

**THEORY AND GENERAL MODELS OF MASS SCREENING  
FOR CONTAGIOUS AND NON-CONTAGIOUS DISEASES**

**Théorie et modèles généraux de dépistage de masse pour  
des maladies contagieuses et non-contagieuses**

*National Contribution of UNITED STATES*

HAU L. LEE

*Department of Industrial Engineering and Engineering Management  
Stanford University, U.S.A.*

WILLIAM P. PIERSKALLA

*The Wharton School  
University of Pennsylvania, U.S.A.*

**Abstract:** We present the formulation of a mathematical theory and models of mass screening of populations for contagious and non-contagious diseases. We describe the stochastic processes underlying the progression of a disease in a population when mass screening programs and compliance regimens are instituted. The resulting models are useful for the analysis of the optimal design of mass screening programs for a country or agency which is attempting to control or eradicate a contagious or non-contagious disease. In the model non-contagious diseases are shown to be special cases of contagious diseases when certain parameters of distributions are held constant.

**Résumé:** Nous présentons une théorie mathématique et des modèles de dépistage de masse dans des populations pour des maladies contagieuses et non-contagieuses. Nous décrivons les processus stochastiques rendant compte de la progression d'une maladie dans une population quand des programmes de dépistage de masse et des régimes obligatoires sont institués. Les modèles qui en résultent peuvent servir à l'analyse de la conception optimale des programmes de dépistage de masse pour un pays ou une institution qui s'efforce de contrôler ou d'éliminer une maladie contagieuse ou non-contagieuse. Dans le modèle, les maladies non-contagieuses sont traitées comme des cas particuliers de maladies contagieuses dans lesquelles certains paramètres ou certaines distributions sont gardés constants.

## 1. INTRODUCTION

A population -- either of human beings, inanimate objects, plants or animals -- are constantly subject to randomly occurring diseases. Whether these diseases are acute or chronic in nature, they may exist and develop within a person, at least for a time, without any manifest symptoms. Early detection of such diseases is usually desirable as this may ameliorate or increase the chance of curing the disease, as well as reduce the chance that the asymptomatic population will contract the disease in the case when the disease is contagious. Modern technological advancement in medical and biological diagnosis has resulted in the introduction of various test procedures to detect different diseases. Periodic administration of these test procedures to large groups of the population, i.e., mass screening programs, may thus be advisable. Currently such mass screening programs are under discussion for the detection and control of HIV (Human Immuno Deficiency Virus), which most often leads to the disease AIDS. They are often used for hepatitis A, B, nonA-nonB, tuberculosis, syphilis, and other infectious diseases.

Monitoring mass screening programs, however, is an expensive task. The cost of mass screening includes easily quantifiable economic costs such as those of the labor and materials needed to administer the testing. Other cost components may be more difficult to quantify. For example, the cost may include the inconvenience and possible discomfort necessitated by the test; the cost of false positives which entails both emotional distress and the need to do unnecessary follow-up testing; and even the risk of physical harm to the testee, e.g., the cumulative effect of X-ray exposure or unnecessary surgery.

To the policy maker, mass screening programs have to be designed in light of the tradeoff of the expenses of testing which increases both with the frequency of test applications and with the cost of the type of test used against the benefits to be achieved from detecting the defect in an earlier stage of development. Such a design must determine which kind of testing technology to be used, as different technologies may have different reliability characteristics and costs. In addition, the frequency of testing must be decided. Moreover, because different subpopulations may have different susceptibility to the disease, the problem of optimal allocation of a fixed testing budget among subpopulations must be considered. Also behavioral problems of attendance at the testing location and compliance with treatment after disease discovery must be included in the analysis.

