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Abdul-Aziz Yakubu (ayakubu@howard.edu) and **Eric Ngang Che***
(ericngangche@yahoo.com), Washington, DC. *A Discrete-Time Risk Structured Model of Cholera Infections In Cameroon*. Preliminary report.

In this talk, unlike the ODE model of Che *et. al.* [1], we introduce a discrete-time cholera model of Cameroon with risk structure and no spatial structure. We use our discrete-time demographic equation to “fit” the total annual population census data of Cameroon. Furthermore, we use our fitted discrete-time cholera model to capture the annually reported cholera cases in Cameroon from 1987-2004. As in the ODE model, we obtain that the basic reproduction number of our fitted discrete-time cholera model, $\mathcal{R}_0 \simeq 1.1832$. The \mathcal{R}_0 of the ODE model with a similar risk structure is 1.1803. That is, the two models have approximately the same value for \mathcal{R}_0 and both predicted cholera endemicity in Cameroon. As in the ODE model, we use our fitted discrete-time cholera model to study the impact of vaccination, treatment and improved sanitation on the number of cholera infections in Cameroon from 2004 to 2019. Furthermore, we use our fitted model to predict future cholera cases.

Reference

[1] E. Che, Y. Kang and A. Yakubu, *Risk structured model of cholera infections in Cameroon*, *Mathematical Biosciences* **320** (2020), 108303.

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