

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 shows how the possibility of migration away from high-prevalence areas affects long-run steady state disease prevalence. We develop a dynamic framework where migration responds to the prevalence of disease, to the costs of migration and to health regulations. The model treats disease prevalence as an endogenous consequence of other characteristics of the areas concerned, notably their environment. It explores how pressure for migration in response to differing equilibrium levels of disease prevalence generates differences in city characteristics such as land rents. Competition for scarce housing in low-prevalence areas can create segregation, with disease concentrated in high-prevalence "sinks". We show that multiple steady states can coexist and explore their comparative static properties. In particular we find that migration can have health benefits, in that it 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 spreading diseases through the effect of crowding, we study its consequences for the composition of populations, which, in turn, affects the evolution of disease. If migration responds to disease incidence as well as influences it, feedback effects may either dampen or magnify initial differences in disease prevalence between locations. We show in particular how, for a large class of infectious endemic diseases, migration can magnify initial differences, 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 because they cannot compete with healthy individuals for scarce space in healthier localities. We show that multiple steady states can exist 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 disease¹. 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)².

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 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 patterns³.

However, migration as a form of preventive behaviour has received very little attention

¹For a recent contribution, see Boily et al. (2007).

²During the Black Death, inhabitants from infected villages frequently migrated to less infected neighboring villages. More recently, after the SARS outbreak in China, numerous workers in urban areas returned to live with their families in safer rural areas (Le Point, 2003).

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

before Mesnard and Seabright (2009), although evidence has accumulated that migration behaviour and epidemics are intrinsically linked. 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. Modern social scientists have not to our knowledge studied the fact that endemic disease may influence migration decisions despite 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 Illinois⁴. 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.

⁴Alexis 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>

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 Organization⁵ 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 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 surprising 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 (Bell et al. 2006, Duncan et al. 1999, Hurd, et al. 2003, Marmot, 2002). And there is strong evidence that epidemic outbreaks cause important economic losses⁶. Furthermore, asset markets may also be affected, as was observed on the housing market in Hong Kong after the SARS outbreak (Wong, 2008). However, among these linkages, migration has attracted 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 land⁷. This requires

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

⁶For 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).

⁷It 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 (2009). 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

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 economy⁸. Individuals 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 decisions about whether to stay in their city of origin or to migrate to the other city, which determines their consumption levels and their risk of being infected in the future. 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 the migration choice 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 and Seabright, 2009, where individuals differ in an individual risk parameter. As individuals may have more information than the health authorities about their probability of being infected, we showed that quarantine measures may have unexpected effects on the spread of diseases, as they may give too high or too low incentives to migrate. This comes from the fact that migrants exert an externality on other individuals living in the destination and origin areas, which depends on their own risk of having caught the disease. The type of externality outlined in that two period model affects the spread of disease in the short run - just after the outbreak of an epidemic disease. In contrast, in the present paper we show that there is a difference between short run and long run externalities. When the costs of migration are prohibitively high, an individual living in a city with zero prevalence imposes a very large externality in the long run if she acquires an infectious disease, because the people she infects directly and indirectly lead to the disease eventually reaching a positive steady state prevalence. However, if the same individual can migrate to a high prevalence city, the long run externality he/she imposes is zero. The fact that migration may lead to a sorting of sick/healthy individuals to high/low infected areas, has thus important policy

easier to define and solve for a steady state.

⁸For 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.

implications that are studied in the present paper.

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 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 in circumstances where migration costs are sufficiently high to discourage migration both in and out of the steady state. As expected we show that cities with a healthier environment will have lower disease prevalence rates.

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 sick individuals to migrate in the opposite direction. Historically there is good reason to think that segregation of neighborhoods by disease incidence has an important influence on the spatial composition of cities and countries, and that relative housing costs play 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 of infectious diseases on migration, it seems likely that they help explain some important characteristics of the geography of development, past and present.

We show that, if all sick individuals do thus migrate, the prevalence rate 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 be-

tween 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 and 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).

A distinctive feature of our model is that 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 the possible role of migration policies in selecting one or the other equilibrium.

The paper proceeds as follows. Section 2 presents the model, Section 3 explains how individuals make their decisions, Section 4 studies the steady-state equilibria and shows that multiple equilibria co-exist. Section 5 discusses the policy implications and concludes. The Appendix contains all mathematical proofs and figures.

2 The model

Consider a discrete time, infinite horizon model with two equally-sized cities in terms of population, indexed by $i \in \{1, 2\}$. We normalize total population size in each city to 1.

Y denotes the constant per-period exogenous income in both cities (income is an endowment, and agents are assumed identical in income). We assume that one city has a less healthy environment, which favors the spread of disease (think for example as low altitude or a high degree of humidity, which may favour airborne or insect born diseases). We will capture the degree of environmental unhealthiness of city i by a parameter α^i and assume, without loss of generality, that $\alpha^1 > \alpha^2$. We also assume that $\alpha^2 < 1$, which ensures interior solutions by ruling out theoretically possible but empirically uninteresting cases of diseases which affect the entire population.

