

CS-7863: Scientific and Statistical Computing
Homework #2
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1.)

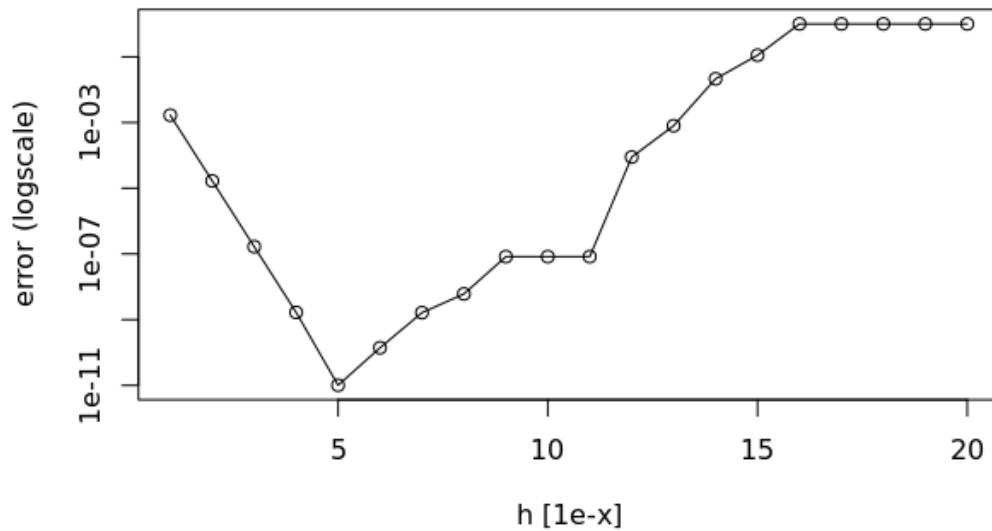
```
## 1. Approximate deriv. of sin(x) at x=pi from h=10^-1 -> 10^-20
forward.approx <- function(func, x, h){
  approx <- (func(x+h)-func(x))/h
}

forward.approx.table <- matrix(nrow = 0, ncol = 3)
colnames(forward.approx.table) <- c("h", "approximation", "error")
for(h in 10^(seq(-1,-20,-1))){
  approx <- forward.approx(sin, pi, h)
  error <- abs(cos(pi)-approx)
  forward.approx.table <- rbind(forward.approx.table, c(h, approx, error))
}
```

	h	approximation	error
[1,]	1e-01	-0.9983342	1.665834e-03
[2,]	1e-02	-0.9999833	1.666658e-05
[3,]	1e-03	-0.9999998	1.666668e-07
[4,]	1e-04	-1.0000000	1.664556e-09
[5,]	1e-05	-1.0000000	1.011558e-11
[6,]	1e-06	-1.0000000	1.396114e-10
[7,]	1e-07	-1.0000000	1.636580e-09
[8,]	1e-08	-1.0000000	6.077471e-09
[9,]	1e-09	-1.0000001	8.274037e-08
[10,]	1e-10	-1.0000001	8.274037e-08
[11,]	1e-11	-1.0000001	8.274037e-08
[12,]	1e-12	-1.0000889	8.890058e-05
[13,]	1e-13	-0.9992007	7.992778e-04
[14,]	1e-14	-1.0214052	2.140518e-02
[15,]	1e-15	-0.8881784	1.118216e-01
[16,]	1e-16	0.0000000	1.000000e+00
[17,]	1e-17	0.0000000	1.000000e+00
[18,]	1e-18	0.0000000	1.000000e+00
[19,]	1e-19	0.0000000	1.000000e+00
[20,]	1e-20	0.0000000	1.000000e+00

```
plot(abs(log(forward.approx.table[, "h"], 10)), forward.approx.table[, "error"],
     xlab="h [1e-x]", ylab="error (logscale)", type="o", log="y",
     main = "Forward Approximation of sin(x) at x=pi")
```

Forward Approximation of $\sin(x)$ at $x=\pi$

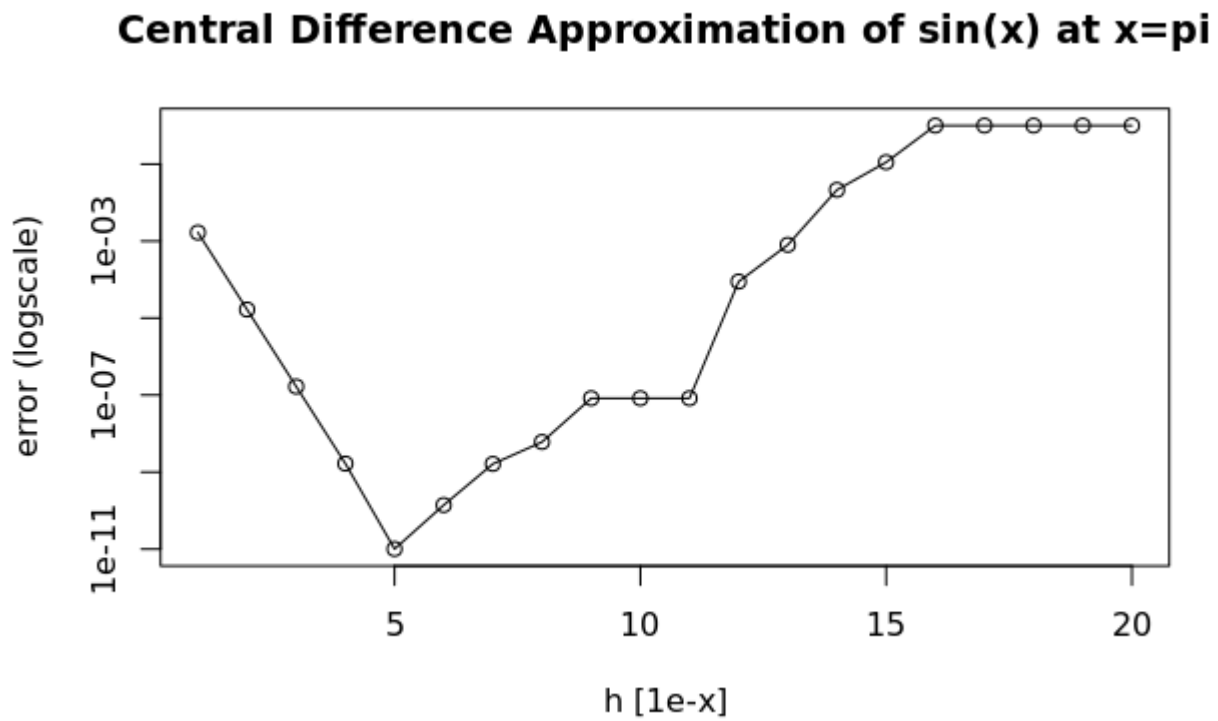


```
# Repeat with central difference approx
central.diff.approx <- function(func, x, h){
  approx <- (func(x+h)-func(x-h))/(2*h)
}
central.diff.table <- matrix(nrow = 0, ncol = 3)
colnames(central.diff.table) <- c("h", "approximation", "error")
for(h in 10^(seq(-1,-20,-1))){
  approx <- central.diff.approx(sin, pi, h)
  error <- abs(cos(pi)-approx)
  central.diff.table <- rbind(central.diff.table, c(h, approx, error))
}
```

	h	approximation	error
[1,]	1e-01	-0.9983342	1.665834e-03
[2,]	1e-02	-0.9999833	1.666658e-05
[3,]	1e-03	-0.9999998	1.666668e-07
[4,]	1e-04	-1.0000000	1.664556e-09
[5,]	1e-05	-1.0000000	1.011546e-11
[6,]	1e-06	-1.0000000	1.396114e-10
[7,]	1e-07	-1.0000000	1.636580e-09
[8,]	1e-08	-1.0000000	6.077471e-09
[9,]	1e-09	-1.0000001	8.274037e-08
[10,]	1e-10	-1.0000001	8.274037e-08
[11,]	1e-11	-1.0000001	8.274037e-08
[12,]	1e-12	-1.0000889	8.890058e-05
[13,]	1e-13	-0.9992007	7.992778e-04
[14,]	1e-14	-1.0214052	2.140518e-02
[15,]	1e-15	-0.8881784	1.118216e-01
[16,]	1e-16	0.0000000	1.000000e+00

```
[17,] 1e-17  0.0000000  1.000000e+00
[18,] 1e-18  0.0000000  1.000000e+00
[19,] 1e-19  0.0000000  1.000000e+00
[20,] 1e-20  0.0000000  1.000000e+00
```

```
plot(abs(log(central.diff.table[, "h"], 10)), central.diff.table[, "error"],
      xlab="h [1e-x]", ylab="error (logscale)", type="o", log="y",
      main = "Central Difference Approximation of sin(x) at x=pi")
```



