

CEACOV RSA - Analyze Noise

August 17, 2020

```
[33]: library(ggplot2)
library(latex2exp)
library(reshape2)

[2]: # This function combines the two output files generated by CEACOV into a single
      →dataframe

read_ceacov_output<- function(f1,f2,h1,h2){

  df1 <- read.table(f1,sep="\t",header=FALSE)
  df1names <- read.csv(h1)
  colnames(df1) <- colnames(df1names)
  df2 <- read.table(f2,sep="\t",header=FALSE)
  df2names <- read.csv(h2)
  colnames(df2) <- colnames(df2names)
  df <- cbind(df1,df2)
  return(df)
}

[3]: # Column headings associated with output from model version v0.6_9_intvs
h1 <- "v6_9_intvs_headings.csv"
h2 <- "v6_9_intvs_state_data_headings.csv"

[4]: KZN_pop <- 11531628
sim_size <- 1e5

# Read in output files from user-specified batch of runs
mypath <- getwd()
batchname <- "R36 8.16.20"

myfolders <- c(paste(rep("CT+IC+QC"),seq(1,10),sep="_"),
               paste(rep("CT+IC+QC+MSS"),seq(1,10),sep="_"))

fnames <- c(rep("CT+IC+QC",10),rep("CT+IC+QC+MSS",10))
out1 <- paste(fnames, ".tsv", sep="")
out2 <- paste(fnames, "_state_data.tsv", sep="")
f1 <- paste(mypath,batchname,myfolders,out1,sep="/")
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f2 <- paste(mypath,batchname,myfolders,out2,sep="/")

strategy <- c(rep("HT+CT+IC+QC",10),rep("HT+CT+IC+QC+MSS",10))

deaths <- numeric(length(f1))
infections <- numeric(length(f1))
nday = 730

AI <- matrix(nrow=20,ncol=nday)
AD <- matrix(nrow=20,ncol=nday)

for (i in seq(1,length(f1))){
  df <- read_ceacov_output(f1[i],f2[i],h1,h2)
  deaths[i] <- df$dead[nday]
  infections[i] <- df$cumulative.infections[nday]
  AI[i,] <- df$cumulative.infections
  AD[i,] <- df$dead
}

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[]:

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[5]: myscale <- function(x){
  n <- length(x)
  mylabel <- numeric(n)
  for (i in seq(1,n)){
    if(is.na(x[i])){
      mylabel[i] <- NA
    } else if (x[i] < 1e3){
      mylabel[i] <- sprintf("%.0f",x[i])
    } else if (x[i] < 1e6){
      mylabel[i] <- sprintf("%.0fk",x[i]/1e3)
    } else{
      mylabel[i] <- sprintf("%.0fM",x[i]/1e6)
    }
  }
  return(mylabel)
}

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[6]: coeff_variation <- function(x){
  sdx <- apply(x,2,sd)
  mx <- apply(x,2,mean)
  cvx <- sdx/mx
  return(cvx)
}

cv_i5 <- coeff_variation(AI[1:10,])
cv_i6 <- coeff_variation(AI[11:20,])

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cv_d5 <- coeff_variation(AD[1:10,])
cv_d6 <- coeff_variation(AD[11:20,])

cv_day <- c(seq(1,nday),seq(1,nday))
cv_strat <- c(rep("HT+CT+IC+QC",nday),rep("HT+CT+IC+QC+MSS",nday))
cv_i <- c(cv_i5,cv_i6)
cv_d <- c(cv_d5,cv_d6)

dfcv <- data.frame(day=cv_day,cv_i=cv_i,cv_d=cv_d,strat=cv_strat)

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[54]: make_df <- function(A){
  rownames(A) <- paste(c(rep("Strategy 5 run ",10),
    rep("Strategy 6 run ",10)),c(seq(1:10),seq(1:
    ↪10)),sep="")
  df <- melt(A)
  df$strategy <- character(length(df$Var1))
  df$strategy[grepl("Strategy 5",df$Var1)] <- "HT+CT+IC+QC"
  df$strategy[grepl("Strategy 6",df$Var1)] <- "HT+CT+IC+QC+MSS"
  colnames(df) <- c("run","day","value","strategy")
  return(df)
}

#dfii <- make_df(AI)
#dfdd <- make_df(AD)

