



**MIGRATION AND THE EQUILIBRIUM PREVALENCE OF INFECTIOUS  
DISEASES**

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# Migration and The Equilibrium Prevalence of Infectious Diseases

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## Abstract

This paper models how migration both influences and responds to differences in disease prevalence between cities, regions and countries, and show how the possibility of migration away from high-prevalence areas affects long-run steady state disease prevalence. We develop a dynamic framework where both migration and prevention behaviour respond to the prevalence of disease, to the costs of migration and of treatment, and to current and anticipated health regulations. The model treats disease prevalence as an endogenous consequence of other features of the areas concerned, notably their economic endowments. It explores how pressure for migration in response to differing equilibrium levels of disease prevalence causes countervailing differences in city characteristics, notably in land rents. Competition for scarce housing in low-prevalence areas can create pressures for segregation, with disease concentrated in high-prevalence "sinks". We show that multiple steady states may exist and explore their comparative static properties. In particular we find that migration can have positive health benefits, in that reductions in barriers to migration can reduce steady-state disease incidence in low-prevalence areas while having no impact on prevalence in high-prevalence areas. This may have important consequences for policy ; in some circumstances, public health measures may need to avoid discouraging migration away from high-disease areas.

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# 1 Introduction

This paper studies the reciprocal causality between migration and the incidence of disease. While it is well known that migration can contribute to disease through the effect of crowding, we study its consequences for the composition of populations and thus for the transmission of disease over time. If migration responds to disease incidence as well as influencing it, then feedback effects may either dampen or magnify initial divergences between localities in disease prevalence. We show how in particular that, for an important class of infectious endemic diseases, migration can magnify initial divergences, since the healthy have a stronger incentive than the sick to flee unhealthy neighborhoods. This can turn some localities into "sinks" whose initial high disease prevalence attracts further sick individuals, not because they are positively drawn to such localities but because they cannot compete with healthy individuals for scarce space in healthier localities. We show the possibility of multiple steady states with different degrees of segregation of sick and healthy individuals. In fact higher segregation is beneficial in the model, since it unambiguously reduces prevalence in low-prevalence locations and does not necessarily increase it in high-prevalence locations. This has implications for public policy towards migration and may provide a case for encouraging or even subsidising migration that has such results.

Epidemiologists have already addressed how individual migration behaviour may contribute, among other factors, to the spread of disease<sup>1</sup>. But much less is known about how migration in turn responds to infectious diseases, although numerous historical instances have been recorded of people fleeing plague or other infectious diseases by migrating to distant areas (see McNeill, 1997)<sup>2</sup>.

Related work has been done on the economic determinants of preventive behaviour (such as vaccination, or the adoption of safe sex). In particular, Philipson (2000) and Geoffard and Philipson (1996) show that, if demand for prevention treatments such as vaccines is prevalence elastic, then initially successful public health efforts typically run into diminishing returns, not simply for technical reasons but because the decline of a disease discourages prevention. Similar considerations apply to the factors determining the adoption of means of contraception as barrier methods for Sexually Transmissible Diseases, and a growing literature now focuses on the microeconomic determinants of such individual decisions, in order to reach a better understanding of epidemiological patterns<sup>3</sup>.

However, migration as a form of preventive behaviour has received very little attention before Mesnard and Seabright (2007), although evidence has accumulated that migration behaviour and epidemics are intrinsically linked.

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<sup>1</sup>For a recent contribution, see Boily et.al. (2007).

<sup>2</sup>During the Black Death, inhabitants from infected villages frequently migrated to neighboring, less infected villages. Much more recently, after the SARS outbreak in China, workers in urban areas returned in large numbers to live with their families in safer rural areas (Le Point, 2003).

<sup>3</sup>See Gersovitz & Hammer (2003) and Pattanayak et al (2007) for overviews and surveys of the evidence on the prevalence elasticity of preventive behavior.

In that paper, we examine the response of health authorities to the outbreak of epidemics, and specifically consider the effectiveness of quarantine measures; we explore how perverse effects may occur if individuals are more accurately informed than the authorities about their previous exposure to infection. Faced with the prospect of costly quarantine restrictions if they subsequently develop symptoms, they may decide to migrate “strategically” into a low prevalence area while still asymptomatic. Such effects were recently observed in China after the SARS outbreak. We show that externalities mean that the migration decisions of individuals may lead to excessively high disease prevalence, but that policy interventions may make matters worse unless they are very carefully designed.

This paper, in contrast, focuses on endemic disease. Although endemic disease as an influence on migration decisions has not to our knowledge been studied by modern social scientists, there is abundant historical evidence of disease as a factor in individuals’ location decisions. Historians have shown that infectious diseases causing high mortality rates among settlers were a key determinant of European colonisation. Among other examples, Acemoglu et al (2001) refer to Crosby (1986 pp143-144) who has shown that the Pilgrim Fathers decided to migrate to the United States rather than to Guyana because of the high mortality rates from infectious diseases in Guyana. We also know from Alexis de Tocqueville and other witnesses of that period that it took the draining of the malarial swamps in the State of Michigan in the mid nineteenth century for the interior of the state to be opened up by settlers on a scale comparable to what had already occurred further west in Illinois<sup>4</sup>. Robert Fogel (2004, p.35) in his discussion of the data on standards of living in the United States in the first half of the nineteenth century, writes that “economic growth, the spread of disease, and the concomitant increase in morbidity and mortality rates were intricately intertwined...the increase in mortality between 1790 and 1860...indicates that a downward adjustment [to GDP per capita] is necessary even if wage rates in high-disease localities fully reflected the extra wage compensation....that workers demanded for the extra risks of living in these areas”. As Fogel’s discussion indicates, higher disease prevalence was a characteristic of high-income localities, since these were more urbanized and urbanization caused crowding; the implied direction of causality was that exogenous productivity shocks induced migration, which raised disease incidence, a phenomenon damping but not fully offsetting the original incentive to migrate.

Even today there is a vast difference between different parts of the world in the incidence of infectious disease. Mortality statistics published by the World Health Organization<sup>5</sup> reveal that deaths from infectious or parasitic disease make up just over 2% of all deaths in Europe, and some 3% of deaths in North America, while they make up over 52% of all deaths in Africa (9% of all deaths

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<sup>4</sup>Alexis de Tocqueville arrived in Detroit in 1831 and was very troubled by mosquitoes during his travels (he speaks in his journal of “inexpressible torment caused by mosquitoes”; Tocqueville 1981, p.140). The initiative shown by Americans in organizing to drain wetlands impressed Tocqueville and was one of the features he contrasted with the French dependence on central government. See <http://www.mackinac.org/article.asp?ID=25>

<sup>5</sup>Downloadable from <http://www3.who.int/whosis>

being due to malaria and 20% of all deaths being due to HIV/AIDS). The world average is a little under 20% of all deaths. Given the importance of infectious disease in mortality it would be extraordinary if individuals did not take variations in its incidence into account in their location decisions. The location of some important cities (Nairobi in Kenya, for example, or Colombo in Sri Lanka) seems likely to have benefited from their low rates of malarial incidence compared to the rest of the country.

