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R. BARTOSZYŃSKI

Branching processes and models of epidemics

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CONTENTS

0. Introduction. In this paper we shall discuss the applications of the theory of branching processes to the description and analysis of the phenomenon of epidemics, the latter being understood as spreading of a disease. We shall be concerned with two groups of problems: spreading of infectious diseases (which corresponds to the standard usage of the term "epidemics"), and spreading of non-infectious diseases.

Thus, the paper will consists of two parts. In the first part, dealing with epidemics of infectious diseases, we shall attempt to build models, which could supply us with predictions concerning real epidemics based on observations of certain parameters. In the second part, dealing with spreading of non-infectious diseases, we shall try to build a model, which explains the observed increase in occurrence of certain diseases (e.g. cancer) by some general hypotheses concerning mechanisms of inheritance of proneness towards these diseases.

In both parts of this paper, the models considered will be based on the theory of branching processes.

PART I

MODELS OF EPIDEMICS FOR INFECTIOUS DISEASES

1. Informal description of the phenomenon of epidemics and construction of mathematical models. Without trying at the moment to define formally the notion of the *branching process*, it is (using the traditional terminology) the process of changes of size of a population of "particles" endowed with the ability of reproduction, the central assumption being that of independence of reproduction of different particles. This informal description of branching processes suggests their possible application for analysis of the phenomenon of epidemics, treated as the process of changes in the size of the population of individuals infected with a given disease. This application consists of interpreting infectives as particles in a branching process, and infections of susceptibles as reproductions of particles. Thus, implicitely, the application discussed will consist of the analysis of consequences of the assumption that the numbers of individuals infected by different infectives are mutually independent.

As regards the phenomenon of epidemics, the attention of mathematicians trying to build models for it is focused on some of the observable variables; the most important variable is the number of individuals infected at a given moment. Other observable variables can be roughly classified into two groups: one consisting of these variables which concern directly the statistical fluctuations of the number of individuals infected (i.e. the number of new infections, number of deaths or recoveries, and so on), and the statistical fluctuations of the migratory movements within the habitat. The second group consists of these observable variables which concern directly the individual's illness, that is the lengths of the periods of incubation and infectiousness, number of contacts with susceptibles, and so on.

All models of epidemics consist, roughly speaking, of constructing a stochastic process whose analysis could yield verifiable information about the behaviour of the basic observable variable, i.e. the number of individuals infected at a given moment. The probability distributions of these processes depend on some parameters whose interpretation is expressed in terms of some other observable variables. This makes it possible to obtain numerical estimates of these parameters and, in consequence, leads to quantitative predictions. Various groups of models utilize in various ways the information contained in the above-mentioned two groups of observable variables, selecting some of them and neglecting others.

All existing models of epidemics can be divided into two groups; the models of the first group (which will be called, somewhat arbitrarily, "classical") are based on the theory of birth-and-death processes. The models of the second group, which will be studied in this paper, are based on the theory of branching processes.

Roughly speaking, classical models utilize parameters, whose interpretation is expressed in terms of the first group of observable variables, that is, in terms of statistical characteristics of fluctuations of populations of infectives and susceptibles, these populations being taken as a whole. On the other hand, the models based on the theory of branching processes use parameters whose interpretation is expressed in terms of the second group of observable variables, i.e. in terms of statistical properties of events pertaining to individuals.

2. General characterization of the classical models of epidemics. As we have already said, the classical models of epidemics are based on the theory of birth-and-death processes. We shall present the general structure of these models in order to be able to discuss later their applicability to the description and analysis of epidemics. In every classical model one considers a classification of individuals into a certain number

of categories. The number of these categories varies depending on the degree of the complexity of the model, in each case, however, one of these categories consists of individuals infected (other possible categories include susceptibles, carriers, and so on). For a given classification into categories, the state of the population at a given moment is described by a vector with nonnegative integer coordinates, the coordinates describing the total number of individuals in a given category at a given moment. The history of epidemics is interpreted as the process of changes of state of a system whose possible states are described by such vectors. The classical models of epidemics are Markov processes of changes of state of such systems, where it is assumed that (1) the transition intensities vanish for pairs of states such that the coordinates of the corresponding vectors differ by more than one, and (2) for the "neighbouring" states it is assumed that the intensity of transition from a state with k infectives to a state with $k-1$ infectives is proportional to k, while the intensity of transition from a state with k infectives and m susceptibles to a state with $k+1$ infectives and $m-1$ susceptibles is proportional to both k and m. This corresponds to the common intuition, according to which the number of deaths and recoveries (in a short time interval) is proportional to the actual size of epidemic, while the number of new cases is proportional to the size of epidemic and to the number of susceptibles. Given the transition intensities, one can easily write down the system of Kolmogorov equations for the transition probabilities. Due to the special form of these intensities, this system can be reduced to a partial differential equation for the generating function of the transition probabilities. In view of the double proportionality appearing in the assumptions on transition probabilities this equation is non-linear, and its solution presented serious difficulties.

An exhaustive presentation of classical models of epidemics can be found in books by Bartlett [2] and Bailey [1], and also in the paper by Kendall [14]. The basic results concerning classical models obtained recently can be summarized as follows. First of all, Gani [12] and Siskind [16] obtained the solution of the equation for "general stochastic epidemic". Before that, the solutions were known only for some particular cases, and the general solution was known for the "deterministic version" of this equation. Williams [19] obtained limit formulas for the case of infinite populations, and Ridler-Rowe [17] found the distribution of the time until the epidemic expires. Finally, Weiss [18] and Dietz [9] considered classical models enriched with the assumption of existence of carriers.

In discussing the practical value of models of epidemics, one is primarily interested in the problem how adequate is the description of reality supplied by these models. As regards the classical models, the central assumption is that of proportionality of number of new cases

in a short time interval to both the number of infectives and the number of susceptibles (which corresponds to the assumption of "perfect mixing" of populations of infectives and susceptibles). In consequence, these models do not take into account the geographical and social inhomogeneity of habitat. One could consider classical models with enriched classification of individuals into categories, by classifying them not only according to their state of health, but also according to some other characteristic, e.g. their actual position in the habitat [2]. Such models, however, are fairly complicated, and there is a little hope of finding solutions under sufficiently general assumptions.

Thus, classical models failed to supply information about the geographical spread of epidemics, and it became necessary to change the basic assumptions in such a way that the resulting models would supply answers to those questions which remained unanswered by classical models. The basic ideas of such a new approach to epidemics are due to Neyman and Scott [15]; these ideas consist of building models based on the theory of branching processes.

3. General characterization of models based on the theory of branching processes. As in the classical theory, the models of epidemics based on the theory of branching processes will consist of constructing a branching process, whose analysis could yield information about the population of infectives. As has already been mentioned at the beginning, the basic assumption will be that of independence of infections of susceptibles by different infectives. In abstract version, it corresponds to the basic in the theory of branching processes assumption of independence of reproduction of particles. As a consequence of accepting models based on the theory of branching processes one obtains the description of epidemic in terms of sizes of its successive "generations". Roughly speaking, the model will consist of defining a stochastic process $Z_0, Z_1, \ldots$, where Z_n is interpreted as the number of infectives in the nth generation of epidemic. The relation between the number of generation and time is, however, rather loose, and this fact determines the direction of search for theorems which could yield predictions concerning observable events in real epidemics. The attention is focussed on two types of theorems: in one type the assertion is of the form

$$P\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1, \tag{3.1}$$

and in the other type, it is of the form

$$P\{\lim Z_n = 0\} = 1. \tag{3.2}$$

Intuitively, the conditions under which (3.1) holds, and (3.2) does not hold correspond, after expressing them in terms of observable variables, to the state of "danger of an outburst of epidemic".

In this paper we shall present three groups of models based on the theory of branching processes. These groups of models will differ in assumptions concerning statistical properties of mechanisms of infection, expressed in terms of distributions of number of susceptibles infected by a single infective.

In the first group of models, the statistical properties of mechanisms of infection will be expressed in terms of probability distributions of statistical fluctuations of migratory movements within the habitat, and probability distributions of "contagiousness" at different points of the habitat.

In the second group of models we shall assume that the statistical properties of mechanisms of infection at a given moment depend on the past history of the process (here we neglect the migratory movements). Such an approach will enable us, to some extent, study the approximations to epidemics on finite populations.

Finally, in the third group of models, the statistical properties of the mechanisms of infection will be expressed in terms of some observable variables, such as the lengths of periods of incubation and infectiousness, and some parameters characterizing the activity of health service, such as, for instance, the efficiency of vaccinations.

To achieve clarity of description and clarity of proofs of theorems, we shall use whatever terminology would be most intuitive in every particular instance. Thus, we shall sometimes use the terms appealing to common intuition connected with real epidemics (that is, we shall use terms such as "illness", "infection", and so on), and sometimes we shall use the traditional in the theory of branching processes terminology of "particles".

4. First group of models: geographical spread of epidemics. The following model of epidemic had been suggested by Neyman and Scott [15]; it was designed to study the influence of migratory movements of individuals within the habitat on the course of epidemic. With this objective in mind, we shall start from the following intuition: every individual infected at a given moment becomes himself infectious after a fixed (and equal for all individuals) period of incubation. During this period individuals may travel within the habitat. After the period of incubation, the individuals infected pass through an infinitely short period of infectiousness, during which they may infect a certain number of susceptibles.

The above intuitive description allows us to define formally the notion of the nth generation of an epidemic originated by a single individual who himself became infected at a given point of the habitat. Incidentally, the assumption about the incubation period being constant and the same for all individuals was made only in order to obtain a clear

time-interpretation of the notion of a given generation of the epidemic: the nth generation consists of those individuals, who became infected n lengths of period of incubation later than the individual who originated the epidemic. This interpretation, however, is not essential, in the sense that it will not be used in the assertions of the theorems; these will concern only the behaviour of sizes of successive generations.

Formally, the description of the process is based on the following assumptions:

I. *The numbers of susceptibles infected by different infectives are independent, and have probability distributions depending only on the point at which the infection occurs.*

II. *The infectives travel within the habitat during their periods of incubation independently of one another, according to a probability distribution depending only on the point where they became infected.*

Thus, the model will be described by two families of probability distributions concerning assumptions I and II. To describe these distributions, we shall denote by X the habitat, and assume that X s a measure space (that is, a certain fixed σ-field $\mathcal{S}$ of subsets of X had been selected).

We assume that:

(i) To each $x \in X$ there corresponds a probability distribution $\{p(k|x)\}$, $k = 0, 1, \ldots$, where $p(k|x)$ is the probability of infecting exactly k susceptibles if the infection occurs at the point x. We assume that for each k the function $p(k|\cdot)$ is $\mathcal{S}$-measurable.

(ii) To each $x \in X$ there corresponds a probability measure $\nu(\cdot|x)$ on $(X, \mathcal{S})$, where for $A \in \mathcal{S}$ the value $\nu(A|x)$ equals to the probability that an individual infected at the point x will be in the set A at the end of his period of incubation. We assume that for every $A \in \mathcal{S}$ the function $\nu(A|\cdot)$ is $\mathcal{S}$-measurable.

To define the process, let E_m, $m = 1, 2, \ldots$, denote the set of all m-tuples $(x_1, \ldots, x_m)$ of points in X (the order of points $x_1, \ldots, x_m$ is irrelevant, and some points may repeat). Let E_0 denote the set consisting of a single point $\emptyset$, and let $E = \bigcup_{m=0}^{\infty} E_m$. The points in E describe the state of epidemic in the following sense: the state $\emptyset$ denotes the extinction of epidemic (no infectives), while the state $(x_1, \ldots, x_m)$ denotes the state with m infectives who became infected at points $x_1, \ldots, x_m$.

The assumptions of the process define the transition probabilities of a homogeneous Markov chain $\xi_0, \xi_1, \ldots$ with values in E, where ξ_n describes the state of epidemic at n lengths of period of incubation after the initial moment.

We shall assume $\xi_0 = u$, that is, we assume that at the beginning we have one infective, who became infected at the point $u \in X$. We shall

denote by P^u the probabilities of events concerning the process $\{\xi_n\}$ conditional upon $\xi_0 = u$.

As we have already mentioned, our aim will be to study the behaviour of the process $\{Z_n\}$ defined by

$$Z_n = \begin{cases} 0 & \text{if} \quad \xi_n = \emptyset, \\ m & \text{if} \quad \xi_n = (x_1, \ldots, x_m) \end{cases}$$

and we shall try to find conditions under which

$$P^u\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1 \tag{4.1}$$

(or a weaker version, in which $\lim Z_n = \infty$ is replaced by $\limsup Z_n = \infty$), and conditions under which

$$P^u\{\lim Z_n = 0\} = 1. \tag{4.2}$$

We shall start with conditions implying (4.1). One could expect, that such conditions can be expressed in form of assumptions about the sets

$$\{x;\ p(0|x) \geqslant c\}, \tag{4.3}$$

i.e. sets with the property that the probability of not infecting anyone for infectives in these sets is uniformly bounded below. Intuitively, we may expect that if for some $c > 0$ the set (4.3) is "attracting" the infectives, we should have (4.1). The property of "attracting" of infectives by subsets of X will be formally described by the following definition.

