

Accelerated Failure Time Model

Example

Parametric regression in SAS

```
proc lifereg data=;
model time*censor(0)=z1,z2 / dist= ;
run;
```

- In MODEL Statement, specify the distribution
 - EXPONENTIAL
 - GAMMA
 - LLOGISTIC
 - LNORMAL
 - LOGISTIC
 - NORMAL
 - WEIBULL (default)

Parametric regression in SAS

```
proc lifereg data=;
class treatment;
model time*censor(0)=X / dist= ;
by center;
output out=outdata quantiles=0.1 0.5 0.9 std=std
p=predtime;
run;
```

- CLASS Statement: names the classification variables to be used in the model
- BY Statement: to obtain separate analyses on observations in groups that are defined by the BY variables.
- OUTPUT Statement:
 - OUT=SAS-data-set specifies the name of output data set keywords=names: specifies the statistics to include in the output data and gives names to the new variables.

Parametric regression in SAS

- Keywords in the output
 - CDF: cdf at observed response
 - CRESIDUAL | CRES: Cox-Snell residuals
 - SRESIDUAL | SRES: standardized residuals
 - QUANTILES | QUANTILE | Q

SAS Example

- Data on 43 bone marrow transplant patients were collected.
- Patients had either Hodgkin's disease or Non-Hodgkin's Lymphoma, and were given either an allogeneic (Allo) transplant (from a HLA match sibling donor) or autogeneic (Auto) transplant (their own marrow was cleansed and returned to them after a high dose of chemotherapy).
- Other covariates are
 - Karnofsky score (a subjective measure of how well the patient is doing, ranging from 0-100)
 - waiting time (in months) from diagnosis to transplant.
- It is of substantial interest to see the difference in leukemia-free survival (in days) between those patients given an Allo or Auto transplant, after adjusting for patients' disease status, Karnofsky score and waiting time.

Data

- allo: transplant type (1=allogenic, 2=autologous)
- hodgkins: disease type (1=Non Hodgkins lymphoma, 2=Hodgkins disease)
- time: time to death or relapse, days
- status: censoring indicator (0=alive, 1=dead)
- kscore: Karnofsky score
- wtime: waiting time

SAS Example

```
data bmt;
input allo hodgkins time status kscore
wtime;
if allo=2 then allo=0;
if hodgkins=2 then hodgkins=0;
cards;
1 1 28 1 90 24 1 1 32 1 30 7 ....
cards;
```

- Here manually coded the indicator variables for **allo** and **hodgkins**. You can use class statement in SAS **Class** **allo** **hodgkins**
- But need to check what does what does 1 mean?

SAS Example

```
/* Fit an exponential model*/
proc lifereg data=bmt;
model time*status(0) = allo hodgkins
kscore wtime / dist=exponential;
run;
```

Type III Analysis of Effects			
Effect	DF	Wald Chi-Square	Pr > ChiSq
allo	1	0.0837	0.7723
hodgkins	1	6.2467	0.0124
kscore	1	64.8976	< .0001
wtime	1	1.6610	0.1975

SAS Example

Analysis of Parameter Estimates					
Parameter	DF	Estimate	Standard Error	Chi-Square	P-value
Intercept	1	2.0018	0.8972	4.98	0.0257
allo	1	0.1333	0.4607	0.08	0.7723
hodgkins	1	-1.3185	0.5275	6.25	0.0124
kscore	1	0.0758	0.0094	64.90	<.0001
wtime	1	0.0093	0.0072	1.66	0.1975
Scale	0	1	0	1	1
Weibull Shape	0	1	0	1	1

Interpretation of regression coefficients

- The coefficient of hodgkins is estimated as -1.3185, interpretation?
- Recall: 1=Non Hodgkins lymphoma, 0=Hodgkins disease
- **Interpretation:** On average, non Hodgkins patients did worse than Hodgkins patients with the average disease-free survival time for Non Hodgkins patients is only $\exp(-1.3185) = 0.27$ of that of the Hodgkins patients, given all the other covariates are the same.

Interpretation of regression coefficients

- The coefficient of kscore is estimated as 0.0758, interpretation?
- The patients with higher Karnofsky scores have better survival that with one point higher of Karnofsky score, the patients' average survival time increases by about 8%:
 $\exp(0.0758)-1=1.078-1=0.078$
