The Impact of Human Mobility on HIV Transmission

Augustino Isdory

Department of Mathematics, University of Dar es Salaam

Department of Mathematics, Uppsala University

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My Advisors

D.T. Sumpter
Main advisor
Uppsala University.
Collective Animal Behaviour.

E. W.Mureithi
Assistant advisor
University of Dar es Salaam.
Fluid Dynamics.

Presentation Outline

1. Introduction
2. The general objective of the study and the gap existing .
3. Model Formulation
4. Analysis of the model
5. Baseline HIV Basic reproduction number for Kenya
6. Numerical results
7. Impact and Applications of the Research

The Impact of Human Mobility on HIV Transmission: A case of Kenya

Introduction

- Human immunodeficiency Virus (HIV) is a virus that affects or destroys the immune system ($CD4^+$ T- cells), so that a body can not fight against infections and diseases.
- HIV is the world's foremost infectious killer.
- Approximately 39 million people have died since the first case of HIV was reported in 1981 (WHO -2014).
- Aproximately 36.7 million people were living with HIV globally at the end of 2016. (WHO and UNAIDS, 2017).

Introduction

- In 2016, approximately 1.8 million people became newly infected, and 1 million died of HIV-related causes. (WHO and UNAIDS, 2017)
- For example, in 2016, on average there about 1.4 million people are living with HIV/AIDS in Tanzania (1.2million – 1.6million).
- This approximately a 6% of the total people living with HIV in Sub-Saharan Africa and a 4% of all people living with HIV globally (UNAIDS DATA 2017).

Introduction

- In the same year, it is also reported that approximately 55,000 (42,000- 67,000) people acquired HIV and 33,000 (26,000-41,000) people died from AIDS-related illness in Tanzania (UNAIDS-DATA-2017)
- It is also reported that 70% of the new infections and more than two third of all HIV- related deaths are from Sub-Saharan Africa (WHO 2013, WHO 2014, Kharsany and Karim. 2016, WHO 2017).

The general objective and the gap existing

- The general objective of this study was to investigate the impact of human mobility on the transmission dynamics of HIV/AIDS using the *SIR* mathematical metapopulation models.
- Since the emergence of HIV, many studies have investigated and explained the impact of human mobility on HIV transmission dynamics (Wang and Mulone 2003, Wang and Zhao 2005, Mundandi *et al.*, 2006, Mmbaga *et al.*, 2008, Vissers *et al.*, 2011)
- Most of these studies do not incorporate the spatial scale mathematical epidemiological models.

- The basic approach is to describe the population in terms of three states i.e *SIR* or four stares i.e *SEIR* if permanent immunity or *SIS* if no permanent immunity upon recovery.
- Under the standard *SIS*, *SIR* or *SEIR* models, the transmission rates, infection periods, contact patterns and removed rates do not account for the spatial spread of the diseases.
- The standard version ignore variations in demographic, social, cultural, economic and geographic factors, such as population mobility.

- Because different regions do not have the same disease prevalence rates, birth and death rates due to different healthcare facilities, mobility rates and social mixing.
- Therefore, spatial scale models are very crucial in understanding the transmission dynamics of diseases
- In this study, we propose an SIR-mathematical model that incorporate movements between different regions (n- patches SIR mathematical meta-population model).

Model Formulation:

- In order to come up with the SIR-mathematical meta-population model, we modify the SI metapopulation model of Keeling and Rohani. 2008.
- We fit the model to the mobility data estimated from mobile phone users from Kenya adopted from the work of Wesolowski *et al.* 2012.

Model Formulation:

Definitions of the model variables:

- We define the adult population who live in region i and currently in region i into susceptible S_{ii}, infectious I_{ii}, removed R_{ii}, and the total adult population to be N_{ii}.
- We define the adult population who live in region j and currently in region j into susceptible S_{jj}, infectious I_{jj}, removed R_{jj},and total adult population N_{jj}.
- We also define the adult population who live in region j and currently are in a visit in region i into susceptible S_{ij}, infectious I_{ij}, removed R_{ij},and the total adult population to be N_{ij}.

Model Formulation:

Definitions of model parameters:

- The model parameter l_{ij} is the rate at which adult individuals who live in region j visit region i per year.
- The model parameter rij represents the return rate from region i to region j per year.
- The parameters β_{ii}, $\gamma_{ii}, \nu_{ii}, \mu_{ii}$ and δ_{ii} are the respectively, infection rate, the recovery, adult recruitment, natural death rate, and the HIV/AIDS induced death rate for adult individuals who live in region i and currently are in region (i).
- We also assume that individuals travel for a next visit after coming back home.

Model Formulation

- For example, the susceptible class in region i are those newly-recruited into the sexually active cohort at the rate $\nu_{ii} = \nu \times p_{ii}$ individuals per year and the total susceptible individuals returning in region i from region j are at the rate $\sum_j r_{ji} S_{ji}$ individuals per year, where ν is the countrywide population growth rate and p_i is the proportion of the total adult population living in region i. Susceptible are lost by becoming HIV infected at the rate $S_{ii}\beta_{ii}\frac{\sum_j I_{ij}}{\sum_j N_{ij}}$, by those dying due to natural causes at the rate $\mu_{ii} S_{ii}$ and the total Susceptible individuals moving from region i to region j are at a rate $\sum_j l_{ji} S_{ii}$ individuals per year,respectively.