DEFINITION. A measurable set $V \subset X$ is called *attractive* if for some $\varepsilon > 0$ and all $x \in X$ we have $\nu(V|x) \geqslant \varepsilon$.

The following theorem was proved in [8]:

THEOREM 4.1. *If there exists $c > 0$ such that the set $\{x;\ p(0|x) \geqslant c\}$ is attractive, then for every $u \in X$ we have*

$$P^u\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1.$$

Paper [8] gives also an example showing that (4.1) may be false under some "non-trivial" assumptions imposed upon the distributions $\{p(k|x)\}$ and measures $\nu(\cdot|x)$. In this example X is a plane, $\mathscr{S}$ is the Borel field of subsets of X, measures $\nu(\cdot|x)$ satisfy the condition $\nu(A|x) > 0$ for every x and every set $A \in \mathscr{S}$ with positive Lebesgue measure, and the function $p(0|x)$ is strictly positive over the whole plane. Yet, for every $x \in X$ we may have $P^x\{\lim Z_n = k\} > 0$ for $k = 0, 1, 2, \ldots, \infty$.

The analysis of this example suggests that the conditions under which the process $\{Z_n\}$ has the property

$$P^u\{\lim Z_n = 0 \text{ or } \limsup Z_n = \infty\} = 1 \tag{4.1}$$

can be expressed in terms of properties of sets of the form

$$\{x;\ p(1|x) < 1-c\}. \tag{4.5}$$

Intuitively, the attractiveness of the set (4.5) for some $c > 0$ introduces to the process $\{Z_n\}$ the amount of randomness sufficient to ensure (4.4). In fact, the following theorem holds (see [4]):

THEOREM 4.2. *If there exists $c > 0$ such that the set*

$$A = \{x;\ p(1|x) < 1-c\} \tag{4.6}$$

is attractive, i.e. there exists $\varepsilon > 0$ such that for all $x \in X$ we have

$$\nu(A|x) \geqslant \varepsilon, \tag{4.7}$$

then for every initial condition $u \in X$ relation (4.4) holds.

Proof. For clarity, we shall use the traditional in the theory of branching processes terminology of "particles". Thus, we shall consider particles which live for a unit of time; during their lives particles can move in the set X, and their movements are governed by measures $\nu(\cdot|x)$. At the end of their life period particles die, giving rise to a random number k ($k = 0, 1, 2, \ldots$) of new particles. If the death occurs at the point x, it gives rise to k new particles with probability $p(k|x)$. The events occurring to different particles are assumed to be independent. We interpret the event of giving rise to k new particles as the event of infecting exactly k susceptibles.

We start from introducing convenient notations. Let S_N, $N = 1, 2, \ldots$, be the set consisting of all finite collections $(x_1, \ldots, x_k)$, $1 \leqslant k \leqslant N$, of points in X (the order of points in $(x_1, \ldots, x_k)$ is irrelevant and some points may repeat). Thus,

$$S_N = \bigcup_{m=1}^{N} E_m.$$

Let $S = \bigcup_{N=1}^{\infty} S_N$. If there are particles at a given time $t = n$, then their position is described by a point $s_n \in S$. The event $s_n \in S_M$ means that $0 < Z_n \leqslant M$, while $s_n \notin S_M$ means that either $Z_n = 0$ or $Z_n > M$.

Since the process is time-homogeneous, to prove (4.4) it suffices to show that under the conditions of the theorem, for every $M > 0$ there exists $\gamma > 0$ and an integer d such that

$$P\{s_k \in S_M,\ k = 1, \ldots, d|s_0\} \leqslant 1-\gamma \tag{4.8}$$

uniformly with respect to $s_0 \in S_M$.

Let us fix $M > 0$ and define d as the smallest integer such that $2^d > M$. We show first that under the conditions of the theorem there exists a number $a > 0$ and a partition of the space X into $d+1$ disjoint

sets $W_0, W_1, \ldots, W_d$ such that each of the following events has probability at least a:

(i) a particle born in W_0 dies giving birth to no offsprings;

(ii) a particle born in W_k ($k = 1, \ldots, d-1$) passes to W_{k-1} and gives birth to at least two offsprings;

(iii) a particle born in W_d passes to $W_{d-1} \cup W_d$ and gives birth to at least two offsprings.

To construct such a partition we may proceed as follows: given the set A defined by (4.6) we partition it into

$$A_0 = A \cap \{x;\ p(0|x) > c/2\}$$

and

$$A_1 = A \cap \{x;\ p(0|x) \leqslant c/2\}.$$

Thus, each particle which reaches the set A_0 dies with no offsprings with probability at least $c/2$, while each particle which reaches A_1 gives birth to at least two offsprings with probability at least $c/2$. Clearly, $A = A_0 \cup A_1$, and by assumption (4.7) we have for all x

$$\nu(A|x) = \nu(A_0|x) + \nu(A_1|x) \geqslant \varepsilon.$$

Define

$$U_0 = \{x;\ \nu(A_0|x) \geqslant \varepsilon/2\},$$

and $V_0 = U_0^c$. Now, on V_0 we have $\nu(A_1|x) \geqslant \varepsilon/2$, and we define U_1 as the subset of V_0 on which $\nu(A_1 \cap U_0|x) \geqslant \varepsilon/4$, and $V_1 = V_0 \cap U_1^c$. In general, having defined U_j and V_j for $j \leqslant k-1$ define

$$U_k = V_{k-1} \cap \{x;\ \nu(A_1 \cap U_{k-1}|x) \geqslant \varepsilon/2^{k+1}\},$$

and $V_k = V_{k-1} \cap U_k^c$.

We now put $W_k = U_k$ for $k = 0, 1, \ldots, d-1$ and $W_d = V_{d-1}$. This clearly defines a partition of space X into $d+1$ disjoint sets, and this partition satisfies requirements (i)-(iii) for a equal $c\varepsilon/2^{d+1}$.

In fact, for particles born in $W_0 = U_0$ the probability of reaching A_0 and dying with no offsprings is at least $\frac{\varepsilon}{2} \cdot \frac{c}{2} \geqslant a$. For particles born in $W_k = U_k$ ($k = 1, \ldots, d-1$) the probability of reaching $U_{k-1} \cap A_1 \subset W_{k-1}$ is at least $\varepsilon/2^{k+1}$, and on A_1 the probability of giving birth to at least two offsprings is $\geqslant c/2$. Finally, we have $V_{d-1} = U_d \cup V_d$ and for all particles born in $W_d = V_{d-1}$ we have either

$$\nu(A_1 \cap U_{d-1}|x) \geqslant \varepsilon/2^{d+1} \quad (\text{if } x \in U_d)$$

or

$$\nu(A_1 \cap V_{d-1}|x) \geqslant \varepsilon/2^{d+1} \quad (\text{if } x \in V_d).$$

Thus, for $x \in W_d$ we have always

$$\nu(A_1 \cap (W_{d-1} \cup W_{d-1}) | x) = \nu(A_1 \cap (W_{d-1} \cup W_d) | x) \geq \varepsilon/2^d,$$

which implies that the probability of the event (iii) is at least $\frac{\varepsilon}{2^d} \cdot \frac{c}{2} = a$.

Next, given the state s of the process (if it has not expired), we define $B(s)$ as the event that for all particles events (i)-(iii) occur simultaneously, whichever of the events is applicable to the given particle (i.e. all particles in W_0 die with no offsprings, all particles in W_k $(k = 1, \ldots, d-1)$ move to W_{k-1} and give birth to at least two new offsprings, and so on). Clearly, if $s \in S_M$, then probability of $B(s)$ is at least $a^M = \beta > 0$, because of the assumed independence of the events occurring to different particles.

To prove inequality (4.8) we proceed as follows: let $s_0 \in S_M$. Then $P\{B(s_0) | s_0\} \geq \beta$ and we can define C_0 as the subset of S_M (possibly empty) consisting of those s_0 for which

$$P\{B(s_0) \cap s_1 \in S_M | s_0\} \geq \beta/2,$$

and let $D_0 = S_M \cap C_0^c$. For $s_0 \in D_0$ we have

$$\beta/2 \leq P\{B(s_0) \cap s_1 \notin S_M | s_0\} \leq P\{s_1 \notin S_M | s_0\}.$$

Next, for $s_1 \in S_M$ we have $P\{B(s_1) | s_1\} \geq \beta$, and using the Markov property of our process we see that for $s_0 \in C_0$

$$P\{B(s_0) \cap s_1 \in S_M \cap B(s_1) | s_0\} \geq \frac{\beta}{2} \cdot \beta = \beta_1$$

(in fact, the left-hand side of the last inequality can be written as the integral

$$\int P\{B(s_1) | s_1\} P(ds_1 | s_0)$$

extended over the set of s_1 which are in S_M and are resulting from the event $B(s_0)$; for $s_1 \in S_M$ the integrand is bounded from below by β).

Let us now define C_1 as the subset of C_0 for which

$$P\{B(s_0) \cap s_1 \in S_M \cap B(s_1) \cap s_2 \in S_M | s_0\} \geq \beta_1/2$$

and $D_1 = C_0 \cap C_1^c$. Thus, on D_1

$$P\{s_2 \notin S_M | s_0\} \geq \beta_1/2.$$

Proceeding in this manner for d steps we define a partition of S_M into sets $D_0, D_1, \ldots, D_{d-1}$ and C_{d-1} such that for some $\gamma > 0$ (γ being the smallest of all bounds obtained in successive steps):

(i) If $s_0 \in D_k$ $(k = 0, 1, \ldots, d-1)$, then

$$P\{s_{k+1} \notin S_M | s_0\} \geq \gamma;$$

(ii) If $s_0 \in C_{d-1}$, then

$$P\{B(s_0) \cap B(s_1) \cap \ldots \cap B(s_{d-1}) | s_0\} \geq \gamma.$$

However, the event $B(s_0) \cap \ldots \cap B(s_{d-1})$ implies that $s_d \notin S_M$; in fact, all descendants of particles located (in location s_0) in the set W_k ($k = 0, 1, \ldots, d-1$) will die with no offsprings in less than d generations, while each particle in W_d will have at least $2^d > M$ descendants. This shows the truth of inequality (4.8), and completes the proof of the theorem.

One could suspect that the assumption of the theorem 4.2 imply stronger assertion (4.1), this problem, however, remains open. For the proof of the basic extinction theorem, i.e. a theorem giving conditions for (4.2), the assertion of theorem 4.2 will be sufficient.

Now we shall turn to the analysis of conditions implying (4.2), i.e.

$$P^u\{\lim Z_n = 0\} = 1.$$

According to the intuition based on a certain analogy with the standard Galton-Watson process (see, for instance, [13]) one could hope that conditions implying (4.2) can be expressed in terms of expected number of susceptibles infected by a single individual; we shall show it to be true under some additional assumptions.

Denote by $E(x) = \sum kp(k|x)$ (finite or infinite) the expected number of susceptibles infected by a single individual if the infection occurs at x. Further, let

$$T(x) = \int E(z)\nu(dz|x).$$

The value $T(x)$ represents the expected number of susceptibles infected by a single individual who himself became infected at x. We shall prove

THEOREM 4.3. *If for some initial state u the process $\{Z_n\}$ satisfies the condition*

$$P^u\{\lim Z_n = 0 \text{ or } \limsup Z_n = \infty\} = 1,$$

and $T(x) \leqslant 1$ for all x, then

$$P^u\{\lim Z_n = 0\} = 1.$$

Proof. It suffices to show that $\limsup E^u(Z_n) < \infty$, where E^u denotes the conditional expectation given the initial state u, i.e. given that the process originated from a single individual who himself became infected at u. Let $\pi^u_{n,k} = P^u\{Z_n = k\}$, and for $\pi^u_{n,k} > 0$ let $\mu^u_{n,k}$ be the probability distribution of the vector $(y_1, \ldots, y_k)$ of positions of members of the nth generation at the moment when they become infectious. We have

$$E^u(Z_{n+2}) = \sum_{k \geqslant 1} \pi^u_{n,k} \int E(Z_{n+2}|y_1, \ldots, y_k)\, d\mu^u_{n,k}. \tag{4.9}$$

Next, we have

$$\begin{aligned} E(Z_{n+2}|y_1,\ldots,y_k) &= \sum_{r_1,\ldots,r_k} [r_1T(y_1)+\ldots+r_kT(y_k)]p(r_1|y_1)\ldots p(r_k|y_k) \\ &\leqslant \sum_{r_1,\ldots,r_k} (r_1+\ldots+r_k)p(r_1|y_1)\ldots p(r_k|y_k) \\ &= E(Z_{n+1}|y_1,\ldots,y_k). \end{aligned}$$

Substituting into (4.9) we get $E^u(Z_{n+2}) \leqslant E^u(Z_{n+1})$. It follows that $E^u(Z_n) \leqslant E^u(Z_1) = T(u) \leqslant 1$, which completes the proof.

