Equilibrium Points and Their Stability of COVID-19 in US

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Supplementary Material
Supplementary Note: 15 pages
Supplementary Figures: 6 figures
Supplementary Tables: 2 tables

Supplementary Note

1. SEIRV compartment model for COVID-19 transmission dynamics

We constructed a compartmental model based on a deterministic system of nonlinear differential equations that considers vaccination. The architecture of the SEIRV is shown in Figure 1.

Let $S(t), E(t), I(t), R(t)$ and $V(t)$ be the number of susceptible, exposed, infectious, recovered and vaccinated individuals at time t. Define the parameters as follows.

Λ: the new birth and new residents per unit of time,

β: transmission rate divided by the total population N,

α: vaccination rate,

μ: natural death rate,

γ: incubation rate by which the exposed individual develops symptoms,

δ: the probability of the recovery or death due to COVID-19,

σ: vaccine inefficiency.

Now we define a set of nonlinear ordinary differential equations as a mathematic model for the transmission dynamics of COVID-19:

$$\frac{dS(t)}{dt} = \Lambda - \beta S(t)I(t) - \alpha S(t) - \mu S(t) , \tag{S1}$$

$$\frac{dE(t)}{dt} = \beta S(t)I(t) - \gamma E(t) + \sigma \beta I(t)V(t) - \mu E(t), \tag{S2}$$

$$\frac{dI(t)}{dt} = \gamma E(t) - \delta I(t) - \mu I(t), \tag{S3}$$

$$\frac{dR(t)}{dt} = \delta I(t) - \mu R(t), \tag{S4}$$

$$\frac{dV(t)}{dt} = \alpha S(t) - \sigma \beta I(t)V(t) - \mu V(t). \tag{S5}$$

Let $N(t) = S(t) + E(t) + I(t) + R(t) + V(t)$ be the total population size.

2. Non-negativity and boundedness of the solutions

In this section we show the non-negativity and boundedness of the solutions of the nonlinear differential equations (S1-S5). Assume that all initial values are non-negative. Since $\Lambda \geq 0$, it follows from equation (S1) that

$$\frac{dS}{dt} \geq -(\beta I(t) + \alpha + \mu)S(t), \tag{S6}$$

which implies that

$$S(t) \geq S(0)e^{-\int_0^t (\beta I(\tau) + \alpha + \mu)d\tau} \geq 0. \tag{S7}$$

By the similar arguments, we can show that all $E(t), I(t), R(t)$ and $V(t)$ are non-negative. For example, using equation (S5) and (S7), we obtain

$$\frac{dV}{dt} \geq -(\sigma \beta I(t) + \mu)V(t)$$

$$\geq V(0)e^{-\int_0^t (\sigma \beta I(\tau) + \mu)d\tau} \geq 0.$$

Summarizing equations (S1-S5), we obtain

$$\frac{dN}{dt} = \Lambda - \mu N(t). \tag{S8}$$

Solving equation (S8) for $N(t)$, we obtain

$$N(t) = \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu}\right)e^{-\mu t}. \tag{S9}$$

We assume that $N(0) \leq \frac{\Lambda}{\mu}$, so we obtain $N(t)$ is bounded by $\frac{\Lambda}{\mu}$ for all t,

$$N(t) \leq \frac{\Lambda}{\mu}. \tag{S10}$$

Equation (S10) indicates that all variables $S(t), E(t), I(t), R(t), V(t)$ are in the region Ω:

$$\Omega = \{N(t) = S(t) + E(t) + I(t) + R(t) + V(t) | 0 \leq N(t) \leq \tfrac{\Lambda}{\mu}\}. \tag{S11}$$

3. Steady state analysis of COVID-19 transmission dynamical systems

Steady state of a dynamic system is the state that will not change without external excitation. Steady state analysis includes the basic reproduction number, critical epidemic equilibrium points, and endemic equilibrium points of the COVID-19 model.

3.1 Reproduction number

Assume that the compartments are divided into two sets. The first set contains infected individuals (E, I). The second set consists of remaining individuals (S, R, V). Let $X(t) = \begin{bmatrix} x_1(t) \\ x_2(t) \end{bmatrix} = \begin{bmatrix} E(t) \\ I(t) \end{bmatrix}$.

Define

$$\frac{dx_i(t)}{dt} = F_i(X) - V_i(X), i = 1, 2, \tag{S12}$$

where $F_i(X)$ is the rate of appearance of new infections in compartment i and $V_i(X)$ includes the rate of transitions between compartment i and other infected compartments.

Recall that

$$\frac{dx}{dt} = \begin{bmatrix} \frac{dE}{dt} \\ \frac{dI}{dt} \end{bmatrix} = \begin{bmatrix} -(\gamma + \mu)E(t) + \beta(S(t) + \sigma V(t))I(t) \\ \gamma E(t) - (\delta + \mu)I(t) \end{bmatrix}. \tag{S13}$$

The rate of appearance of new infections in compartment E is $\beta(S(t) + \sigma V(t))I(t)$ and the rate of appearance of new infections in compartment $I(t)$ is zero. The rate of transitions between compartment $E(t)$ and other infected compartments is $-(\gamma + \mu)E(t)$ and the rate of transitions

between compartment $I(t)$ and other infected compartments includes $\gamma E(t) - (\delta + \mu)I(t)$. Thus, equation (S13) can be written as

$$\frac{dX}{dt} = \begin{bmatrix} \beta(S(t) + \sigma V(t))I(t) \\ 0 \end{bmatrix} - \begin{bmatrix} (\gamma + \mu)E(t) \\ -\gamma E(t) + (\delta + \mu)I(t) \end{bmatrix} = F(X) - V(X) . \qquad (S14)$$

Let

$$F'(X) = \left[\frac{\partial F(X)}{\partial X^T}\right] \text{ and } V'(X) = \left[\frac{\partial V(x)}{\partial X^T}\right].$$

Then, using equation (S14), we obtain

$$F'(X) = \begin{bmatrix} 0 & \beta(S(t) + \sigma V(t)) \\ 0 & 0 \end{bmatrix}, \qquad (S15)$$

$$V'(X) = \begin{bmatrix} (\gamma + \mu) & 0 \\ -\gamma & (\delta + \mu) \end{bmatrix}, V'^{-1}(X) = \frac{1}{(\gamma+\mu)(\delta+\mu)} \begin{bmatrix} \delta + \mu & 0 \\ \gamma & \gamma + \mu \end{bmatrix}. \qquad (S16)$$

Using next generation matrix method (van den Driessche 2017) to calculate the basic reproduction number R_0, we first calculate

$$F'(X)V'^{-1}(X) = \frac{1}{(\gamma+\mu)(\delta+\mu)} \begin{bmatrix} \gamma\beta(S(t) + \sigma V(t)) & (\gamma + \mu)\beta(S(t) + \sigma V(t)) \\ 0 & 0 \end{bmatrix}. \qquad (S17)$$

It is easy to see that the eigenvalues of the matrix $F'(X)V'^{-1}(X)$ are given by

$$\lambda_1 = \frac{\gamma\beta(S(t)+\sigma V(t))}{(\gamma+\mu)(\delta+\mu)}, \lambda_2 = 0 .$$

The basic reproduction number R_0 is defined as the spectral radius of the next-generation matrix $F'(X)V'^{-1}(X)$:

$$R_0 = \frac{\gamma\beta(S(t)+\sigma V(t))}{(\gamma+\mu)(\delta+\mu)} . \qquad (S18)$$

