AIDS Shocks, Families and Development

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(VERY PRELIMINARY and INCOMPLETE)

1 Introduction

The AIDS epidemic is a human tragedy: it kills and maims people (AIDS is the leading cause of deaths in Sub-Saharan Africa (SSA) with 20.1% of all deaths), reduces life expectancy (by 15-20 years) and changes the age composition of Sub-Saharan countries raising the number of dependents (children and old adults) per worker by as much as 20-25% in highly infected countries (see Jamison, Peachem, Makgoba, Bos, Baingana, Hofman, and Rogo (2006) and Stanecki (2004)). This has drastic adverse consequences for economic development delaying the process of industrialization of SSA countries by about a century and reducing the consumption per capita of its people by as much as 12% at the peak of the epidemics, see Santaeulàlia-Llopis (2007). Hence, it is of great importance to assess how much the set of currently implemented AIDS-related Reproductive Health/Family Planning polices may reshape (or not) the development path.

Because AIDS kills mostly young adults, it also kills spouses and parents generating large numbers of widows and orphans. Between one fifth and one fourth of all children in highly infected SSA countries are AIDS orphans (see UNAIDS (2006)). Moreover, the AIDS epidemic is associated with higher divorce rates ((add one number here)) and delays in first marriages ((add one number here)) (see Smith and Watkins (2005) and Reniers (2006)), pushing further the strain of single households. This is, the AIDS epidemic represents an unprecedent seismic demographic shift to the structure of families in African societies that is raising the number of poor (widows and singles) households. In addition, the impact of AIDS on individuals is also very uneven, affecting mostly women at early ages of their adulthood ((elaborate much more on this heterogeneity here)).

Due to the heterogeneity and multiple channels through which the AIDS epidemic affects families and their members, one of the challenges ahead is understanding which of these channels matter for development so that we can design policy. Indeed, the set of Reproductive Health/Family Planning policies proposed to palliate the impact of AIDS is very much tailored to the affected population groups [1]. These policies can: support those families that foster or care for orphans; increase prevention of mother-to-child HIV transmission (at birth and breastfeeding); reduce infection of

adults with counselling on the use of condoms, circumcisions or treatment of genital soars; and treat adults with antiretroviral drugs that extend their lifetimes.

Therefore, if we want to evaluate how much AIDS-related policies accelerate (or not) the process of industrialization or increase (or not) the consumption per capita of SSA countries, we need a model with a richer population process that captures the set of families in a society that is relevant to incorporate the channels through which AIDS distorts the structure and evolution of families. This is the task of this paper.

The thought experiment goes as follows:

1. I construct an exogenous population process (formally, a population projection matrix (a ‘law of motion’)) able to capture the main mechanisms through which AIDS impacts families and their members: mortality rates, birth rates, divorce/marriage rates, infection rates (all by sex, age, marital and health status). This yields a total of $36(N + 1)$ types of families, where $N$ is the maximum number of children per family. I calibrate the population projection matrix to Malawi, a country that suffers from a mature AIDS epidemic (with a HIV prevalence of 12%), using panel data in the Malawi Diffusion and Ideational Change Project.

2. I extend the Hansen and Prescott (2002) development theory with heterogenous families (and incomplete markets) to be able to incorporate the population process constructed previously.

3. I calibrate the model economy to a Northern-African country (also a late starter as the SSA economies) that has already taken-off and it is unaffected by AIDS (for instance, Egypt).

4. I project the initial (and healthy) population distribution of Egypt using the Malawian population projection matrix. This way I obtain the population path of Egypt had it been infected with AIDS at Malawian rates.

5. I solve for the economic development path under the two exogenous population paths: 1) Egypt without AIDS and 2) Egypt infected with the Malawian AIDS.

6. I use the model as a diagnostic device to investigate how much each AIDS population mechanism matters for development in terms of consumption per capita, the agricultural share of output and (perhaps) wealth inequality (shutting channels one by one).

7. I evaluate the effect of AIDS-related Reproductive Health/Family Planning policies on the development path by appropriately modifying parameters of the population projection matrix. For example, setting the mortality rates of children of infected mothers equal to the mortality rates of the children of non-infected mothers can be interpreted as a Reproductive Health policy that eradicates mother-to-child transmissions of HIV.

2 www.malawi.pop.upenn.edu
3 ((Note that the model I present below (Hansen and Prescott (2002) extended with heterogenous families under exogenous market incompleteness) provides an endogenous link between inequality and development. This is, it generates an endogenous distribution of wealth along the development path. I need to talk a lot more about this (perhaps not in this paper but somewhere else). Does a model like mine help us to understand the relationship between inequality and development?, also related, is it interesting to answer: What is the quantitative importance of market incompleteness for development? (the latter is a Victor, or Krusell-Smith type of exercise for another non-stationary environment such as development).))
2 Some Background Data on the Effects of AIDS on Families

Empirical evidence of the effects of AIDS on family dynamics and structure. Families evolve over time via changes on the health status and (possibly premature) death of its members, via the birth of children, and via marriages and divorces among its members. AIDS unambiguously changes these family transitions, creating a very different residual family composition.

(TO BE COMPLETED.)

3 The Model

3.1 Demography of AIDS

I build a population specification on the basis of a large but finite number of family types that can be aggregated nicely both to replicate the demographics of a society as well as the aggregate economic variables. To capture all relevant types of households and its dynamics, I define a household as a vector $z_t$ that subsumes the age, sex, marital status and health status of each of its individuals in period $t$.

Formally, every period $t$ individuals are indexed by age $i \in \{1, 2, 3\}$ that represents childhood, adulthood and old age (a technical device called exponential aging allows to consider time in shorter intervals). Adults differ in sex $g \in G = \{f, m\}$, respectively female and male, and I denote their individual state by $z_{ig}$. The individual state of young adults may take different values depending on his/her health status, $z_{2g} \in \{0, 1, 2\}$, respectively deceased, HIV-positive, or healthy. I assume HIV-infected young adults die before they reach old age and old adults can not be infected with HIV, hence, old adults must be either dead or alive and healthy, in that order, $z_{3g} \in \{0, 2\}$. In addition, the marital status of adults can be single or married, denoted respectively, $k \in \{S, M\}$. For $i \in \{2, 3\}$, households with $z_{if} \neq 0$ and $z_{im} \neq 0$ include a married adult couple of age class $i$; households with $z_{if} \neq 0$ and $z_{im} = 0$ include a single female adult of age class $i$; and households with $z_{if} = 0$ and $z_{im} \neq 0$ include a single male adult of age class $i$. Further, let $z_1 \in [0, N]$ be the number of (asexed) children born by adults in the household, where $N$ is the maximum amount of children a household can host. I consider all children within households are identical and condition their mortality and birth rates on the age-class, marital and health status of the biological mother and on the stock of children in the household.

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4 I will use interchangeably household or family. ((This requires a good discussion yet.))
5 The data counterpart of childhood is individuals below 15 years old, young adulthood includes individuals between 15 and 49 years old, and old age represents 49 years and above.
6 The average time from infection with HIV to developing AIDS is about eight years, and from AIDS to death about one year if no anti-retroviral therapy is available. For children the incubation period is much shorter because their immune systems are not yet fully developed and most children infected at birth develop AIDS and die within 5 years. ((It’d be great to add a state of AIDS (they’d die faster, produce less... all effects would be stressed), unfortunately, I do not know when they develop AIDS in the data. Ask Philip if there is a way to obtain CD4 cells information from the respondents in the next surveys MDCIP-2008.))
7 Married couples and couples that live together are treated equally.
8 I do not consider polygamy (neither polygyny nor polyandry). ((I may be able to make the case that polygamy is not important for my question if there is not data evidence of more or less HIV in the practice polygamy versus monogamy. To be checked!!))
9 An ideal alternative is to explicitly consider the individual health status of each child, but this rises the state
A household consists of a set of people of up to three different generations with at most an elderly couple, and adult couple and maximum number $N$ of children. Any proper subset is also a household type. Formally, a household is a vector that states the relevant properties to each member current demographic fate,

$$z = (z^1, z^{2f}, z^{2m}, z^{3f}, z^{3m}) \in Z = [0, N] \times \{0, 1, 2\}^2 \times \{0, 1\}^2$$

Note the information on the health status of each member is incorporated in the household type.

Therefore, if I abstract from the health status of young adult members, for a given number of children $N$, there are $2^4 (N + 1) = 16 (N + 1)$ possible types of households. If I consider the HIV health status of the young adults, there are $3^2 (N + 1) = 36 (N + 1)$ possible household types.

The population path derived from current HIV/AIDS environmental conditions is a key ingredient of my analysis. This path represents the projected evolution of the HIV/AIDS demographic structure (the measures of family types) over time. For instance, consider a household that consists of $n$ children, a married young couple with a healthy young female adult, a HIV-infected young male, and an old adult female in period $t$. This household is summarized by $z_t = (n, 2, 1, 2, 0)$. If we abstract from aging, the unfortunate events of the young female adult getting HIV-infected and the death of the young male adult and one child represent the transition from $z_t = (n, 2, 1, 2, 0)$ to $z_{t+1} = (n-1, 1, 0, 2, 0)$\(^{[10]}\). This transition obeys rates of survivorship, divorce/marriage and fertility that are all conditioned on HIV/AIDS. In addition, the passage of time will be represented by a natural aging process that makes all members of the family advance age levels: children become young adults, young adults age to old adulthood, and old adults die. Exponential aging allows the construction of this process where periods can be interpreted as being of shorter duration than the year intervals associated with a three age model.

In principal, since we have $36(N + 1)$ family types, there are $(36(N + 1))^2$ possible family transitions from $t$ to $t + 1$. To determine the full set of transitions I pose an exogenous population process that incorporates the demographic channels through HIV/AIDS operates: spreading the disease across the population (infection rates); conditioning survival rates (reducing life expectancy, increasing widowhood and orphanhood); reducing fertility rates; and, raising divorce and (re)marriage rates (increasing marital reshuffling).

3.1.1 Specification of the Population Process

To specify the population process I formulate a population matrix projection model. The matrix formulation permits a discrete analysis that relates the entire population of each period to the preceding as follows

$$\mu^{t+1} = \Gamma \mu^t$$

space by $3^N$ dimensions which is computationally very expensive. Another alternative, would be to HIV-infect an increasing proportion of children as a function of time (starting the date the mother is infected) that we could estimate from the data, or short-cut by HIV-infecting a constant proportion (the limiting one) the date the mother is infected.

\(^{10}\)Consider another example where a household that consists of a healthy single female without dependents marries a healthy young male and bears a child next period. Such household transits from $z_t = (0, 1, 0, 0, 0)$ to $z_{t+1} = (1, 1, 1, 0, 0)$. 

