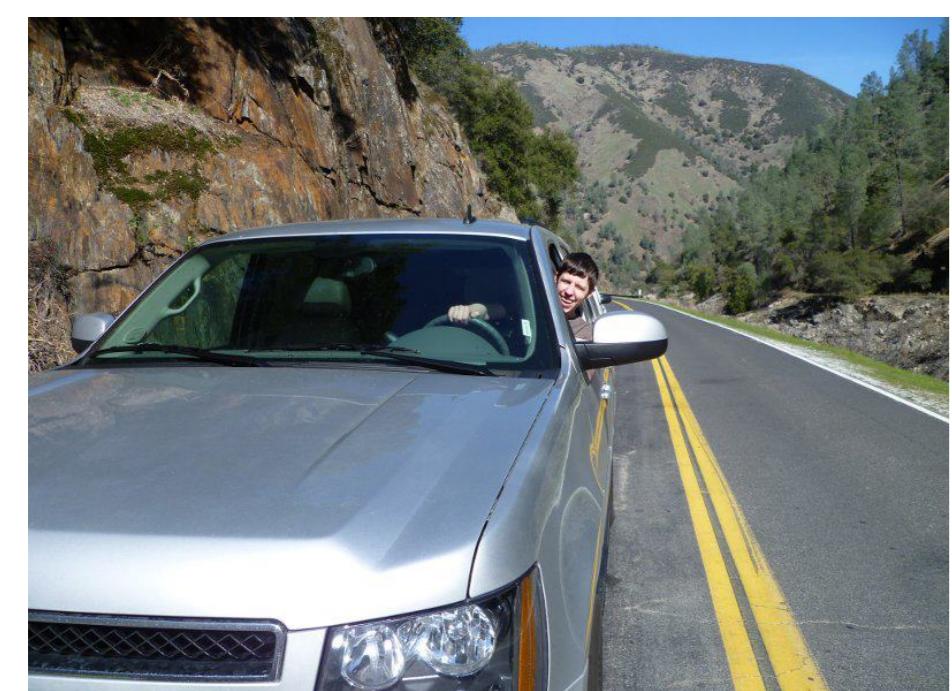


Multilabel classification

Given a set of n samples of input-output pairs $((x^i, y^i) \in (\mathcal{X} \times \mathcal{Y}))_{i=1}^n$, a supervised learning task is defined as searching for the function $f : \mathcal{X} \rightarrow \mathcal{Y}$ in a hypothesis space that minimizes some loss function over the joint distribution of input-output pairs.

In multi-label classification, y^i is a subset of the label space \mathcal{Y} of size p .