As will be discussed in the next section, while there exists a literature concerning the theory of screening, there has not been a comprehensive study on the analysis of a conceptual model of mass screening to consider the above design issues. Most of the past research efforts utilize an approach to develop screening models based on a single individual's decision for screening rather than a large group(s) of individuals. An individual through his lifetime is subject to different probabilities of incurring the disease and screening schedules are consequently evaluated for an individual. In cases when the society (health agency such as a health department, government bureau, or a prepaid group practice) will bear the cost of administering screening programs and when a health agency, or society at large, has only a fixed and limited amount of resources to be used for mass screening, screening tests are not provided continuously throughout the year, but rather periodically. The question of which tests to use and when, which personnel to administer the tests and what utility functions of the group, subgroups or society should be maximized have not been analytically addressed when one considers the different etiology of diseases and different test capabilities and effects.

Most previous works have focused on non-contagious diseases such as cancer. In view of the potential benefit of detecting the existence of contagious diseases in reducing the risk of asymptomatic but susceptible groups in the population, models of screening for contagious diseases and their analyses will be of value to those decision makers responsible for administering such programs.

The purpose of this paper is to describe the development of a general model of mass screening for both contagious and non-contagious diseases with special emphasis on appropriate objectives, false positive and false negative rates of test, subgroup compliance and susceptibility characteristics, disease etiology and the resource allocation of fixed budgets.

## 2. LITERATURE REVIEW

Pierskalla and Voelker [16], and McCall [13] have provided comprehensive reviews of maintenance models for the control and surveillance of deteriorating systems in general. Rather than detail the very large literature on maintenance, in this section we focus on those past efforts which have a bearing on the problem of mass screening.

Kirch and Klein [9] address explicitly a mass screening application that seeks an inspection schedule to minimize expected detection delay (the time from disease incidence until its detection). The methodology is then

applied to determining examination schedules for breast cancer detection [Kirch and Klein, 10]. McCall [14] considers the problem of scheduling dental examinations, where cavities are assumed to occur according to a Poisson process.

Lincoln and Weiss [12] study the statistical characteristics of detection delay under the assumption that the times of examinations form a renewal process and that the probability of detecting the defect is a function of the defect's age. Zelen and Feinleib [27] and Feinleib and Zelen [8] have studied the statistical characteristics of the lead time (the time a disease is detected by screening to the time it is self-detected or symptomatic) provided by a screening program.

Much research has also been done in the etiology and progress of a disease and its relationship to screening effectiveness. Both the reliability of test and the lead time gained from detection can be modelled as a function of the state of the disease rather than the time since the defect's incidence (for example: Prorok [18 and 19], Thompson and Doyle [23], Shwartz and Galliher [20], Thompson and Disney [24], and Voelker [25]). Blumenson [4] develops a mathematical model to evaluate a screening strategy, termed "compromise screening strategy," which consists of two stages of screening examinations with different harmful effects as well as accuracies. The model has also been applied to evaluate different screening intervals for breast cancer detection (Bross and Blumenson [5]). More recently, Shwartz [22] has developed a mathematical model of breast cancer and used it to evaluate the benefits of screening (Shwartz [21]). Again the rate of disease progression is explicitly included in affecting the probability of the disease detection.

Eddy [7], well aware of the complexity of relationships among test reliabilities, disease development, and prognosis of the disease, has constructed a breast cancer screening model by focusing on two attributes that carry information about the effectiveness of the screening tests: the mammogram interval and the patient interval. By modelling these two intervals as random variables, Eddy is able to derive analytical expressions for the sensitivity (true-positive rate) and specificity (true-negative rate) of test procedures, utilizing repeatedly the Bayesian statistical approach. The design of screening strategies to optimally allocate fixed resources, however, has only been briefly discussed. Eddy's work is important as it is one that has been implemented by health agencies.

The above mentioned studies concentrate on incorporating the process of disease progress in their models to evaluate screening programs. Almost all of these studies, however, take a longitudinal view of an individual. An individual through his lifetime is subject to different probabilities of incurring the disease and screening schedules are evaluated (these also with

respect to an individual). For many diseases an important alternative approach is to take the society's or a group practice point of view. Hence, instead of screening program schedules for an individual, mass screening programs must be considered.

The only research on mass screening are the works by Pierskalla and Voelker [17] and Voelker and Pierskalla [26]. Analytical models of a mass screening program are developed and analyzed for both the cases where the test procedures are perfect or imperfect. Optimal allocation of a fixed budget to different sub-populations are given in the perfect test case, whereas optimal decision rules concerning the best choice and frequency test is derived for the imperfect case.

