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Regular Article

Modeling the sexual transmission dynamics of mpox in the United States of America

Musa Rabiu[1,3,a], **Emmanuel Jesuyon Dansu**[2,7], **Oluwaseun Akinlo Mogbojuri**[3,8], **Isaiah Oke Idisi**[2], **Mukhtar Muhammed Yahaya**[4], **Precious Chiwira**[4], **Roseline Toyin Abah**[5], **Adejimi Adesola Adeniji**[6]

[1] Technion Israel Institute of Technology, Haifa, Israel
[2] Department of Mathematical Sciences, Federal University of Technology, Akure, Nigeria
[3] International Centre for Applied Mathematical Modelling and Data Analytics (ICAMMDA) in partnership with the West Africa Mathematical Modeling Capacity Development (WAMCAD), Federal University Oye-Ekiti, Oye-Ekiti, Nigeria
[4] Department of Mathematical Sciences, Stellenbosch University, Stellenbosch, South Africa
[5] Department of Mathematics, University of Abuja, Abuja, FCT, Nigeria
[6] Department of Mathematics and Statistics, Tshwane University of Technology, Pretoria, South Africa
[7] Ecological Integration Lab, Graduate School of Life Sciences, Tohoku University, Sendai, Japan
[8] Department of Mathematical Sciences, Adekunle Ajasin University, Akungba-Akoko, Nigeria

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Abstract In May 2022, an outbreak of mpox, a viral disease that was then popularly known as monkeypox, was first confirmed in the United Kingdom with a cluster of cases. Within a short period of time, the disease spread to the United States, where the index case was recorded on May 17, 2022, in Massachusetts. This outbreak's clinical and epidemiological characteristics are distinct from those of the earlier ones. It has been widely reported that sexual transmission is the primary means of spreading the current outbreak, with the community of men who have sex with men (MSM) being disproportionately and significantly impacted. To this end, we devised a two-group-compartmental model incorporating four distinct sexual transmission routes with focus on the United States. The Bayesian statistical framework with uniform priors was used to fit and capture the spread of the disease in both the men and women communities. Since the data were not disaggregated into men and women populations, some data analyses techniques were used to achieve the disaggregation. Sensitivity and scenario analyses revealed the respective contribution of each sexual transmission route to the basic reproduction number. The results reveal that the major contributing factor to the spread of the disease is the MSM transmission route, and condom usage with a high level of compliance can completely eradicate the spread of mpox in the United States. Since condom usage has shown a promising control measure for the spread of mpox in the MSM community, it is highly recommended that men should be more compliant with the use of condom or abstain completely from having sex with fellow men.

1 Introduction

Mpox (monkeypox) [1] is a disease caused by the monkeypox virus (MPXV), which is a member of the Orthopoxvirus genus within the Poxviridae family and the Chordopoxvirinae subfamily [2]. There are two major types of the mpox virus: Clade I and Clade II [3, 4]. While Clade I from the Congo Basin has a mortality rate of about 10%, Clade II from West Africa has a mortality rate less than 1% [5].

The first human case of the mpox disease was recorded in 1970 in the Democratic Republic of Congo (DRC) from a 9-months-old infant. This was followed by cases in six children in West Africa between 1970–1971 [6]. After the first discovery of the human mpox in the 1970 s, there has not been a significant increase in the number of human cases until the current global outbreak which saw the case number of mpox increasing to about 100 folds worldwide [6]. The current mpox outbreak which started in early 2022 and peaked in August 2022 made the World Health Organization (WHO) declare the disease as a public health emergency of international concerns (PHEIC) on July 23, 2022 [7, 8]. This has led to a growing worldwide emphasis on monitoring and managing the mpox epidemics in recent times [9].

There are several unique features of the ongoing 2022–2023 outbreaks in non-endemic countries. Due to its sequence similarity to the Clade II, the current outbreak strain of mpox has been designated Clade IIb [5]. Infections with the Clade IIb, just like the Clade II, are rarely fatal with less than 1% mortality rate [3, 5]. Also, while there are several routes through which mpox is being transmitted (such as contact with infected animals, respiratory droplets), transmission in the current outbreak is mainly due to sexual contact especially among men having sex with men [7, 10, 11]. The number of such men infected is, at least, 70% of all infected men [6].

[a] e-mail: rabiumusa003@gmail.com (corresponding author)

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As of September 2023, the current mpox outbreak had amounted to more than 91,000 confirmed cases with 157 mortalities in 115 countries across the world [12]. The worst hit countries include the United States of America, Brazil and Spain with 30,636; 10,967; and 9611 cases, respectively. Together, these three countries accounted for about 54% of the reported cases worldwide [12]. The United States of America with over 30,000 morbidity and 50 mortalities was the most affected country globally as of September 2023. It accounts for more than one-third of all mpox cases and about 32% of all deaths globally [12]. In the first 67 days (May 17 to July 22, 2022) of the outbreak in United States, a total of 2891 mpox cases were reported among which 99% of these cases were among men, majority of whom have had sex with other men few weeks before showing symptoms [13].

The West African lineage of the mpox virus is responsible for the greater human mpox outbreak that affected the world in 2022–2023 [14]. The 2022 outbreak occurred in the United States, the fourth country outside of those in Africa with an endemic mpox situation [14]. On May 17, 2022, Boston, Massachusetts, recorded the first case [14] of the current outbreak. As of June 28, the US government was distributing tens of thousands of mpox vaccine doses to clinics around the country [15]. It can be deduced that the full roll-out of mpox vaccine started toward the end of July 2022. An mpox research finding on the US suggested that imperfect vaccines could be assessed against the disease even though they may not completely provide needed protection against the disease, they could reduce the burden [15]. Symptoms of monkeypox include fever, rash, sore throat, headache, swollen lymph nodes, etc. [3, 4]. Mpox has an estimated incubation period (the period between exposure to the disease and the appearance of symptoms) of about 7–21 days [7, 8].

While most studies on mpox transmission concentrated on primary modes such as respiratory or dermal contact, sexual transmission remains an area of growing interest. In recent times, some studies have explored the potential risks associated with specific sexual behaviors, focusing on men having sex with men (MSM) and women having sex with women (WSW) [16–19]. The American region has been significantly affected, accounting for 67 percent of the cumulative cases worldwide [20]. Discrimination in the LGBTQI+ community has been one of the significant determinants of new infections [21]. This raises the need for clinical measures to contain the disease. The Center for Disease Control (CDC) recommends vaccination, using condoms, gloves, covering areas with rashes, and avoiding close contact with infected people as some of the interventions to reduce the spread of mpox [3].

Despite mpox not being considered a sexually transmitted disease, the 2022 global outbreak has been linked to close contact, particularly sexual contacts among men having sex with men and transexual women [18, 22]. This has raised the need to model the sexual transmission of mpox and come up with best strategies in mitigating this disease.

Mathematical modeling has over the years proved to be an indispensable tool in understanding the transmission dynamics of infectious disease. Beginning with the work of Bernoulli in 1760 while researching on smallpox, mathematical models have been used to predict the spread of infectious disease and forecast the impact of various control measures [23]. Several studies have also been dedicated to examining the mpox disease using mathematical modeling approach.

For instance, one of the earliest work on mpox disease dynamics was done by [24] where a deterministic model was developed and analyzed. In addition to the standard compartments, they included an "isolated" compartment. Their model was shown to exhibit backward bifurcation. Their findings show that isolating infected humans will help in reducing the transmission of the disease. The authors in [8] considered a system of nine ODEs to investigate the spread of mpox disease in Germany and Nigeria. The work incorporated the vaccinated and hospitalized compartments and considered the rates of human-to-animal and animal-to-animal transmissions to capture the trend of disease spread in the two countries. They carried out optimal control and cost-effectiveness analyses which showed that behavioral change and personal hygiene are the most effective strategies to halt the spread of the disease.

Idisi et al. [25] developed a compartmentalized mathematical model to assess the impact of heightened awareness on controlling mpox disease following the 2022 outbreak. The model considers the dynamics between humans and host mammals, stratifying the human susceptible population into aware and unaware subgroups. Through rigorous analytical analysis and numerical simulations, the authors found that a robust public awareness campaign could significantly reduce the cumulative incidence of the disease, thereby preventing new cases. They emphasize the importance of a sustained and coherent public awareness program, underscoring the need for ongoing efforts to enhance understanding of mpox disease and recommending strict adherence to established public health measures in reducing mpox disease incidence.

A seven-dimensional system of differential equations was proposed in [26] to describe the transmission and spread of mpox disease between human and rodents populations. The analysis performed in the study shows that the model exhibits backward bifurcation in the presence of quarantined individuals whenever $\mathcal{R}_0 < 1$. The results of the study indicate that an mpox-free state can be achieved if quarantine and isolation guidelines are followed rigorously, as well as preventative measures that can reduce the effective contact rates between humans and rodents.

Bragazzi et al. [27] formulated a compartmental model to understand the transmission dynamics of mpox in Canada. Their model incorporates sexual behavior dynamics and divides the population into high-risk and low-risk groups. Since most of the mpox cases in the high-risk group is believed to occur due to sexual interactions, the authors considered sexual contact in the high-risk group only. They investigated and compared several intervention measures that targeted the high-risk group. Their result shows that adaptive behavioral changes among the high-risk group can be very effective and play a crucial role in controlling the ongoing mpox outbreak in Canada.

The authors in [19] used a mathematical modeling approach to study the transmission dynamics and effects of control measures on the ongoing mpox outbreak among gay and bisexual men in England. They obtained data for all diagnosed mpox cases from May 1 to November 16, 2022. Their findings reveal that about 98% of the cases occur in men and that the mpox outbreak in England

was a result of high numbers of sexual partners among those studied. The authors recommended that a reduction in the number of sexual partners would curb the outbreak.