Let us notice that using the obvious estimate

$$E(x) = \sum_{k=1}^{\infty} kp(k|x) \geqslant \sum_{k=1}^{\infty} p(k|x) = 1-p(0|x)$$

we can formulate the last theorem as follows:

THEOREM 4.4. *If $T(x) \leqslant 1$ for all $x \in X$ and there exists $c > 0$ such that at least one of the sets*

$$\{x;\ p(1|x) \leqslant 1-c\} \quad \text{or} \quad \{x;\ E(x) \leqslant 1-c\}$$

is attractive, then for every u

$$P^u\{\lim Z_n = 0\} = 1.$$

Now we shall prove a theorem, proved in [15], which asserts that the limit properties of the process $\{Z_n\}$ are, in a sense, independent of the initial condition u, namely:

THEOREM 4.5. *If for some u_0 we have $P^{u_0}\{\lim Z_n = 0\} = 1$, then*

$$P^u\{\lim Z_n = 0\} = 1 \quad \text{for} \quad \nu(\cdot|u_0)\text{-almost all points } u.$$

Proof. Let $\varphi(u) = P^u\{\lim Z_n = 0\}$. We have

$$\begin{aligned} \varphi(u) &= \int \sum_k p(k|x)\varphi^k(x)\nu(dx|u) \\ &= \int G(\varphi(x)|x)\nu(dx|u), \end{aligned} \tag{4.10}$$

where $G(s|x) = \sum_k s^k p(k|x)$ is the generating function of the distribution $\{p(k|x)\}$. Since for every x the function $G(s|x) = 1$ if and only if $s = 1$, it follows from (4.10) that if the left-hand side equals 1 for some u_0, then $\varphi(x) = 1$ almost everywhere with respect to $\nu(\cdot|u_0)$.

The model of epidemic described in this section can be slightly generalized by weakening assumptions concerning the probability distributions governing the movements of individuals within X during their

incubation period. This generalization will consists of removing the assumption of independence of movements of individuals infected by the same infective. We shall leave assumption I concerning the independence of numbers of susceptibles infected by different individuals, and assume that

II*. The groups of individuals infected by different infectives move within the habitat X during their incubation periods independently of one another, according to the probability distributions depending only on the point at which the infection occurred. More precisely, we shall assume that to each $x \in X$ and each $k = 1, 2, \ldots$ there corresponds a measure $\mu_k(\cdot|x)$ in the space X^k (with the corresponding product σ-field $\mathscr{G}^k$). We assume that for every k and $C \in \mathscr{G}^k$ the function $\mu_k(C|\cdot)$ is $\mathscr{G}$-measurable, and that the measures $\mu_k(\cdot|x)$ are invariant under permutations of coordinates in the sense that for every $x \in X$, $k = 1, 2, \ldots$, $C_1, \ldots, C_k \in \mathscr{G}$, and every permutation $(i_1, \ldots, i_k)$ of numbers $(1, \ldots, k)$ we have

$$\mu_k(C_1 \times \ldots \times C_k|x) = \mu_k(C_{i_1} \times \ldots \times C_{i_k}|x).$$

The value $\mu_k(C_1 \times \ldots \times C_k|x)$ will be interpreted as the conditional probability, given that the infection occurred at x and k susceptibles were infected, that at the end of their incubation period, first of them will be in the set C_1, ..., kth will be in the set C_k. The invariance of measures $\mu_k(\cdot|x)$ under permutations of coordinates allows us to number these infectives arbitrarily.

Clearly, if measures $\mu_k(\cdot|x)$ and distributions $\{p(k|x)\}$ are arbitrary, one cannot obtain theorems meaningful from the point of view of applications, since by a suitable choice of $\mu_k(\cdot|x)$ and $\{p(k|x)\}$ one can construct the process $\{Z_n\}$ which would with probability one behave in an almost arbitrarily prescribed manner.

To obtain meaningful results, one should impose such conditions on $\mu_k(\cdot|x)$ which introduce sufficient amount of randomness into the migration process. To formulate such conditions we extend the notion of attractiveness of sets as follows:

DEFINITION. A measurable set $V \subset X$ is called *attractive*, if there exists a sequence of positive numbers $\{\varepsilon_k\}$ such that for $k = 1, 2, \ldots$ we have

$$\mu_k(V^k|x) \geqslant \varepsilon_k$$

uniformly in $x \in X$.

The following theorems given in [3] are immediate generalizations of theorems proved at the beginning of this section.

THEOREM 4.6. *If there exists $c > 0$ such that the set $\{x;\ p(0|x) > c\}$ is attractive, then for every $u \in X$*

$$P^u\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1.$$

THEOREM 4.7. *If for some u we have*

$$P^u\{\lim Z_n = 0 \text{ or } \limsup Z_n = \infty\} = 1,$$

and $E(x) \leqslant 1$ for all x, then

$$P^u\{\lim Z_n = 0\} = 1.$$

THEOREM 4.8. *If $E(x) \leqslant 1$ for all x, and there exists $c > 0$ such that the set $\{x;\ E(x) \leqslant 1-c\}$ is attractive, then for all u we have*

$$P^u\{\lim Z_n = 0\} = 1.$$

THEOREM 4.9. *If for some u_0 we have $P^{u_0}\{\lim Z_n = 0\} = 1$, then there exists a set $D \subset X$ such that $P^u\{\lim Z_n = 0\} = 1$, for all $u \in D$ and $p(k \mid u_0) > 0$ implies $\mu_k(D^k \mid u_0) = 1$.*

5. Second group of models: influence of changes of infectiousness on the course of epidemic. The models of this group were designed, generally speaking, as an attempt to study the influence of changes in infectiousness (expressed in terms of changes in the distribution of the number of susceptibles infected by a single individual) on the course of an epidemic. With such models one could (by making suitable assumptions about the changes of these distributions) study epidemics in which the contagiousness is subject to random variations (due, for instance, to climatic changes); one could also (by making other assumptions about changes in the distributions of numbers of susceptibles infected by a single individual) approximate the epidemics on finite populations.

As in the models of the preceding section, we shall define a certain stochastic process $\{Z_n\}$, where Z_n will be interpreted as the number of infectives in the nth generation of epidemic. Intuitively, the process $\{Z_n\}$ will be constructed as follows: Given $Z_j = k$ (i.e. if the jth generation consists of k infectives), one chooses first (according to a probability distribution depending on the whole history of the process) the distribution, say f, of the number of individuals infected by a single infective, and then each of the k infectives of the jth generation infects susceptibles independently according to the distribution f.

Thus, the basic elements of the formal description of the process are: (1) the class of admissible probability distributions of the number of susceptibles infected by a single individual, (2) the rule, depending on the whole past history of the process, of choosing one of these distributions, and (3) the assumption that in each generation all infectives infect susceptibles independently of one another according to the chosen probability distribution.

The processes of this type, which (for the lack of a better name) will be called *generalized branching processes*, were introduced in [5].

Let us note that the standard assumption of the theory of branching processes, namely that of independence of reproductions, is replaced here by the assumption of symmetric dependence (see, for instance, [11]).

We shall now present the formal definition of generalized branching processes. Let S be an arbitrary finite or countable set, and let $\mathscr{F}$ be a class of probability distributions $\{p(k|s)\}$, $s \in S$, $k = 0, 1, 2, \ldots$ over the set of non-negative integers (i.e. for every $s \in S$ we have $p(k|s) \geqslant 0$ and $\sum_k p(k|s) = 1$). Denote by $f(x|s) = \sum_k x^k p(k|s)$, $|x| \leqslant 1$, the generating function of the distribution $\{p(k|s)\}$. Next, let $D(S)$ be the class of all probability distributions on S; thus, each element of $D(S)$ is a function $\pi(\cdot)$ defined on S such that $\pi(s) \geqslant 0$ and $\sum_{s \in S} \pi(s) = 1$.

Let $\mathscr{L}$ be the class of all finite sequences with odd number of elements, of the form

$$(k_0, s_1, k_1, \ldots, s_n, k_n)$$

where $k_0, k_1, \ldots, k_n$ are non-negative integers, and $s_1, \ldots, s_n$ are elements of S. Finally, let Φ be a function mapping $\mathscr{L}$ into $D(S)$.

Definition. A sequence $Z_0, Z_1, Z_2, \ldots$ of non-negative integer-valued random variables will be called a *generalized branching process* if there exist a set S, class $\mathscr{F}$, function $\Phi: \mathscr{L} \to D(S)$ and a probability distribution φ_0 on the set of non-negative integers, such that for every $n = 0, 1, 2, \ldots$ the joint distribution of $(Z_0, Z_1, \ldots, Z_n)$ coincides with the marginal joint distribution of $(Z_0^*, Z_1^*, \ldots, Z_n^*)$ of the process

$$Z_0^*, \xi_1, Z_1^*, \xi_2, \ldots$$

(in which $\xi_1, \xi_2, \ldots \in S$ and $Z_0^*, Z_1^*, \ldots$ are non-negative integers) defined by the following conditions:

(i) Z_0^* has the distribution φ_0;

(ii) given $Z_0^* = k_0, \xi_1 = s_1, Z_1^* = k_1, \ldots, \xi_n = s_n, Z_n^* = k_n$ the random variable ξ_{n+1} has the probability distribution $\Phi(k_0, s_1, k_1, \ldots, s_n, k_n)$;

(iii) given $Z_0^* = k_0, \xi_1 = s_1, \ldots, Z_n^* = k_n, \xi_{n+1} = s_{n+1}$, the random variable Z_{n+1}^* has the distribution with the generating function $[f(x|s_{n+1})]^{k_n}$ (that is, Z_{n+1}^* has the probability distribution of a sum of k_n independent random variables, each with the distribution $\{p(k|s_{n+1})\}$).

As in the preceding section, we shall study conditions under which a generalized branching process $\{Z_n\}$ has the property $P\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1$, and conditions under which $P\{\lim Z_n = 0\} = 1$. We start from a theorem which, in a sense, corresponds to theorem 4.1.

Theorem 5.1. *If a generalized branching process $\{Z_n\}$ satisfies the condition*

$$q = \inf_{s \in S} p(0|s) > 0,$$

then

$$P\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1.$$

Proof. Note first that if $Z_N = 0$ for some N, then $Z_n = 0$ for $n \geq N$. For a fixed $k > 0$ put

$$C_N(k) = \bigcup_{n \geq N} \{Z_n = k\},$$

$$C_N^M(k) = \bigcup_{n=N}^{M} \{Z_n = k\}.$$

To prove the theorem it suffices to show that $P\{\bigcap_N C_N(k)\} = 0$. Since $C_N(k) \supset C_{N+1}(k)$, it suffices to show that

$$\lim_{N \to \infty} P\{C_N(k)\} = 0.$$

Now, we can write

$$C_N^M(k) = \{Z_M = k\} \cup \bigcup_{n=N}^{M-1} \{Z_n = k, Z_{n+1} \neq k, \ldots, Z_M \neq k\}.$$

The events on the right-hand side of the last formula are disjoint, hence

$$\begin{aligned} (5.1) \quad & P\{C_N^M(k)\} \\ &= P\{Z_M = k\} + \sum_{n=N}^{M-1} P\{Z_M \neq k, \ldots, Z_{n+1} \neq k \mid Z_n = k\} P\{Z_n = k\} \\ &= P\{Z_M = k\} + \sum_{n=N}^{M-1} \big(1 - P\{C_{n+1}^M(k) \mid Z_n = k\}\big) P\{Z_n = k\}. \end{aligned}$$

If $\sum_n P\{Z_n = k\} < \infty$ for $k = 1, 2, \ldots$, then passing to the limit with $M \to \infty$ we obtain

$$\lim_{M \to \infty} P\{C_N^M(k)\} = P\{C_N(k)\} \leq \sum_{n=N}^{\infty} P\{Z_n = k\},$$

and it follows that $\lim_{N \to \infty} P\{C_N(k)\} = 0$. If we had $\sum_n P\{Z_n = k\} = \infty$, then passing to the limit with $M \to \infty$ we would obtain from (5.1):

$$\limsup_{n \to \infty} P\{C_{n+1}(k) \mid Z_n = k\} = 1.$$

We have, however, $[C_{n+1}(k)]^c \supset \{Z_{n+1} = 0\}$, hence

$$P\{[C_{n+1}(k)]^c \mid Z_n = k\} \geq P\{Z_{n+1} = 0 \mid Z_n = k\} \geq q^k,$$

which leads to a contradiction and completes the proof.