Out of this income, individuals must pay a rent r_t^i in the city in which they choose to live. To simplify the calculations we assume that land is not scarce at the margin in the poor city, so that $r_t^1 = 0$ for all t . This means we can write $r_t \equiv r_t^2$ for the rent in the rich

city. This rent will be endogenously determined by a land market that clears when the net demand of individuals for migration to the rich city is zero.

Each individual can be in two states of health, denoted by θ : healthy (H) or sick (S). At time t , a proportion p_t^i of city i 's population are sick, the proportion of healthy inhabitants being therefore $(1 - p_t^i)$. We call p_t^i the "prevalence" of the disease in city i at time t . We assume that $p_t^1 + p_t^2 < 1$ to capture the fact that the sick are a minority of the total population.

There is an exogenous utility cost m of migrating from one city to the other. Utility is separable in this cost and in a term $U(c, \theta_t)$ that is increasing and weakly concave in consumption c_t at time t .

The assumption that utility is separable in the migration cost greatly simplifies the calculations because the derivatives of utility with respect to rents and disease prevalence do not depend on whether an individual has migrated in any given period, but it is unlikely that the qualitative findings of the model turn importantly on this restriction.

At the beginning of each period individuals observe their current health status. They also have perfect foresight of the values of all parameters and city-level endogenous variables (namely $Y, m, p,$ and r). They choose whether or not to migrate to the other city and all individuals receive the incomes and pay the rents in the city they have chosen to live in and consume the residual.

Accordingly, individuals living in city i face a per period budget constraint:

$$Y - r_t^i = c_t \quad (1)$$

The health status of individuals evolves as follows:

Healthy individuals' likelihood of becoming infected increases with the local prevalence, p_t^i , and the degree of unhealthiness of their environment:

$$P[\theta_{t+1} = S / \theta_t = H] = \alpha^i p_t^i \quad (2)$$

Sick individuals recover from the disease naturally with exogenous probability π .

$$P[\theta_{t+1} = H / \theta_t = S] = \pi \quad (3)$$

We assume $\pi < \alpha^2 < \alpha^1$ in order to focus on interior solutions (diseases with higher recovery rates never become established as endemic in the population).

The expected present value of current and future utility of individuals of type θ_t in city i at time t is:

$$W_t^i = \sum_{\tau=t}^{\infty} \gamma^{\tau-t} [U(c_\tau, \theta_\tau) - mI_\tau] \quad (4)$$

where I_t is an indicator function taking the value 1 if they migrate in period t , otherwise 0.

We make the following assumptions about the effect of sickness on individual utilities: Sickness lowers current welfare:

$$U(c_t, S) \leq U(c_t, H) \quad (5)$$

The effect of sickness on current welfare is non-decreasing in consumption:

$$\frac{\partial (U(c_t, H) - U(c_t, S))}{\partial c_t} > 0 \quad (6)$$

Note that we do not allow individuals to smooth consumption across time. Allowing for savings in our model would make each individual's decisions in any period dependent on the entire history of their consumption decisions as well as on their entire medical history, which would greatly complexify the model with no extra gains for the understanding of our main results. As it is, individuals' decisions are fully determined by their current health status and their city of residence, which gives us four distinct cases to study. We therefore write the objective function explicitly as a function of current health status as follows:

$$W_t^i = W_t^i(\theta_t)$$

3 Individual decisions

We first note that the objective function can be rewritten as follows, where i is the individual's city at the beginning of the period and k is the city in which they choose to live:

$$W_t^i(\theta_t) = U(Y - r_t^k, \theta_t) - mI_t + \gamma \sum_{\theta_{t+1}} W_{t+1}^k(\theta_{t+1}) P(\theta_{t+1}|\theta_t) \quad (7)$$

from this it follows that $W_t^i(\theta_t)$ is strictly increasing in Y and strictly decreasing in r_t^k , and weakly decreasing in m .

Next, for each value of the current health status, we compare the utility of each individual in case she chooses not to migrate to the utility in case she migrates.

