Forêts aléatoires pour variables structurées

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Contexte

Supervised learning: we are given a dataset $\mathcal{D}_n = \{(X_1, Y_1), \dots, (X_n, Y_n)\}$ where the pairs (X_i, Y_i) are *i.i.d* distributed as (X, Y) and such that

 $\triangleright \mathbf{X} = (X_1, \dots, X_d) \in \mathbb{R}^d \text{ (inputs)}$ $\triangleright \mathbf{Y} \in \mathcal{Y} \text{ (response variable) with}$ $- \mathcal{Y} = \mathbb{R} \text{ in regression,}$ $- \mathcal{Y} = \{1, \dots, K\} \text{ in classification } (k \in \mathbb{N}).$ **Supervised learning:** we are given a dataset $\mathcal{D}_n = \{(X_1, Y_1), \dots, (X_n, Y_n)\}$ where the pairs (X_i, Y_i) are *i.i.d* distributed as (X, Y) and such that

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→ Question: for each $\mathbf{x} \in \mathbb{R}^d$, predict the response $\hat{y} \in \mathcal{Y}$ *i.e.* find a predictor

 $\hat{h}: \mathbb{R}^d \to \mathcal{Y},$

such that $\hat{h}(\mathbf{x}_i) \approx y_i$, for i = 1, ..., n.

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→ Multiple approaches: SVM, random forests, boosting, CNN, etc.

Further assumption: we assume that

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Objective

Develop a random forest method to supervised problems in which ${\bf X}$ has a known group structure.

Gene expression data:



Reynier et al., (2011). Importance of correlation between gene expression levels: application to the type I interferon signature in rheumatoid arthritis. PloS one.

Spectrometry data:



Luabi et al., (2015). Non invasive blood glucose level measurement using nuclear magnetic resonance. Proceedings of the 8th IEEE GCC Conference and Exhibition.

Random forests





Random forests [Breiman, 2001] are a class of algorithms used to solve regression and classification problems

- Large applicability: used in many applied fields since they handle high-dimensional settings.
- Successful methods: good predictive power, can outperform state-of-the-art methods.





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- Successful methods: good predictive power, can outperform state-of-the-art methods.
- → A random forest = aggregation of many random decision trees.

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Prediction rule in each terminal node: mean value (regression) vs. the majory vote (classification). A splitting criterion: maximize the impurity decrease

$$\Delta I(j,\theta) = \mathrm{I}(t) - \left[p_{t_L(j,\theta)} \mathrm{I}(t_L(j,\theta)) + p_{t_R(j,\theta)} \mathrm{I}(t_R(j,\theta)) \right],$$

where

- $t_L(j,\theta) = \{ \mathbf{X} \in t | X_j \le \theta \}$ and $t_R(j,\theta) = \{ \mathbf{X} \in t | X_j > \theta \}$,
- I(t): impurity in node t,
- I(t_z): impurity in node $t_z(j, \theta)$, for $s \in \{L, R\}$,
- p_{t_z} : proportion of observations in t that fall into $t_z(j, \theta)$, for $z \in \{L, R\}$.

→ Several impurity functions (Gini/entropy for classification, variance for regression).

A stopping rule: no stopping rule, grow the maximal tree and then select of the *best* subtree.

- \triangleright A random forest = aggregation of many *random* decision trees.
- \triangleright Random forests algorithm = bagging + features sampling.



Phil Cutler







▷ At each node, preselect a subset of *mtry* variables eligible for splitting.



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Decision trees for grouped inputs

Decision tree are defined by

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Definition of a split based on a group *j*:

- ▷ Via a regularized LDA → Developement of Tree Penalized Linear Discriminant Analysis (TPLDA) [Poterie et al., 2019]
- ▷ Via a CART tree → Extension of CART for Grouped Inputs (CARTGI). [Poterie, 2018, Poterie et al., 202X]

We want to split t into

 $t_L(j, \theta) = \{ \mathbf{X} \in t | f_t^j(\mathbf{X}^j) \le \theta \}$ and $t_R(j, \theta) = \{ \mathbf{X} \in t | f_t^j(\mathbf{X}^j) > \theta \}$

with $j \in \{1, \ldots, J\}$ and $\theta \in \mathbb{R}$.

