

Survival Analysis of Post-Myocardial Infarction Patients

Alvein, Orr, Pham

5/22/2020

Abstract

Background

The rates of myocardial infarction is becoming an increasing common occurrence in the United States. As medical knowledge and techniques improve to meet need of infarction episode, so does the need to understand the survivability of patients who have survived such episodes.

Objectives

Our goal is to provide detailed survival statistics of post-myocardial infarction patients as well as provide an accurate regression model to best prediction of survival outcomes of a single year following an infarction episode.

Methods

Data from 133 post-myocardial infarction patients measure the time in months until death in a one year monitoring period of follow-up. We use a combination of nonparametric (Kaplan-Meier) and parametric methods (Weibull/Cox PH) to determine estimates of survival among gender and myocardial strata (contraction depth, muscular activity,). We consider a slew of statistical and graphical results before determining the most appropriate method of modeling.

Results

Out of all of our methods, we have determined that \square is the most appropriate model for prediction of patient survival. We have AIC values of. We have BIC values. Thus, this model is the best.

Conclusion

summary statistics [review of our model + specific survival rates]

Introduction

Heart disease has become the leader cause of death among the US population among a majority of all racial and ethnic groups (Heron 2019). Myocardial infarctions are becoming largely common among U.S. populations. The number of myocardial infarctions are remarkably increased from [start date] to [end date] by [x] amount (add citation). In 2015, approximately 23% of all fatalities in the United States was related to some degree of heart disease (cdc. cite please). Unsurprisingly, clinical studies have shown harmful symptoms in post-infarction survival patients. Our obtained dataset to examine the tangible difference in survivability rates from the course of year following an infarction episode.

By applying survival analysis techniques to this data set, we seek to achieve improved understanding of the characteristics exhibited by patients in a one year post-infarction interval. We also propose a model to better predict the probability of a survival of patients based on these variable characteristics.

Dataset

We have obtained our data set from Kaggle. The data set contains 133 total patient observations and records 8 variables. Two of the patients as survival times were not given; thus, we elected to remove those values to develop the most accurate portrayal of survival times.

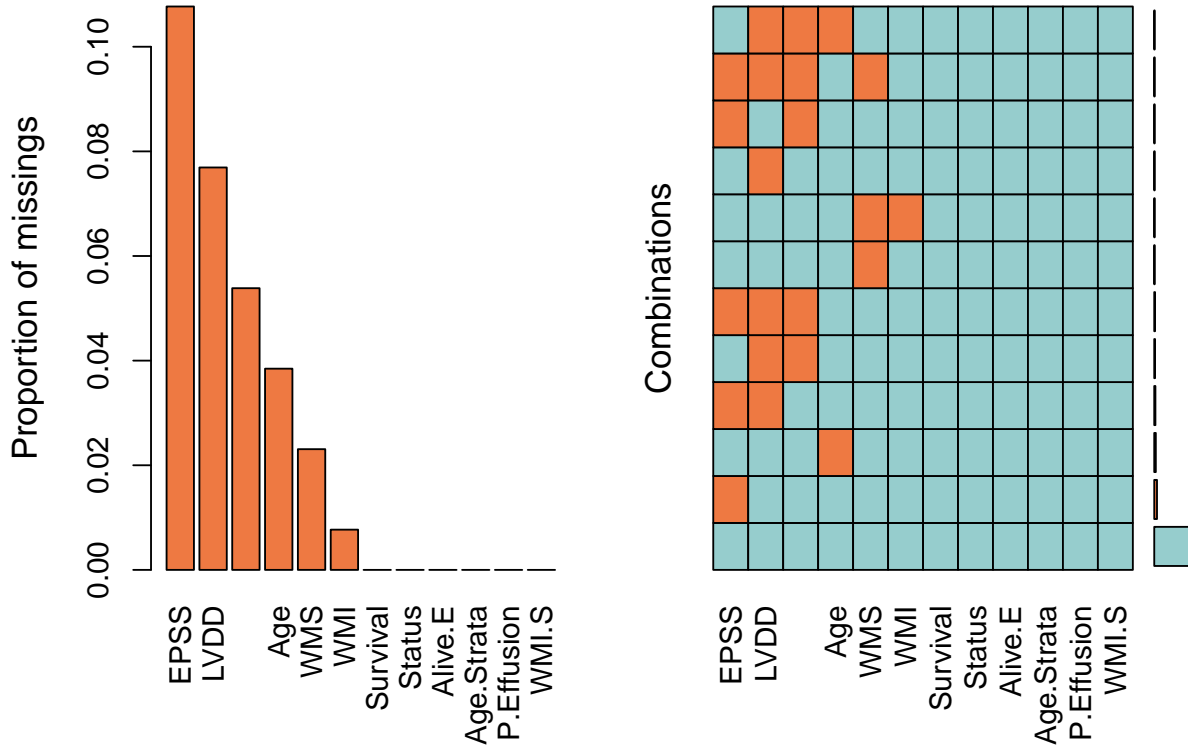
Since the time of infarction varies, some patients were followed for less than a year. This provides a clear censoring and truncation provide. We will address this concern in detail in the later in this section. It should be noted that we have a slew of missing values. Since a single patient has shown as missing, we have opted to impute the values for this data row. With this in mind, our predictive and summary models will have less than ideal accuracy.