3.1 Individual migration choices

A healthy individual who chooses not to migrate and for whom therefore $k = i$ will receive utility:

$$U_N^i(H) \equiv U(Y - r_t^i, H) + \gamma \alpha^i p_t^i W_{t+1}^i(S) + \gamma(1 - \alpha^i p_t^i) W_{t+1}^i(H) \quad (8)$$

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

$$U_M^i(H) \equiv U(Y - r_t^k, H) - m + \gamma \alpha^k p_t^k W_{t+1}^k(S) + \gamma(1 - \alpha^k p_t^k) W_{t+1}^k(H) \quad (9)$$

The agent who is currently sick and chooses not to migrate will receive utility:

$$U_N^i(S) \equiv U(Y - r_t^i, S) + \gamma \pi W_{t+1}^i(H) + \gamma(1 - \pi) W_{t+1}^i(S) \quad (10)$$

A sick individual who chooses instead to migrate from city i to city k will obtain utility equal to:

$$U_M^i(S) \equiv U(Y - r_t^k, S) - m + \gamma \pi W_{t+1}^k(H) + \gamma(1 - \pi) W_{t+1}^k(S) \quad (11)$$

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

$$U_M^i(H) - U_N^i(H) \geq 0 \quad (12)$$

or written out in full as

$$\begin{aligned} 0 \leq & U(Y - r_t^k, H) - U(Y - r_t^i, H) - m + \gamma \alpha^k p_t^k W_{t+1}^k(S) - \gamma \alpha^i p_t^i W_{t+1}^i(S) \dots \\ & \dots + \gamma(1 - \alpha^k p_t^k) W_{t+1}^k(H) - \gamma(1 - \alpha^i p_t^i) W_{t+1}^i(H) \end{aligned} \quad (13)$$

and we note that, from (5) and (6), this condition is more likely to be fulfilled as $p_t^i - p_t^k$ or $r_t^i - r_t^k$ increase, and as m decreases, as we would expect.

Similarly the condition for sick individuals to migrate can be written as

$$U_M^i(S) - U_N^i(S) \geq 0 \quad (14)$$

which when written out in full is

$$\begin{aligned} 0 \leq & U(Y - r_t^k, S) - U(Y - r_t^i, S) - m + \gamma \pi (W_{t+1}^k(H) - W_{t+1}^i(H)) \dots \\ & \dots + \gamma(1 - \pi) (W_{t+1}^k(S) - W_{t+1}^i(S)) \end{aligned} \quad (15)$$

and we note that this condition is more likely to be fulfilled as $p_t^i - p_t^k$ or $r_t^i - r_t^k$ increases and as m decreases, as we would expect.

3.2 Migration flows at steady state

We first define a steady state as a set of values $r_t^i, r_t^k, p_t^i, p_t^k, \phi$ and ψ such that

1) $r_t^i, r_t^k, p_t^i, p_t^k$ remain the same in all periods (we drop the time subscripts to indicate steady state values);

2) ϕ and ψ are consistent with zero net migration (that is, the proportion ϕ of the sick who migrate yields the same absolute number of migrants as the proportion ψ of the healthy who migrate);

3) the values of ϕ and ψ are each consistent with individuals' migration behavior given their migration costs.

For ease of reference we shall sometimes refer to condition 2) as the "adding-up condition", and condition 3) as the "behavioral condition". These are both conditions ensuring that ϕ and ψ represent equilibria of the model. Condition 1) is different: it ensures that the values of $r_t^i, r_t^k, p_t^i, p_t^k$ derived above represent steady state values.

Next we characterise migration flows at such steady states. We can write $V^i(H) \equiv V^i(Y - r^i, H)$ for the indirect steady state utility (excluding any migration cost) of a healthy individual who chooses to reside in city i , and $V^i(S)$ for the corresponding indirect utility of a sick individual.

Let $T^i(H) \equiv V^k(H) - V^i(H)$ be the gain (gross of migration costs) to a healthy individual from migrating from i to k given steady state values of r^i, r^k, p^i and p^k , and $T^i(S) \equiv V^k(S) - V^i(S)$ be the corresponding gross gain for a sick individual.

Note that, whether or not an individual has migrated in period t , she will not migrate in period $t + 1$ unless her health status changes with respect to period t , because her choice of location in t conditional on her health status will remain her optimal choice of location in the next period. Using this insight we can substitute steady state values in (13) and (15) to yield

$$T^i(H) \equiv U(Y - r^k, H) - U(Y - r^i, H) \dots \quad (16)$$

$$\begin{aligned} & + \gamma \alpha^k p^k (V^k(S) + \text{Max}[T^k(S) - m, 0]) - \gamma \alpha^i p^i (V^i(S) + \text{Max}[T^i(S) - m, 0]) \dots \\ & \dots + \gamma(1 - \alpha^k p^k)V^k(H) - \gamma(1 - \alpha^i p^i)V^i(H) \end{aligned} \quad (17)$$

The term on the first line is the gain in present utility (gross of migration costs) for a healthy individual to move from city i to city k ; the term on the second line is the future gain to move from city i to city k if the given that the individual catches the disease with a probability, which depends on the city of residence; the term on the third line is the future gain to move from city i to city k given that the individual does not catch the disease where he/she lives.

