

STAT 886 Final Examination

Part I. Problems

Part II. Analysis of Breast Cancer Data

INTRODUCTION

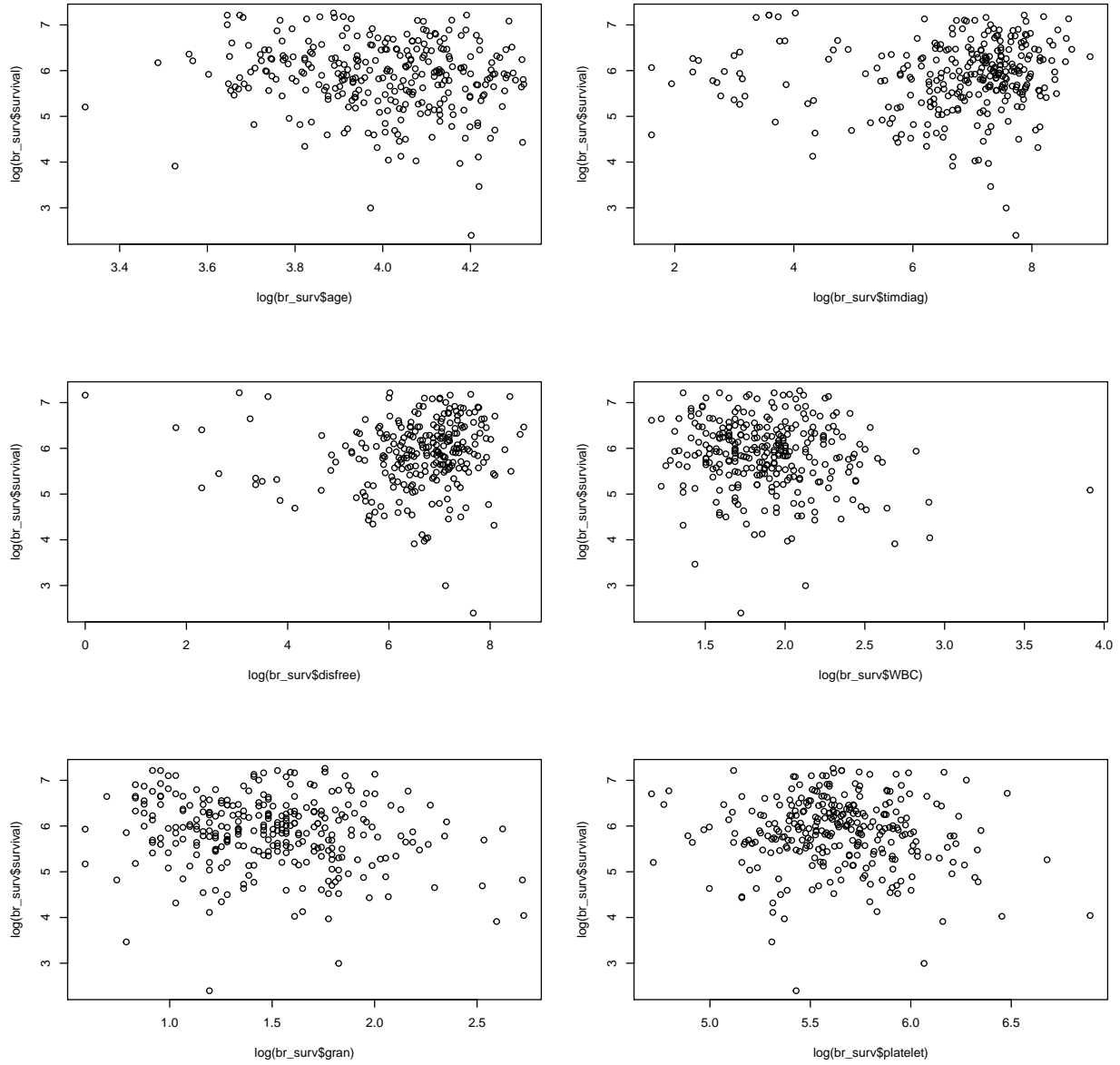
Data were obtained from a randomized Phase III study that compared vinorelbine plus doxorubicin (new treatment) with doxorubicin alone (standard treatment) in 300 patients with disseminated metastatic/recurrent breast cancer. The response failure time is described by the time from recurrence to death. Furthermore, several covariates are collected before treatment, such as age, performance status, pre-menopausal status, tumor measure status, WBC, Blood granulocyte count, and Blood platelet count. This study aims to examine if the investigated treatment could extend the post-progression survival time compared to the standard treatment and to discover the associations with other covariates.

To begin with, we want to see the distribution of each covariate and get a sense of the data set. Next, non-parametric methods such as Kaplan-Meier estimates and (weighted) log-rank tests can be used to examine the differences between each category. In the next step, the parametric model will be fitted into the data and compared to KM-curve to find the optimal fit. After that, we will use the AFT model to determine which covariates are significant. Following that, the semi-parametric model like Cox regression will be applied to identify the significant covariates and show how those variables affect the survival time from recurrence. PH assumption will be verified by model checking at the end.

Preliminary analysis

The 'br_surv' data has 300 observations with 18 feature vectors of interest (excluding ID, time, and status). First, we would like to see how much missing data there are in the dataset. after calculation, we found that there are 2 missing data points in both meno and global categories and 34 in both nodal and er categories. Because 2 missing data is less than 2

For all continuous variables in the dataset, including age, timeddiag, disfree, WBC, granules, and platelets, a scatter plot will be constructed because continuous variables does not have lot missing data. Since the range for x-axis is large, log will be take for each continuous variable to get better view of the data. For categorical data, KM-plot will be generated as this can avoid the effect of missing data. Both method will be use to assess the potential association between each covariate (excluding arm) and survival time.



From the above scatter plots, we can see age, timediag, WBC, and gran seem to have a negative association with survival time. The variable disfree, platelet seems to have a very weak association with survival time. Therefore, we can not eliminate any of the variables for our future analysis.

