Parametric bootstrap for linear and generalized linear models

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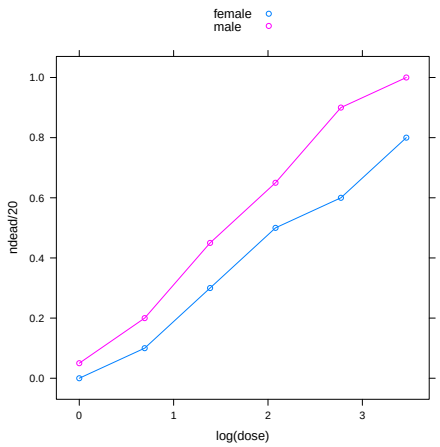
1 budworm

1.1 Linear regression

```
> data(budworm, package='LiSciData')
> library(lattice)
> par(mfrow=c(1,2))
> print(xyplot(ndead/20~log(dose), groups=sex, data=budworm,
+              type="b", auto.key=T))
>
```




```
> lm1 <- lm(ndead/20~sex+log(dose), data=budworm)
> lm0 <- update(lm1,.~.-sex)
> PBmodcomp(lm1, lm0, nsim=999)
```

```
Parametric bootstrap test; bootstrap samples: 999 computing time: 3.09 sec.
large : ndead/20 ~ sex + log(dose)
small : ndead/20 ~ log(dose)
            stat df   p.value   ddf
LRT      16.93364  1 0.0000387    NA
PBtest   16.93364 NA 0.0010010    NA
PBkd     16.93364 NA 0.0010021    NA
Gamma    16.93364 NA 0.0007067    NA
```

```
Bartlett 12.30399  1 0.0004520    NA
F        16.93364  1 0.0040813 7.315
```

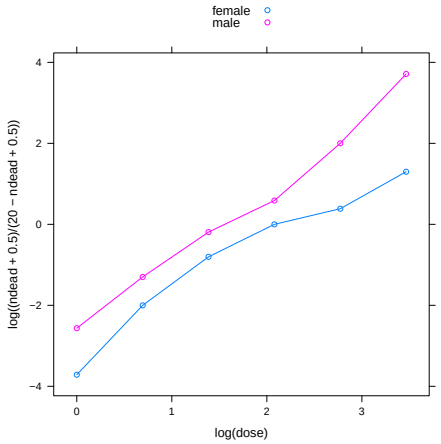
```
> anova(lm1,lm0)
```

```
Analysis of Variance Table

Model 1: ndead/20 ~ sex + log(dose)
Model 2: ndead/20 ~ log(dose)
  Res.Df      RSS Df Sum of Sq      F    Pr(>F)
1      9 0.024256
2     10 0.099464 -1 -0.075208 27.905 0.0005054 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1.2 Logistic regression

```
> library(lattice)
> print(xyplot(log((ndead+.5)/(20-ndead+.5))~log(dose), groups=sex, data=budworm,
+              type="b", auto.key=T))
```




```
> budworm <- transform(budworm, logdose=log(dose))
> lreg1 <- glm(cbind(ndead,ntotal-ndead)~sex+logdose,
+         data=budworm, family=binomial(link=logit))
> lreg0 <- update(lreg1,.~.-sex)
> PBmodcomp(lreg1, lreg0, nsim=999)
```

```
Parametric bootstrap test; bootstrap samples: 947 computing time: 4.51 sec.
large : cbind(ndead, ntotal - ndead) ~ sex + logdose
small : cbind(ndead, ntotal - ndead) ~ logdose
              stat df   p.value    ddf
LRT      10.226968  1 0.0013840     NA
PBtest   10.226968 NA 0.0021119     NA
PBkd     10.226968 NA 0.0021110     NA
Gamma    10.226968 NA 0.0014865     NA
Bartlett  9.531979  1 0.0020192     NA
F        10.226968  1 0.0033005 29.431
```