# The Impact of Current Demographic Trends on the Dynamics and Control of Vaccine Preventable Childhood Infections

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**Summary**. European populations are currently undergoing a number of transformations ranging from the generalized spread of low fertility, the "postponement" of life events, and the increasing role of international immigration, even as a policy to counter population ageing. Even more massive transformations are occurring in the developing world as a consequence of the ongoing fertility transition and fast urbanization. We discuss the impact of demographic change on the dynamics and control of vaccine preventable childhood infections from a modelling perspective. We first clarify the circumstances under which demographic change actually might have an impact on the dynamics of childhood infections. We suggest that to predict the impact of demographic change on infection dynamics we need to understand the relation between population change and critical demographic structures. To figure out such a relation we use an individual-based IBM model where contacts occur in three "arenas" (school, household, and "other" population contacts).

**Introduction and aims**

The age-structure of the population, and the patterns of contact between population (age)-groups which govern age-related processes of infection and serious diseases, have traditionally been considered as the major determinants of the observed epidemiology of infections, including resultant morbidity and mortality (Farrington 1990; Anderson 1985a, Huang 2006). This perspective, somewhat oriented by the availability of infectious diseases data which are typically stratified by age only, has allowed, from the first pioneering contributions (Dietz 1975, Hethcote 1983, Anderson and May 1983, 1985b, 1991, 1992), the emergence of the standard mathematical model for infection transmission and control. The "standard model", despite generating a huge number of scientific contributions (3165 citation for Anderson & May 1992 alone) has rapidly become one of the main supporting tools for public health decisions and policies regarding immunization programmes, with a tremendous progress in the public health sciences. Currently most industrialised countries support their decisions on vaccination policies by mathematical modelling (Brisson et al., 2000; Edmunds et al., 2000; Edmunds & Brisson, 2002; French et al., 2007; Gay et al., 1995; Gay, 1998; Melegaro et al., 2010, Trotter et al., 2005 and 2006).

In contrast, this situation is not shared by the less developed countries, Sub-Saharan Africa (SSA) in the first place, where a poor health situation largely determined by a high burden of preventable infections (Bloom 2004), combines with the lack of modelling skills and infrastructures. The development of an appropriate modelling framework for the transmission and control of vaccine preventable infection in developing countries is made difficult also by the need to model infection transmission in the context of an unstable demographic environment. Indeed, the forecasted demographic changes that are taking place within the ongoing demographic transition (Bongaarts 2008; Bongaarts 2009), ranging from an unexpectedly fast fertility decline to fast rural-to-urban migrations (Montgomery 2008), to mortality decline, will impact strongly upon those population structures, by age, space (between rural and urban areas), and by family size, that are known to play a key role in infection transmission. Furthermore, in high HIV/AIDS prevalence countries there is the further complication that mortality from AIDS, and its direct impact on fertility, together with HIV/AIDS-associated behaviour change influencing age at mortality and fertility (Watkins 2004, Gregson S et al., 2007), will also affect population structures.

Unfortunately, the "standard model" is unable to appropriately take such complex changes in demographic structures into account. Indeed, the standard model postulates a stationary demographic environment, i.e. the population is assumed to be stationary in numbers and age distribution (this is unsurprising: the standard model was developed for industrialised countries in epochs where demographic change, including the low fertility revolution, was considered by most external observers as a transient phenomenon). This stationary distribution is then mapped, usually by a single epidemiological datum at one time point, onto a transmission, or contact matrix by age, which is unchanging over time. This implies that the model is fully unable to predict how changes in fundamental population structures will affect infection transmission.

It is therefore the purpose of this work to fill this gap in the prediction of the impact of demographic change on transmission and control of infectious diseases in SSA countries. In particular, the research question addressed here is the following: what will be the overall impact of the demographic transition on key population structures (eg. household) and on the consequent social contact patterns? and how will the predicted changes in contact patterns might affect the potential for infection transmission? The two case studies of Kenya and Zimbabwe are considered.