Model Formulation:

- The equation describing the dynamics of the susceptible individuals S_{ii} in region i is given by

$$\frac{dS_{ii}}{dt} = \nu_{ii} - \beta_i S_{ii} \frac{\sum_j I_{ij}}{\sum_j N_{ij}} - S_{ii} \sum_j I_{ji} + \sum_j r_{ji} S_{ji} - \mu_{ii} S_{ii}.$$

The SIR Metapopulation Model for region (i)

$$\frac{dS_{ii}}{dt} = \nu_{ii} - \beta_i S_{ii} \frac{\sum_j I_{ij}}{\sum_j N_{ij}} - \sum_j I_{ji} S_{ii} + \sum_j r_{ji} S_{ji} - \mu_{ii} S_{ii}.$$

$$\frac{dS_{ij}}{dt} = -\beta_i S_{ij} \frac{\sum_j I_{ij}}{\sum_j N_{ij}} + I_{ij} S_{jj} - r_{ij} S_{ij} - \mu_{ij} S_{ij}.$$

$$\frac{dI_{ii}}{dt} = \beta_i S_{ii} \frac{\sum_j I_{ij}}{\sum_j N_{ij}} - \gamma_{ii} I_{ii} - \sum_j I_{ji} I_{ii} + \sum_j r_{ji} I_{ji} - \mu_{ii} I_{ii} - \delta_{ii} I_{ii}.$$

$$\frac{dI_{ij}}{dt} = \beta_i S_{ij} \frac{\sum_j I_{ij}}{\sum_j N_{ij}} - \gamma_{ij} I_{ij} + I_{ij} I_{jj} - r_{ij} I_{ij} - \mu_{ij} I_{ij} - \delta_{ij} I_{ij}.$$

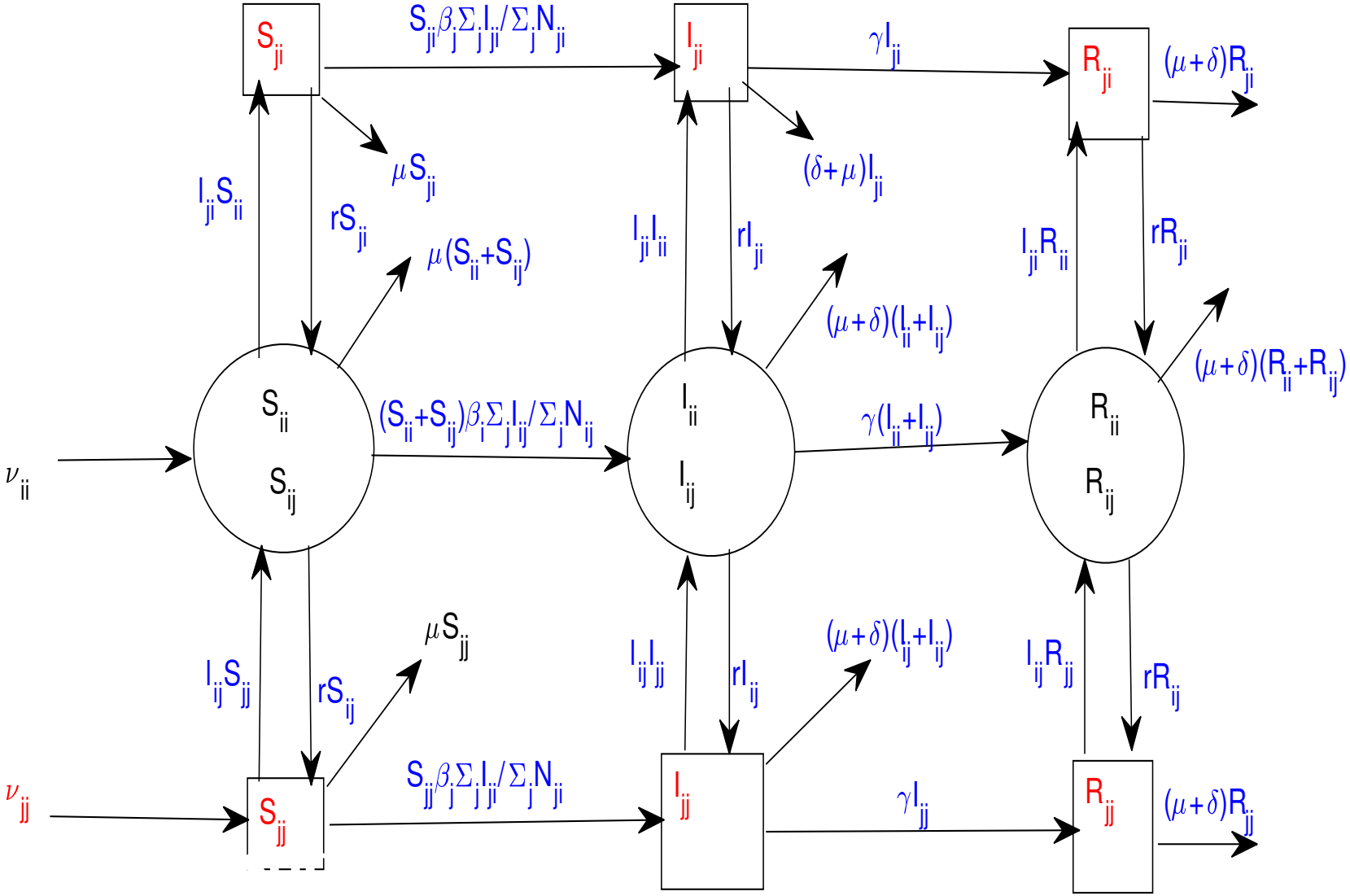
$$\frac{dR_{ii}}{dt} = \gamma_{ii} I_{ii} - \sum_j I_{ji} R_{ii} + \sum_j r_{ji} R_{ji} - \mu_{ii} R_{ii} - \delta_{ii} R_{ii}.$$

$$\frac{dR_{ij}}{dt} = \gamma_{ij} I_{ij} + I_{ij} R_{jj} - r_{ij} R_{ij} - \mu_{ij} R_{ij} - \delta_{ij} R_{ij}.$$

$$\frac{dN_{ii}}{dt} = \nu_{ii} - \sum_j I_{ji} N_{ii} + \sum_j r_{ji} N_{ji} - \mu_{ii} N_{ii} - \delta_{ii} I_{ii} - \delta_{ii} R_{ii}.$$

$$\frac{dN_{ij}}{dt} = I_{ij} N_{jj} - r_{ij} N_{ij} - \mu_{ij} N_{ij} - \delta_{ij} I_{ij} - \delta_{ij} R_{ij}.$$

The Model Compartmental Diagram:



Well Posedness of the SIR n-Patch Metapopulation Model System

- A system is well posed if the solutions of a system remain non-negative for all non-negative initial conditions, the solution exists, unique and depends on the model parameters and the initial conditions (Arino . 2009).
- In this case, the demographic components are positive invariant provided that the positive orthant $\mathbb{R}^{3n^2}$ is invariant.
- Therefore, we need to show that each of the faces of the positive orthant cannot be closed, that is the vector field points inward on the faces (Arino. 2009).

