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CONTROL IN BIOMEDICAL SYSTEMS

Modeling the Impact of Chronic Disease Prevalence on COVID-19 Mortality

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Abstract—A model of the COVID-19 epidemic in a population heterogeneous by chronic non-communicable diseases is presented. A synthetic population is recreated, preserving the causal relationships between chronic diseases, sex, and age. Infection of individuals in the population is simulated, and the effect of the dependence of the course of COVID-19 on the presence and type of specific chronic diseases in infected individuals is modeled. The results of the epidemic modeling in the original population are compared with those in populations with reduced prevalence of chronic non-communicable diseases. Diseases whose reduced prevalence leads to the greatest reduction in COVID-19 mortality, the number of years of life lost, and the load on intensive care equipment are identified.

Keywords: Bayesian network, Markov model, synthetic population

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1. INTRODUCTION

One of the indicators of a population's vulnerability to infectious diseases is the prevalence of chronic non-communicable diseases, which represent the body's decline and decreased resilience. The more chronic diseases a person has, the worse his prognosis for infectious diseases becomes [1, 2]. The distribution of chronic diseases in the population is one of the significant factors determining the differences in COVID-19 mortality rates among countries [3]. Effective control of chronic diseases and the development of policies aimed at reducing their prevalence can help lessen the negative consequences of an infectious disease epidemic.

The impact of chronic diseases on the COVID-19 epidemic was studied using mathematical models with a system of differential equations, or via agent-based modeling. In differential equations models the entire population is divided into groups of people with chronic diseases and those without chronic diseases [4–6]. The [5] proposed that the most cost-effective strategy for reducing COVID-19 burden on population is to lessen the incidence of infection in patients with chronic diseases due to their high vulnerability. Authors of agent-based models usually incorporate chronic diseases in individuals indirectly through age [7]. However in [8] it was shown that the conditional probability of hospitalization of an individual with COVID-19 is higher when taking into account both chronic diseases and age compared to taking into account age alone.

Mathematical models in general do not include the type and number of chronic diseases in individuals, while observational evidences show different increases in the risk of death for different diseases and the presence of a nonlinear cumulative effect [9]. A chronic disease that increases the risk of severe illness and hospitalization may not affect the risk of death [10]. Modeling multiple diseases simultaneously is complicated by the fact that chronic diseases form a causal network in

which the development of one disease increases the probability of the development of a certain type of other diseases over time [11–13].

This paper presents a mathematical model which takes into account the complex interaction mechanisms between multiple chronic diseases and an infectious disease. The aim of the study is to determine how the prevalence of various chronic diseases in a population influences mortality from COVID-19. A series of computational experiments with reduced prevalence levels of various chronic diseases was conducted to determine their contribution to mortality and healthcare resource workload during the COVID-19 epidemic.

2. MODELED MECHANISMS

The model was designed to reproduce the COVID-19 epidemic in a megapolis. The reference was the COVID-19 epidemic in Moscow in 2020–2021. The process of COVID-19 infection in the population was considered random with a uniform probability distribution, and the population was considered uniformly mixed and heterogeneous in terms of sex, age, and chronic diseases.

The presence of various chronic diseases in individuals was considered a dependent random variable. The risk of developing a new chronic disease increases with age. The development of a particular type of chronic disease also depends on sex and the pre-existing chronic diseases. Research [12] has discovered clusters of diseases that occur together with a probability higher than that of a single disease. The sequence of chronic diseases development forms a network with distinct clusters. To reproduce these dependencies, a Bayesian network was created, and its parameters were estimated.

COVID-19 infection causes destruction of pulmonary epithelial cells, leading to respiratory failure and the need for hospitalization. Provided extensive lung damage, COVID-19 leads to the development of L-type pneumonia and, if the condition worsens, H-type pneumonia [14]. In case of L-type pneumonia, a respiratory support using non-invasive ventilation is recommended, while for H-type pneumonia, invasive mechanical ventilation (IMV) is recommended. These methods require monitoring in intensive care units. The average duration of COVID-19 treatment is 2 to 6 weeks [15]. According to these considerations, the course of COVID-19 in an infected patient was modeled as a series of transitions between severity states using a Markov model. The model included the patient's respiratory states (RS): spontaneous breathing, non-invasive ventilation and invasive mechanical ventilation.

