The **R** Package **stagedtrees** for Structural Learning of Stratified Staged Trees

Incontro di Statistica Matematica 27 - 28 January 2020 Sestri Levante

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• In the past twenty years graphical models have become popular for modelling (the absence of) conditional independences. **Bayesian networks** (BNs) are among the most used graphical models, with two main *R* packages: **bnlearn** by Scutari (2009) and **gRain** by Højsgaard (2012).

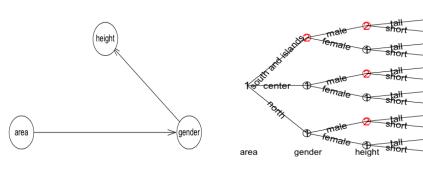
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- Unlike most of its competitors, the chain event graph (CEG) can capture
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 all asymmetric conditional independences in a unique graph, obtained by a
 coalescence over the vertices of an appropriately constructed probability tree,
 called staged tree. Here we consider staged trees for modelling categorical
 variables.
- Only one algorithm and one R package (ceg) are available in the literature for fitting staged trees to a dataset, besides the stagedtrees package presented here.

A first example

Let X = (area, gender, height) be a random vector taking values in a product space $\mathbb{X} = \times_{i=1}^{3} \mathbb{X}_{i}$, where \mathbb{X}_{i} is the sample space of the *i-th* component of X. On a dataset with 2804 units we have:



(a) Bayesian Network

(b) Staged Tree

Main Definitions: floret

Directed Tree

A directed tree $\mathcal{T}=(V,E)$ is a tree with vertex set V and edge set E, where each vertex except for the root has one parent only, all non-leaf vertices have at least two children and all edges point away from the root. For $v,v'\in V$ let $e=(v,v')\in E$ be the edge pointing from v to v'.

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Floret

For a non-leaf v, let $E(v) = \{v' \in V : (v, v') \in E\}$ and call $\mathcal{F}(v) = (v, E(v))$ a floret of the tree.

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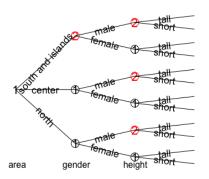
Floret Labels

Let Θ be a non-empty set of labels and $\theta: E \to \Theta$ be a function such that for any non-leaf $v \in V$ the labels in $\theta(E(v))$ are all distinct. The set $\theta(E(v))$ is denoted by θ_v and is called the set of floret labels.

Main Definitions: probability tree

Probability Tree

Assume $\Theta\subseteq [0,1]$. If $\sum_{e\in E(v)}\theta(e)=1$ for all non-leaves v, then $\mathcal T$ together with the θ_v 's is called a *probability tree* and $\theta_e=\theta(e)$ is the probability of the edge $e\in E$, i.e. the transition probability.



Main Definitions: staged tree

Staged Tree

A probability tree where for some $v,v'\in V$ the floret probability sets are equal, $\theta_v=\theta_{v'}$, is called *staged tree*. The vertices v and v' are said to be in the same stage and they have the same color in the graphical representation.

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Statistical Model

The leaf vertices, equivalently the root-to-leaf paths, give the sample space. The product of the edge probabilities on a root-to-leaf path gives its associated probability.

Main Definitions: stratified staged tree

X-compatible Probability Tree

Let X be a discrete random vector with sample space \mathbb{X} . A probability tree is called X-compatible if the sequential factorization

$$p(\mathbf{x}) = \prod_{i=2}^k p(x_i|\mathbf{x}^{i-1})p(x_1)$$

can be associated to the tree. Vertices associated to the same random variable are said to be in the same *stratum*.

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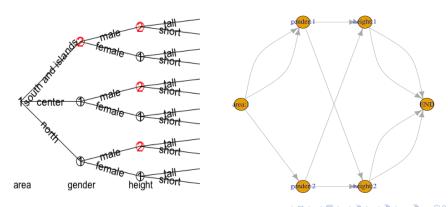
can be associated to the tree. Vertices associated to the same random variable are said to be in the same *stratum*.

Stratified Staged Tree

A staged tree is called *stratified* if it is **X**-compatible and if all non-leaf vertices in the same stage are in the same stratum.

From Stratified Staged Tree to CEG

- Staged trees are very expressive and flexible;
- as the number of variables increases, they cannot succinctly visualize their staging;
- partial solution: chain event graph (CEG).



