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A NOVEL COMPARTMENTAL VSLIT MODEL USED TO ANALYZE THE DYNAMICS OF TUBERCULOSIS IN ALGERIA AND UKRAINE AND THE ASSESSMENT OF VACCINATION AND TREATMENT EFFECTS

НОВА МОДЕЛЬ VSLIT ВІДДІЛЕННЯ, ЯКУ ВИКОРИСТАНО ДЛЯ АНАЛІЗУ ДИНАМІКИ ТУБЕРКУЛЬОЗУ В АЛЖИРІ ТА УКРАЇНІ Й ОЦІНКИ ЕФЕКТІВ ВАКЦИНАЦІЇ ТА ЛІКУВАННЯ

Despite having low rates of tuberculosis (TB) mortality in many countries, like China, Europe, and the United States, other countries, like India continue to struggle to contain the epidemic. This study intends to examine the effects of vaccinations and treatments on the dynamics of TB in two countries, Ukraine and Algeria, with contrasted demographic profiles. A mathematical model called the VSLIT model is considered for this purpose. The stability of both disease-free and endemic equilibrium is discussed qualitatively. For numerical simulations, the parameters are evaluated by the least squares approach according to the TB-reported data for Algeria and Ukraine from 1990 to 2020.

Незважаючи на низькі показники смертності від туберкульозу (ТБ) у багатьох країнах, таких як Китай, європейські країни та Сполучені Штати, інші країни, такі як Індія, продовжують боротися з метою стримування епідемії. Це дослідження має на меті вивчення впливу вакцинації та лікування на динаміку ТБ у двох країнах, Україні та Алжирі, з контрастними демографічними профілями. Для цього застосовано математичну модель під назвою VSLIT. Стабільність як вільної від хвороб, так і ендемічної рівноваги досліджується якісно. Параметри чисельного моделювання оцінюються за допомогою методу найменших квадратів із використанням даних про поширення ТБ в Алжирі та Україні за період з 1990 по 2020 рік.

1. Introduction. Tuberculosis is caused by a bacterium (mycobacterium tuberculosis) which most often affects the lungs. It is a disease that can be prevented and cured. Tuberculosis is transmitted from person to person through the air. One of the top 10 killers in the world, tuberculosis claims 1.8 million lives annually. According to the World Health Organization (WHO), eight nations account for two-thirds of the cases, with India leading the pack, followed by China, Indonesia, the Philippines, Pakistan, Nigeria, Bangladesh, and South Africa. This indicates how the spread of TB endangers human health and negatively affects social and economic life. Therefore, it is crucial to understand the disease's current stage and set up control strategies in order to stop the sickness from spreading.

Bernoulli made the first work on mathematical modelling in 1766 [1]. It was followed by P. D. En'ko who published several significant articles in mathematical epidemiology between 1873 and 1894. However, it might be stated that Ronald Ross's work laid the groundwork for mathematical epidemiology based on compartmental models. The first mathematical model of malaria transmission was presented by Ronald Ross in 1911 [2].

Kermack and McKendrick established the deterministic model Susceptible – Infected – Recovered (SIR) in 1927 [3].

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The development of the first mathematical model of TB was done in 1962 by Waaler and Anderson, who divided the entire population into different groups [4]. Subsequently, diverse mathematical models was developed to explore and manage TB [5, 6].

One of the most important factors in halting and limiting the spread of TB is vaccination. The first human to get the BCG (Bacillus Calmette-Guérin) immunization against tuberculosis was in 1921. The WHO currently suggests immunizing neonates as soon as feasible after birth with a single intradermal injection of BCG [7]. The importance of vaccination in making predictions about the eventual eradication of the illness led to its reliance on the mathematical modelling of TB. This subject has been the subject of numerous prior research, specifically for TB, according to Ucakan et al. [8]. The objective is to ascertain the dynamics of TB in Turkey, its future impact, and the effects of vaccination therapy. Yang and others [9] developed a mathematical model to examine how treatment and immunization affect the dynamics of TB transmission. Egonmwan at al. [10] proposed a mathematical model that incorporates immunization of newborn children and older susceptible individuals in the dynamics of TB transmission in a population.

In this study, a VSLIT compartmental epidemiological model has been used to investigate TB disease in two countries: Ukraine and Algeria with contrasted demographic profiles. Algeria is a country with an increasing young population. Ukraine, a country with stabilized profile of population like other European states, is the home country of O. M. Sharkovsky. We use the new TB infection cases from 1990 to 2020 in Algeria and Ukraine that we obtained from the WHO Global tuberculosis report [11] for the purpose of estimating the biological parameters of the recommended model.

2. Dynamic analysis and mathematical modelling. ***2.1. Formulation of a VSLIT model.*** This section presents the suggested mathematical model of TB infection. Five subgroups are identified among the population: the vaccinated (V), susceptible (S), latent (exposed) (L), infected (TB active) (I), and under treatment (T). The total population is therefore reported as

$$N(t) = V(t) + S(t) + L(t) + I(t) + T(t).$$

The flow chart of the model is shown in Fig. 1.

The dynamics of TB infection describes the system of differential equations

$$\begin{aligned}
\dot{V}(t) &= p\Lambda - (k+\mu)V(t),\\
\dot{S}(t) &= (1-p)\Lambda + kV(t) - \beta S(t)I(t) - \mu S(t),\\
\dot{L}(t) &= \beta S(t)I(t) - (\epsilon+\mu)L(t) + (1-\alpha)\delta T(t),\\
\dot{I}(t) &= \epsilon L(t) + \alpha\delta T(t) - (\gamma+\mu+\sigma)I(t),\\
\dot{T}(t) &= \gamma I(t) - (\mu+\delta+\eta)T(t)
\end{aligned} \tag{2.1}$$

with $V(0) \geq 0$, $S(0) \geq 0$, $L(0) \geq 0$, $I(0) \geq 0$ and $T(0) \geq 0$. Here, Λ is the recruitment rate, p is the vaccination rate $(p \in [0,1])$, μ is the natural death rate, k is the rate of moving from V to S, β is the transmission rate, γ is the recovery rate, ϵ is the progression rate, α is the treatment failure rate, δ is the rate at which the treated population leave the class T, σ and η are the disease death rate in I and the disease death rate in T, respectively.