Finally, to date, the theory of mass screening for contagious diseases has been generally overlooked. From a societal viewpoint, screening for such contagious diseases as tuberculosis of persons in urban ghetto areas and venereal diseases in the sexually active may have very significant benefits for the individuals, but also for their disease-free contacts and for new-borns. However, such mass screening programs are costly, so models must be developed to trade-off the costs and benefits for their most cost-effective implementations.

### 3. A GENERAL MODEL OF MASS SCREENING

In this section, we develop a mathematical model that describes the stochastic processes of the progression of a disease within a population when mass screening programs are instituted. We first describe the epidemic progression of the disease without mass screening, followed by the progression under mass screening. We shall first consider the case when there is only one type of mass screening technology. The model can be easily extended to cases with multiple screening technologies.

For contagious diseases, there may be two distinct stages of the disease that can be identified once a population unit has contracted the disease: the latent and infectious periods. After a unit has contracted a contagious disease, a certain amount of biological development frequently is necessary before it in turn can be passed on to others. This interval is usually termed the "latent period." At the end of the latent period, the infected unit becomes contagious for another period of time, called the "infectious period." The infectious period ends when symptoms of the disease are recognizable and the unit is isolated or removed from the population, or the unit leaves the system by death or other causes. The sum of the latent and infectious periods is called the "incubation period" (see Bailey [1]). We later consider the

case where the infectious unit is not removed from the population but continues to infect others based on a decreasing "compliance" function over time.

There are contagious diseases where the latent period is negligible: for example, scarlet fever and diphtheria. There are also diseases where the latent period may be substantial, such as AIDS. While the assumption that the latent period is negligible could lead to models that are simpler and more tractable for analysis, we shall retain, in the general model, the existence of a latent period for the disease.

(i) Notation

- $W_i(t)$  : number of population units in subgroup  $i$  who are infected but are in the latent period of the disease at time  $t$ ;
- $X_i(t)$  : number of population units in subgroup  $i$  who are infected and are infectious at time  $t$ ;
- $Y_i(t)$  : number of susceptibles in subgroup  $i$  at time  $t$ ;
- $\lambda_j$  : natural incidence rate of the disease for subgroup  $i$ ;
- $\mu_{Xi}$  : rate of leaving the system as an infected unit in the infectious state of the disease for subgroup  $i$  (either by death, self-cure, or removal or isolation after disease is detected without mass screening);
- $\mu_{Wi}$  : rate of leaving the system as an infected unit in the latent state of the disease for subgroup  $i$ ;
- $\mu_{Yi}$  : rate of leaving the system as a susceptible for subgroup  $i$ ;
- $\xi_j$  : rate of transition from the latent stage to the infectious stage for units in subgroup  $i$ ;
- $\alpha_j$  : birth rate of subgroup  $i$ ;
- $\gamma_{ij}$  : rate of transmission of the disease from a contagious unit in subgroup  $j$  to a susceptible in subgroup  $i$ ;

Population subgroups could be homosexuals, alcoholics, men or women in certain age groupings, hospital employees, hospital workers who handle human blood in some manner (drawings, handling, processing), employees on AIDS treatment units, etc.

(ii) Assumptions for the etiology of the disease

- (1) Both the latent period and the infectious periods are exponentially distributed.
- (2) The incidence rates, the rates of transmission of the disease, and the rates of transition from the latent period to the infectious period are stationary over time, and are independent of each other.

- (3) The probability of an increase in the number of infected people at time  $t$  is directly proportional to the number of units in the infectious period of the disease and the number of susceptibles at time  $t$ .
- (4) Once a unit leaves the infectious period, it will never become a susceptible unit again.
- (5) There is negligible transition of units from one subgroup to another over time.