2.)

a) 4th-order Runge-Kutta

```
my_rk4 <- function(f, y0, t0, tfinal, h){
  tspan <- seq(t0,tfinal,h)
  npts <- length(tspan)
  y<-rep(y0,npts) # initialize, this will be a matrix for systems

  for (i in seq(2,npts)){
    k1 <- f(t[i-1], y[i-1])
    k2 <- f(t[i-1] + 0.5 * h, y[i-1] + 0.5 * k1 * h)
    k3 <- f(t[i-1] + 0.5 * h, y[i-1] + 0.5 * k2 * h)
    k4 <- f(t[i-1] + h, y[i-1] + k3*h)
    # Update y
    y[i] = y[i-1] + (h/6)*(k1 + 2*k2 + 2*k3 + k4)
    # Update t
    #t0 = t0 + h
  }
  return(list(t=tspan,y=y))
}
```

b) Numerically solve the decay ode and compare to Euler and RK error

```
decay.f <- function(t,y,k){
  # define the ode model
  # k given value when solver called
  dydt <- -k*y
  as.matrix(dydt)
}

# From class docs:
my_euler <- function(f, y0, t0, tfinal, dt){
  # follow ode45 syntax, dt is extra
  # y0 is initial condition
  tspan <- seq(t0,tfinal,dt)
  npts <- length(tspan)
  y<-rep(y0,npts) # initialize, this will be a matrix for systems
  for (i in 2:npts){
    dy <- f(t[i-1],y[i-1])*dt # t is not used in this case
    y[i] <- y[i-1] + dy
  }
  return(list(t=tspan,y=y))
}

# Solve
t0 <- 0
tfinal <- 100
h <- 10
k <- 0.03
y0 <- 100

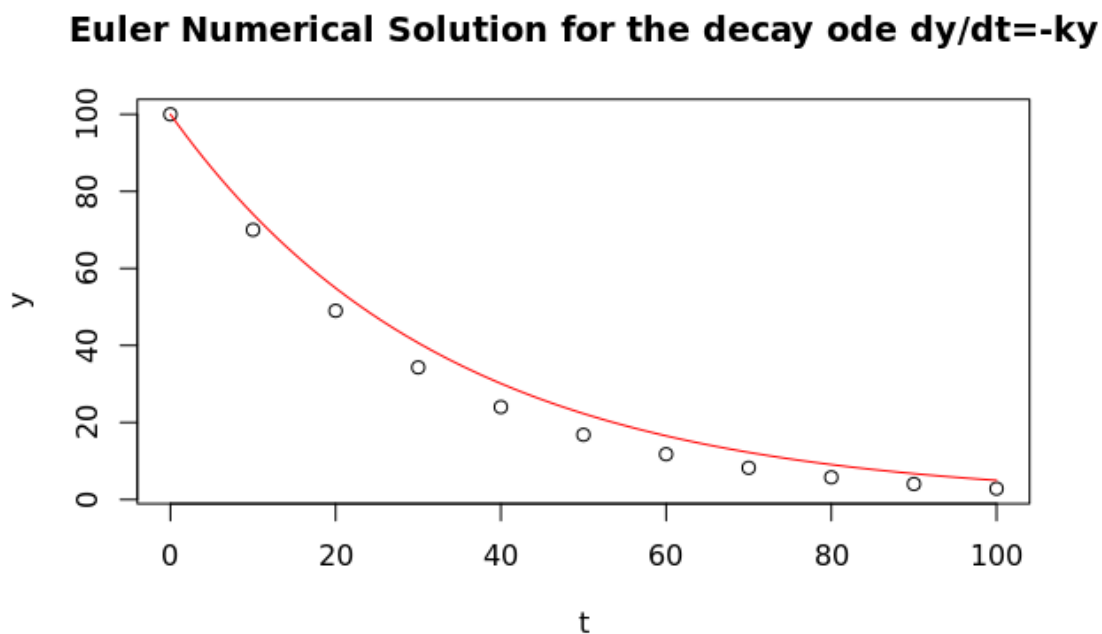
decay.euler.sol <- my_euler(f=function(t,y){decay.f(t,y,k=k)},
                           y0, t0, tfinal, dt=h)

# Exact sol
exact.y <- y0*exp(-k*seq(t0,tfinal,len=100))
exact.y.slice <- exact.y[seq(1,length(exact.y),h)]
# Add in extra point to make lengths even to euler sol
exact.y.slice <- append(exact.y.slice,exact.y[length(exact.y)])
```

```

plot(decay.euler.sol$t,decay.euler.sol$y, xlab="t", ylab="y",
     main="Euler Numerical Solution for the decay ode dy/dt=-ky")
par(new=T)
lines(seq(t0,tfinal,len=100),
      exact.y, col="red")

```



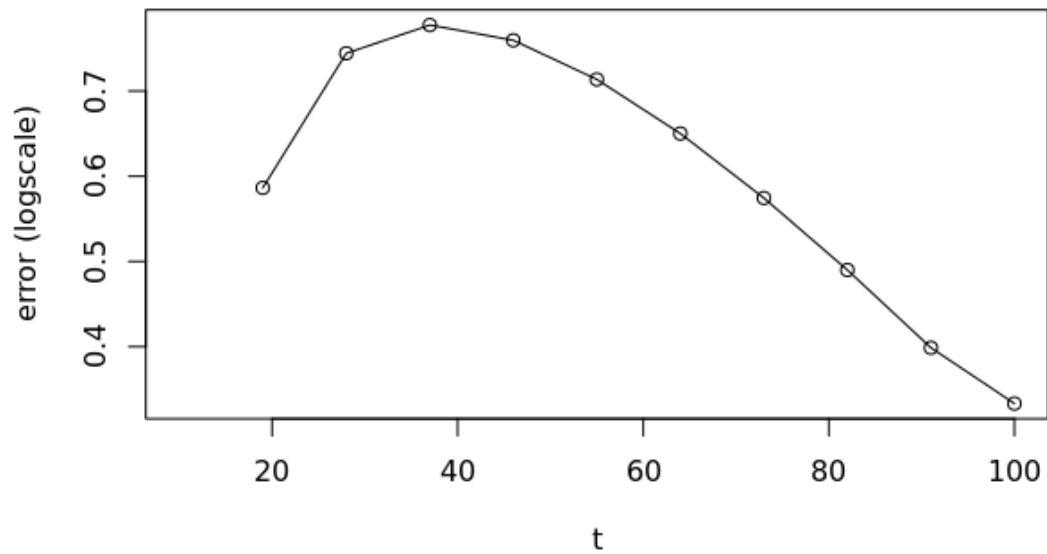
```

# Error
euler.err <- abs(decay.euler.sol$y - exact.y.slice)
euler.log.err <- log(euler.err, 10)
# Unsophisticated way to account for the -Inf error in the logscale
euler.log.err[which(!is.finite(euler.log.err))] <- NA

plot(seq(t0+h,tfinal,len=11), euler.log.err,
     xlab="t", ylab="error (logscale)", type="o",
     main = "Error from Euler Solution vs Exact")