The course of COVID-19 depends on the presence of chronic diseases. Moreover, the severity of COVID-19 depends on both the type and number of chronic diseases. For this model, a risk score for severe COVID-19 was created. The score value was calculated as the sum of the weights of an individual's diseases present; the higher the value, the worse the prognosis. A relative weight was assigned to each disease reflecting its contribution to the increased risk of death. To model the impact on the disease course, the transition probabilities of the Markov model were dependent on the risk score value.

3. MATHEMATICAL DESCRIPTION OF THE MODEL

This section successively describes the creation of a risk score for severe COVID-19, the creation of a Markov model of COVID-19 progression, the generation of a synthetic population using a Bayesian network, and the overall scheme of the computational experiment. This order is determined by the fact that the list of chronic diseases to be modeled in individuals was determined while creating the risk score, and the possible states of individuals at the initial point in time were determined while creating the Markov model. This information was thereafter used to construct a synthetic population. For creating a risk score, a Markov model and a Bayesian network, the data from patients treated with COVID-19 in the infectious diseases department of Moscow hospital from March 2020 to June 2021 were used [16].

3.1. Risk Score for Severe COVID-19

The CoRS-COVID score described in [17] was used as a risk score for severe COVID-19.

Consider $\boldsymbol{x} = (x_1, \ldots, x_n),\ x_i \in \mathbb{R}$ as a list of individual characteristics. The risk of a person to severe course of the disease can be represented with function $\phi_\Pi = f(\boldsymbol{x}),\ \phi \in \mathbb{R}$, where $f(\boldsymbol{x})$ is the ranking function. If a person $\boldsymbol{x_1}$ has higher risk comparing to person $\boldsymbol{x_2}$, then the corresponding function values will be

$$\phi_{\Pi_1} = f(\boldsymbol{x_1}) > \phi_{\Pi_2} = f(\boldsymbol{x_2}).$$

The objective of developing a risk function is to allocate the characteristics $(x_1, \ldots, x_n)$ that impact the infectious disease course and the type of function $f(\boldsymbol{x})$. In particular, the search for the function $f(\boldsymbol{x})$ can be among additive value functions that are composed of the sum of one-dimensional operators $[A]$ of each characteristic:

$$\varphi = f(\boldsymbol{x}) = A_1 x_1 + A_2 x_2 + \cdots + A_n x_n.$$

Consider operators $\{A_i\}$ as

$$A_i x_i = k_i x_i, \quad k_i \in \mathbb{Z}.$$

We will use $x_i \in \{0, 1\}$, where 1 corresponds to chronic disease i's presence and 0 to chronic disease i's absence.

Then

$$\phi_\Pi = \sum_i k_i x_i. \tag{1}$$

We will call ϕ_Π a risk score for a severe disease course and k_i the relative weight of a chronic disease i. For the convenience of clinical use, k_i lies in the domain of integers.

Consider a logistic regression in which the dependent variable is the probability of the lethal outcome of the disease y and the independent variables are the characteristics $\boldsymbol{x}$

$$P(y|\boldsymbol{x}) = \frac{1}{1 + e^{-z(\boldsymbol{x})}}, \tag{2}$$

where

$$z(x) = \boldsymbol{w}^\intercal \boldsymbol{x} + b = w_1 x_1 + w_2 x_2 + \ldots w_n x_n + b, \quad \boldsymbol{w}, b \in \mathbb{R},$$

$z(x)$ is a monotonic function of a linear combination. Thus,

$$\boldsymbol{w}^\intercal \boldsymbol{x_1} > \boldsymbol{w}^\intercal \boldsymbol{x_2} \Rightarrow P(y|\boldsymbol{x_1}) > P(y|\boldsymbol{x_2}).$$

Therefore operators $A_i = w_i$ can be considered as ranking function for health status. Because $w_i, b \in \mathbb{R}$ are real and $k_i \in \mathbb{Z}$ are integers, we shall round

$$k_i = [w_i]\,. \tag{3}$$

To develop ϕ_Π we selected characteristics $\boldsymbol{x}$ as chronic diseases that had odds ratio of a lethal outcome significantly higher than 1.2 or lower than 0.8. The logistic regression (equation (2)) using $\boldsymbol{x}$ was created; the parameters $\boldsymbol{w}$ and b were estimated with maximum likelihood method. The diseases' weights were obtained using equation (3). The final list $\boldsymbol{x}$ consists of 13 diseases (coronary heart disease, hypertension, arrhythmia, cerebrovascular disease, vascular thrombosis, anemia, chronic kidney disease stages 1–3, emphysema, fatty liver disease, metastatic cancer, and autoimmunity) with their weights ranging from -4 to 1.

