Introduction to R and Model Specifications

Jan K. Møller, Henrik Madsen

DTU Compute

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This lecture

- Introduction to R mostly by running R-scripts
- Libraries and information
- Reading Data and Data frames
- Getting subsets of data
- Model specifications in R
- How to get help

Libraries and information

- Homepage: http://www.r-project.org
- Important entry: http://cran.at.r-project.org/
- CRAN family of internet sites: http://CRAN.R-project.org
- R on ETH: stat.ethz.ch/R-manual/
- University of Oxford: http://www.stats.ox.ac.uk/pub/
- Manuals and help are installed with R

Packages and installation

- Important entry: http://stat.ethz.ch/R-manual/R-patched/doc/html/index.html
- Try eg. 'Packages' 'stats' 'StructTS'
- For packages in standard library: library('splines')
- For other packages you must first install: install.packages('tree',dependencies=TRUE)

Reading data from file

```
On Windows:
  worms <-read.table("c:\\data\\worms.txt",header=T,row.names=1)
On Linux/Unix:
  worms<-read.table("./data/worms.txt",header=T,row.names=1)</pre>
```

Typically once the file has been imported to R we want to do two things:

- Use attach to make the variables accessible by name within the R session, and
- Use names to see a list of the variable names

Also to see some information you might want to

- See the contents of the dataframe just type its name
- Use summary {worms} to see a summary of the dataframe

Selecting Parts of a Dataframe

To select all the rows of the first three columns:

• To select the middle 11 rows for all columns:

To select only those rows which have Area>3 and Slope<4:

 Suppose we want the rows of the whole dataframe sorted by Area (the variable in column number one)

 Alternatively, the dataframe can be sorted in descending order by Soil pH, with only Soil pH and Worm density as output:

Specification of models

y: Dependent variable

x: Explanatory variable (continuous)

a: Explanatory variable (factor)

$$y \sim x$$
 or $y \sim 1 + x$

specifies the model

$$y_i = \mu + \beta x_i + e_i$$

and

y
$$\sim$$
 -1 + x

implies no intercept.

$${\tt y}\,\sim\,{\tt a}$$

specifies the model

$$y_{ij} = \alpha_j + e_{ij}; \quad i = 1, \dots, n_j; \quad j = 1, \dots, k$$

the parameterization is however depend on the applied contrast.

Specification of models

• Additive 2-sided model:

y
$$\sim$$
 a1 + a2

2-sided model with interaction

y
$$\sim$$
 a1 + a2 + a1:a2 or y \sim a1*a2

Model specification (cont.)

The construction

is understood by expanding

as ordinary multiplication, ie.

$$(1 + a1 + a2 + a1:a2):(1 + a3)$$

and then

Model specification (cont.)

Further the construction

$$(a1 + a2 + a3)^3$$

is the same as

whereas

$$(a1 + a2 + a3)^2$$

corresponds to

or

$$1 + a1 + a2 + a3 + a1:a2 + a1:a3 + a2:a3$$

Transformation of variables

In general we may write things like

$$log(y) \sim sqrt(x)$$

However – Be careful using $\hat{\ }$, /, and * on continuous variables!! Use the function I() instead, like in

$$log(y) \sim x1 + x2 + I(x1*x2) + I(x4/x5) + I((x6+x7)^2)$$

Analysis of Variance

- summary(lm(...)) : Partial test
- anova(lm(...)) : Sekvential test (alternatively summary(aov())).
- anova(fit.HO, fit.HA): Specific hypotheses.

Examples of more adv. R Model Formulae

• Tree-way ANOVA (not with three-way interaction):

$$y \sim N*P*K-N:P:K$$

Analysis of Covariance

$$y \sim x + gender$$

A common slope for y against x but with two intercepts, one for each gender.

Split-plot ANOVA:

$$y \sim a*b*c+Error(a/b/c)$$

A 3-way factorial setup, but three different error variances.

• Including multiple (polynomial) regression:

$$y \sim poly(x,2)+z$$

Multiple regression

$$y \sim (x+z+w)^2$$

Fit three variables plus all their two-way interactions

Non-parametric model

$$y \sim s(x) + lo(z)$$

u is a function of smoothed x and loess z. Møller and Madsen (Compute)

Tips for building multivariate models

• Consider multivariate relations using eg.

• Then a good way to start is estimating non-parametric models:

```
model = gam(ozone \sim s(rad) + s(temp) + s(wind)); plot(model)
```

• Use tree based methods to identify complex interactions, like:

```
model = tree(ozone ~ .,data=ozone.pollution); plot(model)
```

Now a parametric model can be formulated.

Use R's possibilities for changing the model

• Use R's possibilities for updating or reducing the model:

 When all terms are significant the model assumptions should be checked using eg.

Control of heteroscedasity etc. Transformation is a possible solution.

Error structure

Up to this point we have dealt with statistical analysis of data with gaussian errors. In practice, however, non-Gaussian erros are often seen:

- Poission errors, useful with count data.
- Binomial errors, useful with data on proportions.
- Gamma errors, useful with data showing constant coefficient of variation.
- Exponential errors, useful with data on time-to-death (survival analysis).

The error structure is defined by the **family** directive, and specified as a part of the model formula like:

glm(y
$$\sim$$
 x + z, family = binomial)

Residuals

Standardized residuals (stdres in MASS):

$$e_i' = \frac{e_i}{s\sqrt{1 - h_{ii}}}$$

Studentized residuals (studres in MASS):

$$e_i^* = \frac{y_i - \hat{y}_{(i)}}{\sqrt{Var[y_i - \hat{y}_{(i)}]}}$$

also called jack-knifed residuals. Found alternatively for linear models as

$$e_i^* = \frac{e_i'}{\sqrt{\frac{N-p-(e_i')^2}{N-p-1}}}$$

 h_{ii} can be obtain using lm.influence(...)\$hat.