

Virus Dynamics in R

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Preface

This represents an attempt to write reproduce the code from “Virus Dynamics: Mathematical Principles of Immunology and Virology” by Nowak and May.

No guarantees that anything in this is correct, but just an attempt to reproduce what is in the book.

This book is written in Rmarkdown and rendered using the phenomenal Quarto engine.

To learn more about Quarto books visit <https://quarto.org/docs/books>.

1 Introduction

This is a book created from markdown and executable code.

2 The Basic Model of Virus Dynamics

```
library(deSolve)
library(tidyverse)
```

```
-- Attaching packages ----- tidyverse 1.3.1 --
```

```
v ggplot2 3.3.5.9000      v purrr  0.3.4.9000
v tibble  3.1.5.9000      v dplyr   1.0.7.9000
v tidyr   1.1.4.9000      v stringr 1.4.0.9000
v readr   1.4.0           v forcats 0.5.1
```

```
-- Conflicts ----- tidyverse_conflicts() --
```

```
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
```

Set Up the ODE

```
base_ode <- function(time, state, parameters){
  with(as.list(c(state, parameters)),{

    dx <- lambda - d*x - beta * x * v
    dy <- beta * x * v - a * y
    dv <- k * y - u * v

    return(list(c(dx,dy,dv)))
  })
}

t <- seq(0,30,.1)

params <- c(
  lambda = 1e5, # Uninfected cell production rate
```

```

d = .1, # Cell Death Rate
a = .5, # Infected Cell Death Rate
beta = 2e-7, # "Rate Constant"
k = 100, # Virus productin from Infected cell
u = 5 # Free Virus lifestapn
)

```

Guessing Initial values from a graph

```

x0 <- params["lambda"][1]/params["d"][1]
init <- c(x = unname(x0),
          y = 1, v = 1)

out <- ode(init, t, base_ode, params)

out_df <- as_tibble(as.data.frame(out))

```

Funny side note is that the differences in the scales are almost immediately reproduced as in the book

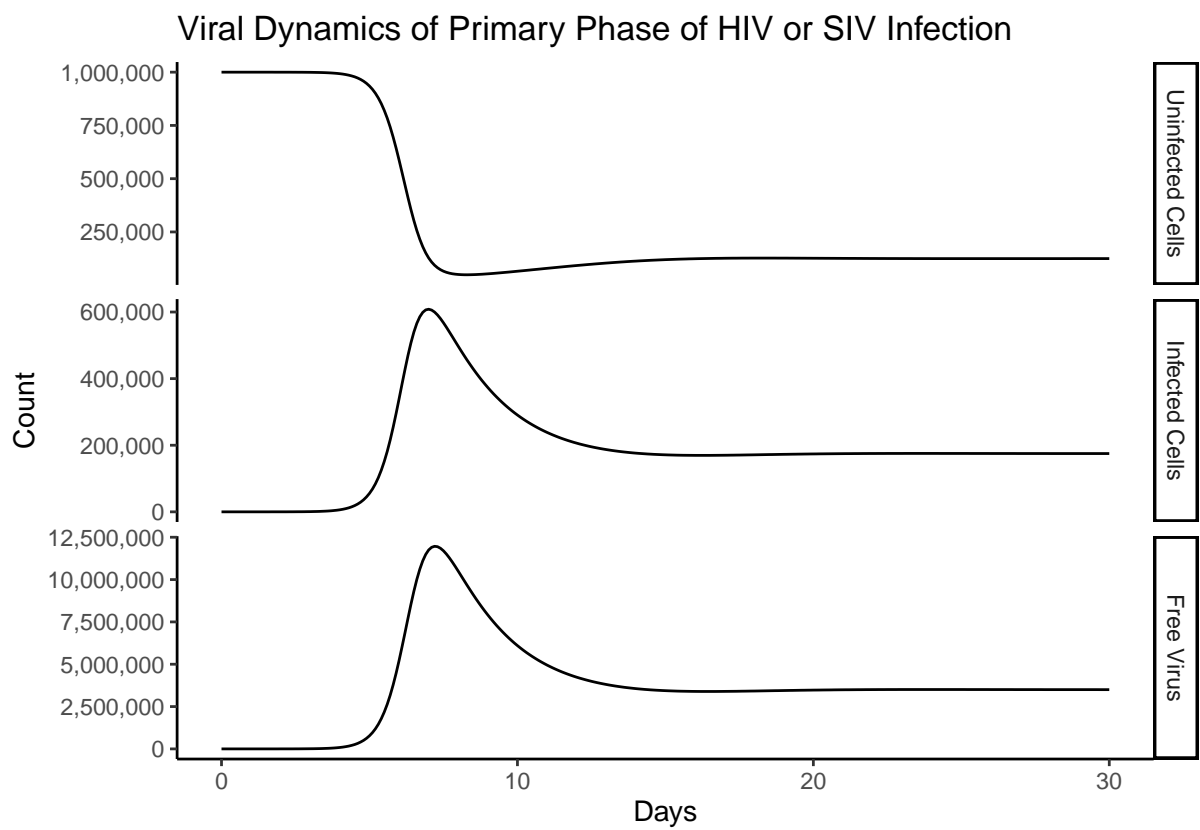
```

p <- out_df %>%
  setNames(c("time", "Uninfected Cells",
             "Infected Cells", "Free Virus")) %>%
  gather(compartment, value, -time) %>%
  mutate(compartment = factor(compartment,
                              c("Uninfected Cells",
                                "Infected Cells",
                                "Free Virus"))) %>%

  ggplot(aes(time, y = value))+
  geom_line()+
  facet_grid(rows = vars(compartment), scales = "free_y")+
  theme_classic()+
  labs(
    title = "Viral Dynamics of Primary Phase of HIV or SIV Infection",
    x = "Days",
    y = "Count"
  )+
  scale_y_continuous(labels = scales::comma_format(accuracy = 1000))

p