Obviously there are correlations between high rates of disease prevalence and a high incidence of poverty, and the complex linkages between poverty and infectious disease make their interaction an interesting area of study. Economists have begun to study the channels through which health outcomes interact with economic factors (Duncan et al. 1999, Hurd, et al. 2003, Marmot, 2002). And there is strong evidence that epidemic outbreaks cause important economic losses<sup>6</sup>. Furthermore, asset markets may also be affected, as was observed on the housing market in Hong Kong after the SARS outbreak (Wong, 2004). However, among these linkages, migration has gained rather little attention and, yet, has been under increasing focus since the SARS outbreak in China.

In this paper we explore the decisions of individuals to live in different areas as being determined by both monetary costs and benefits and by the health environment. We model the long run consequences of migration when the prevalence of endemic disease is considered as part of the quality of life in a particular area. Hence it affects the migration equilibria between different areas and their relative costs of living. To capture the costs of living or of any fixed asset or amenity attached to a given area, the price of which increases with more people settling in the area, we assume that there is a constant stock of land in each city and that rents will vary to clear the market for land<sup>7</sup>. This requires of course a dynamic set-up where the economic and health environment are affected by migration, and in turn determine individual decisions such as migration and preventive behaviour.

At the beginning of each period individuals find themselves in one of two cities, which differ in a number of characteristics including the prevalence of disease. The two cities could also be interpreted as countries or regions, or even in some circumstances as different sectors of the economy<sup>8</sup>. Individuals

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<sup>6</sup>For example, losses associated to the SARS outbreak have been estimated between US\$10 and US\$30 billion, as compared to the 1994 outbreak of plague in India, the costs of which were estimated at around US\$2 billions (Robertson 2003).

<sup>7</sup>It may be more realistic for certain epidemics to consider the possibility of individuals fleeing high-prevalence cities to stay with friends or relatives in lower-prevalence cities, implying an aggregate temporary population shift between cities without any adjustment on the land market. This is captured in the epidemic framework we study in Mesnard and Seabright (2007). Here, by contrast, we consider longer-run location decisions where capacity constraints may play a significant role. In the model total capacity of each city is fixed and cannot be changed by (for instance) construction, but less stringent constraints would preserve the qualitative features of our results. Total capacity constraints also make it easier to define and solve for a steady state.

<sup>8</sup>For instance, decisions of individuals to become sex workers, or within the commercial sex sector to move between street prostitution and the formal brothel-based sector, are likely to be influenced by what is known about relative risks of sexually-transmitted disease.

have characteristics of their own, and in the model we focus on their health status (wealth, which normally differs among individuals, is here assumed to be the same for all individuals in one city so as to focus attention on differences in health). These individuals must make a number of decisions, about consumption levels, about spending on medical care, and about whether to stay in their city of origin or to migrate to the other. Time is infinite and the significance of the future is summarized in terms of a value function whose parameters are the health status of the individual and the characteristics of the city where she lives, both of these considered at the start of the following period. Each individual's decisions therefore involve balancing the impact of varying certain choice variables on her current utility and her future discounted value function.

We assume that healthy individuals in any one city are *ex ante* identical in terms of risk of infection (in this respect we differ from Mesnard & Seabright, 2007). However, individuals once infected spend one period in an asymptomatic state in which they know their own condition but it is not observed by anyone else<sup>9</sup>.

Migration matters in this model even when no migration is actually observed. This is because healthy individuals concerned about their risk of illness may choose either to stay in their city of origin and take medical treatment or to migrate to the other city. Since their risk of illness is increasing in the prevalence of illness in the city where they live, migration to a lower-prevalence city may be the most effective means of reducing their risk, provided the difference in risk between the two cities is great enough. However, the benefits of risk reduction must be balanced against the costs, which here comprise not just migration costs but also any difference in the cost of living in the two cities.

We first present the model and then solve for a steady state in prevalence and wealth levels in circumstances where migration costs are sufficiently high to discourage migration both in and out of the steady state. We show that richer cities will have lower disease prevalence rates and higher land rents. This is in contrast to the historical process described by Fogel, in which incomes and prevalence rates are positively associated. The difference is due to the fact that Fogel described migration from countryside to the city, and the lower prevalence rates in the countryside are due to lower crowding; in contrast, crowding plays no part in our model, and prevalence rates are due to differing health expenditures. One empirical prediction of our model, which we believe to be historically reasonable, is that richer cities should have lower prevalence rates than poorer cities once population density is controlled for.

Next we examine the properties of the steady state when migration costs are sufficiently low that healthy individuals in the high prevalence city will wish to migrate to the low-prevalence city, thereby bidding up rents in that city and encouraging asymptomatic individuals to migrate in the opposite direction. We show that, if all asymptomatic individuals do thus migrate, the prevalence rate

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<sup>9</sup>Thereby we treat information asymmetries about individuals' health risks differently from Mesnard and Seabright (a) where individuals differ in an individual risk parameter  $p^i$ . This greatly simplifies our calculations and does not diminish the insights to be drawn from the results.

in the low-prevalence city declines to zero so that there are no more infected individuals and migration in the steady state no longer occurs. However, the *possibility* of migration is important because it removes potentially infectious individuals from the locality where they can infect the most other people. The possibility of migration strictly lowers steady-state prevalence levels, and it is unambiguously desirable to reduce migration costs to make this possible.

Our prediction that migration may under certain conditions induce sorting by health status has obvious echoes of the literature on segregation by individuals induced by their demand for local public goods such as education. The idea that individuals might sort between locations according to their preferences for local public goods goes back to Tiebout (1956), and there is a substantial more recent literature exploring the conditions under which that sorting would result in segregation of households by income (see Ellickson, 1971, for a pioneering contribution and Epple, 2003, for an overview). As documented by Timmins, 2005, there is much controversy about the strength of such effects and about how to estimate them econometrically. Particular applications have included sorting by preference for education provision (see Bénabou, 1996a, b, and Fernandez & Rogerson, 1996). There is a sense in which our model here documents broadly similar effects, since the prevalence rate of a disease has the relevant characteristics of a public good (or more precisely a public bad). However, our model has certain distinctive features: first, although in our model the willingness of pay of healthy individuals to live close to other healthy individuals exceeds that of sick individuals, this is not a forgone conclusion of models of sorting by health but is true only under certain conditions. Indeed, as we discuss below, under certain alternative assumptions (such as that richer cities have better quality medical care and not just more of it) it could be that sick individuals would have a higher willingness to pay to live in low-prevalence environments, which would act against segregation. And as shown in our companion paper (Mesnard & Seabright 2007), under different assumptions about the distribution of past exposure to the disease and the correlation of past exposure to disease with future risk, migrants to low-prevalence destinations may include a significant proportion of individuals likely to become sick, thereby mitigating segregation effects even if they do not wholly offset them. Secondly, in our model there are multiple equilibria in only some of which there is sorting by migration, with endogenous differences in health status even in the equilibria without sorting. It is also true in our model, unlike in many public-good models, that some of the equilibria can be Pareto-ranked, and that those with the possibility of sorting out of the steady state dominate those without that possibility. These features in our view cast useful light on some of the features of disease incidence as a feature of local environments.

Historically there is good reason to think that segregation of neighborhoods by disease incidence has been an important influence on the spatial composition of cities and countries, and that relative housing costs have played an important part in this process. The East End of London was considered a sink of disease (as well as of other unsavory characteristics) and prosperous citizens paid considerable sums to live in the West End, which thanks to the prevailing (westerly)

winds could escape the noxious odors emanating from the east more easily than the east could avoid those from the west (the winds were thought to transmit disease - through "miasma" - as well as foul odors). Thus although we do not claim that the phenomena we model are the only or even the main influences on migration in the presence of infectious disease, it seems likely that they help to explain some important characteristics of the geography of development, both historically and in disease-ridden countries today.