3. 2. Critical Point and equilibrium of COVID-19 dynamic systems

Critical transition of COVID-19 dynamic systems occurs when restrictions on travel, social gathering and meeting, open of school, mandatory wearing of masks are lifted or poorly adhered to, new variants with strong transmission rates, successfully invade. COVID-19 dynamic system has multiple stable equilibrium points. There must also be unstable equilibrium points between the stable points in the COVID-19 transmission dynamics. Multistability determines the trend of COVID-19 transmission dynamics and provide information on designing public health intervention measures to eradicate CIVID-19 outbreaks. In this section we apply the Jacobian matrix-based linear stability analysis to continuous-time nonlinear dynamical systems. For convenience of discussion, nonlinear differential equations (S1-S5) is rewritten as:

$$\frac{dx}{dt} = f(x) . \tag{S19}$$

A critical point of the system is a point (x_*) such that:

$$f(x_*) = 0 . \tag{S20}$$

In other words, a constant solution x_* at a critical point satisfies both $\frac{dx_*}{dt} = 0$ and $f(x_*) = 0$ and hence

$$\frac{dx_*}{dt} = f(x_*)$$

The solution that begins with critical point x_* and then just stays at the critical point x_*. Therefore, the critical point x_* is also called an equilibrium solution. The critical point (equilibrium) can be found by setting the left sides of differential equations (S1-S5) to be zero. Therefore, the critical points of COVID-19 dynamic system are defined by the following five algebraic equations.

$$\Lambda - \beta S_* I_* - (\alpha + \mu)S_* = 0, \tag{S21}$$

$$\beta S_* I_* + \sigma \beta I_* V_* - (\gamma + \mu)E_* = 0 , \tag{S22}$$

$$\gamma E_* - (\delta + \mu)I_* = 0 , \tag{S23}$$

$$\delta I_* - \mu R_* = 0 , \tag{S24}$$

$$\alpha S_* - \sigma \beta I_* V_* - \mu V_* = 0. \tag{S25}$$

Now we find critical points by solving equations (S21-S25).

Solving equation (S23) yields

$$E_* = \frac{\delta + \mu}{\gamma} I_*. \tag{S26}$$

Substituting equation (S26) into equation (S22), we obtain $\beta S_* I_* + \sigma \beta I_* V_* - (\gamma + \mu)\frac{\delta + \mu}{\gamma} I_* = 0$,

which is reduced to

$$I_* \left(\beta S_* + \sigma \beta V_* - \frac{(\gamma + \mu)(\delta + \mu)}{\gamma}\right) = 0. \tag{S27}$$

Solving equation (S27), we obtain two solutions:

(1) $I_* = 0$, \hfill (S28)

(2) $I_* \neq 0, \beta S_* + \sigma \beta V_* - \frac{(\gamma + \mu)(\delta + \mu)}{\gamma} = 0$. \hfill (S29)

Since the number of new cases I_* determines the disease status, $I_* = 0$ indicates the disease-free, and hence critical point $I_* = 0$ is called *disease-free* critical point or *disease free* equilibrium. The second critical point defined in equation (S29) is called the *endemic* critical point or equilibrium.

In scenario (1), we obtain

$E_* = 0$ (equation S26), $R_* = 0$ (equation S24), $S_* = \frac{\Lambda}{\alpha + \mu}$ (equation S21), and $V_* = \frac{\alpha \Lambda}{\mu(\alpha + \mu)}$

(equations S21 and S25). In summary, *the disease-free critical point* is

$$I_* = 0, E_* = 0, R_* = 0, S_* = \frac{\Lambda}{\alpha + \mu}, V_* = \frac{\alpha \Lambda}{\mu(\alpha + \mu)}, R_0 = \frac{\gamma \beta \Lambda(\mu + \alpha \sigma)}{\mu(\gamma + \mu)(\delta + \mu)(\alpha + \mu)}. \tag{S30}$$

Now we discuss scenario (2) $I_* \neq 0$.

Let

$$a = \frac{\sigma(\gamma+\mu)(\delta+\mu)\beta^2}{\mu}$$

$$b = \frac{(\gamma+\mu)(\delta+\mu)\beta}{\gamma\mu}[\mu + (\alpha + \mu)\sigma] - \frac{\Lambda\sigma\beta^2}{\mu}$$

$$c = \frac{(\gamma+\mu)(\delta+\mu)(\alpha+\mu)}{\gamma} + \beta[\Lambda\sigma - \Lambda - \frac{\alpha+\mu}{\mu}\Lambda]$$

$$d = (\Lambda - \mu)(\alpha + \mu) \,,$$

$$F(\Lambda, \mu, \delta, \gamma, \beta, \alpha, \sigma) = aI^3 + bI^2 + cI + d \,.$$

The parameters are estimated by minimizing

$$\min_{\Lambda,\mu,\delta,\gamma,\beta,\alpha,\sigma} F(\Lambda, \mu, \delta, \gamma, \beta, \alpha, \sigma)^2.$$

Solving equation (S21), we obtain

$$S_* = \frac{\Lambda}{\alpha+\mu+\beta I_*} \,. \tag{S31}$$

Substituting equation (S31) into equation (S25) yields

$$V_* = \frac{\alpha}{\mu+\sigma\beta I_*} S_* = \frac{\alpha\Lambda}{(\mu+\sigma\beta I_*)(\alpha+\mu+\beta I_*)} \,. \tag{S32}$$

Solving equation (S23) yields

$$E_* = \frac{\delta+\mu}{\gamma} I_* \,. \tag{S33}$$

Solving equation (S24) yields

$$R_* = \frac{\delta}{\mu} I_* \,. \tag{S34}$$

Substituting equations (S32-S34) into equation (S22) yields

$$aI_*^2 + bI_* + c = 0, \tag{S35}$$

where

$$a = \frac{(\gamma+\mu)(\delta+\mu)\sigma\beta^2}{\gamma}, \tag{S36}$$

$$b = \frac{(\gamma+\mu)(\delta+\mu)[\mu\beta+(\alpha+\mu)\sigma\beta]}{\gamma} - \sigma\beta^2\Lambda, \tag{S37}$$

$$c = \frac{\mu(\gamma+\mu)(\delta+\mu)(\alpha+\mu)}{\gamma} - \beta\Lambda(\mu + \alpha\sigma). \tag{S38}$$

Solving quadratic equation (S35) for I_*, we obtain

$$I_* = \frac{-b \pm \sqrt{b^2-4ac}}{2a}. \tag{S39}$$

Since $I_* \geq 0$, then we obtain the equilibrium point:

$$I_* = \frac{-b + \sqrt{b^2-4ac}}{2a}, \tag{S40}$$

where $c < 0$.

