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PROJECTION MODELS FOR HEALTH EFFECTS ASSESSMENT IN POPULATIONS EXPOSED TO RADIOACTIVE AND NONRADIOACTIVE POLLUTANTS

Volume I

Introduction to the SPAHR Demographic Model for Health Risk

by

James J. Collins, Robert T. Lundy, Douglas Grahn, and Michael E. Ginevan

ARGONNE NATIONAL LABORATORY, ARGONNE, ILLINOIS

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This is Volume I of a five volume series entitled Projection Models for Health Effects Assessment in Populations Exposed to Radioactive and Nonradioactive Pollutants, NUREG/CR-2364, ANL-81-59. The series presents version 4.1 of the Simulation Package for the Analysis of Health Risk (SPAHR) computer package and model. The complete series of SPAHR documentation is contained in the following five volumes:

Volume I — Introduction to the SPAHR Demographic Model for Health Risk
J. J. Collins, R. T. Lundy, D. Grahn, and M. E. Ginevan

Volume II — SPAHR Introductory Guide
J. J. Collins and R. T. Lundy

Volume III — SPAHR Interactive Package Guide
J. J. Collins

Volume IV — SPAHR User's Guide
J. J. Collins and R. T. Lundy

Volume V — SPAHR Programmer's Guide
J. J. Collins and R. T. Lundy

PROJECTION MODELS FOR HEALTH EFFECTS
ASSESSMENT IN POPULATIONS EXPOSED TO
RADIOACTIVE AND NONRADIOACTIVE POLLUTANTS

ABSTRACT

The Simulation Package for the Analysis of Health Risk (SPAHR) is a computer software package based upon a demographic model for health risk projections. The model extends several health risk projection models by making realistic assumptions about the population at risk, and thus represents a distinct improvement over previous models. Complete documentation for use of SPAHR is contained in this five-volume publication. The demographic model in SPAHR estimates population response to environmental toxic exposures. Latency of response, changing dose level over time, competing risks from other causes of death, and population structure can be incorporated into SPAHR to project health risks. Risks are measured by morbid years, number of deaths, and loss of life expectancy. Comparisons of estimates of excess deaths demonstrate that previous health risk projection models may have underestimated excess deaths by a factor of from 2 to 10, depending on the pollutant and the exposure scenario. The software supporting the use of the demographic model is designed to be user oriented. Complex risk projections are made by responding to a series of prompts generated by the package. The flexibility and ease of use of SPAHR make it an important contribution to existing models and software packages.

FIN #	Title
A2059	Projection models for health effects assessment in populations exposed to radioactive and nonradioactive pollutants

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EXECUTIVE SUMMARY

Prediction of the health consequences to the general population of exposure to airborne and waterborne pollutants is becoming an important feature of environmental impact analyses. Such prediction requires not only knowledge of the dose term and the dose-response function, but also a model for projecting the health risk to some future population. Health risk projections entail considerable uncertainty about the measurement of the dosage that individuals receive and about the magnitude and nature of the biological response at a given population exposure. The uncertainties regarding the individual dose and the dose-response function have received much attention, but the uncertainty associated with the health risk projection model itself has not been fully addressed.

The purpose of this publication is threefold. First, the uncertainties in various health risk projection models will be addressed, and the assumptions inherent in each model will be stated explicitly. Second, a new model that is an extension of earlier models will be introduced. It is argued that this new model, referred to as the demographic model, is superior to previous models because it makes fewer assumptions about the population at risk and the potential of the population to change over time. Third, a computer package referred to as the Simulation Package for Analysis of Health Risk (SPAHR) is presented which facilitates the application of this model for various pollutants and populations at risk.

The core of any risk assessment scheme is the exposure-response model. This is the quantitative relationship between the level of exposure to the hazard of interest and the deleterious effects resulting from that hazard. If the population exposed to the hazard is homogeneous with respect to its likelihood of suffering ill effects from the exposure, estimation of effects is straightforward; we need know only the total number of persons exposed to estimate the effects. However, if the population is heterogeneous (i.e., different persons have differing risks of suffering health effects from exposure to the hazard), then a reasonable assessment of population risk depends upon the distribution of persons by level of risk.

Research indicates that risk levels are often related to the age and sex characteristics of the exposed population. This is true for both radiation and air pollution exposures. When the risk level is a predictable function of age and sex or some other traceable component of the demographic structure of the population, the estimation of projected health effects becomes less straightforward. If one adds to this complexity the long latency periods between exposure and response, the competing risks from other causes of mortality, and the changing demographic structure of the population over time, the projection of health effects becomes even more complex.

Evaluation of the health consequences for populations exposed to pollutants has become an important issue because of the increasing number of known

or suspected carcinogens in the environment. To date, three projection methods have been used in health risk assessments: the single coefficient model, the multi-coefficient model, and the life table model. Each has its own shortcomings, as discussed in Volume I, Chapter 2. This document presents a fourth model that is more useful and realistic than the previous models because it incorporates age, fertility, and mortality structure, and can follow populations through time under changing levels of mortality, fertility, and pollution exposure. This model is referred to as the demographic model.

A sensitivity analysis of the demographic model indicates that population structure alone for a 100-year exposure to 1 rem may introduce more than a factor of 10 variation in the number of excess deaths. This finding substantiates the premise that the population structure may be more important in a health risk projection than the uncertainty inherent in the dose-response functions.

A comparison of the demographic model with the single coefficient model, the most widely used in health risk projections, is presented in Volume I, Chapter 7. It is concluded that the single coefficient model, even in a short-term projection, may seriously underestimate excess deaths since it is unable to accumulate exposure. For instance, comparison of the single coefficient model with the demographic model for continuous exposure to 0.87 ppb of benzene for 50 years yields widely different estimates of excess mortality. The single coefficient model estimates 2,250 deaths, while the demographic model estimates values from 6,386 to 17,568. In the years 2015-2020, the excess leukemia deaths projected by the demographic model are ten times as large as those of the single coefficient model.

The demographic model is also compared with the life table model used in the 1980 BEIR report to estimate excess cancer deaths from exposure to ionizing radiation. The life table model correctly estimates the increased individual probability of death associated with a given radiation scenario. However, the life table model yields misleading results in the estimation of excess deaths for a specific population. The results presented in the 1980 BEIR report underestimate excess deaths by 50% in some instances. For example, using the linear-quadratic, absolute risk model for a continuous exposure of 1 rad per year for 70 years, the life table model estimates 2459 excess male deaths per million while the demographic model estimates 3769 excess male deaths per million.

This document is divided into five volumes:

I. Introduction to the SPAHR Demographic Model for Health Risk

II. SPAHR Introductory Guide

III. SPAHR Interactive Package Guide

IV. SPAHR User's Guide

V. SPAHR Programmer's Guide

The first volume presents the theory behind the SPAHR health risk projection model and several applications of the model to actual pollution episodes. The elements required for an effective health risk projection model are specified, and the models that have been used to date in health risk projections are outlined. These are compared with the demographic model, whose formulation is described in detail. Examples of the application of air pollution and radiation dose-response functions are included in order to demonstrate the estimation of future mortality and morbidity levels and the range of variation in excess deaths that occurs when population structure is changed. Volumes II through V provide the potential user with detailed guidance and appropriate examples to aid in the interpretation of numerical demographic output from the application of the model to realistic circumstances.

1.0 THE HEALTH RISK PROJECTION

What properties should a realistic health risk projection model have? To reduce uncertainty to its lowest level in the health risk projection, the model should incorporate as much information as possible about both the pollutant of interest and the population at risk. Assumptions about either the pollutant or population should be made only when adequate information is not available. In addition, assumptions about unknowns should be made with the best available data.

While our knowledge about the biological effects of many pollutants is scant, in many cases we have indications of the complex effects of specific pollutants on human populations. The Committee on the Biological Effects of Ionizing Radiations (BEIR) and the United Nations Scientific Committee of the Effects of Atomic Radiation (UNSCEAR) have both evaluated the scientific knowledge concerning radiation exposure of human populations (NAS, 1972; NAS, 1980; UN, 1977). An outline of the effects of radiation on human populations reveals the complexity of performing health risk estimates.

Although the mechanisms of chemical or radiation carcinogenesis are not fully known, available information indicates that most, if not all, types of cancer are a result of the combined effects of multiple factors. While the causes of radiogenic cancers are complex, several important relationships have been observed. The most important factor influencing the risk of spontaneous cancer (i.e., a cancer that appears in a population normally) is age. Older persons are more likely to have cancer. There is now considerable evidence in nearly all adult human populations studied that persons irradiated at higher ages have, in general, greater excess risk of cancer than persons irradiated at lower ages (NAS, 1980). It should be noted that there are exceptions. For instance, the time course of the development of excess risk appears to be independent of age at exposure for certain leukemias (NAS, 1980). Second, the period between irradiation and the appearance of the cancer (latency) is often very long and appears to be disease specific. For example, the latency period for leukemia is two years; for bone cancer, four years; and for most other cancers, 20 years (NAS, 1980). Third, it appears that the effect of radiation in producing cancers ends a number of years after exposure, at the end of the plateau period. As with latency, this period is disease specific. Leukemia and bone cancer have plateau periods of 30 years.

Figure 1.1 relates age-specific excess risks, latency period, and plateau period. Irradiation at any age (X_e) adds an increment of cancer incidence to the spontaneous incidence after a minimal latent period (ℓ). However, this increment of cancer incidence lasts only as long as the plateau period (p), after which the spontaneous incidence rates again apply. The increment of cancer incidence and the minimal latent period depend in part on the age at exposure. Therefore, dose response functions and latency periods are age and disease specific.

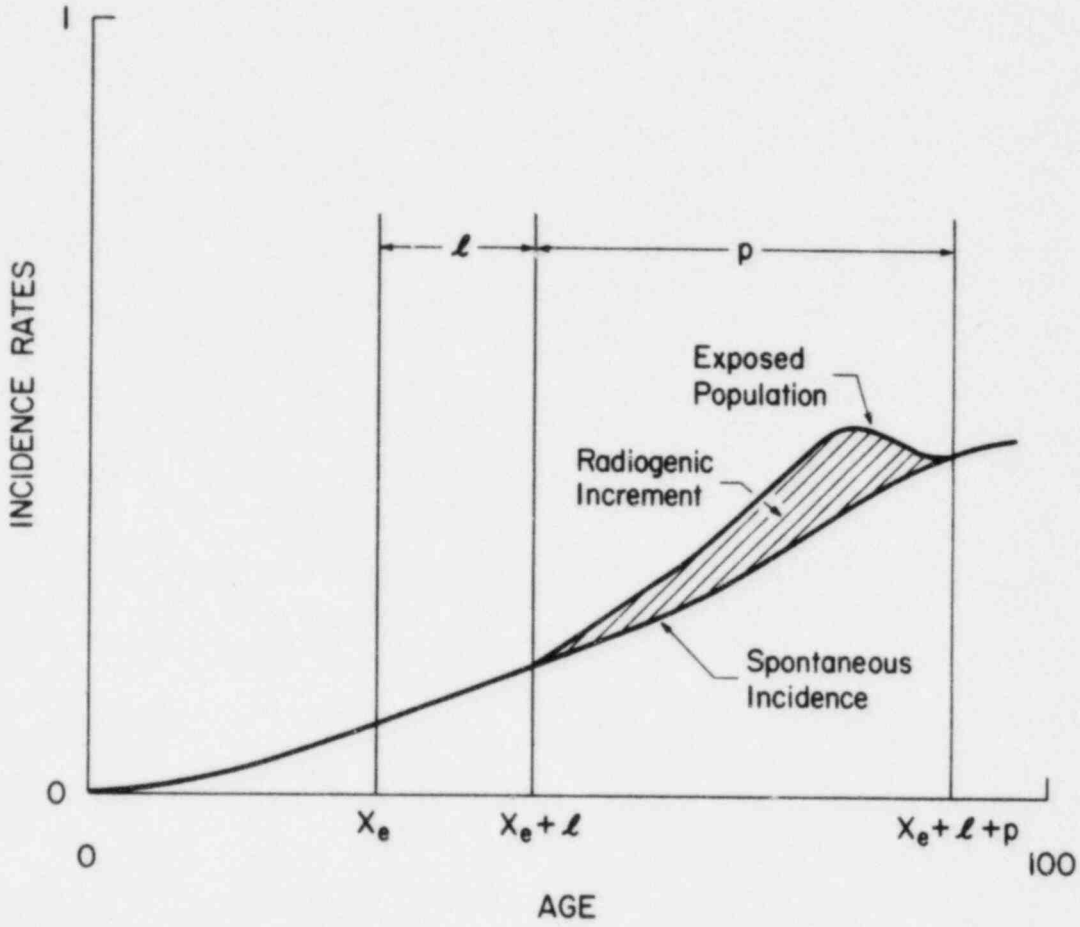

Fig. 1.1. Imposition of a Hypothetical Radiogenic Effect of Spontaneous Incidence

Because of these complex relationships, the model of choice should be able to follow persons by age through time. In Figure 1.1, for instance, exposure at age X_e produces no excess cancers for time ℓ. The excess cancers begin to appear at age $X_e + \ell$ and continue until the plateau period, p, is ended. If we have a cohort of persons at age X_e and we wish to estimate the excess number of deaths, we must follow this hypothetical cohort through time until age $X_e + \ell + p$. Therefore, we must "project" the experience of this cohort over time; hence the term "health risk projection."

In the projection process, uncertainty arises; following persons as they age requires numerous assumptions. For instance, we must take into account competing risks from causes of death other than the radiogenic cancer. If irradiation occurs at an age when the expectation of life is less than the latent period, ℓ, the number of excess deaths for that cohort of persons will approach zero. On the other hand, irradiation at birth will allow nearly the maximum number of excess deaths to occur, because competing risks from other causes are small early in life.

Another assumption is also required. Figure 1.1 demonstrates the case of a single exposure to an excess radiation level. However, excess exposure may also be continuous, for example 1 rad per year for 15 years. A model to estimate excess deaths due to continuous exposure may be based on the approach used in Figure 1.1, with the dose for each cohort accumulating. This approach, however, may seriously underestimate excess deaths because it fails to account for births occurring in the population. Births are important in a health risk projection because newborns are not very susceptible to competing risks from other causes. Therefore, to reduce the uncertainty in the projection and to improve the estimates of risk, we should include a fertility assumption.

In summary, the dose response functions for radiogenic cancers are age specific, and the excess cancers occur in plateau periods following latency periods. There is some evidence that these characteristics may apply to other pollutants. Therefore, the model of choice should follow persons by age through time, account for competing risks from other causes of death, and include an assumption about fertility. Such a model would reduce the uncertainty associated with the projection.

In the next chapter we will review and evaluate the models that have been used to estimate health risk. We will then introduce a new model, built on previous formulations, that meets the above criteria for a model of choice.

2.0 THE MODELS USED IN HEALTH RISK PROJECTIONS

2.1 Introduction

The core of any risk assessment scheme is the exposure-response model. This is the quantitative relationship between the level of exposure to the hazard of interest and the deleterious effects resulting from that hazard. If the population exposed to the hazard is homogeneous with respect to its likelihood of suffering ill effects from the exposure, estimation of effects is straightforward; we need only know the total number of persons exposed to estimate the effects. However, if the population is heterogeneous (i.e., different persons have differing risks of suffering health effects from exposure to the hazard), then in order to arrive at a reasonable assessment of population risk the distribution of persons by level of risk must be considered.

Research indicates that risk levels are often related to the age and sex of the person exposed. This is true for both radiation exposure (NAS, 1972; NAS, 1980) and air pollution (Dixon-Davis et al., 1981; Holland et al., 1979; Gregor, 1976; Lave and Seskin, 1977; Mendelsohn and Orcutt, 1979). When the distribution of risk levels is a predictable function of age and sex or some other tractable component of the demographic structure of the population, the estimation of projected health effects becomes complex. If one adds to this complexity the long latency periods between exposure and response, the competing risks from other causes of mortality, and the changing demographic structure of the population over time, the projection of health effects becomes even less straightforward.

2.2 Risk Projection Models

Assessment of the health consequences for populations exposed to pollution has become an important issue because of the increasing number of known or suspected carcinogens. To date, three projection methods have been used in health risk assessments; each has its own shortcomings. We propose a fourth model that is more useful and realistic because it incorporates age, fertility, and mortality structure and can follow populations through time under changing levels of mortality, fertility, and pollution exposure.

In general, the chance of observing the effects of a given hazard depends on the level of exposure, the duration of exposure, the duration since the onset of exposure, and the intensity of competing risks from other causes of mortality (Neyman, 1977; NAS, 1980; Cook et al., 1978). This suggests that a health risk projection not only should include a dose response function but also should model the population structure, latency of response, and competition from other causes of mortality. In addition, a health risk projection should realistically follow an exposed population through time. Because most pollution exposures are long-lived and latency periods are often long, a mechanism for modeling demographic structured changes through time is necessary. Finally, the model should provide both aggregate mortality levels and individual risk so as to be most useful to the policy maker.

Three types of exposure response models for estimating health risk have been used extensively. These are: (1) the single coefficient model; (2) the multi-coefficient model; and (3) the life table model. We introduce a fourth model, which will be referred to as the demographic model.

2.2.1 Single Coefficient Model

Risk projection models at their most basic level are simple, linear dose response functions. The archetype of the "single coefficient" model was that presented by Wilson (1972). Wilson used a study by Lindberg (1968) relating variations in mortality in the city of Oslo, Norway, with variations in levels of sulfur dioxide (SO_2) to estimate a 1% excess of deaths per ppm of SO_2. This coefficient, by force of repetition, has gained considerable use (e.g., Sagan, 1974; Comar and Sagan, 1976). Other members of this family of risk models include the coefficients generated by the Environmental Protection Agency from the Community Health and Environment Surveillance System (USEPA, 1974) and those developed by Morris (Morris and Novak, 1976; Finch and Morris, 1977) for sulfates.

An example of a single coefficient model would be as follows. First, the exposure, E, is defined as

$$E = Z \cdot t \tag{2.1}$$

where Z is the level of the exposure and t is the length of the time exposed. The number of responses in a specific population, Rp, is then

$$Rp = K \cdot E \cdot P \text{ or } f(E,P) \tag{2.2}$$

where K is the slope of the dose response function, P is the size of the population, and f is any arbitrarily defined function. The arbitrarily defined function, K, is derived from epidemiological studies where a number of deaths are associated with a specific level of mortality.

All of these models have one trait in common: a single coefficient is multiplied by the population exposure integrated over some arbitrary time interval to determine the anticipated "excess" number of deaths or morbid events. The following deficiencies of the single coefficient model are evident when comparing it with characteristics of the ideal model discussed in Chapter 1.

1. The underlying assumption is that the population is homogeneous with respect to risk. The only characteristic of the population that enters into such a model is its total size, and size is important only insofar as it affects the integrated dose estimates. Differences within the population with respect to associated risk factors such as age and sex are ignored.

2. Latency is completely disregarded in the single coefficient model. Depending on the manner in which it is employed, it assumes either that all effects are virtually immediate (i.e., they occur within a year of exposure) or that nothing is known about latency. Most epidemiological studies on air pollution make this assumption (c.f., Buechley et al., 1973; Buechley, 1975), assuming that the responses observed in a population having a long exposure history to the overall level of pollution (as have most of the source study populations) will be identical to those observed in a population in which the exposure history is far shorter, as is likely to be the case for many of the populations for which health risk projections will be made. While it can be argued that air pollution may have an instantaneous impact on the cardiovascular disease mortality rate and thus zero latency (Land and McMillen, 1980), cancers appear to have a latency period exceeding one year (NAS, 1980). Latency periods for cancers resulting from radiation exposure are known to exceed two years for leukemia and 10 years or more for the other cancers (NAS, 1980). In sum, because the issue of latency is not addressed explicitly in the single coefficient model, the assumption is that latency is zero. This assumption is unrealistic, given what is known about mortality resulting from environmental exposures, whether they be air pollutants or radiation.

3. Competing risks are totally ignored. Other risks of death may reduce the apparent effect of a particular hazard by removing persons who might have died of the cause of interest before they had an opportunity to do so. In this sense, automobile accidents prevent cancer. Consequently, the importance of competing risks in a risk assessment is directly related to the importance of latency effects. The longer the potential waiting time between exposure and response, the greater is the opportunity for an unrelated lethal event to intervene. However, latency is not the only source of problems with competing risks. Even if the effect is immediate, variation in susceptibility due to age in the real population will still give a competing risk bias, because the competing risks influence the chance of survival to each age and hence the age structure of the population. For example, the proportion of the population at risk from cardiovascular disease will be lower, all else equal, in a population that has high infant mortality than in one that has low infant mortality, because a smaller proportion of the children will survive into the older years in which risk from cardiovascular disease is significant.

4. Estimates related to individual risk are seriously biased. The alteration in the death rate that is derived from a single coefficient model is, in reality, the mean of several alterations in risk weighted by the arbitrary distribution of several modifying factors such as age. For this reason, and because the issues of structure and latency are neglected in these models, it is impossible for them to generate meaningful estimates of life shortening. Because in a homogeneous, unstructured population we are necessarily assuming the unimportance of age (at least in the context of exposure to the hazard of interest), we are at the same time assuming the equality of the effect across all ages (i.e., that the distribution by age of induced deaths in the population is identical to the age distribution in the population).