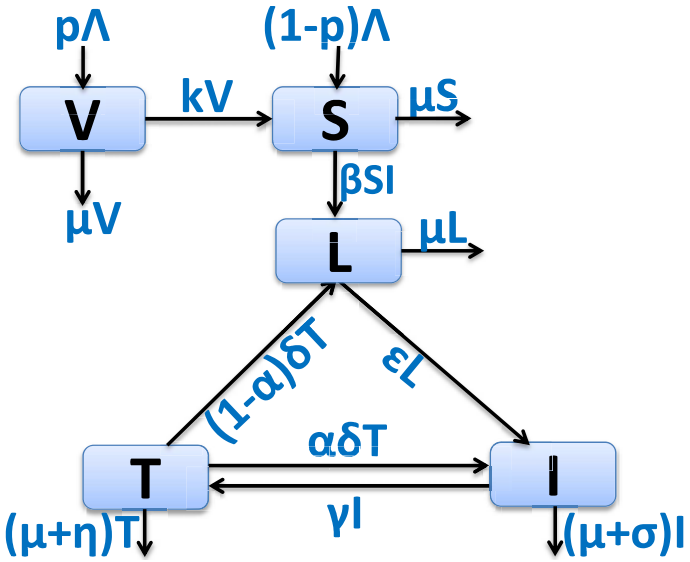

Fig. 1. Flow chart of the proposed VSLIT model.

2.2. Model analysis. Invariance of the feasible region. We will study the TB model (2.1) in a biologically feasible region $\Omega \subset \mathbb{R}^5_+$ provided by

$$\Omega = \left\{ (V(t), S(t), L(t), I(t), T(t)) \in \mathbb{R}^5_+ : N(t) \leq \frac{\Lambda}{\mu} \right\}.$$

Lemma 1. *The TB model's solution is positive whenever it exists for all $t > 0$ and nonnegative initial conditions. Additionally, if $0 \leq N(0) \leq \dfrac{\Lambda}{\mu}$, then*

$$0 \leq N(t) \leq \frac{\Lambda}{\mu} \quad \textit{for all} \quad t > 0.$$

Proof. If the variables $V(t)$, $S(t)$, $L(t)$, $I(t)$, and $T(t)$ are positive, we obtain

$$\dot{V}\,|_{V=0} = p\Lambda \geq 0,$$

$$\dot{S}\,|_{S=0} = (1-p)\Lambda + kV \geq 0,$$

$$\dot{L}\,|_{L=0} = \beta SI + (1-\alpha)\delta T \geq 0,$$

$$\dot{I}\,|_{I=0} = \epsilon L + \alpha\delta T \geq 0,$$

$$\dot{T}\,|_{T=0} = \gamma I \geq 0.$$

As a result, for nonnegative initial conditions, the solution is always positive for all $t \geq 0$.

The addition of the VSLIT model equations (2.1) leads to the conclusion that

$$\begin{aligned}\dot{N}(t) &= \Lambda - \mu(V(t) + S(t) + L(t) + I(t) + T(t)) - (\sigma I(t) + \eta T(t)) \\ &= \Lambda - \mu N(t) - (\sigma I(t) + \eta T(t)) \leq \Lambda - \mu N(t).\end{aligned}$$

Then we have $\frac{dN(t)}{dt} \leq 0$ for $N(t) \leq \frac{\Lambda}{\mu}$. We obtain that $0 \leq N(t) \leq \frac{\Lambda}{\mu}$ for all $t \geq 0$ and $0 \leq N(0) \leq \frac{\Lambda}{\mu}$.

It follows that the feasible region Ω is positively invariant.

Equilibrium points and their stability. To find the equilibrium points of model (2.1). We put the equations of the model equal to zero:

$$\frac{dV}{dt} = \frac{dS}{dt} = \frac{dL}{dt} = \frac{dI}{dt} = \frac{dT}{dt} = 0.$$

We obtain two equilibrium points: the disease-free equilibrium point "DFE"

$$E_1 = (V_1^*, S_1^*, L_1^*, I_1^*, T_1^*) = \left(\frac{p\Lambda}{k+\mu}, \frac{(k+\mu-\mu p)\Lambda}{\mu(k+\mu)}, 0, 0, 0\right),$$

thus, $N = \frac{\Lambda}{\mu}$, and the endemic equilibrium point "EE"

$$\begin{aligned} E_2 &= (V_2^*, S_2^*, L_2^*, I_2^*, T_2^*) \\ &= \left(\frac{p\Lambda}{k+\mu}, \frac{(k+\mu-\mu p)\Lambda}{(k+\mu)(\beta I_2^* + \mu)}, \frac{(\gamma+\mu+\sigma)(\mu+\delta+\eta) - \alpha\delta\gamma}{\epsilon(\mu+\delta+\eta)} I_2^*, I_2^*, \frac{\gamma}{\mu+\delta+\eta} I_2^*\right), \end{aligned}$$

where

$$\begin{aligned} I_2^* &= \frac{(k+\mu-\mu p)\epsilon\Lambda(\mu+\delta+\eta)}{(k+\mu)((\epsilon+\mu)(\gamma+\mu+\sigma)(\mu+\delta+\eta) - (\epsilon+\mu)\alpha\delta\gamma - (1-\alpha)\gamma\delta\epsilon)} - \frac{\mu}{\beta} \\ &= \frac{\mu}{\beta}(\mathcal{R}_0 - 1), \end{aligned}$$

thus, $N = \frac{\Lambda - (\sigma I_2^* + \eta T_2^*)}{\mu} < \frac{\Lambda}{\mu}$.