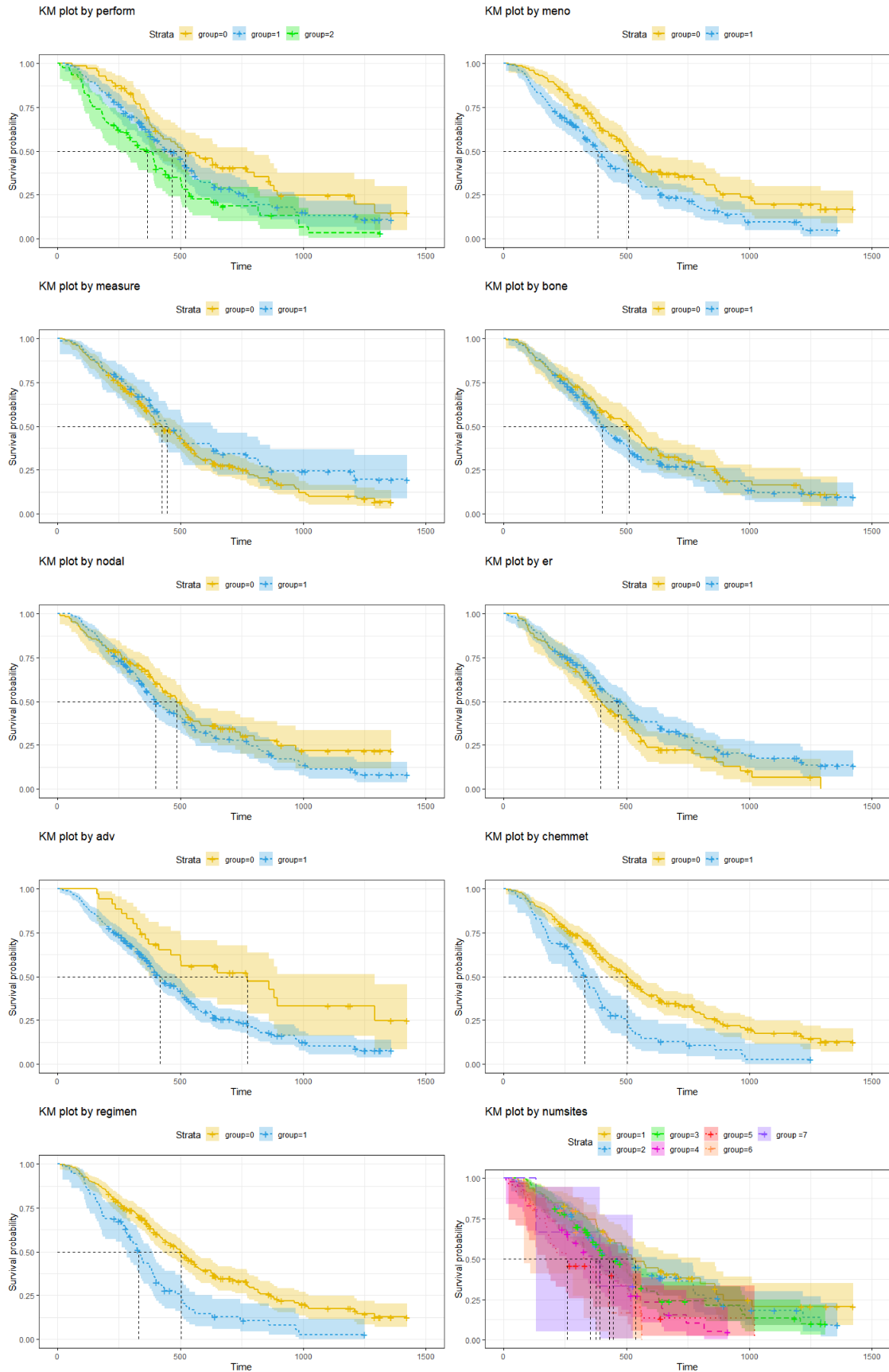


Figure 1: KM plot for covariate

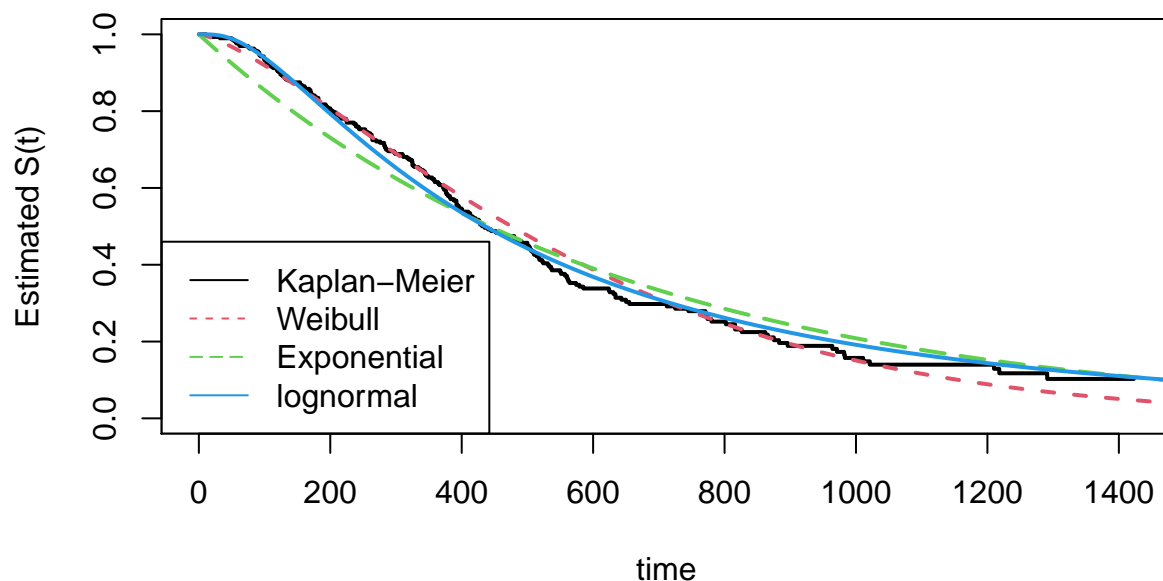
From the KM-plots above, we can see perform, meno, adv, chemmet, regimen and numsites seem to have a big impact on survival time. other variables seem not to have a strong impact. To check the difference, the log-rank and Wilcoxon test will be performed to check which variables are significant.

	wilcx_pval	logrank_pval
perform	0.0007072	0.0019931
meno	0.0011751	0.0015684
measure	0.3736313	0.1766643
numsites	0.0111870	0.0056061
bone	0.2518256	0.2651101
nodal	0.2943026	0.1383021
er	0.1371345	0.0523794
adv	0.0078817	0.0035738
chemmet	0.0000321	0.0000099
regimen	0.0000321	0.0000099

From the Wilcoxon and log-rank test, we can see perform, meno, numsites, adv, chemmet and regimen are statistically significant. Other variables are not statistically significant. For nodal and er, both Wilcoxon and log-rank test have a p-value larger than 0.05 indicating they are important, so we can remove the two columns from our dataset. Interestingly, chemmet and regimen have exactly the same value in the dataset, but we will keep both variables for further analysis.

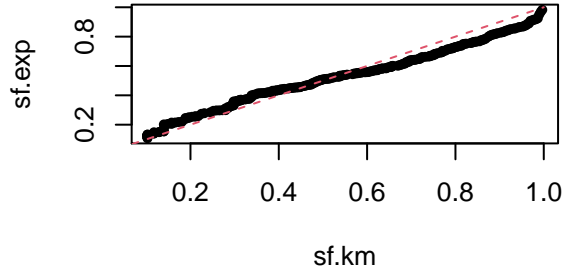
Next, we will use KM-plot to get a sense of the data. Then Parametric model will be included in the plot to see which Parametric model has the best fit for our data. Weibull, Exponential, and lognormal distribution were used here. To assess the effect of the arm, both a Parametric and non-parametric comparison will be performed. The best fit Parametric model will be used for arm comparison.

Breast Cancer

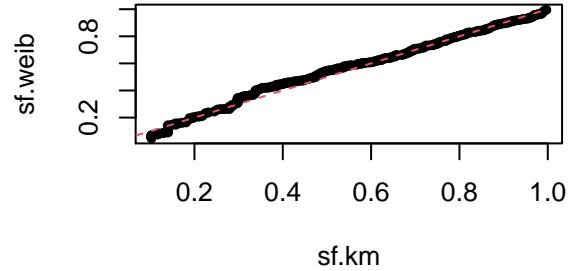


Here, we can see all three Parametric model fits reasonably well. However, the Weibull model does not fit well between $t=500$ to 650 , and after $t=1000$. For exponential mode, the survival probability was underestimated before $t = 400$, and over-estimated between $t=500$ to 1200 . The lognormal model seems to fits better because it has a more closer shape than the KM-plot. To test the fit, a p-p plot will be used here.

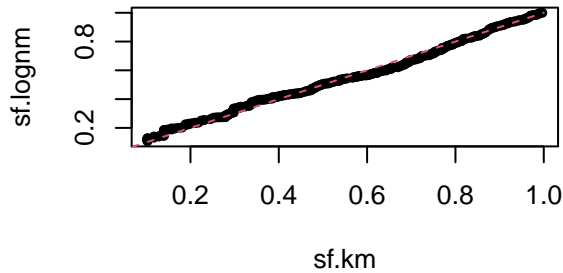
P-P Plot: Exponential vs Kaplan-Meier



P-P Plot: Weibull vs Kaplan-Meier



P-P Plot: LogNormal vs Kaplan-Meier



From the above P-P plot, we can see both exponential and Weibull distributions do not fit the data well in the middle part. the lognormal model has more data lay on the line which means the lognormal model has the best fit. Therefore, we will use the lognormal model and non-Parametric model to assess the effect of arm.