The reader may find a summary of tables and original dataset in the appendix of this paper.

Methodology

Imputation

In addition to the two rows that we removed, we further modified the dataset. The provided data contains 40 missing values that we chose to impute using the random forest algorithm methods in the missForest R package. Below is a summary of the missing data:



```
##
## Variables sorted by number of missings:
## Variable Count
## EPSS 0.107692308
## LVDD 0.076923077
## F.Shortening 0.053846154
## Age 0.038461538
## WMS 0.023076923
```

```

##           WMI 0.007692308
##      Survival 0.000000000
##           Status 0.000000000
##      Alive.E 0.000000000
##      Age.Strata 0.000000000
##      P.Effusion 0.000000000
##           WMI.S 0.000000000

##
## Missings in variables:
##      Variable Count
##           Age      5
##      F.Shortening  7
##           EPSS     14
##           LVDD     10
##           WMS      3
##           WMI      1

```

The algorithmic process used here uses a modified k-nearest neighbor (KNN) approach. Using a training data set, the routines of the missForest algorithm predicts the missing values trained on the observed parts of the dataset (Stekhoven 2012). Refer to Stekhoven, et. al 2012 for more detail.

Following imputation, we verify the imputation accuracy using the normalized root mean squared error as an indicator of accuracy (NRMSE, Oba et al. (2003)). The general performance of our imputed dataset can be expressed by:

$$NRMSE = \sqrt{\frac{\text{mean}((X^{true} - X^{imp})^2)}{\text{var}(X^{true})}}$$

Where X is a matrix of our dataset. Our calculated NRMSE is as follows:

```

## missForest iteration 1 in progress...

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## done!
## missForest iteration 2 in progress...

```

```

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## done!
## missForest iteration 3 in progress...

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## done!
## missForest iteration 4 in progress...

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to

```

```

## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## done!
## missForest iteration 5 in progress...

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =
## mtry, : The response has five or fewer unique values. Are you sure you want to
## do regression?

## done!

```

NRMSE
0.2298817

The full imputed dataset may be found in the appendix of this paper.

Censoring

Fixed study start time and fixed study end time.

Patients can start late.

Left censored: Some values, we are unsure how long ago was their myocardial infarction episode. We only have recorded data from the moment patients entered the study and when the study ends.

Right censored: Additionally, some patients live far beyond the scope of the study.

