

SUPPLEMENT TO “AN EQUILIBRIUM MODEL OF THE AFRICAN HIV/AIDS EPIDEMIC”

(Econometrica, Vol. 87, No. 4, July 2019, 1081–1113)

JEREMY GREENWOOD

Department of Economics, University of Pennsylvania

PHILIPP KIRCHER

Department of Economics, EUI and School of Economics, University of Edinburgh

CEZAR SANTOS

Escola Brasileira de Economia e Finanças, FGV EPGE and Economics and Research Department, Banco de Portugal

MICHÈLE TERTILT

Department of Economics, University of Mannheim

APPENDIX A: TIMING OF EVENTS

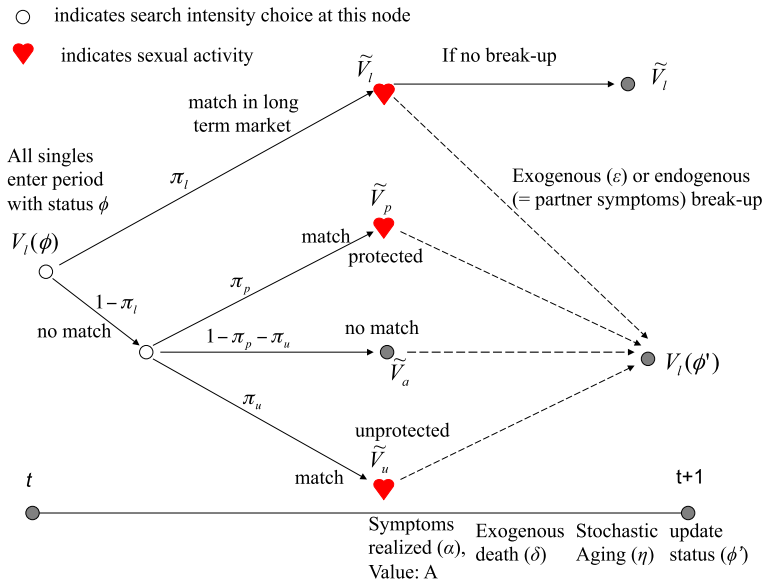


FIGURE 5.—Timing of events.

Jeremy Greenwood: impasse@jeremygreenwood.net
 Philipp Kircher: philipp.kircher@eui.eu
 Cezar Santos: cezarsantos.econ@gmail.com
 Michèle Tertilt: tertilt@uni-mannheim.de

APPENDIX B: DATA

Most of the empirical moments are based on information collected from the interviews of individuals conducted for the Malawi Demographic and Health Survey (MDHS) in 2004, carried out by the Malawi National Statistical Office. In this nationally representative survey, 11,698 women aged 15 to 49 and 3261 men aged 15 to 54 were interviewed. Means are calculated using sample weights. For several figures, means are calculated by age. Since men are underrepresented in the survey, separate means are calculated by sex, and then averaged. Whenever sources other than the MDHS are used, it will be indicated. More details on each figure follow. For the interested reader, the details also include the variable names corresponding to each question.

- Figure 1a: HIV is defined as “Prevalence of HIV, total (% of population ages 15–49).” ART is defined as “Antiretroviral therapy coverage (% of people living with HIV).” HIV data come from UNAIDS and ART coverage is taken from the World Development Indicators.

- Figure 4 is based on the MDHS for the years 1992, 1996, 2000, 2004, 2010, and 2015. The question asked is “What can a person do (to avoid getting AIDS)?” and then various options are given. For 1996, the question on mosquitoes was not asked in a consistent way, and in 2015, no information related to whether abstinence reduces HIV risk was collected. Fractions were computed based on the entire sample (males and females); sample weights were used. The exact list of variables used is as follows. Abstinence: women: s808a (1992), qa509a (1996), v754b (2000–2010), men: mv754b (1992), qma509a (1996), mv754b (2000–2010). Condom use: women: s808c (1992), qa504 (1996), v754c (2000–2015) men: mv754c (1992), qma504 (1996), mv754c (2000–2015). Mosquitoes: women: s804g (1992), v754jp (2000–2015) men: sm504g (1992), mv754jp (2000–2015).

- Figure 6: HIV rate—men versus women, model versus data. In order to calculate the HIV rates by age (MDHS 2004: v012/mv012) and gender, individual information from the MDHS 2004 is matched with the HIV test results (MDHS 2004: hiv03) for those people who agreed on doing the test along with the interview (since not everyone agreed, the sample size is smaller here: 2,404 men and 2,864 women). The resulting HIV rates are smoothed using a third-order polynomial.

- Figure 7: Fraction ever married—model versus data. The fraction of people who have ever been married is derived by dividing the number of people who either are currently married (including cohabitation) or have been formerly married by all people. The corresponding question is “Have you ever been married or lived with a man/woman” (MDHS 2004: v/mv502).

- Figure 8: Sexual behavior by age—model versus data. Singles: Those men and women who reported that they have never been married or are widowed, divorced (living or not living together) are defined as singles (MDHS 2004: v/mv501).

Casual sex: To identify the fraction of sex that occurs in casual relationships, all men and women are considered who had sex in the last year (MDHS 2004: v/mv529). These people are asked with whom they had sex (MDHS 2004: v/mv767a). They are also asked whether they had sex with a second (MDHS 2004: v/mv761b, v/mv767b) and third (MDHS 2004: v/mv761c, v/mv767c) partner. If one of the sex partners was not the spouse or cohabiting partner, then the sex in the last year is categorized as casual sex. Men in addition are asked whether they have ever paid for sex (MDHS 2004: mv792). Those men who have paid for sex in the last year are also defined as being active in the short-term market.

- Figure 9: Deaths by HIV/AIDS by age—model versus data. The data on deaths caused by HIV/AIDS are taken from [Bowie \(2006\)](#), pp. 31–42. He reported the frac-

tion of HIV/AIDS related deaths by age groups, based on the WHO Global Burden of Disease Malawi from 2002.

- Table I: Parameters Chosen Outside the Model. All sources are described in the text.
- Table III: Targeted Moments. The data on the prevalence of HIV/AIDS in Malawi derive from the Demographic and Health Surveys' (MDHS) Final Survey for Malawi in 2004. See MDHS (2004, Table 12.3). The fraction of sex that is casual is the proportion of people—averaged across men and women—who had sex with a non-marital, non-cohabiting partner during the last year, conditional on being sexually active, and is taken from MDHS (2004, Table 11.9). Condom usage for short-term sex also derives from MDHS (2004, Table 11.9)—and is averaged across men and women. The fraction of singles who have casual sex is reported in MDHS (2004, Tables 6.71 and 6.72) and corresponds to the weighted average of never married and divorced/separated/widowed men and women. The proportion of the population that is single is contained in MDHS (2004, Table 6.1), where single is interpreted as anyone who is not currently married nor cohabiting, averaged across men and women. The fraction of males and females that has ever been married by a certain age is the same as in Figure 7. The [World Health Organisation \(2008\)](#) reports that 29% of all deaths in Malawi in 2004 were due to HIV/AIDS.
- Table IV: The cross-country circumcision data come from [Ahuja, Wendell, and Werker \(2009\)](#). The statistics for HIV rates come from UNAIDS, while the numbers for GDP per capita and ART coverage come from the World Bank Development Indicators. The rates for syphilis seropositivity relate to data among antenatal care attendees from the WHO Global Health Observatory. The fractions of populations of different religions are given by the Global Religious Futures Project of the Pew Research Center. Condom prices for different countries are reported in the Global Directory of Condom Social Marketing Projects and Organisations (UNAIDS).
- Table X: Incidence and prevalence numbers are taken from UNAIDS. All numbers on sexual behavior are computed from the MDHS. The 2004 numbers are identical to those in Table III and were calculated as described above. The numbers for 1996 were computed in exactly the same way using data from the MDHS 1996 instead. Model numbers are based on the model simulations.