```

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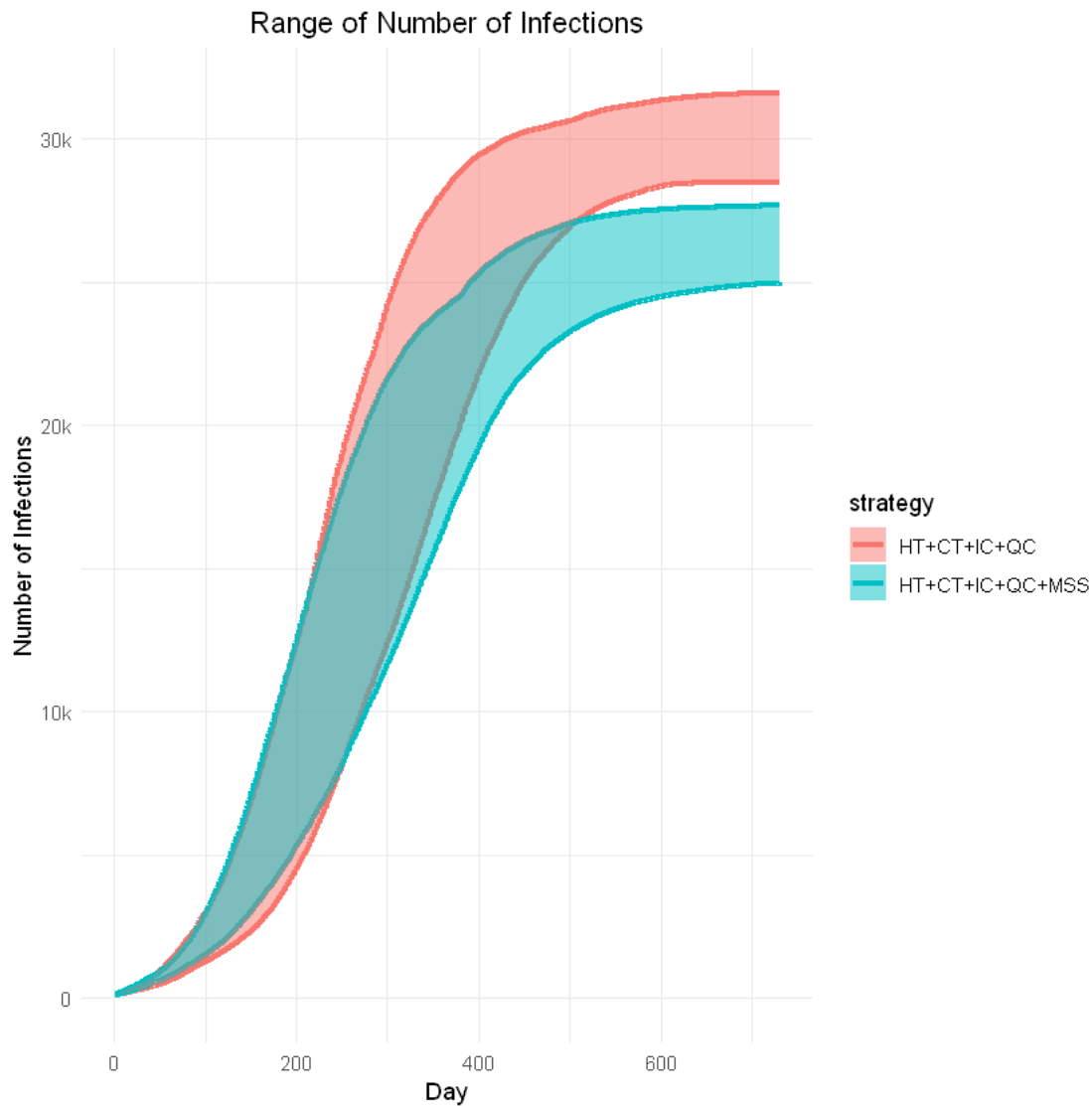
[58]: i5_max <- apply(AI[1:10,],2,max)
i5_min <- apply(AI[1:10,],2,min)
i6_max <- apply(AI[11:20,],2,max)
i6_min <- apply(AI[11:20,],2,min)
d5_max <- apply(AD[1:10,],2,max)
d5_min <- apply(AD[1:10,],2,min)
d6_max <- apply(AD[11:20,],2,max)
d6_min <- apply(AD[11:20,],2,min)

i_min <- c(i5_min,i6_min)
i_max <- c(i5_max,i6_max)
d_min <- c(d5_min,d6_min)
d_max <- c(d5_max,d6_max)

dfr <- data.frame(day <- cv_day,
  strategy = cv_strat,
  i_min = i_min,
  i_max = i_max,
  d_min = d_min,
  d_max = d_max)

