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7.2.

$H_0: \lambda = 0.045$ vs. $H_a: \lambda > 0.045$

① One Sample Log-Rank test

```
##{r}
data(alloauto) # data from section 1.9
help("alloauto")

timevar <- alloauto$time[alloauto$type == 2] # type:2=autologous
delta <- alloauto$delta[alloauto$type == 2]

null_surv <- exp(-0.045 * timevar) #Expected survival probability

survdif(Surv(timevar, delta) ~ offset(null_surv))
#rm(timevar, delta, null_surv)
##{r}
```

```
Call:
survdif(formula = Surv(timevar, delta) ~ offset(null_surv))
```

Observed	Expected	Z	p
28.0000	38.3992	1.6782	0.0933

Therefore, $\chi^2 = 2.816$, $Z = 1.678$

P-value > 0.05 (two sided).

Therefore, we can't reject H_0 . We conclude that $\lambda = 0.045$.

② Using weight function (heavier weight to departures early in time from this hazard rate.)

• Use Fleming & Harrington (1981)

```
##{r}
survdif(Surv(timevar, delta) ~ offset(null_surv), rho=2) # rho=2 should weight earlier heavier
##{r}
```

```
Call:
survdif(formula = Surv(timevar, delta) ~ offset(null_surv),
  rho = 2)
```

Observed	Expected	Z	p
28.000	38.399	0.841	0.400

• The p-value = 0.4 > 0.05 (two sided p-value)

Therefore, we can't reject H_0 . We conclude that $\lambda = 0.045$.

(If using peto-peto, the result wasn't changed, also fail to reject H_0).

7.3 a). $H_0: h_0(x) = h_1(x)$ (0: Routine bath; 1: Body cleaning)
 $H_a: h_0(x) \neq h_1(x)$

```

{r}
data(burn)
help(burn)
survdif(Surv(T3,D3)~Z1,data=burn)

```

Call:
 survdif(formula = Surv(T3, D3) ~ Z1, data = burn)

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
Z1=0	70	28	21.4	2.07	3.79
Z1=1	84	20	26.6	1.66	3.79

Chisq= 3.8 on 1 degrees of freedom, p= 0.0515

• $\chi^2 = 3.8$ with $df = 1$, $P\text{-value} = 0.0515 > 0.05$

Therefore, we don't have enough evidence to reject H_0
 we conclude that $h_0(x) = h_1(x)$, which means there's no difference.

b) + c): Gehan's test & Tarone & Ware weights.

```

{r}
library(survMisc)
fit <- ten(Surv(T3,D3)~Z1,data=burn)
comp(fit)

```

	Q	Var	Z	pNorm
1	-6.6433e+00	1.1695e+01	-1.9426	0.052066
n	-6.9100e+02	1.6781e+05	-1.6868	0.091642
sqrtN	-6.4099e+01	1.3122e+03	-1.7695	0.076811
S1	-5.2057e+00	7.9984e+00	-1.8407	0.065667
S2	-5.1121e+00	7.8261e+00	-1.8274	0.067643
FH_p=1_q=1	-9.4385e-01	2.3082e-01	-1.9646	0.049463

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

	maxAbsZ	Var	Q	pSupBr
1	6.6433e+00	1.1695e+01	1.9426	0.104132
n	7.8300e+02	1.6781e+05	1.9114	0.111911
sqrtN	6.9566e+01	1.3122e+03	1.9204	0.109615
S1	5.2203e+00	7.9984e+00	1.8458	0.129829
S2	5.1791e+00	7.8261e+00	1.8513	0.128245
FH_p=1_q=1	9.4385e-01	2.3082e-01	1.9646	0.098925

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

* From top to bottom we have the test statistics, Q, and the p-values, pNorm for the log-rank, Gehan-Breslow, Tarone-Ware, Peto-Peto, modified Peto-Peto, and Fleming-Harrington weights.

• Gehan's test: $Z = -1.68$, $P\text{-value} = 0.09 > 0.05$. Fail to reject.

Therefore, there's no difference between two treatment.

• Tarone & Ware weights: $Z = -1.77$, $P\text{-value} = 0.076 > 0.05$.

Fail to reject. There's no difference between two treatment.

7.4

a) $H_0: h_1(t) = h_2(t)$ 1: Aneuploid tumor; 2: Diploid tumor.

$H_a: h_1(t) \neq h_2(t)$

```

{r}
data(tongue)
help(tongue)
survdifff(formula = Surv(time, delta) ~ type, data = tongue)

```

Call:
survdifff(formula = Surv(time, delta) ~ type, data = tongue)

	N	Observed	Expected	(O-E) ² /E	(O-E) ² /V
type=1	52	31	36.6	0.843	2.79
type=2	28	22	16.4	1.873	2.79

Chisq= 2.8 on 1 degrees of freedom, p= 0.0949

• $\chi^2 = 2.8$, p-value = 0.0949 > 0.05 . Fail to reject H_0 .

Therefore , the survival rates of patients with cancer of the tongue are the same for patients with aneuploid & diploid tumors.

b) We need a weight method that gives a heavier weight on earlier time , so the Peto & Peto test.

```

{r}
survdifff(formula = Surv(time, delta) ~ type, data = tongue, rho = 1)
# rho = 1 it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

```

Call:
survdifff(formula = Surv(time, delta) ~ type, data = tongue, rho = 1)

	N	Observed	Expected	(O-E) ² /E	(O-E) ² /V
type=1	52	20.2	24.4	0.731	3.3
type=2	28	15.1	10.9	1.643	3.3

Chisq= 3.3 on 1 degrees of freedom, p= 0.0694

• The p-value = 0.0694 > 0.05 , so still fail to reject H_0 .

Therefore , the survival rates of patients with cancer of the tongue are the same for patients with aneuploid & diploid tumors.