Summary statistics

Over the course of the study, there is a $\hat{S}(t)$ Kaplan-Meier We conduct nonparametric Kaplan-Meier fit on our data over multiple strata. We first conduct a fit over all patients in regards to censoring. Then we work on gender groups, age, and general ventricular condition. A survival function can be defined as:

[insert latex equation for survival function, with censored values]

Weibull Fits (+Cox PH)

Log-Normal

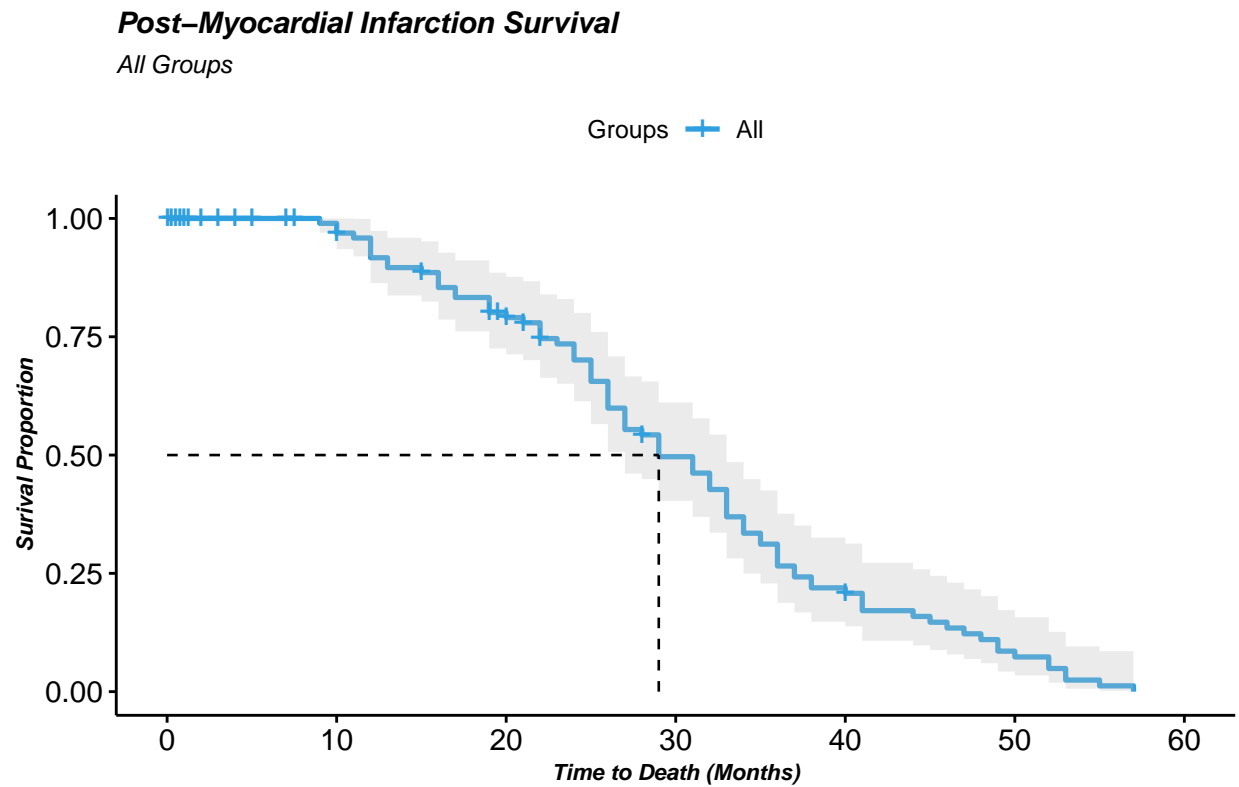
Results

Table of Summary Statistics

KM Curve & Hazard

Survival Curves

KM Overall



Here is the survival curve for all groups within our dataset. We see that a majority of our censored values have very short survival times. This is very intuitive given to our limited interval study time of a single year. We clearly see a median survival time of approximately 29 weeks.

records	n.max	n.start	events	*rmean	*se(rmean)	median	0.95LCL	0.95UCL
130	130	130	88	30.53008	1.249886	29	27	33

Hazard Plots

Weibull Curve

Cox Proportional Hazard

Model Diagnostics

AIC, BIC, and Confidence Intervals

Residual Analysis/QQ Plot

Discussion

References

Heron, M. Deaths: Leading causes for 2017 pdf icon[PDF – 3 M]. National Vital Statistics Reports;68(6). Accessed November 19, 2019.

