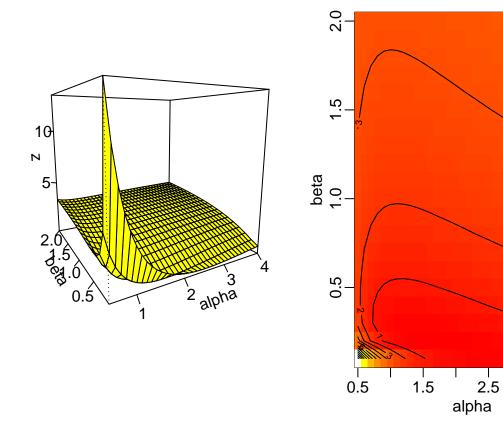
## Question 1 b)

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```
data <- read.csv("Infectious.csv")</pre>
objective.fn <- function(x, y) {
 function(alpha, beta) {
   result <- 0
   for (i in 1:length(x)) {
     result <- result + (y[i] - (1-1/(alpha + beta * x[i])))^2
   return(result)
alpha = seq(0.5, 4, 0.1)
beta = seq(0.1, 2, 0.1)
objective <- objective.fn(data$Infected, data$Deceased.Prop)</pre>
# This is the key computation; there are many ways to achieve this.
z = outer(alpha, beta, objective) # Outer takes advantage of the fact that
                                 # objective.fn is vectorized simultaneously
par(mfrow = c(1, 2), mar = c(3,3,1,1), mgp = c(3, 0.5, 0))
                                      # x-ticks, y-ticks, "height" matrix.
persp(alpha, beta, z,
     theta = -30, phi = 10,
                                # Viewpoint rotation (spherical coordinates).
      col='yellow', expand=1,
      ticktype = 'detailed')
# For an interactive visualization, substitute persp for rgl::persp3d.
image(alpha, beta, z,
                                      # Matrix as heatmap.
                              # Palette with 100 levels; visually continuous.
      col = heat.colors(100),
     useRaster = TRUE,
                               # Less accurate image, but faster.
     ann = FALSE)
mtext(text = "alpha", side = 1, line = 1.5) # Suppress default axis labels, and
mtext(text = "beta", side = 2, line = 1.5) # draw them closer to the axis.
contour(alpha, beta, z, add = TRUE) # Add contours.
```



3.5