jan2021

2024-10-27

1. Graphical Models (6 p) - Using the IC Algorithn

Overview of the IC Algorithm

The IC algorithm consists of three main steps:

1. *Skeleton Discovery*: Construct an undirected graph that represents dependencies between variables.
2. *Edge Orientation with V-Structures*: Identify causal directions by finding V-structures (patterns where A–> B <– C with no edge between A and C).
3. *Propagation of Orientation*: Further orient edges using rules to avoid cycles and preserve conditional independencies.
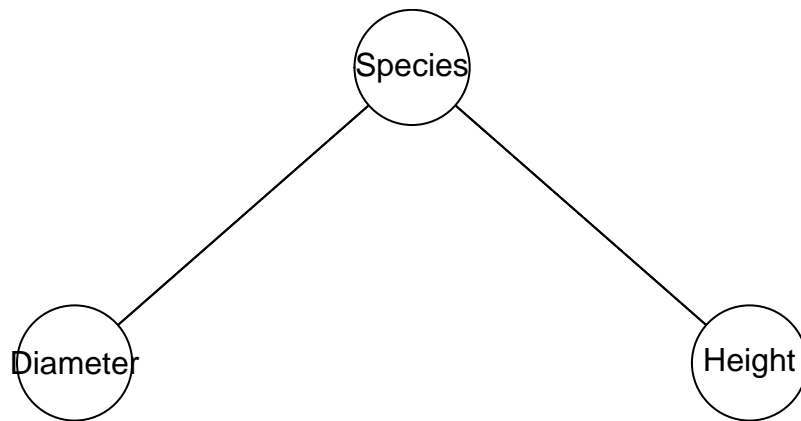
```r
library(bnlearn)

data("lizards")

lizardsnet<-model2network("[Species][Diameter|Species][Height|Species]") # True DAG
plot(lizardsnet)
```
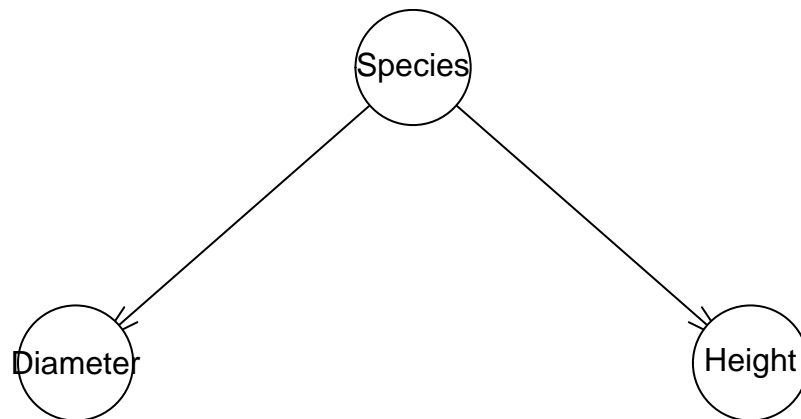


```r
plot(cpdag(lizardsnet)) # Plot the true pattern
```

```r
# Lets assume independence if p-value is > 0.05

# Skeleton discovery
ci.test(x = "Diameter", y = "Species", data = lizards)  # Keep edge D-S.
```

```
##
##  Mutual Information (disc.)
##
## data:  Diameter ~ Species
## mi = 12.606, df = 1, p-value = 0.0003845
## alternative hypothesis: true value is greater than 0
```
```r
ci.test(x = "Diameter", y = "Height", data = lizards)   # Remove edge D-H.
```

```
##
##  Mutual Information (disc.)
##
## data:  Diameter ~ Height
## mi = 0.60771, df = 1, p-value = 0.4357
## alternative hypothesis: true value is greater than 0
```
```r
ci.test(x = "Height", y = "Species", data = lizards)    # Keep edge H-S.
```

```
##
##  Mutual Information (disc.)
##
## data:  Height ~ Species
## mi = 10.405, df = 1, p-value = 0.001257
## alternative hypothesis: true value is greater than 0
```
```r
# The skeleton now looks like this:
currmod = model2network("[Species][Diameter|Species][Height|Species]")
plot(cpdag(currmod))

# Edge Orientation with V-Structures
# Investigate non adjacent vairables
ci.test(x = "Diameter", y = "Height", z = "Species", data = lizards) # Remove edge D-H.
```

```
##
##  Mutual Information (disc.)
##
## data:  Diameter ~ Height | Species
## mi = 2.0256, df = 2, p-value = 0.3632
```

```
## alternative hypothesis: true value is greater than 0
# Since this test showed that D and H are conditionally independent,
# we choose S as an unsheilded collider: D --> S <-- H


plot(model2network("[Diameter][Height][Species|Diameter:Height]"))
```