Oba S, Sato MA, Takemasa I, Monden M, Matsubara K, Ishii S. A Bayesian missing value estimation method for gene expression profile data. *Bioinformatics*. 2003;19(16):2088-2096. doi:10.1093/bioinformatics/btg287

Daniel J. Stekhoven, Peter Bühlmann, MissForest—non-parametric missing value imputation for mixed-type data, *Bioinformatics*, Volume 28, Issue 1, 1 January 2012, Pages 112–118,

Salzberg, S. (1988). Exemplar-based learning: Theory and implementation (Technical Report TR-10-88). Harvard University, Center for Research in Computing Technology, Aiken Computation Laboratory (33 Oxford Street; Cambridge, MA 02138).

Kan, G., Visser, C., Kooler, J., & Dunning, A. (1986). Short and long term predictive value of wall motion score in acute myocardial infarction. *British Heart Journal*, 56, 422-427.

Fryar CD, Chen T-C, Li X. Prevalence of uncontrolled risk factors for cardiovascular disease: United States, 1999–2010 pdf icon[PDF-494K]. NCHS data brief, no. 103. Hyattsville, MD: National Center for Health Statistics; 2012. Accessed May 9, 2019.

Appendix

Dataset Variable Summary

Variable	Label	Definition
Survival	Survival	The number of months the patints survived, post-myocardial infarction.
Status	Status	Censorship status. 0 denotes that a patient is a censored while 1 denotes that a patient is uncensored.
Alive at the end of Survival Period	Alive.E	Binary variable. 0 denotes that patient is alive at the end of the survival period while 1 indicates that a patient is still alive.
Patient Age	Age	The age in years when a myocardial infarction occurs.
Age Group	Age.Strata	0 denotes 49 or younger. 1 denotes 50 or older. 2 denotes 65 or older.
Pericardial Effusion	P.Effusion	Binary variable. Pericardial effusion is excess fluid surrounding the heart. Though excess is not harmful, it is sometimes indicates a porly functioning heart. 0 denotes that pericardial effusion is absent while 1 denotes that fluid is present.
Fractional Shortening	F.Shortening	Fractional shortening is a measure of contractility around the heart. Generally, lower numbers are considered to be abnormal.
E-Point Septal Separation	EPSS	E-point septal separation is an addition measure of heart contractivity. Larger numbers are considered to be abnormal.
Left Ventricular End-Diastolic Dimension	LVDD	Left ventricular end-diastolic dimension is the measure of the heart at the end of disatole. The larger this value is indicates a larger heart. Larger hearts are generally in poor health.
Wall Motion Score	WMS	Wall motion score is a measure of how the segments of the left ventricle are moving during systol.
Wall Motion Index	WMI	Wall motion index is the wall motion score divided by the number of segments that are moving. Normally, 12-13 segments can be seen in an echocardiogram.
Wall Motion Strata	WMI.S	Binary Variable. 0 denotes that WMI is less than or equal to 1.28. 1 denotes that WMI is greater than or equal to 1.28.

Original Dataset

Imputed Dataset

missForest iteration 1 in progress...

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

done! missForest iteration 2 in progress...

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

done! missForest iteration 3 in progress...

