

Recent Development of R package 'predictmeans'

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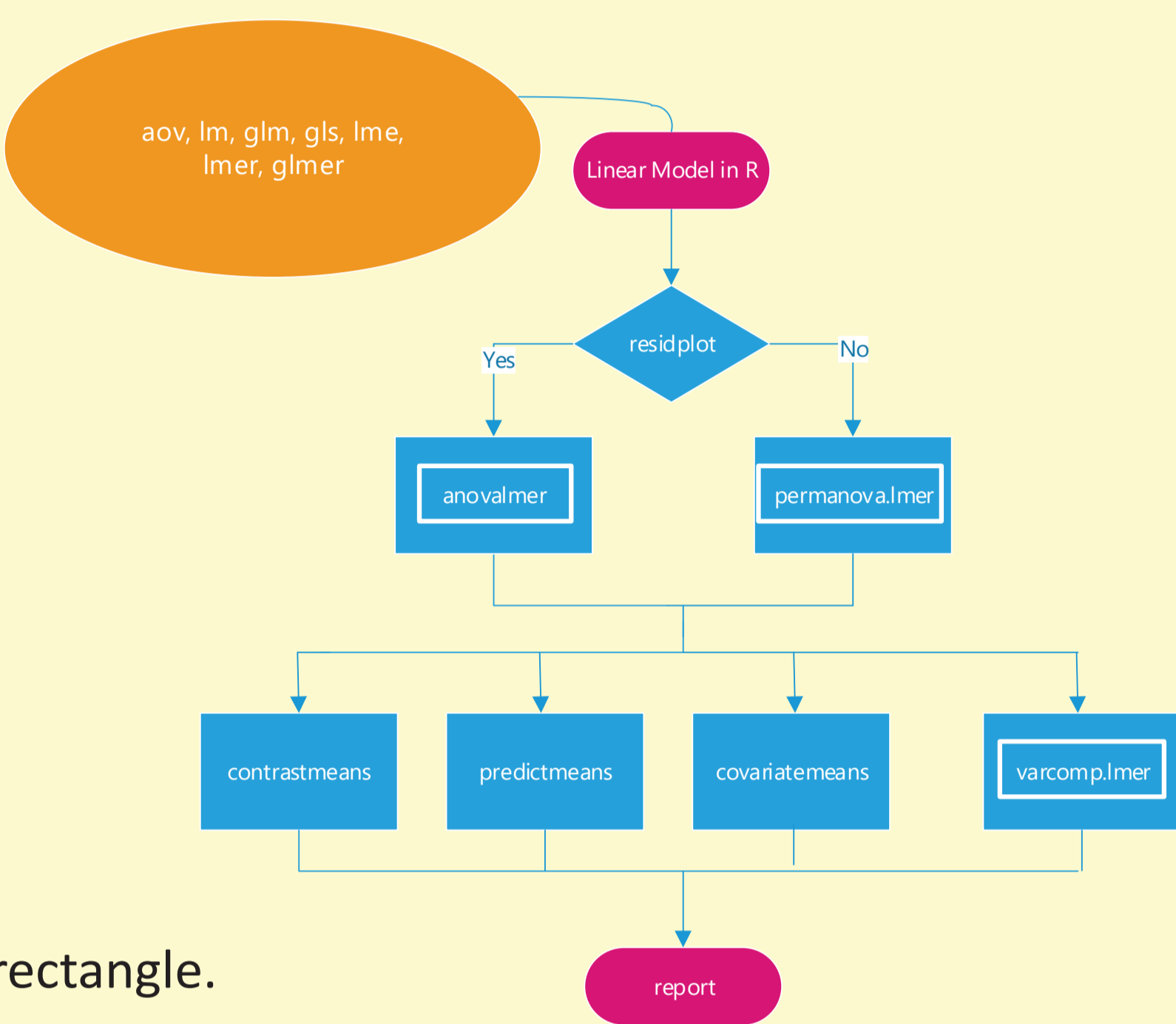