## 2 The model

There are 2 equally-sized cities, 1 and 2.

Time is discrete and infinite.

Individuals can be in three states of health: healthy, infected but asymptomatic, or sick. For a representative individual  $j$  this is denoted by random variable  $\theta_j \in (H, A, S)$ .

In city  $i$  at time  $t$ :

The total population  $n_t^i$  is normalized to unity, of which  $p_t^i$  are sick and  $a_t^i$  are infected but asymptomatic. We assume that there are always more healthy individuals than asymptomatic individuals in the combined population of the two cities (that is, we ignore diseases so infectious but so long latent that most of the population becomes infected without falling sick).

The expected present value of current and future utility of individual  $j$  in city  $i$  at time  $t$  is:

$$U_{jt}^i = U(c_{jt}, x_{jt}, q_t^i, \theta_{jt}) + \gamma E [W(q^i, Y^i, P^i, \theta_j)]$$

where  $U(\cdot)$  is weakly concave in consumption and  $W(\cdot)$  is weakly concave in wealth,  $\gamma$  is a discount factor and the following denotes individual variables:

$c_{jt}$  is consumption in period  $t$ ;

$x_{jt}$  is expenditure on medical care in period  $t$

$\theta_{jt}$  is the state of health in period  $t$ ;

$\theta_j$  is the state of health in period  $t + 1$ .

and the following are city-level variables:

$Y^i$  is the per-period income of the representative agent in city  $i$  (income is considered as an endowment, and agents in each city are assumed identical in income).

$q_t^i \in (0, 1)$  is whether there is a quarantine in force for sick individuals in city  $i$  at date  $t$ . Such quarantine measures also prevent asymptomatic individuals who signal their risk of being infected by taking treatment to migrate to the low prevalence city. As the authorities cannot screen perfectly asymptomatic individuals, they also prevent healthy individuals who adopt treatment from migrating.

$q^i \in (0, 1)$  is whether a quarantine is expected (at  $t$ ) to come into force in period  $t + 1$  for sick individuals in city  $i$ ; this expectation may be based on an announcement or simply on exogenous available information;

$P^i \equiv \frac{p_{t+1}^i}{n_{t+1}^i}$  is the prevalence of the disease in city  $i$  at the beginning of  $t + 1$ .

We make the following assumptions about the effect of sickness on individual utilities:

(A1) Sickness lowers current welfare:

$$U(c_{jt}, x_{jt}, q_t^i, S) < U(c_{jt}, x_{jt}, q_t^i, A), U(c_{jt}, x_{jt}, q_t^i, H)$$

(A2) Sickness lowers future welfare, and to a degree that is non-decreasing in income:

$$W(Y^i, q^i, P^i, S) < W(Y^i, q^i, P^i, A) < W(Y^i, q^i, P^i, H) \text{ and} \\ \frac{\partial(W(Y^i, q^i, P^i, H) - W(Y^i, q^i, P^i, A))}{\partial Y^i} \geq 0, \frac{\partial(W(Y^i, q^i, P^i, A) - W(Y^i, q^i, P^i, S))}{\partial Y^i} \geq 0.$$

(A3) Quarantine lowers current and future welfare of the sick:

$$U(c_{jt}, x_{jt}, 1, S) < U(c_{jt}, x_{jt}, 0, S) \text{ and } W(Y^i, 1, P^i, S) < W(Y^i, 0, P^i, S)$$

(A4) The future welfare of the sick is independent of disease prevalence:  
 $W(q^i, Y^i, P^i, S) = W(q^i, Y^i, P'^i, S) \equiv W(q^i, Y^i, S) \forall P^i, P'^i$

We also assume that expenditure on medical care has no effect on the current utility of those who are healthy but that medical expenditure increases the utility of asymptomatic or sick individuals :

$$(A5) \frac{\partial U(c_{jt}, x_{jt}, q_t^i, H)}{\partial x_{jt}} = 0, \frac{\partial U(c_{jt}, x_{jt}, q_t^i, A)}{\partial x_{jt}} > 0, \frac{\partial U(c_{jt}, x_{jt}, q_t^i, S)}{\partial x_{jt}} > 0$$

It should be noted that (A5) implicitly assumes that the effect of medical care on utility is independent of the city in which it takes place. Under alternative assumptions, such as that the richer city had higher-quality medical care rather than just more of it in equilibrium (ie that the effect of medical care on utility was higher for a given expenditure on care), our segregation result might not hold because sick individuals might have more incentive to migrate than healthy individuals.

Next, individuals face a budget constraint:

$$Y^i - c_{jt} - m^\theta I_{jt} - r_t^i - x_{jt} = 0$$

where

$m^\theta$  is the exogenous migration cost for those choosing to migrate in period  $t$ , with  $m^S > m^H = m^A = m$  to indicate that it is more costly for sick individuals to migrate (in solving the model we shall assume that this is always sufficiently high for no migration to take place by the sick).

$I_{jt}$  is an indicator function taking the value 1 if the individual  $j$  migrates in period  $t$ , otherwise 0.

$r_t^i$  is the rent paid to live in city  $i$ . Without loss of generality we normalize  $r_t^1 = 0$  (city 1 is designated the "low rent city" - it will also turn out to be the "high disease prevalence city"), so we can write  $r_t^2 = r_t$ .

The health status of individuals evolves as follows:

If  $\theta_{jt} = A, \theta_j = S$  with probability 1. All infected individuals in one period become sick in the next period.

If  $\theta_{jt} = H, \theta_j = A$  with probability  $\frac{p_t^i}{1+x_{jt}}$ , otherwise  $\theta_j = H$ . Healthy individuals become infected with a probability that is proportional to the prevalence of the city in which they choose to live in each period, but which can be reduced by expenditure on medical care.

If  $\theta_{jt} = S, \theta_j = H$  with probability  $\pi$ , otherwise  $\theta_j = S$ . We can think of  $\pi$  as the natural recovery rate from the disease.

The order of events in each period  $t$  is as follows:

At the beginning of period  $t$ , individuals observe their current health status.

Next, still in period  $t$ , individuals observe information allowing them to infer whether or not there will be a quarantine in force in period  $t + 1$ .

Next, still in period  $t$ , individuals decide whether or not to migrate from the city in which they currently live to the other city, conditional on disease prevalence levels as observed at the beginning of the period, and on rent levels.

Lastly, in period  $t$ , individuals who have not migrated choose what level of medical treatment to buy (migrators are constrained to choose zero levels of treatment); and all individuals receive the incomes and pay the rents in the cities they have chosen to live in, and decide what level of consumption to undertake.

In period  $t + 1$  representing the future, individuals remain in the city where they have decided to live if their health status has not changed compared to what was expected. However, sick individuals who have recovered in  $t + 1$  and live in the high prevalence city must decide whether to migrate back to the low prevalence city exactly like individuals have not previously been sick. In other words, sickness casts no long-term shadow.

### 3 The decisions of individual agents

We first solve for the consumption and treatment decisions of each individual who chooses not to migrate in the current period, and then compare it with the decisions of those individuals who migrate. All decisions will themselves be contingent on current health status.