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[72]: p5 <- ggplot(dfr,aes(x=day))+
  geom_step(aes(y=i_min,color=strategy),size=1.25)+
  geom_step(aes(y=i_max,color=strategy),size=1.25)+
  geom_ribbon(aes(ymin=i_min,ymax=i_max,fill=strategy),alpha=0.5)+
  labs(x="Day",y="Number of Infections",title="Range of Number of Infections")+
  scale_y_continuous(labels=myscale,limits=c(0,NA))+
  theme_minimal()+
  theme(plot.title = element_text(hjust = 0.5))
p5
ggsave("r_i_100k.png",p5,height=4,width=6,dpi=400)
```

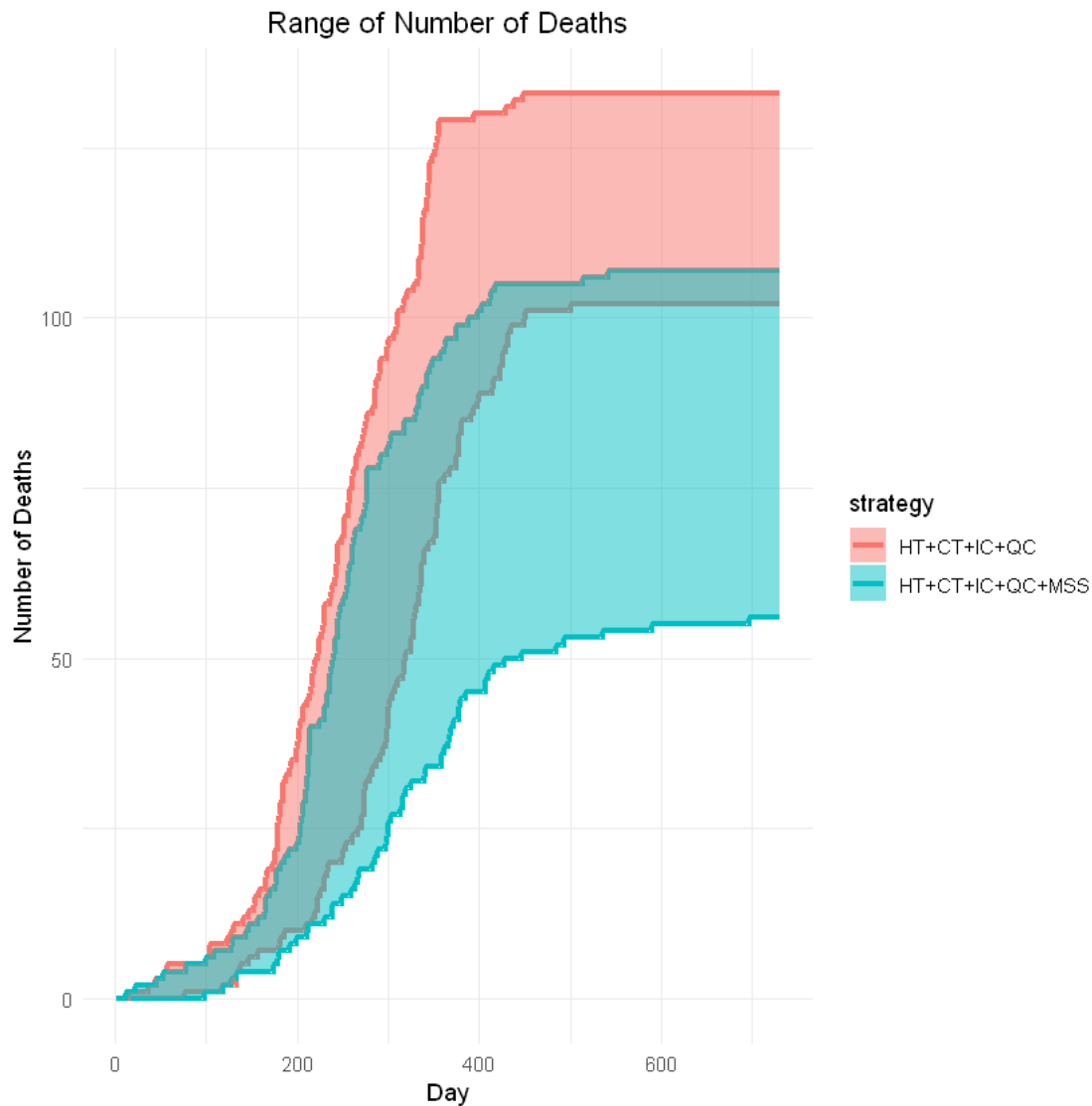


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[71]: p6 <- ggplot(dfr,aes(x=day))+
  geom_step(aes(y=d_min,color=strategy),size=1.25)+
```