5. The use of such a model requires prior knowledge of the size of the population at risk. Consequently, there can be no explicit interaction between the size or composition of the population at risk (and hence the integrated exposure) and the rate at which members are removed as a consequence of the hazard of interest. The size of the population at risk is, in short, treated as an exogenous variable. At very low dose rates this is not a serious problem. It becomes more serious as the exposure level rises, so that at some point (the point being determined by the user's perception of the meaning of "serious") a significant number of people are present in the population and therefore at risk from the hazard who, according to the dose response model, have already died of it.

As a consequence of the factors described above, the applicability of a single coefficient model is severely restricted. If the structure of the population to be analyzed is identical to that of the population that formed the basis for the coefficient estimate and will remain so for the duration of the period during which estimates are to be made, then the estimates of excess events will be unbiased. However, this assumption is violated under almost all circumstances, being true only if both populations have maintained identical birth, death, and migration rates for a long period of time. Furthermore, if one wishes to apply a coefficient derived from a particular population to the same population at a different time, the vital rates that determine structure must have remained constant for the length of time necessary to achieve a stable age structure (typically over 100 years) prior to the earlier of the two times. Whatever the common structure justifying the use of the single coefficient model, it must further be assumed that this structure remains constant for the duration of the time period of the assessment, a proposition that is tenable only if the population has been exposed to nearly constant rates of birth and death for a long time prior to the initiation of the study. Furthermore, with regard to latency, we must either assume an instantaneous effect or assume that the exposure history, relative to the overall level of exposure, has been identical in the two populations as well.

2.2.2 Multi-coefficient Models with Fixed Populations

The next major type of model is called the multi-coefficient constant population model. It represents a considerable improvement over the single coefficient model in that variations in response that depend upon age, duration of exposure, and period since exposure can be estimated. However, the relatively realistic structure on the dose response side of the model is not matched by a corresponding care for structure in its application to the population at risk.

Models in this category are best described as structurally detailed dose response models without an associated demographic framework in which to operate. The best known example of this class of models is that developed in the BEIR report (NAS, 1972), modified and extended in the Reactor Safety Study (USNRC, 1976, Appendix VI), and applied in a number of assessments relating to

the health effects of various aspects of nuclear energy. Also in this category might be placed some of the models derived by Lave and Seskin (Finch and Morris, 1977; Lave and Seskin, 1977) and Mendelsohn and Orcutt (1979). In the BEIR model, exposure to radiation in several different age groups is assumed to result in an increment of risk that begins following a period of latency and lasts for a specific period of time (usually referred to as the "plateau period"). This increment is a linear additive function of dose in the "absolute risk" version of the model, and is linearly proportional to the baseline age-specific rate in the more realistic "relative risk" version.

Although this model has age-specific dose response functions and recognizes latency effects, it has traditionally been used by applying it one time to a population with a particular age distribution, and making the explicit assumption that the most recent available age distribution will remain constant. This use gives the model most of the undesirable features of a single coefficient model. Thus the only real improvement inherent in the multicoefficient model is its ability to define latency effects in cross-sectional projections. The numbers derived with it are biased because the age distribution remains artificially static.

Further, unless the assumed age distribution corresponds by either accident or design to the stationary (life table) age distribution appropriate to the population under study, the projection is no less biased when applied to age cohorts than it is for the total population. When a structured dose response model is used in conjunction with a population whose structure is assumed for convenience to be constant, its projections of excess numbers of events suffer from most of the disadvantages inherent in the single coefficient model. However, the structurally correct dose response model may be used by itself to generate proper life shortening estimates. This fact has been exploited in the next model group to be described.

2.2.3 Life Table Model

Life tables combine mortality rates of a population at different ages into a single statistical model. The life table technique estimates the probability of survivorship of an individual subject to one undifferentiated cause of death. A simple extension of this technique is the multiple decrement life table in which the individual is subject to a number of mutually exclusive hazards such as death from cancer, heart disease, and other causes. Life table methods are used for health risk projection models by classifying the causes of death into two categories: (1) those deaths resulting from exposure to a pollutant, and (2) all other causes of death. In this way the life table model with the multiple decrement extension is used to estimate excess mortality resulting from some pollutant.

The multiple decrement life table represents the fate of a cohort exposed throughout its life to given risks of death. Consequently it is an excellent method of analysis for cohort studies, being by definition correct. It yields

age-specific and time-specific estimates that are not biased in any way (subject to the homogeneity assumption). However, it is limited because the projection dies with the last member of the cohort. It cannot, by definition, be applied for an indefinite time period to any population. The life shortening estimates, being essentially independent of population size, may be applicable to a specific population. However, an estimate of life table deaths for a particular cause cannot be generalized to another population structure. To do so reduces the model to a multi-coefficient model with fixed population structure, which, as we have noted earlier, contains the same biases in cross-sectional projections as does a single coefficient model applied to a totally unstructured population.

2.2.4 Life Table Model With Dynamic Population--The Demographic Model

The demographic model is an extension of the life table model that addresses some of its weaknesses. The demographic model attempts a complete simulation of the dose response function. However, unlike the previous two models, it extends the projection process by dynamically simulating a fully structured population. This projection is accomplished by employing the standard component projection technique (Barclay, 1958; Keyfitz, 1968), which generates periodic cross-sectional estimates of the age structure and size of the population. This is extended to yield age-specific estimates of mortality during the projection interval. The mortality risks used to project the population forward in time are a combination of the baseline mortality rates and the excess mortality rates. This process is repeated until the desired point in time has been reached. It is illustrated graphically in Figure 2.1.

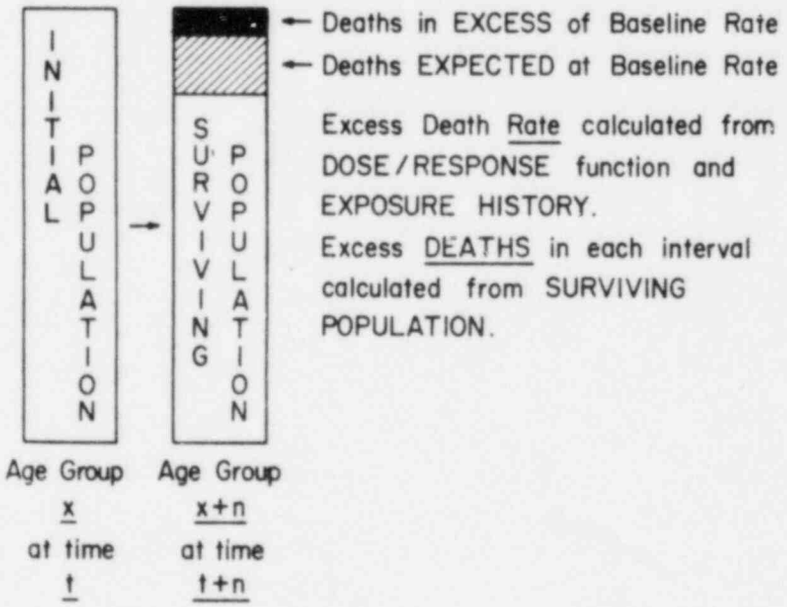

Fig. 2.1. Projecting Excess Deaths and Population at Risk Simultaneously

Many of the problems in the previous models are corrected in the demographic model. Because the population's age distribution is permitted to vary with time, the biases inherent in homogeneous or fixed-structure models are eliminated. In each projection cycle, both the persons who die of "baseline" rates (i.e., the ones who would have died without the added exposure) and the ones who die of the "excess" rates (the ones who would otherwise have lived on) are removed from the population. Consequently, the effects of competing risks are handled as well for the arbitrary age distributions in this model as they are for the cohorts alone in the previous model. No person's death is counted more than once, because changes in population size are tied directly to mortality, in contrast to single coefficient and multi-coefficient fixed-structure models. Life table calculations are a prerequisite for survival calculations. The life table cohort model is therefore a subset of the present model. This demographic model is described fully in the chapter to follow.

3.0 THE DEMOGRAPHIC HEALTH RISK PROJECTION MODEL

This chapter describes the demographic health risk projection model. This model is intended to be a reasonably complete macrodemographic model capable of satisfying most of the requirements of an ideal health effects projection model as outlined earlier in Chapter 1.

Fig. 3.1 illustrates the general approach. The population at risk, in this case the U.S. population of 1970, is subdivided into age and sex groups and is exposed to age-specific fertility rates (i.e., births), mortality rates (i.e., deaths), and environmental pollutants (e.g., radiation exposure). The age-specific mortality and fertility rates age the population or project it forward in time. The age-specific dose response function is applied to the total number of persons in each age-sex group, and the age- and sex-specific excess deaths are estimated. The estimated future population, in this case the population in the year 2000, is used to determine the excess deaths under a particular pollution scenario given specific assumptions on mortality and fertility.

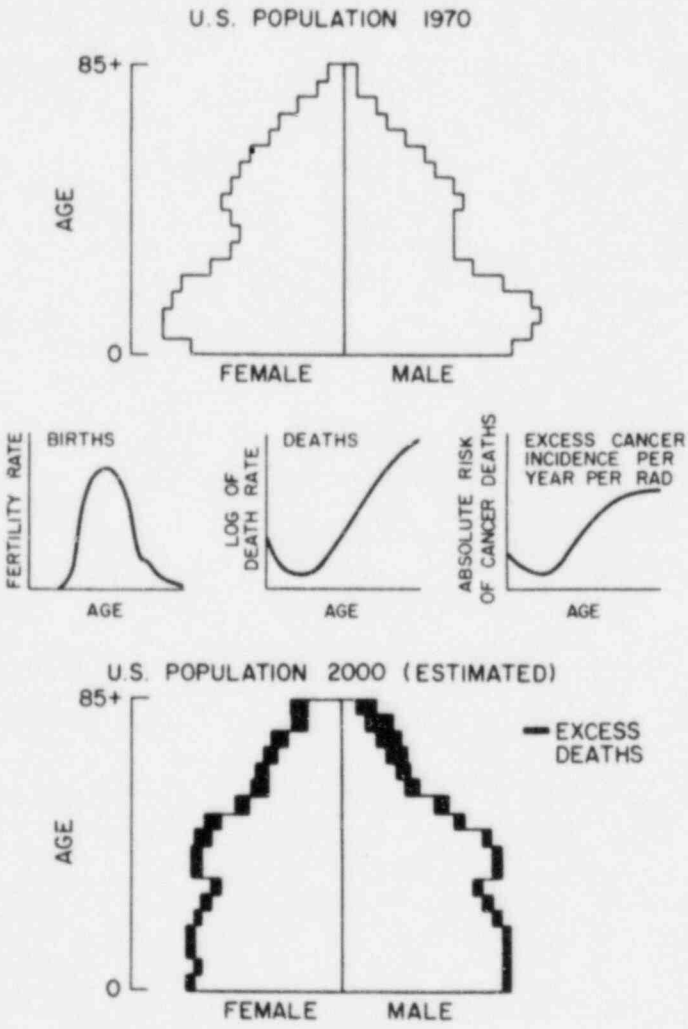

Fig. 3.1

Hueristic Diagram of the SPAHR Model

The demographic projection model begins with the construction of a life table and a multiple decrement life table. From these tables, baseline survivorship (i.e., the proportion of persons surviving a particular interval in the absence of the pollutant) is estimated. Excess death rates are calculated from the dose response functions for the pollutant of interest. These excess death rates are then added to baseline mortality. Fertility enters the model by producing more persons to be exposed. The health risk projection technique used in the demographic model will be included in discussions of the life table, the multiple decrement life table, and the component methods of population projection. The incorporation of the dose response function into the model will follow in Chapter 4.

3.1 The Life Table: The Analysis of Individual Risk

The life table was originally developed to express probabilities pertaining to individual persons. The basic units in a life table are the probability of survival from birth to an exact age x, ℓ_x, and the instantaneous probability of death at exact age x, $\mu(x)$ (Keyfitz, 1968). The two are related to each other as

$$\mu(x) = \frac{-\partial \ln(\ell_x)}{\partial x} \tag{3.1}$$

when ln stands for the natural logarithm of the quantity following it, and

$$\ell_x = \exp^{-\int_0^x \mu(a)\partial a}. \tag{3.2}$$

In most life tables, it is conventional to multiply ℓ_x by some large number, usually 100,000 (called the radix of the life table), and to treat the ℓ_x column as a cohort being followed from birth to extinction.

The number of person-years lived between two exact ages, x and x+n, by the initial cohort is called ${}_nL_x$, and is defined as

$${}_nL_x = \int_x^{x+n} \ell_a \partial a. \tag{3.3}$$

For convenience, the number of deaths, d, in the cohort between age x and x+n is defined as

$${}_nd_x = \ell_x - \ell_{x+n}. \tag{3.4}$$

The future person-years to be lived by the cohort beyond age x is defined as

$$T_x = \int_x^{\infty} \ell_a \partial a \tag{3.5}$$

and the expected years of life remaining per person surviving to age x in the cohort is called the expectation of life, e, at age x

$$e_x = \frac{T_x}{\ell_x}. \tag{3.6}$$

Other quantities of interest which may be derived from a life table are the probability of death between exact age x and x+n,

$${}_nq_x = \frac{{}_nd_x}{\ell_x} \tag{3.7}$$

and the life table age-specific central death rate,

$${}_nm_x = \frac{{}_nd_x}{{}_nL_x}. \tag{3.8}$$

3.1.1 Methods for Calculating Life Tables

In practice, none of the quantities shown above can be taken directly from available data. They are estimated in the following manner (Chiang 1968, Ch. 9; or Keyfitz, 1968, Ch. 3). First assume that the life table central death rate, ${}_nm_x$, is approximated by the observed age-specific death rate, M, in the real population,

$${}_nM_x = \frac{{}_nD_x}{{}_nP_x} \tag{3.9}$$

where ${}_nD_x$ = the observed deaths in the age group x to x+n in the real population during one year, and ${}_nP_x$ = the number of person-years lived in that age group during the year by the population, usually assumed to be the midyear population. This is converted to the probability of death in the age interval by the formula

$${}_nq_x = \frac{n \cdot {}_nm_x}{1 + (n - {}_na_x){}_nm_x} \tag{3.10}$$

where ${}_na_x$ is the average number of years lived in the interval by those who die in it. The number in the hypothetical cohort surviving from birth to exact age x can then be calculated sequentially as

$$\ell_x = \ell_{x-n}\,(1 - {}_nq_x) \tag{3.11}$$

and the person-years lived in the age groups x to x+n by the initial cohort as

$${}_nL_x = n\,\ell_{x+n} + {}_na_x({}_nd_x). \tag{3.12}$$

The total persons-years lived by the starting cohort from age x until extinction is then

$$T_x = \sum_{i=x}^{w} {}_nL_x \tag{3.13}$$

where w represents the final age group.

The final age group, whatever its initial age, must be open-ended, necessitating a different method of computation. It is customarily assumed that the mortality rate in this final age group is constant. The rate at which the risk of death increases with age declines markedly at advanced ages (Barclay, 1958; Bayo, 1972). Assuming this terminal death rate, m_w, to be a constant, the laws of exponential decay apply, and the expectation of life for the final age group becomes

$$e_w = \frac{1}{m_w} \tag{3.14}$$

and

$$L_w = T_w = e_w \ell_w = \frac{\ell_w}{m_w}. \tag{3.15}$$

Since by definition, no one can survive the last age group, the probability of death in that interval is defined as

$$q_w = 1.0. \tag{3.16}$$

3.1.2. An Example of a Life Table

From Table 3.1 it can be seen that in 1970 there were 7,341,007 white females in the 20-24 age group in the United States. During 1970, 4,826 deaths were recorded for this group. Corresponding mortality data for selected causes of death are provided in Table 3.2. The age-specific death rate ${}_5M_{20}$ is thus 4,826/ 7,341,007 = 0.0006574, which is shown rounded to 0.00066 in Table 3.3. The probability of death in the interval is derived from Equation 3.10 as

$${}_5q_{20} = \frac{5 \times 0.0006574}{1 + (2.5)(0.0006574)} = 0.00328.$$

Note from Table 3.3 that 97,572 members of the hypothetical cohort survived to their 20th birthday. An additional

$${}_5d_{20} = 0.00328 \times 97,572 = 320$$

will die in the ensuing five years, so that

$$\ell_{25} = 97,572 - 320 = 97,252.$$

Table 3.1

Raw Data for the White Population of the United States in 1970. This is a copy of the table generated by SPAHR when this data has been entered using the DATA command. Data for population were derived from the U. S. Census of 1970. Data for births and deaths are from the U. S. Vital Statistics for 1970.

<DATOUT> UNITED STATES (WHITE) 1970

AGE	POPULATION		BIRTHS		DEATHS		AGE
GROUP	FEMALE	MALE	FEMALE	MALE	FEMALE	MALE	GROUP
< 1	1433839	1501250			23151	31725	< 1
1- 4	5614968	5873083			3714	4910	1- 4
5- 9	8264333	8633093			2646	4099	5- 9
10-14	8647392	9033725	4648	4865	2410	4382	10-14
15-19	8079090	8291270	266058	278473	4672	12200	15-19
20-24	7341007	6940820	540174	565381	4826	13812	20-24
25-29	5962122	5849792	392685	411009	4360	9897	25-29
30-34	5042368	4925069	166546	174318	4899	9130	30-34
35-39	4936494	4784375	69224	72454	7447	12459	35-39
40-44	5412335	5194497	18776	19652	12557	21819	40-44
45-49	5587023	5257619	1092	1143	20873	35992	45-49
50-54	5169302	4832555			28920	53092	50-54
55-59	4695581	4310921			39009	76502	55-59
60-64	4157467	3647243			50841	98781	60-64
65-69	3491080	2807974			67187	113614	65-69
70-74	2874531	2107552			90091	122829	70-74
75-79	2114943	1437628			113145	124979	75-79
80-84	1314258	805564			116567	101556	80-84
85+	889855	486957			142201	90339	85+
UNKN.	0	0			143	320	UNKN.
TOTAL	91027840	86720864	1459199	1527290	739659	942437	TOTAL

Table 3.2

Raw Data for the U. S. White Population in 1970 for mortality from selected causes of death. Causes shown here correspond to groups defined in the BEIR report (NAS 1972). Data are from the U. S. Vital Statistics for 1970.

<DATOUT> UNITED STATES (WHITE) 1970

DEATHS BY AGE, SEX, AND CAUSE

CAUSE NO.	1 LEUKEMIA	2 LUNG	3 STOMACH	4 ALIMENRY	5 PANCREAS	6 BREAST	7 BONE	8 THYROID	9 OTHER	10 CANCER
FEMALE										
< 1	36	1	0	7	0	0	2	0	31	77
1- 4	195	2	0	7	0	0	6	0	178	388
5- 9	283	3	0	6	0	0	18	1	193	504
10-14	163	2	0	6	0	0	54	0	191	416
15-19	153	3	0	11	1	0	57	3	246	474
20-24	117	5	4	22	3	12	18	3	302	486
25-29	82	13	5	40	5	92	21	2	426	686
30-34	95	47	15	84	27	311	5	4	392	980
35-39	127	187	47	158	78	680	16	8	940	2241
40-44	166	410	83	372	153	1408	18	7	1695	4312
45-49	224	885	167	831	349	2525	25	18	3075	8099
50-54	300	1358	232	1477	657	3181	37	22	4100	11364
55-59	369	1645	375	2228	1014	3657	65	44	4686	14083
60-64	432	1648	484	2847	1314	3360	59	74	6046	16264
65-69	550	1477	668	3714	1506	3220	73	76	6526	17810
70-74	687	1256	823	4379	1430	2884	79	125	6654	18317
75-79	761	1093	985	4607	1292	2626	73	117	6230	17784
80-84	649	711	863	3728	770	1819	63	84	4491	13178
85+	480	450	679	2926	445	1441	53	61	3139	9674
UNKN.	0	1	0	3	1	0	0	0	9	0
TOTAL	5869	11197	5430	27453	9045	27216	742	649	49550	137137
MALE										
< 1	25	3	0	7	0	0	0	0	30	65
1- 4	247	2	0	18	1	0	1	0	233	502
5- 9	344	0	0	3	0	0	14	0	347	708
10-14	229	2	0	2	0	0	54	1	238	526
15-19	211	7	3	27	1	0	121	1	371	742
20-24	155	15	4	32	5	0	54	3	601	869
25-29	120	31	14	51	8	1	15	6	557	803
30-34	117	100	24	80	7	1	15	5	572	921
35-39	153	349	72	164	36	1	14	6	771	1566
40-44	182	1119	142	403	106	4	19	12	1358	3345
45-49	298	2314	266	859	218	12	39	14	2312	6332
50-54	368	4073	461	1606	398	24	54	29	3621	10634
55-59	535	6556	758	2762	571	22	70	42	5374	16690
60-64	695	8312	1027	3762	820	25	88	40	7241	22010
65-69	829	8616	1247	4209	999	39	106	51	8088	24184
70-74	941	7359	1337	4431	1120	28	90	44	8657	24007
75-79	928	5136	1292	4167	1193	36	85	40	8492	21369
80-84	659	2417	978	2908	891	24	68	32	3802	11779
85+	418	972	604	1880	665	15	39	12	1615	6220
UNKN.	0	5	0	2	1	0	0	0	1	0
TOTAL	7454	47388	8229	27373	7040	232	946	338	54281	153272
SUM...	13323.0	58585.0	13659.0	54826.0	16085.0	27448.0	1688.0	987.0	103831.0	290409.0

Table 3.3

Life Table

This is a copy of the female life table generated in response to the 'LIFETAB' command in SPAHR.