Model Fitting and Analysis

Comparison of Failure Time Distribution

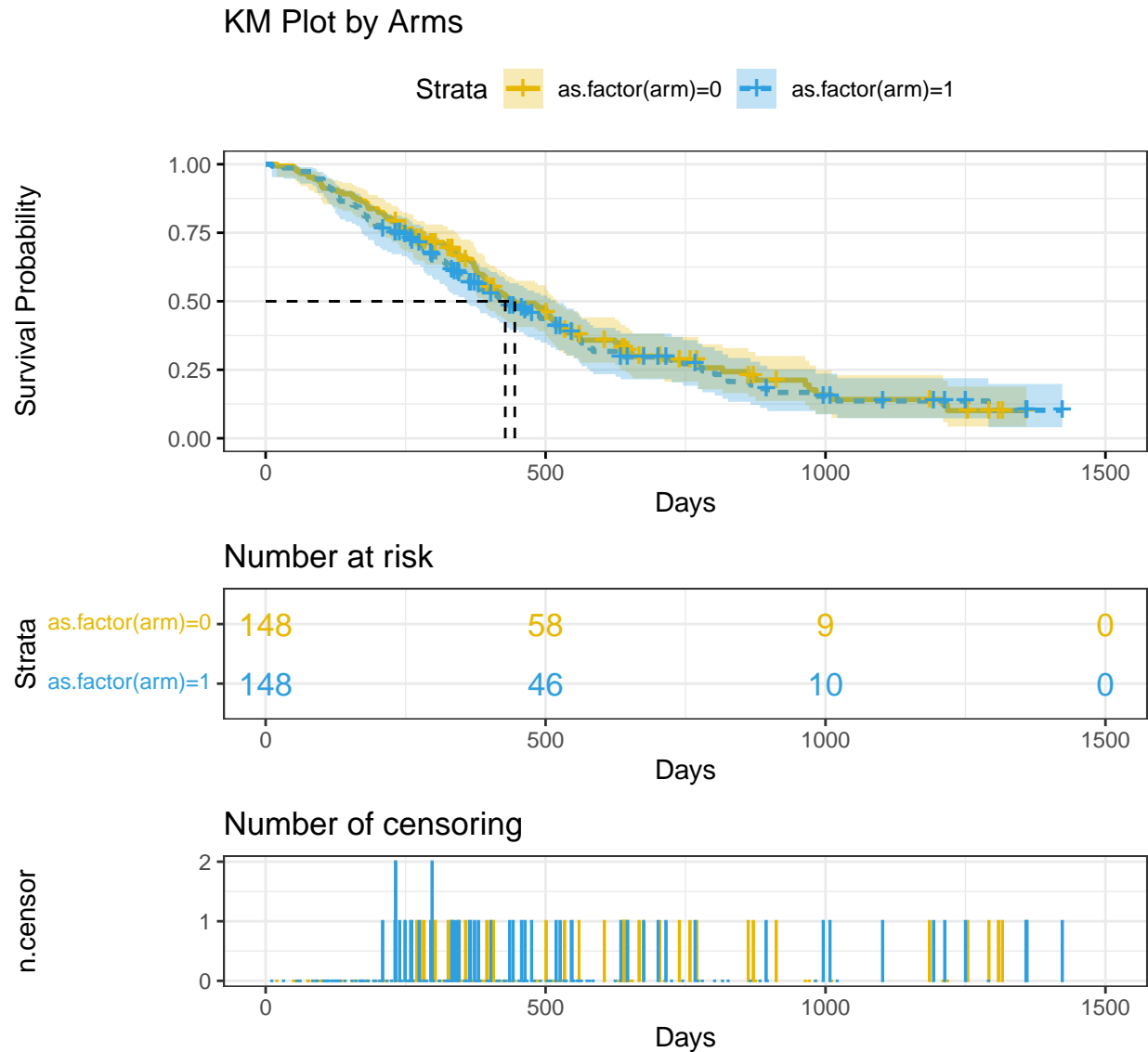
First, I performed a parametric comparison of different treatment groups under the assumption of the log-normal distribution. Next, I conducted a Wilcoxon test and a log-rank test in order to check that the results were consistent.

Parametric Comparison: We test the equality of survival distributions for two arms in two steps. The first one is to test for equality of scale parameters ($H_0 : \sigma_1 = \sigma_2$), If ($H_0 : \sigma_1 = \sigma_2$) is not rejected, then we will perform the second step which is $H_0 : \mu_1 = \mu_2$.

Test for equality	Λ for LR test	p-value
ϕ	0.2843989	0.5938324
μ	0.1607637	0.69

After computing, Λ for LR test for ϕ is 0.28 which correspond with the p-value equals to $0.59 > 0.05$. This means we can not reject the null hypothesis and therefore $\sigma_1 = \sigma_2$. Then Λ for LR test for μ is 0.16 which correspond with the p-value equals to $0.69 > 0.05$. This means we can not reject the null hypothesis and therefore $\mu_1 = \mu_2$. By combining the results, we can conclude that both groups have the same distribution, and there is a high probability that there is no difference in survival distributions between the two groups.

Non-Parametric Comparison: To perform a non-parametric analysis, we will first assume that the data is in the form of $f(x_i; \delta_i) : i = 1, \dots, 296$ and test on the null hypothesis which is $H0 : S_1(t) = S_2(t)$. Here we have 296 data points because we removed 4 patients form the dataset due to missing data.



	Chisquare	pvalue
log-rank test	0.2	0.6
wilcoxon	0.5	0.5

Here, we have a KM-plot for different arms, the yellow line indicates arm = 0 which is Doxorubicin alone group, and the blue line indicates arm = 1 which is Vinorelbine combined with the Doxorubicin group. From the plot, we can see most of the confidence intervals for both groups are largely overlapped. This indicates that the two groups may not have a difference which means the treatments may not have a large impact. However, we can see there is more censoring in arm 1.

From the table above, we can see both the weighted log-rank test and Wilcoxon test give a p-value greater than 0.05 which means we can not reject the null hypothesis. Because there is a lot of slight crossing between the two groups, we can accept the null hypothesis which is both groups have the same distribution.

To conclude, both Parametric and non-Parametric comparison shows the arm(treatment) may not have an impact on the survival without considering other covariates.

The next step is to use the AFT model to perform a parametric regression analysis.

Parametric Regression Analysis (AFT model)

The linear AFT model has the form

$$Y = \log(T) = b_0 + b_1 z_1 + \dots + b_2 z_2 + \dots + b_n z_n + \sigma W$$

where W is a standard location scale distribution.

To evaluate the potential effects of treatments, a number of models will be used. The model selection procedure shown as follows:

- Start with full model includes all covariate
- Construct model by backward selection, add/remove covariates to improve the model by compare the AIC value
- Compute AIC according to the model
- Choose the model with smaller AIC value
- repeat the procedure to find a model with smallest AIC.

Another backward selection was also used following the same procedure as above where the arm is the necessary variable in the model.

After those procedures, we have two models, one has all important covariants without the arm, and another has all important covariants with the arm. For the model with arm, we will check the p-value for all included covariates, if the p-value is greater than 0.05, we will exclude them from the model and check if the new model is better than the old model or not.

	min_AIC	min_BIC
Full model	3017.797	3102.676
Without arm	3001.348	3038.252
With arm	3003.245	3043.839