The analogous estimations yield a slightly more general theorem. For $q > 0$, let

$$S_q = \{s \in S;\ p(0 \mid s) \geq q\},$$

and let $\mathscr{L}_n$ denote the subclass of $\mathscr{L}$ consisting of all sequences $L_n = (k_0, s_1, \ldots, s_n, k_n)$ of length $2n+1$. Write

$$d(L_n, q) = P\{s_{n+1} \in S_q | L_n\} = \sum_{s \in S_q} \pi_{k_0, s_1, \ldots, s_n, k_n}(s),$$

where $\Phi(k_0, s_1, \ldots, s_n, k_n) = \pi_{k_0, s_1, \ldots, s_n, k_n}(\cdot) \in D(S)$. Let

$$d_{n,q} = \inf_{L_n \in \mathscr{L}_n} d(L_n, q).$$

The following theorem holds:

THEOREM 5.2. *If the generalized branching process $\{Z_n\}$ satisfies for some $q > 0$ the condition*

$$\liminf_{n \to \infty} d_{n,q} > 0,$$

then

$$P\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1.$$

We shall now give conditions sufficient for $P\{\lim Z_n = 0\} = 1$. Let $\mathscr{H}_r$ $(r > 0)$ be a subclass of $\mathscr{L}$ consisting of all sequences

$$H_r = (k_0, s_1, \ldots, s_n, k_n)$$

with arbitrary $n = 0, 1, 2, \ldots$ and such that $k_n = r$. Let $\mu(H_r)$ be the expected number of offsprings of a single particle of the last generation given the past history of the process to be H_r. Formally, if $H_r = (k_0, s_1, \ldots, s_n, k_n)$, then, denoting by $\pi_{k_0, s_1, \ldots, s_n, k_K}(\cdot)$ the probability distribution $\Phi(k_0, s_1, \ldots, s_n, k_n) \in D(S)$ and by m_s the expectation of the distribution $p(k|s)\}$, we define

$$\mu(H_r) = \sum_{s \in S} m_s \pi_{k_0, s_1, \ldots, s_n, k_n}(s).$$

Let $\mu_r = \sup_{H_r \in \mathscr{H}_r} \mu(H_r)$. We shall prove

THEOREM 5.3. *If the generalized branching process $\{Z_n\}$ satisfies the conditions $\inf_{s \in S} p(0|s) > 0$, $\mu_r < \infty$ for all r, and $\mu_r \leqslant 1$ for all sufficiently large r, then*

$$P\{\lim Z_n = 0\} = 1.$$

Proof. It follows from theorem 5.1 that with probability one we have either $\lim Z_n = 0$ or $\lim Z_n = \infty$. To exclude the second of these possibilities, it suffices to show that $\limsup E(Z_n) < \infty$. Now, from the proof of theorem 5.1 it follows that for every $k = 1, 2, \ldots$ we have

$\sum_n P\{Z_n = k\} < \infty$. Denoting $R = \max\{r;\ \mu_r > 1\}$ we can write

$$E(Z_{n+1}) = \sum_r E(Z_{n+1}|Z_n = r)P\{Z_n = r\}$$

$$\leqslant \sum_r r\mu_r P\{Z_n = r\}$$

$$\leqslant \sum_r rP\{Z_n = r\} + \sum_{r=1}^{R} r(\mu_r - 1)P\{Z_n = r\} = E(Z_n) + a_n$$

where $A = \sum_n a_n < \infty$. It follows that

$$\limsup E(Z_n) \leqslant E(Z_0) + A,$$

which completes the proof in the case $E(Z_0) < \infty$. In the contrary case, the similar estimates will give for every m

$$\limsup E(Z_n|Z_0 = m) < \infty.$$

6. Third group of models: preventive activity of health service. This group of models is designed to supply information about the effects of preventive methods of health service (expressed in terms of some parameters) on the course of an epidemic. In this section the process $\{Z_n\}$, where Z_n is, as usual, interpreted as the number of infectives in the nth generation of epidemic, will be the standard Galton-Watson process. In other words, we assume that all infectives infect susceptibles independently of one another, and the probability distribution of the number of susceptibles infected by a single individual is the same for all infectives. The process will be defined by assumptions which will allow us to determine this distribution, these assumptions being expressed in terms of some observable variables.

Since from the theory of branching processes (see, for instance, [10]) it is known that the Galton-Watson process $\{Z_n\}$ has the property $P\{\lim Z_n = 0 \text{ or } \lim Z_n = \infty\} = 1$, we shall study only the conditions implying $P\{\lim Z_n = 0\} = 1$. Now, it is well known that the last condition holds if and only if the expected number of "offsprings of a single particle" does not exceed 1. Thus, we shall try to find such conditions imposed on observable variables, under which the expected number of susceptibles infected by a single individual does not exceed 1.

We shall make the following assumptions:

1. Every individual who gets infected passes first through the period of incubation of the length X, followed by the period of infectiousness of the length Y. He can infect others only during the period of infectiousness. We shall measure time in appropriate units (say, days), and assume that X and Y are random variables with the joint probability distribution $p_{m,n} = P\{X = m,\ Y = n\}$, $m = 0, 1, 2, \ldots$, $n = 1, 2, \ldots$

2. During the illness (lasting $X+Y$ days) the individual may be "detected" and isolated from susceptibles. The conditional probability of getting detected on a given day, given that the individual was not detected before, equals $1-\alpha$ during the period of incubation, and $1-\beta$ during the period of infectiousness ($0 < \alpha, \beta \leqslant 1$).

3. During each day of the period of infectiousness each individual who remains undetected makes a certain number of contacts with susceptibles. The numbers of contacts made at different days are assumed to be independent and identically distributed with the distribution $\{r_k\}$, $k = 0, 1, \ldots$ We assume that the expectation $r = \sum k r_k$ satisfies the condition $0 < r < \infty$.

4. Each contact of a susceptible with an infective leads to infection with probability γ ($0 < \gamma \leqslant 1$), independently of the results of other contacts.

5. The events described in assumptions 1-4 are independent for different individuals.

Assumptions 1-5 define a branching process $\{Z_n\}$ of changes of size of generations of individuals who contracted the disease. We start from determining the probability distribution of the number of individuals infected by a single infective.

Let $F(s,t) = \sum_{m=0}^{\infty} \sum_{n=1}^{\infty} p_{m,n} s^m t^n$, $|s| \leqslant 1$, $|t| \leqslant 1$ be the probability generating function of the joint distribution of the lengths of periods of incubation and infectiousness. Let

$$R(t) = \sum_{k=0}^{\infty} r_k t^k, \qquad |t| \leqslant 1$$

be the probability generating function of the number of daily contacts of a single infective, who remains undetected during the period of infectiousness.

We shall prove

THEOREM 6.1. *Under assumptions* 1-4 *the probability generating function of the total number of individuals infected by a single infective equals*

$$G(t) = 1 - \left(1 - \frac{1-\beta}{1-\beta R(\gamma t + 1 - \gamma)}\right)\left[F(\alpha, 1) - F(\alpha, \beta R(\gamma t + 1 - \gamma))\right]. \tag{6.1}$$

To prove (6.1) we shall need a lemma which generalizes theorem 1 from Chapter XI in [10] for the case of bivariate distributions.

For $m, n = 0, 1, 2, \ldots$, write

$$q_{m,n} = p_{m,n+1} + p_{m,n+2} + \ldots = P\{X = m,\ Y > n\},$$

and let

$$Q(s,t) = \sum_{m,n=0}^{\infty} q_{m,n} s^m t^n, \qquad |s| \leqslant 1,\ |t| < 1$$

be the generating function of the sequence $\{q_{m,n}\}$.

LEMMA. *For every* $|s| \leqslant 1$ *and* $|t| < 1$ *we have*

$$Q(s,t) = \frac{F(s,1) - F(s,t)}{1-t}. \tag{6.2}$$

Proof of the lemma. Note first that

$$\sum_{m=0}^{\infty} q_{m,0} s^m = \sum_{m=0}^{\infty} \sum_{n=1}^{\infty} p_{m,n} s^m = F(s,1).$$

Thus we can write

$$\begin{aligned}
Q(s,t) &= \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \sum_{j=n+1}^{\infty} p_{m,j} s^m t^n = \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} q_{m,0} s^m t^n - \sum_{m=0}^{\infty} s^m \sum_{n=1}^{\infty} t^n \sum_{j=1}^{n} p_{m,j} \\
&= \sum_{n=0}^{\infty} t^n \sum_{m=0}^{\infty} q_{m,0} s^m - \sum_{m=0}^{\infty} s^m \sum_{k=1}^{\infty} p_{m,k} \sum_{j=k}^{\infty} t^j \\
&= (1-t)^{-1} F(s,1) - \sum_{m=0}^{\infty} s^m \sum_{k=1}^{\infty} p_{m,k} t^k (1-t)^{-1} \\
&= (1-t)^{-1} \Big[F(s,1) - \sum_{m=0}^{\infty} \sum_{k=1}^{\infty} p_{m,k} s^m t^k \Big] \\
&= (1-t)^{-1} [F(s,1) - F(s,t)].
\end{aligned}$$

Proof of theorem 6.1. Denote by w_n the probability that an infected individual will remain undetected and infectious during exactly n days. For $n \geqslant 1$ we have

$$w_n = \sum_{m=0}^{\infty} p_{m,n} \alpha^m \beta^n + \sum_{m=0}^{\infty} q_{m,n} \alpha^m \beta^n (1-\beta),$$

which expresses the fact that the event under consideration occurs if the person remains undetected during the whole period of incubation and either during the whole period of infectiousness (if $Y = n$), or during the first n days of this period (if $Y > n$). This formula does not hold for $n = 0$ since in that case we must add a term accounting for the possibility

of detection during the period of incubation. To determine w_0 let us add w_n for $n = 1, 2, \ldots$ We obtain

$$\begin{aligned} 1-w_0 &= \sum_{n=1}^{\infty} w_n = \sum_{n=1}^{\infty}\sum_{m=0}^{\infty} p_{m,n}\alpha^m\beta^n + (1-\beta)\sum_{n=1}^{\infty}\sum_{m=0}^{\infty} q_{m,n}\alpha^m\beta^n \\ &= F(\alpha,\beta) + (1-\beta)Q(\alpha,\beta) - (1-\beta)\sum_{m=0}^{\infty} q_{m,0}\alpha^m \\ &= F(\alpha,\beta) + (1-\beta)Q(\alpha,\beta) - (1-\beta)F(\alpha,1), \end{aligned}$$

hence (using (6.2) if $\beta < 1$ or directly if $\beta = 1$):

$$w_0 = 1-\beta F(\alpha,1).$$

Now, the generating function of the number of contractions of the disease under a single contact is obviously $\gamma t+1-\gamma$, and, by the well-known theorem on generating functions of compound distributions (see [10]), $R(\gamma t+1-\gamma)$ is the generating function of the distribution of the number of persons infected by a single individual during one day of his period of infectiousness. Therefore $R^n(\gamma t+1-\gamma)$ is the generating function of the joint number of individuals infected by a single infective who remained undetected during exactly n days of his period of infectiousness.

The required probability generating function equals therefore

$$\begin{aligned} G(t) &= \sum_{n=0}^{\infty} w_n R^n(\gamma t+1-\gamma) \\ &= 1-\beta F(\alpha,1) + \sum_{n=1}^{\infty}\sum_{m=0}^{\infty} p_{m,n}\alpha^m\beta^n R^n(\gamma t+1-\gamma) + \\ &\quad + (1-\beta)\sum_{n=1}^{\infty}\sum_{m=0}^{\infty} q_{m,n}\alpha^m\beta^n R^n(\gamma t+1-\gamma) \\ &= 1-\beta F(\alpha,1) + F\big(\alpha,\beta R(\gamma t+1-\gamma)\big) + \\ &\quad + (1-\beta)Q\big(\alpha,\beta R(\gamma t+1-\gamma)\big) - (1-\beta)\sum_{m=0}^{\infty} q_{m,0}\alpha^m \\ &= 1-F(\alpha,1) + F\big(\alpha,\beta R(\gamma t+1-\gamma)\big) + \\ &\quad + (1-\beta)\frac{F(\alpha,1) - F\big(\alpha,\beta R(\gamma t+1-\gamma)\big)}{1-\beta R(\gamma t+1-\gamma)} \end{aligned}$$

which is equivalent to (6.1).

We shall now prove a theorem which gives necessary and sufficient conditions for the process $\{Z_n\}$ defined by assumptions 1-5 to have the

property $P\{\lim Z_n = 0\} = 1$. To formulate this theorem put

$$D(s) = \frac{\partial}{\partial t} F(s, t)|_{t=1} = \sum_{m=0}^{\infty} s^m \sum_{n=1}^{\infty} n p_{m,n}.$$

Since $F(a, 1)$ is the probability that an infective will remain undetected during the whole incubation period, it follows that $D(a)/F(a, 1)$ is equal to the expected length of infectiousness period for those individuals who remained undetected during their incubation period.

We shall prove the following theorem in which $0 < r = \sum k r_k = R'(1) < \infty$ is the expected number of contacts per day of a single undetected infective.