Well Posedness of the SIR n-Patch Metapopulation Model System

For example, for non-negative initial variables setting $S_{ii} = 0$, we get $\frac{dS_{ii}}{dt} = \nu_{ii} + \sum_{j \neq i} r_{ji} S_{ji} \geq 0$.

This shows that $S_{ii} = 0$ can not be closed from positive to negative S_{ii}.

In a similar manner, we can show that $S_{ij}, I_{ii}, I_{ij}, R_{ii}$ and R_{ij} can also not cross from positive to negative $\forall t \geq 0$.

Equilibrium points and its existence

We resort to the mean field model where we assume regional homogeneity:

$$\begin{aligned}
\frac{dS}{dt} &= \nu - \beta S\frac{I}{N} - \mu S \\
\frac{dI}{dt} &= \beta S\frac{I}{N} - \gamma I - \mu I - \delta I \\
\frac{dR}{dt} &= \gamma I - \mu R - \delta R \\
\frac{dN}{dt} &= \nu - \mu N - \delta I - \delta R
\end{aligned} \tag{1}$$

Equilibrium points and its existence

1. Disease Free Equilibrium point is
$$(S^*, I^*, R^*, N^*) = \left(\frac{\nu}{\mu}, 0, 0, \frac{\nu}{\mu}\right).$$
2. Endemic Equilibrium points
   - The endemic equilibrium point is $\mathrm{EEP} = (S^*, I^*, R^*, N^*)$. Where
$$S^* = \frac{\nu(\gamma + \mu + \delta)}{(\mu + \delta)\beta - \delta(\gamma + \mu + \delta)}. \tag{2}$$

Equilibrium points and its existence

$$I^* = [\frac{\nu}{\gamma+\delta+\mu} - \frac{\nu\mu}{(\mu+\delta)\beta-(\gamma+\mu+\delta)\delta}]. \quad (3)$$

$$R^* = \frac{\gamma\nu\left[\beta-(\gamma+\mu+\delta)\right]}{(\gamma+\mu+\delta)\left[(\mu+\delta)\beta-\delta(\gamma+\mu+\delta)\right].} \quad (4)$$

$$N^* = \frac{\beta\nu}{(\mu+\delta)\beta-\delta(\gamma+\mu+\delta)}. \quad (5)$$

EEP exist if

- $\beta > (\gamma+\mu+\delta)$.

Equilibrium points and its existence

Therefore, the baseline basic reproduction number of the mean field model is

$$R_0 = \frac{\beta}{\gamma + \mu + \delta} \tag{6}$$

Definition

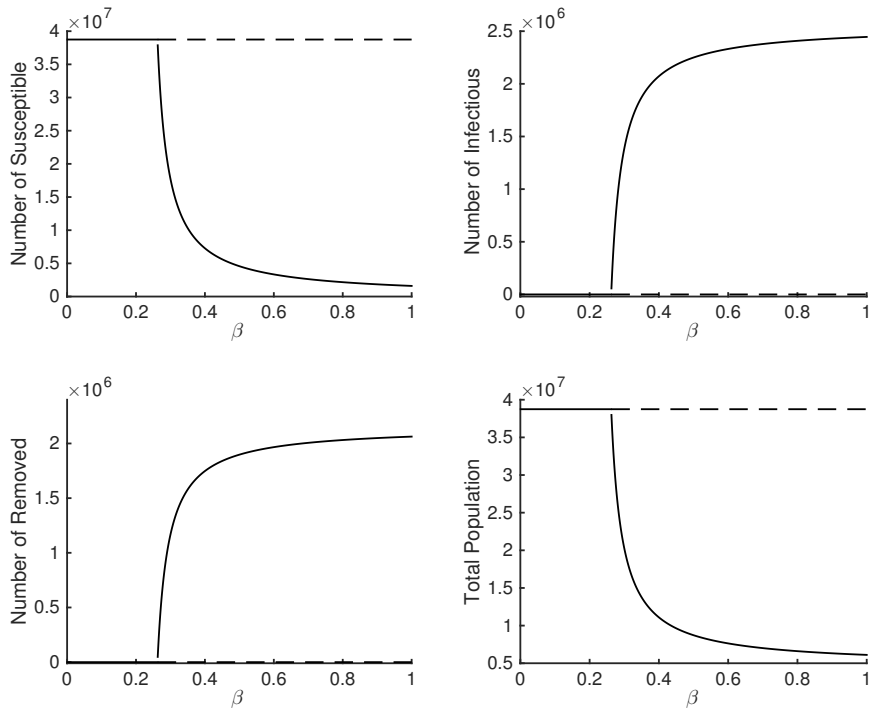
The basic reproduction number R_0: Is the expected number of secondary cases which one case would produce in a completely susceptible population. (van den Driessche and Watmough .2002, Diekmann et al. 2009).

Mathematically:

- If $R_0 < 1$.
  The disease dies in the population.
- If $R_0 > 1$.
  The disease persists in the population.

Baseline R_B for Kenya

- Bifurcation diagram of the equilibrium points : The solid and dotted lines show the values at which the DFEP is stable and unstable, respectively.The solid curves is the stable EEP.

