

# Margin trees for high dimensional classification



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Picture: [www.ruhr-uni-bochum.de](http://www.ruhr-uni-bochum.de)

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# Motivation

- Classifying elements, described by high dimensional features (more than 10,000)
- Organisation of classes lack interpretability
- High quality methods are slow for more than two classes
- Popular application areas like cancer classification

# Margin trees

- Approach of creating meaningful abstractions
- Increase performance of the accurate SVM by divide and conquer
  - Combine classes into two groups
  - Calculate classifier for chosen partition
  - Apply procedure on each group

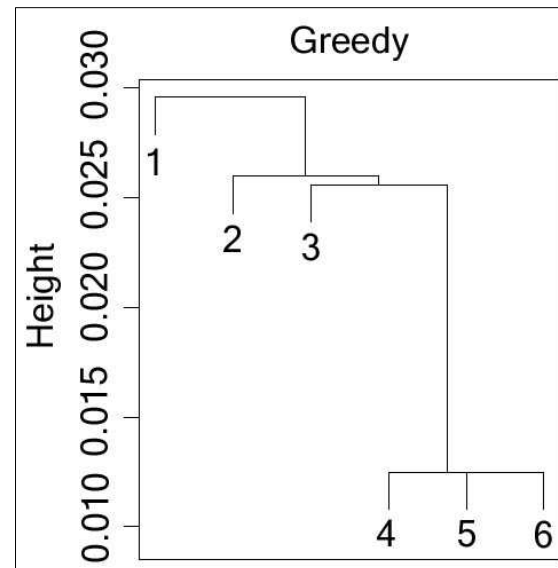
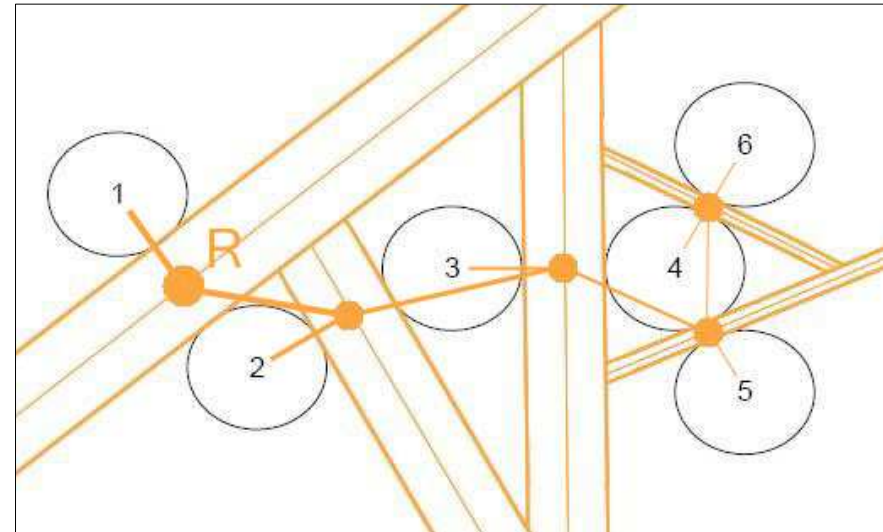
# Linkage constraints