Above are the minimum AIC and BIC for each model, we can see the model without arm has AIC less than the model with arm. this indicates that the arm(treatment) may not have much impact on the model. However, we need to check the p-value before we make a conclusion.

```
survreg(formula = Surv(time, status) ~ as.factor(arm) + age +
  as.factor(perform) + as.factor(meno) + as.factor(measure) +
  as.factor(numsites) + as.factor(bone) + timdiag + disfree +
  global + as.factor(adv) + as.factor(chemmet) + as.factor(regimen) +
  WBC + gran + platelet, data = br_surv)

Value Std. Error z p
(Intercept) 7.54e+00 4.57e-01 16.50 < 2e-16
as.factor(arm)1 -1.06e-02 9.25e-02 -0.11 0.9090
age -8.89e-03 7.68e-03 -1.16 0.2466
as.factor(perform)1 7.27e-02 1.34e-01 0.54 0.5866
as.factor(perform)2 5.17e-02 1.70e-01 0.30 0.7617
as.factor(meno)1 -2.23e-02 1.50e-01 -0.15 0.8815
as.factor(measure)1 1.29e-01 1.17e-01 1.10 0.2717
as.factor(numsites)2 -2.26e-01 1.48e-01 -1.53 0.1266
as.factor(numsites)3 -1.63e-01 1.45e-01 -1.12 0.2619
as.factor(numsites)4 -4.11e-01 1.67e-01 -2.46 0.0139
as.factor(numsites)5 -4.30e-01 2.05e-01 -2.09 0.0362
as.factor(numsites)6 -3.57e-01 2.88e-01 -1.24 0.2156
as.factor(numsites)7 -2.36e-01 4.70e-01 -0.50 0.6158
as.factor(bone)1 -3.99e-02 1.07e-01 -0.37 0.7086
timdiag 2.41e-04 9.15e-05 2.63 0.0085
disfree -6.05e-05 1.20e-04 -0.50 0.6153
global 4.74e-03 2.18e-03 2.17 0.0297
as.factor(adv)1 -4.08e-01 1.75e-01 -2.33 0.0197
as.factor(chemmet)1 -5.48e-01 1.21e-01 -4.53 5.8e-06
as.factor(regimen)1 0.00e+00 0.00e+00 NA NA
WBC -4.41e-02 1.48e-02 -2.97 0.0030
gran -9.91e-03 2.92e-02 -0.34 0.7345
platelet -6.10e-04 4.79e-04 -1.27 0.2027
Log(scale) -4.69e-01 5.46e-02 -8.59 < 2e-16

Scale= 0.626

Weibull distribution
Loglik(model)= -1485.9 Loglik(intercept only)= -1531
Chisq= 90.2 on 22 degrees of freedom, p= 3.2e-10
```

Figure 2: Full model

```
survreg(formula = Surv(time, status) ~ age + as.factor(measure) +
  timdiag + global + as.factor(adv) + as.factor(regimen) +
  WBC + platelet, data = br_surv)

Value Std. Error z p
(Intercept) 7.60e+00 3.78e-01 20.13 < 2e-16
age -1.44e-02 4.86e-03 -2.97 0.00300
as.factor(measure)1 1.71e-01 1.11e-01 1.54 0.12356
timdiag 2.15e-04 4.41e-05 4.88 1.1e-06
global 5.84e-03 1.87e-03 3.12 0.00181
as.factor(adv)1 -4.27e-01 1.57e-01 -2.71 0.00668
as.factor(regimen)1 -4.67e-01 1.05e-01 -4.46 8.2e-06
WBC -4.59e-02 1.20e-02 -3.82 0.00013
platelet -8.56e-04 4.54e-04 -1.88 0.05956
Log(scale) -4.40e-01 5.39e-02 -8.17 3.1e-16

Scale= 0.644

Weibull distribution
Loglik(model)= -1490.7 Loglik(intercept only)= -1531
Chisq= 80.64 on 8 degrees of freedom, p= 3.6e-14
```

Figure 3: Without model

Compare_to	Obs	p_value
intercept only	75.595355	0.0000000
With arm	5.145103	0.0763405

From the above result, we can see the reported coef are almost the same and the included covariates are exactly the same (exclude arm) between them without arm model and with arms model, indicating the arm may not actually do anything. Because the purpose of this analysis is to investigate the arm variable, so we will include the arm in our model. Then from figure 4, we can see measure and platelet variables have a p-value greater than 0.05, so we exclude those two variables in our model. To check whether the

```
survreg(formula = Surv(time, status) ~ as.factor(arm) + age +
  as.factor(measure) + timdiag + global + as.factor(adv) +
  as.factor(regimen) + WBC + platelet, data = br_surv)

Value Std. Error z p
(Intercept) 7.62e+00 3.83e-01 19.89 < 2e-16
as.factor(arm)1 -2.93e-02 9.12e-02 -0.32 0.74774
age -1.45e-02 4.84e-03 -2.99 0.00283
as.factor(measure)1 1.74e-01 1.11e-01 1.56 0.11877
timdiag 2.14e-04 4.45e-05 4.80 1.6e-06
global 5.82e-03 1.87e-03 3.11 0.00190
as.factor(adv)1 -4.29e-01 1.57e-01 -2.72 0.00650
as.factor(regimen)1 -4.67e-01 1.05e-01 -4.47 7.9e-06
WBC -4.63e-02 1.21e-02 -3.83 0.00013
platelet -8.46e-04 4.56e-04 -1.86 0.06332
Log(scale) -4.40e-01 5.39e-02 -8.18 2.9e-16

Scale= 0.644

Weibull distribution
Loglik(model)= -1490.6 Loglik(intercept only)= -1531
Chisq= 80.74 on 9 degrees of freedom, p= 1.2e-13
```

Figure 4: With arm

```
survreg(formula = Surv(time, status) ~ as.factor(arm) + age +
  timdiag + global + as.factor(adv) + as.factor(regimen) +
  WBC, data = br_surv)

Value Std. Error z p
(Intercept) 7.44e+00 3.52e-01 21.11 < 2e-16
as.factor(arm)1 -2.98e-02 9.08e-02 -0.33 0.74298
age -1.42e-02 4.84e-03 -2.94 0.00333
timdiag 2.12e-04 4.47e-05 4.74 2.1e-06
global 6.16e-03 1.87e-03 3.30 0.00098
as.factor(adv)1 -4.57e-01 1.58e-01 -2.88 0.00392
as.factor(regimen)1 -4.90e-01 1.03e-01 -4.74 2.2e-06
WBC -4.93e-02 1.12e-02 -4.41 1.0e-05
Log(scale) -4.39e-01 5.41e-02 -8.11 5.2e-16

Scale= 0.645

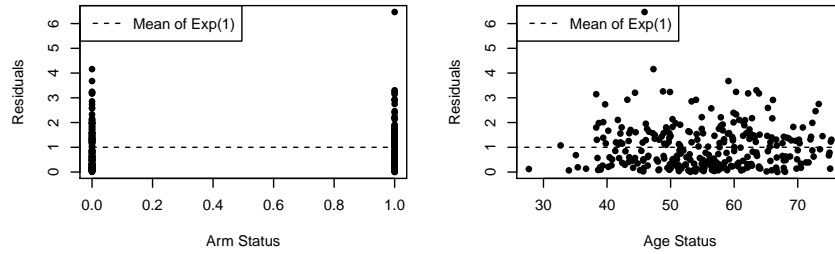
Weibull distribution
Loglik(model)= -1493.2 Loglik(intercept only)= -1531
Chisq= 75.6 on 7 degrees of freedom, p= 1.1e-13
```

Figure 5: selection by p-value from with arm model

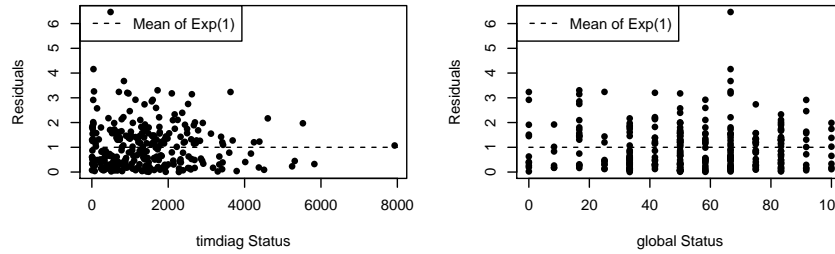
new model is better than the intercept-only model and the arm model, we will use the log-rank test. The null hypothesis for comparing to intercept only model is $h_0 : \beta_{all} = 0$, because the p-value is way less than 0.05, so we can reject the null hypothesis and conclude that there is at least 1 β has a non-zero value. To compare the arm model and the new model, the null hypothesis is with the arm model is as good as the new model. Because the p-value is greater than 0.05, we can not reject the null hypothesis. Then we can conclude with the arm model is as good as the new model, and we will simply choose the new model because it is a simpler model.