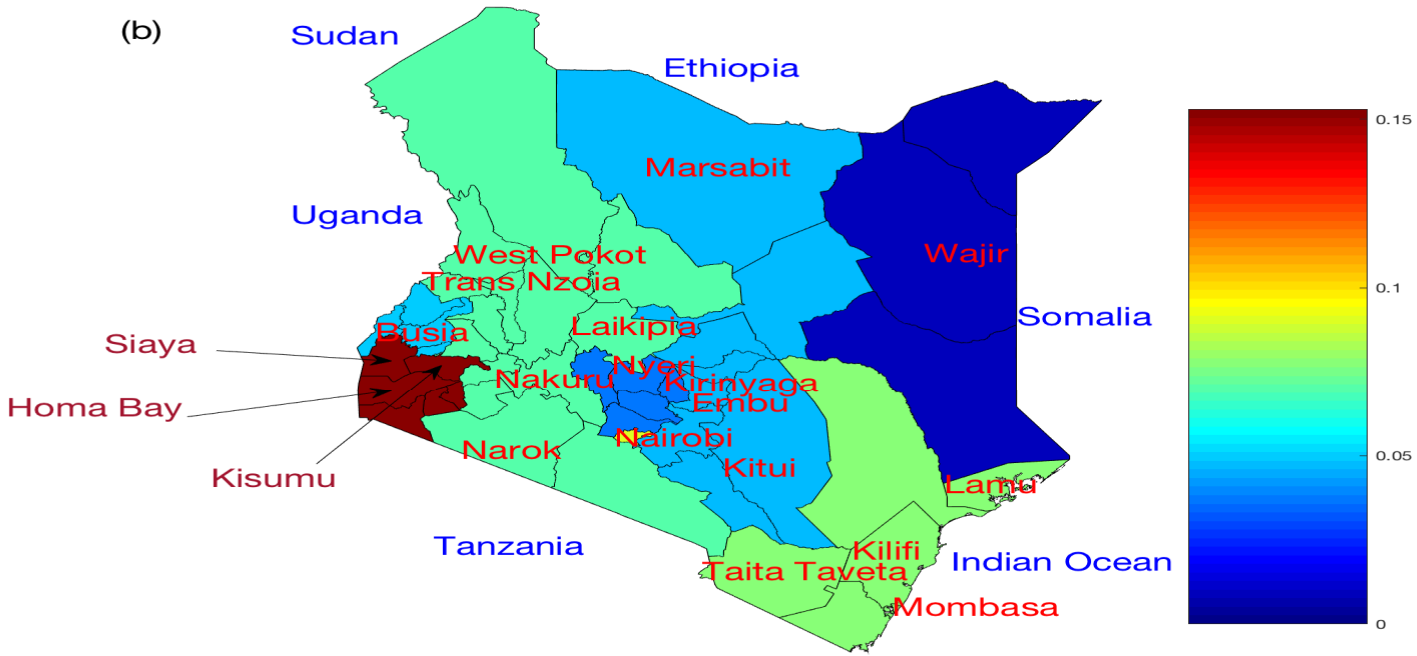


Baseline R_B for Kenya

- $\beta \approx 0.2623$: is the threshold value for the existence or non-existence of the disease for all regions. So that
  - $\beta = 0.22$ gives $R_0 = 0.8388$ and $\beta = 0.42$ gives $R_0 = 1.6014$.
  - $R_B = 0.8388$ for $R_0 < 1$ and $R_B = 1.6014$ for $R_0 > 1$.

HIV prevalence in Kenya, regions by Wesolowski *et al.* 2012.

HIV data Kenya AIDS Indicator Survey-2007



The Role of human mobility on HIV transmission in Kenya

Numerical Results

The Role played by human mobility on HIV transmission in Kenya is based the comparisons between the numerical results of the two scenarios:

1. Coupled and decoupled model for $R_B < 1$.
2. Coupled and decoupled model for $R_B > 1$.

Numerical Results

1. The numerical simulations for the regions with low HIV prevalence:Human mobility tends to slightly increase the number of HIV infectious individuals.
2. The numerical simulations for the regions with high HIV prevalence: Human Mobility tends to slightly decrease the number of HIV infectious individuals.

Regions with high HIV Prevalence for $R_B < 1$: (a) Nairobi, (b) Kisumu, (c) Homa Bay and (d) Siaya.

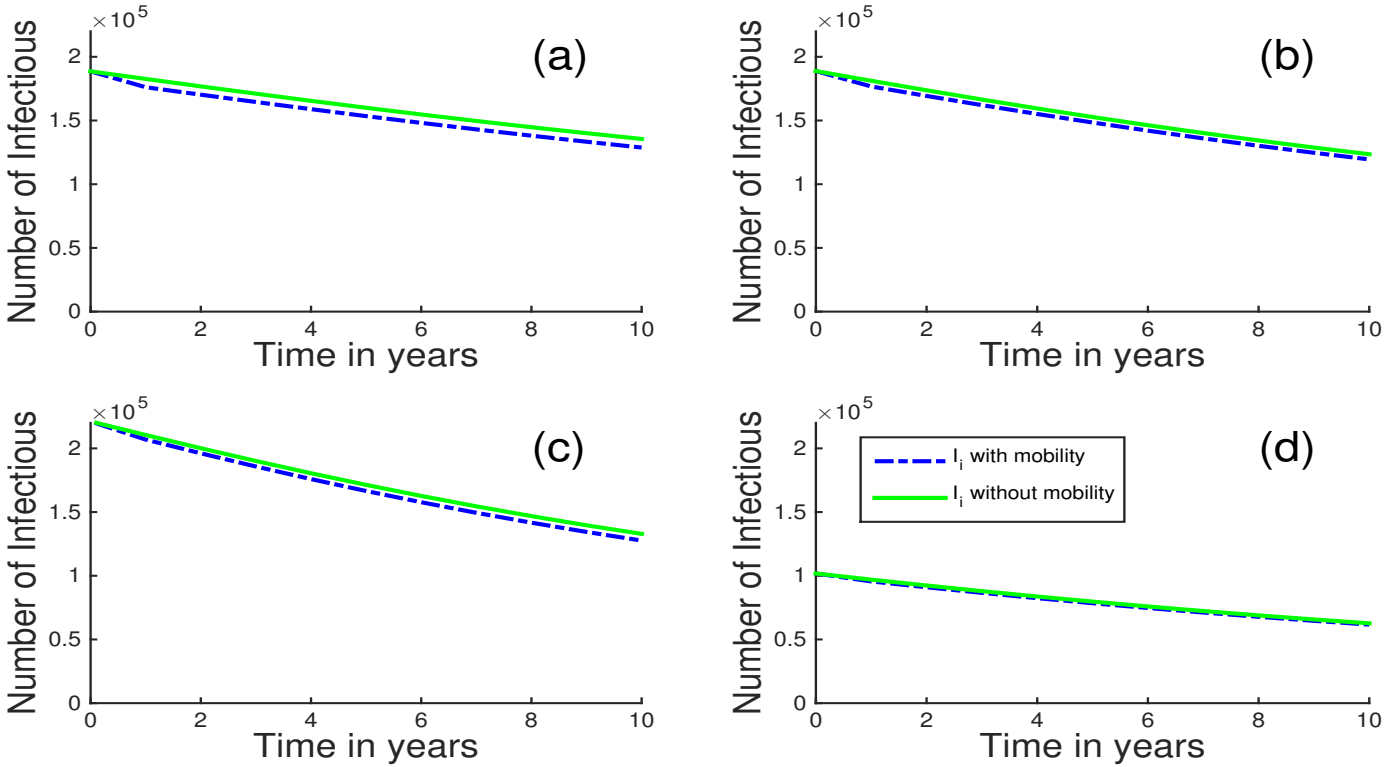


Figure: Example, after 8 -years Siaya - 1.6 % decrease.

