BIOST537_Project

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Directive 1

```
## [1] 782.0292
```

```
## [1] 0.3941606
```

```
##   records     n.max   n.start    events     rmean se(rmean)    median   0.95LCL
##  137.0000  137.0000  137.0000   83.0000 1186.1053  100.5981  481.0000  363.0000
##   0.95UCL
##  748.0000
```

```
## [1] ### SUMMARY OF FITTED WEIBULL MODEL ###
## [1]
## [1] MODEL FIT SUMMARIES
## [1]
## [1] Total number of observations: 137
## [1] Number of events observed: 83
## [1] Number of model parameters: 2
## [1] Maximized loglikelihood value: -657.77
## [1]
## [1] INFERENCE ON MODEL COEFFICIENTS
## [1]
##        estimate ci.lower ci.upper      se
## lambda  0.00068  0.00042  0.00094 0.00013
## p       0.58757  0.47793  0.69720 0.05594
```

```
## [1] ### SUMMARY OF FITTED GENERALIZED GAMMA MODEL ###
## [1]
## [1] MODEL FIT SUMMARIES
## [1]
## [1] Total number of observations: 137
## [1] Number of events observed: 83
## [1] Number of model parameters: 3
## [1] Maximized loglikelihood value: -650.19
## [1]
## [1] INFERENCE ON MODEL COEFFICIENTS
## [1]
##       estimate ci.lower ci.upper      se
## mu     6.22805  5.52109  6.93501 0.36070
## sigma  2.31270  1.88767  2.73774 0.21686
## Q     -0.39609 -1.05804  0.26586 0.33774
```

```
## [1] 9.877379e-05
```

Directive 2

Disease Subgrouping

Table 1: Call: s_bmt ~ disgroup Chisq = 13.803722 on 2 degrees of freedom, p = 0.001006

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
disgroup=1	38	24	21.85	0.2112	0.2893
disgroup=2	54	25	39.97	5.604	11.01
disgroup=3	45	34	21.18	7.756	10.53

	Disease Group 1	Disease Group 2	Disease Group 3
mean_age	24.421	29.407	30.444
sd_age	7.295	8.764	11.220
count_males	26.000	30.000	24.000
prop_males	0.684	0.556	0.533
count_females	12.000	24.000	21.000
prop_females	0.316	0.444	0.467
count_cmv	15.000	26.000	27.000
prop_cmv	0.395	0.481	0.600
count_mtx	17.000	12.000	11.000
prop_mtx	0.447	0.222	0.244
count_hospital	64.000	118.000	81.000
mean_donor_age	26.789	28.074	29.933
sd_donor_age	8.933	9.245	12.057
count_donor_males	26.000	34.000	28.000
prop_donor_males	0.684	0.630	0.622
count_donor_cmv	17.000	22.000	19.000
prop_donor_cmv	0.447	0.407	0.422

```
##              chiSq df pChisq
## 1          13.8037  2      5
## n          16.2407  2      1
## sqrtN      15.6529  2      4
## S1         15.7260  2      3
## S2         15.7781  2      2
## FH_p=1_q=1  9.9331  2      6
## $tft
##                       Q         Var        Z pNorm
## 1              -10.6695     42.7801 -1.63127     5
## n            -1294.0000 439987.8847 -1.95081     1
## sqrtN         -118.1769   4202.2583 -1.82302     4
## S1              -9.2667     23.2023 -1.92379     3
## S2              -9.1996     22.7588 -1.92839     2
## FH_p=1_q=1      -1.0948      1.4957 -0.89516     6
##
## $scores
## [1] 1 2 3
```

FAB Subgrouping

Table 2: Call: s_bmt ~ fab Chisq = 8.435337 on 1 degrees of freedom, p = 0.003680

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
fab=0	92	48	59.83	2.337	8.435
fab=1	45	35	23.17	6.034	8.435