THEOREM 6.2. *The process $\{Z_n\}$ defined by assumptions* 1-5 *has the property $P\{\lim Z_n = 0\} = 1$ if and only if the numbers a, β and γ satisfy (for given $F(s, t)$ and r) the condition $\beta \leqslant \beta^*$, where $\beta^* = \beta^*(a, \gamma)$ equals to the smallest root of the equation*

$$\gamma r x [F(a, x) - F(a, 1)] + 1 - x = 0. \tag{6.3}$$

Equation (6.3) *has always the root $x = 1$. A root $x < 1$ exists if and only if $\gamma D(a) > 1/r$.*

Proof. We shall start from the proof of the second assertion. Consider two functions of β defined for $0 < \beta \leqslant 1$ as

$$h_1(\beta) = F(a, \beta), \qquad h_2(\beta) = F(a, 1) - \frac{1}{\gamma r} \cdot \frac{1-\beta}{\beta}.$$

These functions satisfy conditions $h_1' > 0$, $h_2' > 0$, $h_1'' \geqslant 0$, $h_2'' < 0$. It follows that they are both increasing, the first is convex, and the second concave. Since $h_1(1) = h_2(1)$, the equation $h_1(\beta) = h_2(\beta)$ (that is, equation (6.3)) has no roots $\beta^* < 1$ if $h_1'(1) \leqslant h_2'(1)$. On the other hand, if $h_1'(1) > h_2'(1)$, then there exists exactly one root $\beta^* < 1$ of the equation $h_1(\beta) = h_2(\beta)$. In fact, convexity and concavity of functions h_1 and h_2 exclude the possibility of more than one root smaller than 1, and the existence of the root $\beta^* < 1$ follows from the fact that in the neighbourhood of $\beta = 1$ we have $h_1 < h_2$, while in the neighbourhood of $\beta = 0$ we have the reverse inequality. Finally, $h_1'(1) = D(a)$, $h_2'(1) = 1/\gamma r$, which proves the second assertion of the theorem.

To prove the first assertion it suffices to show that it is satisfied if and only if $G'(1) \leqslant 1$, where $G(t)$ is given by (6.1). Differentiating $G(t)$ and substituting $t = 1$ we obtain for $\beta \neq 1$

$$G'(1) = \gamma r \frac{\beta}{1-\beta} [F(a, 1) - F(a, \beta)],$$

and for $\beta = 1$

$$G'(1) = \gamma r D(a).$$

We shall consider two cases. If $D(\alpha) \leqslant 1/\gamma r$, then $G'(1) \leqslant 1$ for $\beta = 1$, and by the already proved assertion, we have $h_1(\beta) \geqslant h_2(\beta)$ for all $\beta < 1$; thus $G'(1) \leqslant 1$ for all $\beta < 1$. If $D(\alpha) > 1/\gamma r$, then for $\beta = 1$ we have $G'(1) > 1$, and in the interval $0 < \beta < 1$ we have $h_1(\beta) \geqslant h_2(\beta)$ (that is, $G'(1) \leqslant 1$) if and only if $\beta \leqslant \beta^*$. This completes the proof.

The practical interpretation of the theorem above is the following: The model is defined by assumptions expressed in terms of certain observable variables of the phenomenon of epidemic. Thus, the generating function $F(s, t)$ describes those aspects of the disease, which may have some influence on the course of epidemic, namely the distribution of its periods. The generating function $R(t)$ characterizes to a certain degree the social and environmental conditions which may influence the epidemic, namely the number of contacts between infectives and susceptibles. The parameters α, β and γ characterize to a certain degree the attempts of the health servive directed at the prevention of an epidemic. Thus, α measures the efficiency in detecting those who are already infected, but are still non-infectious; β measures the efficiency in detecting the infectious individuals, while γ measures the efficiency in increasing the individual resistance against contacts with the disease.

Theorem 6.2 gives an abstract (and, of course, oversimplified) answer to the following practical problem: given the information about the disease and the environmental conditions, which preventive methods are sufficient for preventing the epidemic.

The model presented above can be generalized, so as to include to a certain degree the migratory movements of population within the habitat. Thus, let us imagine that the habitat is partitioned into N zones, and that the individuals may travel from one zone to another.

As before we assume that the disease is characterized by the joint distribution of the vector (X, Y) of the lengths of periods of incubation and infectiousness. Again we write

$$F(s, t) = \sum_{m=0}^{\infty} \sum_{n=1}^{\infty} p_{m,n} s^m t^n \quad \text{and} \quad Q(s, t) = \sum_{m,n=0}^{\infty} q_{m,n} s^m t^n,$$

where $p_{m,n} = P\{X = m, Y = n\}$, and $q_{m,n} = P\{X = m, Y > n\}$. At each day, the conditional probability of detection and isolation of an infective (given he had not been detected before) equals $1 - \alpha_i$ and $1 - \beta_i$ for individuals in the ith zone during their incubation and infectiousness periods, respectively. The numbers of contacts during each day of the period of infectioussness are independent random variables; in the ith zone, the probability distribution of the number of daily contacts has the generating function $R_i(t)$; independently of the results of other contacts, a contact in the ith zone leads to the disease with probability γ_i. We allow one transition from one zone to another per day, and assume that these transi-

tions are independent of the process of infection, and form a Markov chain with the matrix $[a_{ij}]$ during the period of incubation, and matrix $[b_{ij}]$ during the period of infectiousness. Finally, we assume that the events concerning different individuals are independent.

Let $G_i(t_1, \ldots, t_N)$ be the generating function of the vector $(X_1^i, \ldots, X_N^i)$, where X_j^i equals to the joint number of individuals infected in the jth zone by a person who himself became infected in the ith zone. Let $\boldsymbol{G}(t_1, \ldots, t_N)$ denote the vector whose ith component is $G_i(t_1, \ldots, t_N)$. Proceeding as in the proof of theorem 6.1, we show easily that the following theorem holds:

THEOREM 6.3. *The function* $\boldsymbol{G}(t_1, \ldots, t_N)$ *is given by the formula*

$$\boldsymbol{G}(t_1, \ldots, t_N) = \Psi[F(U, V)+Q(U, V)W+C],$$

where

$$U = [a_{ij}a_j], \qquad W = [b_{ij}(1-\beta_j)],$$
$$V = [b_{ij}\beta_j R_j(\gamma_j t_j + 1-\gamma_j)],$$

C *is a constant matrix* (*whose exact form is of minor interest since we shall need only the derivatives of the vector* $\boldsymbol{G}$), *and* Ψ *is a function, which to a matrix assigns a vector whose successive components equal to the sums of the rows of this matrix.*

To analyse the probability of an outburst of an epidemic we can use the extinction theorem for branching processes with more than one kind of particles (see [13], Chapter II). This theorem asserts that the branching process whose generating functions of the numbers of descendants are given by the vector $\boldsymbol{G}(t_1, \ldots, t_N)$ will become extinct with probability 1 if and only if none of the eigenvalues of the matrix

$$\left[\frac{\partial G_i(t_1, \ldots, t_N)}{\partial t_j}\Bigg|_{t_1=\ldots=t_N=1}\right]$$

lies outside the unit circle.

7. Discussion. We shall now discuss the natural question arising in connection with the presented models, namely how adequate is the description of reality which these models are capable to supply. More precisely, we shall discuss two aspects of the problems: first, which events concerning real epidemics have interpretation in terms of our models, and second, how well can one predict the events in reality on the basis of an analysis of these models. Because of a non-empirical character of this paper, the discussion will concern mainly the first of these problems.

Each of the models presented consists essentially of a set of assumptions which define a certain stochastic process. These assumptions can be interpreted as certain propositions concerning the phenomenon under consideration, while the sample functions of the process are supposed to reflect the changes of number of infectives as a function of a certain parameter.

Now, in models which we called *classical*, the parameter of stochastic process was interpreted as time, while in models based on the theory of branching processes, this parameter was discrete, and was interpreted as the number of successive generation of epidemic. Under somewhat artificial assumptions, (see the model of section 4) that the incubation period is of a constant length and is the same for all individuals, and that the period of infectiousness is "infinitely short", one could arrive at the time-interpretation of the number of successive generation of the epidemic.

The character of the parameter in the stochastic process serving as a model of epidemic determines the class of observable events which can be interpreted in terms of the process; one of the principal aims of building the model is to obtain quantitative information about the probabilities of events of this class. If the parameter can be interpreted as time, this class comprises events defined in terms of the values of the process for a fixed value of the parameter. If the parameter is the number of a successive generation, then the most important event of this class is the termination (extinction) of the epidemic.

In addition to that, with each model we connect another class of observable events (or, more generally, observable variables) which correspond in their abstract version to the notions used in the formulation of assumptions of the model, and assumptions of the theorems. In order for a model to be empirically verifiable, and in order to be able to obtain the predictions of reality, the probabilities of these events (or properties of these observable variables) should be known, at least to the extent necessary for checking whether the propositions concerning reality which correspond to assumptions of the model and assumptions of theorems can be accepted as true.

Thus, we deal with two classes of events; in short, the first class determines the extent of possible applicability of the model, while the second class determines the extent of information about reality necessary for using the model.

In classical models, the first of these classes comprises all events which, in terms of the process, correspond to events of the form $\{Z_t > x\}$; in models based on the theory of branching processes, this class is smaller, and comprises only two events: termination (extinction) of epidemic, interpreted as $\{\lim Z_n = 0\}$, and "outburst of epidemic", interpreted, somewhat arbitrarily, as the event $\{\lim Z_n = \infty\}$.

Now, the restriction of interpretation of real events in terms of the process determines naturally the class of theorems meaningful for practical purposes; in classical models the attention was focussed on determining the probability distribution of the random variable Z_t as a function of some parameters, whose numerical estimates were obtainable from suitable empirical data. This creates a possibility of empirical verification of the model, by studying the deviations between the values predicted and actually observed.

In models based on the theory of branching processes, the attention was focussed mainly on theorems giving the probabilities of events $\{\lim Z_n = 0\}$ and $\{\lim Z_n = \infty\}$. Moreover, in view of difficulties in verification of information contained in numerical values of these probabilities, the problem was further reduced, essentially to finding conditions under which $P\{\lim Z_n = \infty\} > 0$; these conditions, expressed in practical terms, correspond to a state of danger of an epidemic.

Caution should prevent us from reversing this statement: conditions under which $P\{\lim Z_n = \infty\} = 0$ do not necessarily correspond to conditions of "safety" since (except the simplest cases) very little is known about the behaviour of a branching process before it expires.

Thus, in all models considered, the attempts were directed at finding theorems, whose assertions yield verifiable information on reality. In order that these theorems could serve as useful means of predictions, their assumptions have to be formulated in terms corresponding to some observable variables of the phenomenon.

The classical models are built on the main assumption of proportionality, discussed in section 2; thus, their assumptions concern those statistical fluctuations of populations of infectives and susceptibles, in which one neglects the individual case-histories. In models based on the theory of branching processes, the basic assumption is that of independence of events concerning different individuals; this allows us to obtain a description of the behaviour of the population as a whole based on "microscopic" assumptions concerning statistical fluctuations of individual case-histories.

Thus, the models based on the theory of branching processes considered in this paper lead to much smaller class of events, which can be interpreted and predicted, than classical models; one could hope, however, that the predictions will be better, because the assumptions of the models based on the theory of branching processes, being expressed in terms of statistical fluctuations of individual case-histories, are richer than the assumptions of the classical models. The problem whether these predictions are really better, that is, final answer to the question of how adequate are these models, requires of course empirical investigations, lying beyond the scope of this paper.

PART II

SPREADING OF NON-INFECTIOUS DISEASES

8. Introduction. In this part of the paper we shall present a certain model designed for the purpose of explaining the observed changes of the number of occurrences of some non-infectious diseases (e.g. cancer) by some hypotheses concerning inheritance of proneness towards these diseases. Roughly speaking, the increase in occurrence of a given disease is explained by an increase in proportion of individuals who are more prone to develop this disease. The latter increase is, in turn, explained as resulting from two factors: one of them can be, roughly speaking, formulated as a conjecture that the older are the parents at the time when the child is born, the more likely it is that the child will inherit greater proneness towards the given disease. The second factor consists of changes in the social model of the family, where we observe the tendency towards extending the fertility period to older age.

The suggested model consists, in a sense, of two "parts". One of them is the standard multiple-type Galton-Watson process which is to imitate the growth of human population, the types of particles being identified with the given types of proneness towards the disease in question. The second part of the model (which constitutes the main object of our considerations) is aimed at imitating the process of individual reproduction and inheritance of proneness towards the disease.

To formulate the assumptions of the model we shall first present the definition of proneness towards the disease, and then we introduce some simplifications. Generally, the proneness towards the disease is identified with the distribution of the waiting time for some specific events connected with this disease. Formally, let us consider a certain observable event C which may occur during the individual's lifetime. When the model is to be applied to a specific disease, C may denote, for instance, "the occurrence of first symptoms of the disease" or "death due to this disease". To simplify the formulations we shall use this second interpretation of the event C. Let Y denote the waiting time for C to occur (i.e., in this case, waiting time for death due to this disease). We shall consider proneness towards the given disease defined formally as (possibly defective) probability distribution of the random variable Y (which can assume non-negative values or the value $+\infty$).