#### 3.1 Sick individuals:

The choices made by sick individuals involve no considerations of preventive treatment. Rather they must choose whether to migrate and, if not, how much curative treatment to undertake. Curative treatment does not affect the probability of future health status (which can therefore be taken as exogenous to the individual), and therefore is chosen purely for its effect on current utility (see assumption A5). The agent who is currently sick and chooses not to migrate must therefore solve:

$$\text{Max}_{c_{jt}, x_{jt}} [U(c_{jt}, x_{jt}, q_t^i, S) + \gamma ((1 - \pi) W(q^i, Y^i, S) + \pi W(q^i, Y^i, H))]$$

subject to

$$Y^i - c_{jt} - r_t^i - x_{jt} = 0$$

whose first order condition is:

$$\frac{\partial U(S)}{\partial x_{jt}} - \frac{\partial U(S)}{\partial c_{jt}} = 0 \tag{1}$$

where we write  $U(S)$  to indicate that the derivative is evaluated at  $\theta_{jt} = S$ . By assumption (A5) this first order condition yields a strictly positive choice of  $x_{jt}$ .

A sick individual who chooses instead to migrate from city  $i$  to city  $k$  can only do so if  $q_t^i = 0$ , and will consume all her income except that needed to pay the migration cost and the rent in the city of destination, thereby enjoying utility equal to

$$U(Y^i - m^S - r_t^k, 0, 0, S) + \gamma ((1 - \pi) W(q^k, Y^i, S) + \pi W(q^k, Y^i, H)) \tag{2}$$

We can write  $V_M^*(S, 0, q^k, Y^i - m^S - r_t^k)$  for the indirect utility of a sick individual who migrates (provided that  $q_t^i = 0$ ), and note that it is increasing in  $Y^i$  and decreasing in  $q^k, m^S$  and  $r_t^k$ .

Similarly we can write  $V_N^*(S, q_t^i, q^i, Y^i - r_t^i)$  for the indirect utility of a sick individual who does not migrate, and note that it is increasing in  $Y^i$  and decreasing in  $q_t^i, q^i$  and  $r_t^i$ .

Consequently the condition for sick individuals to remain in their city of origin if  $q_t^i = 0$  can be written as

$$V^*(S) \equiv V_N^*(S, 0, q^i, Y^i - r_t^i) - V_M^*(S, 0, q^k, Y^i - m^S - r_t^k) \geq 0$$

and we note that this condition is more likely to be fulfilled as  $q^i - q^k$  or  $r_t^i - r_t^k$  decrease or  $m^S$  increases.

### 3.2 Asymptomatic individuals:

The decision problem for asymptomatic individuals is structurally similar to that for sick individuals. The only difference is that asymptomatic individuals are not affected by quarantine measures at  $t$  and the migration decision differs from that for sick individuals in that asymptomatic individuals can still migrate if  $q_t^i = 1$ . The first-order conditions are

$$\frac{\partial U(A)}{\partial x_{jt}} - \frac{\partial U(A)}{\partial c_{jt}} = 0 \tag{3}$$

As for sick individuals we can write  $V_M^*(A, q^k, Y^i - m - r_t^k)$  for the indirect utility of an asymptomatic individual who migrates, and note that it is increasing in  $Y^i$  and decreasing in  $q^k, m$  and  $r_t^k$ .

We can write  $V_N^*(A, q^i, Y^i - r_t^i)$  for the indirect utility of an asymptomatic individual who does not migrate, and note that it is increasing in  $Y^i$  and decreasing in  $q^i$  and  $r_t^i$ .

Consequently the condition for asymptomatic individuals to remain in their city of origin can be written as

$$V^*(A) \equiv V_N^*(A, q^i, Y^i - r_t^i) - V_M^*(A, q^k, Y^i - m - r_t^k) \geq 0$$

and we note that this condition is more likely to be fulfilled as  $q^i - q^k$  or  $r_t^i - r_t^k$  decrease or  $m$  increases.

### 3.3 Healthy individuals:

The decisions taken by healthy individuals are more complex than in the two preceding cases, since the probability of future health status is now endogenous to the individual's decisions, both via the preventive effect of health care and because it depends on the city in which the individual chooses to live. A healthy individual who chooses not to migrate must solve

$$\begin{aligned} & \text{Max}_{c_{jt}, x_{jt}} [U(c_{jt}, x_{jt}, q_t^i, H) + \\ & \quad \gamma (p_t^i / (1 + x_{jt})) W(q^i, Y^i, P^i, A) + (1 - p_t^i / (1 + x_{jt})) W(q^i, Y^i, P^i, H)] \end{aligned}$$

subject to

$$Y^i - c_{jt} - r_t^i - x_{jt} = 0$$

The first order conditions are

$$\frac{\partial U(H)}{\partial x_{jt}} - \frac{\partial U(H)}{\partial c_{jt}} - \gamma \left( \frac{p_t^i}{(1 + x_{jt})^2} \right) [W(q^i, Y^i, A) - W(q^i, Y^i, H)] = 0 \quad (4)$$

from which by substitution of (A5) we can write:

$$\frac{\partial U(H)}{\partial c_{jt}} = \gamma \left( \frac{p_t^i}{(1 + x_{jt})^2} \right) [W(q^i, C_j, H) - W(q^i, C_j, A)] \quad (5)$$

Thus the utility cost of consumption forgone to pay for treatment is set equal to the utility value of the reduction in the probability of falling sick.

A healthy individual who chooses to migrate will obtain utility equal to:

$$U(Y^i - m - r_t^k, 0, q_t^i, H) + \gamma (p_t^k W(q^k, Y^i, P^k, A) + (1 - p_t^k) W(q^k, Y^i, P^k, H))$$

We can write  $V_M^*(H, p_t^k, q^k, Y_t^i - m - r_t^k)$  for the indirect utility of a healthy individual who migrates, and note that it is increasing in  $Y^i$  and decreasing in  $p_t^k, q^k, m$  and  $r_t^k$ .

Similarly, we can write  $V_N^*(H, p_t^i, q^i, Y^i - r_t^i)$  for the indirect utility of a healthy individual who does not migrate, and note that it is increasing in  $Y^i$  and decreasing in  $p_t^i, q^i$  and  $r_t^i$ .

Consequently the condition for healthy individuals to remain in their city of origin can be written as

$$V^*(H) \equiv V_N^*(H, p_t^i, q^i, Y^i - r_t^i) - V_M^*(H, p_t^k, q^k, Y^i - m - r_t^k) \geq 0$$

and we note that this condition is more likely to be fulfilled as  $p_t^i - p_t^k$ ,  $q^i - q^k$  or  $r_t^i - r_t^k$  decrease or  $m$  increases. Since the utility cost of sickness is non-decreasing in income (Assumption A2) this condition will be less likely to be fulfilled as  $Y^i$  increases: healthy individuals will be more prepared to bear migration costs to reduce their risk of falling sick (just as they are more prepared to bear treatment costs) the richer they are.

Figure 1 represents the relationship between these three no-migration conditions in the space of relative disease prevalence and relative rents. Without loss of generality we assume that  $r_t^1 = 0$  and we can represent  $r_t^2$  on the horizontal axis, with the prevalence differential  $p_t^1 - p_t^2$  on the vertical axis. The non-migration condition for healthy individuals in city 1 is that  $V^*(H) = 0$ , and this is positively sloped, reflecting that a larger prevalence differential is compatible with a greater rent differential. (Note that the slope is decreasing in income.) It also has a positive intercept, reflecting that for low values of the prevalence differential it is more worthwhile for individuals to stay and take medical treatment in their city of origin even if there is no rent differential (there is a direct migration cost, and also an indirect cost in that they cannot take treatment if they migrate).

