L1-based compression of random forest model

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Departement of EE and CS & GIGA-Research
High dimensional supervised learning applications

3D Image segmentation
x=original image  
y=segmented image

Genomics
x=DNA sequence  
y=phenotype

Electrical grid
x=system state  
y=stability

From $10^5$ to $10^9$ dimensions.
Tree based ensemble methods

From a dataset of input-output pairs \( \{(x_i, y_i)\}_{i=1}^n \subset X \times Y \), we approximate \( f : X \to Y \) by learning an ensemble of \( M \) decision trees.

The estimator \( \hat{f} \) of \( f \) is obtained by averaging the predictions of the ensemble of trees.
The complexity of tree based methods is measured by the number of internal nodes and increases with
- the ensemble size $M$;
- the number of samples $n$ in the dataset.

The variance of individual trees increases with the dimension $p$ of the original feature space → $M(p)$ should increase with $p$ to yield near optimal accuracy.

Complexity grows as $nM(p)$ → may require huge amount of storage.

Memory limitation will be an issue in high dimensional problems.
L1-based compression of random forest model (I)

We first learn an ensemble of $M$ extremely randomized trees (Geurts, et al., 2006) . . .

Example

...and associate to each node an indicator function $1_{m,l}(x)$ which is equal to 1 if the sample $(x, y)$ reaches the $l$-th node of the $m$-th tree, 0 otherwise.
L1-based compression of random forest model (II)

The node indicator functions $1_{m,l}(x)$ may be used to lift the input space $\mathcal{X}$ towards its induced feature space $\mathcal{Z}$

$$z(x) = (1_{1,1}(x), \ldots, 1_{1,N_1}(x), \ldots, 1_{M,1}(x), \ldots, 1_{M,N_M}(x)).$$

Example for one sample $x_s$

$$z(x_s) = (1 1 0 0 1 1 0 | 1 1 0 0 1 0 0 | 1 0 1 1 0)$$
A variable selection method (regularization with $L_1$-norm) is applied on the induced space $\mathcal{Z}$ to compress the tree ensemble using the solution of

$$
\left( \beta^*_j(t) \right)_{j=0}^q = \arg \min_{\beta} \sum_{i=1}^{n} \left( y_i - \beta_0 - \sum_{j=1}^{q} \beta_j z_j(x_i) \right)^2
$$

$$\text{s.t. } \sum_{j=1}^{q} |\beta_j| \leq t.
$$

Pruning: a test node is deleted if all its descendants (including the test node itself) correspond to $\beta^*_j(t^*) = 0$. 

$L_1$-based compression of random forest model (III)
Overall assessment on 3 datasets

<table>
<thead>
<tr>
<th>Datasets</th>
<th>Error</th>
<th>Complexity</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ET</td>
<td>rET</td>
</tr>
<tr>
<td>Friedman1</td>
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*ET* Extra trees;  
*rET* L1-based compression of ET.

Table: Parameters of the Extra-Tree method: $M = 100$; $K = p$; $n_{\text{min}} = 1$ on Friedman1 and Two-norm, $n_{\text{min}} = 10$ on SEFTi.
An increase of $t$ decreases the error of rET until $t = 3$ with drastic pruning.

Friedman1: $M = 100$, $K = p = 10$ and $n_{\text{min}} = 1$
Managing complexity in the extra tree method

**Bound $M$**
Restrict the size $M$ of the tree based ensemble.

**Pre-pruning**
Pre-pruning reduces the complexity of tree based methods by imposing a condition to split a node e.g.

- minimum number of samples $n_{\text{min}}$ in order to split,
- minimum decrease of an impurity measure,
- ...
The accuracy and complexity of an rET model does not depend on $n_{\text{min}}$, for $n_{\text{min}}$ small enough ($n_{\text{min}} < 10$)

Friedman1: $M = 100$, $K = p = 10$ and $t = t_{cv}^*$
After variance reduction has stabilized \((M \approx 100)\), further increasing \(M\) keeps enhancing the accuracy of the rET model without increasing complexity.

Friedman1: \(n_{\text{min}} = 10, \ K = p = 10\) and \(t = t_{\text{cv}}^*\)
Conclusion & perspectives

1. Drastic pruning while preserving accuracy.
2. Strong compressibility of the tree ensemble suggests that it could be possible to design novel algorithms suited to very high dimensional input space.
3. Future research will target similar compression ratio without using the complete set of node indicator functions of the forest model.
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