

# STATS3860 Assign1

Jin Zhao 251138547

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## Q1

### (a) MLE of $p$ and its sampling distribution.

$Y \sim \text{Binomial}(n, p)$  means pmf =  $\binom{n}{y} p^y (1-p)^{n-y}$ , so the likelihood function is

$$\begin{aligned} L(p | y) &= \prod_{i=1}^n \binom{n}{y} p^y (1-p)^{n-y} \\ &= \binom{n}{y} p^y (1-p)^{n-y} \\ \ell(p | y) &= \ln L(p | y) = \ln \left( \binom{n}{y} p^y (1-p)^{n-y} \right) \\ &= \ln \binom{n}{y} + y \ln p + (n-y) \ln(1-p) \\ \frac{d\ell(p | y)}{dp} &= \frac{y}{p} - \frac{n-y}{1-p} \end{aligned}$$

Set to 0 for a maximum:

$$\begin{aligned} \frac{d\ell(p | y)}{dp} &= \frac{y}{p} - \frac{n-y}{1-p} = 0 \\ \frac{y}{p} &= \frac{n-y}{1-p} \\ y(1-p) &= p(n-y) \\ y - yp &= np - yp \\ y &= np \\ \therefore \hat{p}_{MLE} &= \frac{y}{n} \end{aligned}$$

The sampling distribution of  $\hat{p}_{MLE}$  is  $N(p, Var(\hat{p}_{MLE}))$ , but we can only estimate for the variance of the estimator, so we use

$$\begin{aligned}\hat{Var}(\hat{p}_{MLE}) &= \frac{1}{I(\hat{p}_{MLE})}, & I(\hat{p}_{MLE}) &= -E\left[\frac{d^2\ell(p)}{dp^2}\right] \\ I(\hat{p}_{MLE}) &= -E\left[\frac{d}{dp}\left(\frac{y}{p} - \frac{n-y}{1-p}\right)\right] \\ I(\hat{p}_{MLE}) &= -E\left[-\frac{y}{p^2} - \frac{n-y}{(1-p)^2}\right]\end{aligned}$$

Since  $E[Y] = np$  for a binomial,

$$\begin{aligned}I(\hat{p}_{MLE}) &= \frac{np}{p^2} + \frac{n(1-p)}{(1-p)^2} \\ I(\hat{p}_{MLE}) &= \frac{n}{p} + \frac{n}{1-p} \\ I(\hat{p}_{MLE}) &= \frac{n(1-p) + np}{p(1-p)} \\ I(\hat{p}_{MLE}) &= \frac{n}{p(1-p)} \\ \hat{Var}(\hat{p}_{MLE}) &= \frac{p(1-p)}{n}\end{aligned}$$

So  $\hat{p}_{MLE} \sim N\left(p, \frac{\hat{p}_{MLE}(1-\hat{p}_{MLE})}{n}\right)$ .

**(b) Wald test statistic and rejection region for this test.**

We use the sampling distribution above to construct the Wald test.

Let Wald test statistic be

$$W = \frac{\hat{p}_{MLE} - p^*}{SE(\hat{p}_{MLE})}$$

where  $SE(\hat{p}_{MLE}) = \sqrt{\frac{\hat{p}_{MLE}(1-\hat{p}_{MLE})}{n}}$ .

So for testing  $H_0 : p = p^*$  vs  $H_1 : p \neq p^*$ , the rejection region at significance level  $\alpha$  is

$$|W| > z_{\alpha/2}$$

where  $z_{\alpha/2}$  is the critical value from the standard normal distribution. Or, we fail to reject  $H_0$  if  $-z_{\alpha/2} \leq W \leq z_{\alpha/2}$ .

**(c) Likelihood ratio test statistic and rejection region for this test.**

Let LRT statistic be

$$LR = -2(\ell(p^*) - \ell(\hat{p}_{MLE})) \sim \chi_1^2$$

and  $p-val = P(T > LR)$ , where  $T \sim \chi_1^2$  under  $H_0$ . So the rejection region at significance level  $\alpha$  is

$$LR > \chi_{1,1-\alpha}^2$$

(d)  $n = 100$ ,  $y = 35$ ,  $p^* = 0.4$  at  $\alpha = 0.05$ .

**Wald test:**  $\alpha/2 = 0.025$ ,  $\hat{p}_{MLE} = \frac{y}{n} = \frac{35}{100} = 0.35$ .

$$SE(\hat{p}_{MLE}) = \sqrt{\frac{0.35 \times (1 - 0.35)}{100}} = 0.04769696$$

$$W = \frac{\hat{p}_{MLE} - p^*}{SE(\hat{p}_{MLE})} = \frac{0.35 - 0.4}{0.04769696} = -1.048284837$$

$$z_{\alpha/2} = z_{0.025} = 1.96$$

We fail to reject  $H_0$  since  $|W| < z_{\alpha/2}$ ,  $-1.96 < -1.048 < 1.96$ . Thus we cannot say the true probability of success differs from our assumption of 0.4.

**LRT test:**

$$\ell(0.35) = \ln \left( \frac{100}{35} \right) + 35 \ln 0.35 + 65 \ln 0.65 = \ln \left( \frac{100}{35} \right) - 64.7447$$

$$\ell(0.4) = \ln \left( \frac{100}{35} \right) + 35 \ln 0.4 + 65 \ln 0.6 = \ln \left( \frac{100}{35} \right) - 65.2738$$

$$LR = -2 (\ell(p^*) - \ell(\hat{p}_{MLE})) \sim \chi^2_1$$

$$LR = -2 (\ell(0.4) - \ell(0.35)) = -2(-65.2738 - (-64.7447)) = 1.0582$$

$$\chi^2_{1,1-0.05} = \chi^2_{1,0.95} = 3.841$$

We fail to reject  $H_0$  since  $LR < \chi^2_{1,1-\alpha}$ ,  $1.0582 < 3.841$ .

```
qnorm(1 - 0.05/2)
```

```
## [1] 1.959964
```

```
qchisq(1 - 0.05, df = 1)
```

```
## [1] 3.841459
```

```
# same for Q2
```

## Q2

(a) MLE of  $\lambda$  and its sampling distribution.

$Y_i \sim \text{Poisson}(\lambda)$  means pmf =  $\frac{e^{-\lambda} \lambda^{y_i}}{y_i!}$ , so the likelihood function is

$$\begin{aligned}
L(\lambda \mid y_i) &= \prod_{i=1}^n f(y_i \mid \lambda) = \prod_{i=1}^n \frac{e^{-\lambda} \lambda^{y_i}}{y_i!} = \frac{e^{-n\lambda} \lambda^{\sum y_i}}{y_1! y_2! \cdots y_n!} \\
\ell(\lambda \mid y_i) &= \ln L(\lambda \mid y_i) = \ln \left( \frac{e^{-n\lambda} \lambda^{\sum y_i}}{y_1! y_2! \cdots y_n!} \right) = -n\lambda + (\sum y_i) \ln \lambda - \sum \ln(y_i!) \\
\frac{\partial \ell(\lambda \mid y_i)}{\partial \lambda} &= -n + \frac{\sum y_i}{\lambda}
\end{aligned}$$

Set to 0 for a maximum:

$$\begin{aligned}
\frac{\partial \ell(\lambda \mid y_i)}{\partial \lambda} &= -n + \frac{\sum y_i}{\lambda} = 0 \\
n &= \frac{\sum y_i}{\lambda} \\
\therefore \hat{\lambda}_{MLE} &= \frac{\sum y_i}{n} = \bar{y}
\end{aligned}$$

The sampling distribution of  $\hat{\lambda}_{MLE}$  is  $N(\lambda, \text{Var}(\hat{\lambda}_{MLE}))$ , we use an estimate for the variance of the estimator,

$$\begin{aligned}
\text{Var}(\hat{\lambda}_{MLE}) &= \frac{1}{I(\hat{\lambda}_{MLE})}, \quad I(\hat{\lambda}_{MLE}) = -E \left[ \frac{\partial^2 \ell(\lambda)}{\partial \lambda^2} \right] \\
I(\hat{\lambda}_{MLE}) &= -E \left[ \frac{\partial}{\partial \lambda} \left( -n + \frac{\sum y_i}{\lambda} \right) \right] \\
I(\hat{\lambda}_{MLE}) &= -E \left[ -\frac{\sum y_i}{\lambda^2} \right]
\end{aligned}$$

Since  $E[Y_i] = \lambda$  for Poisson,

$$\begin{aligned}
I(\hat{\lambda}_{MLE}) &= \frac{n\lambda}{\lambda^2} = \frac{n}{\hat{\lambda}_{MLE}} \\
\text{Var}(\hat{\lambda}_{MLE}) &= \frac{\hat{\lambda}_{MLE}}{n} = \frac{\bar{y}}{n}
\end{aligned}$$

so  $\hat{\lambda}_{MLE} \sim N(\lambda, \frac{\bar{y}}{n})$ .

### (b) Wald test statistic and rejection region for this test.

We use the sampling distribution above to construct the Wald test.

Let Wald test statistic be

$$W = \frac{\hat{\lambda}_{MLE} - \lambda^*}{SE(\hat{\lambda}_{MLE})}$$

where  $SE(\hat{\lambda}_{MLE}) = \sqrt{\frac{\bar{y}}{n}}$ .

So for testing  $H_0 : \lambda = \lambda^*$  vs  $H_1 : \lambda \neq \lambda^*$ , the rejection region at significance level  $\alpha$  is

$$|W| > z_{\alpha/2}$$

where  $z_{\alpha/2}$  is the critical value from the standard normal distribution. Or, we fail to reject  $H_0$  if  $-z_{\alpha/2} \leq W \leq z_{\alpha/2}$ .

**(c) Likelihood ratio test statistic and rejection region for this test.**

Let LRT statistic be

$$LR = -2 \left( \ell(\lambda^*) - \ell(\hat{\lambda}_{MLE}) \right) \sim \chi_1^2$$

and  $p-val = P(T > LR)$ , where  $T \sim \chi_1^2$  under  $H_0$ . So the rejection region at significance level  $\alpha$  is

$$LR > \chi_{1,1-\alpha}^2$$

**(d)  $n = 200$ ,  $\bar{y} = 5$ ,  $\lambda^* = 4$  at  $\alpha = 0.05$ .**

**Wald test:**  $\alpha/2 = 0.025$ ,  $\hat{\lambda}_{MLE} = \bar{y} = 5$ .

$$\begin{aligned} SE(\hat{\lambda}_{MLE}) &= \sqrt{\frac{\bar{y}}{n}} = \sqrt{\frac{5}{200}} = 0.15811 \\ W &= \frac{\hat{\lambda}_{MLE} - \lambda^*}{SE(\hat{\lambda}_{MLE})} = \frac{5 - 4}{0.15811} = 6.324555 \\ z_{\alpha/2} &= z_{0.025} = 1.96 \end{aligned}$$

We reject  $H_0$  since  $|W| > z_{\alpha/2}$ ,  $-1.96 < 1.96 < 6.3246$ . Thus the true  $\lambda$  differs from our assumption of 4.

**LRT test:**

$$\begin{aligned} \ell(4) &= -200(4) + 1000 \ln 4 - \sum \ln(y_i!) = -800 + 1000 \ln 4 - C = 586.2944 - C \\ \ell(5) &= -200(5) + 1000 \ln 5 - \sum \ln(y_i!) = -1000 + 1000 \ln 5 - C = 609.4379 - C \end{aligned}$$

$$\begin{aligned} LR &= -2 \left( \ell(\lambda^*) - \ell(\hat{\lambda}_{MLE}) \right) \sim \chi_1^2 \\ LR &= -2 (\ell(4) - \ell(5)) = -2 (586.2944 - C - (609.4379 - C)) = 46.287 \\ \chi_{1,1-0.05}^2 &= \chi_{1,0.95}^2 = 3.841 \end{aligned}$$

We reject  $H_0$  since  $LR > \chi_{1,1-\alpha}^2$ ,  $46.287 > 3.841$ .

## Q3

(a) Exploring data graphically.

```
library(boot)
data("urine", package = "boot")

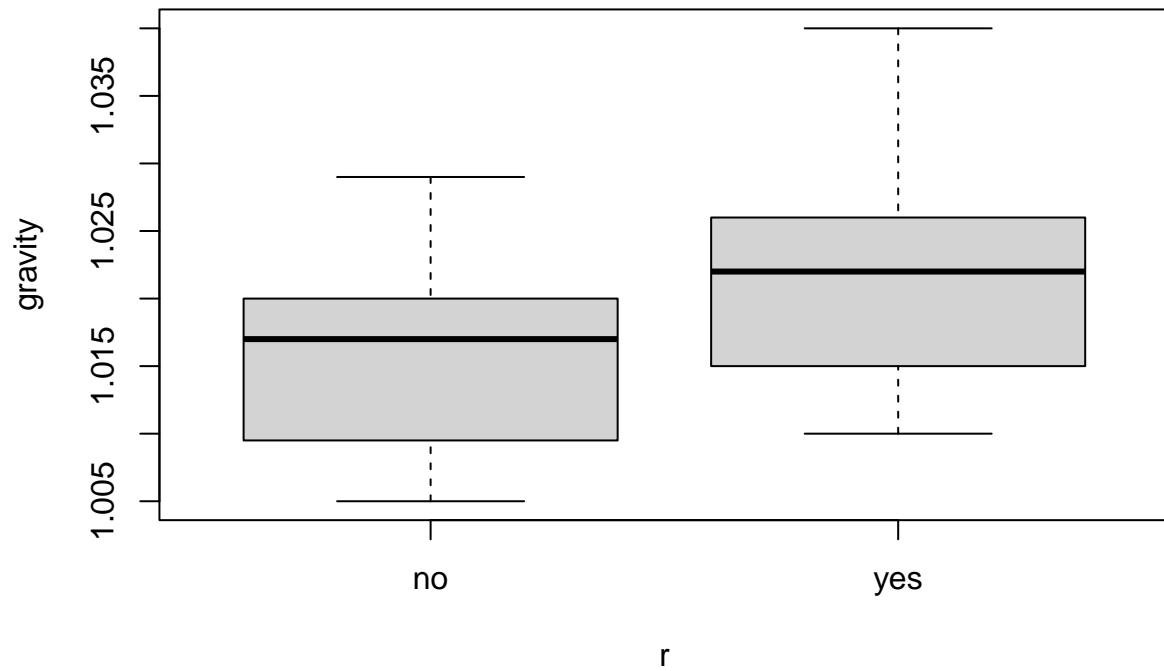
# ?urine

urine <- urine[-c(1, 55), ]
urine$r <- factor(urine$r, levels = c("0", "1"), labels = c("no", "yes"))

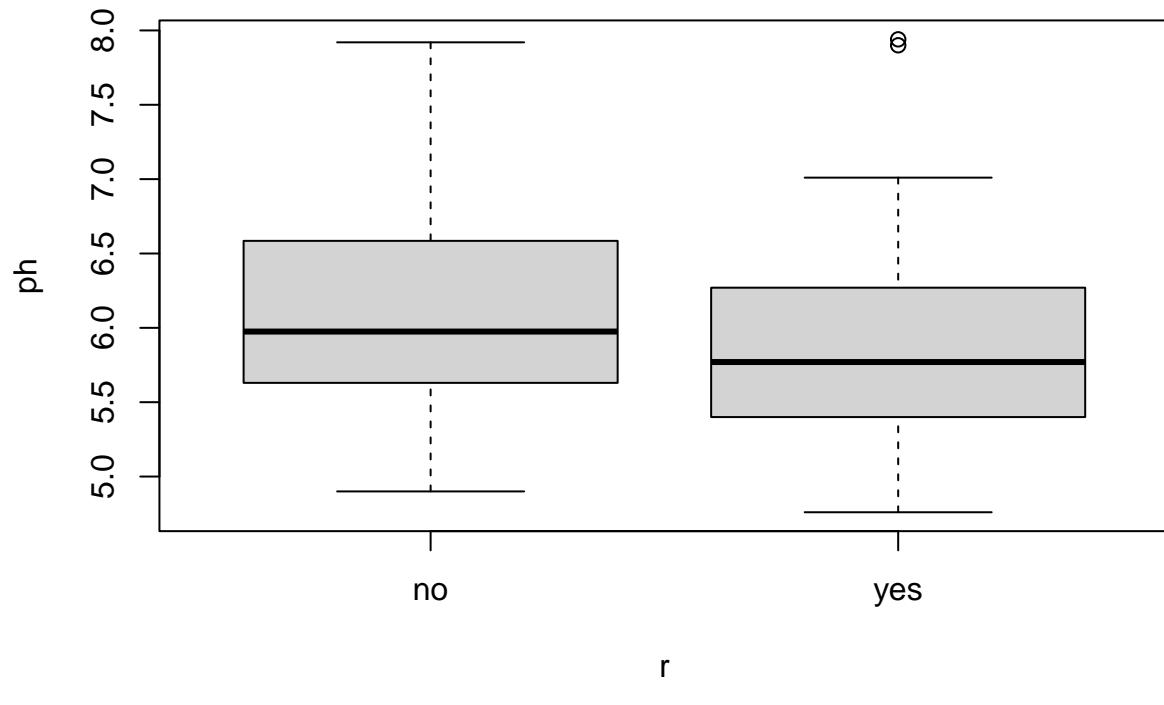
summary(urine)

##      r          gravity          ph          osmo          cond
##  no :44   Min.   :1.005   Min.   :4.760   Min.   :187.0   Min.   : 5.10
##  yes:33   1st Qu.:1.012   1st Qu.:5.530   1st Qu.:410.0   1st Qu.:14.30
##              Median :1.018   Median :5.940   Median :594.0   Median :21.40
##              Mean   :1.018   Mean   :6.041   Mean   :613.6   Mean   :20.91
##              3rd Qu.:1.024   3rd Qu.:6.400   3rd Qu.:803.0   3rd Qu.:27.00
##              Max.   :1.040   Max.   :7.940   Max.   :1236.0  Max.   :38.00
##      urea          calc
##  Min.   : 10.0   Min.   : 0.17
##  1st Qu.:159.0   1st Qu.: 1.45
##  Median :255.0   Median : 3.16
##  Mean   :262.4   Mean   : 4.16
##  3rd Qu.:362.0   3rd Qu.: 6.19
##  Max.   :620.0   Max.   :14.34

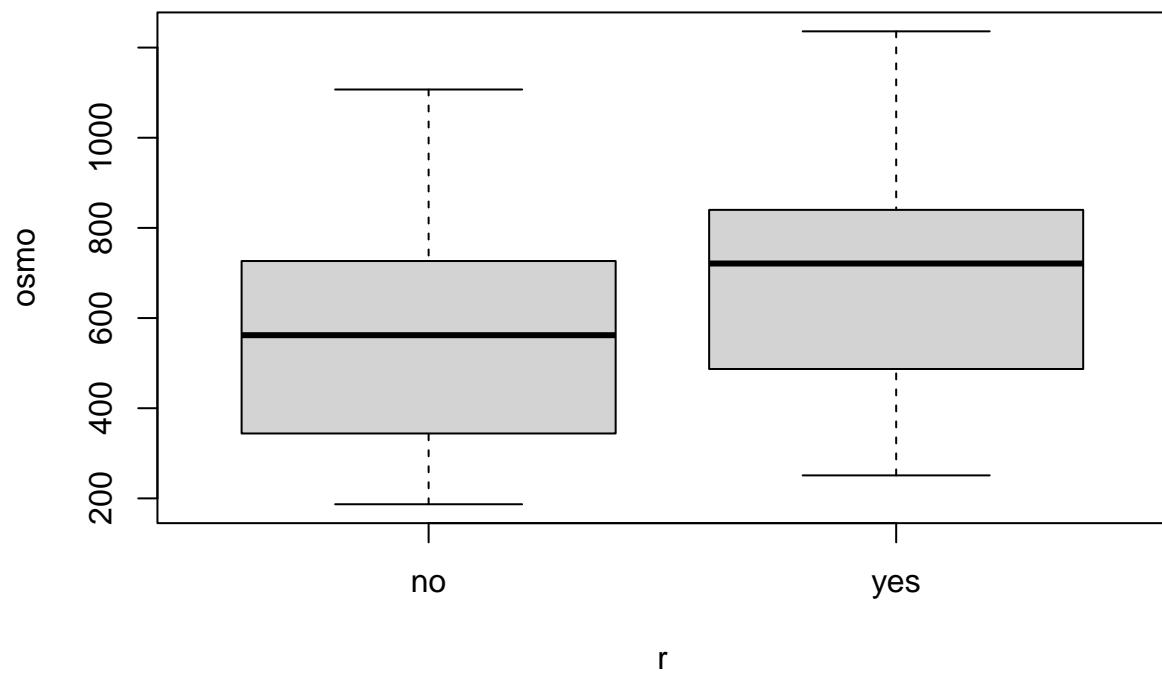
boxplot(gravity ~ r, data = urine)
```



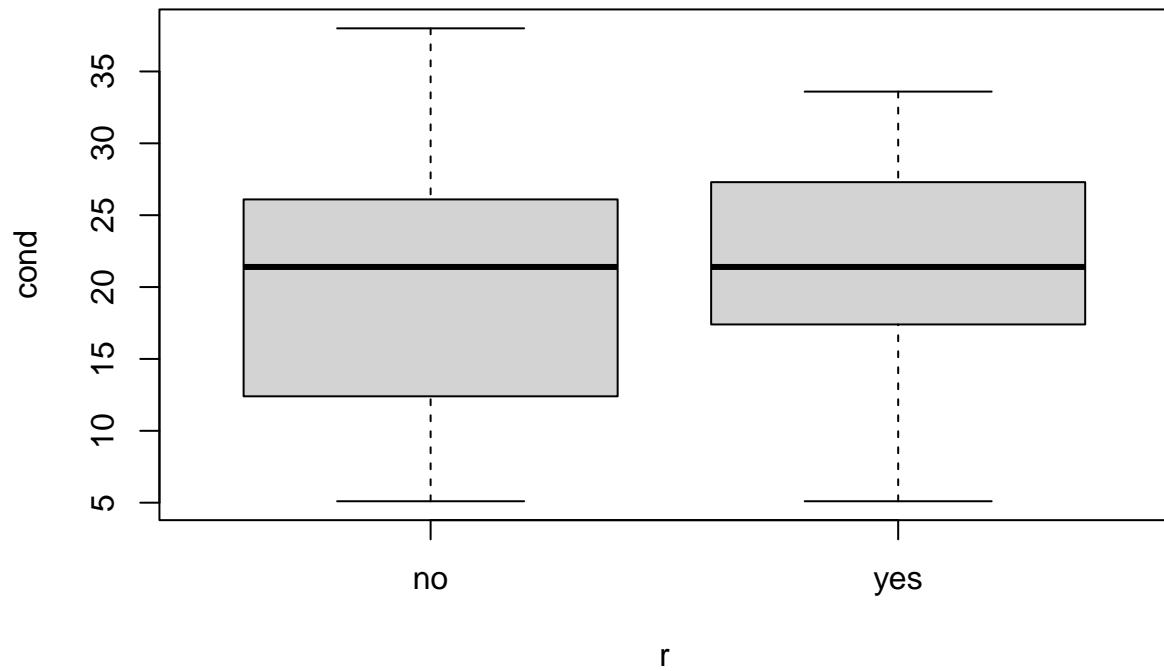
```
boxplot(ph ~ r, data = urine)
```



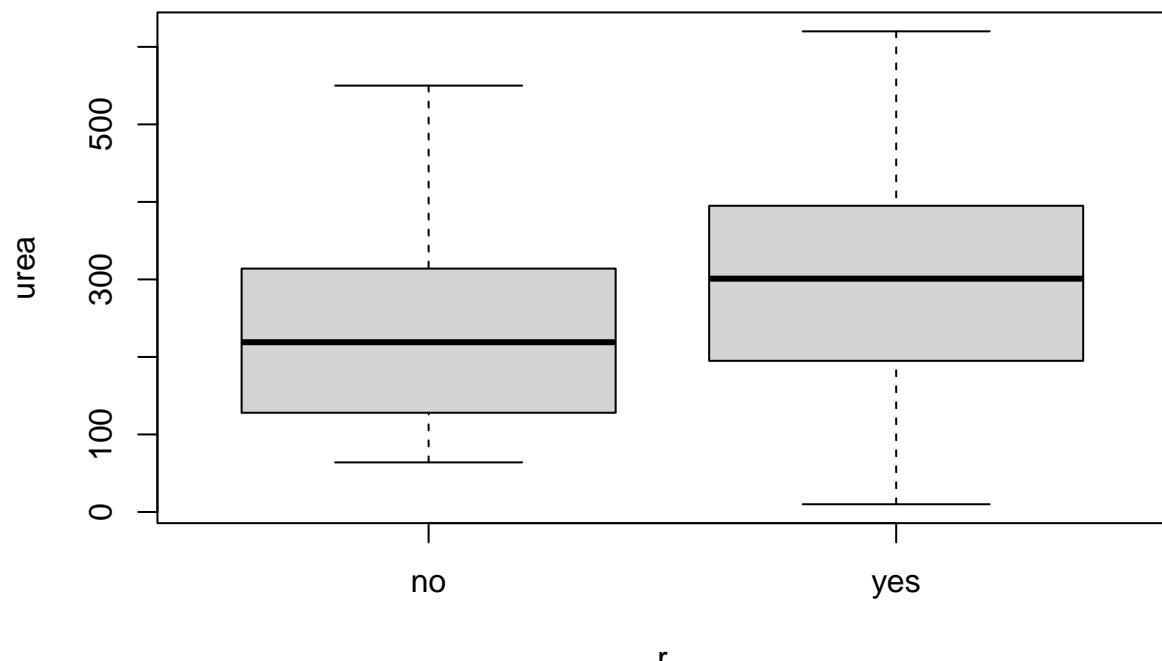
```
boxplot(osmo ~ r, data = urine)
```



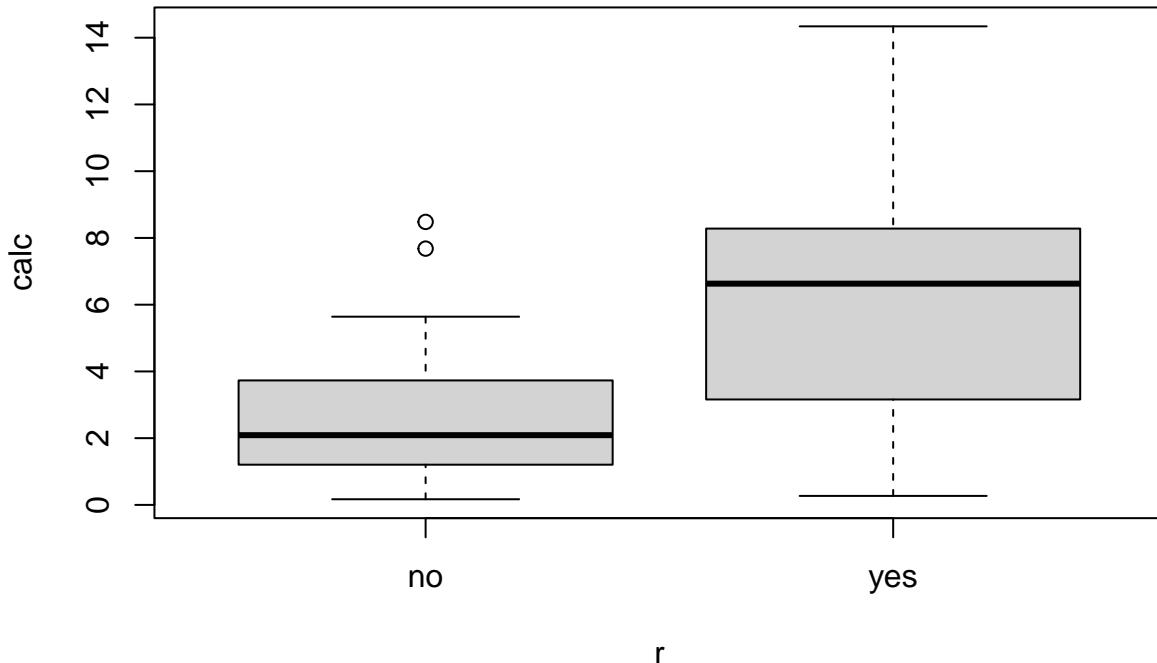
```
boxplot(cond ~ r, data = urine)
```



```
boxplot(urea ~ r, data = urine)
```



```
boxplot(calc ~ r, data = urine)
```



Covariates that visually appear to have an affect on  $r$  and could be useful in predicting for it are: gravity, osmo, urea, calc. ph and cond does not appear to differ as much between the two groups.

### (b) Fit logistic regression model, hypothesis testing.

Hypothesis testing:

- $H_0: \beta_j = 0$ , means that no covariates significant in predicting  $r$
- $H_1: \beta_j \neq 0$ , means that at least one covariate is useful for predicting  $r$ . The test statistic is the likelihood ratio test statistic, which is  $LR = -2(\ell(\hat{\beta}_{null}) - \ell(\hat{\beta}_{full})) \sim \chi_p^2$ , where  $p$  is the number of covariates in the full model, 6 in this case. The p-value is  $P(T > LR)$ , where  $T \sim \chi_p^2$  under  $H_0$ . The rejection region at significance level  $\alpha$  is  $LR > \chi_{p,1-\alpha}^2$ ,  $p = 6$  in this case.

```
# model
lr_full <- glm(r ~ gravity + ph + osmo + cond + urea + calc, data = urine, family = binomial)

# intercept-only model
lr_incp <- glm(r ~ 1, data = urine, family = binomial)

summary(lr_full)

##
## Call:
## glm(formula = r ~ gravity + ph + osmo + cond + urea + calc, family = binomial,
```

```

##      data = urine)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -355.33771  222.76696 -1.595  0.11069
## gravity      355.94379  222.11004  1.603  0.10903
## ph          -0.49570   0.56976 -0.870  0.38429
## osmo         0.01681   0.01782  0.944  0.34536
## cond        -0.43282   0.25123 -1.723  0.08493 .
## urea        -0.03201   0.01612 -1.986  0.04703 *
## calc         0.78369   0.24216  3.236  0.00121 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 105.17  on 76  degrees of freedom
## Residual deviance: 57.56  on 70  degrees of freedom
## AIC: 71.56
##
## Number of Fisher Scoring iterations: 6

# likelihood ratio test
anova(lr_incp, lr_full, test = "Chisq")

```

```

## Analysis of Deviance Table
##
## Model 1: r ~ 1
## Model 2: r ~ gravity + ph + osmo + cond + urea + calc
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       76     105.17
## 2       70     57.56  6    47.608 1.415e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

The p-value is very small, so we reject  $H_0$  and conclude that at least one covariate is useful for predicting  $r$ , the presence of calcium oxalate crystals. The full model does appear to be a significant improvement over the null model. This is shown in the decrease in deviance.

### (c) Backward selection, AIC.

```

library(MASS)

# model obtained using backward selection
bkwd_model <- step(lr_full, direction = "backward")

## Start:  AIC=71.56
## r ~ gravity + ph + osmo + cond + urea + calc
##
##             Df Deviance     AIC
## - ph       1   58.331 70.331

```

```

## - osmo      1  58.502 70.502
## <none>          57.560 71.560
## - gravity   1  60.290 72.290
## - cond      1  60.957 72.957
## - urea      1  62.108 74.108
## - calc      1  79.261 91.261
##
## Step:  AIC=70.33
## r ~ gravity + osmo + cond + urea + calc
##
##           Df Deviance    AIC
## - osmo      1  59.071 69.071
## <none>          58.331 70.331
## - gravity   1  61.224 71.224
## - cond      1  61.369 71.369
## - urea      1  62.352 72.352
## - calc      1  79.801 89.801
##
## Step:  AIC=69.07
## r ~ gravity + cond + urea + calc
##
##           Df Deviance    AIC
## <none>      59.071 69.071
## - urea      1  67.048 75.048
## - cond      1  70.891 78.891
## - gravity   1  75.798 83.798
## - calc      1  79.851 87.851

summary(bkwd_model)

##
## Call:
## glm(formula = r ~ gravity + cond + urea + calc, family = binomial,
##      data = urine)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -500.01090 161.87095 -3.089 0.00201 ***
## gravity      497.12038 161.32939  3.081 0.00206 ***
## cond        -0.20547  0.07105 -2.892 0.00383 **
## urea        -0.01783  0.00723 -2.466 0.01367 *
## calc         0.72232  0.21997  3.284 0.00102 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 105.168 on 76 degrees of freedom
## Residual deviance: 59.071 on 72 degrees of freedom
## AIC: 69.071
##
## Number of Fisher Scoring iterations: 6

```

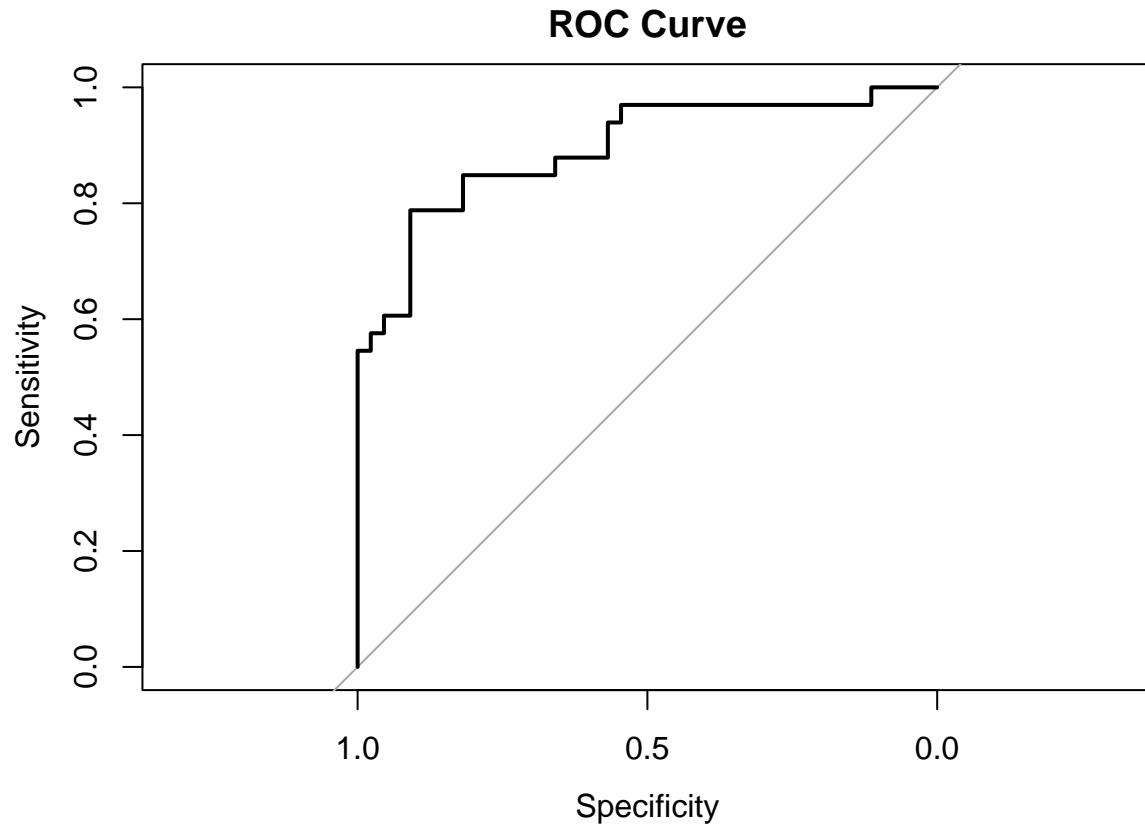
```
AIC(bkwd_model)
```

```
## [1] 69.07103
```

The best subset of variables is calc, gravity, cond, urea.

(d) ROC curve.

```
# Install if needed:  
# install.packages("pROC")  
  
library(pROC)  
  
# Predicted probabilities from selected model  
prob <- predict(bkwd_model, type = "response")  
  
# Create ROC object  
model_roc <- roc(urine$r, prob)  
  
# ROC curve  
plot(model_roc, main = "ROC Curve")
```



```

auc(model_roc)

## Area under the curve: 0.8933

# best probability threshold
best_coords <- coords(model_roc, "best", ret = c("threshold", "sensitivity", "specificity"))

best_coords

## threshold sensitivity specificity
## 1 0.4830697 0.7878788 0.9090909

```

The AUC is 0.8933. The best threshold is 0.4831, with sensitivity 0.7879 and specificity 0.9091.

**(e) Confusion matrix, FP, TP, predictive values.**

```

# Extract optimal threshold
threshold <- 0.4830697

# prediction classes based on threshold above
pred_class <- ifelse(prob > threshold, "yes", "no")
pred_class <- factor(pred_class, levels = c("no", "yes"))

# confusion matrix
conf_matrix <- table(Predicted = pred_class, Actual = urine$r)

conf_matrix

##          Actual
## Predicted no yes
##       no 40   7
##       yes  4  26

TN <- conf_matrix["no", "no"]
TP <- conf_matrix["yes", "yes"]
FP <- conf_matrix["yes", "no"]
FN <- conf_matrix["no", "yes"]

TPR <- TP / (TP + FN)    # Sensitivity
FPR <- FP / (FP + TN)    # False Positive Rate
PPV <- TP / (TP + FP)    # Positive Predictive Value
NPV <- TN / (TN + FN)    # Negative Predictive Value

TPR

## [1] 0.7878788

```

```
FPR
```

```
## [1] 0.09090909
```

```
PPV
```

```
## [1] 0.86666667
```

```
NPV
```

```
## [1] 0.8510638
```

#### (f) Effectiveness of logistic regression model.

The logistic regression model performs well overall in predicting for calcium oxalate crystals.

### Q4

#### (a) Poisson regression model, parameter interpretation.

```
# Read data
elephant <- read.csv("elephant.csv")

# Inspect data
str(elephant)

## 'data.frame':    41 obs. of  2 variables:
##   $ AGE      : num  27 28 28 28 28 29 29 29 29 29 ...
##   $ MATINGS: num  0 1 1 1 3 0 0 0 2 2 ...

summary(elephant)

##          AGE            MATINGS
##  Min.   :27.00   Min.   :0.000
##  1st Qu.:29.00  1st Qu.:1.000
##  Median :34.00  Median :2.000
##  Mean   :35.85  Mean   :2.683
##  3rd Qu.:42.00  3rd Qu.:3.000
##  Max.   :52.00  Max.   :9.000

poisson_model <- glm(MATINGS ~ AGE, data = elephant, family = poisson)

summary(poisson_model)

## 
## Call:
## glm(formula = MATINGS ~ AGE, family = poisson, data = elephant)
```

```

## 
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.58201   0.54462 -2.905  0.00368 **
## AGE          0.06869   0.01375  4.997 5.81e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for poisson family taken to be 1)
## 
## Null deviance: 75.372 on 40 degrees of freedom
## Residual deviance: 51.012 on 39 degrees of freedom
## AIC: 156.46
## 
## Number of Fisher Scoring iterations: 5

```

(b) 95% confidence interval for parameters

```

# Wald CI
confint(poisson_model)

##           2.5 %      97.5 %
## (Intercept) -2.66669764 -0.52892903
## AGE         0.04167776  0.09563762

exp(confint(poisson_model)[ "AGE", ])
##      2.5 %    97.5 %
## 1.042558 1.100360

```

(c) predicted mating rate and CI for prediction.

```

new_data <- data.frame(AGE = 31)

pred <- predict(poisson_model, new_data, se.fit = TRUE)

lambda_hat <- exp(pred$fit)
lambda_hat

##           1
## 1.728872

# 95% CI on log scale
lower_log <- pred$fit - 1.96 * pred$se.fit
upper_log <- pred$fit + 1.96 * pred$se.fit

lower <- exp(lower_log)
upper <- exp(upper_log)

c(lower, upper)

```

```
##      1      1
## 1.299546 2.300033
```

Predicted mating rate for 31-year-old elephant is 1.7289, with 95% CI (1.2995, 2.3000).

#### (d) significance of number of matings.

Hypothesis testing:

- $H_0: \beta_{AGE} = 0$ , means that AGE is not significantly related to the number of matings
- $H_1: \beta_{AGE} \neq 0$ , means that AGE is significantly related to the number of matings

```
anova(poisson_model, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: MATINGS
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL           40    75.372
## AGE     1     24.36       39    51.012 7.991e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

MATINGS is significantly related to AGE, the p-value is very small.

#### (e) quadratic term instead of linear.

```
quad_model <- glm(MATINGS ~ AGE + I(AGE^2),
                     data = elephant,
                     family = poisson)

summary(quad_model)

##
## Call:
## glm(formula = MATINGS ~ AGE + I(AGE^2), family = poisson, data = elephant)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.8574060  3.0356383 -0.941   0.347
## AGE         0.1359544  0.1580095  0.860   0.390
## I(AGE^2)    -0.0008595  0.0020124 -0.427   0.669
##
```

```
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 75.372 on 40 degrees of freedom
## Residual deviance: 50.826 on 38 degrees of freedom
## AIC: 158.27
##
## Number of Fisher Scoring iterations: 5
```

```
anova(poisson_model, quad_model, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: MATINGS ~ AGE
## Model 2: MATINGS ~ AGE + I(AGE^2)
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       39     51.012
## 2       38     50.826  1    0.18544  0.6667
```

```
AIC(poisson_model, quad_model)
```

```
##             df      AIC
## poisson_model 2 156.4578
## quad_model     3 158.2723
```

```
b1 <- coef(quad_model)[ "AGE"]
b2 <- coef(quad_model)[ "I(AGE^2)"]

max_age <- -b1 / (2 * b2)
max_age
```

```
##      AGE
## 79.08861
```

The poisson model has better AIC score, and the anova() does not show a significant improvement with the quadratic term, so we prefer the simpler linear model. Since we don't use the quad\_model, we cannot determine if there is a maximum age.