 \clubsuit Geometric defintion of a split: a linear combination of the variables in group \mathbf{X}^{j}

 $(\beta^j)^\top \mathbf{X}^j = f_t(\mathbf{X}^j)$

TPLDA

Estimation method

▷ For group *j*, find $\beta^j = (\beta_1^j, \dots, \beta_{d_j}^j) \in \mathbb{R}^{d_j}$ by maximizing the Fisher's criterion in node *t*:

$$\max_{\beta^{j} \in \mathbb{R}^{d_{j}}} \left\{ (\beta^{j})^{\top} \widehat{B}_{t}^{j} \beta^{j} - \lambda_{j} \sum_{\ell=1}^{d_{j}} |\widehat{\sigma}_{t,\ell}^{j} \beta_{\ell}^{j}| \right\} \quad \text{subject to} \quad (\beta^{j})^{\top} \widehat{\Sigma}_{t}^{j} \beta^{j} \leq 1,$$

with

- $\hat{\sigma}^{j}_{t,\ell}$: within-class standard deviation estimate of \mathbf{X}^{j}_{ℓ} ,
- \widehat{B}_{t}^{j} : standard estimate of the between-class covariance of \mathbf{X}^{j} ,
- $\lambda_j \in \mathbb{R}^+$: regularization parameter.

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- $\lambda_j \in \mathbb{R}^+$: regularization parameter.
- > Find a split for each group, then select the one that maximizes

$$\Delta I(j,\theta) = \mathsf{pen}(d_j) \left\{ \mathrm{I}\left(t\right) - \left[\mathsf{p}_{t_L(j,\theta)} \mathrm{I}\left(t_L(j,\theta)\right) + \mathsf{p}_{t_R(j,\theta)} \mathrm{I}\left(t_R(j,\theta)\right) \right] \right\},$$

where $pen(d_j)$ is decreasing function of the group size d_j .

We want to split t into several disjoint nodes using information from a group \mathbf{X}^{j} , $(j\in\{1,\ldots,J\}).$

Geometric definition of a split: a partition of the input space defined according to variables of a group X^{j} .

Estimation method

 \triangleright For group *j*, build a CART tree with root *t* and depth **D**_j

CARTGI





> Find a split for each group, then select the one that maximizes

$$\Delta I(j) = \operatorname{pen}(d_j) \left[n_t I(t) - \sum_{l=1}^L n_{t_l(j)} I(t_l(j)) \right]$$

where $pen(d_j)$ is decreasing function of the group size d_j .

Find a pruned subtree of $\mathcal{T}_{\mathrm{max}}$ that minimizes

$$\mathcal{R}_{\alpha}(T) = \mathcal{R}(T, \mathcal{D}_n) + \alpha |\widetilde{T}|, \quad \alpha \in \mathbb{R}^+,$$

where

- $\mathcal{R}(T, \mathcal{D}_n)$: the prediction error,
- $|\widetilde{T}|$: the number of leaves of T,
- α : a tuning parameter which controls the complexity of the tree.

Theorem: Generalized cost-complexity pruning [Poterie, 2018]

For any non-trivial and non-binary tree T with root t_1 , there exist a unique sequence

 $0 = \alpha_1 < \ldots < \alpha_K = \infty$

and a unique sequence of nested subtrees of $\ensuremath{\mathcal{T}}$

 $T \succeq T_1 \succ \ldots \succ T_K = \{t_1\}$

such that for every $1 \le k < K$,

$$\forall \alpha \in [\alpha_k; \alpha_{k+1}[, \quad T_k = \operatorname*{argmin}_{T' \preceq T} \mathcal{R}_{\alpha}(T'), \text{ and}$$
$$\forall \alpha \ge \alpha_K, \quad T_K = \operatorname*{argmin}_{T' \preceq T} \mathcal{R}_{\alpha}(T').$$

➔ In practice, crossvalidation and train-test split can be used to select the best subtree in the sequence.

Random forests for grouped inputs (RFGI)







- $\triangleright~$ At each node, preselect randomly mgrp groups eligible for splitting.
- Build a tree RI on each selected groups by preselecting mvar inputs eligible for splitting at each step.



RFGI algorithm

Input: an observation $\mathbf{x} \in \mathbb{R}^d$, \mathcal{D}_n , ntree, mgrp, mvar_j, D_j , for all $j = 1, \ldots, J$.

Repeat ntree times the following steps:

- 1. Build the bootstrap sample \mathcal{D}_n^b .
- 2. Grow a maximal "random" CARTGI tree $\hat{h}(., \Theta^b, \Theta'^b)$.
 - Use only a random subset of mgrp groups to select a split.
 - Grow random CART trees
 - \Rightarrow at each step, use only a random subset of mvar_i inputs.
 - No pruning phase

Output: prediction of the random forest for observation x

$$\hat{h}_{RFGI}(\mathbf{x}) = aggregation \left\{ \hat{h}(\mathbf{x}, \Theta^1, \Theta'^1), \dots, \hat{h}(\mathbf{x}, \Theta^{\text{ntree}}, \Theta'^{\text{ntree}}) \right\}$$

- \triangleright mgrp/mvar_j = the number of selected groups/variables
 - → Important parameters, analogues of mtry.
 - ➔ Default values:
 - \triangleright mgrp= J/3 and mvar_j = $d_j/3$ in regression,
 - \triangleright mgrp= \sqrt{J} and mvar_j = $\sqrt{d_j}$ in classification.
- \triangleright D_j = the depth of each splitting tree.
 - → Controls the trade-off between adjustment and complexity.
 - → Suggested values: $D_j = 2, 3$ for all j.