The assumption that the latent and the infectious periods are exponentially distributed is a common one in most models (for example, see McKendrick [15], Bartlett [3], Bartholomew [2], and Bailey [1]). Assumption (3) is also one that is generally used in most stochastic models in epidemics, dated as far back as McKendrick [15] (see also the reviews of Dietz [6] and Bailey [1]).

Assumption (4) is not as restrictive as it seems. First, it is reasonable that a unit isolated upon discovery of the disease can be assumed to have a very small probability of contracting the disease again from another infectious unit. Moreover, some diseases, e.g. measles, usually confer life-long immunity from further attack. Assumption (5) implies that the classification into subgroups of the population is stable over time. This would be the case, for example, if the subgroups refer to male and female.

(iii) Etiology of the disease without mass screening

Consider times  $t$  and  $t + \Delta t$ , where  $\Delta t \rightarrow 0$ .

Let  $\Delta X_i$ ,  $\Delta Y_i$  and  $\Delta W_i$  denote the changes in  $X_i$ ,  $Y_i$  and  $W_i$  between times  $t$  and  $t + \Delta t$ . Then, by assumptions (1), (2), (3), and (5), the stochastic processes underlying the dynamics of  $X_i$ ,  $Y_i$  and  $W_i$  can be described by the following equations:

$$\Pr\{\Delta W_i = +1\} = \lambda_i Y_i(t) \Delta t + \sum_j \gamma_{ij} X_j(t) Y_i(t) \Delta t, \quad (1)$$

$$\Pr\{\Delta W_i = -1\} = (\mu_{W_i} + \varepsilon_i) W_i(t) \Delta t, \quad (2)$$

$$\Pr\{\Delta X_i = +1\} = \varepsilon_i W_i(t) \Delta t, \quad (3)$$

$$\Pr\{\Delta X_i = -1\} = \mu_{X_i} X_i(t) \Delta t, \quad (4)$$

$$\Pr\{\Delta Y_i = +1\} = \alpha_i Y_i(t) \Delta t, \quad (5)$$

$$\Pr\{\Delta Y_i = -1\} = [\mu_{Y_i} + \lambda_i + \sum_j \gamma_{ij} X_j(t)] Y_i(t) \Delta t. \quad (6)$$

By assumption (1), it can be seen that the above formulation gives  $1/\xi_i$  and  $1/\mu_{X_i}$  as the means of the latent and infectious periods respectively.

For cases when the size of the population is very large, we can ignore the consideration of  $Y_j$  (equations (5) and (6)), and simplify (1) as

$$\Pr\{\Delta W_i = +1\} = \lambda_i \Delta t + \sum_j \gamma_{ij} X_j(t) \Delta t, \quad (7)$$

where  $\lambda_i$  and  $\gamma_{ij}$  are the appropriately adjusted rates.

(iv) The model with mass screening

Suppose now that at a given point in time, mass screening is given to all units in the population. We have seen, in the literature review, that the effectiveness of a screening test in detecting the disease is usually a function of the state of the disease at the time when the test is given. For simplicity, we assume that here it is a function of whether the disease is in the latent or the infectious period.

Define

$\eta_{W_i}$  = probability that an infected unit of subgroup  $i$  in the latent period would not be detected by the screening test;

$\eta_{X_i}$  = probability that an infected unit of subgroup  $i$  in the infectious period would not be detected by the screening test.

In general,  $\eta_{W_i} \geq \eta_{X_i}$ .

The following additional assumptions on the screening test will also be used:

- (6) The screening test is uniformly effective for population units in the same stage of the disease (latent vs. infectious).
- (7) The use of mass screening will have no impact on the rate of transmission from an infected unit to a susceptible, and the spontaneous incidence rate of the disease.
- (8) The use of mass screening will have no effect on the distribution of the latent and infectious periods.
- (9) Screening takes place in a negligible interval of time.

