

# CatDat HW7

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Code is shown in the appendix.

## 8.2

(a)

$$\begin{aligned} z^2 &= \left( \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}} \right)^2, \\ &= \left( \frac{125 - 2}{\sqrt{125 + 2}} \right)^2, \\ &= 119.13, \quad p < 0.001. \end{aligned}$$

(b)

$$\begin{aligned} SE &= \sqrt{(n_{12} + n_{21}) - (n_{12} - n_{21})^2/n/n} \\ CI &= \text{diff} \pm \alpha_{0.90} SE, \\ &= 0.11 \pm 1.645(0.01), \\ &= (0.094, 0.125). \end{aligned}$$

The lower bound CI is pretty close to zero, but the CIs are also pretty narrow. We also have a lax alpha, so I'd say this is good evidence against the null.

## 4.20

(a)

Response ~ Treatment

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-0.7142	0.1780	-4.01	0.0001
TreatmentDrug	0.4040	0.2514	1.61	0.1080

With Treatment as the only predictor, we get null results.

(b)

Mantel-Haenszel chi-squared test without continuity correction

```
data: trial_partials
Mantel-Haenszel X-squared = 6.3841, df = 1, p-value = 0.01151
alternative hypothesis: true common odds ratio is not equal to 1
95 percent confidence interval:
 1.177590 3.869174
sample estimates:
common odds ratio
      2.134549
```

Because we reject the null ( $\chi^2 = 6.38$ ,  $df = 1$ ,  $p = 0.012$ ), the CMH test on the partial tables of each stratum of center demonstrates potential conditionality on the Center variable. Ignoring Center might not be wise.

(c)

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-1.32	0.66	-2.00	0.05
TreatmentDrug	0.89	0.41	2.14	0.03

Following up on the CMH test, it's likely that there is conditionality on the Center variable, which indicates that we should take measures to hold the effect of Center constant when assessing the effect of Treatment on Response. By not doing so, we risk Type II error.

The odds ratio for the original model was 1.5,  $p = 0.12$ , with 95% CIs (0.915 2.452). Using mixed effects logistic regression with random intercepts and random slopes, the odds ratio comes out to 2.44,  $p = 0.03$ , with 95% CIs (1.078, 5.45).

## Appendix

```
# print good looking p-values
pvalr <- function(pvals, sig.limit = .001, digits = 3, html = FALSE) {

  roundr <- function(x, digits = 1) {
    res <- sprintf(paste0('%.', digits, 'f'), x)
    zzz <- paste0('0.', paste(rep('0', digits), collapse = ''))
    res[res == paste0('-', zzz)] <- zzz
    res
  }

  sapply(pvals, function(x, sig.limit) {
    if (x < sig.limit)
      if (html)
        return(sprintf('&lt; %s', format(sig.limit))) else
        return(sprintf('< %s', format(sig.limit)))
    if (x > .1)
      return(roundr(x, digits = 2)) else
      return(roundr(x, digits = digits))
  }, sig.limit = sig.limit)
}
```

## 8.2

(a)

```
chi_82 <- round(((125-2)/sqrt(125+2))^2, 2)
p_82 <- pvalr(pchisq(chi_82, df=1, lower.tail = FALSE))
```

$$\begin{aligned} z^2 &= \left( \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}} \right)^2, \\ &= \left( \frac{125 - 2}{\sqrt{125 + 2}} \right)^2, \\ &= 119.13, \quad p < 0.001. \end{aligned}$$

(b)

```
# proportions
heaven <- (833+125) / (833+2+160+125)
hell <- (833 + 2) / (833+2+125+160)
# difference
diff <- heaven - hell
# standard error
SE <- sqrt((125+2) - (125-2)^2 / 1120) / 1120
#90% CIs
upper <- diff + (1.645*SE)
lower <- diff - (1.645*SE)
```

$$SE = \sqrt{(n_{12} + n_{21}) - (n_{12} - n_{21})^2/n/n}$$

$$\begin{aligned}
 CI &= \text{diff} \pm \alpha_{0.90} SE, \\
 &= 0.11 \pm 1.645(0.01), \\
 &= (0.094, 0.125).
 \end{aligned}$$

## 4.20

(a)

```
# data
trial <- as.data.frame(rep(c(1:8), each = 2)); names(trial)[1] <- "Center"
trial$Treatment <- rep(c("Drug", "Control"), each = 1)
trial$Success <- c(11,10,16,22,14,7,2,1,6,0,1,0,1,1,4,6)
trial$Failure <- c(25,27,4,10,5,12,14,16,11,12,10,10,4,8,2,1)
# model
Response <- trial$Success / (trial$Success + trial$Failure)
trial_mod <- glm(Response ~ Treatment,
                 weights = Success + Failure,
                 family = binomial,
                 data = trial)

trial_mod$formula
```

Response ~ Treatment

```
xtable::xtable(trial_mod, align = "lrrrr")
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-0.7142	0.1780	-4.01	0.0001
TreatmentDrug	0.4040	0.2514	1.61	0.1080

(b)

```
trial_table <- matrix(c(55, 47, 75, 96), nrow = 2, byrow = T)
rownames(trial_table) <- c("drug", "control")
colnames(trial_table) <- c("success", "failure")
trial_partials <- array(c(11,25,
                          10,27,
                          16,4,
                          22,10,
                          14,5,
                          7,12,
                          2,14,
                          1,16,
                          6,11,
                          0,12,
                          1,10,
                          0,10,
                          1,4,
                          1,8,
                          4,2,
                          6,1),
```

```

dim = c(2,2,8),
dimnames = list(
  response = c("success", "failure"),
  treatment = c("drug", "control"),
  clinic = c("1", "2", "3", "4", "5", "6", "7", "8"))
mantelhaen.test(trial_partials, correct = FALSE)

```

Mantel-Haenszel chi-squared test without continuity correction

```

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95 percent confidence interval:
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sample estimates:
common odds ratio
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```

(c)

```

trial_partials <- array(c(11,25,
  10,27,
  16,4,
  22,10,
  14,5,
  7,12,
  2,14,
  1,16,
  6,11,
  0,12,
  1,10,
  0,10,
  1,4,
  1,8,
  4,2,
  6,1),
  dim = c(2,2,8),
  dimnames = list(
    response = c("success", "failure"),
    treatment = c("drug", "control"),
    clinic = c("1", "2", "3", "4", "5", "6", "7", "8")))
mixed_mod <- lme4::glmer(Response ~ Treatment + (Treatment|Center), family = binomial, weights = trial_partials)
xtable::xtable(summary(mixed_mod)$coef)

```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-1.32	0.66	-2.00	0.05
TreatmentDrug	0.89	0.41	2.14	0.03

```

CIs <- confint.default(trial_mod)
sum <- summary(mixed_mod)
CIs_mixed <- confint(mixed_mod, parm="beta_", method = "Wald")

```

```
OR <- round(exp(0.4040), 2)
OR_mixed <- round(exp(0.89), 2)
CIs_mixed_l <- round(exp(0.07551159), 3)
CIs_mixed_u <- round(exp(1.69556330), 3)
```