Now, we have our final model, and we will do a Cox-Snell residual test for the model.

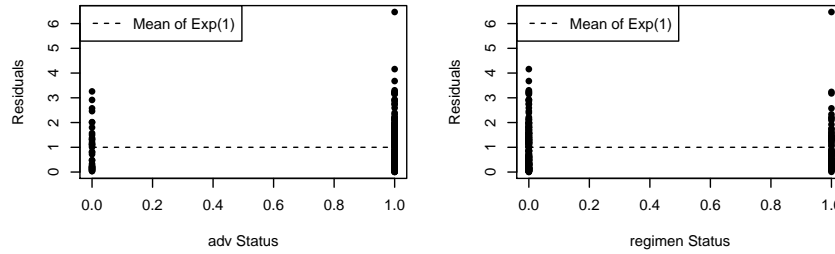
Cox-Snell Residuals: Breast Cancer Cancer Da **Cox-Snell Residuals: Breast Cancer Cancer Da**



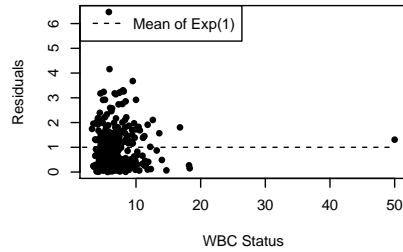
Cox-Snell Residuals: Breast Cancer Cancer Da **Cox-Snell Residuals: Breast Cancer Cancer Da**



Cox-Snell Residuals: Breast Cancer Cancer Da **Cox-Snell Residuals: Breast Cancer Cancer Da**



Cox-Snell Residuals: Breast Cancer Cancer Da



From the cox-snell plots for all relevant covariates, we can see most of the expected values are less than 6 which means AFT model selection may work well. However, for arm, timdiag, age, and global, the dots do not look like random observations from $\exp(1)$. Therefore, AFT model selection may not be a very good choice for this dataset.

Next, we want to try the semi-parametric model for this dataset. The Cox regression model will be used here.

Cox regression model

A Cox regression model is one of the most commonly used approaches to modeling covariate effects for survival analysis, based on the proportional hazards assumption but not requiring a particular probability distribution. The model is referred to as a semi-parametric model of the form

$$h(t|z_i) = h_0(t)\exp(\beta^T z)$$

where z is a covariate vector (p -dimensional), β is a vector of regression coefficients, and $h_0(t)$ is the baseline hazed function.

For the Cox regression model, I will manually choose the best model by dropping all the covariates with a p-value greater than 0.05 excluding the arm variable. The first model will be the full model. In the reported summary, numsites, timdiag, global, chemmet, and WBC are statistically significant. However, the p-value for the adv variable is just slightly over 0.05 which equals 0.052, so I decided to include this variable as well. Then model 2 includes arm, numsites, timdiag, adv, global, chemmet, and WBC. Because adv is not statistically significant, model 3 will be created without the adv variable. Then log-rank comparisons were conducted to see which model is better.

Model	loglikelihood	Compare_to_model	num_of_para	Obs_LR_statistic	p_value
1	-973.6459	NA	21	NA	NA
2	-977.0939	1	12	6.896070	0.6479392
3	-979.4331	2	11	4.678324	0.0305455

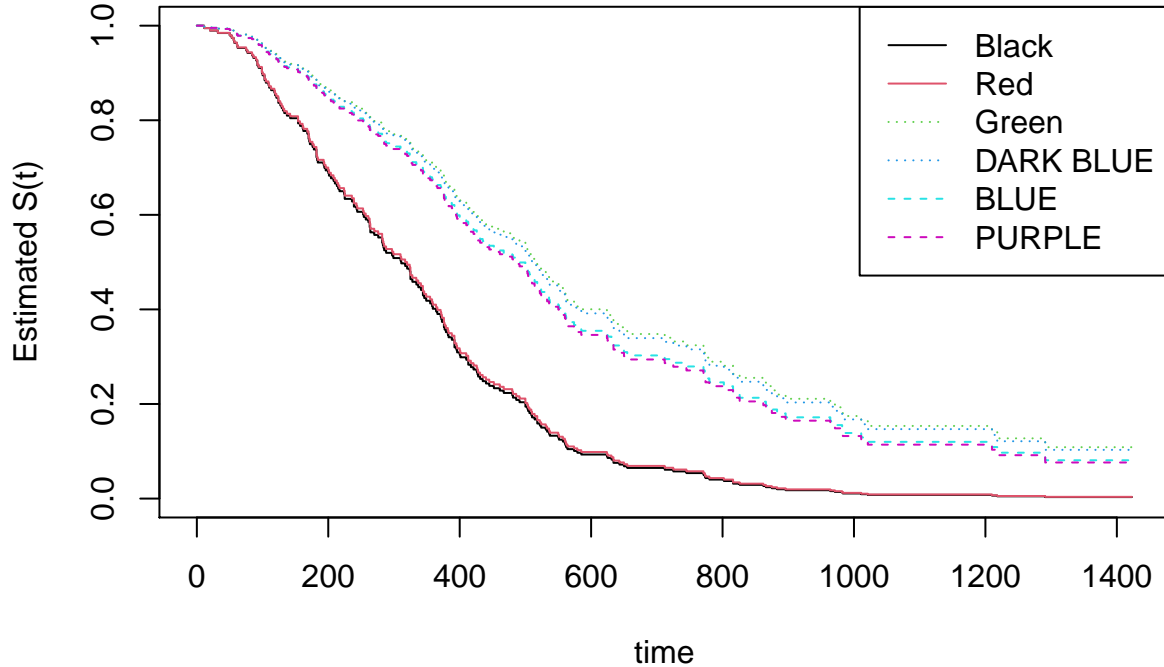
From the log-rank test, we can see the p-value is $0.64 > 0.05$, so we can not reject the null hypothesis and conclude that model 1 is just as good as model 2. When comparing model 2 with model 3, we have a p-value equal to $0.03 < 0.05$ which means we can reject the null hypothesis and conclude that model 3 is not as good as model 2. Therefore, our final model will be model 2.

	coef	exp(coef)	se(coef)	z	Pr(> z)
as.factor(arm)1	0.023700	1.020	1.43e-01	0.166	8.69e-01
as.factor(numsites)2	0.477000	1.610	2.20e-01	2.170	2.99e-02
as.factor(numsites)3	0.353000	1.420	2.18e-01	1.620	1.06e-01
as.factor(numsites)4	0.768000	2.160	2.49e-01	3.080	2.05e-03
as.factor(numsites)5	0.799000	2.220	2.97e-01	2.690	7.07e-03
as.factor(numsites)6	0.817000	2.260	4.24e-01	1.930	5.38e-02
as.factor(numsites)7	0.335000	1.400	7.33e-01	0.457	6.48e-01
timdiag	-0.000298	1.000	6.96e-05	-4.290	1.81e-05
global	-0.007700	0.992	3.05e-03	-2.520	1.17e-02
as.factor(adv)1	0.518000	1.680	2.52e-01	2.060	3.99e-02
as.factor(chemmet)1	0.929000	2.530	1.70e-01	5.470	0.00e+00

	coef	exp(coef)	se(coef)	z	Pr(> z)
WBC	0.076800	1.080	1.76e-02	4.370	1.23e-05

The above is a summary of model 2, we can see all the included covariate has significant p-value except arm. For summary, this model has a reasonable fit. To interpret the arm, we can say, if numsites, timdiag, global, adv, chemmet and WBC keep the same, then the log hazard ratio of patients treated by Vinorelbine combined with Doxorubicin relative to Doxorubicin alone is 0.0237 which suggest that the Vinorelbine combined with Doxorubicin group has higher survival probability comapre to Doxorubicin only group. To check the model visually, estimation plot was created as below. The included line include BLACK: (WBC = wbc, timdiag = timdiag, global = global, numsites = 3, arm = 1, adv = 1, chemmet = 1), RED: (WBC = wbc, timdiag = timdiag, global = global, numsites = 3, arm = 0, adv = 1, chemmet = 1), GREEN: (WBC = wbc, timdiag = timdiag, global = global, numsites = 3, arm = 0, adv = 1, chemmet = 0), DARK BLUE: (WBC = wbc, timdiag = timdiag, global = global, numsites = 3, arm = 1, adv = 1, chemmet = 0), BLUE: (WBC = wbc, timdiag = timdiag, global = global, numsites = 2, arm = 0, adv = 1, chemmet = 0), PURPLE: (WBC = wbc, timdiag = timdiag, global = global, numsites = 2, arm = 1, adv = 1, chemmet = 0).

