

STATS3860 Assign1

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2026-02-26

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 $N(p, \text{Var}(\hat{p}_{MLE}))$, 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 α 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 $p\text{-val} = P(T > LR)$, where $T \sim \chi_1^2$ under H_0 . So the rejection region at significance level α is

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

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

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

$$\begin{aligned} SE(\hat{p}_{MLE}) &= \sqrt{\frac{0.35 \times (1 - 0.35)}{100}} = 0.04769696 \\ W &= \frac{\hat{p}_{MLE} - p^*}{SE(\hat{p}_{MLE})} = \frac{0.35 - 0.4}{0.04769696} = -1.048284837 \\ z_{\alpha/2} &= z_{0.025} = 1.96 \end{aligned}$$

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

LRT test:

$$\begin{aligned} \ell(0.35) &= \ln \binom{100}{35} + 35 \ln 0.35 + 65 \ln 0.65 = \ln \binom{100}{35} - 64.7447 \\ \ell(0.4) &= \ln \binom{100}{35} + 35 \ln 0.4 + 65 \ln 0.6 = \ln \binom{100}{35} - 65.2738 \end{aligned}$$

$$\begin{aligned} LR &= -2(\ell(p^*) - \ell(\hat{p}_{MLE})) \dot{\sim} \chi_1^2 \\ LR &= -2(\ell(0.4) - \ell(0.35)) = -2(-65.2738 - (-64.7447)) = 1.0582 \\ \chi_{1,1-0.05}^2 &= \chi_{1,0.95}^2 = 3.841 \end{aligned}$$

We fail to reject H_0 since $LR \not> \chi_{1,1-\alpha}^2$, $1.0582 < 3.841$.

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

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

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

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

```
# same for Q2
```

Q2

(a) MLE of λ 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

$$L(\lambda | y_i) = \prod_{i=1}^n f(y_i | \lambda) = \prod_{i=1}^n \frac{e^{-\lambda} \lambda^{y_i}}{y_i!} = \frac{e^{-n\lambda} \lambda^{\sum y_i}}{y_1! y_2! \cdots y_n!}$$

$$\ell(\lambda | y_i) = \ln L(\lambda | y_i) = \ln \left(\frac{e^{-n\lambda} \lambda^{\sum y_i}}{y_1! y_2! \cdots y_n!} \right) = -n\lambda + (\sum y_i) \ln \lambda - \sum \ln(y_i!)$$

$$\frac{\partial \ell(\lambda | y_i)}{\partial \lambda} = -n + \frac{\sum y_i}{\lambda}$$

Set to 0 for a maximum:

$$\frac{\partial \ell(\lambda | y_i)}{\partial \lambda} = -n + \frac{\sum y_i}{\lambda} = 0$$

$$n = \frac{\sum y_i}{\lambda}$$

$$\therefore \hat{\lambda}_{MLE} = \frac{\sum y_i}{n} = \bar{y}$$

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,

$$\text{Var}(\hat{\lambda}_{MLE}) = \frac{1}{I(\hat{\lambda}_{MLE})}, \quad I(\hat{\lambda}_{MLE}) = -E \left[\frac{\partial^2 \ell(\lambda)}{\partial \lambda^2} \right]$$

$$I(\hat{\lambda}_{MLE}) = -E \left[\frac{\partial}{\partial \lambda} \left(-n + \frac{\sum y_i}{\lambda} \right) \right]$$

$$I(\hat{\lambda}_{MLE}) = -E \left[-\frac{\sum y_i}{\lambda^2} \right]$$

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

$$I(\hat{\lambda}_{MLE}) = \frac{n\lambda}{\lambda^2} = \frac{n}{\hat{\lambda}_{MLE}}$$

$$\text{Var}(\hat{\lambda}_{MLE}) = \frac{\hat{\lambda}_{MLE}}{n} = \frac{\bar{y}}{n}$$

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

(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

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

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 α 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 $p\text{-val} = P(T > LR)$, where $T \sim \chi_1^2$ under H_0 . So the rejection region at significance level α 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 λ 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")

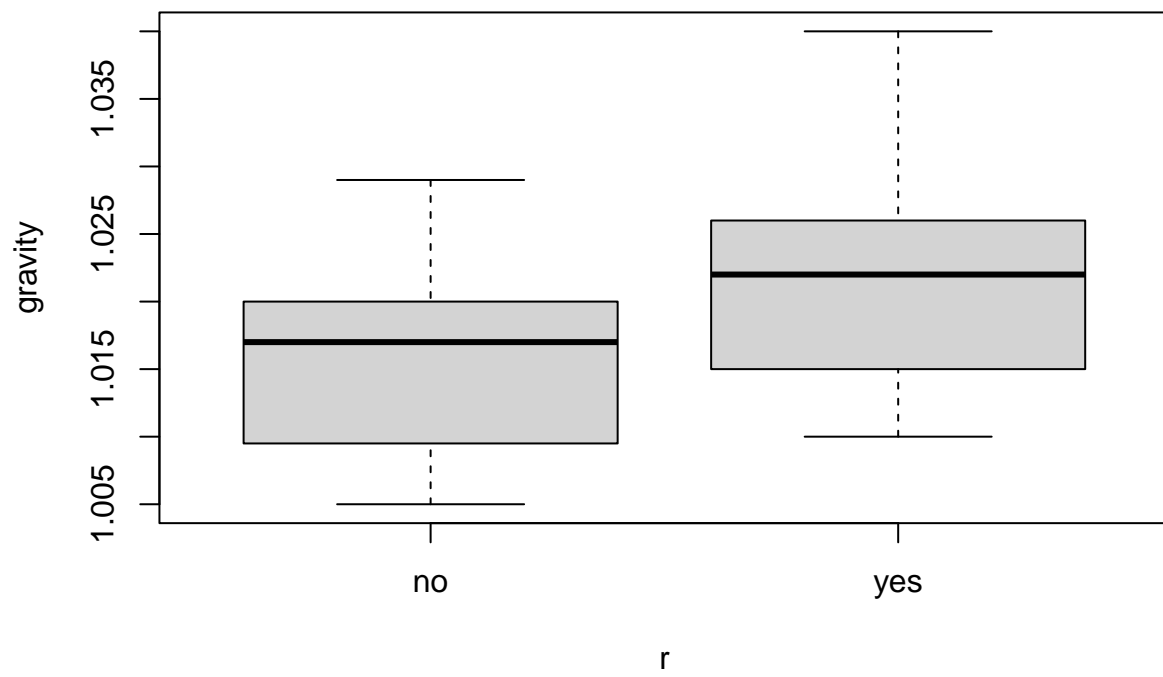
# ?urine

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

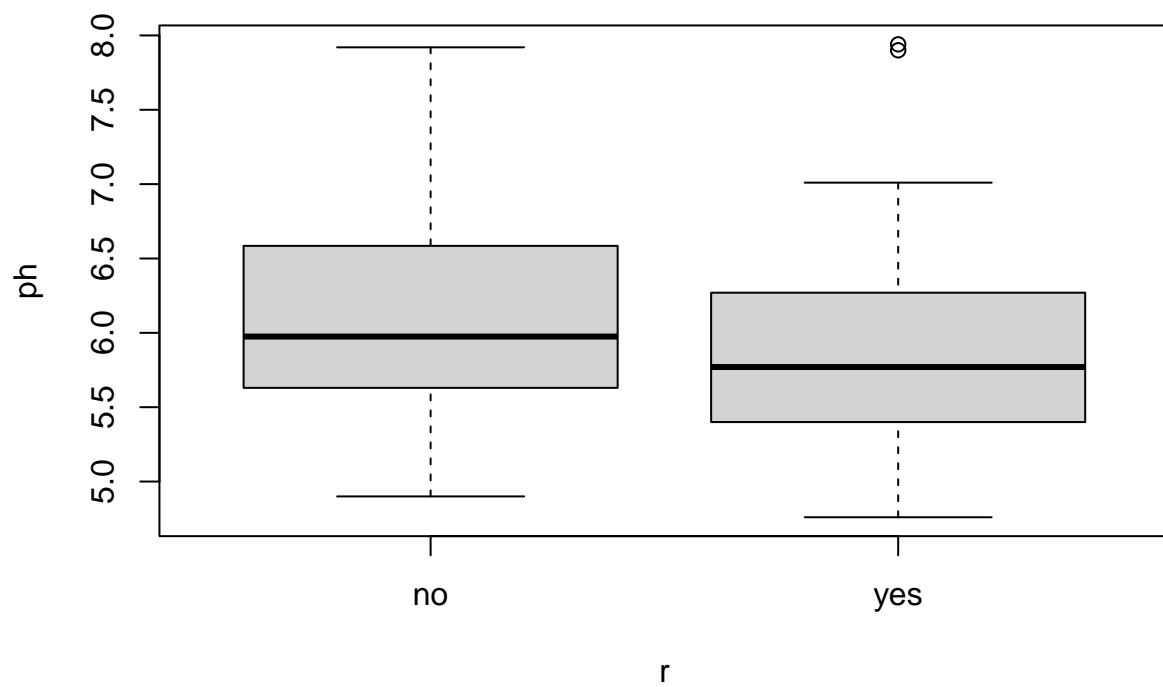
summary(urine)
```

```
##      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
```

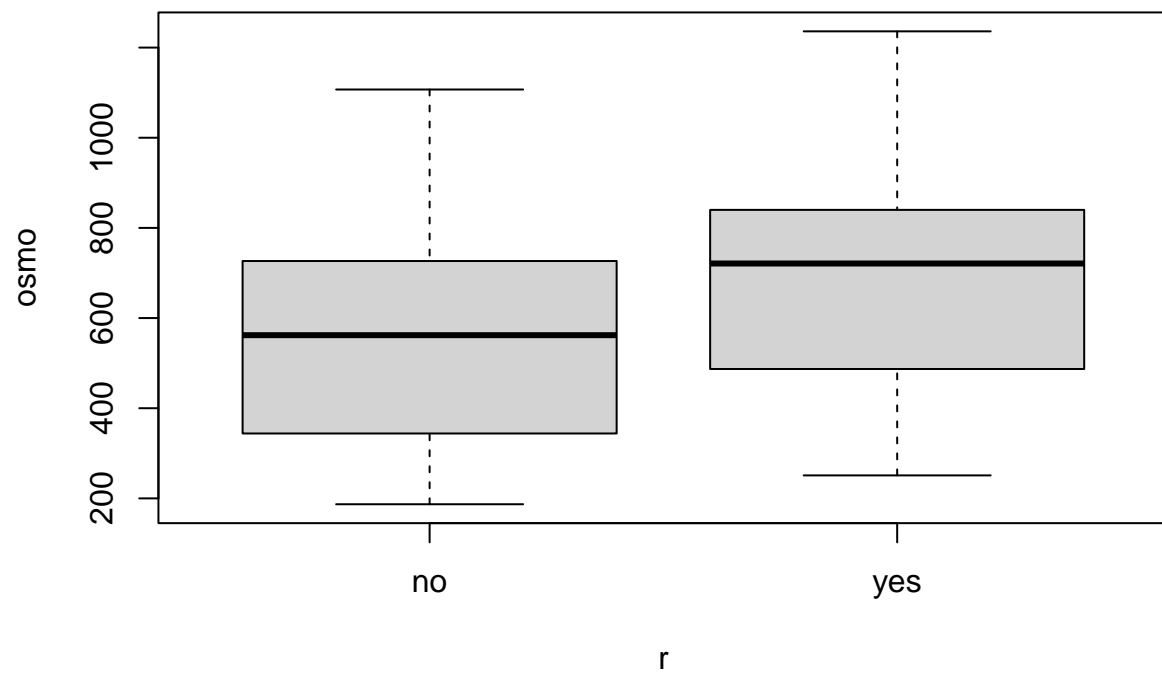
```
boxplot(gravity ~ r, data = urine)
```



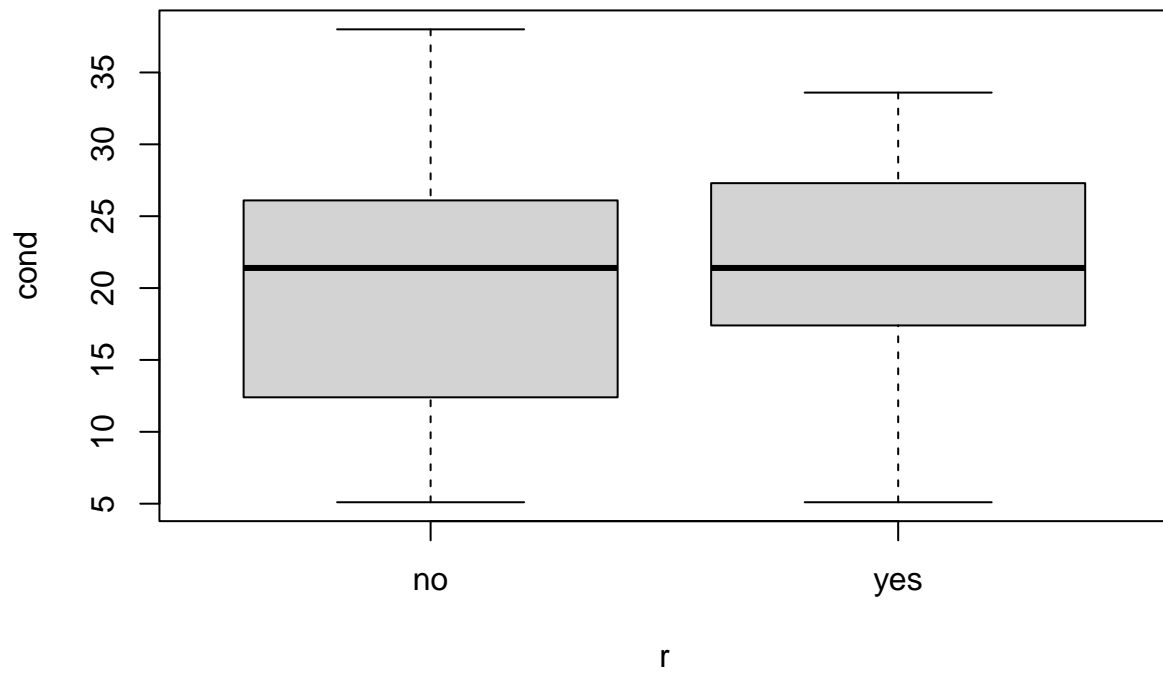
```
boxplot(ph ~ r, data = urine)
```



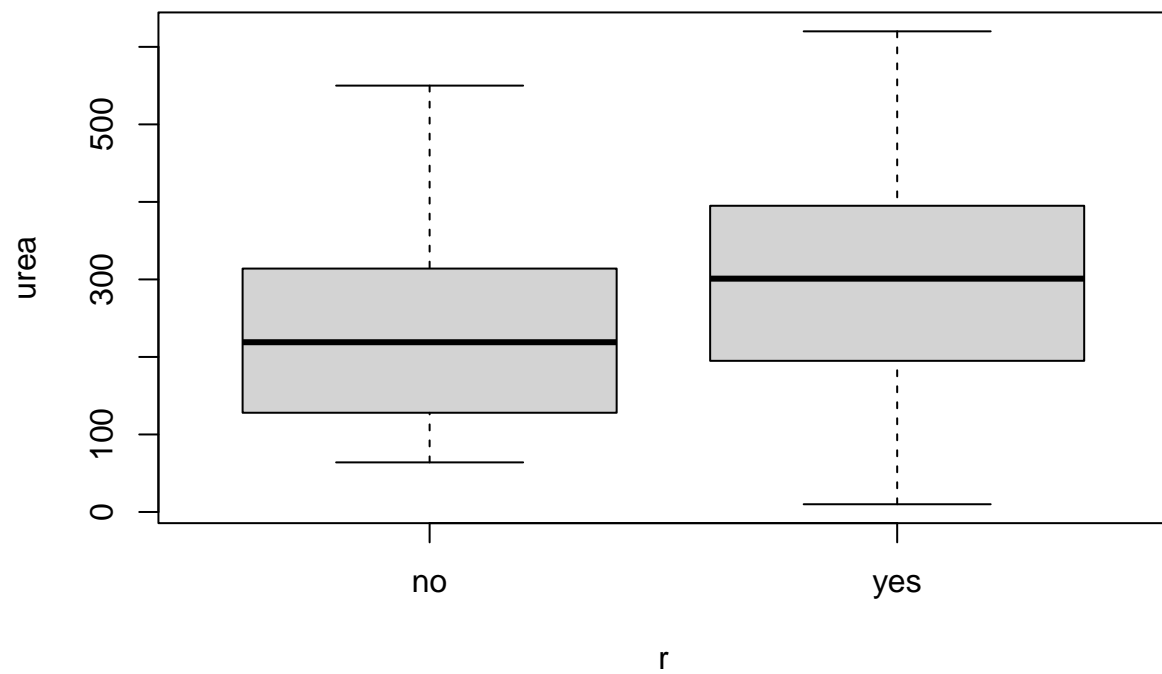
```
boxplot(osmo ~ r, data = urine)
```



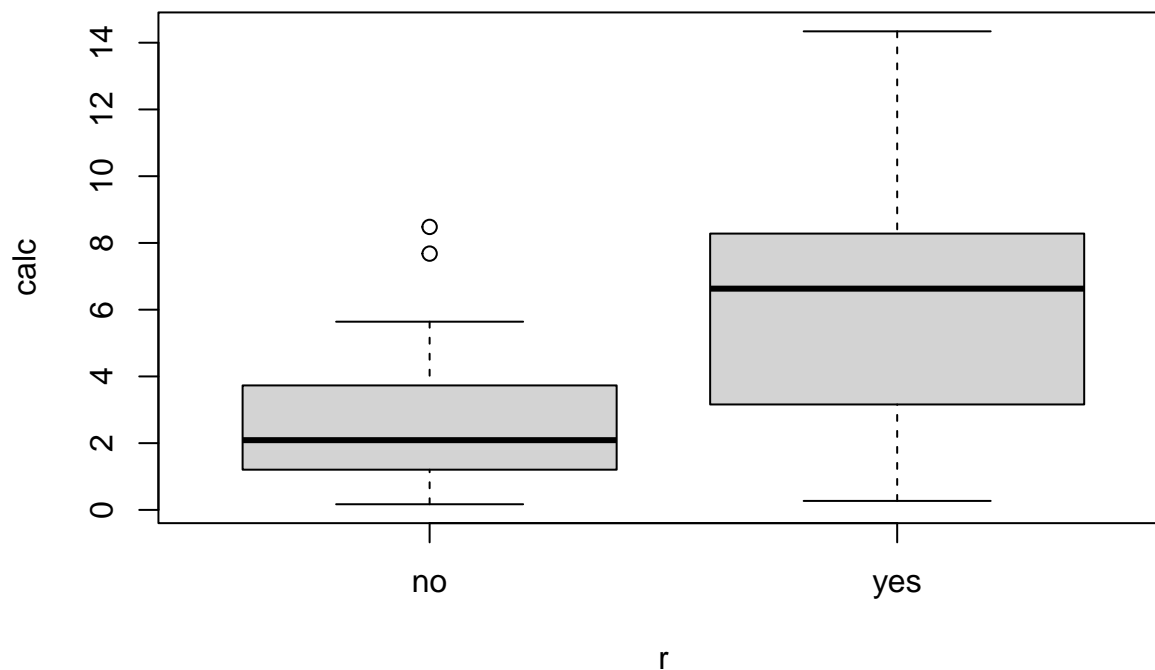
```
boxplot(cond ~ r, data = urine)
```



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



```
boxplot(urea ~ 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 $LR = -2 \left(\ell(\hat{\beta}_{null}) - \ell(\hat{\beta}_{full}) \right) \sim \chi_p^2$, 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 α 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 oxalae 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
```

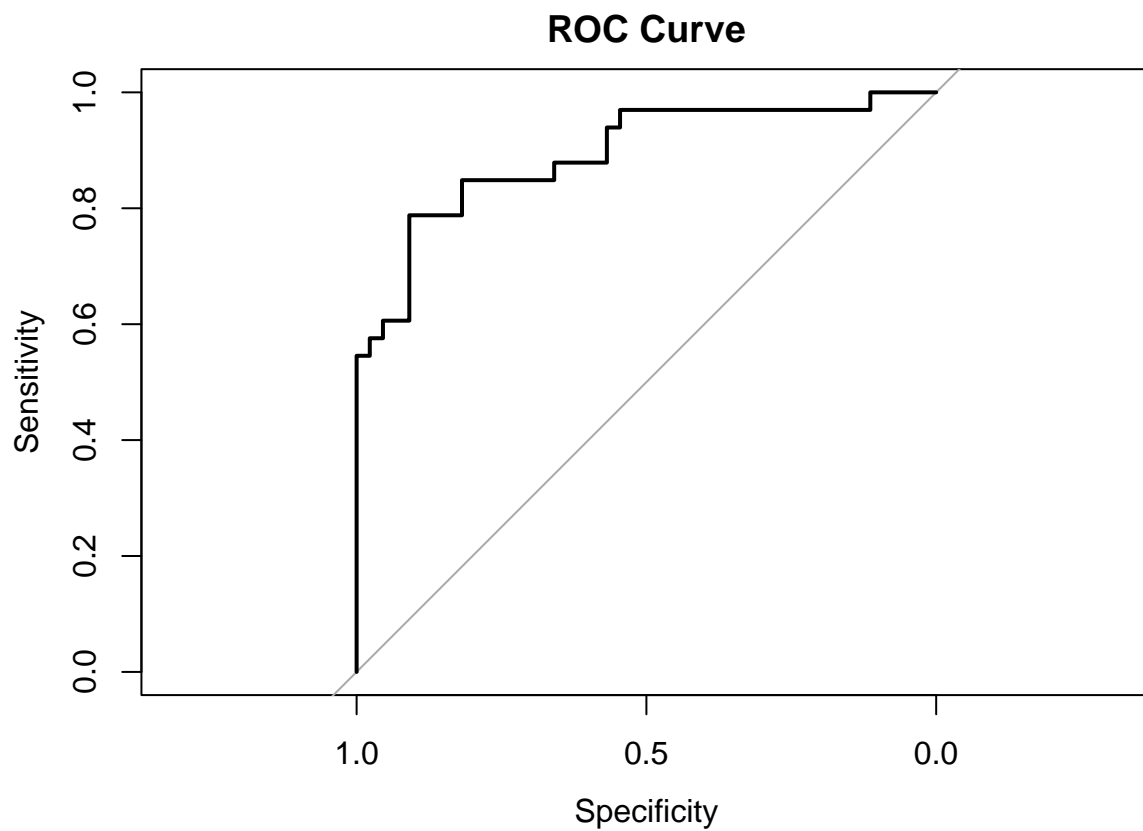
```
AIC(bkwd_model)
```

```
## [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] 0.8666667
```

```
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.