Suppose that mass screening is undertaken at time  $T$ . Then, the numbers of units in the various groups just before screening (say,  $T-\epsilon$ , where  $\epsilon \rightarrow 0$ ), are given by  $W_i(T-\epsilon)$ ,  $X_i(T-\epsilon)$  and  $Y_i(T-\epsilon)$ . As screening does not affect the state of susceptibles (even though false positives could be given by the test),  $Y_i$ 's remain unchanged before and after the test. After the test,  $W_i(T+\epsilon)$  and  $X_i(T+\epsilon)$  are thus binomially distributed, i.e.,



$W_i(T+\epsilon)|W_i(T-\epsilon)$  is binomial with parameter  $W_i(T-\epsilon)$  and  $\eta_{W_i}$ ,

and

$X_i(T+\epsilon)|X_i(T-\epsilon)$  is binomial with parameter  $X_i(T-\epsilon)$  and  $\eta_{X_i}$ .

Furthermore

$$E[W_i(T+\epsilon)] = \eta_{W_i} E[W_i(T-\epsilon)] , \quad (8)$$

$$E[X_i(T+\epsilon)] = \eta_{X_i} E[X_i(T-\epsilon)] , \quad (9)$$

$$\text{Var}[W_i(T+\epsilon)] = \eta_{W_i}(1 - \eta_{W_i}) E[W_i(T-\epsilon)] + \eta_{W_i}^2 \text{Var}[W_i(T-\epsilon)] , \quad (10)$$

$$\text{Var}[X_i(T+\epsilon)] = \eta_{X_i}(1 - \eta_{X_i}) E[X_i(T-\epsilon)] + \eta_{X_i}^2 \text{Var}[X_i(T-\epsilon)] . \quad (11)$$

To prove (8) and (9) is straight forward. For (10) and (11), we make use of the relationship that, for any two random variables  $Z_1$  and  $Z_2$ ,

$$\text{Var}(Z_2) = E_{Z_1}[\text{Var}(Z_2|Z_1)] + \text{Var}_{Z_1}[E(Z_2|Z_1)] . \quad (12)$$

Putting  $Z_1 = W_i(T-\epsilon)$  and  $Z_2 = W_i(T+\epsilon)$  in (12) gives (10), and  $Z_1 = X_i(T-\epsilon)$  and  $Z_2 = X_i(T+\epsilon)$  in (12) gives (11).

After mass screening, the stochastic process of the etiology of the disease resumes to equations (1) to (6), with  $W_i(T+\epsilon)$  and  $X_i(T+\epsilon)$  being the initial values of  $W_i$  and  $X_i$  respectively.

#### (v) The problem of compliance

After mass screening, we have assumed that the units in the population identified as having the disease are then isolated or treated so that they are no longer infectious. In real life, this may not always be the case. For example, for diseases like Hepatitis B and AIDS, the common isolation mechanism is for the patient to exercise self-control and lead a disciplined life to avoid passing the disease to others. Other diseases may require the patients to be treated over an extended time horizon. In this situation, it is possible that a patient may not comply with the prescribed treatment after some time. By doing so, he or she is no longer in isolation from susceptibles, and would begin to transmit the disease if still infectious.

For the evaluation of any mass screening program, it is important to incorporate the behavioral aspects of compliance into the decision processes. The effectiveness of a screening program could be severely hampered by noncompliance of patients identified by screening. While such a behavioral aspect has not been considered in past studies on the economic design of mass

screening efforts, we shall attempt to model its effect on the progression of the disease.

For modelling purposes, we assume that the length of time that a patient complies with the prescribed treatment given to him or her is exponentially distributed with mean  $1/\rho_i$ , for population subgroup  $i$ . Hence, the probability that a patient in subgroup  $i$  would comply for a period of time  $\tau$  periods or longer is given by

$$C_i(\tau) = 1 - \int_0^{\tau} \rho_i \exp(-\rho_i t) dt . \quad (13)$$

It is clear that  $C_i(\tau)$  is exponentially decreasing in  $\tau$ . The function  $C_i(\tau)$  can be viewed as the compliance function of subgroup  $i$ . In what follows, we shall distinguish the compliance functions of units in the latent and the infectious periods of the disease, as there may be behavioral differences between units in these two states of the disease.