The non-migration condition for the other two categories of health status is vertical, reflecting that prevalence has no effect on the incentives to migrate, and the line  $V^*(S) = 0$  lies to the right of  $V^*(A) = 0$  reflecting the higher migration costs of the sick. The various zones of the figure are divided up according to whether they imply zero, one-way, or two-way migration. Note that, if rents clear the land market, only zero or two-way migration can be an equilibrium; one-way migration cannot be. Therefore migration by the healthy from city 1 to city 2 must be matched by migration of at least one of the other two categories from city 2 to city 1. Note also that migration generates a geographic sorting of individuals according to their health status: healthy individuals, if they migrate, go to the high rent and low prevalence city, while sick or asymptomatic individuals choose, if they migrate, the low rent and high prevalence city.

Finally, note that all of these three conditions are affected by migration costs (higher costs shift  $V^*(H) = 0$  upward and the other two curves to the right. They are also affected by future quarantine, but in interestingly different ways. The presence of quarantine in city 1 shifts  $V^*(S) = 0$  infinitely to the right. The expectation of future quarantine in city 1 shifts  $V^*(A) = 0$  and  $V^*(S) = 0$  to the right and  $V^*(H) = 0$  downward, with ambiguous effects on the overall space of two-way migration. The interpretation is interesting: the fear of future quarantine makes the healthy keen to flee the high-prevalence city, but it increases the tenacity with which the other risk categories (with whom the healthy have to compete for scarce land) stay in the low-prevalence city.

## 4 Solving the Model: the steady state

First, note that since individual decisions are contingent only on city-level and health-status exogenous variables we can write  $c^i(\theta)$  and  $x^i(\theta)$  for the values of  $c_{jt}$  and  $x_{jt}$  that solve these programs.

Secondly, in the steady state, populations and the proportion of individuals in each health category remain the same across periods in each city. The fact that populations remain the same implies that  $r_t^2$  clears the migration market so that net migration is zero.

Formally, therefore:

$$\begin{aligned} n_t^i &= n_{t+1}^i = 1 \text{ for } i = 1, 2. \\ p_t^i &= p_{t+1}^i = p^i \text{ for } i = 1, 2. \end{aligned}$$

$$a_t^i = a_{t+1}^i = a^i \text{ for } i = 1, 2.$$

First, we state a trivial proposition:

**Proposition 1** *There exists a steady state with  $p^1 = p^2 = 0$  and with zero gross migration.*

This states no more than the obvious truth that a disease cannot spread if it does not arise in the first place, and follows from the fact that healthy individuals become infected with a probability that is proportional to the prevalence of the city in which they choose to live. The fact that there is zero gross migration follows trivially from the fact that if prevalence is zero there is no motivation for migration from one city to the other.

However, the zero-prevalence steady state is not stable, in the sense that once an infection arises it will spread until the rate of new infections equals the rate at which sick individuals recover from the disease. Our next propositions examine the properties of such positive-prevalence steady states. We begin by examining the elementary case of steady states where the costs of migration are high enough to discourage all migration, both inside and in any relevant neighborhood of the steady state. Call these "high-cost" steady states.

**Proposition 2** *Given the incomes of city 1 and city 2, in any high-cost steady state  $p^i$  is decreasing in income and in the rate of recovery from the disease, and is lower if city  $i$  has announced a future quarantine.*

**Proof:**

Where gross migration is zero, we know that those falling sick in any period consist of those previously asymptomatic in the same city, and in the steady state these will exactly match the numbers recovering from the disease.

Indeed the prevalence rate of disease in city  $i$  in  $t+1$  will be equal to the number of asymptomatic individuals in period  $t$  plus the number of sick individuals in  $t$  who have not recovered from the disease, which is written as :

$$p_{t+1}^i = a_t^i + p_t^i(1 - \pi).$$

Similarly the number of asymptomatic individuals in period  $t+1$  is equal to the number of healthy individuals in  $t$  who have been infected by the disease, which is written as :

$$a_{t+1}^i = \frac{p_t^i}{1+x^i(H)} (1 - p_t^i - a_t^i)$$

Substituting the steady state conditions that  $p_{t+1}^i = p_t^i = p^i$  and  $a_{t+1}^i = a_t^i = a^i$  implies that  $a^i = \pi p^i$ .

Also this shows that  $p^i = \frac{1-\pi(1+x^i(H))}{(1+\pi)} = \frac{1-\pi}{1+\pi} - \frac{\pi x^i(H)}{(1+\pi)}$ , which is decreasing in both  $\pi$  and in  $x^i(H)$ .

$$\text{From (5) we know that } p^i = \frac{A}{\gamma} (1 + x^i(H))^2$$

where  $A = \frac{\frac{\partial U(H)}{\partial c_{jt}}}{[W(q^i, Y^i, H) - W(q^i, Y^i, A)]}$  is the ratio of the marginal utility of consumption to the utility cost of becoming infected.

The solution  $(p^i, x^i)$  to these simultaneous equations in  $p^i$  and  $x^i(H)$  will be unique, with  $p^i$  increasing in  $A$  and decreasing in  $\pi$ . From assumption (A2) we know that the denominator of  $A$  is non-decreasing in income. Therefore from the concavity of  $U$  we can conclude that  $p^i$  is decreasing in income. Since  $W(q^i, Y^i, H) - W(q^i, Y^i, A)$  is increasing in  $q^i$ , it follows also that  $p^i$  is decreasing in  $q^i$ .

### End of proof

This implies richer cities have lower steady state levels of disease prevalence. This is because with greater income the populations can afford higher investment in preventive treatment. Cities with quarantine have lower levels of prevalence (note that this has nothing to do with migration, but reflects the fact that the disutility of quarantine increases the incentive for individuals to take treatment). Diseases with higher rates of natural recovery have lower prevalence in the steady-state.

Figures 2 and 3 illustrate.

We now consider whether there exist steady states that are compatible with positive levels of gross migration. Where gross migration is not zero, two possibilities exist, compatible with the zero net migration implied by clearing of the rental market. One is that some proportion of the healthy migrate from high prevalence to low prevalence cities, and those who migrate in the other direction are a proportion of the asymptomatic (who no longer have anything to

fear from high prevalence). We specify "a proportion" because of our assumption that there are more healthy than asymptomatic individuals, so complete migration by both populations will not be feasible. Denote by  $\phi$  the proportion of the asymptomatic who migrate and by  $\psi$  the proportion of the healthy who migrate. Call any steady state in which costs are low enough that  $\phi$  may be strictly positive a "low cost" steady state.

The second possibility is that migration by the healthy is matched by return migration by both the asymptomatic and the sick. At present we ignore this possibility by assuming  $m^S$  to be sufficiently high, but note it for future work.

