Machine learning for data analysis Assignment 1 Running a classification tree

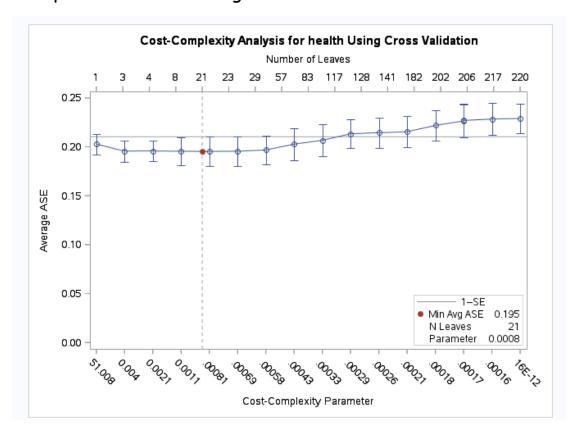
I chose addhealth as my data set and general health (H1GH1) as response variable. H1GH1 is a categorical variable with 5 levels. So I collapsed it into two levels and create a new variable named health. Health equal 1 means this participant is healthy, while health equal 0 means this participant is not healthy.

	The H	HPSPLIT F	Procedu	ire						
	Performance Information									
	Execution	Single-Machine								
	Number of Threads		2							
	Data Access Information									
	Data	Engine	Role	Path						
	WORK.NEW	V9	Input	Or	Client					
	М	odel Infor	mation							
Split Criterion Used					Entropy					
Pruning Method				Cost-Complexity						
Subtree Evaluation Criterion				Cost-Complexity						
Number of Branches				2						
Maxi	imum Tree Dep	sted	10							
Maximum Tree Depth Achieved					10					
Tree Depth					6					
Number of Leaves Before Pruning					330					
Number of Leaves After Pruning					15					
Model Event Level						0				
	Number of Observations Rea				6337					
	Number of C	d	4117							

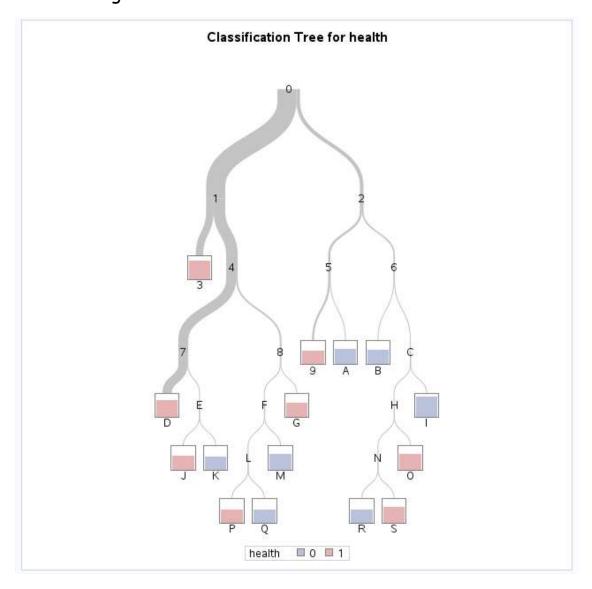
This is the result of *hpsplit* procedure. I used *prune* costcomplexity statement in my code to pruning a large tree

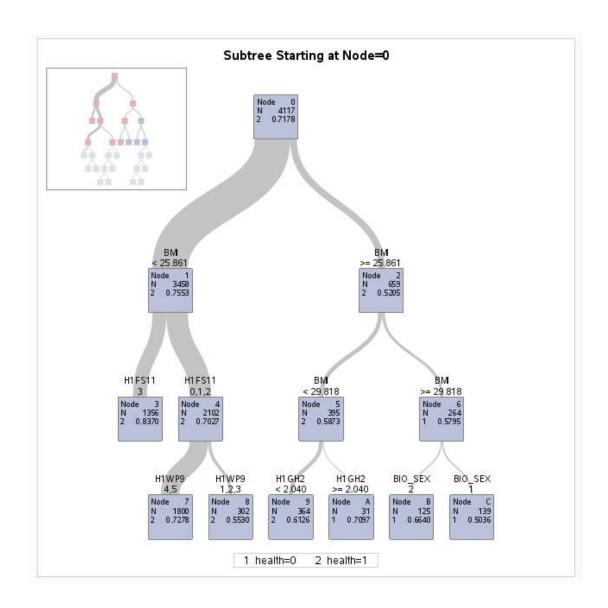
into a smaller tree. As we can see in the model information table, the number of leaves before pruning is 330, while the number of leaves after pruning is only 15, which is much smaller than 330. This result indentifies the function of prune statement.

This plot shows the average line for the standard error.