4
where $\mu^t$ is the $36(N+1)$-dimensional population vector of family measures $\mu^t_z$ and the $36(N+1)$-by-$36(N+1)$ matrix $\Gamma$ is the law of motion of the population. The typical element of the population projection matrix, $\Gamma_{z',z}$, is the mass of families of type $z$ in period $t$ that transit to type $z'$ in period $t+1$. Hence, the measure of families of a particular type $z'$ at period $t+1$ is given by

$$\mu^{t+1}_{z'} = \sum_z \Gamma_{z',z} \mu^t_z$$

Given $\Gamma$ and an initial population vector, iterative multiplications solve the matrix population model (2) and generate the population path via numerical projections. Moreover, standard mathematical tools provide some useful results related to the asymptotic behavior and transient dynamics of the population. The Perron-Frobenius theorem states that if the nonnegative matrix $\Gamma$ has the property of primitivity, then there exists a real positive eigenvalue $\lambda_1$ that is dominant (strictly greater than any other eigenvalue). With regard to the long-term dynamics, the strong ergodic theorem establishes the limiting population grows at a rate equal to the dominant eigenvalue, $\lambda_1$, and converges to a stable population structure equal to the associated right eigenvector of $\lambda_1$, see Keyfitz and Caswell (2005). Stability is a property by which a time can be found when the several household types increase at rates that are arbitrarily close to one another. We can think of this eigenvector as the balanced growth path of the demographic structure. With regard to the transient dynamics, the second eigenvalue governs the asymptotic rate of convergence.

Next, I describe in exhaustive detail how I build the population projection matrix, $\Gamma$. In doing so I will gradually augment the matrix step by step, adding complexity to the analysis. First, I describe the population process for young adults without dependents which includes survival rates, HIV-infection rates and divorce/marriage rates of young adults. Second, I describe how the population of dependents evolves over time via the survivorship of old adults and children and the fertility process. Third, I pose the aging process. Finally, I combine the previous elements to build the population process for the whole economy.

### 3.1.2 Population Process of Young Adults without Dependents.

Here, I specify the survival and HIV-transmission process for the population of young adults of sex $g$. If I abstract from dependents, marriage/divorce, aging and young adults of the opposite sex $g^*$, then the household vector is represented by a single element, $z = z^{2g} \in \{0, 1, 2\}$. Denote the population measure of young adults of sex $g$ who are healthy by $\mu_{z=z^{2g}=2}$, the measure of those who are HIV-infected by $\mu_{z=z^{2g}=1}$, and the measure of those deceased by $\mu_{z=z^{2g}=0}$. Then, I can

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11By definition a population measure is a nonnegative object and human population projection matrices are nonnegative. Nonnegative matrices can be either reducible or irreducible. Irreducible matrices are those in which all stages can contribute, by any developmental path, to some other stage or stages (i.e., the 'American dream, American nightmare' (monotone mixing) condition). A typical example of a reducible matrix is that with postreproductive ages and for this reason I will allow old female adults to bear children with probability measure greater than zero (that if old females happen to be the youngest females in the household). In all, irreducibility is a necessary but not sufficient condition for stability because it does not rule out the possibility of endless cycles. Primitivity is the subset of irreducible matrices without endless cycles. Formally, a primitive matrix is an irreducible matrix that becomes positive (all its elements are greater than zero) when raised to sufficiently high powers. For irreducible stage-classified models, a sufficient condition for primitivity is the presence of at least one positive diagonal element.

12The convergence to the stable structure is asymptotically exponential at a rate at least as faster as $\ln \lambda_1 - \ln |\lambda_2|$ where $\lambda_2$ is the second largest eigenvalue, see Keyfitz and Caswell (2005).
model the evolution of the population of young adults of sex \(g\) as

\[
\begin{bmatrix}
\mu_0 \\
\mu_1 \\
\mu_2
\end{bmatrix}^{t+1} = \Gamma_{2g} \begin{bmatrix}
\mu_0 \\
\mu_1 \\
\mu_2
\end{bmatrix}^t = \begin{bmatrix}
1 & 1 - \gamma_{IIV} & 1 - \gamma_{HIV} \\
0 & \gamma_{IIV} & \lambda_{2g} \gamma_{IIV} \\
0 & 0 & (1 - \lambda_{2g}) \gamma_{IIV}
\end{bmatrix}_{3 \times 3} \begin{bmatrix}
\mu_0 \\
\mu_1 \\
\mu_2
\end{bmatrix}^t
\]

where the law of motion \(\Gamma_{2g}\) combines the survival rate of HIV-infected young adults of sex \(g\), \(\gamma_{IIV}\), the survival rate of healthy young adults of sex \(g\), \(\gamma_{HIV}\), and the HIV-infection rate of healthy young adults of sex \(g\), \(\lambda_{2g}\). The first row and column of \(\Gamma_{2g}\) refers to the absorbing state of death. Although death has trivial dynamics and I will not track the dead in my numerical computations, however, for the construction and parameterization of the population matrix it is convenient to keep households that vanish due to the death of all members explicitly. Actually, the presence of death defines \(\Gamma_{2g}\) as a Markovian transition matrix for the individual \(2g\), what provides a great deal of information. For example, we can compute the average time (or any other moment) that individual \(2g\) spends as healthy or HIV-infected and also the average time to absorption (i.e., to death), that is, life expectancy.

**Survival matrix of young adults**, \(\Gamma^{S2}\). Consider the survival and HIV-transmission of the population of young adults abstracting from dependents, marriage/divorce and aging, then the household vector is given by \(z = (z^{2f}, z^{2m}) \in \{0, 1, 2\}^2\). This implies a total of \(3^2 = 9\) household types with respective measures denoted by \(\mu_z\). I specify the evolution of young adults from \(t\) to \(t + 1\) as the Kronecker product of the transition matrices \(\Gamma_{2f}\) and \(\Gamma_{2m}\), \(^{13}\)

\[
\begin{bmatrix}
\mu_{0,0} \\
\mu_{0,1} \\
\mu_{0,2} \\
\mu_{1,0} \\
\mu_{1,1} \\
\mu_{1,2} \\
\mu_{2,0} \\
\mu_{2,1} \\
\mu_{2,2}
\end{bmatrix}^{t+1} = \Gamma_{2f} \otimes \Gamma_{2m} = \begin{bmatrix}
1 & 1 - \gamma_{IIV} & 1 - \gamma_{HIV} \\
0 & \gamma_{IIV} & \lambda_{2f} \gamma_{HIV} \\
0 & 0 & (1 - \lambda_{2f}) \gamma_{HIV}
\end{bmatrix}_{3 \times 3} \otimes \begin{bmatrix}
1 & 1 - \gamma_{IIV} & 1 - \gamma_{HIV} \\
0 & \gamma_{IIV} & \lambda_{2m} \gamma_{IIV} \\
0 & 0 & (1 - \lambda_{2m}) \gamma_{IIV}
\end{bmatrix}_{3 \times 3}^{18}
\]

The survival 9-by-9 matrix \(\Gamma^{S2} = \Gamma_{2f} \otimes \Gamma_{2m}\) is upper triangular with 36 nonzero elements. This represents survival rates by sex and health status, and HIV-infection rates by sex, which implies 6 parameters. In addition, I condition survival rates and HIV-infections rates of young adults on marital status and on the health status of the spouse (if married) because the odds of getting infected when your partner has HIV increase. This requires some substitutions in \(\Gamma^{S2}\) that raise the total number of parameters to 18: regarding women, for any \(z^{2m} \in \{0, 1, 2\}\), if \(z^{2f} = 2\) then \(\gamma_{2f} = \gamma_{2,z^{2m}}\) and \(\lambda_{2f} = \lambda_{2,z^{2m}}\), while if \(z^{2f} = 1\) then \(\gamma_{2f} = \gamma_{IIV}^{HIV}\). Regarding men, for

\(^{13}\)Note the Kronecker product is the matrix operation that comprehends the full set of possible heterosexual combinations across individuals. In general, given matrices \(A_{m \times n}\) and \(B_{p \times q}\), the Kronecker product \(A \otimes B\) is the \(mp \times nq\) block matrix

\[
A_{m \times n} \otimes B_{p \times q} = \begin{bmatrix}
a_{11}B_{p \times q} & \cdots & a_{1n}B_{p \times q} \\
\vdots & \ddots & \vdots \\
a_{m1}B_{p \times q} & \cdots & a_{mn}B_{p \times q}
\end{bmatrix}_{mp \times nq}
\]

Note the multiplication order is irrelevant because although the Kronecker product is not commutative, \(A \otimes B\) and \(B \otimes A\) are permutation equivalent. Indeed, if \(A\) and \(B\) are square matrices, as it the case for \(\Gamma_{2f}\) and \(\Gamma_{2m}\), they are even permutation similar, that is, we can find a permutation matrix \(P\), such that \(\Gamma_{2f} \otimes \Gamma_{2m} = P(\Gamma_{2m} \otimes \Gamma_{2f})P'\), where \(P'\) is the transpose of \(P\).
any \( z^{2f} \in \{0, 1, 2\} \), if \( z^{2m} = 2 \) then \( \gamma_{2m} = \gamma_{z^{2f}2}^{\ast} \) and \( \lambda_{2m} = \lambda_{z^{2f}2}^{\ast} \), while if \( z^{2m} = 1 \) then \( \gamma_{2m} = \gamma_{z^{2m}1}^{\ast} \). The entire matrix \( \Gamma^{S2} \) is shown explicitly in Appendix C.

**Example 1.** The population of single HIV-infected females in \( t + 1 \) is given by

\[
\mu_{1,0}^{t+1} = \gamma_{1,0}^{HIV} \mu_{1,0}^{t} + (1 - \gamma_{1,1}^{HIV*)} \gamma_{1,1}^{HIV} \mu_{1,1}^{t} + (1 - \gamma_{1,2}^{*}) \gamma_{1,2}^{HIV} \mu_{1,2}^{t} + \\
\gamma_{2,0}^{HIV} \mu_{2,0}^{t} + (1 - \gamma_{2,1}^{HIV*)} \gamma_{2,1}^{HIV} \mu_{2,1}^{t} + (1 - \gamma_{2,2}^{*}) \lambda_{2,2} \gamma_{2,2} \mu_{2,2}^{t}
\]

that is, the sum of period-\( t \) single HIV-infected women that survive, HIV-infected widows of HIV-infected males, HIV-infected widows of healthy males, single healthy women that survived and got HIV-infected and healthy widows that got HIV-infected while married to HIV-infected males or to a healthy males.