Similarly we can write

$$\begin{aligned} T^i(S) \equiv & U(Y - r^k, S) - U(Y - r^i, S) + \gamma(1 - \pi) [V^k(S) - V^i(S)] \quad (18) \\ & + \gamma\pi [V^k(H) + \text{Max}[T^k(H) - m, 0] - V^i(H) - \text{Max}[T^i(H) - m, 0]] \end{aligned}$$

which simplifies to

$$T^i(S) \equiv U(Y - r^k, S) - U(Y - r^i, S) + \gamma(1 - \pi)(T^i(S)) \quad (19)$$

$$+ \gamma\pi(T^i(H) + \text{Max}[T^k(H) - m, 0] - \text{Max}[T^i(H) - m, 0])$$

Figure 1 shows how these two conditions define different zones of migration behavior between cities 1 and 2 in the space of relative disease prevalence and relative rents. Since city 1 is defined as the high-prevalence city, healthy individuals, if they migrate at all, will migrate from city 1 to city 2 while sick individuals, if they migrate at all, will migrate from city 2 to city 1. The horizontal axis plots $\lambda = p^1 - p^2$ which is the relative prevalence of disease in city 1 compared to city 2. The vertical axis plots r^2 the rent in city 2 (which is also the relative rent in city 2 compared to city 1 since $r^1 = 0$). Within this space we define a locus of points $T^1(H) = m$ and $T^2(S) = m$, which we term "migration boundaries", each being (for the relevant agent type) the set of points at which the gross benefits from migration just equal the one-time cost m . We examine how these points vary with λ and r^2 .

First of all, we can show in the Appendix that for the zone in which there is positive migration by healthy individuals, the locus $T^2(S) = m$ is horizontal.

We also show in the Appendix that the locus $T^1(H) = m$ is positively sloped, reflecting that a larger prevalence differential is compatible with a greater rent differential.

It also has a negative intercept, reflecting that for low values of the prevalence differential it is more worthwhile for individuals to stay in their city of origin even if there is no rent differential (as there is a migration cost).

Finally, we show that the migration boundary for sick individuals has a flatter slope than the migration boundary for healthy individuals.

We have thus established the following Lemma:

Lemma 1 :*Sick individuals respond relatively more strongly to a difference in rental rate on the housing market compared to a difference in prevalence rate of the disease, than healthy individuals.*

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 by sick individuals 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 individuals choose, if they migrate, the low rent and high prevalence city.

Finally, note that these conditions are affected by migration costs (higher costs shift $T^1(H)$ downwards and $T^2(S)$ upwards) such that the sizes of the zones with two-way or one-way migration are reduced, as we would expect.

3.3 The distribution of migration costs

We assume that migration costs are realized randomly and independently in every period and are independent of current and past health status. In each period, each individual's migration cost is distributed continuously on the support (m_0, m_1) according to a distribution function $c(m)$. We assume $c(m) > 0 \forall m > m_0$, and $c(m) < 1 \forall m < m_1$.

Define m^* such that $c(m^*) = \frac{\alpha^2 - \pi}{1 - \pi}$.

Define r^{\max} as the rent that discourages all healthy individuals from migrating even at maximum prevalence differential. Thus at $m = 0$ and $p_2 - p_1 = 1$, a healthy individual just prefers not to migrate at r^{\max} .

Define r^{\min} as the rent that just encourages all sick individuals from migrating even at maximum prevalence differential. Thus at $m = m_1$ and $p_2 - p_1 = 1$, a sick individual prefers to migrate at any rent $r > r^{\min}$.

Define $T^i(S, m)$ be the value of $T^i(S)$ for an individual with migration cost m .

We define three types of possible assumption about migration costs: High, Low and Intermediate.

High costs are those where m_0 is sufficiently large that, however high the prevalence gap between cities, nobody will wish to migrate however low the rent in city 2. Specifically:

A High Cost: $r^{\max} \leq 0$

Low costs are those where m_1 is sufficiently small that, however high the prevalence gap between cities, every sick individual will wish to migrate from city 2 given any positive rent. Specifically:

B) Low Cost: $r^{\min} = 0$

Intermediate costs are those where, at the steady state, some but only some individuals in any category will wish to migrate. Specifically:

C) Intermediate Cost: $c(m)$ has two properties:

$$m_0 = 0 \tag{20}$$

$$T^i(S, m^*) < 0 \text{ if } r^2 = r^{\max} \tag{21}$$

Equation (20) implies that the lowest costs are low enough to encourage at least some healthy people to migrate if rents are low enough.

Equation (21) implies that the highest costs are high enough so that less than $\frac{\alpha^2 - \pi}{1 - \pi}$ of sick people will migrate even at a rent high enough to discourage all healthy people from migrating.

Note that these categories of cost distribution are not exhaustive: it is possible for costs to be distributed in such a way that they are neither High, Low nor Intermediate.

