I have three datasets, which contain data of **log(viral loads)** for **Influenza A**, **SARS** and **SARS-CoV-2,** compiled from research articles. The model I am trying to fit is a plain target cell-limited model of viral dynamics (target cells T get contaminated – exposed E cells not yet producing virus – infected I cells actively producing). It is to be expanded to a more complete form.

You would help me a great deal by fitting the model to just one data series from a single patient, with any pathology. Estimation of confidence intervals for parameters would be nice, but of course I could add them later.

I have attached the Python Tellurium code and the data in CSV format. Please use and share the data as you like, though I have yet to learn the precise copyright and academic status of data digitized from figures.

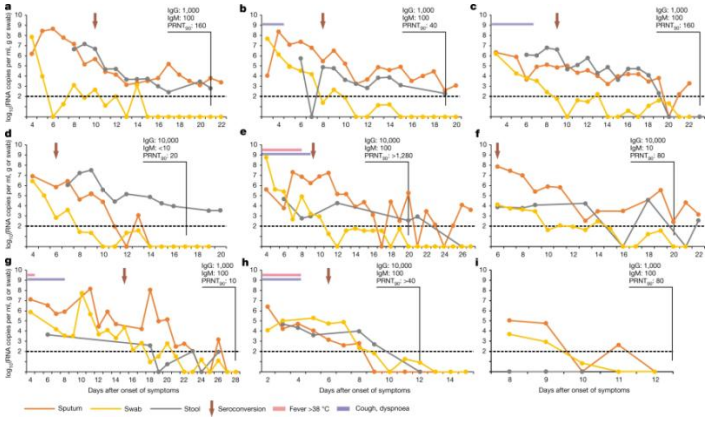
1. The **Influenza** data (from Baccam P et al. 2006, Table 1) is smaller than the one from the CC3D course (Smith AP et al. 2018), data from only five volunteers. Viral levels are in **log10(TCID50 / ml of nasal wash)**, time is in days since exposure. Each line in the array corresponds to a patient.

2. The **SARS-CoV-2** data is from (Wolfel R et al. 2020, figure 2). The corresponding author did not answer email, so I digitized the data from the charts. There are nine patients, viral levels is in **log10 (RNA copies / ml sputum)** and **log10 (RNA copies / nasal swab)**. Time is in days since symptoms onset. Each line in the array corresponds to an individual patient. There are two matching arrays, one with viral loads in the **lungs (sputum)** and the other in the **nasal cavity (swab)**.

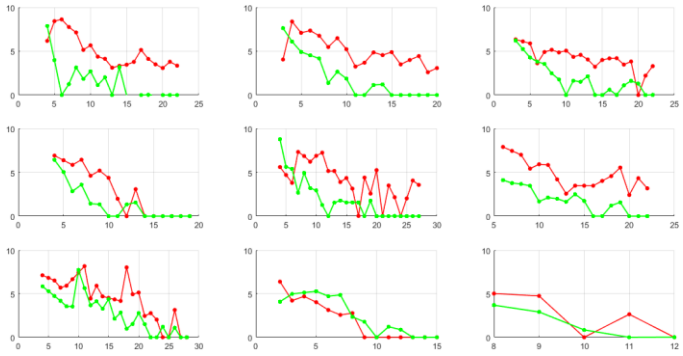
The data is evenly spaced in time. There are no gaps, I did linear interpolation for the cca. 3 datapoints missing from the original data. The patient data aligned and padded with **nan**s at the beginning and the end.

To fit a viral dynamics model, maybe a fixed incubation time for CoV-2 could be added to the time_since_symptoms (the median of 3 days? the average of 5 days?). Alternatively, the incubation time could be a free parameter in a future model.

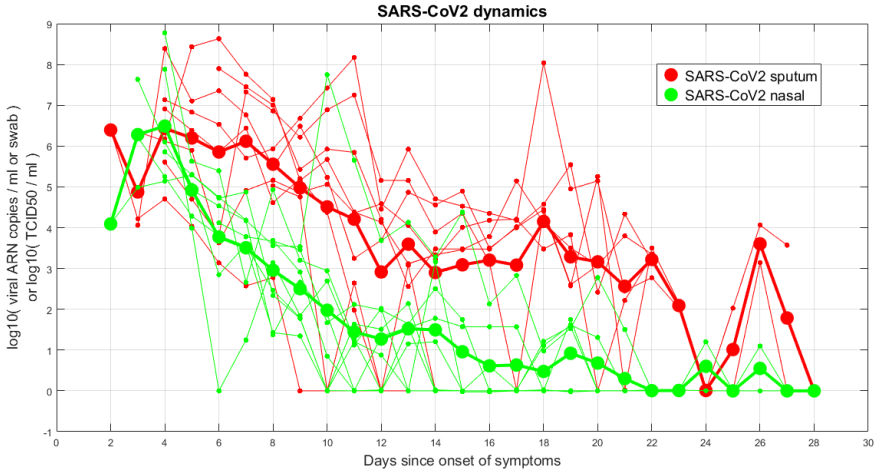
The original figure from [Wolfel et al], each graph is from an individual COVID patient:



To double check, I reconstructed the figure from data (I digitized only traces from viral loads from pulmonary and nasal samples, left out the traces from the GI tract):



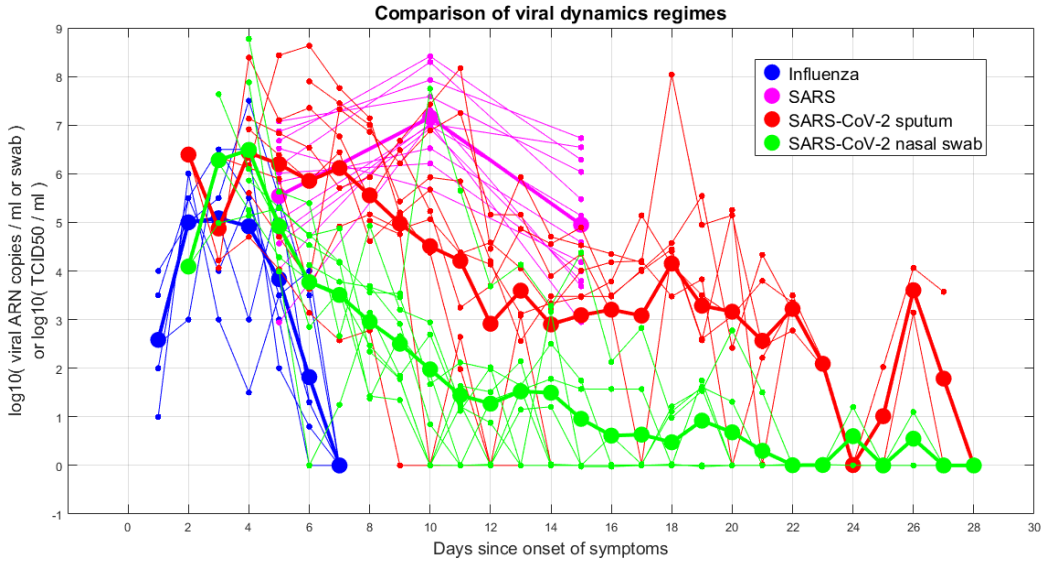
Superposing all the **SARS-CoV-2** data, sputum and nasal swab, shows a pattern (thick lines are category averages):



3. The **SARS** data is from (Peiris et al 2003, fig.4), and has only three data points per patient, at days 5, 10 and 15 since the onset of symptoms. Viral levels are in log10 (RNA copies / ml of nasopharingeal aspirate)l, time in days since symptoms. Just for comparison sake.

The three studies are heterogeneous but still comparable. The **Influenza** is from an experiment on healthy volunteers, with time measured since exposure. **SARS** and **CoV2** are from actual patient data, time is since onset of symptoms, so they miss the increasing phase. The units are also different, log10(TCID / ml), log10(ARN copies/ml sputum or aspirate), log10(ARN copies/nasal swab). Still, the viral levels between studies differ by at most a constant.

A graph with the viral dynamics of all pathologies superposed (thick lines are category averages, thin lines are traces of individual patients):



Influenza decays much faster, SARS reaches peak level a good week later that CoV2. CoV2 levels are higher and more persistent in the lower respiratory tract than in the nasal secretions. Do you think a global model that includes both nasal and sputum data would be possible? Anyway, it's clear that it's not "just like the flu" :).

Many thanks!
Haplea Ioan Stefan.

Sources of the data:

Influenza A, (WT HK/123/77 (H1N1))
Baccam P et al., *Kinetics of Influenza A Virus Infection in Humans*. Journal of Virology. 2006 Aug 1;80(15):7590–9.
From Table 1.
viral levels in log10(TCID50 / ml of nasal wash)

SARS-CoV2
Wölfel R et al. *Virological assessment of hospitalized patients with COVID*-2019. Nature. 2020 May;581(7809):465–9.
From fig.2, digitized
viral levels in log10 (RNA copies / ml sputum) and log10 (RNA copies / swab)

SARS
Peiris J et al. *Clinical progression and viral load in a community outbreak of coronavirus-associated SARS pneumonia: a prospective study.* The Lancet. 2003 May;361(9371):1767–72.
From fig.4, digitized
viral levels in log10 (RNA copies / ml of nasopharingeal aspirate)