**Change point analysis to quantify the impact of African government policy interventions to slow the spread of COVID-19 (a case study of Senegal)**

## INTRODUCTION

During the initial outbreak of an epidemic, reliable short-term forecasts are key to estimate medical requirements and capacities and to inform and advise the public and decision makers (1). During this initial phase, three tasks are important to provide time-critical information for crisis mitigation: (i) establishing central epidemiological parameters, such as the basic reproduction number, that can be used for short-term forecasting; (ii) simulating the effects of different possible interventions aimed at the mitigation of the outbreak; and (iii) estimating the actual effects of the measures taken not only to make rapid adjustments but also to adapt short-term forecasts. Addressing these tasks is challenging because of the large statistical and systematic errors that occur during the initial stages of an epidemic, when case numbers are low. This is further complicated by the fact that mitigation measures are taken rapidly while the outbreak unfolds, but they take effect only after an unknown delay. To obtain reasonable parameter estimates for short-term forecasting and policy evaluation despite these complications, any prior knowledge available needs to be integrated into modeling efforts to reduce uncertainties. This includes knowledge about basic mechanisms of disease transmission, recovery, and preliminary estimates of epidemiological parameters from other countries or from closely related pathogens. The integration of prior knowledge, the quantitative assessment of the remaining uncertainties about epidemiological parameters, and the principled propagation of these uncertainties into forecasts is the domain of Bayesian modeling and inference.

## METHODOLOGY

The SIR/SEIR model employed in this study to explain the parameter dynamics of the disease alongside Bayesian modelling and augmented the model with a time-dependent spreading rate. The time dependence was implemented as potential change points in the spreading rate, which we assume to be driven by governmental interventions and the associated change of individual behavior (non-pharmaceutical interventions) using the methods proposed by Dehning *et al.*,(2020). The SIR/SEIR model is a compartmental model that uses ordinary differential equation to study dynamics of infectious disease. In this project, the model will be used to model the spread in the absence of intervention. The SIR model categorizes each individual in the population into one of the following three groups: Susceptible (S) – people who have not yet been infected and could potentially catch the infection. Infectious (I) – people who are currently infected (active cases) and could potentially infect others they come in contact with. Recovered (R) – people who have recovered (or have died) from the disease and are thereby immune to further infections while in SEIRS (Susceptible - Exposed - Infectious - Recovered - Susceptible) model, recovered people may become susceptible again (recovery does not confer lifelong immunity). These parameters are the solution of differential solution.

$$\frac{dS}{dt} = -\beta I \frac{S}{N} \qquad \frac{dR}{dt} = \gamma I \qquad \frac{dI}{dt} = \beta I \frac{S}{N} - (\gamma + \delta) I$$

Where $\beta$ is the transmission rate, $\gamma$ is the recovery rate.

The data used come from the Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) dashboard.

We estimate the set of model parameters q = {$\lambda_i$, $t_i$, $\mu$, D, $\sigma$, $I_0$, $f_w$, $\Phi_w$} using Bayesian inference with MCMC. The parameter s is the scale factor for the width of the likelihood $P(\hat{C}_t|\emptyset)$ between observed data and model. Our implementation relies on the Python package PyMC3 with NUTS (No- U-Turn Sampling) using multiple, independent Markov chains. The sampling phase consist of chain performs 1500 steps, which are used to approximate the posterior distribution. To ensure that the chains are equilibrated and sampled from the whole posterior distribution (ergodicity), we verified that the R-hat statistic is below 1.05, which is implemented in PyMC3.

The change points effected used in this study include the restrictions on religious activities (10/3/2020), strong social distancing policy implemented on 31st March 2020. The president also lifted the state of emergency and curfew on 30th June 2020.