By employing geo-spatial analysis, topic modeling and sentiment analysis, the authors in [28] found that the current global mpox outbreak is disproportionately affecting the 2SLGBTQIAP+ community and that stigma intensifies the outbreak. The study used Twitter and Facebook to understand mpox stigmatization of the 2SLGBTQIAP+ community. The researchers found that there were country-level variations in topics and sentiments toward mpox and the community and that the number of social media posts with mpox and 2SLGBTQIAP+ keywords had a higher correlation with the number of mpox cases in comparison with the number of posts on mpox.

A dynamic network transmission model was used in [29] to examine the impact of vaccination and change in sexual behavior on mpox reported cases in Washington D.C. Their findings show that although behavior change led to the decline in initial cases, overall reduction in cases is due to vaccination.

In spite of the substantial research carried out in studying the transmission dynamics of mpox using mathematical models, very few studies have utilized modeling approaches to explore the sexual transmission dynamics of the current mpox outbreak. To the best of our knowledge, no research work has disaggregated the mpox community into men and women populations using data analysis.

In this paper, we build upon the existing knowledge by developing a mathematical model that incorporates four sexual routes including the sexual behaviors of the MSM and WSW community in order to capture the current trend of transmission in the ongoing mpox outbreak in the United States. To the best of our knowledge, no research work has studied such. We seek to provide insights into the risks and implications of sexual transmission, contributing to a more comprehensive understanding of mpox disease. Data analysis technique was used to disaggregate the data into both men and women populations since the available data was not disaggregated. By using the Bayesian inference framework, we fit the model to the daily reported mpox data so as to validate the reliability of the model. We also carry out scenario analysis on the reproduction number. Finally, a control strategy (the use of condom) was proposed, and simulations were performed.

The rest of the paper is organized as follows: In Sect. 2, the materials and methods employed in this research are discussed. The basic reproduction number, sensitivity analysis and scenario analysis are performed in Sect. 3. In Sect. 4, condom usage is introduced in the model as a control strategy and numerical simulations are performed. Finally, the discussion of results and the concluding remarks is given in Sect. 5.

2 Materials and methods

2.1 Materials

The main materials used for this research are the demographic data and the daily mpox reported cases data for the USA. We sourced the 7-day rolling average of mpox reported cases from June 1 to August 1, 2022 (equivalent to 62 days) before the implementation of any control intervention. The data are publicly available on *Our World in Data* website [30]. The data contain 15 variables altogether including new cases, new death, smoothed new cases, smoothed new death, total cases, total death, etc. In the USA, the time frame under consideration was prior to the implementation of control intervention.

The obtained data is not disaggregated into men and women population in the United States. So, for disaggregation, we considered the fact that 95% of the reported mpox cases are from sexual contact [31]. Also, most of those in the high-risk group are from the MSM community [27] and the Center for Disease Control (CDC) reported that among mpox cases with available data, 99% occurred among men while 94% occurred among people who reported recent men-to-men sexual or close contact [31]. For these reasons, we attributed 99% of the reported cases to the men population while only 1% of the cases were attributed to the women population. In addition, we also considered the fact that 7.1 million people in the US belongs to the MSM community [32] while the adult population as at 2020 was 258.3 million [32, 33]. Of this population, we assumed that 75% (193,725,000) was sexually active. Further, since 50.4% of the US population were women [33], we assumed that the sexually active population of both men and women in the US was approximately 96,862,500. These estimates are used as initial conditions in our analyses.

2.2 Methods

This section contains the foundation upon which this research is built. We formulate a deterministic compartmental model to study the sexual transmission dynamics of mpox. We stratify the model into two populations- men and women. The men population is further subdivided into four compartments: susceptible men $S_m(t)$, exposed men $E_m(t)$, infectious men $I_m(t)$ and recovered men $R_m(t)$. Similarly, the women population is subdivided into four compartments: susceptible women $S_w(t)$, exposed women $E_w(t)$, infectious women $I_w(t)$ and recovered women $R_w(t)$. We only consider sexual contacts and do not take nonsexual contacts into consideration since majority of transmission in the current outbreak is suspected to be through sexual activities [7]. Furthermore, we do not consider demography (i.e., immigration, birth and death rates) since the study is over a short period of time.

Susceptible men get infected when they have sexual contacts with infectious men or women, with force of infection λ_m, and they moved to the exposed compartment. Exposed men progress to the infectious class after spending $\frac{1}{\alpha_m}$ days in the exposed

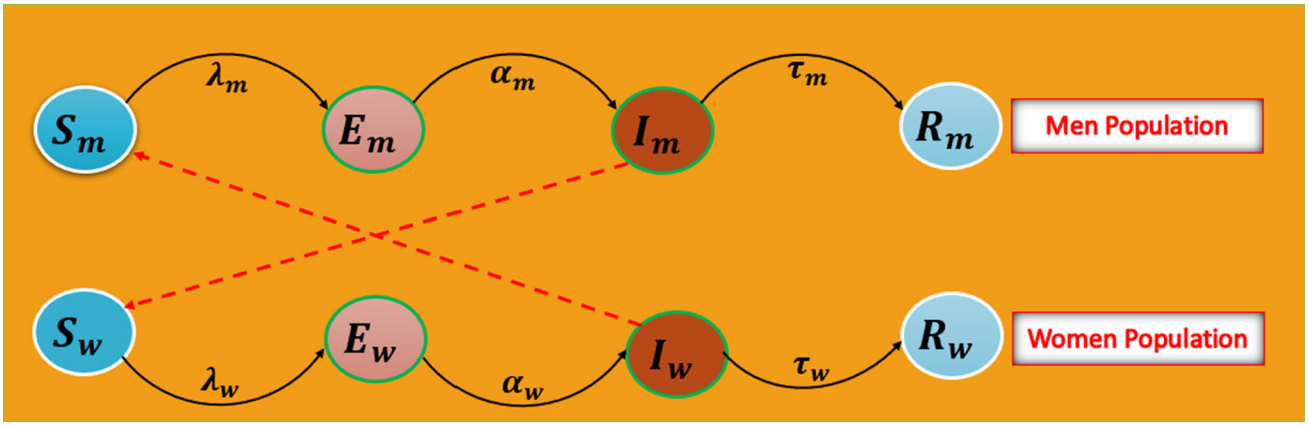

Fig. 1 Schematic diagram for sexual transmission dynamics of mpox. The black curved arrows indicate the progression from one compartment to another. The red dashed arrows indicate the transmission of the disease

compartment while infectious men recover at the rate τ_m. Similar progressions from one compartment to another happen in the women population.

2.3 Model structure

$$\begin{aligned}
\frac{dS_m}{dt} &= -\lambda_m S_m,\\
\frac{dE_m}{dt} &= \lambda_m S_m - \alpha_m E_m,\\
\frac{dI_m}{dt} &= \alpha_m E_m - \tau_m I_m,\\
\frac{dR_m}{dt} &= \tau_m I_m,\\
\frac{dS_w}{dt} &= -\lambda_w S_w,\\
\frac{dE_w}{dt} &= \lambda_w S_w - \alpha_w E_w,\\
\frac{dI_w}{dt} &= \alpha_w E_w - \tau_w I_w,\\
\frac{dR_w}{dt} &= \tau_w I_w,
\end{aligned} \tag{2.1}$$

where the forces of infection within the two populations are defined as

$$\lambda_m = \frac{\beta_{mm} I_m}{N_m} + \frac{\alpha_1 \beta_{wm} I_w}{N_m},\ \lambda_w = \frac{\alpha_2 \beta_{mw} I_m}{N_w} + \frac{\alpha_3 \beta_{ww} I_w}{N_w}, \tag{2.2}$$

and

$$N = N_m + N_w.$$

The first term of λ_m accounts for mpox transmission for men having sex with men (MSM) while the second term of λ_w accounts for transmission for women having sex with women (WSW). The other terms represent transmissions in the context of heterosexual sex (Fig. 1; Table 1).

2.4 Bayesian inference

The model (2.1) was fitted to the daily reported mpox data as earlier described. The Bayesian inference framework in the RStan package [34] in R version 4.3.1 [35] was used to obtain the posterior mean. With the use of this probabilistic framework, we estimated the model parameters while accounting for our prior knowledge, and we assessed probabilistic claims made about the data in the context of the model. Given the model parameters, data generation is involved in the sampling distribution, also known as likelihood. Using the data, we estimated reasonable parameter values using the posterior distribution. The fit summary includes helpful details

Table 1 Description of Variables and Parameters

Variable	Description
S_m, S_w	Population of susceptible men and women
E_m, E_w	Population of exposed men and women
I_m, I_w	Population of infectious men and women
R_m, R_w	Population of recovered men and women
Parameter	**Description**
α_m, α_w	Rates at which exposed men and women, respectively, become infectious
τ_m, τ_w	Rates at which infectious men and women, respectively, recover
β_{mm}	Transmission probability from infectious men having sex with susceptible men (MSM)
β_{ww}	Transmission probability from infectious women having sex with susceptible women (WSW)
β_{mw}	Transmission probability from infectious men having sex with susceptible women (MSW)
β_{wm}	Transmission probability from infectious women having sex with susceptible men (WSM)
α_1, α_2, α_3	Modification parameters for reducing transmission

like the standard deviation, mean, effective sample size, R-hat and more. R-hat is a measure of the degree of convergence of the iteration. R-hat should be very close to 1 to ensure convergence. In general, the Bayesian framework is built upon the relationship

$$p(\eta|\mathcal{U}) \propto p(\mathcal{U}|\eta)p(\eta), \tag{2.3}$$

where $p(\eta|\mathcal{U})$ is the likelihood, $p(\mathcal{U}|\eta)$ is the posterior distribution, and $p(\eta)$ is the prior. The likelihood is constructed as

$$\text{daily\_mpox\_reported\_cases}(t) \sim \text{NegBin}(\text{predict\_cases}(t), \psi), \tag{2.4}$$

where daily_mpox_reported_cases is the daily reported cases of mpox in the US at time t (measured in days), predict_cases(t) is the predicted daily mpox cases computed from the model (2.1), NegBin($\cdot$) is the negative binomial distribution function in RStan, and ψ is the over-dispersion parameter.

