

A SIMULATION MODEL OF THE SPREAD  
OF HIV AND AIDS IN THE  
UNITED KINGDOM

Julia Williams

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IN THE UNITED KINGDOM**

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## ABSTRACT

This paper describes the construction of an integrated demographic and epidemiological model to simulate the spread of HIV and AIDS in the UK as a result of sexual transmission of the virus. Forecasts are produced at the scale of Regional Health Authorities, to reflect the importance of spatial heterogeneity in the distribution of the virus, which is likely to affect the transmission patterns. Forecasting of both population and viral status is carried out using the framework of a multi-regional population projection model. Following a brief description of the HIV/AIDS pandemic, the different modelling approaches applied to this phenomenon are reviewed. The structure of the model which has been developed to combine demographical and epidemiological approaches is then outlined, followed by a more detailed and technical description of the estimation of the inputs to the model and model parameters. Because of uncertainties surrounding several of these parameter values, sensitivity tests were performed to try and assess the impact of changes to these values. Several factors which were influential in determining the impact of the virus on the population were identified, suggesting areas where more accurate and reliable data are needed, as well as strategies which might reduce viral spread. Model predictions were then produced up to the year 2000 to examine the way in which geographical spread might occur. Finally, the paper evaluates the current model and proposes a series of improvements to be implemented in future research.

## 1. INTRODUCTION

This paper details the progress made to date on the construction of a model to simulate the spread, within the UK, of Acquired Immune Deficiency Syndrome (AIDS), and its etiological agent, the Human Immunodeficiency Virus (HIV), of which several types have been identified.

### 1.1. The AIDS pandemic

The first case of AIDS was diagnosed in Los Angeles in 1981, although retrospective diagnoses have since identified possible cases as early as 1969 in Missouri (see Cliff & Haggett 1988). HIV was first identified in 1983 (Wells 1986), and it operates by destroying the immune system, leaving those infected susceptible to opportunistic infections, which the body can otherwise usually overcome. These most commonly include Kaposi's sarcoma (KS), a type of skin cancer, and Pneumocystis carinii pneumonia (PCP), although HIV can also attack the brain and nervous system, causing dementia. The average survival time for people with AIDS (PWAs) diagnosed in 1987 was about 18 months, an improvement on the average of 9-10 months for pre-1987 diagnoses (PHLS 1990). This improvement is thought to be due to greater understanding of the disease, as well as drug treatments such as zidovudine (AZT) which slow down viral replication.

The exact nature of the clinical progression of the disease is still not fully understood, because of the long incubation period between infection and the development of AIDS. Current estimates suggest a median incubation period of 9-10 years, but it is still not certain whether all those infected will eventually progress to AIDS (Rutherford *et al* 1990). During this lengthy incubation period an individual may be asymptomatic, or may suffer from a variety of illnesses and infections which fail to meet the clinical definition of AIDS, and McCormick (1989) has shown that many people may die from HIV-related illness without progressing to AIDS, so that just considering the number of AIDS cases does not give a true picture of the impact of the virus. Several distinct stages in the progression of HIV-related disease have been identified, of which AIDS is the most severe.

There is presently controversy surrounding the geographical origins of the disease. The most widely held view is that HIV first emerged among geographically remote peoples in Africa, and subsequently spread via population movement (Pinching 1986). This theory has been supported by claims of a similarity between HIV and a virus which causes immune deficiency in African green monkeys.

The transmission routes of HIV have been clearly established. HIV has been detected in many different body fluids, including blood, semen, saliva, tears, breast milk, and cervical and vaginal secretions (Acheson 1987). However, HIV cannot survive well outside the body, and therefore transmission requires close contacts. There are only three major transmission routes - sexual contact with an infected person, coming into contact with infected blood or blood products, and from an infected mother to her child,

either in the womb, during birth or while breast feeding (Campbell 1990). There is no evidence of infection via normal, everyday contact (Friedland 1986). This has resulted in HIV infection (at least in the UK) being predominantly concentrated in a number of 'high risk' groups, whose behaviour or medical treatments have placed them at greater risk of acquiring infection, such as homosexuals, intravenous drug users (IDUs), haemophiliacs or transfusion recipients (since the safety of the blood supply could not be ensured before screening measures were introduced). However, it may be misleading to focus attention onto risk groups, when an individuals' behaviour is the major risk factor. In the absence of a cure or vaccine, behavioural change away from risky activities is the only way of preventing further viral spread.

On a global scale, 418,404 AIDS cases were reported to the World Health Authority (WHO) by October 1991 (PHLS & CDSU 1991), although there were estimated to be 1.3 million AIDS cases, and 8-10 million HIV+ adults by the end of 1990, and a conservative forecast predicted 5-6 million adult AIDS cases, and 26-30 million HIV+ individuals (including 10 million children) by the year 2000 (Merson 1991). The majority of reported cases come from North and Latin America (57%), with 13% in Europe and 29% in Africa, although these figures are likely to be biased towards countries with good reporting systems (Europe and USA).

In the UK, the first AIDS cases were reported in 1982, and by the end of September 1991, 5065 AIDS cases and 16,248 HIV+ tests had been reported (see Tables 1 & 2 which contain data from PHLs & CDSU 1991). Within Britain, AIDS cases have been concentrated in London - almost half the cases reported in England and Wales come from 3 London Health Districts (Riverside, Parkside and Bloomsbury), and the 4 Thames Regions account for three quarters of cases (PHLS & CDSU 1991). Trends in the distribution of HIV+ reports are more complicated, with the Thames regions accounting for 52% of reports in 1985, but 70% in 1991. The relative distribution of AIDS cases by exposure category varies across the UK. In Scotland, 32% of AIDS cases were IDUs, compared with 6% in the North Western region. Men who had sex with men represented 90% of AIDS cases reported from NW.Thames, but only about half in the Northern and Oxford Regions and Scotland. Regional variations in HIV+ reports are even more marked, with IDUs accounting for 52% of HIV infections in Scotland, but only between 6% (W.Midlands) and 19% (E.Anglia) in England. In NW.Thames, 78% of infections were in men who had sex with men, compared to 19% in Scotland.

## 1.2. Aims of the research

The main aim of this research is to attempt to construct a comprehensive model of the spatial and temporal diffusion of HIV within the UK, in order to assess its impact on particular population groups (such as age and sex groups, sexual preference groups). The model aims to be comprehensive in the sense that it considers a number of behavioural groups (initially homosexuals and heterosexuals) and the links between these, and it can also produce forecasts at the Regional Health Authority (RHA) scale, so that the spatial spread of the virus can be identified. This is an

important area to research, because although at present the vast majority of PWAs are spatially concentrated in the London region, the distribution of HIV+ reports suggests a wider diffusion of AIDS cases in the future (see Table 1), particularly into Scotland, but also into the West Midlands, Oxford, Trent and Yorkshire RHAs.

Forecasts of the spread of HIV and AIDS in the UK population are likely to prove valuable, not only in the area of managing the allocation of resources for the treatment of future PWAs, but also because any future strategy of preventative health education (and possibly also vaccination) will need to be targeted at specific geographical sub-populations, who have been identified as being at particular risk, in order to be most effective.

### **1.3. Outline of the structure of this paper**

The remainder of this paper is divided into 6 sections. Section 2 briefly reviews the approaches which have been used to model the spread of HIV and AIDS. Section 3 describes the basic structure of the simulation model which has been developed, while Section 4 contains a more technical description of the processes used to estimate the various model inputs and key parameters. Section 5 details the results obtained from sensitivity tests of several key parameter values. Section 6 then looks at the way in which the model predicts geographical spread, and contains a forecast of spread over the rest of the century. Finally, Section 7 is an evaluation of the strengths and weaknesses of the current model, together with suggestions for improvements.

## 2. REVIEW OF APPROACHES TO MODELLING THE SPREAD OF HIV AND AIDS

A wide variety of forecasting methods have been applied to the AIDS epidemic, which can be classified into several groups on the basis of what they actually forecast (prevalence of HIV, prevalence, incidence and deaths associated with AIDS, estimates of the distributions of incubation and survival times), with some methods predicting several of these simultaneously. The direct approach (Hillier 1988), back projection (Day & Gore 1988; Isham 1988, 1989) and transmission models (Anderson 1988; Wilkie 1988; Knox 1986; Dietz 1988) estimate HIV prevalence, while the incidence of AIDS is forecast by extrapolation (DoH 1988) and transmission models, which can also predict AIDS deaths. Estimates of the distributions of the various disease stages (Reeves 1988) are required as inputs by several forecasting methods. This wide variety of approaches were developed in response to the problems caused by a lack of suitable data on which to base forecasts, with each method having its own advantages, disadvantages, and time scale for projections.

### 2.1. Direct approach to estimating HIV prevalence

Estimates of HIV prevalence for the UK were produced by Hillier for the Cox Report (DoH 1988) by estimating the population sizes of the major risk groups and their seroprevalence rate. Despite its apparent simplicity this approach has several problems, including the initial definition of 'risk groups', since members of a group such as male homosexuals are very heterogeneous. Also, some individuals may belong to more than one group, either simultaneously, or because sexual or drug taking behaviours are likely to change over time. A further problem is the lack of reliable data, not only on the size of these groups, but also from unbiased seroprevalence surveys for them, since all current surveys are based to some extent on self selected samples (Beck et al 1990). As a result of these uncertainties, this method produces a wide range of estimates, suggesting that by the end of 1987, between 20,000 and 50,000 people in England and Wales were HIV+ in the Cox Report (DoH 1988).

### 2.2. Back projection

Estimates of the incidence of HIV (DoH 1988; Isham 1989; Anderson 1989) are based on the relationship between the incidence of AIDS cases, the incidence of HIV infections, and the distribution of the incubation period, which can be expressed as

$$\frac{dC(t)}{dt} = \int_0^t I(s) d(t-s), \quad (1)$$

where

$C(t)$  = cumulative number of AIDS cases up to time  $t$  (may be corrected for reporting lags and under reporting),

$dC(t)/dt$  = rate at which new AIDS cases appear,

$I(t)$  = rate at which new HIV infections occur,

$d(t)$  = (assumed) distribution of the incubation times.

If two of these elements are known, then Equation (1) can be used to deduce the third, using the convolution theorem to compound the

two distributions (Bailey 1964). This approach can estimate current numbers infected with HIV, given data on the cumulative numbers of AIDS cases, and an assumed parametric form for the incubation period distribution (usually a Weibull or Gamma distribution, which can represent skewed data). Better information on the shape of this distribution is likely to produce more accurate estimates, although this method cannot cope with changes to this distribution, and the incubation period has been lengthening since the start of the epidemic, possibly due to the use of AZT, or improved understanding of the disease (Osborn 1990; Bannister *et al* 1989).

This methodology can also predict future incidence of HIV and AIDS (Day & Gore 1988). Current numbers infected with HIV are estimated, and it is assumed that the incidence of HIV infection follows a smooth trend which can be extrapolated to forecast new infections. An assumed incubation period distribution is then applied to this seroprevalence data, to forecast future AIDS cases.

### 2.3. Direct Extrapolation

This produces short-term predictions of temporal trends in the incidence of AIDS by extrapolating directly from past trends, using empirical curve fitting techniques, based on the choice of a suitable mathematical function (Anderson 1989; DoH 1988). Popular functions include the exponential and linear logistic, with different types of curve corresponding to different assumptions about the form and growth rate of the epidemic. Parameter estimates are obtained by maximum likelihood and least squares methods (Anderson 1989), and can allow for a variable and temporally changing delay between diagnosis and reporting (Cox & Medley 1989). Unfortunately, many different functions are consistent with the historical data, and a wide range of predictions can be obtained from one data set. Since extrapolation is just an empirical fit to the data, and the approximation is not based on the changing underlying transmission dynamics, the chosen function cannot be expected to apply indefinitely. Other problems with this approach include the different patterns of epidemic growth in different risk groups, changes in the surveillance definition of AIDS, and temporal changes in the distribution of reporting lags (Anderson 1989).

### 2.4 Transmission models

In order to make reliable long-term predictions, more detail on epidemiology and behavioural patterns needs to be included, which can be achieved in transmission models (Hyman & Stanley 1988). Two basic types of mathematical model are suitable for describing the underlying processes behind the epidemics' spread:- deterministic models, based on systems of differential equations which quantify rates of transition between different disease stages, reproducing aggregate patterns and predicting numbers in any stage of the disease, and stochastic models based on probability theory, which predict rates of movement of individuals between different states. To date, most transmission models have been deterministic, and their main application has been to help interpret observed trends,

and focus attention onto areas where better data needs to be collected (Anderson 1988).

At present, the accuracy of their predictions is hampered by uncertainties surrounding vital epidemiological parameters and processes, such as the risks of transmission, behavioural change, and variable infectivity during the incubation period. The first models were highly simplified, for example with assumptions of a single risk group (Wilkie 1988), homogeneous behaviour and constant infectivity (considered by Dietz 1988), but as the epidemic has progressed, models have become increasingly realistic. Table 3 contains a basic classification of features which have been added to these models, including the addition of different risk groups such as heterosexuals and IDUs, heterogeneity of behaviour and complex mixing patterns between these different behavioural or risk groups (Knox 1986), use of a probability distribution to describe incubation or disease periods, behavioural change, variable infectivity, pair formation, age or gender disaggregation, and inclusion of the underlying demographic behaviour of the population (See Table 3 for references).

## 2.5. Models which include population dynamics

Transmission models have recently been extended to try and assess the impact of AIDS on the demographic structure in Africa (Anderson et al 1990; Bongaarts 1989). These models combine demographic, behavioural and epidemiological data, and assess the impact of AIDS by projecting the population in the absence of the disease, and then repeating the projections for different assumptions about the course of the disease. This enables the impact of AIDS on various quantities such as the age structure, fertility rate and final population size to be assessed.

Bongaarts (1989) combined the three sub-models mentioned above, using the demographic framework of a standard cohort-based population projection model. This cohort approach enabled any of the model's parameters to be age specific, and cohorts could also be divided into strata to account for heterogeneity of sexual activity. It is also straightforward to predict future numbers of vertically infected infants using this methodology. However, these models require simplifying assumptions before implementation, and are therefore most useful in identifying factors which influence the demographic impact of AIDS. Anderson (1989) found the potential demographic impact of AIDS to be enhanced by unequal transmission probabilities between males and females, and the tendency for males to have sexual partners who were younger than themselves.

Within the field of Geography, population projection models have been developed which can project the populations of many regions, including age detail and the effects of migration (Rees 1989). The incorporation of an epidemic model of AIDS within a multi-state population projection model was the approach considered by Bongaarts (1989), with several simplifications. It is desirable to extend models in this way since many of the epidemiological, behavioural and demographic determinants of the AIDS epidemic are

age dependant, including sexual activity, the incubation period, non-AIDS mortality, and the probability of giving birth (Bongaarts 1989). A multi-regional model for the UK is desirable because AIDS is not uniformly distributed throughout the country, so that a model which can account for regional variations is required, and it is also important to represent the process of transmission between different places. This occurs when susceptible individuals visit areas away from their permanent homes and become infected via intercourse with infectious partners who are either resident in these regions or also visiting. Susceptibles may also become infected when they have infectious sexual partners who are either resident in, or visiting the area.

Despite their problems, transmission models offer the only option for long-term projections, because they consider the underlying dynamics of the epidemic, and the ways in which these are changing. It is for these reasons that the development of a transmission model incorporating population dynamics will be considered in the rest of this paper, since this will allow an accurate assessment of the impact of AIDS on the demographic structure of the population to be made.

### **3. STRUCTURE OF THE SIMULATION MODEL**

This simulation model aims to predict the future size of the UK population, while taking account of the effects of HIV within the country. The processes applied to the population are displayed in the systems diagram (Figure 1), and basically the models' base population is first subjected to a demographic projection model, followed by an epidemiological transmission model. The resulting final population then becomes the initial population for the next projection period.

#### **3.1. Demographic projection model**

This section of the model projects the RHA populations by period-cohort, gender and viral status. For each period-cohort, the end of period population is projected by forecasting the variables on the RHS of :-

$$\begin{aligned} \text{End-of-period population} &= \text{Start-of-period population} \\ &\quad - \text{non-survivors} \\ &\quad - \text{surviving out-migrants to other RHAs} \\ &\quad + \text{surviving in-migrants from other RHAs.} \end{aligned} \quad (2)$$

A period-cohort consists of the passage of a single age group over one time interval (one year in this model). For the current version, the effects of external migration are ignored. Equation (2) applies to all period-cohorts except the first, in which individuals start off by being born. This is called the 'infant' period-cohort, and a parallel relationship is used to project the numbers of infants forward over the annual interval in which they are born.

$$\begin{aligned} \text{End-of-period population of first period-cohort} &= \text{births} \\ &\quad - \text{infant non-survivors} \\ &\quad - \text{infant surviving out-migrants to other RHAs} \\ &\quad + \text{infant surviving in-migrants from other RHAs.} \end{aligned} \quad (3)$$

The number of births will be unknown at the start of a projection interval, and therefore a fertility model to forecast the number of births within this period is required:

$$\text{Births in projection interval} = \sum_{\text{fertile ages}} \text{age-specific fertility rate} \times \text{population of women at risk of giving birth, by age} \quad (4)$$

The probabilities of non-survival, and of survival and out-migration for the infant period-cohort reflect the shorter period of infants' exposure to these events (on average, half of the projection interval). The terms on the RHS of Equation (2) are produced as follows.

##### 3.1.1. Deaths

These are projected by applying age-specific non-survival

probabilities to the start of period populations. These probabilities account for deaths from all causes except HIV infection, and are calculated outside the model, using life table methods.

### 3.1.2. Migrations between RHAs

The migration process is likely to have significant implications for the spatial spread of the virus, since international population movements have been identified as one of the major causes of the current global spread (Smallman-Raynor & Cliff 1990). Some aspects of population movements were required in the demographic model, and initially a simple measure of inter-RHA migrations was used.

The out-movement from one RHA to the others was calculated by applying age and gender specific probabilities of migration, conditional on survival, to the surviving RHA populations. These probabilities were calculated by dividing the regional probabilities of migration and survival for each age-sex group by their respective survival probabilities. The in-migration to an RHA was computed as the sum of the out-migration from all other RHAs to the one in question, over the projection interval.

### 3.1.3. Births

Births occurring during a projection interval were generated using a female dominant fertility model, to estimate the number of births by region, gender and viral status of the newborn infant. This was achieved by applying age specific fertility rates to the female populations at risk (PAR) of the regions, defined as the average population over the projection interval. These regional fertility rates were estimated using national fertility rates and the numbers of births recorded from each RHA for the base year (1987). The process of vertical transmission from an HIV+ mother to her child is also represented within this section of the model, achieved by applying a vertical transmission rate to children born to HIV+ mothers, in order to estimate how many of these infants will be infected. The processes of survival and migration are then applied to these infants, as for the rest of the population (described above).

### 3.1.4. Ageing of the population

This is the final process in the demographic model, occurring after the population has been subjected to the epidemiological processes. It allows the final population of the current projection period to become the starting population of the next, with the last two period-cohorts added together, and the new births becoming the first period-cohort.

## 3.2. The epidemiological transmission model

The basic epidemiological processes to be represented are the exposure to, and the transmission of HIV within the population, and progression of the disease between the various stages of infection.

### 3.2.1. Exposure to and transmission of HIV

The only transmission routes considered in this model are sexual and vertical ones. The probability of HIV transmission via sexual contact depends on the frequency of contacts, the number of different partners, the probability of choosing an infected partner, and the infectiousness of infected partners (Bongaarts 1989). These processes are represented within the calculation of the 'encounter and infection' rates, obtained outside the model using techniques described by Weyer *et al* (1988) for the calculation of 'suitable contacts' (a contact which leads to certain infection, provided that one partner is susceptible and the other infectious). These rates are dependant on the inter-regional contact patterns (adapted from the migration data), the proportion of the contacts made by any one preference group that are with the other groups (behavioural contact patterns), the risks of transmission for different types of contacts, and the age selectivity that operates during partner choice.

### 3.2.2. Disease progression

The assumed average course of the illness is represented diagrammatically in Figure 2 (adapted from Weyer *et al* 1988). This is a multiple course, where 88% of all asymptomatic HIV+ individuals are first assumed to develop ARC before progressing to AIDS, while 12% develop AIDS in a shorter time. Based on current estimates (PHLS 1990; Rutherford *et al* 1990), the average incubation period was assumed to be about 10 years. The derivation of this pattern of illness is described in greater technical detail in Section 4.8.

#### 4. ESTIMATION OF MODEL INPUTS AND KEY PARAMETERS

This section contains a more technical description of the models' structure, and the various procedures used to obtain, by estimation where necessary, the data sets and parameters required to implement the model. The methodology used is a multistate population projection model, derived from movement data (Rees 1989).

##### 4.1. System description

Table 4 lists the characteristics included within the population data, the encounter and infection rates, the fertility, mortality and migration components, and also the main features of the model. The projection of the population is undertaken using a period cohort framework to project the size and structure of populations by age, gender, and demographic indicators such as RHA and viral status, while permitting model parameters to be age specific.

##### 4.2. Estimation of the population data

The models' base population is the UK population at mid-year 1987, disaggregated by 4 characteristics : sexual preference, RHA of residence, age and viral status. Estimation of these data is based on the manipulation of a wide variety of data sets, and Figure 3 illustrates how these procedures link together.

One basic assumption required for this estimation process is the value of the parameter PREF, the proportion of the adult population who are homo/bisexual, and the initial assumption was that PREF = 0.08 (or 8%).

At present this choice of value is fairly arbitrary, reflecting the lack of accurate survey data on this topic, due to problems of low response rates, recall bias, obtaining unbiased samples, and possible under-reporting of homosexual behaviour. For example, Johnson *et al* (1989) had a 48% response rate to their survey on sexual lifestyle, with only a very small proportion (the same for males and females) reporting any homosexual activity. The (now out of date) US Kinsey Report (1948) estimated that 3.5% of males aged between 15 and 59 were exclusively homosexual, with a further 3.5-10.5% assumed to have some homosexual contacts. In the Cox Report, Hillier (1988) estimated that 4.5% (probable range 3-7%) of adult males were homosexual, based on a survey of GUM clinic attendees. However, her assumptions have been criticised by Rees (1990), who produced an estimate of 6.92% from the same data. Bowie and Ford (1989) conducted a survey among 16 to 21 year olds in Somerset, and found that 2% identified themselves as homo/bisexual, with a further 5% uncertain. The DHSS and Welsh Office (1987) reported the results from several surveys, designed to assess the impact of the Governments' AIDS education campaign, and asked a large sample of adult men about their claimed sexual behaviour. They found that 2% considered themselves to be exclusively homosexual, 1% had fairly frequent sexual contact, 1-3% had infrequent contact, and 2-4% refused/didn't state. Kanouse *et al* (1988) produced estimates of current US sexual behaviour, with 5% of males aged between 18 and 54 mainly homosexual in their

present behaviour, and about 2% bisexual. They also assumed that the proportions who are actively gay decline after age 55, and are greater in large metropolitan areas than elsewhere. There have also been claims made by various AIDS charities and pressure groups that approximately 10% of the British population are homosexual.

Thus the estimate of PREF = 8%, although arbitrary, lies within the range of plausible values. Understandably, given the pattern of HIV spread in the Developed World, these studies are mostly concerned with homosexual activity among men. However, it does not seem unreasonable to assume that a similar proportion of women are homo/bisexual.

#### 4.2.1. Data sets required

Several basic data sets are required for the estimation procedures. Table 5 displays the RHA populations for England and Wales by gender and 5 year age group for ages 0 to 85+, for mid 1987, obtained from the OPCS Mortality Statistics, Series DH1 (OPCS 1989a, Table 2). These data are held as  $P_r^g$ , where

g - gender : 0 = Male, 1 = Female  
r - RHA : 0 = Northern, 1 = Yorkshire..., 14 = Wales  
A - age group : 0 = All, 1 = <1, 2 = 1-4, ..., 18 = 80-84, 19=85+.  
Figure 4 shows the boundaries of the RHAs.