Input \mathcal{X} 800 × 600 pixel



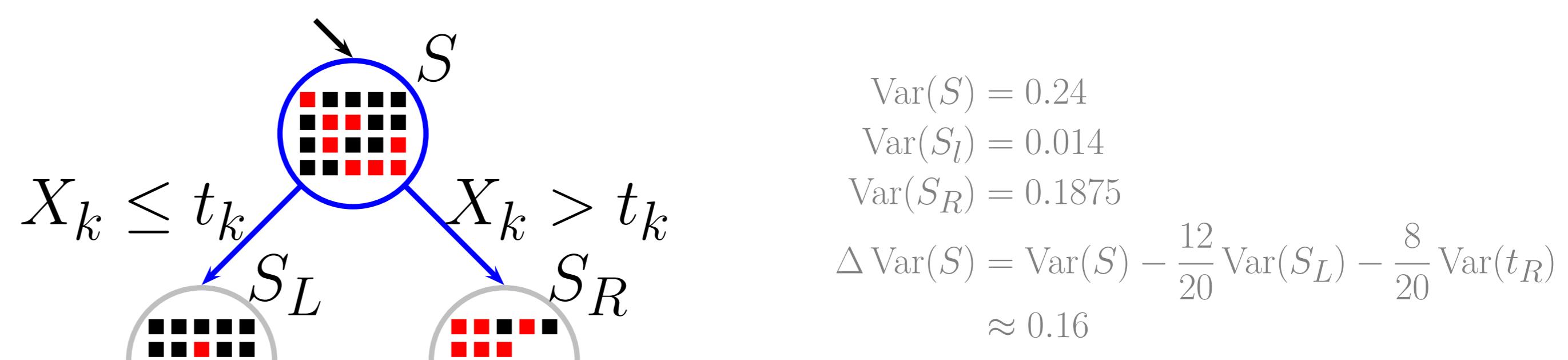
Output \mathcal{Y} labels

This image can be labelled with “car”, “person”, “mountain”, but not with “house” or “elephant”.

If each label corresponds to a wikipedia article, then we have around 4 million labels.

Random forest

Randomized trees are built on a bootstrap copy of the samples by recursively maximizing the reduction of impurity, here the variance Var . At each node, the best split is selected among k randomly selected features.



High dimensional output space \mathcal{Y} is a bottleneck of random forest

Easy to have a very high number of labels...



Tree growing algorithm requires the computation of the sum of the variance

- over the label space
- at each tree node and
- for each candidate split.

Solution Multi-output regression trees in randomly projected output space

Methods

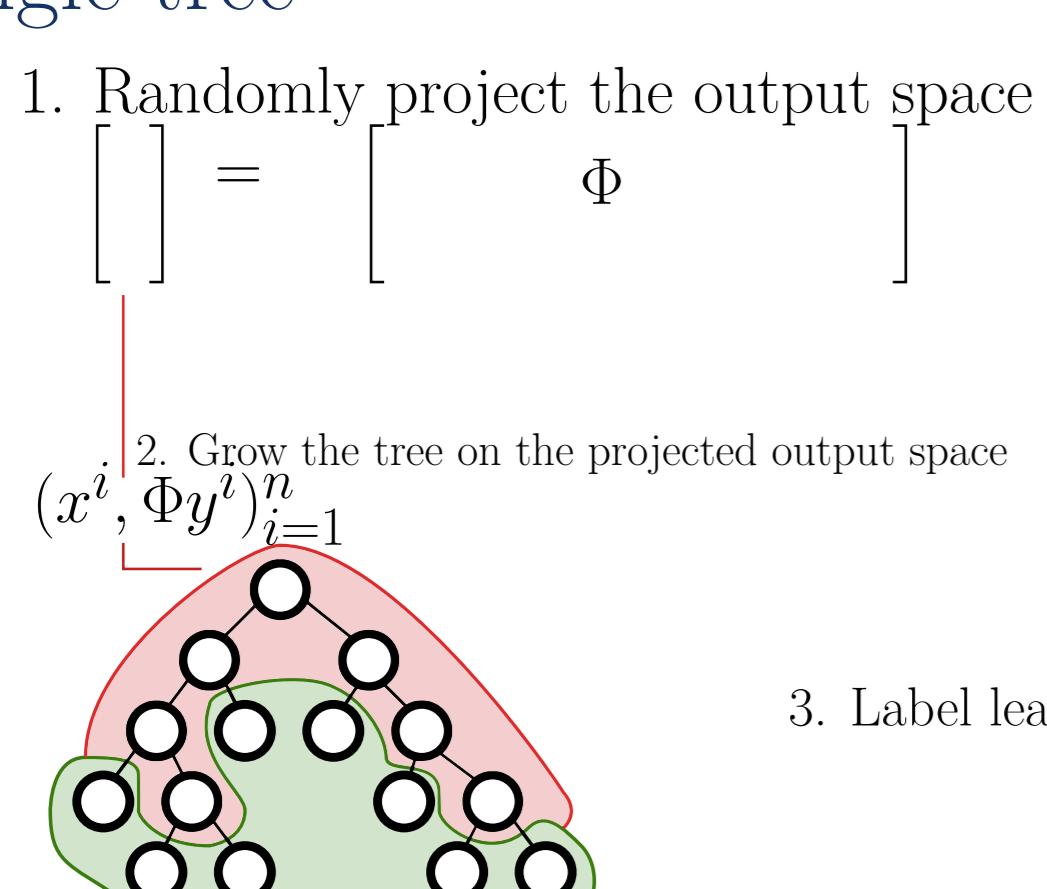
We propose to **approximate the computation** of the variance by using random projection of the output space.

