

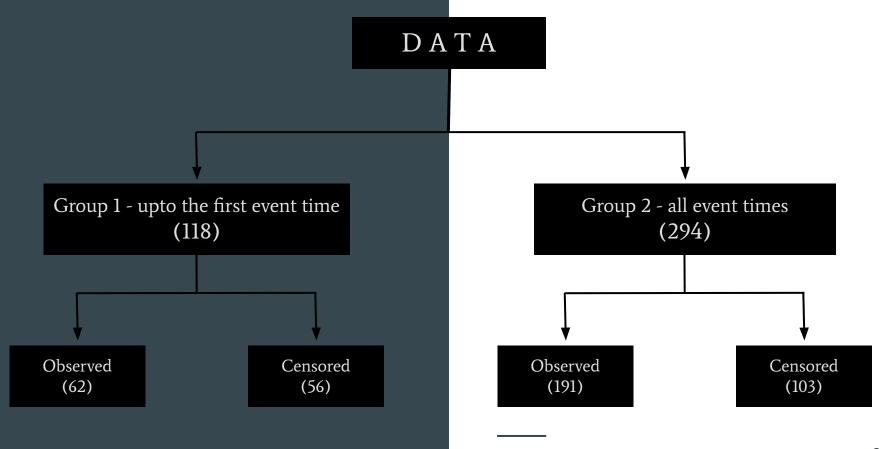
Survival Analysis of Patients with Recurrent Bladder Cancer

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Project objective

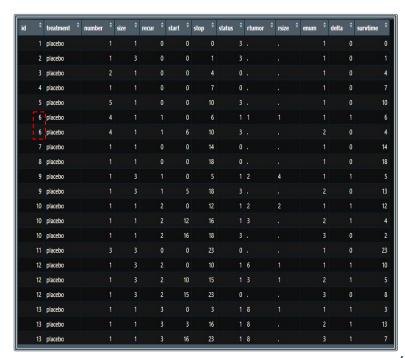
- Estimate and compare survival curves of patients undergoing different treatment methods
 - taking covariates into consideration
 - without taking covariates into consideration
- Frailty modelling for multiple recurrences (dependent time-to-event)



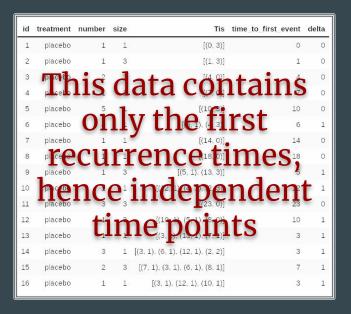
Group 1 - upto the first event time (118)

id	treatment	number	size	Tis	time_to_first_event	delta
1	placebo	1	1	[(0, 3)]	0	0
2	placebo	1	3	[(1, 3)]	1	0
3	placebo	2	1	[(4, 0)]	4	0
4	placebo	1	1	[(7, 0)]	7	0
5	placebo	5	1	[(10, 3)]	10	0
6	placebo	4	1	[(6, 1), (4, 3)]	6	1
7	placebo	1	1	[(14, 0)]	14	0
8	placebo	1	1	[(18, 0)]	18	0
9	placebo	1	3	[(5, 1), (13, 3)]	5	1
10	placebo	1	1	[(12, 1), (4, 1), (2, 3)]	12	1
11	placebo	3	3	[(23, 0)]	23	0
12	placebo	1	3	[(10, 1), (5, 1), (8, 0)]	10	1
13	placebo	1	1	[(3, 1), (13, 1), (7, 1)]	3	1
14	placebo	3	1	[(3, 1), (6, 1), (12, 1), (2, 2)]	3	1
15	placebo	2	3	[(7, 1), (3, 1), (6, 1), (8, 1)]	7	1
16	placebo	1	1	[(3, 1), (12, 1), (10, 1)]	3	1

Group 2 - all event times (294)



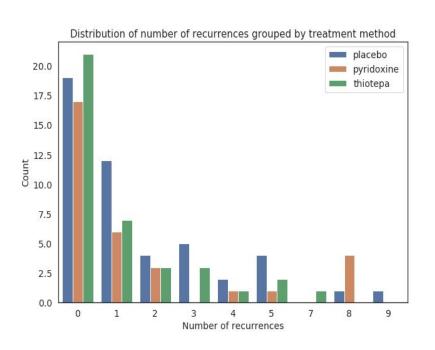
Group 1 - upto the first event time (118)