**Example 2.** The population of healthy women married to HIV-infected men in \( t + 1 \) is given by

\[
\mu_{2,1}^{t+1} = \gamma_{2,1}^{HIV*} (1 - \lambda_{2,1}) \gamma_{2,1} \mu_{2,1}^{t} + \lambda_{2,2}^{HIV*} \gamma_{2,2} \mu_{2,2}^{t}
\]

that is, the sum of period-\( t \) married couples where the wife survives healthy and the HIV-infected husband also survives and healthy married couples where the wife survives and remains healthy while the healthy husband in \( t \) survives but gets HIV-infected.

### 3.1.3 Population Process of Dependents: Old Adults and Children

There are two types of dependents, old adults and children. I assume adults that reach old age are not HIV-infected and will not get HIV-infected\textsuperscript{14}\footnote{The HIV-incidence rate for the population above 46 relatively low.} Young adults may enter as singles or married into old adulthood. If they enter as singles they will remain singles for good, and if they enter as married they can become singles only through widowhood, that is, old adults do not participate in divorce/(re)marriage markets. Children introduce the natural possibility of population growth. I shall assume that the survival and fertility rates of children depend on the health and marital status of the biological mother and on the stock of children in the household.

**Survival Matrix of Old Adults, \( \Gamma^{S3} \).** Consider the survivorship of old adults abstracting from young adults and children. The measure of households with a fixed composition of children and young adults \( z = (z^{1}, z^{2f}, z^{2m}) \), that is, \( \mu_{z} \) with \( z = (z, z^{3f}, z^{3m}) \) and \( z^{bg} \in \{0, 2\} \), evolves according to the survival rates of old adults as

\[
\begin{bmatrix}
\mu_{\gamma_{0,0}} \\
\mu_{\gamma_{0,2}} \\
\mu_{\gamma_{2,0}} \\
\mu_{\gamma_{2,2}}
\end{bmatrix}^{t+1} = 
\begin{bmatrix}
1 & 1 - \gamma_{3f} \\
0 & \gamma_{3f}
\end{bmatrix}_{2 \times 2} \otimes 
\begin{bmatrix}
1 & 1 - \gamma_{3m} \\
0 & \gamma_{3m}
\end{bmatrix}_{2 \times 2} \times 
\begin{bmatrix}
\mu_{\gamma_{0,0}} \\
\mu_{\gamma_{0,2}} \\
\mu_{\gamma_{2,0}} \\
\mu_{\gamma_{2,2}}
\end{bmatrix}_{4 \times 4}^{t}
\]

where \( \gamma_{3f} \) and \( \gamma_{3m} \) are respectively the survival rates of old female and old male adults. Note that I am assuming independence between the survival rates of young and old adults because HIV, the object I am interested in, does not condition significantly the survival of old agents. However, I will condition the survival rates of old adults on their marital status. Hence, their survivorship requires 4 parameters: the survival rates of single and married old females, respectively \( \gamma_{0,0}^{\gamma_{2,0}} \) and \( \gamma_{0,2}^{\gamma_{2,2}} \), and the survival rates of single and married old males, \( \gamma_{0,0}^{\gamma_{2,0}} \) and \( \gamma_{0,2}^{\gamma_{2,2}} \). See \( \Gamma^{S3} \) explicitly in Appendix C.
Survival Matrix of Children, $\Gamma^{S1} \mid \pi^{if}, \pi^{im}$. For a given household composition of adults $\pi = (\pi^{2f}, \pi^{2m}, \pi^{3f}, \pi^{3m})$, denote the measure of households that host a number $z^1$ of children by $\mu_z$ with $z = (z^1, \pi)$ and $z^1 \in \{0,..,N\}$. Then, if I restrict the attention to the survival of children everything else constant, the measure of households with a fixed composition of adult members and children $z^1$ in $t + 1$, is derived as

$$
\mu_{z^1, z}^t = \sum_{z^1} [\Gamma^{S1}_{z^1 \mid z^1} \mid \pi^{if}, \pi^{im}] \mu_{z^1, z}^t
$$

where the survival matrix of children, $\Gamma^{S1} \mid \pi^{if}, \pi^{im}$, conditional on the age, health and marital status of the biological mother is explicitly,

$$
\Gamma^{S1} \mid \pi^{if}, \pi^{im} = \begin{bmatrix}
1 & 1 - \gamma_{1c} & (1 - \gamma_{2c})^2 & (1 - \gamma_{3c})^3 & \cdots & (1 - \gamma_{Nc})^N \\
0 & \gamma_{1c} & 2\gamma_{2c} - (1 - \gamma_{2c}) & 3\gamma_{3c} - (1 - \gamma_{3c})^2 & \cdots & N\gamma_{Nc} - (1 - \gamma_{Nc})^{N-1} \\
0 & 0 & \gamma_{2c} & 3\gamma_{3c} - (1 - \gamma_{3c})^2 & \cdots & N\gamma_{3c} - (1 - \gamma_{Nc})^{N-2} \\
0 & 0 & 0 & \gamma_{3c} & \cdots & N\gamma_{Nc} - (1 - \gamma_{Nc})^{N-3} \\
\vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\
0 & 0 & 0 & 0 & \cdots & \gamma_{Nc}^{N-1} \\
\end{bmatrix}_{(N+1) \times (N+1)}
$$

where $\gamma_{jc}$ is the survival rate of children in a household that has a stock of $j$ children. Also, $(\pi^{if}, \pi^{im}) = (\pi^{2f}, \pi^{2m})$ if $\pi^{2f} \neq 0$, while $(\pi^{if}, \pi^{im}) = (\pi^{3f}, \pi^{3m})$ if $\pi^{2f} = 0$. This way, the survivorship of children depends on the age, health and marital status of the youngest female adult in the household. If only children populate the household, I assume the worst odds and equate the survival matrix of children to the one conditional on single old females.

Fertility Matrix, $\Phi \mid \pi^{if}, \pi^{im}$. If we restrict our attention to fertility, everything else constant, the measure of households with a fixed composition of adult members and children $z^1$ in $t + 1$, is derived as

$$
\mu_{z^1, z}^{t+1} = \sum_{z^1} [\Phi_{z^1 \mid z^1} \mid \pi^{if}, \pi^{im}] \mu_{z^1, z}^t
$$

The fertility matrix, $\Phi \mid \pi^{if}, \pi^{im}$, conditional on the age, health and marital status of the biological mother is explicitly.

$$
\Phi \mid \pi^{if}, \pi^{im} = \begin{bmatrix}
1 - \varphi_1 & 0 & 0 & 0 & \cdots & 0 & 0 \\
\varphi_1 & 1 - \varphi_2 & 0 & 0 & \cdots & 0 & 0 \\
0 & \varphi_2 & 1 - \varphi_3 & 0 & \cdots & 0 & 0 \\
0 & 0 & \varphi_3 & 1 - \varphi_4 & \cdots & 0 & 0 \\
\vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\
0 & 0 & 0 & 0 & \cdots & 1 - \varphi_N & 0 \\
0 & 0 & 0 & 0 & \cdots & \varphi_N & 1 \\
\end{bmatrix}_{(N+1) \times (N+1)}
$$

where $\varphi_j$ is the fertility rate of children when the stock of children in the household is $j$. I assume $(\pi^{if}, \pi^{im}) = (\pi^{2f}, \pi^{2m})$ if $\pi^{2f} \neq 0$, while $(\pi^{if}, \pi^{im}) = (\pi^{3f}, \pi^{3m})$ if $\pi^{2f} = 0$. Also, $\Phi = I$ if $\pi^{2f} = 0$

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15 How does $\varphi_j$ relates to age-specific fertility rates and the total fertility rate?
and \( \bar{z}^{3f} = 0 \). This way, children fertility rates depend on the age, health and marital status of the youngest female adult in the household, and children cannot reproduce by themselves. \(^{16}\)

The assumption that the survival rate of children and fertility rates depend on the stock of children in the household captures 1) the fact that elder children have higher survival rates than younger children via the rise over time of the average survival rate of children in the household without having to keep track of the age of all children\(^{17}\) and 2) the reproductive behavior of women, a humped fertility path with age, without having to keep track of the age of the reproductive female.

With this parameterization of the survivorship of children and fertility, the population of households with a fixed composition of adults, \( \mu_z \) with \( z = (z^1, \bar{z}) \), transits from \( t \) to \( t + 1 \) as

\[
\begin{bmatrix}
\mu_{0,z} \\
\mu_{1,z} \\
\mu_{2,z} \\
\mu_{3,z} \\
\mu_{4,z} \\
\vdots \\
\mu_{N,z}
\end{bmatrix}^{t+1} = 
\begin{bmatrix}
\Phi_1 \\
\Phi_2 \\
\Phi_3 \\
\Phi_4 \\
\vdots \\
\Phi_N
\end{bmatrix} 
\begin{bmatrix}
\mu_{0,z} \\
\mu_{1,z} \\
\mu_{2,z} \\
\mu_{3,z} \\
\mu_{4,z} \\
\vdots \\
\mu_{N,z}
\end{bmatrix}^t
\begin{bmatrix}
\Gamma_1 \\
\Gamma_2 \\
\Gamma_3 \\
\Gamma_4 \\
\vdots \\
\Gamma_N
\end{bmatrix}_{N \times N}
\]

This structures the timing of the evolution of children such that first fertility occurs and then survivorship applies, what allows for post-neonatal mortality. Note women can bear only one child per period, while several may die within one period. In all, given that the survival rates and fertility rates depend on the age, health and marital status of the biological mother, I need a total of \((2^2 + 2)2N = 12N\) parameters.

**Example 3.** Given a composition of adults \( \bar{z} = (\bar{z}^2f, \bar{z}^2m, \bar{z}^3f, \bar{z}^3m) \), the probability of having a stock of one child in \( t \) and remaining with one child in \( t + 1 \) is

\[
\mu^t_{1,\bar{z}}|\mu^t_{1,\bar{z}} = (1 - \varphi_2)\gamma_1 + \varphi_2\gamma_2(1 - \gamma_2)
\]

that is, the sum of the probability of not bearing another child and having the stock children surviving, \((1 - \varphi_2)\gamma_1\), plus the sum of the probability of bearing another child and then having one of them dying, \(\varphi_2\gamma_2(1 - \gamma_2)\). Where recall that the survival rates of children and fertility rates are conditional on the age, health and marital status of the youngest female in the household.

**Example 4.** Given a composition of adults \( \bar{z} = (\bar{z}^2f, \bar{z}^2m, \bar{z}^3f, \bar{z}^3m) \), the probability of having a stock of two children in \( t \) and ending up without children in \( t + 1 \) is

\[
\mu^t_{0,\bar{z}}|\mu^t_{2,\bar{z}} = (1 - \varphi_3)(1 - \gamma_2)^2 + \varphi_3(1 - \gamma_3)^3
\]

that is, the sum of the probability of not bearing a third child between \( t \) and \( t + 1 \) times the probability of having the two children you previously had dying, \((1 - \varphi_3)(1 - \gamma_2)^2\), plus the probability of having a third child and having all three children dying, \(\varphi_3(1 - \gamma_3)^3\).

