AA228 - Decision Making Under Uncertainty Project 1

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Introduction: Bayesian Structure Learning is a method with which we can find the Bayesian network given the data.

Algorithm Implementation:

The algorithm was broken down into below components:

- 1) Initialize an unconnected graph(initial_G) with all the nodes from the given data set.
- 2) Find m_ijk for graph (initial_G). Refer to function find_m_ijk(<data>, <Graph>) in python code.
- 3) Compute Bayesian score for the graph (initial_G) as given by equation below:

$$\sum_{i=1}^{n} \sum_{j=1}^{q_i} \ln \left(\frac{\Gamma(\alpha_{ij0})}{\Gamma(\alpha_{ij0} + m_{ij0})} \right) + \sum_{k=1}^{r_i} \ln \left(\frac{\Gamma(\alpha_{ijk} + m_{ijk})}{\Gamma(\alpha_{ijk})} \right)$$

- a. As the given prior is uniform so the ln(P(G)) term is same for all iterations so it can be omitted.
- b. The alpha_ijk are '1' again because of uniform prior.
- c. alpha_ij0 and m_ij0 are calculated in this iteration itself.

Refer to function *find_bayesian_score(<Graph>, <m_ijk>)* in python code.

- 4) For each node in graph(initial_G):
 - a. Connect a parent to that node. This becomes graph **G**
 - i. Check if graph is cyclic, if not then compute Bayesian score for this new graph(**G**) similar to step 2 & 3.
 - ii. If Bayesian score is better than previous recorded score, update the graph (initial_G) with new optimal graph(G) that will be used for next node iteration.
 - b. Once all nodes are traversed the graph(**G**) will be the final optimal graph and Bayesian score of this graph(**G**) will be the final Bayesian score.

Refer to bottom part of function *compute(infile, outfile)* where graph iterations are carried out.

find m ijk() function:

In this function, for each data sample, parental values of a give node "i" are stored as list (*G.nodes[i]["list_values_at_j"])*) in the "i" node attribute of graph. The indices of the list that stores parental values gives "j". The values of given node 'i' are stored as a list (*G.nodes[i]["value_of_ri"] = []*) in the "i" node attribute of graph. The indices of this list gives "k".

Once for all the data samples the "j" & "k" node information is stored as node attributes. Based on this information we do sample loop iteration(for each sample) to find **m_ijk[index]** which is count of m_ijk[index] based on the "j" & "k" node attributes.

compute(infile, outfile) function:

In the bottom part of this function are the loops that iterate over node list of a given graph and finds the Bayesian score. The 1st loop acts as **Local Directed Graph Search** (algorithm 2.9 from DMU textbook). This loop basically adds a parent to existing best graph available and finds the Bayesian score. If score is better the graph is updated, if not continues.

The 2nd loop and 3rd loop is the **K2Search** (algorithm 2.8 from DMU textbook). The algorithm is described in Step 4 above.

<u>Improvements in the code that must be explored:</u> Have a 4th loop which does **K2Search,** starting at a different node as a starting point. Do this for all nodes in the graph and pick the graph with best Bayesian score.

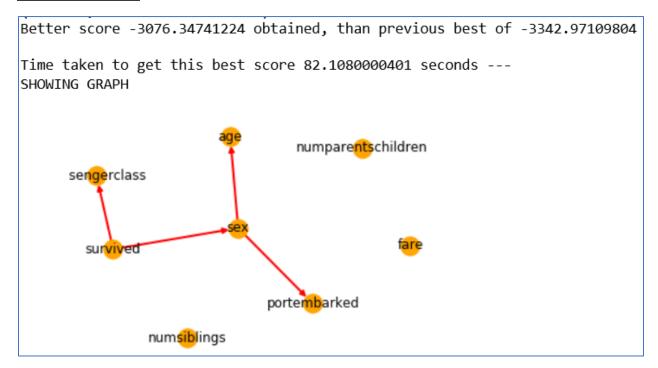
Explore mechanism where m_ijk can be efficiently calculated.

Runtime and Best Bayesian Score Table

<u>Data Set</u>	Best Bayesian Score	Runtime (seconds)
small.csv	-3076.34	82.10
medium.csv	-43133.74	150.55
Large.csv	-426340.15	16027 and running

Graph Outputs:

Data Set: small.csv



Data Set: medium.csv

Better score -43133.7470064 obtained, than previous best of -43987.2344312

Time taken to get this best score 150.558000088 seconds --SHOWING GRAPH

Chlorides
sulphates
alcohol
citricacid
density
fixedacid
ulfurdioxide residualsugar
freesulfurdioxide
volatileacidity
quality

ph

DataSet: large.csv