Synthesized cases data were produced using the proposed model with known parameter values in order to verify that our model (2.1) is accurately programmed in the Stan function and to confirm that the suggested model is properly validated. After fitting the model to the synthesized data, the model's capacity to estimate these parameter values was examined. The biases and coverage of the genuine parameter values utilized to create the synthesized data were checked in the resulting posterior distributions. All analyses and estimates in this section are performed using the adaptive Hamiltonian Monte Carlo method No-U-Turn sampling (NUTS) in RStan with 2000 iterations (where 1000 iterations are discarded for warm up) and 4 chains. For more information about this method, see [36, 37]. For the priors, normal distribution was used for the beta parameters while exponential distribution was used for the over-dispersion parameter.

2.5 Model fitting and parameter estimation

Six of the parameters were estimated because of their unavailability in literature while the remaining ones were picked from reliable literature. In the model equation (2.1), $\alpha_m E_m$ and $\alpha_w E_w$ were directly used as the simulated 7-day rolling average of confirmed cases from the men and the women populations, respectively. The parameter values are available in Table 2. The pairs plots are placed beside the fit in Fig. 2. Other diagnostic plots such as density and trace plots can be found in Appendix A.

3 Basic reproduction number

3.1 Derivation

In epidemiology, the basic reproduction number (R_0) is a measurement used to determine the anticipated number of cases that will be directly caused by one case in a community where everyone is vulnerable to infection. It is neither a rate nor a dimensioned number, and it is crucial for comprehending the idea of herd immunity. When a community reaches the point of herd immunity, a disease cannot spread because, on average, each affected person can only infect one other person at a time. A pathogen's basic reproduction number is not a biological constant because it depends on a number of variables, including the environment and how the infected population behaves [38–40].

Table 2 Table of parameter values and their references. The parameter values from literature are cited while the estimated ones are presented alongside their 95% credible interval (CrI)

Parameter	Value	Reference
α_m	1/8.5	[27]
α_w	1/22	[27]
τ_m	1/8	[27]
τ_w	1/7	[27]
β_{mm}	0.34 (95% CrI : 0.33-0.36)	Estimated
β_{ww}	0.2 (95% CrI : 0.12-0.26)	Estimated
β_{mw}	0.01 (95% CrI : 0.00-0.03)	Estimated
β_{wm}	0.19 (95% CrI : 0.01-0.67)	Estimated
α_1	0.01	Derived from the data
α_2	0.1	Derived from the data
α_3	0.5	Derived from the data
$I_w(0)$	27.00 (95% CrI : 4.17-38.33)	Estimated
$I_m(0)$	28.22 (95% CrI : 4.13-36.38)	Estimated

In order to compute R_0 based on the principle of the next generation matrix, we focus on the exposed and infectious compartments:

$$\begin{aligned}
\frac{\mathrm{d}E_m}{\mathrm{d}t} &= \frac{\beta_{mm} I_m}{N_m} S_m + \frac{\alpha_1 \beta_{wm} I_w}{N_m} S_m - \alpha_m E_m, \\
\frac{\mathrm{d}I_m}{\mathrm{d}t} &= \alpha_m E_m - \tau_m I_m, \\
\frac{\mathrm{d}E_w}{\mathrm{d}t} &= \frac{\alpha_2 \beta_{mw} I_m}{N_w} S_w + \frac{\alpha_3 \beta_{ww} I_w}{N_w} S_w - \alpha_w E_w, \\
\frac{\mathrm{d}I_w}{\mathrm{d}t} &= \alpha_w E_w - \tau_w I_w.
\end{aligned} \tag{3.1}$$

First, we determine the disease-free equilibrium (DFE) which is given by

$$(S_m^*,\ E_m^*,\ I_m^*,\ R_m^*,\ S_w^*,\ E_w^*,\ I_w^*,\ R_w^*) = (N_m,\ 0,\ 0,\ 0,\ N_w,\ 0,\ 0,\ 0).$$

Then, R_0 is derived using the next generation matrix operator [41, 42] on the model compartments (3.1) as used by [8, 43]. The Jacobian matrix for the rates of new infections M_m and that of transfer of infected individuals M_s at the DFE is determined and the product of M_m and M_s^{-1} is given by

$$M_m M_s^{-1} = \begin{pmatrix} 0 & \beta_{mm} & 0 & \alpha_1\beta_{wm} \\ 0 & 0 & 0 & 0 \\ 0 & \alpha_2\beta_{mw} & 0 & \alpha_3\beta_{ww} \\ 0 & 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{\alpha_m} & 0 & 0 & 0 \\ \frac{1}{\tau_m} & \frac{1}{\tau_m} & 0 & 0 \\ 0 & 0 & \frac{1}{\alpha_w} & 0 \\ 0 & 0 & \frac{1}{\tau_w} & \frac{1}{\tau_w} \end{pmatrix}. \tag{3.2}$$

By definition, R_0 is the spectral radius, ρ, of the matrix $M_m M_s^{-1}$. The spectral radius of a matrix is the largest absolute value of its eigenvalues. As such, the basic reproduction number of our model can be expressed as

$$R_0 = \frac{\alpha_3\beta_{ww}\tau_m + \beta_{mm}\tau_w}{2\tau_w\tau_m} + \frac{\sqrt{4\alpha_1\alpha_2\beta_{wm}\beta_{mw}\tau_w\tau_m + \alpha_3^2\beta_{ww}^2\tau_m^2 - 2\alpha_3\beta_{ww}\beta_{mm}\tau_w\tau_m + \beta_{mm}^2\tau_w^2}}{2\tau_w\tau_m}. \tag{3.3}$$

The number of subsequent infections that a single initial infection causes in an otherwise susceptible population is implied by R_0. A disease is endemic if R_0 is greater than unity while its not endemic when R_0 is less than unity. Using the Bayesian inference, the basic reproduction number in the USA is estimated to be 2.72 (95% CrI: 2.45−2.98). The basic reproduction number seems high probably because the data used are a 7-days rolling average of mpox reported cases from June 1 to August 1, 2022 (equivalent to 62 days) before the implementation of control interventions. After the implementation of interventions, the reproduction number is bound to reduce.

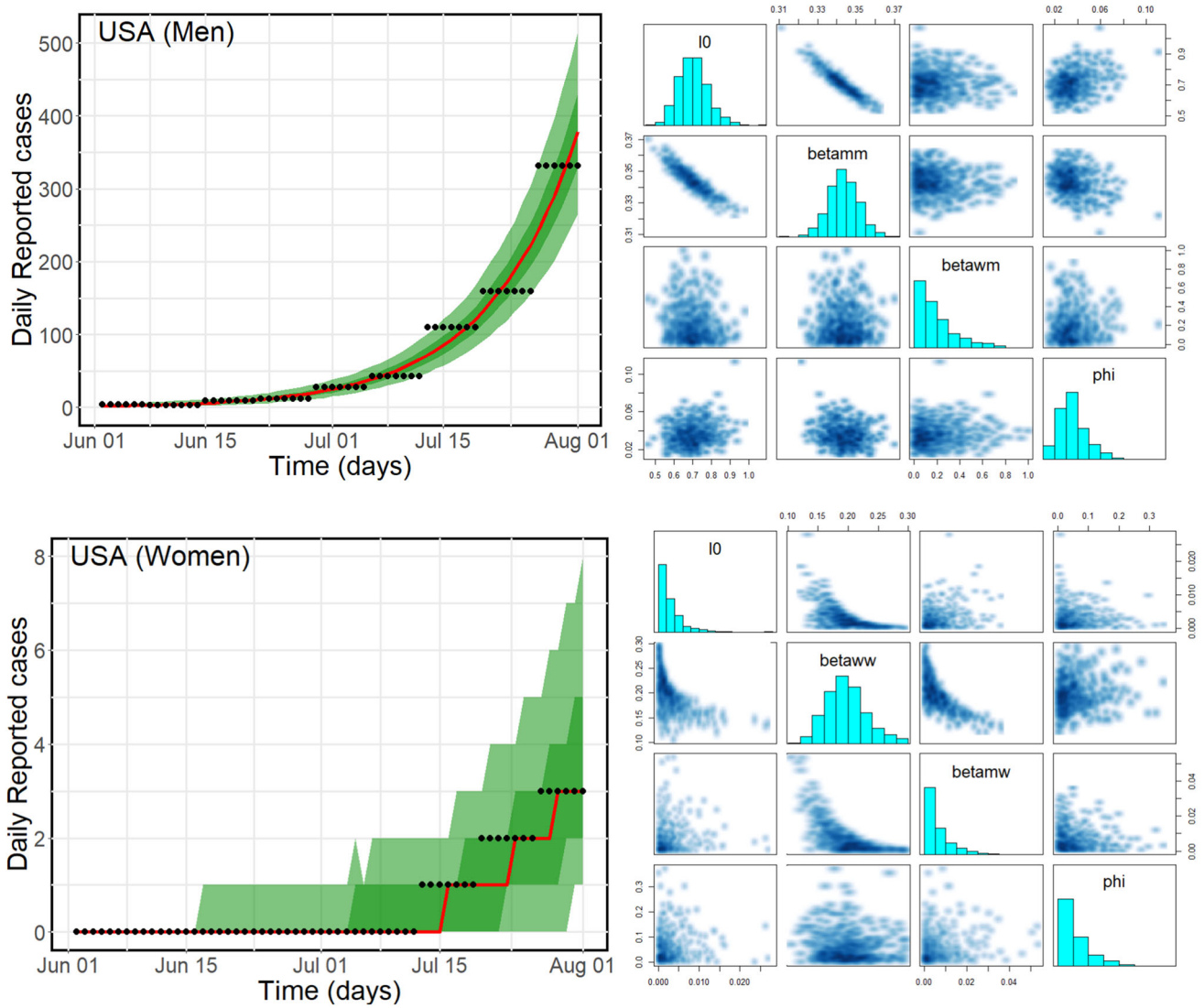

Fig. 2 Model fit using the daily mpox cases for a period of 62 days (June 1–August 1, 2022) for both men and women populations. The dotted lines indicate the reported cases while the red line indicate the model fit. The deeply colored green parts represent the 50% CrI while the lightly colored green parts represent the 95% CrI. Beside the fits are the pair plots of the posterior mean

3.2 Sensitivity analysis

Here, we set out to investigate the sensitivity of the basic reproduction number R_0 to each of its terms. This can be obtained from

$$S_{(\cdot)} = \frac{(\cdot)}{R_0} \times \frac{\partial R_0}{\partial(\cdot)},$$

where $(\cdot)$ represents each parameter (Table 3).

