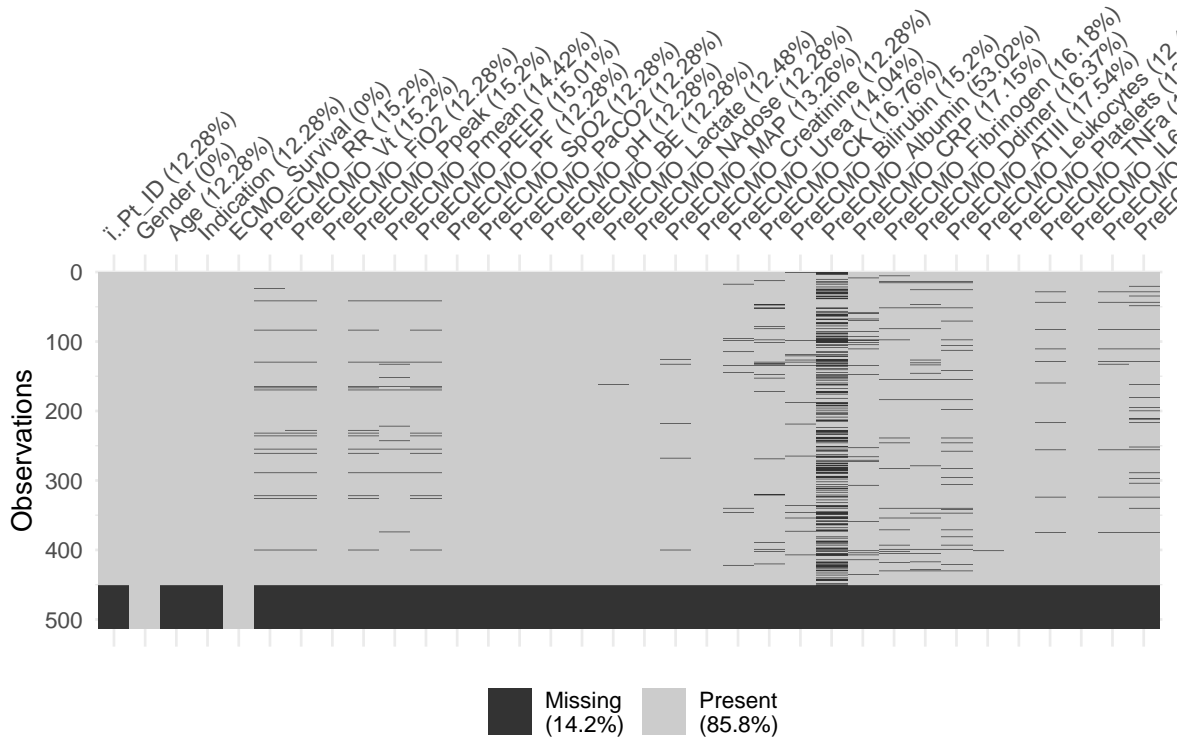
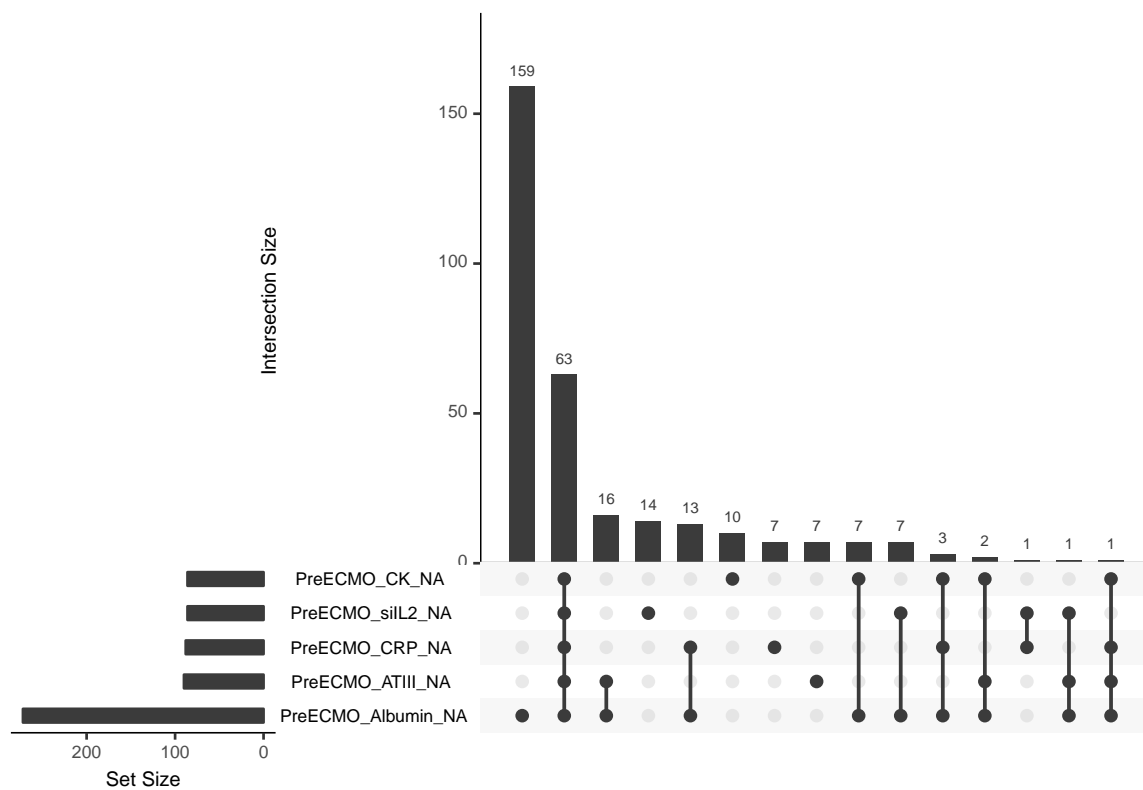