The 1(X) column refers to P_x as defined in the text of Chapter 3.1 and the Equations 3.2 and 3.11. It represents the number of survivors of a hypothetical cohort of 100,000 live births to the beginning of the indicated age interval.

The D(X) column represents the number dying during each age interval, as defined in Equation 3.4.

The Q(X) column represents the probability of death in the interval, as defined in Equation 3.7.

M(X) is the central death rate, defined in Equations 3.8 and 3.9.

L(X) is the person-years lived in each age group, defined in Equations 3.2 and 3.12.

T(X) is as defined in Equation 3.13.

E(X) is the expectation of life at the beginning of the age interval, defined in Equation 3.6.

<LIFE TABLE> UNITED STATES (WHITE) 1970

FEMALE LIFE TABLE

AGE(X)	1(X)	D(X)	Q(X)	M(X)	L(X)	T(X)	E(X)	AGE
< 1	100000.	1592.	0.01592	0.01615	98567.	7561613.	75.616	< 1
1- 4	98408.	260.	0.00264	0.00066	392983.	7463046.	75.838	1- 4
5- 9	98148.	157.	0.00160	0.00032	490348.	7070064.	72.035	5- 9
10-14	97991.	136.	0.00139	0.00028	489614.	6579716.	67.146	10-14
15-19	97855.	283.	0.00289	0.00058	488567.	6090102.	62.236	15-19
20-24	97572.	320.	0.00328	0.00066	487059.	5601536.	57.409	20-24
25-29	97252.	355.	0.00365	0.00073	485371.	5114477.	52.590	25-29
30-34	96897.	470.	0.00485	0.00097	483309.	4629107.	47.774	30-34
35-39	96427.	725.	0.00752	0.00151	480323.	4145799.	42.994	35-39
40-44	95702.	1104.	0.01154	0.00232	475751.	3665477.	38.301	40-44
45-49	94598.	1751.	0.01851	0.00374	468613.	3189727.	33.719	45-59
50-54	92847.	2562.	0.02759	0.00560	457831.	2721114.	29.307	50-54
55-59	90285.	3675.	0.04070	0.00831	442239.	2263284.	25.068	55-59
60-64	86611.	5140.	0.05934	0.01223	420203.	1821045.	21.026	60-64
65-69	81471.	7481.	0.09183	0.01925	388651.	1400842.	17.194	65-69
70-74	73990.	10754.	0.14535	0.03135	343063.	1012191.	13.680	70-74
75-79	63236.	14922.	0.23597	0.05351	278872.	669128.	10.582	75-79
80-84	48314.	17540.	0.36304	0.08871	197718.	390255.	8.078	80-84
85+	30774.	30774.	1.00000	0.15983	192537.	192537.	6.257	85+

These 97,252 survivors each lived five person-years in the interval, while the 320 who died lived on the average half that number of person-years. Thus, the total person-years lived in the interval by this cohort are

$$_5L_{20} = (5 \times 97{,}572) + (2.5 \times 320) = 487{,}059.$$

When this is added to all succeeding members of the $_nL_x$ column, T_{20} (the total person-years to be lived beyond age 20 by the cohort) sums to 5,601,536. The number of person-years lived by each person reaching that age, or the expectation of life e_{20}, is then 5,601,536/97,572 = 57.409 years.

3.2. The Multiple Decrement Life Table

The life table discussed up to this point calculates the probability of survivorship of an individual person subject to the one undifferentiated hazard of death. In multiple decrement tables the individual is subject to a number of mutually exclusive hazards such as death from heart disease, cancer, and other causes. The person is followed to his exit, as in the ordinary life table, but now there is more than one way of exiting.

While the multiple decrement extension of the life table is theoretically simple, the actual calculation is somewhat complicated. A person at any age either lives through the next interval or dies in it. Furthermore, we know that the person now alive will eventually die. In the multiple decrement table, therefore, we allocate each death to its appropriate cause. The number of deaths that may be allocated to a cause of death at a specific age in the life table is proportional to the number of deaths from that cause in the original population. The number of deaths in the age group x to x + n is therefore

$$_nd_x^c = {}_nd_x \cdot \frac{{}_nM_x^c}{{}_nM_x} \tag{3.17}$$

where

$${}_nM_x^c = \frac{{}_nD_x^c}{{}_nP_x} \tag{3.18}$$

and c denotes the cause of interest. (In actuarial notation, a superscript is the equivalent of a subscript and does <u>not</u> imply that the item superscripted is raised to a power.)

The number of persons of age x who will eventually die of cause c is simply the forward accumulation of the deaths due to that cause, or

$$\ell_{x,c} = \sum_{i=x}^{w} n d_x^c. \qquad (3.19)$$

A multiple decrement life table generated by SPAHR is shown in Table 3.4. In its second column, we see the age-specific death rates for leukemia. The fourth column represents the component of the total l_x column ($l_{x,c}$) that is expected to die eventually of the cause in question.

The deaths in the $l_{x,c}$ column are distributed according to the cause-specific death rates, which are in turn directly proportional to the deaths in that age group in the original data. The total death rate for U.S. white females aged 60-64 is 0.01223 (from Table 3.3). From Table 3.4 we see that the death rate from leukemia for this group is 0.000104. The total number dying in this age interval of the life table is 5140. Hence the number dying of leukemia in this life table group is 5140 x (0.000104/0.001223) or 44. Repeating this calculation for every age group, and accumulating backward from the highest age group, we derive that, of our initial hypothetical cohort of 100,000 people, 671 will eventually die of leukemia.

Table 3.4

Multiple Decrement Extension of the Life Table

This table is a copy of the output generated by SPAHR in response to a MULDEC command. The M(X), l(X), and D(X) columns are copied from Table 3.3. The MC(X) column represents the age-specific death rate for the cause of interest (in this case leukemia) as defined in Equation 3.18. The lC(X) column represents the cause of interest, defined in Equation 3.19. The DC(X) column represents the numbers in the D(X) column who will die of the cause of interest, defined as in Equation 3.17.

MULTIPLE DECREMENT RESULTS

AGE(X)	M(X)	MC(X)	l(X)	lC(X)	D(X)	DC(X)
< 1	0.01615	0.000025	100000.	671.	1592.	2.
1- 4	0.00066	0.000035	98408.	668.	260.	14.
5- 9	0.00032	0.000034	98148.	655.	157.	17.
10-14	0.00028	0.000019	97991.	638.	137.	9.
15-19	0.00058	0.000019	97855.	629.	283.	9.
20-24	0.00066	0.000016	97572.	619.	320.	8.
25-29	0.00073	0.000014	97252.	612.	355.	7.
30-34	0.00097	0.000019	96897.	605.	470.	9.
35-39	0.00151	0.000026	96427.	596.	725.	12.
40-44	0.00232	0.000031	95702.	583.	1104.	15.
45-49	0.00374	0.000040	94598.	569.	1751.	19.
50-54	0.00560	0.000058	92847.	550.	2562.	27.
55-59	0.00831	0.000079	90285.	523.	3675.	35.
60-64	0.01223	0.000104	86611.	489.	5140.	44.
65-69	0.01925	0.000158	81471.	445.	7481.	61.
70-74	0.03135	0.000239	73990.	384.	10754.	82.
75-79	0.05351	0.000360	63236.	302.	14922.	100.
80-84	0.08871	0.000494	48314.	201.	17540.	98.
85+	0.15983	0.000539	30774.	104.	30774.	104.

A useful extension of the multiple decrement table is the Associated Single Decrement (ASD) Table. In addition to calculating the effects of several competing causes of death, it is also useful in calculating a life table with one of these causes eliminated. Table 3.5 shows an Associated Single Decrement Table. It bears a strong resemblance to the original life table (Table 3.3) with one difference. It represents the life table for all combined causes as it would appear if leukemia mortality were eliminated without affecting the death rates from all other causes. This condition is known as the assumption of independence between causes of death. This same assumption is used in Chapter 4 to include excess mortality from pollutants. In the present case, however, we will be examining increases in deaths.

Table 3.5

Associated Single Decrement (ASD) Life Table

This table is a copy of the output generated by SPAHR program in response to a MULDEC command. It is identical to an ordinary life table (see Table 3.3) except that it is calculated on the assumption that the mortality rate has been decreased to reflect the total elimination of leukemia. The M(X) column was calculated as the difference between the M(X) column in Table 3.3 and the MC(X) column in Table 3.4, and all other calculations proceeded as described in Chapter 3.1.

<MULDEC> UNITED STATES (WHITE) 1970

MULTIPLE-DECREMENT ANALYSIS FOR FEMALES, CAUSE= LEUKEMIA (1)
ASSOCIATED SINGLE-DECREMENT

FEMALE LIFE TABLE

AGE(X)	l(X)	D(X)	Q(X)	M(X)	L(X)	T(X)	E(X)	AGE
< 1	100000.	1589.	0.01589	0.01612	98570.	7574548.	75.745	< 1
1- 4	98411.	246.	0.00250	0.00063	393027.	7475979.	75.967	1- 4
5- 9	98164.	140.	0.00143	0.00029	490470.	7082953.	72.154	5- 9
10-14	98024.	127.	0.00130	0.00026	489801.	6592483.	67.254	10-14
15-19	97897.	273.	0.00279	0.00056	488799.	6102682.	62.338	15-19
20-24	97623.	313.	0.00320	0.00064	487334.	5613883.	57.506	20-24
25-29	97310.	349.	0.00358	0.00072	485681.	5126550.	52.682	25-29
30-34	96962.	461.	0.00475	0.00095	483657.	4640870.	47.863	30-34
35-39	96501.	713.	0.00739	0.00148	480722.	4157213.	43.079	35-39
40-44	95788.	1090.	0.01138	0.00229	476213.	3676491.	38.382	40-44
45-49	94697.	1734.	0.01831	0.00370	469151.	3200278.	33.795	45-49
50-54	92693.	2539.	0.02731	0.00554	458468.	2731127.	29.379	50-54
55-59	90424.	3646.	0.04032	0.00823	443006.	2272659.	25.133	55-59
60-64	86778.	5107.	0.05885	0.01213	421122.	1829654.	21.084	60-64
65-69	81671.	7441.	0.09111	0.01909	389752.	1408532.	17.246	65-69
70-74	74230.	10713.	0.14432	0.03111	344368.	1018781.	13.725	70-74
75-79	63517.	14899.	0.23457	0.05315	280338.	674413.	10.618	75-79
80-84	48618.	17570.	0.36139	0.08822	199165.	394075.	8.106	80-84
85+	31048.	31048.	1.00000	0.15929	194910.	194910.	6.278	85+

The condition of independence between causes of death is not a completely valid assumption. For example, pneumonia and other infectious diseases often appear in the preclinical stages of leukemia. Consequently, eliminating pneumonia as a cause of death through the introduction of some medical measure would increase the death rates from leukemia. However, eliminating pneumonia statistically through the ASD life table would have no effect on the death rates from leukemia. Thus the improvement in life expectancy that would result from eliminating pneumonia medically would be less than that shown by the statistical elimination in the ASD table. Conversely, the development of a means of medically preventing leukemia would result in an improvement in life expectancy greater than that noted in the ASD table because preleukemic pneumonia would also be eliminated. If medical science were instead to develop a complete cure for all diagnosed cases of leukemia, then the pneumonias that resulted from undiagnosed leukemias would continue to occur as before, and the ASD life table would be an accurate representation of the effect of eliminating leukemia deaths.

One further note concerning ASD life tables is that the change in life expectancy that results from the addition or deletion of a particular set of death rates varies depending on the level of mortality due to other causes. A similar caveat may apply to the interpretation of the multiple decrement life table. Its results are always contingent upon the intensity of the other causes of death that accompany the cause or causes of interest. Indeed, various causes of death may be said to compete. The likelihood that a person will succumb to a particular cause of death, therefore, is a function not only of the likelihood of dying of the cause of interest at each succeeding age, but also of the likelihood that, prior to attaining that age, he has not succumbed to some other competing cause.

3.3 Projecting the Distribution of Characteristics

The life table model and its accompanying extensions merely present the mortality patterns of a population by age and sex at one point in time. However, a health risk projection must model population changes over time. Because the dose response functions of many pollutants are age specific, and because age is the major determinant of mortality and fertility, a health risk projection should be based upon age. Projection of populations by age has a long history in demographic analysis. Most demographic textbooks describe the methods in detail; Keyfitz (1968), Keyfitz and Flieger (1971), and Shryock and Siegel (1975) are all recommended. The salient points will be described here.

3.3.1 Population Projections

Given the age distribution of the present population, it is often desirable to know what it will be n years hence. In the examples that follow, we will refer to Tables 3.6 through 3.8, which are population and mortality projections. The initial conditions are defined by the raw data in Table 3.1.

Table 3.6

Population projection produced in response to the PROJECT command in SPAHR. The first column (U. S. Whites, 1970) is taken directly from the data in Table 3.1. Succeeding columns are generated by the successive application of survival ratios as defined in Equation 3.21.

	POPULATION PROJECTED IN YEAR					
	1970	1975	1980	1985	1990	1995
AGE GROUP			FEMALE			
0- 4	7048807.	7635340.	8419004.	8769810.	8643023.	8451045.
5- 9	8264333.	7031573.	7616672.	8398420.	8748369.	8621891.
10-14	8647392.	8251963.	7021049.	7605272.	8385850.	8735275.
15-19	8079090.	8628885.	8234302.	7006023.	7588995.	8367903.
20-24	7341007.	8054163.	8602262.	8208896.	6984407.	7565580.
25-29	5962122.	7315558.	8026242.	8572441.	8180438.	6960194.
30-34	5042368.	5936794.	7284480.	7992145.	8536024.	8145686.
35-39	4936494.	5011213.	5900113.	7239472.	7942765.	8483283.
40-44	5412335.	4889506.	4963514.	5843953.	7170563.	7867162.
45-49	5587023.	5331132.	4816147.	4889045.	5756274.	7062981.
50-54	5169302.	5458468.	5208465.	4705330.	4776550.	5623825.
55-59	4695581.	4993261.	5272580.	5031091.	4545090.	4613884.
60-64	4157467.	4461611.	4744458.	5009859.	4780403.	4318618.
65-69	3491080.	3845292.	4126599.	4388208.	4633680.	4421453.
70-74	2874531.	3081582.	3394245.	3642555.	3873478.	4090157.
75-79	2114943.	2336680.	2504990.	2759151.	2961000.	3148715.
80-84	1314258.	1499474.	1656684.	1776014.	1956212.	2099321.
85+	889855.	1087423.	1276274.	1447007.	1590113.	1749618.
TOTAL	91027840.	94849776.	99067984.	103284592.	107053152.	110326448.
AGE GROUP			MALE			
0- 4	7374333.	7950465.	8766474.	9131760.	8999741.	8799834.
5- 9	8633093.	7350151.	7924393.	8737726.	9101815.	8970228.
10-14	9033725.	8612391.	7332526.	7905391.	8716773.	9079989.
15-19	8291270.	8989681.	8570401.	7296776.	7866848.	8674275.
20-24	6940820.	8219851.	8912246.	8496578.	7233923.	7799085.
25-29	5849792.	6877179.	8144482.	8830529.	8418672.	7167594.
30-34	4925069.	5798158.	6816477.	8072594.	8752585.	8344364.
35-39	4784375.	4870514.	5733932.	6740971.	7983174.	8655633.
40-44	5194497.	4703803.	4788491.	5637368.	6627448.	7848732.
45-49	5257619.	5053413.	4576047.	4658435.	5484256.	6447445.
50-54	4832555.	5029421.	4834078.	4377431.	4456243.	5246221.
55-59	4310921.	4500064.	4683385.	4501482.	4076253.	4149643.
60-64	3647243.	3858271.	4027553.	4191626.	4028823.	3648243.
65-69	2807974.	3087763.	3266419.	3409734.	3548638.	3410809.
70-74	2107552.	2202784.	2422272.	2562423.	2674850.	2783817.
75-79	1437628.	1478857.	1545681.	1699695.	1798038.	1876927.
80-84	805564.	855390.	879921.	919682.	1011320.	1069834.
85+	486957.	548806.	596224.	626773.	656627.	708213.
TOTAL	86720864.	89986832.	93820896.	97796848.	101435936.	104680736.
TOT.	177748704	184836608.	192888880.	201081440.	208489088.	215007184.

Table 3.7

Mortality Projection by Age

This table is produced in response to the PROJECT command in SPAHR. It is derived as indicated in Equations 3.27 through 3.30.

<PROJECT> UNITED STATES (WHITE) 1970

FEMALE	VITAL EVENTS DURING PROJECTION INTERVALS				
	1970-75	1975-80	1980-85	1985-90	1990-95
AGE GROUP	DEATHS BY AGE - SUMMARY				
0- 4	145052.4	159672.4	167236.2	165743.2	162194.9
5- 9	10055.8	9354.2	10205.0	11001.9	11220.6
10-14	11779.1	10645.2	10194.4	11145.8	11933.4
15-19	24164.1	24388.6	22041.3	21108.4	23077.8
20-24	25312.3	27385.7	27640.3	24980.4	23922.9
25-29	24283.2	28058.2	30356.8	30639.0	27690.5
30-34	26675.1	32122.7	37116.4	40156.8	40530.2
35-39	37525.7	41160.5	49566.2	57271.6	61963.8
40-44	59765.2	57161.4	62698.4	75502.7	87239.9
45-49	101998.7	94797.2	90666.7	99450.1	119758.6
50-54	148675.0	149222.5	138686.4	132644.7	145493.7
55-59	201268.4	213254.3	214040.1	198927.9	190261.7
60-64	263556.2	281505.4	298269.7	299369.1	278232.5
65-69	353047.2	383630.1	409756.6	434159.1	435758.9
70-74	466768.8	507498.1	551460.5	589016.7	624094.2
75-79	595497.4	647673.9	704187.4	765188.6	817301.1
80-84	737956.0	843226.7	933343.1	1026658.6	1117863.0
85+	711285.0	834812.2	946488.9	1040094.4	1144427.0
TOTAL	3944664.0	4345566.0	4703951.0	5023056.0	5322963.0

Table 3.8

Mortality Projections by Cause

This table is produced in response to the PROJECT command. It is derived from the deaths projected by age using the methods described for allocating deaths in multiple decrement life tables.

	1970-75	1975-80	1980-85	1985-90	1990-95
CAUSE GROUP	DEATHS BY CAUSE - SUMMARY				
LEUKEMIA	30683.0	33029.1	35245.2	37281.2	39133.1
LUNG	58405.0	62061.4	65050.9	67692.1	70516.2
STOMACH	29027.5	31787.8	34298.5	36580.3	38628.5
ALIMENRY	146130.9	159405.2	171196.9	181591.0	190782.4
PANCREAS	47662.6	51381.5	54585.4	57231.3	59398.3
BREAST	141754.3	150597.0	158382.1	165958.6	174210.7
BONE	3869.6	4120.5	4329.0	4536.3	4743.6
THYROID	3452.3	3769.8	4061.5	4315.3	4528.0
OTHER	260286.9	279539.8	296769.8	312564.8	327262.4
CANCER	721272.1	775692.5	823919.1	867750.9	909203.1

The probability that a person of exact age x will be alive exactly n years later is

$$1 - {}_nq_x = \frac{\ell_{x+n}}{\ell_x}. \tag{3.20}$$

However, in an actual population one generally knows only that there are ${}_nP_x$ people in a given age group distributed more or less randomly among all possible ages between x and x + n. Definition of the survival ratio,

$$n S_x = \frac{{}_nP_{x+n}^{t+n}}{{}_nP_x^t} \tag{3.21}$$

is necessary to project all living members of an actual population age group into the next older age group during one projection interval of n years. It is also necessary to estimate the number of those yet unborn. These considerations are discussed in the next two sections.

3.3.2. Decrements to the Population and the Stationary Assumption

If the 100,000 people who composed the initial cohort of the life table are instead an annual cohort of 100,000 births appearing at regular intervals over the course of a year, and if this condition has prevailed for at least a hundred years, then the resulting "stationary" population thus defined has several very useful properties. The number of births and deaths each year is constant, the crude birth and death rates are equal to the inverse of the expectation of life at birth, and, most importantly, the age distribution ${}_nP_x$ at any time is equal to the person-years lived in the age group ${}_nL_x$ in the life table. The survival ratio for a stationary population is therefore

$$n S_x = \frac{{}_nL_{x+n}}{{}_nL_x}. \tag{3.22}$$

If the age distribution within the n-year age group in the actual population does not differ greatly from that of the stationary population of the same age group (this assumption will be referred to henceforth as "piecewise stationary"), we may use the derived survival ratio to project any living population forward in time. The error introduced by this assumption is very small and may be ignored either if the long-term rate of growth of the population is relatively small, or if the age groups are narrow. The population of the United States now has a very low long-term growth rate, but even if fertility were to return to the levels of the postwar baby boom the error would not be great enough to cause concern.