Define

$V_{Wi}(t)$  : number of infected units in subgroup  $i$  in the latent period of the disease who have been identified by a previous screening test, and who are currently complying with the treatments at time  $t$ ;

$V_{Xi}(t)$  : same as above for units in the infectious period of the disease;

$1/\rho_{Wi}$  : mean of the length of compliance time for units of subgroup  $i$  in the latent period of the disease;

$1/\rho_{Xi}$  : mean of the length of compliance time for units of subgroup  $i$  in the infectious period of the disease;

$\mu_{W_i}$  : rate of leaving the system of units in  $V_{Wi}$ ;

$\mu_{X_i}$  : rate of leaving the system of units in  $V_{Xi}$ ;

$\xi_{Vi}$  : rate of transition from the latent stage to the infectious stage for units in subgroup  $i$  who have been complying with treatments after being identified in mass screening.

The stochastic process of the etiology of the disease would have to be modified now. First, consider mass screening at time  $T$  as before. Then,

$$V_{Wi}(T+\epsilon) = V_{Wi}(T-\epsilon) + Z_{Wi}(T) , \quad (14)$$

$$V_{Xi}(T+\epsilon) = V_{Xi}(T-\epsilon) + Z_{Xi}(T) , \quad (15)$$

where  $Z_{Wi}(T)$  and  $Z_{Xi}(T)$  are the number of infected units identified in the screening test at  $T$  in the latent and infectious periods respectively.

It is clear that

$$Z_{W_i}(T) | W_i(T-\varepsilon) = W_i(T-\varepsilon) - [W_i(T+\varepsilon) | W_i(T-\varepsilon)] , \quad (16)$$

and

$$Z_{X_i}(T) | X_i(T-\varepsilon) = X_i(T-\varepsilon) - [X_i(T+\varepsilon) | X_i(T-\varepsilon)] . \quad (17)$$

We recall that  $W_i(T+\varepsilon) | W_i(T-\varepsilon)$  and  $X_i(T+\varepsilon) | X_i(T-\varepsilon)$  are binomially distributed with parameters  $W_i(T-\varepsilon)$ ,  $\eta_{W_i}$  and  $X_i(T-\varepsilon)$ ,  $\eta_{X_i}$  respectively.

Based on (14) to (17), we obtain

$$E[Z_{W_i}(T)] = (1 - \eta_{W_i}) E[W_i(T-\varepsilon)] , \quad (18)$$

$$E[Z_{X_i}(T)] = (1 - \eta_{X_i}) E[X_i(T-\varepsilon)] , \quad (19)$$

$$\text{Var}[Z_{W_i}(T)] = \eta_{W_i}(1 - \eta_{W_i}) E[W_i(T-\varepsilon)] + (1 - \eta_{W_i})^2 \text{Var}[W_i(T-\varepsilon)] , \quad (20)$$

and

$$\text{Var}[Z_{X_i}(T)] = \eta_{X_i}(1 - \eta_{X_i}) E[X_i(T-\varepsilon)] + (1 - \eta_{X_i})^2 \text{Var}[X_i(T-\varepsilon)] . \quad (21)$$

Equations (20) and (21) are obtained using (12), in a similar way as the derivation of (10) and (11).

Second, after mass screening, the stochastic process follows the following equations describing the etiology of the disease,

$$\text{Pr}(\Delta V_{W_i} = +1) = 0 , \quad (22)$$

$$\text{Pr}(\Delta V_{W_i} = -1) = (\mu_{V_{W_i}} + \xi_{V_i} + \rho_{W_i}) V_{W_i}(t) \Delta t , \quad (23)$$

$$\text{Pr}(\Delta V_{X_i} = +1) = \xi_{V_i} V_{W_i}(t) \Delta t , \quad (24)$$

$$\text{Pr}(\Delta V_{X_i} = -1) = (\mu_{V_{X_i}} + \rho_{X_i}) V_{X_i}(t) \Delta t , \quad (25)$$

$$\begin{aligned} \text{Pr}(\Delta W_i = +1) &= \lambda_i Y_i(t) \Delta t + \sum_j \gamma_{ij} X_j(t) Y_i(t) \Delta t \\ &\quad + \rho_{W_i} V_{W_i}(t) \Delta t , \end{aligned} \quad (26)$$