Classification of Acute Respiratory Distress Syndrome

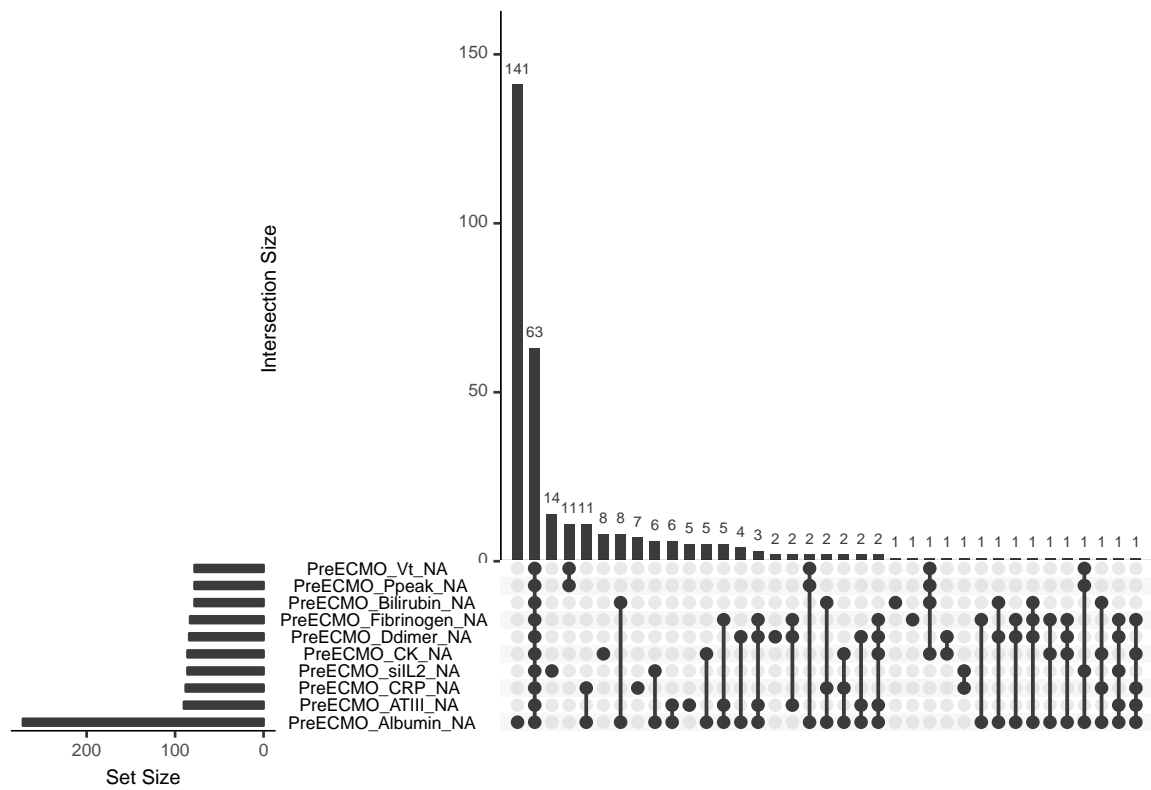
Robert Edwards



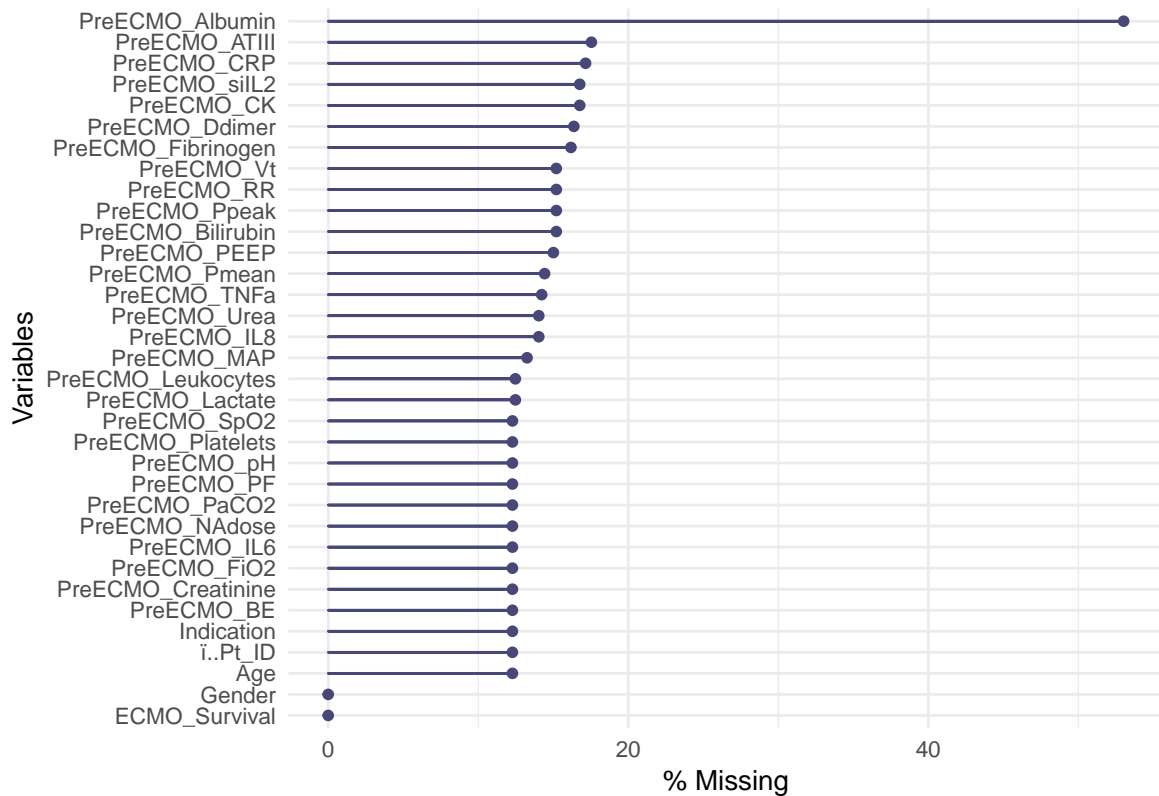
An upSet plot from the **UpSetR** package can be used to visualise the patterns of missingness, or rather the combinations of missingness across cases. To see combinations of missingness and intersections of missingness amongst variables, use the `gg_miss_upset` function:



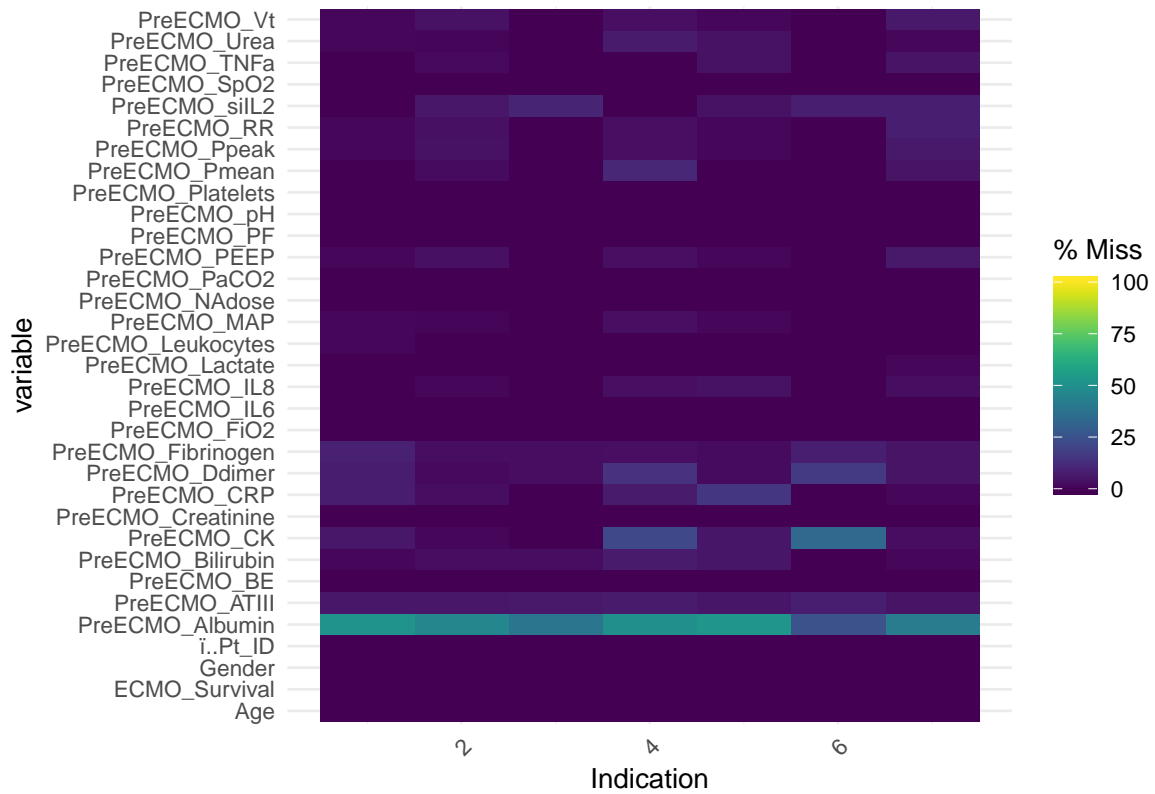
If there are 40 intersections, there will be up to 40 combinations of variables explored. The number of sets and intersections can be changed by passing arguments `nsets = 10` to look at 10 sets of variables, and `nintersects = 50` to look at 50 intersections.



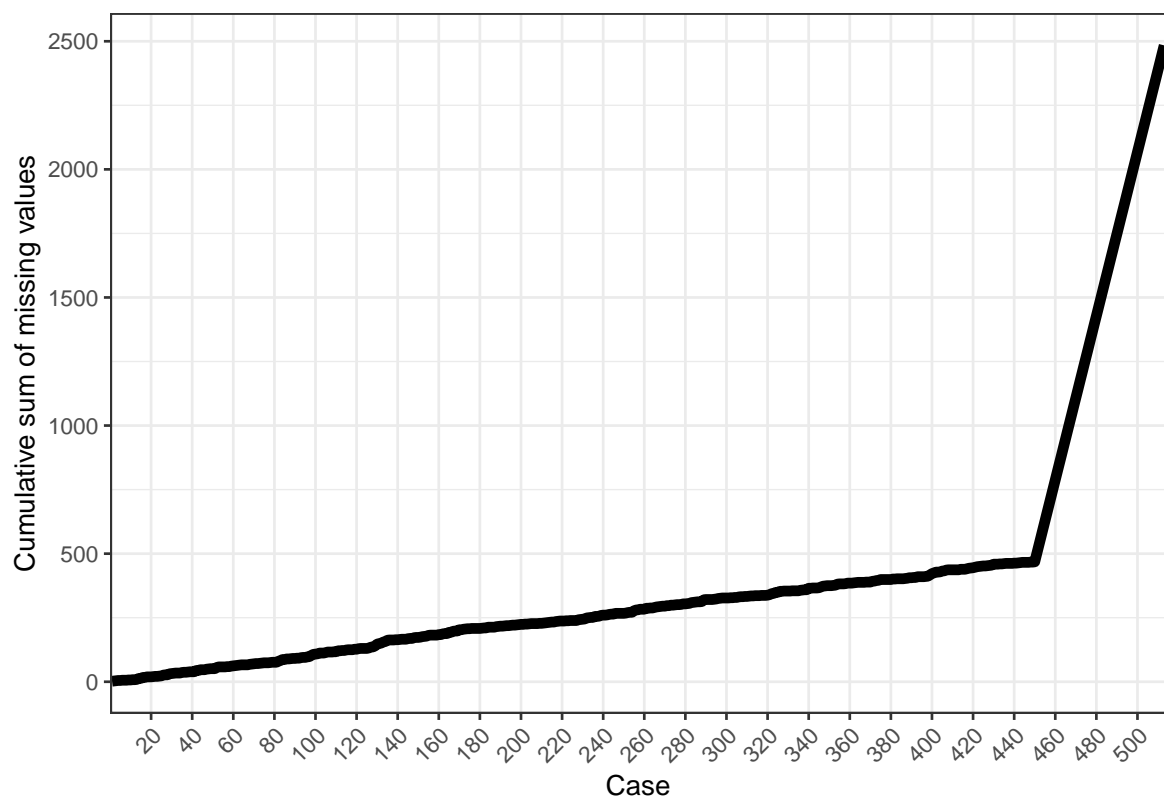
This plot shows the number of missing values in each variable in a dataset. It is powered by the `miss_var_summary()` function.



