

## 流行病學與生物統計計算 Homework 8

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### # Homework8

#### # EX 20-1

**Q1 : use Newton-Raphson method to find MLE of the regression coefficient of logistic regression**

```
# EX 20-1

setwd("/Users/raymond/Desktop/")
resp <- read.csv("/Users/raymond/Desktop/resp.csv", header = TRUE)
head(resp)
dim(resp)

# Q1 : use NR to find maximum likelihood estimate of beta

# convert treatment to numeric, setting "P" be 1, "A" be 0
respma <- as.data.frame(resp)
for (i in 1 : length(resp$treatment)) {
  if (respma[i, 3] == "P") {
    respma[i, 3] <- 1
  } else {
    respma[i, 3] <- 0
  }
}
head(respma)
(treatment <- as.numeric(respma[, 3]))

# constructing matrix
X <- cbind(rep(1, length(resp$outcome)), treatment, resp$page,
resp$baseline) # nolint
Y <- resp$outcome # nolint

# ftn
ftn <- function(betacoeff) {
  pil <- exp(X %*% betacoeff) / (1 + exp(X %*% betacoeff))
}
```

```

        gradient <- t(X) %*% (Y - pi1)
        hessian <- - t(X) %*% diag(c(pi1 * (1 - pi1)),
length(resp$outcome)) %*% X # nolint

        return(list(gradient, hessian))
    }

# highorder Newton-Raphson method
highnew <- function(ftn, x0, tol, maxiter) {
    x <- x0
    fx <- ftn(x)
    iter <- 0

    while ((max(abs(fx[[1]])) > tol) && (iter < maxiter)) {
        x <- x - (solve(fx[[2]]) %*% fx[[1]])
        fx <- ftn(x)
        iter <- iter + 1
    }

    if (max(abs(fx[[1]])) > tol) {
        cat("algorithm failed to converge\n")
        return(NULL)
    } else {
        cat("algorithm converges to\n")
        return(x)
    }
}

highnew(ftn, x0 = c(0, 0, 0, 0), tol = 1e-9, maxiter = 100)

```

```

> highnew(ftn, x0 = c(0, 0, 0, 0), tol = 1e-9, maxiter = 100)
algorithm converges to
      [,1]
0.43670552
treatment -1.23475884
      [,1]
-0.01140389
      [,1]
1.98241179

```

### # Q2 : find the variance-covariance matrix

```
(beta <- highnew(ftn, c(0, 0, 0, 0), tol = 1e-9, maxiter = 100))  
solve(-ftn(beta)[[2]])
```

```
> solve(-ftn(beta)[[2]])  
               treatment  
0.09951118 -2.070235e-02 -2.168930e-03 -1.289550e-02  
treatment -0.02070235  5.133126e-02 -3.292548e-05 -1.351023e-02  
          -0.00216893 -3.292548e-05  6.630252e-05 -2.084783e-05  
          -0.01289550 -1.351023e-02 -2.084783e-05  5.426992e-02
```

### # Q3 : find the log likelihood

```
X <- cbind(rep(1, length(resp$outcome)), treatment, resp$age, resp$baseline)  
Y <- resp$outcome  
ftn <- function(betacoeff) {  
  pi1 <- exp(X %*% betacoeff) / (1 + exp(X %*% betacoeff))  
  gradient <- t(X) %*% (Y - pi1)  
  hessian <- - t(X) %*% diag(c(pi1 * (1 - pi1)), length(resp$outcome)) %*%  
X # nolint  
  loglike <- sum(Y * log(pi1 / (1 - pi1)) + log(1 - pi1))  
  
  return(list(gradient, hessian, loglike))  
}  
  
ftn(beta)[[3]]
```

```
> ftn(beta)[[3]]  
[1] -247.9434
```