Section2_PartA&B

Section 2 — Predicting Good Health (UNSDG 3)

Part A: Building the Model with Maximum Likelihood

Task 1 - Log-likelihood

We model whether life expectancy exceeds the median using a binary response and a single predictor (log GDP per capita).

- Data: (y_i, x_i) for $i = 1, \dots, n$, where $y_i \in \{0, 1\}$ and $x_i = \log(\text{gdpPercap}_i)$.
- $\bullet \ \ \mathrm{Model: \ logit}(p_i) = \beta_0 + \beta_1 x_i, \ \mathrm{where} \ p_i = \Pr(Y_i = 1 \mid x_i).$

Likelihood

$$\begin{split} L(\beta_0, \beta_1) &= \prod_{i=1}^n p_i^{y_i} \, (1-p_i)^{\, 1-y_i}, \\ p_i &= \frac{\exp(\beta_0 + \beta_1 x_i)}{1 + \exp(\beta_0 + \beta_1 x_i)}. \end{split}$$

Log-likelihood

$$\ell(\beta_0, \beta_1) = \sum_{i=1}^{n} \left[y_i (\beta_0 + \beta_1 x_i) - \log(1 + \exp(\beta_0 + \beta_1 x_i)) \right].$$

Task 2 - Implement log-likelihood

```
loglik_logistic <- function(par, y, x){
beta0 <- par[1]
beta1 <- par[2]
eta <- beta0 + beta1 * x
sum(y * eta - log(1 + exp(eta)))
}</pre>
```

This function loglik_logistic takes the parameter vector par = c(beta0, beta1) together with the data vectors y (binary 0/1) and x = log(gdpPercap), forms the linear predictor i= 0+1xi_i= 0+1x_i i= 0+1xi, and returns the single numeric value of the logistic/Bernoulli log-likelihood

Data preparation

```
library(dplyr)

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':
    filter, lag

The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union

library(ggplot2)
library(gapminder)

data <- gapminder %>%
    filter(year == 2007) %>%
mutate(
high_lifeExp = ifelse(lifeExp > median(lifeExp), 1, 0),
log_gdp = log(gdpPercap)
)
```

Response and Predictor

```
y <- data$high_lifeExp
x <- data$log_gdp
stopifnot(length(y) == length(x))</pre>
```

Task 3 - Maximise log-likelihood with optim()

```
# Initial values for beta0 and beta1
par0 <- c(0, 0)
# Maximise the log likelihood
optim_fit <- optim(</pre>
par = par0,
fn = loglik_logistic,
y = y,
x = x,
method = "BFGS",
control = list(fnscale = -1),
hessian = TRUE
# Estimates and checks
beta_hat <- optim_fit$par</pre>
names(beta_hat) <- c("beta0_hat", "beta1_hat")</pre>
ll_max <- optim_fit$value</pre>
conv <- optim_fit$convergence</pre>
beta_hat
```

beta0_hat beta1_hat -20.38243 2.34889

ll_max

[1] -42.44485

conv

[1] 0

Task 4 - Fit the model with glm()

```
model_glm <- glm(high_lifeExp ~ log_gdp, data = data, family = binomial)
coef_glm <- coef(model_glm)
coef_glm</pre>
```

```
(Intercept) log_gdp
-20.382309 2.348878
```

Task 5 - Compare optim() and glm() coefficients

```
# Comparison
comp <- rbind(optim = beta_hat,
glm = coef_glm)
comp

    beta0_hat beta1_hat
optim -20.38243   2.348890
glm    -20.38231   2.348878

# Numerical differences
diff <- comp["optim", ] - comp["glm", ]
diff</pre>
```

```
beta0_hat beta1_hat -1.228719e-04 1.234431e-05
```

The estimates from optim() and glm() are essentially identical, differing only by numerical tolerance: about 10^{-4} for $\hat{\beta}_0$ and 10^{-5} for $\hat{\beta}_1$. This confirms that our log-likelihood implementation and maximisation with optim() (BFGS, fnscale = -1) recover the same MLEs as the built-in glm() fit.

Part B: Estimating Uncertainty with Fisher Information

Task 1 - Extract and display the Hessian matrix

```
H <- optim_fit$hessian
H</pre>
```

```
[,1] [,2]
[1,] -13.12452 -114.6084
[2,] -114.60837 -1007.5049
```

Task 2 - Compute and display the Fisher information matrix

```
I_hat <- -H
I_hat
```

```
[,1] [,2]
[1,] 13.12452 114.6084
[2,] 114.60837 1007.5049
```

Task 3 - Compute and display the standard errors

```
V_hat <- solve(I_hat)
se <- sqrt(diag(V_hat))
names(se) <- c("beta0","beta1")
se</pre>
```

beta0 beta1 3.3848272 0.3863266

Task 4 - Manually construct the 95% confidence intervals

```
beta_hat_vec <- setNames(optim_fit$par, c("beta0","beta1"))
z <- 1.96
CI <- cbind(
lower = beta_hat_vec - z * se,
upper = beta_hat_vec + z * se
)
CI</pre>
```

lower upper beta0 -27.01669 -13.74817 beta1 1.59169 3.10609