Online Supplement:

Title: Prognostic and Predictive Value of Endothelial Dysfunction Biomarkers in Sepsis-Associated Acute Kidney Injury: Risk Stratified Analysis from a Prospective Observational Cohort of Pediatric Septic Shock.

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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"))
```