APPENDIX C: THEORY

C.1. Value Functions for Young Individuals, $d = \iota$

The value functions for young individuals follow a similar structure as those for old individuals, namely, equations (1) to (6). The required adjustments are outlined in the main body in connection with (1).

In particular, for young abstinent individuals of health status ϕ , the analog to (1) replaces the high discount factor, β , with the low discount factor, ι , and treats continuation values as the average of the continuation with a low and a high discount factor, so that

$$\begin{aligned} \tilde{V}_a^\iota(\phi, x) = & \ln(y) + \alpha_\phi \iota A \\ & + (1 - \alpha_\phi) \iota \left\{ \frac{Q(\phi)[\eta V_i^\beta(t, x) + (1 - \eta)V_i^\iota(t, x)]}{+ [1 - Q(\phi)][\eta V_i^\beta(\phi, x) + (1 - \eta)V_i^\iota(\phi, x)]} \right\}. \end{aligned} \quad (9)$$

Similarly, for short-term sex, either for infected or treated individuals ($\phi = 0, t$), the analog to (2) is

$$\begin{aligned} \tilde{V}_s^t(\phi, x) &= \ln(y - z_s) + pI(s) + u[1 - I(s)] + \alpha_\phi \iota A \\ &+ (1 - \alpha_\phi) \iota \left\{ \frac{Q(\phi)[\eta V_l^\beta(t, x) + (1 - \eta)V_l^t(t, x)]}{+ [1 - Q(\phi)][\eta V_l^\beta(\phi, x) + (1 - \eta)V_l^t(\phi, x)]} \right\}, \end{aligned} \quad (10)$$

for $s = p, u$. For young healthy individuals ($\phi = 1$), the analog to (3) is

$$\begin{aligned} \tilde{V}_s^t(1, x) &= \ln(y - z_s) + pI(s) + u[1 - I(s)] \\ &+ \sum_{\hat{\phi}} R_s(\hat{\phi})[1 - \gamma_s(\hat{\phi})] \\ &\times \chi(c) \iota \left\{ \frac{q[\eta V_l^\beta(t, x) + (1 - \eta)V_l^t(t, x)]}{+ (1 - q)[\eta V_l^\beta(0, x) + (1 - \eta)V_l^t(0, x)]} \right\} \\ &+ \left\{ 1 - \sum_{\hat{\phi}} R_s(\hat{\phi})[1 - \gamma_s(\hat{\phi})] \chi(c) \right\} \\ &\times \iota [\eta V_l^\beta(1, x) + (1 - \eta)V_l^t(1, x)]. \end{aligned} \quad (11)$$

For long-term sex, note that the transition probabilities $Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, c, \hat{c})$ in Appendix C.2 are not affected by the discount factor, and therefore the young individual's analog of (6) is

$$\begin{aligned} \tilde{V}_l^t(\phi, \hat{\phi}, \hat{c}, x) &= \ln(y - z_l) + u + l + \alpha_\phi \iota A \\ &+ (1 - \alpha_\phi)(1 - \epsilon)(1 - \delta)(1 - \alpha_{\hat{\phi}}) \iota \\ &\times \sum_{\phi', \hat{\phi}'} Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, c, \hat{c}) \left[\frac{\eta \tilde{V}_l^\beta(\phi', \hat{\phi}', x)}{+ (1 - \eta) \tilde{V}_l^t(\phi', \hat{\phi}', x)} \right] \\ &+ (1 - \alpha_\phi)[1 - (1 - \epsilon)(1 - \delta)(1 - \alpha_{\hat{\phi}})] \iota \\ &\times \sum_{\phi', \hat{\phi}'} Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, c, \hat{c}) \left[\frac{\eta V_l^\beta(\phi', x)}{+ (1 - \eta)V_l^t(\phi', x)} \right]. \end{aligned} \quad (12)$$

C.2. Transition Probabilities in Long-Term Relationships

The transition probabilities, $Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, c, \hat{c})$, from the situation where a relationship is currently characterized by the quadruple $(\phi, \hat{\phi}, c, \hat{c})$ to one where the couple's health status next period is $(\phi', \hat{\phi}')$, are now presented. Start with the situation where the person is currently healthy ($\phi = 1$) but his partner is infected ($\hat{\phi} \in \{0, t\}$). The following

lists all possible cases for this situation:

$$\begin{aligned}
Y(1, t|1, \widehat{\phi}, c, \widehat{c}) &= \{1 - [1 - \gamma_u(\widehat{\phi})]\chi(c)\}Q(\widehat{\phi}); \\
Y(1, 0|1, \widehat{\phi}, c, \widehat{c}) &= \{1 - [1 - \gamma_u(\widehat{\phi})]\chi(c)\}[1 - Q(\widehat{\phi})]; \\
Y(0, t|1, \widehat{\phi}, c, \widehat{c}) &= [1 - \gamma_u(\widehat{\phi})]\chi(c)(1 - q)Q(\widehat{\phi}); \\
Y(0, 0|1, \widehat{\phi}, c, \widehat{c}) &= [1 - \gamma_u(\widehat{\phi})]\chi(c)(1 - q)[1 - Q(\widehat{\phi})]; \\
Y(t, t|1, \widehat{\phi}, c, \widehat{c}) &= [1 - \gamma_u(\widehat{\phi})]\chi(c)qQ(\widehat{\phi}); \\
Y(t, 0|1, \widehat{\phi}, c, \widehat{c}) &= [1 - \gamma_u(\widehat{\phi})]\chi(c)q[1 - Q(\widehat{\phi})].
\end{aligned} \tag{13}$$

The chance that the individual remains healthy is given by $\{1 - [1 - \gamma_u(\widehat{\phi})]\chi(c)\}$, while the odds that they will not are $[1 - \gamma_u(\widehat{\phi})]\chi(c)$. In the latter case, the person will get treated with probability q and not with $1 - q$. The term $Q(\widehat{\phi})$ reflects the odds of the partner being treated, while the one $1 - Q(\widehat{\phi})$ gives the odds that the companion is not.