4 Steady state equilibria

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:

$$n_t^i = n_{t+1}^i = 1 \text{ for } i = 1, 2 \text{ after normalisation.}$$

$$p_t^i = p_{t+1}^i = p^i \text{ for } i = 1, 2.$$

We can thus infer easily that:

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

This simply states 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:

Proposition 2 *Given the differences in environment between city 1 and city 2, in any steady state with High Costs p^i is increasing in the degree of unhealthiness of the environment and decreasing in the rate of recovery from the disease such that $p^i = 1 - \pi/\alpha^i$.*

This implies cities with lower α (as for example low degree of humidity for the case of malaria) have lower steady state levels of disease prevalence and diseases with higher rates of natural recovery have lower prevalence in the steady-state.

We now consider whether there exist steady states that are compatible with positive levels of gross migration. Where gross migration is not zero, the zero net migration implied by clearing of the rental market implies 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 sick (who no longer have anything to fear from high prevalence). We specify "a proportion" because of our assumption that there are more healthy than sick individuals, so complete migration by both populations will not be feasible. Denote by ϕ the proportion of the sick who migrate and by ψ the proportion of the healthy who migrate, and note that $\psi > \phi$ when migration is strictly positive, because $p_t^1 + p_t^2 < 1$ which implies that the sick in city 2 are less numerous than the healthy in city 1. Call any steady state in which costs are low enough that ϕ may be strictly positive a "low cost" steady state.

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

$$p_{t+1}^1 = (1 - p_t^1)(1 - \psi)\alpha^1 p_t^1 + \phi p_t^2(1 - \pi) + p_t^1(1 - \pi) \quad (22)$$

$$p_{t+1}^2 = \alpha^2 p_t^2(1 - p_t^2) + \psi(1 - p_t^1)\alpha^2 p_t^2 + (1 - \phi)p_t^2(1 - \pi) \quad (23)$$

In order for equations (22) and (23) to characterise the steady state equilibria the values of p_t^1 and p_{t+1}^1 must be the same and the values of ψ and ϕ have to be consistent with steady state equilibrium. In order for the values of ψ and ϕ to be consistent with steady state equilibrium :

1) the "adding up condition" has to hold, which implies that the proportion ϕ of the sick who migrate yields the same absolute number of migrants as the proportion ψ of the

healthy who migrate, so that

$$\phi p^2 = \psi (1 - p^1) \quad (24)$$

2) the "behavioural condition" implies that the demand for migration by proportion ϕ of the sick is generated by the same r^2 in city 2 as generates the demand for migration by a proportion ψ of the healthy.

Replacing (24) into (22) and (23) and rewriting these equations at the steady state gives:

$$p^1 = (1 - p^1)(1 - \psi)\alpha^1 p^1 + \psi (1 - p^1) (1 - \pi) + p^1(1 - \pi) \quad (25)$$

$$p^2 = \frac{\alpha^2 - \pi - \phi(1 - \pi)}{\alpha^2(1 - \phi)} \text{ or } p^2 = 0 \quad (26)$$

If p^2 is 0 we can show easily the following proposition:

Proposition 3 *If migration costs are distributed according to the Low Cost assumption, so that non-zero gross migration occurs in equilibrium out of the steady state, there exists a steady state which has $p^1 = 1 - \pi/\alpha^1$ and $p^2 = 0$. This steady state has zero gross migration and Pareto dominates the steady state with zero gross migration out of steady state.*

Note how the possibility of migration makes the crucial difference between the steady states described in Propositions 2 and 3 *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.

Furthermore, when non-zero gross migration is possible out of the steady-state, there may exist steady states with non-zero gross migration. Specifically this will happen when migration costs are Intermediate as shown in Appendix.

Prevalence in city 1 is the same in the steady states defined by Propositions 2 and 3; only that in city 2 differs. Propositions 2 and 3 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. We can interpret migration costs as the effects of quarantine measures. If quarantine measures are so severe that there is zero migration, then global

prevalence rate will be higher than if quarantine is not so severe that there is two-way migration out of the steady state.

The fact that the steady state with non zero gross migration out of equilibrium Pareto-dominates that with zero migration has important implications for policy. In this model it is a good thing for there to be outmigration of sick 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

Our analysis indicates that differences in disease prevalence rates can emerge as the equilibrium outcome of more fundamental differences in environment, with migration behaviour acting as a means of arbitrage between locations with different 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.

In our model the willingness to pay of healthy individuals to live close to other healthy individuals exceeds that of sick individuals, which leads to sorting by health and higher costs of living in healthier areas. This, however, is true only under certain conditions. Indeed, as we discussed, 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 high-prevalence environments, which would act against segregation. Moreover, as shown in Mesnard and Seabright (2009), 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 on the short run even if they do not wholly offset

them.