The endemic equilibrium point exists if $\mathcal{R}_0 > 1$.

The basic reproduction number, $\mathcal{R}_0$. The basic reproduction number, denoted by $\mathcal{R}_0$, is the expected number of secondary infections generated by a typical infected individual during its period of infection in a fully susceptible population [12]. If $\mathcal{R}_0 < 1$, it means that the disease will not be spread in the population, while $\mathcal{R}_0 > 1$, implies that the disease can spread in the population and becoming endemic.

The basic reproduction number $\mathcal{R}_0$ is calculated using the next generation matrix method (see [13]), where $\mathcal{R}_0 = \rho(FV^{-1})$, with the Jacobian matrices F and V of the new infection in the infected compartments $\mathcal{F}$ and the remaining transfer terms $\mathcal{V}$, respectively, given by

$$\mathcal{F} = \begin{bmatrix} \beta SI \\ 0 \\ 0 \end{bmatrix},$$

$$\mathcal{V} = \begin{bmatrix} (\epsilon+\mu)L - (1-\alpha)\delta T \\ -\epsilon L - \alpha\delta T + (\gamma+\mu+\sigma)I \\ -\gamma I + (\mu+\delta+\eta)T \end{bmatrix} = \begin{bmatrix} k_1 L - (1-\alpha)\delta T \\ -\epsilon L - \alpha\delta T + k_2 I \\ -\gamma I + k_3 T \end{bmatrix}.$$

Here, $k_1 = \epsilon + \mu$, $k_2 = \gamma + \mu + \sigma$, $k_3 = \mu + \delta + \eta$.

The Jacobian matrices of $\mathcal{F}$ and $\mathcal{V}$ are evaluated at the equilibrium so that F is nonnegative and V is a nonsingular matrix. One has

$$J(\mathcal{F}) = \begin{pmatrix} 0 & \beta S & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad \text{and} \quad J(\mathcal{V}) = \begin{pmatrix} k_1 & 0 & -(1-\alpha)\delta \\ -\epsilon & k_2 & -\alpha\delta \\ 0 & -\gamma & k_3 \end{pmatrix}.$$

Thus, at E_1 one gets

$$F = J(\mathcal{F}) = \begin{pmatrix} 0 & \dfrac{(k+\mu-\mu p)\Lambda\beta}{\mu(k+\mu)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad \text{and} \quad V = J(\mathcal{V}) = \begin{pmatrix} k_1 & 0 & -(1-\alpha)\delta \\ -\epsilon & k_2 & -\alpha\delta \\ 0 & -\gamma & k_3 \end{pmatrix}.$$

Then, $\mathcal{R}_0$ is the spectral radius (dominant eigenvalue) of the matrix FV^{-1}:

$$\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\epsilon(k+\mu-\mu p)\Lambda\beta k_3}{\mu(k+\mu)(k_1k_2k_3 - \alpha\gamma\delta k_1 - (1-\alpha)\delta\gamma\epsilon)}.$$

Global stability analysis of DFE.

Theorem 1. *The model's disease-free equilibrium point E_1 (DFE) is globally asymptotically stable if and only if $\mathcal{R}_0 < 1$ and it becomes unstable if $\mathcal{R}_0 > 1$.*

Proof. To demonstrate the theorem, we assume the Lyapunov function that follows:

$$V(t) = b_1L + b_2I + b_3T,$$

where b_i, $i = 1, 2, 3$, are positive constants to be chosen later. By calculating the time derivative of $V(t)$ along the solutions of system (2.1), we get

$$\frac{dV(t)}{dt} = b_1\frac{dL}{dt} + b_2\frac{dI}{dt} + b_3\frac{dT}{dt},$$

$$\begin{aligned} \frac{dV(t)}{dt} &= b_1[\beta SI - k_1L + (1-\alpha)\delta T] + b_2[\epsilon L + \alpha\delta T - k_2I] + b_3[\gamma I - k_3T] \\ &\le b_1\left[\frac{\Lambda\beta}{\mu}I - k_1L + (1-\alpha)\delta T\right] + b_2[\epsilon L + \alpha\delta T - k_2I] + b_3[\gamma I - k_3T] \\ &\le \frac{(b_2k_2 - b_3\gamma)(k+\mu-\mu p)}{(k+\mu)}\left[\frac{b_1\Lambda\beta}{\mu(b_2k_2 - b_3\gamma)} - 1\right]I \\ &\quad + [b_2\epsilon - b_1k_1]L + [b_1(1-\alpha)\delta + b_2\alpha\delta - b_3k_3]T, \quad S \le \frac{\Lambda}{\mu}. \end{aligned}$$

Now choosing $b_1 = \dfrac{\epsilon k_3(k+\mu)}{k+\mu-\mu p}$, $b_2 = \dfrac{k_1k_3(k+\mu)}{k+\mu-\mu p}$, and $b_3 = \dfrac{((1-\alpha)\epsilon + \alpha\delta k_1)(k+\mu)}{k+\mu-\mu p}$, we obtain $\dfrac{dV(t)}{dt} \le \dfrac{b_1\Lambda\beta}{\mu\mathcal{R}_0}(\mathcal{R}_0 - 1)I$. Hence, if $\mathcal{R}_0 < 1$ then $\dfrac{dV(t)}{dt}$ is negative. By LaSalle's invariant principle, it implies that E_1 is globally asymptotically stable.