Recall that 1 denotes the high prevalence and 2 the low prevalence city. We can then state the following proposition:

**Proposition 3** *In any low-cost steady-state in which net migration is zero but a proportion  $\psi$  of healthy individuals in city 1 migrate and a proportion  $\phi$  of asymptomatic individuals in city 2 migrate,  $p^2$  is decreasing in  $\phi$ , and is equal to zero for  $\phi$  sufficiently close to 1.*

**Proof:**

We know that those falling sick in any period consist of those previously asymptomatic in the same city who have not migrated outwards, plus any previously asymptomatic in the other city who have migrated inwards, plus those who were previously sick in the same city and who have not recovered. We can therefore write the equations governing the evolution of prevalence rates in the two cities as follows:

$$p_{t+1}^1 = a_t^1 + \phi a_t^2 + p_t^1(1 - \pi) \quad (6)$$

$$p_{t+1}^2 = (1 - \phi)a_t^2 + p_t^2(1 - \pi) \quad (7)$$

Analogously, the asymptomatic in any city consist of those who were previously healthy and who have caught the disease, less those who have out-migrated, plus those who have in-migrated. We can write the equations governing the evolution of the proportion of asymptomatic individuals as follows:

$$a_{t+1}^1 = \frac{p_t^1}{1 + x^1(H)} (1 - \psi) (1 - p_t^1 - a_t^1) \quad (8)$$

$$a_{t+1}^2 = \frac{p_t^2}{1 + x^2(H)} (1 - p_t^2 - a_t^2) + \psi p_t^2 (1 - p_t^1 - a_t^1) \quad (9)$$

In the steady state those newly sick in each city in any period just equal the numbers who recover, so (recalling that the asymptomatic migrate only from city

2 to city 1) we can write  $\pi p^1 = a^1 + \phi a^2$  and  $\pi p^2 = (1 - \phi)a^2$ . The condition that net migration is zero implies that the gross migration flows in each direction are the same, so that  $\phi a^2 = \psi(1 - p^1 - a^1)$ . Substituting the second steady state condition in the form  $a^2 = \frac{\pi p^2}{(1 - \phi)}$  and the net migration condition into equation

9 and rearranging yields that  $p^2 = \text{Max} \left[ \frac{1 - \pi \left( \frac{1 + x^2(H)}{1 - \phi} \right)}{(1 + \frac{\pi}{1 - \phi})}, 0 \right]$ , which is strictly

decreasing in  $\phi$ , and is equal to 0 for  $\phi$  sufficiently close to 1. In addition, and unsurprisingly, as  $\phi$  tends to 0,  $p^2$  tends to  $\frac{1 - \pi(1 + x^2(H))}{(1 + \pi)}$ , which is the no-migration solution.

**End of proof**

In the presence of two-way migration, therefore, there is no longer a single prevalence function, common to the two cities. Instead there are two prevalence functions, one for each city, in which prevalence is a function both of the level of treatment and of the rate of migration. Migration for city 1 provides for an additional source of asymptomatic individuals, who raise the prevalence rate since they replace healthy individuals only some of whom would have caught the disease. For city 2 migration replaces some asymptomatic individuals in city 2 (who will develop the disease with probability 1) with healthy individuals, thereby reducing the prevalence rate both in the next period and in the steady state. The two phenomena interact, of course, in ways that affect the steady state prevalence in both cities. In particular, since in the steady state  $p^2$  is decreasing in  $\phi$ , so will be the rate at which individuals in city 2 catch the disease, and therefore the rate at which the city generates potential migrants to city 1. This means that, unlike  $p^2$ ,  $p^1$  will not be monotonic in  $\phi$ . Indeed, as  $\phi$  tends to 1,  $a^2$  will tend to zero and therefore the absolute numbers of migrants from city 2 to city 1 will tend to zero. The result will be a new steady state with  $p^1$  at the same level as in the absence of gross migration, but with  $p^2 = 0$ .

To see this, note that substituting the steady state conditions in equation 8 and re-arranging yields:

$$Q(p^1) \equiv \left( \frac{1 + \pi}{1 + x^1(H)} \right) (p^1)^2 + \left( \pi - \frac{1}{1 + x^1(H)} \right) p^1 - \phi a^2 = 0 \quad (10)$$

which is a quadratic with one strictly positive root and one non-positive root for all non-negative values of  $\phi a^2$ . Indeed  $\phi a^2 = 0$  both when  $\phi = 0$  and when  $\phi = 1$ , since in the latter case  $p^2 = 0$ . Figure 4 illustrates, showing  $p^1$  on the horizontal axis and  $Q(p^1)$  on the vertical axis: the positive root is the same for both  $\phi = 0$  and  $\phi = 1$ . Note that, as  $\phi$  increases,  $\phi a^2$  first increases then decreases, as  $a$  is endogeneous, until it reaches 0 when  $\phi = 1$ . Figure 5 shows, for given values of  $\pi$  and  $x^1(H)$ , the steady state value of  $p^1$  as a function of

$\phi$ . Call this function  $p(\phi)$  and define  $P(\phi) \equiv p(\phi) - \frac{1 - \pi \left( \frac{1 + x^2(H)}{1 - \phi} \right)}{(1 + \frac{\pi}{1 - \phi})}$ . We can call

$P(\phi)$  the "prevalence gap" between cities 1 and 2 and note that it is continuous, strictly positive and has an interior maximum in  $\phi$ . Figure 5 also plots  $P(\phi)$ ; note that  $P(\phi) > P(0)$  for all  $\phi > 0$ .

Using equation 10 we can show the following proposition:

**Proposition 4** *If migration costs are sufficiently low that non-zero gross migration occurs in equilibrium out of the steady state, the only steady state with positive prevalence and  $\phi = 1$  has  $p^2 = 0$  and  $p^1 = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$ . This steady state has zero gross migration and has strictly lower prevalence than the steady state in which migration costs are high enough to rule out gross migration out.*

**Proof**

From Proposition 3 we know that the only steady state with  $\phi = 1$  has  $p^2 = 0$ . From equation 9 it follows that  $a^2 = 0$  and that therefore gross migration is zero. Substituting  $a^2 = 0$  in equation 10 yields the solutions  $p^1 = 0$  and  $p^1 = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$ . From Proposition 2 we know that this is the same value for  $p^1$  as in the steady state where there is zero gross migration outside the steady state, but that  $p^2$  is strictly lower (namely zero) when gross migration is positive outside the steady state. Since there is no migration, and therefore no migration cost, and since it has the same prevalence in city 1 and a strictly lower prevalence in city 2, the steady state with non-zero gross migration out of steady state Pareto-dominates the steady state with zero gross migration out of steady state.

**End of proof**

Note how the possibility of migration makes the crucial difference between the two steady states *even though in the steady state no actual migration takes place*. This is because any infected individuals who arise in city 2, instead of remaining in city 2 where they progressively infect the rest of the population, migrate out immediately to city 1. This keeps the prevalence rate at zero in city 2. It has no lasting effect on the prevalence in city 1, though, because in the steady state there is no further in-migration and the prevalence in city 1 is determined in exactly the same way as it was in the non-migration steady state.

Propositions 2 and 4 have merely characterized two steady states according to whether or not migration costs are low enough for gross migration to occur out of steady state. It has not been shown that such steady states actually exist. This is the task of Proposition 5, which shows that not only will one or the other always exist but there may for some levels of migration costs exist multiple steady states.