The conditions described in our model are thus not general but they do constitute an important class of cases for public policy to bear in mind and warn policy makers to take into account positive externalities generated by migration in the presence of endemic diseases. Public policy needs to model very carefully the interactions between disease and migration in order to ensure that policy interventions do not have counter-productive consequences on the short run (Mesnard Seabright 2009) and on the long run, as highlighted in the present paper. 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. Given the startling differences in disease prevalence between different regions of the world, it remains of real significance today. And given the likely emergence of new forms of antibiotic-resistant infections in years to come, some of which may become endemic in certain parts of the world, the problem can only grow in importance in the future.

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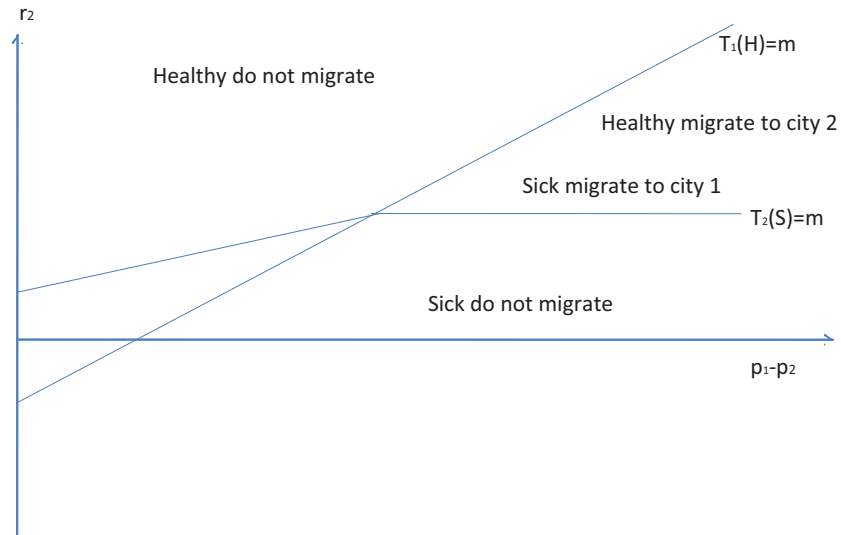
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Figure 1 : migration choices at steady states



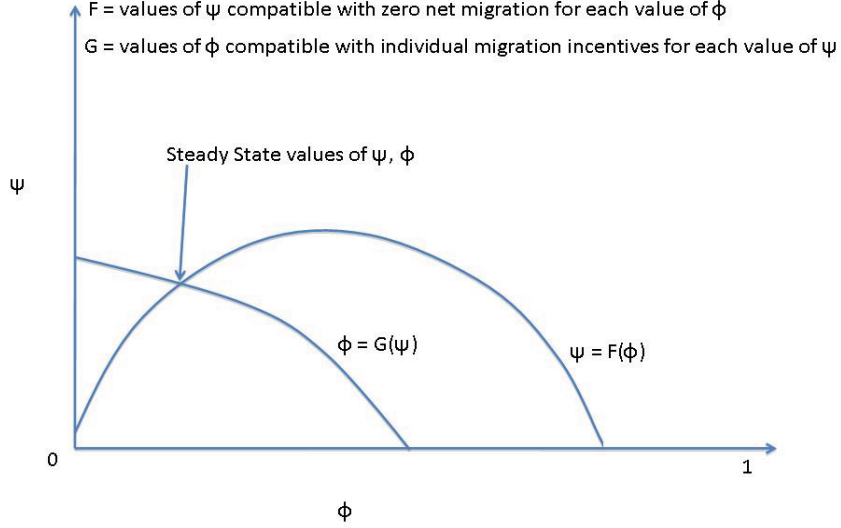
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7 APPENDIX

Figures

Figure 2: Existence of steady state with $\phi, \psi > 0$



Proofs of section 3:

To see that for the zone in which there is positive migration by healthy individuals (ie where $T^1(H) - m > 0$), the locus $T^2(S) = m$ is horizontal, rewrite equation (19) for $i = 2$ and note that $Max [T^1(H) - m, 0] = T^1(H) - m$ and $Max [T^2(H) - m, 0] = 0$:

$$T^2(S) \equiv U(Y - r^1, S) - U(Y - r^2, S) + \gamma\pi (T^2(H) + T^1(H) - m) + \gamma(1 - \pi) (T^2(S)) \quad (27)$$

Since $T^2(H) + T^1(H) = 0$, this simplifies to

$$T^2(S) \equiv U(Y - r^1, S) - U(Y - r^2, S) - \gamma\pi m + \gamma(1 - \pi) (T^2(S)) \quad (28)$$

Differentiating with respect to λ yields

$$\frac{\partial T^2(S)}{\partial \lambda} = \gamma(1 - \pi) \frac{\partial T^2(S)}{\partial \lambda} \quad (29)$$

which implies that $\frac{\partial T^2(S)}{\partial \lambda} = 0$ unless fortuitously $\pi = (1 - \frac{1}{\gamma})$. As $T^2(S) + T^1(S) = 0$ we find $\frac{\partial T^1(S)}{\partial \lambda} = 0$.