If we assume that natural death rate μ is zero, then we obtain

$$a = \delta\sigma\beta^2, b = \sigma\beta(\alpha\delta - \beta\Lambda), c = -\alpha\beta\sigma\Lambda. \tag{S41}$$

Substituting equation (S41) into equation (S40), we obtain

$$I_* = \frac{\Lambda}{\delta}. \tag{S42}$$

After I_* is found, we can obtain

$$S_* = \frac{\Lambda}{\alpha+\mu+\beta I_*} \text{ (from equation S21),}$$

$$V_* = \frac{\alpha\Lambda}{(\mu+\sigma\beta I_*)(\alpha+\mu+\beta I_*)} \text{ (from equation S32),}$$

$$E_* = \frac{\delta+\mu}{\gamma} I_* \text{ (from equation S23),}$$

$$R_* = \frac{\delta}{\mu} I_* \text{ (from equation S24)} \tag{S43}$$

In summary, we obtain two equilibrium points:

(1) Disease free critical (equilibrium) point:

$$I_* = 0, E_* = 0, R_* = 0, S_* = \frac{\Lambda}{\alpha+\mu}, V_* = \frac{\alpha\Lambda}{\mu(\alpha+\mu)}, R_0^{free} = \frac{\gamma\beta\Lambda(\mu+\alpha\sigma)}{\mu(\gamma+\mu)(\delta+\mu)(\alpha+\mu)}. \tag{S44}$$

(2) Endemic critical (equilibrium) point:

$$I_* = \frac{-b+\sqrt{b^2-4ac}}{2a},$$

$$a = \frac{(\gamma+\mu)(\delta+\mu)\sigma\beta^2}{\gamma}, b = \frac{(\gamma+\mu)(\delta+\mu)[\mu\beta+(\alpha+\mu)\sigma\beta]}{\gamma} - \sigma\beta^2\Lambda,$$

$$c = \frac{\mu(\gamma+\mu)(\delta+\mu)(\alpha+\mu)}{\gamma} - \beta\Lambda(\mu+\alpha\sigma) ,$$

$$S_* = \frac{\Lambda}{\alpha+\mu+\beta I_*}, \ V_* = \frac{\alpha\Lambda}{(\mu+\sigma\beta I_*)(\alpha+\mu+\beta I_*)}, E_* = \frac{\delta+\mu}{\gamma} I_*, \ R_* = \frac{\delta}{\mu} I_* .$$

$$R_0^{end} = \frac{\gamma\beta\Lambda}{(\gamma+\mu)(\delta+\mu)(\alpha+\mu+\beta I_*)} \left[1 + \frac{\alpha\sigma}{(\mu+\sigma\beta I_*)} \right] \tag{S45}$$

3.3. Classification of Critical Points

Stability analysis for the general nonlinear dynamic systems is complicated. In this paper, we will focus on isolated critical point and almost linear systems. If there is only critical point in its neighborhood, then this critical point is called an isolated critical point. A system is called almost linear at a critical point if the Jacobian matrix of linearized system at an isolated critical point is invertible. Let x_* be an isolated critical point. Assume that the Jacobian matrix of the nonlinear dynamic system (S19) is invertible. Consider almost linear system of the nonlinear system at the isolated critical point:

$$\frac{dx}{dt} \approx \frac{\partial f}{\partial x^T}\bigg|_{x=x_*} (x - x_*). \tag{S46}$$

Denote the Jacobian matrix at the critical point x_* as $J = \left.\frac{\partial f}{\partial x^T}\right|_{x=x_*}$. Using equations (S1-S5), we

obtain

$$J = \begin{bmatrix} -\varepsilon_1 & 0 & -\beta S_* & 0 & 0 \\ \beta I_* & -\varepsilon_2 & \beta(S_* + \sigma V_*) & 0 & \sigma\beta I_* \\ 0 & \gamma & -\varepsilon_3 & 0 & 0 \\ 0 & 0 & \delta & -\mu & 0 \\ \alpha & 0 & -\sigma\beta V_* & 0 & -\varepsilon_4 \end{bmatrix},$$

(S47)

where

$$\varepsilon_1 = \alpha + \mu + \beta I_*, \varepsilon_2 = \gamma + \mu, \varepsilon_3 = \delta + \mu \text{ and } \varepsilon_4 = \mu + \sigma\beta I_*.$$

(S48)

Once the Jacobian matrix is calculated, we then calculate its eigenvalues and classify the critical

points. We first consider disease-free critical point.

3.3.1 Disease-free critical point

Substituting equation (S44) into equation (S48), we obtain

$$\varepsilon_1^0 = \alpha + \mu, \varepsilon_2 = \gamma + \mu, \varepsilon_3 = \delta + \mu \text{ and } \varepsilon_4^0 = \mu.$$

(S49)

Again, substituting equation (S49) into equation (S47) yields the Jacobian matrix at the disease-

fee critical point:

$$J^0 = \begin{bmatrix} -\varepsilon_1^0 & 0 & -\beta S_* & 0 & 0 \\ 0 & -\varepsilon_2 & \beta(S_* + \sigma V_*) & 0 & 0 \\ 0 & \gamma & -\varepsilon_3 & 0 & 0 \\ 0 & 0 & \delta & -\mu & 0 \\ \alpha & 0 & -\sigma\beta V_* & 0 & -\varepsilon_4^0 \end{bmatrix}.$$

(S50)

Its characteristic polynomial is given by

$$|\lambda I - J^0| = (\lambda + \varepsilon_1^0)(\lambda + \mu)(\lambda + \varepsilon_4^0)[(\lambda + \varepsilon_2)(\lambda + \varepsilon_3) - \gamma\beta(S_* + \sigma V_*)].$$

(S51)

Using equation (S18), we obtain

$$\gamma\beta(S_* + \sigma V_*) = \varepsilon_2\varepsilon_3 R_0, \tag{S52}$$

where R_0 is the basic reproduction number.

Substituting equation (S52) into equation (S51) yields

$$|\lambda I - J^0| = (\lambda + \varepsilon_1^0)(\lambda + \mu)(\lambda + \varepsilon_4^0)[\lambda^2 + (\varepsilon_2 + \varepsilon_3)\lambda + (1 - R_0)\varepsilon_2\varepsilon_3]. \tag{S53}$$

The solutions to characteristic equation (S53) are

$$\lambda_1 = -\varepsilon_1^0 = -(\alpha + \mu), \tag{S54}$$

$$\lambda_2 = \frac{-(\varepsilon_2+\varepsilon_3)+\sqrt{(\varepsilon_2-\varepsilon_3)^2+4\varepsilon_2\varepsilon_0 R_0}}{2} = \frac{-(\gamma+\delta+2\mu)+\sqrt{(\gamma-\delta)^2+4(\gamma+\mu)(\delta+\mu)R_0}}{2}, \tag{S55}$$

$$\lambda_3 = \frac{-(\varepsilon_2+\varepsilon_3)-\sqrt{(\varepsilon_2-\varepsilon_3)^2+4\varepsilon_2\varepsilon_0 R_0}}{2} = \frac{-(\gamma+\delta+2\mu)-\sqrt{(\gamma-\delta)^2+4(\gamma+\mu)(\delta+\mu)R_0}}{2}, \tag{S56}$$

$$\lambda_4 = \lambda_5 = -\varepsilon_4^0 = -\mu. \tag{S57}$$

Eigenvalues λ_1, λ_3, λ_4 and λ_5 are negative. Now we investigate λ_2. When $R_0 < 1$, then

$$(\gamma - \delta)^2 + 4(\gamma + \mu)(\delta + \mu)R_0 < (\gamma - \delta)^2 + 4(\gamma + \mu)(\delta + \mu)$$

$$= (\gamma + \delta + 2\mu)^2. \tag{S58}$$

Using equation (S58), we obtain

$\sqrt{(\gamma - \delta)^2 + 4(\gamma + \mu)(\delta + \mu)R_0} < \gamma + \delta + 2\mu$, which implies that

$$-(\gamma + \delta + 2\mu) + \sqrt{(\gamma - \delta)^2 + 4(\gamma + \mu)(\delta + \mu)R_0} < 0.$$

Therefore, λ_2 is negative. In other words, when $R_0 < 1$, then all solutions are negative, the system is locally asymptotically stable. By the similar arguments, when $R_0 = 1$, then $\lambda_2 = 0$ the system is unstable. When $R_0 > 1$, then $\lambda_2 > 0$. The system is unstable.