```

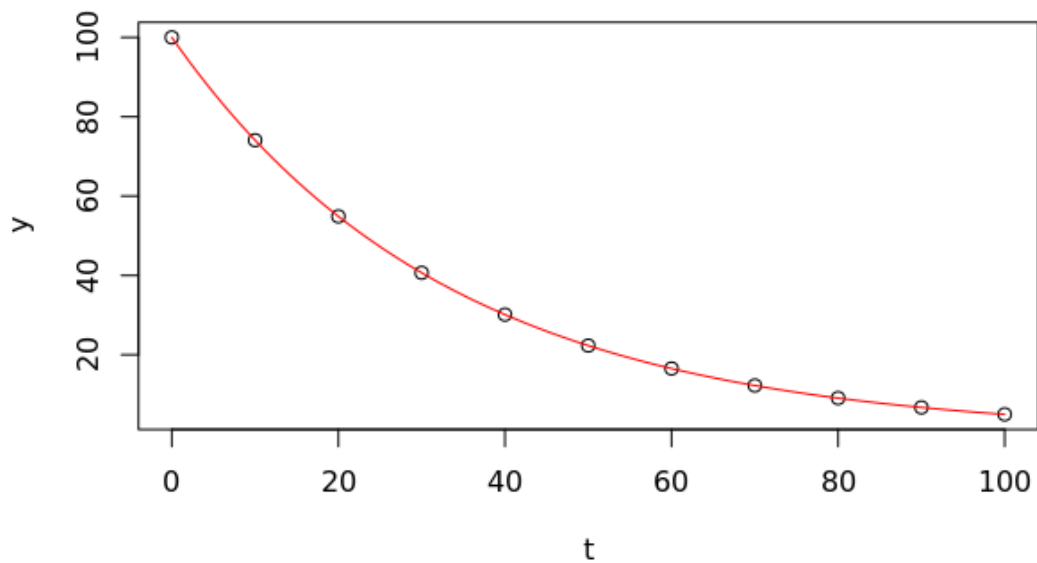
Error from Euler Solution vs Exact



Repeat with RK4

```
decay.rk4.sol <- my_rk4(f=function(t,y){decay.f(t,y,k=k)},  
                        y0, t0, tfinal, h)  
plot(decay.rk4.sol$t,decay.rk4.sol$y, xlab="t", ylab="y",  
      main="RK4 Numerical Solution for the decay ode dy/dt=-ky")  
par(new=T)  
lines(seq(t0,tfinal,len=100),  
      exact.y, col="red")
```

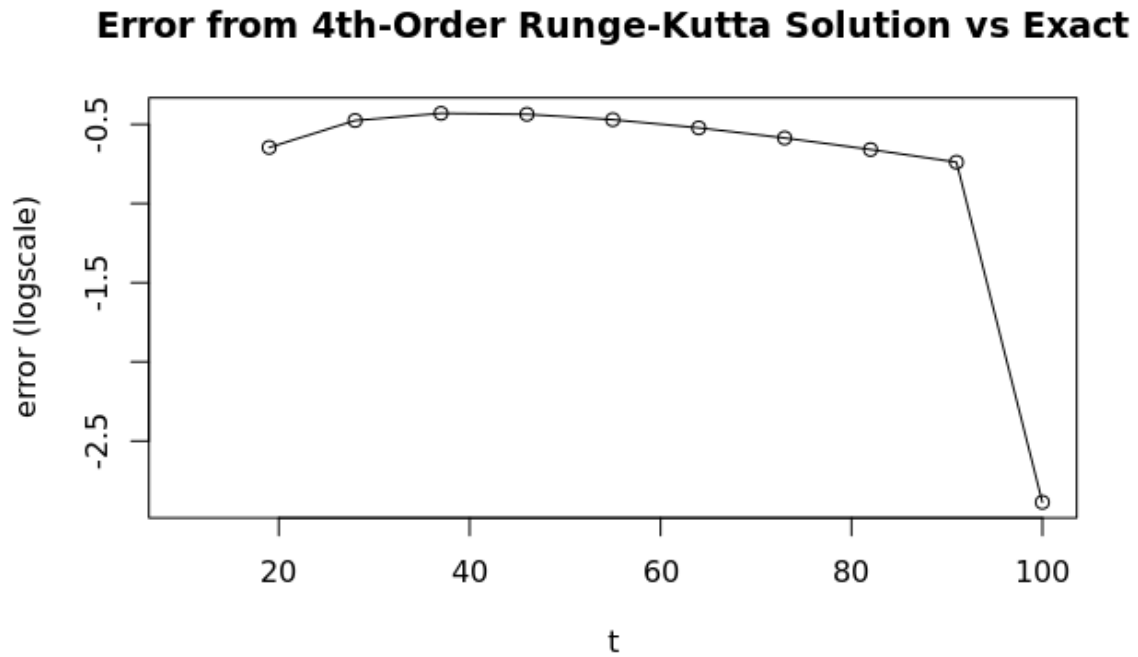
RK4 Numerical Solution for the decay ode $dy/dt = -ky$



Error

```
rk4.err <- abs(decay.rk4.sol$y - exact.y.slice)
rk4.log.err <- log(rk4.err, 10)
# Unsophisticated way to account for the -Inf error in the logscale
rk4.log.err[which(!is.finite(rk4.log.err))] <- NA

plot(seq(t0+h,tfinal,len=11), rk4.log.err,
     xlab="t", ylab="error (logscale)", type="o",
     main = "Error from 4th-Order Runge-Kutta Solution vs Exact")
```



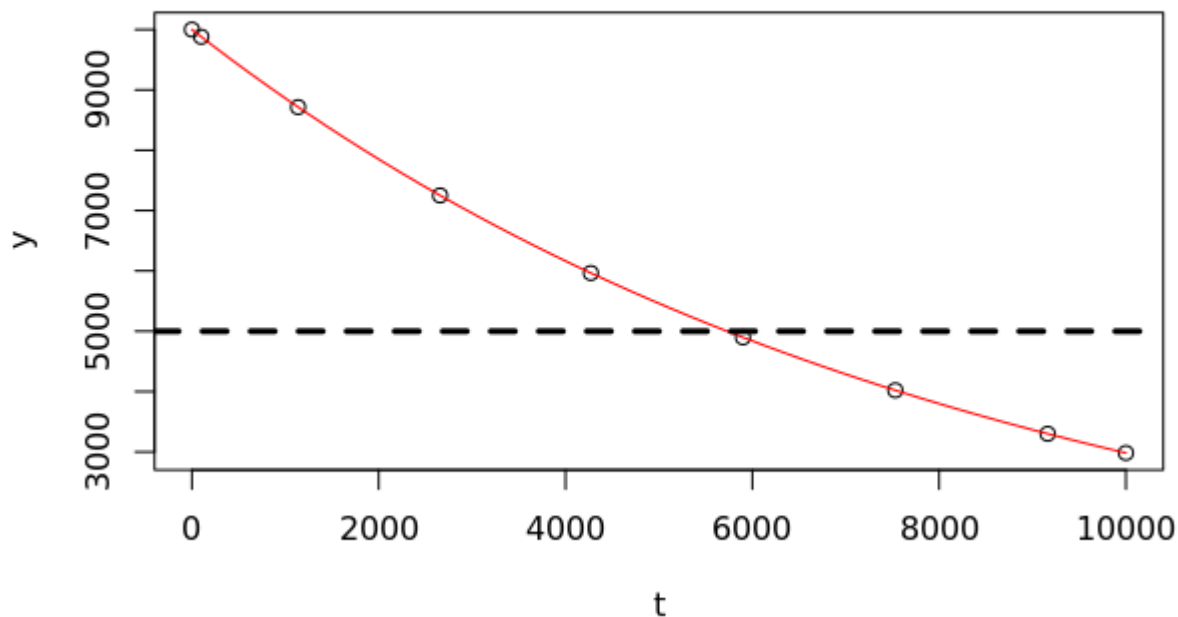
Comparing the exact solution (in red) to the Euler solution and the Runge-Kutta solution shows a noticeable difference in error. When plotting the error of each, it is observable that the Runge-Kutta is substantially more accurate.