Total populations for England and Wales by gender and single year ages for mid 1987, were also obtained from OPCS (1989a, Table 1) - see Table 6, and are held as  $P^{ag}$ , where

a - age : 0-89, 90+  
g - gender : 0 = Male, 1 = Female

The populations of Scotland and Northern Ireland by gender and single year ages for mid 1987, were obtained from the Annual Reports (Registrar General Scotland 1988, Table A2.1; Registrar General Northern Ireland 1989) - see Table 7. Each have the form  $P^{ag}$ , where

a - age : 0-89, 90+, Total  
g - gender : 0 = male, 1 = Female

RHA totals of cumulative AIDS reports up to the end of 1987 were obtained from the PHLS Quarterly Surveillance Tables (PHLS & CDSU 1991, Table 4). The national number of AIDS-deaths in the same period was obtained from the UK public access AIDS data file, which is prepared from voluntary confidential reports by clinicians sent directly to the PHLS, and these deaths were then allocated to RHAs in proportion to the number of AIDS cases they reported. The regional distribution of total HIV+ reports for the end of 1987 was obtained from the PHLS (PHLS & CDSU 1991), and these data are listed in Table 8.

The total number of UK AIDS reports to the end of 1987, by transmission route (PHLS & CDSU 1991), and AIDS-related deaths by transmission route (AIDS data file), were available for the following preference groups:

- 0 - Male homo/bisexual
- 1 - IDU
- 2 - Male haemophiliac
- 3 - Transfusion

- 4 - Male heterosexual
- 5 - Female heterosexual
- 6 - Infant
- 7 - Other/Not known

The transmission route distributions of HIV+ reports for Scotland and the rest of the United Kingdom for the end of 1987 (PHLS & CDSU 1991) were available for the following groups:

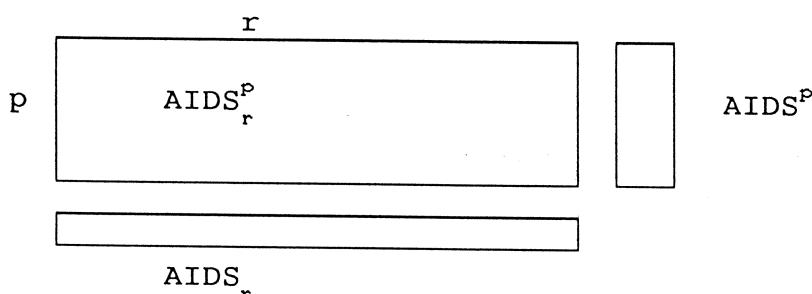
- 0 - Male homo/bisexual
- 1 - Male heterosexual
- 2 - Female heterosexual
- 3 - Male IDU
- 4 - Female IDU
- 5 - Infant
- 6 - Blood
- 7 - Other/Not known

These data are displayed in Tables 9 and 10.

#### 4.2.2. Estimation of the HIV/AIDS/Deaths joint RHA and transmission route distribution

The joint distribution for each disease stage was estimated using an iterative proportional fitting (IPF) routine, constrained by the two single distributions, a procedure based on the following methodology.

Firstly an initial (crude) estimate of the joint distribution is made, which is then improved iteratively, by adjusting to the known RHA and transmission route totals, until further adjustments create only marginal improvements in the estimates. The diagram below represents the data for the AIDS distributions, with similar processes applied to the HIV and deaths data.



for  $r = \text{RHA}, 0-16,$   
 $p = \text{transmission route}, 0-7.$

##### Stage 0 : Initial Guess

Guess that the 1166 AIDS cases have a uniform distribution over the 17 regions and 8 transmission routes.

$$\text{AIDS}_{r,0}^p = 1166 / (17 \times 8), \forall r,p. \quad (5)$$

##### Stage 1 : Adjust to regional data.

$$\text{AIDS}_{r,1}^p = \text{AIDS}_{r,0}^p \times \left( \frac{\text{AIDS}_r}{\sum_p \text{AIDS}_{r,0}^p} \right) \quad (6)$$

Stage 2 : Adjust to transmission route data.

$$\text{AIDS}_{r^{(2)}}^p = \text{AIDS}_{r^{(1)}}^p \times \left[ \frac{\text{AIDS}_{r^{(1)}}^p}{\sum_r \text{AIDS}_{r^{(1)}}^p} \right] \quad (7)$$

Stage 3 : Check for convergence.

$$\text{diff} = |\text{AIDS}_{r^{(2)}}^p - \text{AIDS}_{r^{(1)}}^p|, \forall r, p. \quad (8)$$

If  $\text{diff} > c$ , where  $c$  is some small constant, reset  $\text{AIDS}_{r^{(2)}}^p$  to  $\text{AIDS}_{r^{(1)}}^p$  and continue iteration; in this case  $c = 0.5$ , so that the process will converge to the nearest integer, representing a whole case or person.

The final output from this procedure consists of tables - Tables 11 to 13, and an array of data,  $P_{rv}$ ,  $r=0-16$ ,  $p=0-2$  ( $p$  refers to a combination of preference and gender categories: 0=male homo/bisexual, 1=male heterosexual, 2=female heterosexual),  $v=0-3$  (HIV+, ARC, AIDS, DEAD), to be used by other programs. The tables contain the full joint distribution for the 17 regions and 8 transmission routes, and also a condensed form of this distribution, for just the 3 transmission routes mentioned above, to be used within other procedures. In producing these condensed distributions several assumptions have been made.

For the AIDS and deaths data, male haemophiliacs were assigned to sexual preference groups according to the value of PREF, since this is a model to examine the impact of spread via sexual contact. Also, an adjustment was made to allow for 20% under-reporting in these data (Cox Report, DoH 1988).

For the HIV data, 90% of those in the blood category were assumed to be male haemophiliacs, with the remainder transfusion cases with an equal number of males and females, and these reports were then allocated to sexual preference groups. These assumptions agree broadly with observed features of the epidemic. Sexual transmission was assumed to be responsible for 75% of the other/not stated category, with 75% of these homo/bisexual males. There was also assumed to be a significant amount of non-testing, so that the true number who were HIV+ by 1987 was 27,500.

This figure of 27,500 has been chosen fairly arbitrarily, since there is little consensus on the level of seroprevalence in 1987. The Cox Report (DoH 1988) estimated that by the end of 1987, between 20,000 and 50,000 people in England and Wales were HIV+ (with the most plausible figure towards the lower end of these projections). The Day Report (PHLS 1990) produced much lower figures, estimating that by the end of 1988, only between 12,250 and 26,400 were HIV+. Rees (1990) also criticised the Cox Report, but estimated that approximately 90,000 people in England and Wales were HIV+ by the end of 1987, a figure which would be increased by at least 10% if diagnosed instead of reported AIDS cases were used as a basis for estimation. Fewer estimates are available for

Scotland and Northern Ireland, but by the end of 1987, Scotland had produced 1381 HIV+ tests (PHLS & CDSU 1991), 16% of all the UK positive tests, while Northern Ireland had 43 results, or about 0.005%.

The final stage of this procedure was to divide the HIV+ category into two: asymptomatic HIV infection and AIDS-related complex (ARC). This division produces a more realistic representation of the incubation period distribution (see Bongaarts 1988), and also allows for the fact that in some areas of the UK (especially the Thames regions), the virus is more firmly established, with a greater proportion of those who are HIV+ likely to be in more advanced stages of infection.

In a longitudinal study of homosexual men in San Francisco in 1989, Rutherford *et al* (1990) discovered that of those who had become infected between 1977 and 1980 ( $n=341$ ), 46% of those who had not developed AIDS had ARC, compared to 35% of those infected between 1981 and 1983 ( $n=73$ ), 44% of those infected between 1984 and 1986 ( $n=17$ ), and 0% of those infected since 1987 ( $n=11$ ). In England and Wales, various evidence suggests that the HIV epidemic is more advanced in the Thames regions. Bannister *et al* (1989) noted that a higher proportion of (homosexual) males were ill when tested for HIV, the cumulative incidence of AIDS/HIV disease was greater, and the prevalence of HIV was higher within London than elsewhere.

Based on this information, the following proportion of each region's HIV+ population were allocated to the ARC category.

North.....0.3	SE.Thames...0.5	Mersey.....0.3
Yorkshire..0.3	SW.Thames...0.4	N.West.....0.3
Trent.....0.3	Wessex.....0.3	Wales.....0.2
E.Anglia...0.3	Oxford.....0.3	Scotland...0.3
NW.Thames..0.5	S.West.....0.3	N.Ireland..0.2
NE.Thames..0.5	W.Midlands..0.3	

These figures give an average of about 35% of those who are HIV+ having ARC (implied by the structure of the transmission diagram, Figure 2). However, there was also differentiation between preference groups, since the epidemic is more firmly established within the homosexual than the heterosexual community. Therefore, for male homo/bisexuals, the above figures were used, while they were further reduced by a factor of about 70% for heterosexuals. Although these are arbitrary divisions since no detailed data is available, they are consistent with the few known facts.

#### 4.2.3. Estimation of single year of age RHA populations for England and Wales

Estimates of population sizes by single year of age and gender for the RHAs of England and Wales,  $P_{rg}^{ag}$ , are based on the RHA populations by gender and 5 year ages, and the national populations by gender and single year of age, as shown below. Data for Scotland and Northern Ireland are already in single years of age.

$$P_r^{ag} = \frac{P_n^{ag}}{P_n^{Ag}} \times P_r^{Ag}, \text{ for } a \in A, \quad (9)$$

where n = nation (England & Wales),  
r = RHA,  
a = single year of age,  
A = 5 year age group,  
g = gender.

An example of the results from these calculations is given in Table 14. The size of the adult (aged 16+) population of each region was also estimated, because this information was required by subsequent procedures - see Table 15.

#### 4.2.4. Estimation of the total size of the homo/bisexual population for RHAs

This estimation is based on the regional numbers of AIDS cases among homo/bisexual men (estimated previously), and the sizes of the sexually active (aged 16+) populations. Instead of using the actual number of AIDS cases reported from a region, these data were recoded, to try and overcome the problems caused by the great range in the number of AIDS cases for different regions.

Number of AIDS cases	Recoded value (recode <sup>r</sup> )
0 - 10.39	1.00
10.40 - 26.83	1.25
26.84+	1.50

These divisions were chosen to represent natural break points in the frequency distribution of AIDS cases.

The new values were then standardized to sum to 1.0, and have a mean of 1/17.

$$\text{recode}^{r(1)} = \text{recode}^{r(0)} / \sum_r \text{recode}^{r(0)} \quad (10)$$

They were then adjusted so that their mean equalled PREF, the assumed probability of being homo/bisexual.

$$\text{recode}^{r(2)} = \text{recode}^{r(1)} \times (\text{PREF}/(1/17)) \quad (11)$$

These values then represent the probability of being homo/bisexual, given region of residence. In order to obtain population numbers instead of probabilities, the size of the adult population of each region is then multiplied by its respective probability. Table 16 lists the results from each stage of these calculations.

#### 4.2.5. Estimation of the distribution of the population according to single year of age, RHA and sexual preference.

An IPF routine is used to estimate the distribution of  $P_r^{ap}$ , where

$p$  = sexual preference and gender  
 (0=Male heterosexual, 1=Male homo/bisexual,  
 2=Female heterosexual, 3=Female homo/bisexual),  
 $a$  = age (16+),  
 $r$  = RHA,

given  $P_r^{ag}$ ,  $P(r, p=\text{homosexual})$ ,  $P(p=\text{homosexual}, g)$ , which were calculated earlier. Note that  $P(p=\text{homosexual}, g) = \text{PREF} \times P(g)$ . The basic IPF process is the same used in Section 4.2.2, although it is now a 3 dimensional array being estimated, using the constraints of the known regional and gender distributions for homo/bisexuals. Also, IPF is only used to estimate the size of the gay population, with the heterosexual population obtained by subtraction, using  $P_r^{ag}$ . The example below illustrates the procedure for  $p=1$  (male homo/bisexuals), and a similar procedure is used for  $p=3$  (females).

Stage 0 : Initial Guess - 8% of adult population are homo/bisexual.

$$P_r^{a,p=1}_{(0)} = \text{PREF} \times P_r^{ag}, \forall g \in p, r, a \geq 16 \quad (12)$$

Stage 1 : Adjust to regional data.

$$P_r^{a1}_{(1)} = P_r^{a1}_{(0)} \times \left[ \frac{P_r^{p=1}}{\sum_a P_r^{a1}_{(0)}} \right] \quad (13)$$

Stage 2 : Adjust to gender data.

$$P_r^{a1}_{(2)} = P_r^{a1}_{(1)} \times \left[ \frac{P_r^{p=1}}{\sum_a \sum_r P_r^{a1}_{(1)}} \right] \quad (14)$$

Stage 3 : Check for convergence.

$$\text{diff} = |P_r^{a1}_{(2)} - P_r^{a1}_{(1)}| \quad (15)$$

If  $\text{diff} > c$  ( $c=0.5$ ), then reset  $P_r^{a1}_{(2)}$  to  $P_r^{a1}_{(1)}$ , and continue iteration.

The distribution for the heterosexual population (males in this case) is then estimated as follows.

$$P_r^{ao} = P_r^{ag} - P_r^{a1}, \forall a, r, g \in p. \quad (16)$$

The final distribution is illustrated in Table 17.

#### 4.2.6 Estimation of the distribution of the population according to single year of age, RHA, sexual preference and viral status

This procedure also uses an IPF routine to estimate the distribution of  $P_r^{av}$ , where  $v$  = viral status (0=HIV+, 1=ARC, 2=AIDS,

3=DEAD), given information on  $P_{rv}^p$ , for  $p=0-2$  ( $0=\text{male homo/bisexual}$ ,  $1=\text{male heterosexual}$ ,  $2=\text{female heterosexual}$ ). In estimating these data, it was assumed that no female homo/bisexuals had HIV, to reflect this groups' minimal risk of infection from sexual activity, although some may have been infected via drug use or blood transfusions (Chu et al 1990). The results from this stage are illustrated in Table 18.

The final estimate of the base population data, for input into the demographic and epidemiological model, produces  $P_{av}^{ap}$ , given  $P_{rv}^{ap}$  for  $a=0-90+$ , and  $P_{rv=1-4}^{ap}$ , where  $v=0-4$  ( $0=\text{HIV-}$ ,  $1=\text{HIV+}$ ,  $2=\text{ARC}$ ,  $3=\text{AIDS}$ ,  $4=\text{DEAD}$ ). An extract from this distribution is contained in Table 19. The calculations are based on the assumptions that only those aged between 16 and 65 may become infected with HIV via sexual activity, since the vast majority of AIDS/HIV reports are from this age group (PHLS & CDSU 1991), and no female homo/bisexuals become infected. Also, sexual preferences are not allocated to those below the age of 16. Finally, once the estimates of the cumulative number of HIV/AIDS cases have been produced, these data need to be altered by subtraction, to obtain estimates of current prevalences for each of the viral states, since this is the form in which the data are required by the epidemiological model.

#### 4.3. Mortality component

This section of the model consists of a general procedure for computing life-tables (derived from a program in Keyfitz & Fleiger 1971). National non-survivorship rates (for England and Wales, Scotland and Northern Ireland) are obtained from the survivorship rates, one of the life-table variables produced, and the rates for England and Wales then broken down to RHA level, using ratios of standardised mortality ratios (SMRs) as an indication of a regions relative mortality experience. These non-survival probabilities reflect the chances of dying from all causes except HIV-related ones, which are dealt with separately in the epidemiological model.

The data on which these calculations are based are the national populations and deaths for 1986,  $P_{ag}^n$  and  $D_{ag}^n$  ( $a=0-90+$ ), which are used to calculate age-specific occurrence exposure rates of mortality for people dying between (period) ages  $a$  and  $a+n$ ,

$${}^n M_{ag} = D_{ag}^n / P_{ag}^n \quad (17)$$

The age interval,  $n$ , is set to 1 year. Calculation of the survivorship rates,  ${}^n S_{ag}$ , (the probability of surviving from age group  $a$  to  $a+n-1$  at last birthday, to age group  $a+n$  to  $a+2n-1$ ) then proceeds as follows for the different ages,  $a$ .

$$a=0: {}^n S_{0g} = {}^n L_{0g} / {}^1 l_{0g} \quad (18)$$

$$1 \leq a \leq 88: {}^n S_{ag} = {}^n L_{a+1 g} / {}^n L_{ag} \quad (19)$$

$$a=89: \bar{n}S_{89g} = (1 - \frac{1}{2} \bar{n}M_g) / (1 + \frac{1}{2} \bar{n}M_g) \quad (20)$$

$$a=90: \bar{n}S_{90g} = (\bar{n}L_{90g} - (\bar{n}S_{89g} \times \bar{n}L_{89g})) / \bar{n}L_{90g} \quad (21)$$

where

$\bar{n}M_g$  = average death rate for individuals of gender g, for ages 89 and 90,  
 $= 1/2(\bar{n}M_{89g} + \bar{n}M_{90g})$ ,

$\bar{n}L_{ag}$  = life years lived between exact ages a and a+n, by people of gender g,

$\bar{l}_{ag}$  = probability of survival to exact age, a by people of gender g,

which are calculated as follows:

$$a=0: \bar{l}_{0g} = 100,000 \quad (22)$$

$$1 \leq a \leq 90: \bar{l}_{ag} = \bar{l}_{a-1g} \cdot \bar{n}px_{ag} \quad (23)$$

$$a=0: \bar{n}L_{0g} = sep_g \bar{l}_{0g} + (1 - sep_g) \bar{l}_{1g} \quad (24)$$

$$1 \leq a \leq 89: \bar{n}L_{ag} = 1/2 (\bar{l}_{a+1g} + \bar{l}_{ag}) \quad (25)$$

$$a=90: \bar{n}L_{90g} = \bar{l}_{90g} / \bar{n}M_{90g} \quad (26)$$

where

$\bar{n}px_{ag}$  = probability of surviving between exact ages,

$sep_g$  = fraction of deaths from age 0-1 that fall in the second age cohort triangle,

$$= 0.07 + 1.7 \bar{n}M_{ag},$$

and  $\bar{n}px_{ag}$  is computed as follows:

$$a=0: \bar{n}px_{0g} = (1 - sep_g \bar{n}M_{0g}) / (1 + (1 - sep_g) \bar{n}M_{0g}) \quad (27)$$

$$1 \leq a \leq 89: \bar{n}px_{ag} = (1 - \frac{1}{2} \bar{n}M_{ag}) / (1 + \frac{1}{2} \bar{n}M_{ag}) \quad (28)$$

$$a=90: \bar{n}px_{ag} = 0.0 \quad (29)$$

Once the survival rates,  $\bar{n}S_{ag}$ , have been calculated, the regional non-survival rates can be estimated by modifying the non-survivorship rates for England and Wales,

$$non\_S_{ag}^{EW} = 1 - S_{ag}^{EW}, \quad (30)$$

using ratios of the SMRs of the 15 RHAs of England and Wales,

obtained from OPCS mortality statistics (OPCS 1989a), displayed in Table 20, as follows,

$$\text{non-}S_{\alpha g}^r = \left( \frac{\text{SMR}_r}{(\sum_r \text{SMR}_r) / 1.5} \right) \times \text{non-}S_{\alpha g}^{\text{EW}} . \quad (31)$$

The results of these calculations are contained in Table 21.

#### 4.4. Migration component

The basic data available were the number of moves between the 97 Family Practitioner Committee Areas (FPCA) for individuals, and the in and out-migration totals for FPCAs for 1976-89. These data sets have the following basic structure.

```
inter_f pca(i,j,y),
  where i = origin,          0-96, 97=Total
        j = destination,      0-96, 97=Total
        y = year,             0-13: 0=1975/76, ..., 13=1988/89

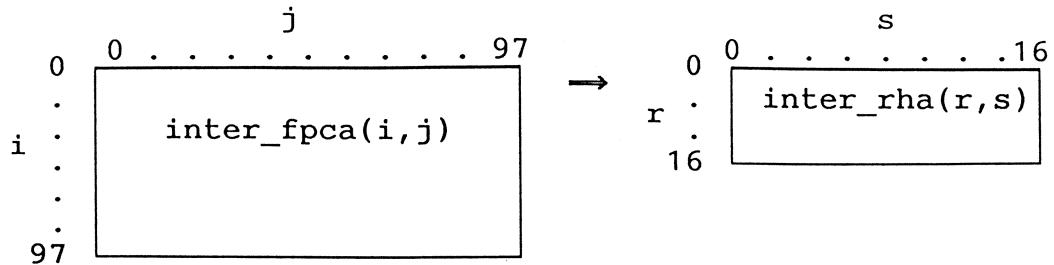
tot_f pca(i,g,A,d,y),
  where i = FPCA,           0-96
        g = gender,           0=males, 1=females
        A = age group,        0=0-4, 1=5-9, ..., 15=75+
        d = direction,        0=in-migration, 1=out-migration
        y = year,              0-13: 0=1975/76, ..., 13=1988/89
```

These data have been assembled by P.Boden from the National Health Service Central Register (NHSCR) migration information, which are records of all moves made by NHS patients which involve re-registering with a doctor in a new FPCA. Since these files are extremely large, the initial stages in utilising these data were to extract information for a single year, 1987/88, and condense this to the RHA scale. Figure 5 illustrates the procedures involved in the estimation of the migration data required by the model, the probabilities of migration between RHAs, conditional on survival. Estimation of these probabilities requires several stages.

##### 4.4.1. Aggregation of the NHSCR data

The FPCA data is assigned to RHAs according to a membership list containing, for each FPCA, a number assigning it to an RHA. The elements of the RHA data set are then the sums of all out or in-migrations relating to FPCAs within that RHA. An illustration of the procedure for the `inter_f pca` data is given below, with a similar process used for the `tot_f pca` data (the `y` subscript has been dropped from the following notation for clarity, since the data now refer to a single year).

$$\text{inter\_rha}(r,s) = \sum_{i \in r} \sum_{j \in s} \text{inter\_f pca}(i,j), \quad 0 \leq r,s \leq 16 \quad (32)$$



This procedure produces two data files containing the arrays `inter_rha` and `tot_rha` - see Tables 22 and 23, and manipulation of these data into a form suitable to be used as model inputs is performed as follows.

#### 4.4.2. Estimation of inter-RHA migrations, by gender and single year of age

Data on inter-RHA migrations by individuals, and total in and out migrations by gender and 5 year age group are combined using an IPF routine to produce a migration matrix,  $M_{rs}^{Ag}$ , for  $r,s=0-16$ ,  $g=0-1$ ,  $A=0-16$ , as in the previous section. The initial guess is of an equal age and sex distribution of migrants, so that

$$M_{rs}^{Ag} = M_{rs}^{\cdot\cdot} / (16 \times 2), \forall r,s,A,g. \quad (33)$$

This crude estimate is then adjusted to the known in and out migration totals, by age and gender, until convergence is reached (with a convergence criterion of  $c=0.5$ ).