\(^{16}\)Note that although fertility introduces the possibility of population growth, here the units of measurement are households (not individuals) and fertility does not alter the Markovian properties of the population projection matrix. Fertility offsets the absorbing power of death, and now, given an initial demographic structure we may reach an invariant distribution where not everybody ends up dead. In other terms, fertility implies irreducibility of the matrix.

\(^{17}\)In this version of the paper, children mortality rates reflect under-16 mortality rates without explicit shorter age-interval distinctions. However, conditioning these rates on the number of children in the household intends to capture distinctions between neonatal, postneonatal, infant and child mortality; the reason being that the presence of more children in the household is likely to rise the survival rate of the average child simply because of the elder children face lower mortality rates than those younger. ((Reference this!!!))
So far we have described the survivorship for each age class and the fertility process. Next we turn to adding the divorce/marriage process and the aging process. The Markovian properties will be violated by the introduction of marital reshuffling and also of the aging process.\footnote{We deal with households, not individuals as standardly done in human demography in which the introduction of the aging process (probability of changing stages) does not alter the Markovian properties. Unlike fertility, marriage/divorce and aging change the total mass of the households altering the Markovian properties of the population projection matrix. When households divorce they double, when households marry they halve, when households age a matrilocal structure (man do not carry dependents) or the fact that children become independent as single young adults generates new households.}

### 3.1.4 Divorce/Marriage Process

Only young adults change marital status. First, I consider households composed only by young adults, $z_t = (z^f, z^m)$ and study the changes in the household composition due only to marriages and divorces, abstracting from the survivorship and HIV transmission of young adults, dependents and the process of aging. This way, tomorrow’s population (of young adults) is given by

\[
\begin{pmatrix}
1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & -m_{1,1} + d_{1,1} & 0 & 0 & -m_{2,1} + d_{2,1} & 0 \\
0 & 0 & 1 & 0 & -m_{1,2} + d_{1,2} & 0 & 0 & -m_{2,2} + d_{2,2} & 0 \\
0 & 0 & 0 & 1 & -m_{1,1} + d_{1,1} & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 + m_{1,1} - d_{1,1} & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 + m_{1,2} - d_{1,2} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 1 + m_{2,1} - d_{2,1} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 + m_{2,2} - d_{2,2} & 0 \\
\end{pmatrix}
\begin{pmatrix}
\mu_{0,0} \\
\mu_{0,1} \\
\mu_{0,2} \\
\mu_{1,0} \\
\mu_{1,1} \\
\mu_{1,2} \\
\mu_{2,1} \\
\mu_{2,2} \\
\end{pmatrix}
\]

The divorce and marriage rates depend on the health status of the individuals of interest, what yields a total of 8 parameters: the marriage and divorce rates of healthy individuals denoted by $m_{2,2}$ and $d_{2,2}$, of healthy wives and HIV-infected husbands, $m_{2,1}$ and $d_{2,1}$, of HIV infected wives and healthy husbands $m_{1,2}$ and $d_{1,2}$, and of HIV-infected wives and HIV-infected husbands, $m_{2,2}$ and $d_{2,2}$.\footnote{Note that marriage rates include first marriages and re-marriages. Further, I do not allow re-marriage within periods. One can easily incorporate re-marriage by having a 9x9 marriage matrix multiplying a 9x9 divorce matrix. Data suggest re-marriage is not that immediate though. (Reference this!!))}

**Example 1 (continued).** If I restrict the attention to the marriage/divorce market, then the population of single HIV-infected females in $t + 1$ is given by

$$
\mu^{t+1}_{1,0} = \mu^t_{1,0} - m^t_{1,1} \mu^t_{1,1} - m^t_{1,2} \mu^t_{1,2} + d^t_{1,1} \mu^t_{1,1} + d^t_{1,2} \mu^t_{1,2}
$$

that is, the amount of single HIV-infected women in $t$, minus those single HIV-infected women who marry single HIV-infected men or healthy men, plus those HIV-infected married women who divorce HIV-infected or healthy men.

**Example 2 (continued).** If I restrict the attention to the marriage/divorce market, then the population of healthy women married to a HIV-infected male in $t + 1$ is given by

$$
\mu^{t+1}_{2,1} = \mu^t_{2,1} + m^t_{2,1} \mu^t_{2,1} - d^t_{2,1} \mu^t_{2,1}
$$

that is, the amount healthy women married to a HIV-infected male in $t$, minus those healthy women that divorce their HIV-infected husband, plus those healthy women that marry a HIV-infected husband.
I will assume divorce and marriage are unconditional on the stock of dependents, that is, the divorce and marriage rate of household \((z^1, z^{2f}, z^{2m}, z^{3f}, z^{3m})\) is independent of \(z^1, z^{3f}\) and \(z^{3m}\):

\[
(m_{z^2 f, z^2 m} - d_{z^2 f, z^2 m}) \mu_{z^2 f, z^2 m} = \sum_{z^1, z^3 f, z^3 m} (m_{z^1, z^2 f, z^2 m, z^3 f, z^3 m} - d_{z^2 f, z^2 m}) \mu_{z^1, z^2 f, z^2 m, z^3 f, z^3 m}
\]

\[
= \sum_{z^1, z^3 f, z^3 m} (m_{z^2 f, z^2 m} - d_{z^2 f, z^2 m}) \mu_{z^1, z^2 f, z^2 m, z^3 f, z^3 m}
\]

\[
= (m_{z^2 f, z^2 m} - d_{z^2 f, z^2 m}) \sum_{z^1, z^3 f, z^3 m} \mu_{z^1, z^2 f, z^2 m, z^3 f, z^3 m}
\]

This way, the divorce/marriage matrix, \(\Gamma^M_{36(N+1)\times 36(N+1)}\), is constructed by setting the following elements:

\[
\Gamma^M_{(z_{t+1}, z^2 f_{t+1}, z^2 m_{t+1}, z^3 f_{t+1}, z^3 m_{t+1}) \rightarrow (z_{t}, z^2 f_{t}, z^2 m_{t}, z^3 f_{t}, z^3 m_{t})} = 1 + m_{z^2 f, z^2 m} - d_{z^2 f, z^2 m}
\]

for married couples in period \(t\), that is, households where \(z^2 f_{t} \neq 0\), \(z^2 m_{t} \neq 0\), and

\[
\Gamma^M_{(z_{t}, z^2 f_{t}, z^2 m_{t}, z^3 f_{t}, z^3 m_{t}) \rightarrow (z_{t+1}, z^2 f_{t+1}, z^2 m_{t+1}, z^3 f_{t+1}, z^3 m_{t+1})} = -m_{z^2 f, z^2 m} + d_{z^2 f, z^2 m}
\]

for single households in period \(t\), that is, households where \(z^2 f_{t} \neq 0\) and \(z^2 m_{t} = 0\), or \(z^2 f_{t} = 0\) and \(z^2 m_{t} \neq 0\). Setting the rest of elements of the matrix to zero yields a divorce/marriage matrix of 48\((N + 1)\) nonzero elements.

### 3.1.5 The Aging Process

There are three possible age stages defined as childhood, young adulthood and old age. Childhood represents individuals below 16, young adulthood includes individuals between 16 and 45, and old age 46 and above. All members within the household are subject to an aging process that carries individuals from childhood to young adulthood, from young adulthood to old adulthood, and from old adulthood to death. The fact that age intervals are not of the same size is irrelevant as long as the probability (common to all individuals) of advancing one age level, \(\pi\), is chosen such that the life expectancy of individuals in the model coincides with the data, which is what I do.

Formally, I specify a process of aging in which age intervals do not coincide with time (projection) intervals. This falls in the category of population models usually denoted as size-classified life-cycle models. An individual in a size class \(i\) may survive and grow to size class \(i + 1\) with probability \(P_i\), or may survive and remain in size class \(i\) with probability \(G_i\) \((\neq 1 - P_i)\). This hybrid three age OLG setup allows to consider shorter periods than the intervals associated with the three age groups. Also, I do not allow individuals to shrink, or to grow two size classes in a single time interval. It is perhaps helpful to look at the life cycle graph in ??, a description of the population that is isomorphic to the population projection matrix.

---

20 Life expectancy = \(f(\pi, \gamma_1, \gamma_2, \gamma_3)\), where \(\pi\) is the aging probability, \(\gamma_i\) is the survival rate within age-class \(i\), see Section ?? for the calibration of \(\pi\).

21 This contrasts with the standard modelization of OLG models where the age interval coincides with the time (projection) interval (age-classified population models) even though the process of aging may be probabilistic.

22 That is, agents can not become younger over time and neither do they age from childhood to old age, or from young adulthood to death in a single step of the aging process.
The aging process, requires the determination of the living arrangements for the elder. I assume these arrangements are such that a daughter will host her parents after aging. Note that only those members of the household are recognized as family and, hence, when a household ages, previous relatives (respective brothers, sisters, sons and daughters) that leave the household lose their lineage.

The matrix of aging is a $36(N+1)$-by-$36(N+1)$ matrix with $1 - \pi$ in its diagonal. For a given family composition $z_t = (z_t^1, z_t^2, z_t^m, z_t^{3f}, z_t^{3m}) \in Z = [0, N] \times \{0, 1, 2\}^2 \times \{0, 2\}^2$, if the family ages, then $z_t$ disappears and aging creates $z^t_1$ new households in $t + 1$. But not all households age, $1 - \pi$ will remain in the same stage while $\pi$ households will age. In detail, if $z^1 \neq 0$ then a total number of $z^1\pi$ households will be created as the sum of: $1\pi$ households of type $z_{t+1} = (0, z_{t+1}^{2f}, 0, z_{t+1}^{3m})$ where $(z_{t}^{2f}, z_{t}^{2m}) = (z_{t+1}^{3f}, z_{t+1}^{3m})$ (this way, I allocate old adults to one of their daughters); $z^{1-1}\pi$ households of type $z_{t+1} = (0, z_{t+1}^{2f}, 0, 0, 0)$; and, $z^{1-\pi}$ households of type $z_{t+1} = (0, 0, z_{t+1}^{2m}, 0, 0)$. If $z^1 = 0$ and $(z_{t}^{2f}, z_{t}^{2m}) \neq (0, 0)$, then $1 - \pi$ will remain in the same stage, while $\pi$ households of type $z_{t+1} = (0, 0, z_{t+1}^{2f}, z_{t+1}^{2m})$ will be created. Also, orphans become single HIV-free households with equal gender probability if they age. The rest of elements in this matrix are zeros.