3.2. Markov Model of COVID-19 Progression

The modeling of COVID-19 course was carried out using the Markov model of COVID-19 progression [18].

Let $\{S_t, t = 0, 1, 2, 3, \dots\}$ be a homogeneous Markov chain defined in measurable space $(E, \mathfrak{F})$ with transition probabilities

$$\mathbb{P}(s, B) = \mathbb{P}(D = S_{t+1} \in B | S_t = s),\ s \in E,\ B \in \mathfrak{F},$$

and the initial probabilities distribution

$$\pi_0(B) = \mathbb{P}(S_0 \in B),\ B \in \mathfrak{F}. \tag{4}$$

We defined the state space E for the Markov model of COVID-19 progression as consisting of five states: hospital stay without respiratory support s_1, hospital stay on non-invasive ventilation s_2, hospital stay on invasive mechanical ventilation s_3, recovery s_4, and death in the hospital s_5. The transition probability matrix T is

$$T = \begin{pmatrix} p_{11} & p_{12} & p_{13} & p_{14} & p_{15} \\ p_{21} & p_{22} & p_{23} & p_{24} & p_{25} \\ p_{31} & p_{32} & p_{33} & p_{34} & p_{35} \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix}, \quad \text{where } p_{ij} = \mathbb{P}(S_{t+1} = s_j | S_t = s_i).$$

The transition probabilities p_{ij} were estimated using the multinomial logistic regressions, that have the transition probabilities $P(S_t, B)$ from the current state as the dependent variable and the value of a risk score for severe COVID-19 ϕ_Π (equation (1)) as the independent variable:

$$\begin{aligned} p_{il}(\phi_\Pi) &= \mathbb{P}(S_{t+1} = s_l | S_t = s_i) = \frac{e^{-\beta^i_{0l} - \beta^i_l \phi_\Pi}}{1 + \sum_{k=1}^5 e^{-\beta^i_{0k} - \beta^i_k \phi_\Pi}}, \\ p_{i5}(\phi_\Pi) &= \mathbb{P}(S_{t+1} = s_5 | S_t = s_i) = \frac{1}{1 + \sum_{k=1}^5 e^{-\beta^i_{0k} - \beta^i_k \phi_\Pi}}, \end{aligned} \qquad l = 1, \dots, 4, \forall i. \tag{5}$$

The prediction of COVID-19 course for one individual n within one day time step is

$$S_{t,n} = T^t(\phi_{\Pi,n}) S_{0,n}.$$

The parameters $\{\beta\}$ for transition probabilities p_{ij} were estimated using the maximum likelihood method based on data of patients treated in a hospital with COVID-19.

3.3. Synthetic Population

Consider a population $\mathcal{P}$ of individuals $\{a_n\}_{n=1}^N$. Each individual has the list V^n of random variables, denoting characteristics of individuals. The list of characteristics consisted of V_1^n as age group; V_2^n as sex; V_{3-16}^n as presence of chronic diseases, partially corresponding to the characteristics x_i of risk score equation (1); and $V_{17}^n = S_0^n$ as the type of respiratory status at the moment of hospitalization, which corresponds to the first state π_0 of the Markov model in equation (4).

A synthetic population was created using a Bayesian network [19]. The Bayesian network was a directed acyclic graph; its nodes were random variables V_i denoting the characteristics of individuals, and its edges r_i denoted the dependent relations between the random variables. At each root node, the probability distribution $\mathbb{P}(V_i)$ of the values of the corresponding random variable V_i was determined. At each child node, the conditional probability distributions of the values of the random variables were determined depending on the value of the parent node: $\mathbb{P}(V_i | parents(V_i))$.

The unconditional joint probability of all random variables in the network is expressed through the product of all probabilities of the parents and parents of the parents of the nodes:

$$\mathbb{P}(V_1, \dots, V_n) = \prod_{i=1}^n \mathbb{P}(V_i | parents(V_i)). \tag{6}$$

This equation can be used to generate a list of individuals with given characteristics via a sequential calculation.