The symmetric probabilities for when the partner is healthy ($\widehat{\phi} = 1$) but the individual is infected or treated ($\phi = 0, t$) are

$$\begin{aligned}
Y(t, 1|\phi, 1, \widehat{c}, c) &= \{1 - [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})\}Q(\phi); \\
Y(0, 1|\phi, 1, \widehat{c}, c) &= \{1 - [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})\}[1 - Q(\phi)]; \\
Y(t, 0|\phi, 1, \widehat{c}, c) &= [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})(1 - q)Q(\phi); \\
Y(0, 0|\phi, 1, \widehat{c}, c) &= [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})(1 - q)[1 - Q(\phi)]; \\
Y(t, t|\phi, 1, \widehat{c}, c) &= [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})qQ(\phi); \\
Y(0, t|\phi, 1, \widehat{c}, c) &= [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})q[1 - Q(\phi)].
\end{aligned} \tag{14}$$

In the above equations, the term $[1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})$ gives the odds that the partner will become infected.

Next, both partners might be infected ($\phi \in \{0, t\}$ and $\widehat{\phi} \in \{0, t\}$), in which case a healthy future is no longer an option. The only question that remains is whether the future sees treatment or not, so that

$$Y(\phi', \widehat{\phi}'|\phi, \widehat{\phi}, c, \widehat{c}) = \begin{cases} [1 - Q(\phi)]Q(\widehat{\phi}), & \text{for } (\phi', \widehat{\phi}') = (0, t); \\ [1 - Q(\phi)][1 - Q(\widehat{\phi})], & \text{for } (\phi', \widehat{\phi}') = (0, 0); \\ Q(\phi)Q(\widehat{\phi}), & \text{for } (\phi', \widehat{\phi}') = (t, t); \\ Q(\phi)[1 - Q(\widehat{\phi})], & \text{for } (\phi', \widehat{\phi}') = (t, 0). \end{cases} \tag{15}$$

The last remaining case is where both partners are currently healthy. Here, $Y(1, 1|1, 1, c, \widehat{c}) = 1$, implying that $Y(\phi', \widehat{\phi}'|1, 1, c, \widehat{c}) = 0$, when $\phi' \in \{0, t\}$ and/or $\widehat{\phi}' \in \{0, t\}$.

C.3. Stationary Equilibrium

A stationary equilibrium for the developed framework is formulated now. First, the equilibrium distributions for singles will be specified. Let $\mathcal{S}^d(\phi; x)$ represent the (non-normalized) stationary distribution of singles at the beginning of a period. It denotes the

measure of type- x singles that have health status ϕ and discount factor d . Similarly, let $\mathcal{L}^d(\phi, \widehat{\phi}; x, \widehat{x})$ stand for the measure of long-term relationships for type- x individuals with health status ϕ and discount factor d who are coupled with a partner of type \widehat{x} and health status $\widehat{\phi}$. Given some distributions \mathcal{S} and \mathcal{L} of singles and married people, the sexual behavior of individuals according to their decision rule Π [$\Pi_r^d = \Pi_r^d(\phi, x)$ for each status and type] gives rise to a new distribution of singles and married people, which can be described by a mapping \mathbf{T} that is characterized fully in Section C.4. In steady state, the distributions of singles and married people remain constant, and are determined by a fixed point of this operator:

$$(\mathcal{S}^\beta, \mathcal{L}^\beta, \mathcal{S}^\iota, \mathcal{L}^\iota) = \mathbf{T}(\mathcal{S}^\beta, \mathcal{L}^\beta, \mathcal{S}^\iota, \mathcal{L}^\iota; \Pi). \quad (16)$$

Next, the expectations over the fraction of types in each market have to be consistent with the aggregation of individual choices in equilibrium. It is now useful to introduce the subscript g (for $g = f, m$) to a function or variable to denote the gender of the person in question. The number of market participants for sexual activity r ($= l, p, u$), who are of gender g , type- x with status ϕ , and discount factor d , is given by

$$\mathcal{M}_{g,r}^d(\phi, x) \equiv \begin{cases} \Pi_{g,l}^d(\phi, x) \mathcal{S}_g^d(\phi; x), & \text{if } r = l, \\ [1 - \Pi_{g,l}^d(\phi, x)] \Pi_{g,r}^d(\phi, x) \mathcal{S}_g^d(\phi; x), & \text{if } r = p, u. \end{cases} \quad (17)$$

The number of market participants equals the number of singles times their probability of participating in a particular market. For the short-term market, this also entails the probability of not previously finding a long-term partner within the current period. Then the fraction $R_{s,r}(\phi)$ of agents with health status ϕ in market s of gender g is given by

$$R_{g,s}(\phi) = \frac{\sum_d \sum_x \mathcal{M}_{g,s}^d(\phi, x)}{\sum_d \sum_x \sum_{\phi'} \mathcal{M}_{g,s}^d(\phi', x)}, \quad \text{for all } g \text{ and } s \in \{p, u\}. \quad (18)$$

For the long-term market, the relevant fraction is given by

$$R_{g,l}(\phi, c) = \frac{\sum_d \sum_x \mathcal{M}_{g,l}^d(\phi, x) \mathcal{I}(c(x) = c)}{\sum_d \sum_x \sum_{\phi'} \mathcal{M}_{g,l}^d(\phi', x)}, \quad \text{for all } g, \quad (19)$$

where $c(x)$ is a slight abuse of notation that denotes the circumcision status of the agent that is contained in his or her type x . The function $\mathcal{I}(\cdot)$ is an indicator function that takes the value of 1 if its argument is true. Note that $R_{f,s}(\phi)$ and $R_{f,l}(\phi, c)$ denote the distributions among women, which are relevant for *men* when determining their odds of getting infected. Similarly, $R_{m,s}(\phi)$ and $R_{m,l}(\phi, c)$ refer to the odds among men, but are relevant for *women* when making their decisions.

Market clearing requires that the number of female participants equals the number of male participants in any market:

$$\sum_d \sum_x \sum_{\phi} \mathcal{M}_{f,r}^d(\phi, x) = \sum_d \sum_x \sum_{\phi} \mathcal{M}_{m,r}^d(\phi, x), \quad \text{for all } r. \quad (20)$$

Additionally, a transfer paid by one gender on a market is a transfer earned by the other so that

$$z_{f,r} + z_{m,r} = 0, \quad \text{for all } r. \quad (21)$$

This leads to the following formal definition of equilibrium.

