spore-print-color population

## habitat class

Test mode:10-fold cross-validation

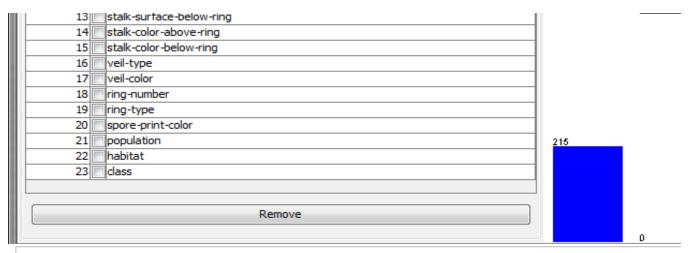
=== Classifier model (full training set) ===
J48 pruned tree
----odor = a: e (332.0)
odor = c: e (0.0)
odor = f: e (0.0)
odor = l: e (323.0)
odor = m: e (0.0)
odor = n: e (183.0)
odor = p: p (95.0)
odor = s: e (0.0)

What do you think about this tree? Are you satisfied with the result? Why or why not?

odor = y: e (0.0)

Preliminarily, this tree looks good, but it appears to be over fit. Every possible category seems to have a node, which is why I am apprehensive to how this would perform on non-training data.

2. Remove the "odor" attribute and reconstruct the tree. What is this second tree? Current relation Selected attribute Relation: mushroom Name: cap-shape Instances: 933 Attributes: 23 Missing: 0 (0%) Attributes Label 1 b None Invert Pattern 2 c 3 f No. Name 4 k cap-shape 5 s 2 cap-surface 6 x 3 cap-color 4 bruises? 5|| odor gill-attachment 6 7 gill-spacing 8 gill-size 9 gill-color 10 stalk-shape Class: class (Nom) 11 stalk-root 12 stalk-surface-above-ring The ch



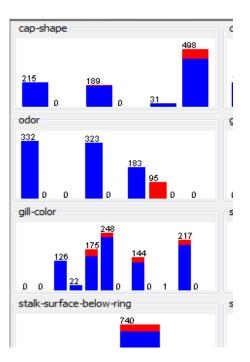
Preliminary Analysis: In this data set there are 933 examples represented in 23 attributes. Some attributes are

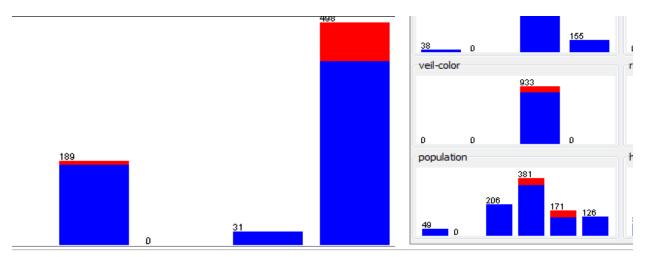


/hat do you think about this tree

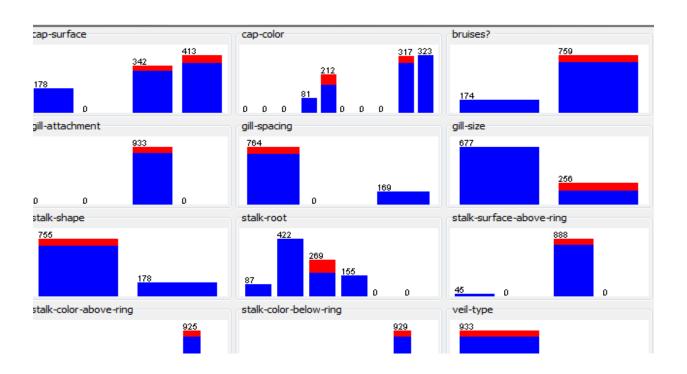
result? Why

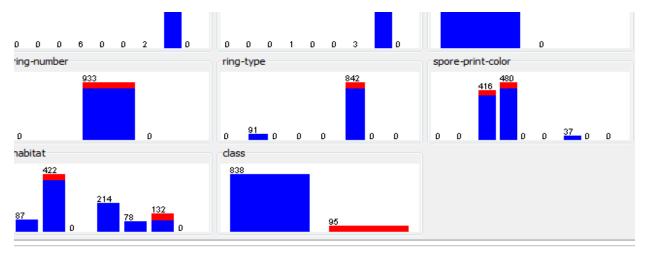
Distinct: 4	Type: Nominal Unique: 0 (0%)
	Count
	215
	0
	189
	0
	31
	498
	▼ Visualize All
nosen attribute will also be	used as the class attribute when a filter is





binary, like bruises, gill-size, veil - type, stalk shape, and class, ye other attributes are categorical or con-





tinuous. I assume that the class attribute is the identifier of poisonous and non-poisonous. Visually, it