An example of a SPAHR-generated population projection is given in Table 3.6. The initial population used is the 1970 U. S. population (from Table 3.1). One might wish to estimate the number of women in the 25-29 age group in 1975 given only that 7.341×10^6 women were in the 20-24 age group in 1970. Using the life table from Table 3.3, we calculate ${}_5S_{20}$ as 485,371/487,059 = 0.99653. Multiplying this by our 7.341×10^6 initial women gives 7315558, shown in the second column of Table 3.6.

The number of infants born during the projection interval who survive to be counted at the end of that projection interval as members of the population age < n is estimated by assuming piecewise stationary (i.e., we assume that within small age groups the age distribution does not matter) between the stationary population and that being projected. In the stationary population, the births in the previous n years number ${}_n\ell_0$, while the population in the first age group is ${}_nL_0$. The survival-from-birth ratio is therefore

$$ {}_nS_0 = \frac{{}_nL_0}{{}_n\ell_0}. \tag{3.23} $$

Using our life table from Table 3.3, we calculate this ratio for our example projection as

$${}_5S_0 = {}_5L_0/5\ell_0 = ({}_4L_1 + {}_1L_0)/5(100,000) = (98,567 + 392,983)/ 500,000$$

$$= 491,550/500,000 = 0.9831.$$

This value is applied to the number of female births calculated for the projection interval, 7.766×10^6 (we will show how these were computed in the next section), to generate our estimate of $0.9831(7.766 \times 10^6) = 7.635 \times 10^6$ for the number of girls age 0-4 in 1975.

The terminal age group w also requires special treatment. The people w-n years and older at the beginning of the projection interval will be w years and older at the end of the projection interval. Therefore, the appropriate projection procedure for the last two age groups is to merge the two groups and project their sum jointly into the final age group n years later, so that

$$ P_w^{t+n} = ({}_nP_{x-n}^t + P_w^t)S_w. \tag{3.24} $$

Once again the piecewise stationary assumption is made, and

$$ S_w = \frac{T_w}{T_{w-n}}. \tag{3.25} $$

For example, the population of women over age 85 in 1975 could be projected as $(1.314 \times 10^6 + 0.89 \times 10^6) \times (192,537/390,255) = 1.087 \times 10^6$.

3.3.3. Increments to the Population

Presently the SPAHR projection model ignores migration. Hence, the only way the projected population increases is through births. Births are estimated in the following way. The age-specific fertility rate is defined as

$$ {}_nf_x = \frac{{}_nB_x}{{}_nP_{x,f}} \tag{3.26} $$

where ${}_nB_x$ = the number of children born to women aged x to x+n, and ${}_nP_{x,f}$ = the person-years at risk lived by women in the same time interval.

The number of person-years at risk of giving birth in any projected age group is estimated as the length of the interval multiplied by the mean number of women in the age group at the beginning and end of the interval. Thus the number of births to women in each age group during the projection interval of length n is

$$ {}_nB_{x,t} = \frac{n}{2}\left({}_nP_x^t + {}_nP_x^{t+n}\right){}_nf_x. \tag{3.27} $$

The number of births to women in the 25-29 age group between 1970 and 1975, for example, can be computed as follows. Note from Table 3.6 that there will be 7.316×10^6 women 25-29 years old in 1975, and that there were 5.962×10^6 women in this age group in 1970. The age-specific fertility rate for female children is ${}_5f_{25} = 411{,}009/5{,}962{,}122 = 0.0689367$. Thus the number of female children born to women in this age group over the five-year interval is $2.5 \times (5.962 \times 10^6 + 7.316 \times 10^6) \times 0.06894 = 2241.9 \times 10^3$. Repeating this procedure for each age group gives the 7766.4×10^3 total female births in the interval. Of these babies, however, a few will die before they can be counted in the 0-5 age group in 1970. By applying the survival-from-birth ratio, it becomes clear that 2241.9×10^3 (0.9831) = 2204.0×10^3 of these children will survive to be counted as part of the 0-5 age group in 1975.

3.3.4 Allocation of Deaths by Age and Cause

Because our interest in the structure of the projected population is primarily in its impact on mortality and other health measures, it is desirable to project mortality by age and cause as well. Published analyses in the literature concerning population projections (including the more general category of Markov processes with absorbing states) stop at this point. We know that a certain number of people expired during the transition from one age group to the next, but not in which of the age groups their deaths occurred. Unfortunately, the data with which we will wish to compare the results of our projections are usually presented as events occurring within age groups rather than between them. This is an especially important consideration when we are estimating distributions of deaths by cause.

We might assume that about half of the deaths during the projection interval occur in each age group. However, in most age groups the risk of death increases with age, and thus there will be a bias in favor of dying in the later age group. Returning to the piecewise stationary assumption, we recall that the distribution of population within an age group is assumed to be proportional to that in the life table. It follows then, that the deaths should likewise be proportional to those in the life table. Let us define ${}_nZ_x$ as the proportion of those starting out in age group x to x+n who die in the following age group. Then

$$ {}_nZ_x = \frac{{}_nd_{x+n}}{{}_nd_x + {}_nd_{x+n}}. \tag{3.28} $$

Of our initial cohort ${}_nP_x$,

$$ D = {}_nP_x(1 - {}_nS_x) $$

will die during the projection interval. Of these,

$$ D_1 = D(1 - {}_nZ_x) \tag{3.29} $$

will die while still in the x to x+n age group, while

$$ D_2 = D({}_nZ_x) \tag{3.30} $$

will die in the age group that follows.

To estimate the number of female deaths occurring within the age group 70-74 during the 1970-75 projection interval, we return to our sample projection in Table 3.6. Of the 3.491×10^6 females in the 65-69 age group in 1970, 3.082×10^6 lived for five years and 409×10^3 died. Of the 2.875×10^6 in the 70-74 age group in 1970, 2337×10^6 survived until 1975 and 538×10^3 died. Going back to our life table (Table 3.3), we calculate ${}_5Z_{65}$ as 10,754/(7,481 + 10,754) = 0.5897. We then compute ${}_5Z_{70}$ as 14,922/(10,754 + 14,922) = 0.58117. The number dying in the 70-74 age group during the projection interval is then the sum of the 409×10^3 (0.5897) = 241.2×10^3 deceased members of the original 65-69 age group who died after age 70 and the $538 \times 10^3(1 - 0.58117)$ = 225.3×10^3 members of the initial 70-74 age group who died before age 75, for a total of 466.5×10^3. This number is shown as 466768.8 in Table 3.7. The difference can be traced to few digits of precision. Table 3.8 provides the total number of deaths by cause for five-year intervals from 1970 to 1990.

The ${}_nZ_x$ calculations outlined above depend strongly upon the assumption that deaths in the life table are uniformly distributed within each age interval. This is, of course, an oversimplification. However, it is adequate for all age groups except the first.

In the first n years of life, when the death rate is changing very rapidly, a different formula is employed to allocate deaths. Because all entries into this group arrive via birth rather than transition through a previous age group, the difference between the number of births computed and the size of the 0-n age group at the end of the interval is assigned to deaths in the 0-n age group. By applying a chain of reasoning similar to that used to derive Equations 3.28-3.30 to the life table in the first n years, we conclude that in the special case of n = 5,

$$ {}_5z_0 = \frac{0.2_1d_0 + 1.2_4d_1}{{}_5d_5 + 1.2d_1 + 0.2_1d_0}. \qquad (3.31) $$

When the deaths are distributed by age, they can easily be distributed by cause. The proportional distribution of deaths by cause within an age group is assumed to remain constant. This is not strictly true, of course, but it works well for small age groups such as those used here under the piecewise stationary assumption. Deaths by cause for the age group are therefore derived from the estimated total deaths for the age group by multiplying the ratio of the age-specific deaths for each cause by the number of age-specific deaths for all causes, much as we did in calculating multiple decrement life tables.

The results of such calculations may be printed out for each projection interval. Consider, for example, deaths from leukemia among females in the 70-74 age group. Our previous example showed that a total of 0.4668×10^6 women in this age group died during the first projection interval. The female age-specific death rate in that age group from leukemia (calculated from the data in Table 3.2) is 687/2,874,531 = 0.000239, while Table 3.3 reveals that the overall death rate in this age group is 0.03135. Consequently, we estimate the number of leukemia deaths in the age group as $(466.8 \times 10^3)(0.000239)/0.03135 = 3500$. We note that the sum of all such calculations is 30683 deaths, given in Table 3.8.

3.4 Error Bounds on the Projection

Earlier it was mentioned that some uncertainty is associated with health risk projections. This uncertainty is associated with the projection model itself. It is often desirable to specify the upper and lower limits of the results of a projection in addition to the expected values, especially if the interpretation of the projection is critically dependent on a relatively small number of events. Such a situation might arise, for example, if one were attempting to replicate a long-term epidemiological study.

Binomial or Poisson approximations of the error components for relatively rare events may be used whenever the initial conditions are known. Thus, for a single exposure situation, the numbers of radiogenic cancers that will occur in the population may be treated as a Poisson variate. However, when a long-term exposure situation is to be analyzed, random factors act multiplicatively, and the conditions that justify a Poisson assumption no longer hold. Indeed, an

analytic solution to the variance of a population projection is very complex, if not impossible, for most cases. Consequently, a Monte Carlo approach is taken in the SPAHR model for estimating variances in the long term.

3.4.1 Use of the Monte Carlo Simulation to Bound the Projection

The projected population can vary in the following ways:

1. The number of survivors from any given starting number is randomly distributed. As a consequence, the number of parents available in any projection interval is random.

2. The number of births per parent is a random variable.

3. The distribution of exact ages at death within each projection interval is random.

4. The distribution of deaths by cause within each exact age interval is random.

In a classical Monte Carlo scheme, the events that will happen to each individual are computed by using a random number generator. Consequently, each individual must be polled, calculated for, and acted upon at least once in his or her lifetime, and (especially when conditions can vary over time) often must be addressed during each time step. The POPSIM and SOCSIM family of programs (Hammel el al., 1976) that have been developed in North Carolina and Berkeley respectively, make extensive use of such procedures. However, the requirements for large data arrays and/or frequent treatment of individuals render this approach prohibitively costly when the populations become large. These two program systems generally are used for populations of less than 1,000. The SPAHR model, on the other hand, can be used for populations that range into the hundreds of millions.

In SPAHR, the random perturbations are handled by treating all of the components of the projection process as binomial random events and by selecting the outcome that has the same probability as a generated uniform random number. This is generally known as the inverse method. The binomial distribution assumes that in n independent trials, there is probability q of a "success" and 1-q of a failure. The probability of i successes is distributed as

$$P(i) = \binom{n}{i}(1-q)^{n-i}\, q^{i}. \qquad (3.32)$$

A single binomial random partitioning model is used in all of the randomized calculations. The expected value E is calculated based on the probability of the event q and the number of trials N as

$$E = qN. \qquad (3.33)$$

Then, if N is greater than 36, the normal approximation to the binomial distribution is invoked, and the perturbed value E* is computed as

$$E^* = E + Nq(1-q)\ R \tag{3.34}$$

where

R is a random unit normal deviate, defined as a random number from a normal (or Gaussian) distribution with an expected value = 0 and variance = 1,

and

Nq(1-q) is the binomial variance.

If, on the other hand, E is less than 36, the normal approximation deteriorates, because the binomial distribution becomes asymmetrical, and the risk that Equation 3.34 will yield a number outside the range of possible values becomes large enough to merit concern. When E is less than 36, we generate a uniform random number and choose that E* whose cumulative probability is closest to the random number, using the binomial recursion formula. We select the largest number, E*, of events (deaths, births, males among total births, etc.) such that

$$p\ (k \leq E^*) \leq R_u$$

where R_u is a uniform random deviate, $0 < R < 1$ (this means that all random numbers within the indicated range are equally likely to occur), and

$$P\ (K \leq E^*) = \sum_{i=0}^{k} \binom{N}{i} (1-q)^{N-i} q^i. \tag{3.35}$$

To minimize the number of iterations, the partitioning is performed on either q or 1-q, whichever is less.

The sequence of events in the randomized projection follows the deterministic projection very closely. Indeed, the random partitioning algorithm begins in most cases with the deterministically calculated values for E. First, random survival is calculated. From this comes the randomized mortality. Then the deaths in each age group are calculated by randomly partitioning the deaths in the projection interval. After the random living population at the end of the interval has been computed, the person-years in each age group at risk of giving birth are computed as the length of the projection interval multiplied by the mean of the initial and projected populations in each age group. Then the number of births in the interval is calculated by randomly partitioning the number of person-years at risk of giving birth into birth years and nonbirth years based on the annual age-specific birth rates for the age group. Surviving newborns (distributed randomly) are added to the living population in the first age group.

3.4.2 Justification for the Binomial Assumption

Mortality is a simple binary phenomenon. During any time interval, a person will either live or die. If death is the event, the death will only fit into one category. If we further assume that the time step is small enough that the risk of the event is approximately uniform throughout the interval, then the binomial assumption is justified. The probability of death rises exponentially with age; however, in a 5-year interval the death rate typically changes by only about one third.

Births, on the other hand, are a far more complex phenomenon. The gestation period for humans is only about 3/4 of a year, rather than a full year. Consequently, it is possible for a woman who gives birth at the beginning of a year to do so again before the year has ended. In addition, a small proportion of pregnancies can result in multiple births. Furthermore, since births are subject to voluntary control, the risk of birth for any woman is in part a function of the number of children already born. Marital status provides another major source of heterogeneity, especially at younger ages.

We note, however, that the incidence of multiple births is negligibly small, approximately 1% of all births. In addition, for a number of reasons, the risk of pregnancy in the first few months following a birth is greatly reduced. Therefore, the likelihood of two separate live births in a single year is negligible, and the person-year is, in fact, a reasonable binary unit to use for the random projection of discrete births.

The last potential cause for concern is heterogeneity by birth order. Within any age group, the women may be classified according to the number of children already born (parity). The degree to which heterogeneity in parity will affect the variance used in the random partitioning procedure will depend on the degree to which the probability of giving birth varies with parity. This probability can be shown to be a function of the square of the deviation of the risk of giving birth for each individual parity group. For a population of N persons in k states (where state denotes parity group), the probability of a "success" (where "success" denotes a birth), p, is state dependent. Thus, the number of "successes," S, is

$$S = \sum_{i=1}^{k} N_i p_i \tag{3.36}$$

and the variance of the number of "successes," V(S), is

$$V(S) = \sum_{i=1}^{k} N_i p_i \left(1-p_i\right). \tag{3.37}$$

In SPAHR, we assume a homogeneous population, with probability $\hat{P}_t$ of "success" at a point in time t defined as

$$\hat{P}_t = \frac{\Sigma N_i P_i}{\Sigma N_i} \tag{3.38}$$

and

$$\hat{V}(S) = (\Sigma N_i)\, \hat{P}_t(1-\hat{P}_t). \tag{3.39}$$

The validity of the assumption depends on $V(S) - \hat{V}(S)$.

The various p_i can be expressed in terms of P_t as

$$p_i = P_t + \delta_i \tag{3.40}$$

so that

$$\begin{aligned} V(S) &= \Sigma N_i\, (P_t + \delta_i)(1 - P_t - \delta_i) \\ &= \Sigma N_i P_t(1 - P_t - \delta_i^2 + S_i - 2P_t\delta_i) \\ &= (\Sigma N_i)P_t(1 - P_t) - \Sigma\delta_i^2 \\ &= \hat{V}(S) - \Sigma\delta_i^2. \end{aligned} \tag{3.41}$$

The true variance will always be less than the assumed variance by $\Sigma\delta_i^2$. Because this is a sum of squares of numbers that are in most cases considerably less than one, only a very slight upward bias in the variance is expected. The magnitude of this bias for the United States was calculated explicitly for confirmation. Inspection of Table 3.9 shows that in the United States, this component of variation is relatively small in comparison with the variation attributable to age. Most of the large deviations take place in numerically unimportant parity groups. Table 3.9 also shows a comparison of the standard deviations for births calculated by using the assumption of homogeneity for an age group containing 1000 women (column 4) with standard deviations calculated from the sums of the variances for each parity group individually (column 3). The differences are sufficiently small to justify neglecting them.

Table 3.9. Effect of Heterogeneity in Fertility Rates by Birth Order on the Estimates Variance in 1000 Person-years of Risk of Birth

Mother's Age Group	Expected Number of Births	Hetero-geneous	Homo-geneous	Differ-ence		Birth Order							
						0	1	2	3	4	5	6	7+
15-19	66	7.75182	7.85479	0.10297	% in group	0.934	0.056	0.009					
					birth rate	0.057	0.229	0.000					
20-24	163	11.61596	11.68227	0.06631	% in group	0.563	0.256	0.129	0.038	0.011	0.003		
					birth rate	0.133	0.222	0.168	0.192	0.217	0.000		
25-29	139	10.90117	10.95284	0.05167	% in group	0.230	0.224	0.284	0.156	0.066	0.025	0.010	0.006
					birth rate	0.129	0.198	0.120	0.113	0.126	0.146	0.170	0.000
30-34	72	8.17827	8.19595	0.01768	% in group	0.101	0.130	0.260	0.234	0.140	0.070	0.034	0.031
					birth rate	0.070	0.100	0.065	0.059	0.064	0.079	0.090	0.132
35-39	32	5.54269	5.56249	0.01980	% in group	0.084	0.101	0.225	0.228	0.160	0.090	0.050	0.062
					birth rate	0.024	0.034	0.023	0.024	0.030	0.038	0.050	0.083
40-44	8	2.84647	2.85593	0.00947	% in group	0.105	0.113	0.228	0.211	0.143	0.082	0.047	0.070
					birth rate	0.004	0.005	0.004	0.006	0.008	0.011	0.015	0.033

4.0 DOSE AND RESPONSE

The projection model outlined in the Chapter 3 becomes a health risk projection model when a dose response function is incorporated into the calculations. The demographic model incorporates age-specific dose response data together with the projection technique to produce a realistic simulation of population exposure. The form of the model in matrix notation is

$$P_{t+1} = \left[L \sum_{i=1}^{n} D_t^i \right] P_t \qquad (4.1)$$

where P_t and P_{t+1} are the age- and sex-structured populations at times t and t+1, L is the Leslie matrix incorporating fertility and baseline mortality, and the D_t^i values are square matrices with negative elements on the subdiagonal that deflate the age-specific survivorship of the population at risk. The D_t^i matrix represents sex- and disease-specific dose response functions that change over time depending on the level of the dose, the latency period of the particular disease, and the duration of exposure.

The dose response function defines a relationship between the level of exposure to a hazardous agent and the excess mortality risk observed as a result. Most simply,

$$\Delta\mu = B\Delta p, \qquad (4.2)$$

where μ = risk of death, B = proportionality factor, and p = exposure index. However, few, if any, hazardous agents have a strictly linear function as indicated above. Since the risk of death, or indeed of any other outcome, is a probability and cannot exceed unity or decline to less than zero, the linear assumption is automatically constrained as an approximation over a relatively narrow range. Furthermore, different agents have different modes of action; if a nonlinear form is found suitable for one agent, it will not necessarily be appropriate for others.

The hazardous agents of interest in the context of energy analysis fall into five major categories: air pollution, radiation, accidental injury, chemical toxicity, and chemical carcinogans. The first two of these are most commonly treated in studies of the impacts on the general public, while the remaining three are generally considered as aspects of occupationally related impacts. As such, their analysis is usually conducted in a fashion that is not strictly age related. Only the first two are currently treated in the demographic model.

4.1. Air Pollution

Air pollution is generally of concern in the analysis of the public health impacts of fossil fuel systems. The effluents of interest are the direct products or secondary by-products of combustion, consisting of a complex aggregate of particulates of varying composition, SO_2, NO_x, and polycyclic hydrocarbons. Most studies of air pollution and health can be divided into two groups: (1) those that have ignored the time-related aspects of the damage function, assuming that the dose has remained reasonably stable over time and thus that the damage has reached an equilibrium state, and (2) those that have focused on the short-term impacts of daily or weekly variations in the pollution level. Age and other structural features of the populations at risk are usually treated inadequately, at least with regard to applicability of results to age-structured populations.

Winkelstein's study of Buffalo, NY (Winkelstein et al., 1968), for example, treated only two very broad age groups (45-69 and 70+). Based on a static analysis of mortality and air pollutants in 1960, it provides a data point at older ages, but not enough information to fit a fully age-structured line. The studies of Lave and Seskin (1977) covered a much broader age range, but only five age groups: infants, 4-15, 15-45, 45-65, and 65+. For individual causes of death, the studies were limited to age-adjusted death rates, which are generally of little use in an age-structured model. Epidemiological studies such as these, based on case-control designs in which individual cases are matched by age, race, and sex with a selected control group, are reasonably good methods for identifying a risk factor. Unless age-specific results are reported, however, these studies are not useful in fitting an age-structured model. The same is true if the study is "self-controlled," i.e. the same population is observed at different exposure levels on different days or at different times of the day. Variation in age is considered to be adequately controlled for in these cases and hence is omitted from the analysis. A discussion of the reasoning involved is given in Lave and Seskin's book.