Regions with low HIV Prevalence for $R_B < 1$: (a) Wajir, (b) Laikipia, (c) Kirinyaga, (d) Marsabit.

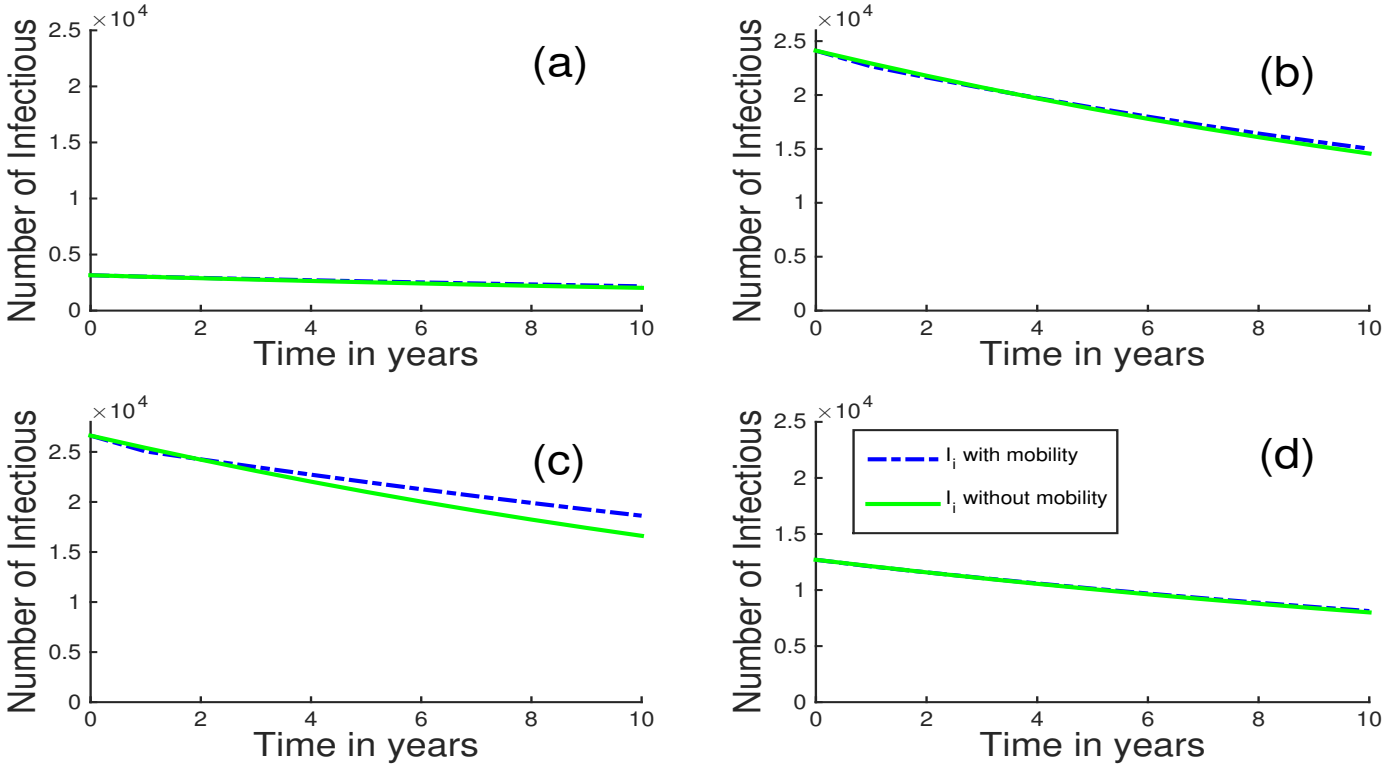


Figure: Example, after 8 -years Wajir - 5 % increase.

Regions with high HIV Prevalence for $R_B > 1$: (a) Nairobi, (b) Kisumu, (c) Homa Bay and (d) Siaya.