**Method**

In order to answer the above questions, we are proceeding in the following two areas of work:

1. Analysis of DHS data for Kenya (KE) and Zimbabwe (ZW) to characterise these two countries from the socio-demographic point of view and taking into consideration the various heterogeneities that are present within the country. This also allows to capture important effects of the demographic transition on those social structures that are expected to be relevant for childhood infectious diseases transmission (eg. household, schools)
2. Development of an agent-based model (ABM) (Merler et al., 2010) parameterised with the gathered socio-demographic data for Kenya and Zimbabwe and capable of reproducing relevant demographic structures and of projecting how demographic changes over time might affect these structure and consequently individual social interactions. The model will provide projections of the impact of population changes on social structures and contact patterns relevant for disease transmission for whatever patterns of population change, including for example those embedded in official population projections which usually assume time-varying demographic rates, thereby yielding complex transient population behaviour. Secondly, the model will allow us to specify how changing contact patterns might evolve in social structures (i.e. schools and workplaces) which may differ for urban or rural setting. These investigations would allow projections for the evolution of contact patterns triggered by demographic changes currently ongoing and, consequently, the production of *time-varying* social contact matrices that are one of the most important components for realistic epidemiological modelling of infections and control programmes.

**Preliminary results**

Comprehensive analyses of the available socio-demographic data for both Kenya and Zimbabwe have been undertaken and an important change in population age structure is being observed (Figure 1). This is driven by reductions in the Total Fertility Rate (TFR), which, however, appear to remains above 4 in recent years though with significant heterogeneities in the urban/rural settings (Figure 2). Heterogeneities in the social structure have been identified, especially in households (Figure 3-4) and schools (Figure 5), which need to be taken into account. In particular, type and structure of the household is typically much more complex in SSA countries in respect to European countries (Figure 4) and relevant differences can be identified among different settings such as urban and rural area. For instance, rural areas are characterised by larger household and by schools with a larger pupils per classroom ratio.

In order to reproduce the rules of evolution of socio-demographic structures over time and, thus, being able to predict how changes in important demographic processes (eg. changes in the fertility pattern in the urban/rural setting) might affect these structures; critical parameters for household environment have been derived. In particular, the various mechanisms for household formation and dissolution (eg. marriage, partnership, cohabitation, leaving parental home, etc) (Figure 6) have been identified and the related statistics have been extracted from the DHS data. We build a population of individuals structured in complex households that are compliant with the extracted descriptive statistics on household structure. Examples of what type of statistics have been used to model household in KE and ZW are the following: the probability of having a certain martial status by age of the individual; the probability of having a certain number of children by age and marital status. Also, given the age of the head (ie. normally the oldest household member), we derived the

probability for each household to be characterised by a certain structure (eg. whether the following are present: head's parents and/or head's brother(s)/sister(s) and/or head's grandchildren and/or the head's son-in-law or parent–in-law).

The model produces a population which is compliant not only with the age structure of the total population but also with the expected age structure within households. Examples of what type of statistics have been used to model household age structures are the difference in age between husbands and wives and, given the cardinality of the son or daughter (i.e. if he/she is the 1st, the 2nd, the 3rd, etc birth of the couple), the difference in age between the mother and the children, the difference in age usually characterizing the parents of an individual or his brothers and sister. In this way we are able to account for a complex social structure within the household.

The household has been widely shown as one of the main sources of infection for different diseases, with an estimated 30% of influenza cases generated from household transmission. However, the heterogeneity in the type and size of households together with the differences in the school structures have been responsible for different epidemic pattern throughout Europe. These aspects will be even more crucial for SSA countries for the following reasons: 1) the social structures in these countries are extremely more complex and usually larger in respect with European households; 2) the fast pace in which the demographic transition is occurring in developing countries is expected to play an important role in changing the household size and the age distribution of household members and thus the role of different social structures in the infection transmission process. See empirical evidence of changes in the household size over time in Figure 7 for both countries.