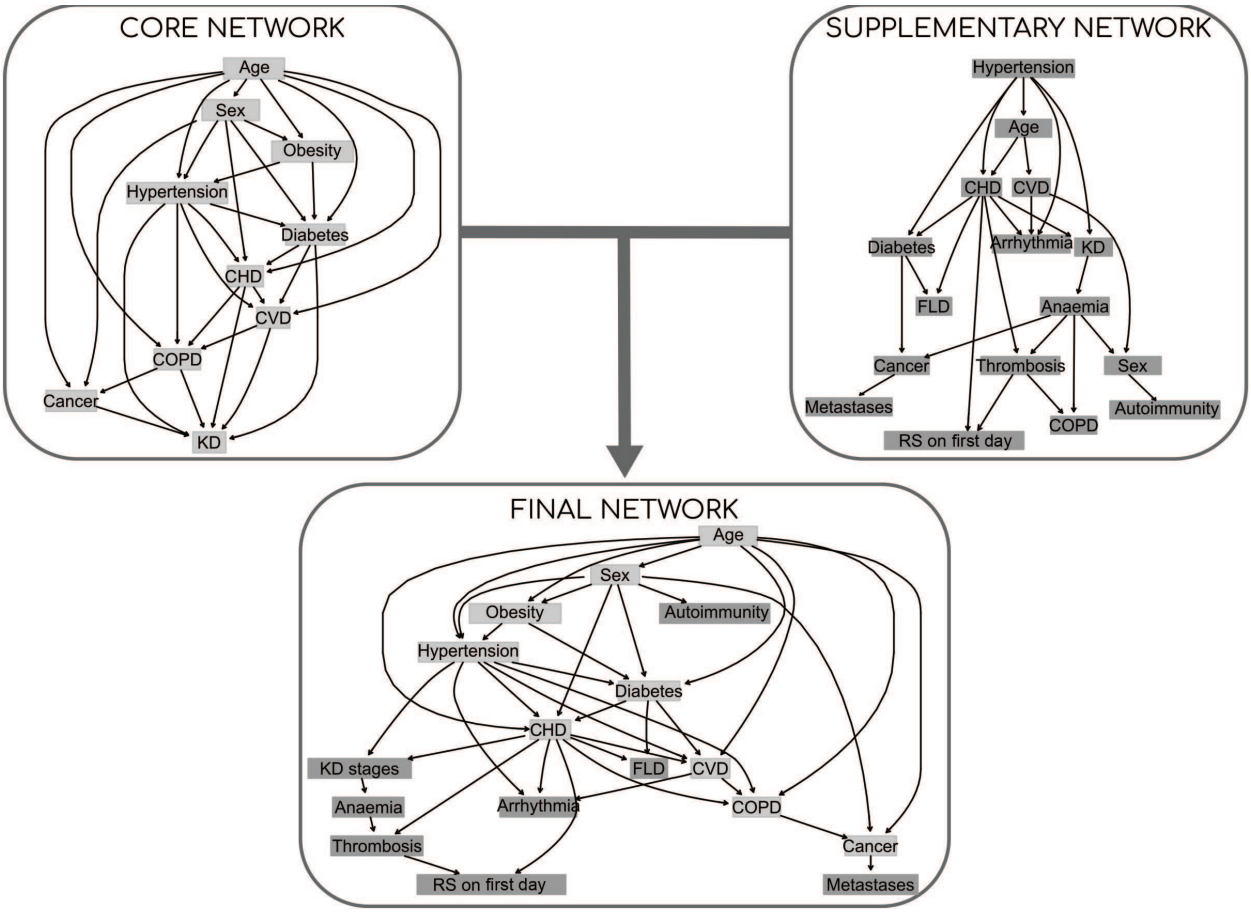

Fig. 1. A diagram of the merging of the Bayesian network graph based on the data of questionnaires (core network) and the Bayesian network graph based on the data of hospitalized patients (supplementary network). CHD—coronary heart disease, CVD—cerebrovascular disease, COPD—chronic obstructive pulmonary disease, KD—kidney disease, FLD—fatty liver disease, RS—respiratory support.