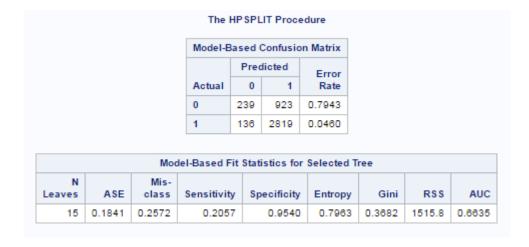


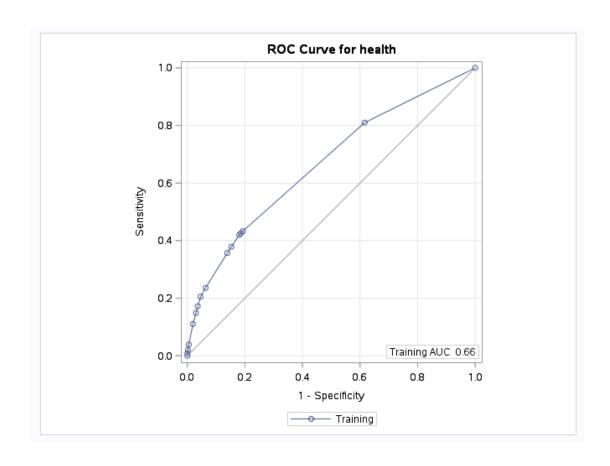
This is the general model and the final classification tree.





This shows how well the tree fit the model.





This table shows the most important variables to determine the response variable health. It shows BMI (body mass index) contributes the most to the health.

	Variable Im	portance			
	Variable	Tra			
Variable	Label	Relative	Importance	Count	
ВМІ		1.0000	8.5911	3	
H1FS11	feeling happy	0.6809	5.8493	3	
H1GH2	frequency of headache	0.5078	4.3625	4	
H1WP9	how close with mother	0.4627	3.9753	1	
H1GI20	grade	0.2864	2.4607	2	
BIO_SEX	gender	0.2142	1.8403	1	

Code:

```
1 LIBRAME mydata "/courses/d1406aeSba27fe300" access=readonly;
2 data new; set mydata.addhealth_pds;
   4 if HIGI20=97 then delete; if HIGI20=99 then delete; if HIGI20=96 then delete;
S if HIGI20=98 then delete;
Sif HiGH20-98 then delete;

81f HiGH26 then HiGH1=,; if HiGH28 then HiGH2=.;

71f HiGH26 then HiGH2=.; if HiGH288 then HiGH2=.;

81f HiGH266 then HiGH6-.; if HiGH688 then HiGH6-.;

91f HiGH59A-96 then HiGH59A-.; if HiGH59A-98 then HiGH59A-.; if HiGH59A-99 then HiGH59A-.;

101f HiGH59B-96 then HiGH59B-.; if HiGH59B-98 then HiGH59B-.; if HiGH59B-99 then HiGH59B-.;

111f HiGH60-996 then HiGH60-.; if HiGH50-998 then HiGH60-.; if HiGH60-999 then HiGH50B-.;

121f HiFS11-6 then HiFS11-.; if HiFS11-8 then HiFS11-.;
13 if Himp3=6 then Himp9=,; if Himp9=7 then Himp9=,;
14 if Himp9=8 then Himp9=,; if Himp9=9 then Himp9=,;
15 if Himp13=6 then Himp13=,; if Himp13=7 then Himp13=,;
16 if Himp13=8 then Himp13=,; if Himp13=9 then Himp13=,;
 18
 19 HIGH59-HIGH59A * 12 + HIGH59B;/*add a new variable*/
20 BMI=HIGH60 * 0.454/(HIGH59 * 0.0254)**2;/*body mass index*/
 22 if HIGH1 c= 2 then health = 1;
23 else health = 0;
 25 label AID="respondent ID"
26 BIO_SEX="gander"
27 H1G120="grade"
                        H1GH1="general health"
                       HIGH1="general health"
HIGH2="frequency of headache"
HIGH6="frequency of feeling weak"
HIGH59A="height in feet"
HIGH59B="height in inch"
HIGH60="weigt (pound)"
HIF311="feeling happy"
HIW99="how close with mother"
 29
30
  31
  32
  33
  34
                       HIWP13="how close with father"
HIGH59="height (inch)";
  36
  38
  39
  40 proc sort; by AID;
  43 ods graphics on:

46 proo hpsplit seed = 10000;

45 class health BIO_SEX HIFS11 HIMPS HIMP13;

46 model health = BIO_SEX BMI HIFS11 HIMPS HIMP13 HIGI20 HIGH2;
  47 grow entropy;
48 prune costcomplexity;
 49 run;
50
```