$$\text{Pr}(\Delta W_i = -1) = (\mu_{W_i} + \xi_i) W_i(t) \Delta t , \quad (27)$$

$$\text{Pr}(\Delta X_i = +1) = \xi_i W_i(t) \Delta t + \rho_{X_i} V_{X_i}(t) \Delta t , \quad (28)$$

$$\text{Pr}(\Delta X_i = -1) = \mu_{X_i} X_i(t) \Delta t , \quad (29)$$

$$\Pr\{\Delta Y_i = +1\} = \alpha_i Y_i(t) \Delta t, \quad (30)$$

$$\Pr\{\Delta Y_i = -1\} = [\mu_{Y_i} + \lambda_i + \sum_j \gamma_{ij} X_j(t)] Y_i(t) \Delta t. \quad (31)$$

#### (vi) A Model for Non-Contagious Diseases

For diseases that are not contagious, a special case of the model in the last section can be used. First, we do not have to distinguish between  $W_i$  and  $X_i$ , as the meaning of latent and infectious period does not exist for non-contagious diseases. Let  $W_i$  denote the number of infected units, and ignore  $X_i$ . It is clear that, for non-contagious diseases,  $\gamma_{ij} = 0$ . Therefore, the stochastic process describing the epidemics of the disease, based on (1) to (6), can be written as

$$\Pr\{\Delta W_i = +1\} = \lambda_i Y_i(t) \Delta t \quad (32)$$

$$\Pr\{\Delta W_i = -1\} = \mu_{W_i} W_i(t) \Delta t \quad (33)$$

$$\Pr\{\Delta Y_i = +1\} = \alpha_i \Delta t \quad (34)$$

$$\Pr\{\Delta Y_i = -1\} = \mu_{Y_i} Y_i(t) \Delta t. \quad (35)$$

When the size of the population is large, we can simplify the process by

$$\Pr\{\Delta W_i = +1\} = \lambda_i \Delta t \quad (36)$$

$$\Pr\{\Delta W_i = -1\} = \mu_{W_i} W_i(t) \Delta t \quad (37)$$

Similar modifications can be made to the contagious model with compliance (equations (22) to (31)). Compliance may still be an important factor in determining the optimal tests to use and the optimal testing frequency-- particularly when compliance affects the benefits and costs of testing.

Voelker and Pierskalla [1980] and Pierskalla and Voelker [1978] have analyzed the mass screening model with non-contagious diseases as described by (36) and (37).

#### 4. SUMMARY

In this paper we have described the stochastic processes underlying the progression of a disease when mass screening is used and when the compliance rate of patients identified by the screening tests may be less than 100%.

The model formulated, however, is extremely complicated, and may be mathematically intractable. There are two approaches that could be taken from this point onwards. First, we can resort to the use of simulation to analyze the operating characteristics of mass screening programs, which can then be used for economic analysis to tackle the issues outlined in the introduction. Second, in many cases, simplifying assumptions can be made so as to facilitate mathematical analysis. The appropriateness of these simplifying assumptions, however, is an empirical question that depends on circumstances and specific diseases. These two approaches are investigated in later papers. In Lee and Pierskalla [11], the special case of diseases with no latent period is studied. Currently work is ongoing to simulate the contagious diseases Hepatitis B and AIDS, under the general framework of this paper.