Therefore, **the disease-free critical point can be classified as three cases:**

(1) when $R_0 < 1$, the disease-free critical point is classified as a asymptotically stable node;

(2) when $R_0 = 1$, the disease-free critical point is classified as an unstable node; and

(3) when $R_0 > 1$, the disease-free critical point is classified as an unstable saddle point.

3.3.2 Endemic equilibrium point

Recall from the Jacobian matrix in equation (S47) that under the endemic equilibrium point condition, we have $I_* \neq 0$, which implies

$\varepsilon_1 = \alpha + \mu + \beta I_*, \varepsilon_2 = \gamma + \mu, \varepsilon_3 = \delta + \mu$ and $\varepsilon_4 = \mu + \sigma\beta I_*$. Thus,

$$J_* = \begin{bmatrix} -\varepsilon_1 & 0 & -\beta S_* & 0 & 0 \\ \beta I_* & -\varepsilon_2 & \beta(S_* + \sigma V_*) & 0 & \sigma\beta I_* \\ 0 & \gamma & -\varepsilon_3 & 0 & 0 \\ 0 & 0 & \delta & -\mu & 0 \\ \alpha & 0 & -\sigma\beta V_* & 0 & -\varepsilon_4 \end{bmatrix}. \tag{S59}$$

Its characteristic polynomial is

$$|\lambda I - J_*| = (\lambda + \mu)\{(\lambda + \varepsilon_4)[(\lambda + \varepsilon_1)(\lambda + \varepsilon_2)(\lambda + \varepsilon_3) + \gamma\beta[\beta I_* S_* - (\lambda + \varepsilon_1)((S_* + \sigma V_*)]$$

$$+\gamma\beta^2[(\lambda + \varepsilon_1)\sigma^2 I_* V_* + \alpha\sigma I_* S_*]\}, \tag{S60}$$

Or

$$|\lambda I - J_*| = (\lambda + \mu)\{\lambda^4 + (\varepsilon_1 + \varepsilon_2 + \varepsilon_3 + \varepsilon_4)\lambda^3 + [\varepsilon_4(\varepsilon_1 + \varepsilon_2 + \varepsilon_3) + \varepsilon_1(\varepsilon_2 + \varepsilon_3) + \varepsilon_2\varepsilon_3$$

$$-\gamma\beta(S_* + \sigma V_*)]\lambda^2 + [\varepsilon_2\varepsilon_3\varepsilon_4 + \varepsilon_1(\varepsilon_2\varepsilon_3 + \varepsilon_2\varepsilon_4 + \varepsilon_3\varepsilon_4) - \gamma\beta(\varepsilon_1 + \varepsilon_4)(S_* + \sigma V_*) + \gamma\beta^2 S_* I_* +$$

$$\gamma\beta^2\sigma^2 V_*]\lambda + \varepsilon_1\varepsilon_2\varepsilon_3\varepsilon_4 - \gamma\beta(S_* + \sigma V_*)\varepsilon_1\varepsilon_4 + \gamma\sigma^2\beta^2\varepsilon_1 I_* V_* + \gamma\beta^2\varepsilon_4 I_* S_* + \alpha\gamma\sigma\beta^2 I_* S_*\}. \tag{S61}$$

Using equations (S45) and (S59), we obtain

$$\gamma\beta(S_* + \sigma V_*) = \varepsilon_2\varepsilon_3 R_0^{end}, \tag{S62}$$

where

$$R_0^{end} = \frac{\gamma\beta\Lambda}{(\gamma+\mu)(\delta+\mu)(\alpha+\mu+\beta I_*)}[1 + \frac{\alpha\sigma}{(\mu+\sigma\beta I_*)}]. \tag{S63}$$

Again, substituting equation (S62) into equation (S60) yields

$$|\lambda I - J_*| = (\lambda + \mu)(\lambda + \varepsilon_4)\{(\lambda + \varepsilon_1)[(\lambda + \varepsilon_2)(\lambda + \varepsilon_3) - \varepsilon_2\varepsilon_3 R_0^{end} + \gamma\beta^2\sigma^2 I_* V_*]$$

$$+\gamma\beta^2(1 + \alpha\sigma)I_* S_* \}. \tag{S64}$$

It follows from equation (S64) that the positive solution to characteristic equation (S64) comes from the equation

$$(\lambda + \varepsilon_1)[(\lambda + \varepsilon_2)(\lambda + \varepsilon_3) - \varepsilon_2\varepsilon_3 R_0^{end} + \gamma\beta^2\sigma^2 I_* V_*] + \gamma\beta^2(1 + \alpha\sigma)I_* S_* = 0. \tag{S65}$$

Considering that when dynamic system reaches stationary status, number of new cases I_* is small. Thus, equation (S65) can be reduced to

$$(\lambda + \varepsilon_1)[(\lambda + \varepsilon_2)(\lambda + \varepsilon_3) - \varepsilon_2\varepsilon_3 R_0^{end}] = 0. \tag{S66}$$

Equation (S66) can be further reduced to

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0, \tag{S67}$$

where $a_1 = \varepsilon_1 + \varepsilon_2 + \varepsilon_3, a_2 = \varepsilon_1\varepsilon_2 + \varepsilon_1\varepsilon_3 + \varepsilon_2\varepsilon_3 - \varepsilon_2\varepsilon_3 R_0^{end}, a_3 = \varepsilon_1\varepsilon_2\varepsilon_3(1 - R_0^{end}).$

Using Routh-Hurwitz stability criterion, we obtain that all roots in characteristic equation (S67) have negative real parts if and only if

$$H_1 = a_1 > 0, H_2 = \begin{vmatrix} a_1 & a_3 \\ 1 & a_2 \end{vmatrix} = a_1 a_2 - a_3 > 0, H_3 = \begin{vmatrix} a_1 & a_3 & 0 \\ 1 & a_2 & 0 \\ 0 & a_1 & a_3 \end{vmatrix} a_3(a_1 a_2 - a_3) > 0. \tag{S68}$$

After some algebra, we can obtain from equation (S67) that

$$H_1 = \varepsilon_1 + \varepsilon_2 + \varepsilon_3, \tag{S69}$$

$$H_2 = (\varepsilon_1 + \varepsilon_2 + \varepsilon_3)(\varepsilon_1\varepsilon_2 + \varepsilon_1\varepsilon_3) + (\varepsilon_2 + \varepsilon_3)\varepsilon_2\varepsilon_3(1 - R_0^{end}), \tag{S70}$$

$$H_3 = \varepsilon_1\varepsilon_2\varepsilon_3(1 - R_0^{end})H_2. \tag{S71}$$

Recall that

$$\varepsilon_1 = \alpha + \mu + \beta I_*, \varepsilon_2 = \gamma + \mu, \varepsilon_3 = \delta + \mu,$$

which implies

$$H_1 > 0 \text{ for all cases.} \tag{S72}$$

It is clear that if $R_0^{end} < 1$ then

$$H_2 > 0, H_3 > 0.$$

Using Routh-Hurwitz stability criterion, we obtain that all roots in characteristic equation (S67) have negative real parts. Therefore, if $R_0^{end} < 1$ then the endemic equilibrium point is stable.