DEFINITION: A stationary equilibrium is described by a set of decision rules for search effort, $\Pi_{g,r}^d(\phi, x)$, a set of transfer payments, $z_{g,r}$, a set of stationary distributions, $\mathcal{S}_g^d(\phi; x)$ and $\mathcal{L}_g^d(\phi, \hat{\phi}; x, \hat{x})$, and status/type prevalence in each market, $R_{g,s}(\phi)$ and $R_{g,l}(\phi, c)$, for all $d = \{\iota, \beta\}$, $g \in \{f, m\}$, $r \in \{l, p, u\}$, $s \in \{p, u\}$, such that:

1. The decision rules for search intensities, $\Pi_{g,r}^d(\phi, x)$, satisfy the appropriately gender subscripted versions of the generic problems (4) and (8), taking as given transfer payments and HIV/AIDS prevalence rates.
2. The stationary distributions, $\mathcal{S}_g^d(\phi; x)$ and $\mathcal{L}_g^d(\phi, \hat{\phi}; x, \hat{x})$, solve the appropriately gender subscripted version of (16).
3. The distributions over health status for each market, $R_{g,s}(\phi)$ and $R_{g,l}(\phi, c)$, are given by (18) and (19) using (17).
4. The transfer payments, $z_{r,g}$, are such that the markets for all types of relationships clear according to (20). Additionally, the flow of transfers across the genders must balance as specified by (21).

C.4. Stationary Distributions

The transition operator \mathbf{T} defined in Section C.3 is now fully characterized. Before starting, recall that $\mathcal{I}(\cdot)$ is an indicator function that takes the value of 1 if its argument is true, and 0 otherwise. Focus on a particular gender so that the gender subscript can be omitted. Again, $\mathcal{S}^d(\phi; x)$ denotes the beginning-of-period mass of singles with discount factor d , health status ϕ , and type x . Next, $\mathcal{L}^d(\phi, \hat{\phi}; x, \hat{x})$ represents the beginning-of-period measure of long-term relationships for individuals of type x with health status ϕ and discount factor d who are coupled with a partner of type \hat{x} and health status $\hat{\phi}$. Finally, \mathcal{A} is the mass of individuals with the final symptoms of AIDS. The sexual behavior of individuals is governed by their decision rules, $\pi_r^d = \Pi_r^d(\phi, x)$.

Assume temporarily that only people who are of health status $\phi = t$ will be treated next period. Moreover, suppose that the individual's discount factor does not change. Given the beginning of period distributions \mathcal{S}^d , \mathcal{L}^d , and \mathcal{A} , one can compute the distributions at the beginning of next period under these assumptions. Call these \mathcal{S}'^d , \mathcal{L}'^d , and \mathcal{A}' . These will be adjusted subsequently for changing treatment status and discount factors. Before proceeding, define the following variable to represent the infectiousness of each short-term market:

$$\hat{\theta}_s = \sum_{\hat{\phi}} R_s(\hat{\phi})[1 - \gamma_s(\hat{\phi})], \quad \text{for } s \in \{p, u\}. \quad (22)$$

First consider *next period's distribution of single individuals*. Take up first the distribution of healthy singles next period:

$$\begin{aligned} \mathcal{S}'^d(1, x) &= (1 - \delta) \\ &\times \left\{ \mathcal{S}^d(1, x)[1 - \Pi_l^d(1, x)] \right\} \left\{ 1 - \Pi_p^d(1, x) - \Pi_u^d(1, x) \right\} \end{aligned}$$

$$\begin{aligned}
& + \sum_s \Pi_s^d(1, x) [1 - \widehat{\theta}_s \chi(c)] \Big\} \\
& + \sum_{\widehat{\phi}, \widehat{x}} [\mathcal{L}^d(1, \widehat{\phi}; x, \widehat{x}) + R_l(\widehat{\phi}, \widehat{c}) \Pi_l^d(1, x) \mathcal{S}^d(1, x)] \{1 - [1 - \gamma_u(\widehat{\phi})] \chi(c)\} \\
& \times [1 - (1 - \delta)(1 - \alpha_{\widehat{\phi}})(1 - \varepsilon)] \Big\} \\
& + \mu(x) \mathcal{I}(d = \iota). \tag{23}
\end{aligned}$$

Singles survive into the next period with probability $(1 - \delta)$, as captured by the first line. The second and third lines account for healthy singles this period that continue as healthy singles next period. There are $\mathcal{S}^d(1, x)$ such singles this period. They remain healthy singles if they do not successfully enter the long-term market, which is represented by the term in the first bracket, and if they either do not enter the short-term market or enter but do not get infected, as presented by the terms in braces. The fourth and fifth lines account for those who exit from marriage as healthy singles. The terms in the first bracket give the stock of individuals married to a partner of status $\widehat{\phi}$ at the start of the period plus those singles who newly marry such a partner this period. They remain healthy with probability $\{1 - [1 - \gamma_u(\widehat{\phi})] \chi(c)\}$, but the marriage breaks up with the probability in the bracket on the fifth line, $[1 - (1 - \delta)(1 - \alpha_{\widehat{\phi}})(1 - \varepsilon)]$. The final line is the inflow of newborns.

Consider next the distribution of infected individuals without treatment next period:

$$\begin{aligned}
\mathcal{S}^{dI}(0, x) & = (1 - \delta) \\
& \times \left\{ \mathcal{S}^d(1, x) [1 - \Pi_l^d(1, x)] \sum_s \Pi_s^d(1, x) \widehat{\theta}_s \chi(c) \right. \\
& + \sum_{\widehat{\phi}, \widehat{x}} [\mathcal{L}^d(1, \widehat{\phi}; x, \widehat{x}) + R_l(\widehat{\phi}, \widehat{c}) \Pi_l^d(1, x) \mathcal{S}^d(1, x)] [1 - \gamma_u(\widehat{\phi})] \chi(c) \\
& \times [1 - (1 - \delta)(1 - \alpha_{\widehat{\phi}})(1 - \varepsilon)] \\
& + \mathcal{S}^d(0, x) (1 - \alpha_0) [1 - \Pi_l^d(0, x)] \\
& + (1 - \alpha_0) \sum_{\widehat{\phi}, \widehat{x}} [\mathcal{L}^d(0, \widehat{\phi}; x, \widehat{x}) + R_l(\widehat{\phi}, \widehat{c}) \Pi_l^d(0, x) \mathcal{S}^d(0, x)] \\
& \left. \times [1 - (1 - \delta)(1 - \alpha_{\widehat{\phi}})(1 - \varepsilon)] \right\}. \tag{24}
\end{aligned}$$

The first four lines detail the same elements as in the previous equation, but now healthy individuals only transit to the untreated infected state, $\phi = 0$. Line five captures currently infected singles, who do not develop final-stage symptoms with probability $1 - \alpha_0$ and who do not enter the long-term market with probability $1 - \Pi_l^d(0, x)$, and therefore survive as infected singles. Lines six and seven account for individuals that either started in marriage or got married, similar to lines three and four, except now these individuals are currently infected. Again, they return as infected singles, if they do not develop final-stage symptoms, and if the marriage does not survive.