3.)

```
## 3. Use library function ode45 to solve the decay numerically
if (!require("pracma")) install.packages("pracma")
library(pracma)
# specify intial conds and params
k <- 1.21e-4
tmin <- 0
tmax <- 10000
y.init <- 10000

decay.ode45.sol <- ode45(f=function(t,y){decay.f(t,y,k=k)},
                        y=y.init, t0=tmin, tfinal=tmax)
plot(decay.ode45.sol$t,decay.ode45.sol$y, xlab="t", ylab="y",
     main="Decay Model Solution Using Pracma ODE45")
par(new=T)
lines(seq(tmin,tmax,len=50),
      y.init*exp(-k*seq(tmin,tmax,len=50)), col="red")
abline(h=y.init/2, lty="dashed", lwd=3)
```

Decay Model Solution Using Pracma ODE45



#Solve for half-life with bisection

```
findZeroBisect <- function(func, xl, xr, tol, maxsteps=1e6){
  steps <- 0
  if (func(xl) * func(xr) >= 0){
    stop("Bad interval: try again with different endpoints")
  }
  repeat{
    xm <- (xl + xr)/2
    if(abs(func(xm)) < tol || steps >= maxsteps){
      break
    }
  }
```

```

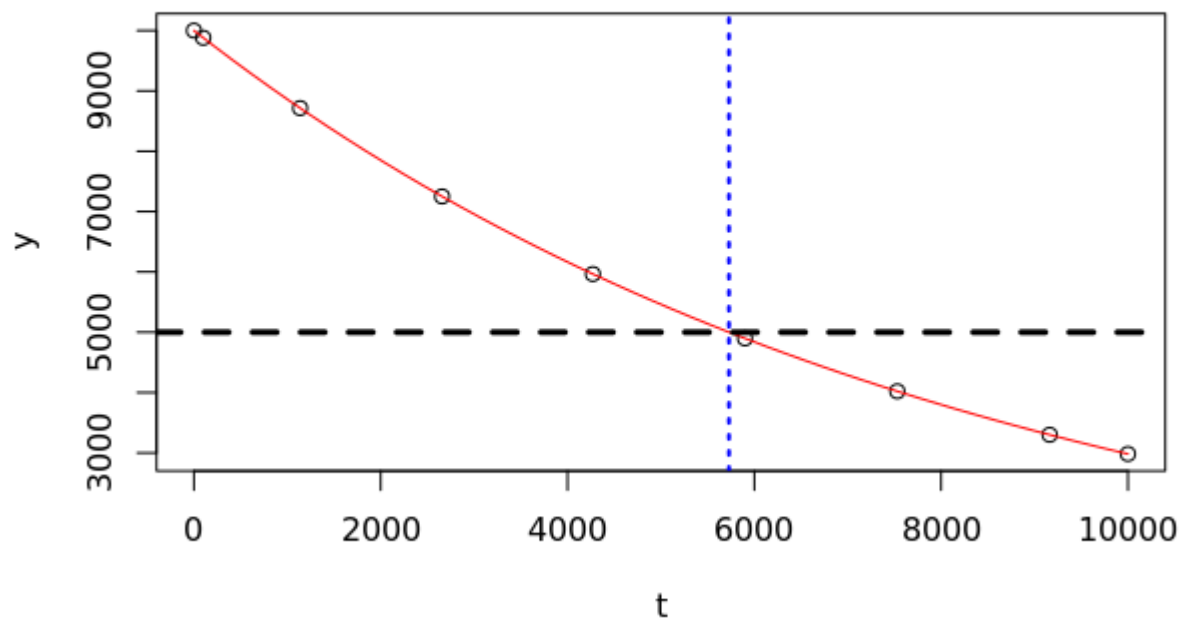
    }

    ifelse(func(xl) * func(xm) > 0, xl<-xm, xr<-xm)
    steps <- steps + 1
  }
  return(c(xm, func(xm), steps))
}
fun.hl <- function(x) {-5000+(y.init)*exp(-k*x)}

halflife <- findZeroBisect(fun.hl, 5000, 6500, 1e-8)[1]
abline(v=halflife, lty="dotted", lwd=2, col="blue")

```

Decay Model Solution Using Pracma ODE45



```

> halflife
[1] 5728.489

```

4.)

```
## 4. Solve the predator-prey model numerically
# pred-prey ode system with ode45
pp.f <- function(t,y,k){
  # k is a vector of model params
  # y is a vector of length equal to the number of odes
  prey <- y[1]
  pred <- y[2]
  dPrey <- -k[1]*prey*pred + k[2]*prey
  dPred <- k[3]*prey*pred - k[4]*pred
  return(as.matrix(c(dPrey, dPred)))
}

# a) k1=0.01, k2=0.1, k3=0.001, k4=0.05, prey(0)=50, pred(0)=15. t=0 -> 200
tmin <- 0; tmax<-200;
pp.params <- c(.01, .1, .001, .05)
prey0 <- 50
pred0 <- 15

pp.sol <- ode45(f = function(t,y){pp.f(t,y,k=pp.params)},
               y = c(prey0, pred0),
               t0 = tmin, tfinal = tmax)

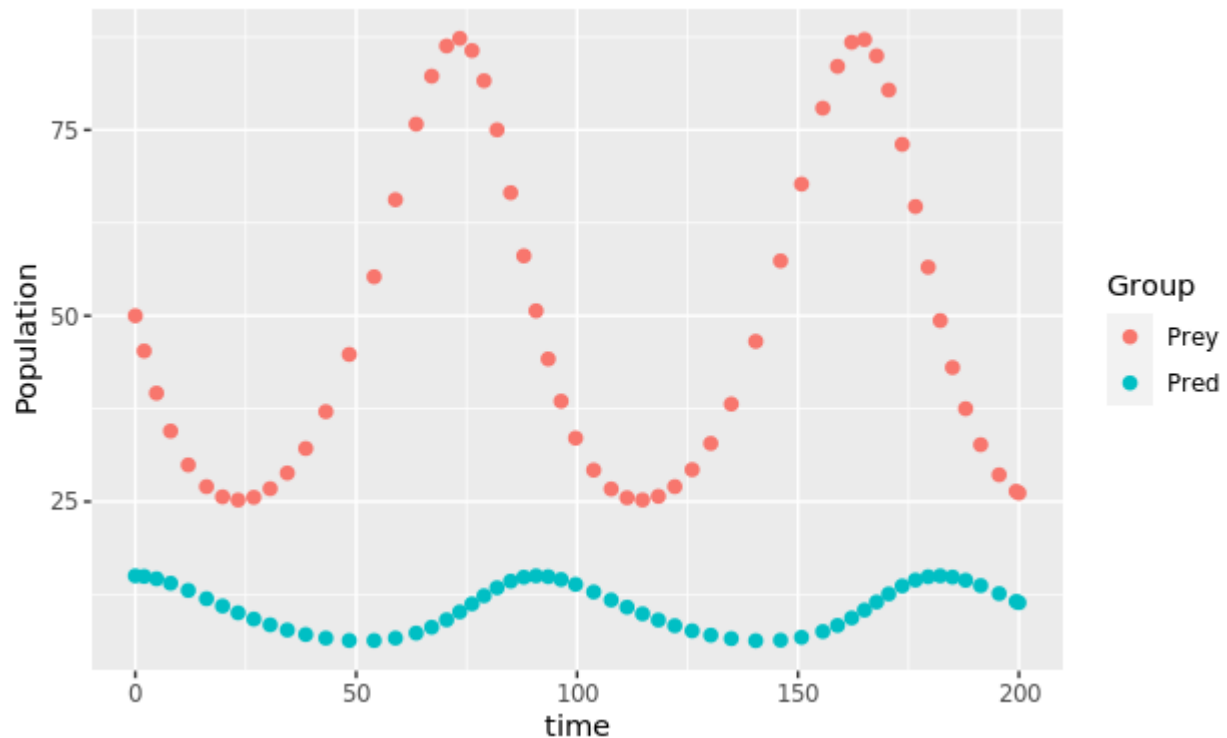
# plot
if (!require("reshape")) install.packages("reshape")
library(reshape)
if (!require("ggplot2")) install.packages("ggplot2")
library(ggplot2)

plot.pred.prey <- function(sol, method){
  # - pred/prey columns melted to 1 column called "value"
  sol.melted <- melt(data.frame(time=sol$t,
                                Prey=sol$y[,1],
                                Pred=sol$y[,2]),
                    id = "time") # melt based on time
  # New column created with variable names, called "variable"
  colnames(sol.melted)[2] <- "Group" # used in legend

  g <- ggplot(data = sol.melted,
              aes(x = time, y = value, color = Group))
  g <- g + geom_point(size=2)
  g <- g + xlab("time") + ylab("Population")
  g <- g + ggtitle(paste("Predator-Prey Model Using", method))
  show(g)
}

plot.pred.prey(pp.sol, "ODE45")
```