From the sensitivity analysis, we have the following observations:

1. α_1, which denotes a transmission-reducing modification factor, has a sensitivity index of 0.0053 which signifies a small impact on R_0. This suggests that a small change can be anticipated in the disease's basic reproduction number (R_0) if a slight change to α_1 is made (which could represent interventions like public health initiatives or behavioral changes). Therefore, altering the transmission through α_1 has a discernible but not particularly powerful effect on the disease's spread.
2. Like α_1, α_2 is a modification factor that helps to lower transmission. With a sensitivity index of 0.0005, it has a little less significant impact on R_0 than α_1. Accordingly, modifications to α_2 have a lower effect on R_0 compared to α_1 though it still has a discernible impact on the spread of disease.
3. A further adjustment factor that lowers transmission is α_3. With a sensitivity index of 0.0000, α_3 has negligible impact on R_0. The relationship between α_3 and R_0 shows that α_3 has nearly no influence on making mpox break out.

Table 3 Sensitivity index of R_0 to each parameter

Parameter	Sensitivity index
α_1	0.0053
α_2	0.0005
α_3	0.0000
β_{mm}	7.9998
β_{mw}	0.0053
β_{wm}	0.0003
β_{ww}	0.0001
τ_m	− 21.7599
τ_w	− 0.0005

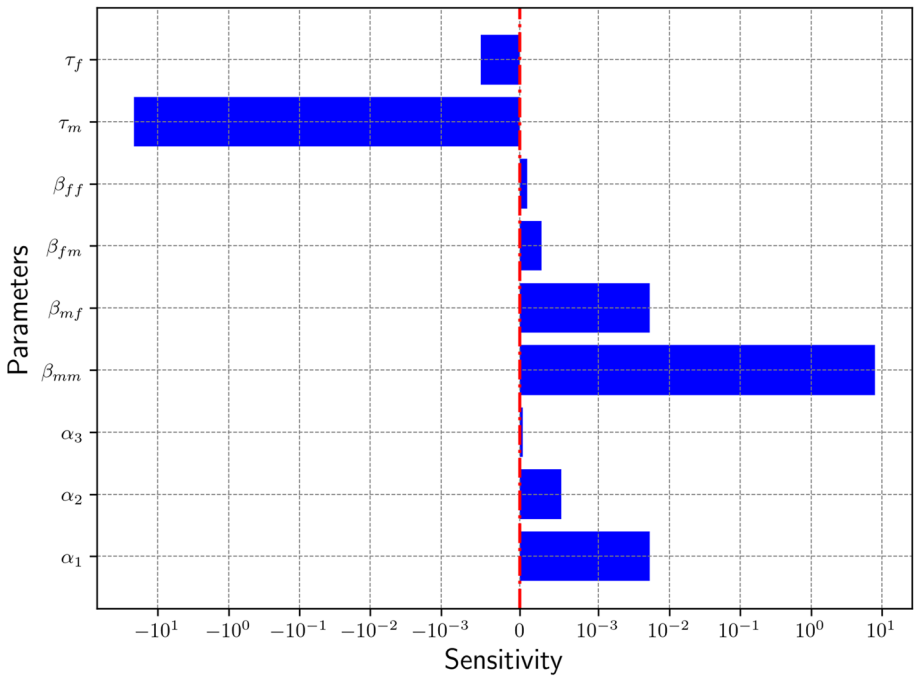

Fig. 3 Plot of the sensitivity index of R_0 to each parameter

4. β_{mm} measures the likelihood that an infectious man will transmit the disease to a susceptible man. It has a sensitivity index of 7.9998 and a significant impact on R_0. This shows that variations in the probability of transmission between infectious and susceptible men have a great positive impact on the disease's basic reproduction number (R_0).
5. β_{ww} measures the likelihood of disease transmission from infected to susceptible women. It has a very low sensitivity index of 0.0001 and an insignificant positive impact on R_0.
6. β_{mw}: This parameter depicts the likelihood of infection spreading from infected men to susceptible women. It has a sensitivity index of 0.0053 and a little impact on R_0. The basic reproduction number (R_0) is somewhat affected by changes in this transmission probability, demonstrating that this feature of transmission has a little influence (Fig. 3).
7. Similar to β_{mw}, β_{wm} measures the likelihood of transmission, but from infected women to susceptible men. It has a negligible impact on R_0, with a sensitivity index of 0.0003. This indicates that changes in the likelihood of disease transmission from infectious women to susceptible men have insignificant effect on the spread of mpox.
8. τ_m measures how quickly infected men recover. With a high sensitivity index of -21.75899, it has a major negative impact on R_0. The spread of the disease is greatly decreased by an increase in the rate of recovery for infectious men. This shows that reducing the length of men's infectious periods can aid in disease management.
9. τ_w is the rate of recovery for infected women and it weakly affects R_0 with a very negative sensitivity index at -0.0005. Insignificantly less disease spread occurs when infectious women recover more quickly. This suggests that shorter women's infectious periods have a minute impact on disease control and insignificantly lower R_0.

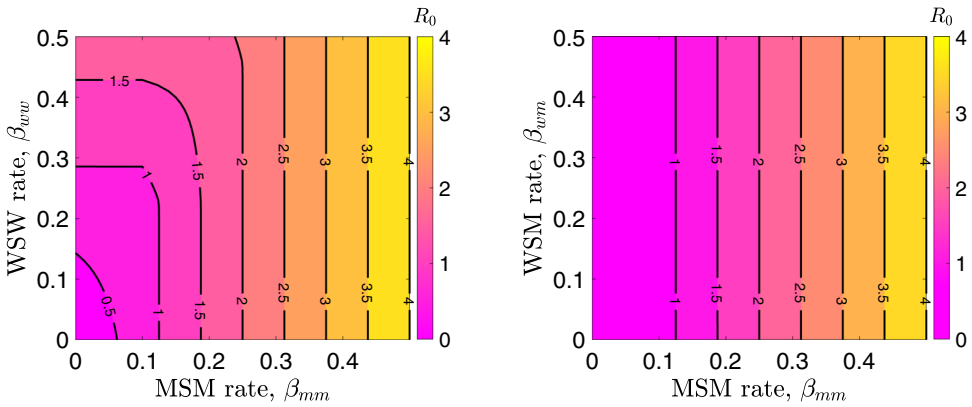

Fig. 4 Left panel: Effect of the MSM and WSW transmission rates on the basic reproduction number. Right panel: Effect of MSM and WSM transmission rates on the basic reproduction number

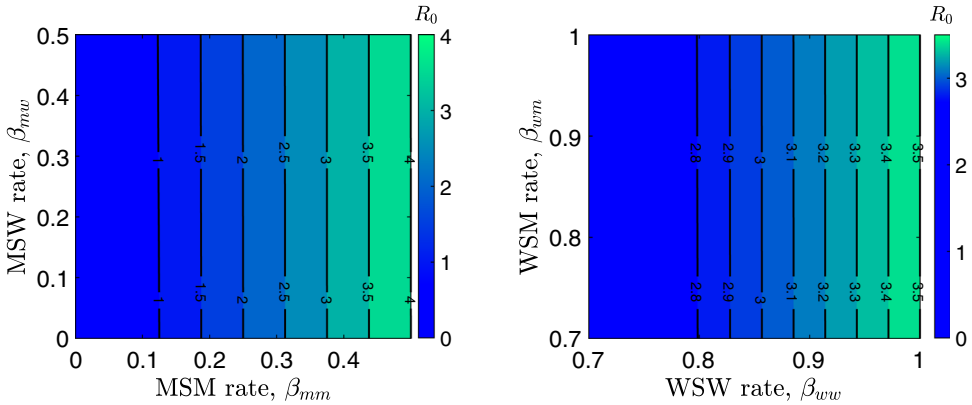

Fig. 5 Left panel: Effect of the MSM and MSW transmission rates on the basic reproduction number. Right panel: Effect of WSW and WSM transmission rates on the basic reproduction number

3.3 Scenario analysis with contour plots

In this section, we carry out some scenario analyses on the basic reproduction number R_0 using contour plots. Baseline parameter values are as described in Table 2 while the varied parameter values are in the closed interval [0, 1]. We varied parameters such as β_{mm}, β_{ww}, β_{mw}, and β_{wm} to have a grasp of their respective effects on R_0. The main reason for this is that majority of the recent mpox spread, especially in the US, is attributed to the MSM community. As such, it is imperative and instructive to check the effects of all the considered four sexual contact routes on R_0.