Next we consider $R_0^{end} = 1$. In this case, we have $a_3 = 0$, which implies that

$$H_3 = 0$$

and Routh-Hurwitz stability criterion is violated. Thus, the endemic equilibrium point is unstable.

Finally, we consider $R_0^{end} > 1$. The condition

$$R_0^{end} > 1$$

Implies that

$$a_3 = \varepsilon_1 \varepsilon_2 \varepsilon_3 \left(1 - R_0^{end}\right) < 0. \tag{S73}$$

Since $H_3 = \varepsilon_1 \varepsilon_2 \varepsilon_3 \left(1 - R_0^{end}\right) H_2$, which implies that H_2 and H_3 have opposite sign. Therefore, if $R_0^{end} > 1$ then again Routh-Hurwitz stability criterion is violated and the endemic equilibrium point is unstable.

Therefore, in summary, the **endemic equilibrium point can be classified as three cases:**

(1) when $R_0^{end} < 1$, the endemic equilibrium point is classified as a asymptotically stable node;

(2) when $R_0^{end} = 1$, the endemic equilibrium point is classified as an unstable node; and

(3) when $R_0^{end} > 1$, the endemic equilibrium point is classified as an unstable saddle point.
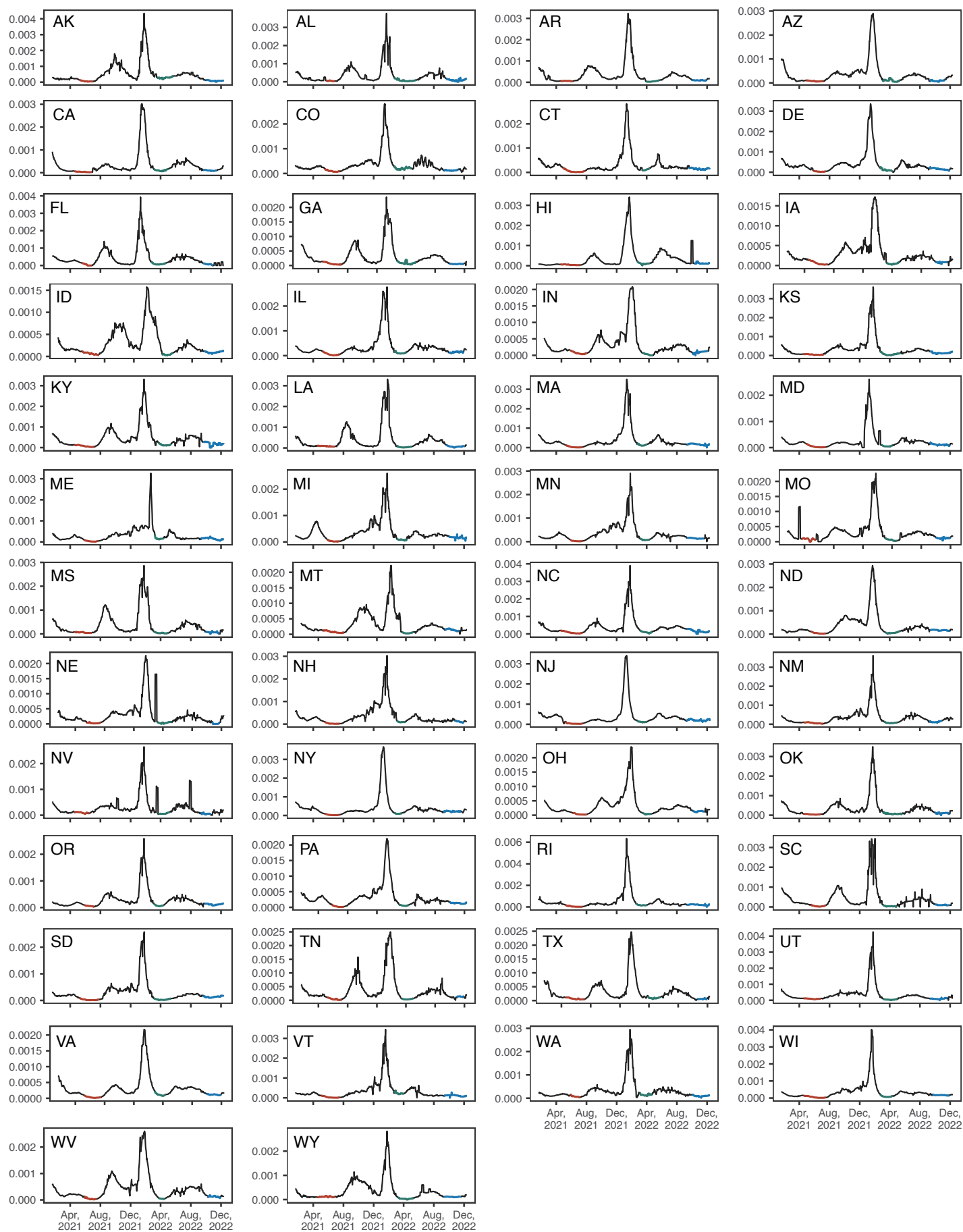
Figure S1. Three steady state periods (April – July, 2021; March – May, 2022; and September – November, 2022) are selected from January 12, 2021 to December 12, 2022. Three periods are represented in red, green and blue colors.
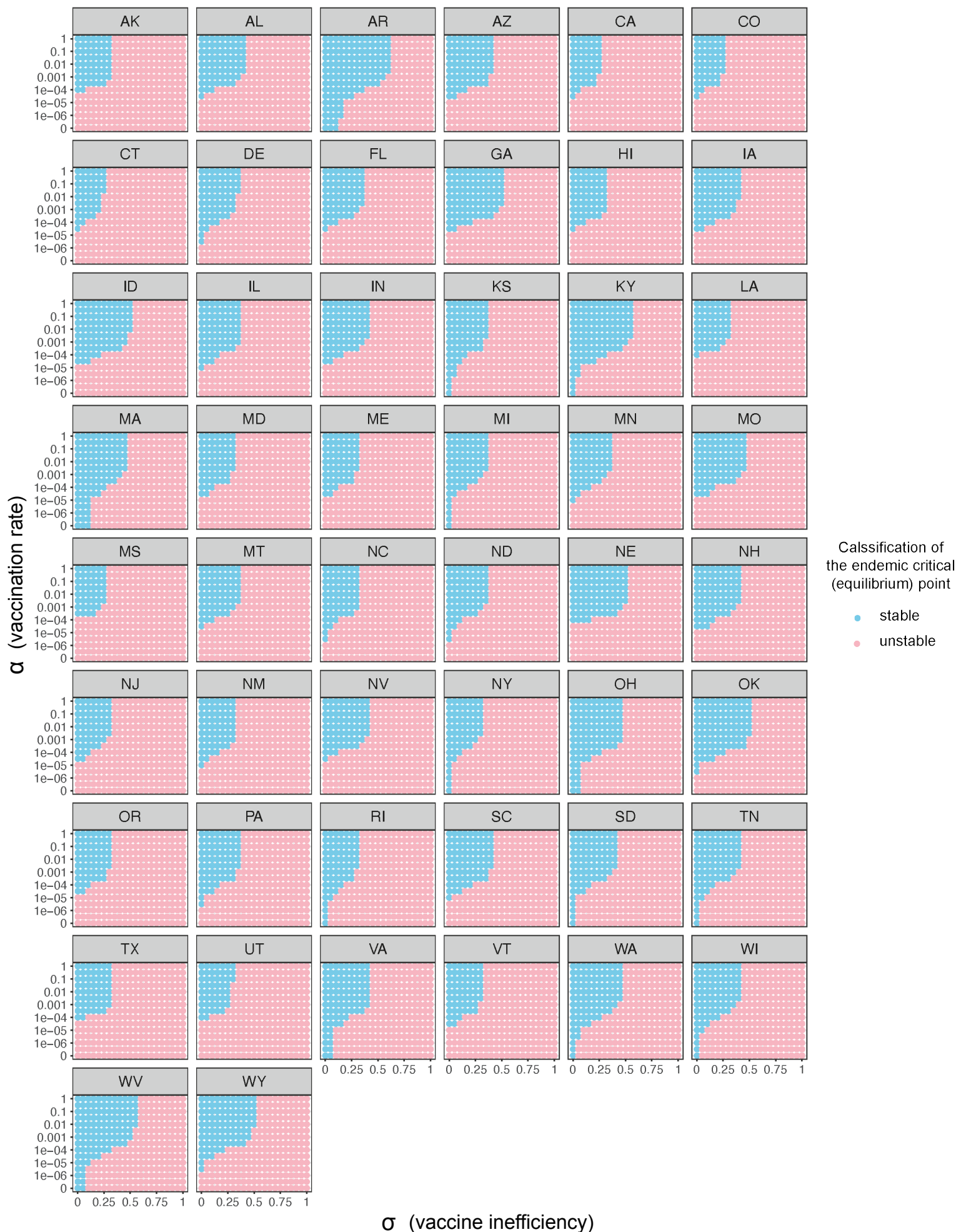
Figure S2. Impact of simultaneously changing changing parameters α (vaccination rate) and σ (vaccine inefficiency) while keeping the current values of other parameters unchanged on the stability of COVID-19 dynamics in the steady periods (September – November 2022) across 50 states in the US. Vertical axis represented α and horizontal axis represented σ.
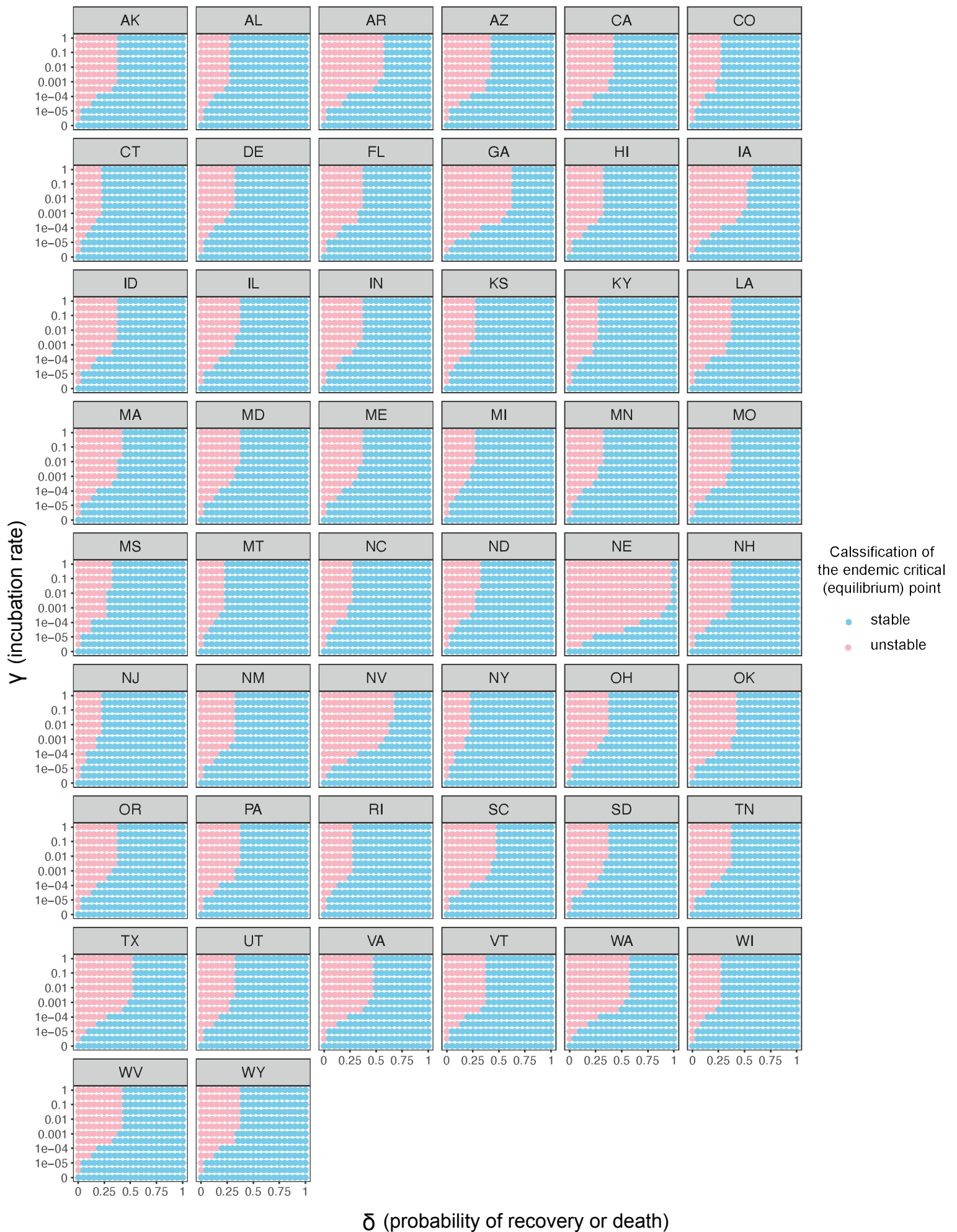
Figure S3. Impact of simultaneously changing changing parameters γ (incubation rate) and δ (probability of recovery or death) while keeping the current values of other parameters unchanged on the stability of COVID-19 dynamics in the steady periods (September – November 2022) across 50 states in the US. Vertical axis represented γ and horizontal axis represented δ.