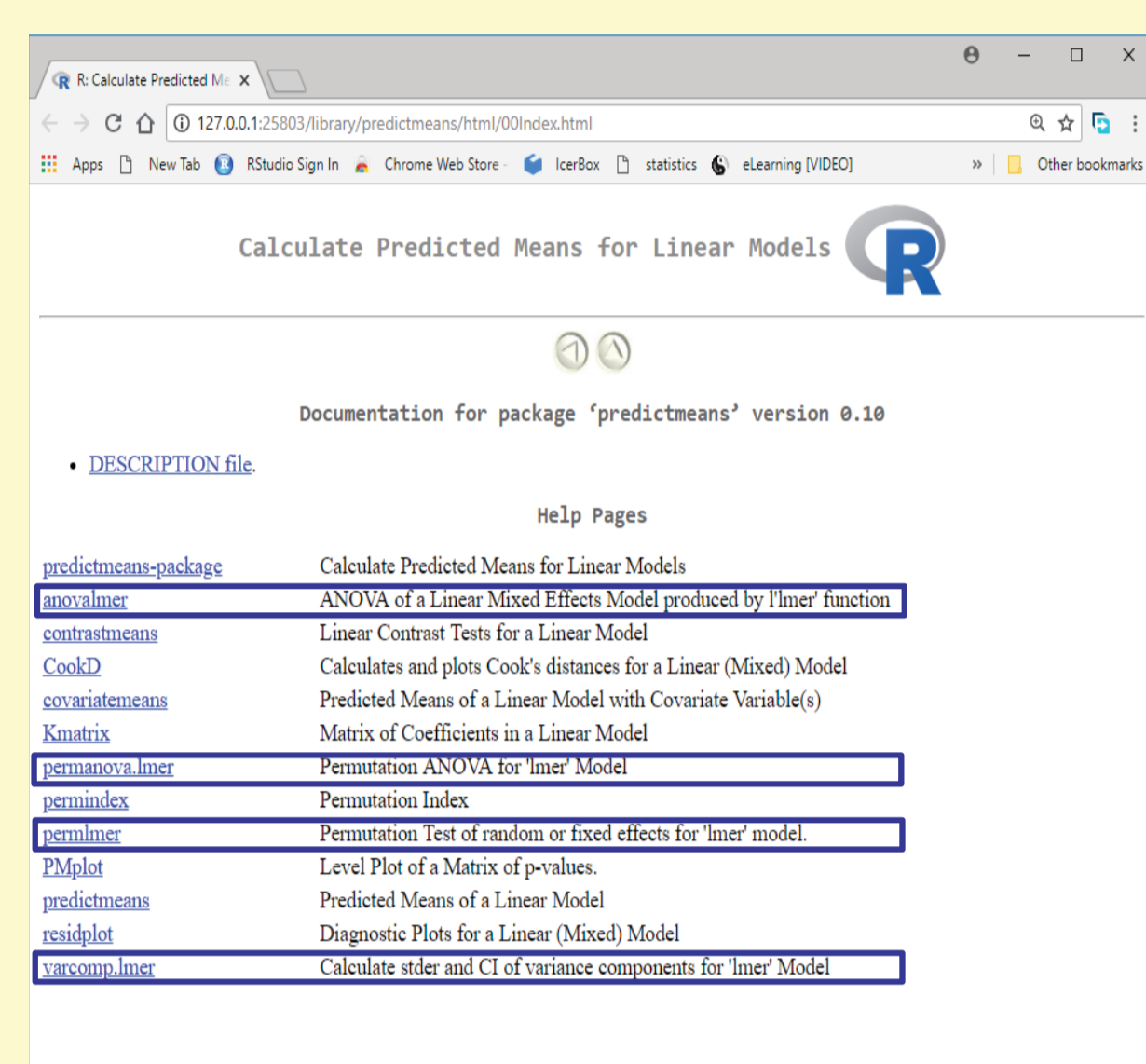
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INTRODUCTION:

R package 'predictmeans' is used to calculate predicted means for linear models (including 'aov', 'lm', 'glm', 'gls', 'lme', and 'lmer'). It provides functions to diagnose and make inferences such as predicted means and standard errors, contrasts, multiple comparisons, permutation tests and graphs. This poster will highlight some major improvement of the package by examples, especially, output presentation and permutation test.

Overview

```
> install.packages("predictmeans")
> library(predictmeans)
> help(package=predictmeans)
```



* The new functions are highlighted by rectangle.

Example1 split plot design (Oats data)

- In the split-plot design shown here, the treatments are three varieties of oats (Victory, Golden rain and Marvellous) and four levels of nitrogen (0, 0.2, 0.4 and 0.6 cwt). As it is feasible to work with smaller plots for fertiliser than for varieties, the six blocks were initially split into three whole-plots and then each whole-plot was split into four subplots. The varieties were allocated (at random) to the whole-plots within each block, and the nitrogen levels (at random) to the subplots within each whole-plot. In a randomized-block design, we have a hierarchical structure with blocks and then plots within blocks.

```
> data(Oats, package="nlme")
> Oats$nitro <- factor(Oats$nitro)
> fm <- lme(yield ~ nitro*Variety, random=~1|Block/Variety, data=Oats)
> residplot(fm, level=1) # from package 'predictmeans'
> anova(fm)
> predictmeans(fm, "nitro:Variety", atvar="Variety", adj="BH", barplot=TRUE)
```

	Variety Golden Rain	Marvellous	Victory
nitro 0	80.0000	86.6667	71.5000
0.2	98.5000	108.5000	89.6667
0.4	114.6667	117.1667	110.8333
0.6	124.8333	126.8333	118.5000

\$`Standard Error of Means`
All means have the same Stder
9.10696

\$`Standard Error of Differences`
Max.SED Min.SED Avg.SED
9.715030 7.682956 9.160828
attr("For the Same Level of Factor")
nitro Variety
Avg.SED 9.71503 7.682956
Min.SED 9.71503 7.682956
Max.SED 9.71503 7.682956

\$LSD
Max.LSD Min.LSD Avg.LSD
19.56707 15.47427 18.45085
attr("Significant level")
[1] 0.05
attr("Degree of freedom")
nitro:Variety
45

\$`Pairwise comparison p-value (adjusted by 'BH' method)`
[1] "For variable 'nitro' at each level of 'Variety'"