Global stability analysis of EE. In this part, we demonstrate the global asymptotic stability of the EE of the model (2.1). Utilizing the technique explained in [14], from the system (2.1) at the EE, we get

$$\begin{aligned}
&p\Lambda = (k+\mu)V_2^*,\\
&kV_2^* = -(1-p)\Lambda + \beta S_2^* I_2^* + \mu S_2^*,\\
&k_1 L_2^* = \beta S_2^* I_2^* + (1-\alpha)\delta T_2^*,\\
&k_2 I_2^* = \epsilon L_2^* + \alpha\delta T_2^*,\\
&\gamma I_2^* = k_3 T_2^*.
\end{aligned}$$

Theorem 2. *If $\mathcal{R}_0 > 1$, the endemic equilibrium point E_2 (EE) of the model* (2.1) *is globally asymptotically stable.*

Proof. To demonstrate the theorem, we consider the Lyapunov function

$$\begin{aligned}
D = k\left[V(t) - V^* - V^* \ln\frac{V(t)}{V^*}\right] + \epsilon\left[S(t) - S^* - S^* \ln\frac{S(t)}{S^*}\right]\\
+ \epsilon\left[L(t) - L^* - L^* \ln\frac{L(t)}{L^*}\right] + k_1\left[I(t) - I^* - I^* \ln\frac{I(t)}{I^*}\right]\\
+ \frac{\delta T^*(k_1\alpha + \epsilon(1-\alpha))}{\gamma I^*}\left[T(t) - T^* - T^* \ln\frac{T(t)}{T^*}\right].
\end{aligned}$$

Computing the time derivative of $V(t)$ along the system (2.1) solutions, we get

$$\begin{aligned}
\frac{dD}{dt} = k\left[\left(1 - \frac{V^*}{V}\right)V'\right] + \epsilon\left[\left(1 - \frac{S^*}{S}\right)S' + \left(1 - \frac{L^*}{L}\right)L'\right]\\
+ k_1\left[\left(1 - \frac{I^*}{I}\right)I'\right] + \frac{\delta T^*(k_1\alpha + \epsilon(1-\alpha))}{\gamma I^*}\left[\left(1 - \frac{T^*}{T}\right)T'\right].
\end{aligned}$$

From a simple calculation, it follows that

$$\begin{aligned}
k\left(1 - \frac{V^*}{V}\right)V' &= k\left(1 - \frac{V^*}{V}\right)[p\Lambda - (k+\mu)V]\\
&= k(k+\mu)V^*\left(2 - \frac{V^*}{V} - \frac{V}{V^*}\right),\\
\epsilon\left(1 - \frac{S^*}{S}\right)S' &= \epsilon\left(1 - \frac{S^*}{S}\right)[(1-p)\Lambda + kV - \beta SI - \mu S]\\
&= \epsilon\mu S^*\left(2 - \frac{S^*}{S} - \frac{S}{S^*}\right) + \epsilon\beta S^* I^*\left(1 - \frac{S^*}{S} + \frac{I}{I^*}\right) - \epsilon\beta SI,
\end{aligned}$$

$$\epsilon\left(1-\frac{L^*}{L}\right)L' = \epsilon\left(1-\frac{L^*}{L}\right)[\beta SI - k_1 L + (1-\alpha)\delta T]$$

$$= \epsilon\beta SI - \epsilon\beta SI\frac{L^*}{L} - k_1\epsilon L + \epsilon\beta S^* I^*$$

$$+ (1-\alpha)\delta\epsilon T^* + (1-\alpha)\epsilon\delta T - (1-\alpha)\delta\epsilon\frac{TL^*}{L},$$

$$k_1\left(1-\frac{I^*}{I}\right)I' = k_1\left(1-\frac{I^*}{I}\right)[\epsilon L + \alpha\delta T - k_2 I]$$

$$= k_1\epsilon L - \epsilon\beta S^* I^*\frac{LI^*}{L^*I} - (1-\alpha)\epsilon\delta T^*\frac{LI^*}{L^*I} + k_1\alpha\delta T - k_1\alpha\delta T\frac{I^*}{I} + \epsilon\beta S^* I^*$$

$$+ k_1\alpha\delta T^* + \epsilon(1-\alpha)\delta T^* - \epsilon\beta S^* I^*\frac{I}{I^*} - (1-\alpha)\epsilon\delta T^*\frac{I}{I^*} - k_1\alpha\delta T^*\frac{I}{I^*},$$

$$\frac{\delta T^*(k_1\alpha+\epsilon(1-\alpha))}{\gamma I^*}\left(1-\frac{T^*}{T}\right)[\gamma I - k_3 T]$$

$$= \frac{\delta T^*(k_1\alpha+\epsilon(1-\alpha))}{I^*}\left(1-\frac{T^*}{T}\right)\left[I - \frac{I^*}{T^*}T\right]$$

$$= \delta\alpha k_1 T^*\frac{I}{I^*} + \delta(1-\alpha)\epsilon T^*\frac{I}{I^*} - \delta\alpha k_1 T^*\frac{IT^*}{I^*T}$$

$$- \delta(1-\alpha)\epsilon T^*\frac{IT^*}{I^*T} - \delta\alpha k_1 T - \delta(1-\alpha)\epsilon T$$

$$+ \delta\alpha k_1 T^* + \delta(1-\alpha)\epsilon T^*.$$

By using the previous equations, we obtain

$$\frac{dD}{dt} = k(k+\mu)V^*\left(2-\frac{V^*}{V}-\frac{V}{V^*}\right) + \epsilon\mu S^*\left(2-\frac{S^*}{S}-\frac{S}{S^*}\right)$$

$$+ \epsilon\beta S^* I^*\left(3-\frac{S^*}{S}-\frac{I}{I^*}-\frac{LI^*}{L^*I}-\frac{SIL^*}{S^*I^*L}\left(1-\frac{LS^*}{L^*S}\right)\right)$$

$$+ (1-\alpha)\epsilon\delta T^*\left(3-\frac{I^*L}{IL^*}-\frac{L^*T}{LT^*}-\frac{T^*I}{TI^*}\right)$$

$$+ \delta\alpha k_1 T^*\left(2-\frac{I^*T}{IT^*}-\frac{IT^*}{I^*T}\right). \tag{2.2}$$