**Proposition 5** Let  $m^*(Y^1, Y^2, p)$  be the value of  $m$  such that, given the income levels in the two cities and the induced equilibrium rental in city 2, and given that  $p_t^1 - p_t^2 = p$ , asymptomatic individuals in city 2 are just indifferent between remaining in city 2 and migrating to city 1. It is immediate that  $m^*(Y^1, Y^2, p)$  is increasing in  $p$ . Then:

i) If  $m < m^*(Y^1, Y^2, p^L)$  where  $p^L = \frac{1-\pi(1+x^1(H))}{(1+\pi)} - \frac{1-\pi(1+x^2(H))}{(1+\pi)}$ , there exists one and only one positive-prevalence steady state with zero gross migration, with  $p^1 = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$  and with  $p^2 = 0$ .

ii) If  $m > m^*(Y^1, Y^2, p^H)$  where  $p^H = \max_\phi [P(\phi)]$ , there exists one and only one positive-prevalence steady state with zero gross migration, with  $p^1 = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$  and with  $p^2 = \frac{1-\pi(1+x^2(H))}{(1+\pi)}$ .

iii) If  $m^*(Y^1, Y^2, p^L) \leq m \leq m^*(Y^1, Y^2, p^M)$  where  $p^M = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$ , there exist two positive-prevalence steady states with zero gross migration, both with  $p^1 = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$ , one with  $p^2 = \frac{1-\pi(1+x^2(H))}{(1+\pi)}$  and the other with  $p^2 = 0$ . The latter Pareto-dominates the former. In addition, there exists a third steady state with positive gross migration at  $0 < \phi < 1$ .

iv) If  $m^*(Y^1, Y^2, p^M) < m \leq m^*(Y^1, Y^2, p^H)$ , there exist one positive-prevalence steady state with positive gross migration, with  $p^1 = \frac{1-\pi(1+x^1(H))}{(1+\pi)}$  and with  $p^2 = \frac{1-\pi(1+x^2(H))}{(1+\pi)}$ . In addition, there exist two steady states with positive gross migration at  $0 < \phi < 1$ .

**Proof.** The proof of (i) follows from noting that  $P(0) = p^L$  and that  $P(\phi) > P(0)$  for all  $\phi > 0$ , so that when  $m < m^*(Y^1, Y^2, p^L)$  all asymptomatic individuals will always wish to migrate at (strictly positive) steady state prevalence levels regardless of the value of  $\phi$ . Thus the only steady state has  $\phi = 1$  at which gross migration in the steady state is zero.

The proof of (ii) follows similarly from noting that  $p^H = \max_\phi [P(\phi)]$  so that asymptomatic individuals will never wish to migrate at (strictly positive) steady state prevalence levels regardless of the value of  $\phi$ . Thus the only steady state has  $\phi = 0$  at which gross migration in the steady state is also zero.

The proof of (iii) follows from noting that  $P(1) = p^M$  so for values of  $m$  intermediate between  $m^*(Y^1, Y^2, p^L) \leq m \leq m^*(Y^1, Y^2, p^M)$  asymptomatic individuals will not wish to migrate at steady-state prevalence levels if  $\phi = 0$  and will always wish to do so if  $\phi = 1$ . The Pareto-dominance of the steady state with  $\phi = 1$  follows from the fact that migration (and thus migration costs) are zero in both steady states and  $p^1$  is the same in the two steady states, but  $p^2$  is unambiguously lower when  $\phi = 1$ . The existence of the third steady state follows from the continuity of  $P(\phi)$ .

Finally, the proof of (iv) follows likewise from the continuity of  $P(\phi)$ , noting also that for  $m > m^*(Y^1, Y^2, p^M)$  asymptomatic individuals will not wish to migrate at steady-state prevalence levels if  $\phi = 1$ , so that  $\phi = 1$  is not a steady state. ■

Figure 6 provides geometrical intuition for this proof, plotting  $P(\phi)$  against  $\phi$ , showing on the vertical axis the threshold levels of the prevalence gap. The case illustrated is case (iii), and  $p^m$  denotes the level of  $p$  at which the asymptomatic are just indifferent given actual migration costs  $m$ ; thus  $m \equiv m^*(Y^1, Y^2, p^m)$ . The two steady states at  $\phi = 0$  and  $\phi = 1$  are illustrated as is the one in between where  $p^m = P(\phi)$ .

The fact that the steady state with  $\phi = 1$  Pareto-dominates that with  $\phi = 0$  has important implications for policy. In this model it is a good thing for there to be outmigration of asymptomatic individuals from city 2 (driven by the higher rents due to competition from individuals in-migrating from city 1). The reason for this is that outmigration of such individuals removes them from where they would contribute to new infections and places them in a city in which the disease is already established and to which their presence will bring no lasting deterioration in the prevalence. In these circumstances, action by the authorities should not be to discourage migration but rather actively to encourage it. In the steady state there will in fact be no migration, but out of the steady state such migration is an important means of reducing the risk that the disease established in city 1 also establishes itself in city 2.

## 5 Conclusion: What Have We Learned?

Our dynamic model has indicated that differences in prevalence rates of disease may emerge as the equilibrium outcome of more fundamental differences in economic endowments, with migration behaviour acting as a means of arbitrage between places with difference prevalence levels. We have also shown that whether migration takes place out of the steady state has important implications for steady state prevalence levels even if there is no migration at the steady state. In particular, it is desirable for infected individuals to migrate away from low-prevalence localities since these are the ones in which they create the greatest negative externalities. This has potentially important implications for policy since it suggests that, far from seeking to discourage voluntary migration in conditions of endemic disease, it may sometimes be desirable to encourage it. We do not pretend that the conditions described in our model are general (indeed in our paper Mesnard & Seabright 2007 we describe conditions under which it is preferable to discourage migration). However, we do believe it is important to model very carefully the interactions between disease and migration in order to ensure that policy interventions do not have counter-productive consequences. We also believe that segregation by disease-prevalence of neighborhoods within cities, and of regions within countries, has been a phenomenon of historical significance which models of this kind can help us to understand.