- Greedy

- Top down
- Choose partition which provides widest margin

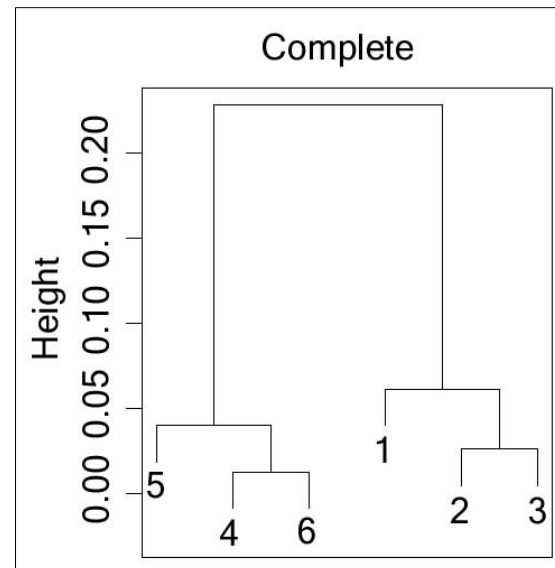
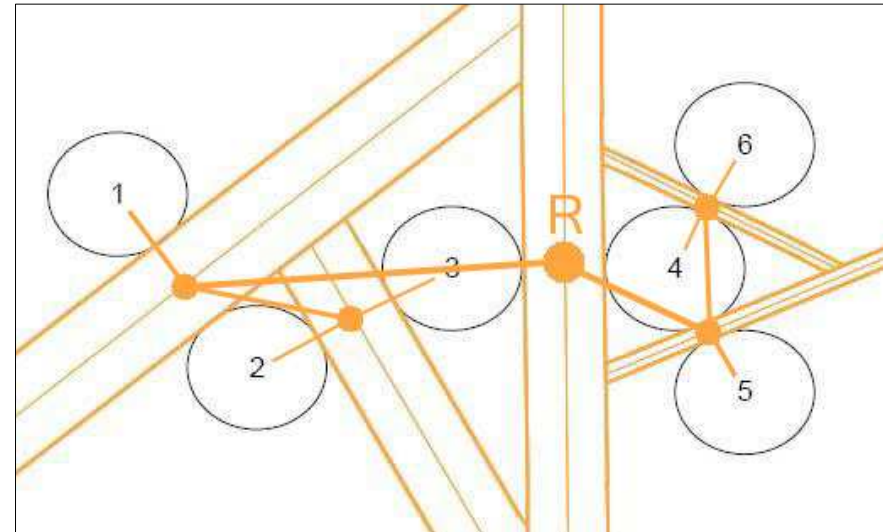
- Requires computation of  $O(\sum_{k=1}^{n-1} \binom{n}{k})$  classifiers  
(own estimation)

- 14 classes  $\square$  16,382 possible classifiers



# Linkage constraints

- Complete linkage
  - Bottom up
  - At first each class is in its own group
  - Combine groups having least widest margin
  - Requires computation of only  $O(n^2)$  classifiers



# Organisation of classes

- Greedy does not care about distances between classes in the same group
  - Produces stringy trees by splitting off single classes
- Complete linkage produces groups having same size but differs in shapes (Brian T. Luke)
  - Might be more interpretable because of balanced hierarchy

# Kill two birds with one stone?

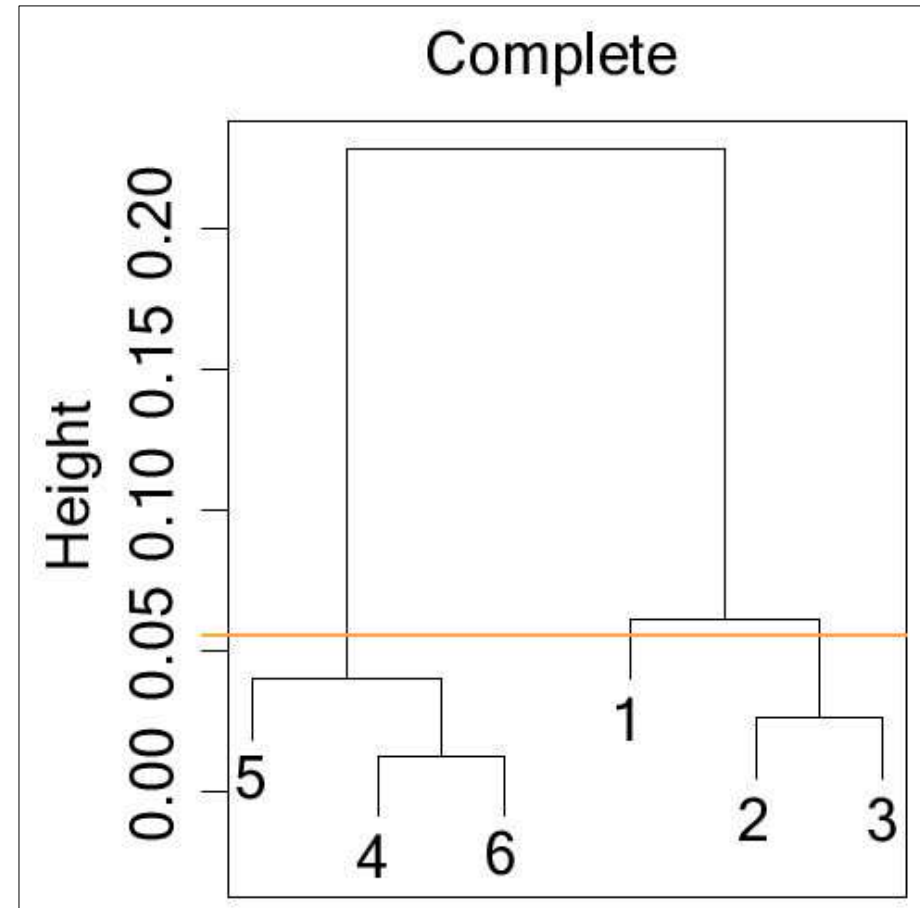
- Complete linkage trees turn out to be competitive to the greedy tree's robustness
- Constructed computationally fast
- Mostly balanced □ Fast classification