R package **stagedtrees**

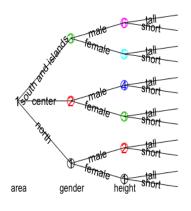
Various methods for fitting a stratified staged tree are implemented:

- hill-climbing,
- entropy,
- penalized log-likelihood (AIC and BIC index),
- distances and divergences among pair of discrete density distributions:
 - symmetrized Kullback-Leibler divergence,
 - symmetrized Renyi divergence,
 - L^p norm,
 - total variation,
 - Hellinger distance,
 - Bhattacharyya distance,
 - Chan-Darwiche distance,
 - user defined distance.

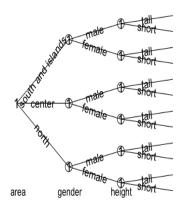
Stepwise Procedure

A backward and a forward procedure are implemented:

- backward: it starts from the saturated model, i.e. all edge labels are colored differently, and at each step it identifies the two nodes with the most marked independence relationship, until a stop criterion is reached:
- forward: it starts from the full-independence model, i.e. all edge labels have the same color, and at each step it identifies the two nodes with the most marked dependence relationship, until a stop criterion is reached.



(a) Saturated Model



(b) Full-Independence Model

R package stagedtrees

- Dataset format: data.frame, table, list.
- Initialize a sevt object: full or indep; order of variables can be specified with the order option;
 - full returns a sevt object where each vertex is in a different stage (a saturated model);
 - **indep** returns a sevt object where vertices in the same stratum are in the same stage (all variables are marginally independent of each other).

R package stagedtrees

Algorithms:

- hill-climbing:
 - hc.sevt
 - bhc.sevt
 - fbhc.sevt
 - bhcr.sevt

for which we can specify the *score* to maximize (AIC, BIC, ...), the max number of iterations *max_iter* and if we want to display or not each step of algorithm (*trace*);

• distance-based: **bj.sevt**, where the *distance* and the threshold *thr* have to be specified.

Querying the Estimated Model

- print and plot;
- **summary**: returns for each stratum all the estimated stages, the number of paths and observations starting from the root that arrives to each stage and their corresponding probability distributions;
- prob.sevt: computes the probability (its logarithm if log = TRUE) of any event of interest (x);
- compare.sevt: checks if two staged trees are equal and returns a plot where nodes in different stages are colored in red;
- sample.sevt: generates observations according to the stage probability distributions;
- predict: returns a vector of labels predicting the class specified by the option class over the observations specified by newdata; If prob = TRUE, it returns the probabilities (their logarithm if log = TRUE) of observing all the class labels;
- get_stage: returns the stage of a given path in a staged tree (object);
- get_path: returns the paths that starting from the root arrive at a given stage, for the specified variable (var) in a staged tree (object);
- ceg.sevt: constructs the CEG corresponding to a given staged tree (object);
- **subtree.sevt**: it constructs a subtree having as root the explicited *path*.

Creating a Staged Tree

```
devtools::install_github("gherardovarando/stagedtrees",
                         ref = "master", force = TRUE)
library(stagedtrees)
data("Titanic")
str(Titanic)
m.indep <- indep(Titanic, lambda = 0.5)
m.full <- full(Titanic, lambda = 0.5)
```

Structural Learning Algorithms

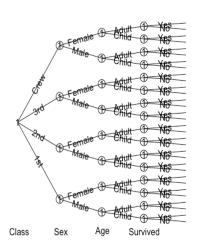
```
mod1 <- hc.sevt(m.indep)
mod2 <- bj.sevt(m.full, thr = 0.1)
mod2 <- stndnaming.sevt(mod2)

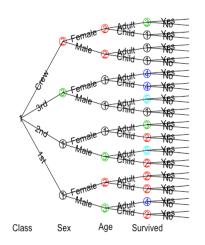
par(mfrow = c(1, 2))
plot(m.indep)
text(m.indep, y = -0.05, xlim = c(0.01, 1))
plot(mod1, col = "stages")
text(mod1, y = -0.05, xlim = c(0.01, 1))</pre>
```

Structural Learning Algorithms

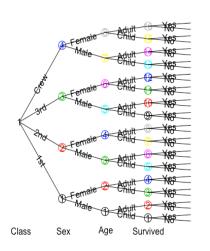
```
mod1 <- hc.sevt(m.indep)</pre>
mod2 \leftarrow bj.sevt(m.full, thr = 0.1)
mod2 <- stndnaming.sevt(mod2)</pre>
par(mfrow = c(1, 2))
plot(m.indep)
text(m.indep, y = -0.05, x \lim_{x \to 0} c(0.01, 1))
plot(mod1, col = "stages")
text(mod1, y = -0.05, x = c(0.01, 1))
plot(m.full)
text(m.full, y = -0.05, xlim = c(0.01, 1))
plot(mod2, col = "stages")
text(mod2, y = -0.05, x = c(0.01, 1))
```