The next stage is to factor down these 5 year rates to single year of age rates, using a model migration schedule (MMS), which is a parameterised representation of the profile of age-specific migration rates (Willekens 1990). In this model, a simplified basic standard migration schedule (Rogers & Castro 1981) is used, and the basic equation for this curve is

$$mx(x) = a_1 \exp(-\alpha_1 x) + a_2 \exp(-\alpha_2 (x-\mu_2)) - \exp(-\lambda_2 (x-\mu_2)) + c \quad (34)$$

where  $mx(x)$  is the migration rate for age  $x$ . The parameter values used in this implementation are the general MMS parameter values, although at a later stage it may be possible to use some of the parameters derived by Boden (1989).

$$\begin{array}{llll} a_1 = 0.02 & \alpha_1 = 0.10 & \mu_2 = 20 & c = 0.003 \\ a_2 = 0.06 & \alpha_2 = 0.10 & \lambda_2 = 0.40 & \end{array}$$

These values of  $mx$  are used as follows, assuming an even population distribution.

$$M_{rs}^{Ag} = M_{rs}^{\cdot\cdot} \times \left[ \frac{mx^\alpha}{\sum_{\alpha \in A} mx^\alpha} \right] \quad (35)$$

#### 4.4.3 Calculation of probabilities of migration, given survival

Calculation of an S 'matrix' of migration and survival probabilities is one of the stages of multistate population projection models. However, for this model the effects of migration and survival have been separated out so that they can be examined independently. To do this, their joint probability was altered to obtain the conditional probability of migration, given survival. Calculation of S is carried out as follows (the a and g superscripts have been dropped from the notation for clarity).

$$S = (I + \frac{1}{2} M)^{-1} (I - \frac{1}{2} M) \quad (36)$$

where I = the identity matrix,

$$M = \begin{pmatrix} (\sum_{s \neq 1} m_{1s} + d_1) & -m_{21} & \dots & -m_{n1} \\ -m_{12} & (\sum_{s \neq 2} m_{2s} + d_2) & \dots & -m_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ -m_{1n} & -m_{2n} & \dots & (\sum_{s \neq n} m_{ns} + d_n) \end{pmatrix} \quad (37)$$

$m_{rs}$  = crude migration rate from RHA r to s  
 $= M_{rs} / P_r$ ,

$d_r$  = non-survival rate for RHA r.

Once these joint probabilities of migration and survival ( $s_{rs}^{ag}$ ) have been calculated, the conditional probabilities are calculated by dividing through by the survival probabilities.

$$m_{rs}^{ag} = s_{rs}^{ag} / (1 - d_r^{ag}) \quad (38)$$

The results from these calculations are illustrated in Table 24.

#### **4.5. Fertility component**

In order to project future population sizes, the number of new births needs to be estimated, which is achieved using a female dominant fertility model to estimate the number of births by region, gender and viral status of the newborn infant, by applying fertility rates to the female populations at risk (PAR):

$$B_{rv}^g = z^g \sum_{\alpha=\alpha_1}^{\alpha_2} f_r^\alpha PAR_{rv}^\alpha \quad (39)$$

$$B_{ri}^g = r_v B_{rv}^g \quad (40)$$

where

$B_{ri}^g$  = births occurring in region r, by gender g and infant viral status i,

$B_{rv}^g$  = births occurring in region  $r$ , by gender  $g$  and maternal viral status  $v$ ,  
 $r_v$  = probability of vertical transmission of HIV (Currently set in the model to 13%),  
 $f_r^a$  = fertility rate for women of period-cohort  $a$ , in region  $r$ ,  
 $PAR_{rv}^a$  = PAR of women in region  $r$ , period-cohort  $a$ , and viral status  $v$ ,  
 $a_1$  = first fertile period-cohort (ages 15-16),  
 $a_2$  = last fertile period-cohort (ages 45-46),  
 $z^g$  = proportion of all births that are of gender  $g$  (Currently set in the model as 0.513 for males, 0.487 for females).

The following data are available as a basis for the calculations of Equations (39) and (40):

$PAR_{rv}^a$  - extracted from the initial population matrix, and the population matrix after the migration and survival probabilities have been applied,  
 ie. Average population size over the year,  
 $PAR_{rv}^a = 1/2 ( PAR_{rv}^a(t) + PAR_{rv}^{a-1}(t+1) )$ ,  
 $B_n^g$  = National totals of births (England and Wales, Scotland and Northern Ireland), by gender,  
 $f_n^a$  = National fertility rates for period-cohort  $a$ ,  
 $B_r^A$  = RHA births, by 5 year age group of mother, A.

These fertility data were obtained from the OPCS Fertility and Marriage Statistics for England and Wales (OPCS 1989b), and the equivalent statistics from the annual reports (Registrar General Scotland 1988; Registrar General Northern Ireland 1989), and the rates required for Equation (39) were derived as follows:

$$z^g = \sum_n B_n^g / \sum_g \sum_n B_n^g \quad (41)$$

$$f_r^a = f_n^a \left[ \frac{B_r^A}{\sum_{a \in A} f_n^a PAR_{rv}^a} \right] \quad (42)$$

$$B_{rv}^g = z^g \sum_{a=a_1}^{a_2} f_r^a PAR_{rv}^a \quad (43)$$

In performing these calculations, several assumptions and simplifications have been made. The vertical transmission probability of 13% was chosen as being the most up-to-date estimate (European Collaborative Study 1991), and probably also the most reliable, since it is based on a prospective study of all children born to a group of HIV+ women, and is therefore less prone to recruitment bias. It is also unlikely to be affected by bias due to the effects of treatment. A further assumption is that women with AIDS have a reduced fertility rate (half the normal rate), to reflect the fact that many women in this situation may be less willing to have children, when they are aware that they may pass on the virus, that pregnancy may further weaken their immune system, and that women in advanced stages of infection may be more likely to pass on the virus (Campbell 1990).

#### 4.6. Ageing of the population

This final process in the demographic model takes place after the epidemiological processes. At the end of the projection interval, the final population needs to be transferred into the initial population of the next interval,

$$IP_{rv}^{ap}(t+1) = FP_{rv}^{a-1,p}(t) \quad (44)$$

except in the case of the last period cohort, A, where the final population of the last, open-ended period cohort is added in as well.

$$IP_{rv}^{Ap}(t+1) = FP_{rv}^{A-1,p}(t) + FP_{rv}^{Ap}(t) \quad (45)$$

Also, surviving births which occurred during the projection period need to be transferred into the first period cohort.

$$IP_{rv}^{op}(t+1) = B_{rv}^g(t), \text{ for } g \in p. \quad (46)$$

The final process is assignment of sexual preferences to those newly aged 16, using the parameter PREF, the proportion of the population who are homo/bisexual.

#### 4.7. Estimation of encounter and infection rates

In order to model the transmission dynamics of AIDS, the 'suitable contacts' approach is used (Hethcote & Yorke 1984; Weyer et al 1988). A suitable contact is one which leads to certain infection, provided that one partner is susceptible and the other infectious. The number of actual contacts can be converted into an equivalent number of suitable contacts as follows. If

$\lambda_{rs}^{Abpq}$  = contact rate of infectious person (age b, preference q, RHA s) with any person of age group A, preference p, RHA r,

then

$$\lambda_r^{Ap} = \sum_b \sum_s \sum_q \lambda_{rs}^{Abpq} \left( P_{ro}^{Ap} / \sum_{v=0}^3 P_{rv}^{Ap} \right) \quad (47)$$

$=$  proportion of suitable contacts within  $\lambda_{rs}^{Abpq}$ .

Calculation of the contact rate is based on the following parameters,

- $a^q$  = average number of sexual encounters/partners for preference q per year (sexual encounter rate),  
 $q^{pq}$  = probability that an infectious person of preference q infects a healthy person of preference p, during a sexual partnership,  
 $n_{rs}^{Abpq}$  = proportion of sexual contacts of age b, RHA s, preference q, that are with age group A, RHA r, preference p. (sexual selectivity).

If no contact paths exist between groups p and q, then the above parameters equal zero, as therefore do their encounter and infection rates. However, if two groups do have contact, then

$$\lambda_{rs}^{Abpq} = n_{rs}^{Abpq} \cdot a^q \cdot q^{pq}. \quad (48)$$

Initial estimates for these parameters are listed in Table 25, based on data from a variety of sources. Further research and investigation are needed to try and locate more accurate, reliable estimates, since at present most are arbitrary estimates, consistent with the few known facts.

Numerous surveys of sexual behaviour, have tried to estimate the average number of sexual partners per year, a vital model parameter. However, because of the problems associated with these surveys, such as low response rates, recall bias, and obtaining unbiased samples (Johnson *et al* 1989), this aspect of the models' data is still problematic. Table 26 lists the results from a selection of these surveys.

For heterosexuals the survey data are fairly consistent, averaging between 1 and 2 partners a year, with a tendency for women to have slightly fewer partners, and for men to have greater variability in the number of partners recorded. There also seems to be variation between different age groups, with the average number of partners decreasing with increasing age.

There have been no surveys for lesbians, and most studies of homosexual males give very high values (5 to 20 a year). However, Hunt *et al* (1991) have questioned the definition of 'sexual partner' used within these surveys, and identified a difference between sexual partners and penetrative sexual partners (PSP), and behaviour which may transmit the virus only occurs within these latter partnerships. They found that homosexual men had an average of 11 partners per year, but only 2 PSPs. Within this model a fairly low value for the number of partners per year has been assumed, consistent with the results from this work. For female homosexuals, an arbitrary guess has been made, which is higher than

that for female heterosexuals, but not as high as that for male homosexuals.

At present it is just this simple average number of partners which is included in the model, although Anderson and May (1988) believe that it is better to replace the 'effective average' rate of acquiring new sexual partners, with the mean rate plus the variance to mean ratio. This is because of the great variability that these surveys have revealed (with many people having few partners, while a minority have a larger number).

The uncertainty surrounding the values of the transmission risk parameters ( $q^{pq}$ ) is revealed by Longini *et al* (1990), who reviewed studies on the risks of transmission during partnerships, and noted that because the duration of partnerships and the rate of sexual contact per partnership vary considerably, these studies are difficult to compare. They noted the following variations in the risks of transmission:

Male to female : 0.03-0.73  
Female to male : 0.08-0.71  
Male to male : 0.10-0.60

Estimates of the probability of infection during the course of heterosexual partnerships are usually based on partner studies of couples of discordant sero-status. Anderson *et al* (1991) reviewed a large number of published studies, and discovered that the average patterns recorded in most published studies suggest transmission probabilities per partnership of 20% from male to female, and 11% from female to male (and these are the figures used in the model). There was however great variability in these transmission studies, with some recording equal probabilities for both sexes, and they also revealed that the likelihood of vertical or sexual transmission was positively correlated with the severity of the disease symptoms in the mother or infected sexual partner.

For homosexuals, evidence about transmission risks is more indirect, coming mainly from epidemiological models which analyse serological data, combined with information about rates of acquiring new partners (Anderson & May 1988), which have produced estimates of  $q \geq 0.1$ . It is probable that the transmission probability per contact is higher for homosexuals, but the average duration of partnerships, and number of acts are higher for heterosexuals in these models. Within these models, a relatively high number of partners per year for male homosexuals (8.7) was assumed, based on the survey data mentioned above. However, as Hunt *et al* (1991) have shown, there are differences between the definitions of sexual partners and penetrative sexual partners. Since this model utilises the concept of PSPS, the value of  $q$  used in this model needs to be higher, to compensate for the fact that fewer partnerships of a greater duration are used, in order to maintain a comparable level of risk with the earlier models. Adjustment suggests that the value of  $q$  for male homosexuals should be about 0.43.

A further assumption was that patterns of sexual behaviour (average number of partners) were irrespective of region of

residence and age, in order to simplify estimation of the inter-regional contact rates. It has been discovered that age has a significant confounding effect on patterns of behaviour, and Lagrange (1991) found that men seem to 'settle down' at age 45, to have on average, just over one partner per year, while women do so at 25. He also discovered that a significant proportion of women had many partners when young, followed by monogamy or abstinence in later life.

#### 4.7.1. Estimation of the sexual selectivity parameters

One of the first elements which needed to be incorporated into these parameters was some measure of the inter-regional contact patterns between individuals from different preference groups. The migration data,  $M_{rs}^{bg}$ , of the number of moves between different regions was used as a surrogate data source for the pattern of inter-regional sexual contacts, based on the assumption that the pattern of inter-regional visits and permanent migrations are likely to be similar (since visits often follow migrations and vice versa). However, the migration matrix only contains information about the number of inter-regional moves, so that a proportion of all contacts,  $\gamma_s$ , are assigned to be within a region, with the remainder,  $(1 - \gamma_s)$ , taking place between regions, in proportion to the number of migrations between them. Let

$$\begin{aligned} C_{rs}^{bg} &= \text{proportion of contacts made by people from RHA } s, \text{ gender } g, \\ &\quad \text{age } b, \text{ that are with region } r, \\ M_{rs}^{bg} &= \text{number of migrations from origin region } r \text{ to destination} \\ &\quad \text{region } s, \text{ by age } b \text{ and gender } g, \\ r=s: \quad C_{rs}^{bg} &= \gamma_s \\ r \neq s: \quad C_{rs}^{bg} &= \left[ 1 - \gamma_s \right] \left[ m_{sr}^{bg} / \sum_r m_{sr}^{bg} \right] \end{aligned} \quad (49)$$

There is very little information to suggest what proportion of all visits or migrations should take place within an RHA, and therefore initially the assumption that  $\gamma_s = 0.8, \forall s$ , was made, which seemed intuitively plausible.

Behavioural elements were then added to these contact rates, assuming independence between sexual behaviour patterns and region of residence. If

$$\begin{aligned} b^{pq} &= \text{proportion of contacts made by group } q \text{ that are with } p, \\ \text{then } n_{rs}^{bpq} &= C_{rs}^{bg} \cdot b^{pq}, \text{ for } g \leq q. \end{aligned} \quad (50)$$

The final feature added to these sexual selectivity parameters was a measure of the age selectivity which operates within partner choice (since heterosexual males tend to have partners slightly younger than themselves). As a rough indication of the age combinations within a sexual partnership, data on the ages of

partners at marriage was used for all heterosexual contacts (OPCS 1989c, Table 14), displayed in Table 27. For homosexual contacts, a more simplified assumption about the ages of partners was made: 40% of contacts occur within each age group, 20% with the next highest/lowest group, and 5% with each of the next two highest/lowest. For both types of contacts, data are available for 9 five-year age groups, <20, 20-24, ..., 55-59. These data were utilised by calculating the proportion of contacts made by an individual of age group B and gender/preference q, that were with someone of age group A and gender/preference p.

$$n_{rs}^{Abpq} = n_{rs}^{bpq} \cdot m^{Abpq}, \text{ for } b \in B. \quad (51)$$

where

$m^{Abpq}$  = proportion of contacts made by B,q, that are with A,p.

#### 4.8. Transmission of HIV and disease progression

Using the encounter and infection rates, the number of new infections for those of age a, RHA r and preference p,  $\text{Inf}_r^{ap}$ , for the sexually active population ( $a=16-60$ ), can be calculated as follows:

$$\text{Inf}_r^{ap} = \sum_b \sum_s \sum_q \left( \lambda_{rs}^{Abpq} \left[ P_{ro}^{ap} / \sum_{v=0}^3 P_{rv}^{ap} \right] \sum_{v=1}^2 P_{sv}^{bq} \right), \forall a \in A. \quad (52)$$

Within this process, PWAs ( $v=3$ ) were assumed to be too ill to contribute to further viral spread, so that the infectious and incubation periods were identical, which simplified calculations. The transmission equations below represent the transfer of the population between the different stages of infection, between times t and t+1.

$$P_{ro}^{ap}(t+1) = P_{ro}^{ap}(t) - \text{Inf}_r^{ap} \quad (53)$$

$$P_{r1}^{ap}(t+1) = (1-1/D1) \cdot P_{r1}^{ap}(t) + \text{Inf}_r^{ap} \quad (54)$$

$$P_{r2}^{ap}(t+1) = (1-1/D2) \cdot P_{r2}^{ap}(t) + \beta \cdot (1/D1) \cdot P_{r1}^{ap}(t) \quad (55)$$

$$P_{r3}^{ap}(t+1) = (1-1/D3) \cdot P_{r3}^{ap}(t) + (1-\beta)(1/D1) \cdot P_{r1}^{ap}(t) \\ + (1/D2) \cdot P_{r2}^{ap}(t) \quad (56)$$

$$P_{r4}^{ap}(t+1) = P_{r4}^{ap}(t) + (1/D3) \cdot P_{r3}^{ap}(t) \quad (57)$$

For the non-sexually active population, the process is similar, although there are no new infections, only the progression of existing ones. The various parameters concerning disease progression have been defined as follows:

$\beta$  = Proportion of HIV+ who develop ARC before AIDS,  
 $D1, D2, D3$  = Average duration of HIV+, ARC, AIDS stages (years).

The initial value of  $\beta$  was 88%, (from Weyer *et al* 1988), while  $D_1=7.0$ ,  $D_2=3.5$ ,  $D_3=1.6$ . These parameters were chosen to be consistent with the estimate that the average duration of the incubation period in this country is about 10 years (PHLS 1990).  $D_3$  represents the duration of AIDS, and defining this parameter posed problems because this duration has been increasing due to the effects of treatments such as AZT, and improved understanding of the disease. For example, in the Day report (PHLS 1990), AIDS cases diagnosed in 1987 had a median survival time of 18 months, while prospects for those diagnosed after 1988 had improved further. Different disease progression parameters are needed for those under 16, and for new born infants, because the disease progresses more rapidly in children than in adults (European Collaborative Study 1991). After the first 12 months of life, about 60% of infected children were found to be showing signs of HIV infection, of whom 7% had AIDS and 26% were dead from HIV-related disease, although subsequently the disease progressed more slowly, and most children remained stable or even improved during their second year. Among those infants where AIDS does not develop very early, the incubation period has been found to be 6.4 years (see Panos 1990), giving rise to progression parameters of  $D_1=4.4$ ,  $D_2=2.2$  for this age group, while the value of  $D_3$  was set to 1.0, because children with AIDS have a shorter survival time than adults (Anderson & May 1988).

## 5. SENSITIVITY TESTING

Given the uncertainties surrounding several key model parameters, it is useful to utilise epidemiological models to identify factors likely to have a major impact on the future epidemic, the parameters which projections are most sensitive to. It is also essential to examine the effects of various assumptions because predictions from transmission models depend critically on the values of unknown parameters (Isham 1988).

Several of the parameters likely to have an impact on the future size of the epidemic, and whose values were not known with any certainty, were chosen, their values systematically altered from the initial ones described in Section 4, and the impacts on predictions examined. This procedure is based on the assumption of no interaction between the various parameters, which greatly reduces the number of sets of parameter values to be tested. The parameters chosen were

PREF : Proportion of population assumed to be homo/bisexual,  
TOTHIV : Total number assumed to be HIV+ in 1987,  
 $\gamma$  : Level of inter-regional migration/visiting,  
 $D_1, D_2, D_3$  : Length of incubation and disease periods,  
 $q_{pq}$  : Infection probabilities (per partner),  
 $a^q$  : Average number of sexual partners per year.

Their values were altered in turn to 50% and 200% of their baseline values, as shown in Table 28, and the impact on model outputs assessed. The analysis was carried out by looking at variations in the total numbers in each stage of infection, and also at any differences in their regional and preference group distributions. For the number of AIDS cases and deaths, it was also possible to compare the various predictions to the observed data for the years 1988-1990, using goodness of fit statistics to compare the two distributions. The statistic chosen was the mean absolute percentage deviation of the prediction from the observed figure, calculated as follows for the regional distribution ( $n$  = number of regions)

$$MAD_v = \frac{1}{n} \sum_r \left[ |pred_{rv}(t) - obs_{rv}(t)| / obs_{rv}(t) \right] \times 100 \quad (58)$$

However, it should be remembered that there are problems associated with the reliability of the observed data when using these statistics. It has been suggested (McCormick 1989) that there may be nearly as many deaths as are reported to CDSC among people who have developed AIDS but not been reported to CDSC, and people who die because of HIV infection without developing AIDS. There are also problems of reporting delays in the surveillance data, so that observed figures need to be treated with caution. In order to ensure that this observed data was as comparable as possible to the output from the model, it was adjusted in the same way as the models' input data (For the AIDS and deaths data, male haemophiliacs were assigned to sexual preference groups according to the value of PREF, and an adjustment was made to allow for 20% under-reporting. For the HIV data, 90% of those in the blood

category were assumed to be male haemophiliacs, and the remainder transfusion cases, with an equal number of males and females, and these reports were then allocated to sexual preference groups. Sexual transmission was assumed to be responsible for 75% of the other/not-stated category, with 75% of these being homo/bisexual males, and there was also assumed to be a significant amount of non-testing, so that the true number who were HIV+ by 1987 was 27,500).

### 5.1. Variation produced by changing sexual preference parameters

The results of varying the value of PREF are shown in Table 29. Varying this parameter had a small effect on the numbers of HIV+, but only a marginal impact on the numbers in the other stages. This can be seen more clearly in Table 30, which gives the predictions from the model variants for 1990 as a percentage of the baseline predictions. These tables show that a higher value of PREF slightly increased the impact of the epidemic (possibly because the risk of viral transmission is higher among homosexuals), but the impact is only negligible. Also these variants had little effect on the goodness of fit statistics - see Table 29, or on the distribution of cases between different RHAs or preference groups. It is thus possible to conclude that PREF is not a critical parameter in determining the final form of the epidemic, since large alterations in its value have little impact on final predictions.

### 5.2. Variation produced by changing assumptions about the total number who were HIV+ in 1987

Changes to the value of TOTHIV produced the greatest variation of any of the model variants tested in the numbers within the ARC, AIDS and DEAD categories, and one of the greatest for those HIV+, and the magnitude of these differences can be seen in Table 31. As expected, these variations had their greatest impact on the numbers who were HIV+, or had ARC and AIDS, and slightly less on the number of deaths, as the effects take time to work through the model. The critical importance of this parameter can be seen because a 50% or 100% alteration to its value produces an even greater change in the model predictions. The goodness of fit statistics also show the importance of this parameter - for the high variant the MAD statistic for the AIDS cases has been increased over fivefold, indicating a large discrepancy between these predictions and the observed data. However, despite this effect on the total number of cases predicted, there was very little impact on the distribution of cases between RHAs or preference groups. For example the baseline version predicted that 19.94% of the HIV+ population in 1990 would live in North West Thames, compared to 19.09% for the low variant and 19.43% for the high variant.

### 5.3. Variation produced by changing assumptions about inter regional migration or visiting

The parameter  $\gamma$  has little impact on the total figures shown in Table 32, and also on the goodness of fit statistics in Table 29. However, despite this lack of an overall effect, if the regional

and preference group distributions for the HIV+ and AIDS categories are examined (Tables 33 and 34), it can be seen that the level of inter-regional movement within the contact rates affects the proportion of cases recorded from each region (although the preference group distribution is unaffected).

As expected, increasing levels of inter-regional contacts results in more rapid diffusion of the epidemic from its epicentres (eg NW.Thames) to the rest of the country. However, if all contacts take place within an RHA, then the epidemic becomes increasingly concentrated in its 'stronghold regions', and as prevalence increases within these RHAs, the rates of increase are likely to increase. There is a greater impact on the HIV than the AIDS figures because it takes time for the effects to filter through the stages of infection.

#### **5.4. Variation produced by changing assumptions about the incubation or survival times**

Variation of the parameters controlling incubation time affected the numbers in all of the stages of infection, while variation of the survival time with AIDS only affected the numbers of AIDS cases and deaths. Table 35 shows the substantial percentage differences from the baseline predictions produced by these variants.

The effect of increasing the values of D1 and D2 (the incubation period) is to reduce the number of AIDS cases and deaths predicted, while a decrease in the parameter values increases the predictions, with the largest impact being on the number of AIDS cases recorded. This occurs because reducing the incubation period means that those infected will progress to AIDS more quickly, while with a longer incubation period, individuals will remain in the HIV+ and ARC stages for longer, and thus the true impact of the disease, in terms of the number of PWAs, will take longer to become apparent. Variation of these parameters also produced up to a 2% variation in the regional and preference groups distributions of AIDS cases (see Tables 36 and 37). This happens because the longer incubation period means that a greater proportion of AIDS cases will be reported from those RHAs or preference groups where the epidemic is more advanced (and a greater proportion have ARC), than those areas where most are in the first stages of infection.

Lengthening the survival time (D3) produced an increased number of AIDS cases, and fewer deaths, while a reduction resulted in fewer AIDS cases and more deaths, since increasing this parameter means that PWAs survive with AIDS for longer. However, this parameter had less effect on the regional or preference distributions, only producing about a 1% variation, probably because the effects have had to filter through the stages of infection.

