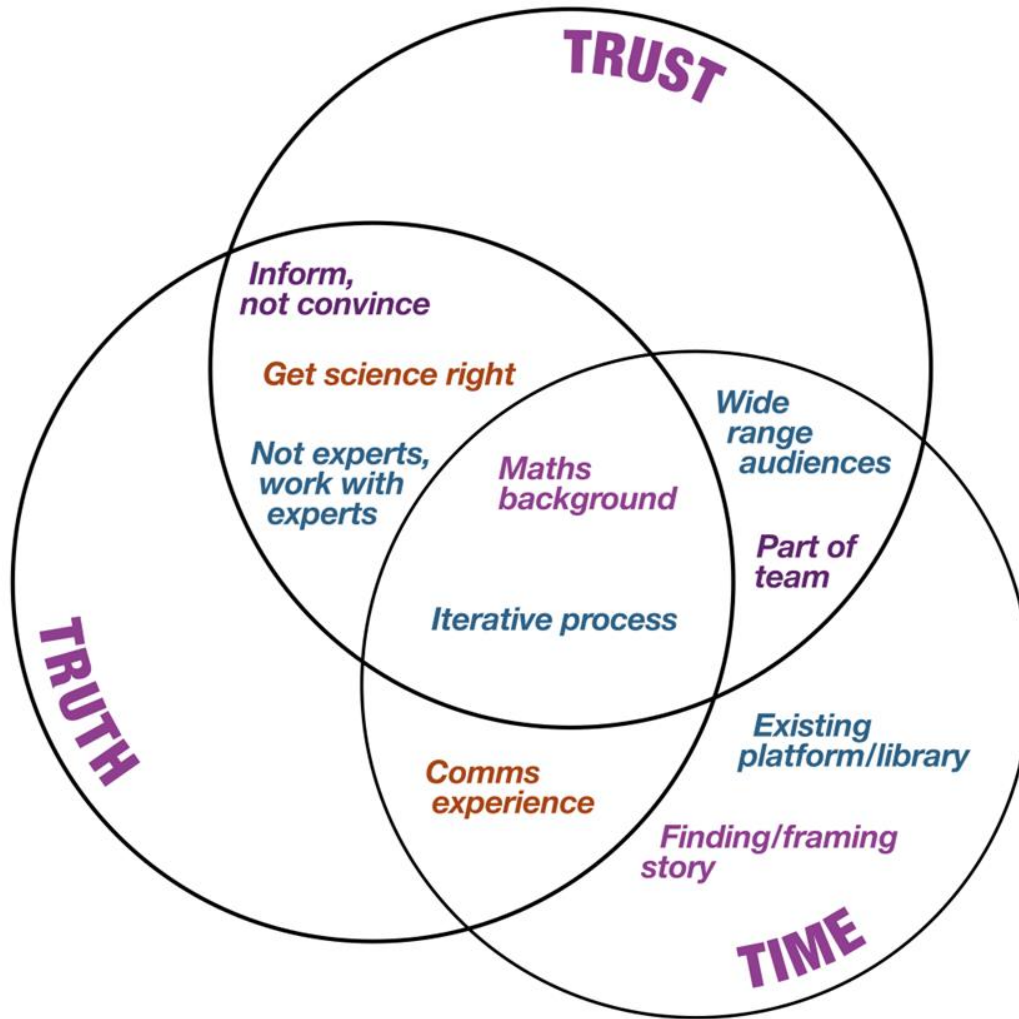
The *Mathematical frontline* podcast is about the mathematicians who are grappling with the unprecedented challenge of studying a live pandemic unfolding in front of their eyes. In this podcast series we interview our colleagues in the [JUNIPER modelling consortium](#), whose research and insights feed into the [Scientific Pandemic Influenza Modelling](#)















## The growth rate

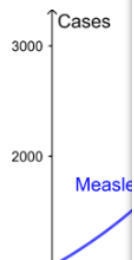
Julia Gog, Rachel Thomas, M

### Why isn't $R$ enough?

We have all become used to thinking about  $R$ , the *reproduction number* of a disease. That's the number of people infected by one infected person. As we saw in [previous articles](#),  $R < 1$  means the epidemic will grow,  $R = 1$  means it will stay the same, and  $R > 1$  means the epidemic will decline.

(Note that the  $R$  we hear about on the news each day is the *effective reproduction number*,  $R_t$ , rather than the *basic reproduction number*,  $R_0$ , that we hear about [here](#).)

One thing that  $R$  does not tell us, though, is how *quickly* the epidemic is growing. For example, if  $R=2$  for some disease then the number of cases doubles every day. For diseases like HIV or TB, where there can be months between infections, this is a slow growth. However for influenza or measles, where there is a short incubation period, this is a very fast growth.



## About $R$ and growth rate

### $R$

The reproduction number ( $R$ ) is the average number of people produced by a single infected person.

An  $R$  value of 1 means that on average each infected person infects 1 other person, meaning the total number of infected people stays the same. If  $R > 1$ , on average, each infected person infects more than 1 other person, meaning the total number of infected people grows. If  $R < 1$ , on average, each infected person infects fewer than 1 other person, meaning the total number of infected people shrinks. The higher  $R$  is above 1, the faster the epidemic grows, and so the faster the epidemic grows.