The Bayesian network for the considered synthetic population $\mathcal{P}$ was created in three stages. At the first stage, a core network was created using data from the 2021 Behavioral Risk Factor Surveillance System (BRFSS) collected by the US Centers for Disease Control and Prevention. The data represent the results of telephone surveys of 438 693 US residents on the presence of chronic diseases diagnosed by their physicians; their behavior; diet; living conditions; as well as information on state of residence, sex, age, survey date, and other information. We selected the responses on the following: sex, age group, presence of high blood pressure (hypertension), heart attack and coronary heart disease, stroke, cancer, chronic obstructive pulmonary disease, kidney disease, diabetes, and obesity using a BMI value. These characteristics formed the nodes of the core Bayesian network; the core network contained a total of 10 nodes. However, these data did not contain information on all the necessary chronic diseases included in the ϕ_Π index.

At the second stage, a supplementary network was created, for which data from patients treated with COVID-19 in the infectious diseases department of Moscow from March 2020 to June 2021 was used [16]. The data consist of the patient's sex, age, date of hospitalization, duration of treatment, type of respiratory support used for each day of treatment, treatment outcome and chronic diseases present. For the supplementary Bayesian network, we selected data on age, sex, diseases present in the BRFSS questionnaire (hypertension, coronary heart disease, stroke, kidney disease, diabetes, cancer, and chronic obstructive pulmonary disease); additional diseases included in the ϕ_Π index

(arrhythmia, vascular thrombosis, anemia, fatty liver disease, metastases, and autoimmunity); and the patient's initial type of respiratory status s_0 at the time of hospitalization. The age of the patients was divided into groups corresponding to the BRFSS questionnaire categories. These characteristics formed 16 nodes of the supplementary network.

Optimization of both the core and supplementary networks was performed using the hill-climbing algorithm and maximization of the Bayesian Information Criterion

$$BIC(G|D) = \ln(P(D|G,\Theta)) - \frac{d}{2}\log m \xrightarrow[g,\Theta]{} \max,$$

where G is a graph structure, D is observation data, Θ are estimates of parameters given a structure, d is the number of free parameters, and m is the size of observation D.

At the third stage the two networks were merged together into one by adding the six absent nodes from the supplementary network to the core network, preserving parent edges and conditional probabilities (Fig. 1).

3.4. Computational Experiment Scheme

Figure 2 presents an overview of the experiment. Using the equation (6), a population of 100 000 individuals with randomly assigned characteristics was generated. For each individual, the risk score for severe COVID-19 was calculated by $\phi^n_\Pi = \sum_j k_j x^n_j$. The proportion p of the population was deemed infected with COVID-19, and the course of COVID-19 for all infected individuals was simulated using a Markov model. The probability of infection p was estimated as the ratio of the total number of detected COVID-19 cases as of January 2025 to the total number of Moscow residents in 2025 and amounted to 0.295. For each infected individual, transition probabilities in the model were calculated depending on the risk score value (equation (5)). Based on the transition