To simplify the matter we shall consider individuals of one sex only (say, males), and assume that there exist only two possible probability distribution functions of the random variable Y, say $G_0(t)$ and $G_1(t)$. The generalization to the case of two sexes, and more than two types of proneness presents only computational difficulties, while all essential features remain the same. It will be convenient to introduce the auxiliary

index variable I which assumes value i ($i = 0, 1$) for individuals with distribution $G_i(t)$. We shall also speak of "individuals of type i". In the sequel we shall tacitly assume that all random variables under consideration are non-negative, that is, their probability distribution functions vanish for negative values of the argument.

The model will consist of describing the mechanism of inheritance of type by offsprings. The basic assumption will be that of conditional independence of reproduction and life-histories of different individuals, given any combination of types of these individuals. Further assumptions will allow us to determine the probability that an individual of the type i will have m sons of type 0 and n sons of type 1. These probabilities define a certain branching process with two types of "particles", 0 and 1; this process serves as a model of growth of the population. We shall not, however, study this process in detail; our aim will be to analyse the possibility of statistical inference and estimation connected with mechanisms of inheritance of type I, where we assume that we can observe certain events, whose probabilities depend on the type I, while the value of I itself is not observable. Our population will consist of independent observations of beginnings of such processes, each originating from a single individual (father). The father's type I in each of these processes will be assumed to be unknown, and will constitute the initial condition. For our purposes it will turn out to be sufficient to study only first two generations, i.e. it will be sufficient to study "families" consisting of a father and the set his sons. We shall assume that the father's type I is a random variable, whose distribution will have to be estimated. In practice, it corresponds to a situation when we sample families out of a large population of families, and our aim is to evaluate the fraction of those families, where father is of type 0.

9. Formal presentation of the model of reproduction and inheritance of types. Formally, when considering the family histories, we shall be dealing with the following probabilistic setup: the sample space Ω consists of points of the form

$$\omega = (D, V_1, \ldots, V_D, X, I, Y, \xi(\cdot), S_1, \ldots, S_D)$$

where $D, V_1, \ldots, V_D, X, I, Y, S_1, \ldots, S_D$ are non-negative numbers and $\xi(\cdot)$ is a function of t, defined for $t \geqslant 0$ and assuming values 0 and 1. In the space Ω we distinguish a σ-field $\mathcal{B}$ of measurable subsets, generated by cylinders with Borel bases. In the measure space $(\Omega, \mathcal{B})$ we define a probability measure P by the following conditions:

(i) The random variable D assumes non-negative integer values $0, 1, 2, \ldots$ We write $d_k = P\{D = k\}$, and we interpret D as the number of sons the individual would have if he lived indefinitely.

(ii) Given $D = k > 0$, the random variables $V_1, \ldots, V_k$ form an order statistic from a sample of independent identically distributed random variables $U_1, \ldots, U_k$. We write $H(t) = P\{U_j \leqslant t\}$, $j = 1, 2, \ldots$ (in other words, V_j is equal to the jth in magnitude among $U_1, \ldots, U_k$). We shall interpret V_j as the father's age at the moment of the birth of his jth son if the father were to live indefinitely.

(iii) The random variable X is independent of the remaining random variables, and has the distribution $F(t) = P\{X \leqslant t\}$. We shall interpret X as the father's age at the time when he is to die for reasons other than connected with the disease under consideration.

(iv) The random variable I is independent of D, $V_1, \ldots, V_D$ and X, and assumes values 0 or 1 with probabilities π and $1-\pi$, respectively. We shall interpret I as the "type" of father.

(v) Given $I = i$, the random variable Y (possibly defective) is independent of the remaining random variables, and has the conditional probability distribution function $G_i(t) = P\{Y \leqslant t \mid I = i\}$. We shall interpret Y as the father's age at the time when he is to die from the disease under consideration (i.e. at the time of occurrence of the event C).

(vi) Given $I = i$, the stochastic process $\xi(\cdot)$ is independent of random variables $D, V_1, \ldots, V_D, X$ and Y, and its sample functions assume values 0 and 1. We write

$$p^i_{j_1,\ldots,j_n}(t_1, \ldots, t_n) = P\{\xi(t_k) = j_k,\ k = 1, \ldots, n \mid I = i\}.$$

We shall interpret the process $\xi(\cdot)$ as follows: the value $\xi(t)$ determines the type of son born at the time when the father was of age t, in the sense that the son born at the moment V_j is of the type $\xi(V_j)$.

(vii) Given $D, V_1, \ldots, V_D, I$ and sample function $\xi(\cdot)$, the random variables $S_1, \ldots, S_D$ are independent (and independent of X and Y). Their probability distribution functions are

$$P\{S_j \leqslant t\} = \begin{cases} 1-\big(1-F(t)\big)\big(1-G_0(t)\big) & \text{if} \quad \xi(V_j) = 0, \\ 1-\big(1-F(t)\big)\big(1-G_1(t)\big) & \text{if} \quad \xi(V_j) = 1. \end{cases}$$

We shall interpret S_j as the life-length of the jth son, provided father's lifelength exceeded the moment V_j when the jth son was to be born.

Assumptions (i)-(vii) define a probability measure P on $(\Omega, \mathscr{B})$. Next, to each point $\omega \in \Omega$ there corresponds its "observable part". Formally, the space Ω is mapped into the space Ω^* consisting of points of the form

$$f(\omega) = \omega^* = (K, t_1, \ldots, t_K, Z, \varepsilon, W_1, \ldots, W_K)$$

where for $\omega = (D, V_1, \ldots, V_D, X, I, Y, \xi(\cdot), S_1, \ldots, S_D)$ we have

$$K(\omega) = \begin{cases} 0 & \text{if} \quad \min(X, Y) < V_1, \\ \max\{j;\ V_j \leqslant \min(X, Y)\} & \text{if} \quad \min(X, Y) \geqslant V_1, \end{cases}$$

$$t_j(\omega) = V_j \quad \text{for} \quad j = 1, \ldots, K(\omega),$$

$$Z(\omega) = \min(X, Y),$$

$$\varepsilon(\omega) = \begin{cases} +1 & \text{if} \quad X \geqslant Y, \\ -1 & \text{if} \quad X < Y, \end{cases}$$

$$W_j(\omega) = S_j \quad \text{for} \quad j = 1, \ldots, K(\omega).$$

Clearly, the mapping f is measurable, and carries the measure P from $(\Omega, \mathscr{B})$ into a measure P^* on $(\Omega^*, \mathscr{B}^*)$, where $\mathscr{B}^*$ is the corresponding σ-field of measurable subsets of Ω^*.

Coming back to the intuitive interpretation of our model, $\mathscr{B}^*$ is the class of observable events, and we shall assume that the measure P^* can be estimated experimentally by sampling families ω^*. In intuitive terms, K is the actual number of sons, $t_1, \ldots, t_K$ denote father's age at the time of the birth of these sons, and $S_1, \ldots, S_K$ denote the life-lengths of these sons. The variable Z denotes the father's life-length, and ε assumes values $+1$ or -1 according to whether father died of causes connected with the considered disease, or from other causes. The remaining variables in ω are not observable.

Our basic object will be to analyse the possibilities of statistical inference concerning the distributions appearing in (i)-(vii), based on samples from Ω^*. For such an inference to be possible, it is necessary for different distributions appearing in (i)-(vii) to determine different measures P^* in the sample space of observable events. We shall show that, under some conditions, the measure P^* determines uniquely these distributions.

In the sequel we shall adopt the convention of denoting with an asterisk the probabilities of observable events, and functions of these probabilities.

10. Tests for detecting time-dependent inheritance mechanisms. To find methods of detecting the existence of inheritance mechanisms depending on individual's age we shall show that every such mechanism must result in the dependence of the life-length distribution of offsprings on the age of the parents at the time when these offsprings were born.

Formally, let $Q(t)$ denote the event

$$Q(t) = \{\omega;\ \text{there exists exactly one } j \text{ with } V_j = t\}.$$

Let $t \leqslant T$. Consider the event

$$A(t, T) = Q(t) \cap \{Z > T\}.$$

In intuitive terms, the event $A(t, T)$ occurs if and only if the father outlives the age T and exactly one of his sons is born at the father's age t.

Given the event $A(t, T)$ occurred, let L denote the life-length of the son born at the moment when the father was of age t (i.e. $L = W_j$, where j is determined by condition $V_j = t$).

Let $\Psi_0(x)$ and $\Psi_1(x)$ denote respectively the conditional, given $I = i$, tails of the life-length distributions, i.e.

$$\Psi_i(x) = \big(1-F(x)\big)\big(1-G_i(x)\big).$$

Consider the function

$$m^*(x, t, T) = P^*\{L > x \,|\, A(t, T)\}.$$

Empirically, $m^*(x, t, T)$ can be estimated as the fraction of sons who outlived age x in the population of all sons born at the time when their fathers were of age t, these fathers known to have outlived age T.

We shall prove the following theorem:

THEOREM 10.1. *Suppose that assumptions* (i)-(vii) *of the model are satisfied. Then*

(1) *If* $\Psi_0(x) \equiv \Psi_1(x)$, *then the function* $m^*(x, t, T)$ *does not depend on variables* t *and* T;

(2) *If* $p_0^i(t) \equiv \text{const}$, $i = 0, 1$, (*where* $p_0^i(t)$ *is defined in condition* (vi)), *then the function* $m^*(x, t, T)$ *does not depend on* t;

(3) *If* $p_0^0(t) \equiv p_0^1(t)$, *then the function* $m^*(x, t, T)$ *does not depend on* T.

Proof. We have

$$\begin{aligned}
m^*(x, t, T) &= P^*\{L > x \,|\, Q(t), Z > T\} \\
&= P\{L > x \,|\, Q(t), Z > T, I = 0\}P\{I = 0 \,|\, Q(t), Z > T\} + \\
&\quad + P\{L > x \,|\, Q(t), Z > T, I = 1\}P\{I = 1 \,|\, Q(t), Z > T\} \\
&= P\{L > x \,|\, Q(t), I = 0\}P\{I = 0 \,|\, Z > T\} + \\
&\quad + P\{L > x \,|\, Q(t), I = 1\}P\{I = 1 \,|\, Z > T\} \\
&= [p_0^0(t)\Psi_0(x) + p_1^0(t)\Psi_1(x)]\pi_0(T) + \\
&\quad + [p_0^1(t)\Psi_0(x) + p_1^1(t)\Psi_1(x)]\pi_1(T) \\
&= \Psi_1(x) + \big(\Psi_0(x) - \Psi_1(x)\big)\big[p_0^0(t)\pi_0(T) + p_0^1(t)\big(1 - \pi_0(T)\big)\big],
\end{aligned}$$

where $\pi_i(T) = P\{I = i \,|\, Z > T\}$.

This theorem allows us to make the following inference from empirical data: estimating the values of $m^*(x, t, T)$ for different values of arguments x, t, T we could apply standard statistical procedures for testing the hypothesis concerning the dependence of $m^*(x, t, T)$ of variables t and T. If these tests should lead to rejection of the hypothesis that $m^*(x, t, T)$ does not depend on t, and rejection of the hypothesis that $m^*(x, t, T)$ does not depend on T, we could infer that the population of all men is heterogeneous in the sense that it splits into two subpopulations, say 0 and 1 (these subpopulations may, in turn, be also heterogeneous), and this partition satisfies the following properties: first, the probability that a son of a father from a given subpopulation will belong to subpopulation 0 depends on the father's age at the time when this son was born, and, second, the probability that the son will belong to subpopulation 0 depends on the subpopulation of his father.