Finally, the distribution of treated individuals next period is given by

$$\begin{aligned}
\mathcal{S}^d(t, x) &= (1 - \delta) \\
&\times \left\{ \mathcal{S}^d(t, x)(1 - \alpha_t)[1 - \Pi_l^d(t, x)] \right. \\
&+ (1 - \alpha_t) \sum_{\widehat{\phi}, \widehat{x}} [\mathcal{L}^d(t, \widehat{\phi}; x, \widehat{x}) + R_l(\widehat{\phi}, \widehat{c})\Pi_l^d(t, x)\mathcal{S}^d(t, x)] \\
&\left. \times [1 - (1 - \delta)(1 - \alpha_{\widehat{\phi}})(1 - \varepsilon)] \right\}. \tag{25}
\end{aligned}$$

The four lines here correspond to lines one, five, six, and seven in the previous expression. The reason the intermediate lines are dropped is the temporary assumption that only individuals who were already in treatment at the beginning of the period are eligible for treatment next period. This will be adjusted later.

The mass of individuals with final-stage symptoms next period is

$$\mathcal{A} = \sum_{d, \phi, x} (1 - \delta) \left\{ (1 - \delta_2)\mathcal{A} + \left[\mathcal{S}^d(\phi, x) + \sum_{\widehat{\phi}, \widehat{x}} \mathcal{L}^d(\phi, \widehat{\phi}, x, \widehat{x}) \right] \alpha_{\phi} \right\}. \tag{26}$$

It comprises those that started the period in the final stage and neither died of natural causes nor of AIDS-related reasons. It also includes all other individuals who develop final-stage symptoms, which occurs with probability α_{ϕ} .

Now consider the *distribution of long-term marriages next period* for type- x individuals with health status ϕ and discount factor d who are coupled with a type- \widehat{x} partner with health status $\widehat{\phi}$. Start with a marriage between two healthy individuals. The marriage survives if neither spouse dies of natural causes or the marriage does not break up exogenously. The stock of marriages next period includes marriages in the current period made up from both old and new ones. The mass of such marriages next period is

$$\begin{aligned}
&\mathcal{L}^d(1, 1; x, \widehat{x}) \\
&= (1 - \delta)^2(1 - \varepsilon) \\
&\times \left\{ \mathcal{L}^d(1, 1; x, \widehat{x}) + [1 - R_l(0, \widehat{c}) - R_l(t, \widehat{c})]\Pi_l^d(1, x)\mathcal{S}^d(1, x) \right\}. \tag{27}
\end{aligned}$$

Next, move onto the case where the partner is infected or treated. The terms are similar to before, only now marriages break up for one additional reason, namely, the partner develops AIDS (probability $\alpha_{\widehat{\phi}}$). The person stays healthy with probability $\{1 - [1 - \gamma_u(\widehat{\phi})]\chi(c)\}$. So,

$$\begin{aligned}
\mathcal{L}^d(1, \widehat{\phi}; x, \widehat{x}) &= (1 - \delta)^2(1 - \varepsilon)(1 - \alpha_{\widehat{\phi}}) \{1 - [1 - \gamma_u(\widehat{\phi})]\chi(c)\} \\
&\times [\mathcal{L}^d(1, \widehat{\phi}; x, \widehat{x}) + R_l(\widehat{\phi}, \widehat{c})\Pi_l^d(1, x)\mathcal{S}^d(1, x)]. \tag{28}
\end{aligned}$$

A similar expression obtains for partnerships where the individual under consideration is infected or treated but the partner is healthy:

$$\begin{aligned}
\mathcal{L}^d(\phi, 1; x, \widehat{x}) &= (1 - \delta)^2(1 - \varepsilon)(1 - \alpha_{\phi}) \{1 - [1 - \widehat{\gamma}_u(\phi)]\chi(\widehat{c})\} \\
&\times [\mathcal{L}^d(\phi, 1; x, \widehat{x}) + R_l(1, \widehat{c})\Pi_l^d(\phi, x)\mathcal{S}^d(\phi, x)]. \tag{29}
\end{aligned}$$

In the case where both spouses are infected or treated, there is no longer the need to take into account the transmission of the disease. Now there is a chance that either person will develop symptoms. So,

$$\begin{aligned} \mathcal{L}^{nd}(\phi, \widehat{\phi}; x, \widehat{x}) &= (1 - \delta)^2(1 - \varepsilon)(1 - \alpha_\phi)(1 - \alpha_{\widehat{\phi}}) \\ &\quad \times [\mathcal{L}^d(\phi, \widehat{\phi}; x, \widehat{x}) + R_t(\widehat{\phi}, \widehat{c})\Pi_t^d(\phi, x)\mathcal{S}^d(\phi, x)]. \end{aligned} \quad (30)$$

Finally, introduce the *adjustments for a changing discount factor and changing treatment status*, which are mechanical parts of the model that do not involve any choices. Incorporate discount factor changes first. To do this, let D^{nd} represent generic auxiliary distributions that result from incorporating the transitions from the previous D^d due to changing discount factors. High-discount-factor individuals stay with a high discount factor, but low-discount-factor people switch to a high discount factor with probability η . Hence,

$$D^{n\beta}(\phi, \dots) = D^{\beta}(\phi, \dots) + \eta D^u(\phi, \dots), \quad (31)$$

$$D^{nu}(\phi, \dots) = (1 - \eta)D^i(\phi, \dots). \quad (32)$$

To give examples, $\mathcal{S}^{n\beta}(\phi, x) = \mathcal{S}^{\beta}(\phi, x) + \eta\mathcal{S}^u(\phi, x)$ counts the number of type- x singles of health status ϕ that end up with the high discount, β . Another example would be $\mathcal{L}^{nu}(\phi, \widehat{\phi}; x, \widehat{x}) = (1 - \eta)\mathcal{L}^u(\phi, \widehat{\phi}; x, \widehat{x})$.

The analysis focuses on steady states for the model. Therefore, the fixed point of the operator \mathbf{T} in (16) is being sought. The stationary distributions for singles and marrieds can now be recovered by taking into account changes in treatment status, since infected individuals with status 0 change to a treated status t with probability q :

$$\mathcal{S}^d(1, x) = \mathcal{S}^{nd}(1, x),$$

$$\mathcal{S}^d(0, x) = \mathcal{S}^{nd}(0, x)(1 - q),$$

$$\mathcal{S}^d(t, x) = \mathcal{S}^{nd}(0, x)q + \mathcal{S}^{nd}(t, x),$$

$$\mathcal{L}^d(1, 1, x, \widehat{x}) = \mathcal{L}^{nd}(1, 1, x, \widehat{x}),$$

$$\mathcal{L}^d(1, 0, x, \widehat{x}) = \mathcal{L}^{nd}(1, 0, x, \widehat{x})(1 - q),$$

$$\mathcal{L}^d(0, 1, x, \widehat{x}) = \mathcal{L}^{nd}(0, 1, x, \widehat{x})(1 - q),$$

$$\mathcal{L}^d(0, 0, x, \widehat{x}) = \mathcal{L}^{nd}(0, 0, x, \widehat{x})(1 - q)^2,$$

$$\mathcal{L}^d(1, t, x, \widehat{x}) = \mathcal{L}^{nd}(1, 0, x, \widehat{x})q + \mathcal{L}^{nd}(1, t, x, \widehat{x}),$$

$$\mathcal{L}^d(t, 1, x, \widehat{x}) = \mathcal{L}^{nd}(0, 1, x, \widehat{x})q + \mathcal{L}^{nd}(t, 1, x, \widehat{x}),$$

$$\mathcal{L}^d(0, t, x, \widehat{x}) = \mathcal{L}^{nd}(0, t, x, \widehat{x})(1 - q) + \mathcal{L}^{nd}(0, 0, x, \widehat{x})(1 - q)q,$$

$$\mathcal{L}^d(t, 0, x, \widehat{x}) = \mathcal{L}^{nd}(t, 0, x, \widehat{x})(1 - q) + \mathcal{L}^{nd}(0, 0, x, \widehat{x})q(1 - q),$$

$$\mathcal{L}^d(t, t, x, \widehat{x}) = \mathcal{L}^{nd}(t, t, x, \widehat{x}) + \mathcal{L}^{nd}(0, t, x, \widehat{x})q + \mathcal{L}^{nd}(t, 0, x, \widehat{x})q + \mathcal{L}^{nd}(0, 0, x, \widehat{x})q^2.$$

