Modeling Ebola Outbreak

It is no longer news that, in the current century new viruses and virus-related diseases have threatened the health of humans and many animal species. Unarguably, the Ebola virus makes this list by all measurements.

The Ebola virus disease (EVD) is an acute disease that affect humans and other animals. The disease caused by ebolaviruses, is transmitted to humans from wild animals and then propagates in the human population via direct contact with the blood, secretions, faeces or other bodily discharges of the infected person, and with surfaces and materials (e.g. bedlinens) maculated with these fluids. Symptoms of this disease include but are not limited to fever, diarrhoea, fatigue, headache, abdominal pain and sore throat [1].

Ebola-the very name evokes fear and panic. And no wonder, because Ebola is the virus of horror movies and nightmares. It appears as if from nowhere, striking suddenly and unpredictably, and produces agonizing symptoms. And with no specific treatment available, it kills over half its victims. Until 2014 most people in the world had never heard of Ebola, but the epidemic in West Africa changed all that by posing a global threat.

The first Ebola outbreak ever recorded occurred some four decades ago in a remote village in Zaire (Zaire is now called the Democratic Republic of Congo (DRC)). Although the virus may have struck isolated communities in Central Africa before this time, all previous outbreaks went unnoticed by the international community.

Perhaps, even locally the deadly effects of Ebola were unrecognizable against a background of killer microbes that target poor and isolated communities in Sub Saharan Africa. The epidemiology of EVD is of utmost necessity because the study of this disease have provided insights into the behaviour of the disease and have generated measures to contain an outbreak. The countless lives saved by the study of EVD cannot in any way be overlooked. Also, the risk of death from pneumonia, tuberculosis (TB), meningitis, influenza, whooping cough, and diphtheria declined dramatically all thanks go in part to epidemiology.

In this paper, we are modelling the ongoing outbreak in DRC through the INLA-SPDE approach. The use of Bayesian models and computational methods in application to studies in spatial biostatistics is a relatively new trend, that has gained widespread acceptance [4]. It should be noted that this acceptance is triggered and facilitated to a large extent by the development of fast computers and better algorithms that were simply absent or not accessible 25 years ago. Bayesian methods to deal with spatial and spatio-temporal data started to appear around the year 2000, with the development of Markov chain Monte Carlo (MCMC) simulative methods. Until this time, the Bayesian approach was almost only used for theoretical models and found little or sometimes no applications in real life case studies due to the lack of numerical/analytical or simulative tools to compute posterior distributions. It should be pertinent to note that (INLA)-Integrated Nested Laplace Approximation method is widely applied when building and analyzing Bayesian models. The reason is not far-fetched.

INLA uses approximation methods for fitting Mixed Effect Models, it is as efficient as MCMC

method plus it is computationally faster [5].