

Survival Analysis

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This document show how to analyze the **time to seed germination** using **Survival Analysis**. The data used here correspond to seeds of 38 plants of *Ipomoea hederacea* (Convolvulaceae) obtained after the application of the following experiments:

- Hand-self pollination: flowers were manually pollinated with pollen from the two longest anthers of the flower.
- Hand-cross pollination: emasculated flowers were manually pollinated with pollen obtained from the two longest anthers of two-three donor plants.

Data

```
germination <- read.table("../data/germination.csv", header = TRUE, sep = ",")
head(germination)
```

##	plant	year	treatment	fruit	weight	germination	day
## 1	5	2012	HCP	3	11.0	0	122
## 2	9	2012	HSP	2	12.8	0	122
## 3	10	2012	HCP	3	13.5	1	7
## 4	7	2012	HCP	3	13.7	1	4
## 5	5	2012	HCP	3	15.1	0	122
## 6	10	2012	HSP	2	16.3	0	122

Cure model

A parametric mixture cure model is applied to compare probability survival curves per treatment by year. The analysis required the creation of survival objects, which are created using the `surv` function. A survival object consists of two columns:

- First column is the time or censored time.- Second column is the censoring indicator, indicating right censored data.

```
g12 <- filter(germination, year == "2012")
surv_cure12 <- flexsurvcure(
  Surv(day, germination) ~ treatment,
  data = g12, link = "logistic",
  dist = "lnorm",
```

```

mixture = T
)
surv_cure12_null <- flexsurvcure(
  Surv(day, germination) ~ 1,
  data = g12,
  link = "logistic",
  dist = "lnorm",
  mixture = T
)
mp_norm1 <- surv_cure12$loglik
mp_norm0 <- surv_cure12_null$loglik
chisq <- 2 * (mp_norm1 - mp_norm0)
chisq

```

```
## [1] 2.829155
```

```

g13 <- filter(germination, year == "2013")
surv_cure13 <- flexsurvcure(
  Surv(day, germination) ~ treatment,
  data = g13,
  link = "logistic",
  dist = "lnorm",
  mixture = T
)
surv_cure13_null <- flexsurvcure(
  Surv(day, germination) ~ 1,
  data = g13,
  link = "logistic",
  dist = "lnorm",
  mixture = T
)
mp_norm1 <- surv_cure13$loglik
mp_norm0 <- surv_cure13_null$loglik
chisq <- 2 * (mp_norm1 - mp_norm0)
chisq

```

```
## [1] 8.523345
```

Plotting cumulative incidence by treatment

Calculate the cumulative germination between treatments