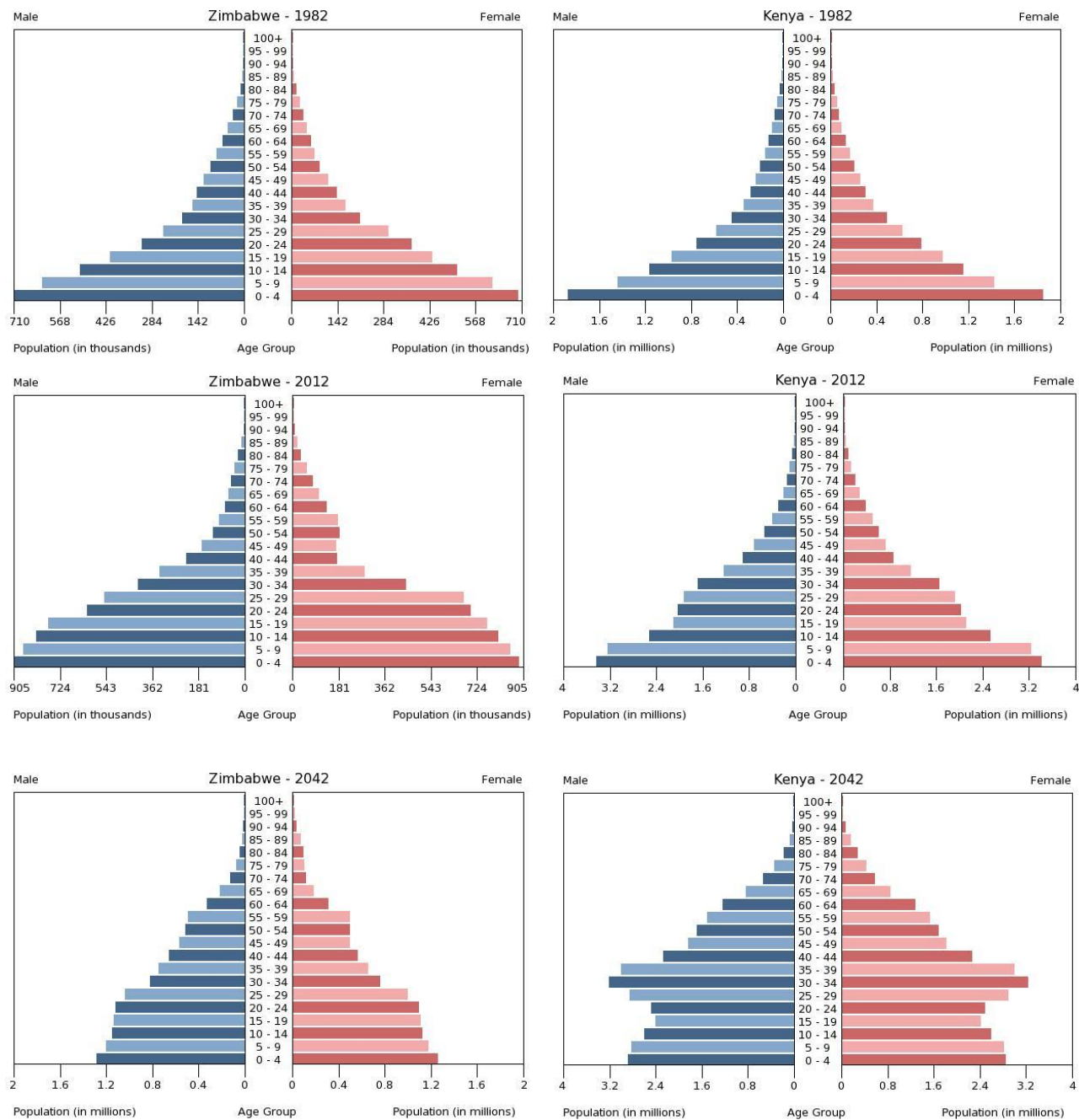*Figure 1 – Population pyramids for Zimbabwe and Kenya (Source: http://www.census.gov/)*