RESULTS AND DISCUSSION

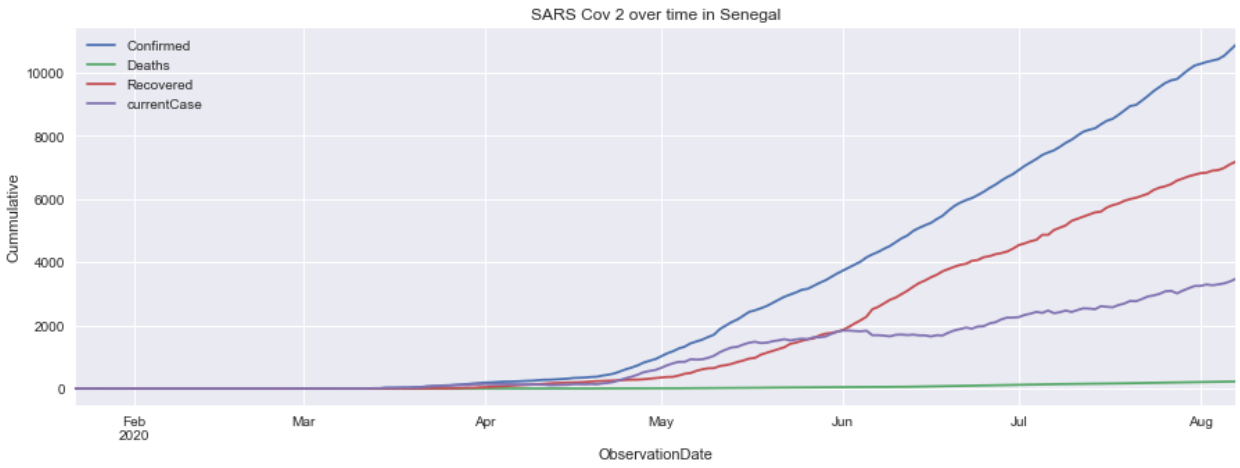


Figure 1: Plot of Covid-19 spread over time in Senegal

Figure 1 shows the distribution of the Covid-19 situation in Senegal. A noticeable increase in cases started in early April. The parameter dynamics of the disease from the SIR model is shown in the figure 2 below. The equation derived above are thought of as directions that tell us what happens to the population the next day. This means that if 20 people are infected and γ=0.2, then the number of recovered individuals the next day should increase by (0.2* 20 = 4).

The transitions from one state to another is described in simple terms as

Rate ⟶ probability ⟶ population.

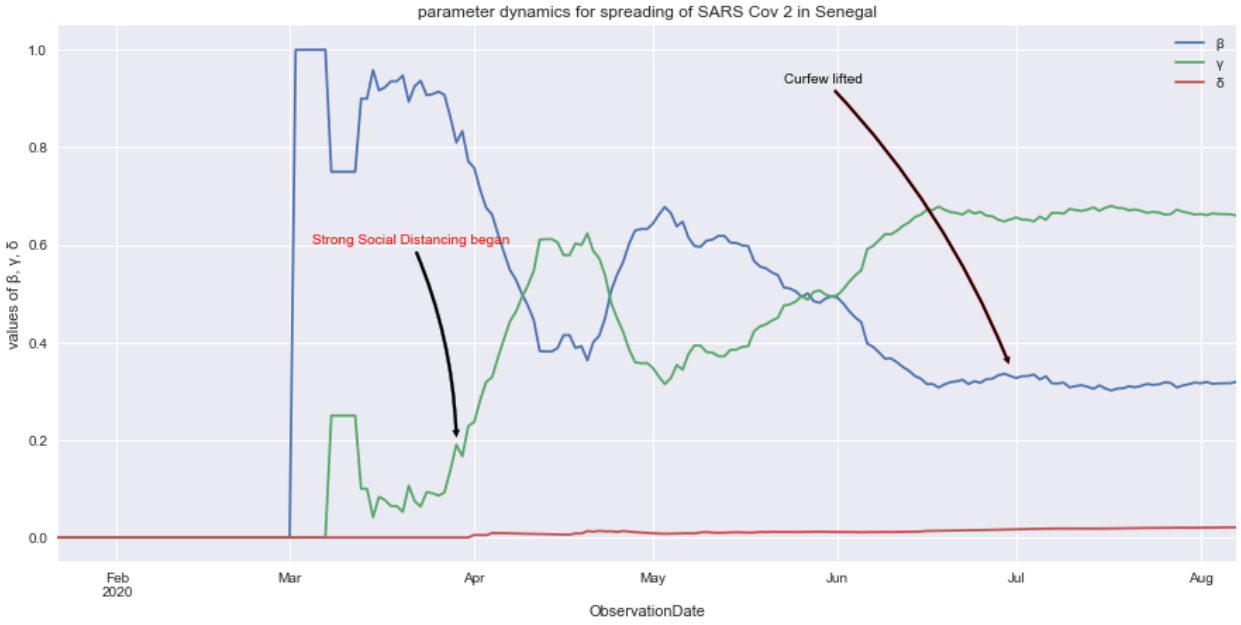


Figure 2: Plots showing the parameter dynamics

The buffer zone is the zone where transmission rate and recovery rate are very near i.e. $\beta(t)-\gamma(t)-\delta(t)\approx 0$β(t)−γ(t)−δ(t)≈0. This zone can exist as cross over points where there is a rise in recovery rate of infected patient as against transmission rate.