### 3.1.6 The Population Projection Matrix

We now have all the ingredients to build the population matrix for the whole economy. The population projection matrix is the following $36(N+1)$-by-$36(N+1)$ square matrix

\[
\Gamma_{36(N+1) \times 36(N+1)} = \\
\left[ \Gamma^{S2}_{9 \times 9} \otimes \Gamma^{S3}_{4 \times 4} \otimes \left[ \Gamma^{S1} \times \Phi \right]_{(N+1) \times (N+1)} \right]_{36(N+1) \times 36(N+1)} \times \Gamma^{M}_{36(N+1) \times 36(N+1)} \times \Gamma^{A}_{36(N+1) \times 36(N+1)}
\]

where each of the matrices in the right hand side of (3) have been defined above.  \(^{23}\)

In addition, empirical evidence on living arrangements suggests that less than 20% of all children do not live with their biological mother while only 3% of all children live alone with their biological father (see Malawi DHS 2004), perhaps, as the result of a strong matrilocal social structure which I shall assume here. In this line, in the case of marital dissolution I will attach children to their biological mother, in the case of mother orphanhood I will attach children to the biological grandmother, and in the very unlikely absence of any maternal lineage children will become heads of their own household. This requires that for a given household composition of young male adults with dependents, $z_t = (z_t^1, 0, z_t^{2m}, z_t^{3f}, z_t^{3m})$ with $z_t^{2m} \neq 0$ and $(z_t^{1}, z_t^{3f}, z_t^{3m}) \neq (0, 0, 0)$, we change (realloccate and increase) the population mass with the following substitutions in the population matrix (3). For any household type, $z_t$, that transits to a household that consists of a single male

\(^{23}\)This population matrix is very different from the standard age-classified population models (Leslie matrix type) where the age interval coincides with the projection interval as applied for instance in Rios-Rull (2001). There, age-specific fertilities appear in the first row of the population matrix and age-specific survival rates in the subdiagonal. Here, fertilities appear in the subdiagonal while survival rates in the diagonal, because although agents may survive to next period they may stay in the same stage again.
with dependents we substitute

\[
\Gamma_{(0,0,z_{t+1}^{2m},0,0)}(z_t) = \Gamma_{(0,0,z_{t+1}^{2m},0,0)} + \Gamma_{(z_{t+1}^{1},0,z_{t+1}^{2m},z_{t+1}^{3m})}(z_t) + \Gamma_{(z_{t+1}^{1},0,z_{t+1}^{2m},z_{t+1}^{3m})}(z_t)
\]

Finally, I drop the households composed of young male adults with dependents and, hence, the total household types in the economy are

\[
36(N + 1) - (6(N + 1) + 2N) = 28N + 30.
\]

Taking stock of this section, we have specified a population process as a matrix projection mode suitable for the incorporation of the three channels through which HIV/AIDS affects most the demographic fate of households. HIV/AIDS alters the population dynamics conditioning 1) the life expectancy of young adults by age, sex and marital status, \(\Gamma_{S2}\), 2) the divorce/(re)marriage rates of the young adults involved in marital reshuffling, \(\Gamma_{M}\), and 3) the survival of children and associated fertility, respectively \(\Gamma_{S1}\) and \(\Phi\), by the age and marital status of the biological mother. In addition, we have assumed a societal system that has a matrilocal structure to define the living arrangements of the children, allocated exclusively to the mother’s lineage and the living arrangements of the elder, allocated exclusively to one daughter.

### 3.2 Technology

(To be completed.)


Below I define a competitive equilibrium as a set of sequences of distributions, prices, firms allocations and household policy functions that determine a transition path between the Malthusian and the Solowian stationary equilibria (see Section 4). To this end, I cast the households problem as a sequence of recursive problems. Further, institutional market arrangements that do not allow individuals to perfectly insure risk at no cost represent, perhaps, a more accurate description of these economies.

### 3.3 The Household Problem

(To be completed.)

I build an incomplete markets version of the hybrid OLG model in Santaeulalia-Llopis (2007) (see also Hong and Rios-Rull (2007)).

\(^{24}\)(I need to put the transition in the context of other epidemiology models (such the one used by UNAIDS, the EPP), recent more sophisticated ones (check how the U.S. Census Bureau is doing it) and some others that include sexual behavior such as Oster (2005).)

\(^{25}\)In social anthropology the term matrilocal is sometimes used in a more strict sense to define societies in which the offspring of a mother live in the mother’s house when they become adults forming large households of at least three generations. ([What’s the % of matrilocality in Malawi? and in SSA?]) Here, I have built families in which households host three generations but only one child (a daughter) remains in the household when members age.
Households consist of families with at most three overlapping generations. Young adults of a \(z\)-type family at period \(t\) solve
\[
V^y_t(z,a) = \max_{c \geq 0, x' \in \mathcal{A}, s_k \in [0,1]} \{ u^y_t(c) + \beta \sum_{z' \in Z} \Gamma(z'|z) \{ \pi V^0_{t+1}(z',a') + (1-\pi) V^y_{t+1}(z',a') \} \}
\]
subject to the budget constraint,
\[
c + x' = w_t \epsilon_z + \left( (1 + r^K_t - \delta) s_k + \frac{q_t + r^L_t}{q_{t-1}} (1 - s_k) \right) a
\]
The current felicity of young adults is the sum of their utility functions:
\[
u^y_z(c) = \sum_{g \neq g^*, g \in G} \omega^{y,z,g} u^y_z \left( \frac{c}{(1 + n^\nu) (\alpha(1 + \omega^{o,m} + 1_1) (1 + 1_{z^o,g^* \neq 0}))} \right)
\]
where \(c = c_{y,m} + c_{y,f}\), that is, spouses’ consumption and own consumption are perfect substitutes. Young adults with dependants face larger expenditures to enjoy the same consumption than without dependants: young adults face a proportional cost \(\alpha\) of consumption due to the presence of old individuals, and a proportional cost \((1 + n^\nu)\) due to \(n\) children. ((A discussion on the choice between equivalence scales and subsistence level is required!!)).

Households supply labor inelastically, but not all hours across individuals are the same.

The household state space is its demographic and health status, \(z\), and its wealth, \(a\). Households choose consumption, \(c\), next period’s wealth, \(x'\), and the share of current wealth allocated to capital, \(s_k\). \(V^y_t\) is the value function of young adults, \(u^y_z\) is the utility function for young adults, and \(V^0_t\) is the value function of old adults.

Old adults are not involved in the savings decision of the household, and their optimal choice is trivial: consume all their budget (all they get from young adults). Young adults internalize the problem of old adults,
\[
V^o_t(z,a) = \max_{\bar{c} \in [0,\alpha(1 + \omega^{o,m} + 1_1) \bar{c}]} u^o_z(\bar{c}) + \beta \sum_{z' \in Z} \Gamma(z'|z) \left( (1 - \pi) V^0_{t+1}(z',a') \right)
\]
\[
u^o_z(\bar{c}) = \sum_{g \neq g^*, g \in G} \omega^{o,z,g} u^o_z \left( \frac{\bar{c}}{1 + 1_1} \right)
\]

In order to solve their maximization problem, young adults need to know the sequences of prices \(\{w_t, r^K_t, r^L_t, q_t\}_{t=0}^T\). This is why I index value functions by time. In addition, households need to forecast the wealth of prospective spouses, \(x'^{*}\). Rules \(a'(x', x'^{*})\) define how family wealth changes in case of marital reshuffling.

First Order Conditions

1. FOC\((s_k)\): arbitrage condition that yields identical returns for capital and land,
\[
(1 + r^K_t - \delta) = \frac{q_t + r^L_t}{q_{t-1}} \tag{4}
\]
which is a first order difference equation in \(q_t\).
2. FOC\( (x') \): The Euler equation for young agents,

\[
\frac{\partial u_y^z(c)}{\partial c} = \beta \sum_{z' \in Z} \Gamma \{z' | z\} \{ (1 + r^K_{t+1} - \delta) \frac{\partial u(x', x'^*)}{\partial x'} \left[ \pi \frac{\partial u^c_{z'}(\bar{c})}{\partial c'} + (1 - \pi) \frac{\partial u^y_{z'}(c')}{\partial c'} \right] \}
\]

(5)

with

\[
\begin{align*}
c &= w_t \epsilon_z + (1 + r^K_t - \delta) a - x' \\
c' &= w_{t+1} \epsilon_{z'} + (1 + r^K_{t+1} - \delta) a' \left( x', x'^* \right) - x'' \\
\bar{c} &= \alpha (1_{z_{0,\mu}} + 1_{z_{0,\pi}}) c
\end{align*}
\]

Since we know function \( x'' \) at \( T \), we can solve for \( x' \) backwards. That is, (5) is a functional equation in \( x' \). For each period \( t \) we have to find a solution for the function \( x'(z, a) \), a functional equation in \( x_{t+1}(z, a) \), evaluated at every family state \( z \) and wealth state \( a \).

Thus, the household problem is summarized by a system of \( 2 \times (T + 1) \) equations with \( T + 1 \) unknown prices \( q_t \) and \( T + 1 \) unknown functions \( x' \).

4 Equilibrium

There is a requirement that agents decisions are consistent with their understanding of the evolution of the economy. From their point of view this includes not only the evolution of the epidemics and family composition, but also the prices they face and an assessment of the wealth of prospective spouses. A stationary equilibrium (one with constant rates of return, wage rates and savings) can be easily defined and solved. However, our central interest is the process of development and for this the evolution of the population and of savings have to be jointly determined. This requires the non stationary notion of equilibrium, that for non stationary population environments (but still quite different from mine) has been defined for example in Rios-Rull (2001) or Storesletten (2000).

**Equilibrium.** Given the initial distribution of wealth \( \chi_0 \), the amount of land \( L_0(= 1) \), the initial population structure \( \mu_0 \) and the population dynamics \( \{\Gamma_t\}_{t \geq 0} \), a competitive equilibrium in this economy consists of sequences of prices, \( \{q_t\}_{t \geq 0} \) and \( \{w_t, r^K_t, r^L_t\}_{t \geq 0} \), sequences of firm allocations, \( \{K_{mt}, K_{st}, N_{mt}, N_{st}, Y_{mt}, Y_{st}\}_{t \geq 0} \), sequences of household functions, \( \{c_t, x_{t+1}, s^k_t, V_t\}_{t \geq 0} \), and sequences of wealth distributions \( \{\chi_t\}_{t \geq 0} \) and population measures \( \{\mu_t\}_{t \geq 0} \) such that the following are true:

1. Firms optimize: Factor prices \( w_t \), \( r^K_t \) and \( r^L_t \) equate marginal productivities.

2. Households optimize: Decision rules \( \{c_t, x_{t+1}, s^k_t\} \) generate the value function \( \{V_t\} \).
3. Markets clear:

\[
\int_{Z \times A} c_t(z,a) \mu_{z,t} \, d\chi_t + K_{t+1} = Y_t + (1 - \delta)K_t
\]

\[
A_{t+1} = \int_{Z \times A} x_{t+1}(z,a) \mu_{z,t} \, d\chi_t
\]

\[
K_{t+1} = A_{t+1} - q_t \, L_{t+1} = A_{t+1} - q_t
\]

\[
N_t = \sum_{z_t} \epsilon_{z_t} \mu_{z,t}
\]

\[
K_t = K_{mt} + K_{st}, \quad N_t = N_{mt} + N_{st}
\]

\[
Y_t = A_{mt}F(K_{mt}, N_{mt}, L_t) + A_{st}F(K_{st}, N_{st})
\]

4. The wealth distribution that agents use to forecast prices is consistent with individual behavior,

\[
\chi_{t+1}(B) = M_t(\chi_t) = \sum_{z \in Z} \Gamma(z' | z) \int_A 1_{x_{t+1}(z,a) \in B} \chi_t(d(a))
\]

where, \(M_t\) is the wealth distribution transition law.