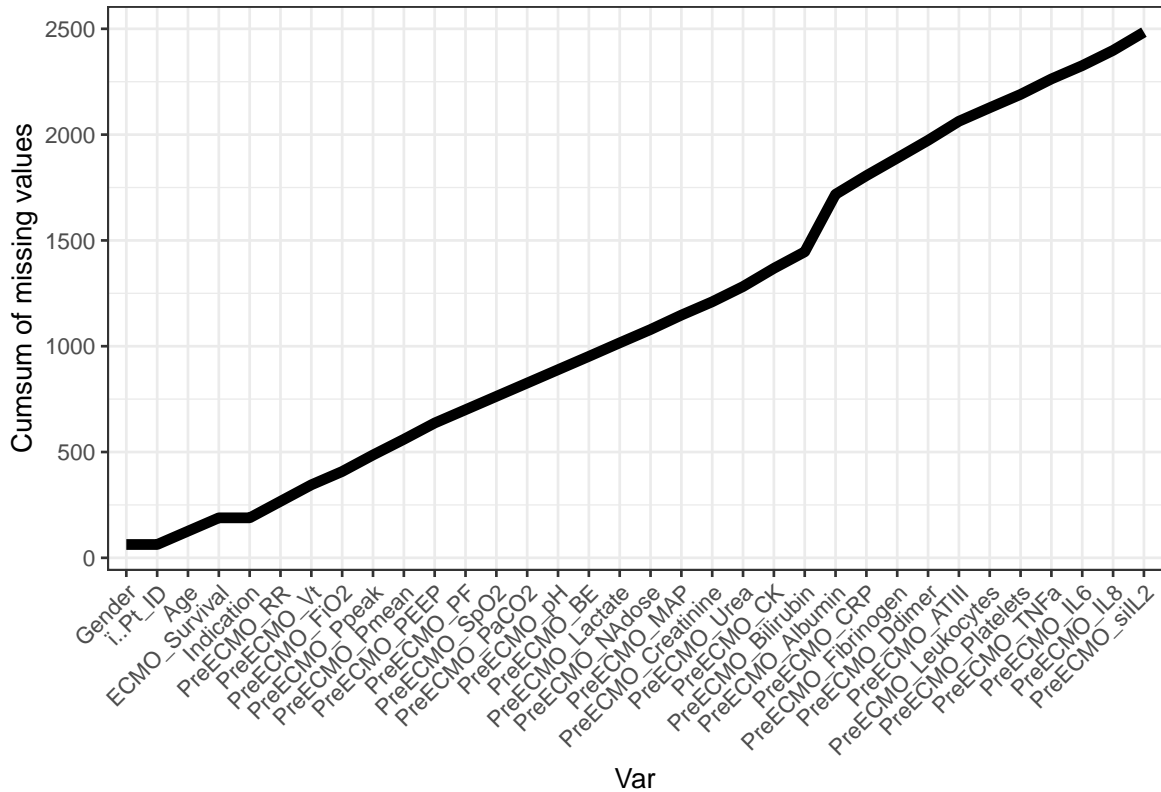
This plot shows the number of missings in each column, broken down by a categorical variable from the dataset. It is powered by a `dplyr::group_by` statement followed by `miss_var_summary()`.



This plot shows the cumulative sum of missing values, reading the rows of the dataset from the top to bottom. It is powered by the `miss_case_cumsum()` function.



This plot shows the cumulative sum of missing values, reading columns from the left to the right of your dataframe. It is powered by the `miss_var_cumsum()` function.



Exploratory Data Analysis

We first visually explore the data to get a sense of the features and distributions of the data. Then we will conduct hypothesis tests for each feature based on `ECMO_Survival` as a rough idea how relevant each feature will be.

Boxplot

All continuous features are normally scaled to be comparable.

Observations: 513

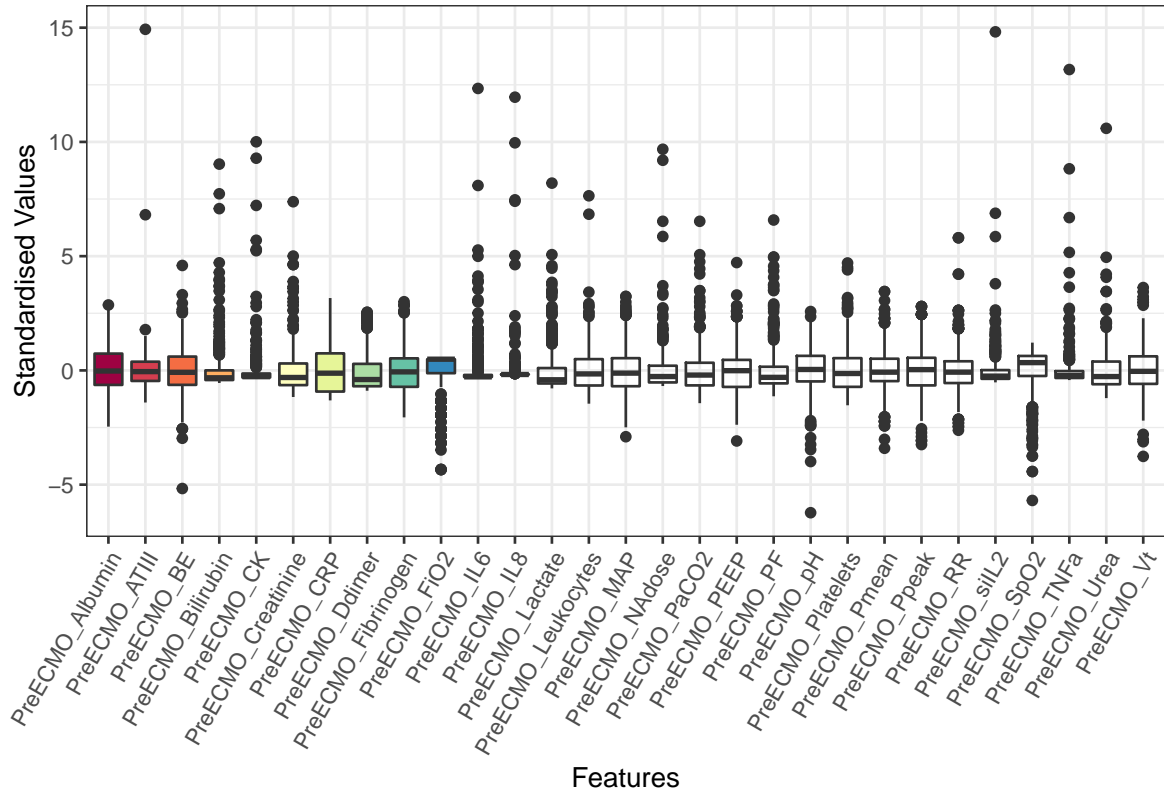
Variables: 29

```
$ PreECMO_RR      <dbl> <matrix[25 x 1]>
$ PreECMO_Vt      <dbl> <matrix[25 x 1]>
$ PreECMO_FiO2    <dbl> <matrix[25 x 1]>
$ PreECMO_Ppeak   <dbl> <matrix[25 x 1]>
$ PreECMO_Pmean   <dbl> <matrix[25 x 1]>
$ PreECMO_PEEP    <dbl> <matrix[25 x 1]>
$ PreECMO_Pf      <dbl> <matrix[25 x 1]>
$ PreECMO_SpO2    <dbl> <matrix[25 x 1]>
$ PreECMO_PaCO2   <dbl> <matrix[25 x 1]>
$ PreECMO_pH      <dbl> <matrix[25 x 1]>
$ PreECMO_BE      <dbl> <matrix[25 x 1]>
```

```

$ PreECMO_Lactate      <dbl> <matrix[25 x 1]>
$ PreECMO_NAdose      <dbl> <matrix[25 x 1]>
$ PreECMO_MAP          <dbl> <matrix[25 x 1]>
$ PreECMO_Creatinine  <dbl> <matrix[25 x 1]>
$ PreECMO_Urea         <dbl> <matrix[25 x 1]>
$ PreECMO_CK           <dbl> <matrix[25 x 1]>
$ PreECMO_Bilirubin   <dbl> <matrix[25 x 1]>
$ PreECMO_Albumin     <dbl> <matrix[25 x 1]>
$ PreECMO_CRP          <dbl> <matrix[25 x 1]>
$ PreECMO_Fibrinogen  <dbl> <matrix[25 x 1]>
$ PreECMO_Ddimer       <dbl> <matrix[25 x 1]>
$ PreECMO_ATIII       <dbl> <matrix[25 x 1]>
$ PreECMO_Leukocytes  <dbl> <matrix[25 x 1]>
$ PreECMO_Platelets   <dbl> <matrix[25 x 1]>
$ PreECMO_TNFa        <dbl> <matrix[25 x 1]>
$ PreECMO_IL6         <dbl> <matrix[25 x 1]>
$ PreECMO_IL8         <dbl> <matrix[25 x 1]>
$ PreECMO_siIL2       <dbl> <matrix[25 x 1]>