\$`Golden Rain`

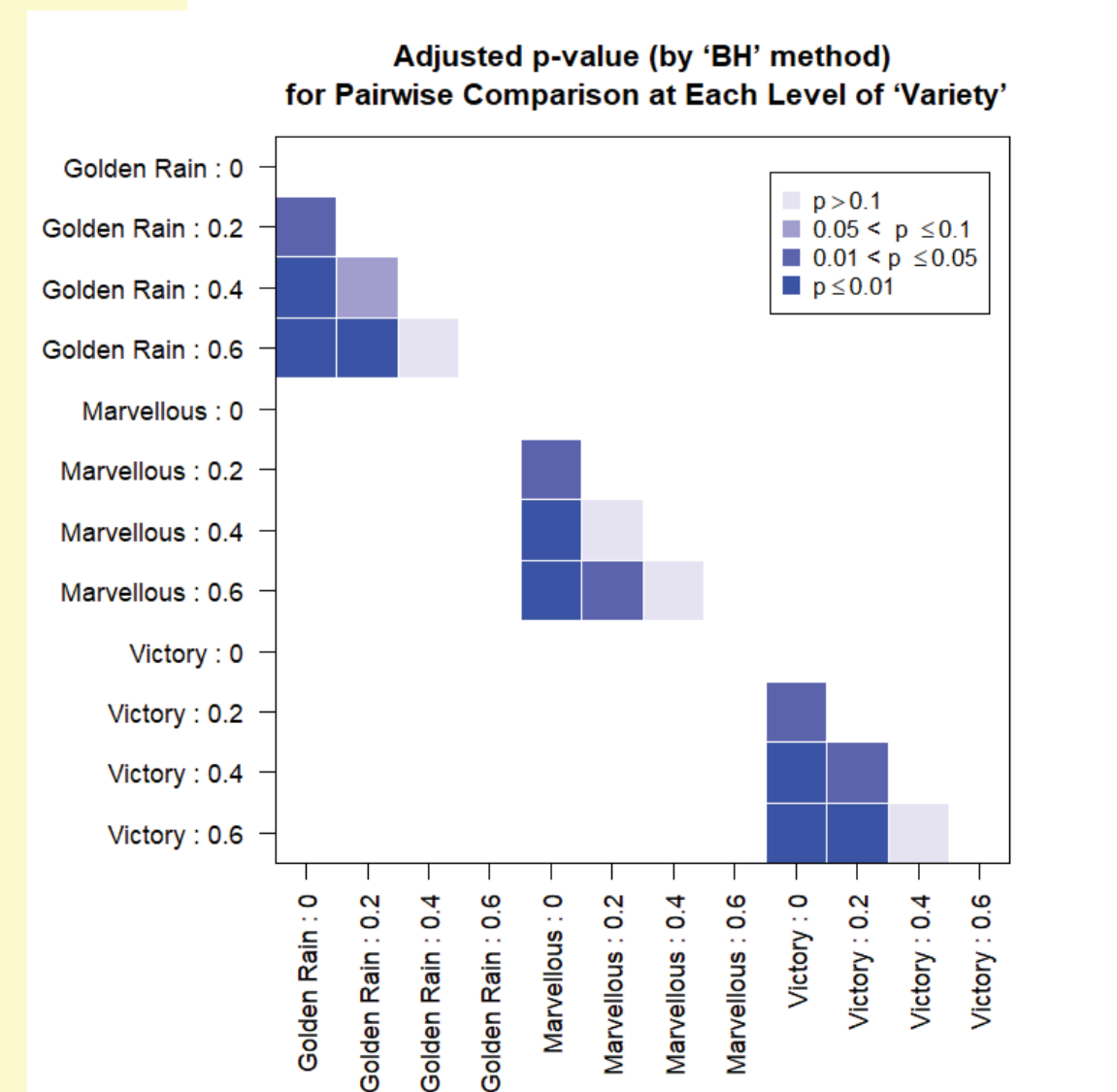
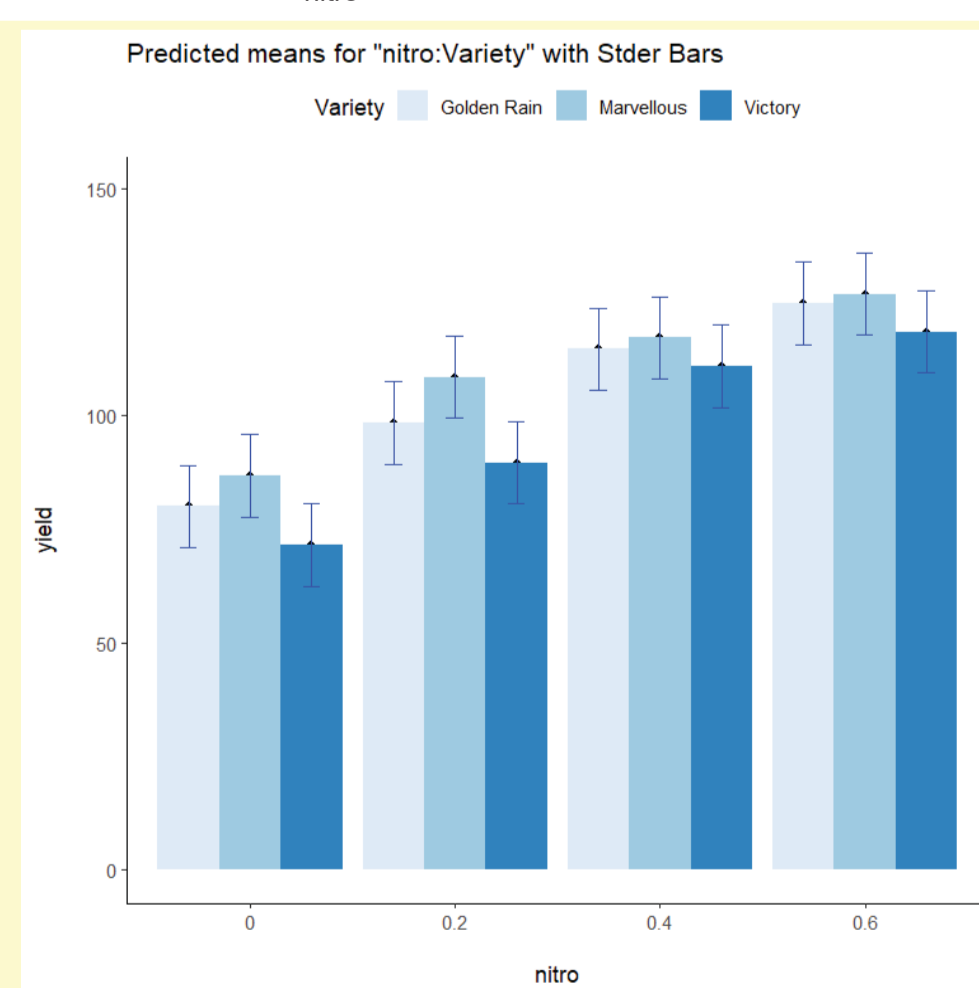
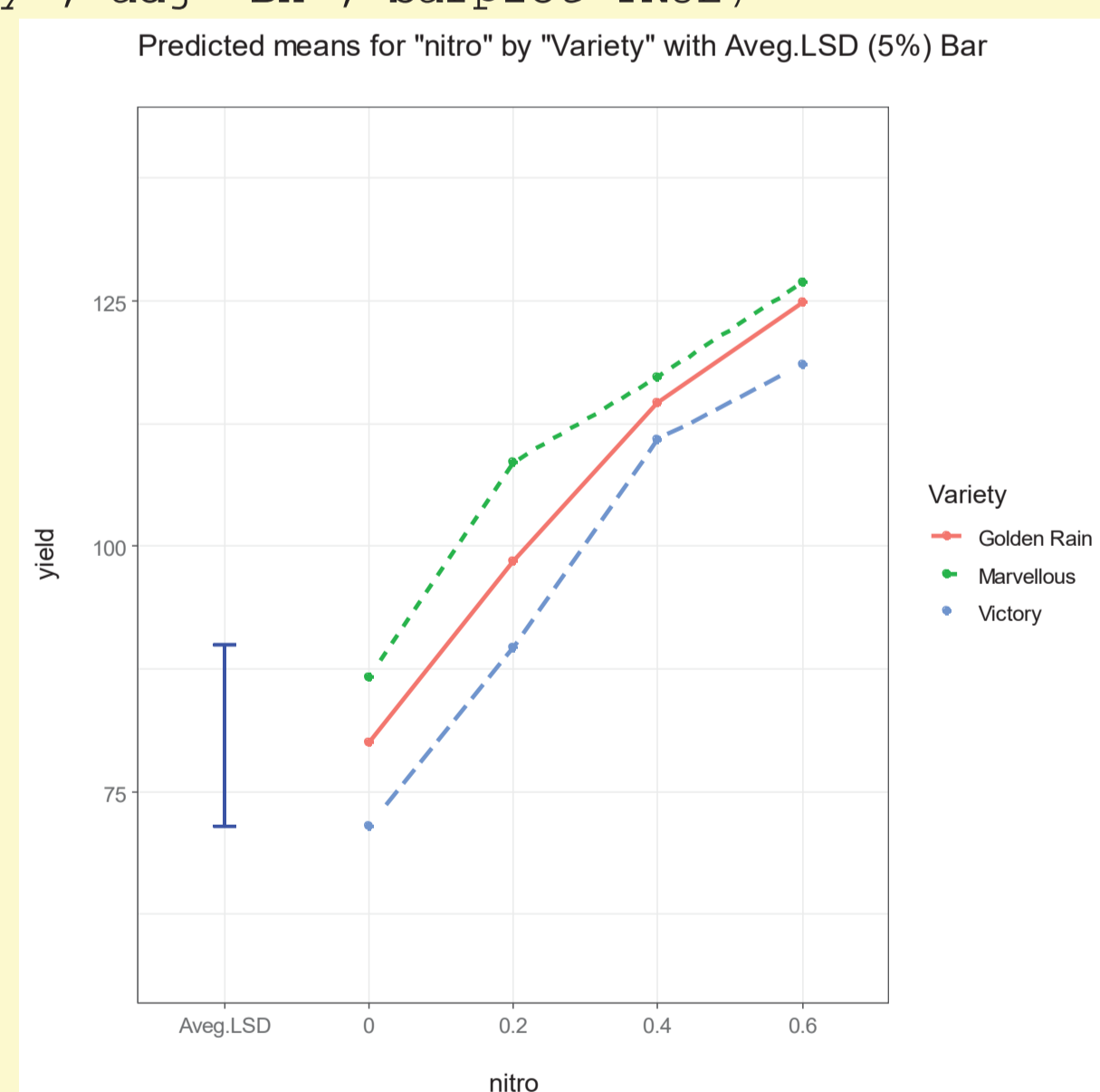
	0	0.2	0.4	0.6	Group
0	1				C
0.2	0.0311	1			B
0.4	0.0002	0.0527	1		AB
0.6	0.0001	0.003	0.2309	1	A