Figure S4. Impact of simultaneously changing changing parameters γ (incubation rate) and β (transmission rate) while keeping the current values of other parameters unchanged on the stability of COVID-19 dynamics in the steady periods (September – November 2022) across 50 states in the US. Vertical axis represented γ and horizontal axis represented β.

Figure S5. Impact of simultaneously changing changing parameters β (transmission rate) and δ (probability of recovery or death) while keeping the current values of other parameters unchanged on the stability of COVID-19 dynamics in the steady periods (September – November 2022) across 50 states in the US. Vertical axis represented β and horizontal axis represented δ.
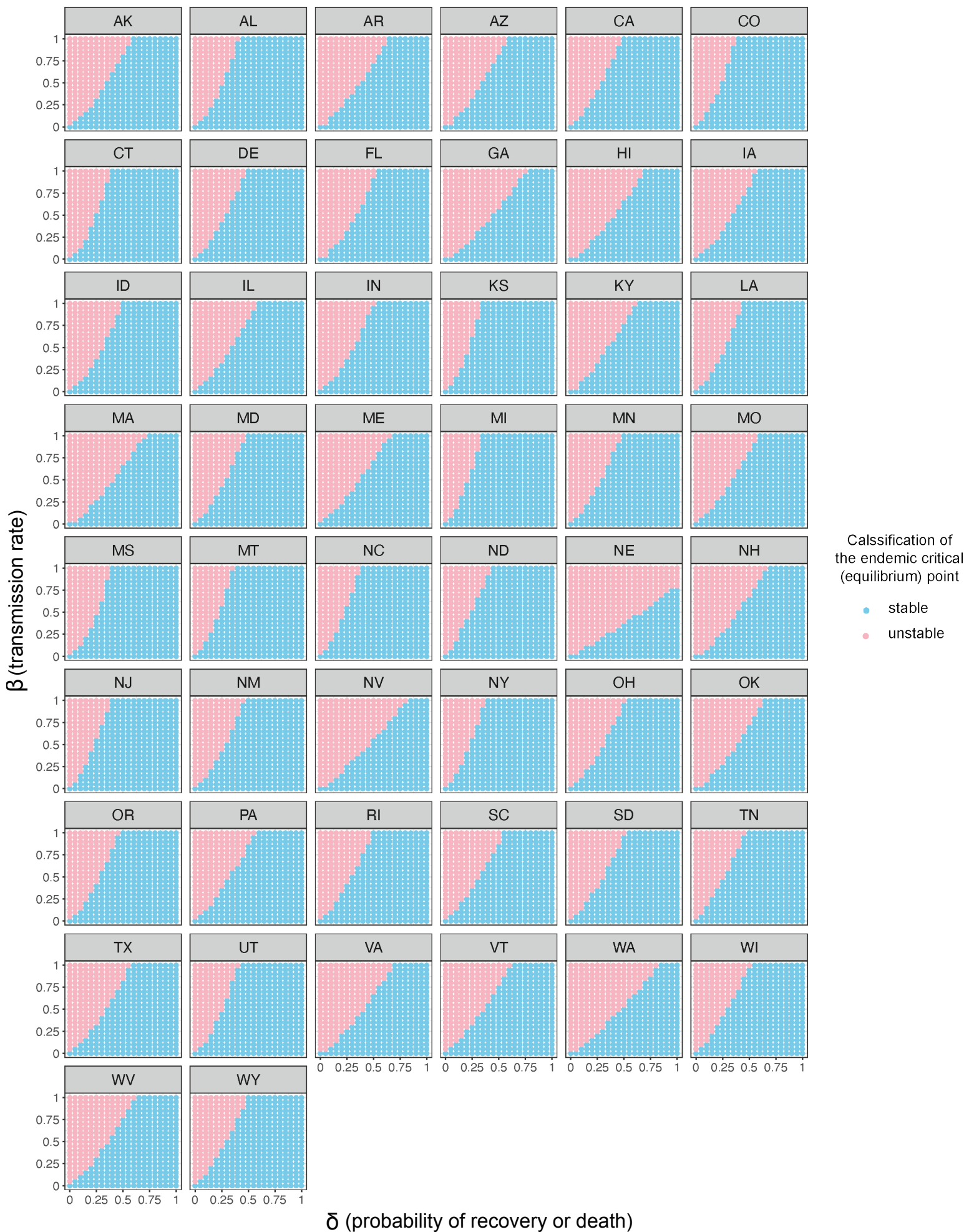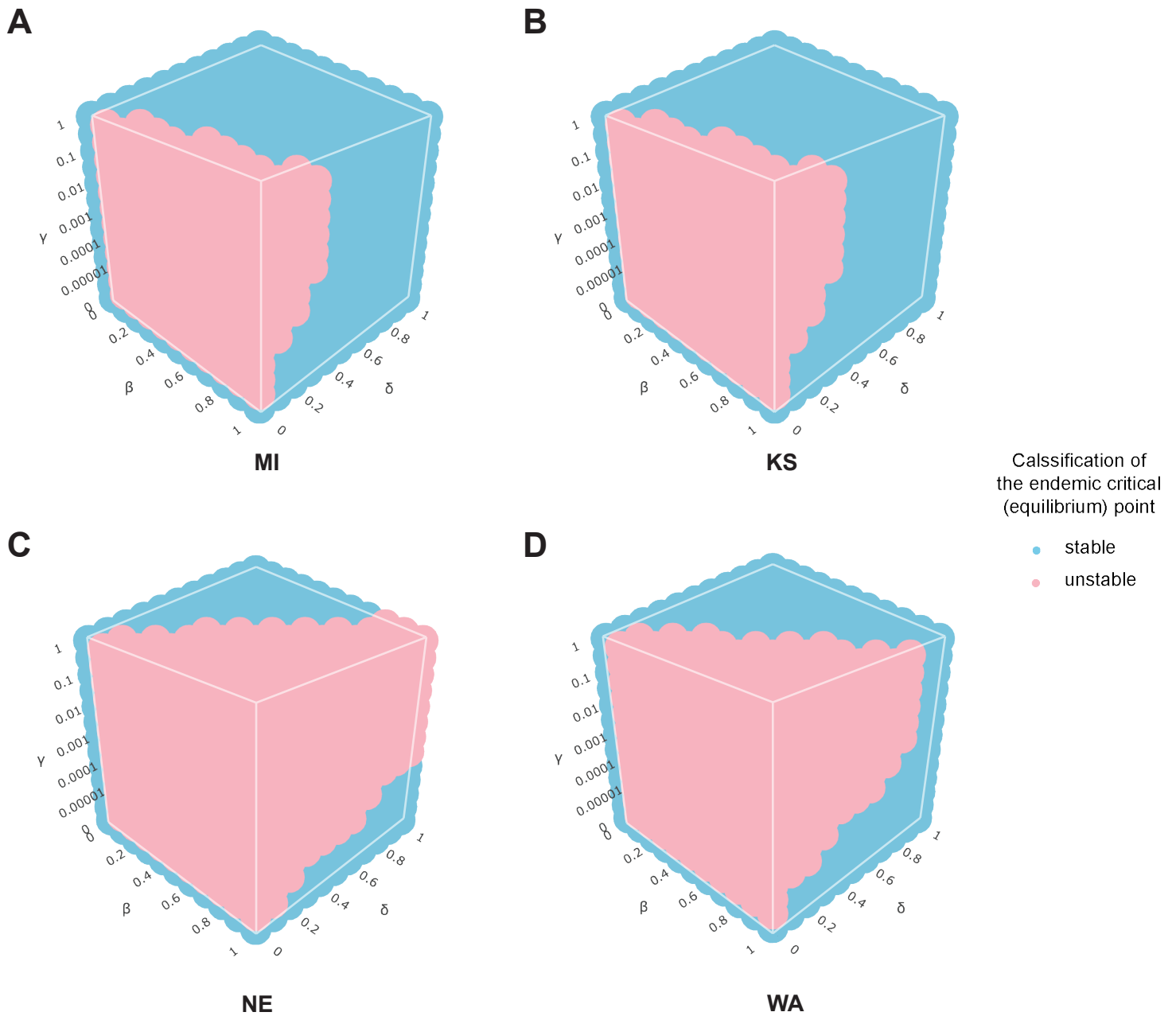
Figure S6. Impact of simultaneously changing parameters β (transmission rate), γ (incubation rate) and δ (probability of recovery or death) while keeping the current values of other parameters unchanged on the stability of COVID-19 dynamics in the steady periods (September – November 2022). Axis x represented parameter β, axis y represented parameter δ and axis z represented parameter γ. (A) MI, the state with the largest stability region, (B) KS, the state with the second largest stability region, (C) NE, the state with the smallest stability region, and (D) WA, the state with the second smallest stability region.