Similarly we can rewrite equation (16) for $i = 1$.

$$T^1(H) \equiv U(Y - r^2, H) - U(Y - r^1, H) + \gamma\alpha^2 p^2 (V^2(S) + Max [T^2(S) - m, 0]) - \gamma\alpha^1 p^1 (V^1(S) + Max [T^1(S) - m, 0]) + \gamma(1 - \alpha^2 p^2) V^2(H) - \gamma(1 - \alpha^1 p^1) V^1(H) \quad (30)$$

It is evident from equation (16) that where $\frac{\partial T^1(S)}{\partial \lambda} = \frac{\partial T^2(S)}{\partial \lambda} = 0$, $T^1(H)$ is decreasing in r^2 and increasing in λ . Therefore the locus $T^1(H) = m$ is positively sloped.

Next we show that, where there is no migration by healthy individuals (ie where $T^1(H) - m < 0$ and where $T^2(H) - m < 0$), the locus $T^2(S) = m$ is more shallow sloped than $T^1(H) = m$.

To see this, note that equation (19) for $i = 2$ simplifies to

$$T^2(S) \equiv U(Y - r^1, S) - U(Y - r^2, S) + \gamma\pi(T^2(H)) + \gamma(1 - \pi)(T^2(S))$$

Differentiating, and noting that $T^2(H) = -T^1(H)$, we obtain

$$\frac{\partial T^2(S)}{\partial \lambda} = -\gamma\pi \frac{\partial T^1(H)}{\partial \lambda} + \gamma(1 - \pi) \frac{\partial T^2(S)}{\partial \lambda} \quad (31)$$

Therefore we obtain

$$\frac{\partial T^2(S)}{\partial \lambda} = \frac{-\gamma\pi}{(1 - \gamma + \gamma\pi)} \frac{\partial T^1(H)}{\partial \lambda} \quad (32)$$

Since $\frac{\gamma\pi}{(1 - \gamma + \gamma\pi)} < 1$ and since $T^1(S) = -T^2(S)$ we find that $\frac{\partial T^1(S)}{\partial \lambda} < \frac{\partial T^1(H)}{\partial \lambda}$.

Analogous differentiation with respect to r^2 yields

$$\frac{\partial T^2(S)}{\partial r^2} = \frac{U'}{(1 - \gamma + \gamma\pi)} - \frac{\gamma\pi}{(1 - \gamma + \gamma\pi)} \frac{\partial T^1(H)}{\partial r^2} \quad (33)$$

which implies that

$$\frac{\frac{\partial T^2(S)/\partial \lambda}{\partial T^2(S)/\partial r^2}}{\frac{\partial T^1(H)/\partial \lambda}{\partial T^1(H)/\partial r^2}} < 1 \quad (34)$$

Proofs of propositions

Proof of Proposition 2:

Where gross migration is zero, we know that those falling sick in any period consist of those previously healthy who fall sick 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 period $t + 1$ will be equal to the proportion of healthy individuals in period t who fell sick plus the proportion of sick individuals in t who have not recovered from the disease, which is written as :

$$p_{t+1}^i = \alpha^i p_t^i (1 - p_t^i) + p_t^i (1 - \pi) \quad (35)$$

Substituting the steady state conditions that $p_{t+1}^i = p_t^i = p^i$ implies that $p^i = 1 - \pi/\alpha^i$

Proof of Proposition 3:

If $p^2 = 0$ at the steady state there will no longer be migration. Furthermore as $p^1 + p^2 < 1$, $1 - p^1 > 0$. Therefore equation (24) implies that $\psi = 0$. Substituting $\psi = p^2 = 0$ into (25), we show that

$$p^1 = 1 - \frac{\pi}{\alpha^1} \tag{36}$$

As p^1 is the same as in the steady state with no migration out of the equilibria and $p^2 = 0$ is below the prevalence level in city 2 in the steady state with no migration out of the equilibria, we have shown that, in this equilibrium, prevalence levels are strictly below those in the high cost steady state. Since in addition no migration costs are occurred at this steady state, it is Pareto improving at the steady state for migration to be possible out of steady state.

Existence of steady states with non-zero gross migration

We need first to establish that there exist real non zero solutions to the equations for the prevalence levels in the two cities in the steady state (25) and (26) as stated below.

Lemma For any given pair (ϕ, ψ) such that $0 < \phi < \frac{\alpha^2 - \pi}{1 - \pi}$ and $0 < \psi < 1$, there exist solutions to equations (25) and (26) with $0 < p^i < 1$, $i = 1, 2$.