Predator-Prey Model Using ODE45



b) Use Euler and RK to solve with h=10

h <- 10

```
my_euler2 <- function(f, y0, t0, tfinal, dt){
  # follow ode45 syntax, dt is extra
  # y0 is a vector of initial conditions
  # this y determines the number of dependent variables to solve for
  tspan <- seq(t0,tfinal,dt)
  npts <- length(tspan)
  nvars <- length(y0)
  # initialize, this will be a matrix for systems
  y <- matrix(0,nrow=npts, ncol=nvars)
  y[1,] <- y0
  for (i in seq(2,npts)){
    y_prev <- y[i-1,] # vector at previous time
    dy <- f(t[i-1],y_prev)*dt # also a vector/matrix
    y[i,] <- y_prev + dy # Euler update
  }
  return(list(t=tspan, y=y))
}
```

```
my_rk4_2 <- function(f, y0, t0, tfinal, h){
  tspan <- seq(t0,tfinal,h)
  npts <- length(tspan)
  nvars <- length(y0)
  # initialize, this will be a matrix for systems
  y <- matrix(0,nrow=npts, ncol=nvars)
  y[1,] <- y0
  for (i in seq(2,npts)){
```

```

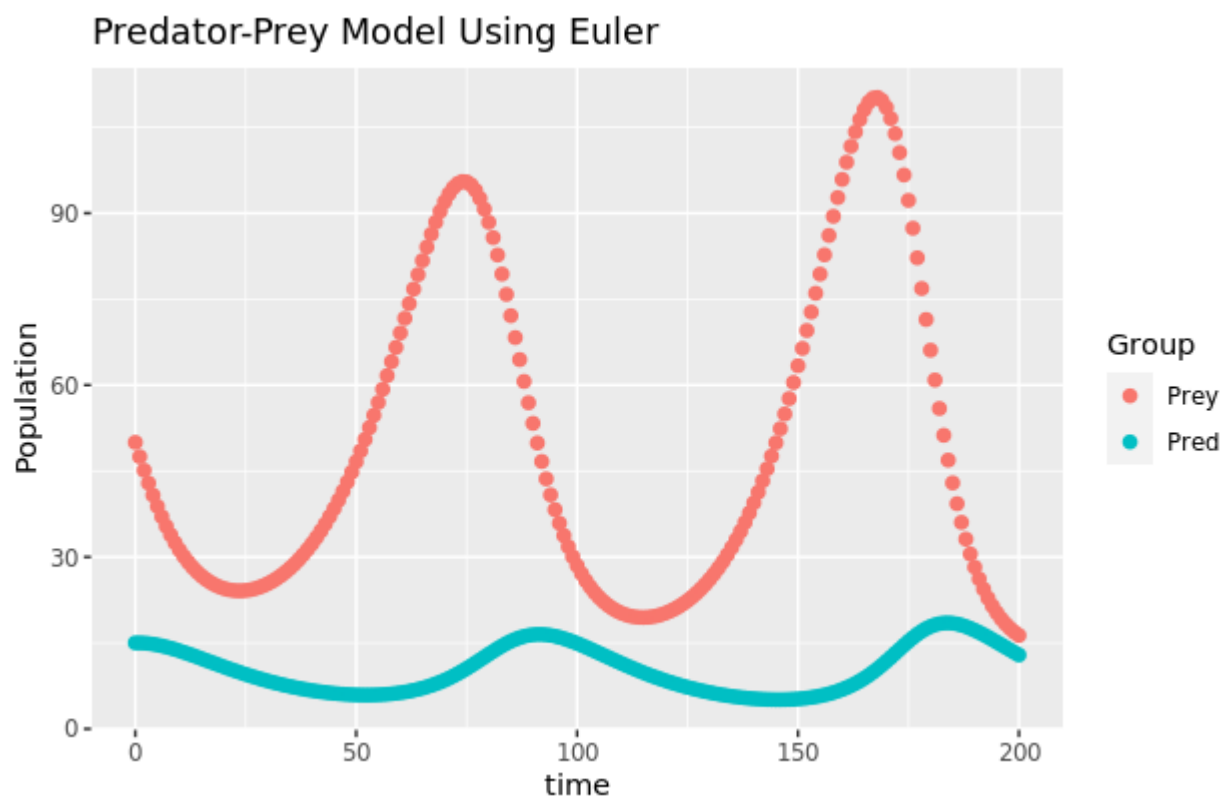
y_vec_prev <- y[i-1,] # both y values at previous time point

k1 <- f(t[i-1], y_vec_prev)
k2 <- f(t[i-1] + 0.5 * h, y_vec_prev + 0.5 * k1 * h)
k3 <- f(t[i-1] + 0.5 * h, y_vec_prev + 0.5 * k2 * h)
k4 <- f(t[i-1] + h, y_vec_prev + k3*h)

y[i,] <- y_vec_prev + (h/6)*(k1 + 2*k2 + 2*k3 + k4)
}
return(list(t=tspan,y=y))
}

pp.euler.sol <- my_euler2(f = function(t,y){pp.f(t,y,k=pp.params)},
  y = c(pre0, pred0),
  t0 = tmin, tfinal = tmax, dt=h)
plot.pred.prey(pp.euler.sol, "Euler")

```

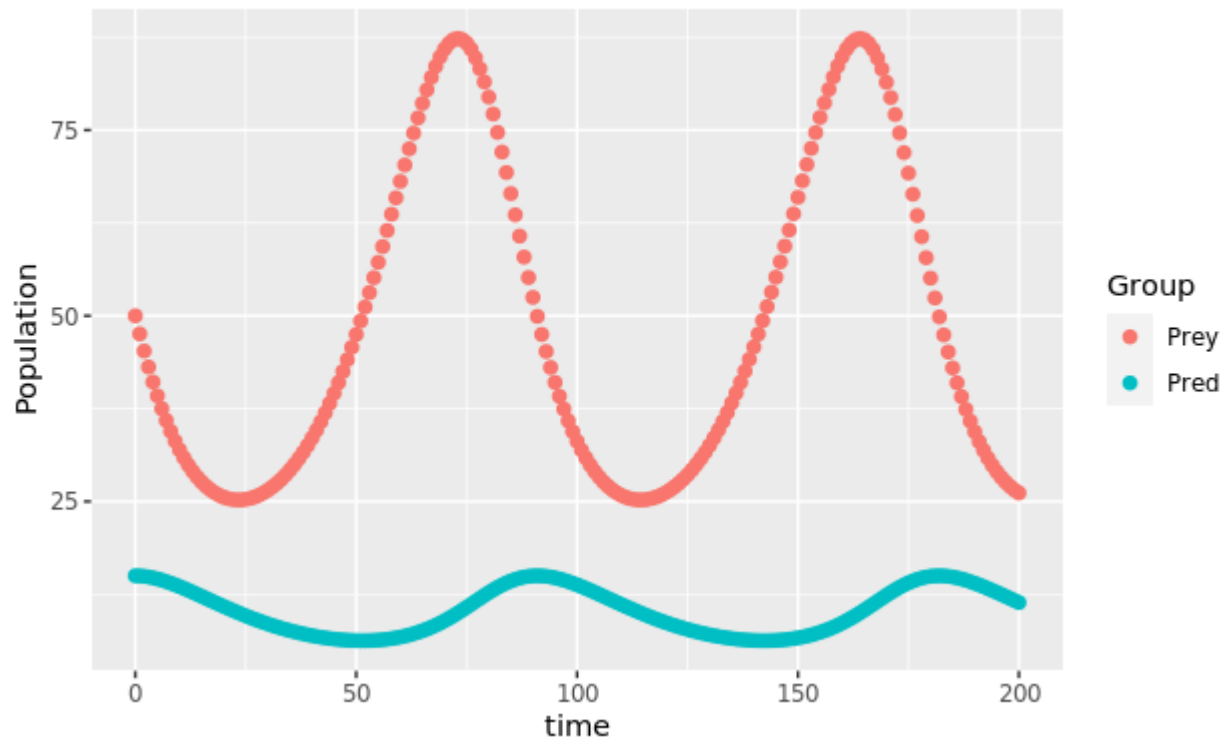


```

pp.rk4.sol <- my_rk4_2(f = function(t,y){pp.f(t,y,k=pp.params)},
  y = c(pre0, pred0),
  t0 = tmin, tfinal = tmax, h)
plot.pred.prey(pp.rk4.sol, "RK4")

```

Predator-Prey Model Using RK4



```
# plot comparing Prey solutions to ode45
```

```
plot(pp.sol$t, pp.sol$y[,1], type="l", col="green", lwd=3, ylim=c(20,120),  
      xlim=c(0,200), main="Comparing Prey solutions")
```

```
par(new=T)
```