\$`Marvellous`

	0	0.2	0.4	0.6	Group
0	1				C
0.2	0.0134	1			B
0.4	0.0008	0.2809	1		AB
0.6	0.0001	0.0311	0.2417	1	A

\$`Victory`

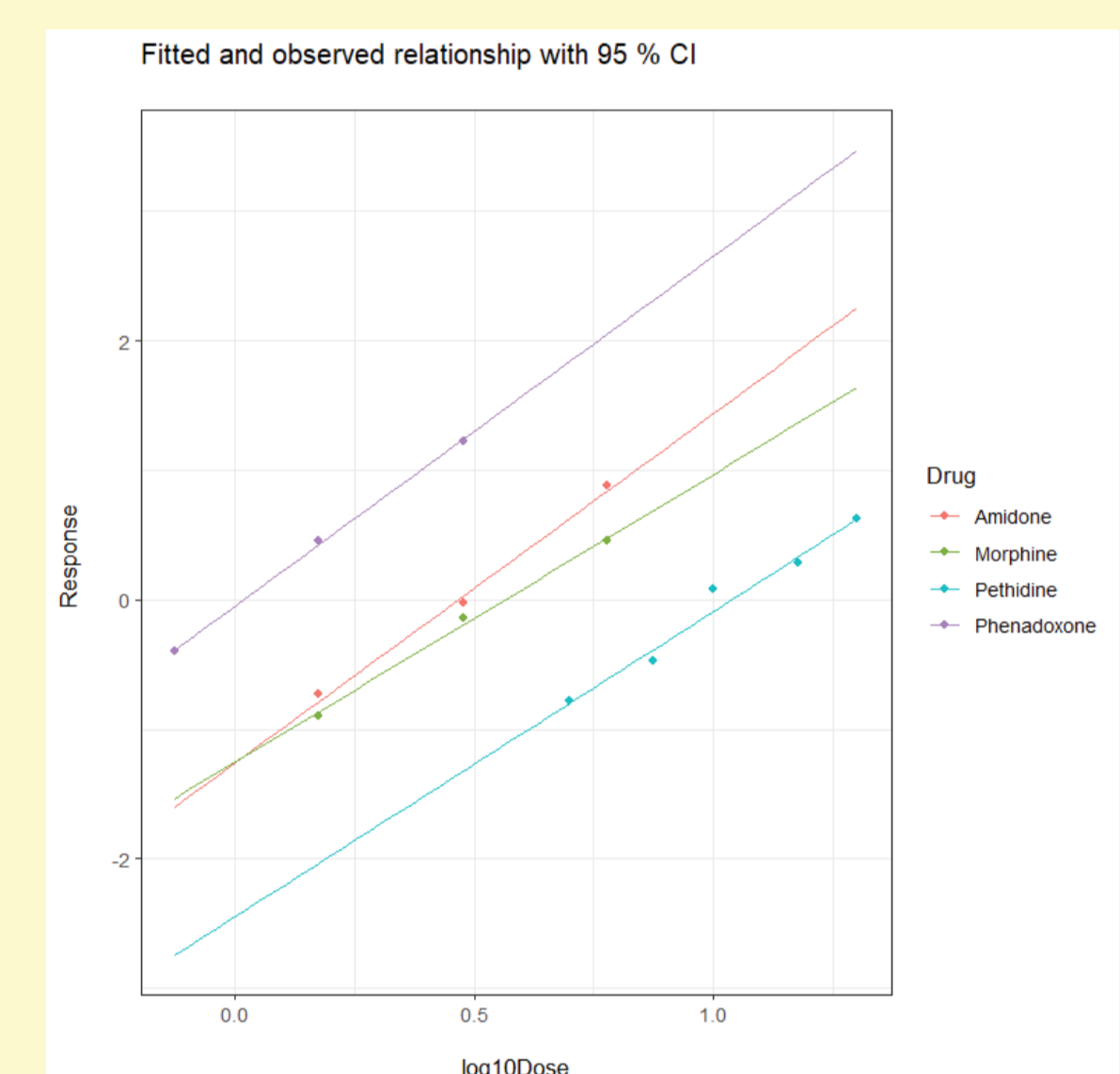