Proof

For equations (26) to be satisfied with strictly positive migration in the steady state it must be the case that

$$p^2 = \frac{\alpha^2 - \pi - \phi(1 - \pi)}{\alpha^2(1 - \phi)} \quad (37)$$

and this is satisfied with $0 < p^2 < 1$ if $0 < \phi < \frac{\alpha^2 - \pi}{1 - \pi}$ (after noting that $\frac{\alpha^2 - \pi}{1 - \pi} < \frac{\pi}{\alpha^2 - 1 + \pi}$ as $\alpha^2 < 1$).

As there is zero net migration, necessarily p^1 must satisfy (24), which means that $p^1 = 1 - \frac{\phi}{\psi}p^2$.

Using (37) we can write

$$p^1 = 1 - \frac{\phi}{\psi} \frac{\alpha^2 - \pi - \phi(1 - \pi)}{\alpha^2(1 - \phi)} \quad (38)$$

We also know that at such two-way migration steady states p^1 satisfies (25) which is an equation of degree 2 of the form

$$(1 - \psi)\alpha^1 (p^1)^2 + p^1(-(1 - \psi)\alpha^1 + \psi(1 - \pi) + \pi) - \psi(1 - \pi) = 0 \quad (39)$$

$$A (p^1)^2 + (\pi - C - A)p^1 + C = 0 \quad (40)$$

where $A = \alpha^1(1 - \psi)$, $C = -\psi(1 - \pi)$, $B = \pi - C - A$.

The general form of the solution to that equation is:

$$p^1 = \frac{-B + \sqrt{B^2 - 4AC}}{2A} \quad (41)$$

$$p^1 = \frac{A - \pi + C \pm \sqrt{(A - \pi + C)^2 - 4AC}}{2A} \quad (42)$$

Note first of all that since $A > 0$ and $C \leq 0$, $4AC \leq 0$ so the solution always has real roots. At least one of these roots is always non-negative and weakly less than one. To see this note that we can rewrite

$$(A - \pi + C)^2 - 4AC = (A + \pi - C)^2 - 4\pi A \quad (43)$$

Thus, since $4\pi A > 0$

$$p^1 < \frac{A - \pi + C + \sqrt{(A + \pi - C)^2}}{2A} \quad (44)$$

Since $\sqrt{(A + \pi - C)^2} = (A + \pi - C)$

$$p^1 < \frac{A - \pi + C + (A + \pi - C)}{2A} \quad (45)$$

which implies that $p^1 < 1$.

Thus we have shown that for all values of ψ such that $0 < \psi < 1$, there exists a solution for p^1 that satisfies (25) and for which $0 < p^1 < 1$.

End of the proof

We now need to examine the "adding up" and "behavioural conditions" under which solutions to these equations with strictly positive levels of ϕ and ψ are steady states. By studying the consistency of these two conditions, which necessarily have to be satisfied at steady states, we can establish the conditions under which such non-zero gross migration steady states exist, as stated below:

Conditions under which non-zero gross migration steady states exist : *If the lowest migration costs are low enough to encourage some healthy individuals to migrate at low rents and the highest migration costs are high enough so that less than $\frac{\alpha^2 - \pi}{1 - \pi}$ of sick people migrate at high rents, there exists a steady state with non-zero gross migration, which has $p^2 = \frac{\alpha^2 - \pi - \phi(1 - \pi)}{\alpha^2(1 - \phi)}$ where $0 < \phi < \frac{\alpha^2 - \pi}{1 - \pi}$, $0 < \psi < 1$ and $p^1 = 1 - \frac{\phi}{\psi}p^2$.*

Proof

We can summarize the first "adding up" requirement in the function $F(\cdot)$ which is derived from the zero net migration condition (equation (24)):

$$\psi = F(\phi) = \frac{\phi p^2}{(1 - p^1)} \quad (46)$$

We know, for p^1 and p^2 lying strictly between zero and unity, that if ϕ is zero then ψ must be zero too. We also know that if ϕ approaches $\frac{\alpha^2 - \pi}{1 - \pi}$ then p^2 approaches zero again, so ψ must also approach zero. In between these two points $F(\cdot)$ is continuous and positive. A simple illustration of F is given in Figure 2. Note that F can be more highly non linear than in this figure.

We can summarize the second "behavioural" requirement in the function G . $G(\cdot)$ is defined as follows. For any value of ψ , let $r(\psi)$ be the value of r^2 at which the proportion

of healthy people wishing to migrate is just equal to ψ . Then let $G(r(\psi))$ be the value of ϕ , the proportion of sick people wishing to migrate, given that $r^2 = r(\psi)$.

Equation (20) implies that $G^{-1}(0)$ is strictly positive and equation (21) 2 implies that $G(0) < \frac{\alpha^2 - \pi}{1 - \pi}$. In between these two points $G(\cdot)$ is continuous and positive, as illustrated in Figure 2.

This implies that $G(\psi)$ and $F(\varphi)$ must cross at least once. The point(s) where they cross is (are) the steady state(s) with non-zero gross migration. This is the proof of existence of at least one steady state such as characterised by Proposition.