The right-hand sides of these equations together with (23) to (32) fully describe the fixed point of the operator \mathbf{T} in (16).

APPENDIX D: DETAILS ON MODEL EXTENSIONS

D.1. *The Diffusion of Better Information*

To capture uninformed individuals, consider a type- x person with $i = 0$. Let $\hat{s} \in \{a, p, u\}$ and define $\hat{I}(\hat{s}) = 1$, for $\hat{s} = p$, and $\hat{I}(\hat{s}) = 0$, otherwise. Likewise, define $J(\hat{s}) = 0$, if $\hat{s} = a$, and $J(\hat{s}) = 1$, otherwise. If healthy, the value from short-term sex, for $\hat{s} = \{a, u, p\}$, is now given by

$$\begin{aligned} \tilde{V}_s^\beta(1, x) &= \ln(y - z_s) + \{p\hat{I}(\hat{s}) + u[1 - \hat{I}(\hat{s})]\}J(\hat{s}) \\ &\quad + \sum_{\hat{\phi}} R_u(\hat{\phi})[1 - \gamma_u(\hat{\phi})]\beta[qV_i^\beta(t, x) + (1 - q)V_i^\beta(0, x)] \\ &\quad + \left\{1 - \sum_{\hat{\phi}} R_u(\hat{\phi})[1 - \gamma_u(\hat{\phi})]\right\}\beta V_i^\beta(1, x), \end{aligned} \quad (33)$$

where $z_a = 0$. Compared to the value function for informed individuals (3), uninformed people perceive all sex as being as risky as unprotected sex without circumcision. In the case of abstinence, the uninformed now worry about infection even when they do not have sex—cf. (1).

In the long-term market, an uninformed individual thinks that transmissions are governed as if people are not circumcised. That means that, for a uninformed type- x individual (so that $i = 0$),

$$\begin{aligned} \tilde{V}_i^\beta(\phi, \hat{\phi}, \hat{c}, x) &= \ln(y - z_i) + u + l + \alpha_\phi \beta A \\ &\quad + (1 - \alpha_\phi)(1 - \epsilon)(1 - \delta)(1 - \alpha_{\hat{\phi}})\beta \sum_{\phi', \hat{\phi}'} Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, 0, 0) \tilde{V}_i^\beta(\phi', \hat{\phi}', \hat{c}, x) \\ &\quad + (1 - \alpha_\phi)[1 - (1 - \epsilon)(1 - \delta)(1 - \alpha_{\hat{\phi}})]\beta \sum_{\phi', \hat{\phi}'} Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, 0, 0) V_i^\beta(\phi', x). \end{aligned}$$

(Note that c and \hat{c} have been set to 0 in the transition probability Y .) Similar adjustments need to be made for young uninformed type- x individuals. Now,

$$\begin{aligned} \tilde{V}_s^\iota(1, x) &= \ln(y - z_s) + \{p\hat{I}(\hat{s}) + u[1 - \hat{I}(\hat{s})]\}J(\hat{s}) \\ &\quad + \sum_{\hat{\phi}} R_u(\hat{\phi})[1 - \gamma_u(\hat{\phi})]\iota \left\{ \begin{aligned} &q[\eta V_i^{\beta\iota}(t, x) + (1 - \eta)V_i^{\iota\iota}(t, x)] \\ &+ (1 - q)[\eta V_i^{\beta\iota}(0, x) + (1 - \eta)V_i^{\iota\iota}(0, x)] \end{aligned} \right\} \\ &\quad + \left\{1 - \sum_{\hat{\phi}} R_u(\hat{\phi})[1 - \gamma_u(\hat{\phi})]\right\}\iota [\eta V_i^{\beta\iota}(1, x) + (1 - \eta)V_i^{\iota\iota}(1, x)], \end{aligned}$$

for $\hat{s} = \{a, u, p\}$. Last, the value function for a young uninformed individual in a long-term relationship is

$$\begin{aligned} \tilde{V}_i^\iota(\phi, \hat{\phi}, \hat{c}, x) &= \ln(y - z_i) + u + l + \alpha_\phi \iota A \\ &\quad + (1 - \alpha_\phi)(1 - \epsilon)(1 - \delta)(1 - \alpha_{\hat{\phi}})\iota \end{aligned}$$

TABLE XI
IMPROVED INFORMATION—MODEL VERSUS DATA

	Bench.	Condoms	Circumcision	ART		STDs
		$p = 5.5$	100%	$q = 0.01$	$q = 0.075$	$\gamma_u^m = 0.9$
Panel (a): 1996 benchmark						
HIV prevalence, %	14.4	20.7	4.5	12.7	7.0	11.1
Sex that is casual, %	19.8	34.6	26.2	21.6	35.0	20.2
Condom use (singles), %	27.9	48.8	25.8	26.4	26.0	26.4
Fraction of singles, %	47.4	58.9	50.3	47.5	58.1	46.2
Non-abstinent singles, %	66.8	72.2	82.1	73.1	86.1	71.7
Panel (b): 2004 benchmark						
HIV prevalence, %	10.3	15.8	5.6	11.3	8.1	9.5
Sex that is casual, %	15.7	34.0	28.9	20.5	41.5	18.7
Condom use (singles), %	32.8	59.2	22.4	27.2	24.1	27.6
Fraction of singles, %	48.0	62.4	56.7	51.1	65.7	49.6
Non-abstinent singles, %	53.6	66.4	75.6	62.5	83.6	60.3

$$\begin{aligned}
& \times \sum_{\phi', \hat{\phi}'} Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, 0, 0) \left[\begin{array}{c} \eta \tilde{V}_l^\beta(\phi', \hat{\phi}', x) \\ + (1 - \eta) \tilde{V}_l^\beta(\phi', \hat{\phi}', x) \end{array} \right] \\
& + (1 - \alpha_\phi) [1 - (1 - \epsilon)(1 - \delta)(1 - \alpha_{\hat{\phi}})] \iota \\
& \times \sum_{\phi', \hat{\phi}'} Y(\phi', \hat{\phi}' | \phi, \hat{\phi}, 0, 0) \left[\begin{array}{c} \eta V_l^\beta(\phi', x) \\ + (1 - \eta) V_l^\beta(\phi', x) \end{array} \right].
\end{aligned}$$

Table XI reports the results of selected policy experiments using the environment with uninformed individual as a starting point—Panel (a): 1996 benchmark. For ease of comparison, the table also reports the results using the benchmark calibration—Panel (b): 2004 benchmark. As discussed in Section 6, in general, policies implemented when there are uninformed agents tend to have stronger effects. The reason is that uninformed agents do not change their behavior in response to the policy change.