Table S1. The largest eigenvalue at the endemic equilibrium points in three steady periods across 50 states in the US.

state	N	λ_4		
		April - July, 2021	March - May, 2022	September - November, 2022
AK	733,391	1.56E-01	6.10E-02	1.90E-01
AL	5,024,279	1.71E-01	1.17E-01	1.12E-01
AR	3,011,524	1.22E-01	2.61E-01	6.73E-02
AZ	7,151,502	1.35E-01	6.94E-02	1.36E-01
CA	39,538,223	2.11E-01	1.18E-01	1.55E-01
CO	5,773,714	1.36E-01	6.24E-02	9.90E-02
CT	3,605,944	1.32E-01	1.53E-01	1.10E-01
DE	989,948	2.41E-01	1.00E-01	9.05E-02
FL	21,538,187	1.29E-01	1.41E-01	1.36E-01
GA	10,711,908	9.10E-02	1.11E-01	1.80E-01
HI	1,455,271	1.85E-01	1.05E-01	1.62E-01
IA	3,190,369	1.72E-01	1.59E-01	1.74E-01
ID	1,839,106	1.19E-01	1.86E-01	1.11E-01
IL	12,812,508	8.04E-02	1.36E-01	1.24E-01
IN	6,785,528	9.64E-02	3.55E-01	1.46E-01
KS	2,937,880	1.66E-01	1.57E-01	1.86E-02
KY	4,505,836	1.83E-01	9.89E-02	8.74E-02
LA	4,657,757	8.99E-02	2.25E-01	1.66E-01
MA	7,029,917	1.90E-01	7.80E-02	7.56E-02
MD	6,177,224	1.78E-01	3.46E-01	1.00E-01
ME	1,362,359	2.96E-01	9.65E-02	1.42E-01
MI	10,077,331	3.05E-01	2.14E-01	5.51E-02
MN	5,706,494	2.36E-01	1.84E-01	9.80E-02
MO	6,154,913	5.65E-02	2.22E-01	1.50E-01
MS	2,961,279	1.35E-01	2.10E-01	1.40E-01
MT	1,084,225	1.33E-01	2.96E-01	9.10E-02
NC	10,439,388	1.10E-01	8.09E-02	6.41E-02
ND	779,094	2.02E-01	2.29E-01	7.88E-02
NE	1,961,504	2.20E-01	2.11E-01	2.56E-01
NH	1,377,529	2.73E-01	1.41E-01	1.59E-01
NJ	9,288,994	2.75E-01	1.26E-01	7.17E-02
NM	2,117,522	1.80E-01	2.01E-01	8.91E-02

NV	3,104,614	5.38E-02	1.87E-01	2.70E-01
NY	20,201,249	2.23E-01	1.75E-01	5.63E-02
OH	11,799,448	1.84E-01	2.50E-01	8.04E-02
OK	3,959,353	1.73E-01	1.27E-01	1.24E-01
OR	4,237,256	2.36E-01	1.33E-01	1.20E-01
PA	13,002,700	2.99E-01	3.09E-01	1.13E-01
PR	3,285,874	1.78E-01	1.08E-01	5.07E-02
RI	1,097,379	6.73E-02	8.17E-02	6.55E-02
SC	5,118,425	1.40E-01	2.51E-01	1.21E-01
SD	886,667	2.08E-01	2.25E-01	9.39E-02
TN	6,910,840	1.38E-01	2.35E-01	8.61E-02
TX	29,145,505	1.15E-01	2.99E-02	2.14E-01
UT	3,271,616	9.34E-02	2.78E-01	1.31E-01
VA	8,631,393	1.72E-01	8.09E-02	1.18E-01
VT	643,077	1.44E-01	6.34E-02	1.18E-01
WA	7,705,281	1.78E-01	6.34E-02	1.30E-01
WI	5,893,718	1.52E-01	1.43E-01	7.52E-02
WV	1,793,716	2.29E-01	2.19E-01	8.74E-02
WY	576,851	1.86E-02	2.22E-01	1.05E-01

Table S2. The reproduction number at the endemic equilibrium point in three steady periods across 50 states in the US.

state	N	R_0^{end}		
		April - July, 2021	March - May, 2022	September - November, 2022
AK	733,391	1.4882	1.2717	1.6087
AL	5,024,279	1.6356	1.4859	1.4873
AR	3,011,524	1.3871	1.5872	**0.7592**
AZ	7,151,502	1.2515	1.4992	**1.1714**
CA	39,538,223	3.2000	1.4639	1.1679
CO	5,773,714	1.4619	0.9392	1.2262
CT	3,605,944	1.6514	1.1172	1.4204
DE	989,948	2.3482	1.4158	**0.9796**
FL	21,538,187	1.6243	1.3346	1.6129
GA	10,711,908	1.4301	1.3906	1.4375
HI	1,455,271	1.5330	1.2221	1.3806
IA	3,190,369	1.4979	2.3558	1.0906
ID	1,839,106	1.2902	1.5004	1.1492
IL	12,812,508	1.1010	1.2427	1.0303
IN	6,785,528	1.4808	2.0483	1.3011
KS	2,937,880	1.6181	1.5825	**0.8463**
KY	4,505,836	1.5401	1.1988	**0.9389**
LA	4,657,757	1.2269	1.5380	1.7963
MA	7,029,917	2.4008	1.0846	**0.7365**
MD	6,177,224	1.8112	1.4433	1.1016
ME	1,362,359	2.2400	1.4987	1.1074
MI	10,077,331	2.5159	1.2283	**0.9385**
MN	5,706,494	2.1400	1.6076	1.0471
MO	6,154,913	1.3783	1.3245	1.1722
MS	2,961,279	1.3353	1.7490	2.5765
MT	1,084,225	1.3814	1.9140	1.2367
NC	10,439,388	1.5884	0.8518	0.9769
ND	779,094	1.8152	1.6852	**0.9715**
NE	1,961,504	2.4089	2.8713	2.4377
NH	1,377,529	2.1694	1.1846	1.1882
NJ	9,288,994	1.8680	1.1596	1.0438
NM	2,117,522	1.2206	1.2357	1.0108

NV	3,104,614	0.9301	1.3862	1.5088
NY	20,201,249	1.8802	1.3264	**0.9069**
OH	11,799,448	1.6439	2.0173	**0.8531**
OK	3,959,353	1.6449	1.9003	**1.0150**
OR	4,237,256	1.4383	1.1184	1.0886
PA	13,002,700	2.4117	1.3496	**0.9778**
PR	3,285,874	4.1541	1.1200	**0.9633**
RI	1,097,379	1.2908	1.2471	**0.8438**
SC	5,118,425	1.5699	2.0826	1.0259
SD	886,667	1.7168	1.6564	**0.9446**
TN	6,910,840	1.6918	2.0071	**0.9094**
TX	29,145,505	1.2565	0.8002	1.5579
UT	3,271,616	1.2628	1.8566	1.4559
VA	8,631,393	2.3099	1.0337	0.8755
VT	643,077	1.7794	1.5289	1.1950
WA	7,705,281	1.4924	0.7499	0.9286
WI	5,893,718	1.5690	1.6867	**0.9044**
WV	1,793,716	1.8349	1.4470	**0.8511**
WY	576,851	0.7828	2.0850	0.9964