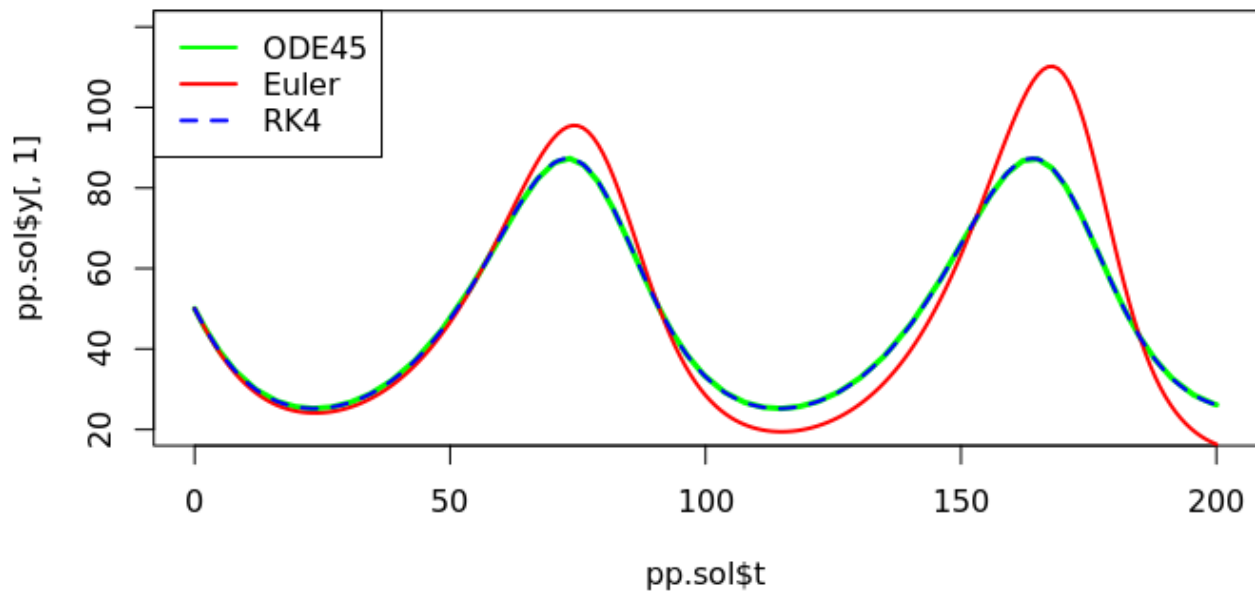
```
lines(pp.euler.sol$t,pp.euler.sol$y[,1], col="red", lwd=2)
```

```
par(new=T)
```

```
lines(pp.rk4.sol$t,pp.rk4.sol$y[,1], col="blue", lty="dashed", lwd=2)
```

```
legend(x = "topleft",  
       legend = c("ODE45", "Euler", "RK4"),  
       lty = c(1, 1, 2),  
       col = c("green", "red", "blue"),  
       lwd = 2)
```

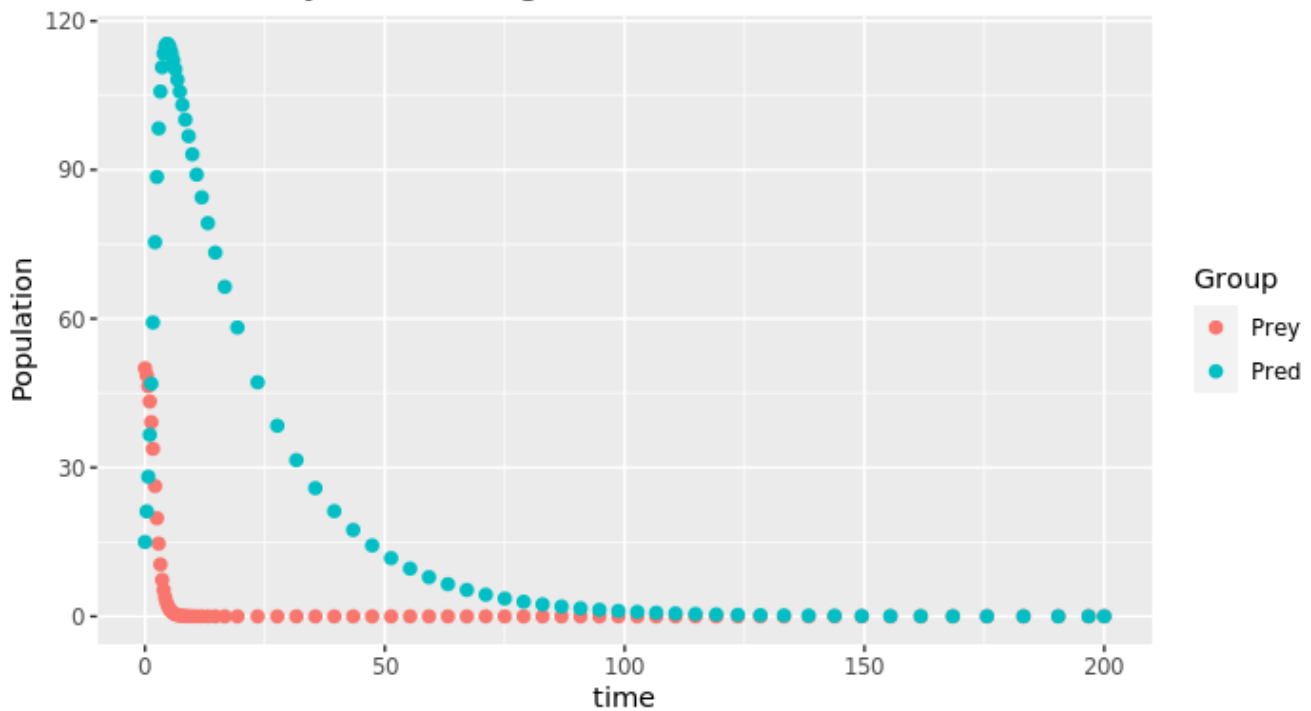
Comparing Prey solutions



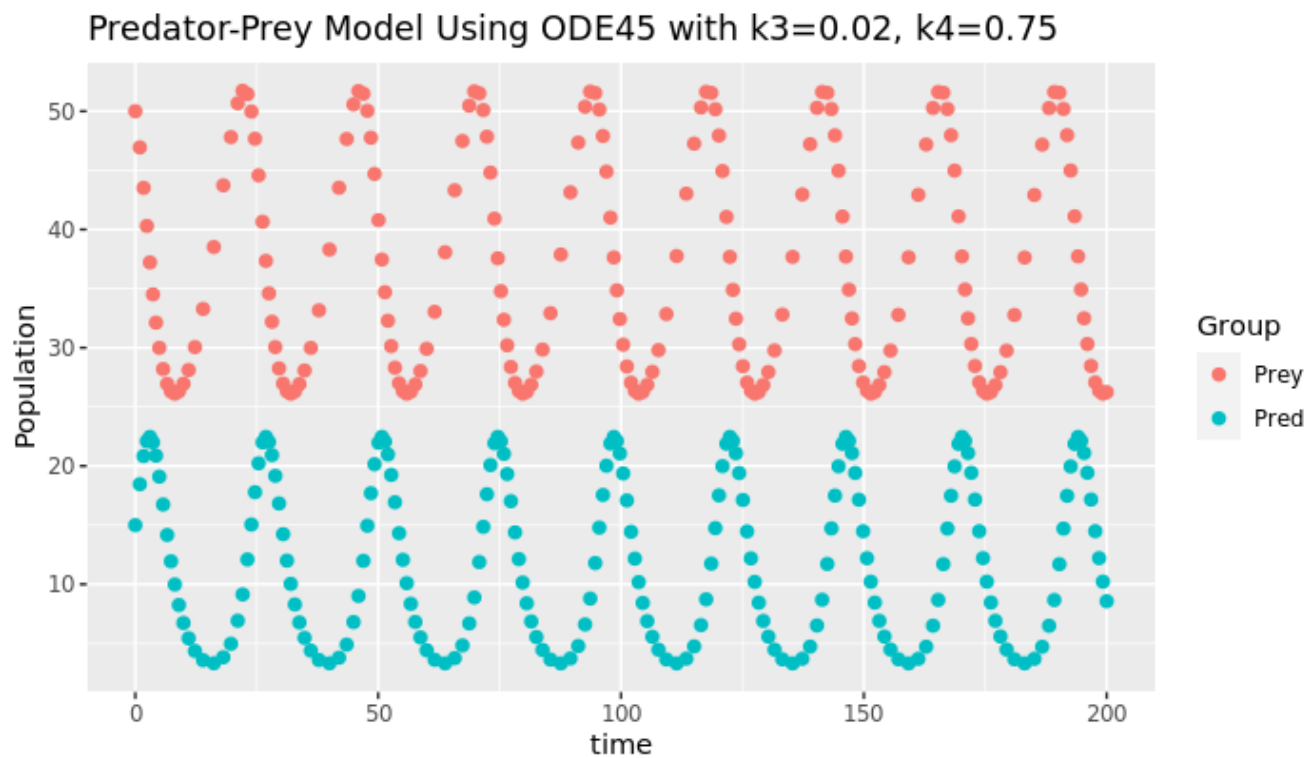
c) Use $k_3=0.02$

```
pp.params.c <- c(.01, .1, .02, .05)
pp.sol.c <- ode45(f = function(t,y){pp.f(t,y,k=pp.params.c)},
  y = c(pre0, pred0),
  t0 = tmin, tfinal = tmax)
plot.pred.prey(pp.sol.c, "ODE45 with  $k_3=0.02$ ")
```