$R$  can change over time. For example, if the number of contacts between people increases when the numbers of contacts increase, then  $R$  increases when the numbers of contacts increase. This can lead to a rise in viral transmission.

### Growth rate

The growth rate reflects how quickly the number of infections changes day by day. It is an approximation of the percentage change in the number of infections each day. If the growth rate is positive, the epidemic is growing. If the growth rate is negative, the epidemic is shrinking. However, at a growth rate of 0, the epidemic does not hold.

The size of the growth rate indicates the speed of change. A growth rate of +5% indicates the epidemic is growing faster than a growth rate of +1%. Likewise, a growth rate of -4% indicates the epidemic is shrinking faster than a growth rate of -1%. Further technical information on growth rate can be found on [Plus magazine](#).



## Why the generation time

Rachel Thomas

Living through a pandemic we all know by now that the growth rate is important. But what do you need to know to calculate it?

Knowing  $R$ , the average number of people infected by one infected person, we can understand what is happening with the disease. If  $R > 1$ , the epidemic is growing, if  $R < 1$  it is shrinking, and if  $R = 1$  it is plateauing, and  $R < 1$  means that the epidemic is also giving an intuitive way for predicting the spread of the epidemic.

But  $R$  is not easy to measure in practice, particularly for a disease where it is much easier to estimate the *growth rate* of the epidemic. We then use this to estimate the value of  $R$ . But in addition to  $R$ , another important aspect of the disease – the incubation period – is the time between a person being infected, and when they go on to infect others.

### The generation time

The generation time isn't one single number for a disease. It is the time between a person being infected (the infector) and when they go on to infect others. This will be different for different pairs of people.

The range of values the generation time takes for a disease is often described by a *gamma distribution*. This is a probability distribution such as the mean and variance of the generation time.

This all sounds very promising but there's a hitch. The generation time is often measured in hours or even the day, that someone becomes infectious.

## SPI-M-O Consensus statement on COVID-19

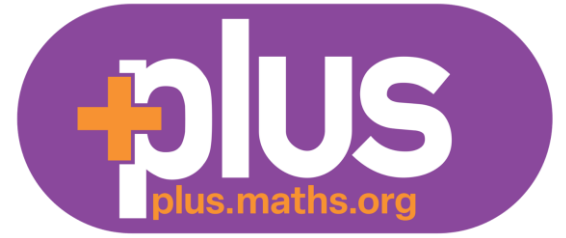
Date: 6<sup>th</sup> January 2022

All probability statements are in line with the framework given in Annex 2.

### Generation times, serial intervals, and growth rates

1. The generation time is the average time between someone becoming infected and that person infecting others<sup>1</sup>. The serial interval is the average time between someone developing symptoms, and those they infect developing symptoms themselves.
2. If the epidemic is growing at a given rate, a shorter generation time would mean the reproduction number is smaller and so less stringent measures or a smaller amount of behavioural change would be needed to curb the spread of the variant. Similarly, if the epidemic is shrinking at a given rate (for example as a result of interventions or behaviour change), a shorter generation time would mean the reproduction number is larger and that there is therefore greater scope for a return to growth as any control measures are relaxed or mixing behaviours increase. In brief, shorter generation times lead to estimated reproduction numbers that are closer to 1.
3. Generation times and serial intervals are context dependent; the same variant can have different serial intervals in different groups of people or if behaviour changes as a result of measures, such as the isolation of infectious people. It is therefore very difficult to measure serial intervals in a robust way as it requires transmission events to be observed in an unbiased way. Generation times are usually inferred from serial intervals as infection events cannot be observed directly. A recent study from South Korea<sup>2</sup> estimated that the mean serial interval for omicron was 2.2 days (with a standard deviation of 1.62 days), compared to 3.3 days with delta.
4. Early analysis from the UK Health Security Agency (UKHSA) has estimated that the distribution of serial intervals for omicron has a **median** that is about half a day shorter than for delta (3.1 to 3.2 days versus 3.5 to 3.6 days), but a much heavier tail, so a larger proportion of omicron serial intervals are greater than 8 days. This means that the **mean** serial intervals are similar, at 3.64 days (95% CI: 3.60, 3.68) for omicron and 3.87 days (95% CI: 3.84, 3.90) for delta. Note that a shorter serial interval does **not** necessarily mean that people with omicron stop being infectious sooner than those with delta.
5. UKHSA have cautioned that omicron's average serial interval could be shorter than they have estimated, as a result of the nature of the contact tracing data. This could also mean that the differences between omicron and delta are underestimates. UKHSA suggest this as one reason why their estimates are longer than those from South Korea.

<sup>1</sup> More information on generation times and serial intervals is available from Plus magazine: [Why the generation time of COVID-19 is important | plus.maths.org](#)  
<sup>2</sup> [Serial interval and basic reproduction number of SARS-CoV-2 Omicron variant in South Korea](#), Kim et al, 2021



## Things to reflect on for the future:

- What's our measure of success? Why are we doing this work?
- What expertise are we lacking?
- What audiences didn't we reach? Could we encourage secondary use?