

Online Supplement:

Title: Biomarkers of Endothelial Dysfunction in Sepsis Associated-Acute Kidney Injury: A Risk Stratified Analyses from a Prospective Observational Cohort of Critically Ill Children.

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R code for PERSEVERENCE CART Tree to predict D3 Sepsis Associated-Acute Kidney Injury among children with septic shock.

```
Install.package(dplyr)
library(dplyr)
```

```
#load in you CSV file
data <- ***
```

```
#add the terminal node designations
```

```
data <- data %>% mutate(Terminal_Node =
  case_when(
    data$`Tie-2` <= 28599 & data$`D1 SAAKI` <= 0 & data$`Tie-2` <= 11070 ~ "TN1",
    data$`Tie-2` <= 28599 & data$`D1 SAAKI` <= 0 & data$`Tie-2` > 11070 ~ "TN2",
    data$`Tie-2` <= 28599 & data$`D1 SAAKI` <= 1 & data$`Ang-2/Tie-2` <= 0.35 ~ "TN3",
    data$`Tie-2` <= 28599 & data$`D1 SAAKI` >= 1 & data$`Ang-2/Tie-2` > 0.35 & data$`sTM` <=
    11830 ~ "TN4",
    data$`Tie-2` <= 28599 & data$`D1 SAAKI` >= 1 & data$`Ang-2/Tie-2` > 0.35 & data$`sTM` >
    11830 ~ "TN5",
    data$`Tie-2` > 28599 ~ "TN6"))
```

```
#now add the D3 SA-AKI risk
```

```
data <- data %>% mutate(D3_SAAKI_Prob=
  case_when(data$Terminal_Node == "TN1" ~ "0.714",
    data$Terminal_Node == "TN2" ~ "0.118",
    data$Terminal_Node == "TN3" ~ "0.333",
    data$Terminal_Node == "TN4" ~ "0.720",
    data$Terminal_Node == "TN5" ~ "1.000",
    data$Terminal_Node == "TN6" ~ "0.087",))
```

```
#now you can add the mortality risk class.
```

```
data <- data %>% mutate(D3_SAAKI_PREDICTED_Class =
  case_when(data$D3_SAAKI_Prob >= 0.714 ~ "HIGH",
    TRUE ~ "LOW"))
```