I choose those values because most people have numsites = 2 or 3, and chemmet is the most significant covariate in our model. Also, we want to compare the treatment, so we have 6 lines in total. WBC, timdiag, and global covariates are scattered with no obvious patterns therefore mean is taken. It is clear that chemmet and numsites have a great impact on post-progression survival time (line3-6) as the lines are high above. Then we can compare horizontally (arm = 1 vs arm = 0), the line with arm = 0 is always above the line with arm = 1. This means the Doxorubicin-only group generally does better in surviving breast cancer.



After this, we will perform model checking using Schoenfeld Residual.

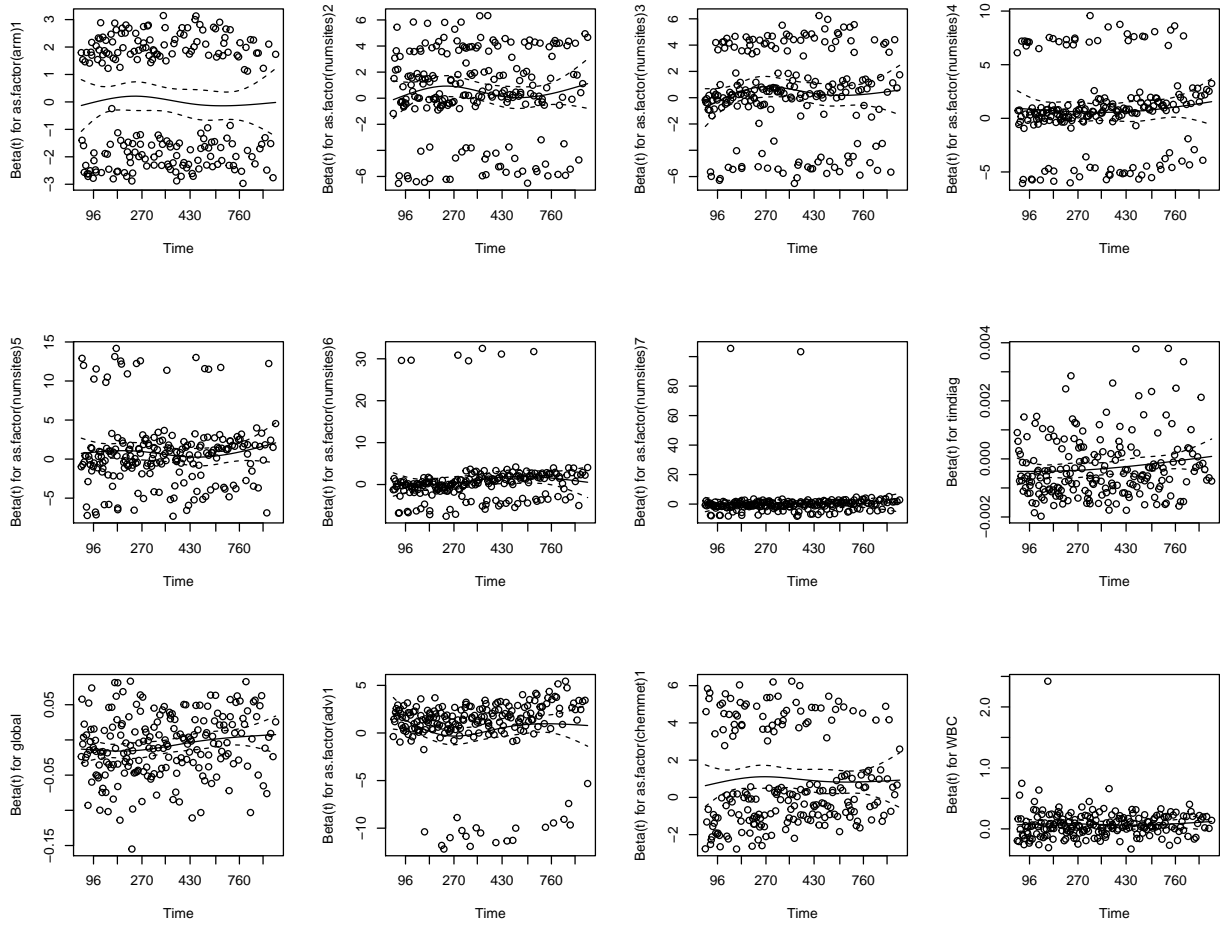
Model Checking and Schoenfeld Residual

To test the validity and PH assumption of the model, I used Schoenfeld residual analysis.
The Schoenfeld residuals are defined by:

$$\hat{s}_{ik} = \delta_i(z_{ik} - \sum_{j=1}^n z_{jk} \hat{w}_{ij})$$

for subject $i = 1 \dots n$, with $\delta_i = 1$, for covariate $k = 1 \dots p$

PH model assumption is not violated if there is no significant time trend in Schoenfeld residual versus time plot.



```
##               chisq df    p
## as.factor(arm)1      0.7095  1 0.400
## as.factor(numsites)2 0.3577  1 0.550
## as.factor(numsites)3 0.5991  1 0.439
## as.factor(numsites)4 0.1214  1 0.728
## as.factor(numsites)5 1.1129  1 0.291
## as.factor(numsites)6 4.3611  1 0.037
## as.factor(numsites)7 0.0055  1 0.941
```



```
## timdiag          2.8786  1 0.090
## global           4.3236  1 0.038
## as.factor(adv)1   0.0208  1 0.885
## as.factor(chemmet)1 0.0439  1 0.834
## WBC              0.1332  1 0.715
## GLOBAL           15.1396 12 0.234
```

From the Schoenfeld Residual plots, we can see some variable has a time trend. However, no significant time trends were observed for the global test(0.234). Therefore, the PH assumption is valid. we can then conclude the Cox model fits reasonably well for this dataset.

Conclusion

In this analysis, we first explore the data with a scatter plot, and KM-plot, Wilcoxon, and weighted log-rank tests were used to test covariate significant. As a result, Perform, meno, adv, chemmet, regimen and numsites show significant differences in survival time distribution. From the scatter plot, we can not exclude any covariate since all four continuous variables seem to have some association with survival time.

The next step we did is to use the parametric and non-parametric comparison methods to assess the effect of different arms(treatments). Both results show there is no clear relationship between arm and survival time. After this, we performed an AFT model parametric regression analysis. the resulting model also shows the arm does not have a large impact on survival time. However, the residual test for some of the covariates does not appear to have an $\exp(1)$ distribution. Therefore, this AFT model may not fit the dataset very well. Hence, a Cox model has been constructed.

From the Cox regression model, we have manually selected statistically significant covariates by looking at the p-value and used the LR test to select the best model. Then Schoenfeld Residual analysis was performed to check whether there is a time trend in the model. As a result, the global p-value is greater than 0.05, which means there is no clear time trend in this model, so the PH assumption is not violated, so the Cox model has a good fit. Because there is no time trend, so we don't need to perform further analysis.

In conclusion, if there is an association between survival time and the type of treatment, the treatment should prolong survival time. However, in previous models, 'arm' did not seem to matter much in explaining post-progression survival time. Notice that the most important covariates are numsites, timdiag, global, adv, chemmet, and WBC. Both timdiag and global have negative relationships to survival probability, while arm, numsites, adv, chemmet, and WBC have positive relationships. It suggests that patients with good global scores and a long er timdiag have a better chance of surviving breast cancer.

Overall, the treatment with Doxorubicin only has a slight effect on prolonging survival time after disseminated metastatic/recurrent breast cancer compare to vinorelbine combined with the doxorubicin group. Nonetheless, this is not a judgemental approach to the treatment of breast cancer.