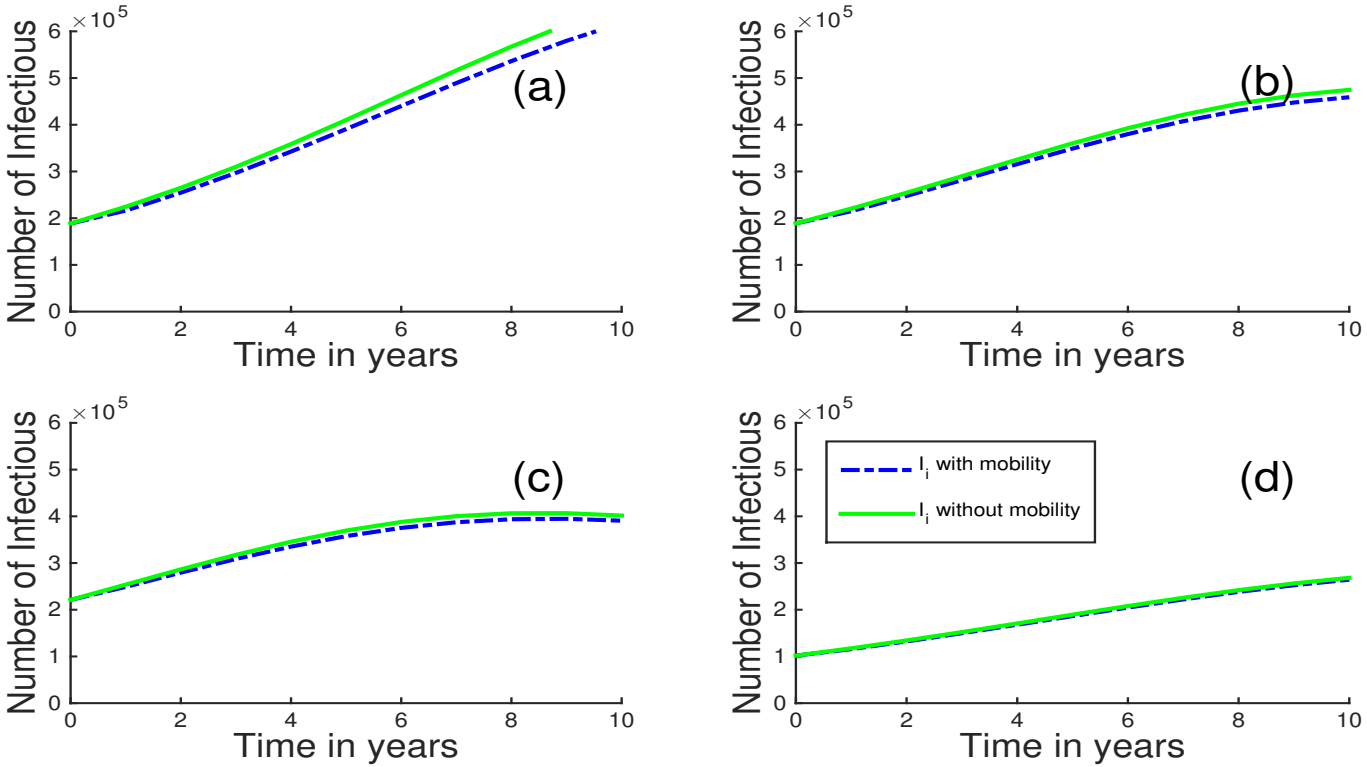


Figure: Example, after 8 -years Nairobi - 5.5 % decrease.

Regions with high low Prevalence for $R_B > 1$: (a) Wajir, (b) Laikipia, (c) Kirinyaga, (d) Marsabit.