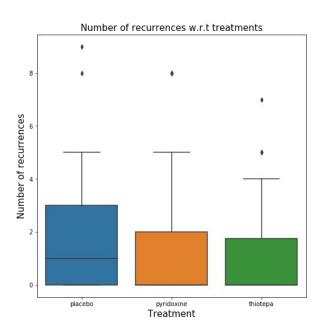


Group 2 - all event times (294)

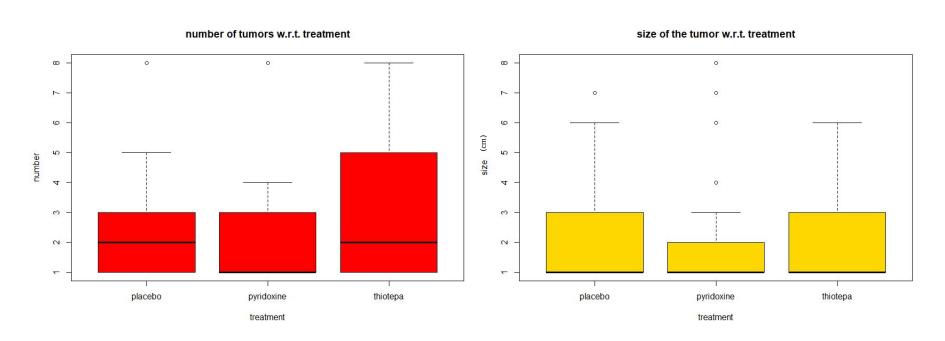


Treatment-wise distribution of recurrences

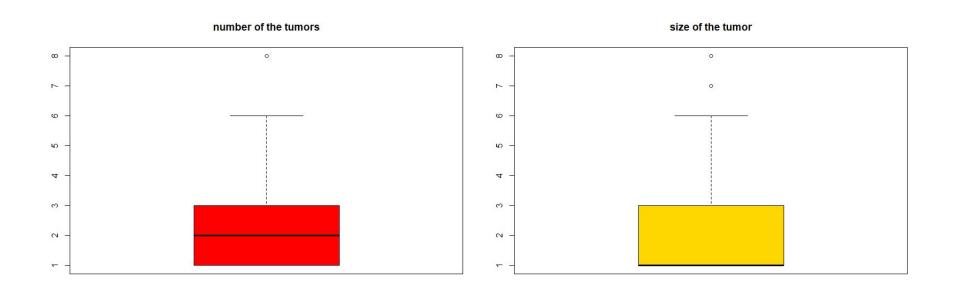




Outlier Detection in the Covariates



Outlier Detection in the Covariates



Kaplan-Meier Estimation (no covariates into consideration)

Kaplan-Meier estimator

The Kaplan–Meier estimator is a non-parametric statistic used to estimate the survival function from time-to-event data.

$$\hat{S}(t) = \prod_{t_i \leqslant t, \, i=1}^n igg(1 - rac{d_i}{Y_i}igg)$$

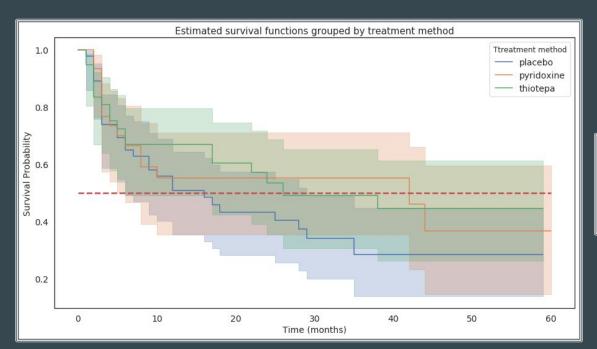
Log-rank test

The log-rank test is a non-parametric hypothesis test to compare survival distributions from two samples.