Figure 4 (left panel) shows the effects of the transmission rates of both the MSM and WSM communities. It can be observed that both rates increase R_0 as they increase. When β_{mm} is low, an increase in β_{ww} does not have much effect on R_0 compared to when βww is low and β_{mm} is varied. It can also be observed that the MSM transmission rate has more effect on R_0 compared to the WSW contact rate. When the MSM transmission rate is 0.3 while the WSM transmission rate is 0, the corresponding R_0 is approximately 2.5. However, when the MSM transmission rate is 0 while the WSW transmission rate is 0.3, R_0 is slightly above 1. This shows that the β_{mm} has more significance on R_0 over β_{ww}. The biological implication of this is that the MSM community strongly drives mpox spread in the US, and this is in consonance with the findings in [27, 31, 32]. The right panel shows the effects of the MSM and WSM transmission rates on R_0. The figure shows that the MSM transmission rate has more impact on R_0 than the WSM transmission rate. Again, this shows that MSM are key drivers in the spread of mpox.

The left panel in Fig. 5 shows the effect of the MSM and MSW transmission rates on R_0. The figure shows that the MSM transmission rate has greater effect than the MSW transmission rate on the reproduction number. Very smaller values of the MSM transmission rate (< 0.1) do not really have much effect on R_0 even if the MSW transmission rate is increased. In both Figs. 4 and 5, increase in MSW and WSM transmission rates do not impact significantly on R_0. What can be inferred from this is that the 2022 mpox spread across the world is not so much dependent on MSW and WSM sexual contact rates. This result looks like the one on the right panel of Fig. 5 where we examined the effect of the WSW and WSM transmission rates on R_0 though the WSW transmission rate has more impact on the R_0 compared to the WSM transmission rate.

A similar result is obtained in Fig. 6 where we check the effects of WSW and MSW transmission rates on R_0. The figure shows that the WSW transmission rate has more impact on R_0 than the MSW transmission rate. Smaller values of the WSW transmission rate (< 0.8) does not have so much effect even when the MSW rate is increased.

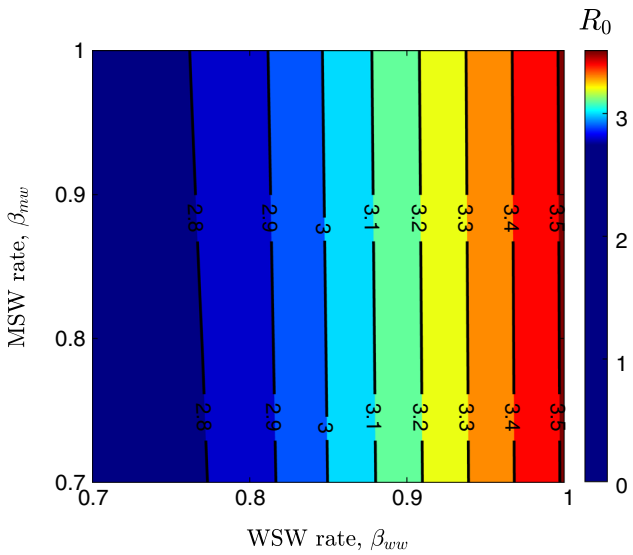

Fig. 6 Effect of the WSW and MSW transmission rates on the basic reproduction number

4 Numerical simulations

4.1 Condom use as a control strategy

Condom use is one of the common control measures for sexually transmitted infections (STIs). According to [44–47], one of the best ways to contain the spread of STIs like HIV and mpox is to use condoms properly and regularly, even in same-sex interactions. However, it has not been embraced by some people due to various reasons [25, 48].

Just like the case with HIV/AIDS [49, 50], MSM tend to have the lion share of mpox infections [22, 51, 52]. As such, [53] sought to identify the causes of inconsistent use of condoms among MSM in their systematic analysis and meta-synthesis. Six major themes were found after the analysis of 39 qualitative investigations and were grouped according to the socioecological model. These themes covered individual-level obstacles such as physical discomfort, a lack of awareness about HIV/STIs, and substance abuse, while interpersonal-level difficulties resulted from the stigma surrounding condoms, which was related to trust, conventional attitudes of sex, and humiliation. Situational inaccessibility, the high cost of condoms, and power inequalities in intimate relationships were among the environmental and structural barriers. The study's results highlight the need for diverse treatments, notably in addressing the condom stigma, and shed light on the complexity of barriers to condom use among MSM.

In using condom as a control strategy for model (2.1), we have $0 \leq \mu \leq 1$ representing condom use for the susceptible men and women populations, respectively. As such, we have

$$\lambda_m = (1-\mu)\left(\frac{\beta_{mm} I_m}{N_m} + \frac{\alpha_1 \beta_{wm} I_w}{N_m}\right), \ \lambda_w = (1-\mu)\left(\frac{\alpha_2 \beta_{mw} I_m}{N_w} + \frac{\alpha_3 \beta_{ww} I_w}{N_w}\right). \tag{4.1}$$

The initial conditions used are $S_w(0) = 96862500$, $E_w(0) = 0$, $I_w(0) = 27$, $R_w(0)$=0, $S_m(0) = 96862500$, $E_m(0) = 0$, $I_m(0) = 28$, $R_m(0)$=0, and the baseline parameters are as referenced in Table 2.

To explore the dynamics of the mpox disease further, we solved the system (2.1) with the new forces of infection (4.1) numerically using the Runge–Kutta Fourth Order Scheme. This helped to investigate the evolution of the disease within the MSM and WSW populations over the course of time with special attention on the control parameter μ.

In Fig. 7, we graphed the incidence function for the men population over a defined time frame, and it was noticed that when the condom control parameter μ decreases, there is a rapid rise in the number of new mpox cases. A gradual decline from the peak is observed as the control increases from 0.1 to 0.4.

As depicted in Fig. 8, the infection in the women population declines in significantly shorter time and with less condom use control efforts. This is understandable because the women population has an insignificant contribution to the mpox disease burden compared to the men population and a little control effort can eradicate the disease among the women population.

4.2 Temporal variation of the population

Here, we are interested in the temporal variation of the population of each compartment in the system (2.1) over time. Figure 9 shows that the susceptible men class S_m has the largest population of the four compartments at initial time with a total population of 76 million individuals and it gradually declines to a level below 20 million within the simulated time interval. The exposed men population gradually decreases over the simulated time interval; this is attributed to a rise in the number of both infected and recovered individuals. However, the converse is observed in the infected compartment as it reveals a sudden rise at initial time from

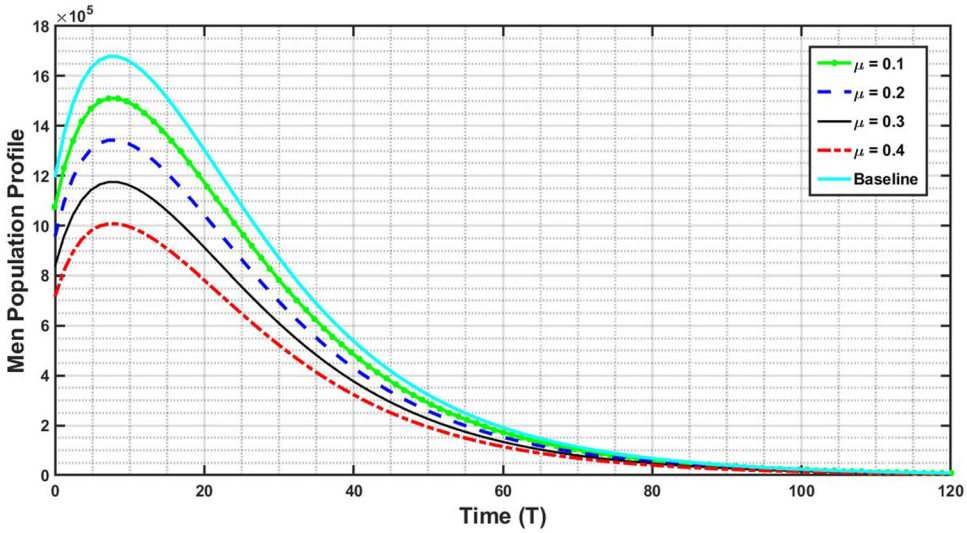

Fig. 7 Condom control on the men population with variations in the value of μ using the incidence function (4.1) as a baseline when $R_0 > 1$

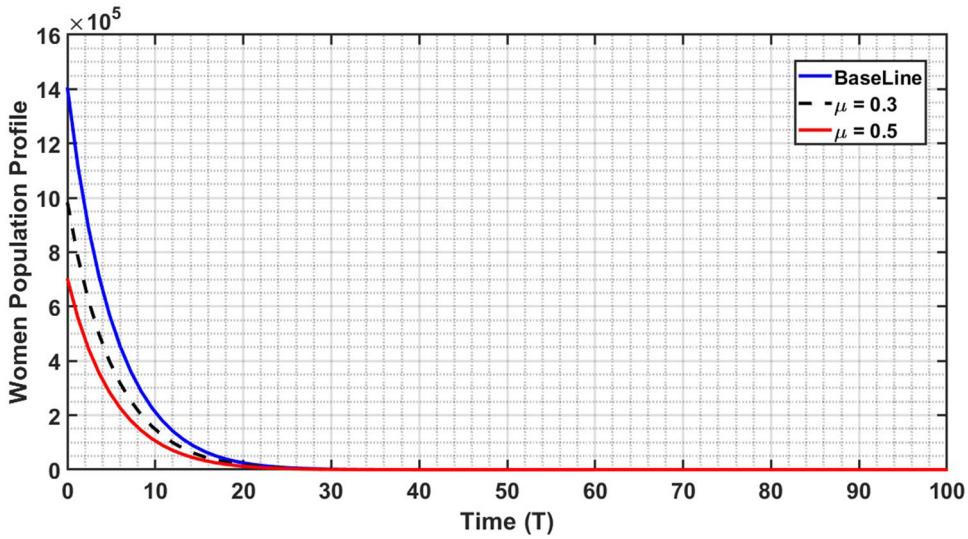

Fig. 8 Condom control on the women population with variations in the value of μ using the incidence function (4.1) as a baseline when $R_0 > 1$

7.3 million to attain a peak of 14 million and gradually declines. It is further observed that the men recovered compartment shows a steady increase in the number of recovered individuals over time from almost 0 to 80 million.