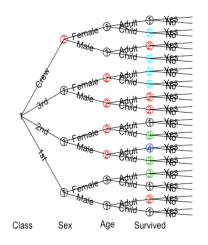
m.indep and mod1





m.full and mod2





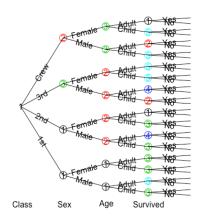
Re-fitting a Staged Tree

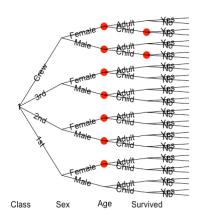
```
mod3 <- hc.sevt(mod2)

par(mfrow = c(1, 1))
plot(mod3, col = "stages")
text(mod3, y = -0.015, xlim = c(0.01, 1))

compare.sevt(mod1, mod3, plot = TRUE)
text(mod3, y = -0.015, xlim = c(0.01, 1))</pre>
```

mod3 and compare.sevt between mod1 and mod3



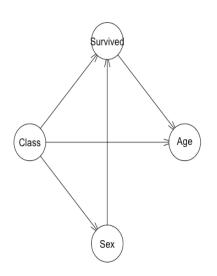


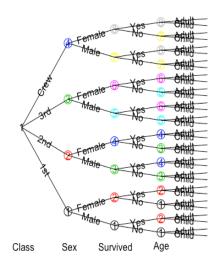
Bayesian Network as Staged Tree

```
tit <- as.data.frame(Titanic)
tit <- tit[rep(row.names(tit), tit$Freq), 1:4]

library(bnlearn)
mod.bn <- bnlearn::hc(tit)
plot(mod.bn)

mod.bn <- bn.fit(mod.bn, tit)
bn.tree <- fit.sevt(full(mod.bn, lambda = 0.5), data = tit)
plot(bn.tree)
text(bn.tree, y = -0.05, xlim = c(0.01, 1))</pre>
```





Refining a BN to a Staged Tree & Model Comparison

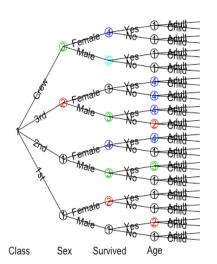
```
mod4 <- hc.sevt(bn.tree)</pre>
mod4 <- stndnaming.sevt(mod4)</pre>
results <- cbind(df = AIC(mod1, mod2, mod3, bn.tree, mod4)[, 1],
                logLik = c(mod1\$11, mod2\$11, mod3\$11, bn.tree\$11, mod4\$11),
                AIC = AIC(mod1, mod2, mod3, bn.tree, mod4)\lceil, 2\rceil,
                BIC = BIC(mod1, mod2, mod3, bn.tree, mod4)[, 2])
rownames(results) <- c("mod1", "mod2", "mod3", "bn.tree", "mod4")</pre>
#
           df logLik AIC
                                        BT(
# mod1 14 -5167.385 10362.77 10442.52
# mod2 12 -5192.397 10408.79 10477.15
# mod3 14 -5168.066 10364.13 10443.89
# bn.tree 23 -5162.628 10371.26 10502.28
# mod4 15 -5158.697 10347.39 10432.84
```

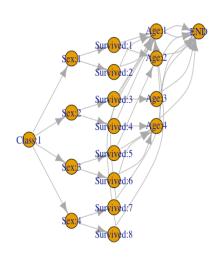
From Staged Tree to CEG

```
library(igraph)
ceg <- ceg.sevt(mod4)
A <- ceg2adjmat(ceg)
gr <- graph_from_adjacency_matrix(A)
lay <- layout.reingold.tilford(gr)

par(mfrow = c(1, 2))

plot(mod4)
text(mod4, y = -0.015, xlim = c(0.01, 1))
plot.igraph(gr, layout = -lay[, 2:1])</pre>
```