Intuitively one could expect that the analysis of the joint distribution of the life-lenghts of brothers should yield some information about the probability distributions of the process $\{\xi(t)\}$ determining the types of offsprings. For $t_1 \leqslant t_2$ denote by $Q(t_1, t_2)$ the event

$$Q(t_1, t_2) = \{\omega;\ \text{there exists exactly one pair } (j, k) \text{ such that } V_j = t_1, \text{ and } V_k = t_2\}.$$

For $T \geqslant t_2$ consider the event

$$A(t_1, t_2, T) = Q(t_1, t_2) \cap \{Z > T\}.$$

Given $A(t_1, t_2, T)$ occurred, denote by L_1 and L_2 the life-lengths of sons born at the moments when their father was at the age t_1 and t_2 respectively (i.e. $L_1 = V_j, L_2 = V_k$ with j and k defined by conditions $V_j = t_1$, $V_k = t_2$). Let $m_1^*(x, t_1, t_2, T)$ and $m_2^*(x, t_1, t_2, T)$ denote respectively the tails of the marginal distributions of L_1 and L_2 in the joint distribution of the pair (L_1, L_2) given the event $A(t_1, t_2, T)$ occurred. The following theorem holds:

THEOREM 10.2. *Suppose that conditions* (i)-(vii) *of the model are satisfied. If* $p_{01}^i(t_1, t_2) = p_{10}^i(t_1, t_2)$ *for* $i = 0, 1$, *then for every* x *and* T *we have*

$$m_1^*(x, t_1, t_2, T) = m_2^*(x, t_1, t_2, T).$$

Proof. Using the notations of the proof of the preceding theorem we obtain after simple transformations

$$m_1^*(x, t_1, t_2, T) = \pi_0(T)[(p_{00}^0 + p_{01}^0)\Psi_0(x) + (p_{10}^0 + p_{11}^0)\Psi_1(x)] + \\ + (1 - \pi_0(T))[(p_{00}^1 + p_{01}^1)\Psi_0(x) + (p_{10}^1 + p_{11}^1)\Psi_1(x)],$$

and

$$m_2^*(x, t_1, t_2, T) = \pi_0(T)[(p_{00}^0 + p_{10}^0)\Psi_0(x) + (p_{01}^0 + p_{11}^0)\Psi_1(x)] + \\ + (1 - \pi_0(T))[(p_{00}^1 + p_{10}^1)\Psi_0(x) + (p_{01}^1 + p_{11}^1)\Psi_1(x)].$$

In the sequel we shall make the following assumption about the finite-dimensional probability distributions of the process $\{\xi(t)\}$:

(viii) There exist two (perhaps defective) probability distribution functions $U_0(t)$ and $U_1(t)$ such that for all n and all $t_1 < t_2 < \ldots < t_n$ we have

$$P\{\xi(t_1) = \ldots = \xi(t_n) = 0 \mid I = i\} = 1 - U_i(t_n),$$

$$P\{\xi(t_1) = \ldots = \xi(t_j) = 0, \xi(t_{j+1}) = \ldots = \xi(t_n) = 1 \mid I = i\} = U_i(t_{j+1}) - U_i(t_j), \quad j = 1, 2, \ldots, n-1,$$

$$P\{\xi(t_1) = \ldots = \xi(t_n) = 1 \mid I = i\} = U_i(t_1)$$

(and $P\{\xi(t_1) = j_1, \ldots, \xi(t_n) = j_n \mid I = i\} = 0$ for all other combinations of $j_1, \ldots, j_n$).

Intuitively, condition (viii) means that there exists a random variable ξ (possibly defective) with conditional (given $I = i$) distribution $U_i(t)$, which determines the types of offsprings in the following sense: all sons born at moments t with $\xi > t$ are of type 0, and all remaining sons are of type 1.

11. Possibility of estimating distributions appearing in the assumptions of the model. We shall start from the problem of estimating these probability distributions which depend on the value assumed by the random variable I, that is, the type of the father. Using the notations of the last section, we may express the function $m^*(x, t, T)$, using assumption (viii), as follows:

$$m^*(x, t, T) = \Psi_1(x) + \left(\Psi_0(x) - \Psi_1(x)\right)\left[\left(1 - U_0(t)\right)\pi_0(T) + \left(1 - U_1(t)\right)\left(1 - \pi_0(T)\right)\right].$$

Next, we have formally

$$\pi_0(T) = P\{I = 0 \mid Z > T\} = \frac{P\{I = 0\}P\{Z > T \mid I = 0\}}{P^*\{Z > T\}} = \frac{\pi\Psi_0(T)}{\Psi^*(T)}$$

and after simple transformations we get

$$m^*(x, t, T) = \Psi_0(x) + U_1(t)\left(\Psi_1(x) - \Psi_0(x)\right) + \frac{\pi\Psi_0(T)}{\Psi^*(T)}\left(\Psi_1(x) - \Psi_0(x)\right)\left(U_1(t) - U_0(t)\right).$$

Thus, if $0 < \pi < 1$, this formula allows us to estimate (using, for instance, the method of least squares or maximum likelihood) the number π, and functions Ψ_0, Ψ_1, U_0 and U_1 for these values of arguments, for which there are available the corresponding estimates of $m^*(x, t, T)$, i.e. for all x such that $x < M^* = \inf\{T;\ \Psi^*(T) = 0\}$, and all t for which there

are sons born at the time when the father was of age t. The partial overlapping of the domains of arguments x and T for which we have available observations of $m^*(x, t, T)$ makes it possible to obtain the number of equations exceeding the number of unknowns.

Now we shall formulate the theorem concerning the possibility of estimating the probability distribution $\{d_k\}$ appearing in assumption (i) and the probability distribution function $H(t)$ appearing in assumption (ii). Clearly, if $M^* = \inf\{t;\ \Psi^*(t) = 0\} = \sup\{t:\ P^*\{Z > t\} < 1\}$ is finite, we cannot obtain any information about the values of the distribution function $H(t)$ for values of argument exceeding M^*.

Let P^* be an arbitrary measure in the space of observable events Ω^* described in section 9. We shall say that the distribution $\{d_k\}$ from assumption (i) and distribution $H(t)$ from assumption (ii) satisfy condition $W(P^*)$ if the distribution $H(t)$ has the density $h(t)$ such that $h(t) = 0$ for $t > b$, where $b < M^*$, and measure P^* can be obtained from assumptions (i)-(vii) in the manner described in section 9 for some distributions pertaining to (iii)-(vii). One can easily prove the following theorem.

THEOREM 11.1. *For any measure P^* in $(\Omega^*, \mathscr{B}^*)$ there exists at most one pair of distributions $\{d_k\}$, $H(t)$ satisfying condition $W(P^*)$.*

We shall now turn to the problem of determining the probability distributions of the random variables X and Y described in assumptions (iii) and (v). Write $G(t) = \pi G_0(t) + (1-\pi)G_1(t)$. Thus, $G(t)$ is the distribution function of (possibly defective) random variable Y described in (v), equal to the waiting time for the event C to occur. Let $F(t) = P\{X \leqslant t\}$ be the (proper) probability distribution function of the random variable X described in (iii), equal to the waiting time for death for reasons other that connected with the disease under consideration.

In abstract formulation, the problem can be formulated as follows: for a given pair of random variables (X, Y) define

$$Z = \min(X, Y), \qquad \varepsilon = \begin{cases} +1 & \text{if} \quad Y \leqslant X, \\ -1 & \text{if} \quad Y > X, \end{cases} \tag{11.1}$$

and let

$$\Phi(t) = P^*\{Z \leqslant t\}, \qquad A(t) = P^*\{Z \leqslant t \mid \varepsilon = +1\}, \qquad Q = P^*\{\varepsilon = +1\} \tag{11.2}$$

(where, for convenience, we omitted the asterisks over distribution functions $\Phi(t)$ and $A(t)$ and number Q). The problem is to find conditions under which the distribution functions $\Phi(t)$ and $A(t)$ and the number Q determine uniquely the distribution functions F and G of random variables X and Y. Write

$$\sup\{t;\ \Phi(t) < 1\} = M \leqslant +\infty \tag{11.3}$$

(here, again, M should be marked with an asterisk, as being observable).

We shall prove first

THEOREM 11.2. *Suppose that the random variables X and Y are independent and let their distribution functions have densities $f(t) = F'(t)$ and $g(t) = G'(t)$ respectively, such that the following conditions are satisfied:*

$$F(0) = G(0) = 0, \quad F(\infty) = 1, \quad G(\infty) \leqslant 1,$$

and $0 < G(t) < 1$ for all $t > 0$. Then $0 < Q < 1$, the distribution functions $\Phi(t)$ and $A(t)$ given by (11.1) *and* (11.2) *are differentiable, and*

$$F(t) < \Phi(t) < A(t) \quad \text{for} \quad 0 < t < M,$$
$$F(t) = \Phi(t) = A(t) = 1 \quad \text{for} \quad t \geqslant M.$$

Proof. We have

$$Q = P^*\{Y \leqslant X\} = \int_0^\infty G(u)f(u)\,du$$

and the inequality $0 < Q < 1$ follows from the fact that $0 < G(u) < 1$ for all $u > 0$. Next, we have

$$1-\Phi(t) = P^*\{\min(X, Y) > t\} = \big(1-F(t)\big)\big(1-G(t)\big), \tag{11.4}$$

and it follows that $\Phi(t)$ is differentiable. Finally, for $t > 0$ we have

$$\begin{aligned} A(t) &= P^*\{Z \leqslant t \mid \varepsilon = +1\} = P^*\{Y \leqslant t \mid Y \leqslant X\} \\ &= \int_0^\infty P\{Y \leqslant t \mid Y \leqslant u\}f(u)\,du \\ &= \int_0^t P\{Y \leqslant t \mid Y \leqslant u\}f(u)\,du + \int_t^\infty P\{Y \leqslant t \mid Y \leqslant u\}f(u)\,du \\ &= F(t)+G(t)\int_t^\infty \frac{f(u)}{G(u)}\,du \end{aligned} \tag{11.5}$$

and it follows that $A(t)$ is differentiable. Now, from (11.4) we obtain

$$\Phi(t) = F(t)+G(t)\big(1-F(t)\big)$$

and in view of the inequality $G(t) < 1$ we have $\Phi(t) = 1$ if and only if $F(t) = 1$. Thus, for $t \geqslant M$ we have $\Phi(t) = F(t) = 1$, hence $f(t) = 0$, and by (11.5) we must have $A(t) = F(t) = 1$. For $0 < t < M$ we can write

$$\begin{aligned} A(t) &= F(t)+G(t)\int_t^\infty \frac{f(u)}{G(u)}\,du = F(t)+G(t)\int_t^M \frac{f(u)}{G(u)}\,du \\ &> F(t)+G(t)\int_t^M f(u)\,du = F(t)+G(t)\big(1-F(t)\big) = \Phi(t) > F(t), \end{aligned}$$

which completes the proof.

Let now $A(t)$ and $\Phi(t)$ be arbitrary distribution functions, and let $0 < Q < 1$ be arbitrary. We shall say that the distribution functions F and G *satisfy the condition* $W(\Phi, A, Q)$ if these distribution functions have densities, $0 < G(t) < 1$ for all $t > 0$, and for a pair of independent random variables X and Y with distribution functions F and G formulas (11.1) and (11.2) hold.

We shall prove the following uniqueness theorem:

THEOREM 11.3. *Let $A(t)$ and $\Phi(t)$ be arbitrary distribution functions with densities $a(t)$ and $\varphi(t)$ respectively, satisfying the conditions*

$$\begin{aligned} &\Phi(0) = A(0) = 0, \\ &\Phi(t) < A(t) \qquad \text{for } 0 < t < M, \\ &\Phi(t) = A(t) = 1 \qquad \text{for } t \geqslant M. \end{aligned} \tag{11.6}$$

Suppose, moreover, that the density $a(t)$ is continuous in the open interval $0 < t < M$. If the pairs (F_1, G_1) and (F_2, G_2) satisfy the condition $W(\Phi, A, Q)$ for some $0 < Q < 1$, then $F_1(t) = F_2(t)$ for all t, and $G_1(t) = G_2(t)$ for all $t < M$.

Proof. If a pair (F, G) satisfies the condition $W(\Phi, A, Q)$, then by theorem 11.2 we must have $F(t) = 1$ for $t \geqslant M$ and $F(t) < 1$ for $t < M$. In view of the conditions $G(t) < 1$ it follows from (11.4) that

$$F(t) = 1 - \frac{1-\Phi(t)}{1-G(t)}, \tag{11.7}$$

and hence the problem of uniqueness of $F(t)$ for $t < M$ reduces to that of uniqueness of $G(t)$ in this interval. For $0 < t < M$ we obtain from (11.5)

$$A(t) - F(t) = G(t) \int_t^\infty \frac{f(u)}{G(u)}\, du. \tag{11.8}$$

Differentiating, we get

$$a(t) = g(t) \int_t^\infty \frac{f(u)}{G(u)}\, du. \tag{11.9}$$

Since

$$\int_t^\infty \frac{f(u)}{G(u)}\, du = \int_t^M \frac{f(u)}{G(u)}\, du > \int_t^M f(u)\, du = 1 - F(t) > 0,$$

we may divide (11.9) by (11.8) obtaining

$$g(t) = G(t) \frac{a(t)}{A(t) - F(t)}$$

and using (11.7) we get after simple reductions

$$g(t) = \frac{a(t)G(t)\big(1-G(t)\big)}{A(t)-\Phi(t)+\big(1-A(t)\big)G(t)}. \tag{11.10}$$

In view of assumption (11.6) this equation determines uniquely the derivative $g(t)$ of function $G(t)$ in the interval $0 < t < M$. Since by assumption the function $a(t)$ is continuous in the open interval $0 < t < M$, the right-hand side of (11.10) is a continuous function of t. To prove the uniqueness of solutions we shall show that it satisfies the Lipschitz condition in every domain of the form $0 \leqslant G \leqslant 1$, $c \leqslant t \leqslant M-c$ with $c > 0$. Let

$$h = \max_{c \leqslant t \leqslant M-c} [A(t)-\Phi(t)] > 0$$

and

$$r = \max_{c \leqslant t \leqslant M-c} |a(t)|.$$

Differentiating formally the right-hand side of (11.10) with respect to G we get

$$\frac{a(1-2G)[A-\Phi+(1-A)G]-aG(1-G)(1-A)}{[A-\Phi+(1-A)G]^2}.$$

Since $1-A \geqslant 0$, we can write for $c \leqslant t \leqslant M-c$ and $0 \leqslant G \leqslant 1$:

$$[A-\Phi+(1-A)G]^2 \geqslant h^2$$

while the numerator of the derivative of the right-hand side of (11.10) with respect to G can easily be estimated from above by

$$r|1-2G|(1-\Phi)+rG(1-G)(1-A) \leqslant r\left(1+\tfrac{1}{4}\right).$$

Let us note first that every solution of equation (11.10) satisfying for some $0 < t_0 < M$ the condition $0 < G(t_0) < 1$ is non-decreasing in the whole interval $0 < t < M$ and satisfies in this interval the inequality $0 < G(t) < 1$. The first property is obvious in view of the fact that the assumptions (11.6) imply that the derivative $g(t)$ of $G(t)$ is non-negative. The second property follows from the fact that $G(t) \equiv 1$ and $G(t) \equiv 0$ are solutions of (11.10), hence within the interval $(0, M)$ no other solution can reach values 0 or 1.