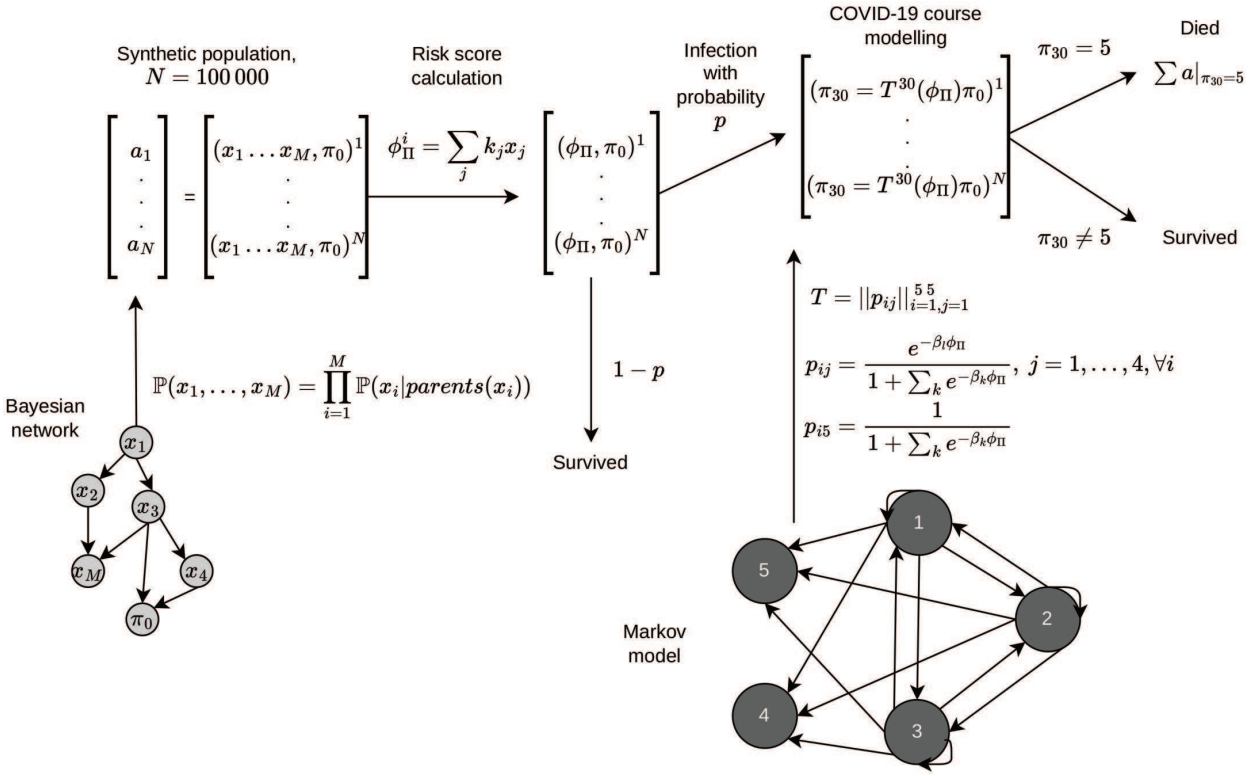

Fig. 2. An overview of the computational experiment: creating a population using a Bayesian network, calculating a risk score for each individual, randomly infecting the population, and simulating the course of COVID-19 in infected individuals using a Markov model.

probabilities, for each one-day time step the next state in the model was randomly chosen for each infected individual. The disease course for the infected was simulated for 30 days.

Estimates of the number of survivors and deceased, their sex, average age, and average length of stay were obtained. The prevalence of chronic diseases among deceased individuals and the relative risks of death for different diseases were calculated. For deceased individuals, estimates of years of life lost were obtained based on life expectancy in age groups calculated from data on mortality in Moscow for 2014 from the Human Mortality Database. To obtain reliable estimates, 100 random runs of the model were carried out, the results were averaged and confidence intervals were calculated.

A series of simulations of the COVID-19 epidemic were conducted in a population with a reduced prevalence of chronic diseases. In the original Bayesian network, the conditional probabilities $\mathbb{P}(V_i|parents(V_i))$ were lowered by 50% at one or more nodes V_i corresponding to chronic diseases, and a new synthetic population was generated. For individuals in the new population, infection with COVID-19 was randomly assigned, and a 30-day infection course was simulated; mortality, the sum of years of life lost, and the average length of stay were estimated. Epidemics in populations with a reduced prevalence of hypertension, obesity, diabetes, cancer, coronary heart disease, chronic obstructive pulmonary disease, and cerebrovascular disease were simulated. We also simulated a decrease in the prevalence of several diseases simultaneously, specifically hypertension and diabetes; hypertension and coronary heart disease and cerebrovascular disease; all cardiovascular diseases (hypertension, coronary heart disease, cerebrovascular disease, anemia, arrhythmia, and vascular thrombosis); and all diseases in the population. The obtained estimates were compared with the corresponding estimates from the original population.

4. RESULTS

Following 100 model runs, the average number of hospitalizations among 100 000 individuals was 29 470 people, and the number of deceased individuals amounted to 3682 people. Thus, the overall COVID-19 fatality rate in the synthetic population was 0.037, and the fatality rate among hospitalized was 0.125. The average age of the deceased was 57.6 years; the average age of deceased females was two years older than males. The number of years of life lost averaged to 23.61 years per person; the highest number of years of life lost was observed in the 60 to 69 age group.