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geom_step(aes(y=d_max,color=strategy),size=1.25)+
geom_ribbon(aes(ymin=d_min,ymax=d_max,fill=strategy),alpha=0.5)+
labs(x="Day",y="Number of Deaths",title="Range of Number of Deaths")+
scale_y_continuous(labels=myscale,limits=c(0,NA))+
theme_minimal()+
theme(plot.title = element_text(hjust = 0.5))
p6
ggsave("r_d_100k.png",p6,height=4,width=6,dpi=400)

```



```

[31]: p3 <- ggplot(dfcv,aes(x=day,y=cv_i,color=strat))+
geom_step(size=1.25)+
labs(x="Day",
y=TeX("$\\frac{\\sigma}{\\mu}$"),

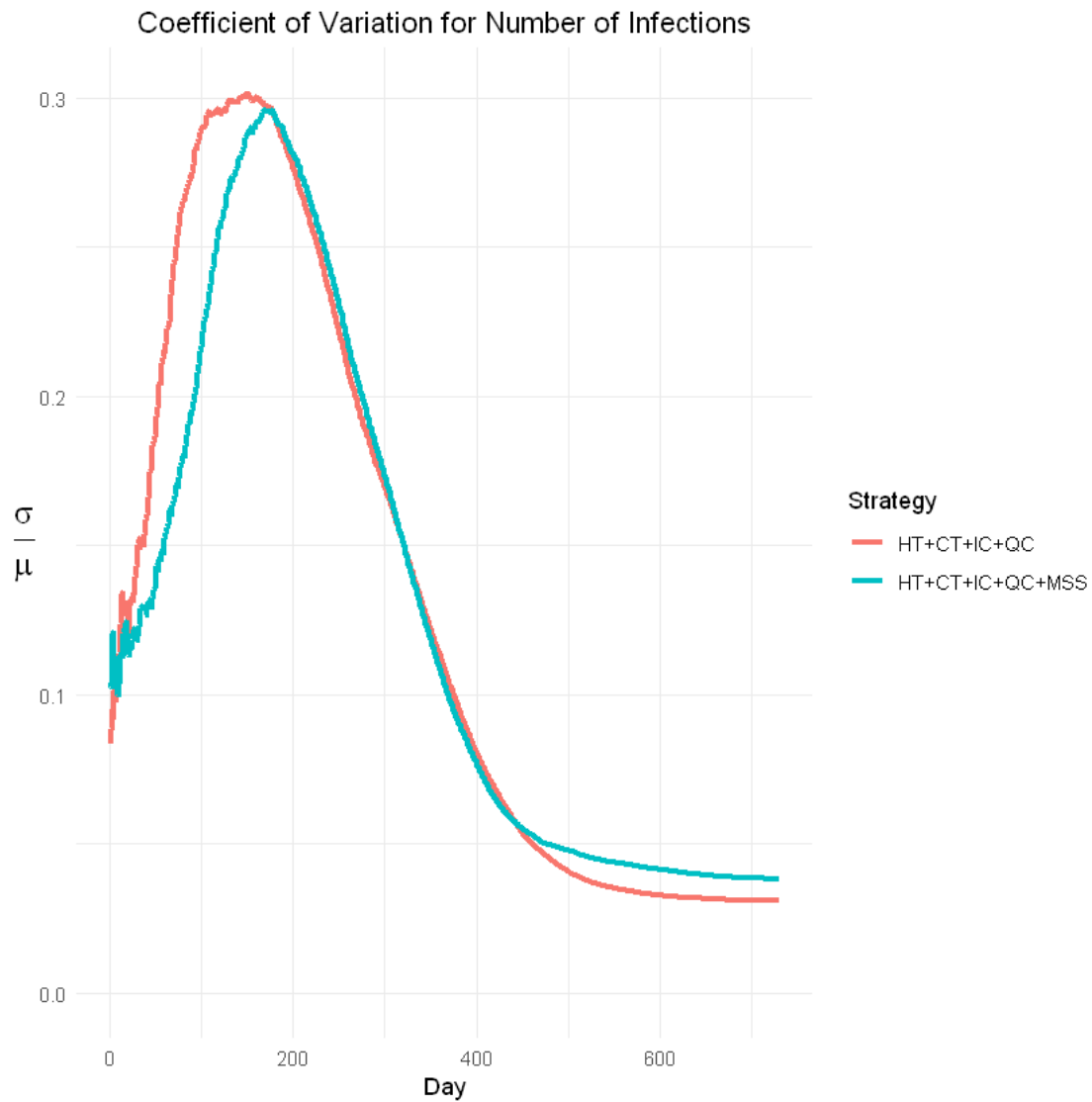
```

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    title="Coefficient of Variation for Number of Infections",
    color="Strategy")+
scale_y_continuous(limits=c(0,NA))+
theme_minimal()+
theme(plot.title = element_text(hjust = 0.5))+
theme(axis.title.y = element_text(angle = 0,vjust=0.5,size = 15))
p3

#ggsave("cv_i_100k.png",p3,height=4,width=6,dpi=400)