Basically, in Fig. 10 the WSW community reveals a sharp decline in the respective compartments (Susceptible, Exposed, Infectious and Recovered). It is observed in the susceptible women compartment that there is a sharp decline in the number of from 73 million to as low as 63 million. However, the initial increase in the exposed women compartment resulted from the sharp decline in the susceptible compartment as depicted in Fig. 10 with an initial population of 20 million slowly declining through the stipulated time interval to 5 million. Furthermore, in the recovered compartment, as shown in Fig. 10, a quick rise is seen in the recovered population within a short period of time after which the population declines gradually. However, the final population level in the recovered compartment is remarkably higher than that of the infected compartment (I_w) in comparison.

To explore deeper, the impact of transmission probability β_{mm} on the prevalence of mpox disease, as depicted in Fig. 11, was examined. This plot reveals an initial increase on the population as (β_{mm}) increases through the baseline to 0.55, thus revealing a sharp increase in the prevalence of mpox disease in the population having high saturation within a very short time; afterward, it slowly declines. However, decreasing the value of β_{mm} (say β_{mm}= 0.35) elongates the time for infection to reach its peak (i.e., prolonged rapid spread of the disease) which also increases the time for the disease to die out.

Figure 12 depicts the impact of varying β_{ww} on the spread of mpox; it reveals a slight change in the prevalence of the disease in the WSW population when in comparison with the MSM population. This is a pointer to the kind of policies required to mitigate the spread of mpox in both MSM and WSW communities.

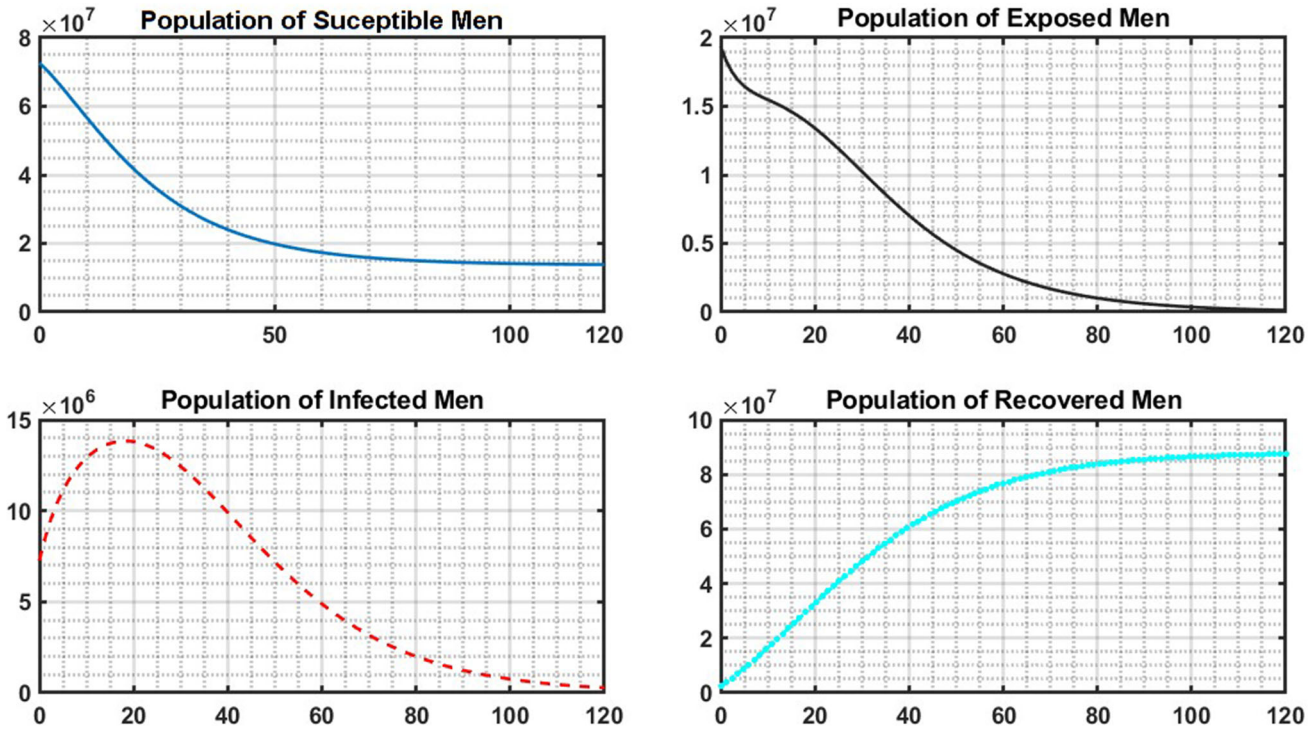

Fig. 9 Men population using baseline parameters

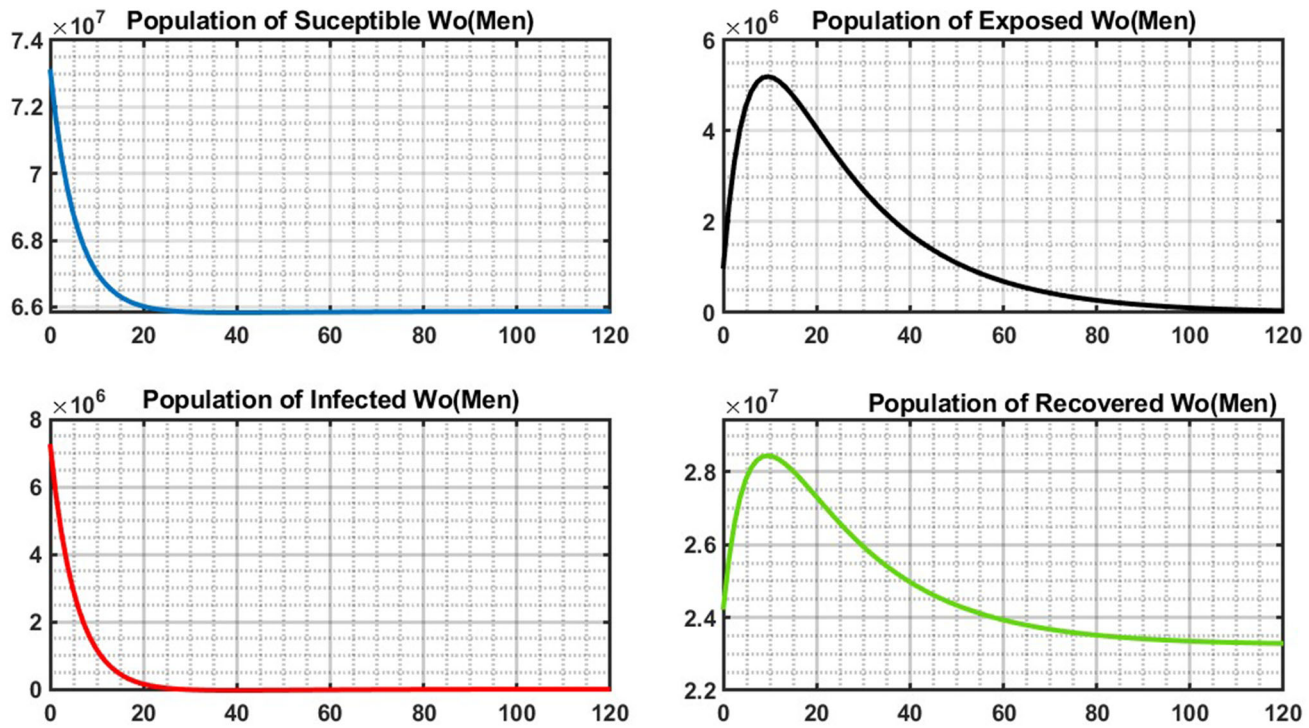

Fig. 10 Women population using baseline parameters

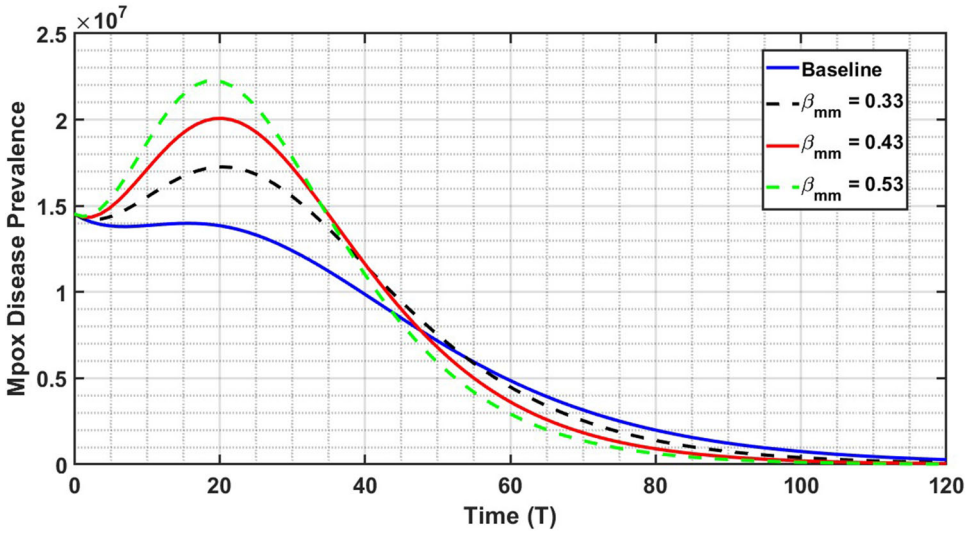

Fig. 11 Effect of varying β_{mm} on Mpox disease prevalence. Right panel: Effect of varying β_{ww} on Mpox disease prevalence