Group importance measure

Mean decrease in Accuracy (MDA) for group \mathbf{X}^{j} : weighted difference between the forest error $err(\hat{h}_{RFGI})$ and the permuted forest error $\widetilde{err}^{j}(\hat{h}_{RFGI})$

$$MDA(\mathbf{X}^{j}) = \frac{1}{d_{i}} \left\{ \widetilde{err}^{i}(\hat{h}_{RFGI}) - err(\hat{h}_{RFGI}) \right\}.$$

→ Adaptation of the measure of grouped importance [Gregorutti et al., 2015].

Numerical experiments

Numerical experiments

Model 1: no "real" group structure (block covariance matrix).

• n = 500, J = 10 groups including 5 predictive groups, $d_j = 10$.

Model 2: group structure, non-linear relationship + interactions in groups.

• n = 1000, J = 10 groups including 2 predictive groups, $d_j = 5$.

Model 3: group structure, linear relationship in groups.

• n = 1000, J = 10 groups including 2 predictive groups, $d_j = 5$ or $d_j = 50$.

	RFGI	RF	CARTGI	TPLDA	CART	Group-Lasso
Model 1						
AUC	0.83 (0.01)	0.83 (0.01)	0.69 (0.03)	0.76 (0.02)	0.68 (0.03)	0.67 (0.02)
Error	0.24 (0.01)	0.23 (0.01)	0.33 (0.02)	0.28 (0.02)	0.33 (0.02)	0.35 (0.03)
Model 2						
AUC	0.94 (0.02)	0.85 (0.04)	0.78 (0.04)	0.61 (0.09)	0.73 (0.06)	0.50 (0.03)
Error	0.15 (0.03)	0.24 (0.04)	0.25 (0.04)	0.41 (0.09)	0.31 (0.06)	0.49 (0.02)
Model 3						
AUC	0.86 (0.03)	0.82 (0.03)	0.73 (0.03)	0.78 (0.03)	0.71 (0.04)	0.90 (0.02)
Error	0.21 (0.03)	0.25 (0.03)	0.30 (0.03)	0.23 (0.03)	0.32 (0.04)	0.15 (0.02)

Tuning parameters are selected by using cross-validation and a validation sample.

Model 1: no "real" group structure (block covariance matrix), Gaussian mixture.

- J = 10 groups with each $d_i = 10$ variables.
- No between-group correlation.
- 5 relevant groups = groups with ood index.
- $I(X^1) > I(X^3) > I(X^5) > I(X^7) > I(X^9)$.

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Applications to real data

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Gene expression data 1: colitis data [Burczynski et al., 2006].

- n = 127 patients whom 85 patients with Crohn's disease or ulcerative colitis
- d = 7818 genes grouped into J = 275 groups including (average size: 30 genes).

Gene expression data 2: breast cancer data [Ma et al., 2004].

- n = 60 patients whom 28 with cancer recourence.
- d = 4246 genes grouped into J = 268 groups including (average size: 18.5 genes).

Extreme weather event data : Flash Flood Information Retrieval data [Wilkho et al., 2023]

- n = 14420 webpages whom 1560 are related to flash flood (10,8%).
- d = 40 synthetic variables grouped into J = 8 groups including (group size between 3 and 10 variables).

	RFGI	RF	Sparse-group lasso*	Group-Lasso*
colitis data				
Accuracy	0.93 (0.04)	0.93 (0.04)	0.87	0.84
breast cancer data				
Accuracy	0.53 (0.12)	0.48 (0.12)	0.70	0.60
flood data				
Accuracy	0.95 (2E-3)	0.95 (2E-3)	-	-

Results from [Simon et al., 2013].



Normalized MDA for variables in RF

Applications to real data: group/variable importance



Normalized MDA for groups in RFGV

Conclusions, perspectives

- Development of decision-tree and random forests methods for groups of variables.
- Methods implemented in R and Python.
 - In R: TPLDA and dtrfgv (available on github).
 - Fast implemention in Cython: extension of the library scikit-learn (available on github).

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Actual questions:

- How to automatically define the group structure ?
- How to build random forest for data with spatio-temporal data ?

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