Varying these two parameters also produced significant alterations to the goodness of fit statistics (see Table 29), suggesting that accurate information about the progression of the disease is a vital model element, necessary for the production of accurate results.

## 5.5. Variation produced by changing assumptions about the transmission risks, or average number of partners.

These two variants produced almost identical predictions - see Table 29, probably due to the way that they are used within the model to calculate the encounter and infection rates, so that a 50% reduction in either parameter probably has a very similar effect on the final rates. Table 38 therefore shows the percentage variations produced by the transmission probability variations (although they would have been similar for partner numbers). This table shows that the greatest influence is on the number who are HIV+, with less effect on subsequent stages of infection, due to the way in which individuals move unidirectionally through the stages of infection. In fact, a 100% increase in their value results in more than a 100% increase in predictions, showing how important these parameters are in determining the size of the predictions. Once again however, there is very little impact on the regional or preference group distributions.

## 5.6. Summary of results from sensitivity testing

For the seven parameters tested:

- PREF - Very little impact.
- TOTHIV - Major impact, probably the most important parameter tested.
- $\gamma$  - Little overall effect, but important for the regional distribution.
- D1,D2 - Important, especially for the number of AIDS cases and deaths predicted. Also has small effect on regional distribution.
- D3 - Important for the number of AIDS cases and deaths predicted.
- a,q - Important for determining the number of new infections.

Now that these important parameters have been identified, it will be necessary to ensure that the estimates of these parameters used in the model are the best possible.

## 6. GEOGRAPHICAL SPREAD SIMULATED

In order to get some idea of the ways in which the model predicts the geographical spread of the virus, forecasts were produced to cover the period until the year 2000. However, before this was done, several alterations were made to the parameter values described in Section 4, in order to reflect known patterns of behaviour and behavioural change. These changes included a reduction in the average yearly number of sexual partners for gay men from 3 to 2, reflecting reductions in the average numbers of partners reported in surveys (DHSS 1987). The transmission probabilities per partnership for this group were also reduced from 0.43 to 0.25, reflecting behavioural change towards safer sex and greater use of condoms, as has also been reported (DHSS 1987). At the same time it was assumed that male homo/bisexuals in NW.Thames had one and a half times as many partners as the national average, while for the other Thames regions this figure was one and a quarter. This assumption was made because surveys have shown that levels of homosexual activity tend to be higher in the capital (McManus & McEvoy 1986). If these assumptions were not incorporated, then there was predicted an almost even distribution of the virus across the country by 2000, with most of the male homo/bisexual population infected, reflecting the importance of behavioural change in determining the outcome of the epidemic.

By the end of the century, 49,368 people are predicted to have died from AIDS, with a cumulative figure of 247,696 having been infected with the virus. The model also predicts that there will be gradual diffusion throughout the regions, in terms of increasing numbers affected from all regions, although the Thames regions still dominate in the overall picture - see Table 39. For example in 1987, the Thames regions were predicted to contain 63% of the currently infected population, but by 2000 this figure had fallen to 47%. Also, in 1987 it was estimated that Yorkshire had a cumulative total of 676 affected, and had experienced 23 cases of AIDS, and by 2000 these figures were predicted to be 9578 and 2455 respectively. The region predicted to be least affected is Northern Ireland, perhaps because it is separated from the rest of the UK by the physical barrier of the Irish Sea, and there are therefore less inter-regional contacts, and also because this RHA has relatively few HIV+ residents (122 by 1987, 1232 by 2000).

In terms of preference groups, homosexual and bisexual men are predicted to be the major group affected, making up over 90% of the caseload in 2000 - see Table 40. However, as with the regional spread, there is considerable diffusion in terms of the numbers affected in different groups, although not necessarily in terms of the proportion of the caseload. For example, by 1987 a cumulative total of 1022 heterosexual women had been infected, of whom 28 had developed AIDS, while by 2000 the figures were 15,346 and 5118 respectively. Another feature revealed by the model output is that while the numbers of infections are increasing among heterosexual women (from 994 in 1987 to 10,228 in 2000), among male heterosexuals, prevalence appears to be decreasing (from 3889 to 1891).

## 7. EVALUATION

### 7.1. Assessment of the weaknesses of the current model

Examining the predictions in Section 6, there appear to be several problems with the model. Firstly, it seems to be too dominated by London, with the future case-load comprising of too many homo/bisexual men, and not enough heterosexual transmission occurring to be realistic, and there may be several reasons why this pattern has emerged. Firstly, there is no representation in the model of any ongoing process of behavioural change, for example a reduction in the number of partners, or wider use of condoms, while significant behavioural changes are known to have taken place, especially among homo/bisexual men (Hunt *et al* 1991) and especially in London (Weatherburn *et al* 1991), and these are likely to become more widespread as the perceived severity of the epidemic increases. Also, one of the fastest growing epidemics is currently occurring in the IDU community who are not included in this model, and this group may have a different geographical distribution to homosexual men. Importantly, this group has been identified as one of the major diffusion poles for the spread of the virus into the rest of the heterosexual community, and the absence of this group may be one of the reasons for the lower than expected level of diffusion into the heterosexual community.

The reduction in prevalence among heterosexual men possibly reflects the fact that initially, haemophiliacs were included in the heterosexual category, as they may contribute to sexual spread, so there were higher than expected numbers of heterosexual males who were infected initially. It may also reflect the theory that the probability of transmission from women to men is about half that from men to women. Also, heterosexual women in this model have some contact with bisexual men, and may therefore be at a higher risk of acquiring infection. The situation which has been forecast does seem slightly unrealistic at present, but may be improved when the behavioural group of IDUs is added, and heterosexual males may then have direct contact with a 'higher risk group', namely female IDUs.

### 7.2. Improvement strategy for the current model

This analysis has suggested several ways in which the current model may be improved, which are listed below (in no particular order):

1. Extension of the model to include transmission via intravenous drug use, and take account of the links between IDUs and the other groups in the model, which will involve searching for more data on the mixing patterns between different behavioural groups.
2. Some way of modelling the impact of behavioural change should be investigated, as this could have important implications, especially for the transmission of the virus in the homosexual community, and in the Thames regions.
3. The heterogeneity of rates of partner change within groups could

also be extended, to try and account for the very high variability which has been recorded in surveys of sexual behaviour (DHSS 1987).

4. The results also suggest that the division into the HIV+ and ARC categories should be reviewed, possibly with greater regional differentiation, since at present, there seem to be too many in the ARC stage at the start of the model run. This will require more data on the regional proportions of those who were ill when tested.

5. Introduction of variable levels of infectivity during the incubation period could also be considered, since several researchers have identified that this is important in determining the final outcome of the epidemic (Anderson 1988).

6. It will be necessary to conduct extensive searches, to try and identify more accurate estimates of the various model parameter values, since the sensitivity analysis of Section 5 identified the importance of several parameter values in determining the final form of the epidemic. For example it may be possible to get a more accurate idea of the numbers who were HIV+ in 1987 when more results from the anonymous serosurveys that are currently being undertaken are made available. It may also be possible to use the model to gain some understanding of the true numbers who were HIV+ by 1987. The accuracy of the HIV/AIDS data in the model might also be improved by taking account of the cross boundary flows which exist, particularly in the Thames regions, so that the region where an AIDS case is reported is not necessarily the region of residence (PHLS & CDSU 1991).

7. It may also be possible to divide the male homo/bisexual category into two separate groups (see Anderson & Johnson 1990), to reflect of the different patterns of behaviour in these two groups.

8. Develop computerised mapping techniques to help display the results clearly, maybe using packages such as ARC/INFO.

9. Start the model run using an earlier base year, for example 1985, because a longer time series of observed data would then be available, to allow predictions to be evaluated more extensively.

10. Possibly include some representation of external migration in the model, since international sexual contacts are extremely important in determining the spread of the virus between countries. Several infections in UK residents have been identified as being due to overseas contacts (PHLS & CDSU 1991).

### 7.3. Policy implications of the current model

Despite the problems identified above, this model shows that even with fairly conservative estimates about the number of partners, transmission probabilities and other model parameters, it is still possible to produce forecasts which demonstrate the potential that exists for the large-scale spread of HIV within this country, as can be seen in Figure 6, a graph showing the spread of the disease as forecast by this model.

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## APPENDIX 1. Glossary of terms used in this paper

AIDS	- Acquired Immune Deficiency Syndrome
ARC	- AIDS-related complex
AZT	- Zidovudine
CDSC	- Communicable Disease Surveillance Centre (UK)
CDSU	- Communicable Diseases (Scotland) Unit
DoH	- Department of Health
DHSS	- Department of Health and Social Security
FPCA	- Family Practitioner Committee Area
HIV	- Human Immunodeficiency Virus
IDU	- Intravenous drug user
IPF	- Iterative proportional fitting
KS	- Kaposi's sarcoma
MAD	- Mean absolute deviation
MMS	- Model migration schedule
NHSCR	- National Health Service Central Register
OPCS	- Office of Population Censuses and Surveys
PAR	- Population at risk
PCP	- Pneumocystis carinii pneumonia
PHLS	- Public Health Laboratory Service
PSP	- Penetrative sexual partner
PWA	- People with AIDS
RHA	- Regional Health Authority
SMR	- Standardised mortality ratio
WHO	- World Health Authority

TABLE 1. Regional distribution of AIDS cases and HIV+ reports, cumulative totals to September 1991 (UK residents)

Region	AIDS	(%)	HIV+	(%)
Northern	91	(2)	366	(2)
Yorkshire	127	(3)	422	(3)
Trent	98	(2)	422	(3)
E.Anglia	58	(1)	210	(1)
NW.Thames	1861	(37)	4882	(30)
NE.Thames	878	(17)	2845	(18)
SE.Thames	553	(11)	1770	(11)
SW.Thames	190	(4)	513	(3)
Wessex	111	(2)	352	(2)
Oxford	109	(2)	436	(3)
S.Western	104	(2)	347	(2)
W.Midlands	114	(2)	544	(3)
Mersey	67	(1)	192	(1)
N.Western	198	(4)	715	(4)
Wales	75	(1)	241	(1)
Scotland	258	(5)	1906	(12)
N.Ireland	24	(1)	85	(1)
TOTAL	4916	(100)	16248	(100)

Source : PHLS & CDSU (1991)

TABLE 2. Transmission route distribution of AIDS cases and HIV+ reports, cumulative totals to September 1991

Probable route of transmission	AIDS	(%)	HIV+	(%)
Sexual intercourse				
between men	3295	(78)	9587	(59)
between men and women	387	(8)	1644	(11)
IDU	223	(4)	2179	(13)
IDU & sexual intercourse between men	79	(2)	180	(1)
Haemophiliacs	272	(5)	1275	(8)
Blood transfusion	71	(1)	148	(1)
Mother to infant	45	(1)	97	(1)
Other/undetermined	63	(1)	1138	(7)
TOTALS	5065	(100)	16248	(100)

Source : PHLS & CDSU (1991)

### BLE 3 THE CHARACTERISTICS OF TRANSMISSION MODELS

EL FEATURE	1	2	3	4	5	6	7	MODEL NUMBER (SEE KEY)														
C MODEL STRUCTURE	1987	1990	1990	1989	1988	1986	1988	1988	1989	1988	1990	1990	1988	1988	1988	1990	1990	1990	1990	1988	1988	
Year developed	1987	1990	1990	1989	1988	1986	1988	1988	1989	1988	1990	1990	1988	1988	1988	1990	1990	1990	1990	1988	1988	
Geographic Location	Eng. Wales	Africa	UK	UK	UK	W. Ger.	U.K.	San.	U.S.A.	San.	W. GER.	Africa	NE USA	USA	USA	USA	USA	USA	USA	USA	USA	USA
ministic / Stochastic	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	S	S	S	S	S	D	
Aggregate / Individual Scale	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	I	I	I	I	A	
past incidence of HIV / AIDS / Deaths	HA	HA	AD	HAD	HA	HAD	HA	HAD	HA	HAD	HA	HAD	HAD	HAD	HAD	H	H	H	H	H	HAD	
scale projections (years)	30	60	100	100	5	50	75	5	25			6	23	200	25	5	10	7	10	7		
idence Intervals / Sensitivity Analysis			S.A.	S.A.												C.I.	C.I.	C.I.				
Equilibrium attained																						
<b>POPULATION</b>																						
a / Multi risk-group	S	S	M	S	S	M	M	S	S	S	S	S	M	M	M	S	S	S	S	S	M	
Homosexual	✓	✓		✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	*		✓	✓	✓		
Bisexual	✓						✓	✓		✓		✓	✓	✓	✓							✓
Us (Injection / Sexual)																✓	*	✓	✓	✓	✓	✓
aemophiliacs																						
Transfusion																						
eterosexual			✓				✓	✓								✓	✓	✓				✓
stitutes								✓	✓							✓	✓					
erinatal			✓																			
Population size: Constant (with recruitment) / Variable	Cr	Cr	V	Cr	Cr	Cr		Cr	Cr	C	Cr	C	Cr	V	V	Cr	C	Cr	V		✓	
Initial population size	100,000	500,000	16.6 M	500,000	500,000	2.5 M	1 M		100,000		1 M		100 M									200,503,000
Spatial disaggregation																					*	✓
disaggregation (years)			✓					✓	✓						✓	✓	✓					✓
ter disaggregation			✓					✓							✓	✓	✓					✓
Heterogeneous behavior (no. of classes)	✓	✓	6	Age	6	6				2	5				2	10						Age
ng	Random																					✓
Restricted																						✓
Proportionate	✓	✓		✓	✓			✓		✓	✓	✓				✓	✓	✓	✓	✓	✓	✓
Preferred	✓	Age																				*
Complex choice								✓							✓							
Partner choice age-dependent			✓						✓	✓										*		✓
non-AIDS mortality included			✓						✓	✓	✓											✓
ulation dynamics included				Some											Some	✓	✓			✓	*	✓
lement Into / From risk population	In	In		In	In	In		In/From	In/From		In				*	In			Some	*		✓
<b>TRANSMISSION FACTORS</b>																						
able Infectivity		✓			✓	✓				✓					✓							✓
s vary with Behaviour / Gender / Age		G						✓	✓	✓					G							ABG
ions per Contact / Partner	P	P	P	P	P	P	P		C	C	C	C	P	C	C	C	C	C	C	C	C	
Variable number of contacts								✓			✓	✓			✓	✓	✓	✓	✓	✓	✓	✓
formation																						
mission ceases when AIDS develops	✓	✓		✓	✓			✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
fectious immediately after infection	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
behavioural change occurs				✓	✓	*		✓	✓						*	✓	✓	*	*	*	*	✓
tments available						*		✓	✓						*							*
sible immune stage	✓																					
cofactors for injection															*							✓
account of effects of testing															✓							
<b>EASE PROGRESSION</b>																						
istributed Incubation or Disease periods	✓	✓	✓	✓	✓	✓			✓	✓	✓				✓						✓	✓
Complex stage transitions allowed															✓	✓						✓
ression dependant on Age / Route /Clinical manifestation			A					A	A	C											C	
What proportion of infecteds develop AIDS	0.3		1.0	1.0	1.0			1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9				1.0	1.0		1.0
age length of inoculation period (yrs.)	5	8	8	8				8		5.2 ±0.6		9.125	11.4	8	9.3							7 3/4

El \* - The inclusion of these processes has been discussed in theory, but not applied in practice

KEY TO MODELS																		
1. May and Anderson (1987)	11. Ahlgren et al (1990)																	
2. Anderson et al (1990)	12. Weyer et al (1988)																	
3. Anderson et al (1989)	13. Anderson et al (1988)																	
4. Blyth and Anderson (1988)	14. Bongaarts (1989)																	
5. Knox (1986)	15. Kaplan (1990)																	
6. Dietz (1988)	16. Allard (1990)																	
7. Wilkie (1988)	17. Peterson et al (1990)																	
8. Institute of Actuaries (1989)	18. Leslie and Brunham (1990)																	
9. Bailey (1988)	19. Mode et al (1990)																	
10. Sattenspiel et al (1990)	20. Kanouse et al (1990)																	

TABLE 4. Basic model characteristics

Population : $p_{rv}^{ap}$ Non-survival probabilities : $d_r^{ag}$ Age-specific fertility rates : $f_r^{af}$ Inter regional migration probabilities, given survival : $m_{rs}^{ag}$			
Code	Name	no.	Description
a af p	Age Age Sexual preference	91 30 4	Single years of age, 0-90+ Female single years of age, 15-44 Male heterosexual, Male homo/bisexual Female heterosexual Female homo/bisexual
r,s	RHA of residence	17	15 Health Regions plus 3 countries
v	Viral status	5	HIV-, Asymptomatic HIV+, ARC, AIDS, DEAD from AIDS.
g	Gender	2	Male, female
Encounter and infection rates : $\lambda_{rs}^{Abpq}$			
Code	Name	no.	Description
A b	Age of target pop Age of infected population	9 44	Five year age groups, <20, 20-24, 25-29, . . . . . , 50-59 Single year of age, 16-60
p,q	Preference	4	Preferences of target and infected populations (see above)
r,s	RHA	17	RHAs of residence of target and infected populations
System characteristics			
Projection period = 1 year Base year = 1987 Demographic processes : births, deaths, in and out migration Transmission methods : sexual (homosexual and heterosexual) vertical transmission			

TABLE 5. RHA populations for England and Wales, by gender and five year age groups, for mid 1987 (hundreds)

RHA & gender	All	Age Groups											
		<1	1-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	
North M	14,986	203	805	988	983	1152	1267	1178	1046	1070	1049	863	
	F	15,782	194	765	935	929	1135	1249	1161	1015	1050	1024	855
York M	17,541	245	953	1162	1166	1416	1513	1371	1216	1251	1231	998	
	F	18,505	235	914	1108	1100	1372	1477	1344	1188	1238	1200	986
Trent M	22,851	302	1197	1470	1482	1803	1986	1806	1592	1648	1635	1318	
	F	23,612	293	1126	1387	1399	1728	1912	1767	1542	1620	1581	1291
E. An M	9,868	130	528	655	634	798	868	746	661	694	685	550	
	F	10,268	124	506	622	604	727	795	751	693	712	674	536
N.W.T M	17,036	246	929	1091	1027	1309	1564	1435	1246	1268	1239	989	
	F	17,846	236	884	1042	982	1281	1539	1438	1267	1298	1231	983
NET M	18,308	274	1011	1175	1125	1376	1654	1513	1317	1336	1294	1030	
	F	19,407	260	969	1124	1060	1362	1663	1531	1319	1358	1295	1028
S.E.T M	17,501	248	921	1096	1071	1372	1521	1392	1227	1248	1214	975	
	F	18,854	237	879	1043	1016	1334	1496	1380	1209	1255	1215	985
S.W.T M	14,285	190	726	877	856	1131	1172	1126	1014	1065	1047	835	
	F	15,311	178	695	838	817	1041	1150	1100	999	1078	1051	850
Wessex M	14,167	185	726	896	888	1215	1288	1137	957	979	946	766	
	F	14,889	179	684	837	834	1069	1145	1068	953	1003	974	795
Oxf M	12,425	174	696	854	817	1111	1170	1032	894	924	894	702	
	F	12,594	164	658	801	770	979	1085	1016	907	932	882	687
S.W M	15,478	198	777	967	967	1249	1299	1153	1029	1076	1067	869	
	F	16,578	189	737	918	920	1168	1249	1153	1040	1102	1073	880
W.Mid M	25,642	363	1393	1695	1710	2070	2199	2008	1765	1837	1842	1501	
	F	26,334	344	1315	1601	1602	1969	2126	1946	1694	1799	1775	1455
Mers M	11,666	164	646	785	795	935	999	918	807	823	816	674	
	F	12,421	158	614	741	746	916	988	917	795	826	813	675
N.W M	19,402	285	1086	1297	1290	1536	1693	1537	1353	1395	1375	1107	
	F	20,509	269	1035	1235	1221	1498	1653	1500	1298	1358	1326	1081
Wal M	13,771	191	742	901	918	1115	1171	1044	902	962	932	793	
	F	14,591	182	706	853	865	1065	1152	1025	874	964	932	783

**Table 5. cont.**

RHA & gender	Age Groups								
	50 -54	55 -59	60 -64	65 -69	70 -74	75 -79	80 -84	85+	
Nor M	844	820	820	705	521	364	189	88	
	F	848	882	892	844	716	604	408	279
York M	954	947	909	799	613	444	239	115	
	F	958	983	984	949	840	735	515	376
Tren M	1258	1248	1207	1058	808	582	308	143	
	F	1238	1259	1267	1216	1053	897	608	428
E.An M	520	511	506	477	383	286	158	78	
	F	514	533	553	538	480	413	282	211
NWT M	939	913	846	708	553	408	219	108	
	F	925	906	868	823	727	635	442	338
NET M	989	983	939	814	634	467	254	123	
	F	983	995	988	951	848	744	525	403
SET M	931	928	916	837	673	506	282	143	
	F	955	989	1024	1020	928	831	592	466
SWT M	794	778	736	652	530	409	228	121	
	F	811	820	823	800	737	664	481	380
Wess M	740	733	725	676	546	412	231	121	
	F	765	796	820	807	727	638	450	344
Oxf M	648	612	563	485	372	267	142	69	
	F	626	609	586	548	468	399	272	205
S.W M	838	838	840	780	633	480	273	143	
	F	860	900	943	933	844	742	522	404
W.Mi M	1436	1416	1342	1152	858	606	311	137	
	F	1390	1409	1413	1338	1137	952	635	436
Mers M	657	650	604	516	389	278	143	66	
	F	662	676	669	636	552	474	326	236
N.W M	1049	1036	990	866	666	476	252	115	
	F	1040	1070	1094	1065	953	837	577	399
Wal M	752	748	763	680	512	362	192	93	
	F	760	779	839	814	698	597	410	294

Source : OPCS (1989a)

TABLE 6. Total populations of England and Wales, by gender and single year age groups (hundreds)

Age	Male	Female	Age	Male	Female
0	3399	3244	45	2862	2829
1	3357	3185	46	2643	2630
2	3340	3179	47	2819	2792
3	3211	3058	48	2823	2817
4	3228	3066	49	2822	2801
5	3223	3057	50	2775	2753
6	3266	3109	51	2725	2720
7	3303	3136	52	2677	2669
8	3185	3012	53	2583	2587
9	2931	2770	54	2589	2606
10	2884	2719	55	2667	2687
11	2997	2837	56	2690	2746
12	3127	2958	57	2660	2766
13	3238	3065	58	2608	2718
14	3484	3286	59	2566	2688
15	3703	3501	60	2583	2717
16	3952	3744	61	2589	2752
17	3898	3698	62	2540	2743
18	4002	3836	63	2515	2776
19	4034	3864	64	2479	2784
20	4178	3999	65	2562	2915
21	4229	4091	66	2637	3063
22	4349	4203	67	2689	3182
23	4355	4222	68	1731	2116
24	4249	4164	69	1586	2002
25	4136	4091	70	1718	2195
26	4027	3969	71	1788	2319
27	3866	3790	72	1814	2447
28	3739	3674	73	1740	2422
29	3626	3575	74	1631	2327
30	3506	3476	75	1493	2206
31	3434	3370	76	1372	2115
32	3333	3272	77	1278	2047
33	3386	3336	78	1163	1963
34	3365	3337	79	1040	1834
35	3299	3297	80	906	1672
36	3367	3360	81	780	1548
37	3463	3482	82	683	1430
38	3594	3596	83	570	1266
39	3851	3857	84	481	1128
40	4230	4192	85	389	970
41	3317	3289	86	315	867
42	3279	3229	87	246	737
43	3300	3244	88	177	577
44	3141	3092	89	136	458
			90+	402	1591

Source : OPCS (1989a)

TABLE 7. Scottish and Northern Irish populations (hundreds), by gender and single year of age, mid 1987