Static analysis, in which mortality rates are compared in populations exposed at the same time to varying pollution levels, is far more likely to take explicit account of such components of variation as age, race, and socioeconomic status. However, this is often done in a way that prevents its use in fitting an age-structured dose response model. For example, studies on grade school children (as Hammer's Nashville study cited in [NAS 1978]) have solved the problem of age variation quite effectively. However, the effect of age is not easily recovered. One can in this case extrapolate to other age groups only with the use of additional assumptions. Other studies use age-standardized data and show the potential for being useful. However, as in the case of a limited age range study, the age-standardized data alone cannot be used to fit an age-specific model without making some additional assumptions.

Most studies, unfortunately, fall into one of the groups described above. Only rarely do full-scale, age-specific studies of interesting environmental

hazards appear. Examples are the studies of Lave and Seskin (1977) and Mendelsohn and Orcutt (1979). The Lave and Seskin study dealt mostly with infant mortality or with total age-adjusted mortality. However, in two tables, the age groups infant, 4-15, 15-44, 45-64, and 65+ were identified. The Mendelsohn-Orcutt study used more age groups. Both of these studies, however, relied almost totally on least-squares multiple linear regressions, which led to some anomalous results: at some ages, some air pollutants seemed to actually improve health. This apparent result was justifiably dismissed by the authors as indicative of the unimportance of the effect in that age group (the phenomenon usually occurred in the age groups including adolescence through the early 30's, where one would expect to see relatively little effect). However, the anomaly does highlight the importance of having a reasonable theoretical model of the effect being studied. The practices of treating the death rates in each age group as if they were unrelated to the death rates in adjacent groups, and of combining age groups across which there are order-of-magnitude increases in mortality rates with no attention to age adjustment within the groups, are likely to produce artifactual results.

Another source of air pollution, the cigarette, has been investigated at some length. Of course, cigarette smoke and smoke from fossil fuel sources differ in composition, most notably in the much greater concentration of CO and polycyclic hydrocarbons in cigarette smoke. In addition, ordinary air pollution is breathed at a relatively even level over protracted periods of time, while exposures to cigarette smoke are generally short, pulsed periods of very high exposure alternating with periods of relatively mild exposure. Finally, air pollution studies have suggested a threshold for air pollution damage, while data on cigarette smoke, which generated a curve that resembles a decreasing power function, have suggested quite the opposite.

Nevertheless, cigarette smoke is used as an archetype for constructing an air pollution dose response curve with the following justification: No single overriding component in either cigarette smoke or air pollution makes it harmful. The damage done by both results from the toxic and irritant properties of the combination of components. Variation in the relative concentration of the various components probably affects only the relative toxicity of a given total quantity. As will be shown later, the conversion of air pollution into cigarette-equivalent doses is done in a way that does not depend on the composition of the air pollutants, but rather on the observable toxic properties of the air pollution being analyzed.

Of some concern is the apparent nonlinearity of the dose response function for cigarette smoke in the Hammond data (1966) used for fitting the cigarette smoke model. Hammond indicates, however, that the higher slope for lower dose rates is probably an artifact introduced by the manner in which the data were collected. He feels that a linear assumption is probably justified. If there is a threshold dose for cigarette smoke, it cannot be observed in any of the studies we have seen.

Threshold dose levels for air pollution data have generally been derived from dynamic analyses of short-term effects rather than from static analyses of long-term effects. The quality of the data and the nature of the models fitted have precluded, in our view, the detection of any threshold effects that may be present. The conservative analysis, therefore, would assume no threshold effect for long-term damage resulting from air pollution.

Table 4.1 gives the basic data from the Hammond cigarette study (1966), rearranged to show the mean effects for each age group. It should be noted that if Hammond's view of the reporting bias is correct, the mean number of cigarettes smoked per day will be an underestimate, so that the effect per cigarette per day will be somewhat overstated. The magnitude of the error is not large--the very light smokers are a small minority in the reported data, and would be an even smaller minority in Hammond's conjecture.

Table 4.1. Effects of Cigarette Smoking on Mortality from All Causes by Age

Age Group	Death Rate/100,000 person-years[a]				Mean Cigarettes/day,[b] All Smokers		Increase in Death Rate/100,000/ Cigarette/day	
	Nonsmokers		Smokers					
	Female	Male	Female	Male	Female	Male	Female	Male
35-39	136	173	143	285	20.6	28.5	0.34	3.9
40-44	178	230	206	435	20.3	28.8	1.3	7.1
45-49	254	271	310	645	20.0	28.9	3.1	14.6
50-54	352	541	479	1,089	19.5	28.6	6.0	19.2
55-59	561	859	730	1,768	18.7	27.3	9.0	33.3
60-64	1,492	1,638	1,082	2,811	17.6	26.4	12.2	46.1
65-69	1,492	2,493	1,965	4,185	16.4	23.4	28.8	72.3
70-74	2,585	4,202	3,348	6,189	14.9	21.0	51.1	94.6
75-79	4,790	5,542	5,073	9,063	14.2	18.0	19.9	139.2
80-84	8,404	11,230	10,473	14,504	12.0	17.4	172.4	188.2

From Lundy and Grahn (1977).
[a]Data from Hammond, 1966, Appendix Tables 2.a and 2.b, pp. 176-178.
[b]Calculated as means of midpoints weighted by person-years from data in Hammond, 1966, Appendix Tables 3.a and 3.b.

The data upon which the cigarette smoke dose response function for total mortality is based are displayed in the last two columns of Table 4.1. Keeping in mind that the average male smoker in the Hammond study started smoking at about age 15, and that the average female smoker started at about age 20, it appears that the increase in the death rate rises exponentially with age. The ill effects associated with smoking tend to be latent effects; a long time elapses between the initiation of damage and the time when it becomes apparent.

In the absolute risk formulation, a reasonable representation of the effect of cigarette smoke on the risk of death is given by

$$\Delta\mu(x) = \frac{pgae^{bx}}{1 + c\ e^{-d(x-x_0)'}} \qquad (4.3)$$

where x = current age, x_0 = age at onset of exposure, p = exposure level of the pollutant of interest in micrograms per cubic meter, g = multiplier specific to the index pollutant and source study that converts the effluent exposure level into an equivalent value for cigarettes per day, and a, b, c, and d are fitted constants determining the rate at which risk increases with age and the duration of the period of latency.

In the relative risk formulation of the air pollution model, the most reasonable function appears to be

$$\Delta\mu(x) = \frac{pga\mu'(x)^b}{1 + ce^{-d(x-x_0)'}} \qquad (4.4)$$

where $\mu'(x)$ is the mortality rate at age x in the absence of the air pollution dose.

The a, b, c, and d coefficients were initially fitted to the cigarette smoke data in Table 4.1 using an ad hoc procedure (log-linear regression on the region that appears log-linear to get a and b, and then visual selection for c and d). Nonlinear regression was later employed using these ad hoc coefficients as initial values, and the results converged to very similar values. The ad hoc values are given in Table 4.2.

Table 4.2. Fitted Coefficients of Equations 4.3 and 4.4 Using Data of Table 4.1

Coefficient	Females	Males
a	6.24×10^{-7}	9.14×10^{-6}
b	8.84×10^{-2}	6.44×10^{-2}
c	100.0	100.0
d	0.2	0.2
x_0	20	15

From Lundy and Grahn (1977).

The values of g, the conversion coefficients found in Table 4.3, were derived by estimating the cigarette dose necessary to emulate the effects of a 1 $\mu g/m^3$ dose based on the cited study in a population having a defined age distribution (Northeastern U. S. whites in 1960 for the Winkelstein studies, total U. S. whites in 1965 for Lave and Seskin).

Table 4.3. Conversion Coefficients Used to Convert Various Index Air Pollutants to Cigarette-per-day Equivalent Values

Source Study	Index Pollutants(s)	g
Morris and Novak (1976)	Suspended sulfates (SO_4)	0.21
Winkelstein et al. (1968)	Total suspended particulates (TSP)	0.35
Lave and Seskin (1977)	Sulfur dioxide (SO_2) and TSP[a]	0.09
Carnow and Meier (1973)	Benzo[a]pyrene (BAP)	1052.3

From Lundy and Grahn (1977).
[a] SO_2 and TSP = 0.715 x SO_2 + 0.815 x TSP

4.2 Radiation

Two sets of radiation models have been widely used. These models are taken from the Biological Effects of Ionizing Radiation (BEIR) Committee Reports of 1972 (NAS, 1972) and 1980 (NAS, 1980). Because the BEIR 1980 report extends the BEIR 1972 conclusions and is based on more information, the models of the BEIR 1980 report may be more appropriate for estimating risk. However, the BEIR 1972 models have been used widely in the literature, and both models have been incorporated into SPAHR.

4.2.1 BEIR 1972

The Mortality Adjustment Models indexed to radiation doses and adopted from BEIR 1972 are derived from two sources, the BEIR report (NAS, 1972) and the Reactor Safety Study, (WASH-1400), sometimes referred to as the Rasmussen report (USNRC, 1975). The coefficients for lung cancer are based on more recent data provided by the Environmental Protection Agency (Gotchy, personal communication).

The principal adverse effect of ionizing radiation on human health is the induction of cancer. The mechanisms of radiation carcinogenesis are still subject to dispute, but a few generalizations seem reasonable: different organ systems have different susceptibilities to damage, and damage is to a large extent a function of the total dose accumulated during the exposure period. A malignant neoplasm, whether induced by radiation or some other factor, rarely appears as an immediate response to the carcinogen. Usually several years elapse between the time of exposure and the time the tumor becomes apparent.

Beyond these generalizations, a great number of models have been advanced to explain or predict the carcinogenic response of various organ systems to radiation. The two used here are both developed in the BEIR report and are called the absolute risk and relative risk models. Both models are based on simple association with no reference to possible causal mechanisms. Both models assume an initial latency period following the exposure during which no effect is observable. This interval is assumed constant with respect to dose but variable with respect to age at exposure. This is followed by the so-called plateau period during which the excess risk of death is elevated by a constant factor. Following the plateau period, the increase in risk returns to zero.

The main conceptual difference between the two models is that in the case of the absolute risk model, the degree of the response is assumed independent of the spontaneous rate of occurrence of the tumor, while in the relative risk model, interdependence is assumed. In the absolute risk formulation, the increase in risk of death from each of the tumor types is a linear function of the dose accumulated during the interval defined by the latency and plateau periods. The change in risk as a function of exposure is given by

$$\Delta\mu(x) = \sum_{i=x_0}^{x} r(i)h(i-x_0)B(i,x) \qquad (4.5)$$

where $\mu(x)$ = risk of death from the neoplasm of interest (in deaths per person-year); x_0 = age at onset of exposure; $r(i)$ = level of exposure to radiation at age i (in rem); h = latency multiplier for duration $(i-x_0)$ because exposure = 1 if $(i-x_0)$ is greater than the period of latency but less than the sum of the latency and plateau periods, and exposure = 0 otherwise; $B(i,x)$ = response coefficient relating the absolute increase in $\mu(x)$ with the exposure at age i (in deaths per person-year per rem).

In the relative risk model, the proportional increase in risk of death over the spontaneous rate, $\Delta\mu(x)$, varies linearly with respect to dose, so that

$$\Delta\mu(x) = \mu'(x) \sum_{i=x_0}^{x} r(i)h(i-x_0)C(i,x) \qquad (4.6)$$

where $\mu'(x)$ = spontaneous risk of death from the neoplasm of interest (in deaths per person-year), and $C(i,x)$ = response coefficient relating the proportional increase in $\mu(x)$ to exposure accumulated at age i.

4.2.1.1 Sources of Coefficients and Constants

In the BEIR 1972 report and WASH-1400 (USNRC, 1975), two alternative assumptions are made concerning the duration of the period of elevated risk. In the first assumption (generally labelled "a" in the BEIR 1972 report), the plateau period is assumed to last 30 years for cancers other than leukemia. The conservative ("b") assumption for all tumors except for leukemia is that the plateau period exceeds the human life-span. In the case of leukemia this period is assumed to last from 10 to 25 years under both assumptions. Both options are available in SPAHR under the control of the LPLAT (Long PLATeau) switch parameter of the ADJUST subcommand of PROJECT.

The duration of the period of latency following each increment of exposure is retained at the values given in WASH-1400 for both the relative and absolute risk models. WASH-1400 gives absolute risk coefficients for eight tumor types and for a residual group. These coefficients with the exception of those for breast cancer were carried over unchanged in the absolute risk model used here. We have considered breast cancer as sex-specific by reversing the logic of the BEIR 1972 report. The given coefficient was doubled and made specific to females. For males, the spontaneous death rate for breast cancer is about one hundredth of the rate for females, so the absolute risk coefficient for males was set at one hundredth of the female value.

WASH-1400 does not give relative risk estimates. The BEIR 1972 report gives both absolute and relative risk coefficients, but the latter are confined to leukemia and "all other tumors." Furthermore, no attempt was made in

the BEIR report to force consistency between two models. Hence the BEIR relative risk model predicts a greater number of excess deaths at any dose level than does the absolute risk model.

The relative risk coefficients for leukemia resulting from exposure at all ages, and for all other tumors resulting from exposure below the age of 10 years, were used directly from the BEIR 1972 report. However, the coefficients for in utero exposure were multiplied by 0.6 to reflect the later modifications that were incorporated in WASH-1400.

The coefficients for nonleukemic tumors resulting from exposure above age 10 for the present relative risk model were determined from the BEIR 1972 relative risk model and the WASH-1400 absolute risk model by first calculating excess deaths using the absolute risk model. Then relative risk coefficients were calculated from excess deaths and the spontaneous death rates in the U.S. vital statistics of 1970 by a procedure based on secant iteration: An arbitrary value is selected to initiate the procedure, and a hypothetical number of deaths for the tumor of interest is computed following the procedure summarized in Table 3.3 of the BEIR 1972 report. (Such a table can be calculated using the PROJECT and DATA commands in SPAHR.) The number of deaths thus generated is compared with the criterion number estimated from the absolute risk model. The coefficient is then divided by the ratio of the derived to desired number of deaths, and the cycle is repeated until convergence is obtained.

Finally, the relative risk coefficients were increased by the proportion by which the total cancers exclusive of leukemia (BEIR 1972 relative risk model) exceeded those predicted in the BEIR absolute risk model. That is, if

$N_{i,a}$ = number of excess cancer deaths of type i in the absolute risk model (BEIR 1972),

$N_{T,a}$ = number of total nonleukemic excess cancer deaths predicted in the absolute risk model (BEIR 1972),

$N_{i,r}$ = number of cancer deaths of type i generated in the relative risk model (BEIR 1972),

$N_{T,r}$ = number of total nonleukemic excess cancer deaths predicted in the relative risk model (BEIR 1972), and

C_i = relative risk coefficient for tumor type i,

then

$$C_i = C_i^* \frac{N_{i,a}}{N_{i,r}} \cdot \frac{N_{T,r}}{N_{T,a}} \qquad (4.7)$$

where C_i^* is the trial value of C_i that generated $N_{i,r}$.

4.2.1.2 Implementation in the SPAHR System

The absolute and relative risk models described above are constructed on the assumption that age and time are continuously variable. In the context of a projection system such as this, however, both age and time are divided into discrete intervals. Therefore, some assumptions must be made regarding the relationship between continuous time and discrete time in projection intervals. As is the case for variable baseline mortality, we assume that the mortality rate calculated for each age group at the midpoint of the projection interval represents the mortality rate for that age group throughout the interval. Thus for a 25-year projection in 5-year intervals, the model would be evaluated a total of five times, assuming exposure durations (or, at any rate, durations since initial exposure) of 2.5, 7.5, 12.5, 17.5, and 22.5 years.

Discrete age groups are treated as in the BEIR 1972 report by assuming that when only a fraction of the age interval is subject to a particular increased risk, the risk is diluted evenly over the entire interval; i.e., the increment in the death rate Δm_i for each age i in the interval (x, x+n) becomes an increment to the total age-specific death rate $\Delta_n m_x$ by

$$\Delta_n m_x = \frac{\Delta m_i}{n}.$$

For example, if in the 35- through 39-year age group, the mortality rates of persons aged 35 and 36 were raised by 2%, while the rates for persons aged 37, 38, and 39 were not changed at all, the rate for the entire age group would be raised by 2% x 2/5 = 0.08%.

4.2.2 BEIR 1980

This synopsis presents the step-by-step procedures that have been used for quantifying the Biological Effects of Ionizing Radiation (BEIR) 1980 Committee Report for use in the Simulation Package for Assessing Health Risks (SPAHR). The procedures outlined below have been suggested by staff of both the Nuclear Regulatory Commission and the National Cancer Institute.* Three principles were used in developing these coefficients. First, we attempted to utilize as much information as possible from the report of the BEIR committee. Secondly, we wanted the SPAHR results to agree with the committee's results for whole body exposure even at the sacrifice of logical consistency in the site-, sex-, and age-specific risk coefficients. Finally, priority was given to matching mortality results with the BEIR committee report. Morbidity was estimated independently using the morbidity models in SPAHR.

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*We would especially like to thank Drs. Branagan, Gotchy, and Willis at the Nuclear Regulatory Commission and Dr. Land at the National Cancer Institute for their suggestions. Of course, any errors are solely the responsibility of the author.

The SPAHR computer program requires three types of information for health risk assessments: (1) coefficients of risk for the sex-, age-, disease-specific dose response, (2) the duration of the latent period, and (3) the duration of the effect (i.e., the plateau period). Deriving this information from the BEIR 1980 report is somewhat difficult because the committee placed more emphasis on the method of estimation than on the numerical estimates themselves. In addition, the committee proposed three model types: (1) a linear quadratic model, (2) a linear model, and (3) a quadratic model. While the committee generally agreed that the linear quadratic model best described the dose response relationship for low doses of low-LET radiation, arguments can be made for the other models (NAS, 1980:190). The committee therefore decided to present an envelope of estimates bounded by the linear, the linear quadratic, and the quadratic models. Consequently, each of three models will be operationalized to provide the SPAHR user with this envelope of estimates.

4.2.2.1 The Baseline Population

The BEIR 1980 report estimated excess cancer incidence from low level radiation for 13 sites. Because some of the site-specific cancers occurred very rarely, it was necessary to provide stable baseline rates for subsequent calculations in SPAHR. The age-, sex-, race-specific cancer rates were therefore calculated for three years of mortality (i.e., 1969, 1970, and 1971) using the 1970 census count as the population at risk. These same cancer rates were used in the BEIR 1980 report. SPAHR uses the 1970 census population for all calculations unless the user specifies otherwise.

Table 4.4 presents the names for cancer deaths used in the BEIR 1980 report along with the comparable listings from the International Classification of Disease (ICDA) provided in the mortality data. Most of these disease categories corresponded directly to causes of death listed, with one important

Table 4.4. Sites of Radiation-Induced Cancers Specified in BEIR 1980 Report

BEIR 1980 Name	International Classification of Disease, Adapted, 1965 (ICDA), Eighth Revision	
	Category number	Causes of death
Thyroid	193	Cancer of thyroid gland
Breast	174	Cancer of breast
Lung	162	Cancer of trachea, bronchus, and lung
Esophagus	150	Cancer of esophagus
Stomach	151	Cancer of stomach
Intestine	152, 153	Cancer of large intestine Cancer of small intestine
Pancreas	157	Cancer of pancreas
Urinary	188, 189	Cancer of urinary organs
Lymphoma	200, 203	Lymphosarcoma, recticulum cell sarcoma, and multiple myeloma
Leukemia	204-207	Leukemia
Bone	170	Cancer of bone
All malignant neoplasms	140-209	Malignant neoplasms, including neoplasms of lymphatic and hematopoietic tissues

exception. In the case of leukemia and bone cancer, the BEIR committee chose to use incidence instead of mortality, assuming that incidence and mortality were the same. Because SPAHR is a mortality based model, however, the use of incidence is clearly inappropriate, especially for leukemia, which has a relatively high survival rate (Axtell, et al., 1976). Therefore, since SPAHR estimates mortality from incidence coefficients, the resulting estimate of excess number of deaths is conservative.

Table 4.5 presents the coefficient estimates for the three models and two risk types derived from the BEIR 1980 report. The latency period is ten years for all disease and age groups with the following exceptions. Breast cancer is assumed to have a 5-year latency period for ages 20 and above (NAS, 1980:339). Lung cancer has a 30-year latency for the age group 0-9, a 20-year latency for ages 10-19, and a 15-year latency for ages 20-24 (NAS, 1980:243, 251). Both leukemia and bone cancer have a two-year latency period (NAS, 1980:403, 498-500). The plateau period for all categories is assumed to be life long (i.e., 101 years) except for leukemia and bone cancer, where the plateau is assumed to be 25 years (NAS, 1980:191, 243).

