Dose-Time Response Modeling of Rabbit Brain AChE Activity: Methiocarb Dermal Dosing

June 24, 2005

1 Preamble

Here is some code to set up the analysis: loading required libraries and datasets, and defining some functions.

First, `CarbamateData` loads the full dataset for this risk assessment, and causes the library `DRUtils` to be loaded.

```
> library(CarbamateData)

Loading required package: DRUtils
Loading required package: nlme
Loading required package: tcltk
```

Set up lattice to use B&W instead of color:

```
> library(lattice)
> ltheme <- canonical.theme(color = FALSE)
> ltheme$strip.background$col <- "transparent"
> lattice.options(default.theme = ltheme)
```

Use package `Hmisc` for some formatting support.

```
> library(Hmisc)

Hmisc library by Frank E Harrell Jr

Type library(help='Hmisc'), ?Overview, or ?Hmisc.Overview')
to see overall documentation.

NOTE:Hmisc no longer redefines [.factor to drop unused levels when
subsetting.  To get the old behavior of Hmisc type dropUnusedLevels().

Attaching package 'Hmisc':


        The following object(s) are masked from package:stats :

         ecdf
```

The dermal data for this analysis are in `AggData`. The following code prints out documentation for the datasets in use:

```
> printDataDoc(AggData)
```

```
----------------------------------------
Data set: AggData

Dataset creation date: Wed Jun 22 12:07:24 2005
Script name: /home/setzer/tasks/CarbamateCRA/EmpiricalDoseResponsesFinal/Data/getdata.R
Script last modified: 2005-06-22 12:05:47
sysname: Linux
release: 2.4.24-openmosix2
version: #1 Wed Jul 28 14:33:52 CEST 2004
nodename: node24.cluster2.org
machine: i686
login: unknown
user: setzer
----------------------------------------
```

The following function turns out to be quite useful on subsetted dataframes. It just eliminates unused levels of all factors in the data frame:

```
> CleanUp <- function(x) {
+     for (nm in names(x)) {
+         if (is.factor(x[, nm]))
+             x[, nm] <- factor(x[, nm])
+     }
+     x
+ }
```

To get starting values, we often have to extract values from a previously fit model. The following function simplifies that. The argument `what` is a regular expression:

```
> getParms <- function(what, Par) {
+     Par[grep(what, names(Par))]
+ }
```

This script is for modeling the dose-time response for rat brain. via dermal exposure.

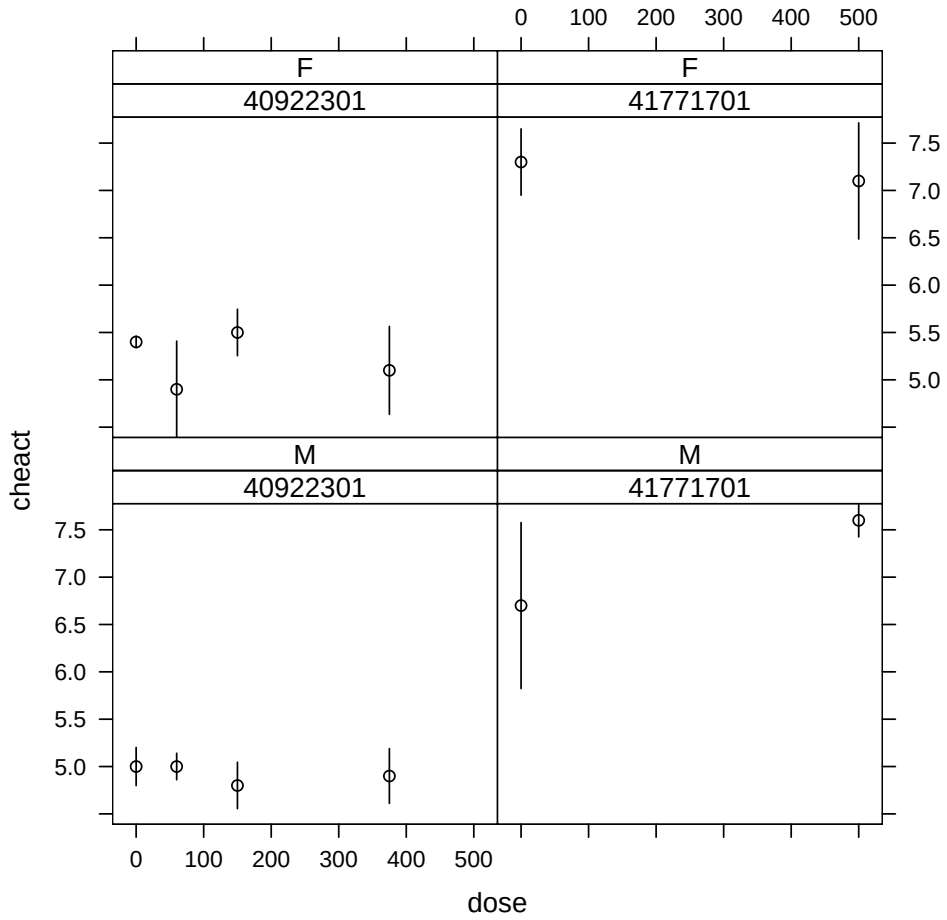
Set up the analysis dataset.

```
> dta <- CleanUp(subset(AggData, chemical %in% "METHIOCARB" & dsmtd ==
+     "DERMAL" & sctn %in% "WHOLEBRAIN", select = c("cheact", "sd",
+     "n", "dose", "tmpstds", "tmonstdy", "mrid", "sex", "species")))
```

Summary of this dataset:

```
> summary(dta)

     cheact            sd               n          dose          tmpstds
 Min.   :4.800   Min.   :0.0700   Min.   :5   Min.   :  0.0   Min.   : NA
 1st Qu.:4.975   1st Qu.:0.2225   1st Qu.:5   1st Qu.:  0.0   1st Qu.: NA
 Median :5.250   Median :0.3050   Median :5   Median :105.0   Median : NA
 Mean   :5.775   Mean   :0.3967   Mean   :5   Mean   :180.8   Mean   :NaN
 3rd Qu.:6.800   3rd Qu.:0.5425   3rd Qu.:5   3rd Qu.:375.0   3rd Qu.: NA
 Max.   :7.600   Max.   :1.0000   Max.   :5   Max.   :500.0   Max.   : NA
                                                              NA's   : 12
    tmonstdy        mrid   sex     species
 Min.   :21   40922301:8   F:6   RABBIT:12
 1st Qu.:21   41771701:4   M:6
 Median :21
 Mean   :21
 3rd Qu.:21
 Max.   :21
```



Plots of the dose-response
There is no evidence for a dose-response in this dataset, and it will not be modeled further.

2 Summary

There is no evidence for a dose-response, so no BMD is calculated.

species RABBIT

mrid `[1] "40922301" "41771701"`

Save everything:

```
> save.image(file = "DermalBrainDR.RData")
```

Save the results for incorporating into a database:

```
> methiocarb.dermal.brain <- list(mrid = levels(dta$mrid), species = levels(dta$species))
> save(methiocarb.dermal.brain, file = file.path("..", "..", "01Summaries",
+     "methiocarb.dermal.brain.RData"))
```