```



The boxplot shows many highly skewed variables indicating that these likely need to be transformed in some fashion (likely log transformation). For **logistic regression**, first a model will be fit without transformations and then the not significant variables will be transformed and model fit will be evaluated.

To get an idea of the distribution of the data, the following summary statistics were obtained for the categorical variable ECMO_Survival (Table 1) and for the continuous variables (Table 2).

Table 1: Numbers of smokers and nonsmokers.

	ECMO_Survival	n
		63
N		109
Y		341

Table 1 shows that out of the 513 individuals, only 0% of the individuals in the study sample smoke (0 survivors vs 0 non-survivors).

[1] TRUE

Table 2: Summary statistics on insurance charges, age and bmi.

Variable	n	Mean	SD	Minimum	1st quartile	Median	3rd quartile	Maximum
PreECMO_Albumin	513	8.6e-17	1	-2.46	-0.64	-0.027	0.73	2.86
PreECMO_ATIII	513	2.2e-17	1	-1.41	-0.46	-0.053	0.38	14.93
PreECMO_BE	513	2e-17	1	-5.17	-0.63	-0.083	0.6	4.59
PreECMO_Bilirubin	513	1.7e-17	1	-0.55	-0.42	-0.32	0.0013	9.03
PreECMO_CK	513	3.4e-17	1	-0.33	-0.31	-0.27	-0.14	10
PreECMO_Creatinine	513	1.7e-17	1	-1.16	-0.64	-0.31	0.3	7.38
PreECMO_CRP	513	1.1e-17	1	-1.31	-0.93	-0.12	0.75	3.17
PreECMO_Ddimer	513	2.5e-17	1	-0.89	-0.69	-0.4	0.29	2.54
PreECMO_Fibrinogen	513	2e-16	1	-2.06	-0.72	-0.065	0.53	3
PreECMO_FiO2	513	1.5e-16	1	-4.34	-0.12	0.49	0.49	0.49
PreECMO_IL6	513	9e-18	1	-0.29	-0.29	-0.28	-0.2	12.34
PreECMO_IL8	513	6.2e-18	1	-0.18	-0.18	-0.18	-0.17	11.96
PreECMO_Lactate	513	1e-16	1	-0.79	-0.57	-0.41	0.1	8.2
PreECMO_Leukocytes	513	3.1e-18	1	-1.46	-0.66	-0.15	0.49	7.64
PreECMO_MAP	513	-1.7e-16	1	-2.9	-0.69	-0.12	0.53	3.24
PreECMO_NAdose	513	4.4e-18	1	-0.68	-0.53	-0.27	0.2	9.68
PreECMO_PaCO2	513	-1.7e-16	1	-1.43	-0.66	-0.2	0.33	6.53
PreECMO_PEEP	513	-1.5e-17	1	-3.09	-0.72	-0.013	0.46	4.72
PreECMO_PF	513	1.1e-16	1	-1.13	-0.57	-0.31	0.16	6.58
PreECMO_pH	513	1.3e-15	1	-6.23	-0.48	0.04	0.64	2.58
PreECMO_Platelets	513	2.9e-17	1	-1.53	-0.72	-0.14	0.54	4.7
PreECMO_Pmean	513	-3.5e-16	1	-3.41	-0.47	-0.077	0.51	3.45
PreECMO_Ppeak	513	-4.1e-16	1	-3.25	-0.66	0.034	0.55	2.8
PreECMO_RR	513	6.5e-17	1	-2.62	-0.55	-0.077	0.4	5.8
PreECMO_siIL2	513	-1.2e-17	1	-0.52	-0.37	-0.25	0.014	14.82
PreECMO_SpO2	513	-5.6e-17	1	-5.69	-0.24	0.34	0.63	1.22
PreECMO_TNFa	513	-9.8e-18	1	-0.42	-0.33	-0.23	-0.031	13.17
PreECMO_Urea	513	-9.8e-17	1	-1.21	-0.61	-0.27	0.39	10.59
PreECMO_Vt	513	-1.1e-16	1	-3.76	-0.59	-0.041	0.62	3.63

Looking at Table 2

Imputation

Here I will try various methods for data imputation.