Table 4.5. Percent Excess Cancer Mortality Per Rad, All Cancers Except Leukemia and Bone, for Continuous Exposure to 1 rad per Year by Age at Exposure, Sex, and Dose Response Model

	Dose Response Model					
	Linear		Linear Quadratic*		Pure Quadratic	
Age at exposure	Male	Female	Male	Female	Male	Female
0-9	0.528	0.576	0.221	0.234	0.00331	0.00349
10-19	0.528	0.576	0.221	0.234	0.00331	0.00349
20-34	0.298	0.415	0.122	0.165	0.00191	0.00239
35-49	0.0994	0.188	0.0428	0.0784	0.00036	0.00067
50-64	0.0831	0.171	0.0325	0.0649	0.00042	0.0009
65-110	0.0790	0.156	0.0309	0.0593	0.00042	0.0009

*For the coefficient of the quadratic term, multiply these values by 0.008614.

4.2.2.2 Absolute Risk Model

The disease-aggregate risk coefficients are provided in Tables V-16 through V-21 of the BEIR 1980 report. In order to derive disease-specific coefficients, the disease-specific data in Table V-14 must be adjusted to give the same results as data for total body exposure (NAS, 1980). Therefore, the disease-specific coefficients of Table V-14 were normalized to the "correct" total risk value by first multiplying each of the sex-, age-, and disease-specific incidence coefficients of Table V-14 by the sex- and disease-specific mortality ratios in Table V-15 (NAS, 1980:250-2). This produces estimates of nonnormalized sex-, age-, and disease-specific mortality coefficients. Secondly, we added the products by age for each sex and then divided each sex-,

age-, and disease-specific cell by this total. This produced an estimate of the fraction of total excess mortality due to a specific disease group by age and sex. Finally, we multiplied these cell fractions by the corresponding sex- and age-specific total mortality coefficient from Tables V-19 to V-21 (NAS, 1980:258-260). This produced the sex-, age-, and disease-specific normalized mortality coefficients needed for SPAHR.

The above procedure was used for the following cancer types: thyroid, breast, lung, esophagus, stomach, intestine, liver, pancreas, urinary, and lymphoma. Mortality coefficients for the category of "other cancers" were estimated in the same way by assuming that the ratio of mortality to incidence was 1. Leukemia and bone cancer coefficients for mortality are presented in the BEIR committee report in Tables V-16, V-17, and V-18 (NAS, 1980:255-7), and therefore no estimation was needed.

4.2.2.3 Relative Risk Model

Site-specific mortality coefficients for the relative risk model do not appear in the BEIR 1980 report. Therefore, the SPAHR coefficients were based upon the BEIR committee report and information in Table 4.5. As Willis (1981) pointed out, there is no completely satisfactory way of obtaining disease-specific coefficients for the relative risk models. One possible approach is to repeat the procedure used for the absolute risk model. Although there is no real justification for basing disease-specific coefficients for the relative risk model on the absolute model coefficients provided in Table V-14(NAS, 1980:250), this is the best that can be done with the available data.

Neither leukemia nor bone cancer has a relative risk formulation. Therefore a problem arises in using absolute risk formulations for leukemia and bone cancer and relative risk formulations for the rest of the cancers. In order to properly account for competing risks, one should use two separate ADJUST subparagraphs in the PROJECT paragraph of SPAHR, one to specify an absolute risk formulation for leukemia and bone cancers, and a second to specify a relative risk formulation for the other cancers.

4.2.2.4 Testing of the Coefficient Estimates

Table 4.6 presents the coefficient estimates for the two risk formulations for three dose response models. These coefficients are used in SPAHR to replicate results presented in the BEIR Committee Report of 1980. The committee used the life table model of health risk developed by the Environmental Protection Agency (Cook et al., 1978; Bunger et al., 1981). Because SPAHR is based in part on a similar life table model, we should be able to replicate some of the risk assessments presented in the BEIR report (NAS, 1980:255-60). Table 4.7 presents the results of the comparisons. For almost all cancers other than leukemia and bone, there is very close agreement between the two computer programs. This is especially reassurring when one keeps in mind that

Table 4.6. Coefficients of Risk, Latency Periods, and Plateau Periods Used for SPAMR

Cause of Death	Coefficient Name	Latency Period (years)	Plateau Period (years)	Coefficients of Risk											
				Absolute Risk						Relative Risk					
				Linear		Linear Quadratic*		Pure Quadratic		Linear		Linear Quadratic*		Pure Quadratic	
				Female	Male	Female	Male	Female	Male	Female	Male	Female	Male	Female	Male
Thyroid	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	8.6817E-07	2.8675E-07	3.9399E-07	1.3400E-07	5.5710E-09	1.9326E-09	1.9413E-02	7.8856E-02	7.8863E-03	3.3006E-03	1.1762E-04	4.9435E-05
	10-19 yr	10	101	3.4669E-07	1.9692E-07	1.4080E-07	8.2376E-08	1.8531E-09	1.1054E-09	1.0214E-02	7.1361E-03	4.1496E-03	2.9869E-03	6.1890E-05	4.4736E-05
	20-34 yr	10	101	7.2858E-07	2.8468E-07	2.8995E-07	1.1671E-07	3.7389E-09	1.5343E-09	5.2068E-03	1.9606E-03	2.0702E-03	8.0266E-05	2.9986E-05	1.2566E-05
	35-49 yr	10	101	6.5268E-07	2.1944E-07	2.7276E-07	9.4476E-08	3.6301E-09	1.2819E-09	1.2819E-09	1.7277E-03	7.2050E-04	1.7751E-04	6.1574E-06	1.4930E-06
	50+ yrs	10	101	7.0164E-07	2.1200E-07	2.6640E-07	8.2940E-08	3.3037E-09	1.0487E-09	1.0148E-03	2.0001E-04	3.8515E-04	7.8223E-05	5.3411E-06	1.0109E-06
Breast	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	10-19 yr	10	101	8.5088E-07	0.0	3.4558E-07	0.0	4.5482E-09	0.0	2.5070E-02	0.0	1.0184E-02	0.0	1.5190E-04	0.0
	20-34 yr	5	101	1.6167E-06	0.0	6.4339E-07	0.0	8.2964E-09	0.0	1.1554E-02	0.0	4.5936E-03	0.0	6.6538E-05	0.0
	35-49 yr	5	101	1.4483E-06	0.0	6.0525E-07	0.0	8.0550E-09	0.0	2.2518E-03	0.0	1.5988E-03	0.0	1.3663E-05	0.0
	50+ yrs	5	101	1.5569E-06	0.0	5.9113E-07	0.0	7.3309E-09	0.0	2.2518E-03	0.0	8.5473E-04	0.0	1.1852E-05	0.0
Lung	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	30	101	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	10-19 yr	20	101	1.2104E-07	2.2288E-07	4.9160E-08	9.3235E-08	6.4700E-10	1.2511E-09	3.5663E-03	8.0768E-03	1.4488E-03	3.3806E-03	2.1608E-05	5.0633E-05
	20-34 yr	15	101	1.1541E-06	1.4619E-06	4.5930E-07	5.9934E-07	5.9225E-09	7.8786E-09	8.2478E-03	1.0068E-02	3.2793E-03	4.1217E-03	4.7500E-05	6.4529E-05
	35-49 yr	10	101	2.1522E-06	2.3456E-06	8.9941E-07	1.0099E-06	1.1970E-08	1.3703E-08	5.6971E-03	4.4066E-03	2.3758E-03	1.8974E-03	2.0303E-05	1.5960E-05
	50+ yrs	10	101	3.0802E-06	3.0170E-06	1.1695E-06	1.1804E-06	1.4504E-08	1.4924E-08	4.4551E-03	2.8465E-03	1.6908E-03	1.1132E-03	2.3448E-05	1.4386E-05
Esophagus	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	5.2390E-08	5.0688E-08	2.3775E-08	2.3686E-08	3.3618E-10	3.4162E-10	1.1714E-03	1.3939E-03	4.7590E-04	5.8344E-04	7.0978E-06	8.7384E-06
	10-19 yr	10	101	2.0921E-08	3.4809E-08	8.4968E-09	1.4561E-08	1.1183E-10	1.9540E-10	6.1639E-04	1.2614E-03	2.5041E-04	5.2799E-04	3.7347E-06	7.9078E-06
	20-34 yr	10	101	8.1651E-08	9.3456E-08	3.2494E-08	3.8315E-08	4.1901E-10	5.0367E-10	5.8352E-04	6.4363E-04	2.3200E-04	2.6350E-04	3.3605E-06	4.1253E-06
	35-49 yr	10	101	1.1816E-07	1.1637E-07	4.9379E-08	5.0101E-08	6.5717E-10	6.7982E-10	3.1278E-04	2.1861E-04	1.3044E-04	9.4132E-05	1.1147E-06	7.9176E-07
	50+ yrs	10	101	3.3872E-07	2.9979E-07	1.2861E-07	1.1729E-07	1.5949E-09	1.4830E-09	4.8990E-04	2.8284E-04	1.8593E-04	1.1062E-04	2.5784E-06	1.4295E-06
Stomach	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	2.3351E-07	2.1724E-07	1.0597E-07	1.0151E-07	1.4984E-09	1.4641E-09	5.2213E-03	5.9740E-03	2.1212E-03	2.5005E-03	3.1636E-05	3.7450E-05
	10-10 yr	10	101	9.3248E-08	1.4918E-07	3.7871E-08	6.2406E-08	4.9843E-10	8.3744E-10	2.7473E-03	5.4061E-03	1.1161E-03	2.2628E-03	1.6646E-05	3.3891E-05
	20-34 yr	10	101	3.7723E-07	4.1516E-07	1.5012E-07	1.7021E-07	1.9358E-09	2.2375E-09	2.6959E-03	2.8592E-03	1.0719E-03	1.1705E-03	1.5526E-05	1.8326E-05
	35-49 yr	10	101	5.5781E-07	5.2781E-07	2.3293E-07	2.2724E-07	3.1000E-09	3.0835E-09	1.4754E-03	9.9157E-04	6.1528E-04	4.2696E-04	5.2582E-06	3.5912E-06
	50+ yrs	10	101	1.5807E-06	1.3450E-06	6.0009E-07	5.2623E-07	7.4420E-09	6.6535E-09	2.2859E-03	1.2690E-03	8.6758E-04	4.9630E-04	1.2031E-05	6.4137E-06
Intestine	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	1.0702E-07	9.7901E-08	4.8568E-08	4.5748E-08	6.8677E-10	6.5981E-10	2.3931E-03	2.6923E-03	9.7220E-04	1.1269E-03	1.4500E-05	1.6878E-05
	10-19 yr	10	101	4.2738E-08	6.7231E-08	1.7358E-08	2.8124E-08	2.2845E-10	3.7741E-10	1.2592E-03	2.4364E-03	5.1155E-04	1.0198E-03	7.6295E-06	1.5273E-05
	20-34 yr	10	101	1.7963E-07	1.9439E-07	7.1488E-08	7.9696E-08	9.2182E-10	1.0476E-09	1.2837E-03	1.3387E-03	5.1041E-04	5.4808E-04	7.3931E-06	8.5806E-06
	35-49 yr	10	101	2.5995E-07	2.4204E-07	1.0863E-07	1.0421E-07	1.4458E-09	1.4140E-09	6.8812E-04	4.5472E-04	2.8696E-04	1.9579E-04	2.4523E-06	1.6469E-06
	50+ yrs	10	101	7.4186E-07	6.2078E-07	2.8167E-07	2.4287E-07	3.4931E-09	3.0708E-09	1.0730E-03	5.8569E-04	4.0723E-04	2.2906E-04	5.672E-06	2.9601E-06
Liver	in utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	5.2390E-07	5.0688E-07	2.3775E-07	2.3686E-07	0.3618E-09	3.4162E-09	1.1714E-02	1.3939E-02	4.7590E-03	5.8344E-03	7.0978E-05	8.7385E-05
	10-19 yr	10	101	2.0921E-07	3.409E-07	8.4968E-08	1.4561E-07	0.1183E-09	1.9540E-09	6.1639E-03	1.2614E-02	2.5041E-03	5.2799E-03	3.7347E-05	7.9078E-05
	20-34 yr	10	101	4.3966E-07	5.0322E-07	1.7497E-07	2.0631E-07	0.2562E-09	2.7121E-09	3.1420E-03	3.4657E-03	1.2492E-03	1.4188E-03	1.8095E-05	2.2213E-05
	35-49 yr	10	101	3.9386E-07	3.8789E-07	1.6460E-07	1.6700E-07	0.1906E-09	2.2661E-09	1.0426E-03	7.2872E-04	4.3479E-04	3.1377E-04	3.7156E-06	2.6392E-06
	50+ yrs	10	101	4.2340E-07	3.7474E-07	1.6076E-07	1.4661E-07	0.9936E-09	1.8537E-09	6.1238E-04	3.5355E-04	2.3242E-04	1.3827E-04	3.2231E-06	1.7869E-06

Table 4.6 (Contd.)

Cause of Death	Coefficient Name	Latency Period (years)	Plateau Period (years)	Coefficients of Risk											
				Absolute Risk						Relative Risk					
				Linear		Linear Quadratic*		Pure Quadratic		Linear		Linear Quadratic*		Pure Quadratic	
				Female	Male	Female	Male	Female	Male	Female	Male	Female	Male	Female	Male
Pancreas	In utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	1.6166E-07	1.5815E-07	7.3362E-08	7.3901E-08	1.0374E-09	1.0658E-09	3.6147E-03	4.3491E-03	1.4685E-03	1.8203E-03	2.1902E-05	2.7264E-05
	10-19 yr	10	101	6.4556E-08	1.0860E-07	2.6219E-08	4.5432E-08	2.4507E-10	6.0966E-10	1.9020E-03	3.9357E-03	7.7269E-04	1.6473E-03	1.1524E-05	2.4672E-05
	20-34 yr	10	101	2.5437E-07	2.9439E-07	1.0123E-07	1.2069E-07	1.3054E-09	1.5866E-09	1.8179E-03	2.0274E-03	7.2278E-04	8.3002E-04	1.0469E-05	1.2995E-05
	35-49 yr	10	101	3.7979E-07	3.7819E-07	1.5872E-07	1.6283E-07	2.1123E-09	2.2094E-09	1.0054E-03	7.1050E-04	4.1926E-04	3.0593E-04	3.5829E-06	2.5732E-06
	50+ yrs	10	101	1.0724E-06	9.5971E-07	4.0718E-07	3.7547E-07	5.0496E-09	4.7473E-09	1.5511E-03	9.0545E-04	5.8868E-04	3.5412E-04	8.1635E-06	4.5763E-06
Urinary	In utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	1.3771E-08	1.0717E-08	6.2493E-09	5.0079E-09	8.8367E-11	7.2228E-11	3.0792E-04	2.9472E-04	1.2509E-04	1.2336E-04	1.8657E-06	1.8476E-06
	10-19 yr	10	101	3.1620E-09	4.2318E-08	1.2842E-08	1.7703E-08	1.6902E-10	2.3755E-10	9.3163E-04	1.5335E-03	3.7848E-04	6.4188E-04	5.6448E-06	9.6137E-06
	20-34 yr	10	101	1.4446E-07	1.3299E-07	5.7490E-08	5.4526E-08	7.4122E-10	7.1676E-10	1.0324E-03	9.1593E-03	4.1047E-04	3.7498E-04	5.9455E-06	5.8706E-06
	35-49 yr	10	101	2.3812E-07	1.8863E-07	9.911E-08	8.1211E-08	1.3244E-09	1.1020E-09	6.3033E-04	3.5436E-04	2.6286E-04	1.5258E-04	2.2464E-06	1.2834E-06
	50+ yrs	10	101	4.5074E-07	3.2088E-07	1.7114E-07	1.2554E-07	2.1224E-09	1.5873E-09	6.5192E-04	3.0274E-04	2.4743E-04	1.1840E-04	3.4312E-06	1.5301E-06
Lymphoma	In utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	1.5156E-07	1.4272E-07	6.8777E-08	6.6694E-08	9.725E-10	9.6190E-10	3.3888E-03	3.9249E-03	1.3767E-03	1.6428E-03	2.0533E-05	2.4605E-05
	10-19 yr	10	101	6.0521E-08	9.8012E-08	2.4580E-08	4.1001E-08	3.2350E-10	5.5020E-10	1.7831E-03	3.5518E-03	7.2440E-04	1.4867E-03	1.0804E-05	2.2266E-05
	20-34 yr	10	101	1.2719E-07	1.4169E-07	5.0616E-08	5.8092E-08	6.5269E-10	7.6364E-10	9.0895E-04	9.7584E-04	3.6139E-04	3.9950E-04	5.2347E-06	6.2545E-06
	35-49 yr	10	101	1.1394E-07	1.0922E-07	4.7616E-08	4.7023E-08	6.3370E-10	6.3806E-10	3.0161E-04	2.0519E-04	1.2578E-04	8.8350E-05	1.0749E-06	7.4313E-07
	50+ yrs	10	101	1.2248E-07	1.0552E-07	4.6505E-08	4.1282E-08	5.7673E-10	5.2195E-10	1.7715E-04	9.9550E-05	6.7235E-05	3.8934E-05	9.3238E-07	5.0314E-07
Leukemia	In utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	2	25	1.1920E-06	1.8490E-06	5.0670E-07	7.8550E-07	6.8930E-09	1.0680E-08	0.0	0.0	0.0	0.0	0.0	0.0
	10-19 yr	2	25	1.1920E-06	1.8490E-07	5.0670E-07	7.8550E-07	6.8930E-09	1.0680E-08	0.0	0.0	0.0	0.0	0.0	0.0
	20-34 yr	2	25	1.6660E-06	2.5960E-06	7.3010E-07	1.1380E-06	1.0130E-08	1.5790E-08	0.0	0.0	0.0	0.0	0.0	0.0
	35-49 yr	2	25	1.2370E-06	1.9210E-06	5.4830E-07	8.5110E-07	7.6210E-09	1.1820E-08	0.0	0.0	0.0	0.0	0.0	0.0
	50+ yrs	2	25	2.7600E-06	4.3190E-06	1.2380E-06	1.9370E-06	1.7290E-08	2.7060E-08	0.0	0.0	0.0	0.0	0.0	0.0
Bone	In utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	2	25	2.6600E-07	4.1300E-07	1.1320E-08	1.7540E-08	1.5370E-10	2.3820E-10	0.0	0.0	0.0	0.0	0.0	0.0
	10-19 yr	2	25	2.6600E-07	4.1300E-07	1.1320E-08	1.7540E-08	1.5370E-10	2.3820E-10	0.0	0.0	0.0	0.0	0.0	0.0
	20-34 yr	2	25	3.7200E-07	5.8000E-07	1.6300E-08	2.5410E-08	2.2590E-10	3.5190E-10	0.0	0.0	0.0	0.0	0.0	0.0
	35-49 yr	2	25	2.7600E-07	4.2900E-07	1.2240E-08	1.9010E-08	1.7000E-10	2.6360E-10	0.0	0.0	0.0	0.0	0.0	0.0
	50+ yrs	2	25	6.1600E-07	9.6400E-07	2.7650E-08	4.3260E-08	3.8560E-10	6.0350E-10	0.0	0.0	0.0	0.0	0.0	0.0
Other	In utero	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	0-9 yr	10	101	4.6402E-07	4.4895E-07	2.1058E-07	2.0979E-07	2.9776E-09	3.0258E-09	1.0376E-02	1.2346E-02	4.2151E-03	5.1676E-03	6.2866E-05	7.7398E-05
	10-19 yr	10	101	1.1357E-07	1.8896E-07	4.6125E-08	7.9048E-08	6.0707E-10	1.0608E-09	3.3461E-03	6.8478E-03	1.3594E-03	2.8662E-03	2.0274E-05	4.2928E-05
	20-34 yr	10	101	7.0345E-07	7.7578E-07	2.7995E-07	3.3010E-07	3.6099E-09	4.3393E-09	5.0273E-03	5.5451E-03	1.9988E-03	2.2701E-03	2.8952E-05	3.5541E-05
	35-49 yr	10	101	7.8772E-07	7.7578E-07	3.2920E-07	3.3401E-07	4.3811E-09	4.5321E-09	2.0852E-03	1.4574E-03	8.6957E-04	6.2753E-04	7.4313E-06	5.2784E-06
	50+ yrs	10	101	1.7541E-06	1.5525E-06	6.6600E-07	6.0739E-07	8.2593E-09	7.6796E-09	2.3370E-03	1.4647E-03	9.6287E-04	5.7284E-04	1.3353E-05	7.4029E-06

*This coefficient represents the linear term of the model. The quadratic term of this model is the linear term times 0.008614.

Table 4.7. Comparison of the 1980 BEIR Committee Report with SPAHR on Normal Expectation and Excess Life Table Deaths per Million Persons for a Continuous Exposure to 1 Rad per Year for Lifetime

	Absolute Risk Model				Relative Risk Model			
	BEIR 1980		SPAHR		BEIR 1980		SPAHR	
Cancers Other Than Leukemia and Bone	Males	Females	Males	Females	Males	Females	Males	Females
Normal expectation	165,700	149,200	161,168	149,920	165,700	149,200	161,168	149,920
LQ-L excess**	2,459	4,243	2,470	4,440	10,220	12,820	11,830	12,910
LL excess**	5,827	10,400	5,800	10,760	24,210	30,540	28,550	31,470
Q-L excess**	*	*	30	50	*	*	170	180
Leukemia and Bone								
Normal expectation	10,600	9,050	8,060	7,110				
LQ-L	1,592	1,209	1,470	1,130				
LL excess	3,568	2,709	3,960	3,060				
Q-L excess	*	*	20	20				

*Estimates not provided in the BEIR Committee Report.