Age	Scotland		N.Ireland		Age	Scotland		N.Ireland	
	Male	Female	Male	Female		Male	Female	Male	Female
0	33,558	31,981	140	130	47	28,112	29,568	80	80
1	33,850	32,230	140	130	48	28,305	29,461	80	80
2	32,872	31,698	140	130	49	28,370	29,443	80	80
3	31,982	30,419	140	130	50	27,541	29,542	70	80
4	32,640	30,998	140	130	51	27,416	29,277	70	80
5	33,160	31,772	130	130	52	27,159	28,887	70	70
6	34,327	32,357	140	130	53	26,895	28,352	70	80
7	33,372	31,984	140	130	54	26,447	28,536	70	70
8	32,560	30,516	130	130	55	27,195	29,706	70	80
9	29,894	28,704	130	120	56	27,008	29,576	70	80
10	30,048	28,208	130	120	57	26,587	29,671	70	70
11	32,852	30,925	130	120	58	26,143	29,209	60	70
12	33,082	31,618	130	120	59	25,653	28,513	70	80
13	34,162	32,366	140	130	60	25,519	28,749	60	80
14	36,873	34,746	140	130	61	25,874	29,332	60	70
15	39,258	37,892	140	130	62	24,732	28,244	60	70
16	42,022	40,090	150	140	63	24,553	28,531	60	70
17	41,637	40,299	150	140	64	23,424	27,896	60	70
18	42,767	41,155	150	140	65	24,500	29,342	60	70
19	43,612	42,503	150	140	66	23,681	29,900	60	70
20	45,204	42,890	150	130	67	24,656	31,598	50	70
21	44,946	42,901	150	130	68	16,387	22,064	40	60
22	47,316	44,520	150	130	69	15,442	21,064	40	60
23	45,544	43,303	140	130	70	16,289	22,068	40	60
24	44,448	42,151	140	130	71	16,392	23,161	40	60
25	43,803	41,208	130	120	72	16,946	24,602	40	60
26	42,425	40,694	130	120	73	16,090	24,076	40	60
27	41,077	39,126	120	120	74	15,106	22,764	40	60
28	39,943	38,790	120	110	75	13,803	21,682	30	60
29	38,529	37,912	110	110	76	12,716	20,916	30	50
30	37,439	36,640	110	110	77	11,677	20,205	30	50
31	36,573	35,720	100	110	78	10,479	19,171	20	40
32	34,747	34,462	100	100	79	9,358	17,938	20	40
33	34,701	34,404	100	100	80	7,992	15,961	20	40
34	34,132	33,863	100	100	81	6,957	15,233	10	30
35	32,638	32,719	90	100	82	5,922	13,554	10	30
36	33,855	33,648	100	90	83	4,927	12,158	10	20
37	34,223	33,884	100	90	84	4,047	10,506	10	20
38	35,316	35,181	100	100	85	3,286	9,070	10	20
39	36,888	36,764	100	100	86	2,574	8,024	10	20
40	40,242	40,214	100	100	87	2,004	6,869	10	20
41	31,276	31,237	90	90	88	1,389	4,998	0	10
42	29,874	30,059	90	90	89	1,069	4,169	0	10
43	31,154	31,168	90	90	90+	3,051	13,044	10	30
44	30,495	31,142	90	100					
45	28,561	29,575	80	80	Tot	2470,645	2641,484	7710	8020
46	27,085	28,218	80	80					

Source : Registrar General Northern Ireland (1989) & Registrar General Scotland (1988)

**TABLE 8. RHA cumulative HIV+, AIDS and AIDS-deaths reports to the end of 1987**

Region	HIV+	AIDS	DEAD
Northern	239	30	18
Yorkshire	242	19	18
Trent	197	19	12
E.Anglia	122	14	9
NW.Thames	2444	512	310
NE.Thames	1258	219	133
SE.Thames	921	108	66
SW.Thames	183	43	26
Wessex	198	27	16
Oxford	253	22	13
S.Western	166	20	12
W.Midlands	295	20	12
Mersey	113	15	9
N.Western	377	40	24
Wales	66	18	11
Scotland	1381	37	22
N.Ireland	42	3	5

Source : PHLS & CDSU (1991)

**TABLE 9. AIDS cases (A) and deaths (D) by transmission route and age, up to the end of 1987**

Transmission route	A	Age group											
		<1	1-	5-	10-	15-	20-	25-	30-	35-	40-	50-	60+
Male homo/bisexual	A	0	0	0	0	2	45	119	224	230	291	74	14
	D	0	0	0	0	1	25	59	123	134	196	49	11
IDU	A	0	0	0	0	0	3	20	6	4	5	0	0
	D	0	0	0	0	0	0	10	6	2	4	0	0
Male haemophiliac	A	0	0	1	1	5	9	4	9	7	9	10	12
	D	0	0	0	1	5	6	2	5	5	7	10	11
Transfusion	A	0	1	1	0	0	1	0	0	1	4	1	4
	D	0	1	0	0	0	0	0	0	1	2	1	4
Male heterosexual	A	0	0	0	0	0	0	3	5	4	0	3	0
	D	0	0	0	0	0	0	2	1	1	0	1	0
Female heterosexual	A	0	0	0	0	0	5	2	1	3	4	1	1
	D	0	0	0	0	0	3	1	1	4	1	1	0
Infant	A	2	6	1	0	0	0	0	0	0	0	0	0
	D	0	2	0	0	0	0	0	0	0	0	0	0
Other	A	0	0	0	0	0	0	0	0	1	2	1	0
	D	0	0	0	0	0	0	0	0	1	1	0	0

Source : PHLS & CDSU (1991)

TABLE 10. HIV+ reports by transmission route, for Scotland and the rest of the UK, December 1987

Transmission Route	Rest of UK	Scotland
Male homo/bisexual	4462	206
Male heterosexual	145	26
Female heterosexual	163	35
Male IDU	414	505
Female IDU	188	269
Infant	28	64
Blood	1108	85
Other	608	191

Source : PHLS & CDSU (1991)

**TABLE 11. HIV+ and ARC joint regional and transmission route distributions, cumulative to end of 1987**

**ESTIMATED DISTRIBUTION OF HIV REPORTS**

RHA	Group number							
	1	2	3	4	5	6	7	8
Northern	149.9	4.9	5.5	13.9	6.3	0.9	37.2	20.4
Yorkshire	151.7	4.9	5.5	14.1	6.4	0.9	37.7	20.7
Trent	123.5	4.0	4.5	11.5	5.2	0.8	30.7	16.8
E.Anglian	76.5	2.5	2.8	7.1	3.2	0.5	19.0	10.4
NW.Thames	1532.5	49.8	56.0	142.2	64.6	9.6	380.5	208.8
NE.Thames	788.8	25.6	28.8	73.2	33.2	4.9	195.9	107.5
SE.Thames	577.5	18.8	21.1	53.6	24.3	3.6	143.4	78.7
SW.Thames	114.8	3.7	4.2	10.6	4.8	0.7	28.5	15.6
Wessex	124.1	4.0	4.5	11.5	5.2	0.8	30.8	16.9
Oxford	158.6	5.2	5.8	14.7	6.7	1.0	39.4	21.6
S.Western	104.1	3.4	3.8	9.7	4.4	0.6	25.8	14.2
W.Midland	185.0	6.0	6.8	17.2	7.8	1.2	45.9	25.2
Mersey	70.9	2.3	2.6	6.6	3.0	0.4	17.6	9.6
N.Western	236.4	7.7	8.6	21.9	10.0	1.5	58.7	32.2
Wales	41.4	1.3	1.5	3.8	1.7	0.3	10.3	5.6
Scotland	206.0	26.0	35.0	505.0	269.0	64.0	85.0	191.0
N.Ireland	26.3	0.9	1.0	2.4	1.1	0.2	6.5	3.6

The key to these group numbers is as follows:

- |                             |               |
|-----------------------------|---------------|
| 1: Male homosexual/bisexual | 5: Female IDU |
| 2: Male heterosexual        | 6: Infant     |
| 3: Female heterosexual      | 7: Blood      |
| 4: Male IDU                 | 8: Other      |

**CUMULATIVE HIV+ AND ARC DATA ADJUSTED TO ALLOW FOR NON-TESTING**

RHA	Groups for HIV data			Groups for ARC data		
	A	B	C	A	B	C
Northern	371.6	115.8	26.3	159.3	11.4	2.6
Yorkshire	376.3	117.2	26.7	161.3	11.6	2.6
Trent	306.3	95.4	21.7	131.3	9.4	2.1
E.Anglian	189.7	59.1	13.4	81.3	5.8	1.3
NW.Thames	2714.3	1105.8	251.7	2714.3	195.1	44.4
NE.Thames	1397.1	569.2	129.6	1397.1	100.4	22.9
SE.Thames	1022.9	416.7	94.8	1022.9	73.5	16.7
SW.Thames	243.9	85.7	19.5	162.6	11.7	2.7
Wessex	307.9	95.9	21.8	131.9	9.5	2.2
Oxford	393.4	122.5	27.9	168.6	12.1	2.8
S.Western	258.1	80.4	18.3	110.6	7.9	1.8
W.Midland	458.7	142.9	32.5	196.6	14.1	3.2
Mersey	175.7	54.7	12.5	75.3	5.4	1.2
N.Western	586.2	182.6	41.6	251.2	18.1	4.1
Wales	117.3	33.0	7.5	29.3	2.1	0.5
Scotland	827.5	359.6	168.5	206.9	22.9	10.7
N.Ireland	65.3	20.3	4.6	28.0	2.0	0.5

The key to these group numbers is as follows:

- |                             |                        |
|-----------------------------|------------------------|
| A: Male homosexual/bisexual | C: Female heterosexual |
| B: Male heterosexual        |                        |

**TABLE 12. AIDS joint regional and transmission route distributions, cumulative to end of 1987**

**ESTIMATED DISTRIBUTION OF AIDS CASES**

RHA	GROUP NUMBER							
	1	2	3	4	5	6	7	8
Northern	25.70	0.98	1.72	0.33	0.39	0.44	0.23	0.10
Yorkshire	16.28	0.62	1.09	0.21	0.24	0.28	0.15	0.07
Trent	16.28	0.62	1.09	0.21	0.24	0.28	0.15	0.07
E.Anglian	11.99	0.46	0.80	0.16	0.18	0.20	0.11	0.05
NW.Thames	438.67	16.69	29.42	5.71	6.59	7.46	3.95	1.76
NE.Thames	187.63	7.14	12.58	2.44	2.82	3.19	1.69	0.75
SE.Thames	92.53	3.52	6.21	1.20	1.39	1.57	0.83	0.37
SW.Thames	36.84	1.40	2.47	0.48	0.55	0.63	0.33	0.15
Wessex	23.13	0.88	1.55	0.30	0.35	0.39	0.21	0.09
Oxford	18.85	0.72	1.26	0.25	0.28	0.32	0.17	0.08
S.Western	17.14	0.65	1.15	0.22	0.26	0.29	0.15	0.07
W.Midland	17.14	0.65	1.15	0.22	0.26	0.29	0.15	0.07
Mersey	12.85	0.49	0.86	0.17	0.19	0.22	0.12	0.05
N.Western	34.27	1.30	2.30	0.45	0.51	0.58	0.31	0.14
Wales	15.42	0.59	1.03	0.20	0.23	0.26	0.14	0.06
Scotland	31.70	1.21	2.13	0.41	0.48	0.54	0.29	0.13
N.Ireland	2.57	0.10	0.17	0.03	0.04	0.04	0.02	0.01

The key to these group numbers is as follows:

- |                             |                        |
|-----------------------------|------------------------|
| 1: Male homosexual/bisexual | 5: Male heterosexual   |
| 2: IDU                      | 6: Female heterosexual |
| 3: Male haemophiliac        | 7: Infant              |
| 4: Transfusion recipient    | 8: Other               |

**CUMULATIVE DATA ADJUSTED TO ALLOW FOR 20% UNDER-REPORTING**

RHA	GROUP NUMBER		
	A	B	C
Northern	31.01	2.51	0.66
Yorkshire	19.64	1.59	0.42
Trent	19.64	1.59	0.42
E.Anglian	14.47	1.17	0.31
NW.Thames	529.23	42.76	11.33
NE.Thames	226.37	18.29	4.85
SE.Thames	111.63	9.02	2.39
SW.Thames	44.45	3.59	0.95
Wessex	27.91	2.25	0.60
Oxford	22.74	1.84	0.49
S.Western	20.67	1.67	0.44
W.Midland	20.67	1.67	0.44
Mersey	15.50	1.25	0.33
N.Western	41.35	3.34	0.89
Wales	18.61	1.50	0.40
Scotland	38.24	3.09	0.82
N.Ireland	3.10	0.25	0.07

The key to these group numbers is as follows:

- |                             |                        |
|-----------------------------|------------------------|
| A: Male homosexual/bisexual | C: Female heterosexual |
| B: Male heterosexual        |                        |

TABLE 13. AIDS-deaths joint regional and transmission route distributions, cumulative to end of 1987

ESTIMATED DISTRIBUTION OF AIDS-DEATHS

RHA	GROUP NUMBER							
	1	2	3	4	5	6	7	8
Northern	15.03	0.55	1.31	0.23	0.13	0.28	0.05	0.05
Yorkshire	15.03	0.55	1.31	0.23	0.13	0.28	0.05	0.05
Trent	10.02	0.37	0.87	0.15	0.08	0.18	0.03	0.03
E.Anglian	7.52	0.28	0.65	0.11	0.06	0.14	0.03	0.03
NW.Thames	258.91	9.53	22.51	3.90	2.16	4.76	0.87	0.87
NE.Thames	111.08	4.09	9.66	1.67	0.93	2.04	0.37	0.37
SE.Thames	55.12	2.03	4.79	0.83	0.46	1.01	0.18	0.18
SW.Thames	21.72	0.80	1.89	0.33	0.18	0.40	0.07	0.07
Wessex	13.36	0.49	1.16	0.20	0.11	0.25	0.04	0.04
Oxford	10.86	0.40	0.94	0.16	0.09	0.20	0.04	0.04
S.Western	10.02	0.37	0.87	0.15	0.08	0.18	0.03	0.03
W.Midland	10.02	0.37	0.87	0.15	0.08	0.18	0.03	0.03
Mersey	7.52	0.28	0.65	0.11	0.06	0.14	0.03	0.03
N.Western	20.04	0.74	1.74	0.30	0.17	0.37	0.07	0.07
Wales	9.19	0.34	0.80	0.14	0.08	0.17	0.03	0.03
Scotland	18.37	0.68	1.60	0.28	0.15	0.34	0.06	0.06
N.Ireland	4.18	0.15	0.36	0.06	0.03	0.08	0.01	0.01

The key to these group numbers is as follows:

- |                             |                        |
|-----------------------------|------------------------|
| 1: Male homosexual/bisexual | 5: Male heterosexual   |
| 2: IDU                      | 6: Female heterosexual |
| 3: Male haemophiliac        | 7: Infant              |
| 4: Transfusion recipient    | 8: Other               |

CUMULATIVE DATA ADJUSTED TO ALLOW FOR 20% UNDER-REPORTING

RHA	GROUP NUMBER		
	A	B	C
Northern	18.17	1.62	0.36
Yorkshire	18.17	1.62	0.36
Trent	12.11	1.08	0.24
E.Anglian	9.08	0.81	0.18
NW.Thames	312.85	27.97	6.23
NE.Thames	134.22	12.00	2.67
SE.Thames	66.61	5.96	1.33
SW.Thames	26.24	2.35	0.52
Wessex	16.15	1.44	0.32
Oxford	13.12	1.17	0.26
S.Western	12.11	1.08	0.24
W.Midland	12.11	1.08	0.24
Mersey	9.08	0.81	0.18
N.Western	24.22	2.17	0.48
Wales	11.10	0.99	0.22
Scotland	22.20	1.99	0.44
N.Ireland	5.05	0.45	0.10

The key to these group numbers is as follows:

- |                             |                        |
|-----------------------------|------------------------|
| A: Male homosexual/bisexual | C: Female heterosexual |
| B: Male heterosexual        |                        |

TABLE 14. Estimated RHA populations of England and Wales, by single year of age and gender : the data for Yorkshire

Age	Male	Female	Age	Male	Female
0	24,500	23,500	45	20,447	20,112
1	24,322	23,263	46	18,883	18,698
2	24,199	23,220	47	20,140	19,849
3	23,264	22,336	48	20,169	20,027
4	23,388	22,394	49	20,161	19,913
5	23,542	22,454	50	19,833	19,779
6	23,856	22,836	51	19,476	19,542
7	24,127	23,034	52	19,133	19,176
8	23,265	22,123	53	18,461	18,587
9	21,408	20,346	54	18,504	18,723
10	21,378	20,120	55	19,147	19,413
11	22,216	20,994	56	19,312	19,839
12	23,179	21,889	57	19,097	19,984
13	24,002	22,681	58	18,723	19,637
14	25,825	24,316	59	18,422	19,420
15	26,767	25,764	60	18,479	19,425
16	28,567	27,552	61	18,522	19,676
17	28,177	27,213	62	18,171	19,611
18	28,929	28,229	63	17,993	19,776
19	29,160	28,435	64	17,735	19,904
20	29,593	28,564	65	18,267	20,831
21	29,954	29,221	66	18,802	21,903
22	30,804	30,021	67	19,173	22,739
23	30,846	30,157	68	12,342	15,121
24	30,096	29,743	69	11,308	14,306
25	29,238	28,788	70	12,119	15,746
26	28,468	27,930	71	12,613	16,635
27	27,330	26,670	72	12,796	17,553
28	26,432	25,854	73	12,274	17,374
29	25,633	25,157	74	11,505	16,692
30	25,041	24,593	75	10,446	15,954
31	24,527	23,843	76	9,599	15,296
32	23,806	23,150	77	8,942	14,804
33	24,184	23,603	78	8,137	14,197
34	24,034	23,610	79	7,276	13,264
35	23,482	23,201	80	6,330	12,224
36	23,967	23,644	81	5,449	11,318
37	24,650	24,502	82	4,772	10,455
38	25,582	25,305	83	3,982	9,256
39	27,412	27,141	84	3,360	8,247
40	30,157	29,511	85	2,688	7,014
41	23,648	23,154	86	2,177	6,269
42	23,377	22,731	87	1,700	5,329
43	23,526	22,837	88	1,223	4,172
44	22,393	21,767	89	940	3,312
			90+	2,879	11,434
			Total	1,754,100	1,850,500

TABLE 15. The size of the adult (aged 16 plus) RHA populations

RHA	Population size
Northern Yorkshire	2,455,245
Trent	2,863,585
E.Anglian	3,715,938
NW.Thames	1,604,179
NE.Thames	2,796,557
SE.Thames	3,019,692
SW.Thames	2,930,211
Wessex	2,398,617
Oxford	2,337,624
S.Western	1,971,083
W.Midlands	2,589,415
Mersey	4,123,102
N.Western	1,909,489
Wales	3,163,189
Scotland	2,259,647
N.Ireland	4,069,215
	1,150,000

TABLE 16. Results from the calculations to estimate the total size of the RHA homo/bisexual populations

RHA	Estimated no AIDS cases among homo/ bisexual men	Recoded value	Standardised values (mean=1/17)	Adjusted values (mean=PREF)	Estimated size of homo/bisexual population
Northern Yorkshire	31.01	1.50	0.0652	0.0887	217,770
Trent	19.64	1.25	0.0543	0.0739	211,656
E.Anglian	19.64	1.25	0.0543	0.0739	274,656
NW.Thames	4.47	1.25	0.0543	0.0739	118,750
NE.Thames	529.93	1.50	0.0652	0.0887	248,042
SE.Thames	226.37	1.50	0.0652	0.0887	267,833
SW.Thames	111.63	1.50	0.0652	0.0887	259,897
Wessex	44.45	1.50	0.0652	0.0887	212,747
Oxford	27.91	1.50	0.0652	0.0887	207,337
S.Western	22.74	1.25	0.0543	0.0739	145,689
W.Midland	20.67	1.25	0.0543	0.0739	191,391
Mersey	20.67	1.25	0.0543	0.0739	304,751
N.Western	15.50	1.25	0.0543	0.0739	141,136
Wales	41.35	1.50	0.0652	0.0887	280,561
Scotland	18.61	1.25	0.0543	0.0739	167,017
N.Ireland	38.24	1.50	0.0652	0.0887	360,922
	3.10	1.00	0.0435	0.0591	68,000

TABLE 17. Estimated RHA population distribution, by single year of age, gender and sexual preference : data for NW.Thames

Age	Male		Female	
	Heterosexual	Homo/Bisexual	Heterosexual	Homo/Bisexual
16	24,097	2,312	23,474	2,250
17	23,767	2,280	23,186	2,222
18	24,402	2,341	24,051	2,305
19	24,597	2,360	24,227	2,322
20	27,912	2,678	27,160	2,603
21	28,253	2,711	27,785	2,663
22	29,055	2,788	28,546	2,736
23	29,095	2,791	28,675	2,749
24	28,387	2,723	28,281	2,711
25	27,924	2,679	28,108	2,694
26	27,188	2,608	27,270	2,614
27	26,101	2,504	26,040	2,496
28	25,244	2,422	25,243	2,420
29	24,481	2,349	24,563	2,354
30	23,413	2,246	23,935	2,294
31	22,932	2,200	23,205	2,224
32	22,258	2,135	22,530	2,160
33	22,612	2,169	22,971	2,202
34	22,471	2,156	22,978	2,202
35	21,718	2,084	22,197	2,128
36	22,166	2,127	22,622	2,168
37	22,798	2,187	23,443	2,247
38	23,660	2,270	24,210	2,321
39	25,352	2,432	25,968	2,489
40	27,695	2,657	27,625	2,648
41	21,718	2,084	21,674	2,078
42	21,469	2,060	21,279	2,040
43	21,606	2,073	21,378	2,049
44	20,565	1,973	20,376	1,953
45	18,489	1,774	18,297	1,754
46	17,074	1,638	17,010	1,630
47	18,211	1,747	18,058	1,731
48	18,237	1,750	18,220	1,746
49	18,231	1,749	18,116	1,736
50	17,813	1,709	17,428	1,670
51	17,492	1,678	17,219	1,650
52	17,183	1,649	16,896	1,619
53	16,580	1,591	16,377	1,570
54	16,619	1,594	16,497	1,581
55	16,843	1,616	16,327	1,565
56	16,989	1,630	16,686	1,599
57	16,799	1,612	16,807	1,611
58	16,471	1,580	16,516	1,583
59	16,206	1,555	16,333	1,566

TABLE 17. cont.