I. KNN Imputation

Observations: 513

Variables: 68

```
$ i..Pt_ID          <int> 1397, 811, 1224, 1060, 1526, 653, 655, ...
$ Gender            <fct> m, m, m, w, m, m, m, w, m, m, w, m, ...
$ Age              <int> 19, 20, 22, 23, 29, 31, 34, 36, 37, 37, ...
$ Indication       <int> 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, ...
$ ECMO_Survival    <fct> Y, Y, Y, Y, Y, Y, N, Y, Y, Y, Y, N, ...
$ PreECMO_RR      <int> 22, 22, 15, 25, 25, 27, 34, 20, 32, 20, ...
$ PreECMO_Vt      <int> 554, 560, 567, 500, 456, 443, 631, 425, ...
$ PreECMO_FiO2    <dbl> 0.90, 1.00, 0.90, 0.95, 1.00, 1.00, 0.9...
$ PreECMO_Ppeak   <int> 38, 30, 35, 33, 32, 47, 31, 42, 33, 47, ...
$ PreECMO_Pmean   <int> 20, 25, 22, 20, 19, 33, 22, 28, 22, 40, ...
$ PreECMO_PEEP    <int> 15, 16, 15, 15, 12, 26, 13, 17, 15, 25, ...
$ PreECMO_PF      <int> 82, 38, 87, 75, 51, 75, 77, 43, 42, 61, ...
$ PreECMO_SpO2    <int> 92, 49, 94, 86, 72, 93, 92, 68, 63, 93, ...
$ PreECMO_PaCO2   <int> 76, 88, 85, 70, 65, 64, 82, 67, 58, 53, ...
$ PreECMO_pH      <dbl> 7.09, 6.96, 7.15, 7.25, 7.12, 7.19, 7.1...
$ PreECMO_BE      <dbl> -6.0, -17.2, -1.3, 2.7, -5.0, -3.9, 1.1...
$ PreECMO_Lactate <int> 31, 105, 15, 29, 34, 12, 16, 16, 11, 62...
$ PreECMO_NAdose  <dbl> 0.598, 0.427, 1.667, 0.208, 0.746, 0.19...
$ PreECMO_MAP     <int> 78, 71, 67, 78, 71, 64, 72, 65, 45, 79, ...
$ PreECMO_Creatinine <dbl> 2.0, 1.7, 1.0, 0.7, 1.9, 1.5, 1.1, 1.3, ...
$ PreECMO_Urea    <int> 157, 58, 33, 113, 44, 40, 28, 42, 19, 2...
$ PreECMO_CK      <int> 145, 278, 192, 58, 529, 7348, 111, 4344...
$ PreECMO_Bilirubin <dbl> 0.6, 0.2, 0.3, 0.4, 2.4, 0.6, 0.9, 13.2...
$ PreECMO_Albumin <int> 25, 18, 18, 22, 12, 32, 28, 20, 29, 14, ...
$ PreECMO_CRP     <int> 11, 1, 87, 339, 251, 125, 22, 269, 273, ...
$ PreECMO_Fibrinogen <int> 109, 191, 314, 421, 156, 471, 417, 224, ...
$ PreECMO_Ddimer  <int> 2, 5, 3, 9, 32, 4, 8, 4, 3, 2, 28, 4, 1...
$ PreECMO_ATIII   <int> 109, 67, 61, 49, 18, 85, 80, 34, 88, 15...
$ PreECMO_Leukocytes <dbl> 22.8, 11.3, 12.4, 15.5, 12.0, 4.4, 27.9...
$ PreECMO_Platelets <int> 149, 371, 283, 315, 10, 205, 272, 59, 4...
$ PreECMO_TNFa    <int> 25, 24, 26, 14, 83, 35, 25, 25, 10, 246...
$ PreECMO_IL6     <int> 71, 4304, 2850, 26, 38994, 43, 1137, 21...
$ PreECMO_IL8     <int> 27, 2136, 118, 18, 659, 31, 93, 172, 24...
$ PreECMO_siIL2   <int> 2111, 356, 1476, 839, 14803, 3990, 1830...
$ i..Pt_ID_imp    <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ Gender_imp      <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ Age_imp         <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ Indication_imp  <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ ECMO_Survival_imp <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_RR_imp  <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Vt_imp  <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_FiO2_imp <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Ppeak_imp <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
```

```

$ PreECMO_Pmean_imp      <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_PEEP_imp       <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_PF_imp         <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_SpO2_imp       <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_PaCO2_imp      <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_pH_imp         <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_BE_imp         <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Lactate_imp    <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_NAdose_imp     <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_MAP_imp        <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Creatinine_imp <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Urea_imp       <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_CK_imp         <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Bilirubin_imp  <lgl> TRUE, FALSE, FALSE, FALSE, FALSE, FALSE...
$ PreECMO_Albumin_imp    <lgl> TRUE, TRUE, TRUE, TRUE, FALSE, FALSE, F...
$ PreECMO_CRP_imp        <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Fibrinogen_imp <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, TRUE...
$ PreECMO_Ddimer_imp     <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_ATIII_imp      <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Leukocytes_imp <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_Platelets_imp  <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_TNFa_imp       <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_IL6_imp        <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_IL8_imp        <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...
$ PreECMO_siIL2_imp      <lgl> FALSE, FALSE, FALSE, FALSE, FALSE, FALS...