Applying the characteristics of the geometric and arithmetic means in Eq. (2.2), we have

$$2-\frac{V}{V^*}-\frac{V^*}{V} \le 0,$$

$$2-\frac{S}{S^*}-\frac{S^*}{S} \le 0,$$

$$3-\frac{S^*}{S}-\frac{I}{I^*}-\frac{LI^*}{L^*I}-\frac{SIL^*N^*}{S^*I^*NL}\left(1-\frac{LS^*}{L^*S}\right) \le 0,$$

Table 1. Parameters and initial data of the model (2.1)

Parameter	Description	Algerian value	References	Ukrainian value	References
$V(0)$	Initial number of vaccinated	8,109,389	Assumed	5,980,291	Assumed
$S(0)$	Initial number of susceptible	17,368,226	Calculated	45,564,208	Calculated
$L(0)$	Initial number of latent	8,852	Assumed	8,852	Assumed
$I(0)$	Initial number of infected	11,607	[11]	16,465	[11]
$T(0)$	Initial number of treated	20,000	Assumed	20,000	Assumed
Λ	Recruitment rate	811,085	[15]	344214	[21]
μ	Natural death rate	0.00498	[15]	0.0121	[21]
k	Rate of moving from V to S	0.25	[16]	0.25	[17]
β	Transmission rate	6.6752×10^{-11}	Fitted	5.83×10^{-10}	Fitted
γ	Recovery rate	0.0043	Fitted	0.00012	Fitted
ϵ	Progression rate	0.0656	Fitted	0.225	Fitted
α	Treatment failure rate	0.1095	[19]	0.4033	[20]
δ	Rate at which the treated population leave the class T	0.1325	Fitted	0.208	Fitted
σ	Disease death rate in I	0.0136	Fitted	0.019	Fitted
η	Disease death rate in T	4.2327×10^{-6}	Fitted	0.0006	Fitted
p	Vaccination rate	0.977	[16]	0.899	[17]

$$3 - \frac{I^*L}{IL^*} - \frac{L^*T}{LT^*} - \frac{T^*I}{TI^*} \leq 0,$$

$$2 - \frac{I^*T}{IT^*} - \frac{IT^*}{I^*T} \leq 0.$$

The parameters are all positive, so it follows that $\dfrac{dD}{dt} \leq 0$ when $\mathcal{R}_0 > 1$. As a result, according to the LaSalle's invariance principle, $(V, S, L, I, T) \to (V^*, S^*, L^*, I^*, T^*)$ as $t \to \infty$.

3. Parameters estimation and numerical solution. This section estimates six model parameters using data from the WHO Global tuberculosis report [11] between 1990 and 2020 (see Table 1) and the other parameters are based on statistical data in the literature. Using the data of Algeria's and Ukraine's population from [15] one takes the death rate μ as the average death rate per year from 1990 to 2020, $\mu = 0.00498$ and $\mu = 0.0150875$, and the recruitment rate Λ, as the average birth per year from 1990 to 2020, $\Lambda = 811{,}085$ and $\Lambda = 434{,}687$, for Algeria's and Ukraine's, respectively.

The child immunization rate, BCG, is the ratio of children aged 12 – 23 months who have received BCG vaccination. Figures 2 and 3 display the percentage of one-year-old children who have received BCG immunization in Algeria and Ukraine between 1990 and 2020, according to data from officially recognized sources compiled by the World Bank [16, 17]. Hence, one gets the average vaccination rate for Algeria and Ukraine $p = 0.977$ and $p = 0.899$, respectively. The BCG has shown efficiency of overall 70% to 80% against childhood tuberculosis, namely meningitis and miliary tuberculosis [18]. Hence, in this paper one takes the average rate of moving from V to S as the BCG immunization failure $k = 1 - 0.75 = 0.25$. The treatment success from 2000 to 2020 [19, 20] is used to calculate the treatment failure rate $\alpha = 1 - 0.8905 = 0.1095$ and $\alpha = 1 - 0.59 = 0.4033$, for Algeria and Ukraine, respectively.

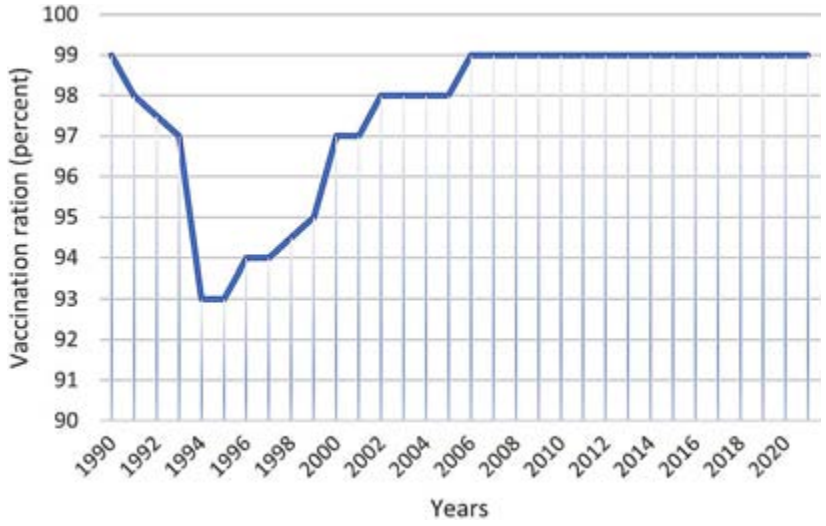

Fig. 2. Percentage of one-year-old children in Algeria receiving BCG vaccination during the time period 1990 – 2020.