Age	Male		Female	
	Heterosexual	Homo/Bisexual	Heterosexual	Homo/Bisexual
60	156,93	1,506	15,637	1,499
61	157,29	1,509	15,838	1,518
62	154,31	1,481	15,786	1,513
63	152,80	1,466	15,919	1,526
64	150,61	1,445	16,022	1,536
65	147,70	1,417	16,485	1,580
66	15,202	1,459	17,333	1,661
67	15,502	1,487	17,995	1,725
68	9,979	957	11,966	1,147
69	9,143	877	11,322	1,085
70	9,976	957	12,435	1,192
71	10,382	996	13,138	1,259
72	10,533	1,011	13,863	1,329
73	10,103	969	13,721	1,315
74	9,470	909	13,183	1,264
75	8,759	840	12,578	1,206
76	8,049	772	12,059	1,156
77	7,497	719	11,671	1,119
78	6,823	655	11,192	1,073
79	6,101	585	10,457	1,002
80	5,292	508	9,574	918
81	45,56	437	8,864	850
82	3,990	383	8,188	785
83	3,329	319	7,249	695
84	2,810	270	6,459	619
85	2,304	221	5,754	551
86	1,865	179	5,143	493
87	1,457	140	4,371	419
88	1,048	101	3,422	328
89	,805	77	2,717	260
90+	2,551	245	10,062	964
Tot	1,231,661	118,167	1,320,188	126,542

**TABLE 18. Estimated RHA HIV+/AIDS populations, by single year of age, gender and sexual preference : data for NW.Thames males**

Age	Heterosexual				Homo/Bisexual			
	HIV+	ARC	AIDS	DEAD	HIV+	ARC	AIDS	DEAD
0	2.31	0.41	0.53	0.00	0.00	0.00	0.00	0.00
1	2.24	0.39	0.40	0.13	0.00	0.00	0.00	0.00
2	2.23	0.39	0.40	0.13	0.00	0.00	0.00	0.00
3	2.14	0.38	0.39	0.13	0.00	0.00	0.00	0.00
4	2.15	0.38	0.39	0.13	0.00	0.00	0.00	0.00
5	2.31	0.41	0.15	0.00	0.00	0.00	0.00	0.00
6	2.34	0.41	0.15	0.00	0.00	0.00	0.00	0.00
7	2.37	0.42	0.16	0.00	0.00	0.00	0.00	0.00
8	2.28	0.40	0.15	0.00	0.00	0.00	0.00	0.00
9	2.10	0.37	0.14	0.00	0.00	0.00	0.00	0.00
10	1.97	0.35	0.09	0.09	0.00	0.00	0.00	0.00
11	2.04	0.36	0.09	0.09	0.00	0.00	0.00	0.00
12	2.13	0.38	0.10	0.10	0.00	0.00	0.00	0.00
13	2.21	0.39	0.10	0.10	0.00	0.00	0.00	0.00
14	2.38	0.42	0.11	0.11	0.00	0.00	0.00	0.00
15	6.75	1.19	0.49	0.49	0.00	0.00	0.00	0.00
16	6.57	1.16	0.48	0.47	20.88	20.88	0.31	0.18
17	6.48	1.14	0.47	0.47	20.60	20.60	0.31	0.18
18	6.66	1.17	0.49	0.48	21.15	21.15	0.32	0.18
19	6.71	1.18	0.49	0.48	21.32	21.32	0.32	2.18
20	36.77	6.49	0.85	0.56	93.05	93.05	4.71	2.59
21	37.22	6.57	0.86	0.57	94.18	94.18	4.77	2.62
22	38.28	6.75	0.89	0.58	96.86	96.86	4.91	2.70
23	38.33	6.76	0.89	0.58	96.99	96.99	4.91	2.70
24	37.40	6.60	0.87	0.57	94.63	94.63	4.79	2.63
25	54.24	9.57	0.75	0.43	137.26	137.26	13.41	6.55
26	52.81	9.32	0.73	0.41	133.64	133.64	13.06	6.38
27	50.70	8.95	0.70	0.40	128.30	128.30	12.53	6.13
28	49.03	8.65	0.68	0.38	124.08	124.08	12.12	5.93
29	47.55	8.39	0.66	0.37	120.33	120.33	11.76	5.75
30	43.27	7.64	1.44	0.60	109.49	109.49	24.39	13.20
31	42.38	7.48	1.41	0.59	107.25	107.25	23.89	12.93
32	41.13	7.26	1.37	0.57	104.09	104.09	23.18	12.55
33	41.79	7.37	1.39	0.58	105.75	105.75	23.55	12.75
34	41.53	7.33	1.38	0.58	105.09	105.09	23.41	12.67
35	31.14	5.49	1.03	0.55	78.79	78.79	22.81	13.11
36	31.78	5.61	1.05	0.56	80.42	80.42	23.28	13.38
37	32.69	5.77	1.08	0.57	82.71	82.71	23.94	13.76
38	33.92	5.99	1.13	0.60	85.84	85.84	24.85	14.28
39	36.35	6.41	1.21	0.64	91.98	91.98	26.62	15.30
40	24.38	4.30	0.59	0.46	61.70	61.70	20.94	13.91
41	19.12	3.37	0.47	0.36	48.38	48.38	16.42	10.91
42	18.90	3.34	0.46	0.35	47.83	47.83	16.23	10.78
43	19.02	3.36	0.46	0.36	48.13	48.13	16.34	10.85
44	18.10	3.19	0.44	0.34	45.81	45.81	15.55	10.33

TABLE 18. cont.

Age	Heterosexual				Homo/Bisexual			
	HIV+	ARC	AIDS	DEAD	HIV+	ARC	AIDS	DEAD
45	11.33	2.00	0.40	0.30	28.67	28.67	13.98	9.29
46	10.46	1.85	0.37	0.28	26.47	26.47	12.91	8.58
47	11.16	1.97	0.39	0.30	28.24	28.24	13.77	9.15
48	11.17	1.97	0.39	0.30	28.28	28.28	13.79	9.16
49	11.17	1.97	0.39	0.30	28.27	28.27	13.78	9.16
50	6.90	1.22	0.68	0.56	17.45	17.45	4.15	2.73
51	6.77	1.20	0.67	0.55	17.14	17.14	4.08	2.68
52	6.65	1.17	0.65	0.54	16.83	16.83	4.01	2.63
53	6.42	1.13	0.63	0.52	16.24	16.24	3.87	2.54
54	6.43	1.14	0.63	0.52	16.28	16.28	3.88	2.54
55	1.63	0.29	0.64	0.53	4.12	4.12	3.93	2.58
56	1.64	0.29	0.65	0.53	4.16	4.16	3.96	2.60
57	1.63	0.29	0.64	0.53	4.11	4.11	3.92	2.57
58	1.59	0.28	0.63	0.52	4.03	4.03	3.84	2.52
59	1.57	0.28	0.62	0.51	3.97	3.97	3.78	2.48
60	1.52	0.27	0.35	0.32	3.84	3.84	0.48	0.37
61	1.52	0.27	0.35	0.32	3.85	3.85	0.48	0.37
62	1.49	0.26	0.35	0.31	3.78	3.78	0.47	0.37
63	1.48	0.26	0.34	0.31	3.74	3.74	0.46	0.36
64	1.46	0.26	0.34	0.31	3.69	3.69	0.46	0.36
65	1.43	0.25	0.33	0.30	3.62	3.62	0.45	0.35
66	1.47	0.26	0.34	0.31	3.72	3.72	0.46	0.36
67	1.50	0.26	0.35	0.31	3.80	3.80	0.47	0.37
68	0.97	0.17	0.22	0.20	2.44	2.44	0.30	0.24
69	0.88	0.16	0.20	0.19	2.24	2.24	0.28	0.22
70	0.97	0.17	0.22	0.20	2.44	2.44	0.30	0.24
71	1.00	0.18	0.23	0.21	2.54	2.54	0.32	0.25
72	1.02	0.18	0.24	0.21	2.58	2.58	0.32	0.25
73	0.98	0.17	0.23	0.20	2.47	2.47	0.31	0.24
74	0.92	0.16	0.21	0.19	2.32	2.32	0.29	0.23
75	0.85	0.15	0.20	0.18	2.14	2.14	0.27	0.21
76	0.78	0.14	0.18	0.16	1.97	1.97	0.24	0.19
77	0.73	0.13	0.17	0.15	1.84	1.84	0.23	0.18
78	0.66	0.12	0.15	0.14	1.67	1.67	0.21	0.16
79	0.59	0.10	0.14	0.12	1.49	1.49	0.19	0.15
80	0.51	0.09	0.12	0.11	1.30	1.30	0.16	0.13
81	0.44	0.08	0.10	0.09	1.12	1.12	0.14	0.11
82	0.39	0.07	0.09	0.08	0.98	0.98	0.12	0.09
83	0.32	0.06	0.07	0.07	0.82	0.82	0.10	0.08
84	0.27	0.05	0.06	0.06	0.69	0.69	0.09	0.07
85	0.22	0.04	0.05	0.05	0.56	0.56	0.07	0.05
86	0.18	0.03	0.04	0.04	0.46	0.46	0.06	0.04
87	0.14	0.02	0.03	0.03	0.36	0.36	0.04	0.03
88	0.10	0.02	0.02	0.02	0.26	0.26	0.03	0.02
89	0.08	0.01	0.02	0.02	0.20	0.20	0.02	0.02
90+	0.25	0.04	0.06	0.05	0.62	0.62	0.08	0.06
Tot	1105.82	195.14	42.76	27.97	2714.32	2714.32	529.14	312.81

TABLE 19. Estimated RHA populations according to single year of age,  
sexual preference & disease stage : data for Yorkshire males

Age	Heterosexual					Homo/bisexual				
	HIV-	HIV+	ARC	AIDS	DEAD	HIV-	HIV+	ARC	AIDS	DEAD
0	24,499.7	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1	24,322.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	24,198.8	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	23,264.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	23,387.4	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
5	23,542.1	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
6	23,856.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
7	24,126.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
8	23,264.6	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
9	21,409.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
10	21,377.7	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
11	22,215.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
12	23,178.9	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
13	24,001.7	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
14	25,825.2	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
15	26,766.5	0.7	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
16	26,482.4	0.7	0.1	0.0	0.0	2,079.9	2.9	1.2	0.0	0.0
17	26,120.6	0.7	0.1	0.0	0.0	2,051.5	2.8	1.2	0.0	0.0
18	26,817.5	0.7	0.1	0.0	0.0	2,106.2	2.9	1.2	0.0	0.0
19	27,031.9	0.7	0.1	0.0	0.0	2,123.1	2.9	1.3	0.0	0.0
20	27,429.6	3.9	0.4	0.0	0.0	2,140.4	12.7	5.4	0.0	0.2
21	27,764.5	3.9	0.4	0.0	0.0	2,166.5	12.9	5.4	0.0	0.2
22	28,552.3	4.0	0.4	0.0	0.0	2,228.0	13.2	5.6	0.0	0.2
23	28,591.7	4.0	0.4	0.0	0.0	2,231.1	13.3	5.6	0.0	0.2
24	27,895.8	3.9	0.4	0.0	0.0	2,176.8	12.9	5.4	0.0	0.2
25	27,098.9	5.7	0.5	0.0	0.0	2,105.8	18.5	7.7	0.1	0.4
26	26,384.7	5.6	0.5	0.0	0.0	2,050.3	18.0	7.5	0.1	0.4
27	25,329.9	5.3	0.5	0.0	0.0	1,968.3	17.3	7.2	0.1	0.4
28	24,497.8	5.2	0.5	0.0	0.0	1,903.7	16.8	6.9	0.1	0.3
29	23,757.4	5.0	0.5	0.0	0.0	1,846.1	16.2	6.7	0.1	0.3
30	23,209.5	4.5	0.4	0.0	0.0	1,805.1	14.3	5.6	0.1	0.8
31	22,732.9	4.4	0.4	0.0	0.0	1,768.1	14.0	5.5	0.1	0.8
32	22,064.3	4.3	0.4	0.0	0.0	1,716.1	13.6	5.3	0.1	0.7
33	22,415.1	4.4	0.4	0.0	0.0	1,743.3	13.8	5.4	0.1	0.7
34	22,276.1	4.4	0.4	0.0	0.0	1,732.5	13.7	5.4	0.1	0.7
35	21,765.8	3.3	0.3	0.0	0.0	1,697.5	10.1	3.8	0.1	0.8
36	22,214.4	3.3	0.3	0.0	0.0	1,732.5	10.3	3.9	0.1	0.8
37	22,847.8	3.4	0.3	0.0	0.0	1,781.9	10.6	4.0	0.1	0.8
38	23,712.1	3.6	0.3	0.0	0.0	1,849.3	11.0	4.2	0.1	0.8
39	25,407.7	3.8	0.3	0.0	0.0	1,981.5	11.8	4.5	0.1	0.9
40	27,953.7	2.6	0.2	0.0	0.0	2,187.8	7.8	2.9	0.0	0.8
41	21,920.2	2.0	0.2	0.0	0.0	1,715.6	6.1	2.3	0.0	0.6
42	21,669.1	2.0	0.2	0.0	0.0	1,695.9	6.0	2.2	0.0	0.6
43	21,807.9	2.0	0.2	0.0	0.0	1,706.8	6.1	2.3	0.0	0.6
44	20,757.1	1.9	0.2	0.0	0.0	1,624.5	5.8	2.1	0.0	0.6

TABLE 19. cont.

Age	Heterosexual					Homo/bisexual				
	HIV-	HIV+	ARC	AIDS	DEAD	HIV-	HIV+	ARC	AIDS	DEAD
45	18,954.3	1.2	0.1	0.0	0.0	1,486.0	3.5	1.2	0.0	0.5
46	17,503.9	1.1	0.1	0.0	0.0	1,372.3	3.2	1.1	0.0	0.5
47	18,669.5	1.2	0.1	0.0	0.0	1,463.7	3.4	1.2	0.0	0.5
48	18,696.0	1.2	0.1	0.0	0.0	1,465.7	3.4	1.2	0.0	0.5
49	18,689.4	1.2	0.1	0.0	0.0	1,465.2	3.4	1.2	0.0	0.5
50	18,385.6	0.7	0.0	0.0	0.0	1,443.4	2.3	0.9	0.0	0.2
51	18,054.4	0.7	0.0	0.0	0.0	1,417.4	2.2	0.9	0.0	0.2
52	17,736.3	0.7	0.0	0.0	0.0	1,392.4	2.2	0.9	0.0	0.2
53	17,113.5	0.7	0.0	0.0	0.0	1,343.6	2.1	0.8	0.0	0.1
54	17,153.3	0.7	0.0	0.0	0.0	1,346.7	2.1	0.8	0.0	0.1
55	17,749.8	0.1	0.0	0.0	0.0	1,396.0	0.4	0.1	0.0	0.2
56	17,902.9	0.1	0.0	0.0	0.0	1,408.0	0.4	0.1	0.0	0.2
57	17,703.2	0.1	0.0	0.0	0.0	1,392.3	0.4	0.1	0.0	0.2
58	17,357.1	0.1	0.0	0.0	0.0	1,365.1	0.4	0.1	0.0	0.1
59	17,077.6	0.1	0.0	0.0	0.0	1,343.1	0.4	0.1	0.0	0.1
60	17,130.8	0.1	0.0	0.0	0.0	1,347.3	0.5	0.2	0.0	0.0
61	17,170.6	0.1	0.0	0.0	0.0	1,350.5	0.5	0.2	0.0	0.0
62	16,845.6	0.1	0.0	0.0	0.0	1,324.9	0.5	0.2	0.0	0.0
63	16,679.8	0.1	0.0	0.0	0.0	1,311.9	0.5	0.2	0.0	0.0
64	16,441.0	0.1	0.0	0.0	0.0	1,293.1	0.5	0.2	0.0	0.0
65	16,934.5	0.1	0.0	0.0	0.0	1,331.9	0.5	0.2	0.0	0.0
66	17,430.3	0.1	0.0	0.0	0.0	1,370.9	0.5	0.2	0.0	0.0
67	17,774.0	0.2	0.0	0.0	0.0	1,397.9	0.5	0.2	0.0	0.0
68	11,441.7	0.1	0.0	0.0	0.0	899.9	0.3	0.1	0.0	0.0
69	10,483.3	0.1	0.0	0.0	0.0	824.5	0.3	0.1	0.0	0.0
70	11,234.7	0.1	0.0	0.0	0.0	883.6	0.3	0.1	0.0	0.0
71	11,692.5	0.1	0.0	0.0	0.0	919.6	0.3	0.1	0.0	0.0
72	11,862.5	0.1	0.0	0.0	0.0	933.0	0.4	0.1	0.0	0.0
73	11,378.6	0.1	0.0	0.0	0.0	894.9	0.3	0.1	0.0	0.0
74	10,665.8	0.1	0.0	0.0	0.0	838.9	0.3	0.1	0.0	0.0
75	9,683.7	0.1	0.0	0.0	0.0	761.6	0.3	0.1	0.0	0.0
76	8,898.9	0.1	0.0	0.0	0.0	699.9	0.3	0.1	0.0	0.0
77	8,289.2	0.1	0.0	0.0	0.0	651.9	0.2	0.1	0.0	0.0
78	7,543.3	0.1	0.0	0.0	0.0	593.3	0.2	0.1	0.0	0.0
79	6,745.5	0.1	0.0	0.0	0.0	530.5	0.2	0.1	0.0	0.0
80	5,867.7	0.1	0.0	0.0	0.0	461.5	0.2	0.1	0.0	0.0
81	5,051.7	0.0	0.0	0.0	0.0	397.3	0.2	0.1	0.0	0.0
82	4,423.5	0.0	0.0	0.0	0.0	347.9	0.1	0.1	0.0	0.0
83	3,691.6	0.0	0.0	0.0	0.0	290.3	0.1	0.0	0.0	0.0
84	3,115.2	0.0	0.0	0.0	0.0	245.0	0.1	0.0	0.0	0.0
85	2,492.3	0.0	0.0	0.0	0.0	196.0	0.1	0.0	0.0	0.0
86	2,018.1	0.0	0.0	0.0	0.0	158.7	0.1	0.0	0.0	0.0
87	1,576.1	0.0	0.0	0.0	0.0	124.0	0.0	0.0	0.0	0.0
88	1,134.0	0.0	0.0	0.0	0.0	89.2	0.0	0.0	0.0	0.0
89	871.3	0.0	0.0	0.0	0.0	68.5	0.0	0.0	0.0	0.0
90+	2,669.0	0.0	0.0	0.0	0.0	209.9	0.1	0.0	0.0	0.0
Tot	1,653,728	115.6	10.1	0.5	1.6	99,765	356.6	141.6	2.1	18.2

TABLE 20. Standardised mortality ratios for the RHAs of England and Wales

Region	Males	Females
Northern	112	110
Yorkshire	105	104
Trent	102	101
E.Anglian	90	92
NW.Thames	92	93
NE.Thames	96	93
SE.Thames	96	96
SW.Thames	90	93
Wessex	91	92
Oxford	91	96
S.Western	93	95
W.Midlands	104	105
Mersey	108	106
N.Western	114	112
Wales	105	102

Source : OPCS (1989a)

TABLE 21. Estimated RHA non-survival rates, by single year of age  
 (This extract shows data for males from 8 Regions)

Age	Region							
	Nor	York	Tren	E.An	NWT	NET	SET	SWT
0	0.01127	0.01056	0.01026	0.00905	0.00926	0.00966	0.00966	0.00905
1	0.00065	0.00061	0.00059	0.00052	0.00053	0.00055	0.00055	0.00052
2	0.00045	0.00042	0.00041	0.00036	0.00037	0.00038	0.00038	0.00036
3	0.00034	0.00032	0.00031	0.00027	0.00028	0.00029	0.00029	0.00027
4	0.00025	0.00023	0.00023	0.00020	0.00020	0.00021	0.00021	0.00020
5	0.00025	0.00023	0.00022	0.00020	0.00020	0.00021	0.00021	0.00020
6	0.00022	0.00021	0.00020	0.00018	0.00018	0.00019	0.00019	0.00018
7	0.00022	0.00021	0.00020	0.00018	0.00018	0.00019	0.00019	0.00018
8	0.00023	0.00021	0.00021	0.00018	0.00019	0.00019	0.00019	0.00018
9	0.00023	0.00022	0.00021	0.00019	0.00019	0.00020	0.00020	0.00019
10	0.00023	0.00022	0.00021	0.00019	0.00019	0.00020	0.00020	0.00019
11	0.00024	0.00022	0.00021	0.00019	0.00019	0.00020	0.00020	0.00019
12	0.00024	0.00022	0.00022	0.00019	0.00020	0.00020	0.00020	0.00019
13	0.00028	0.00027	0.00026	0.00023	0.00023	0.00024	0.00024	0.00023
14	0.00041	0.00038	0.00037	0.00033	0.00034	0.00035	0.00035	0.00033
15	0.00054	0.00051	0.00049	0.00044	0.00045	0.00046	0.00046	0.00044
16	0.00076	0.00071	0.00069	0.00061	0.00062	0.00065	0.00065	0.00061
17	0.00093	0.00087	0.00085	0.00075	0.00076	0.00080	0.00080	0.00075
18	0.00100	0.00094	0.00091	0.00081	0.00082	0.00086	0.00086	0.00081
19	0.00104	0.00098	0.00095	0.00084	0.00086	0.00089	0.00089	0.00084
20	0.00098	0.00092	0.00089	0.00079	0.00081	0.00084	0.00084	0.00079
21	0.00093	0.00087	0.00085	0.00075	0.00076	0.00080	0.00080	0.00075
22	0.00090	0.00085	0.00082	0.00073	0.00074	0.00078	0.00078	0.00073
23	0.00087	0.00082	0.00080	0.00070	0.00072	0.00075	0.00075	0.00070
24	0.00085	0.00080	0.00077	0.00068	0.00070	0.00073	0.00073	0.00068
25	0.00086	0.00081	0.00079	0.00069	0.00071	0.00074	0.00074	0.00069
26	0.00091	0.00086	0.00083	0.00073	0.00075	0.00078	0.00078	0.00073
27	0.00100	0.00093	0.00091	0.00080	0.00082	0.00085	0.00085	0.00080
28	0.00099	0.00093	0.00090	0.00079	0.00081	0.00085	0.00085	0.00079
29	0.00090	0.00084	0.00082	0.00072	0.00074	0.00077	0.00077	0.00072
30	0.00091	0.00085	0.00083	0.00073	0.00075	0.00078	0.00078	0.00073
31	0.00102	0.00096	0.00093	0.00082	0.00084	0.00087	0.00087	0.00082
32	0.00112	0.00105	0.00102	0.00090	0.00092	0.00096	0.00096	0.00090
33	0.00116	0.00109	0.00106	0.00093	0.00095	0.00100	0.00100	0.00093
34	0.00123	0.00115	0.00112	0.00099	0.00101	0.00105	0.00105	0.00099
35	0.00126	0.00118	0.00114	0.00101	0.00103	0.00108	0.00108	0.00101
36	0.00133	0.00125	0.00121	0.00107	0.00109	0.00114	0.00114	0.00107
37	0.00149	0.00140	0.00136	0.00120	0.00123	0.00128	0.00128	0.00120
38	0.00163	0.00153	0.00149	0.00131	0.00134	0.00140	0.00140	0.00131
39	0.00177	0.00166	0.00161	0.00142	0.00145	0.00152	0.00152	0.00142
40	0.00196	0.00184	0.00179	0.00158	0.00161	0.00168	0.00168	0.00158
41	0.00223	0.00209	0.00203	0.00179	0.00183	0.00191	0.00191	0.00179
42	0.00253	0.00238	0.00231	0.00204	0.00208	0.00217	0.00217	0.00204
43	0.00289	0.00271	0.00263	0.00232	0.00237	0.00248	0.00248	0.00232
44	0.00328	0.00307	0.00299	0.00263	0.00269	0.00281	0.00281	0.00263

TABLE 21. cont.