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?
```

Table 1: Dataset

Survival	Status	Alive.E	Age	Age.Strata	P.Effusion	F.Shortening	EPSS	LVDD	WMS	WMI	WMI.S	
11.00	1	0	71.00	2	0	0.260	9.000	4.600	14.00	1.000	0	
19.00	1	0	72.00	2	0	0.380	6.000	4.100	14.00	1.700	1	
16.00	1	0	55.00	1	0	0.260	4.000	3.420	14.00	1.000	0	
57.00	1	0	60.00	1	0	0.253	12.062	4.603	16.00	1.450	1	
19.00	0	1	57.00	1	0	0.160	22.000	5.750	18.00	2.250	1	
26.00	1	0	68.00	2	0	0.260	5.000	4.310	12.00	1.000	0	
13.00	1	0	62.00	1	0	0.230	31.000	5.430	22.50	1.875	1	
50.00	1	0	60.00	1	0	0.330	8.000	5.250	14.00	1.000	0	
19.00	1	0	46.00	0	0	0.340	0.000	5.090	16.00	1.140	0	
25.00	1	0	54.00	1	0	0.140	13.000	4.490	15.50	1.190	0	
10.00	0	1	77.00	2	0	0.130	16.000	4.230	18.00	1.800	1	
52.00	1	0	62.00	1	1	0.450	9.000	3.600	16.00	1.140	0	
52.00	1	0	73.00	2	0	0.330	6.000	4.000	14.00	1.000	0	
44.00	1	0	60.00	1	0	0.150	10.000	3.730	14.00	1.000	0	
0.50	0	1	62.00	1	0	0.120	23.000	5.800	11.67	2.330	1	
24.00	1	0	55.00	1	1	0.250	12.063	4.290	14.00	1.000	0	
0.50	0	1	69.00	2	1	0.260	11.000	4.650	18.00	1.640	1	
0.50	0	1	62.53	1	1	0.070	20.000	5.200	24.00	2.000	1	
22.00	0	1	66.00	2	0	0.090	17.000	5.819	8.00	1.333	1	
1.00	0	1	66.00	2	1	0.220	15.000	5.400	27.00	2.250	1	
0.75	0	1	69.00	2	0	0.150	12.000	5.390	19.50	1.625	1	
0.75	0	1	85.00	2	1	0.180	19.000	5.460	13.83	1.380	1	
0.50	0	1	73.00	2	0	0.230	12.733	6.060	7.50	1.500	1	
5.00	0	1	71.00	2	0	0.170	0.000	4.650	8.00	1.000	0	
48.00	1	0	64.00	1	0	0.190	5.900	3.480	10.00	1.110	0	
29.00	1	0	54.00	1	0	0.300	7.000	3.850	10.00	1.667	1	
29.00	1	0	35.00	0	0	0.300	5.000	4.170	14.00	1.000	0	
29.00	1	0	55.00	1	0	NA	7.000	NA	2.00	1.000	0	
0.25	0	1	75.00	2	0	NA	NA	NA	NA	1.000	0	
36.00	1	0	55.00	1	1	0.210	4.200	4.160	14.00	1.560	1	
1.00	0	1	65.00	2	0	0.150	NA	5.050	10.00	1.000	0	
1.00	0	1	52.00	1	1	0.170	17.200	5.320	14.00	1.170	0	
3.00	0	1	NA	2	0	NA	12.000	NA	6.00	3.000	1	
27.00	1	0	47.00	0	0	0.400	5.120	3.100	12.00	1.000	0	
35.00	1	0	63.00	1	0	NA	10.000	NA	14.00	1.170	0	
26.00	1	0	61.00	1	0	0.610	13.100	4.070	13.00	1.625	1	
16.00	1	0	63.00	1	1	NA	NA	5.310	5.00	1.000	0	
1.00	0	1	65.00	2	0	0.060	23.600	NA	21.50	2.150	1	
19.00	1	0	68.00	2	0	0.510	NA	3.880	15.00	1.670	1	
31.00	1	0	80.00	2	0	0.410	5.400	4.360	NA	1.000	0	
32.00	1	0	54.00	1	0	0.350	9.300	3.630	11.00	1.222	0	
16.00	1	0	70.00	2	1	0.270	4.700	4.490	22.00	2.000	1	
40.00	1	0	79.00	2	0	0.150	17.500	4.270	13.00	1.300	1	
46.00	1	0	56.00	1	0	0.330	NA	3.590	14.00	1.000	0	
2.00	0	1	67.00	2	1	0.440	9.000	3.960	17.50	1.450	1	
37.00	1	0	64.00	1	0	0.090	NA	NA	12.00	2.000	1	
19.50	0	1	81.00	2	0	0.120	NA	NA	9.00	1.250	0	
20.00	0	1	59.00	1	0	0.030	21.300	6.290	17.00	1.310	1	
0.25	0	1	63.00	1	1	NA	NA	NA	23.00	2.300	1	
2.00	0	1	56.00	1	1	0.040	14.000	5.000	NA	NA	1	
7.00	0	1	61.00	1	1	0.270	NA	NA	9.00	1.500	1	
10.00	1	0	57.00	1	10	0	0.240	14.800	5.260	18.00	1.380	1
12.00	1	0	58.00	1		0	0.300	9.400	3.490	14.00	1.000	0
1.00	0	1	60.00	1		0	0.010	24.600	5.650	39.00	3.000	1
10.00	1	0	66.00	2	0	0.290	15.600	6.150	14.00	1.000	0	

```
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?  
  