Theorem

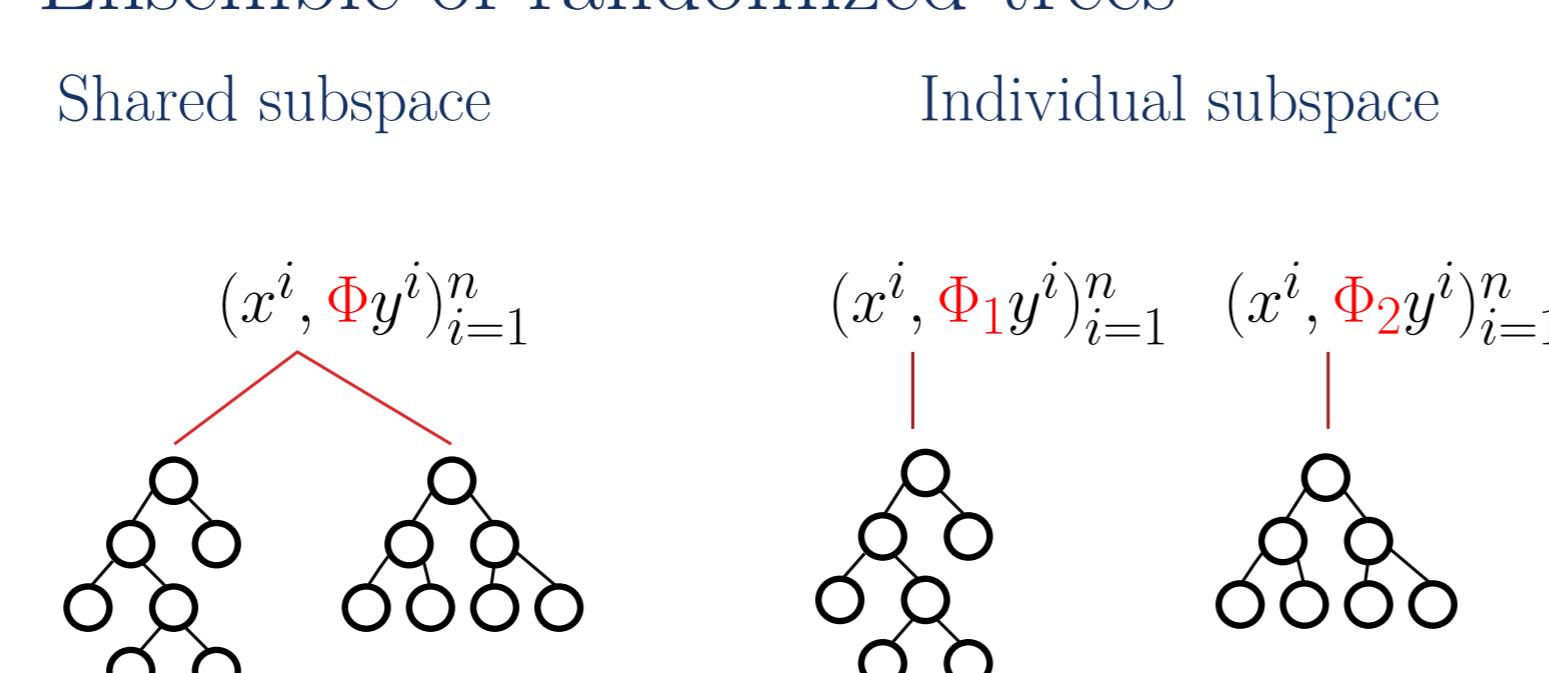
Given $\epsilon > 0$, a sample $(y^i)_{i=1}^n$ of n points $y \in \mathbb{R}^d$, and a projection matrix $\Phi \in \mathbb{R}^{m \times d}$ such that for all pairs of points the Johnson-Lindenstrauss lemma holds, we have also

$$(1 - \epsilon) \text{Var}((y^i)_{i=1}^n) \leq \text{Var}((\Phi y^i)_{i=1}^n) \leq (1 + \epsilon) \text{Var}((y^i)_{i=1}^n).$$

