CaMML MB prior test

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```r
source('~/PhDProjects/RStudioProjects/local2global/scripts/load_libraries.R')
```

```
## Loading required package: causalbn

## Loading required package: bnlearn

##
## Attaching package: 'bnlearn'

## The following object is masked from 'package:stats':
##
##     sigma

## Loading required package: entropy

##
## Attaching package: 'entropy'

## The following object is masked from 'package:bnlearn':
##
##     discretize

## Loading required package: reshape2

## Loading required package: ggplot2

## Loading required package: Rgraphviz

## Loading required package: graph

## Loading required package: BiocGenerics

## Loading required package: parallel

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB

## The following object is masked from 'package:bnlearn':
##
##     score

## The following objects are masked from 'package:stats':
##
##     IQR, mad, xtabs

## The following objects are masked from 'package:base':
##
##     anyDuplicated, append, as.data.frame, cbind, colnames,
##     do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##     grepl, intersect, is.unsorted, lapply, lengths, Map, mapply,
```

```
##      match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##      Position, rank, rbind, Reduce, rownames, sapply, setdiff,
##      sort, table, tapply, union, unique, unsplit, which, which.max,
##      which.min

##
## Attaching package: 'graph'

## The following objects are masked from 'package:bnlearn':
##
##      degree, nodes, nodes<-

## Loading required package: grid

## Loading required package: magic

## Loading required package: abind

## Loading required package: expm

## Loading required package: Matrix

##
## Attaching package: 'expm'

## The following object is masked from 'package:Matrix':
##
##      expm

## Loading required package: gtools

## Loading required package: readr

## Loading required package: networkD3

## dirichletMultinomial.R :
## findCMB.R :
## findMB.R :
## getCumSumMmlMD.R :
## getPCMB.R :
## logFactorial.R :
## mb2stage.R :
## mbAccuracy.R :
## mmlCPT_fast.R :
## mmlCPT.R :
## mmlCPTRevised.R :
## mmlMultinomialDirichlet.R :
## mmlPC.R :
## multiParentsComputation.R :
## nodeToIndex.R :
## numeric2Nominal.R :
## proftable.R :
## singleParentComputation.R :
## symmetryCorrection.R :
## generateCPTsWithAsymmetricDir.R :
## randAdjmtx.R :
## randCPTs.R :
## randDag.R :
## randSeed.R :
## checkArc.R :
```

```
## computeRatio.R :
## cpts2dag.R :
## dagIsom.R :
## editDistDags.R :
## estProb.R :
## findCollider.R :
## isDag.R :
## learnBN.R :
## makePaString.R :
## matrix2dag.R :
## netica2bnlearn.R :
## parentsList2BN.R :
## powerset.R :
## threeWayInteraction.R :
## fisherMatrix.R :
## getIndicator.R :
## getInteractData.R :
## getInteractionIndices.R :
## intersectIndices.R :
## logDeterminant.R :
## makeFormula.R :
## mmlLogit.R :
## mmlLogit2ndOrder_addOneTermEachTime.R :
## mmlLogit2ndOrder_noParameterPrior.R :
## mmlLogit2ndOrder_revised1.R :
## mmlLogit2ndOrder_revised2.R :
## mmlLogit2ndOrder.R :
## negLogLike.R :
## getDataInfo.R :
## mbBackwardElemination.R :
## mbForwardSelection_fast.R :
## mbForwardSelection.R :
## mbForwardSelectionForMML2ndOrderLogit.R :
## mbForwardSelectionUsingMMLMultinomialDirichlet.R :
## mbGreedySearchNonDeterministic.R :
## mbGreedySearchWithLookAhead.R :
## mbSimulatedAnnealing.R :
## addArcs_greedy.R :
## arcCount.R :
## arcPrior.R :
## cammlPrior.R :
## computeCI.R :
## computeMMLMatrix.R :
## count2Prior.R :
## cpdag2dag.R :
## dfs_cycle.R :
## enumerateMBPTs.R :
## enumWithNoSp.R :
## extractArcs.R :
## featureUncertainty.R :
## find_bidirected_arcs.R :
## format_camml_prior.R :
## get_arcs.R :
## isDag.R :
```

```
## learnMBPT.R :
## mbEditDist.R :
## mBlkt.R :
## mbLocalStr.R :
## mergeDags.R :
## mergeMBPTs.R :
## mmlDag_fast.R :
## mmlDag.R :
## nMBPTs.R :
## polytree_exhaustive.R :
## randPolytree.R :
## refineMergedMBPT.R :
## sa.R :
## strAccuracy.R :
## string2numeric.R :
## substituteVar.R :
## txt2csv.R :
## varLevels.R :
```

Generate models and data

```r
seed = randSeed()
set.seed(seed)
nvars = 15
maxPar = 3
maxArity = 3
beta = 1
n = 10000
dag = randDag(nvars, maxPar)
cpts = randCPTs(dag, maxArity, beta)
data = rbn(cpts, n)
name = paste0(c(nvars, maxPar, maxArity, beta, n, seed), collapse = "_")
write.csv(data, paste0("~/Experiments/CaMML/MB prior test/Data/", name, ".csv"), row.names = FALSE)
```

Get the Markov blanket of each node. Firstly, test camml by giving the connections in each mb. That is by telling camml the true arcs in dag.

```r
arcList = bnlearn::arcs(dag)
priors = rep(1, nrow(arcList))
text = "arcs {"
for (i in 1:nrow(arcList)) {
  text = paste(text, "\n", arcList[i, 1], "->", arcList[i, 2], priors[i], ";")
}
text = paste(text, "\n }")
write_file(text, paste0("~/Experiments/CaMML/MB prior test/Prior/", name, ".txt"))
```