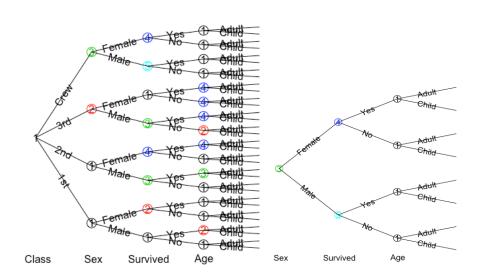




Querying the Model: subtree.sevt

```
subtree.crew <- subtree.sevt(mod4, path = c("Crew"))
plot(mod4)
text(mod4, y = -0.05, x = c(0.01, 1))
plot(subtree.crew, col = "stages")
text(subtree.crew, y = -0.05, x = c(0.01, 1))
summary(mod4)
```

mod4 and subtree.crew



Querying the Model: get_path and get_stage

```
get_path(mod4, var = "Survived", stage = "3")
    Class Sex
     2nd
           Male
# 5
     3rd Male
get_path(mod4, var = "Survived", stage = "4")
    Class
            Sex
           Female
     2nd
           Female
    Crew
get_path(mod4, var = "Age", stage = "1")
     Class
                         Survived
                Sex
      1st
               Male
                           No
      1st
            Female
                           No
      1st
             Female
                          Yes
# 5
       2nd
                Male
                           No
             Female
       2nd
                           No
# 13
                Male
     Crew
                           No
# 14
                Male
     Crew
                           Yes
# 15
     Crew
              Female
                           No
# 16 Crew
              Female
                           Yes
get_stage(mod4, path = c("Crew", "Female"))
# [1] "4"
```

Querying the Model: prob.sevt

```
prob.sevt(mod4, x = c(Class = "Crew", Sex = "Female"))
 Γ17 0.0104498
paths_grid <- expand.grid(mod4$tree[2:1])[, 2:1]</pre>
cbind(paths_grid,
     Stage = get_stage(mod4, paths_grid),
     Prob = round(prob.sevt(mod4, paths_grid), 4))
#
    Class
            Sex
                   Stage
                          Prob
# 1 1st Male 1
                         0.0869
# 2 1st Female 2 0.0608
# 3 2nd Male
                         0.0762
# 4 2nd Female
                         0.0533
          Male
# 5 3rd
                         0.2317
# 6 3rd
           Female
                         0.0891
# 7
    Crew
          Male
                         0.3916
         Female
# 8
    Crew
                    4
                         0.0104
```

Querying the Model: sample.sevt

```
set.seed(1234)
bootstrap <- sample.sevt(mod4, n = NROW(tit))
summary(tit[, names(mod4$tree)])
# Class
              Sex
                 Survived
                                   Age
# 1st :325 Male :1731 No :1490 Child: 109
# 2nd :285 Female: 470 Yes: 711 Adult:2092
# 3rd :706
# Crew: 885
summary(bootstrap)
# Class
              Sex
                   Survived Age
# 1st :312 Female: 487 No :1482 Adult:2087
# 2nd :268 Male :1714 Yes: 719 Child: 114
# 3rd :726
# Crew: 895
```

Querying the Model: predict

```
p1 <- predict(mod4, newdata = bootstrap,
              class = "Survived", prob = F)
# [1] No No No No Yes No
# Levels: No Yes
p2 <- predict(mod4, newdata = bootstrap,
              class = "Survived", prob = T)
# No
           Yes
# F1.7 0.77726218 0.2227378
# [2.] 0.84636664 0.1536334
# F3.7 0.84636664 0.1536334
# [4,] 0.84636664 0.1536334
# F5.7 0.02758621 0.9724138
# F6.7 0.84636664 0.1536334
p3 <- predict(mod4, newdata = bootstrap,
              class = "Survived", prob = T, loa = T)
# No
             Yes
# F1.7 -0.2519776 -1.50175990
# \[ \Gamma_1, \Gamma_0.1668026 \] \[ -1.87318632 \]
# F3.7 -0.1668026 -1.87318632
# F4.7 -0.1668026 -1.87318632
# [5,] -3.5904394 -0.02797385
# \[ \( \) \[ \] \ -0.1668026 \[ -1.87318632 \]
table(p1, bootstrap$Survived)
# p1 No Yes
# No 1465 451
# Yes
        17
              268
```

Conclusions

- stagedtrees is an R package which provides a free implementation of staged trees and CEGs structures.
- stagedtrees is designed to support users in staged tree modelling of categorical experimental data and analizying the learned models to untagle complex dependence structures. It provides a set of utility functions to perform descriptive statistics and basic inference procedures.
- Various structure learning algorithms for *stratified staged trees* are currently implemented.
- Exploring the model space of non-stratified trees lies in the exponential explosion of its size with the number of variables. Fast euristic model search procedures are currently investigated.

References

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