Fig. 3. Percentage of one-year-old children in Ukraine receiving BCG vaccination during the time period 1990 – 2020.

The following initial conditions have been carefully chosen: The total beginning population, $N(0)$, has been set at $25{,}518{,}074$ and $51{,}589{,}817$, respectively, which corresponds to Algeria's and Ukraine's respective populations in 1990, according to [15]. The WHO Global tuberculosis report [11] has been used to determine the beginning infected population, $I(0)$. We have chose the initial latent population $L(0)$, the initial treated population $T(0)$, and the total number of vaccine recipients $V(0)$. The initial susceptible population can be estimated as $S(0) = N(0) - L(0) - I(0) - T(0) - V(0)$ as a result of these values. To provide accurate and trustworthy numerical simulations of the system under study, these initial conditions have been carefully selected. The parameters β, γ, ϵ, σ, α, δ, k, and η are estimated by minimizing the error between the solution of the proposed model and the actual TB incidence data (2.1). This parameter estimation's objective function is given by

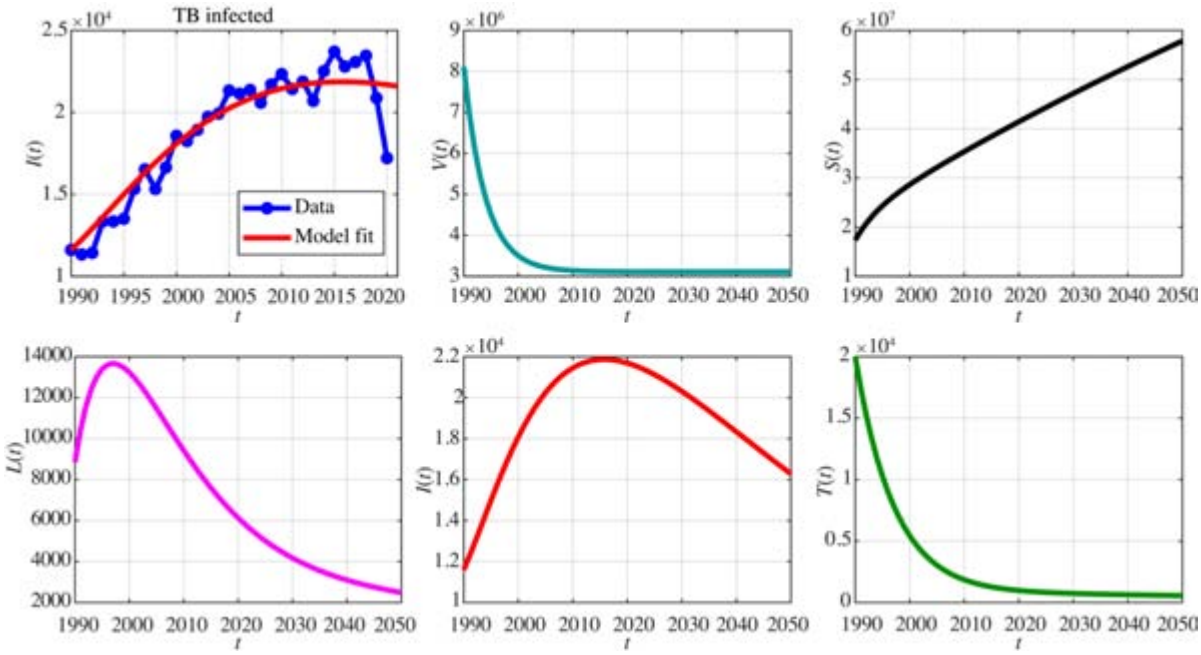

Fig. 4. Data fitting of the number of TB cases in Algeria.

$$\psi = \sum_{i=1}^{n} (I_{t_i} - I^*_{t_i})^2, \tag{3.1}$$

where $I^*_{t_i}$ denotes the actual TB infected case and I_{t_i} are the corresponding model solution at time t_i, n is the number of available actual data. The MATLAB function "fitnlm" which solves nonlinear regression problems based on the Levenberg – Marquardt algorithm in MATLAB R2020b, was employed to minimize the function (3.1).

In Fig. 4, the incidence data are displayed along with the model-fitted curve, obtained using the values in Table 1.

4. Sensitivity analysis. The examination of disease spread involves assessing the sensitivity of each parameter. This analysis is commonly used to measure the reliability of a model's predictions when considering errors in data collection and assumed parameters. By studying the effects of various model parameters, we can assess the relative significance of these factors in influencing disease transmission. The partial derivatives of the basic reproduction number $\mathcal{R}_0$ are studied in relation to the model parameters β, γ, k, and ϵ. Since $\dfrac{\partial \mathcal{R}_0}{\partial \beta} > 0$, it follows that by decreasing the rate of transmission (by adopting an isolation strategy for example), the endemic free equilibrium can be stabilized meaning that the spread of disease can be controlled. However, taking into account that $\dfrac{\partial \mathcal{R}_0}{\partial \gamma} < 0$, we deduce that tuberculous infection can be controlled by increasing the treatment rate γ. The increase of the immunization failure rate k causes an increase of $\mathcal{R}_0$ because $\dfrac{\partial \mathcal{R}_0}{\partial k} > 0$, leading to a faster grow of the diseased population. Finally, we have $\dfrac{\partial \mathcal{R}_0}{\partial \alpha} > 0$. As a result, by lowering the treatment failure rate α, the cumulative number of infected people can be minimized.

To estimate the relative change in a variable when the parameters change we calculate the sensitivity index.