5. The measure of families of type \(z_t\) evolves according to

\[
\mu_{t+1} = \sum_z \Gamma(z' | z) \mu_t
\]

A stationery equilibrium around a BGP is an equilibrium such that all elements of the equilibrium are invariant with respect to time.

5 Calibration

(TO BE COMPLETED.)

5.1 Technology Parameters

5.2 Preference Parameters

5.3 Efficiency Units of Labor

5.4 Population Parameters

I calibrate the population projection matrix, \(\Gamma\), using transition frequency data from the last two waves of the Malawi Diffusion and Ideational Project data set,\(^{26}\) MDICP-2004 and MDICP-2006. This is a rich panel data where individuals can be identified and followed, and then the entries in

\(^{26}\)www.malawi.pop.upenn.edu
the projection matrix can be computed by recording the state of individuals at time \( t \) and then returning to measure their fate at time \( t + 1 \). \footnote{Instead, if we knew the next stable population (say, in 200 years ahead), we could back out the elements of the population matrix. This is not my case.} \footnote{It should we clear now why we need panel data to identify these rates which we cannot using two cross-section data sets.}

### 5.4.1 Survival Rates and HIV Infection Rates of Young Adults: 18 parameters.

Here I restrict the attention to young adults above 15 and below 46 years old, and abstract from the process of divorce/marriage and aging.

**Healthy Single Women:** \( z_t = (2, 0) \). The survival rate of single healthy women in the age interval 16-45, \( \gamma_{2,0} \), is computed as the number of single women alive in \( t + 1 \) conditional on being single and healthy in \( t \) divided by number of single and healthy woman in period \( t \),

\[
\gamma_{2,0} = \frac{\mu_{1,0}(t+1|2,0)_t + \mu_{2,0}(t+1|2,0)_t}{\mu_{2,0}(t)}
\]

Note the numerator includes all woman that survived to \( t + 1 \) and were single and HIV-infected in \( t \) independently of the fact the they may or not have been infected during the transition.

The HIV infection rate of single healthy women, \( \lambda_{2,0} \), is computed as the number of single women that got HIV-infected from \( t \) to \( t + 1 \) divided by the total number of single and healthy woman in \( t \) that survived to \( t + 1 \),

\[
\lambda_{2,0} = \frac{\mu_{1,0}(t+1|2,0)_t}{\mu_{1,0}(t+1|2,0)_t + \mu_{2,0}(t+1|2,0)_t}
\]

**HIV-Infected Single Women:** \( z_t = (1, 0) \). The survival rate of single HIV infected women, \( \gamma_{1,HIV} \), is the fraction of single women alive in period \( t + 1 \) conditional on being single HIV-infected women in period \( t \) over the number of single HIV-infected women in period \( t \)

\[
\gamma_{1,HIV} = \frac{\mu_{1,0}(t+1|1,0)_t}{\mu_{1,0}(t)}
\]

The rates associated with married take into account the health status of corresponding partner.

**Healthy Women Married to Healthy Husbands:** \( z_t = (2, 2) \). The survival rate of healthy women married to healthy men, \( \gamma_{2,2} \), is computed as the number of married women alive in \( t + 1 \) conditional on being healthy woman married to a healthy man in \( t \) and divided by number of healthy woman married to healthy men in period \( t \),

\[
\gamma_{2,2} = \frac{\mu_{1,0}(t+1|2,2)_t + \mu_{1,1}(t+1|2,2)_t + \mu_{1,2}(t+1|2,2)_t + \mu_{2,0}(t+1|2,2)_t + \mu_{2,1}(t+1|2,2)_t + \mu_{2,2}(t+1|2,2)_t}{\mu_{2,2}(t)}
\]

Note the numerator includes all woman that survived to \( t + 1 \) and were healthy and married to a healthy husband in \( t \) independently of the fact the they may or not have been infected during the transition and their respective husbands may or not have been infected or even die in the transition.
The HIV infection rate of healthy women married to healthy husbands, $\lambda_{2,2}$, is computed as the number of healthy woman married to healthy husbands in $t$ that survive to $t + 1$ and get infected women during the transition divided by the total number of healthy women married to healthy men in $t$ that survived from $t$ to $t + 1$,

$$\lambda_{2,2} = \frac{\mu_{(1,0)_{t+1}|(2,2)} + \mu_{(1,1)_{t+1}|(2,2)} + \mu_{(1,2)_{t+1}|(2,2)}}{\mu_{(1,0)_{t+1}|(2,2)} + \mu_{(1,1)_{t+1}|(2,2)} + \mu_{(1,2)_{t+1}|(2,2)} + \mu_{(2,0)_{t+1}|(2,2)} + \mu_{(2,1)_{t+1}|(2,2)} + \mu_{(2,2)_{t+1}|(2,2)}}$$

**HIV-Infected Women Married to Healthy Husbands**: $z_\ell = (1, 2)$. The survival rate of HIV-infected woman married to healthy men is equal to the number of woman that were HIV-infected and married to healthy men in $t$ and survived independently of the evolution of the health status of her partner from $t$ to $t + 1$ divided by the total number of HIV-infected woman married to healthy men in $t$.

$$\gamma_{1,2}^{HIV} = \frac{\mu_{(1,0)_{t+1}|(1,2)} + \mu_{(1,1)_{t+1}|(1,2)} + \mu_{(1,2)_{t+1}|(1,2)}}{\mu_{(1,2)}}$$

**Healthy Women Married to HIV-Infected Husbands**: $z_\ell = (2, 1)$. The survival rate of healthy women married to HIV-infected men, $\gamma_{2,1}$, is computed as the number of married women alive in $t + 1$ conditional on being healthy woman married to a HIV-infected man in $t$ and divided by number of healthy woman married to HIV-infected men in period $t$,

$$\gamma_{2,1} = \frac{\mu_{(1,0)_{t+1}|(2,1)} + \mu_{(1,1)_{t+1}|(2,1)} + \mu_{(2,0)_{t+1}|(2,1)} + \mu_{(2,1)_{t+1}|(2,1)}}{\mu_{(2,1)}}$$

The HIV infection rate of healthy women married to HIV-infected husbands, $\lambda_{2,1}$, is computed as the number of healthy woman married to HIV-infected husbands in $t$ that survive to $t + 1$ and get infected women during the transition divided by the total number of healthy women married to HIV-infected men in $t$ that survived from $t$ to $t + 1$,

$$\lambda_{2,1} = \frac{\mu_{(1,0)_{t+1}|(2,2)} + \mu_{(1,1)_{t+1}|(2,2)} + \mu_{(2,0)_{t+1}|(2,2)} + \mu_{(2,1)_{t+1}|(2,2)}}{\mu_{(1,0)_{t+1}|(2,2)} + \mu_{(1,1)_{t+1}|(2,2)} + \mu_{(1,2)_{t+1}|(2,2)} + \mu_{(2,0)_{t+1}|(2,2)} + \mu_{(2,1)_{t+1}|(2,2)} + \mu_{(2,2)_{t+1}|(2,2)}}$$

**HIV-Infected Women Married to HIV-Infected Husbands**: $z_\ell = (1, 1)$. The survival rate of HIV-infected woman married to HIV-infected men is equal to the number of woman that were HIV-infected and married to HIV-infected men in $t$ and survived independently of the evolution of her partner from $t$ to $t + 1$ divided by the total number of HIV-infected woman married to healthy men in $t$.

$$\gamma_{1,1}^{HIV} = \frac{\mu_{(1,0)_{t+1}|(1,1)} + \mu_{(1,1)_{t+1}|(1,1)}}{\mu_{(1,1)}}$$

Analogously, I obtain the survival rates of single health men, $\gamma_{0,2}^*$, of single HIV-infected men, $\gamma_{0,1}^{HIV^*}$, of healthy men married to healthy women, $\gamma_{2,2}^*$, of healthy men married to HIV-infected woman, $\gamma_{1,2}^{HIV^*}$, of HIV-infected men married to healthy women, $\gamma_{2,1}^*$, of HIV-infected men married to HIV-infected women $\gamma_{1,1}^{HIV^*}$ and the infection rates of single healthy man $\lambda_{0,2}^*$, of healthy men married to healthy woman $\lambda_{2,2}^*$, and of healthy men married to HIV-infected women, $\lambda_{1,2}^*$. 

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5.4.2 Survival Rates of Old Adults: 4 parameters.

Here I restrict the attention to young adults, \( z = (z^3_f, z^3_m) \), and abstract from the process of aging. The survival rate of single old women above 46, \( \gamma^o_{2,0} \), is computed as the number of old women alive in \( t+1 \) conditional on being single in \( t \) divided by number of single old women in period \( t \), where numerator includes all woman that survived to \( t+1 \) and were single in \( t \), independently of marital reshuffling from \( t \) in \( t+1 \). The survival rate of married old women, \( \gamma^o_{2,2} \), is computed as the number of old women alive in \( t+1 \) conditional on being married in \( t \) divided by number of married old woman in period \( t \). I obtain analogous rates for single and married old men, respectively, \( \gamma^{ox}_{0,2} \) and \( \gamma^{ox}_{2,2} \).

5.4.3 Survival Rates of Children and Fertility Rates: 12N + 1 parameters.

I group mothers by age, health and marital status (these generates 6 types of potential biological mothers: single or married healthy or sick young adults and single or married old adults). For each type of biological mother, define the total number of child \( j \)-th births in the interval \( (t, t+1) \) as \( B_{j(t,t+1)} \), then the birth rate of the \( j \)-th child is for each type of mother is

\[
\varphi_j = \frac{B_{j(t,t+1)} \mid \mu_{(j-1)t}}{\mu_{(j-1)t}}
\]

where \( \mu_{jt} \) is the measure of households with \( j \) children in period \( t \) per type of mother.

