### **Practicals**

#### **Practical 1: Marginal Models Continuous**



• We will use the PBC dataset; this is available as the object <a href="pbc2">pbc2</a> in the R workspace available on GitHub

- To load this workspace and make the data available execute the following steps:
  - 1. Open a new Rstudio session
  - 2. Create a new R script file (File  $\rightarrow$  New File  $\rightarrow$  R Script)
  - 3. Copy-paste and execute the following three lines

```
con <- url("https://raw.github.com/drizopoulos/Repeated_Measurements/master/Data.RData")
load(con)
close(con)</pre>
```



- The data are available in the data frame pbc2 we will need the following variables
  - \* id: patient id number
  - \* prothrombin: prothrombin time in sec (the response variable of interest)
  - \* year: follow-up times in years
  - \* drug: the randomized treatment
  - \* sex: the gender of the patients
  - \* age: the age of the patients

Aim: To build an appropriate marginal model to investigate the relationships between the prothrombin time and the aforementioned variables



- Q1: We will start by producing some descriptive plots for the prothrombin time, similar to those we have seen in Chapter 1, i.e.,
  - > spaghetti plot per treatment group including the loess curve
  - > spaghetti plot per sex including the loess curve

(hint: see code for Section 1.1)

What observations can you make?



- We will continue by starting our model building exercise
   Remember
  - > we start with a full specification of the mean structure, and investigate the covariance structure
  - based on our chosen covariance structure we can make inferences for the mean structure
- Q2: Start by fitting a marginal model with independent error terms using gls() and the following specification of the mean structure (hint: see code for Section 2.4)
  - > nonlinear time evolutions using natural cubic splines with 3 degrees of freedom
  - ▷ correct for sex, drug and age
  - interactions of the time effect with sex and drug



- Q2:
  - interpret the results you obtained
  - > should we simplify the model by excluding the non-significant terms?
- Q3: Continue with the same mean structure and try different covariance structures

  - by then extend the above structures by assuming heteroscedastic errors, i.e., that the variance increases (or decreases) with time

(hint: see code for Section 2.9)



- Q4: Using appropriate tools (hypothesis tests, information criteria) decide which structure is the best
  - > which models are nested to which models?
- For the remainder we will use the covariance structure you have chosen in Q4
- Q5: Check if we can drop all the interaction terms

(hint: see code for Section 2.9)



- Q6: Continue and check whether you can drop the nonlinear terms for the time effect
  - > to do that fit a model that assumes a linear time trend, and
  - > then do the likelihood ratio test to compare it to the model that includes the nonlinear terms
- Q7: Interpret the results of your final model
  - > regression coefficients
  - > covariance structure



- Q8: Use an Effect Plot to depict the model with the following settings

  - ▷ sex: both males and females

(hint: see code for Section 2.4 – Effect Plot)

#### **Practical 2: Mixed Models Continuous**



# Practical 2: Mixed Models Continuous (cont'd)



# Practical 3: Marginal Models Discrete



# Practical 3: Marginal Models Discrete (cont'd)



#### **Practical 4: Mixed Models Discrete**



# Practical 4: Mixed Models Discrete (cont'd)