Single tree



Ensemble of randomized trees



Bias-variance analysis

Averaging over the learning set LS , algorithm randomization ϵ and output subspace randomization Φ , the square error Err of t multi output tree models can be decomposed into:

Single shared subspace (Algo 1)

$$E_{LS, \Phi, \epsilon^t} \{ Err(f_1(x; LS, \Phi, \epsilon^t)) \} = \sigma_R^2(x) + B^2(x) + V_{LS}(x) + \frac{V_{Algo}(x)}{t} + V_{Proj}(x).$$

Individual subspace (Algo 2)

$$E_{LS, \Phi, \epsilon^t} \{ Err(f_2(x; LS, \Phi^t, \epsilon^t)) \} = \underbrace{\sigma_R^2(x)}_{\text{residual error}} + \underbrace{B^2(x)}_{\text{bias}} + \underbrace{V_{LS}(x) + \frac{V_{Algo}(x) + V_{Proj}(x)}{t}}_{\text{variance}}.$$

If the additional computational burden needed to generate a different random projection for each tree is not problematic, then individual subspace should always be preferred to single shared subspace.

Conclusion

- Lower computing time, without affecting accuracy.
- Optimizing input and output randomization could improve prediction performance.

Source code is available @ github.com/arjoly.

Future work

Develop efficient technique to adjust random output space parameters so to reach the best accuracy and computing time trade-off.

