[7] studbookR: Inbreeding depression

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Introduction

- Neonatal survival and fitness
- Survival analysis
- Lethal equivalents

Neonatal survival and fitness

```
inbreeding.depression()
```

```
## ================================================
## Inbreeding depression in age group 0 - 30
## ================================================
##
## Inbreeding of parents: none
## Inbreeding depression ID: 0.06023732 [F(mean) = 0.02076399 ]
##
## ------------------------------------------------
##             Survival
## Factor       Survived Died
##   inbred          464  136
##   non-inbred      618  133
##
##  2-sample test for equality of proportions with continuity
##  correction
##
## data:  table2x2
## X-squared = 4.8331, df = 1, p-value = 0.02792
## alternative hypothesis: two.sided
## 95 percent confidence interval:
##  -0.094285720 -0.004853206
## sample estimates:
##    prop 1    prop 2
## 0.7733333 0.8229028
##
## H0: inbred and non-inbred survival are the same. => rejected
## [alpha =  0.05 ]
##
## Adjust for potential litter effect
## ---------------------------------
##
## Type: Donner
##
## N = 660 clusters, n = 1351 subjects, m = 269 cases, I = 2 groups.
```

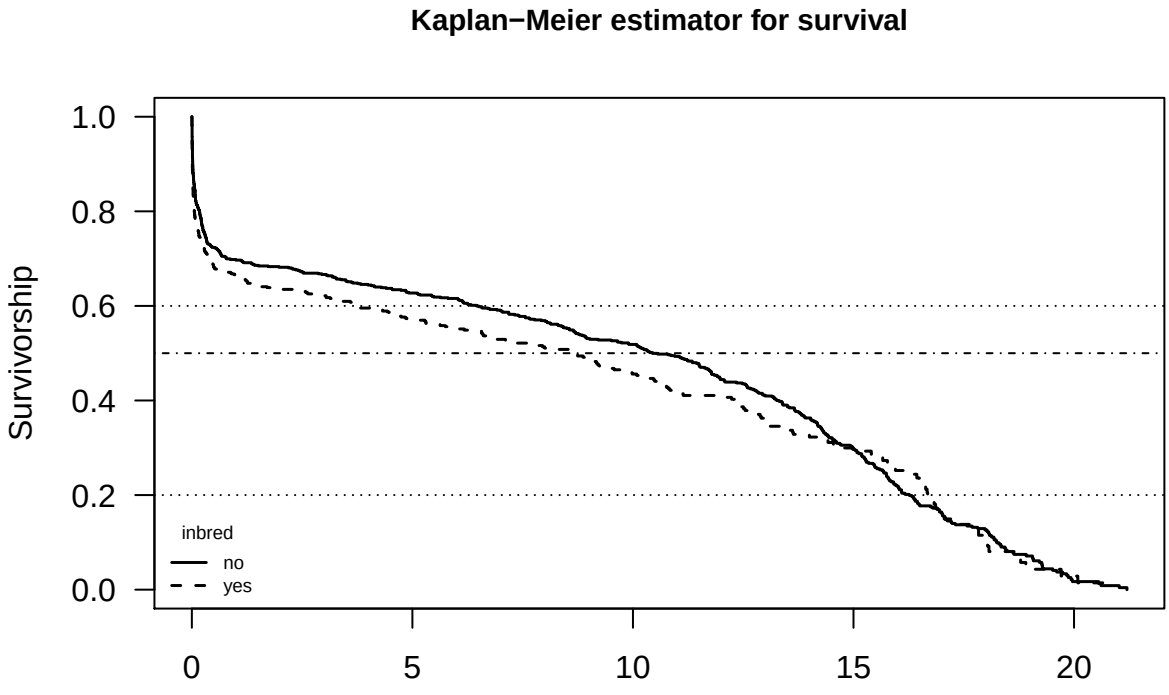
```
##
## Data and correction factors:
##   INBRED   N   n   m     mu     C
## 1  FALSE 381 751 133 0.1771 1.684
## 2   TRUE 279 600 136 0.2267 1.803
##
## Adjusted chi2 test:
## X2 = 2.9,
##       df = 1,
##       P(> X2) = 0.0865
##
## Intra-cluster correlation (anova estimate): 0.5321
```