Some of the offspring born during the interval will not survive to time \( t+1 \). The survival rate of the \( j \)-th child for each type of biological mother is

\[
\gamma_j = \frac{\mu_{j(t,t+1)} \mid \mu_{(j-1)t}}{\mu_{(j-1)t}}
\]

To treat the data and model consistently, I redefine \( \mu_{(j')t+1} = \sum_j \Phi_{j'j} \mu_{jt} \) in (13) before the computation of \( \gamma_j \), allowing for neonatal mortality.

I calibrate the maximum number of children, \( N \), large enough to ensure the stock of children of healthy married females aged 16-45 in the model matches the data. Its model counterpart is the mean of the invariant distribution of the children’s survival matrix times the fertility matrix associated with these females. \(^{29}\) \(^{30}\)

Note the MDICP panel data has a two years interval while the time interval in the model is one year. However, the MDICP-2006 questionnaire covers in detail how many children have been born within each of the previous two years. This way, since a woman may have born more than one child during the two years between surveys, she may provide us with more than one observation. \(^{31}\)

\(^{29}\) The total fertility rate (TFR) adds up the age-specific fertility rates for a given cross-section, where age-specific fertility rates are the total number of children born within the age interval of interest.

\(^{30}\) Alternatively, we could make sure that females in their reproductive years produce offspring at a rate that is average of the maternity function for the those females, where the maternity function is defined as the expected offspring per individual aged \( a \) per unit of time \( t \).

\(^{31}\) For example, assume a household is formed by a single healthy mother and 2 children in 2004. In the case that she bears two more children between 2004 and 2006, she has formally transited twice, ceteris paribus, due to the evolution of the stock of children in the household. First, this households has transited from \( z_{2004} = (2,2,0,0,0) \)}
5.4.4 Divorce/Marriage Rates: 8 parameters.

In the model, only young adults, \( z_t = (z_2^{2f}, z_2^{2m}) \), enter the divorce/marriage market. The marriage and divorce rates between \( t \) and \( t + 1 \) are computed, as the amount of marriages and divorces between \( t \) and \( t + 1 \) divided by the number of married couples in period \( t \). Denote the total number of divorces and marriages of a given type of couple \((z_2^{2f}, z_2^{2m})\) respectively by \( M(z_2^{2f}, z_2^{2m})(t,t+1) \) and \( D(z_2^{2f}, z_2^{2m})(t,t+1) \). This way, the marriage rate of couples \((z_2^{2f}, z_2^{2m})\) is given by

\[
m_{z_2^{2f},z_2^{2m}} = \frac{M(z_2^{2f}, z_2^{2m})(t,t+1)}{\mu_{z_2^{2f},z_2^{2m}}} \tag{14}\]

and the divorce rate by

\[
d_{z_2^{2f},z_2^{2m}} = \frac{D(z_2^{2f}, z_2^{2m})(t,t+1)}{\mu_{z_2^{2f},z_2^{2m}}} \tag{15}\]

We have used data from 2004 and 2006, a two years interval. For convenience we adjust the computed two-years survival rates for adults and children, and the divorce/marriage rates to one-year rates using the geometric mean.

5.4.5 Probability of Aging.

I calibrate the probability of aging, \( \pi \), such that the life expectancy of a woman in the model matches the data. Define the transition matrix associated with the three age-classes of a female,\[\Gamma_f = \begin{bmatrix} \gamma_{1f} & 0 & 0 \\ \pi & \gamma_{2f} & 0 \\ 0 & \frac{\pi}{2} & \gamma_{3f} \end{bmatrix}\]

where \( \gamma_{1f} \), \( \gamma_{2f} \) and \( \gamma_{3f} \), are, respectively, the survival rates of girls (< 16 years old), young adult females (\( \geq 16 \) and < 46), and old adult females (\( \geq 46 \)), and \( \pi \) is the probability of aging.

The life expectancy (or time to death) of a woman is computed using the fundamental matrix of \( \Gamma_f \), \( N = I + \Gamma_f + \Gamma_f^2 + \Gamma_f^3 + \cdots = (I - \Gamma_f)^{-1} \). The element \( N(1, 1) \) is the average duration (in years) a woman stays as a kid, \( N(2, 1) \) is the average duration a woman is a young adult, and \( N(3, 1) \) represents the average duration a woman is an old adult. Then, the life expectancy of a woman (at the time of birth) is the sum of the elements of the first column in \( N \). This yields to \( z_{2005}^{2005} = (3, 2, 0, 0, 0) \), which will contribute to the computation of \( \varphi_1 \), and second, from \( z_{2005}^{2005} = (3, 2, 0, 0, 0) \) to \( z_{2006}^{2006} = (4, 2, 0, 0, 0) \), which will contribute to the computation of \( \varphi_4 \). This way, even though there is a sequence of bearing that goes beyond the one year interval of the model I assume constancy of the fertility rates between 2004-2005 and 2005-2006 in order to make use of the full information available in the data.

\[\text{Note that the number of females } z_2^{2f} \text{ that marry males } z_2^{2m} \text{ is given by,} \]

\[
m_{z_2^{2f},z_2^{2m}} \mu_{z_2^{2f},z_2^{2m}} = m_{z_2^{2f},z_2^{2m}}' \mu_{z_2^{2f},0} \]

where \( m_{z_2^{2f},z_2^{2m}}' = \frac{M(z_2^{2f}, z_2^{2m})(t,t+1)}{\mu_{z_2^{2f},0}} \) is the marriage rate for females.

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an expression for the life expectancy as a function of the survival rates within age groups and the ageing probability (not of the population structure) that I can solve for \( \pi \).

5.5 Initial Population Distribution

(TO BE COMPLETED.)

I obtain the initial distributions, \( \mu_0 \), from nationally representative Demographic and Health Surveys (DHS).

6 Findings

6.1 Population Projection with and without HIV/AIDS

(TO BE COMPLETED.)

The population matrix \( \Gamma \) is constant. This means that transition rates are independent of density and have no inherent time variation.

(What are the assumptions of the population analysis so far? First, the construction of the model assumes implicitly that it is appropriate to classify individuals by age, sex, marital, and health status. This is equivalent to assuming that properties other than these are irrelevant to an individual’s demographic fate. This is not an innocuous assumption. Second, the discrete nature of the model discards all information on the age dependency of vital rates within age classes.)

(Interpreted as projections, the results of demographic analyses reveal something about present conditions (more precisely, about the relation between present conditions and the population experiencing them), not about the future behavior of the population. One of the most powerful ways to study present conditions is to examine their eventual consequences were they to remain as they are. Population projections are particularly revealing because they integrate the impact of environmental

\[
LE = N(1, 1) + N(2, 1) + N(3, 1) = f(\gamma_{1f}, \gamma_{2f}, \gamma_{3f}) \left( (1 - \gamma_{2f} - \gamma_{3f} + \gamma_{2f} \gamma_{3f}) + (\pi(1 - \gamma_{3f})) + \left( \frac{\pi^2}{2} \right) \right)
\]

where \( f(\gamma_{1f}, \gamma_{2f}, \gamma_{3f}) = \frac{1}{1 - \gamma_{1f} - \gamma_{2f} - \gamma_{3f} + \gamma_{1f} \gamma_{2f} + \gamma_{1f} \gamma_{3f} + \gamma_{2f} \gamma_{3f} - \gamma_{1f} \gamma_{2f} \gamma_{3f}} \).

Assuming that the probability of aging is identical across demographic groups I have given up the possibility of solving for the \( \pi \) that would correspond to each demographic group. However, given the calibrated common \( \pi \), I can check how close the modelled life expectancies of each demographic group match their corresponding data counterparts.

The criticism that the real world is neither linear nor time-invariant applies to stage-classified models just as it does to age-classified models. How can we justify the analysis then? The distinction between forecasting of future population dynamics and projecting the hypothetical consequences of present environmental conditions remains the appropriate response to this criticism. Well, this is not a forecast exercise (an attempt to predict what will happen), this is, i’m not using the projection model to forecast actual future population dynamics. No such assumptions are required to interpret the growth rate and population structure as answers to they hypothetical question “how would the population behave if the present conditions were to be maintained indefinitely?” To assert that ”the present demographic properties of this population are such that, were they to remain constant, the population would eventually grow at such-and-such a rate with such-and-such structure” is not to claim that the first, hypothetical clause (constancy of \( \Gamma \)) is true.
conditions on vital rates throughout the life cycle. To know the survival probabilities and fertilities of every age class under a particular set of circumstances is to possess a great deal of biological information about these circumstances. This information is most valuable when coupled with a comparative approach, in which vital rates are measured under two or more different conditions.}

6.2 Economic Development Path with and without HIV/AIDS

(TO BE COMPLETED.)

Compare alternative development time paths of:

1. Consumption per capita,
2. Agricultural share of output, and
3. Wealth inequality.

7 Policy Evaluation

(TO BE COMPLETED.)

I compare the alternative economic development paths generated by a set of three AIDS-related policies that alter the population projections.

We know that mother-to-child transmission rates are about zero in the U.S. or Europe. So, what would happen to the economic development of Malawi if we were to bring the U.S. reproductive health system to Malawi? Would then Malawi transit faster to an industrial regime? If yes, by how many years? Would consumption per capita increase or decrease during this transition? These are the types of questions I aim to answer. Specifically,

1. The population matrix has parameters that represent mother-to-child transmission in terms of the mortality rates of children of infected versus non-infected mothers. We can think of changes in those parameters as a reduced form implementation of reproductive health policies, which in the extreme example of assume that we can bring the reproductive health system of the U.S. or Europe to Malawi. This requires setting the mortality rates of children of infected mothers equal to the children of non-infected mothers.

2. I also have parameters that represent adult infection rates of different individuals (by age, sex, marital) in the population matrix. It is very easy then to see how changes in these infection rates may change the development path of an economy. We can think of changes in the infection rates as a reduced form implementation of a policy that enforces, for example, the use of condoms (Bracher, Santow, and Watkins (2004)), circumcisions, abstention or the treatment of genital soars (Oster (2005)).

3. We can extend the lives providing universal free-access to anti-retrovirals (this is, 'bring Brazil or Uganda to Malawi') by decreasing the mortality rates (which are parameters in the population matrix) of infected individuals.
4. Evaluate policies that support the fosterhood and care of orphans.

To the best of my knowledge, this is the first analysis that will kick out macroeconomic evaluations (in terms of years to complete the process of industrialization, and consumption per capita time path) of AIDS-related Reproductive Health policies targeted at the micro level.