Experiments

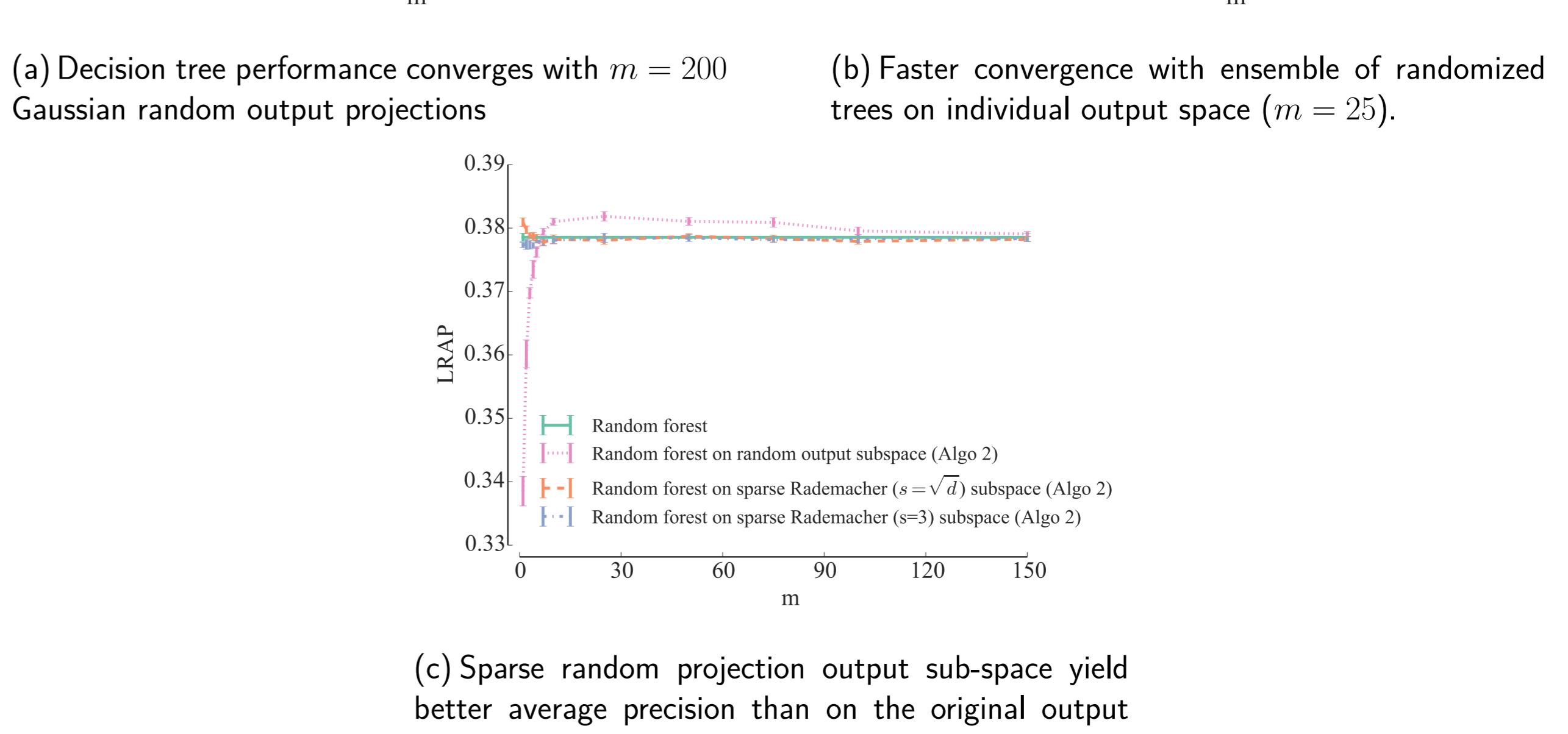
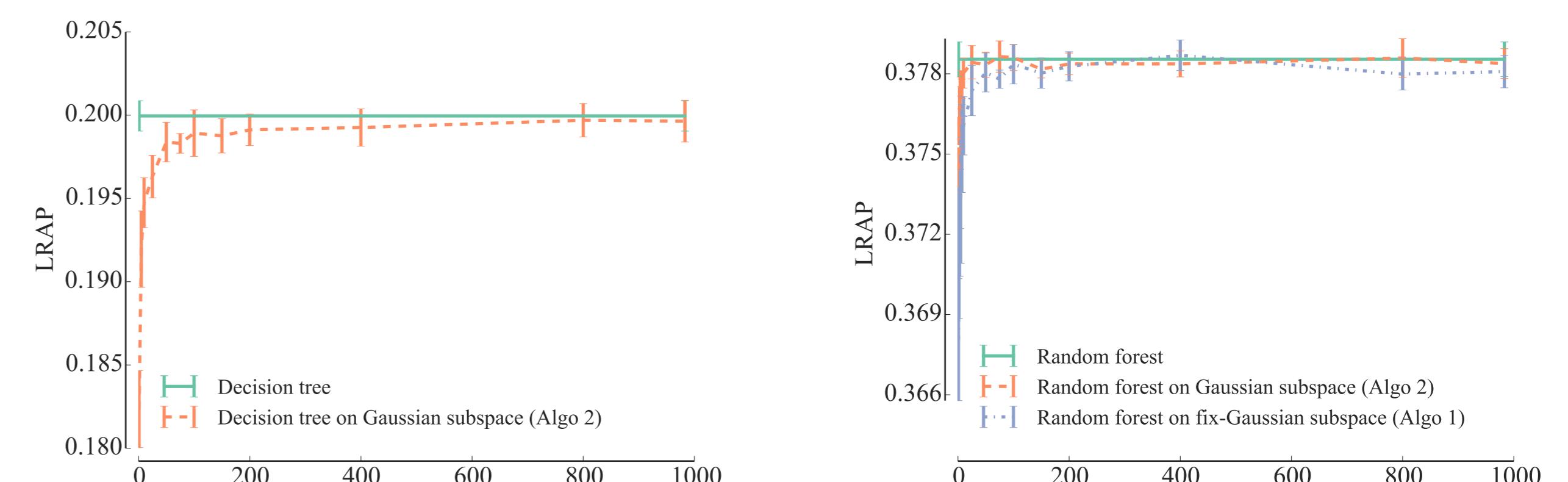
Label ranking average precision to assess performance