The null hypothesis is that the two groups have identical hazard functions, ie :

$$H_0: h_1(t) = h_2(t)$$

Kaplan-Meier estimator of survival functions of the 3 treatment groups



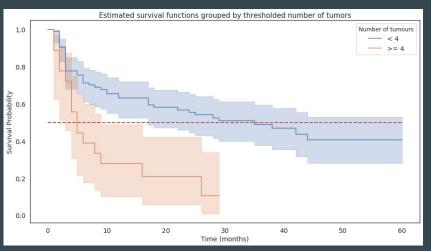
		test_statistic	р	-log2(p)
placebo	pyridoxine	1.326279	0.249468	2.003072
	thiotepa	1.520945	0.217477	2.201068
pyridoxine	thiotepa	0.001407	0.970077	0.043828

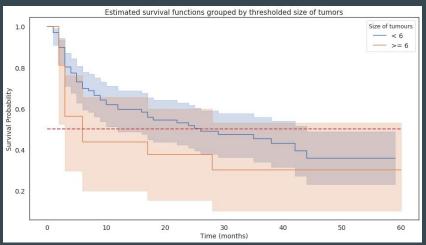
Thresholding on on

```
p-value when threshold on number of tumours is 2 : 0.0017939330834322697 p-value when threshold on number of tumours is 3 : 0.007020162822710038 p-value when threshold on number of tumours is 4 : 0.0002594167683235225 p-value when threshold on number of tumours is 5 : 0.002688648730418267 p-value when threshold on number of tumours is 6 : 0.0010422478423726767 p-value when threshold on number of tumours is 7 : 0.02283357735020892 p-value when threshold on number of tumours is 8 : 0.02283357735020892
```

```
p-value when threshold on size of tumours is 2 : 0.5199524395300987 p-value when threshold on size of tumours is 3 : 0.3024758137141664 p-value when threshold on size of tumours is 4 : 0.23865366312441283 p-value when threshold on size of tumours is 5 : 0.1682752207760559 p-value when threshold on size of tumours is 6 : 0.1570410142894633 p-value when threshold on size of tumours is 7 : 0.9146316972988796 p-value when threshold on size of tumours is 8 : 0.3025414266710924
```

Kaplan-Meier estimator of survival functions of the thresholded groups

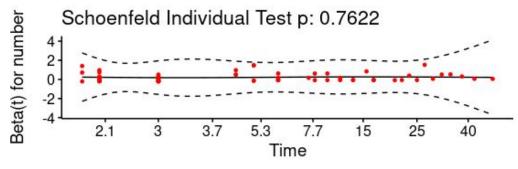


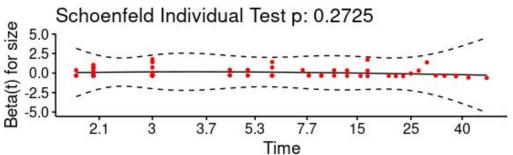


Cox Proportional Hazard Model (taking covariates into consideration)

Proportional Hazard Assumption : Schoenfeld Test







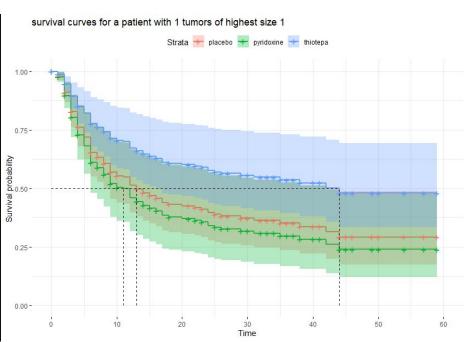
 H_0 : Hazards are proportional

H₁: Hazards are not proportional

```
chisq df p
number 0.0915 1 0.76
size 1.2041 1 0.27
GLOBAL 1.3589 2 0.51
```

Cox Proportional Hazard Model

```
> summary(cox)
Call:
coxph(formula = survobj1 ~ treatment + number + size, data = group22,
    cluster = id)
  n= 254, number of events= 162
                        coef exp(coef) se(coef) robust se
                                                              z Pr(>|z|)
treatmentpyridoxine 0.14967
                              1.16145 0.18418
                                                 0.24514 0.611 0.541516
treatmentthiotepa
                   -0.51959
                              0.59476 0.21593
                                                 0.26281 -1.977 0.048036 *
number
                     0.26014
                              1.29712 0.06319
                                                 0.07655 3.398 0.000678 ***
                    0.06854
                              1.07094 0.07729
                                                 0.09234 0.742 0.457983
size
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
                   exp(coef) exp(-coef) lower .95 upper .95
treatmentpyridoxine
                                 0.8610
                                           0.7183
                                                     1.8779
                       1.1614
treatmentthiotepa
                      0.5948
                                 1.6813
                                           0.3553
                                                     0.9955
                      1.2971
                                 0.7709
                                                     1.5071
number
                                           1.1164
                      1.0709
                                 0.9338
                                           0.8936
                                                     1.2834
size
Concordance= 0.602 (se = 0.025)
Likelihood ratio test= 23.47 on 4 df,
                    = 22.79 on 4 df,
                                        p=1e-04
Score (logrank) test = 23.67 on 4 df,
                                        p=9e-05,
                                                   Robust = 12.36 p=0.01
  (Note: the likelihood ratio and score tests assume independence of
     observations within a cluster, the Wald and robust score tests do not).
```