8 Conclusion

(TO BE COMPLETED.)
References


A Appendix: Derivation of the Euler Equation

Given the non-standard features of this model it is perhaps useful to derive in some detail the Euler equation (5) using the Envelope theorem. First, derive the first order condition for young adults with respect to consumption, \( \bar{c} \),

\[
\frac{\partial u_y(z, a)}{\partial c} = \beta \sum_{z' \in Z} \Gamma (z'|z) \left\{ \pi \frac{\partial V_{t+1}^y(z', a')}{\partial a'} \frac{\partial a'(x', x^*)}{\partial x'} + (1 - \pi) \frac{\partial V_{t+1}^y(z', a')}{\partial a'} \frac{\partial a'(x', x^*)}{\partial x'} \right\} \tag{16}
\]

Second derive the first order condition for old adults with respect to consumption, \( \bar{c} \),

\[
\frac{\partial u_z(\bar{c})}{\partial c} = \beta \sum_{z' \in Z} \Gamma (z'|z) \left\{ (1 - \pi) \frac{\partial V_{t+1}^o(z', a')}{\partial a'} \frac{\partial a'(x', x^*)}{\partial x'} \frac{\partial x'(z, a)}{\partial c} \right\} \tag{17}
\]

At optimum,

\[
V_t^y(z, a) = u_y^y(c(z, a)) + \beta \sum_{z' \in Z} \Gamma (z'|z) \left\{ \pi V_{t+1}^y(z', a'(x'(z, a), x^*)) + (1 - \pi) V_{t+1}^y(z', a'(x'(z, a), x^*)) \right\}
\]

and

\[
V_t^o(z, a) = u_z^o(\bar{c}(c(z, a))) + \beta \sum_{z' \in Z} \Gamma (z'|z) \left\{ (1 - \pi) V_{t+1}^o(z', a'(x'(z, a), x^*)) \right\}
\]

Then 1),

\[
\frac{\partial V_t^y(z, a)}{\partial a} = \frac{\partial u_y^y(c(z, a))}{\partial c(a, z)} \left( 1 + r_t^K - \delta \right) - \frac{\partial x'(z, a)}{\partial a} + \beta \sum_{z' \in Z} \Gamma (z'|z) \left\{ \pi \frac{\partial V_{t+1}^y(z', a'(x'(z, a), x^*))}{\partial a'(x'(z, a), x^*)} + (1 - \pi) \frac{\partial V_{t+1}^y(z', a'(x'(z, a), x^*))}{\partial a'(x'(z, a), x^*)} \right\} \frac{\partial a'(x'(z, a), x^*)}{\partial x'(z, a)} \frac{\partial x'(z, a)}{\partial a}
\]

which using (16) becomes,

\[
\frac{\partial V_t^y(z, a)}{\partial a} = \frac{\partial u_y^y(c(z, a))}{\partial c(a, z)} \left( 1 + r_t^K - \delta \right) \tag{18}
\]

and 2),

\[
\frac{\partial V_t^o(z, a)}{\partial a} = \frac{\partial u_z^o(c(z, a))}{\partial c(a, z)} \frac{\partial \bar{c}(c(z, a))}{\partial c(a, z)} \left( 1 + r_t^K - \delta \right) - \frac{\partial x'(z, a)}{\partial a} + \beta \sum_{z' \in Z} \Gamma (z'|z) \left\{ (1 - \pi) \frac{\partial V_{t+1}^o(z', a'(x'(z, a), x^*))}{\partial a'(x'(z, a), x^*)} \right\} \frac{\partial a'(x'(z, a), x^*)}{\partial x'(z, a)} \frac{\partial x'(z, a)}{\partial a}
\]

which using (17) becomes,

\[
\frac{\partial V_t^o(z, a)}{\partial a} = \frac{\partial u_z^o(\bar{c}(c(z, a)))}{\partial c(a, z)} \left( 1 + r_t^K - \delta \right) \tag{19}
\]

Third, forward equations (18) and (19) one period and plug them into (16) to get (5).
B Appendix: Data

B.1 Malawi Diffusion and Ideational Change Project

(TO BE COMPLETED.)

I use intensively the Malawi Diffusion and Ideational Change Project (MDCIP) panel data conducted by the Population Studies Center at UPENN available at http://www.malawi.pop.upenn.edu. In http://www.malawi.pop.upenn.edu, the reader may find excellent descriptions of the MDICP sample selection, data collection and data quality. This survey is ideal for my purposes because it tracks the same individual and household over time, a feature that is essential for the estimation of the transition matrices that represent how an individual evolves over different demographic states.

The most relevant elements of the MDICP for my purposes are: household rosters, including basic demographic information on all members usually residing in the sample households; marriage and partnership histories; cash income, labor market participation and small business activity of the households.

B.2 Sampling Strategy, Selection and Attrition

(TO BE COMPLETED.)

From http://www.malawi.pop.upenn.edu: “The sampling strategy was not designed to be representative of the national population of rural Malawi, although the sample characteristics closely match the characteristics of the rural population of the Malawi Demographic and Health Survey. The target sample for the first MDICP wave was 500 ever married women age 15-49 in each district, plus their husbands. The third survey wave added a sample of approximately 400 adolescents age 15-29 in each district.”
C  Appendix: Survival Matrices of Adults

C.1  Survival Matrix of Young adults, $\Gamma^{S2}$, where $z = (z^2 f, z^2 m)$.

$$\Gamma^{S2} =
\begin{pmatrix}
1 & 1 - \gamma^{HV*} & 1 - \gamma & (1 - \gamma^{HV*}) (1 - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV*}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & \lambda & \lambda & \gamma^{HV} & (1 - \gamma^{HV*}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & 0 & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & 0 & 0 & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & (1 - \gamma^{HV*} - \gamma^{HV}) & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & (1 - \gamma^{HV*} - \gamma^{HV}) \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\end{pmatrix}_{9 \times 9}
$$

C.2  Survival Matrix of Old adults, $\Gamma^{S3}$, where $z = (z^3 f, z^3 m)$.

$$\Gamma^{S3} = [\Gamma_{3m} \otimes \Gamma_3f]_{4 \times 4} =
\begin{pmatrix}
1 & 1 - \gamma^* & 1 - \gamma & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) \\
0 & \gamma & \gamma & \gamma^2 & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) \\
0 & 0 & 0 & \gamma^2 & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) \\
0 & 0 & 0 & 0 & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) & (1 - \gamma - \gamma^2) \\
\end{pmatrix}_{4 \times 4}
$$
\[
\left[ t^{S_2} \times t^M \right]_{9 \times 9} \otimes \left[ t^{S_2} \right]_{4 \times 4} \otimes \left[ t^{S_1} \times \Phi \right]_{N \times N} \right]_{36(N+1) \times 36(N+1)} \times \Gamma_{26(N+1) \times 36(N+1)}^{A}
\]
D Appendix: Computation Algorithm

I assume the transition from Malthus to Solow takes place after $T$ periods. To compute the equilibrium transition we follow these steps:

1. Choose $T$

2. Solve the stationary Malthusian economy with prices $\{w_0, r^K_0, r^L_0, q_0\}$, household functions $\{c_0, x_1, s^K_0, V_0\}$, wealth distribution $\chi_0$, population structure $\mu_0$ and aggregate total wealth $A_0$. Incorporate Malthusian BGP.

3. Solve the stationary Solowian economy with prices $\{w_T, r^K_T, r^L_T, q_T\}$, household functions $\{c_T, x_{T+1}, s^K_T, V_T\}$, wealth distribution $\chi_T$, population structure $\mu_T$ and aggregate total wealth $A_T$. Incorporate Solowian BGP.

4. Generate the sequence $\{N_t = \sum_z \epsilon_z \mu_{z,t}\}_{t=0}^{T}$ iterating forward the initial population structure $\mu_0$ with the population law of motion $\{\Gamma_t\}_{t=0}^{T}$.

5. Guess a sequence for the aggregate demand of capital stock $\{\hat{K}_t\}_{t=0}^{T}$, where $\hat{K}_0 = \hat{K}_1$ is the stationary Malthusian capital stock and $\hat{K}_T$ the stationary Solowian capital stock.

6. Given $\{\hat{K}_t, N_t\}_{t=0}^{T-1}$, generate the sequences of factor prices $\{w_t, r^K_t, r^L_t\}_{t>0}$.

7. Given $\{w_t, r^K_t, r^L_t\}_{t=0}^{T}$ and $q_0$, solve for sequence of the relative price of land $\{\hat{q}_t\}_{t>0}$ in arbitrage condition $[4]$, a first order difference equation that we solve forward. If $q_t < 0$, go back to step 5 and update (raise) the guess $\{\hat{K}_t\}_{t=0}^{T}$.

8. Given $\{w_t, r^K_t, r^L_t\}_{t=0}^{T}$, solve for sequence of decision rules $\{\hat{x}_{t+1}(z,a)\}_{t>0}$ in Euler equation, $[5]$. Since we know the stationary Solowian decision rule, $x_{T+1}(z,a)$, we can solve for the decision rule at $T - 1$, $\hat{x}_T(z,a)$ (a nonlinear function that I approximate using collocation methods) and proceed backwards to obtain the whole sequence $\{\hat{x}_{t+1}(z,a)\}_{t>0}$.

9. Given the implied sequence of decision rules $\{\hat{x}_{t+1}\}_{t=0}^{T}$, compute the sequence of transitions functions $\{\hat{M}_t\}_{t=0}^{T}$. Then, iterate forward the initial distribution $\chi_0$ to get the sequence of wealth distributions, $\{\hat{\chi}_{t+1} = \hat{M}_t(\hat{\chi}_t)\}_{t=0}^{T}$.

10. Given the sequence of decision rules $\{\hat{x}_{t+1}\}_{t=0}^{T}$, the sequence of wealth distributions, $\{\hat{\chi}_t\}_{t=0}^{T}$, and the sequence of population measures, $\{\mu_t\}_{t=0}^{T}$, we can compute the aggregate supply of capital as

$$\hat{K}^S_{t+1} = \hat{A}_{t+1} - \hat{q}_t = \int \hat{a}_{z,t+1} \mu_{z,t} d\hat{\chi}_t - \hat{q}_t$$

11. Check the transition of the excess of demand of capital,

$$\max_{1 \leq t < T} |\hat{K}_t - \hat{K}^S_{t+1}| < \epsilon \quad (20)$$

If (20) holds, go to step 12. If not, go back to step 5 and update the guess for the aggregate demand of capital (I use Gauss-Seidel algorithm for updating).
12. Check if $T$ is large enough. Check if the aggregate supply of capital (chosen at $T - 1$) is close to the aggregate demand of the stationary Solowian economy,

$$|\hat{K}^S_T - K_T| < \epsilon$$  \hspace{1cm} (21)

If (21) holds, we are done. Otherwise go to step 1 and increase $T$. 