	FAB Classification 1	FAB Classification 2
mean_age	28.598	27.889
sd_age	9.478	9.810
count_males	56.000	24.000
prop_males	0.609	0.533
count_females	36.000	21.000
prop_females	0.391	0.467
count_cmv	44.000	24.000
prop_cmv	0.478	0.533
count_mtx	32.000	8.000
prop_mtx	0.348	0.178
count_hospital	178.000	85.000
mean_donor_age	29.000	26.956
sd_donor_age	9.669	11.133
count_donor_males	58.000	30.000
prop_donor_males	0.630	0.667
count_donor_cmv	44.000	14.000
prop_donor_cmv	0.478	0.311

```
##                      Q        Var      Z pNorm
## 1          1.1825e+01 1.6590e+01 2.9033     1
## n          1.0830e+03 1.6628e+05 2.6559     6
## sqrtN      1.1217e+02 1.6047e+03 2.8001     2
## S1         7.9035e+00 8.7832e+00 2.6668     4
## S2         7.8227e+00 8.6118e+00 2.6657     5
## FH_p=1_q=1 2.1652e+00 6.0024e-01 2.7948     3
##                maxAbsZ        Var      Q pSupBr
## 1          1.2047e+01 1.6590e+01 2.9578      1
## n          1.0850e+03 1.6628e+05 2.6608      6
## sqrtN      1.1283e+02 1.6047e+03 2.8167      3
## S1         7.9834e+00 8.7832e+00 2.6938      4
## S2         7.8946e+00 8.6118e+00 2.6902      5
## FH_p=1_q=1 2.2184e+00 6.0024e-01 2.8633      2
```

```
## [1] 0.007909707
```

Directive 3

Sex Subgrouping

Table 3: Call: s_bmt ~ male Chisq = 1.078766 on 1 degrees of freedom, p = 0.298974

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
male=0	57	36	31.42	0.6662	1.079
male=1	80	47	51.58	0.4059	1.079

CMV Subgrouping

Table 4: Call: s_bmt ~ cmv Chisq = 0.497423 on 1 degrees of freedom, p = 0.480635

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
cmv=0	69	40	43.2	0.2375	0.4974
cmv=1	68	43	39.8	0.2579	0.4974

Donor Sex Subgrouping

Table 5: Call: s_bmt ~ donormale Chisq = 0.001359 on 1 degrees of freedom, p = 0.970591

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
donormale=0	49	30	29.84	0.0008686	0.001359
donormale=1	88	53	53.16	0.0004875	0.001359

Donor CMV Subgrouping

Table 6: Call: s_bmt ~ donorcmv Chisq = 0.043347 on 1 degrees of freedom, p = 0.835073

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
donorcmv=0	79	48	48.93	0.01772	0.04335
donorcmv=1	58	35	34.07	0.02544	0.04335

Hospital Subgrouping

Table 7: Call: s_bmt ~ hospital Chisq = 13.680494 on 3 degrees of freedom, p = 0.003374

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
hospital=1	76	50	47.71	0.1101	0.2613
hospital=2	17	13	5.905	8.524	9.258
hospital=3	23	13	13.62	0.02779	0.03339
hospital=4	21	7	15.77	4.879	6.076