$$\text{LRAP}(\hat{f}) = \frac{1}{|TS|} \sum_{i \in TS} \frac{1}{|y^i|} \sum_{j \in \{k: y_k^i = 1\}} \frac{|\mathcal{L}_j^i(y^i)|}{|\mathcal{L}_j^i(1_d)|}, \text{ with } \mathcal{L}_j^i(q) = \{k : q_k = 1 \text{ and } \hat{f}(x^i)_k \geq \hat{f}(x^i)_j\}$$

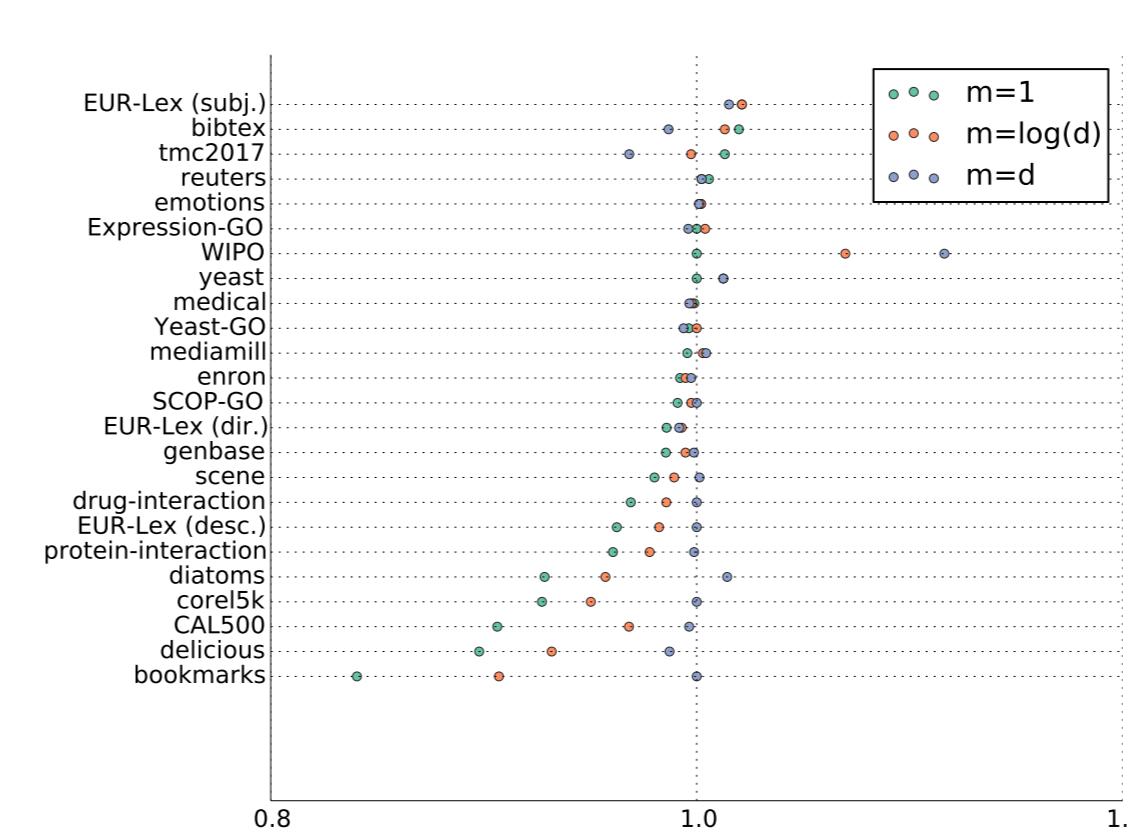
where $\hat{f}(x^i)_j$ is the probability (or the score) associated to the label j by the learnt model \hat{f} applied to x^i , 1_d is a d -dimensional row vector of ones. Higher score if true labels have a higher probability (score) than the false labels.