Age	Region								
	Nor	York	Tren	E. An	NWT	NET	SET	SWT	
45	0.00360	0.00338	0.00328	0.00290	0.00296	0.00309	0.00309	0.00290	
46	0.00390	0.00366	0.00355	0.00313	0.00320	0.00334	0.00334	0.00313	
47	0.00451	0.00423	0.00411	0.00363	0.00371	0.00387	0.00387	0.00363	
48	0.00521	0.00489	0.00475	0.00419	0.00428	0.00447	0.00447	0.00419	
49	0.00579	0.00543	0.00527	0.00465	0.00475	0.00496	0.00496	0.00465	
50	0.00638	0.00598	0.00581	0.00513	0.00524	0.00547	0.00547	0.00513	
51	0.00693	0.00650	0.00631	0.00557	0.00569	0.00594	0.00594	0.00557	
52	0.00788	0.00739	0.00718	0.00633	0.00647	0.00675	0.00675	0.00633	
53	0.00904	0.00847	0.00823	0.00726	0.00742	0.00775	0.00775	0.00726	
54	0.01022	0.00958	0.00931	0.00821	0.00839	0.00876	0.00876	0.00821	
55	0.01154	0.01082	0.01051	0.00927	0.00948	0.00989	0.00989	0.00927	
56	0.01281	0.01201	0.01166	0.01029	0.01052	0.01098	0.01098	0.01029	
57	0.01437	0.01347	0.01309	0.01155	0.01180	0.01232	0.01232	0.01155	
58	0.01635	0.01533	0.01489	0.01314	0.01343	0.01402	0.01402	0.01314	
59	0.01821	0.01707	0.01658	0.01463	0.01496	0.01561	0.01561	0.01463	
60	0.02026	0.01899	0.01845	0.01628	0.01664	0.01736	0.01736	0.01628	
61	0.02245	0.02105	0.02045	0.01804	0.01844	0.01925	0.01925	0.01804	
62	0.02478	0.02323	0.02256	0.01991	0.02035	0.02124	0.02124	0.01991	
63	0.02655	0.02489	0.02418	0.02133	0.02181	0.02276	0.02276	0.02133	
64	0.02913	0.02731	0.02653	0.02341	0.02393	0.02497	0.02497	0.02341	
65	0.03337	0.03129	0.03039	0.02682	0.02741	0.02860	0.02860	0.02682	
66	0.03648	0.03420	0.03322	0.02931	0.02996	0.03127	0.03127	0.02931	
67	0.03977	0.03729	0.03622	0.03196	0.03267	0.03409	0.03409	0.03196	
68	0.04307	0.04038	0.03923	0.03461	0.03538	0.03692	0.03692	0.03461	
69	0.04663	0.04371	0.04247	0.03747	0.03830	0.03997	0.03997	0.03747	
70	0.05101	0.04782	0.04645	0.04099	0.04190	0.04372	0.04372	0.04099	
71	0.05620	0.05268	0.05118	0.04516	0.04616	0.04817	0.04817	0.04516	
72	0.06238	0.05848	0.05681	0.05013	0.05124	0.05347	0.05347	0.05013	
73	0.06839	0.06412	0.06228	0.05496	0.05618	0.05862	0.05862	0.05496	
74	0.07537	0.07065	0.06864	0.06056	0.06191	0.06460	0.06460	0.06056	
75	0.08216	0.07703	0.07483	0.06602	0.06749	0.07042	0.07042	0.06602	
76	0.08927	0.08369	0.08130	0.07173	0.07333	0.07652	0.07652	0.07173	
77	0.09743	0.09134	0.08873	0.07829	0.08003	0.08351	0.08351	0.07829	
78	0.10547	0.09888	0.09606	0.08476	0.08664	0.09041	0.09041	0.08476	
79	0.11613	0.10887	0.10576	0.09332	0.09539	0.09954	0.09954	0.09332	
80	0.12587	0.11800	0.11463	0.10114	0.10339	0.10789	0.10789	0.10114	
81	0.13453	0.12612	0.12252	0.10811	0.11051	0.11531	0.11531	0.10811	
82	0.14687	0.13769	0.13375	0.11802	0.12064	0.12589	0.12589	0.11802	
83	0.15846	0.14855	0.14431	0.12733	0.13016	0.13582	0.13582	0.12733	
84	0.17165	0.16092	0.15632	0.13793	0.14100	0.14713	0.14713	0.13793	
85	0.18705	0.17536	0.17035	0.15031	0.15365	0.16033	0.16033	0.15031	
86	0.20254	0.18988	0.18446	0.16276	0.16637	0.17361	0.17361	0.16276	
87	0.21512	0.20168	0.19592	0.17287	0.17671	0.18439	0.18439	0.17287	
88	0.22360	0.20962	0.20363	0.17967	0.18367	0.19165	0.19165	0.17967	
89	0.25164	0.23591	0.22917	0.20221	0.20670	0.21569	0.21569	0.20221	
90+	0.27281	0.25576	0.24845	0.21922	0.22409	0.23384	0.23384	0.21922	

TABLE 22. Inter-RHA migrations, persons, 1987

Origin	Destination Region									
	North	Yorks	Trent	E.Ang	NWT	NET	SET	SWT	Wess	Oxfor
Nor	34599	9577	5318	2241	4944	2442	2270	3596	2743	3517
Yorks	8103	40349	13861	3144	5537	2500	2622	4144	3184	3874
Trent	4694	15508	43481	6957	7550	3556	3608	5339	4703	7317
E.Ang	1875	3433	8381	14570	7065	5901	3035	4067	3096	4773
NWT	3822	5454	9433	14961	60134	27505	13860	35748	13669	28590
NET	2130	2969	5890	14587	19494	43819	8876	9123	5000	5007
SET	2304	3439	5678	5378	8643	6108	27086	21232	7529	5635
SWT	2823	4010	6400	6720	23543	10285	36406	59405	21695	12643
Wess	2374	3439	4906	3306	6796	3114	5453	13839	18586	10106
Oxf	2607	3778	7815	5548	14263	3632	4955	9967	14544	20832
S.Wes	2240	3570	5104	3275	7148	3285	4835	7633	16620	7688
W.Mid	3323	5437	13075	3482	8538	3845	3789	5988	6253	8187
Mers	2865	3398	3797	1552	3900	1894	2006	3514	2413	3165
N.Wes	5870	8400	7910	2067	6382	2945	2550	4059	2966	3866
Wales	1469	2030	3174	1525	3980	1794	2241	3499	3747	3497
Scot	6104	4600	4508	3267	7587	3591	3405	6003	4368	4699
N.Ire	788	825	823	447	2611	980	873	1673	868	843

Origin	Destination region						
	S.Wes	W.Mid	Mers	N.Wes	Wales	Scot	N.Ire
Nor	2663	3527	2464	5133	1552	5031	378
Yorks	3745	5273	2725	7879	2131	3578	495
Trent	6188	11776	3287	6729	3562	3388	425
E.Ang	3527	3031	1123	1753	1909	2042	207
NWT	13116	8338	2777	4243	5351	4118	1117
NET	5960	3854	1313	2350	2881	2124	439
SET	8242	4636	1691	2397	3873	2410	741
SWT	14225	6302	2700	3317	4788	3537	586
Wess	19356	6139	1828	2631	5492	3164	547
Oxf	11790	8589	2112	2960	4705	2988	377
S.Wes	30805	10036	2164	3164	7947	2762	369
W.Mid	12294	87030	5038	5740	9633	2822	877
Mers	3130	5720	22333	12581	6856	1723	325
N.Wes	4032	6349	13375	55518	4935	3402	781
Wales	6524	7550	4589	3292	26777	1366	303
Scot	3657	3512	2288	4520	2006	0	1180
N.Ire	578	1033	545	1153	487	1292	0

SOURCE : NHSCR (Boden 1989)

TABLE 23. Total RHA migrations, by direction, gender and single year of age, 1987

This extract shows total in-migrations to RHAs for males

Age	Region									
	North	Yorks	Trent	E.Ang	NWT	NET	SET	SWT	Wess	Oxfor
0-4	3323	4636	5681	3367	5391	4574	4234	5619	4992	4999
5-9	3191	4155	5262	3116	5030	4188	4030	5532	4630	4618
10-14	3212	4045	4731	2519	8058	5166	4024	7112	4321	4414
15-19	3143	3767	4602	2248	7626	4849	3789	6844	4038	4075
20-24	2733	3985	4712	2941	3949	3274	3315	4106	4225	4029
25-29	2708	3672	4507	2842	3661	3281	3276	3833	3989	3744
30-34	2773	3463	4180	2139	6173	4074	3135	5326	3585	3639
35-39	2710	3341	3996	2007	5862	3937	3061	4961	3382	3511
40-44	2097	3079	3681	2518	2917	2321	2720	3378	3493	3869
45-49	1937	2724	3361	2155	2772	2186	2615	2915	3097	2967
50-54	2091	2726	3277	1856	4630	3015	2629	4433	3289	3434
55-59	2022	2495	3056	1624	4207	2756	2247	3874	2806	2711
60-64	3919	5461	7239	3516	5787	3443	3778	5206	4758	5449
65-69	4645	7108	8219	4063	8338	4642	4882	7415	5784	6655
70-74	3979	5010	5926	2892	6085	3608	4114	5945	4305	4827
75+	5058	6268	7658	3571	7805	4611	5197	7694	5540	5743

Age	Region						
	S.Wes	W.Mid	Mers	N.Wes	Wales	Scot	N.Ire
0-4	4886	7012	2980	4891	3356	1822	565
5-9	4725	6814	2744	4466	3070	1796	534
10-14	4036	6811	2862	5071	2622	2606	718
15-19	3789	6402	2592	4715	2408	2329	685
20-24	4658	5636	2369	3923	2939	1752	400
25-29	4322	5361	2306	3729	2782	1666	394
30-34	3355	5477	2288	4302	2301	2188	548
35-39	3146	5232	2211	3981	2080	2125	530
40-44	4180	4618	1714	2883	2318	1197	229
45-49	3741	4077	1535	2575	2114	1172	222
50-54	2906	4361	1756	3157	1770	1570	312
55-59	2606	3977	1676	2848	1517	1447	296
60-64	5991	7716	2515	4638	3736	1582	199
65-69	7545	9199	3467	6299	4826	1967	387
70-74	5198	7623	3448	5339	3529	2267	847
75+	6463	9589	4458	6923	4782	2957	1124

Source : NHSCR (Boden 1989)

TABLE 24. Inter-RHA migration probabilities given survival, for males aged 20

Origin Region	Destination Region					
	North	Yorks	Trent	E.Ang	NWT	NET
Northern	0.96515	0.00498	0.00296	0.00132	0.00446	0.00197
Yorkshire	0.00356	0.96509	0.00606	0.00146	0.00397	0.00161
Trent	0.00170	0.00521	0.96312	0.00261	0.00441	0.00186
E.Anglia	0.00124	0.00213	0.00544	0.95789	0.00745	0.00551
NW.Thames	0.00101	0.00135	0.00247	0.00403	0.94206	0.01008
NE.Thames	0.00050	0.00066	0.00138	0.00352	0.00727	0.97436
SE.Thames	0.00071	0.00100	0.00175	0.00173	0.00431	0.00269
SW.Thames	0.00098	0.00131	0.00222	0.00242	0.01285	0.00505
Wessex	0.00101	0.00138	0.00209	0.00148	0.00469	0.00193
Oxford	0.00117	0.00159	0.00345	0.00257	0.01012	0.00236
S.Western	0.00113	0.00169	0.00255	0.00172	0.00577	0.00238
W.Midlands	0.00097	0.00149	0.00375	0.00106	0.00399	0.00161
Mersey	0.00190	0.00212	0.00252	0.00109	0.00419	0.00182
N.Western	0.00211	0.00284	0.00284	0.00079	0.00372	0.00154
Wales	0.00096	0.00125	0.00206	0.00104	0.00416	0.00168
Scotland	0.00176	0.00126	0.00131	0.00100	0.00355	0.00151
N.Ireland	0.00091	0.00090	0.00096	0.00055	0.00482	0.00163

	SET	SWT	Wessex	Oxford	S.West	W.Mid
Northern	0.00159	0.00281	0.00150	0.00239	0.00138	0.00184
Yorkshire	0.00146	0.00257	0.00139	0.00210	0.00154	0.00218
Trent	0.00164	0.00271	0.00167	0.00319	0.00206	0.00393
E.Anglia	0.00249	0.00374	0.00199	0.00379	0.00214	0.00187
NW.Thames	0.00450	0.01270	0.00347	0.00886	0.00315	0.00204
NE.Thames	0.00257	0.00298	0.00115	0.00145	0.00129	0.00085
SE.Thames	0.96766	0.00892	0.00226	0.00212	0.00233	0.00134
SW.Thames	0.01514	0.93639	0.00712	0.00524	0.00446	0.00204
Wessex	0.00290	0.00806	0.95607	0.00515	0.00742	0.00244
Oxford	0.00277	0.00615	0.00620	0.94988	0.00477	0.00354
S.Western	0.00301	0.00530	0.00793	0.00463	0.95174	0.00463
W.Midlands	0.00138	0.00243	0.00177	0.00287	0.00324	0.96903
Mersey	0.00167	0.00325	0.00157	0.00255	0.00192	0.00352
N.Western	0.00116	0.00206	0.00106	0.00171	0.00135	0.00213
Wales	0.00182	0.00316	0.00236	0.00274	0.00384	0.00451
Scotland	0.00124	0.00243	0.00124	0.00166	0.00099	0.00096
N.Ireland	0.00126	0.00268	0.00098	0.00120	0.00063	0.00111

TABLE 24. cont.

Origin Region	Destination Region				
	Mersey	N.West	Wales	Scot	N.Ire
Northern	0.00124	0.00280	0.00079	0.00263	0.00018
Yorkshire	0.00109	0.00340	0.00085	0.00150	0.00019
Trent	0.00107	0.00238	0.00116	0.00116	0.00014
E.Anglia	0.00067	0.00114	0.00113	0.00127	0.00012
NW.Thames	0.00066	0.00110	0.00126	0.00102	0.00025
NE.Thames	0.00028	0.00055	0.00061	0.00048	0.00009
SE.Thames	0.00047	0.00073	0.00107	0.00071	0.00020
SW.Thames	0.00084	0.00113	0.00148	0.00115	0.00018
Wessex	0.00071	0.00111	0.00208	0.00127	0.00020
Oxford	0.00085	0.00130	0.00187	0.00126	0.00015
S.Western	0.00098	0.00156	0.00351	0.00131	0.00016
W.Midlands	0.00131	0.00163	0.00247	0.00078	0.00022
Mersey	0.95853	0.00806	0.00401	0.00108	0.00019
N.Western	0.00428	0.96944	0.00159	0.00116	0.00024
Wales	0.00264	0.00208	0.96469	0.00084	0.00017
Scotland	0.00060	0.00129	0.00053	0.97838	0.00030
N.Ireland	0.00057	0.00130	0.00051	0.00140	0.97859

TABLE 25. Parameter values for  $a$  (number of partners per year), and  $q$  (probability of infection per partner) used in the model

Preference group	No. partners, a	Probability of infection during partnership, $q^{pq}$
0. Male heterosexual	1.60	Male to male - 0.43
1. Male homo/bisexual	3.00	Male to female - 0.20
2. Female heterosexual	1.20	Female to male - 0.11
3. Female homo/bisexual	2.00	

TABLE 26. Estimates of the number of sexual partners (SP) per year

Preference	Sex	No. partners/yr	Notes	Reference
Heterosexual	M F	1.10 0.89	variance=1.46 variance=0.21	Johnson et al 1989
	Both	1.50		Anderson 1988
	M F	1.90 1.60	Ages 16-21	Bowie & Ford 1989
	Both	0.90		DHSS 1987
	M F	1.13-1.80 0.77-1.40	Different age groups	Lagrange 1991
	Both	1.50	Students	Anderson 1988
	Both	2.10	USA	Baldwin & Baldwin 1988
Homosexual	M	10.50 8.70 7.10 4.80	Feb '86 Apr '86 Nov '86 Feb '87	BMRB 1987
	M	8.00		Lagrange 1991
	M	16.00 20.80	1984 (N. 1985/6 Ireland)	Maw et al 1987 (Northern Ireland)
	M	11.00 2.00	Sexual Partners Penatratve SP	Hunt et al 1991

TABLE 27. The number of marriages in 1987, by age of the partners, for those aged <60

Females	Males									
	<20	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	
<20	5572	20832	5679	1102	314	122	38	23	6	
20-24	2714	77377	52235	11361	3518	1211	374	131	61	
25-29	448	13268	37230	17884	6995	2889	855	312	119	
30-34	99	2251	7454	10301	7038	3539	1353	544	231	
35-39	27	625	2085	3756	5285	4263	2131	943	377	
40-44	10	177	617	1273	2463	3730	2783	1700	812	
45-49	2	38	136	313	728	1468	2007	1893	1175	
50-54	0	5	15	57	172	373	744	1386	1211	
55-59	0	2	7	14	33	61	161	410	766	

Source : OPCS (1989c)

TABLE 28. The parameter values used for the sensitivity testing

Parameter	Baseline value	Low Variant	High Variant
PREF : <i>Proportion of population assumed to be homo/bisexual</i>			
PREF	0.08	0.04 (1)	0.16 (2)
TOTHIV : <i>Total number assumed to be HIV+ in 1987</i>			
TOTHIV	27,500	13,750 (3)	55,000 (4)
$\gamma$ : <i>Level of inter-regional migration/visiting</i>			
$\gamma$	0.8	0.5 (5)	1.0 (6)
D1,D2,D3 : <i>Length of incubation and disease periods</i>			
D1 }      7.0 }	10.08	3.64 } 5 (7)	13.8 } 20.0 (8)
D2 }      3.5 }		1.75 }	7.0 }
D3	1.6	0.8 (9)	3.2 (10)
$q^{pq}$ : <i>Infection probabilities (per partner)</i>			
$q^{pq}$	MM 0.43 } FM 0.20 } FM 0.11 }	0.22 } 0.10 } 0.05 }	0.86 } 0.40 } 0.22 }
$a^q$ : <i>Average number of sexual partners per year</i>			
$a^q$	q=0 1.6 } q=1 3.0 } q=2 1.2 } q=3 2.0 }	0.8 } 1.5 } 0.6 } 1.0 }	3.2 } 6.0 } 2.4 } 4.0 }

KEY: (1) - Variation number 1  
 (Baseline run = (0))

**TABLE 29. Results from sensitivity analysis, showing numbers in each stage of infection, and goodness-of-fit statistics**

Version	HIV+	ARC	AIDS	DEAD	MAD (AIDS)	MAD (DEAD)
		1988				
(0)Baseline	21,655	6,183	2237	1140	22.2	15.3
(1)Lo homo/bisexual	21,459	6,161	2226	1140	22.1	15.3
(2)Hi homo/bisexual	21,764	6,225	2288	1140	22.6	15.3
(3)Lo initial HIV+	9,555	2,601	1042	1139	48.9	15.4
(4)Hi initial HIV+	45,605	13,447	4669	1142	128.5	15.2
(5)Hi mobility	21,689	6,183	2237	1140	22.2	15.3
(6)Lo mobility	21,632	6,183	2237	1140	22.2	15.3
(7)Short incubation	19,779	6,026	4269	1140	112.1	15.3
(8)Long incubation	22,558	6,291	1225	1140	40.9	15.3
(9)Short disease	26,555	6,183	1910	1467	23.8	18.6
(10)Long disease	21,655	6,183	2401	976	24.7	24.8
(11)Lo infection prob	16,514	6,183	2237	1140	22.2	15.3
(12)Hi infection prob	32,157	6,183	2237	1140	22.2	15.3
(13)Few SP	16,404	6,183	2237	1140	22.2	15.3
(14)Many SP	32,157	6,183	2237	1140	22.2	15.3
		1989				
(0)Baseline	34,115	7,127	2974	2541	26.5	50.4
(1)Lo homo/bisexual	33,312	7,087	2961	2535	26.3	50.1
(2)Hi homo/bisexual	34,697	7,170	2995	2553	27.0	51.1
(3)Lo initial HIV+	14,949	3,054	1296	1792	48.0	13.4
(4)Hi initial HIV+	71,245	15,311	6368	4068	147.9	143.3
(5)Hi mobility	34,241	7,131	2975	2541	27.5	50.4
(6)Lo mobility	34,010	7,124	2974	2541	26.0	50.4
(7)Short incubation	28,403	7,595	5706	3808	136.7	128.2
(8)Long incubation	37,082	6,822	1563	1901	40.3	16.7
(9)Short disease	34,122	7,127	1668	3848	32.0	129.3
(10)Long disease	34,112	7,127	3780	1735	50.6	12.9
(11)Lo infection prob	20,507	6,481	2886	2541	23.4	50.4
(12)Hi infection prob	71,131	8,445	3154	2542	33.9	50.5
(13)Few SP	20,243	6,468	2884	2541	23.3	50.4
(14)Many SP	71,130	8,445	3154	2452	33.8	50.5
		1990				
(0)Baseline	52,966	9,357	3728	4407	28.1	102.5
(1)Lo homo/bisexual	50,788	9,228	3698	4393	27.8	102.3
(2)Hi homo/bisexual	54,542	9,461	3758	4432	28.6	103.9
(3)Lo initial HIV+	23,254	4,051	1611	2606	40.1	21.0
(4)Hi initial HIV+	108,824	19,844	7965	8062	144.2	277.5
(5)Hi mobility	53,298	9,376	3732	4407	33.8	104.0
(6)Lo mobility	52,626	9,342	3725	4407	25.3	101.9
(7)Short incubation	40,974	10,453	7428	7376	144.4	255.4
(8)Long incubation	59,650	8,194	1889	2897	44.4	30.9
(9)Short disease	53,016	9,358	2214	5925	33.6	176.7
(10)Long disease	52,937	9,357	5200	2932	59.9	34.6
(11)Lo infection prob	25,305	7,191	3278	4350	23.8	99.2
(12)Hi infection prob	152,915	14,934	4804	4523	60.0	110.2
(13)Few SP	24,823	7,148	3269	4349	23.8	99.1
(14)Many SP	152,909	14,938	4804	4523	59.9	110.2

TABLE 30. Changes produced by altering the value of PREF, the proportion of the population assumed to be homo/bisexual (1990, %)

	MODEL VARIANTS		
	(0) Baseline	(1) Lo homo/bisexual	(2) Hi homo/bisexual
ASSUMPTIONS : PREF	100.0	50.0	200.0
OUTCOMES : HIV+	100.0	95.9	103.0
ARC	100.0	98.6	101.1
AIDS	100.0	99.2	100.8
DEAD	100.0	99.7	100.6

TABLE 31. Changes produced by altering value of TOTHIV, the total number assumed HIV+ in 1987 (1990, %)

	MODEL VARIANTS		
	(0) Baseline	(3) Lo initial HIV+	(4) Hi initial HIV+
ASSUMPTIONS : TOTHIV	100.0	50.0	200.0
OUTCOMES : HIV+	100.0	43.9	205.5
ARC	100.0	43.3	212.1
AIDS	100.0	43.2	213.7
DEAD	100.0	59.1	182.9

TABLE 32. Changes produced by altering the value of GAMMA, the level of inter-regional migration or visiting (1990, %)

	MODEL VARIANTS		
	(0) Baseline	(5) Hi mobility	(6) Lo mobility
ASSUMPTIONS : $\gamma$ (value)	100.0	0.5	1.0
OUTCOMES : HIV+	100.0	100.6	99.4
ARC	100.0	100.2	99.8
AIDS	100.0	100.1	99.9
DEAD	100.0	100.0	100.0

**TABLE 33. Percentage change in the regional distribution of HIV+ and AIDS reports, produced by altering the level of inter-regional migration**

Region	HIV+			AIDS		
	Baseline (0)	Hi mobility (5)	Lo mobility (6)	(0)	(5)	(6)
North	3.58	3.53	3.63	3.03	3.02	3.03
Yorkshire	4.08	4.38	3.86	3.36	3.42	3.31
Trent	4.30	5.31	3.47	3.18	3.43	3.01
E.Anglia	3.46	4.57	2.41	2.45	2.76	2.22
NW.Thames	19.94	15.90	23.40	26.04	24.93	26.82
NE.Thames	13.14	10.57	15.25	16.53	15.92	16.96
SE.Thames	10.47	8.91	11.90	12.70	12.29	13.00
SW.Thames	5.85	8.46	3.71	4.26	4.97	3.74
Wessex	4.18	5.29	3.32	3.15	3.40	2.97
Oxford	5.33	6.42	4.34	4.30	4.62	4.08
S.West	4.09	5.41	3.02	2.87	3.17	2.66
W.Midlands	5.09	5.42	4.88	4.23	4.30	4.19
Mersey	2.09	2.44	1.79	1.58	1.67	1.52
N.West	5.17	4.76	5.56	4.64	4.54	4.72
Wales	1.96	2.83	1.26	1.15	1.35	1.01
Scotland	6.48	5.23	7.56	5.96	5.66	6.18
N.Ireland	0.61	0.56	0.65	0.57	0.56	0.58

**TABLE 34. Percentage change in the preference group distribution of HIV+ and AIDS reports, produced by altering the level of inter-regional migration**