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?  
  
## Warning in randomForest.default(x = obsX, y = obsY, ntree = ntree, mtry =  
## mtry, : The response has five or fewer unique values. Are you sure you want to  
## do regression?  
  
done!
```

Survival	Status	Alive.E	Age	Age.Strata	P.Effusion	F.Shortening	EPSS	LVDD	WMS	WMI	WMI.S	
11.00	1.00	0.00	71.00	2.00	0.00	0.26	9.00	4.60	14.00	1.00	0.00	
19.00	1.00	0.00	72.00	2.00	0.00	0.38	6.00	4.39	16.41	1.70	1.00	
16.00	1.00	0.05	55.00	1.00	0.00	0.26	4.00	3.42	14.00	1.00	0.00	
57.00	1.00	0.01	60.00	1.02	0.00	0.25	12.06	4.60	16.00	1.45	1.00	
19.00	0.00	1.00	57.00	1.00	0.00	0.10	22.00	5.75	18.00	2.25	1.00	
26.00	1.00	0.00	68.00	2.00	0.00	0.26	5.00	4.31	12.00	1.04	0.00	
13.00	1.00	0.00	62.00	1.00	0.00	0.23	31.00	5.43	22.50	1.88	1.00	
37.15	1.00	0.00	60.00	1.00	0.00	0.33	8.00	5.25	14.00	1.00	0.00	
19.00	1.00	0.00	46.00	0.00	0.00	0.21	0.00	5.09	16.00	1.14	0.00	
25.00	1.00	0.00	59.79	1.00	0.00	0.14	13.00	4.52	15.50	1.19	0.00	
2.94	0.00	1.00	77.00	2.00	0.00	0.13	16.00	4.23	18.00	1.80	1.00	
52.00	1.00	0.00	62.00	1.00	1.00	0.45	9.00	3.60	16.00	1.14	0.00	
52.00	1.00	0.00	73.00	2.00	0.00	0.33	6.00	4.56	14.00	1.00	0.00	
44.00	1.00	0.00	60.00	1.00	0.00	0.15	10.00	3.73	14.00	1.12	0.00	
8.62	0.00	1.00	62.00	1.00	0.00	0.12	23.00	5.80	11.67	2.33	1.00	
24.00	1.00	0.00	55.00	1.00	1.00	0.25	12.06	4.29	9.75	1.00	0.00	
0.50	0.00	0.98	69.00	2.00	1.00	0.26	11.00	4.65	18.00	1.74	1.00	
0.50	0.00	1.00	62.53	1.00	1.00	0.07	20.00	5.20	24.00	2.00	1.00	
22.00	0.00	1.00	66.00	1.71	0.00	0.09	17.00	5.82	8.00	1.33	1.00	
1.00	0.00	1.00	66.00	2.00	1.00	0.22	15.00	5.40	27.00	2.25	1.00	
0.75	0.00	1.00	69.00	2.00	0.00	0.15	12.00	5.39	19.50	1.62	1.00	
0.75	0.00	1.00	85.00	1.87	1.00	0.18	19.00	5.46	13.83	1.38	1.00	
0.50	0.03	1.00	72.82	1.91	0.00	0.23	12.73	6.06	7.50	1.50	1.00	
5.00	0.00	1.00	71.00	2.00	0.00	0.22	0.00	4.65	8.00	1.00	0.00	
48.00	1.00	0.00	64.00	1.00	0.00	0.19	5.90	4.95	10.00	1.11	0.00	
29.00	1.00	0.00	54.00	1.00	0.00	0.30	8.46	3.85	10.00	1.67	1.00	
