

## Question 1 c)

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```
data <- read.csv("Infectious.csv")
```

```
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)  
  }  
}
```

```
# Narrow the ranges  
alpha = seq(0.5, 1.6, 0.01)  
beta = seq(0.1, 0.5, 0.01)  
objective <- objective.fn(data$Infected, data$Deceased.Prop)  
# 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))  
persp(alpha, beta, z, # x-ticks, y-ticks, "height" matrix.  
  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.  
  col = heat.colors(100), # Palette with 100 levels; visually continuous.  
  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.
```