**Abbreviations: LQ-L, linear quadratic model; LL, linear model; Q-L, quadratic model.

SPAHR uses disease-specific dose response functions estimated in the procedures outlined above, while the life table model used by the BEIR committee estimates all causes with a single dose response function. We can therefore conclude that our estimates of the dose response functions for individual causes of death produce the "correct" number of excess deaths (as presented by the BEIR committee) when summed.

As one might suspect, the leukemia and bone cancer comparisons do not agree as closely. First, the normal expectation of deaths is somewhat higher in the BEIR report. This is because the BEIR committee used incidence instead of mortality, and incidence in a specific year is likely to be higher than mortality. However, the excess death estimates from both computer programs are reasonably close. In summary, the computer packages appear to produce similar results, providing a validity test for the computational ability of both. In addition, the estimations of the disease-specific dose response functions replicate summary findings presented in the BEIR report, indicating a degree of validity for these procedures. Therefore, the disease-specific dose response functions incorporated into SPAHR appear to provide reasonable estimates of increased health risk due to ionizing radiation.

5.0 MORBIDITY ESTIMATION

In the current version of SPAHR two approaches are used for morbidity estimation. Both approaches are derived from morbidity rates. The first is an age-specific model indexed to mortality for all causes of death combined. This approach is based upon the work of Thomas (1973). The second approach is cause specific and was developed to provide morbidity estimates for individual disease groups.

5.1 The Thomas Model

Thomas related age-specific morbidity rates by type (i.e., restricted activity, bedridden, and hospitalized) to age-specific mortality rates by the equation

$$y_j = b_0 + b_1 x^{b_2} \tag{5.1}$$

where

y_j = morbidity rate by type j

x = mortality rate, and

b_0, b_1, and b_2, are fitted coefficients.

A nonlinear regression procedure was utilized to estimate the coefficients. These coefficients, along with the squared multiple correlation coefficient for both sexes for each type of morbidity, are presented in Table 5.1.

Table 5.1. Coefficient Estimates and Explained Variance (R^2) for Both Sexes and Each Morbidity Type

Dependent Variable	Coefficients			R^2
	b_0	b_1	b_2	
Males, Restricted Activity	6.97	0.112	0.661	0.9919
Males, Bedridden	2.85	0.021	0.781	0.9964
Males, Hospitalized	0.29	0.007	0.866	0.9989
Females, Restricted Activity	9.50	0.360	0.544	0.9649
Females, Bedridden	5.01	0.008	0.892	0.9954
Females, Hospitalized	0.68	0.004	0.919	0.9969

The Thomas model was derived independently of time. In the usual course of events, morbid states precede mortal ones. However, as Thomas noted, the mortality variable drives the morbidity variable. This makes the morbidity variable ideally suited for incorporation into the SPAHR model, which is primarily a mortality-oriented system. However, derivation of a time series of estimates is at best a suspect procedure that is implemented only in the calculation of the summary tables for the projection rather than in the individual interval calculations.

Thomas calculated his morbidity groups inclusively, so that each morbid group included all persons in higher states of severity. SPAHR, however, separates each group into individual states of severity. The age-specific morbidity rates are then applied to the age-specific person-years to derive person-years spent in the various morbid states. In this way, cost for a particular pollution episode can be estimated for each of the morbid components.

It should be noted that the Thomas model assumes that the relationship between morbidity and mortality does not depend on age. As a result, it appears to overestimate morbid episodes at the older ages (Thomas, 1973:118). The Thomas model may, however, be a useful indicator of the effect of changes in the levels of pollutants that cause a generalized deterioration of health status and mimic to an extent the effects of accelerated aging. Therefore, this model appears suited for estimating life shortening from respiratory diseases that might result from air pollution, the purpose for which it was proposed. However, the model is not well suited for determining morbidity effects resulting from highly specific influences such as radiation-induced cancers. A disease-specific model is needed for estimating morbid effects of radiation exposure.

5.2 Cause-Specific Morbidity

Overall levels of morbidity as defined in the Thomas model may be of little use in describing the effects of a particular disease. For this reason, we have derived a second morbidity model that relates incidence and duration of illness to mortality rates for specific causes. This model is very useful for estimating morbidity for pollutants such as radiation that cause cancer.

The cause-specific morbidity model is based upon the assumptions that the disease resulting from the pollutant occurs only once to each victim, and that there are only two outcomes, death and recovery. Recovery is assumed complete if the duration in the morbid state exceeds 20 years.

With these assumptions, a cause-specific morbidity model based upon cause-specific mortality is constructed in the following way. First, incidence for a specific disease, I^k, in an interval is defined as

$$I^k = D^k \cdot C^k \qquad (5.2)$$

where

D^k = number of deaths from disease k and

C^k = the inverse of the case fatality ratio for disease k.

The number of morbid years spent by survivors of the disease, SY^k, is then estimated as

$$SY^k = (I^k - D^k) \cdot SM^k \tag{5.3}$$

where SM^k is the mean of the morbid years for survivors of disease k. The number of morbid years for persons dying of disease k, DY^k, is

$$DY^k = D^k \cdot DM^k \tag{5.4}$$

where DM^k is the mean of the morbid years for those who die of disease k. The sum of SY^k and DY^k then yields an estimate of the total morbid years lost in a specific projection interval due to disease k.

In order to estimate these morbid years lost, three coefficients for each disease are needed: (1) an incidence multiplier, (2) the mean morbid years of survivors, and (3) the mean morbid years of those that die. The incidence multiplier is simply the inverse of the case fatality ratio of a particular disease. For instance, breast cancer for white females has a case fatality ratio of 0.65 (Axtell, et al., 1976). The incidence multiplier, therefore, would be 1.53.

The mean morbid years of the survivors of a particular cancer are assumed to be 5 years, based upon the medical definition of recovery. An exception to this assumption is made for thyroid cancer, however, where the rate of recovery is very high and the length of morbidity associated with survivors is generally on the order of two weeks.

The mean survival time for persons dying of a particular disease is estimated by fitting a Weibull distribution to the distribution of persons dying within 5 years of diagnosis. The method for fitting this distribution is taken from Gross and Clark (1975:106-7). The data are taken from Cancer Patient Survival (Axtell, et al., 1976).

For the Weibull distribution, the hazard function is

$$H(t) = \lambda\gamma t^{\gamma-1} \tag{5.5}$$

the survival function is

$$S(t) = \exp(-\lambda t^{\gamma}) \tag{5.6}$$

and the mean time until death is given by

$$\bar{t} = \frac{(1 + 1/\gamma)}{\lambda(1/\gamma)} \tag{5.7}$$

where λ and γ are constants and t is a measure of time.

Table 5.2 gives the intermediate calculations for fitting the Weibull distribution to the data for female breast cancer. The columns Years (t) and S_i are copied directly from the table on page 161 of Cancer Patient Survival, (Axtell et al., 1976). The S_i' column represents the S_i column assuming a 37% recovery rate, obtained by assuming that the 20-year case fatality ratio of 38% would drop only 1% in the coming years. The x_i column shows the natural logs of the t column entries, and the y_i column is the log of the log of the inverse of the survival probability assuming a 37% recovery rate (S_i'). The least squares estimates $\tilde{\gamma}$ and $\tilde{\lambda}$ of γ and λ are obtained by

$$\tilde{\gamma} = \frac{\sum_{i=1}^{n} (x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^{n} (x_i - \bar{x})^2} \tag{5.8}$$

and

$$\log_e \tilde{\lambda} = \bar{y} - \tilde{\gamma}\,\bar{x}. \tag{5.9}$$

Table 5.3 presents the sex-specific morbidity coefficients for various types of cancer. Generally, women appear to suffer more morbid years from cancer than do men.

Table 5.2. Intermediate Results for Fitting the Weibull Distribution to the Data for Female Breast Cancer

Interval	Years (t)	x_i	y_i	S_i	S_i'	$E(S_i')$
1	1	0.0	-1.755	0.90	0.841	0.839
2	5	1.609	0.008	0.60	0.365	0.392
3	10	2.303	0.610	0.47	0.159	0.146
4	15	2.708	1.014	0.41	0.063	0.053
5	20	2.996	1.421	0.38	0.016	0.019

Lambda	0.1760
Gamma	1.0382
Mean Survival	5.2489

Table 5.3. Morbidity Coefficients Used in SPAHR for Various Types of Cancer

Cause of Death (Cancer)	Incidence Multiplier[1]		Average Morbid Years Lived for Survivors	Average Morbid Years Lived by Those Who Die	
	Males	Females		Males	Females
Leukemia	1.163	1.176	5	1.767	1.581
Lung	1.087	1.149	5	0.703	0.927
Stomach	1.136	1.163	5	0.953	1.357
Alimentary[4]	1.852	1.887	5	2.397	2.561
Pancreas	1.010	1.020	5	0.593	0.686
Breast	2.128	1.429	5	5.249[2]	5.249
Bone	1.299	1.429	5	1.567	2.108
Thyroid	5.000	7.692	0.038[3]	0.357	3.231
Esophagus	1.031	1.064	5	0.656	0.945
Intestines[4]	1.852	1.887	5	2.397	2.251
Liver	1.042	1.075	5	1.279	0.526
Urinary[5]	1.695	1.754	5	2.952	2.927
Lymphoma[6]	1.515	1.587	5	2.293	3.124
Other[7]	1.695	1.695	5	1.181	1.181

[1] The inverse of the relative survival rate after 5 years minus 1.

[2] Males are assumed to have the same relative survivorship and mean morbid years as females.

[3] The average morbid years lived by survivors of thyroid cancer is assumed to be 2 weeks, or 0.038 of a year.

[4] Rates for cancer of the colon are used.

[5] Rates for cancer of the kidney are used.

[6] Rates for lymphosarcoma are used.

[7] Rates for all other cancers combined are used.

It should be noted that the morbidity estimates are generally applicable only to nonrecurring conditions such as cancer or well-defined infectious conditions to which the victim becomes immune following recovery. Secondly, the data from which the Weibull distribution is fitted are not age specific, even though the process of recovery probably is. Hence these estimates have an implied age distribution corresponding to that of the NCI sample. The severity of this problem is related to the overall lethality of the disease. Finally, the morbidity definition used is not consistent with that of the Thomas model. A diagnosis of cancer does not necessarily imply any particular number of restricted days, although most cancer patients are hospitalized as part of their treatment, and in many cases a permanent change in lifestyle occurs.

6.0 SENSITIVITY ANALYSIS--THE VARIATION INTRODUCED BY CONSIDERING POPULATION STRUCTURE

The importance of considering mortality, fertility, and age structure for the estimation of excess deaths due to a pollution scenario can be illustrated by applying the demographic model to a number of diverse populations and then comparing estimates of excess risk.

6.1 Methods

The results of applying the demographic model to 36 diverse populations are shown in Table 6.1. The data are those collected by Keyfitz and Flieger (1968) for the years shown, with the exception of the United States data, which are derived from the U. S. Census and Vital Statistics. Each population was normalized to an initial size of 1 million and projected forward 200 years. During the first hundred years, a constant exposure rate of 1 rem per year was assumed. It was further assumed that no excess exposure occurred in the second hundred years, so that the only radiation-induced cancers reported in the second hundred years are a result of exposure accumulated in the first hundred years. All leukemias and lung cancers that could result from the assumed excess exposure were permitted to occur. The age-specific coefficients of risk and the latency period for the absolute and relative risk models with lifetime plateaus were derived from the first BEIR committee report (NAS, 1972) and from WASH-1400 (USNRC, 1975).

Except for the United States black population (1970), age-specific cancer deaths rates for the U. S. white population were used. This eliminated a source of variation that could occur in the use of a relative risk model. Consequently, the variation shown reflects only the increased age dependence of the dose response model, compared to the absolute risk model. If baseline cancer rates had also been permitted to vary, even greater variations in excess deaths in the relative risk model would have been observed.

In addition to the selected excess mortality measures in Table 6.1, three other indicators describe the structures of the populations: the expectation of life at birth (e_o) for males and females, the net reproduction rate (NRR), and the percent of the population less than 15 years of age (LT15).

6.2 Results

The following general conclusions can be drawn from Table 6.1. First, populations with high fertility have more excess deaths. The Fiji Islands and the Japanese populations have similar values for e_o, but the Fiji Islands have a higher NRR and consequently two to six times as many deaths. Second, high e_o means more excess deaths. For example, Nicaragua and Ecuador have similar values for NRR, but Nicaragua has a higher e_o. Nicaragua exhibits substantially more excess deaths from leukemia and lung cancer, however, because the competing risks from other causes of death are much lower. Third,

populations with low mortality and low fertility exhibit more excess deaths from lung cancer than from leukemia, at least in the absolute risk formulation. For example, the ratio of excess deaths, lung cancer to leukemia, for Sweden is 1.12, while that of Madagascar is 0.63. Excess deaths from lung cancer are more likely to occur in an "older" population such as Sweden's, whereas excess leukemia deaths are more frequent in proportionally younger populations, such as Madagascar's.

Table 6.1. Leukemia and Lung Cancer Risk Projections for 200 Years, with 1 Rem/Year for the First 100 Years, for an Initial Population of 1 Million Using the Absolute and Relative Risk Models Proposed by the BEIR Committee (NAS, 1980)

Country, by Continent	e_o[1] Females	e_o[1] Males	Net Reproduction Rate	% of Population < age 15	Absolute Excess Deaths Leukemia	Absolute Excess Deaths Lung Cancer	Relative Excess Deaths Leukemia	Relative Excess Deaths Lung Cancer
United States								
(White) 1970	75.62	67.94	1.132	27.57	3856	4239	6706	11034
(Black) 1970	68.84	59.84	1.446	35.38	7510	6948	8003	17277
Africa								
Algeria 1965	67.99	63.25	2.657	47.23	31800	27740	31560	62900
Cameroon (West) 1964	38.23	34.44	1.729	48.57	12450	7560	10738	12921
Central African Republic 1960	38.62	34.63	1.404	40.02	5638	4071	4757	6655
Guinea 1955	27.51	24.61	1.502	42.12	6198	3347	4540	5123
Madagascar 1966	38.65	37.70	1.884	46.51	12030	7581	9505	13408
Togo 1961	40.33	33.71	2.143	47.94	15630	9633	11347	14378
Tunisia 1960	63.95	55.85	2.358	40.85	20900	18380	21478	43830
North America								
Barbados 1965	71.24	66.98	1.647	38.92	9906	9766	9738	21840
Dominican Republic 1966	66.17	63.76	2.191	44.57	18020	17110	17554	28391
Honduras 1966	60.57	59.23	2.646	51.48	34050	25870	26280	53333
Mexico 1966	62.85	59.54	2.713	46.26	33670	26620	31450	58370
Nicaragua 1965	68.09	64.48	2.571	48.34	34730	28840	29740	59141
South America								
Brazil 1950	44.36	41.44	1.842	41.68	11420	8376	10305	16538
Chile 1967	69.65	63.36	1.665	39.84	9891	10140	7201	14272
Colombia 1965	61.81	58.36	1.984	46.64	14950	13290	16301	30759
Ecuador 1965	60.85	57.17	2.592	46.98	30130	24820	25528	51259
Asia								
Ceylon 1961	63.63	62.06	2.131	41.86	17310	14930	16463	32745
China (Mainland) 1956	44.25	43.83	1.894	35.95	10420	7789	9709	16395
China (Taiwan) 1966	69.87	65.25	2.203	43.69	20320	17620	20082	38704
Hong Kong	72.75	65.84	2.070	40.45	14840	13520	15615	29671
India 1961	44.24	46.21	1.782	41.09	11400	8661	10872	19031
Japan 1964	72.95	67.73	0.949	24.97	3043	3409	5566	9442
Malaysia (West) 1966	66.92	63.63	2.411	44.17	24580	20690	23751	45511
Pakistan 1961	42.69	44.60	2.090	44.79	17860	12560	15388	25913
Philippines 1960	58.79	55.50	2.437	45.69	24630	19920	23518	44186
Turkey 1960	48.90	48.48	2.211	41.25	17950	13280	16106	27772
United Arab Republic 1960	48.68	40.76	2.191	42.76	15300	11000	12951	19924
Europe								
England and Wales 1968	74.79	68.62	1.205	23.20	3693	3971	6041	10316
France 1967	75.49	68.03	1.251	25.28	4147	4470	6785	11483
Italy 1965	73.16	67.67	1.176	24.30	3701	4036	6327	10877
Sweden 1965	76.12	71.72	1.150	20.94	3343	3737	6275	10651
U.S.S.R. 1959	72.73	67.69	1.149	29.88	4170	4532	6657	11987
Oceania								
Fiji Islands 1966	73.67	68.15	2.166	52.86	20340	18360	23128	42892
New Zealand 1966-68	74.32	68.18	1.593	32.59	8214	8176	10658	19839

[1]The e_o = expectation of life at birth.

The differences between the absolute and relative risk formulations (Table 6.1) are striking. Most importantly, the widely held belief that the relative risk formulation generates more excess deaths than does the absolute formulation (NAS, 1972 and NAS, 1980) is an artifact of the population structure itself. Seventeen populations exhibit more excess leukemia deaths in the absolute risk formulation than in the relative risk formulation.

Summary measures for the estimates of excess deaths for the 36 populations are presented in Table 6.2. In the relative risk formulation, values for excess leukemia deaths are lower than in the absolute risk formulation. In contrast, excess lung cancer deaths are consistently higher in the relative risk formulation, the means differing by a factor of two.

Table 6.2. Summary Measures of Excess Deaths for Leukemia and Lung Cancer for the Absolute and Relative Risk Formulations Presented in Table 6.1

Summary Measure	Absolute Risk Model		Relative Risk Model	
	Leukemia	Lung	Leukemia	Lung
Mean	14946	12361	14406	26630
Median	13645	9953	11109	19882
Standard Deviation	9554	7756	8129	16917
Maximum	34730	28840	31560	62900
Minimum	3043	3347	4540	5123
Range	31687	25493	27020	57777

The range of the excess death estimations shows the importance of considering the population structure. For each measure in Table 6.2, the range exceeds 25 thousand deaths. The population structure, therefore, may be more important than the uncertainty inherent in the dose response functions. The same conclusion was reached in a study comparing this demographic model with a single coefficient model to assess the health effects of benzene exposure (Collins et al., 1981).

A multiple linear regression using ordinary least squares was performed to evaluate more precisely the effects of competing risks from other causes of death, of initial age structure, and of fertility levels on health risk projections. The regression equations included projections of 15, 50, and 200 years for exposure periods of 15, 50, and 100 years, respectively, relating the dependent variable (number of excess deaths) to the independent variables (life expectancy at birth for females, the net reproduction rate, and the percentage of the population less than age 15). The dose level of 1.0 rem/year was used for all projections. The lengths of exposure periods were chosen to fit realistic scenarios usually requested by regulatory analysts. Fifteen and 50 years are typical exposure lengths requested. The 15- and 50-year projections underestimated the total number of excess deaths, because the

projections ended during the latency period. Nevertheless, these projection intervals allowed us to estimate the importance of competing risks, age structure, and fertility patterns upon excess deaths at specific time points. Results from the 100-year exposure with the 200-year projection are presented in Table 6.1.

The standardized regression coefficients for each projection interval, risk model, and disease type are presented in Table 6.3. Only coefficients for leukemia are given for the first projection interval, 15 years, because lung cancer has a 20-year latency period in the present model formulation, and no excess lung cancer deaths occur within 15 years after the beginning of exposure. Data for the absolute risk model in the first projection interval indicate that both age structure (LT15) and fertility patterns (NRR) are the important determinants of excess deaths in this model. For the relative risk model in the first projection interval, only NRR is a significant determinant. Because leukemia is to some extent a childhood disease, a relative risk model tends to have a large number of excess deaths at the early ages, so that the fertility element in the demographic model takes on added significance. In both risk models, the fertility level largely determines the number of excess deaths that will occur, even in a 15-year period. Therefore, even for a very short exposure, the fertility level is far more important in determining future levels of mortality from leukemia than are competing risks from other causes of mortality, as is indicated by the value for e_o. Thus the demographic model incorporating a fertility element is useful for providing realistic estimates, even if the duration of exposure is relatively short.