Predator-Prey Model Using ODE45 with $k_3=0.02$



```
pp.params.c2 <- c(.01, .1, .02, .75)
pp.sol.c2 <- ode45(f = function(t,y){pp.f(t,y,k=pp.params.c2)},
  y = c(pre0, pred0),
  t0 = tmin, tfinal = tmax)
plot.pred.prey(pp.sol.c2, "ODE45 with k3=0.02, k4=0.75")
```



Not balanced, but better.

5.)

```
## 5. Solve SIR model numerically from t=0 -> 20
sir.f <- function(t, y, k) {
  dS <- -k[1] * y[1] * y[2]
  dI <- k[1] * y[1] * y[2] - k[2] * y[2]
  dR <- k[2] * y[2]
  return(as.matrix(c(dS, dI, dR)))
}

# a) a=0.5, b=1, S(0)=0.9, I(0)=0.1, R(0)=0
sir.params <- c(0.5, 1)
S0 <- 0.9
I0 <- 0.1
R0 <- 0.0
tmin <- 0
tmax <- 20

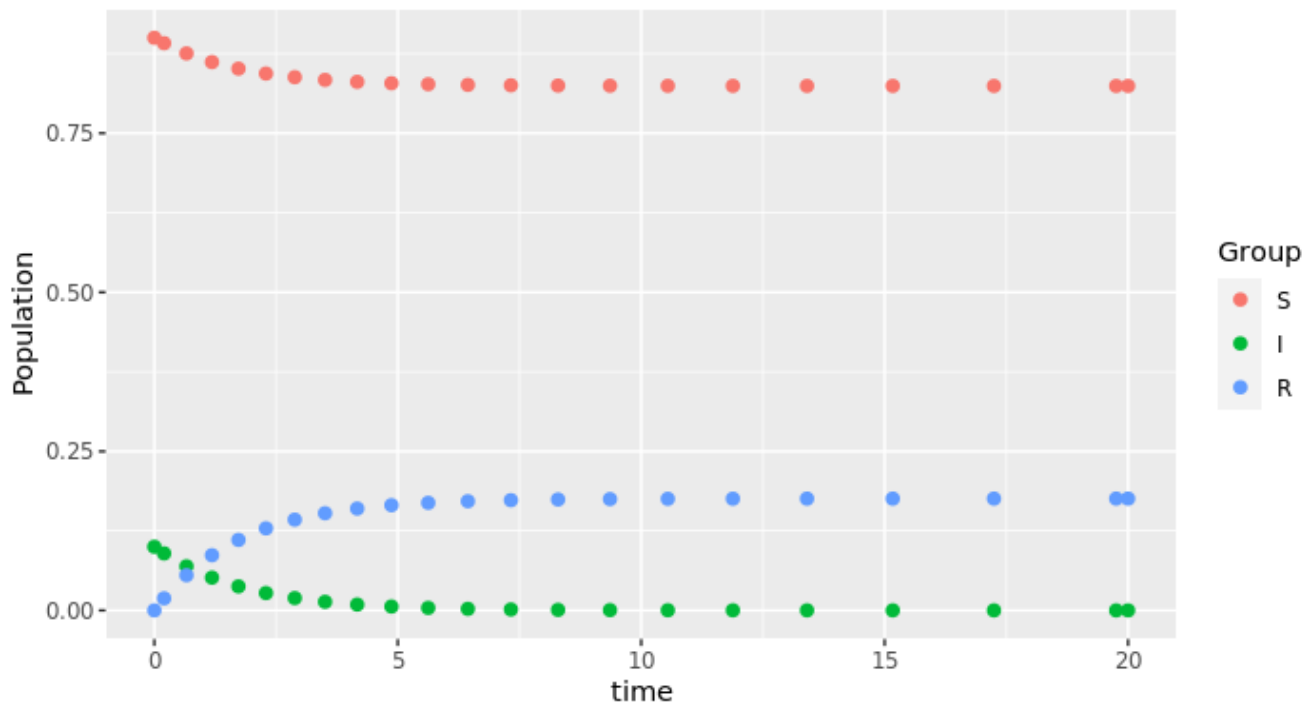
sir.ode.sol <- ode45(f = function(t,y){sir.f(t,y,k=sir.params)},
  y = c(S0, I0, R0),
  t0 = tmin, tfinal = tmax)

# plot
plot.sir <- function(sol, method){
  # - pred/prey columns melted to 1 column called "value"
  sol.melted <- melt(data.frame(time=sol$t,
                                S=sol$y[,1],
                                I=sol$y[,2],
                                R=sol$y[,3]),
                    id = "time") # melt based on time
  # New column created with variable names, called "variable"
  colnames(sol.melted)[2] <- "Group" # used in legend

  g <- ggplot(data = sol.melted,
              aes(x = time, y = value, color = Group))
  g <- g + geom_point(size=2)
  g <- g + xlab("time") + ylab("Population")
  g <- g + ggtitle(paste("SIR Model Using", method))
  show(g)
}

plot.sir(sir.ode.sol, "ODE45")
```