*Figure 2 – Total fertility rate for Kenya (left panel) and Zimbabwe (right panel) over time and among different settings (Source: DHS data)*
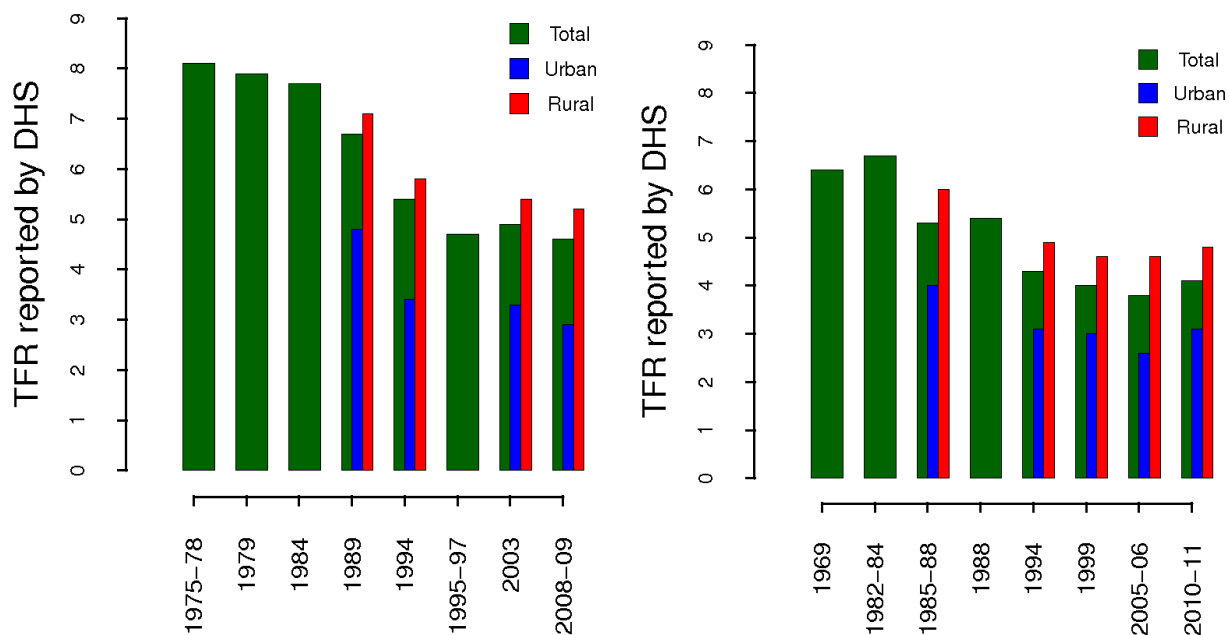


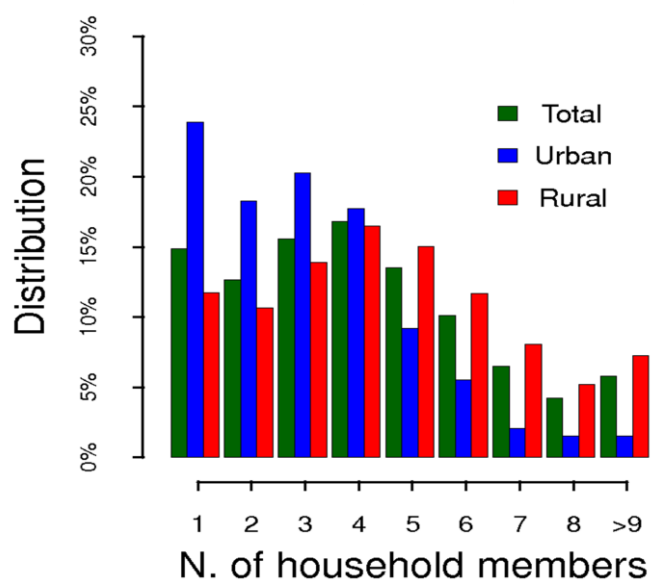*Figure 3 – Household size for Kenya by settings (Source: DHS data)*