D.2. Fertility

This little appendix describes how the model is parameterized when there is heterogeneous utility for fertility within marriage, as described in Section 5.3. Note that, conditional on an individual's circumcision status, there is only one source of permanent heterogeneity in the benchmark model: the time discount factors, β and ι . Since there is a one-to-one correspondence between β and ι , think about β as summarizing this heterogeneity. To keep the computational complexity fixed, leave the number of types constant. That is, for each type- x person with a different discount factor, β , assign a different level of utility from fertility $f(x)$; again, $f(x)$ is really just changing with β . Now, the instantaneous utility from a long-term relationship is given by $u + l + f(x)$.

Assume a quadratic form for the utility from fertility such that $f(x) = \theta_0 + \theta_1\beta + \theta_2\beta^2$, regardless of the value for c and ι . Note that θ_0 and l cannot be separately identified given the linear form of utility. Thus, three values must be calibrated: $\theta_0 + l$, θ_1 , and θ_2 . These are picked such that the new model fits the baseline data targets as closely as possible. The resulting parameters are: $\theta_0 = 28,207$, $\theta_1 = -58,380$, and $\theta_2 = 30,201$. The

TABLE XII
CALIBRATION—FERTILITY

Observation	Data	Model <i>Benchmark</i>	Model <i>w./Fertility</i>
HIV prevalence, %	11.8	10.3	10.0
Males	10	8.6	8.3
Females	13	12.1	11.8
Sex that is casual, % (of all)	18	16	18
Condom use for casual sex, %	39	33	29
Singles that had casual sex in past year, %	47	54	65
Singles, %	33	48	47
Married by age 22, %			
Males	58	57	54
Females	90	63	58
Married by age 50, %			
Males	100	98	78
Females	100	98	88
Deaths related to HIV, %	29	25	32

fertility benefit $f(x)$ ranges from -1.55 to 21.23 . Table XII reports results from this new parameterization.

APPENDIX E: LIFE-CYCLE IMPLICATIONS

Figure 6 plots HIV/AIDS prevalence by age.⁴³ Both the data and model agree on a hump-shaped infection pattern, despite the fact that individuals in the model become sexually active earlier than is observed in the Malawian data, which shifts the model's life-cycle predictions on HIV/AIDS infections to the left. The hump-shaped pattern is explained by two opposing forces. First, the rise in HIV/AIDS infection is due to the fact that older people have been sexually active for a longer period of time. Therefore, a larger percentage of the older population is infected with HIV/AIDS. Second, people who are infected early in life will die before they make it to old age. Put differently, people who have made it to old age must be those who have engaged in less risky sexual behavior and so are less likely to be infected with HIV/AIDS. This second effect explains the eventual drop in HIV/AIDS prevalence seen at older ages. Figure 6 also illustrates the differential patterns of infection between the sexes. The figure shows that women get infected earlier than men, in both the data and model.

Figure 7 compares the fraction of the population that has ever married in the model versus the data. The model generates the earlier marriage of women (relative to men) via their higher infection risk. Men eventually “catch up,” and by age 50 almost everyone is married, in both the data and model.

The model also does a very nice job of matching the decline in risky activity over the life cycle. Older people are less likely to be single; see Figure 8. As people age, they are thus less likely to engage in casual sex; this is also reported in Figure 8. The fact that the discount factor stochastically rises with age helps to generate this pattern.

An additional prediction of the model relates to the causes of death, since individuals may die either due to HIV/AIDS or due to other natural causes. Figure 9 compares the

⁴³The data are fitted with a third-order polynomial. The somewhat choppy raw data are due to the small sample sizes.

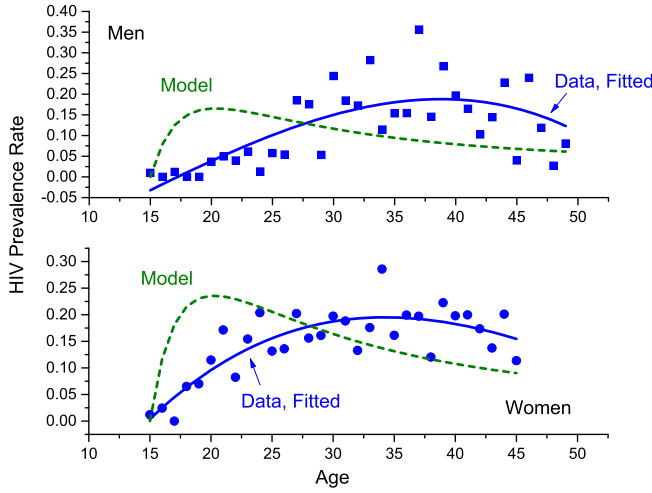


FIGURE 6.—HIV prevalence rate—men versus women, model versus data.

model prediction over the life cycle with its data counterpart. Both the data and model exhibit a hump-shaped pattern of HIV/AIDS-caused deaths; this is consistent with the hump-shaped pattern of infection rates.

APPENDIX F: ROBUSTNESS

This appendix provides some sensitivity analysis regarding the parameters estimated in Section 4. Recall that 11 parameters were chosen by fitting the model to a specific set of data moments from Malawi. These are listed on the different rows of Tables XIII and XIV. Each of these two tables has three columns besides the first that lists the parameters. The column labeled “HIV—Benchmark” provides the HIV prevalence rate when the pa-

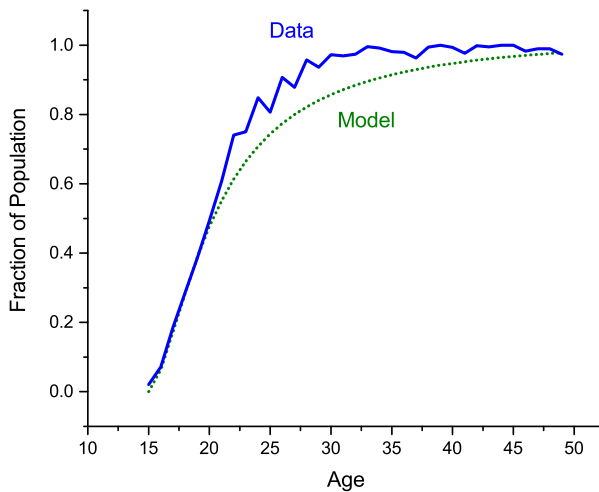


FIGURE 7.—Fraction of population ever married—model versus data.