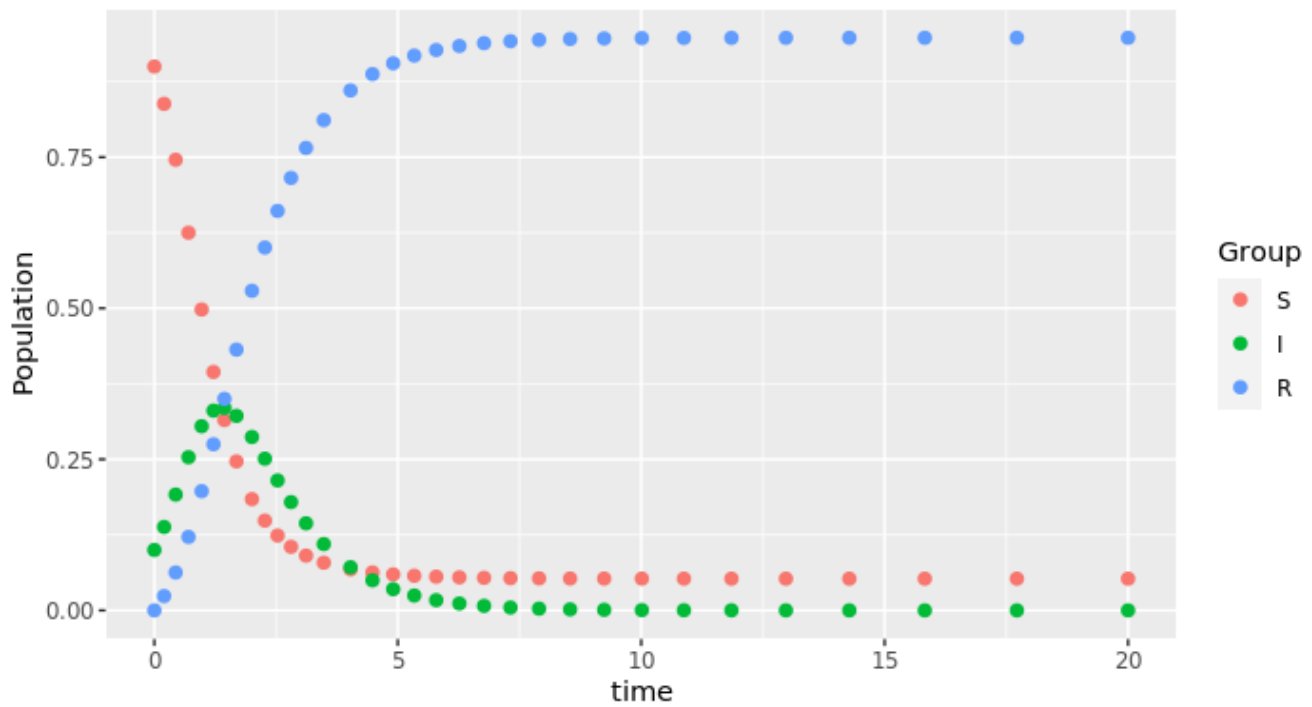
SIR Model Using ODE45



b) $a=3$

```
sir.params.b <- c(3, 1)
sir.ode.sol.b <- ode45(f = function(t,y){sir.f(t,y,k=sir.params.b)},
                      y = c(S0, I0, R0),
                      t0 = tmin, tfinal = tmax)
plot.sir(sir.ode.sol.b, "ODE45 with a=3")
```

SIR Model Using ODE45 with $a=3$



The infected group quickly rises to 0.35 at $t=1.43$, and decreases back to 0 where it remains for the duration of the time modeled. The susceptible group decreases at this time, and the recovered group rises.

6.)

6. Decomp of dinitrogen pentoxygen into nitrogen dioxide and molecular oxygen

```
decomp.f <- function(t, y, k) {
  dA <- -k[1]*y[1] + k[2]* y[2]*y[4]
  dB <- k[1]*y[1] - k[2]*y[2]*y[4] + 2*k[4]*y[4]*y[5]
  dC <- k[3]*y[2]*y[4]
  dD <- k[1]*y[1] - k[2]*y[2]*y[4] - k[3]*y[2]*y[4] - k[4]*y[4]*y[5]
  dE <- k[3]*y[2]*y[4] - k[4]*y[4]*y[5]
  return(as.matrix(c(dA, dB, dC, dD, dE)))
}

# a) k1=1.0, k2=0.5, k3=0.2,k4=1.5, [N2O5]o=1, all other IC's=0, t=0 -> 10
decomp.params <- c(1.0, 0.5, 0.2, 1.5)
A0 <- 1
B0 <- 0; C0 <- 0; D0 <- 0; E0 <- 0;
tmin <- 0
tmax <- 10

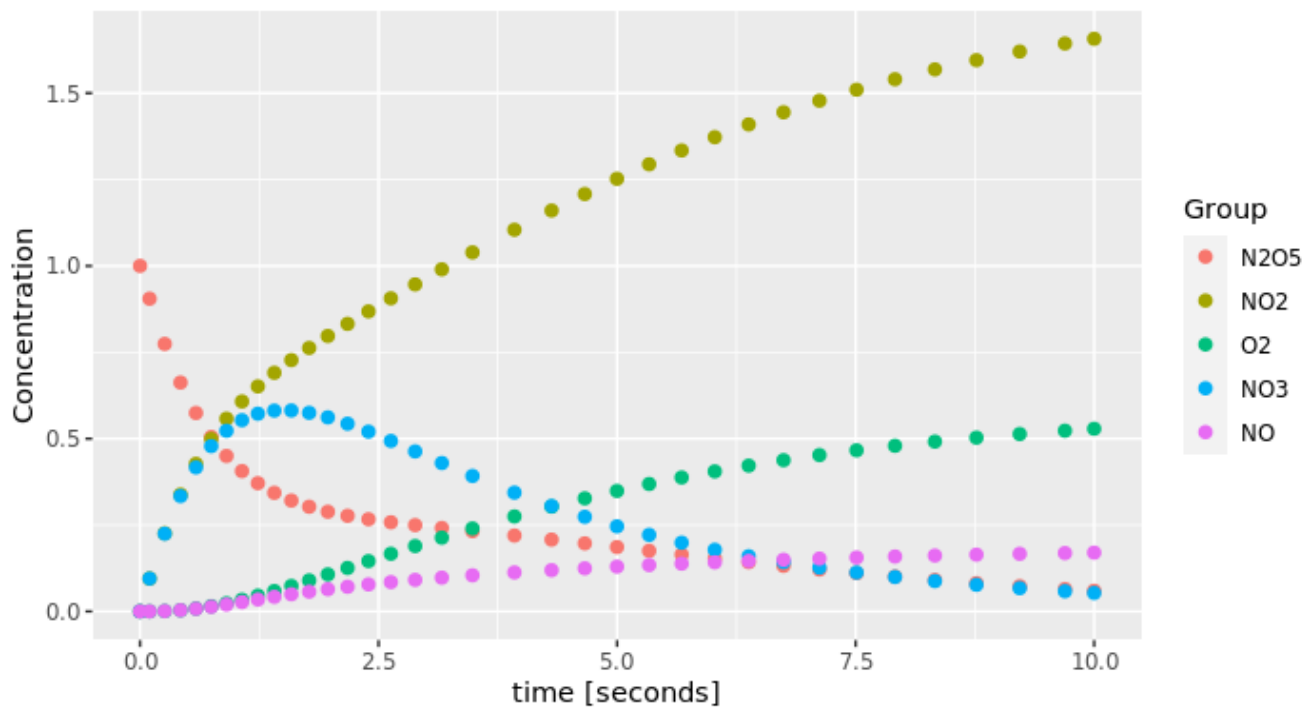
decomp.ode.sol <- ode45(f = function(t,y){decomp.f(t,y,k=decomp.params)},
  y = c(A0, B0, C0, D0, E0),
  t0 = tmin, tfinal = tmax)

# plot
plot.decomp <- function(sol, method){
  # - pred/prey columns melted to 1 column called "value"
  sol.melted <- melt(data.frame(time=sol$t,
                                N2O5=sol$y[,1],
                                NO2=sol$y[,2],
                                O2=sol$y[,3],
                                NO3=sol$y[,4],
                                NO=sol$y[,5]),
                    id = "time") # melt based on time
  # New column created with variable names, called "variable"
  colnames(sol.melted)[2] <- "Group" # used in legend

  g <- ggplot(data = sol.melted,
              aes(x = time, y = value, color = Group))
  g <- g + geom_point(size=2)
  g <- g + xlab("time [seconds]") + ylab("Concentration")
  g <- g + ggtitle(paste("Decomposition Model Using", method))
  show(g)
}

plot.decomp(decomp.ode.sol, "ODE45")
```

Decomposition Model Using ODE45



```
# b) Increase k4 to make the intermediate species -> 0
k4.mono.table <- matrix(nrow = 0, ncol = 2)
for(k in 10^(seq(-1, 4, 1))){
  k4 <- k
  decomp.params.b <- c(1.0, 0.5, 0.2, k4)
  decomp.ode.sol.b <- ode45(f = function(t,y){decomp.f(t,y,k=decomp.params.b)},
    y = c(A0, B0, C0, D0, E0),
    t0 = tmin, tfinal = tmax)
  #plot.decomp(decomp.ode.sol.b, paste("ODE45 Using k4 =", k4))
  # Is NO monotonically increasing?
  mono.check <- all(decomp.ode.sol.b$y[,5] == cummax(decomp.ode.sol.b$y[,5]))
  k4.mono.table <- rbind(k4.mono.table, c(k4, mono.check))
}
```

```
k4.mono.table
```

```
> k4.mono.table
```

```
  [,1] [,2]
[1,] 1e-01 1
[2,] 1e+00 1
[3,] 1e+01 1
[4,] 1e+02 1
[5,] 1e+03 1
[6,] 1e+04 0
```

NO stops monotonically increasing at k=1e04

Setting $dE/dt=0$ in the model is not a good idea since it is not accurate to the decomposition. NO is the hypothesized intermediate, and its change is dependent on the other steps of the reaction. Fully removing dE/dt ignores the reaction process and sets it to the ideal, which may not be the case.