## REFERENCES

- [1] Bailey, N.T.J., The Mathematical Theory of Infectious Disease and Its Applications, Charles Griffin & Co. Ltd., London [1975].
- [2] Bartholomew, D.J., Stochastic Models for Social Processes, John Wiley & Sons, London [1967].
- [3] Bartlett, M.S., "Some Evolutionary Stochastic Processes," Journal of the Royal Statistical Society, Series B, Vol. 11 [1949], 211-29.
- [4] Blumenson, L.E., "Compromise Screening Strategies for Chronic Disease," Mathematical Biosciences, 34 [1977], 79-94.
- [5] Bross, I.D.J. and L.E. Blumenson, "Screening Random Asymptomatic Women Under 50 by Annual Mammographies: Does it Make Sense," Journal of Surgical Oncology, 8 [1976], 437-445.
- [6] Dietz, K., "Epidemic and Rumors: A Survey," Journal of the Royal Statistical Society, Series A, 130, [1967], 505-528.
- [7] Eddy, D.M., Screening for Cancer: Theory, Analysis, and Design, Prentice-Hall, Inc., Englewood Cliffs, New Jersey [1980].
- [8] Feinleib, M. and M. Zelen, "Some Pitfalls in the Evaluation of Screening Programs," Arch. Environ. Health, 19 [1969], 412-415.
- [9] Kirch R. and M. Klein, "Surveillance Schedules for Medical Examinations," Management Science, 20 [1974], 1403-1409.
- [10] Kirch R. and M. Klein, "Examination Schedules for Breast Cancer," Cancer, 33 [1974], 1444-1450.
- [11] Lee, H.L. and W.P. Pierskalla, "Mass Screening Models for Contagious Diseases with No Latent Period," Working paper submitted to Operations Research, 1987.
- [12] Lincoln, T. and G.H. Weiss, "A Statistical Evaluation of Recurrent Medical Examinations," Operations Research, 12 [1964], 187-205.

- [13] McCall, J., "Maintenance Policies for Stochastically Failing Equipment: A Survey," Management Science, [1965], 493-524.
- [14] McCall, J., "Preventive Medicine Policies," Rand Corporation P-3368-1, 1969.
- [15] McKendrick, A.G., "Applications of Mathematics to Medical Problems," Proceedings of Edinburgh Mathematical Society, Vol. 14, [1926], 98-130.
- [16] Pierskalla, W.P. and J.A. Voelker, "A Survey of Maintenance Models: The Control and Surveillance of Deteriorating Systems," Naval Research Logistics Quarterly, 23, 3 [1976], 353-388.
- [17] Pierskalla, W.P. and J.A. Voelker, "A Model for Optimal Mass Screening and the Case of Perfect Test Reliability," Technical Report No. 3, Northwestern University, Department of Industrial Engineering and Management Sciences [1978].
- [18] Prorok, P., "The Theory of Periodic Screening, I: Lead Time and Proportion Detected," Advances in Applied Probability, 8 [1976], 127-143.
- [19] Prorok, P., "The Theory of Periodic Screening, II: Doubly Bounded Recurrence Times and Mean Lead Time and Detection Probability Estimation," Advances in Applied Probability, 8 [1976], 460-476.
- [20] Schwartz, M. and H. Galliker, "Analysis of Serial Screening in an Asymptomatic Individual to Detect Breast Cancer," Technical Report, Department of Industrial and Operations Engineering, College of Engineering, University of Michigan, 1975.
- [21] Schwartz, M., "An Analysis of the Benefits of Serial Screening for Breast Cancer Based Upon a Mathematical Model of the Disease," Cancer, 41 [1978], 1550-1564.
- [22] Schwartz, M. "A Mathematical Model Used to Analyze Breast Cancer Screening Strategies," Operations Research, 26, 6 [1978], 937-955.
- [23] Thompson, D.E. and T.C. Doyle, "Analysis of Screening Strategies for Colorectal Cancer: A Description of an Approach," Michigan Cancer Foundation, Detroit, Michigan, March [1976].
- [24] Thompson, D.E. and R. Disney, "A Mathematical Model of Progressive Diseases and Screening," Vector Research, Inc., Ann Arbor, Michigan, November [1976].
- [25] Voelker, J.A., "Contributions to the Theory of Mass Screening," Ph.D. dissertation, Northwestern University, 1976.
- [26] Voelker, J.A. and W.P. Pierskalla, "Test Selection for a Mass Screening Program," Naval Research Logistics Quarterly, 27, 1 [1980], 43-56.
- [27] Zelen, M. and M. Feinleib, "On the Theory of Screening for Chronic Diseases," Biometrika, 56 [1969], 601.