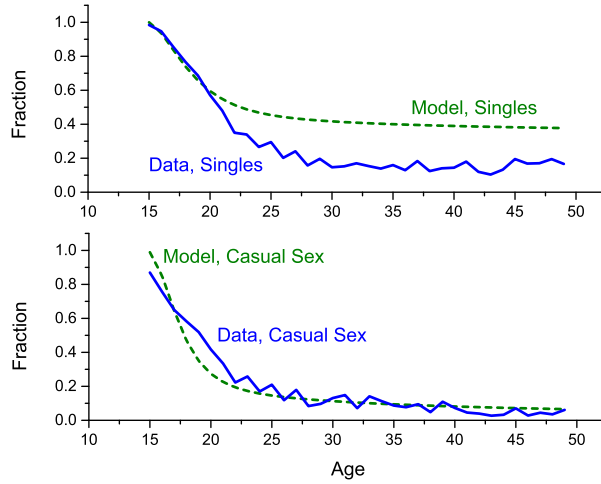


FIGURE 8.—Sexual behavior by age—model versus data.

parameter of each corresponding row is changed by 1% (Table XIII) or 10% (Table XIV).⁴⁴ The column “ Δ HIV—Circumcision (50%)” reports the change in the percentage HIV rate under the intervention that circumcises 50% of the males in the economy. Finally, the last column (Δ HIV—ART ($q = 5\%$)) presents the change in the percentage HIV rate when the infected have a 5% probability of receiving ART in each period.

Table XIII shows that the benchmark is quite robust when the parameters are changed by 1%. The HIV prevalence rate is always remarkably close to the 10.3% found in the benchmark calibration. Moreover, the results from the two main policy experiments (male circumcision and ART) are also very close to the changes found in the benchmark. Jux-

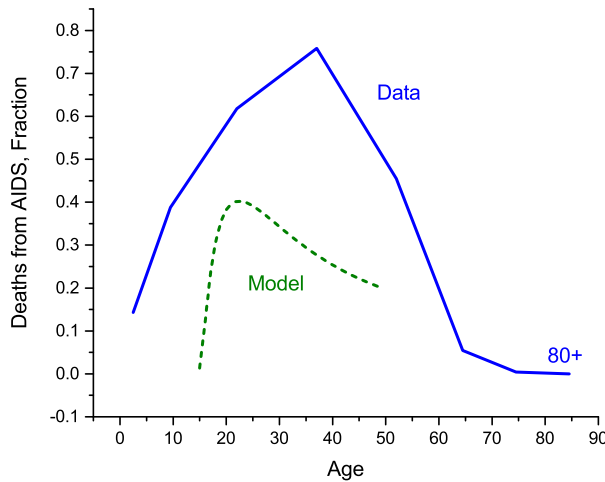


FIGURE 9.—Deaths by HIV/AIDS by age, fraction—model versus data.

⁴⁴To be precise, the rows for the discount factors (β_{\max} and β_{\min}) report changes on the discount rates $\rho = (1 - \beta)/\beta$.

TABLE XIII
ROBUSTNESS—1%

	HIV—Benchmark	Δ HIV—Circumcision (50%)	Δ HIV—ART ($q = 5\%$)
Main calibration	10.3	-1.2	-0.8
p	10.3	-1.2	-0.7
u	10.2	-1.2	-1.1
l	10.1	-1.2	-1.0
β_{\max}	10.3	-1.2	-0.8
β_{\min}	10.4	-1.3	-0.8
ι_{change}	10.2	-1.2	-0.7
A	10.3	-1.2	-0.9
η	10.2	-1.2	-0.7
ω_s	10.2	-1.2	-0.9
ω_l	10.3	-1.2	-0.7
κ	10.3	-1.2	-0.8

tapose these numbers with the ones reported in Table XIV, in which each parameter is changed by 10%. The percentage change now is considerably larger. Correspondingly, the HIV prevalence rate now changes compared with the main calibration. This suggests that, in order to fit the moments targeted in the calibration, the parameters should be close to the ones found in the estimation. At the same time, the percentage changes in the policy experiments are remarkably similar, even if individual parameters are changed by 10%.

APPENDIX G: COMPUTATIONAL DETAILS

A capsule summary of the numerical algorithm used to solve the benchmark model is provided here. There are two key steps. The first step involves solving the model for a given set of parameter values. In the second step, the algorithm picks the parameter values to match the model's output with the data targets as closely as possible. The first step proceeds as follows:

1. The static problems (4) and (8) that yield the meeting probabilities are solved. The solution to these problems implies that each π can be implicitly written as a nonlinear

TABLE XIV
ROBUSTNESS—10%

	HIV—Benchmark	Δ HIV—Circumcision (50%)	Δ HIV—ART ($q = 5\%$)
Main calibration	10.3	-1.2	-0.8
p	10.3	-1.2	-0.8
u	9.1	-1.5	0.0
l	8.8	-1.3	0.3
β_{\max}	10.3	-1.2	-0.8
β_{\min}	11.4	-1.5	-1.8
ι_{change}	9.0	-0.5	0.5
A	10.3	-1.2	-0.8
η	9.8	-1.1	-0.3
ω_s	9.8	-1.3	-0.5
ω_l	10.9	-1.3	-1.3
κ	10.1	-1.2	-0.7

function of the difference between either two \tilde{V} 's or a \tilde{V} and V . Given a grid of values for the \tilde{V} 's and V 's, the π 's can be computed at each grid point using the bisection method. The values for the π 's when the \tilde{V} 's and V 's lie off the grid can be obtained using an interpolation scheme.

2. One outer loop solves for the market-clearing prices using the NEWUOA algorithm. This algorithm picks the prices to minimize excess demand in the three relationship markets.

3. In an inner loop, the value functions and stationary distributions are determined computationally, given prices, using standard iterative procedures. First, the "matched" value functions (the \tilde{V} 's) are computed for each type of individual. Then, the ex ante value functions (the V 's) are calculated using a linear interpolation scheme for the π 's that employs the results from 1. The stationary distributions are computed using the formulas in Appendices C.3 and C.4.

In the second step, the parameter values are calibrated using a Pattern Search algorithm. The calibration algorithm and the solutions to the static problems in 1 are implemented in MATLAB, while the more computationally demanding loops in 2 and 3 are coded in FORTRAN.

REFERENCES

- AHUJA, A., B. WENDELL, AND E. WERKER (2009): "Male Circumcision and AIDS: The Macroeconomic Impact of a Health Crisis," Harvard Business School Working Paper, vol. 07-025. [3]
 BOWIE, C. (2006): "The Burden of Disease in Malawi," *Malawi Medical Journal*, 18 (3), 103–110. [2]
 WORLD HEALTH ORGANISATION (Ed.) (2008): *The Global Burden of Diseases: 2004 Update*. WHO Press. [3]

Co-editor Fabrizio Zilibotti handled this manuscript.

Manuscript received 3 April, 2013; final version accepted 12 February, 2019; available online 4 March, 2019.