Appendix

```
# read data first
br_surv <- read.table("br_surv.txt", header = T, na.strings = ".")
ncol(br_surv)

# NA represent missing data, check missing data
# need to check which variable is significant
colSums(is.na(br_surv))

# scatter plot for continuous variable because continuous
# variables does not have lot missing data
# since the range for x-axis is large, log will be take for each variable.
par(mfrow = c(3,2))
plot(log(br_surv$age), log(br_surv$survival))
plot(log(br_surv$timdiag), log(br_surv$survival))
plot(log(br_surv$disfree), log(br_surv$survival))
plot(log(br_surv$WBC), log(br_surv$survival))
plot(log(br_surv$gran), log(br_surv$survival))
plot(log(br_surv$platelet), log(br_surv$survival))
mtext(~italic("my caption"), side=1, outer=TRUE, adj=0, line=3)

library(survival)
library(ggplot2)
library(survminer)

##### Variable checking #####
time <- br_surv$survival
status <- br_surv$dead

# the missing data is over 10% for certain binary data, so a scatter
# plot may not be effective in investigate the effect, so KM plots will
# be generated for all binary variables to check whether a variable will
# affect the survival or not.

fitCov <- function(br_surv, Cov, name, opt = 0){
  temp <- length(unique(na.omit(Cov)))
  col <- c("#E7B800", "#2E9FDF", "#04e700", "#e700d0",
           "#FF1616", "#FF914D", "#8C52FF")
  if(opt == 1){
    lab <- c("group=1", "group=2", "group=3", "group=4",
             "group=5", "group=6", "group=7")
  }else{
    lab <- c("group=0", "group=1", "group=2", "group=3",
             "group=4", "group=5", "group=6")
  }
  fit_arm<-survfit(Surv(time, status)~eval(as.name(paste(name))),
                  conf.type="log-log", data = br_surv)
  result <- ggsurvplot(fit_arm,
                       title = paste("KM plot by", name),
                       conf.int = TRUE,
                       linetype = "strata", # Change line type by groups
                       surv.median.line = "hv", # Specify median survival
```

```

        ggtheme = theme_bw(), # Change ggplot2 theme
        legend.labs=lab[1:temp],
        palette = col[1:temp])

  return(result)
}

fitCov(br_surv=br_surv, Cov = br_surv$perform, name = "perform")
fitCov(br_surv=br_surv, Cov = br_surv$meno, name = "meno")
fitCov(br_surv=br_surv, Cov = br_surv$measure, name = "measure")
fitCov(br_surv=br_surv, Cov = br_surv$bone, name = "bone")
fitCov(br_surv=br_surv, Cov = br_surv$nodal, name = "nodal")
fitCov(br_surv=br_surv, Cov = br_surv$er, name = "er")
fitCov(br_surv=br_surv, Cov = br_surv$adv, name = "adv")
fitCov(br_surv=br_surv, Cov = br_surv$chemmet, name = "chemmet")
fitCov(br_surv=br_surv, Cov = br_surv$regimen, name = "regimen")
fitCov(br_surv=br_surv, Cov = br_surv$numsites, name = "numsites", opt = 1)

## willcoxon test
pval <- c()
names <- c("perform","meno","measure","numsites","bone",
           "nodal","er","adv","chemmet","regimen")
wilcx<-survdifff(Surv(time,status)~as.factor(perform), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(meno), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(measure), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(numsites), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(bone), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(nodal), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(er), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(adv), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(chemmet), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

wilcx<-survdifff(Surv(time,status)~as.factor(regimen), data=br_surv,rho=1)
pval <- c(pval, pchisq(wilcx$chisq, length(wilcx$n)-1, lower.tail = FALSE))

pval <- as.data.frame(pval); row.names(pval) <- names
knitr::kable(pval)

```

```
##### Explore data with KM curve #####

# KM estimate
fit<-survfit(Surv(time, status)~1, conf.type="log-log", data = br_surv)
plot(fit, xlab = "Time", ylab = "Estimated Survival",
     mark.time = T, conf.int = T, main="kM plot")

# Weibull
fit.weib <- survreg(Surv(time, status)~1, data = br_surv)
sig1<-fit.weib$scale
mu1<-fit.weib$coef

# Exp
fit.exp <- survreg(Surv(time, status)~1, dist = "exp", data = br_surv)
mu2 <- fit.exp$coef

# lognormal
fit.lognm<-survreg(Surv(time,status)~1,data=br_surv, dist="lognormal")
mu3<-fit.lognm$coeff
sig3<-fit.lognm$scale

time1 <- fit$time

# draw parametric curve
t<-0:1500
st.weib<-exp(-exp((log(t)-mu1)/sig1))
st.exp<-exp(-exp(log(t)-mu2))
st.lognm<-1-pnorm((log(t)-mu3)/sig3)
plot(fit,xlab="time",
     ylab="Estimated S(t)",main="Breast Cancer",
     conf.int=F,lty=1,lwd=2)
lines(t,st.weib,lty=2,lwd=2, col=2)
lines(t,st.exp,lty=5,lwd=2, col=3)
lines(t,st.lognm,lty=7,lwd=2, col=4)
legend("bottomleft", c("Kaplan-Meier", "Weibull", "Exponential", "lognormal"),
     col=c(1,2,3,4), lty=c(1,2,5,7))
par(mfrow = c(2,2))

# P-P plot
sf.km <- fit$surv
sf.exp <- exp(-exp((log(time1)-mu2)))
sf.weib<-exp(-exp((log(time1)-mu1)/sig1))
sf.lognm<-1-pnorm((log(time1)-mu3)/sig3)

plot(sf.km, sf.exp, main="P-P Plot: Exponential vs Kaplan-Meier")
lines(seq(0,1,0.1),seq(0,1,0.1), lty=2)
plot(sf.km, sf.weib, main="P-P Plot: Weibull vs Kaplan-Meier")
lines(seq(0,1,0.1),seq(0,1,0.1), lty=2)
plot(sf.km, sf.lognm, main="P-P Plot: LogNormal vs Kaplan-Meier")
lines(seq(0,1,0.1),seq(0,1,0.1), lty=2)

##### Arm comparison #####
```

```

##### Parametric comparison (lognormal will be used)
# split by arm
fitall<-survreg(Surv(time, status)~as.factor(arm), data = br_surv)
fit0<-survreg(Surv(time, status)~1, subset = arm == 0, data = br_surv)
fit1<-survreg(Surv(time, status)~1, subset = arm == 1, data = br_surv)
# Test on phi
lambda_obs <- 2*(fit0$loglik[2] + fit1$loglik[2] - fitall$loglik[2])
sigmap <- pchisq(0.2004501,df=1, lower.tail = F)
# Test on mu
mu_obs <- 2*(fitall$loglik[2] - fitall$loglik[1])

##### Non-Parametric comparison
fit_arm<-survfit(Surv(time, status)~as.factor(arm), conf.type="log-log",
               data = br_surv)
ggsurvplot(fit_arm,
            title="KM Plot by Arms",
            xlab = "Days",
            ylab= "Survival Probability",
            pval = TRUE, conf.int = TRUE,
            ncensor.plot = TRUE,
            risk.table = TRUE, # Add risk table
            risk.table.col = "strata", # Change risk table color by groups
            linetype = "strata", # Change line type by groups
            surv.median.line = "hv", # Specify median survival
            ggtheme = theme_bw(), # Change ggplot2 theme
            surv.plot.height = 10,
            palette = c("#E7B800", "#2E9FDF"))
wilcx <- survdiff(Surv(time,status)~as.factor(arm), data=br_surv,rho=1)
lgrk <- survdiff(Surv(time,status)~as.factor(arm), data=br_surv)
result <- data.frame(Chisquare = c(0.3, 0.5),
                    pvalue = c(0.5, 0.6),
                    row.names = c("log-rank test", "wilcoxon"))
# We cannot reject the null hypothesis that they have the same distribution.
knitr::kable(result)

##### AFT #####
aftall <- survreg(Surv(time,status)~age+as.factor(perform)+
                as.factor(meno)+as.factor(measure)+
                as.factor(numsites)+as.factor(bone)+
                timdiag+disfree + global +as.factor(adv)+
                as.factor(chemmet)+as.factor(regimen)+
                WBC+gran+platelet, data=br_surv)

aft2 <- step(aftall, trace = 0, direction = c("backward"))

aftall1 <- survreg(Surv(time,status)~as.factor(arm)+age+as.factor(perform)+
                as.factor(meno)+as.factor(measure)+
                as.factor(numsites)+as.factor(bone)+
                timdiag+disfree + global +as.factor(adv)+
                as.factor(chemmet)+as.factor(regimen)+
                WBC+gran+platelet, data=br_surv)
aft21 <- step(aftall1, trace = 0, direction = c("backward"),
             scope = list(lower = as.formula(Surv(time,status)~as.factor(arm)),