```



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[32]: p4 <- ggplot(dfcv,aes(x=day,y=cv_d,color=strat))+
geom_step(size=1.25)+
labs(x="Day",

```

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y=TeX("$\\frac{\\sigma}{\\mu}$"),
title="Coefficient of Variation for Number of Deaths",
color="Strategy")+
scale_y_continuous(limits=c(0,1.0))+
theme_minimal()+
theme(plot.title = element_text(hjust = 0.5))+
theme(axis.title.y = element_text(angle = 0,vjust=0.5,size = 15))
p4

#ggsave("cv_d_100k.png",p4,height=4,width=6,dpi=400)

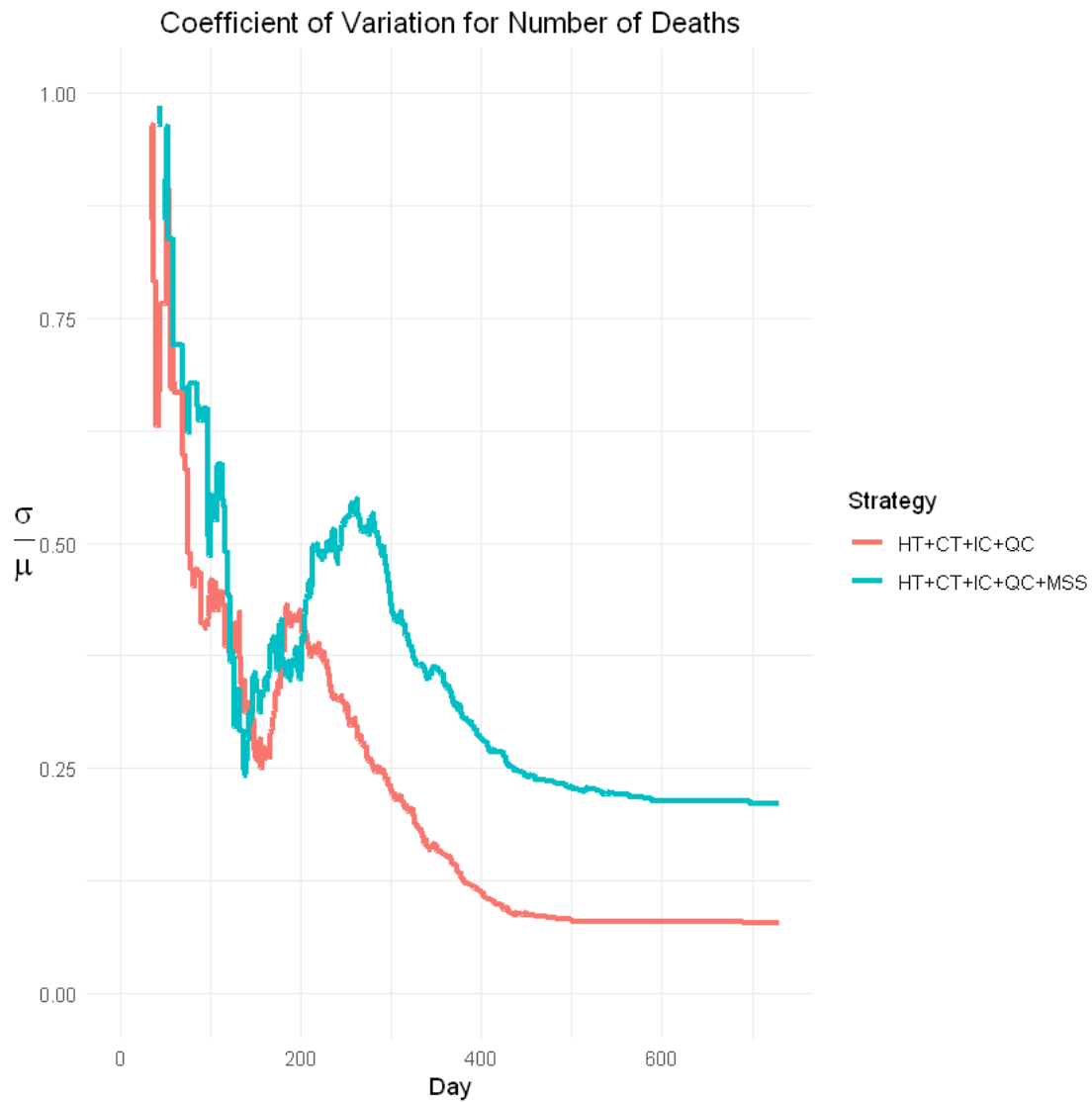
```