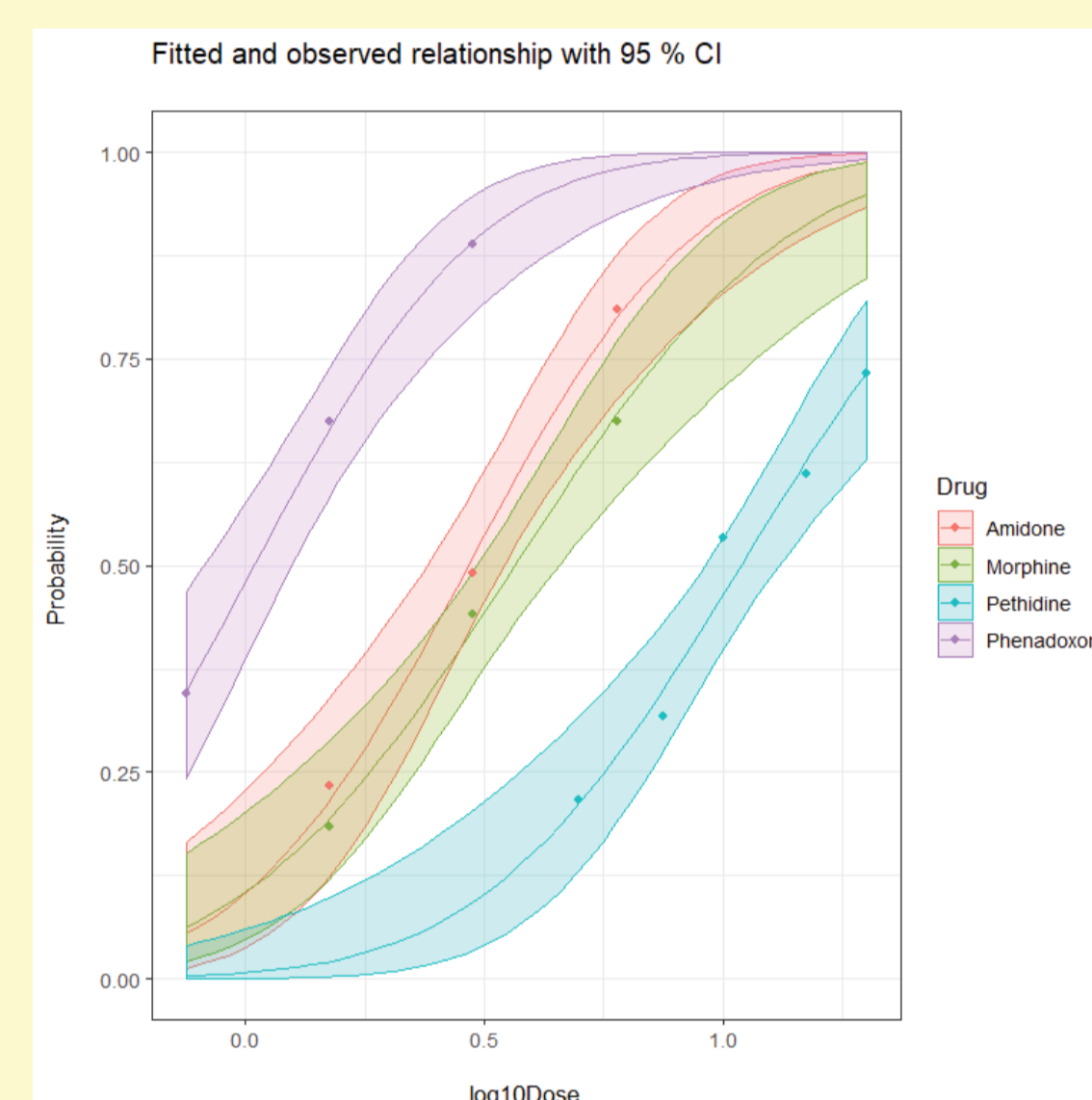
	0	0.2	0.4	0.6	Group
0	1				C
0.2	0.0311	1			B
0.4	0.0001	0.0152	1		A
0.6	0.0001	0.0013	0.3237	1	A



