## Introduction

This is a summary of analysis in relation to the potential outcome of an Mpox outbreak among the population of men who have sex with men (MSM) population of Victoria. Victoria has an estimated MSM population of 36,000.

Mpox spreads with prolonged skin contact, so Victoria’s MSM population is at-risk during an Mpox outbreak.

This analysis looks at two scenarios: fast and slow Mpox, and the assumptions of each are below:

|  |  |  |
| --- | --- | --- |
|  | Fast | Slow |
| (expected new infections per infection, at start of outbreak) | 2.4 | 1.1 |
| infectious period, days) | 14 | 28 |
| (incubation period, days) | 1 | 7 |

Additionally, these assumptions were used:

* There are no information campaigns
* No one is vaccinated
* No change in sexual behaviour due to Mpox
* Population is closed (no natural mortality)
* No mortality due to the disease
* Infected become recovered, always

## Findings

We expect these results, calculated directly based on the assumptions:

|  |  |  |
| --- | --- | --- |
|  | Fast | Slow |
| (growth rate) | 0.12499 | 0.00457 |
| doubling time, days) | 5.55 | 151.67 |

Given the assumptions, the SEIR model is appropriate for use. The population of MSM will have these compartments that affect each other:

Susceptible -> Exposed -> Infectious -> Recovered.

A simulation of this scenario, using the assumptions, finds these expected outcomes:

|  |  |  |
| --- | --- | --- |
|  | Fast | Slow |
| Peak infectious population (on a single day) | 7337 | 124 |
| Peak infectious day (after outbreak) | 125 | 2288 |
| Eventual population who are infected (%) | 87.9% | 17.6% |

A graph of a number of different colored lines

Description automatically generatedA graph of a graph showing the results of a model

Description automatically generated with medium confidence

## Code used in simulation

# SEIR Epidemic in a Closed Population

library(deSolve)

SEIRmodel <- function(time, state, parameters) {

with(as.list(c(state, parameters)), {

dS <- -beta\*(S\*I)/N

dE <- beta\*(S\*I)/N -sigma\*E

dI <- sigma\*E -gamma\*I

dR <- gamma\*I

return(list(c(dS, dE, dI, dR)))

})

}

diseaseFreePopulation = 36000

infectedAtStart = 1

init <- c(S=diseaseFreePopulation, E=0, I=infectedAtStart, R=0)

times <- seq(1,365,0.1)

#### FAST MPOX

SEIRpars\_fastMpox <- c(beta=2.4/14,

sigma=1,

gamma=1/14,

N=diseaseFreePopulation-infectedAtStart)

out\_fastMpox <- ode(y=init, times=times, func=SEIRmodel, parms=SEIRpars\_fastMpox, method="ode45")

out\_fastMpox <- as.data.frame(out\_fastMpox)

print(c("Total recovered population of fast mpox:", tail(out\_fastMpox$R, n=1)))

maxInfection = max(out\_fastMpox$I)

indexOfMaxInfection = match(maxInfection, out\_fastMpox$I)

print(c("Max infectious on a single day:", maxInfection))

print(c("Day of peak infectious:", times[indexOfMaxInfection]))

plot(out\_fastMpox$time, out\_fastMpox$S, ylim = c(0, 36000), type='l', lty=1, col="red", lwd=2, xlab="Day of epidemic",

ylab="", main="SEIR model - fast mpox")

lines(out\_fastMpox$time, out\_fastMpox$E, type='l', lty=2, col="blue", lwd=2, xlab="Day of epidemic",

ylab="")

lines(out\_fastMpox$time, out\_fastMpox$I, type='l', lty=3, col="green", lwd=2, xlab="Day of epidemic",

ylab="")

lines(out\_fastMpox$time, out\_fastMpox$R, type='l', lty=4, col="black", lwd=2, xlab="Day of epidemic",

ylab="")

legend(190, 22000, legend=c("Susceptible", "Exposed", "Infectious", "Recovered"),

col=c("red", "blue", "green", "black"), lty=1:4, cex=1.2)

#### SLOW MPOX

diseaseFreePopulation = 36000

infectedAtStart = 1

init <- c(S=diseaseFreePopulation, E=0, I=infectedAtStart, R=0)

times <- seq(1,6000,0.1)

SEIRpars\_slowMpox <- c(beta=1.1/28,

sigma=1/7,

gamma=1/28,

N=diseaseFreePopulation-infectedAtStart)

out\_slowMpox <- ode(y=init, times=times, func=SEIRmodel, parms=SEIRpars\_slowMpox, method="ode45")

out\_slowMpox <- as.data.frame(out\_slowMpox)

print(c("Total recovered population slow mpox:", tail(out\_slowMpox$R, n=1)))

maxInfection = max(out\_slowMpox$I)

indexOfMaxInfection = match(maxInfection, out\_slowMpox$I)

print(c("Max infectous on a single day:", maxInfection))

print(c("Day of peak infectious:", times[indexOfMaxInfection]))

plot(out\_slowMpox$time, out\_slowMpox$S, ylim = c(0, 36000), type='l', lty=1, col="red", lwd=2, xlab="Day of epidemic",

ylab="", main="SEIR model - slow mpox")

lines(out\_slowMpox$time, out\_slowMpox$E, type='l', lty=2, col="blue", lwd=2, xlab="Day of epidemic",

ylab="")

lines(out\_slowMpox$time, out\_slowMpox$I, type='l', lty=3, col="green", lwd=2, xlab="Day of epidemic",

ylab="")

lines(out\_slowMpox$time, out\_slowMpox$R, type='l', lty=4, col="black", lwd=2, xlab="Day of epidemic",

ylab="")

legend(190, 22000, legend=c("Susceptible", "Exposed", "Infectious", "Recovered"),

col=c("red", "blue", "green", "black"), lty=1:4, cex=1.2)