Survival analysis

```
inbreeding.survival(method="kaplan")
```

```
## ================================================
## Kaplan-Meier estimator for survival
## ================================================
##
## Sex      : all
## Unknown  : include
## Age range: [0-Inf] (days)
## Group    : inbreeding
## Parents  : none inbred
## Formula  : survival.object ~ INBRED
##
## Call: survfit(formula = as.formula(formula.km), data = survival.data,
##     subset = subset, na.action = na.omit)
##
##              n events *rmean *se(rmean) median 0.95LCL 0.95UCL
## INBRED=no  751    578   3328       99.1   3812    3259    4297
## INBRED=yes 600    361   3077      121.9   3171    2407    3726
##     * restricted mean with upper limit =  7654
##
##
## * Last age group in Kaplan-Meier estimator
##     time risk event survivorship
## 932 7569    1     0   0.01437578
##
## [ Mantel-Haenszel (logrank) test ]
## Call:
## survival::survdiff(formula = as.formula(formula.km), data = survival.data,
##     subset = subset, na.action = na.omit, rho = rho)
##
##              N Observed Expected (O-E)^2/E (O-E)^2/V
## INBRED=no  751      578      599     0.755      2.16
## INBRED=yes 600      361      340     1.331      2.16
##
##  Chisq= 2.2  on 1 degrees of freedom, p= 0.142
## H0: Samples are from the same distribution => not rejected
```

```
## [alpha =  0.05 ]
```



Survival differences between inbred and non−inbred groups.

Lethal equivalents

```
studbook.lethaleqv(method=c("glm"))
```

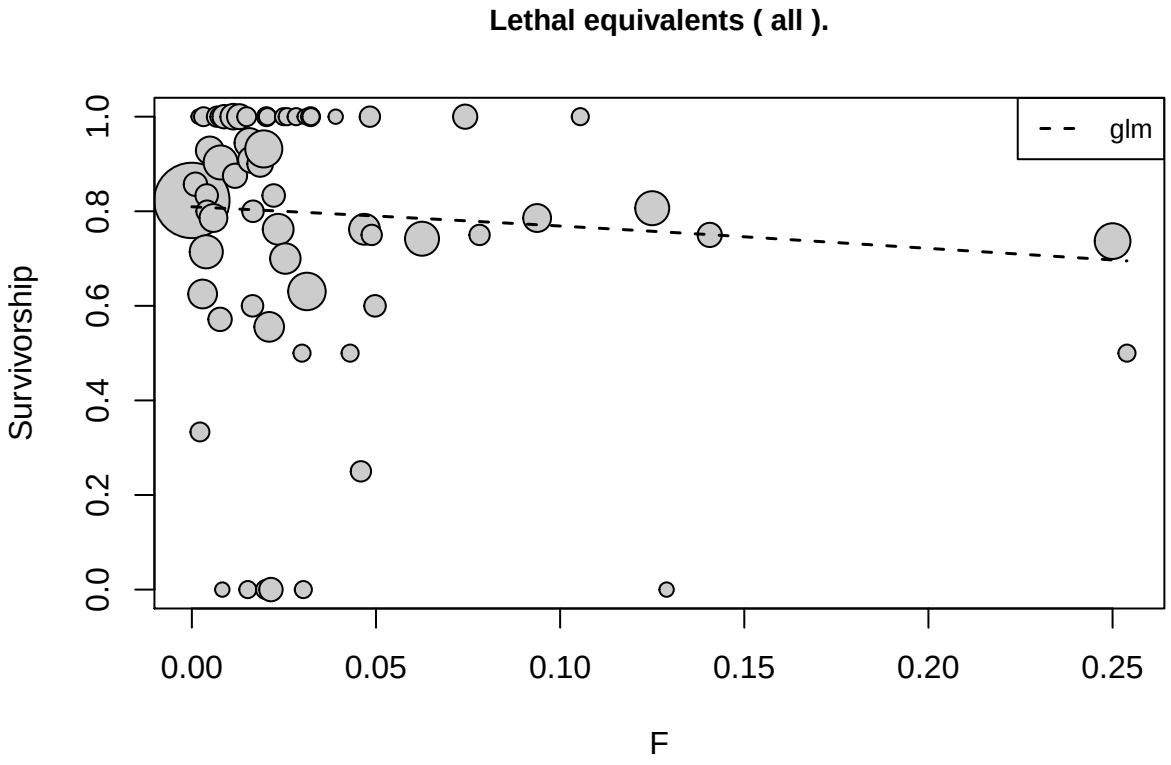
```
## ================================================
## Lethal equivalents in all (Inbred parents: none )
## ================================================

## Waiting for profiling to be done...

## [ Generalised linear model (Amstrong and Cassey, 2007) ]

## Warning in log(B[2:3]): NaNs produced

## Family/link                : binomial / logit
## Residual deviance (df)     : 134.556 ( 62 )
## Overdispersion(*)          : 2.170258
## Survivorship of non-inbred : 0.81 [0.79,0.83]
## Lethal equivalents diploid : 1.8 [-Inf,3.18]
## AIC: 230.0535
## ----------------------------------------------------------------
## * Crawley (p273, 2007)
```


Lethal equivalents (all).
glm
Survivorship
0.0
0.2
0.4
0.6
0.8
1.0
0.00
0.05
0.10
0.15
0.20
0.25
F

```
## [1] FALSE
```