MTX Subgrouping

Two of the hospitals appear to be significant, but since each has little data, the power might be low, the SE might be high, and the CI may cross.

```
## Call:
## coxph(formula = s_bmt ~ deltaa + age + cmv + donorcmv + strata(hospital),
##     data = bmt_df)
##
##   n= 137, number of events= 83
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## deltaa    0.32446   1.38328  0.29323  1.106    0.269
## age       0.01983   1.02003  0.01310  1.515    0.130
## cmv      -0.10680   0.89871  0.24115 -0.443    0.658
## donorcmv -0.10844   0.89723  0.23607 -0.459    0.646
##
##          exp(coef) exp(-coef) lower .95 upper .95
## deltaa      1.3833     0.7229    0.7786     2.458
## age         1.0200     0.9804    0.9942     1.047
## cmv         0.8987     1.1127    0.5602     1.442
## donorcmv    0.8972     1.1145    0.5649     1.425
##
## Concordance= 0.572  (se = 0.041 )
## Likelihood ratio test= 3.55  on 4 df,   p=0.5
## Wald test            = 3.68  on 4 df,   p=0.5
## Score (logrank) test = 3.71  on 4 df,   p=0.4

## Call:
## coxph(formula = s_relapse ~ deltaa + age + cmv + donorcmv, data = bmt_df)
##
##   n= 137, number of events= 42
##
##               coef exp(coef)  se(coef)      z Pr(>|z|)
## deltaa   -0.507186  0.602188  0.482812 -1.050    0.293
## age       0.004592  1.004603  0.017577  0.261    0.794
## cmv       0.475670  1.609093  0.334449  1.422    0.155
## donorcmv -0.028186  0.972208  0.325574 -0.087    0.931
##
##          exp(coef) exp(-coef) lower .95 upper .95
## deltaa      0.6022     1.6606    0.2338     1.551
## age         1.0046     0.9954    0.9706     1.040
## cmv         1.6091     0.6215    0.8354     3.099
## donorcmv    0.9722     1.0286    0.5136     1.840
##
## Concordance= 0.598  (se = 0.046 )
## Likelihood ratio test= 3.55  on 4 df,   p=0.5
## Wald test            = 3.4  on 4 df,   p=0.5
## Score (logrank) test = 3.46  on 4 df,   p=0.5

## Warning in .add_surv_median(p, fit, type = surv.median.line, fun = fun, : Median
## survival not reached.

## Warning in .add_surv_median(p, fit, type = surv.median.line, fun = fun, : Median
## survival not reached.

## Warning in .add_surv_median(p, fit, type = surv.median.line, fun = fun, : Median
## survival not reached.
```

```
## Warning in .add_surv_median(p, fit, type = surv.median.line, fun = fun, : Median
## survival not reached.
```

```
## Call:
## coxph(formula = s_gvhd ~ mtx + donorcmv + strata(hospital), data = bmt_df)
##
##   n= 137, number of events= 26
##
##             coef exp(coef) se(coef)     z Pr(>|z|)
## mtx           NA        NA   0.0000    NA       NA
## donorcmv 0.7177    2.0497   0.4028 1.782   0.0748 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##          exp(coef) exp(-coef) lower .95 upper .95
## mtx             NA         NA        NA        NA
## donorcmv      2.05     0.4879    0.9307     4.514
##
## Concordance= 0.637  (se = 0.054 )
## Likelihood ratio test= 3.22  on 1 df,   p=0.07
## Wald test            = 3.17  on 1 df,   p=0.07
## Score (logrank) test = 3.3  on 1 df,   p=0.07
```

```
## Warning in .add_surv_median(p, fit, type = surv.median.line, fun = fun, : Median
## survival not reached.
```

```
## Call: survfit(formula = s_gvhd ~ mtx, data = bmt_df, conf.type = "log-log")
##
##                 mtx=0
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##     7     96       0    1.000  0.0000           NA           NA
##    14     96       0    1.000  0.0000           NA           NA
##    21     92       6    0.937  0.0249        0.865        0.971
##    28     86       5    0.884  0.0328        0.801        0.934
##    35     81       3    0.853  0.0363        0.764        0.910
##    42     80       1    0.842  0.0374        0.752        0.902
##    49     79       0    0.842  0.0374        0.752        0.902
##    56     78       1    0.832  0.0384        0.740        0.893
##
##                 mtx=1
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##     7     39       0    1.000  0.0000           NA           NA
##    14     36       2    0.949  0.0353        0.810        0.987
##    21     36       0    0.949  0.0353        0.810        0.987
##    28     36       0    0.949  0.0353        0.810        0.987
##    35     35       1    0.922  0.0431        0.778        0.974
##    42     31       3    0.841  0.0596        0.680        0.925
##    49     31       0    0.841  0.0596        0.680        0.925
##    56     30       0    0.841  0.0596        0.680        0.925
```

```
## Call:
## coxph(formula = s_bmt ~ deltap + age + donorcmv + strata(hospital),
##     data = bmt_df)
```

```
##
##   n= 137, number of events= 83
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## deltap   -1.60327   0.20124  0.32830 -4.883 1.04e-06 ***
## age       0.01959   1.01978  0.01223  1.602    0.109
## donorcmv -0.24138   0.78554  0.23819 -1.013    0.311
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##          exp(coef) exp(-coef) lower .95 upper .95
## deltap      0.2012     4.9692    0.1057     0.383
## age         1.0198     0.9806    0.9956     1.045
## donorcmv    0.7855     1.2730    0.4925     1.253
##
## Concordance= 0.615  (se = 0.042 )
## Likelihood ratio test= 21.54  on 3 df,   p=8e-05
## Wald test            = 26.16  on 3 df,   p=9e-06
## Score (logrank) test = 29.21  on 3 df,   p=2e-06

## Call:
## coxph(formula = s_relapse ~ deltap + age + donorcmv + strata(hospital),
##     data = bmt_df)
##
##   n= 137, number of events= 42
##
##               coef exp(coef)  se(coef)      z Pr(>|z|)
## deltap   -0.612551  0.541966  0.642941 -0.953    0.341
## age       0.009407  1.009451  0.017443  0.539    0.590
## donorcmv -0.021436  0.978792  0.320631 -0.067    0.947
##
##          exp(coef) exp(-coef) lower .95 upper .95
## deltap      0.5420     1.8451    0.1537     1.911
## age         1.0095     0.9906    0.9755     1.045
## donorcmv    0.9788     1.0217    0.5221     1.835
##
## Concordance= 0.584  (se = 0.058 )
## Likelihood ratio test= 1.07  on 3 df,   p=0.8
## Wald test            = 1.2  on 3 df,   p=0.8
## Score (logrank) test = 1.22  on 3 df,   p=0.7

## Saving 6.5 x 4.5 in image
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