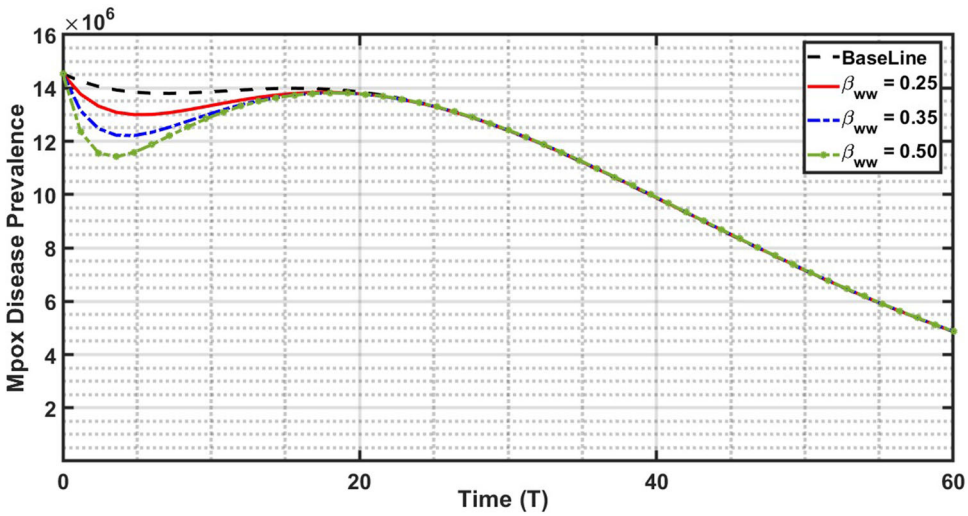

Fig. 12 Effect of varying β_{ww} on mpox disease prevalence

5 Conclusion

Mpox is a developing zoonotic disease caused by an orthopoxvirus which is related to the Variola or smallpox virus, in terms of both genetic and physical characteristics [54]. Although, the smallpox disease was declared extinct in the 1980 s, the former is still in circulation, having become endemic in several African nations since 1970 s [55]. It has also been occasionally seen outside of Africa, in places including the Germany, Israel, Singapore, the United Kingdom, and the United States of America.

There has been an mpox outbreak that began at the end of April 2022. This outbreak differs from the previous ones in terms of its epidemiological and clinical characteristics. The community of men who have sex with men (MSM) is disproportionately affected by sexual transmission, which has been proposed as the main mode of transmission for the current pandemic. A comprehensive, multi-national study revealed that 95% of 528 cases of mpox infections were thought to have been transmitted through sexual activities [7].

Semen samples taken from patients who had seminal viral shedding during the early stages of infection have also been shown to contain the mpox virus [56]. Other routes of transmission, however, have also been documented. These include social and household contact, occupational exposures, travel to endemic areas, and contact with infected animals.

This study examined the spread of mpox disease in the United States using some data analysis and mathematical modeling techniques. A two-group compartmental model made up of a system of nonlinear ordinary differential equations incorporating four different sexual transmission routes was developed. The two groups are the men and women populations. The basic reproduction

number was determined using the next generation matrix approach. Data analysis techniques were used to disaggregate the data used into men and women populations.

The Bayesian inference framework and the RStan package [34] in R version 4.3.1 [35] were used to obtain the posterior mean. With the use of this probabilistic framework, we were able to estimate the model parameters while accounting for our prior knowledge, and we were able to assess probabilistic claims made about the data in the context of the model. Given the model parameters, data generation is involved in the sampling distribution, also known as likelihood. Using the data we have, we were able to estimate reasonable parameter values using the posterior distribution. The proposed model was able to accurately predict the mpox spread in the United States in both the men and women populations.

This study's strength spans a wide range, from a strong fit of model and data to credible estimated parameter values. Data analysis technique was used to disaggregate the data into both men and women population. The basic reproduction number of the mpox disease in the USA for the period under consideration was estimated to be 2.72 (95% CrI: 2.45−2.98) using the Bayesian inference method. This basic reproduction number is seemingly high, probably due to the use of a 7-day rolling average data of mpox reported cases for about 62 days before the implementation of control interventions. Control interventions do not only reduce the basic reproduction number; they also help in eradicating diseases. The highest parameter value is the MSM transmission rate β_{mm} which was estimated to be 0.34 (95% CrI: 0.33−0.36).

The sensitivity analysis shows that the most sensitive parameter on the basic reproduction number is the MSM transmission rate, and efforts must be made to put this in check. Furthermore, the contour plots for scenario analyses show that the MSM transmission rate has greater effect on the basic reproduction number and on the overall disease dynamics. In all, condom usage with high compliance rate was found to be effective in controlling the spread of the disease.

This study is not without limitations. Although we included the primary population currently afflicted by mpox in the USA (the MSM population), we excluded other populations such as travelers, children and healthcare personnel. Also, the model does not capture the age-structure of the population as well as demography. Lastly, future models should account for vaccination in addition to other control measures.

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Data Availability The data are publicly available on *Our World in Data* website [30].

Declarations

Conflict of interest The authors declare that there is no competing interest.

Appendix: Diagnostic plots for the fitting

See Figs. 13, 14, 15 and 16.