```



3 Anti-viral Drug Therapy

From pages 35-37.

```
library(deSolve)
library(tidyverse)
```

```
-- Attaching packages ----- tidyverse 1.3.1 --
```

```
v ggplot2 3.3.5.9000      v purrr  0.3.4.9000
v tibble  3.1.5.9000      v dplyr   1.0.7.9000
v tidyr   1.1.4.9000      v stringr 1.4.0.9000
v readr   1.4.0           v forcats 0.5.1
```

```
-- Conflicts ----- tidyverse_conflicts() --
```

```
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
```

Set Up the ODE Represents infected cells becoming: * Latently infected: do not produce new virions, but contain replication competent virus that can be re-activated to become virus producing * long-lived chronic producers: produce small amounts of virus over long periods * cells which harbor defective provirus

```
base_ode <- function(time, state, parameters){
  with(as.list(c(state, parameters)),{

    dx <- lambda - d*x - beta * x * v
    dy1 <- q1*beta * x * v - a1 * y1 + alpha * y2
    dy2 <- q2*beta * x * v - a2 * y2 - alpha * y2
    dy3 <- q3*beta * x * v - a3 * y3
    dv <- k * y1 - u * v

    return(list(c(dx, dy1, dy2, dy3, dv)))
  })
}
```



```

t <- seq(0,30,.1)

params <- c(
  lambda = 1e7, # Uninfected cell production rate
  d = .1, # Cell Death Rate
  a1 = .5, # Infected Cell Death Rate
  a2 = .01, # Infected Cell Death Rate
  a3 = .008, # Infected Cell Death Rate
  beta = 5e-10, # "Rate Constant"
  alpha = .3, # Virus Production rate of reactivated latent
  k = 500, # Virus productin from Infected cell
  u = 5, # Free Virus lifestapn
  q1 = .55, # P(Infected State | Infected)
  q2 = .05, # P(Latent State | Infected)
  q3 = .4 # P(Defective Provirus | Infected)
)

#' Guessing Initial values from a graph
x0 <- params["lambda"][1]/params["d"][1]
init <- c(x = unname(x0),
          y1 = 1, y2=0, y3=0, v = 1)

out <- ode(init, t, base_ode, params)

out_df <- as_tibble(as.data.frame(out))

