Safe Blues: A Method for Estimation and Control in the Fight Against COVID-19

https://safeblues.org/

Shane G. Henderson¹, Marijn Jansen², James McCaw³, Sarat Moka², Yoni Nazarathy², Chris Rackauckas⁴, Peter G. Taylor³, Aapeli Vuorinen^{2,3}

(1) Cornell University. (2) The University of Queensland. (3) The University of Melbourne. (4) Massachusetts Institute of Technology.

April 13, 2020

There is a dire need for timely information about the spread of the COVID-19 virus. Such information can feed into predictive models that could be used by governments as part of their decision-making process. In general, the spread of a virus depends on both the biological properties of the virus and on the behavioural properties of the population. Biological properties of COVID-19 have been studied since the start of the outbreak. On the other hand, population behaviour is changing rapidly due to unprecedented social distancing measures and is hard to observe and to predict. As a consequence, achieving tight real-time estimates of R_0 , the expected number of individuals infected by an infected person, is a difficult task. Importantly, inaccurate estimates of R_0 at different stages of the pandemic can result in suboptimal decisions, affecting human life and having significant economic consequences.

In an imaginary world, one may seek to engineer a benign biological virus that has similar spreading properties as COVID-19 and is traceable via cheap and reliable diagnosis. Then by spreading such an imaginary virus throughout the population, the spread of COVID-19 could be easily estimated because the benign virus would respond to population behaviour in a similar manner to COVID-19. However, such a benign biological virus doesn't exist. Instead, we propose a safe and privacy-preserving digital alternative that we call *Safe Blues*.

The Safe Blues method would use Bluetooth signals in a similar way to the suite of existing and new contact tracing apps. Such apps, deployed on personal mobile devices, are aimed at monitoring viral threats and collecting data about potential contacts. One example is the Singaporean "TraceTogether" app. The focus of TraceTogether and other similar apps is to protect the population from specific infected individuals. However, such apps may also be adapted to transmit Safe Blues signals in a privacy-preserving manner and without any danger to the software or hardware of individuals.

The Safe Blues idea is that mobile devices mimic virus spread via the safe exchange of Bluetooth signals. Then, aggregated counts are reported to a server without recording private information. By periodically creating various strands of Safe Blues and repeatedly spreading them through the (mobile device) population, our analysis of the signals will help government easily obtain aggregate estimates of population contact. The result will be a near-real-time measure of the level of social distancing. Further, when additional aggregated information is available, it will also be used.

At the moment, when government adjusts social distancing directives, it is not clear what the population compliance is and, even if compliance is widespread and immediate, it often takes weeks to see the effect of the measures on the spread of COVID-19. In such a scenario this makes it difficult to place optimal social distancing measures in a way that balances objectives with an optimal R₀ target. However, the Safe Blues idea will produce a much faster feedback loop because the measurement of social contact will be timelier and more precise. This is because, in contrast to COVID-19, the observations and diagnosis of Safe Blues spread will be in near-real-time.

Importantly, if Safe Blues is implemented early during the COVID-19 pandemic, information obtained during that period will be highly beneficial for decision making near the end game of the battle against COVID-19 as well as for the efforts to mitigate second or third waves of attack. In fact, our initial simulation analysis hints that Safe Blues data may help improve predictions of COVID-19 infection within the asymptomatic population. For this, statistical machine learning and artificial intelligence methods, mixed with solid epidemiological models, will help build estimates of COVID-19 spread as a function of live measurements of Safe Blues spread. As COVID-19 progresses, the estimates will become more and more precise. A consequence is that within 3 to 6 months of deployment of Safe Blues, estimates of the time-varying R_0 of COVID-19 will be much tighter than what they are today. Similarly, the effect of various forms of social distancing government directives on R_0 will be much better understood. As an end result, government will have a better grasp of how to optimally "flatten the curve" (or keep the curve below the health care system threshold).

The implementation of Safe Blues within an existing contact tracing software platform is straightforward and does not require complicated software design. Our team includes applied mathematicians, machine learning experts, and biological modellers, and also has some expertise in native iOS and Android app development. We do not seek to develop an independent app, but rather to help software teams integrate the Safe Blues idea, easily and simply. Then, on the server side, our team (as well as potentially other teams), will be able to analyse the Safe Blues data and inform government accordingly. Note that we may supply the back end (server side) in a timely manner and if needed we are prepared to handle the needed ethics approvals.

We also mention a potential extra benefit of the Safe Blues idea. In a second or third generation of apps, one may also consider presenting individual users with an up to date count of how many strands of Safe Blues their devices are "infected" with. One may envision that this will enable users to get a feel for the level of social distancing that they are practising and to stay socially responsible as advised by government.

For further information, visit <u>https://safeblues.org/</u>, contact A/Prof. Yoni Nazarathy, The School of Mathematics and Physics, The University of Queensland via <u>v.nazarathy@uq.edu.au</u>, or any other author of this note via, <u>sqh9@cornell.edu</u>, <u>h.m.jansen@uq.edu.au</u>, <u>jamesm@unimelb.edu.au</u>, <u>s.babumoka@uq.edu.au</u>, <u>contact@chrisrackauckas.com</u>, <u>taylorpg@unimelb.edu.au</u>, or <u>contact@aapelivuorinen.com</u>.