```

Observations: 513

Variables: 30

```

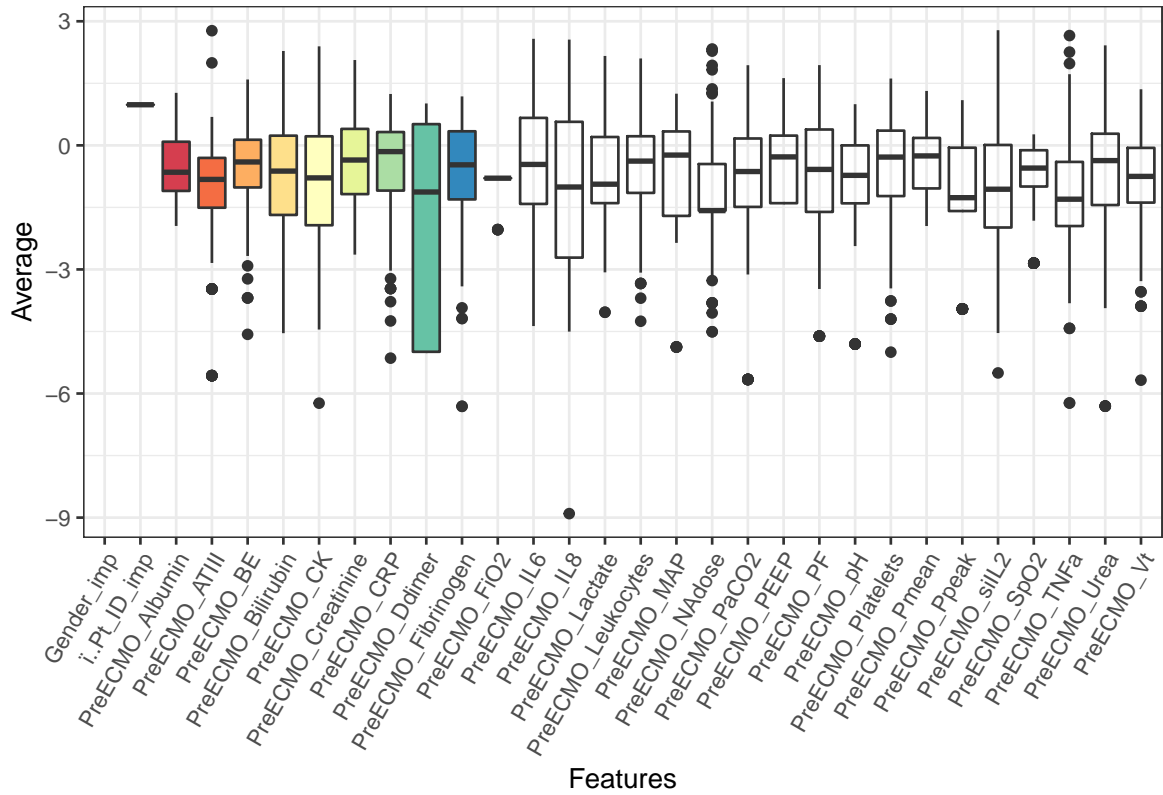
$ PreECMO_Vt      <dbl> <matrix[25 x 1]>
$ PreECMO_FiO2    <dbl> <matrix[25 x 1]>
$ PreECMO_Ppeak   <dbl> <matrix[25 x 1]>
$ PreECMO_Pmean   <dbl> <matrix[25 x 1]>
$ PreECMO_PEEP    <dbl> <matrix[25 x 1]>
$ PreECMO_PF      <dbl> <matrix[25 x 1]>
$ PreECMO_SpO2    <dbl> <matrix[25 x 1]>
$ PreECMO_PaCO2   <dbl> <matrix[25 x 1]>
$ PreECMO_pH      <dbl> <matrix[25 x 1]>
$ PreECMO_BE      <dbl> <matrix[25 x 1]>
$ PreECMO_Lactate <dbl> <matrix[25 x 1]>
$ PreECMO_NAdose  <dbl> <matrix[25 x 1]>
$ PreECMO_MAP     <dbl> <matrix[25 x 1]>
$ PreECMO_Creatinine <dbl> <matrix[25 x 1]>
$ PreECMO_Urea    <dbl> <matrix[25 x 1]>
$ PreECMO_CK      <dbl> <matrix[25 x 1]>
$ PreECMO_Bilirubin <dbl> <matrix[25 x 1]>
$ PreECMO_Albumin <dbl> <matrix[25 x 1]>
$ PreECMO_CRP     <dbl> <matrix[25 x 1]>
$ PreECMO_Fibrinogen <dbl> <matrix[25 x 1]>
$ PreECMO_Ddimer  <dbl> <matrix[25 x 1]>
$ PreECMO_ATIII   <dbl> <matrix[25 x 1]>
$ PreECMO_Leukocytes <dbl> <matrix[25 x 1]>
$ PreECMO_Platelets <dbl> <matrix[25 x 1]>

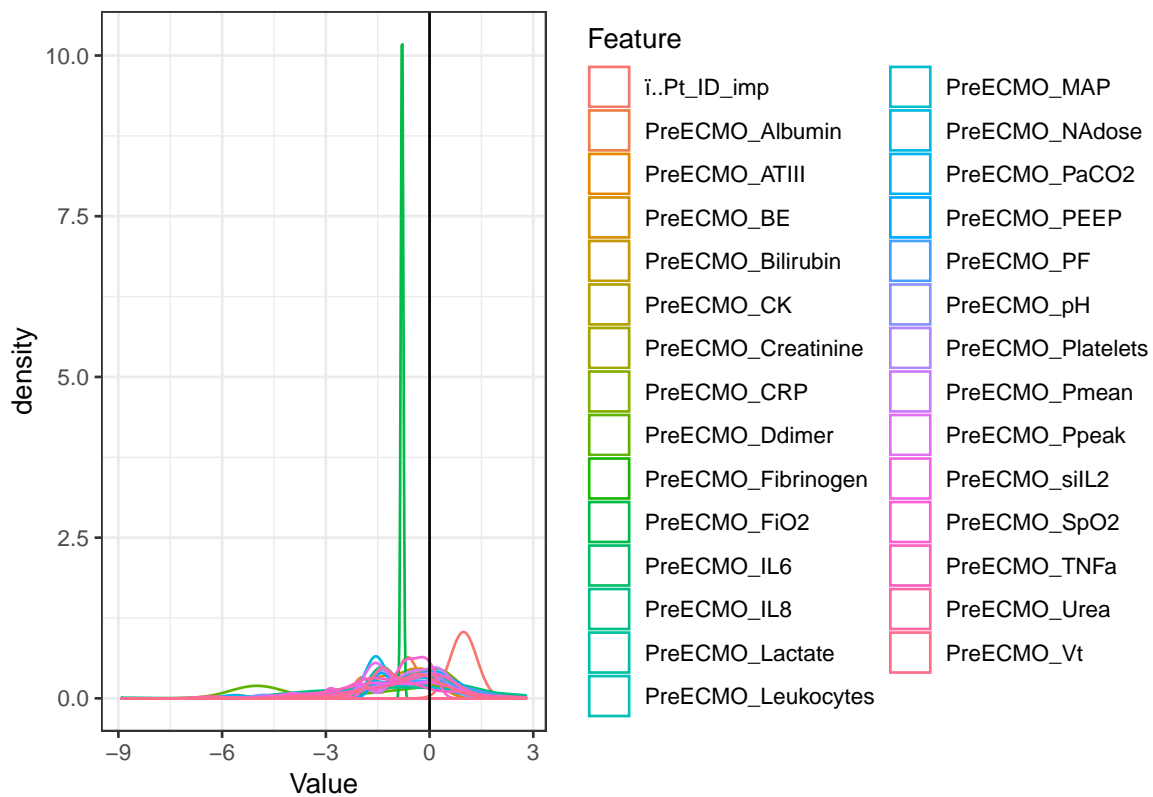
```

```

$ PreECMO_TNFa      <dbl> <matrix[25 x 1]>
$ PreECMO_IL6       <dbl> <matrix[25 x 1]>
$ PreECMO_IL8       <dbl> <matrix[25 x 1]>
$ PreECMO_siIL2     <dbl> <matrix[25 x 1]>
$ i..Pt_ID_imp      <dbl> <matrix[25 x 1]>
$ Gender_imp        <dbl> <matrix[25 x 1]>

