A stochastic model for Meningococcal Disease in the African Meningitis belt

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1 Introduction

The mathematical description of populations and disease dynamics is a field which can be extremely complex. It is a subject of much research, relevant to policy makers and medical researchers. An accurate model that can predict future dynamics can be of immense value, both to prepare for and deal with epidemics, and to evaluate different vaccination policies. However, accuracy is in itself not enough. The model must also be precise enough, as well as capable of evaluating several possible scenarios within a reasonable time frame. This leads to a need for a balance between accuracy, which means several different interactions must be considered, and swiftness, which calls for approximations and numerical efficiency.

A common practise for population dynamics are to approximate the system, according to the central limit theorem and the law of large numbers, to a continuous and deterministic system. It is obvious that in a given population, the number of individuals is a discrete number. Furthermore, it is intuitively clear that events such as contagion and infection are fundamentally random. Models that incorporate this randomness into their structure are in general significantly slower to evaluate. Firstly, a single evaluation will take longer, and secondly more evaluations are needed to increase precision and accuracy (in correspondence to the Monte Carlo framework). Consequently, an approximation is made to a deterministic system governed by differential equations. A part of this approximation is letting the populations vary continuously. By the law of large numbers and the central limit theorem, this is no issue if the population is large enough. A continuous population will, while not entirely accurate, be at least as specific as a realisation of a discrete random system.

1.1 Background

This report focuses on meningococcal disease, which are any diseases caused by *Neisseria Meningitidis*. The infection of N. Meningitidis can take many forms, of which two common (and severe) are meningococcal septicaemia and meningitis [source]. Meningitis is an infection of the thin lining surrounding the brain and the spinal cord, and is a serious condition that untreated leads to death in about 50% of cases. Early diagnosis and adequate treatment reduces the fatality rate to about 5-10%, with permanent disabilities in about 10-20% of cases. The incubation time varies from 2-10 days, but is on average 4 days [source: WHO]. Meningococcal septicaemia is the infection of the bloodstream, and is often even more severe than meningitis. The infection damages the walls of blood vessels and leads to bleeding into the skin and other organs. The treatment is similar, but possible consequences include amputation[source]. In rare cases, N. Meningitidis can cause arthritis and similar diseases[source].

Humans are the only known reservoir for N. Meningitidis. At a given time, about 2-50% of the population are likely to be carriers of the bacterium. Carriage can last both for a very short period of time as well as for several months, during which the bacterium is present in the nasopharynx of the carrier [4]. In general, carriage does not lead to invasive disease, but it has been linked to a subsequent immune response to the bacterium. Immune response can take several different forms, but research has shown that a significant part of the adult population have an immune response that is putatively protective towards the disease [source: human immunity to the meningococcus]. Another bacterium frequently theorized as potentially leading to immunity to the disease is *Neisseria Lactamica*, often present in the nasopharynx of young children [source]. While immunity protects towards invasive disease, it has not been shown that there is any reduction of carriage caused by the immune response. [sources]

N. Meningitidis is genetically variable. It is classified, based on surface-level structures, into different serogroups, most commonly A, B, C, W-135, X, and Y [source]. Note however that it is fairly common for the bacterium to be non-serogroupable[source?]. Of the main serotypes, most epidemics have historically been caused by serogroups A and B, and serogroups C and W-135 have also been the cause of some epidemics.

The African meningitis belt was first described by Lapeyssonnie in 1968 [1]. This region is shown in **??** and has been characterized by semi-regular epidemics documented since the early 20th century. Its specific geographical area is defined be the WHO as the region in Africa between Senegal in the west and Ethiopia in the east [source], which coincides fairly well with the area described by Lapeyssonnie.

Meningitis dynamics in the region have some characteristics. Firstly, there are recurring epidemics with intervals of about 5-15 years. Secondly, the incidence rates of disease is higher than in other regions of the world. Thirdly, the disease is most commonly caused by a serogroup which does not usually cause epidemics in the rest of the world. All of these properties are also affected by a strong seasonality, so that there are three distinguishable states for the disease in a population. There is the hypoendemic state, with a low incidence rate of about [] which occurs during the wet season. During the dry season, the system falls into a hyperendemic state with increased incidence rate, or occasionally an epidemic state. An epidemic state is defined as a rate of disease above []. [3]

The reason for the specific dynamics in this region is often considered to be some climatic factors. One such factor frequently considered is the total precipitation. The region coincides fairly well with the area between the 300mm and 1100mm isohyets [2]. Another common cilmate factor for the area, as defined by the WHO, is that

it is affected by the Harmattanm a dry wind from the Saharan desert. As there are links between factors that irritate the airways and subsequent infection by *N. Meningitidis* [sources on smoking, colds], a link between the Harmattan and the hyperendemic meningitis season would seem plausible. Is is an area of active research [?], and finding any climactic factors that could be driving the epidemics is outlined as an area of priority by the WHO [source: research priorities].

Historically, epidemics in the meningitis belt have been caused by serogroup A, while most epidemics and infections in the rest of the world has been casued by serogroup B [source]. To tackle the disease dynamics in the meningitis belt, vaccines towards serogroup A have been introduced, and since the introduction of these, no new epidemics caused by this serogroup has occurred in the area. However, there have been incidences of other serogroups causing epidemics, most notably W-135. [sources]

1.2 Terminology

2 Methods

The goal of this project is to develop methods to understand the dynamics characterizing meningococcal diseases in the meningitis belt. The degree of urbanization is comparatively low in this region [source] and so any applicable method must be accurate also for smaller communities. Traditional methods using deterministic dynamics and non-discrete populations become gradually more imprecise when dealing with decreasing population sizes [source], and as such a different approach is required.

Hence, we develop a dynamical model for integer-valued populations following a Markov-Jump process. The model is subsequently simulated using the Feller-Kendall algorithm, and it's behaviour is validated by comparing to real-world data as well as to previous models (on an appropriate scale).

2.1 Model

2.1.1 Populations

2.1.2 Time dependency

2.2 Implementation

3 Results and analysis

4 Conclusions

References

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