“Delicious” dataset (983 labels, 100 trees, $k = \sqrt{p}$, no pruning)

Randomly projecting the output space reduces computing time of random forest from 3458 seconds (no projection) to 311 seconds ($m = 25$, Gaussian individual subspace) without accuracy degradation.

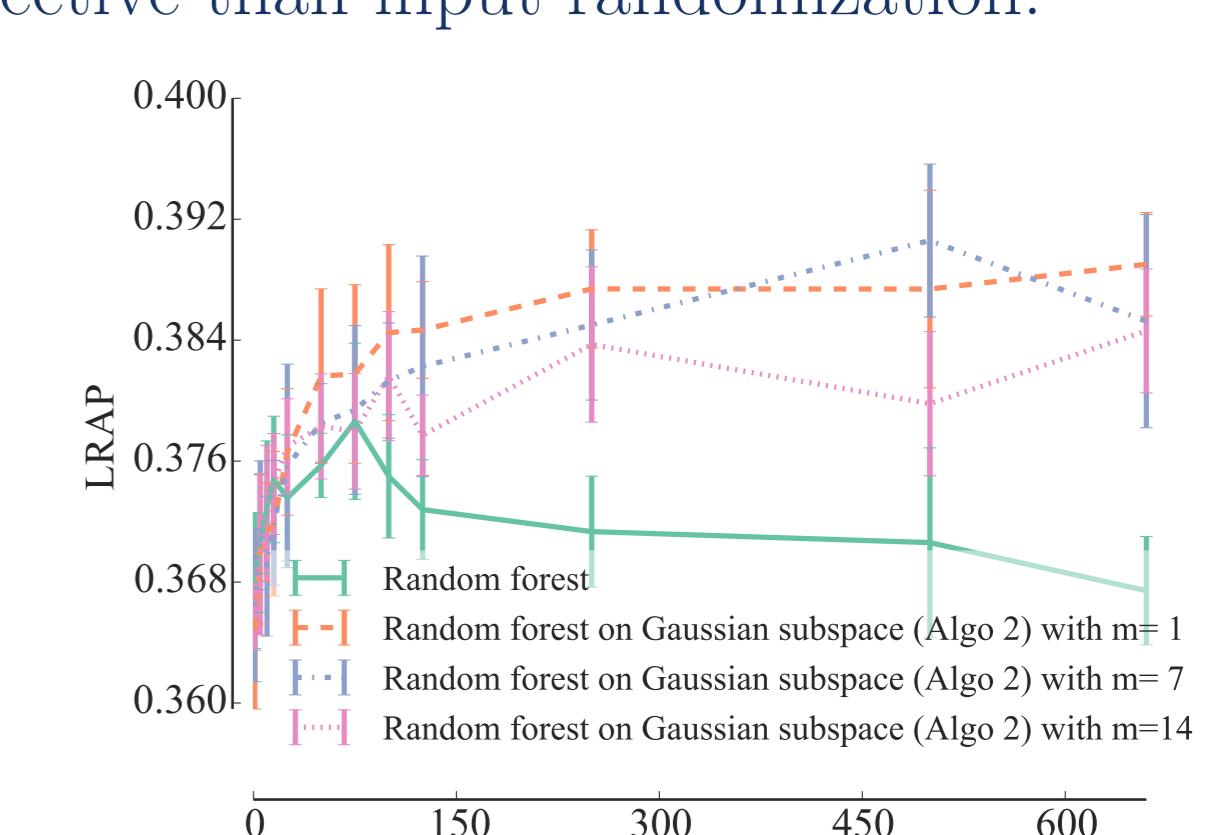


Systematic analysis on 24 datasets



(100 trees, no pruning, $k = \sqrt{p}$)

Output randomization could be more effective than input randomization.



Drug-interaction dataset (1554 labels, 100 trees, no pruning)