Warning message:

"Removed 73 rows containing missing values (geom_path)."

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"Removed 73 rows containing missing values (geom_path)."



```
[ ]:
[ ]: p1 <- ggplot(df,aes(x=strategy,y=deaths,fill=strategy))+
geom_boxplot(width=0.25,size=1.25)+
geom_jitter(width=0.1,height=0,color="purple",size=2)+
labs(x="Strategy",y="Number of Deaths",title="Distribution of Number of
↳Deaths")+
scale_y_continuous(labels=myscale,limits=c(0,NA))+
theme_minimal()+
theme(plot.title = element_text(hjust = 0.5))+
theme(legend.position = "none")
p1

[ ]: p2 <- ggplot(df,aes(x=strategy,y=infections,fill=strategy))+
geom_boxplot(width=0.25,size=1.25)+
geom_jitter(width=0.1,height=0,color="purple",size=2)+
labs(x="Strategy",y="Number of Infections",title="Distribution of Number of
↳Infections")+
scale_y_continuous(labels=myscale,limits=c(0,NA))+
theme_minimal()+
theme(plot.title = element_text(hjust = 0.5))+
theme(legend.position = "none")
p2

[ ]: hh <- 4
ww <- 6
dpi <- 400
#ggsave("dist_deaths_100k.png",p1,height=hh,width=ww,dpi=dpi)
#ggsave("dist_infections_100k.png",p2,height=hh,width=ww,dpi=dpi)
```

1 Manuscript

	Path 1	Path 2	Path 3	Path 4
Pre-infectious	2.6	2.6	2.6	2.6
Asymptomatic	9.5	2.0	2.0	2.0
Mild/Moderate	—	10.0	6.5	3.0
Severe	—	—	10.5	7.1
Critical	—	—	—	11.9
Recuperation	—	—	—	5.7

2 Model

	Path 1	Path 2	Path 3	Path 4
Pre-infectious	2.6	2.6	2.6	2.6
Asymptomatic	9.5	2.0	2.0	2.0
Mild/Moderate	—	10.0	6.5	3.0
Severe	—	—	10.5	9.0
Critical	—	—	—	20.0
Recuperation	—	—	—	5.7

3 Length of Disease State

	Presentation to care over duration of health state	Presentation to care over one day	Implied duration of health state
Susceptible	0 %	0 %	—
Pre-infectious	10 %	3.34 %	3.1 days
Asymptomatic	10 %	2.44 %	4.26 days
Mild/Moderate	40 %	4.79 %	10.4 days
Severe	100 %	100 %	—
Critical	100 %	100 %	—
Recuperation	0 %	100 %	—

[]: