

Epidemiological exercises in R

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2019-08-02

Contents

Prerequisites	5
1 Exercise 4	7
1.1 Load packages	7
1.2 Import data	7
1.3 First mixed model	8
1.4 Second mixed model	13
2 Exercise 9.4	19
2.1 Load packages	19
2.2 Data	19
2.3 Autocorrelation statistics	20
2.4 First variogram	23
2.5 Second variogram	24
2.6 Variogram model selection	26
3 Exercise 9.5	31
3.1 Load packages	31
3.2 Data	31
3.3 Autocorrelation statistics	32
3.4 First variogram	35
3.5 Second variogram	36
3.6 Variogram model selection	38

4	Yield loss	43
4.1	Load packages	43
4.2	Data	43
4.3	Mixed model for response variable DS	44
4.4	Mixed model for response variable YIELD	51
4.5	Linear regression between YIELD and DS	58
4.6	Mixed model for RY2	61
4.7	Linear regression between RY2 and CDS	63
A	SAS code	65
A.1	Exercise 4	65
A.2	Exercise 9.4	68
A.3	Exercise 9.5	69
A.4	Yield loss	72

Prerequisites

To run these exercises, you will need to install the latest version of R (<https://cloud.r-project.org/>) and RStudio (<https://www.rstudio.com/products/rstudio/download/>) on your computer. Please click on the above mentioned links to go to the download pages of R and RStudio.

These exercises are a work in progress, and are an attempt to translate SAS code written by Tim Todd into R.

Chapter 1

Exercise 4

1.1 Load packages

Here is the R code to download the required packages for this exercise.

```
# install package manager 'pacman'  
if (!require(pacman)){  
  install.packages('pacman')  
}
```

Loading required package: pacman

Load the packages needed for this exercise:

```
pacman::p_load(tidyverse,  
               nlme,  
               emmeans)
```

1.2 Import data

Our data is located in `ex4.csv` file, which can be found on my github repo. Import the data and create new variables using the code below.

```
# import data  
a <- read_csv("https://raw.githubusercontent.com/luckymehra/epidem-exercises/master/data/ex4.csv")  
col_types = cols(  
  blk = col_factor(), # parse blk as a factor
```

Table 1.1: The first 6 rows of dataset *a*.

plot	t	blk	trt	pctsev	y	ystar	wt
101	0	1	2	9	0.09	-2.313635	0.0819
102	0	1	1	6	0.06	-2.751535	0.0564
103	0	1	3	2	0.02	-3.891820	0.0196
201	0	2	2	7	0.07	-2.586689	0.0651
202	0	2	3	5	0.05	-2.944439	0.0475
203	0	2	1	3	0.03	-3.476099	0.0291

```

      trt = col_factor() # parse trt as a factor
    ))

# create new variables
a$y <- a$pctsev/100
a$ystar <- log(a$y/(1-a$y))
a$wt <- a$y*(1-a$y)

# print the data
knitr::kable(head(a),
               caption = "The first 6 rows of dataset *a*.")

# get a glimpse of data
glimpse(a)

```

```

## Observations: 72
## Variables: 8
## $ plot      <dbl> 101, 102, 103, 201, 202, 203, 301, 302, 303, 401, 402, ...
## $ t         <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 7, 7, 7, 7, 7, 7, 7...
## $ blk       <fct> 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4, 1, 1, 1, 2, 2, 2, 3...
## $ trt       <fct> 2, 1, 3, 2, 3, 1, 3, 2, 1, 1, 2, 3, 2, 1, 3, 2, 3, 1, 3...
## $ pctsev    <dbl> 9, 6, 2, 7, 5, 3, 4, 2, 6, 1, 1, 4, 4, 6, 10, 2, 5, 3, ...
## $ y         <dbl> 0.09, 0.06, 0.02, 0.07, 0.05, 0.03, 0.04, 0.02, 0.06, 0...
## $ ystar     <dbl> -2.313635, -2.751535, -3.891820, -2.586689, -2.944439, ...
## $ wt        <dbl> 0.0819, 0.0564, 0.0196, 0.0651, 0.0475, 0.0291, 0.0384, ...

```

1.3 First mixed model

1.3.1 Fit the model

Run the mixed model analysis using **nlme** package in R. The function used to fit the mixed model is called `lme()`.


```

# fit the model

mm_1 <- lme(ystar ~ trt*t, # fixed effects
            data = a,
            random = list(blk = ~ 1, plot = ~ 1), # random effects
            correlation = corAR1(form = (plot = ~ 1)), # specify that observations within a plot
            contrasts = list(trt = "contr.SAS"), # specify this option to get parameter estimates
            weights = ~ I(1/wt))

# output the summary
summary(mm_1)

## Linear mixed-effects model fit by REML
## Data: a
##      AIC      BIC    logLik
## 210.5257 232.4222 -95.26285
##
## Random effects:
## Formula: ~1 | blk
##      (Intercept)
## StdDev: 0.1887117
##
## Formula: ~1 | plot %in% blk
##      (Intercept) Residual
## StdDev: 4.604287e-05 0.2519511
##
## Correlation Structure: AR(1)
## Formula: ~1 | blk/plot
## Parameter estimate(s):
##      Phi
## 0.06205463
## Variance function:
## Structure: fixed weights
## Formula: ~I(1/wt)
## Fixed effects: ystar ~ trt * t
##              Value Std.Error DF   t-value p-value
## (Intercept) -2.5689859 0.3629604 57 -7.077868 0.0000
## trt2         -0.1948084 0.5193013  6 -0.375136 0.7205
## trt1         -0.5406041 0.5136249  6 -1.052527 0.3331
## t            0.0992675 0.0142177 57  6.981964 0.0000
## trt2:t       -0.0221696 0.0202998 57 -1.092109 0.2794
## trt1:t       0.0437431 0.0212717 57  2.056398 0.0443
## Correlation:
##      (Intr) trt2   trt1   t      trt2:t
## trt2  -0.652

```

```
## trt1    -0.658  0.459
## t       -0.888  0.621  0.627
## trt2:t   0.623 -0.924 -0.439 -0.700
## trt1:t   0.592 -0.413 -0.913 -0.667  0.466
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -2.1518915 -0.6900213 -0.4024653  0.4132408  2.7733450
##
## Number of Observations: 72
## Number of Groups:
##           blk plot %in% blk
##           4      12
```

```
# extract covariance parameter estimates
VarCorr(mm_1)
```

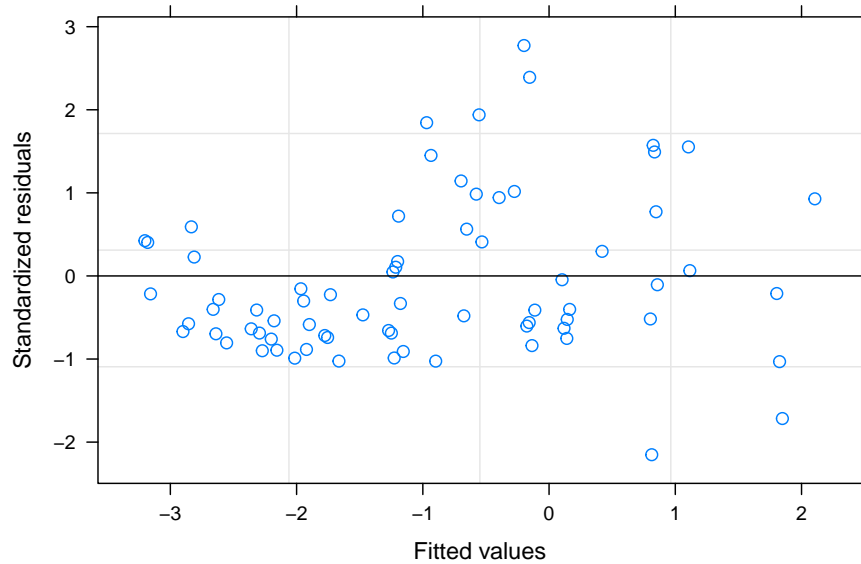
```
##           Variance      StdDev
## blk =      pdLogChol(1)
## (Intercept) 3.561212e-02 1.887117e-01
## plot =      pdLogChol(1)
## (Intercept) 2.119946e-09 4.604287e-05
## Residual    6.347936e-02 2.519511e-01
```

```
# extract type3 fixed effects anova
anova.lme(mm_1, type = 'marginal')
```

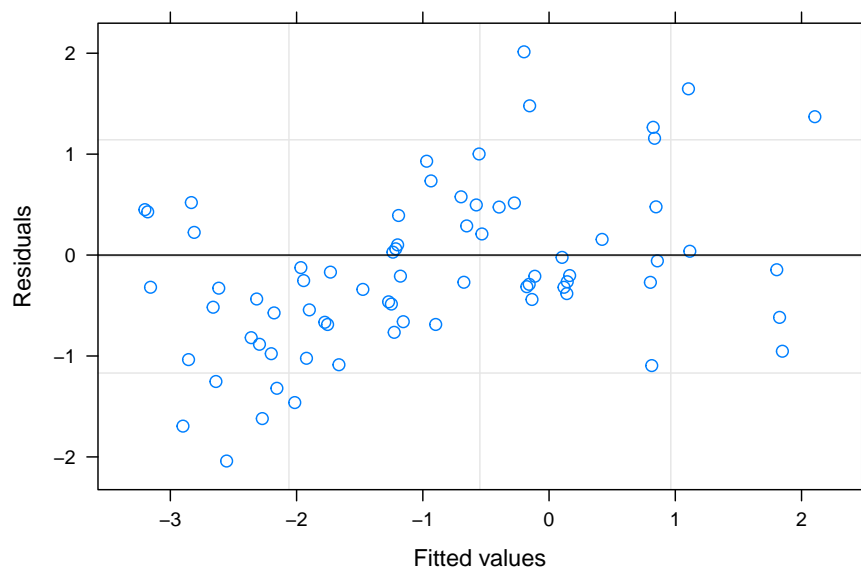
```
##           numDF denDF  F-value p-value
## (Intercept)      1    57 50.09622 <.0001
## trt              2     6  0.56135  0.5977
## t                1    57 48.74782 <.0001
## trt:t            2    57  4.80110  0.0118
```

1.3.2 Diagnostic plots

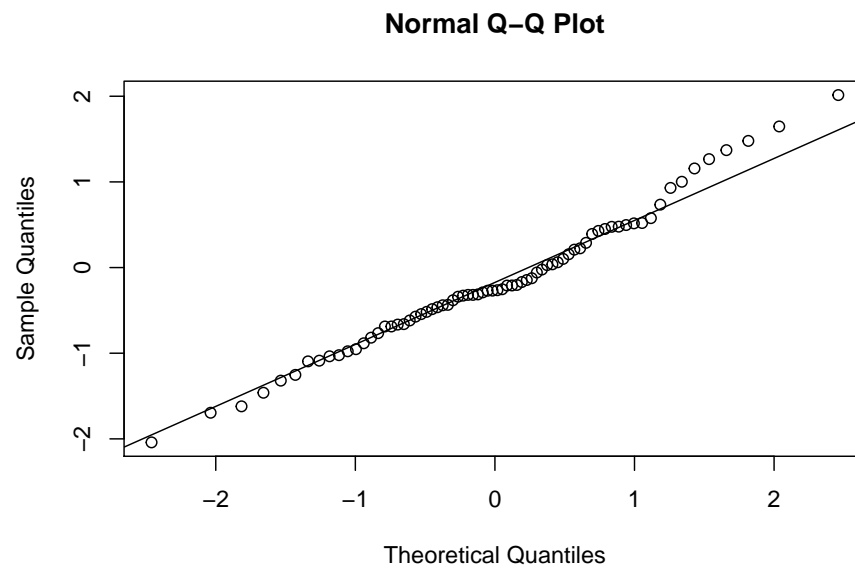
```
# pearson residuals vs. fitted values
plot(mm_1, resid(., type="pearson") ~ fitted(.), abline = 0)
```



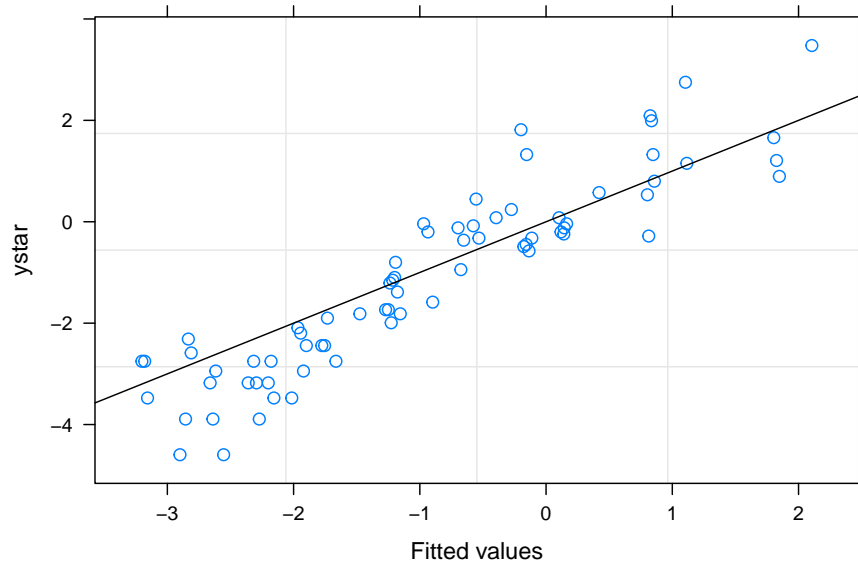
```
# standardized residuals vs. fitted values  
plot(mm_1, resid(., scaled=TRUE) ~ fitted(.), abline = 0)
```



```
# qq plot  
qqnorm(residuals(mm_1))  
qqline(residuals(mm_1))
```



```
#observed vs. fitted values  
plot(mm_1, ystar ~ fitted(.), abline = c(0,1))
```



1.4 Second mixed model

1.4.1 Fit the model

Run the mixed model analysis using **nlme** package in R. The function used to fit the mixed model is called `lme()`. Here we will specify no intercept. We will also use **emmeans** package to get least squared means and contrasts.

```
# fit the model
#library(nlme)
mm_2 <- update(mm_1, fixed = ystar ~ - 1 + trt + trt:t) # update fixed effects in mm_1, -1 indicates no intercept

# output the summary
summary(mm_2)

## Linear mixed-effects model fit by REML
## Data: a
##      AIC      BIC    logLik
## 210.5257 232.4222 -95.26285
##
## Random effects:
## Formula: ~1 | blk
```

```

##          (Intercept)
## StdDev:   0.1887117
##
## Formula: ~1 | plot %in% blk
##          (Intercept) Residual
## StdDev: 4.603147e-05 0.2519511
##
## Correlation Structure: AR(1)
## Formula: ~1 | blk/plot
## Parameter estimate(s):
##          Phi
## 0.06205463
## Variance function:
## Structure: fixed weights
## Formula: ~I(1/wt)
## Fixed effects: ystar ~ trt + trt:t - 1
##          Value Std.Error DF   t-value p-value
## trt2    -2.7637943 0.3944803   6 -7.006165 4e-04
## trt1    -3.1095900 0.3877657   6 -8.019250 2e-04
## trt3    -2.5689859 0.3629604   6 -7.077868 4e-04
## trt2:t    0.0770979 0.0144893  58  5.321034 0e+00
## trt1:t    0.1430106 0.0158560  58  9.019328 0e+00
## trt3:t    0.0992675 0.0142177  58  6.981964 0e+00
## Correlation:
##          trt2   trt1   trt3   trt2:t trt1:t
## trt1      0.057
## trt3      0.062  0.065
## trt2:t   -0.901  0.001  0.001
## trt1:t    0.001 -0.881 -0.002 -0.001
## trt3:t    0.000 -0.002 -0.888  0.000  0.002
##
## Standardized Within-Group Residuals:
##          Min          Q1          Med          Q3          Max
## -2.1518915 -0.6900213 -0.4024653  0.4132408  2.7733450
##
## Number of Observations: 72
## Number of Groups:
##          blk plot %in% blk
##          4          12

```

```

# extract covariance parameter estimates
VarCorr(mm_2)

```

```

##          Variance      StdDev
## blk =      pdLogChol(1)

```

```
## (Intercept) 3.561212e-02 1.887117e-01
## plot =      pdLogChol(1)
## (Intercept) 2.118896e-09 4.603147e-05
## Residual    6.347936e-02 2.519511e-01
```

```
# extract type3 fixed effects anova
anova.lme(mm_2, type = 'marginal')
```

```
##      numDF denDF  F-value p-value
## trt      3      6 48.57698 1e-04
## trt:t    3     58 52.74601 <.0001
```

```
# compare the slopes for different treatments
#library(emmeans)
```

```
emtrends(mm_2, pairwise ~ trt, var="t", adjust = "none")
```

```
## $emtrends
##   trt t.trend      SE df lower.CL upper.CL
## 2    0.0771 0.0145 58    0.0481    0.106
## 1    0.1430 0.0159 58    0.1113    0.175
## 3    0.0993 0.0142 58    0.0708    0.128
##
## d.f. method: containment
## Confidence level used: 0.95
##
## $contrasts
##   contrast estimate      SE df t.ratio p.value
## 2 - 1      -0.0659 0.0215 58   -3.067  0.0033
## 2 - 3      -0.0222 0.0203 58   -1.092  0.2793
## 1 - 3       0.0437 0.0213 58    2.056  0.0443
```

```
# get the treatment difference at various time points
```

```
emmeans(mm_2, pairwise ~ trt|t, nesting = NULL, at = list(t = c(0, 7, 14, 21, 28, 35)), adjust =
```

```
## $emmeans
## t = 0:
##   trt emmean      SE df lower.CL upper.CL
## 2    -2.7638 0.394   6    -3.729  -1.7985
## 1    -3.1096 0.388   6    -4.058  -2.1608
## 3    -2.5690 0.363   6    -3.457  -1.6809
##
## t = 7:
##   trt emmean      SE df lower.CL upper.CL
```

```

## 2 -2.2241 0.306 6 -2.974 -1.4746
## 1 -2.1085 0.295 6 -2.830 -1.3873
## 3 -1.8741 0.278 6 -2.555 -1.1931
##
## t = 14:
## trt emmean SE df lower.CL upper.CL
## 2 -1.6844 0.229 6 -2.246 -1.1232
## 1 -1.1074 0.219 6 -1.644 -0.5712
## 3 -1.1792 0.207 6 -1.687 -0.6719
##
## t = 21:
## trt emmean SE df lower.CL upper.CL
## 2 -1.1447 0.179 6 -1.582 -0.7072
## 1 -0.1064 0.184 6 -0.556 0.3437
## 3 -0.4844 0.168 6 -0.896 -0.0726
##
## t = 28:
## trt emmean SE df lower.CL upper.CL
## 2 -0.6051 0.179 6 -1.042 -0.1680
## 1 0.8947 0.210 6 0.380 1.4095
## 3 0.2105 0.183 6 -0.237 0.6581
##
## t = 35:
## trt emmean SE df lower.CL upper.CL
## 2 -0.0654 0.229 6 -0.626 0.4948
## 1 1.8958 0.282 6 1.207 2.5850
## 3 0.9054 0.242 6 0.314 1.4968
##
## d.f. method: containment
## Confidence level used: 0.95
##
## $contrasts
## t = 0:
## contrast estimate SE df t.ratio p.value
## 2 - 1 0.3458 0.537 6 0.644 0.5435
## 2 - 3 -0.1948 0.519 6 -0.375 0.7205
## 1 - 3 -0.5406 0.514 6 -1.053 0.3331
##
## t = 7:
## contrast estimate SE df t.ratio p.value
## 2 - 1 -0.1156 0.404 6 -0.286 0.7843
## 2 - 3 -0.3500 0.392 6 -0.893 0.4062
## 1 - 3 -0.2344 0.383 6 -0.613 0.5625
##
## t = 14:
## contrast estimate SE df t.ratio p.value

```



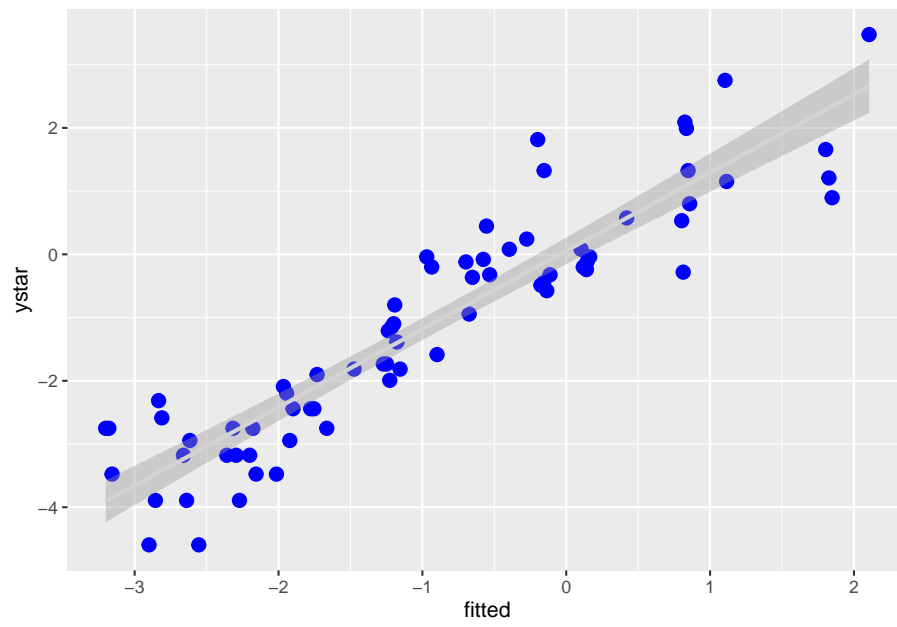
```
## 2 - 1      -0.5770 0.288  6 -2.004  0.0919
## 2 - 3      -0.5052 0.279  6 -1.811  0.1201
## 1 - 3       0.0718 0.271  6  0.265  0.7996
##
## t = 21:
## contrast estimate      SE df t.ratio p.value
## 2 - 1      -1.0384 0.219  6 -4.739  0.0032
## 2 - 3      -0.6604 0.206  6 -3.204  0.0185
## 1 - 3       0.3780 0.211  6  1.794  0.1229
##
## t = 28:
## contrast estimate      SE df t.ratio p.value
## 2 - 1      -1.4998 0.242  6 -6.204  0.0008
## 2 - 3      -0.8156 0.218  6 -3.741  0.0096
## 1 - 3       0.6842 0.245  6  2.795  0.0314
##
## t = 35:
## contrast estimate      SE df t.ratio p.value
## 2 - 1      -1.9611 0.338  6 -5.806  0.0011
## 2 - 3      -0.9707 0.305  6 -3.184  0.0190
## 1 - 3       0.9904 0.346  6  2.861  0.0288
```

1.4.2 Plot observed versus predicted model values

```
# add fitted and residuals in to a new dataset called b
b = cbind(a, resid = resid(mm_2), fitted = fitted(mm_2))

# fit linear regression
b.lm <- lm(ystar ~ fitted, data=b)

# plot using ggplot2 package
ggplot(b, aes(x=fitted, y = ystar)) +
  geom_point(color="blue", size = 3) +
  geom_smooth(method = lm, color = "lightgrey")
```



Chapter 2

Exercise 9.4

2.1 Load packages

Here is the R code to download the required packages for this exercise.

```
# install package manager 'pacman'  
if (!require(pacman)){  
  install.packages('pacman')  
}
```

Loading required package: pacman

```
# load packages needed for this exercise  
library(pacman)  
p_load(tidyverse,  
       lctools, # to calculate Moran's I  
       spdep, # to calculate geary's c  
       geoR, # to compute variogram  
       gridExtra, # to stack plots  
       gstat, automap, # packages for variogram model selection  
       sp # need a function called `coordinates`  
       )
```

2.2 Data

This is equivalent to data step in SAS. Here, the data is entered inside a function called `tibble`.

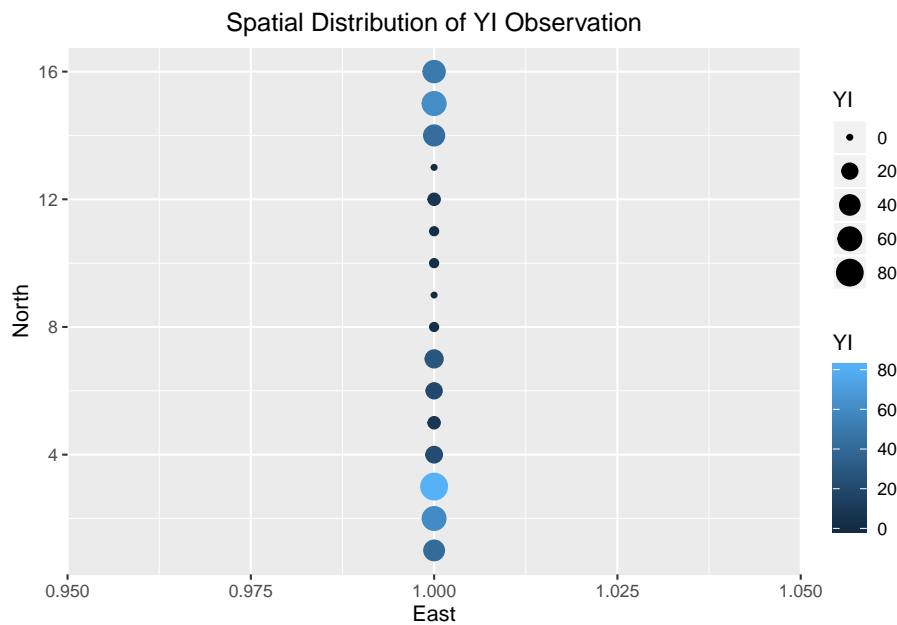
```
# Enter data
a <- tibble(I = 1:16, YI = c(41, 60, 81, 22, 8, 20, 28, 2,
                           0, 2, 2, 8, 0, 43, 61, 50)) %>%
  # creat new variable East and North
  mutate(East = 1,
         North = I)

# print the data
a
```

```
## # A tibble: 16 x 4
##       I     YI East North
##   <int> <dbl> <dbl> <int>
## 1     1    41     1     1
## 2     2    60     1     2
## 3     3    81     1     3
## 4     4    22     1     4
## 5     5     8     1     5
## 6     6    20     1     6
## 7     7    28     1     7
## 8     8     2     1     8
## 9     9     0     1     9
## 10    10     2     1    10
## 11    11     2     1    11
## 12    12     8     1    12
## 13    13     0     1    13
## 14    14    43     1    14
## 15    15    61     1    15
## 16    16    50     1    16
```

2.3 Autocorrelation statistics

```
# visualize the data
ggplot(data = a) +
  geom_point(mapping = aes(x = East, y = North, size = YI, color = YI)) +
  ggtitle("Spatial Distribution of YI Observation") +
  theme(plot.title = element_text(hjust = 0.5))
```



```
# calculate Moran's I
Coords <- a %>%
  dplyr::select(East, North)

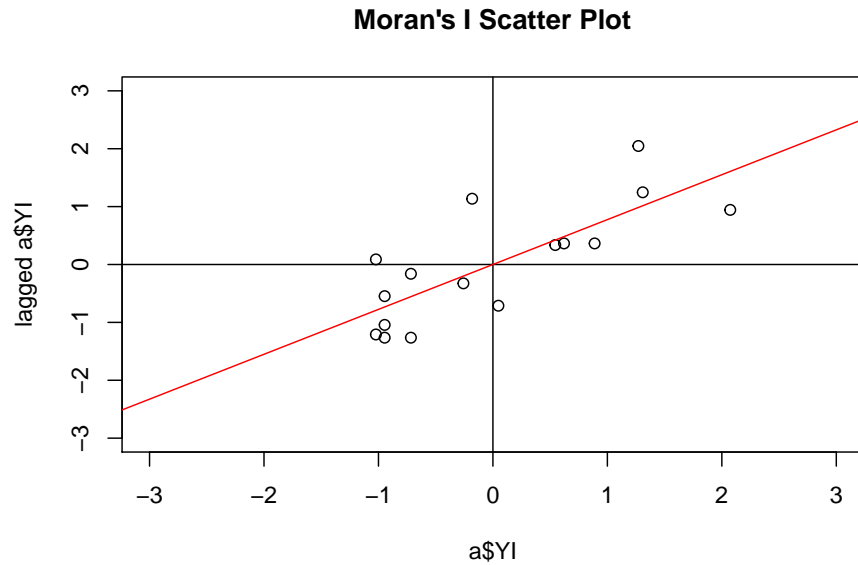
mI <- moransI(Coords, Bandwidth = 1, a$YI)

# print Moran's I table
moran.table <- tribble(
  ~`Moran's I`, ~`Expected I`, ~`Z randomization`, ~`P value randomization`,
  #-----/-----/-----/-----
  mI$Morans.I, mI$Expected.I, mI$z.randomization, mI$p.value.randomization
)

moran.table
```

```
## # A tibble: 1 x 4
##   `Moran's I` `Expected I` `Z randomization` `P value randomization`
##   <dbl>      <dbl>      <dbl>      <dbl>
## 1     0.625    -0.0667      2.81      0.00499
```

```
# create Moran's I scatter plot
l.moran <- l.moransI(Coords, Bandwidth = 1, a$YI)
```



```
# calculate geary's c
Coords_num <- coordinates(Coords)

# create an object of class 'nb' so that it can be used with function from package 'sp'
Coords_nb <- knn2nb(knearneigh(Coords_num))

# create a 'listw' object for use in the function 'geary.test'
coords_listw <- nb2listw(Coords_nb)

gearyC <- geary.test(a$YI, coords_listw, alternative = "two.sided")
gearyC
```

```
##
## Geary C test under randomisation
##
## data: a$YI
## weights: coords_listw
##
## Geary C statistic standard deviate = 2.5826, p-value = 0.009806
## alternative hypothesis: two.sided
## sample estimates:
## Geary C statistic      Expectation      Variance
##      0.37085605      1.00000000      0.05934473
```

2.4 First variogram

We will use the package `geoR` to construct empirical variogram, and then draw them using package `ggplot2`.

```
v1 <- variog(coords = Coords_num, data = a$YI, breaks = seq(0.5, 15.5),
             max.dist = 11)
```

```
## variog: computing omnidirectional variogram
```

```
# extract data from object v1 for plotting
v1_plot_data <- cbind(v1$u, v1$v, v1$n) %>%
  as.data.frame() %>%
  dplyr::rename(Distance = V1,
                Semivariance = V2,
                Pair_count = V3)

# in the table below, gamma is semivariance
v1_plot_data
```

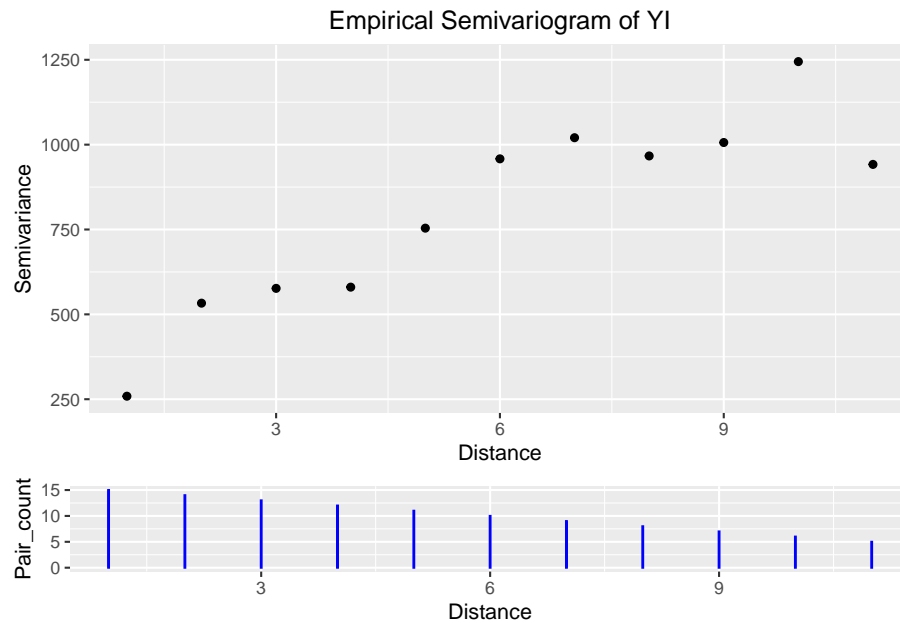
##	Distance	Semivariance	Pair_count
## 1	1	258.8333	15
## 2	2	533.0000	14
## 3	3	576.6154	13
## 4	4	580.1667	12
## 5	5	754.0000	11
## 6	6	958.2000	10
## 7	7	1020.4444	9
## 8	8	966.7500	8
## 9	9	1006.2857	7
## 10	10	1244.6667	6
## 11	11	941.8000	5

```
# plot variogram
v1_plot_vario <- ggplot(data = v1_plot_data) +
  geom_point(mapping = aes(x = Distance, y = Semivariance)) +
  ggtitle("Empirical Semivariogram of YI") +
  theme(plot.title = element_text(hjust = 0.5))

# plot pair counts
v1_plot_pair_count <- ggplot(data = v1_plot_data) +
  geom_col(mapping = aes(x = Distance, y = Pair_count), width = 0.01, color = "blue")

# stack two plots
```

```
grid.arrange(v1_plot_vario, v1_plot_pair_count,
              ncol = 1, heights = c(3, 1))
```



2.5 Second variogram

Plot robust and classical variogram together.

```
# fit robust variogram
v1_robust <- variog(coords = Coords_num, data = a$YI, breaks = seq(0.5, 15.5),
                  max.dist = 11, estimator.type = "modulus")
```

```
## variog: computing omnidirectional variogram
```

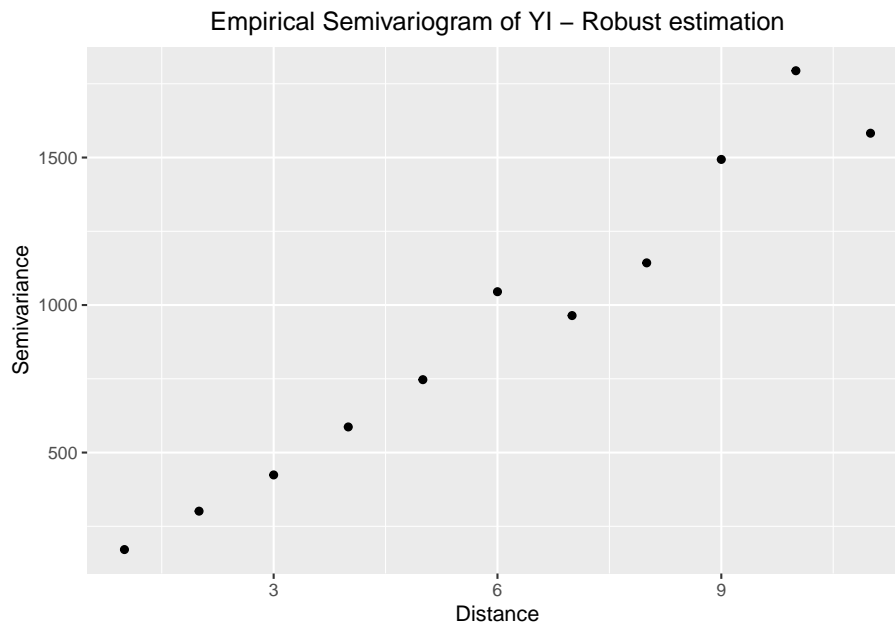
```
# extract the data
v1_robust_data <- cbind(v1_robust$u, v1_robust$v, v1_robust$n) %>%
  as.data.frame() %>%
  dplyr::rename(Distance = V1,
                Semivariance = V2,
                Pair_count = V3)

# plot robust variogram
```



```
v1_robust_vario <- ggplot(data = v1_robust_data) +
  geom_point(mapping = aes(x = Distance, y = Semivariance)) +
  ggtitle("Empirical Semivariogram of YI - Robust estimation") +
  theme(plot.title = element_text(hjust = 0.5))

v1_robust_vario
```

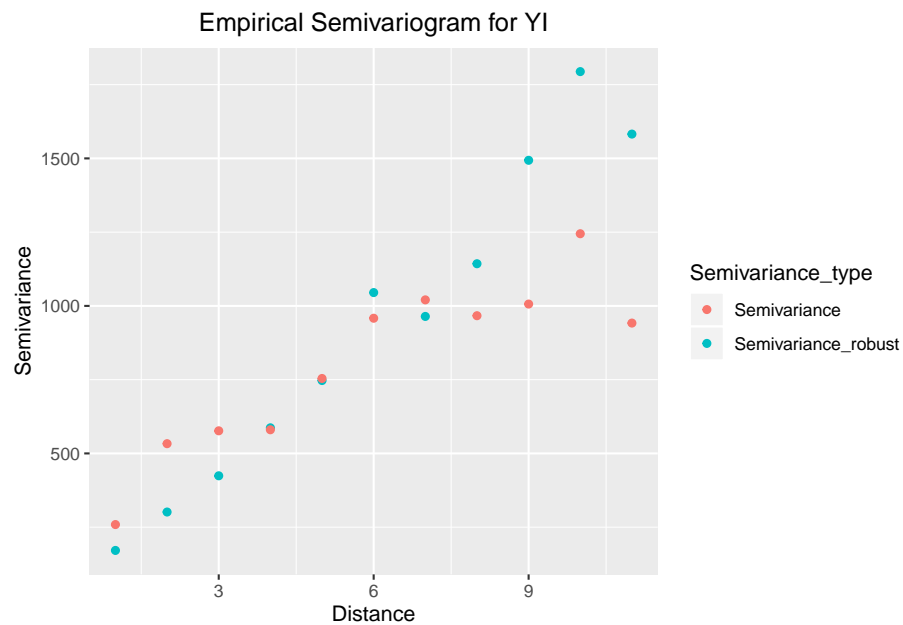


```
# combine robust and classical variogram
var_comb <- v1_robust_data %>%

  # combine robust and classical variogram datasets
  dplyr::rename(Semivariance_robust = Semivariance) %>%
  bind_cols(dplyr::select(v1_plot_data, Semivariance)) %>%
  gather(key = "Semivariance_type", value = "Semivariance", -c(Distance, Pair_count)) %>%

  # plot
  ggplot() +
  geom_point(mapping = aes(x = Distance, y = Semivariance, color = Semivariance_type)) +
  ggtitle("Empirical Semivariogram for YI") +
  theme(plot.title = element_text(hjust = 0.5))

var_comb
```



2.6 Variogram model selection

We will use the package `gstat` and `automap` for variogram model selection

```
# specify coordinates in the dataset
coordinates(a) = ~East+North

# select the best model out of exponential, spherical, and gaussian
autofitVariogram(YI ~ East + North, a, model = c("Sph", "Exp", "Gau"))
```

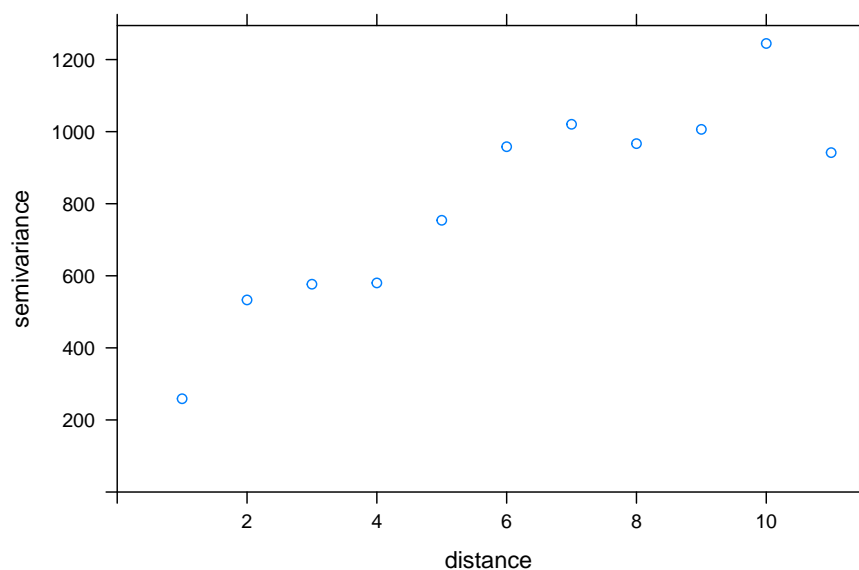
```
## $exp_var
##   np dist    gamma dir.hor dir.ver   id
## 1  15    1 258.8333      0      0 var1
## 2  14    2 533.0000      0      0 var1
## 3  13    3 576.6154      0      0 var1
## 4  12    4 580.1667      0      0 var1
## 5  11    5 754.0000      0      0 var1
##
## $var_model
##   model    psill    range
## 1  Nug    0.0000 0.000000
## 2  Exp  854.3133 2.575499
##
```

```
## $sserr
## [1] 28783.32
##
## attr("class")
## [1] "autofitVariogram" "list"
```

```
# fit empirical variogram
v_emp <- variogram(YI ~ East + North, data = a, cutoff = 11)
v_emp
```

```
##      np dist      gamma dir.hor dir.ver   id
## 1  15    1 258.8333      0      0 var1
## 2  14    2 533.0000      0      0 var1
## 3  13    3 576.6154      0      0 var1
## 4  12    4 580.1667      0      0 var1
## 5  11    5 754.0000      0      0 var1
## 6  10    6 958.2000      0      0 var1
## 7   9    7 1020.4444     0      0 var1
## 8   8    8 966.7500      0      0 var1
## 9   7    9 1006.2857     0      0 var1
## 10  6   10 1244.6667     0      0 var1
## 11  5   11 941.8000      0      0 var1
```

```
plot(v_emp)
```



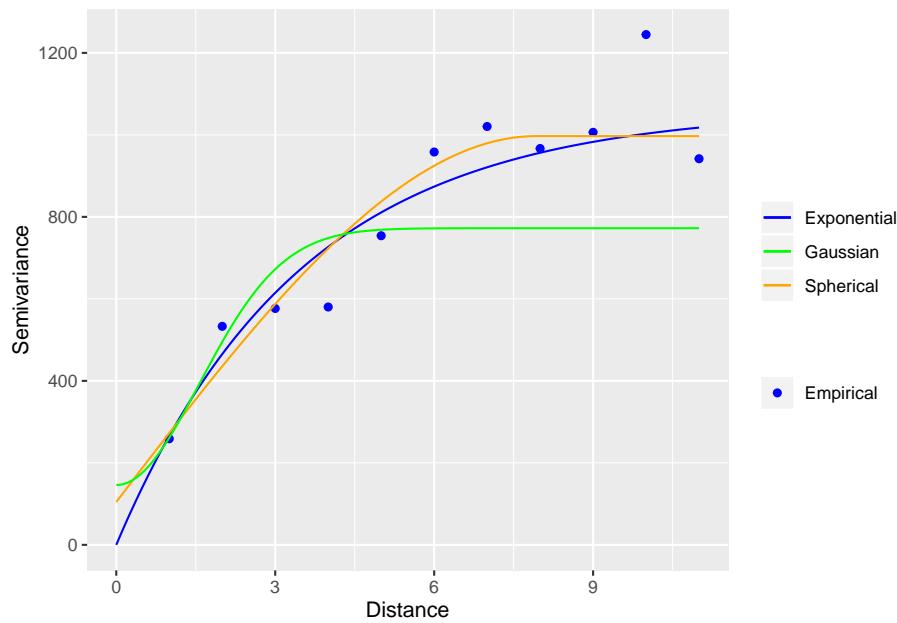
```
# fit exponential variogram
v_exp <- fit.variogram(v_emp, vgm("Exp"))
v_exp
```

```
##   model    psill   range
## 1  Nug     0.000 0.00000
## 2  Exp 1062.461 3.47171
```

```
# fit spherical and gaussian
v_sph <- fit.variogram(v_emp, vgm("Sph"))
v_gau <- fit.variogram(v_emp, vgm("Gau"))

# extract plotting data from fitted variograms
v_exp_line <- variogramLine(v_exp, maxdist = 11)
v_sph_line <- variogramLine(v_sph, maxdist = 11)
v_gau_line <- variogramLine(v_gau, maxdist = 11)

# plot empirical and fitted variograms together
# specify color for legends
legend_color <- c("Empirical" = "blue", "Exponential" = "blue",
                  "Spherical" = "orange", "Gaussian" = "green")
ggplot(data = v_emp) +
  geom_point(mapping = aes(x = dist, y = gamma, fill = "Empirical"), color = "blue") +
  geom_line(data = v_exp_line, mapping = aes(x = dist, y = gamma, color = "Exponential"))
  geom_line(data = v_sph_line, mapping = aes(x = dist, y = gamma, color = "Spherical"))
  geom_line(data = v_gau_line, mapping = aes(x = dist, y = gamma, color = "Gaussian"))
  scale_color_manual(name = "", values = legend_color) +
  scale_fill_manual(name = "", values = legend_color) +
  labs(x = "Distance",
       y = "Semivariance")
```



Chapter 3

Exercise 9.5

3.1 Load packages

Here is the R code to download the required packages for this exercise.

```
# install package manager 'pacman'  
if (!require(pacman)){  
  install.packages('pacman')  
}
```

Loading required package: pacman

```
# load packages needed for this exercise  
library(pacman)  
p_load(tidyverse,  
       lctools, # to calculate Moran's I  
       spdep, # to calculate geary's c  
       geoR, # to compute variogram  
       gridExtra, # to stack plots  
       gstat, automap, # packages for variogram model selection  
       sp # need a function called `coordinates`  
)
```

3.2 Data

This is equivalent to data step in SAS. Here, the data is imported from a file `data.csv` using the function `read_csv`. This function will download the file directly from here.

```
# Import data
a <- read_csv("https://raw.githubusercontent.com/luckymehra/epidem-exercises/master/data.csv")

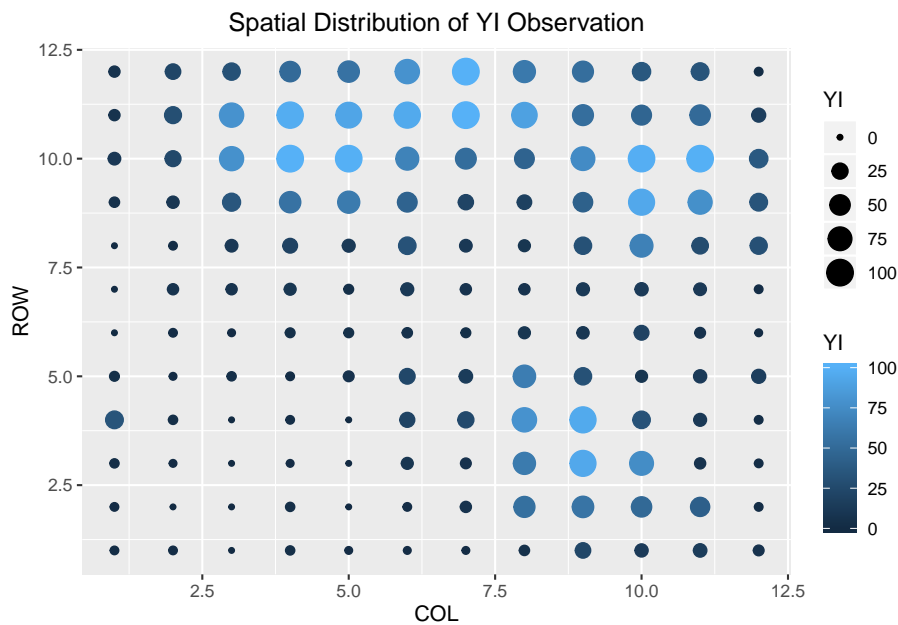
## Parsed with column specification:
## cols(
##   COL = col_double(),
##   ROW = col_double(),
##   YI = col_double()
## )

# print the data
a
```

```
## # A tibble: 144 x 3
##   COL ROW YI
##   <dbl> <dbl> <dbl>
## 1     1     1     2
## 2     2     1     2
## 3     3     1     0
## 4     4     1     3
## 5     5     1     1
## 6     6     1     1
## 7     7     1     1
## 8     8     1     5
## 9     9     1    22
## 10    10     1    13
## # ... with 134 more rows
```

3.3 Autocorrelation statistics

```
# visualize the data
ggplot(data = a) +
  geom_point(mapping = aes(x = COL, y = ROW, size = YI, color = YI)) +
  ggtitle("Spatial Distribution of YI Observation") +
  theme(plot.title = element_text(hjust = 0.5))
```

```
# calculate Moran's I
Coords <- a %>%
  dplyr::select(COL, ROW)

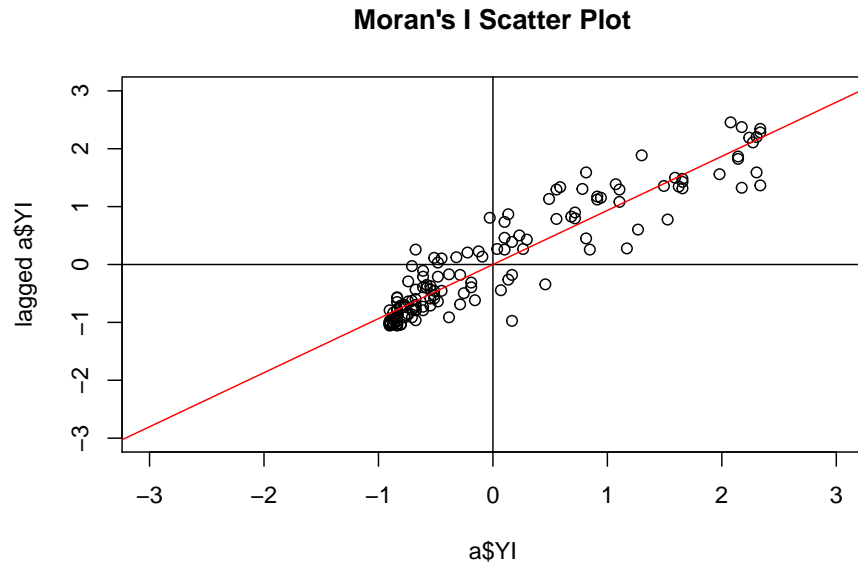
mI <- moransI(Coords, Bandwidth = 1, a$YI)

# print Moran's I table
moran.table <- tribble(
  ~`Moran's I`, ~`Expected I`, ~`Z randomization`, ~`P value randomization`,
  #-----/-----/-----/-----
  mI$Morans.I, mI$Expected.I, mI$z.randomization, mI$p.value.randomization
)

moran.table
```

```
## # A tibble: 1 x 4
##   `Moran's I` `Expected I` `Z randomization` `P value randomization`
##   <dbl>      <dbl>      <dbl>      <dbl>
## 1    0.782    -0.00699      13.0      1.28e-38
```

```
# create Moran's I scatter plot
l.moran <- l.moransI(Coords, Bandwidth = 1, a$YI)
```



```
# calculate geary's c
Coords_num <- coordinates(Coords)

# create an object of class 'nb' so that it can be used with function from package 'sp'
Coords_nb <- knn2nb(knearneigh(Coords_num))

# create a 'listw' object for use in the function 'geary.test'
coords_listw <- nb2listw(Coords_nb)

gearyC <- geary.test(a$YI, coords_listw, alternative = "two.sided")
gearyC
```

```
##
## Geary C test under randomisation
##
## data: a$YI
## weights: coords_listw
##
## Geary C statistic standard deviate = 8.8657, p-value < 2.2e-16
## alternative hypothesis: two.sided
## sample estimates:
## Geary C statistic      Expectation      Variance
##      0.235058006      1.000000000      0.007444457
```

3.4 First variogram

We will use the package `geoR` to construct empirical variogram, and then draw them using package `ggplot2`.

```
v1 <- variog(coords = Coords_num, data = a$YI, breaks = seq(0.5, 15.5),
             max.dist = 12)
```

```
## variog: computing omnidirectional variogram
```

```
# extract data from object v1 for plotting
v1_plot_data <- cbind(v1$u, v1$v, v1$n) %>%
  as.data.frame() %>%
  dplyr::rename(Distance = V1,
                Semivariance = V2,
                Pair_count = V3)

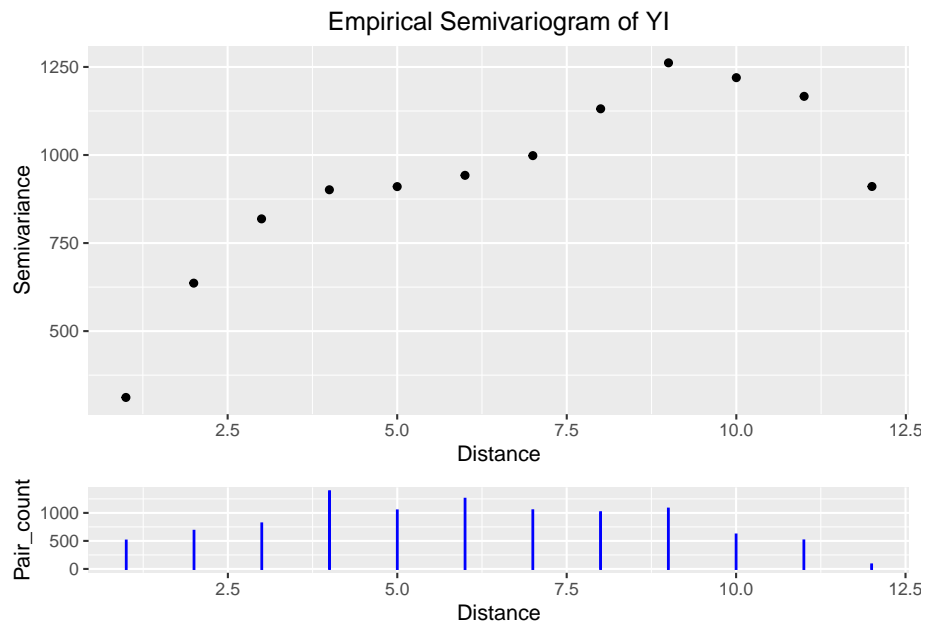
# in the table below, gamma is semivariance
v1_plot_data
```

##	Distance	Semivariance	Pair_count
## 1	1	311.7154	506
## 2	2	636.2074	680
## 3	3	818.7044	812
## 4	4	901.3218	1386
## 5	5	910.2773	1044
## 6	6	942.3219	1252
## 7	7	998.2290	1046
## 8	8	1131.2105	1012
## 9	9	1261.6817	1076
## 10	10	1219.6067	614
## 11	11	1166.5541	508
## 12	12	910.6250	80

```
# plot variogram
v1_plot_vario <- ggplot(data = v1_plot_data) +
  geom_point(mapping = aes(x = Distance, y = Semivariance)) +
  ggtitle("Empirical Semivariogram of YI") +
  theme(plot.title = element_text(hjust = 0.5))

# plot pair counts
v1_plot_pair_count <- ggplot(data = v1_plot_data) +
  geom_col(mapping = aes(x = Distance, y = Pair_count), width = 0.01, color = "blue")
```

```
# stack two plots
grid.arrange(v1_plot_vario, v1_plot_pair_count,
             ncol = 1, heights = c(3, 1))
```



3.5 Second variogram

Plot robust and classical variogram together.

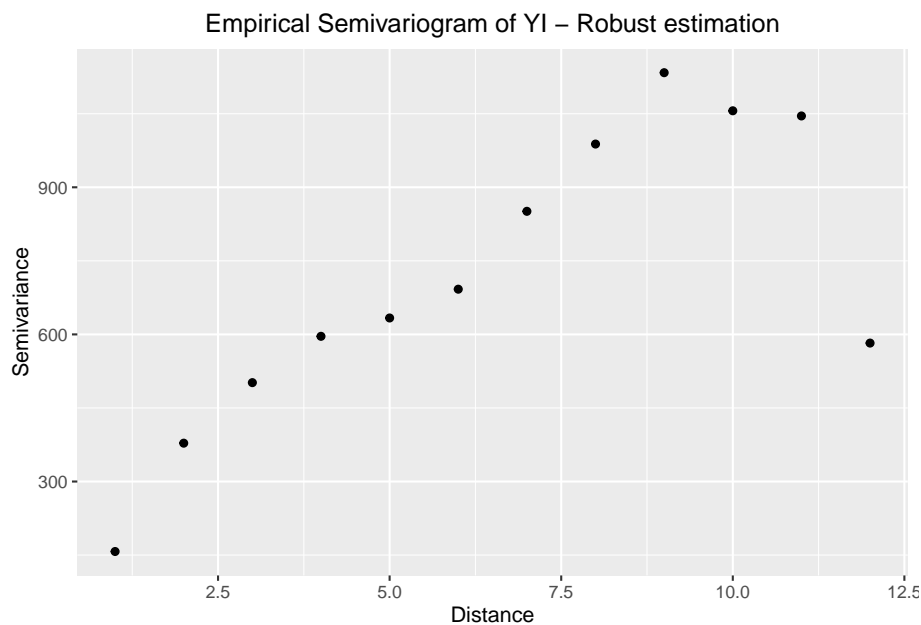
```
# fit robust variogram
v1_robust <- variog(coords = Coords_num, data = a$YI, breaks = seq(0.5, 15.5),
                  max.dist = 12, estimator.type = "modulus")
```

```
## variog: computing omnidirectional variogram
```

```
# extract the data
v1_robust_data <- cbind(v1_robust$u, v1_robust$v, v1_robust$n) %>%
  as.data.frame() %>%
  dplyr::rename(Distance = V1,
                Semivariance = V2,
                Pair_count = V3)
```

```
# plot robust variogram
v1_robust_vario <- ggplot(data = v1_robust_data) +
  geom_point(mapping = aes(x = Distance, y = Semivariance)) +
  ggtitle("Empirical Semivariogram of YI - Robust estimation") +
  theme(plot.title = element_text(hjust = 0.5))

v1_robust_vario
```

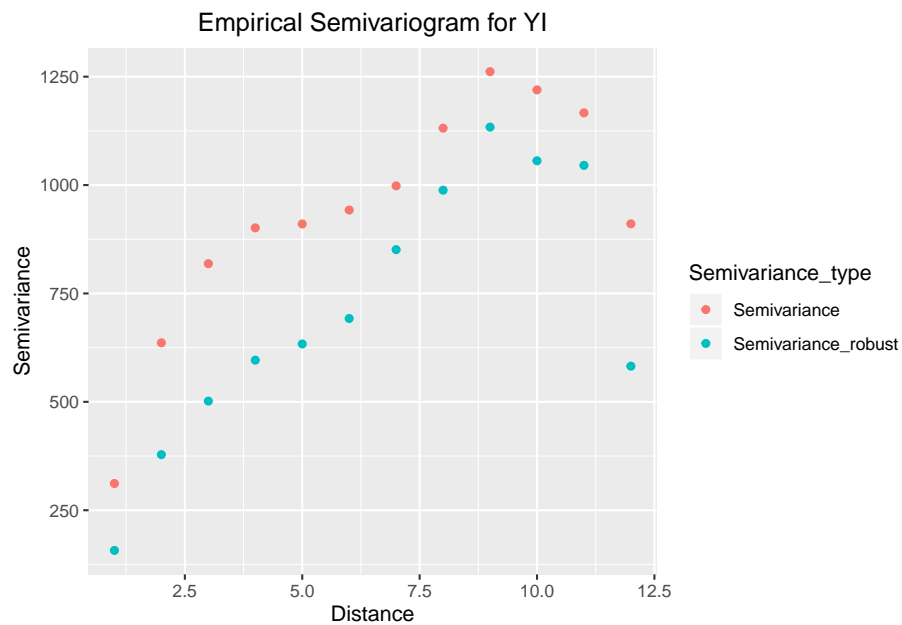


```
# combine robust and classical variogram
var_comb <- v1_robust_data %>%

  # combine robust and classical variogram datasets
  dplyr::rename(Semivariance_robust = Semivariance) %>%
  bind_cols(dplyr::select(v1_plot_data, Semivariance)) %>%
  gather(key = "Semivariance_type", value = "Semivariance", -c(Distance, Pair_count)) %>%

  # plot
  ggplot() +
  geom_point(mapping = aes(x = Distance, y = Semivariance, color = Semivariance_type)) +
  ggtitle("Empirical Semivariogram for YI") +
  theme(plot.title = element_text(hjust = 0.5))

var_comb
```



3.6 Variogram model selection

We will use the package `gstat` and `automap` for variogram model selection

```
# specify coordinates in the dataset
coordinates(a) = ~COL+ROW

# select the best model out of exponential, spherical, and gaussian
autofitVariogram(YI ~ COL + ROW, a, model = c("Sph", "Exp", "Gau"), cutoff = 12)
```

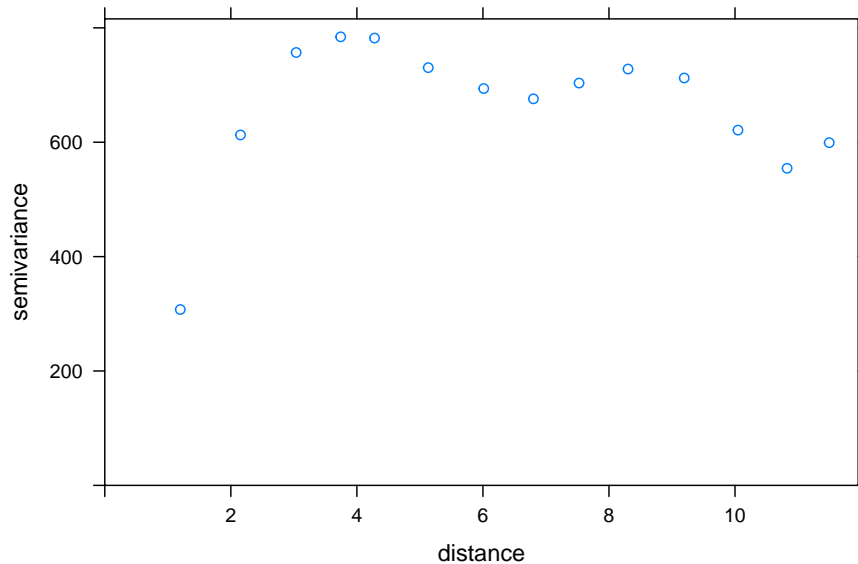
```
## $exp_var
##      np      dist      gamma dir.hor dir.ver  id
## 1  264  1.000000  233.2400      0      0 var1
## 2  242  1.414214  388.5222      0      0 var1
## 3  680  2.152750  612.6985      0      0 var1
## 4  812  3.036881  756.8971      0      0 var1
## 5 1066  3.944315  783.1461      0      0 var1
## 6 1364  4.977586  742.6252      0      0 var1
##
## $var_model
##   model  psill  range
## 1  Nug  0.0000 0.000000
## 2  Sph 782.9935 4.019145
```

```
##
## $sserr
## [1] 1247749
##
## attr("class")
## [1] "autofitVariogram" "list"
```

```
# fit empirical variogram
v_emp <- variogram(YI ~ COL + ROW, data = a, cutoff = 12)
v_emp
```

```
##      np      dist      gamma dir.hor dir.ver  id
## 1   506  1.198102  307.5054      0      0 var1
## 2   680  2.152750  612.6985      0      0 var1
## 3   812  3.036881  756.8971      0      0 var1
## 4   552  3.742751  784.3027      0      0 var1
## 5   834  4.280245  782.1560      0      0 var1
## 6  1044  5.132514  730.3844      0      0 var1
## 7  1028  6.012860  693.9058      0      0 var1
## 8   878  6.801676  675.9157      0      0 var1
## 9   836  7.525735  703.4337      0      0 var1
## 10  852  8.302717  728.0099      0      0 var1
## 11  792  9.194510  712.3311      0      0 var1
## 12  542 10.047104  621.2100      0      0 var1
## 13  452 10.826377  554.3985      0      0 var1
## 14  208 11.494850  599.2237      0      0 var1
```

```
plot(v_emp)
```



```
# fit exponential variogram
v_exp <- fit.variogram(v_emp, vgm("Exp"))
```

```
# fit spherical and gaussian
v_sph <- fit.variogram(v_emp, vgm("Sph"))
v_sph
```

```
##  model    psill    range
## 1  Nug     0.0000 0.000000
## 2  Sph    745.8602 3.765221
```

```
v_gau <- fit.variogram(v_emp, vgm("Gau"))
```

```
## Warning in fit.variogram(v_emp, vgm("Gau")): No convergence after 200
## iterations: try different initial values?
```

```
# extract plotting data from fitted variograms
v_exp_line <- variogramLine(v_exp, maxdist = 12)
v_sph_line <- variogramLine(v_sph, maxdist = 12)
# v_gau_line <- variogramLine(v_gau, maxdist = 12)

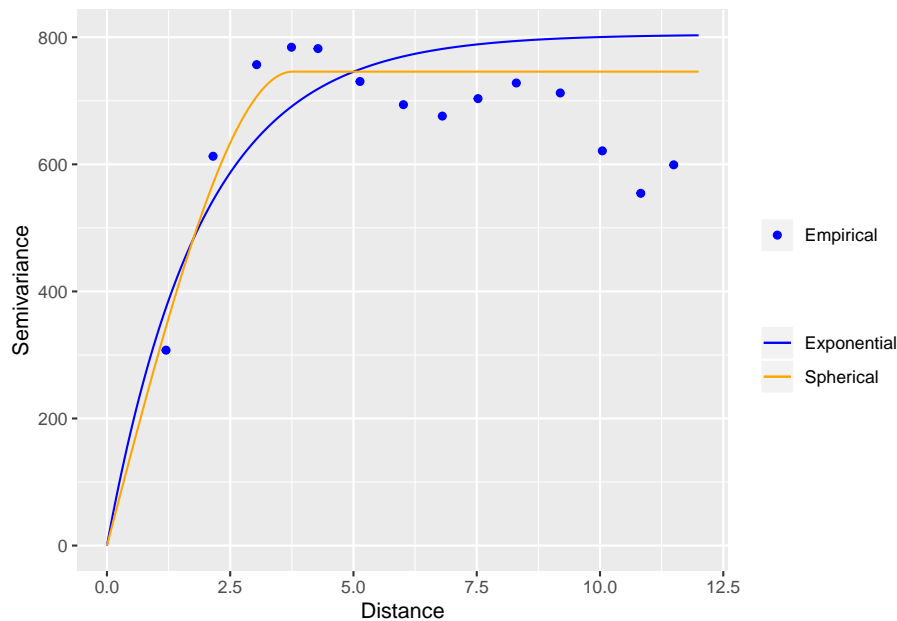
# plot empirical and fitted variograms together
# specify color for legends
```



```

legend_color <- c("Empirical" = "blue", "Exponential" = "blue",
                  "Spherical" = "orange")
ggplot(data = v_emp) +
  geom_point(mapping = aes(x = dist, y = gamma, fill = "Empirical"), color = "blue") +
  geom_line(data = v_exp_line, mapping = aes(x = dist, y = gamma, color = "Exponential")) +
  geom_line(data = v_sph_line, mapping = aes(x = dist, y = gamma, color = "Spherical")) +
  # geom_line(data = v_gau_line, mapping = aes(x = dist, y = gamma, color = "Gaussian")) +
  scale_color_manual(name = "", values = legend_color) +
  scale_fill_manual(name = "", values = legend_color) +
  labs(x = "Distance",
       y = "Semivariance")

```



Chapter 4

Yield loss

4.1 Load packages

Here is the R code to download the required packages for this exercise.

```
# install package manager 'pacman'  
if (!require(pacman)){  
  install.packages('pacman')  
}
```

Loading required package: pacman

```
# load packages needed for this exercise  
pacman::p_load(tidyverse,  
               nlme,  
               emmeans,  
               predictmeans  
)
```

4.2 Data

This is equivalent to the data step in SAS. Here, the data is imported from a file `yield_loss.csv` using the function `read_csv`. This function will download the data file directly from here.

```
# Import data  
a <- read_csv("https://raw.githubusercontent.com/luckymehra/epidem-exercises/master/data/yield_loss.csv")
```

```
## Parsed with column specification:
## cols(
##   WP = col_double(),
##   SP = col_character(),
##   BLK = col_double(),
##   TRT = col_double(),
##   FUNG = col_double(),
##   DS = col_double(),
##   YIELD = col_double()
## )
```

```
# print the data
a
```

```
## # A tibble: 24 x 7
##       WP SP      BLK TRT FUNG    DS YIELD
##   <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1  101 A      1     1     0    43   205
## 2  101 B      1     1     1     1   399
## 3  102 A      1     2     1     2   426
## 4  102 B      1     2     0    92   102
## 5  103 A      1     3     1     2   385
## 6  103 B      1     3     0     7   355
## 7  201 A      2     2     1     4   412
## 8  201 B      2     2     0    75   224
## 9  202 A      2     3     1     3   425
## 10 202 B      2     3     0    10   352
## # ... with 14 more rows
```

```
# specify that FUNG, TRT, and BLK are factors
a$FUNG <- as.ordered(as.factor(a$FUNG))
a$TRT <- as.ordered(as.factor(a$TRT))
a$BLK <- as.ordered(as.factor(a$BLK))
```

4.3 Mixed model for response variable DS

```
# fit the model
mm_1 <- lme(DS ~ TRT*FUNG, # fixed effects
            data = a,
            random = ~1|BLK/TRT) # read mm_1 as mixed model 1

# summary output
summary(mm_1)
```

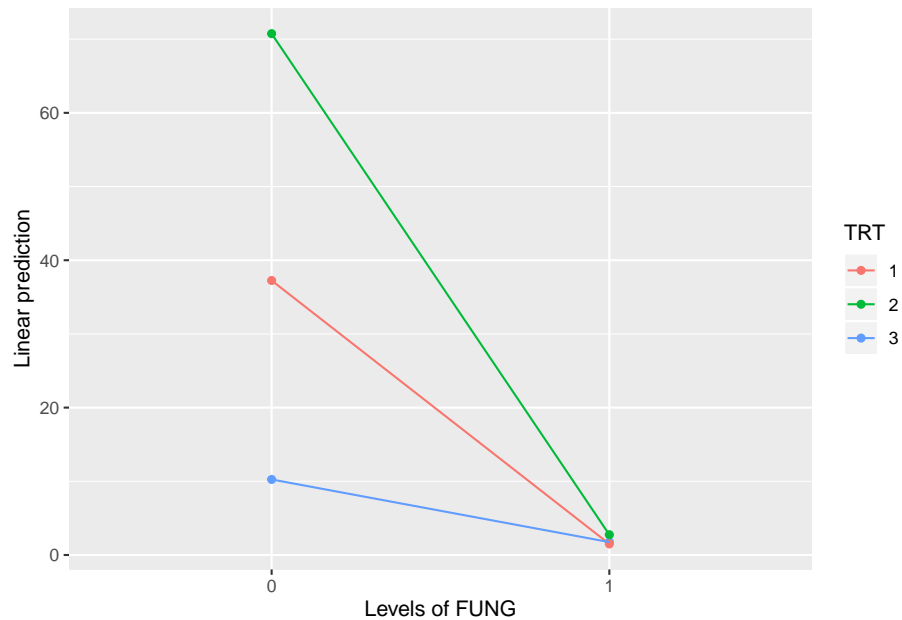
```
## Linear mixed-effects model fit by REML
## Data: a
##      AIC      BIC    logLik
## 156.1691 164.1825 -69.08456
##
## Random effects:
## Formula: ~1 | BLK
##      (Intercept)
## StdDev: 0.0009561632
##
## Formula: ~1 | TRT %in% BLK
##      (Intercept) Residual
## StdDev: 0.001007113 7.918859
##
## Fixed effects: DS ~ TRT * FUNG
##              Value Std.Error DF   t-value p-value
## (Intercept) 20.708333  1.616430  9 12.811150  0.0000
## TRT.L       -9.457553  2.799740  6  -3.378012  0.0149
## TRT.Q       -19.646949  2.799740  6  -7.017420  0.0004
## FUNG.L      -26.457579  2.285978  9 -11.573857  0.0000
## TRT.L:FUNG.L 13.625000  3.959430  9   3.441152  0.0074
## TRT.Q:FUNG.L 26.485944  3.959430  9   6.689333  0.0001
## Correlation:
##      (Intr) TRT.L TRT.Q FUNG.L TRT.L:
## TRT.L      0
## TRT.Q      0      0
## FUNG.L      0      0      0
## TRT.L:FUNG.L 0      0      0      0
## TRT.Q:FUNG.L 0      0      0      0      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.241484e+00 -9.471064e-02 -1.590814e-08  1.736361e-01  2.683467e+00
##
## Number of Observations: 24
## Number of Groups:
##      BLK TRT %in% BLK
##      4      12
```

```
# type 3 tests of fixed effects
anova(mm_1)
```

```
##      numDF denDF   F-value p-value
## (Intercept)    1     9 164.12557 <.0001
## TRT            2     6  30.32757  7e-04
```

```
## FUNG          1      9 133.95416 <.0001
## TRT:FUNG      2      9  28.29435  1e-04
```

```
# visualize interaction
emmip(mm_1, TRT ~ FUNG)
```



```
# to do anova for random effects, we need to compare mm_1 with a model that only has f
# we can use `gls()` function in `nlme` to fit the fixed effects model
fixed_model <- gls(DS ~ TRT * FUNG,
                   data = a)
```

```
# test the random effects in the model
anova(mm_1, fixed_model)
```

```
##          Model df      AIC      BIC    logLik  Test      L.Ratio
## mm_1          1  9 156.1691 164.1825 -69.08456
## fixed_model    2  7 152.1691 158.4017 -69.08456 1 vs 2 1.250038e-08
##          p-value
## mm_1
## fixed_model    1
```

```
# least square means
test(emmeans(mm_1, "TRT"))
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## TRT emmean SE df t.ratio p.value
## 1      19.4 2.8 3  6.920  0.0062
## 2      36.8 2.8 3 13.126  0.0010
## 3       6.0 2.8 3  2.143  0.1215
##
## Results are averaged over the levels of: FUNG
## d.f. method: containment
```

```
test(emmeans(mm_1, "FUNG"))
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## FUNG emmean SE df t.ratio p.value
## 0      39.4 2.29 3 17.243  0.0004
## 1       2.0 2.29 3  0.875  0.4460
##
## Results are averaged over the levels of: TRT
## d.f. method: containment
```

```
# pairwise difference
test(emmeans(mm_1, pairwise ~ TRT), adjust = "none")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## $emmeans
## TRT emmean SE df t.ratio p.value
## 1      19.4 2.8 3  6.920  0.0062
## 2      36.8 2.8 3 13.126  0.0010
## 3       6.0 2.8 3  2.143  0.1215
##
## Results are averaged over the levels of: FUNG
## d.f. method: containment
##
## $contrasts
## contrast estimate SE df t.ratio p.value
## 1 - 2      -17.4 3.96 6 -4.388  0.0046
## 1 - 3       13.4 3.96 6  3.378  0.0149
## 2 - 3       30.8 3.96 6  7.766  0.0002
##
## Results are averaged over the levels of: FUNG
```

```
test(emmeans(mm_1, pairwise ~ FUNG))
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## $emmeans
##   FUNG emmean    SE df t.ratio p.value
## 0      39.4 2.29  3 17.243  0.0004
## 1       2.0 2.29  3  0.875  0.4460
##
## Results are averaged over the levels of: TRT
## d.f. method: containment
##
## $contrasts
## contrast estimate    SE df t.ratio p.value
## 0 - 1          37.4 3.23  9 11.574  <.0001
##
## Results are averaged over the levels of: TRT
```

```
test(emmeans(mm_1, pairwise ~ TRT*FUNG), adjust = "none")
```

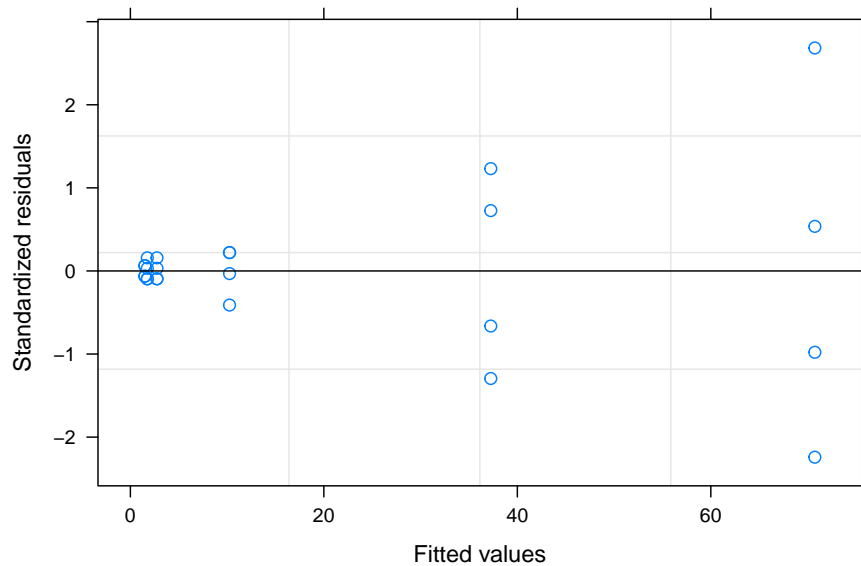
```
## $emmeans
## TRT FUNG emmean    SE df t.ratio p.value
## 1  0      37.25 3.96  3  9.408  0.0025
## 2  0      70.75 3.96  3 17.869  0.0004
## 3  0      10.25 3.96  3  2.589  0.0812
## 1  1       1.50 3.96  3  0.379  0.7300
## 2  1       2.75 3.96  3  0.695  0.5373
## 3  1       1.75 3.96  3  0.442  0.6884
##
## d.f. method: containment
##
## $contrasts
## contrast estimate    SE df t.ratio p.value
## 1,0 - 2,0    -33.50 5.6  6 -5.983  0.0010
## 1,0 - 3,0     27.00 5.6  6  4.822  0.0029
## 1,0 - 1,1     35.75 5.6  9  6.385  0.0001
## 1,0 - 2,1     34.50 5.6  6  6.161  0.0008
## 1,0 - 3,1     35.50 5.6  6  6.340  0.0007
## 2,0 - 3,0     60.50 5.6  6 10.805  <.0001
## 2,0 - 1,1     69.25 5.6  6 12.367  <.0001
## 2,0 - 2,1     68.00 5.6  9 12.144  <.0001
## 2,0 - 3,1     69.00 5.6  6 12.323  <.0001
## 3,0 - 1,1      8.75 5.6  6  1.563  0.1692
## 3,0 - 2,1      7.50 5.6  6  1.339  0.2289
```



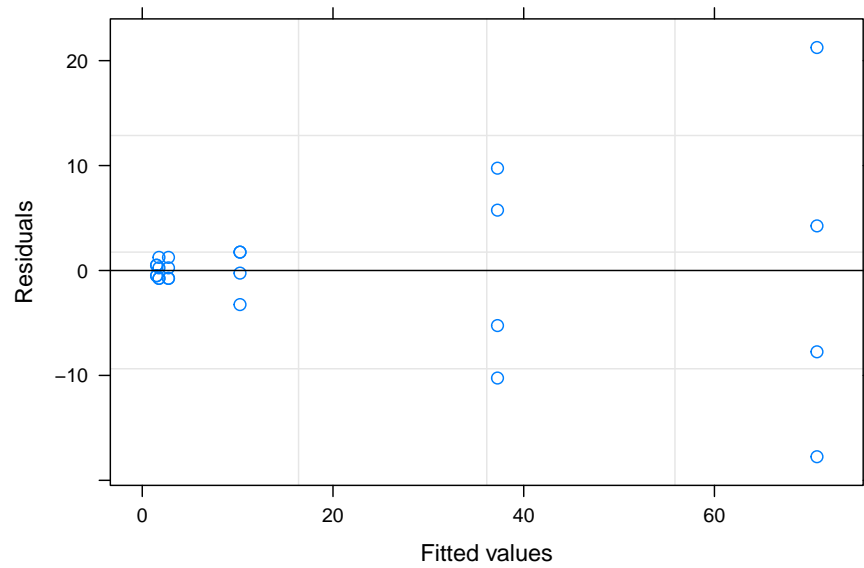
```
## 3,0 - 3,1      8.50 5.6  9  1.518  0.1633
## 1,1 - 2,1      -1.25 5.6  6 -0.223  0.8308
## 1,1 - 3,1      -0.25 5.6  6 -0.045  0.9658
## 2,1 - 3,1       1.00 5.6  6  0.179  0.8641
```

4.3.1 Diagnostic plots

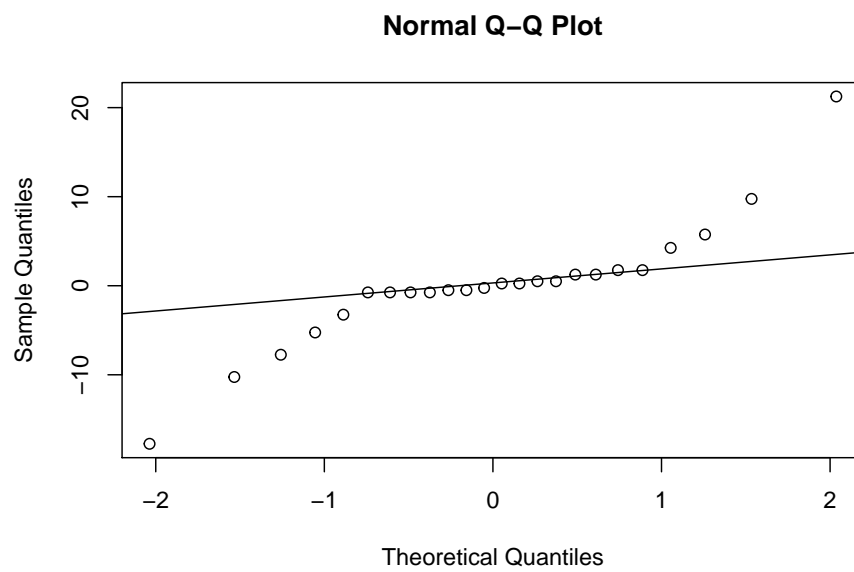
```
# pearson residuals vs. fitted values
plot(mm_1, resid(., type="pearson") ~ fitted(.), abline = 0)
```



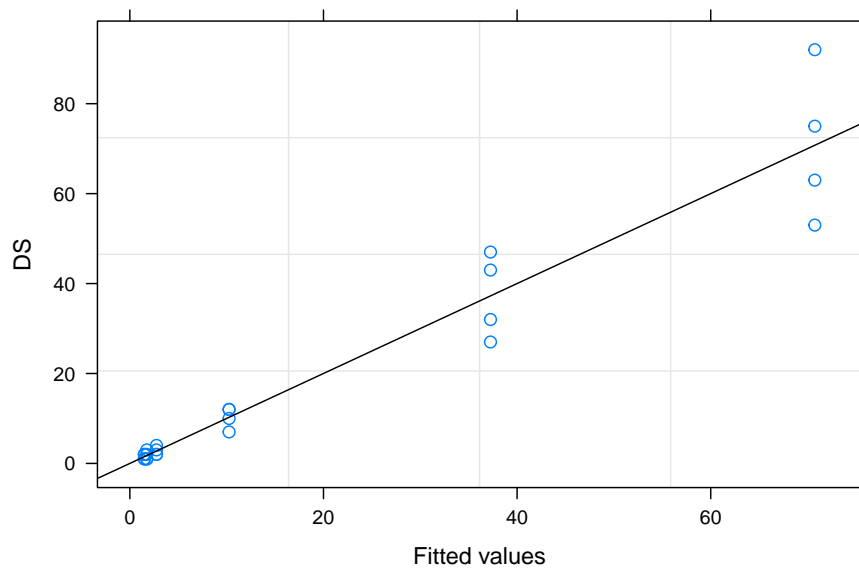
```
# standardized residuals vs. fitted values
plot(mm_1, resid(., scaled=TRUE) ~ fitted(.), abline = 0)
```



```
# qq plot  
qqnorm(residuals(mm_1))  
qqline(residuals(mm_1))
```



```
#observed vs. fitted values
plot(mm_1, DS ~ fitted(.), abline = c(0,1))
```



4.4 Mixed model for response variable YIELD

```
# fit the model
mm_2 <- lme(YIELD ~ TRT*FUNG, # fixed effects
            data = a,
            random = ~1|BLK/TRT) # read mm_2 as mixed model 2
```

```
# summary output
summary(mm_2)
```

```
## Linear mixed-effects model fit by REML
## Data: a
##      AIC      BIC   logLik
## 209.9214 217.9348 -95.9607
##
## Random effects:
## Formula: ~1 | BLK
##      (Intercept)
```

```

## StdDev:      11.99815
##
## Formula: ~1 | TRT %in% BLK
##           (Intercept) Residual
## StdDev: 0.001914579 33.61779
##
## Fixed effects: YIELD ~ TRT * FUNG
##              Value Std.Error DF   t-value p-value
## (Intercept) 335.1667  9.114752  9 36.77189  0.0000
## TRT.L        21.3016 11.885682  6  1.79221  0.1233
## TRT.Q        54.5522 11.885682  6  4.58974  0.0037
## FUNG.L       93.9274  9.704619  9  9.67862  0.0000
## TRT.L:FUNG.L -31.8750 16.808893  9 -1.89632  0.0904
## TRT.Q:FUNG.L -75.2720 16.808893  9 -4.47811  0.0015
## Correlation:
##              (Intr) TRT.L TRT.Q FUNG.L TRT.L:
## TRT.L          0
## TRT.Q          0      0
## FUNG.L          0      0      0
## TRT.L:FUNG.L    0      0      0      0
## TRT.Q:FUNG.L    0      0      0      0      0
##
## Standardized Within-Group Residuals:
##              Min          Q1          Med          Q3          Max
## -2.04399017 -0.33265713  0.07191314  0.49972251  1.20545632
##
## Number of Observations: 24
## Number of Groups:
##              BLK TRT %in% BLK
##              4      12

```

```

# type 3 tests of fixed effects
anova(mm_2)

```

```

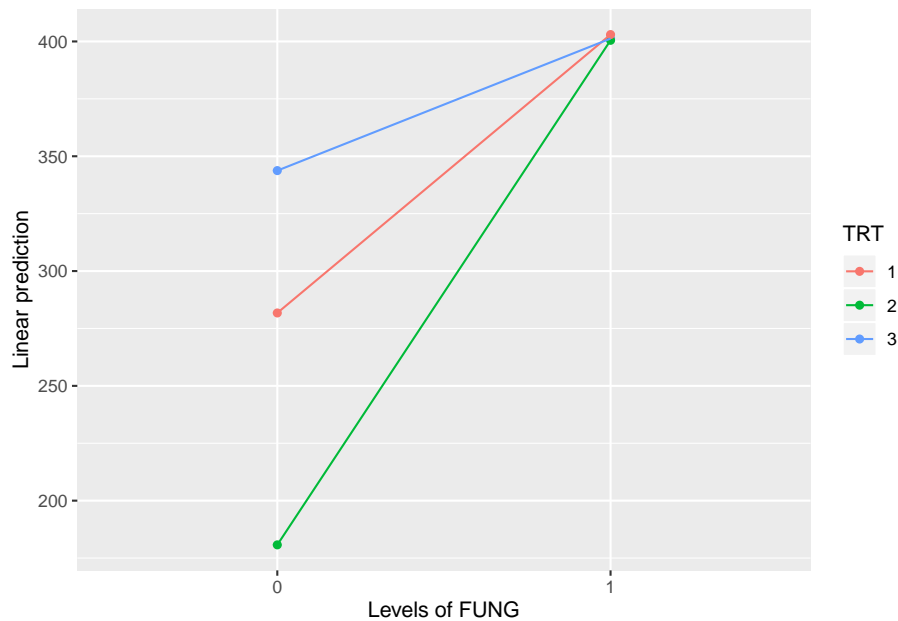
##              numDF denDF   F-value p-value
## (Intercept)      1     9 1352.1720 <.0001
## TRT              2     6  12.1389  0.0078
## FUNG             1     9  93.6757 <.0001
## TRT:FUNG         2     9  11.8247  0.0030

```

```

# visualize interaction
emmip(mm_2, TRT ~ FUNG)

```



```
# to do anova for random effects, we need to compare mm_1 with a model that only has fixed effects
# we can use `glsl()` function in `nlme` to fit the fixed effects model
fixed_model_YIELD <- glsl(YIELD ~ TRT * FUNG,
                           data = a)
```

```
# test the random effects in the model
anova(mm_2, fixed_model_YIELD)
```

```
##           Model df      AIC      BIC    logLik  Test  L.Ratio
## mm_2           1  9 209.9214 217.9348 -95.96070
## fixed_model_YIELD  2  7 206.3763 212.6089 -96.18815 1 vs 2 0.4548877
##           p-value
## mm_2
## fixed_model_YIELD 0.7966
```

```
# least square means
test(emmeans(mm_2, "TRT"))
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## TRT emmean SE df t.ratio p.value
## 1      342 13.3  3 25.716 0.0001
## 2      291 13.3  3 21.829 0.0002
```

```
## 3      372 13.3  3 27.978  0.0001
```

```
##
```

```
## Results are averaged over the levels of: FUNG
```

```
## d.f. method: containment
```

```
test(emmeans(mm_2, "FUNG"))
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## FUNG emmean    SE df t.ratio p.value
```

```
## 0      269 11.4  3 23.556  0.0002
```

```
## 1      402 11.4  3 35.198  0.0001
```

```
##
```

```
## Results are averaged over the levels of: TRT
```

```
## d.f. method: containment
```

```
# pairwise difference
```

```
test(emmeans(mm_2, pairwise ~ TRT), adjust = "none")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## $emmeans
```

```
## TRT emmean    SE df t.ratio p.value
```

```
## 1      342 13.3  3 25.716  0.0001
```

```
## 2      291 13.3  3 21.829  0.0002
```

```
## 3      372 13.3  3 27.978  0.0001
```

```
##
```

```
## Results are averaged over the levels of: FUNG
```

```
## d.f. method: containment
```

```
##
```

```
## $contrasts
```

```
## contrast estimate    SE df t.ratio p.value
```

```
## 1 - 2      51.8 16.8  6  3.079  0.0217
```

```
## 1 - 3     -30.1 16.8  6 -1.792  0.1233
```

```
## 2 - 3     -81.9 16.8  6 -4.871  0.0028
```

```
##
```

```
## Results are averaged over the levels of: FUNG
```

```
test(emmeans(mm_2, pairwise ~ FUNG))
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

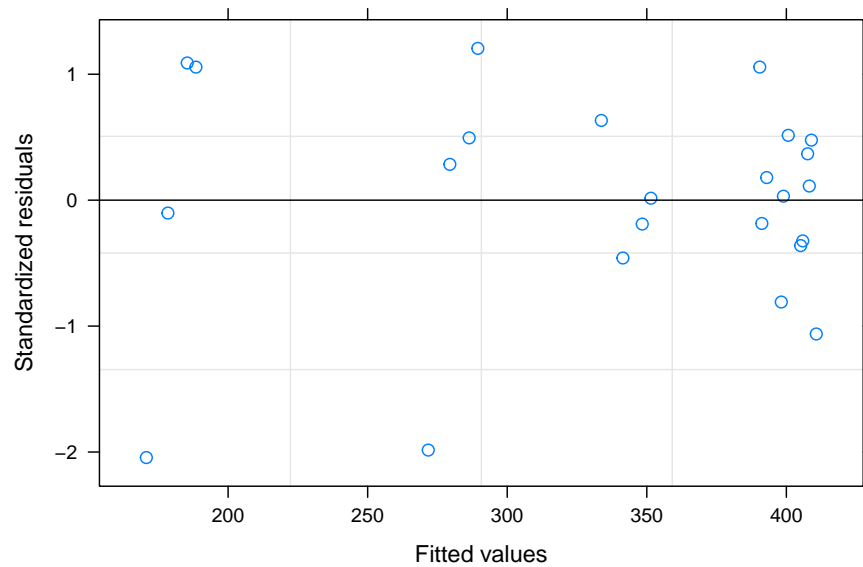
```
## $emmeans
##   FUNG emmean    SE df t.ratio p.value
##    0      269 11.4   3 23.556  0.0002
##    1      402 11.4   3 35.198  0.0001
##
## Results are averaged over the levels of: TRT
## d.f. method: containment
##
## $contrasts
##   contrast estimate    SE df t.ratio p.value
##    0 - 1      -133 13.7   9 -9.679  <.0001
##
## Results are averaged over the levels of: TRT
```

```
test(emmeans(mm_2, pairwise ~ TRT*FUNG), adjust = "none")
```

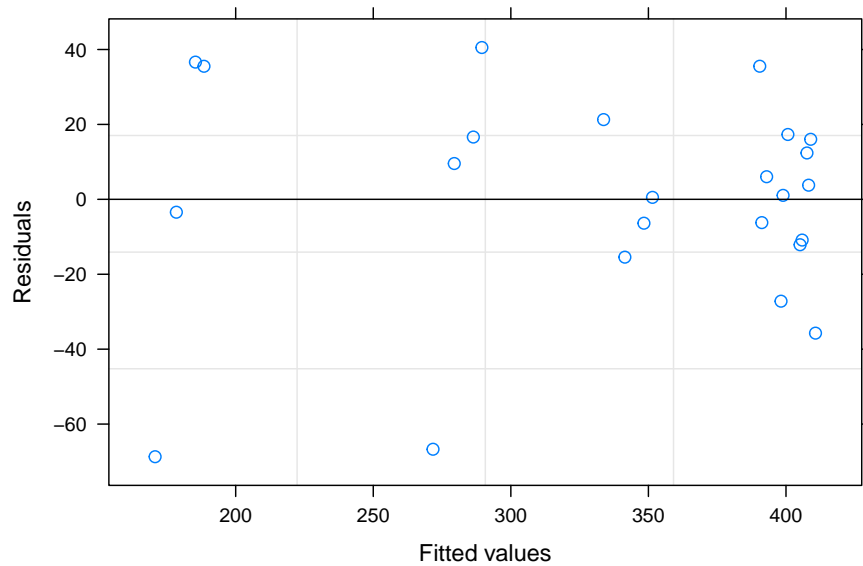
```
## $emmeans
##   TRT FUNG emmean    SE df t.ratio p.value
##    1    0      282 17.8   3 15.787  0.0006
##    2    0      181 17.8   3 10.128  0.0021
##    3    0      344 17.8   3 19.261  0.0003
##    1    1      403 17.8   3 22.580  0.0002
##    2    1      400 17.8   3 22.440  0.0002
##    3    1      401 17.8   3 22.482  0.0002
##
## d.f. method: containment
##
## $contrasts
##   contrast estimate    SE df t.ratio p.value
##    1,0 - 2,0    101.00 23.8   6  4.249  0.0054
##    1,0 - 3,0    -62.00 23.8   6 -2.608  0.0402
##    1,0 - 1,1   -121.25 23.8   9 -5.101  0.0006
##    1,0 - 2,1   -118.75 23.8   6 -4.996  0.0025
##    1,0 - 3,1   -119.50 23.8   6 -5.027  0.0024
##    2,0 - 3,0   -163.00 23.8   6 -6.857  0.0005
##    2,0 - 1,1   -222.25 23.8   6 -9.349  0.0001
##    2,0 - 2,1   -219.75 23.8   9 -9.244  <.0001
##    2,0 - 3,1   -220.50 23.8   6 -9.276  0.0001
##    3,0 - 1,1    -59.25 23.8   6 -2.492  0.0470
##    3,0 - 2,1    -56.75 23.8   6 -2.387  0.0542
##    3,0 - 3,1    -57.50 23.8   9 -2.419  0.0387
##    1,1 - 2,1     2.50 23.8   6  0.105  0.9197
##    1,1 - 3,1     1.75 23.8   6  0.074  0.9437
##    2,1 - 3,1    -0.75 23.8   6 -0.032  0.9759
```

4.4.1 Diagnostic plots

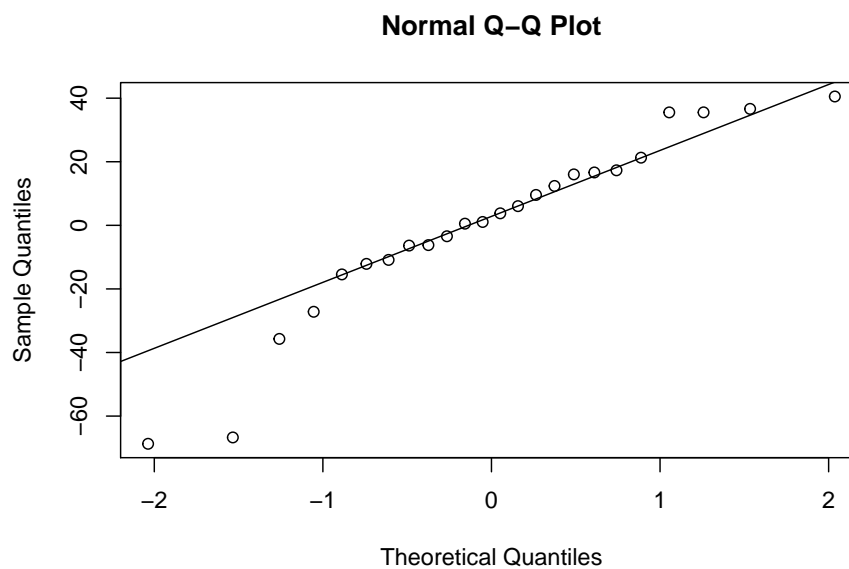
```
# pearson residuals vs. fitted values  
plot(mm_2, resid(., type="pearson") ~ fitted(.), abline = 0)
```



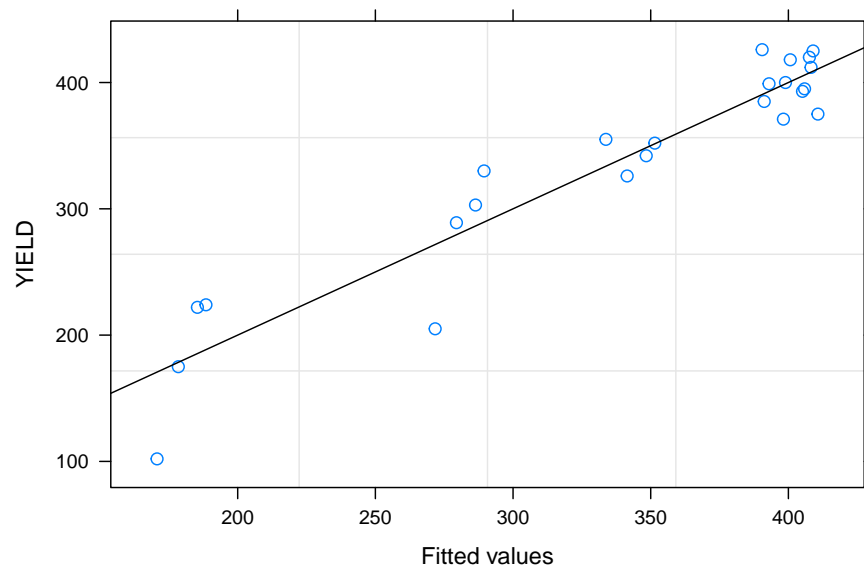
```
# standardaized residuals vs. fitted values  
plot(mm_2, resid(., scaled=TRUE) ~ fitted(.), abline = 0)
```

```
# qq plot  
qqnorm(residuals(mm_2))  
qqline(residuals(mm_2))
```



```
#observed vs. fitted values
plot(mm_2, YIELD ~ fitted(.), abline = c(0,1))
```



4.5 Linear regression between YIELD and DS

```
# fit `lm` model
lm_1 <- lm(YIELD ~ DS, data = a)
summary(lm_1)
```

```
##
## Call:
## lm(formula = YIELD ~ DS, data = a)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -61.196 -18.565   0.856  22.676  56.812
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  399.2384     8.0711   49.47  < 2e-16 ***
## DS           -3.0940     0.2399  -12.90 9.81e-12 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 31.17 on 22 degrees of freedom
## Multiple R-squared:  0.8832, Adjusted R-squared:  0.8779
## F-statistic: 166.4 on 1 and 22 DF,  p-value: 9.809e-12
```

```
anova(lm_1)
```

```
## Analysis of Variance Table
##
## Response: YIELD
##           Df Sum Sq Mean Sq F value    Pr(>F)
## DS           1 161600  161600   166.38 9.809e-12 ***
## Residuals    22  21368     971
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# diagnostic plots
residplot(lm_1)
```

4.5.1 Linear regression between RY1 and DS

```
b <- a %>%
  mutate(RY1 = YIELD/399.23843)
```

```
# fit linear regression model
lm_2 <- lm(RY1 ~ DS, data = b)
summary(lm_2)
```

```
##
## Call:
## lm(formula = RY1 ~ DS, data = b)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.153282 -0.046502  0.002143  0.056798  0.142301
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.0000000  0.0202162   49.47  < 2e-16 ***
## DS          -0.0077498  0.0006008  -12.90 9.81e-12 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07806 on 22 degrees of freedom
## Multiple R-squared:  0.8832, Adjusted R-squared:  0.8779
## F-statistic: 166.4 on 1 and 22 DF,  p-value: 9.809e-12
```

```
anova(lm_2)
```

```
## Analysis of Variance Table
##
## Response: RY1
##           Df Sum Sq Mean Sq F value    Pr(>F)
## DS           1  1.01385   1.01385   166.38 9.809e-12 ***
## Residuals    22  0.13406   0.00609
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# diagnostic plots
residplot(lm_2)
```

4.5.2 Transform dataset a

```
a_yield <- a %>%
  dplyr::select(BLK, TRT, YIELD) %>%
  arrange(BLK, TRT, YIELD) %>%
  group_by(BLK, TRT) %>%
  summarise(RY2 = YIELD[1]/YIELD[2]) %>%
  ungroup()

a_ds <- a %>%
  dplyr::select(BLK, TRT, DS) %>%
  arrange(BLK, TRT, DS) %>%
  group_by(BLK, TRT) %>%
  summarise(CDS = DS[2]) %>%
  ungroup()

a_new <- a_yield %>%
  inner_join(a_ds) %>%
  ungroup() %>%
  mutate(BLK = parse_factor(as.character(BLK)),
         TRT = parse_factor(as.character(TRT)))
```

```
## Joining, by = c("BLK", "TRT")
```

```
# print the data
a_new
```

```
## # A tibble: 12 x 4
##   BLK   TRT   RY2   CDS
##   <fct> <fct> <dbl> <dbl>
## 1 1     1     0.514 43
## 2 1     2     0.239 92
## 3 1     3     0.922 7
## 4 2     1     0.88 27
## 5 2     2     0.544 75
## 6 2     3     0.828 10
## 7 3     1     0.721 47
## 8 3     2     0.565 63
## 9 3     3     0.866 12
## 10 4     1     0.691 32
## 11 4     2     0.472 53
## 12 4     3     0.815 12
```

4.6 Mixed model for RY2

```
# fit the model
mm_3 <- lme(RY2 ~ TRT, # fixed effects
            data = a_new,
            random = ~1|BLK) # read mm_3 as mixed model 3

# summary output
summary(mm_3)
```

```
## Linear mixed-effects model fit by REML
## Data: a_new
##      AIC      BIC    logLik
## 2.04077 3.026893 3.979615
##
## Random effects:
## Formula: ~1 | BLK
##      (Intercept) Residual
## StdDev: 0.05297273 0.1134963
##
## Fixed effects: RY2 ~ TRT
```

```
##              Value Std.Error DF   t-value p-value
## (Intercept)  0.7016501 0.06262490  6 11.204012  0.0000
## TRT2        -0.2467228 0.08025398  6 -3.074274  0.0218
## TRT3         0.1561339 0.08025398  6  1.945497  0.0997
## Correlation:
##      (Intr) TRT2
## TRT2 -0.641
## TRT3 -0.641  0.500
##
## Standardized Within-Group Residuals:
##      Min          Q1          Med          Q3          Max
## -1.50508335 -0.38516867 -0.01698779  0.58195830  1.29565814
##
## Number of Observations: 12
## Number of Groups: 4
```

```
# type 3 tests of fixed effects
anova(mm_3)
```

```
##              numDF denDF   F-value p-value
## (Intercept)      1     6 254.00333  <.0001
## TRT              2     6  12.81141  0.0068
```

```
# to do anova for random effects, we need to compare mm_1 with a model that only has f
# we can use `glms()` function in `nlme` to fit the fixed effects model
fixed_model_RY2 <- gls(RY2 ~ TRT,
                       data = a_new)
```

```
# test the random effects in the model
anova(mm_3, fixed_model_RY2)
```

```
##              Model df          AIC          BIC   logLik   Test   L.Ratio
## mm_3              1  5 2.0407705 3.026893 3.979615
## fixed_model_RY2    2  4 0.3057644 1.094663 3.847118 1 vs 2 0.2649939
##
##              p-value
## mm_3
## fixed_model_RY2  0.6067
```

```
# pairwise difference
test(emmeans(mm_3, pairwise ~ TRT), adjust = "none")
```

```
## $emmeans
## TRT emmean      SE df t.ratio p.value
## 1      0.702 0.0626  3 11.204  0.0015
```

```
## 2    0.455 0.0626  3  7.264  0.0054
## 3    0.858 0.0626  3 13.697  0.0008
##
## d.f. method: containment
##
## $contrasts
## contrast estimate      SE df t.ratio p.value
## 1 - 2          0.247 0.0803  6  3.074  0.0218
## 1 - 3         -0.156 0.0803  6 -1.945  0.0997
## 2 - 3         -0.403 0.0803  6 -5.020  0.0024
```

```
# diagnostic plots
residplot(mm_3)
```

4.7 Linear regression between RY2 and CDS

```
# fit linear regression model
lm_3 <- lm(RY2 ~ CDS, data = a_new)
summary(lm_3)
```

```
##
## Call:
## lm(formula = RY2 ~ CDS, data = a_new)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.13338 -0.05085 -0.01090  0.06530  0.12439
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.9386111  0.0467991  20.056 2.09e-09 ***
## CDS         -0.0067778  0.0009845  -6.884 4.28e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09061 on 10 degrees of freedom
## Multiple R-squared:  0.8258, Adjusted R-squared:  0.8083
## F-statistic: 47.39 on 1 and 10 DF,  p-value: 4.275e-05
```

```
anova(lm_3)
```

```
## Analysis of Variance Table
```

```
##
## Response: RY2
##           Df Sum Sq Mean Sq F value    Pr(>F)
## CDS         1  0.38914  0.38914   47.394 4.275e-05 ***
## Residuals  10  0.08211  0.00821
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# diagnostic plots
residplot(lm_3)
```


Appendix A

SAS code

A.1 Exercise 4

Copy and paste the below code into a SAS editor, and hit run to see the output.

```
DATA A;
INPUT PLOT AN T BLK TRT PCTSEV;
Y=PCTSEV/100;
YSTAR=LOG(Y/(1-Y));
WT=Y*(1-Y);
DROP AN;
CARDS;
101 1 0 1 2 9
102 1 0 1 1 6
103 1 0 1 3 2
201 1 0 2 2 7
202 1 0 2 3 5
203 1 0 2 1 3
301 1 0 3 3 4
302 1 0 3 2 2
303 1 0 3 1 6
401 1 0 4 1 1
402 1 0 4 2 1
403 1 0 4 3 4
101 2 7 1 2 4
102 2 7 1 1 6
103 2 7 1 3 10
201 2 7 2 2 2
202 2 7 2 3 5
203 2 7 2 1 3
```

301	2	7	3	3	11
302	2	7	3	2	6
303	2	7	3	1	4
401	2	7	4	1	8
402	2	7	4	2	3
403	2	7	4	3	6
101	3	14	1	2	8
102	3	14	1	1	20
103	3	14	1	3	15
201	3	14	2	2	13
202	3	14	2	3	12
203	3	14	2	1	14
301	3	14	3	3	15
302	3	14	3	2	8
303	3	14	3	1	25
401	3	14	4	1	17
402	3	14	4	2	14
403	3	14	4	3	49
101	4	21	1	2	24
102	4	21	1	1	38
103	4	21	1	3	61
201	4	21	2	2	31
202	4	21	2	3	42
203	4	21	2	1	79
301	4	21	3	3	48
302	4	21	3	2	23
303	4	21	3	1	86
401	4	21	4	1	52
402	4	21	4	2	45
403	4	21	4	3	56
101	5	28	1	2	28
102	5	28	1	1	89
103	5	28	1	3	44
201	5	28	2	2	41
202	5	28	2	3	49
203	5	28	2	1	79
301	5	28	3	3	45
302	5	28	3	2	47
303	5	28	3	1	63
401	5	28	4	1	94
402	5	28	4	2	52
403	5	28	4	3	64
101	6	35	1	2	36
102	6	35	1	1	77
103	6	35	1	3	88
201	6	35	2	2	42

```

202 6   35  2   3   69
203 6   35  2   1   71
301 6   35  3   3   43
302 6   35  3   2   39
303 6   35  3   1   84
401 6   35  4   1   97
402 6   35  4   2   47
403 6   35  4   3   76
;
PROC MIXED DATA=A COVTEST;
CLASS BLK TRT;
MODEL YSTAR=TRT|T/ SOLUTION DDFM=bw RESIDUAL;
RANDOM BLK;
WEIGHT WT;
REPEATED/SUBJECT=BLK*TRT TYPE=AR(1) R RCORR;
quit;

PROC MIXED DATA=A;
CLASS BLK TRT;
MODEL YSTAR=TRT TRT*T/NOINT SOLUTION DDFM=bw OUTPM=B;
RANDOM BLK;
WEIGHT WT;
REPEATED/SUBJECT=BLK*TRT TYPE=AR(1);
LSMEANS TRT/DIFF AT T=0;
LSMEANS TRT/DIFF AT T=7;
LSMEANS TRT/DIFF AT T=14;
LSMEANS TRT/DIFF AT T=21;
LSMEANS TRT/DIFF AT T=28;
LSMEANS TRT/DIFF AT T=35;

ESTIMATE 'TRT1 S VS TRT2 S' TRT*T 1 -1 0;
ESTIMATE 'TRT1 S VS TRT3 S' TRT*T 1 0 -1;
ESTIMATE 'TRT2 S VS TRT3 S' TRT*T 0 1 -1;
quit;

PROC PRINT DATA=B;

PROC REG DATA=B;
MODEL YSTAR=PRED;

RUN;

```

A.2 Exercise 9.4

Copy and paste the below code into a SAS editor, and hit run to see the output.

```
DATA A;
INPUT I YI;
EAST=1;
NORTH=I;
CARDS;
1 41
2 60
3 81
4 22
5 8
6 20
7 28
8 2
9 0
10 2
11 2
12 8
13 0
14 43
15 61
16 50
;
PROC VARIOGRAM PLOTS=MORAN OUTVAR=B;
COMPUTE LAGD=1 MAXLAG=11 AUTOCORR(ASSUM=RANDOM);
COORDINATES XC=EAST YC=NORTH;
VAR YI;

PROC PRINT;
run;

PROC VARIOGRAM DATA=A PLOTS=FIT;
COMPUTE LAGD=1 MAXLAG=11 CL ROBUST;
COORDINATES XC=EAST YC=NORTH;
MODEL FORM=AUTO(MLIST=(SPH EXP GAU) NEST=1);
VAR YI;

RUN;
```

A.3 Exercise 9.5

Copy and paste the below code into a SAS editor, and hit run to see the output.

```
DATA A;
INPUT COL ROW YI;
CARDS;
1 1 2
2 1 2
3 1 0
4 1 3
5 1 1
6 1 1
7 1 1
8 1 5
9 1 22
10 1 13
11 1 14
12 1 6
1 2 2
2 2 0
3 2 0
4 2 3
5 2 0
6 2 2
7 2 7
8 2 54
9 2 57
10 2 49
11 2 42
12 2 2
1 3 3
2 3 1
3 3 0
4 3 1
5 3 0
6 3 9
7 3 6
8 3 62
9 3 94
10 3 75
11 3 7
12 3 2
1 4 33
2 4 3
```

3	4	0
4	4	2
5	4	0
6	4	20
7	4	25
8	4	79
9	4	95
10	4	32
11	4	12
12	4	2
1	5	4
2	5	1
3	5	3
4	5	2
5	5	6
6	5	23
7	5	14
8	5	64
9	5	31
10	5	9
11	5	13
12	5	16
1	6	0
2	6	2
3	6	1
4	6	4
5	6	4
6	6	5
7	6	4
8	6	9
9	6	10
10	6	19
11	6	6
12	6	1
1	7	0
2	7	7
3	7	7
4	7	9
5	7	4
6	7	12
7	7	7
8	7	7
9	7	12
10	7	13
11	7	11
12	7	2

1	8	0
2	8	2
3	8	11
4	8	19
5	8	12
6	8	32
7	8	11
8	8	9
9	8	31
10	8	67
11	8	27
12	8	30
1	9	5
2	9	10
3	9	35
4	9	56
5	9	62
6	9	45
7	9	21
8	9	18
9	9	43
10	9	94
11	9	77
12	9	33
1	10	11
2	10	24
3	10	78
4	10	100
5	10	99
6	10	68
7	10	52
8	10	45
9	10	74
10	10	98
11	10	99
12	10	37
1	11	7
2	11	29
3	11	79
4	11	97
5	11	92
6	11	95
7	11	100
8	11	89
9	11	53
10	11	46

```

11 11 50
12 11 16
1 12 7
2 12 22
3 12 31
4 12 50
5 12 56
6 12 79
7 12 100
8 12 61
9 12 53
10 12 36
11 12 33
12 12 2
;

```

```

PROC VARIOGRAM DATA=A PLOTS=MORAN OUTVAR=B;
COMPUTE LAGD=1 MAXLAG=12 AUTOCORR(ASSUM=RANDOM);
COORDINATES XC=COL YC=ROW;
VAR YI;

```

```
PROC PRINT;
```

```

PROC VARIOGRAM DATA=A PLOTS=FIT;
COMPUTE LAGD=1 MAXLAG=12 CL ROBUST;
COORDINATES XC=COL YC=ROW;
MODEL FORM=AUTO(MLIST=(SPH EXP GAU) NEST=1);
VAR YI;

```

```
RUN;
```

A.4 Yield loss

Copy and paste the below code into a SAS editor, and hit run to see the output.

```

DATA A;
INPUT WP SP $ BLK TRT FUNG DS YIELD;
CARDS;
101 A 1 1 0 43 205
101 B 1 1 1 1 399
102 A 1 2 1 2 426
102 B 1 2 0 92 102
103 A 1 3 1 2 385
103 B 1 3 0 7 355

```



```

201 A 2 2 1 4 412
201 B 2 2 0 75 224
202 A 2 3 1 3 425
202 B 2 3 0 10 352
203 A 2 1 0 27 330
203 B 2 1 1 2 375
301 A 3 1 1 2 420
301 B 3 1 0 47 303
302 A 3 3 0 12 342
302 B 3 3 1 1 395
303 A 3 2 0 63 222
303 B 3 2 1 3 393
401 A 4 3 0 12 326
401 B 4 3 1 1 400
402 A 4 1 0 32 289
402 B 4 1 1 1 418
403 A 4 2 1 2 371
403 B 4 2 0 53 175
;
PROC MIXED COVTEST METHOD=TYPE3;
CLASS BLK TRT FUNG;
MODEL DS=TRT|FUNG/RESIDUAL;
RANDOM BLK BLK*TRT;
LSMEANS TRT|FUNG/DIFF;
run;

PROC MIXED COVTEST METHOD=TYPE3;
CLASS BLK TRT FUNG;
MODEL YIELD=TRT|FUNG/RESIDUAL;
RANDOM BLK BLK*TRT;
LSMEANS TRT|FUNG/DIFF;

PROC REG;
MODEL YIELD=DS;

DATA B;
SET A;
RY1=YIELD/399.23843;

PROC REG;
MODEL RY1=DS;

PROC SORT DATA=A; BY BLK TRT FUNG;
PROC TRANSPOSE DATA=A OUT=T1A; BY BLK TRT;
VAR YIELD;

```

```
run;

DATA T2A;
SET T1A;
RY2=COL1/COL2;
DROP _NAME_ COL1 COL2;
run;

PROC TRANSPOSE DATA=A OUT=T1B; BY BLK TRT;
VAR DS;
run;

DATA T2B;
SET T1B;
CDS=COL1;
DROP _NAME_ COL1 COL2;
run;

DATA T3;
MERGE T2A T2B;
BY BLK TRT;

PROC PRINT;
run;

PROC MIXED COVTEST;
CLASS BLK TRT;
MODEL RY2=TRT/RESIDUAL;
RANDOM BLK;
LSMEANS TRT/DIFF;

PROC REG;
MODEL RY2=CDS;

RUN;
```