Shared Frailty Modelling

Unobserved covariates, (U):

$$h(t) = h_0(t)e^{x'\beta + u'\beta^*}$$

$$h(t \mid z) = zh_0(t)e^{x'\beta}$$

where $z = e^{u'\beta^*}$

Conditional survival function:

$$S(t|z) = \exp(-zH_0(t))e^{x'\beta}$$

where $H_0(t)$ integrated hazard.

Unconditional survival function:

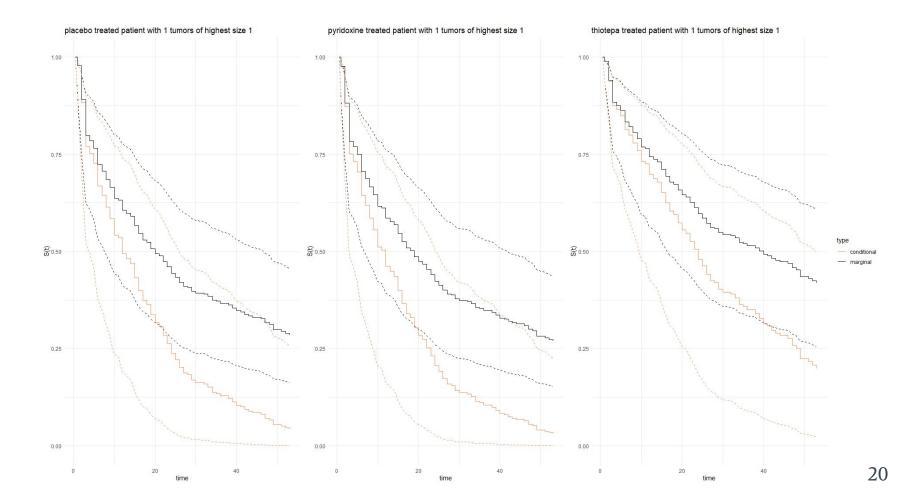
$$S(t) = E_z \left[e^{-zH_0(t)e^{x'\beta}} \right] = L_z \left[H_0(t)e^{x'\beta} \right]$$

Commenges-Anderson Test :

```
> ca_test(cox)
tstat var pval
9.377964e+01 5.482473e+02 6.197441e-05
>
```

Gamma Frailty Model:

```
> summary(gam)
Call:
emfrail(formula = Surv(start, stop, delta) ~ number + size +
    treatment + cluster(id), data = group22)
Regression coefficients:
                       coef exp(coef) se(coef) adj. se
number
                    0.3181
                              1.3745
                                       0.1203 0.1204 2.6426 0.01
size
                    0.0446
                              1.0456
                                       0.1342 0.1343 0.3324 0.74
                                       0.3573 0.3573 0.2579 0.80
treatmentpyridoxine 0.0922
                              1.0965
treatmentthiotepa -0.6704
                              0.5115 0.3599 0.3600 -1.8622 0.06
Estimated distribution: gamma / left truncation: FALSE
Fit summarv:
Commenges-Andersen test for heterogeneity: p-val 5.71e-11
no-frailty Log-likelihood: -663.099
Log-likelihood: -636.731
LRT: 1/2 * pchisq(52.7), p-val 1.91e-13
Frailty summary:
                   estimate lower 95% upper 95%
Var[Z]
                      1.296
                               0.710
                                          2.222
Kendall's tau
                     0.393
                               0.262
                                         0.526
Median concordance
                     0.396
                               0.259
                                         0.541
E[logZ]
                     -0.773
                              -1.435
                                        -0.395
Var[logZ]
                     2.431
                               1.016
                                         5.917
                     0.772
                               0.450
                                         1.409
theta
Confidence intervals based on the likelihood function
```



Thank You!