```





Training/Test Data

Dropping NAs from dataset

```
[1] 314
```

Call:

```
glm(formula = ECMO_Survival ~ ., family = binomial(link = "logit"),
     data = train.ARDS)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.11299	0.01256	0.20365	0.50838	1.66856

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	7.459e-01	1.166e+00	0.640	0.52224
ï..Pt_ID	6.577e-04	7.042e-04	0.934	0.35031
Gender1	1.684e-01	7.360e-01	0.229	0.81908
Indication2	1.135e+00	8.017e-01	1.416	0.15689
Indication3	1.345e+00	1.307e+00	1.029	0.30354
Indication4	1.256e+00	1.655e+00	0.759	0.44776
Indication5	-1.461e+00	1.114e+00	-1.311	0.19000

Indication6	1.646e+01	1.581e+03	0.010	0.99169
Indication7	5.297e-01	1.100e+00	0.482	0.63000
Age	-1.085e+00	3.756e-01	-2.888	0.00388 **
PreECMO_RR	-2.376e-01	3.484e-01	-0.682	0.49520
PreECMO_Vt	3.141e-01	3.721e-01	0.844	0.39868
PreECMO_FiO2	3.898e-01	4.905e-01	0.795	0.42681
PreECMO_Ppeak	-1.130e+00	4.727e-01	-2.389	0.01687 *
PreECMO_Pmean	7.336e-01	6.227e-01	1.178	0.23878
PreECMO_PEEP	-1.887e-01	5.087e-01	-0.371	0.71070
PreECMO_PF	8.158e-01	5.133e-01	1.589	0.11199
PreECMO_SpO2	-2.124e+00	7.278e-01	-2.919	0.00352 **
PreECMO_PaCO2	3.202e-02	7.263e-01	0.044	0.96483
PreECMO_pH	-2.309e-01	7.183e-01	-0.321	0.74789
PreECMO_BE	-4.730e-01	5.845e-01	-0.809	0.41844
PreECMO_Lactate	-1.316e+00	5.334e-01	-2.467	0.01362 *
PreECMO_NAdose	-1.859e+00	5.764e-01	-3.226	0.00126 **
PreECMO_MAP	1.740e-01	3.096e-01	0.562	0.57412
PreECMO_Creatinine	4.600e-01	5.693e-01	0.808	0.41907
PreECMO_Urea	-1.766e-01	4.272e-01	-0.413	0.67936
PreECMO_CK	4.441e-01	4.518e-01	0.983	0.32560
PreECMO_Bilirubin	3.551e-01	4.558e-01	0.779	0.43603
PreECMO_CRP	4.630e-01	4.280e-01	1.082	0.27938
PreECMO_Fibrinogen	-1.365e+00	5.002e-01	-2.728	0.00637 **
PreECMO_Ddimer	-1.467e-01	4.432e-01	-0.331	0.74073
PreECMO_ATIII	-2.063e-01	2.586e-01	-0.798	0.42493
PreECMO_Leukocytes	5.937e-01	4.333e-01	1.370	0.17069
PreECMO_Platelets	-5.491e-02	3.347e-01	-0.164	0.86969
PreECMO_TNFa	1.099e-01	2.507e-01	0.438	0.66121
PreECMO_IL6	-1.285e-01	5.114e-01	-0.251	0.80155
PreECMO_IL8	5.989e-01	5.304e-01	1.129	0.25886
PreECMO_siIL2	-2.470e-01	6.808e-01	-0.363	0.71672

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 169.07 on 156 degrees of freedom
Residual deviance: 102.11 on 119 degrees of freedom
AIC: 178.11

Number of Fisher Scoring iterations: 15

A quick note about the `plogis` function: The `glm()` procedure with `family="binomial"` will build the logistic regression model on the given formula. When we use the `predict` function on this model, it will predict the $\log(\text{odds})$ of the Y variable. This is not what we ultimately want because, the predicted values may not lie within the 0 and 1 range as expected. So, to convert it into prediction probability scores that is bound between 0 and 1, we use the `plogis()`. For more info see (blog on logistic regression)[<http://r-statistics.co/Logistic-Regression-With-R.html>].

Optimal Prediction Probability Cutoff for the Model

The default cutoff prediction probability score is 0.5 or the ratio of — in the training data. But sometimes, tuning the probability cutoff can improve the accuracy in both the development and validation samples. The `InformationValue::optimalCutoff` function provides ways to find the optimal cutoff to improve the prediction of —, —, both — and — and o reduce the misclassification error. Let's compute the optimal score that minimizes the misclassification error for the above model.

Model Diagnostics

```
[1] 0.6923077
      0      1
0.3333333 0.8000000
[1] 0.6923077
      0      1
0.3333333 0.8000000
```

Imputed Dataset

```
Call:
glm(formula = ECMO_Survival ~ ., family = binomial(link = "logit"),
    data = train.ARDS)
```

```
Deviance Residuals:
      Min       1Q   Median       3Q      Max
-2.8586  -0.4973   0.3646   0.7091   2.1184
```

```
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.060050   0.829839  -0.072  0.942313
i..Pt_ID      0.001466   0.000497   2.949  0.003189 **
Gender1      -0.799568   0.412103  -1.940  0.052354 .
Indication2  -0.233507   0.654411  -0.357  0.721227
Indication3   0.177572   0.946911   0.188  0.851246
Indication4   1.821782   1.318526   1.382  0.167070
Indication5  -0.744931   0.771846  -0.965  0.334480
Indication6  -1.601984   1.111825  -1.441  0.149624
Indication7  -0.406773   0.852536  -0.477  0.633267
Age          -0.434630   0.221073  -1.966  0.049298 *
PreECMO_RR   -0.335603   0.256910  -1.306  0.191449
PreECMO_Vt   -0.111969   0.229660  -0.488  0.625874
PreECMO_FiO2  0.038171   0.318198   0.120  0.904515
PreECMO_Ppeak 0.098373   0.293356   0.335  0.737371
PreECMO_Pmean -0.515321   0.343718  -1.499  0.133808
PreECMO_PEEP -0.001138   0.292004  -0.004  0.996891
PreECMO_PF   -0.038376   0.368887  -0.104  0.917144
PreECMO_SpO2 -0.538799   0.257553  -2.092  0.036439 *
```

PreECMO_PaCO2	0.883239	0.494137	1.787	0.073867	.
PreECMO_pH	1.238998	0.641423	1.932	0.053404	.
PreECMO_BE	-1.029121	0.454843	-2.263	0.023661	*
PreECMO_Lactate	-0.096827	0.243589	-0.398	0.690996	
PreECMO_NAdose	0.113347	0.183294	0.618	0.536320	
PreECMO_MAP	0.510472	0.248319	2.056	0.039810	*
PreECMO_Creatinine	-0.463896	0.289247	-1.604	0.108757	
PreECMO_Urea	0.047146	0.221012	0.213	0.831078	
PreECMO_CK	0.102874	0.191989	0.536	0.592075	
PreECMO_Bilirubin	0.071551	0.199401	0.359	0.719722	
PreECMO_CRP	0.015786	0.243725	0.065	0.948358	
PreECMO_Fibrinogen	0.409629	0.280282	1.461	0.143881	
PreECMO_Ddimer	-0.653350	0.178722	-3.656	0.000256	***
PreECMO_ATIII	0.085969	0.413616	0.208	0.835349	
PreECMO_Leukocytes	0.523626	0.270487	1.936	0.052884	.
PreECMO_Platelets	-0.013206	0.289883	-0.046	0.963665	
PreECMO_TNFa	-0.218696	0.182107	-1.201	0.229780	
PreECMO_IL6	0.217920	0.253810	0.859	0.390563	
PreECMO_IL8	-0.293109	0.205400	-1.427	0.153575	
PreECMO_siIL2	0.245615	0.262684	0.935	0.349778	

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 333.19 on 255 degrees of freedom
Residual deviance: 221.28 on 218 degrees of freedom
AIC: 297.28

Number of Fisher Scoring iterations: 5

Model Diagnostics

```
[1] 0.6640625
      0      1
0.500000 0.744186
[1] 0.6640625
      0      1
0.500000 0.744186
```