Preference Grp	HIV+			AIDS		
	Baseline (0)	Hi mobility (5)	Lo mobility (6)	(0)	(5)	(6)
M.Heterosexual	4.35	4.33	4.38	11.82	11.81	11.83
M.Homo/bisexual	88.91	88.97	88.84	83.12	83.13	83.11
F.Heterosexual	5.91	5.88	5.94	4.81	4.80	4.81
F.Homo/bisexual	0.83	0.83	0.84	0.26	0.26	0.26

**TABLE 35. Changes produced by altering values of D1,D2,D3, the length of the incubation and disease periods (1990, %)**

		MODEL VARIANTS		
		(0) Baseline	(7) Short incubation	(8) Long incubation
<b>ASSUMPTIONS : D1,D2</b>		100.0	50.0	200.0
OUTCOMES : HIV+		100.0	77.3	112.6
ARC		100.0	111.7	87.6
AIDS		100.0	199.2	50.7
DEAD		100.0	167.4	65.7
		MODEL VARIANTS		
		(0) Baseline	(9) Short disease	(10) Long disease
<b>ASSUMPTIONS : D3</b>		100.0	50.0	200.0
OUTCOMES : HIV+		100.0	100.0	99.9
ARC		100.0	100.0	100.0
AIDS		100.0	59.4	139.5
DEAD		100.0	134.4	66.5

**TABLE 36. Variation in the regional distribution of AIDS reports, produced by altering the length of the incubation periods (1990, %)**

Region	Baseline (0)	Short incubation (7)	Long incubation (8)
North	3.03	3.30	2.85
Yorkshire	3.36	3.64	3.17
Trent	3.18	3.45	3.01
E.Anglia	2.45	2.62	2.35
NW.Thames	26.04	24.12	27.27
NE.Thames	16.53	15.34	17.28
SE.Thames	12.70	11.81	13.25
SW.Thames	4.26	4.39	4.20
Wessex	3.15	3.40	2.99
Oxford	4.30	4.57	4.13
S.West	2.87	3.11	2.73
W.Midlands	4.23	4.56	4.02
Mersey	1.58	1.73	1.49
N.West	4.64	5.03	4.39
Wales	1.15	1.33	1.04
Scotland	5.96	6.99	5.28
N.Ireland	0.57	0.61	0.54

**TABLE 37. Variation in the preference group distribution of AIDS reports, produced by altering the length of the incubation periods (1990, %)**

Preference Group	Baseline (0)	Short incubation (7)	Long incubation (8)
M.Heterosexual	11.82	13.50	10.54
M.Homo/bisexual	83.12	80.22	84.95
F.Heterosexual	4.81	5.92	4.30
F.Homo/bisexual	0.26	0.36	0.21

**TABLE 38. Changes produced by altering the value of the infection probabilities, q (1990, %)**

	MODEL VARIANTS		
	(0) Baseline	(11) Lo infection prob	(12) Hi infection prob
ASSUMPTIONS : $q^{pq}$	100.0	50.0	200.0
OUTCOMES : HIV+	100.0	47.8	288.7
ARC	100.0	76.9	159.6
AIDS	100.0	87.9	128.9
DEAD	100.0	98.7	102.6

**TABLE 39. Regional distribution for 1987, and predictions for 2000**

RHA	1987				2000			
	HIV+	ARC	AIDS	DEAD	HIV+	ARC	AIDS	DEAD
North	480	140	14	20	4,488	1195	515	1536
Yorks	499	154	3	20	5,632	1491	640	1815
Trent	402	121	8	13	7,476	1939	824	2108
E.Ang	246	73	6	10	6,563	1734	740	1846
NWT	3849	2380	237	347	22,617	6197	2671	9903
NET	1846	1273	101	149	16,730	4637	2018	6910
SET	1411	991	49	74	15,267	4091	1759	5546
SWT	300	130	20	29	13,299	3317	1379	3328
Wessex	395	114	13	18	7,788	2022	859	2170
Oxford	519	159	11	15	8,252	2218	953	2614
S.West	334	98	9	13	8,116	2086	882	2143
W.Mids	611	191	9	13	7,420	1963	843	2344
Mersey	226	65	7	10	3,111	806	343	932
N.West	765	228	19	27	5,839	1576	684	2156
Wales	137	16	8	12	4,450	1125	473	1083
Scot	1313	199	18	25	5,896	1691	753	2654
N.Ire	87	27	2	6	677	192	85	278
Total	13060	6358	535	802	143,623	38282	16423	49368

**TABLE 40.** Preference group distribution for 1987, and predictions for 2000

preference group	1987				2000			
	HIV+	ARC	AIDS	DEAD	HIV+	ARC	AIDS	DEAD
M.heterosexual	3560	429	34	65	1,266	625	341	3,285
M.homo/bisexual	8607	5828	487	722	132,439	34,623	14,698	41,571
F.heterosexual	893	101	14	14	7,758	2,470	1,144	3,974
F.homo/bisexual	0	0	0	0	2,161	564	240	538

**TABLE 41.** Predicted regional distribution for 2000, giving each RHA figure as a percentage of the total in that category

RHA	HIV+		ARC		AIDS		DEATHS	
	no	%	no	%	no	%	no	%
North	4,488	3.1	1195	3.1	515	3.1	1536	3.1
Yorks	5,632	3.9	1491	3.9	640	3.9	1815	3.7
Trent	7,476	5.2	1939	5.1	824	5.0	2108	4.3
E.Ang	6,563	4.6	1734	4.5	740	4.5	1846	3.7
NWT	22,617	15.7	6197	16.2	2671	16.3	9903	20.1
NET	16,730	11.6	4637	12.1	2018	12.3	6910	14.0
SET	15,267	10.6	4091	10.7	1759	10.7	5546	11.2
SWT	13,299	9.3	3317	8.7	1379	8.4	3328	6.7
Wessex	7,788	5.4	2022	5.3	859	5.2	2170	4.4
Oxford	8,252	5.7	2218	5.8	953	5.8	2614	5.3
S.West	8,116	5.6	2086	5.4	882	5.4	2143	4.3
W.Mids	7,420	5.2	1963	5.1	843	5.1	2344	4.7
Mersey	3,111	2.2	806	2.1	343	2.1	932	1.9
N.West	5,839	4.1	1576	4.1	684	4.2	2156	4.4
Wales	4,450	3.1	1125	2.9	473	2.9	1083	2.2
Scot	5,896	4.1	1691	4.4	753	4.6	2654	5.4
N.Ire	677	0.5	192	0.5	85	0.5	278	0.6

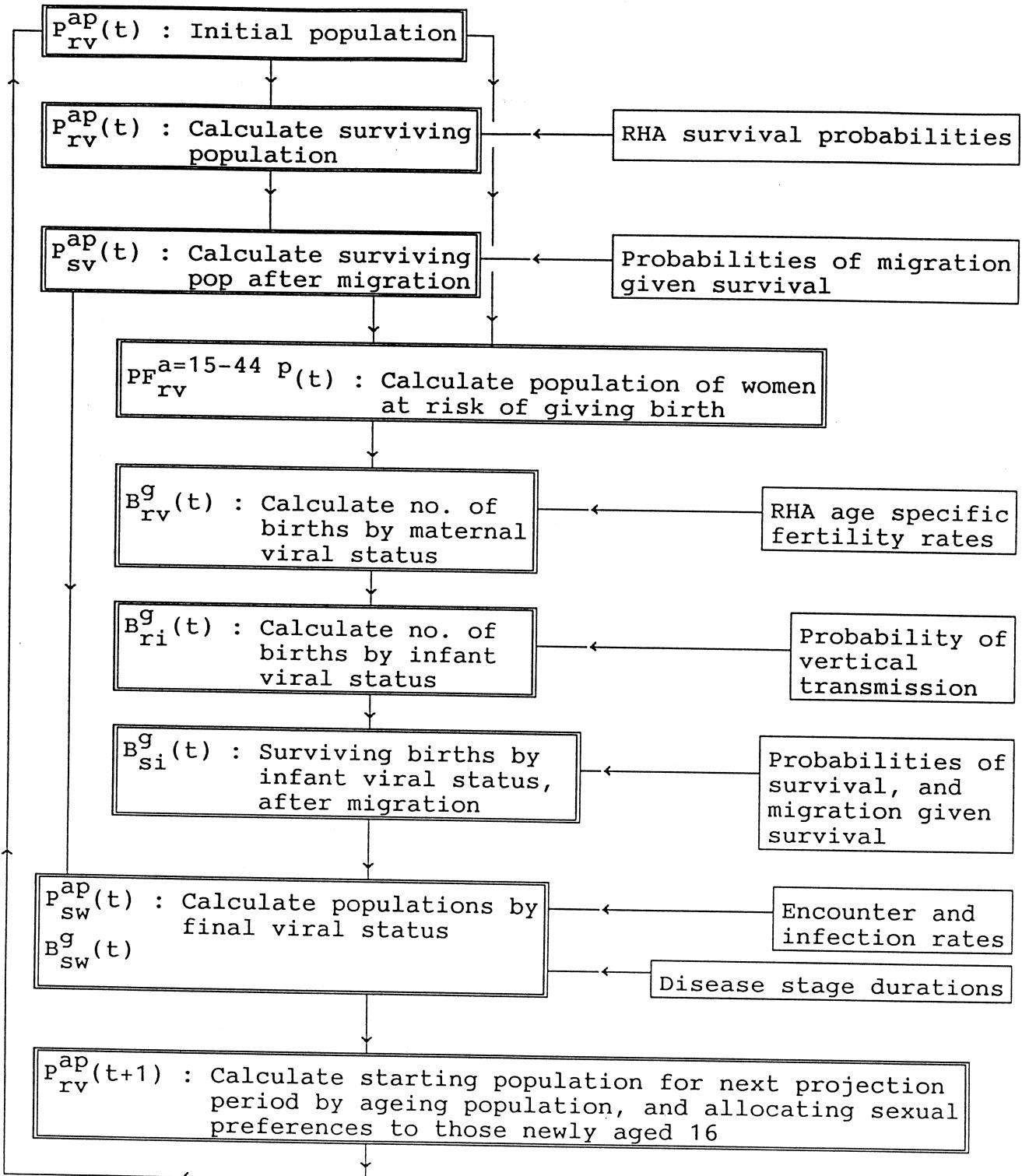
**TABLE 42.** Predicted preference group distribution for 2000, giving each group figure as a percentage of the total in that disease stage

pref	HIV+		ARC		AIDS		DEATHS	
	no	%	no	%	no	%	no	%
M.Het	1,266	0.9	625	1.6	341	2.1	3,285	6.6
M.Hom	132,439	92.2	34,623	90.4	14,698	89.5	41,571	84.2
F.Het	7,758	5.4	2,470	6.4	1,144	7.0	3,974	8.0
F.Hom	2,161	1.5	564	1.5	240	1.5	538	1.1

**FIGURE 1. Systems diagram for the simulation model**

**STAGES OF MODEL CALCULATIONS**

**INPUTS REQUIRED**



KEY :

- a - Age group
- p - Sexual preference
- r - Initial RHA
- s - Final RHA
- v - Initial viral status
- w - Final viral status

g - gender  
 i - Infants viral status  
 t - Year  
 P - Population  
 PF - Population of women  
 B - Births

**FIGURE 2. Diagram to represent the average course of the disease, with mean stage durations (years).**

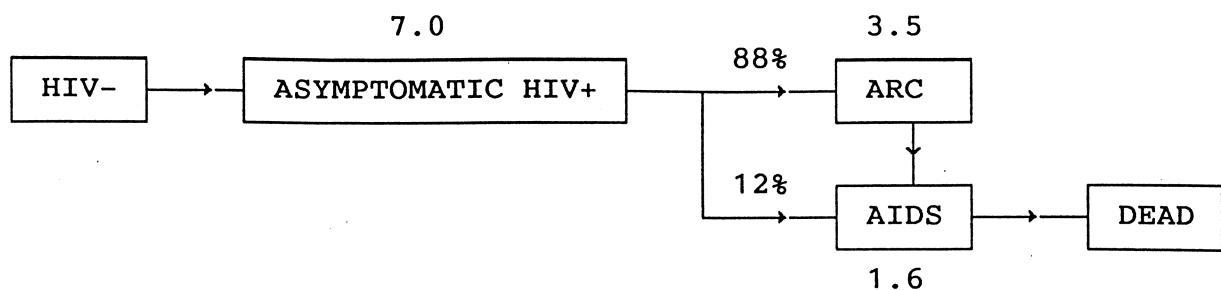
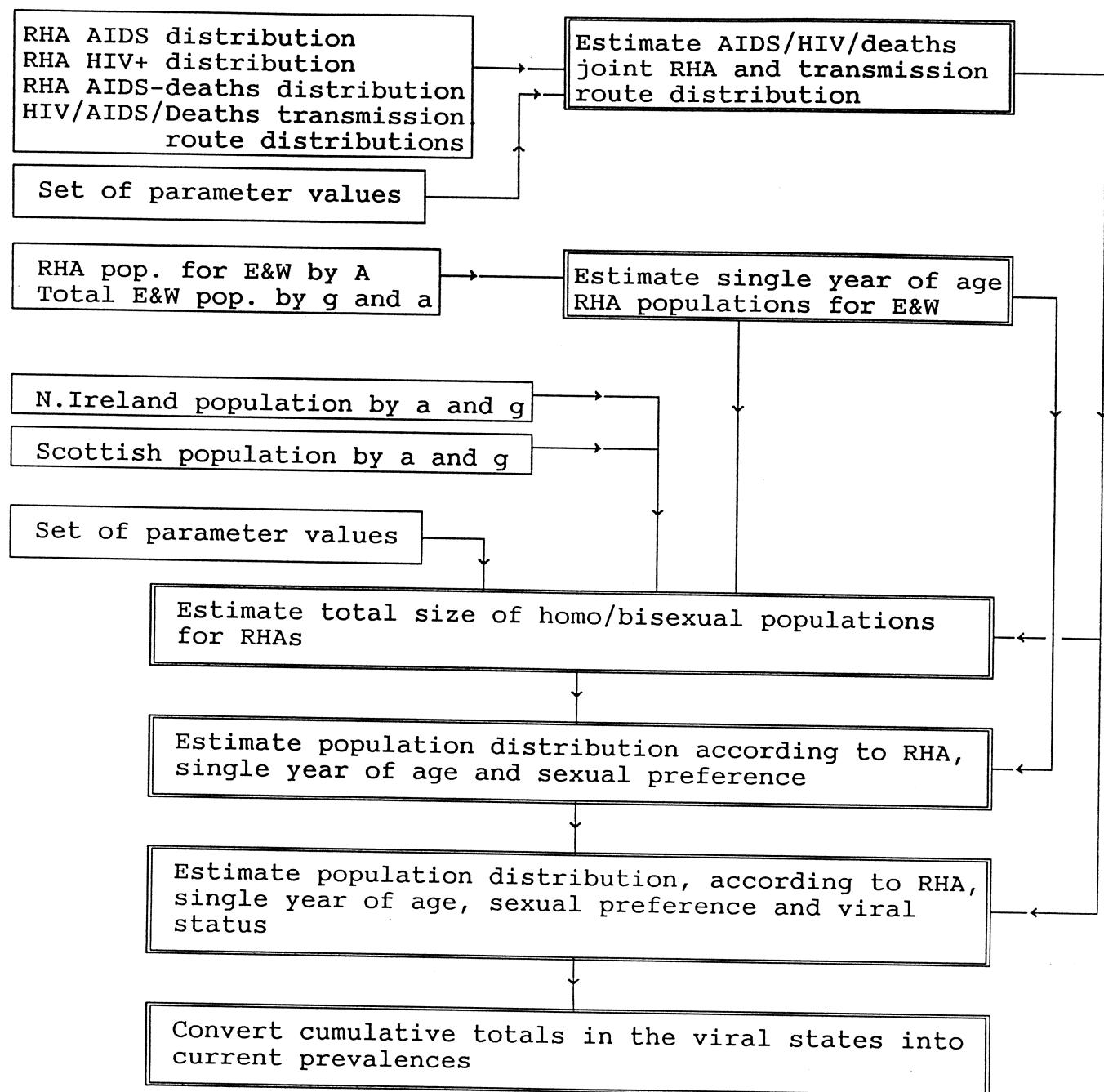


FIGURE 3. Procedures involved in estimating the population data

DATA SETS / PARAMETER VALUES

PROCESSES



KEY : g - gender

a - single year age groups

A - five year age groups

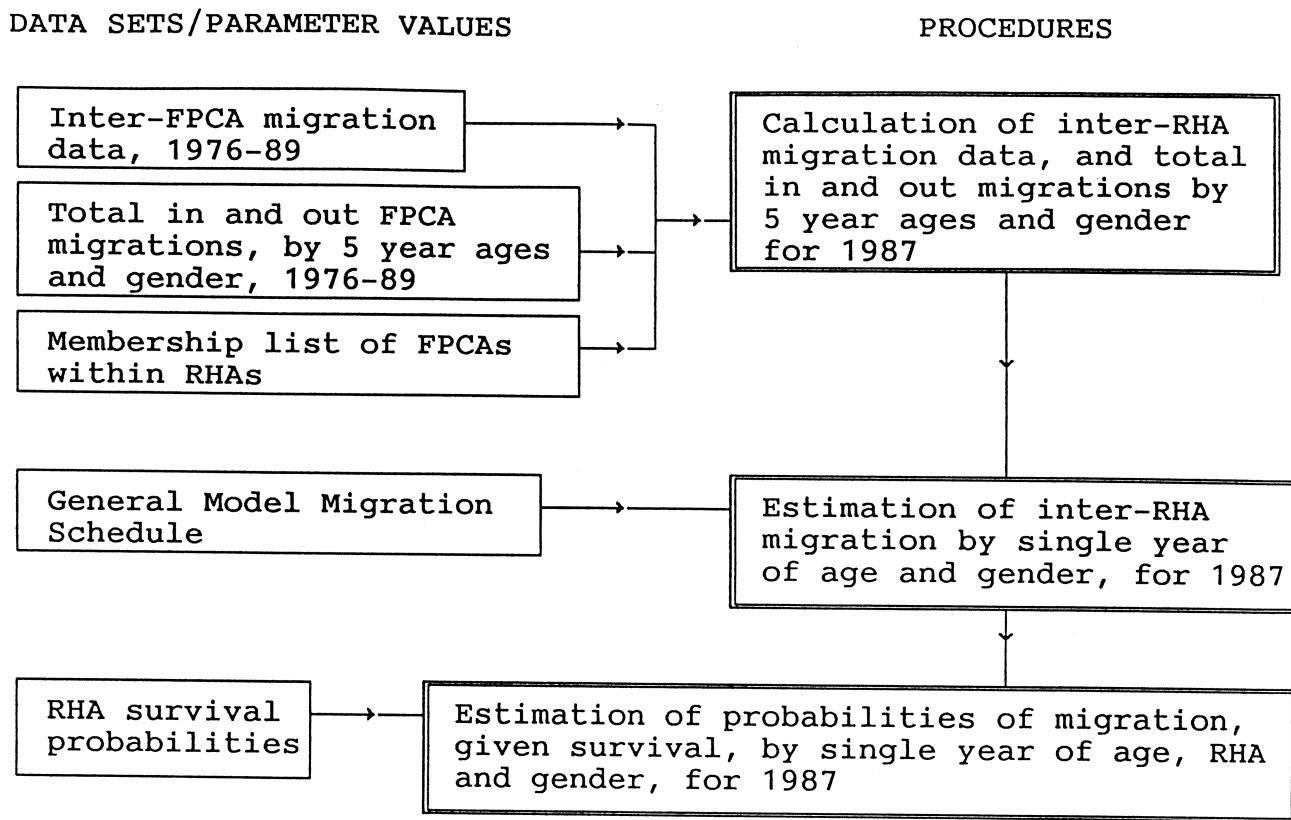
E&W - England and Wales

→-- - Arrows represent the transfer of data

FIGURE 4  
REGIONAL HEALTH AUTHORITIES (ENGLAND & WALES), SCOTLAND & NORTHERN IRELAND



**FIGURE 5. Procedures involved in estimating the migration data**



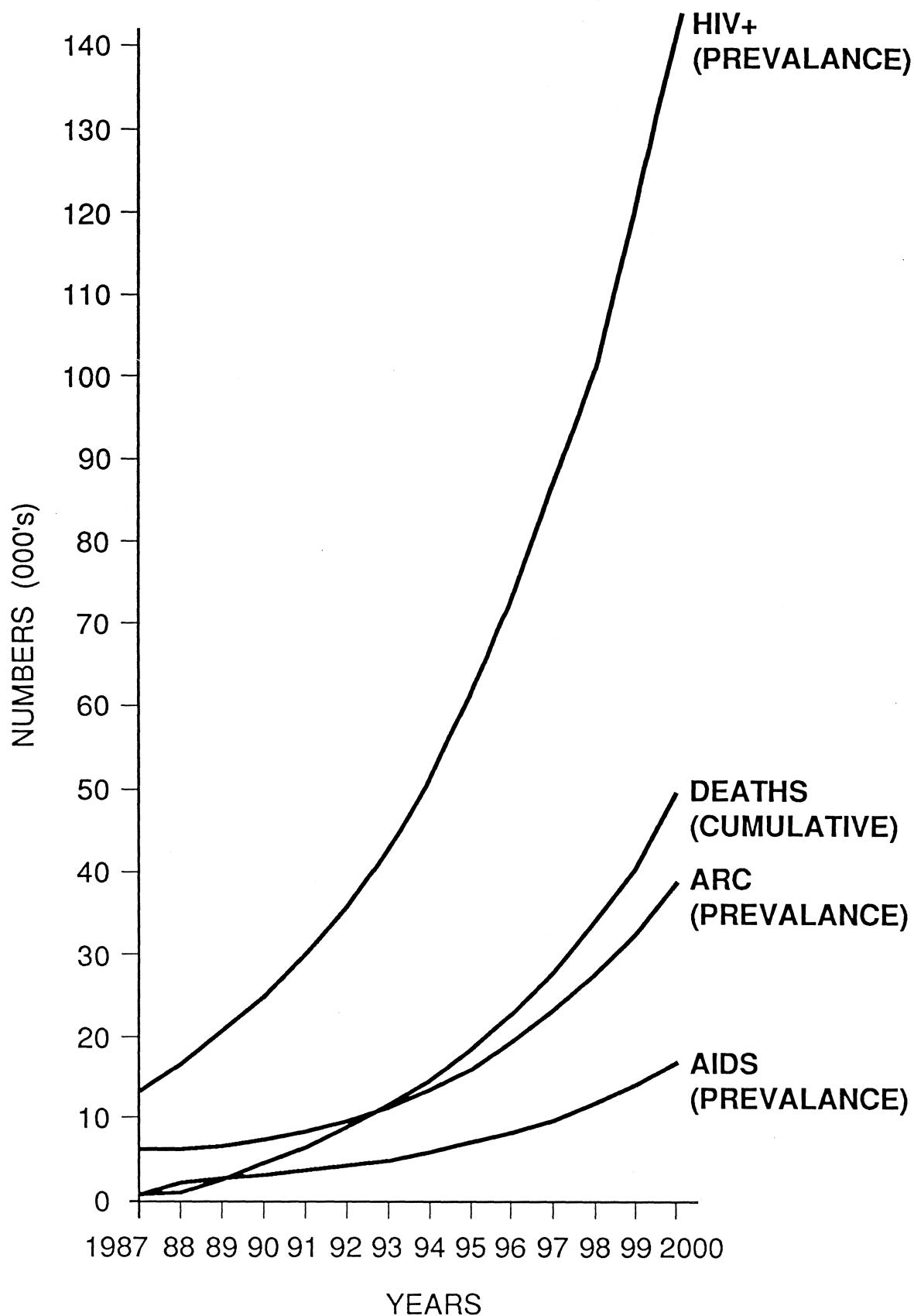


FIGURE 6 GRAPH TO SHOW THE NUMBERS PREDICTED FOR THE DIFFERENT DISEASE STAGES, UP TO 2000.

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