The social distancing change points effected on 31st of March was responded to by an increase in recovery rate as against transmission rate. The curfew was also lifted at a time when the recovery rate was higher than the transmission rate (figure 2).

Furthermore, the timing of an intervention matters: Apart from the strength of an intervention, its onset time has great impact on the total case number.

From the model, it can be predicted that the reported case will be above 10,000 as shown in figure 3 below.

As it has been said, all model are wrong. The implication of this method is that the predictions are limited to short and medium term. This study is based on the basic SEIR framework (or, in some cases, its simple variations), exclusively focused on the direct, human-to-human transmission pathway. It has been commonly accepted that COVID-19 can be transmitted through direct contact between human hosts, and both the symptomatic and asymptomatic individuals are capable of infecting others. In contrast, the indirect transmission pathway from the environment to human hosts is also a highly possible route to spread the coronavirus but has not been sufficiently addressed in the literature. Another limitation of the current COVID-19 models is that the transmission rates are typically fixed as constants, rendering simplicity for both mathematical analysis and data fitting. In practice, however, the transmission rates may change with the epidemiological and socioeconomic status and may be impacted by the outbreak control.

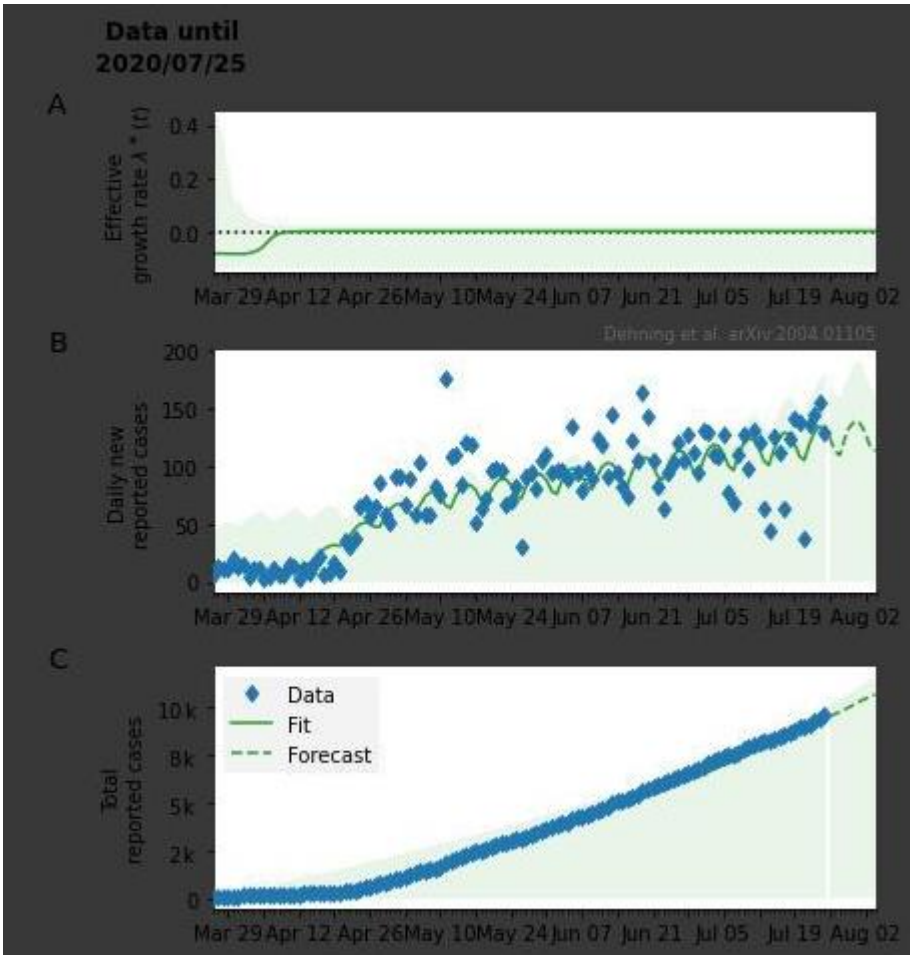


Figure 3: A Time series plot of the Bayesian model