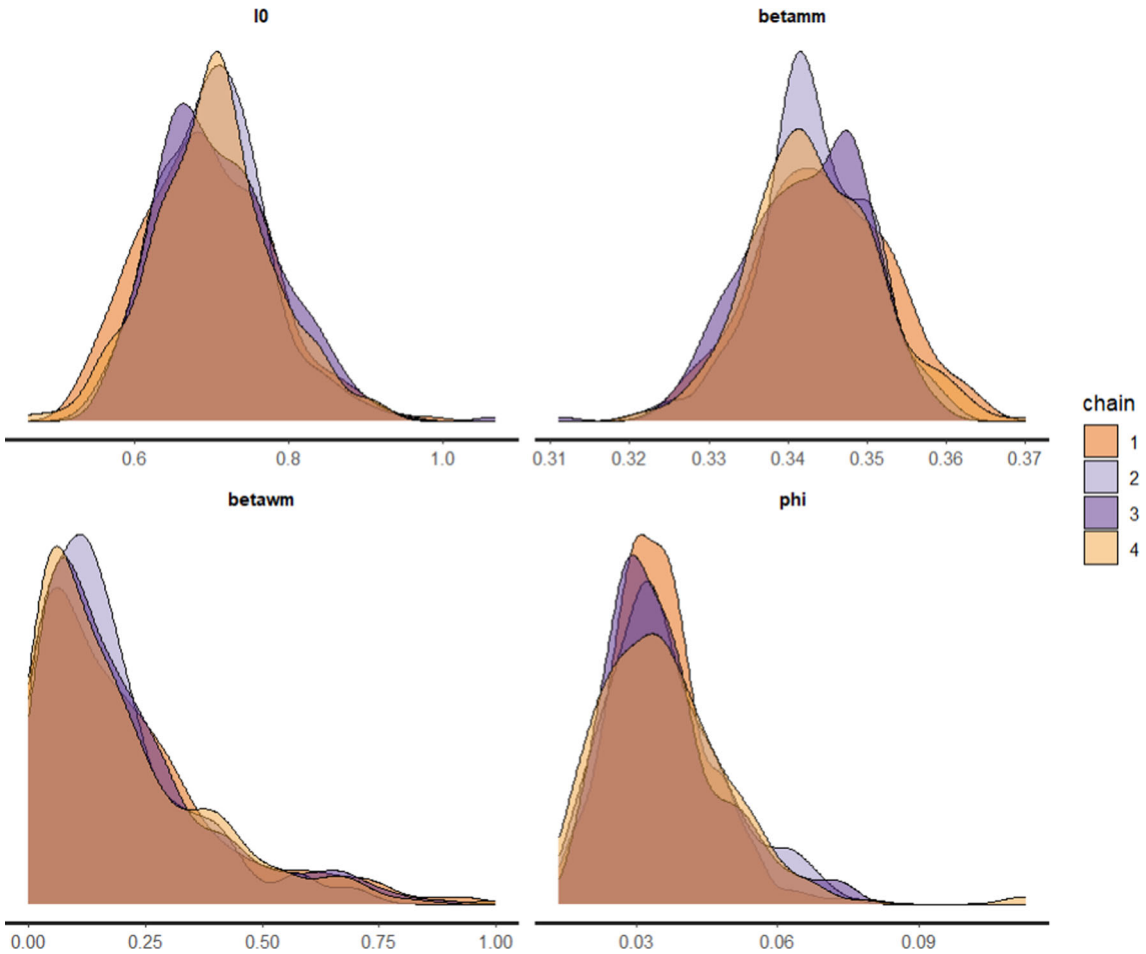

Fig. 13 Density plot of the male population fit

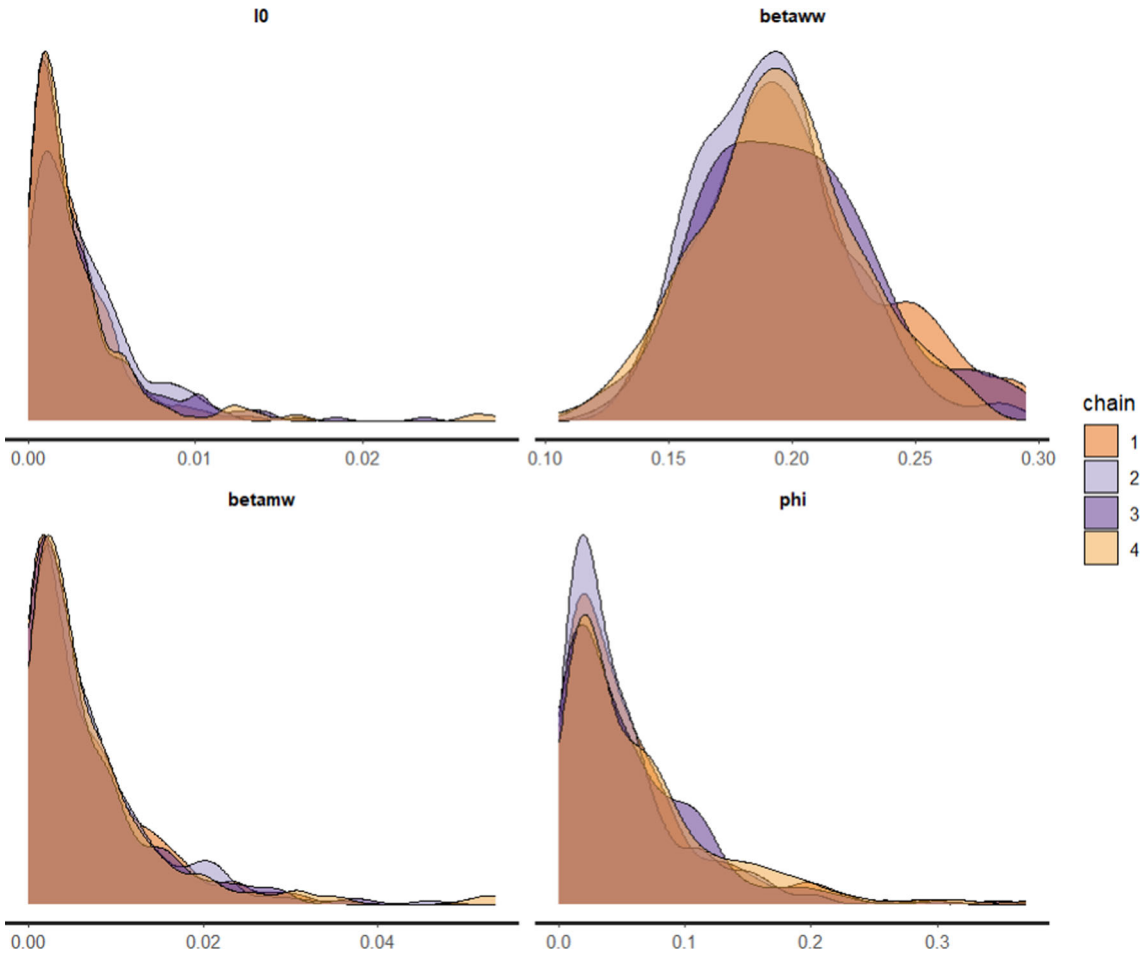

Fig. 14 Density plot of the female population fit

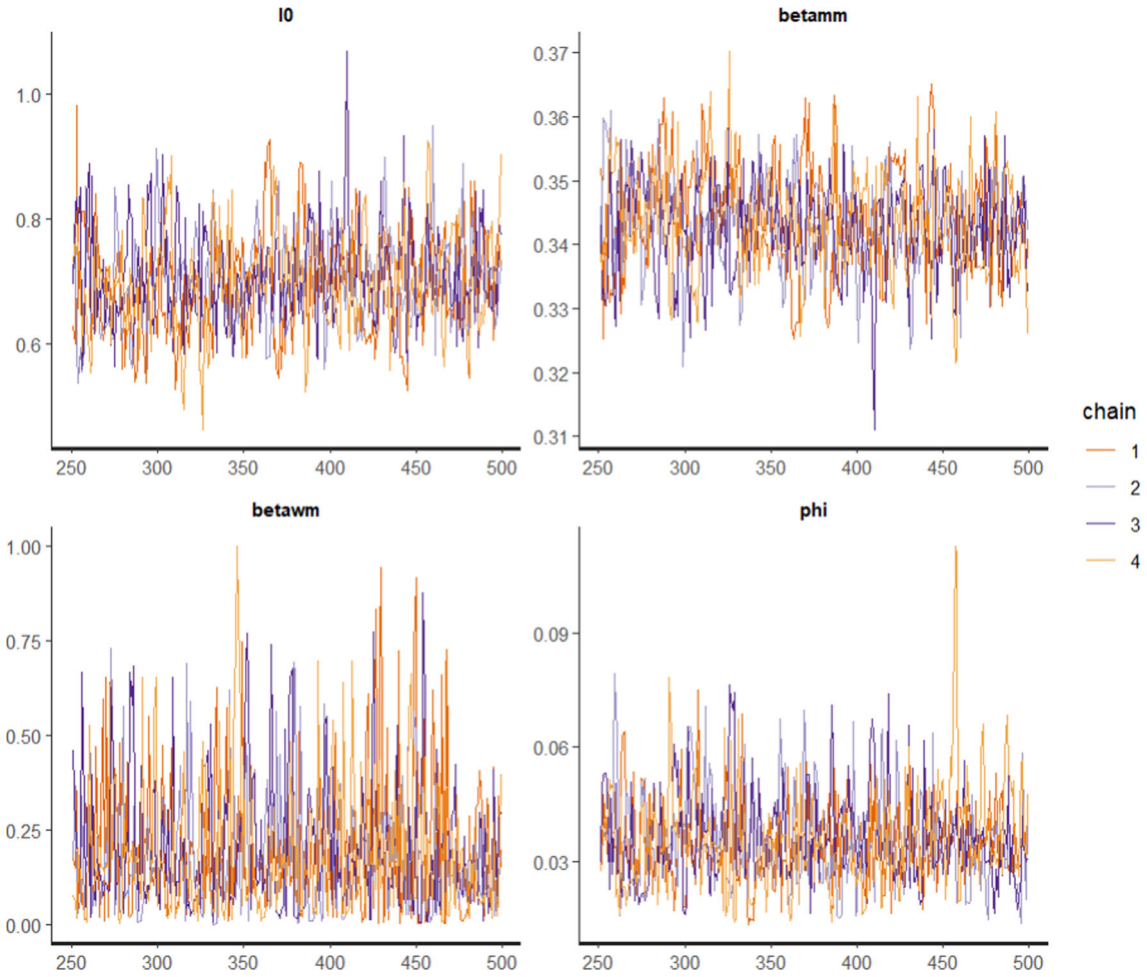

Fig. 15 Trace plot of the male population fit

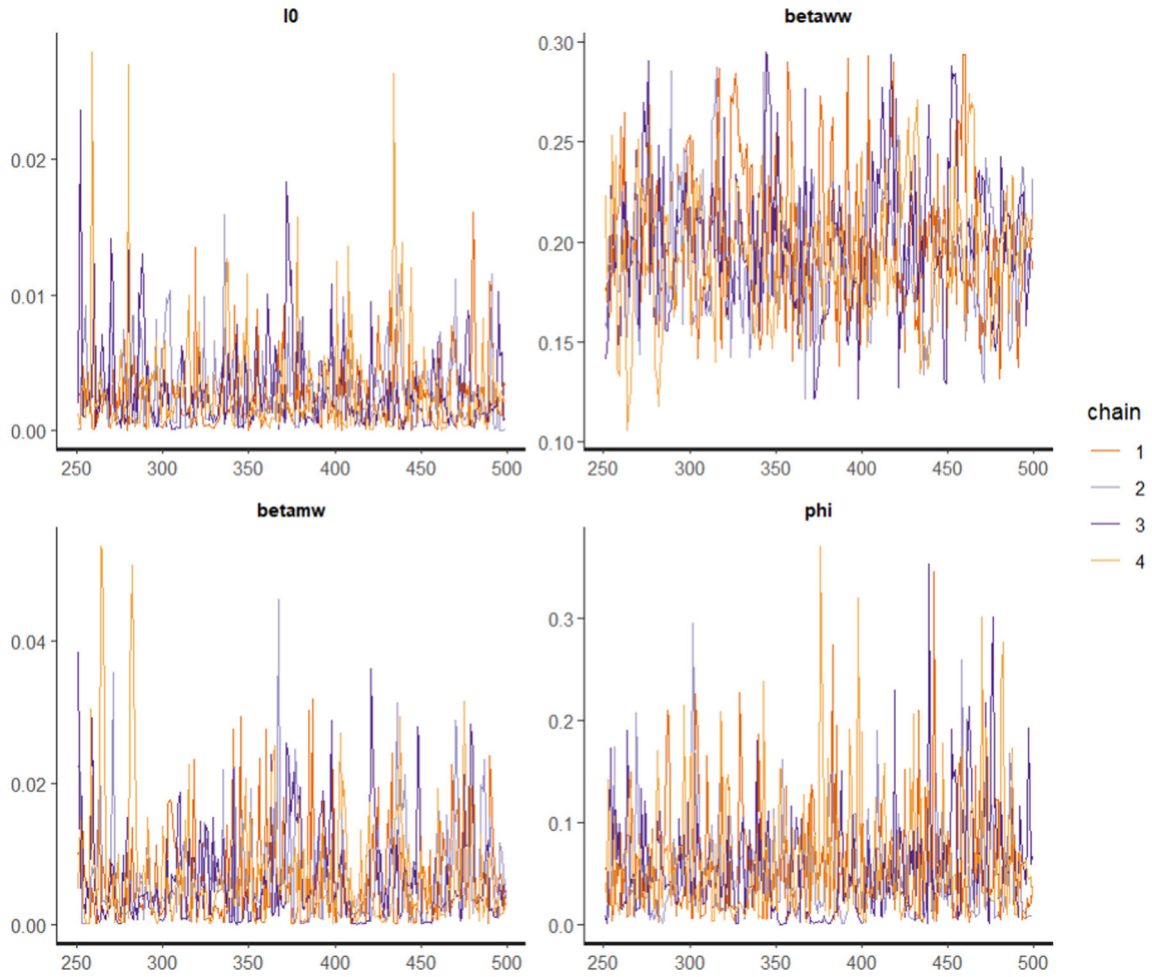

Fig. 16 Trace plot of the female population fit

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