Example2 GLM (Drug data)

- Comparison of the effectiveness of three analgesic drugs to a standard drug, morphine (Finney, Probit analysis, 3rd Edition 1971, p.103). 14 groups of mice were tested for response to the drugs at a range of doses. N is total number of mice in each group, R is number responding.

```
> str(Drug)
'data.frame': 14 obs. of 5 variables:
 $ Drug : Factor w/ 4 levels "Morphine","Amidone",...: 1 1 1 2 2 3 3 3 4 ...
 $ Dose : num 1.5 3 6 1.5 3 6 0.75 1.5 3 5 ...
 $ N : int 103 120 123 60 110 100 90 80 90 60 ...
 $ R : int 19 53 83 14 54 81 31 54 80 13 ...
 $ log10Dose: num 0.176 0.477 0.778 0.176 0.477 ...
> fm <- glm(cbind(R, N-R) ~ log10Dose*Drug, family=binomial(link="probit"), data=Drug)
> residplot(fm)
> car: Anova(fm)
> summary(fm)
> covariatemeans(model=fm, modelterm="Drug", covariate="log10Dose", trellis = F)
> covariatemeans(model=fm, modelterm="Drug", covariate="log10Dose", trans=function(x) x, trellis = F, ci=F)
```



```
> predictmeans(fm, "Drug", adj="BH", jitterv = 0.2) # Output has the similar style as example # one
```

Example3 Permutation Test (Sleep study data)

- The data set is about the average reaction time per day for subjects in a sleep deprivation study (Belenky et al. 2003). On day 0 the subjects had their normal amount of sleep. Starting that night they were restricted to 3 hours of sleep per night. The response variable, Reaction, represents average reaction times in milliseconds (ms) on a series of tests given each Day to each Subject.

```
> str(sleepstudy)
'data.frame': 180 obs. of 3 variables:
 $ Reaction: num 250 259 251 321 357 ...
 $ Days : num 0 1 2 3 4 5 6 7 8 9 ...
 $ Subject : Factor w/ 18 levels "308","309","310",...: 1 1 1 1 1 1 1 1 1 1 ...
> fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
> fm2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
> fm3 <- update(fm1, ~ . - (Days | Subject) + (1 | Subject))
> anova(fm1, fm2, fm3) # Chisq Test
> perm.lmer(fm3, fm2) # permutation test
refitting model(s) with ML (instead of REML)
Data: sleepstudy
Models:
lmer0: Reaction ~ Days + (1 | Subject)
lmer1: Reaction ~ Days + ((1 | Subject) + (0 + Days | Subject))
Df AIC BIC logLik deviance Chisq Chi Df Pr(>Chisq)
lmer0 4 1802.1 1814.8 -897.04 1794.1
lmer1 5 1762.0 1778.0 -876.00 1752.0 42.075 1 8.7822e-11
Perm-p
```

```
lmer0
lmer1 0.001
> perm.lmer(fm2, fm1) # permutation test
refitting model(s) with ML (instead of REML)
Data: sleepstudy
Models:
lmer0: Reaction ~ Days + ((1 | Subject) + (0 + Days | Subject))
lmer1: Reaction ~ Days + (Days | Subject)
Df AIC BIC logLik deviance Chisq Chi Df Pr(>Chisq)
lmer0 5 1762.0 1778.0 -876.00 1752.0
lmer1 6 1763.9 1783.1 -875.97 1751.9 0.0639 1 0.80042
Perm-p
```

```
lmer0
lmer1 0.842
```