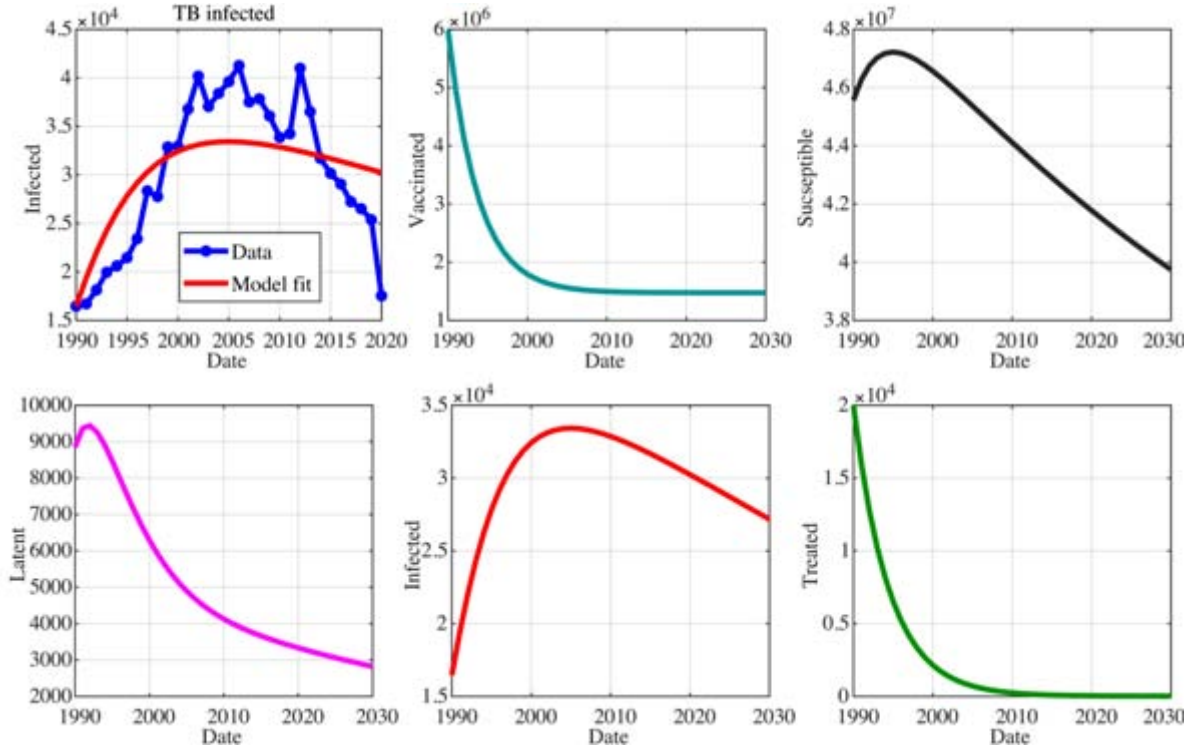

Fig. 5. Data fitting of the number of TB cases in Ukraine.

Definition. *For a specific parameter σ, the normalized $\mathcal{R}_0$ term sensitivity index is determined by*

$$S_{\sigma}^{\mathcal{R}_0} = \frac{\sigma}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \sigma}. \tag{4.1}$$

The computed sensitivity indices of the basic reproduction number $\mathcal{R}_0$ are displayed in Table 2 for the baseline model parameters established by the formula (4.1).

The values of $S_{\beta}^{\mathcal{R}_0}$ and $S_{\Lambda}^{\mathcal{R}_0}$ are exactly $+1$, as we can see in Table 2. This implies that an increase in $\mathcal{R}_0$ proportionate to both β and Λ will accompany an increase in both parameters. Furthermore, we show that the parameters k, ϵ, α, and δ are directly proportional to $\mathcal{R}_0$ due to the fact that $S_{k}^{\mathcal{R}_0} > 0$, $S_{\epsilon}^{\mathcal{R}_0} > 0$, $S_{\alpha}^{\mathcal{R}_0} > 0$ and $S_{\delta}^{\mathcal{R}_0} > 0$. Additionally, $S_{\mu}^{\mathcal{R}_0} < 0$, $S_{\gamma}^{\mathcal{R}_0} < 0$, $S_{\sigma}^{\mathcal{R}_0} < 0$, $S_{p}^{\mathcal{R}_0} < 0$, and $S_{\eta}^{\mathcal{R}_0} < 0$ indicate that the parameters μ, γ, σ, p, and η are inversely proportional to $\mathcal{R}_0$.

5. Results and discussion. Table 1 reports the results of the estimation of the parameters, and Figs. 4 and 5, illustrate the incidence data of Algeria and Ukraine, respectively, with the model-fitted curve, obtained using the values in Table 1. $\mathcal{R}^2$ values of 0.9016 and 0.6036 for Algeria and Ukraine, respectively, show that our model has a decent fit to the supplied real data.

Using the estimate parameters value, one obtains values for Algeria and Ukraine of $\mathcal{R}_0 = 0.5228$ and $\mathcal{R}_0 = 0.4306$, respectively, both of which are less than 1. By maintaining effective treatment and isolation procedures in the future, as shown by the model-fitted curve for the period of $2020-2050$ in Figs. 4 and 5, it is possible to reduce or eradicate the disease.