*Figure 4 – Proportion of households by presence of specific household members (Source: DHS data for Kenya)*
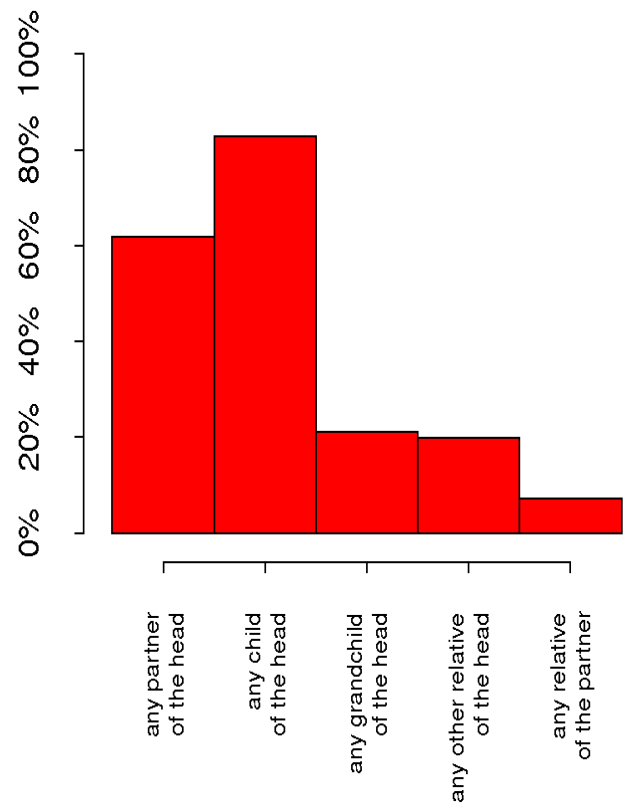