If a pair (F, G) satisfies the condition $W(\Phi, A, Q)$, then in the interval $0 < t < M$ the function $G(t)$ is a solution of equation (11.10). We shall show that this equation has at most one solution satisfying the condition imposed by Q, i.e. the condition $Q = \int_0^\infty G(u)f(u)du$. We have

(from probabilistic considerations, or integrating by parts)

$$Q = P^*\{Y \leqslant X\} = \int (1-F(u))g(u)du = \int_0^M \frac{1-\Phi(u)}{1-G(u)}\, g(u)du,$$

and in view of equation (11.10) we obtain

$$(11.11) \qquad Q = \int_0^M a(u)(1-\Phi(u))\, \frac{G(u)du}{A(u)-\Phi(u)+(1-A(u))G(u)}.$$

Let t_0 be an arbitrary fixed point with $0 < t_0 < M$, and let $0 < c < 1$. There exists exactly one solution of (11.10) which assumes the value c at the point t_0; let us denote this solution by $G(t, c)$. Next, let us consider the functional Q defined by (11.11) as a function of c. To complete the proof of the theorem it suffices to show that this functional cannot assume the same value for different values of c. To prove this property, note first that for every $0 < t < M$ the function $G(t, c)$ is strictly increasing and differentiable in c. Differentiating formally the integrand in (11.11) we obtain

$$\frac{a(u)(1-\Phi(u))G'_c(u, c)(A(u)-\Phi(u))}{[A(u)-\Phi(u)+(1-A(u))G(u, c)]^2}.$$

For $0 < u < M$ all factors in the last expression except perhaps $a(u)$ are strictly positive. Since $a(u) \geqslant 0$ and $\int a(u)du = 1$, we have $\frac{d}{dc}Q(G(t, c)) > 0$, which completes the proof.

Now, the theorems of this section assert that, under some conditions (which can be assumed to hold in practical situations to which the model was designed to be applied), different distributions appearing in (i)-(viii) yield different measures P^* in the space of observable events. The question of existence, however, remains open: what conditions should be imposed on measure P^* in order to assure the existence of distributions appearing in (i)-(viii) which yield this particular measure P^*. In particular, in connection with the last theorem, the problem is to find such conditions for the distributions $\Phi(t)$ and $A(t)$ (besides conditions (11.6)) which would imply the existence of solutions $G(t)$ of (11.10) "admissible" from probabilistic point of view, i.e. such solutions $G(t)$ for which

$$F(t) = 1 - \frac{1-\Phi(t)}{1-G(t)}$$

is also a distribution function.

12. Probability generating function of the number of offsprings of different types. In this section we shall use assumptions (i)-(viii) and derive the formula for probability generating function of the joint distribution of the number of actually born sons of types 0 and 1, given the type of the father. In other words, we shall obtain the probability generating function for the branching process which serves as a model for the growth of the considered population.

Let C_0 and C_1 denote the numbers of actually born sons of types 0 and 1, respectively, and let $p_i(m, n) = P\{C_0 = m, C_1 = n \mid I = i\}$. Let $L_i(u, v) = \sum p_i(m, n) u^m v^n$ be the probability generating function of the distribution $\{p_i(m, n)\}$. Write

$$\Phi_i(x) = P\{Z \leqslant x \mid I = i\} = 1 - \big(1 - F(x)\big)\big(1 - G_i(x)\big).$$

We shall prove

THEOREM 12.1. *Under assumptions* (i)-(viii) *the functions* $L_i(u, v)$ *are given by formulas*

$$L_i(u, v) = \int_0^\infty \int_0^T D\big(1 + H(t)(u - v) - H(T)(1 - v)\big)\, dU_i(t)\, d\Phi_i(T) +$$

$$+ \int_0^\infty D\big(1 - H(T)(1 - u)\big)\big(1 - U_i(T)\big)\, d\Phi_i(T).$$

Proof. Consider the event $\{C_0 = m, C_1 = n\}$, and suppose first that $n > 0$. Given the values $D = r$, $Z = T$, $\xi = t$, this event can occur only if $r \geqslant m + n$ and $t < T$, and in this case its probability equals

$$\frac{r!}{m!\, n!\, (r - m - n)!} H(t)^m \big(H(T) - H(t)\big)^n \big(1 - H(T)\big)^{r - m - n}. \tag{12.1}$$

If $n = 0$, this event may occur also if $t > T$, and in this case we have to add the term

$$\frac{r!}{m!\, (r - m)!} H(T)^m \big(1 - H(T)\big)^{r - m}. \tag{12.2}$$

Using assumptions of conditional (given $I = i$) independence of random variables D, Z and ξ we obtain

$$p_i(m, 0) = \int_0^\infty \int_0^T \sum_{r \geqslant m} d_r \frac{r!}{m!\, (r - m)!} H(t)^m \big(1 - H(T)\big)^{r - m} dU_i(t)\, d\Phi_i(T) +$$

$$+ \int_0^\infty \sum_{r \geqslant m} d_r \frac{r!}{m!\, (r - m)!} H(T)^m \big(1 - H(T)\big)^{r - m} \big(1 - U_i(T)\big)\, d\Phi_i(T)$$

and for $n > 0$

$$p_i(m, n) = \int_0^\infty \int_0^T \sum_{r \geqslant m+n} d_r \frac{r!}{m!\, n!\, (r-m-n)!} H(t)^m \times$$

$$\times [H(T) - H(t)]^n \left(1 - H(T)\right)^{r-m-n} dU_i(t)\, d\Phi_i(t).$$

Multiplying by $u^m v^n$ and adding for all m, n we easily obtain the desired formulas.

13. Discussion. As in the discussion of models for spreading of infectious diseases, we shall try to analyse how adequate to reality is the proposed model of spreading of non-infectious diseases. In other words, we shall discuss the interpretational and predictive value of this model. As before, because of a non-empirical character of this paper, the discussion will be confined mainly to the first of these problems.

To analyse the interpretational value of the proposed model we shall start from stating once more the basic aim of constructing it. Generally speaking, the object was to create the possibility of testing the hypothesis asserting that the mechanisms of inheritance of certain traits (that is, the probability distribution of the offspring's trait) depend, among other factors, on the parent's age at the time when the offspring is born. Incidentally, one could venture to interpret this hypothesis in genetic terms: it would assert that the genetic code of a given organism may undergo some changes as the organism grows older.

To create the possibility of testing this hypothesis, we have suggested a model whose construction is the following: it consists of defining a branching process, where it is additionally assumed that, besides the reproduction of particles, one can observe certain variables connected with these particles such as the age of particle at the time of a birth of its offspring, the life-length of a particle, "cause" of its death, and so on. In order to be able to test the hypothesis on the age-dependence of the mechanisms of inheritance, the central problem of the model was to build methods which would allow us to infer, that the particles are not identical in their probability distributions of the numbers of offsprings, i.e. that there is more than one "kind" of particles in the considered process.

To describe the process of reproduction, we constructed a certain "sub-model" which consists of defining random mechanisms generating the individual life-histories of particles. This sub-model was expressed in terms of a certain number of random variables, in such a way that their probability distributions determine the probability distributions of reproductions of particles of different kinds in the branching process.

To create the possibility of building actual estimates, these random variables were interpreted in terms of certain events connected with families in human populations.

Thus, the model consists of defining a branching process of reproduction of particles, whose individual life-histories are described by the sub-model. The interpretation into the reality of the studied phenomenon of the spreading of non-infectious diseases is the following: particles are interpreted as individuals (more precisely, individuals of a given sex), and the random variables of the sub-model are identified with certain observable variables connected with life-histories of human beings such as life-length, cause of death, and so on.

Now, the degree to which any model is adequate to reality, which it attempts to describe, depends on the degree to which the assumptions concerning the notions of the model approximate the real properties of those observable variables which are interpreted in terms of these notions. In the present case the answer as to how adequate is the proposed model depends on the answer to the question how well the assumptions of branching processes (i.e. independence of reproductions and invariance of the distribution of the number of offsprings) describe the development of human populations. The objections to these assumptions are well known and we shall not dwell on this point; it is much more interesting to analyse how adequate are the assumptions about the variables of sub-model since the measurements of those observable variables of the phenomenon studied which are interpreted in terms of variables of sub-model are not always available (more precisely, the problem which variables can be observed in a specific situation and which cannot depends on the values of these variables). The theorems proved in sections 10 and 11 show that under some assumptions one can study the properties of these variables even though one cannot always observe them. This creates the possibility of empirical verification of the model.

It may be worthwhile to compare the presented model of inheritance with the well-known genetic models. In most general terms, in all standard genetic models one can distinguish three basic groups of assumptions:

(1) First group consists of postulating the existence of a certain classification of individuals with respect to genotypes and making some assumptions concerning the relation between genotypes and fenotypes. In more abstract terminology, one introduces two classifications: the (unobservable) genotype classification $\mathscr{G} = \{G_1, G_2, \ldots\}$ into groups $G_1, G_2, \ldots$ and (observable) fenotype classification $\mathscr{F} = \{F_1, F_2, \ldots\}$ into groups $F_1, F_2, \ldots$ These two classifications are connected by a certain (usually not one-to-one) function $\mathscr{G} \to \mathscr{F}$.

(2) The second group consists of assumptions concerning the probability distributions of the offspring's genotype given the genotypes of his parents. In abstract terminology, these assumptions can be expressed as a function $\mathcal{G} \times \mathcal{G} \to \mathcal{M}(\mathcal{G})$, where $\mathcal{M}(\cdot)$ denotes the class of all probability distributions over the corresponding set.

(3) The third group of assumptions concerns the mating process; it is assumed that the probability of mating of a given pair (specified in each model) depends only on the fenotypes of the members of this pair.

From the point of view of the model presented, we shall not discuss the third group of assumptions since our model is restricted to one sex only.

As regards assumptions (1), the situation is the following: the role of (unobservable) genotype classification is played by the classification with respect to type I, that is, $\mathcal{G} = \{G_0, G_1\}$.

The role of fenotype classification is played by a certain space Ω^* of observable events, and the mapping $\mathcal{G} \to \mathcal{M}(\Omega^*)$, which in this case reduces to a pair of probability distributions over Ω^*. Thus, our assumptions are more general than in standard models since it is not required that these probability measures are concentrated on disjoint subsets of the space Ω^*.

As regards assumptions (2), the situation in our model is the following: in view of restriction of considerations to one sex only, the probability distribution of the offspring's "genotype" depends on the "genotype" of one of his parents only (father); we assume, however, that — in distinction with the standard models — this distribution depends also on the father's age at the time of the birth of the offspring. In abstract terms, the model consists of assuming the existence of a certain function $\mathcal{G} \times [0, \infty) \to \mathcal{M}(\mathcal{G})$.

Formally, such an assumption could be incorporated in (2) by suitable enrichment of the genotype classification (by adding the individual's age as one of the characteristics). This, however, would require violating the traditional terminology, by accepting that the individual's genotype changes during his life.

At the conclusion, it may be worthwhile to discuss from a more general point of view the differences between models for infections diseases presented in Part I and models for non-infectious diseases, presented in Part II. In the first part of the paper, because of the nature of questions concerning epidemics of infectious diseases, the main object was to study the limit properties of given types of branching processes, the assumptions of theorems being expressed in terms of the distributions of the number of offsprings (i.e. in terms of the distribution of the number of susceptibles

infected by a given infective). In the second part of the paper the limit properties of the branching process were of a secondary interest only; in view of the character of the question posed, the main object was to analyse the mechanisms of reproduction and the methods of infering about the heterogeneity of the population, caused by the specific mechanisms of inheritance of certain traits which determine the probabilities of some observable events.

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