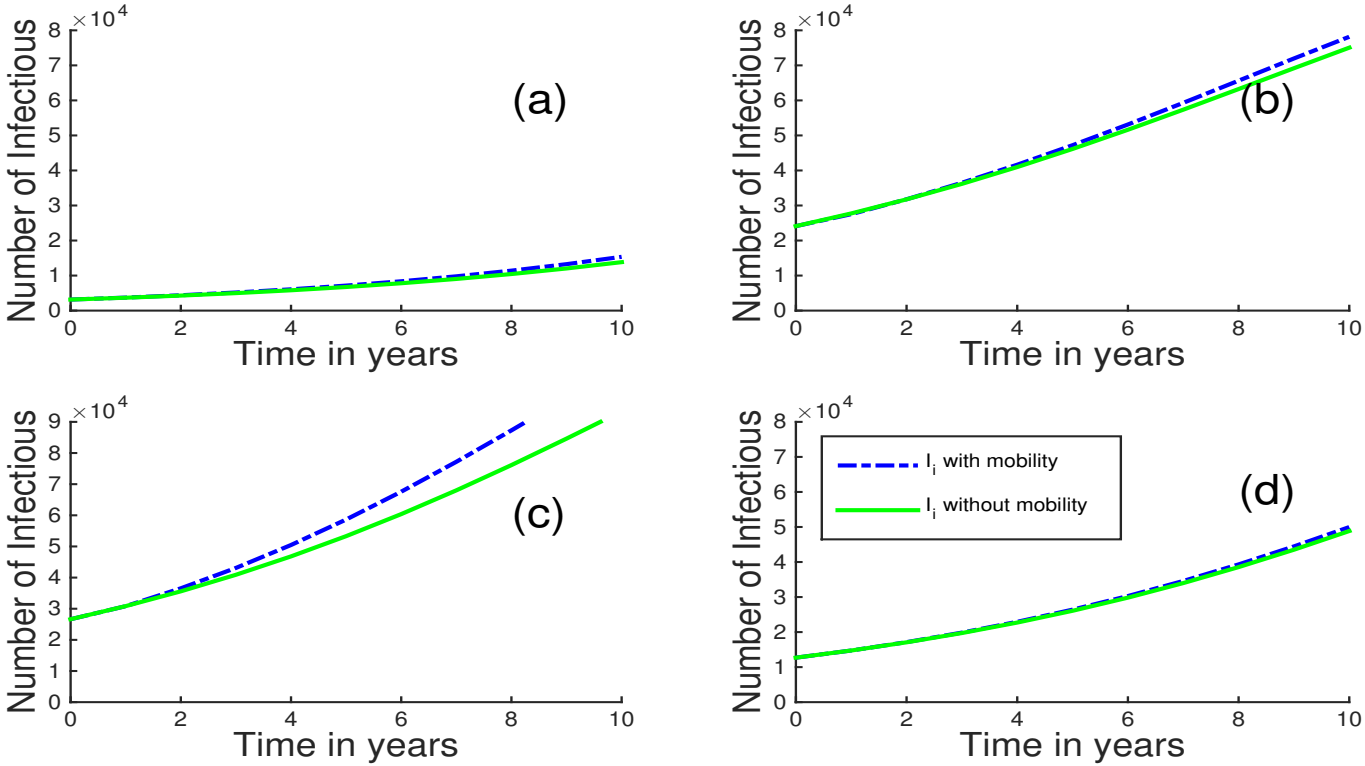


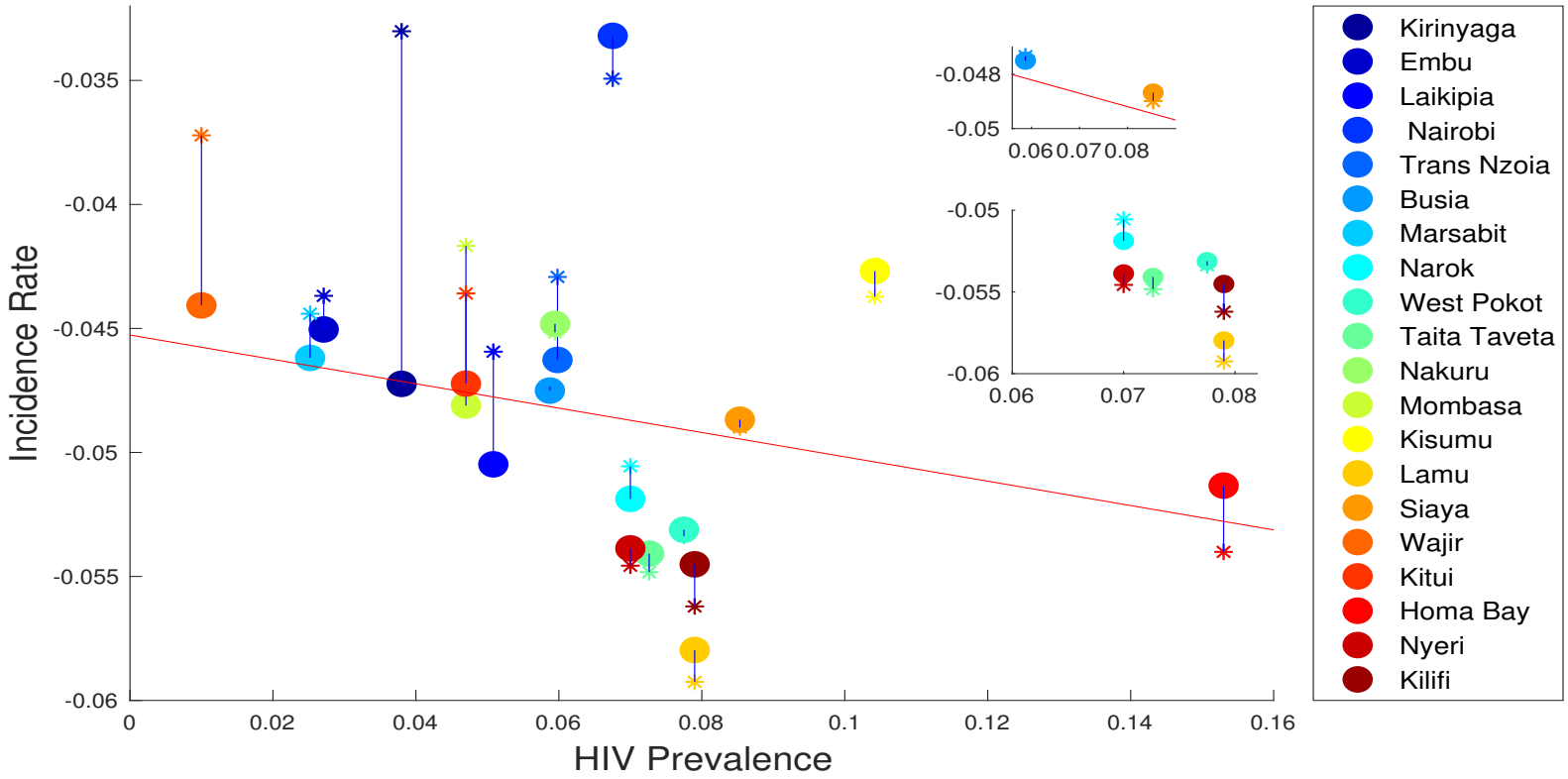
Figure: Example, after 8 -years Marsabit - 2% increase.