Table 6.3. Standardized Regression Coefficients for Specific Projection Intervals, Risk Models, and Disease Types for Total Numbers of Excess Deaths for Exposure to 1.0 rem/year

Model Attributes				Standardized Regression Coefficients				
Length of Projection	Length of Exposure	Absolute Model	Disease Type	Net Reproduction Rate (NRR)	e_o (Females)	% of Population less than age 15 (LT15)	R^2	Mean of Dependent Variable
15	15	Absolute	Leukemia	0.569*	-0.042	0.445*	0.970*	123.08
		Relative	Leukemia	0.808*	0.027	-0.282	0.351*	104.39
50	50	Absolute	Leukemia	0.740*	0.175*	0.313*	0.968*	1874.69
		Absolute	Lung	0.455*	0.846*	0.340*	0.904*	710.94
		Relative	Leukemia	0.728*	0.379*	0.162	0.746*	1664.10
		Relative	Lung	0.469*	0.775*	0.057	0.703*	1223.25
200	100	Absolute	Leukemia	0.942*	0.158*	0.047	0.930*	14945.53
		Absolute	Lung	0.903*	0.330*	0.092	0.941*	12360.85
		Relative	Leukemia	0.940*	0.309*	0.031	0.921*	14406.44
		Relative	Lung	0.920*	0.399*	0.036	0.923*	26629.63

*t value significant at 0.05.

For the 50-year projection interval, both excess leukemia and lung deaths were examined. As with the 15-year interval, NRR is a significant determinant in all cases. However, the standardized regression coefficients are somewhat larger for excess deaths from leukemia than from lung cancer. Because lung cancer mortality occurs at relatively more advanced ages than does leukemia mortality, fertility levels are far more likely to affect leukemia deaths. The coefficients for life expectancy (e_o) for the 50-year projection interval are also all significant. However, in this case the coefficients for e_o for the excess lung cancer deaths are substantially larger than those for leukemia. It appears that competing risks, therefore, affect lung cancer deaths more than they do leukemia mortality. Again, this is probably because lung cancer is primarily a disease of the old, and competing risks from other causes of mortality are far more likely to affect excess lung cancer deaths than leukemia deaths. Another manifestation of the strong positive relationship between excess deaths and e_o values is seen in the implications of declining mortality, which has been observed in most countries and is likely to continue. In an environment of declining mortality, excess deaths are necessarily underestimated because higher life expectancy means that more persons will survive to die of the pollution-induced mortality. In this sense, then, the excess deaths projected here are underestimated.

Age structure as represented by LT15 is a significant determinant in the 50-year projection interval only for the absolute risk model. In fact, in no case is the LT15 coefficient significant for a relative risk model. This finding is somewhat difficult to interpret, because one would expect the initial age structure to be an important determinant of excess mortality, at least in the short term. However, the relative risk model essentially estimates increased risk as a percentage increase in the age-specific death rate, while the absolute risk model estimates an "absolute" increase over a very wide age group. It seems likely that the relative risk model is more sensitive to a small age interval than is the absolute risk model. Therefore, while the percentage of persons aged 0 to 15 adequately represents the dynamics of age structure in the absolute risk model, a more sensitive indicator of age structure may be required for the relative risk model. This possible inadequacy of the indicator of age structure may also explain the poor fit of the relative risk equations to the data.

The final panel of Table 6.3 presents coefficients for the 200-year projection with 100-year exposure. In this final set of equations the fertility indicator, NRR, clearly dominates. In fact, NRR is on the order of three times as important as the competing risk indicator (e_o). Nevertheless, the significance of e_o in each case suggests that competing risks are still important. The age structure indicators (LT15) are all insignificant, suggesting that the original age structure has been removed from the population by the projection process.

7.0 COMPARISON OF THE DEMOGRAPHIC MODEL WITH A SINGLE COEFFICIENT MODEL

The utility of the demographic model is demonstrated by a comparison with what was referred to earlier as a single coefficient model (Collins et al., 1981). In the single coefficient model, a coefficient is multiplied by the population exposure integrated over some time interval to determine the excess number of deaths. Such a model, employing a relative risk nonthreshold formulation, has been used to estimate that about 90 excess leukemia deaths will occur each year if the U. S. population is exposed to 1 ppb of benzene (Albert et al., 1979). These workers estimated the change in the leukemia rate per lifetime average ppm of benzene, B, as

$$B = P \cdot (R-1)/I \qquad 7.1$$

where P = the probability of dying of leukemia at age zero, R = relative risk of leukemia for workers exposed to benzene, and I = industrial level of exposure.

The expected number of leukemia deaths per year, N, is then estimated as

$$N = B \cdot D/L \qquad 7.2$$

where D = the dose, and L = the average life expectancy.

The deficiencies of the single coefficient model were outlined in Chapter 1. Briefly, this approach ignores the age and fertility structures of populations and models mortality patterns only very crudely. In addition, it assumes that the population is static both in size and structure. Finally, it cannot incorporate competing risks from other causes of death, and latency is assumed to be zero.

7.1 Methods

The same population size and dose levels can be used to estimate excess deaths in both the single coefficient and demographic models. The difference between the models is in the explicit assumptions about mortality, fertility, and age structure made in the demographic model. The relative risk nonthreshold formulation in the demographic model is defined as the proportional increase in risk of death over the underlying rate, which varies linearly with respect to dose, so that

$$\mu(x) = \mu'(x) \sum_{i=x_0}^{x} r(i)h(i - x_0)B(i,x) \qquad 7.3$$

where: $\mu'(x)$ = the underlying risk of death from leukemia (in deaths per person-year); $\mu(x)$ = the excess risk associated with benzene exposure; $r(i)$ = the level of exposure to benzene at age i(in ppm); h = latency multiplier for

duration $(i - x_0)$, because exposure = 1 if $(i - x_0)$ is greater than the period of latency and less than the sum of the latency and plateau periods, and exposure = 0 otherwise; $B(i,x)$ = response coefficient relating the proportional increase in $\mu(x)$ to exposure accumulated at age i.

The latency period for benzene exposure is assumed to be two years, the same as that for radiation exposure (NAS, 1980). Because leukemia mortality generally increases with age, the relative risk formulation produces larger excess death rates at higher ages.

To demonstrate the importance of mortality, fertility, and age structure, several diverse populations from Keyfitz and Flieger (1968) were selected based upon life expectancy, net reproduction rate, and percentage of population under age 15. Each population was normalized to an initial size equal to the 1973 U. S. population for comparison with the single coefficient model. To eliminate another source of variation, the leukemia mortality rates of the 1970 U. S. white population were used for each population. This means that in the relative risk formulation the baseline cancer rates of the U. S. white population were used to generate excess risk data for each population.

7.2 Results of the Comparison

Comparison of the single coefficient model with the demographic model for continuous exposure to 0.87 ppb of benzene for 15 or 50 years yields widely varying estimates of excess mortality. Table 7.1 compares the results obtained with the demographic model for eight populations with results of the

Table 7.1. Comparison of the Single Coefficient Model with the Demographic Model for Estimated Excess Leukemia Deaths After 15 or 50 Years of Exposure of Various Populations to 1 ppb of Benzene

Country and Year	Female e_0	Net Reproduction Rate	% of Population < 15	Total Excess Leukemia Deaths for Females	
				After 15 yrs.	After 50 yrs.
United States (White) 1970	75.62	1.446	28	974	15,000
United States (Black) 1970	68.84	1.132	35	655	11,676
Algeria, 1965	67.99	2.643	47	701	17,144
Guinea (African), 1955	27.51	1.467	42	453	6,386
Honduras, 1966	60.57	2.675	51	701	17,568
Japan, 1964	72.95	0.995	25	747	13,760
Sweden, 1965	76.12	1.153	21	1053	14,584
Togo, 1961	40.33	2.057	48	523	12,436
Single Coefficient Model of Albert et al., 1979	-	-	-	675	2,250

single coefficient model. The demographic model gave numbers of excess deaths after 15 years of exposure ranging from a low of 523 (Togo) to a high of 1053 (Sweden). The single coefficient model gave a value in the lower part of this range, an estimated 675 excess deaths. However, after 50 years of exposure, the demographic model with the diverse population structures and the single coefficient model yielded widely varying estimates of excess deaths. The single coefficient model estimated 2250 deaths, while the demographic model estimated values ranging from 6386 to 17,568. It therefore appears that the model used to project excess deaths is very important. The demographic model, since it makes explicit assumptions concerning mortality, fertility, and the resulting age structure, is able to dynamically follow the population through time. The single coefficient model has made hidden assumptions about mortality, fertility, and age structure and, in addition, is static in that it can only project estimates for a single year and cannot allow the dose to accumulate over time. In the short term, differences are small. Long-term risks, however, at least in the case of benzene, may be grossly underestimated in the single coefficient model.

To further demonstrate the inability of the single coefficient model to simulate dose over time, Figure 7.1 is presented. The y axis represents the number of excess leukemia deaths, and the x axis represents the projection by year. In the second 5-year interval, both models estimate about the same number of deaths. However, beginning with the third 5-year interval, the demographic model's projection for each population exceeds the total number of leukemia deaths in the single coefficient model's projection. In fact, in the

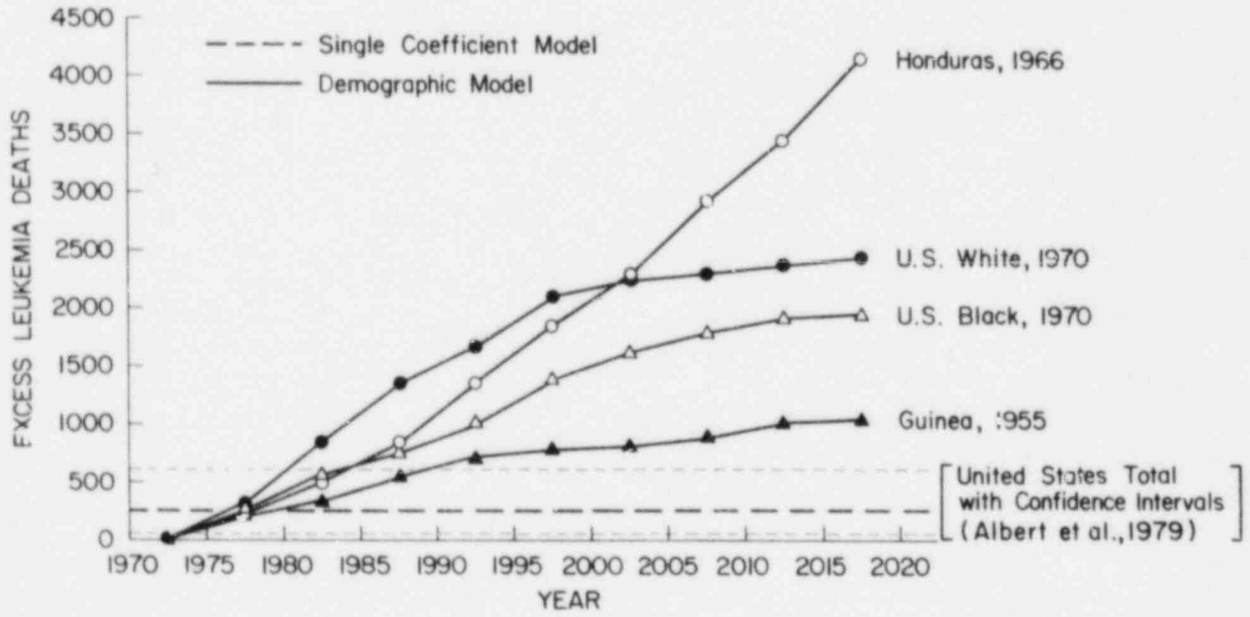

Fig. 7.1. Comparison of the Single Coefficient Model with the Demographic Model for Estimating Excess Female Deaths from Leukemia Resulting from a Continuous Exposure to 1 ppb of Benzene

interval 2015-20, the excess leukemia deaths projected by the demographic model in the U. S. white population are ten times those projected by the single coefficient model.

The excess mortality levels projected for diverse population structures by the demographic model vary widely over time. The following observations can be made:

1. Older populations initially produce more excess deaths because their age structure exposes more persons to higher risk.

2. Populations with low life expectancies have lower levels of excess deaths because competing risks from other causes of death eliminate large segments of the population before they can succumb to the benzene-induced leukemia.

3. Populations with high fertility levels produce large numbers of excess deaths in the long term because more persons are born to be exposed.

7.3 Conclusions

In conclusion, the single coefficient model and the demographic model yield widely varying estimates of excess mortality. The confidence intervals for the single coefficient model encompass only the first 20 years of excess deaths estimated by the demographic model. The demographic model is able to follow populations over time while incorporating specific assumptions about age, fertility, and mortality structure. Comparisons with other projection models of health risk indicate that variations introduced into the estimation of excess deaths resulting from age, fertility, and mortality structure may equal or exceed the variance inherent in estimating a dose response function.

8.0 COMPARISON OF THE DEMOGRAPHIC MODEL WITH A LIFE TABLE MODEL

The purpose of this chapter is to explain the meaning of the estimates of excess risk appearing in the BEIR 1980 report (NAS, 1980) and to show how these estimates, if interpreted incorrectly, can be misleading. The model used to estimate excess deaths in the BEIR 1980 report is the life table model proposed by Cook et al. (Cook et al., 1978; Bunger et al., 1981). In addition to the cautions issued for the use of a life table model, a more versatile model, referred to as the Simulation Package for the Analysis of Health Risk (SPAHR), will be presented and compared to the life table model. The results of this comparison will demonstrate when use of the life table model is appropriate.

8.1 The Life Table Model

There appears to be a great deal of misunderstanding about the life table model results presented in the BEIR Committee Report of 1980 (NAS, 1980). The results have two interpretations. First, the life table model can be viewed as depicting the lifetime mortality experience of a single cohort of newborn babies, who are subject to the age-specific mortality rates on which the table is based. Of course, this description does not have to be limited to newborns. We could just as easily depict the mortality experience of persons over 18, for instance. In the second interpretation, the life table model is viewed as a "stationary" population resulting from the unchanging schedule of age-specific mortality rates shown and a constant annual number of births.

The age and fertility structures of the stationary population of the life table are, in almost all cases, very different from those of the actual population from which the table was derived. A stationary population is defined as a population whose total number and distribution by age do not change with time. Such a hypothetical population could be obtained if the number of births per year remained constant (usually assumed to be 100,000) for a long period of time and if each cohort of births experienced the currently observed mortality rates throughout life. The annual number of deaths would also equal 100,000, and there would be no change in the size of the population; thus the term stationary population. The stationary population, therefore, accounts only for the mortality structure of the population. Fertility and age structure are not considered.

8.2 The Demographic Model--SPAHR

Table 8.1 compares estimates of excess mortality resulting from a 70-year exposure to 1 rad per year per million males and females for life table populations and actual populations. The results of the Cook et al. (1978) program that was used in the BEIR committee report are compared with the SPAHR results, which use the actual population structures. As can be seen, the Cook et al.

Table 8.1. Comparison of Estimates of Excess Mortality of the 1980 BEIR Committee Report with the SPAHR Model, 1969-1971 Total U. S. Population and 1970 Black U. S. Population, on Normal Life Expectation and Excess Deaths for One Million Males and Females with a Continuous Exposure of 1 Rad per Year for 70 Years Using an Absolute Risk Model for the BEIR Committee Report of 1980

Causes of Death and Model Type	Life Table Populations (Stationary Population)						Actual Population Structures			
	Cook et al. (1978) Used in BEIR 1980 (1969-1971 U. S. Total)		SPAHR Replication (1969-1971 U. S. Total)		SPAHR Estimates for 1970 U. S. Black Population		Total U. S. Population 1969-1971		Total U. S. Black Population 1970	
	Males	Females	Males	Females	Males	Females	Males	Females	Males	Females
Cancers Other than Leukemia and Bone										
LQ-L excess*	2459	4243	2470	4440	1980	3870	3769	6458	4805	8571
LL excess*	5827	10400	5800	10760	4570	9250	8756	15569	11069	20488
Q-L excess*	**	**	30	50	30	50	50	84	64	112
Leukemia and Bone										
LQ-L excess	1592	1209	1470	1130	1250	1010	2091	1526	2780	2049
LL excess	3568	2709	3960	3060	3360	2720	5665	4121	7551	5562
Q-L excess	**	**	20	20	10	10	28	20	37	27
Summary Measures of Population Structure										
e_o	67.052	74.650	67.048	74.787	59.836	68.838	67.048	74.787	59.836	68.838
% Less than age 15	15	15	15	15	16	14	25	28	35	32
Crude Birth Rate (X1000)	14.10		14.10		15.54		18.13		25.73	

*Abbreviations: LQ-L, linear quadratic model; LL, linear model; Q-L, quadratic model; e_o, expectation of life.
**Estimate not provided in the BEIR report.

program and SPAHR yield similar results for the life table model of the 1969-1971 population of the United States. The summary measures of population structure are also very similar for these two models, indicating the validity of both computer packages.

8.3 The Results of the Comparison

Returning to the two interpretations of the life table (Chapter 8.1), the results can be understood as follows. First, in examining the results of the linear quadratic model (LQ-L excess) for this exposure scenario, the number for males (2459) can be interpreted to mean either (1) that for newborn males the increased probability of dying from the exposure scenario is 2459 divided by 1 million, or 0.002459, or (2) that there will be 2459 excess deaths from the stationary population of 1 million males. The first interpretation is powerful in that it represents an individual's increased probability of death, which applies only to birth cohorts born into this exposure scenario. However, it tells nothing of the expected number of deaths in an actual population. The second interpretation refers to the excess number of deaths in a stationary population, and this interpretation is valid only if the actual and the stationary populations are identical. The actual population structure is also presented in Table 8.1. The total U. S. population, 1969-1971, was used to construct the life table populations for both the Cook et al. program and SPAHR.

Examining the summary measures of population structure reveals the differences between the life table population and the actual population from which the life table was derived. There is, of course, no difference in life expectancy at birth (e_0) for the SPAHR life table model and the actual total U. S. population. In addition, the difference in the crude birth rates is small, 14.10 compared to 18.13. However, the age structures appear radically different. The life table model has 15% of both males and females younger than age 15, whereas the actual population has 25% of males and 28% of the females less than 15 years of age. The actual population is much younger than the life table population. This results in lower life table estimates of excess deaths than those estimated in the actual population, because the younger population is less susceptible to the diluting effect of competing risks from other causes of death. The estimates of excess deaths are approximately 50% higher in the actual population than in the life table population for both groupings of cancer deaths. Therefore, if we want to estimate probabilities for specific birth cohorts, the life table model is useful. However, if we wish to estimate excess deaths for a specific population, the life table model yields misleading results, underestimating excess deaths by 50% in the present example.

A further demonstration of the importance of population structure is given by comparison of the life table populations with the actual population structure for blacks in the United States. In 1970, blacks had a much lower life expectancy than did the total population. For males, life expectancy was

59.839 (blacks) compared with 67.048 (whites); for females, life expectancy was 68.838 (blacks) compared with 74.787 (whites). The black population should experience fewer life table deaths because competing risks from other causes of death are greater. The results in Table 8.1 confirm this. For cancers other than leukemia and bone cancer in males, the linear life table model (LL) estimates about 5800 excess deaths for the 1969-1971 U. S. total population and only 4570 excess deaths for the 1970 U. S. black population. That is, an individual black male born into this exposure scenario has a lower probability of dying of an excess cancer than does the average male in the total popula-tion, because the black male is more likely to die from other causes than from the radiation-induced cancer.

If we examine the actual population structure, a very different picture emerges. First, a comparison of the summary measures for the life table and actual populations presents a striking contrast. While the expectation of life (e_o) is the same, the actual population is much younger and has a higher birth rate than does the life table population. The excess death estimates are therefore much higher for the actual population than for the life table population; this difference is in all cases greater than 100%.

This contrast between the life table and actual populations for blacks brings into focus the appropriateness of the two approaches. The life table model provides an estimate of increased probability of death for an individual in a specific birth cohort under a particular radiation scenario. The SPAHR model provides a further estimate of the number of expected deaths in the actual population under a particular radiation scenario. For the black population, the individual probability of dying of a radiation-induced cancer is small compared to that of the total population, while the excess deaths in the black population are much greater than in the total population. While the black population has a lower probability of dying from the radiation-induced cancer, the age and fertility structure of the black population exposes more persons to greater risk and results in larger numbers of excess deaths.

In summary, the life table population is appropriate when an estimate of the increased probability of dying from a radiation-induced cancer for a particular birth cohort is needed. However, more general estimates such as excess numbers of deaths for a particular population under a particular radiation scenario should be derived from actual populations and not from the stationary populations of the life table.

8.4 Replication of BEIR 1980 Estimates of Excess Mortality

To replicate with SPAHR the results of the Cook et al. (1978) life table model used in the BEIR 1980 report, the user should invoke the interactive package called WORKER and specify a life table model. The WORKER program will prompt the user for this option. The user should then follow the populations for 70 years after the beginning of the exposure. Because the life table model of Cook et al. (1978) estimates a lifetime risk, the excess deaths for

males occur 65 years after exposure, and those for females 70 years after exposure. (Males have a life expectancy of 65 and females of 70.) In other words, excess life table deaths for females appear in the year 2040 (70 years after exposure), while those for males appear in the year 2035 (65 years after initial exposure). Excess deaths for the actual population structures are calculated in the same way by not selecting the life table model option.

To maintain comparability of the population sizes at risk, the SPAHR user should specify a total population size of 2 million. Keep in mind that the life table model begins with 1 million males and 1 million females at risk, or 2 million persons. Of course, specifying a total population size of 2 million does not expose a million males and a million females, because the sex ratio of the population is rarely 1:1. Nevertheless, the bias introduced by this approach is very small.

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