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## 7 List of Figures

**Figure 1: No-migration constraints for healthy, asymptomatic and sick individuals**

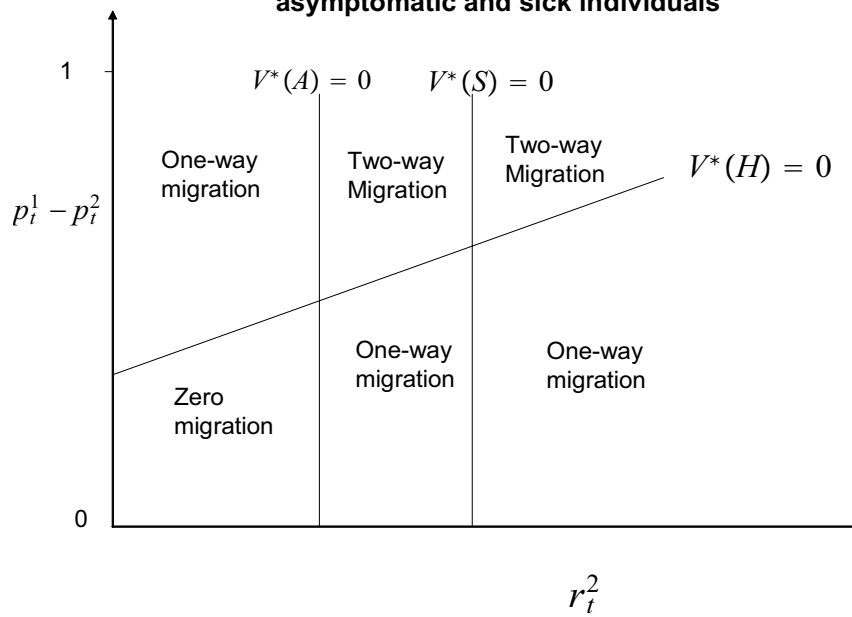
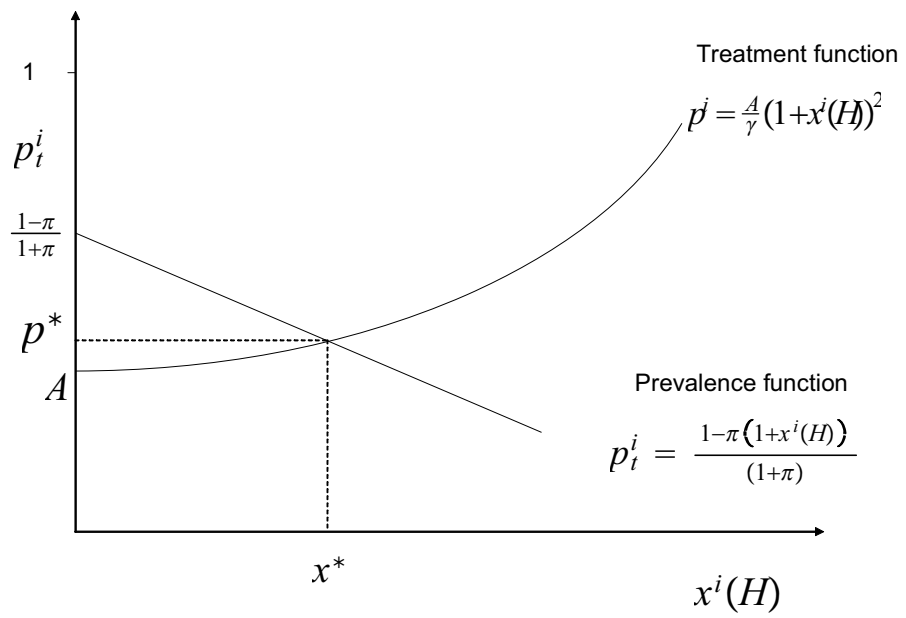
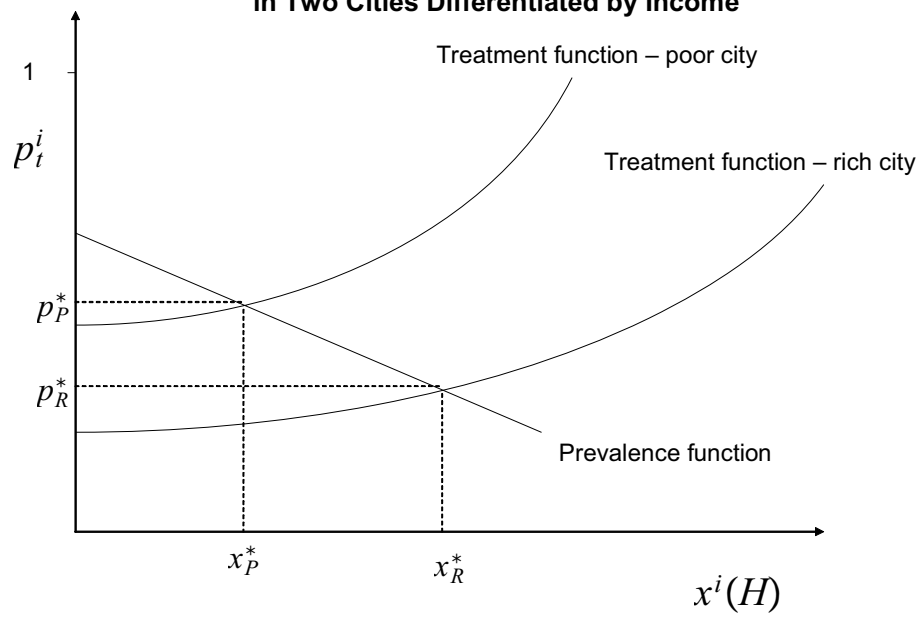


Figure 2: Determinants of Steady State Disease Prevalence



**Figure 3: Determinants of Steady State Disease Prevalence in Two Cities Differentiated by Income**



**Figure 4: Values of  $Q(p^1)$  and  $p^1$**

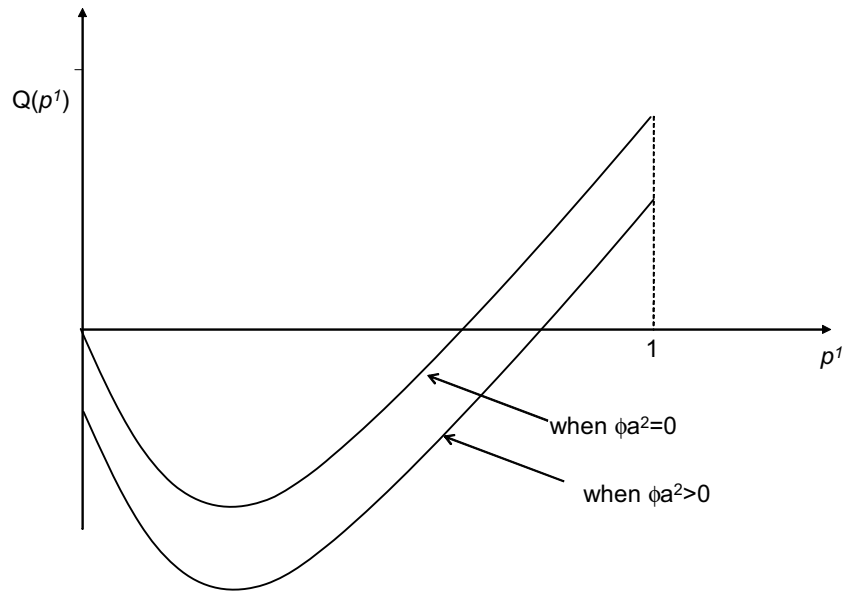


Figure 5: Prevalence and Prevalence Gaps as a function of  $\phi$

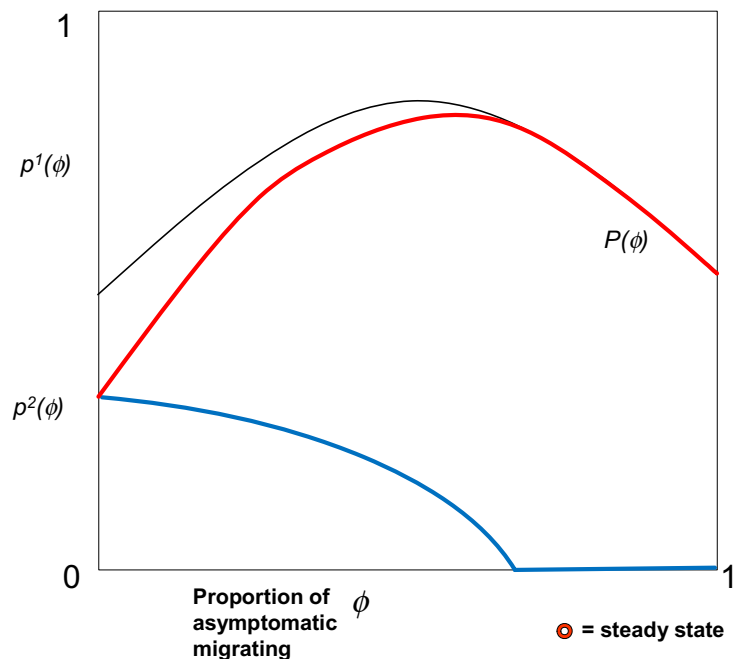


Figure 6: Prevalence Gaps and Migration: steady states