*Figure 5 – Average classroom size of primary schools in Kenya. Urban Pupil Classroom Ratio in Nairobi (left panel) and rural Pupil Classroom Ratio in North Eastern (right panel) (Source: Kenya Open Data, 2007)*
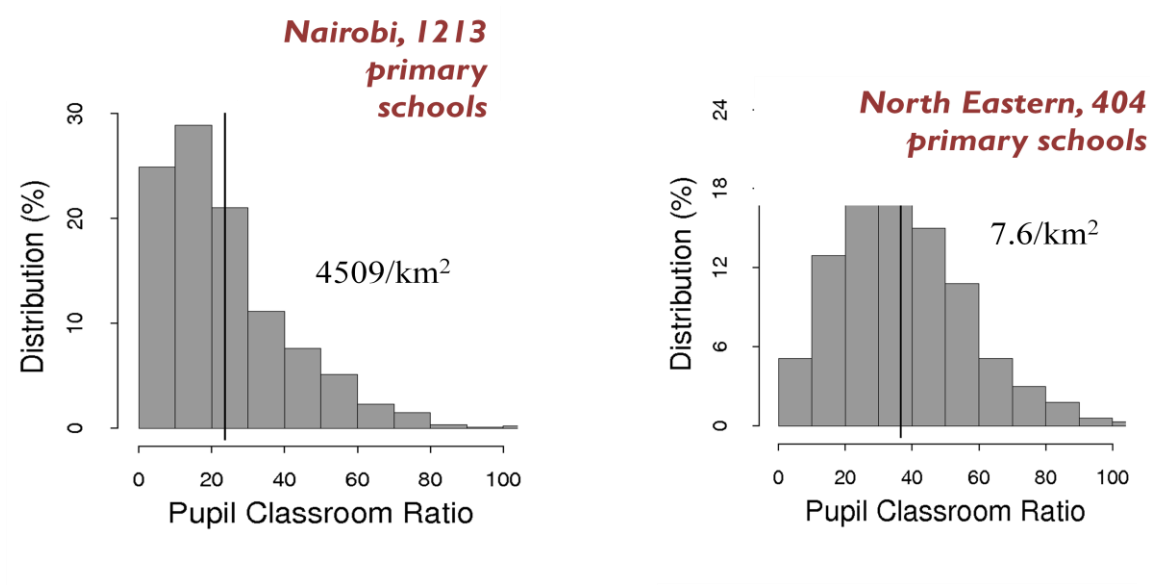
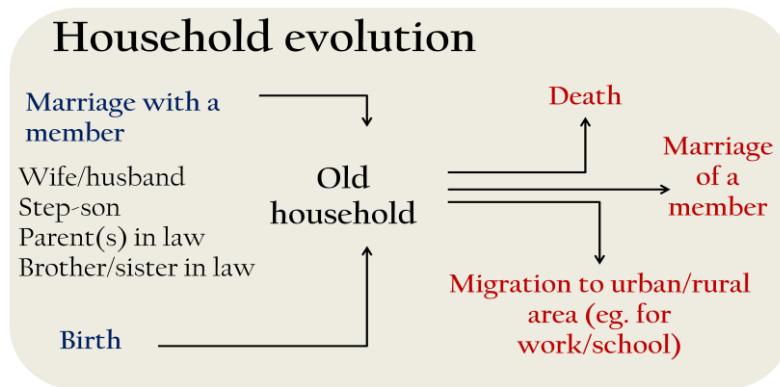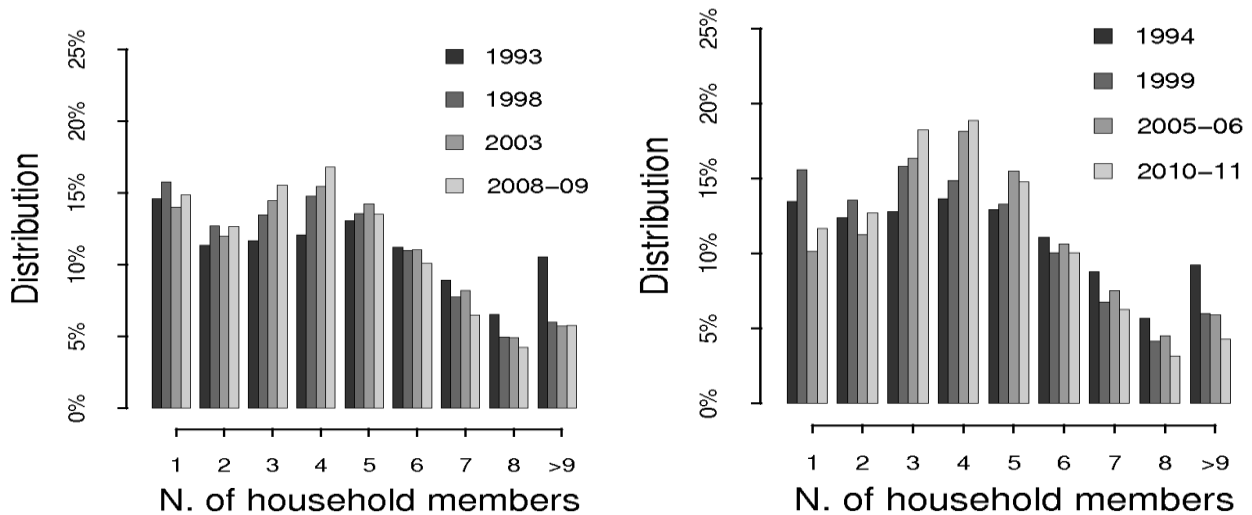*Figure 6 – Schematic representation of DHS-based observed mechanisms for household evolution*



*Figure 7 – Changes in the household size over time for Kenya (left panel) and Zimbabwe (right panel) as a consequence of the demographic transition*



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