35.62	1.00	0.00	54.25	0.00	0.00	0.30	5.00	4.17	14.00	1.00	0.00	
29.00	1.00	0.04	55.00	1.00	0.00	0.23	7.00	4.60	2.00	1.00	0.00	
0.25	0.00	1.00	71.35	2.00	0.00	0.17	10.80	4.96	12.42	1.00	0.00	
36.00	1.00	0.00	55.00	1.00	1.00	0.21	4.20	4.16	14.00	1.56	1.00	
1.00	0.00	1.00	65.00	2.00	0.00	0.15	11.24	5.05	10.00	1.00	0.00	
1.00	0.00	1.00	52.00	1.00	1.00	0.13	17.20	5.32	14.00	1.17	0.00	
3.00	0.00	1.00	67.78	2.00	0.00	0.16	12.00	5.20	6.00	3.00	1.00	
35.01	1.00	0.00	47.00	0.00	0.00	0.40	5.12	3.10	12.00	1.00	0.00	
35.00	1.00	0.00	63.00	1.00	0.00	0.19	10.00	4.44	14.00	1.17	0.00	
26.00	1.00	0.00	61.00	1.00	0.00	0.61	13.10	4.07	13.00	1.62	1.00	
21.65	1.00	0.05	63.00	1.00	0.36	0.21	10.58	5.31	5.00	1.00	0.00	
1.00	0.00	1.00	65.00	2.00	0.00	0.06	23.60	5.81	21.50	2.15	1.00	
19.00	1.00	0.00	68.00	2.00	0.00	0.51	7.66	4.31	15.78	1.67	1.00	
31.00	1.00	0.00	80.00	2.00	0.00	0.41	5.40	4.35	12.13	1.00	0.00	
32.00	1.00	0.00	54.00	0.92	0.00	0.35	9.30	3.63	12.33	1.22	0.00	
16.00	1.00	0.07	70.00	2.00	1.00	0.27	4.70	4.49	22.00	2.00	1.00	
40.00	1.00	0.00	79.00	1.74	0.00	0.15	17.50	4.27	13.00	1.30	1.00	
46.00	1.00	0.00	56.00	1.00	0.00	0.33	7.77	3.59	14.00	1.00	0.00	
2.00	0.00	1.00	67.00	2.00	0.29	0.44	9.00	3.96	17.50	1.45	1.00	
26.40	1.00	0.00	64.00	1.00	0.00	0.09	15.52	5.05	12.00	2.00	0.84	
9.12	0.19	1.00	81.00	1.94	0.00	0.12	11.65	5.02	12.82	1.08	0.00	
20.00	0.00	1.00	59.00	1.00	0.00	0.03	21.30	6.29	17.00	1.31	1.00	
2.66	0.00	1.00	63.00	1.00	1.00	0.13	18.44	5.19	23.00	2.30	1.00	
2.00	0.00	1.00	56.00	1.00	1.00	0.04	14.00	5.00	17.09	1.62	1.00	
6.89	0.00	1.00	61.00	1.14	1.00	0.27	9.29	4.91	9.00	1.74	1.00	
10.00	1.00	0.00	57.00	1.06	0.44	0.24	14.80	5.26	16.10	1.61	1.00	
12.00	1.00	0.06	58.00	1.00	0.00	0.30	9.40	3.49	14.00	1.00	0.00	
1.00	0.00	1.00	60.00	1.00	12	0.00	24.60	6.02	39.00	3.00	1.00	
37.16	1.00	0.02	66.00	2.00		0.00	0.29	15.60	6.15	14.00	1.00	0.00
45.00	1.00	0.00	63.00	1.00		0.00	0.15	13.00	4.57	13.00	1.08	0.00
28.39	1.00	0.00	59.05	1.00		0.00	0.13	18.60	4.37	12.33	1.37	0.77
52.00	1.00	0.00	72.00	2.00	0.00	0.12	0.00	5.12	22.00	2.25	1.00	

R Code