The results of computational experiments in the original population and in populations with a 50% reduced prevalence of chronic diseases are given in the table. The greatest effect was observed for a reduction in the conditional probability of hypertension: a decrease in the number of individuals with hypertension from 39 018 people to 19 603 led to a decrease in the number of deaths from COVID-19 by 8.73% and the number of years of life lost by 6.9%. When comparing the effect relative to the number of individuals, the greatest effect was observed for a reduction in the conditional probability of coronary heart disease: a decrease in the number of individuals with coronary heart disease from 8096 to 4021 led to a decrease in the number of deaths from COVID-19 by 4.61% and the number of years of life lost by 2.9%; in addition, it caused the greatest effect on the decrease of the number of infected people requiring invasive mechanical ventilation on the first day of hospitalization—by 6%. Reductions in the prevalence of coronary artery disease and hypertension had the same effect on the number of days of invasive mechanical ventilation use—the decrease by 3.31%.

Diseases that do not directly influence COVID-19 severity contributed to mortality indirectly by being the causes of other diseases with a direct negative impact. For example, a reduction in the prevalence of obesity or diabetes, which were not included in the risk score for severe COVID-19, led to a decrease in COVID-19 mortality due to their relationships with other diseases in the Bayesian network.

Relative changes in epidemic parameters caused by a 50% decrease in the prevalence of chronic diseases in a synthetic population. CHD—coronary heart disease, COPD—chronic obstructive pulmonary disease, CVD—cerebrovascular disease, IMV—invasive mechanical ventilation

The disease with reduced prevalence	Change in number of deaths	Change in number of patients on IMV at the admission	Change in number of IMV usage days	Change in number of total years of life lost
Hypertension	−8.73%	−2.57%	−3.31%	−6.9%
Obesity	−1.38%	−0.47%	−0.49%	−1.3%
Diabetes	−0.51%	−0.82%	−0.37%	−0.3%
Cancer	−0.52%	=	−0.26%	−0.4%
CHD	−4.61%	−5.87%	−3.31%	−2.9%
COPD	−1.96%	=	−1.02%	−1.5%
CVD	−1.25%	=	−0.59%	−0.9%
Hypertension and diabetes	−9.06%	−3.20%	−3.58%	−7.1%
Hypertension, CVD, CHD	−12.97%	−7.45%	−6.31%	−9.6%
All cardiovascular diseases	−22.31%	−20.74%	−12.95%	−19.5%
All diseases	−23.1%	−21.24%	−12.35%	−19.7%

Reduction in the prevalence of several diseases simultaneously has a smaller effect than the sum of the effects of individual disease prevalence reductions. A 50% reduction in the prevalence of all diseases led to a 23% decrease in the number of deaths, a 12% decrease in the number of IMV days, and a 20% decrease in years of life lost. Thus, a 1% reduction in the quantity of people with chronic diseases leads to a 0.4% decrease in the number of COVID-19 deaths. Moreover, up to 96% of mortality was attributable to the high prevalence of cardiovascular diseases.

Model results showed that the high prevalence of chronic diseases in the population leads to a significant increase in mortality from infectious disease. In addition, chronic diseases increase the workload on healthcare resources, as illustrated by the prolonged usage of artificial lung ventilation and intensive care equipment due to the increased likelihood of high severity of the condition upon hospitalization. The relative decrease in years of life lost was smaller than that of the number of deaths. This is due to the fact that the decrease in the number of deaths mainly occurs in older age groups.

5. CONCLUSION

A model of the COVID-19 epidemic in a population heterogeneous in terms of chronic diseases was developed. According to the model's findings, a high prevalence of chronic non-communicable diseases is a major risk factor for increased mortality from infectious diseases in the population.

The model helped identify the diseases that have the greatest impact on mortality: hypertension and coronary heart disease. It was noted that a reduction in the prevalence of obesity and diabetes, which do not directly influence the course of COVID-19, also leads to a decrease in COVID-19 mortality in the population.

The ratio of the reduction in the prevalence of chronic diseases to the consequential decrease in the number of COVID-19 deaths was estimated to be 1% to 0.4%. Moreover, up to 96% of mortality was attributable to cardiovascular diseases.

This work is one of the first to study the relationship between infection parameters in a population and the prevalence of chronic diseases. This analysis can be applied when developing policies to reduce the burden of chronic diseases in the population. The proposed approach can be broadened and applied in the study of the influence of chronic diseases on the course and outcomes of other infectious diseases, such as influenza, rhinovirus, and hepatitis C.

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