Infection rate versus the initial HIV prevalence rate

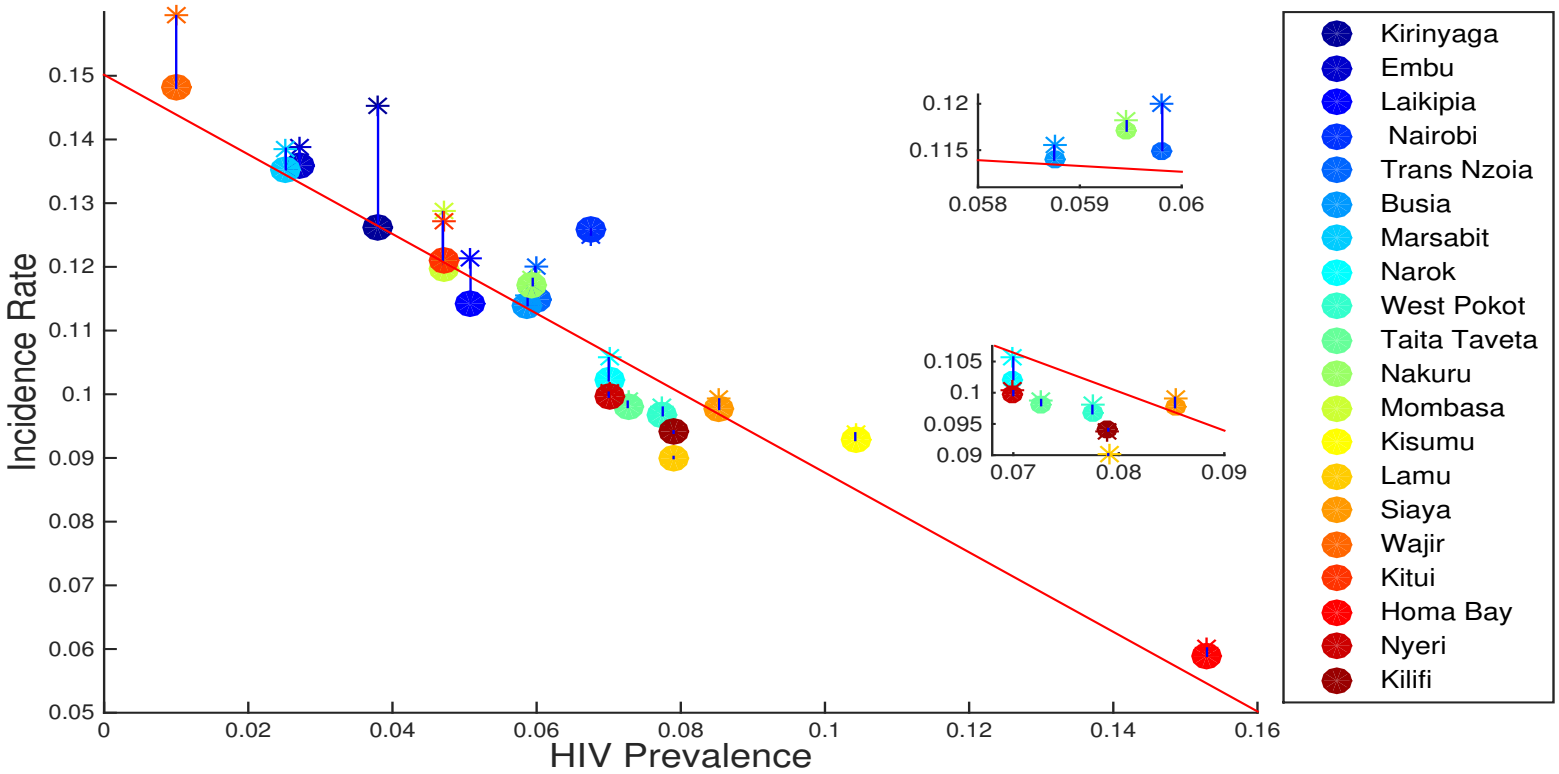
Numerical Results

1. When $R_B < 1$ human mobility: Tends to increase the HIV infection rate to the regions with initially low HIV prevalence.
2. When $R_B < 1$ human mobility: Tends to decrease the infection rate of the regions with initially high HIV prevalence.
3. With the exceptions of Nairobi and Narok : When $R_B < 1$, 7% is a threshold value of initial HIV prevalence above which human mobility decreases the HIV infection rate.
4. When $R_B > 1$ human mobility: Tends to slightly increase the HIV infection rate to all the regions. However, much increase in the infection rate is observed to regions with initially low HIV prevalence.

Incidence rate versus the HIV prevalence rate: Dots for decoupled and stars for coupled model for $R_B < 1$.



Incidence rate versus the HIV prevalence rate: Dots for decoupled and stars for coupled model $R_B > 1$.



Country-wide impact of human mobility on HIV infections $R_B > 1$.

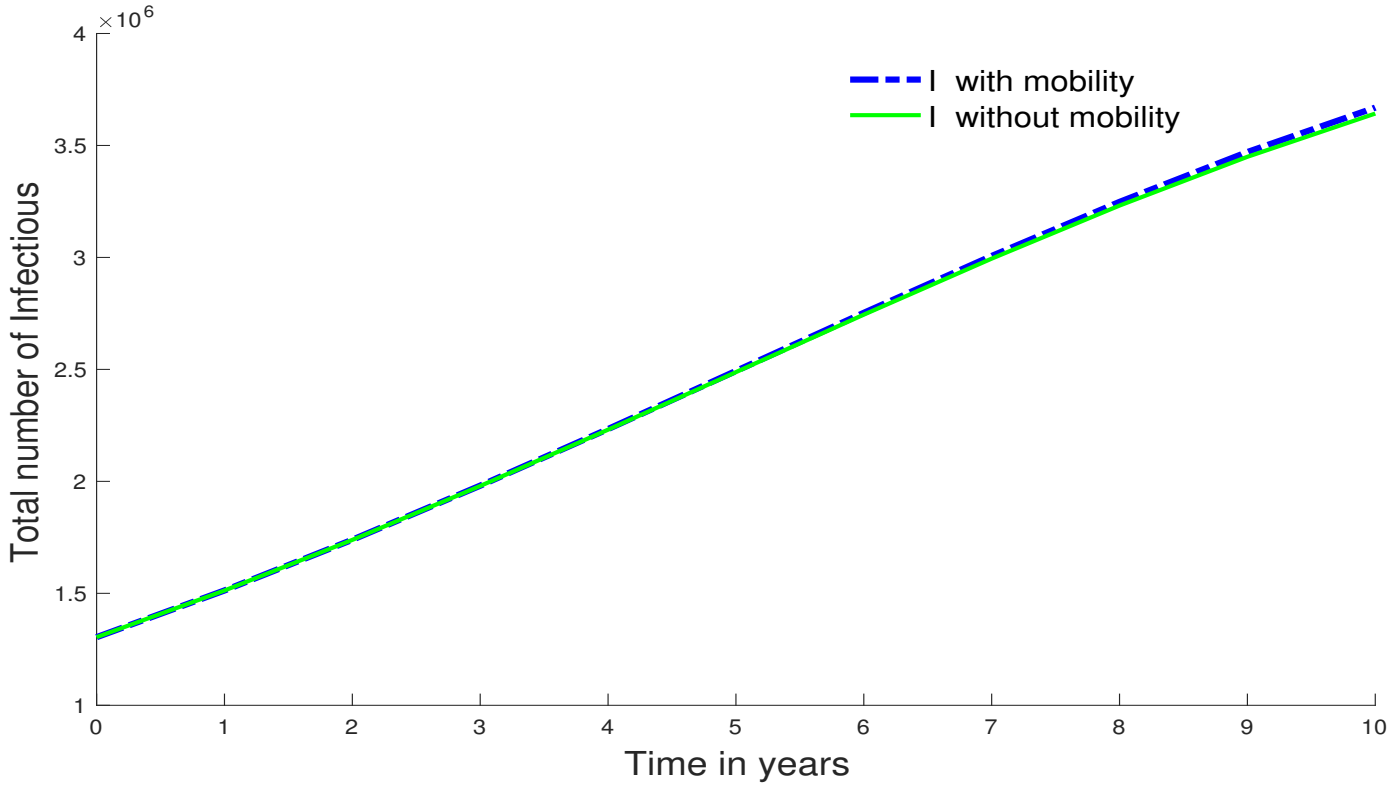


Figure: Example, after 8 -years Kenya would have a 0.5% increase.

Conclusion

Conclusion:

1. Our results show, using countrywide data, human mobility can influence the transmission of HIV in Kenya.
2. Mobility does play an important role in local dynamics of HIV. Specifically,
   - Regions with initially low HIV prevalence experience an increase in the number of infectious.
   - Regions with initially high HIV prevalence experience a slight decrease.
   - To the regions with initial low HIV prevalences it tends to increase their HIV incidence rates more than in the regions with initial high HIV prevalence.

Impact and Applications of this Research

1. The outcome of this work will help the community understand the role played by human mobility on the transmission dynamics of HIV (conscientization).
2. The *SIR* mathematical metapopulation model presented in this study can also be used in different areas of science and engineering, for example, in the analysis of social networks.
3. Through this study, suggestions are given to the authority organs, such as the policy-makers.
4. The study will also contribute to the existing literature at the same time serve as a guide for future research on the impact of human mobility on the transmissions dynamics of HIV as well as for other diseases.

Tack så mycket!

Thank you!

Asante Sana!