```

```

upper = as.formula(Surv(time,status)~as.factor(arm)+
                    age+as.factor(perform)+
                    as.factor(meno)+
                    as.factor(measure)+
                    as.factor(numsites)+
                    as.factor(bone)+timdiag+disfree+
                    global +as.factor(adv)+
                    as.factor(chemmet)+
                    as.factor(regimen)+ WBC+
                    gran+platelet)))

df <- data.frame(min_AIC = c(AIC(aftall), AIC(aft2), AIC(aft21)),
                 min_BIC = c(BIC(aftall), BIC(aft2), BIC(aft21)),
                 row.names = c("Full model", "Without arm", "With arm"))
knitr::kable(df)

aft23 <- survreg(formula = Surv(time, status) ~ as.factor(arm) + age
                 + timdiag + global + as.factor(adv) +
                 as.factor(regimen) + WBC, data = br_surv)

1- pchisq(2*abs(aft23$loglik[2] - aft23$loglik[1]), 7) #reject H0: all beta = 0
1- pchisq(2*abs(aft23$loglik[2] - aft21$loglik[2]), 2)

# This shows model 3 is just as good as model 2, therefore, we can remove
# platelet and measure from the model

# reported coef are almost the same indicate the arm
# may not actually do anything.

##### COX-snell #####
b<-aft23$coef
mu <- b[1] + b[2]*br_surv$arm + b[3]*br_surv$age + b[4]*br_surv$timdiag +
      b[5]*br_surv$global + b[6]*br_surv$adv + b[7]*br_surv$regimen +
      b[8]*br_surv$WBC
sig = aft23$scale
r<-exp((log(time)-mu)/sig)+1-status
par(mfrow = c(4,2))
plot(br_surv$arm,r,pch=16,xlab="Arm Status", ylab="Residuals",
      main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(0,1,0.1),rep(1,11),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)
plot(br_surv$age,r,pch=16,xlab="Age Status", ylab="Residuals",
      main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(20,80,10),rep(1,7),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)
plot(br_surv$timdiag,r,pch=16,xlab="timdiag Status", ylab="Residuals",
      main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(0,8000,1000),rep(1,9),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)
plot(br_surv$global,r,pch=16,xlab="global Status", ylab="Residuals",
      main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(0,100,10),rep(1,11),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)

```

```

plot(br_surv$adv,r,pch=16,xlab="adv Status", ylab="Residuals",
     main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(0,1,0.1),rep(1,11),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)
plot(br_surv$regimen,r,pch=16,xlab="regimen Status", ylab="Residuals",
     main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(0,1,0.1),rep(1,11),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)
plot(br_surv$WBC,r,pch=16,xlab="WBC Status", ylab="Residuals",
     main="Cox-Snell Residuals: Breast Cancer Cancer Data")
lines(seq(0,50,5),rep(1,11),lty=2)
legend("topleft","Mean of Exp(1)",lty=2)

##### COX modle #####
fit1<-coxph(Surv(time,status)~as.factor(arm)+age+as.factor(perform)+
            as.factor(meno)+as.factor(measure)+
            as.factor(numsites)+as.factor(bone)+
            timdiag+disfree + global +as.factor(adv)+
            as.factor(chemmet)+as.factor(regimen)+
            WBC+gran+platelet, data=br_surv)

fit2<-coxph(Surv(time,status)~ as.factor(arm)+as.factor(numsites)+
            timdiag+global+as.factor(adv)+
            as.factor(chemmet)+ WBC, data=br_surv)

lr1 <- 2*(fit1$loglik[2] - fit2$loglik[2]) # Observed LR statistic
p1 <- 1 - pchisq(2*(fit1$loglik[2] - fit2$loglik[2]), 9) # p-value

fit3<-coxph(Surv(time,status)~ as.factor(arm)+as.factor(numsites)+
            timdiag+global+ as.factor(chemmet)+ WBC, data=br_surv)

lr2 <- 2*(fit2$loglik[2] - fit3$loglik[2]) # Observed LR statistic
p2 <- 1 - pchisq(2*(fit2$loglik[2] - fit3$loglik[2]), 1) # p-value
# can reject the null, so choose model 2 as final model

df <- data.frame(Model = c(1,2,3),
                 loglikelihood = c(fit1$loglik[2], fit2$loglik[2], fit3$loglik[2]),
                 Compare_to_model = c(NA, 1,2),
                 num_of_para = c(21, 12, 11),
                 Obs_LR_statistic = c(NA, lr1, lr2),
                 p_value = c(NA, p1, p2))
knitr::kable(df)

##### COX estimation #####
wbc <- mean(br_surv$WBC)
timdiag <- mean(br_surv$timdiag)
global <- mean(br_surv$global)

#Table for numsites
# 1 2 3 4 5 6 7
#58 80 81 40 24 10 3

```

```

#estimate survival by arm
sf.M2.type1<-survfit(fit2,newdata=data.frame(WBC = wbc,timdiag = timdiag,
                                             global = global,
                                             numsites = 3, arm = 1,
                                             adv = 1, chemmet = 1))
plot(sf.M2.type1,conf.int=F,xlab="time",ylab="Estimated S(t)")
sf.M2.type2<-survfit(fit2,newdata=data.frame(WBC = wbc,timdiag = timdiag,
                                             global = global,
                                             numsites = 3, arm = 0,
                                             adv = 1, chemmet = 1))

lines(sf.M2.type2,conf.int=F, col = 2)
sf.M2.type3<-survfit(fit2,newdata=data.frame(WBC = wbc,timdiag = timdiag,
                                             global = global,
                                             numsites = 3, arm = 0,
                                             adv = 1, chemmet = 0))

lines(sf.M2.type3,conf.int=F, lty = 3, col = 3)
sf.M2.type4<-survfit(fit2,newdata=data.frame(WBC = wbc,timdiag = timdiag,
                                             global = global,
                                             numsites = 3, arm = 1,
                                             adv = 1, chemmet = 0))

lines(sf.M2.type4,conf.int=F, lty = 3, col = 4)
sf.M2.type3<-survfit(fit2,newdata=data.frame(WBC = wbc,timdiag = timdiag,
                                             global = global,
                                             numsites = 2, arm = 0,
                                             adv = 1, chemmet = 0))

lines(sf.M2.type3,conf.int=F, lty = 2, col = 5)
sf.M2.type4<-survfit(fit2,newdata=data.frame(WBC = wbc,timdiag = timdiag,
                                             global = global,
                                             numsites = 2, arm = 1,
                                             adv = 1, chemmet = 0))

lines(sf.M2.type4,conf.int=F, lty = 2, col = 6)

##### Schoenfeld residuals #####
# Scaled Schoenfeld residuals.
resid.scaledsch=residuals(fit2, type="scaledsch")

# Run cox.zph for scaled Schoenfeld residuals.
zph=cox.zph(fit2,terms=F)

# Plot scaled Schoenfeld residuals versus time.
par(mfrow=c(3,4))
plot(zph)

print(zph)

# no significant time trends observed for global test(0.234),
# therefore, the PH assumption is valid

```