One plots $\mathcal{R}_0$ versus six parameters, as illustrated in Fig. 6, to better understand how specific parameters impact the spread of the disease. It is obvious that the three parameters β, ϵ, and α have a proportionate relationship to the fundamental reproduction number $\mathcal{R}_0$. This means that an increase

Table 2. Parameters and initial data of the model (2.1)

Parameter	Sensitivity index for Algeria	Sensitivity index for Ukraine
Λ	$+1$	$+1$
μ	-1.6502	-0.2053
k	$+0.0012$	$+0.0035$
β	$+1$	$+1$
γ	-0.1671	-3.0296
ϵ	$+0.0005$	$+0.06294$
α	$+2.1364 \times 10^{-10}$	$+8.7236 \times 10^{-05}$
δ	$+1.4003 \times 10^{-09}$	$+8.1145 \times 10^{-10}$
σ	-0.4043	-0.5647
η	-2.5311×10^{-11}	-3.3821×10^{-11}
p	-0.0194	-0.0527

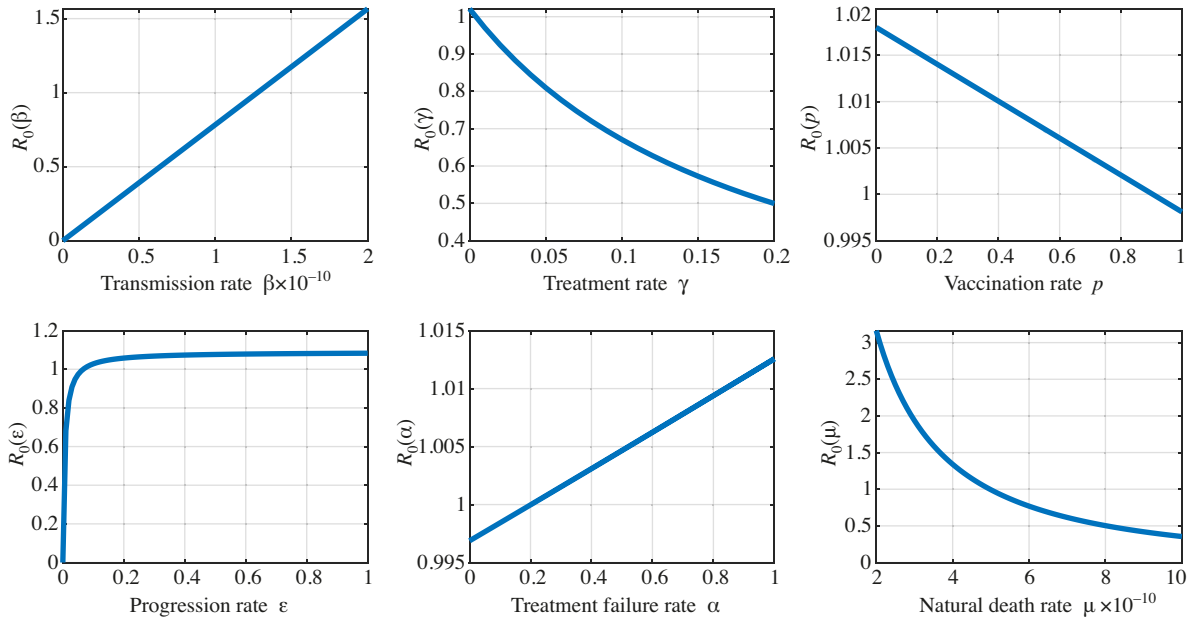

Fig. 6. Influence of the parameters β, γ, p, ϵ, α, and μ, respectively, on the basic reproduction number $\mathcal{R}_0$.

in any of these factors will raise the basic reproduction rate, which will then cause the disease to spread more widely.

On the other hand, the study found that there is an inverse relationship between the basic reproduction number $\mathcal{R}_0$ and the other three parameters γ, p and μ. This implies that an increase in any of these parameters will result in a decrease in the basic reproduction number, which will lead to a slower spread of the disease. It is important to note that these results are in good agreement with the reality.

The results show that four elements must be taken into account in any strategy intended to stop the spread of TB:

- TB diagnoses should be made more accurate and thorough so that infected persons can receive the proper care.
- Imposing isolation restrictions on diseased people and medically observing their families to prevent contact with contagious patients.
- Maintaining a high immunization rate for kids to give them protection.
- Increasing the treatment rate through the education of expert medical personnel, the acquisition of powerful drugs, and the construction of facilities specifically designed to treat this illness.

6. Conclusion. To assess the dynamics of TB disease transmission in Algeria and in Ukraine, we created a mathematical VSLIT model that considers the biological aspects of tuberculosis and some grounded assumptions. The model parameters were computed using the least-squares method with the supplied infection data. According to the results, some system parameters are crucial for controlling and preventing the spread of TB, especially: the contact parameter β, the treatment parameter γ, and the vaccine parameter p. By using the estimated model parameters for Algeria and for Ukraine, we found that the basic reproduction number was less than one, indicating that TB can be eradicated by upholding excellent vaccination, top-notch treatment, and isolation practices. Through the results of this study, we notice that most of the parameter values of the proposed model (whether those extracted from the published data or those estimated using the proposed model) indicate some progress in favor of Algeria in combating the disease compared to Ukraine. For example, the vaccination rate p as well as the recovery rate γ in Algeria is greater than in Ukraine, and the transmission rate β in Algeria is less than in Ukraine. However, we found a higher value of the basic reproduction number $\mathcal{R}_0$ for Algeria than in Ukraine, which means that Ukraine has a greater chance than Algeria to control or eliminate the disease. This can be explained by the fact that Ukraine has recorded a largest number of infections, with annual cases ranging between 33,000 and 41,000 during the period 2001 – 2013, and it even exceeded its peak during this period. Meanwhile, Algeria, by implementing relatively more stringent measures, was able to relatively reduce the number of annual infections, but that led to a delay in the peak, and infections remained on a rise until its peak in 2018, where it began to decline.

This study can help develop more effective prevention and treatment techniques to reduce the impact of tuberculosis in Algeria, Ukraine, and other affected communities.

On behalf of all authors, the corresponding author states that there is no conflict of interest.

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