**Multimedia Appendix 6.** Technical details of decision tree based modeling.

First, a general technique of bootstrap aggregating (bagging) was applied for building multiple decision trees by repeatedly and randomly resampling training cohort with replacement, and voting the trees for a consensus prediction. Second, the survival trees were grown based on the randomly selected predictors via Log-rank survival splitting rule on each survival tree node, which maximizes survival differences across daughter nodes.

$$F_{x,c} = i = 1 N_{t_i - Y_i, 1 Y_i = 1 Y_i - Y_i, 1 Y_i - di}$$

Here, \( c \) is the split value for predictor \( x \); \( di, j \) and \( Yi, j \) for node \( h \) equal the number of patient who visited ED and had no ED visit before time \( ti \) in next 6 months period for daughter nodes \( j = 1, 2 \). Hence, \( Yi, 1 = \# T_i \geq ti \text{ & } x \leq c \) and \( Yi, 2 = \# T_i \geq ti \text{ & } x > c \), where \( Ti \) is ED visit time in next 6 month for the individual \( l \). The value \( F_{x,c} \) is the measure of node separation, the greater difference between case and control groups and the better the split for the predictor is. Therefore, the optimized predictor \( x^* \) and split value \( c^* \) at node \( h \) is determined by maximizing the \( F_{x^*,c^*} \) such that \( F_{x^*,c^*} \geq F_{x,c} \) for all \( x \) and \( c \).

Third, an ensemble cumulative hazard estimate by combining information from the survival trees so that each individual will be assigned one estimate.

$$H_{ht} = (t_i \leq t_d l h \ Y_l h)$$

Where \( H_{ht} \) is the cumulative hazard estimate for node \( h \), \( t_d l h \) is the distinct ED visit times in node \( h \), \( d_l h \) and \( Y_l h \) represent the number of patients who visited ED and had no ED visit before time \( t_d l h \). \( H_{ht} \) was computed for terminal node for each predictor \( x_i \) for individual sample \( i \) drop down into in the tree. Therefore,

$$H_{t|x_i} = H_{ht}, \text{ if } x_i \in h$$

To compute individual estimate for all trees, ensemble average for all tree cumulative hazard estimate score.

$$H_{e|x} = 1 n_{tree} \ b = 1 n_{tree} H b t|x_i$$

Here, \( b \) denotes the individual tree and \( n_{tree} \) is the number of trees in survival forest.