```

Funny side note is that the differences in the scales are almost immediately reproduced as in the book.

```

compartment_names <- c("Uninfected Cells",
  "Actively Infected Cells",
  "Latently Infected Cells",
  "Cells Infected with Defective Virus",
  "Free Virus")

p <- out_df %>%
  setNames(c("time", compartment_names)) %>%
  gather(compartment, value, -time) %>%
  mutate(compartment = factor(compartment,
                              compartment_names)) %>%
  ggplot(aes(time, y = value))+
  geom_line()+

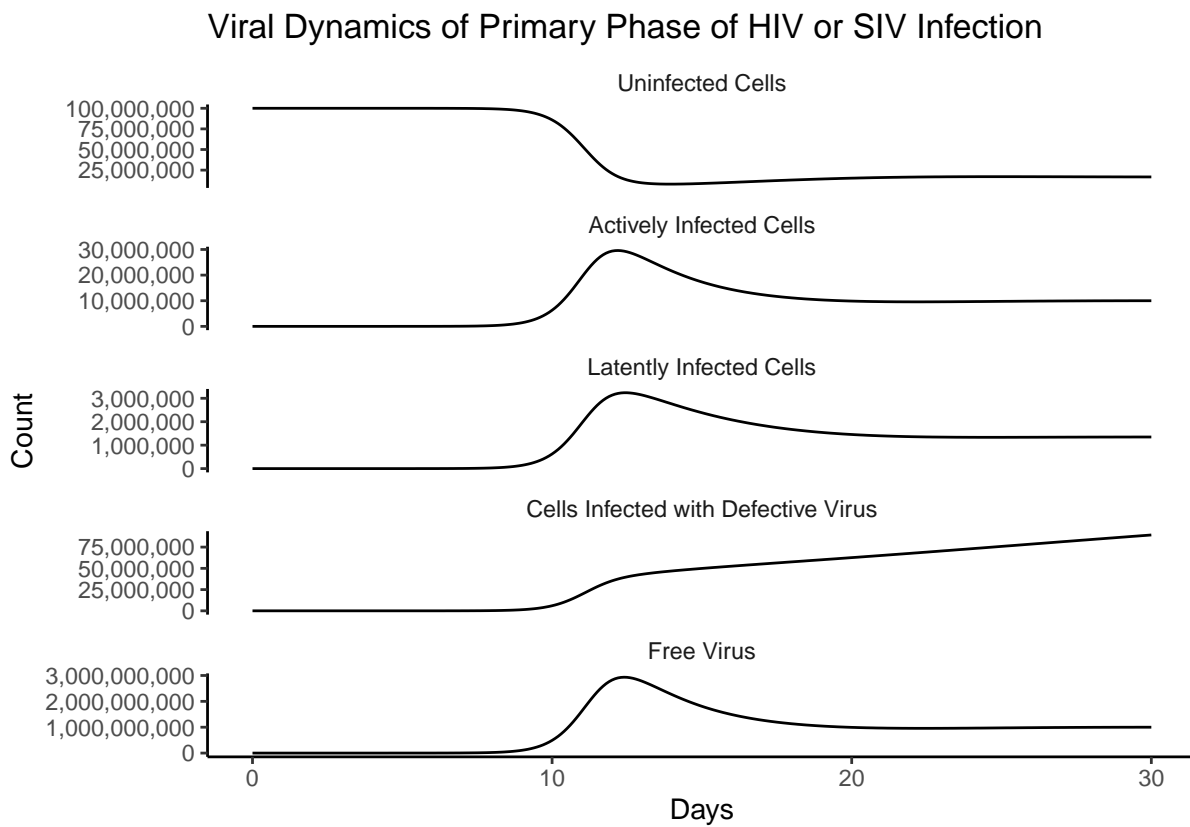
```

```

facet_wrap(~compartment, ncol = 1,scales = "free_y")+
theme_classic()+
labs(
  title = "Viral Dynamics of Primary Phase of HIV or SIV Infection",
  x = "Days",
  y = "Count"
)+
scale_y_continuous(labels = scales::comma_format(accuracy = 1000))+
theme(strip.background = element_blank())

```

p



4 Summary

In summary, this book has no content whatsoever.

References