*and*

- Yields an exact algorithm for the greedy criterion

# Base of exact algorithm for greedy criterion

- Margin between elements of different groups is greater or equal than margin between those groups
- Cut in complete linkage tree at height  $M$  implies less margins in subtrees





# Exact algorithm for greedy criterion

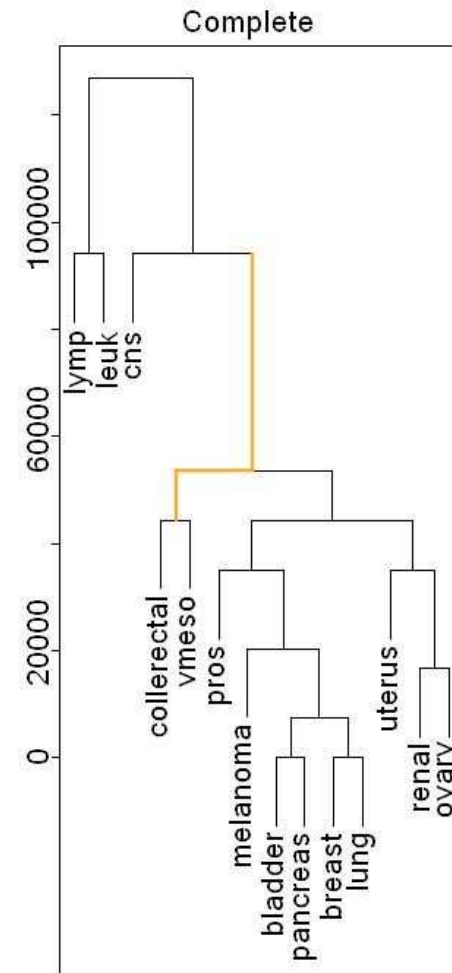
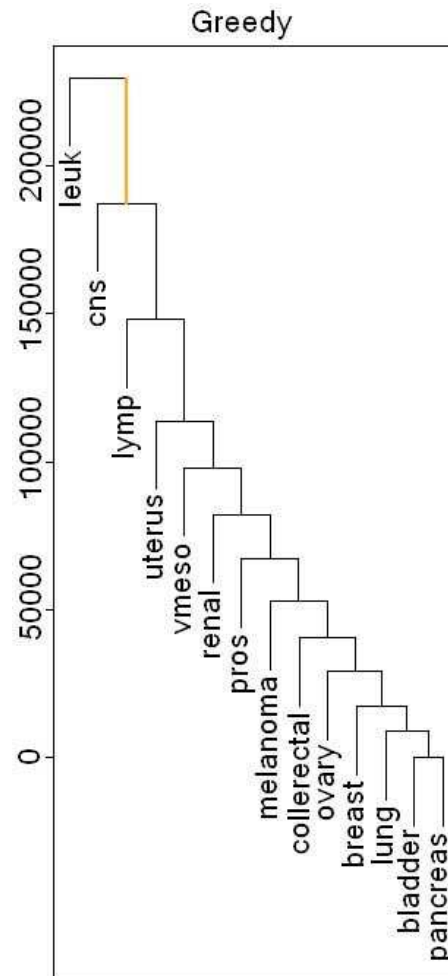
- Greedy criterion according to a monoton decreasing sequence of margins
  - Build complete linkage tree
  - Determine the widest margin achieved by one versus the rest classifiers and the margin of complete linkage tree
  - Cut tree at found height, collapse nodes and proceed with subtrees
- Terminates in  $O(n^2 + n \cdot n + n) \approx O(n^2)$  (own estimation)

# Experiment

- Microarray cancer data set of Ramaswamy
  - Samples: 198 tumours (144 for training and 54 for testing)
  - Features: 16,063 genes
  - Classes: 14 types
- Comparison of all-pairs SVM, exact greedy, complete linkage and nearest centroid classifiers

# Experiment

- Approximation of greedy tree can fail performing wide margins!



# Experiment

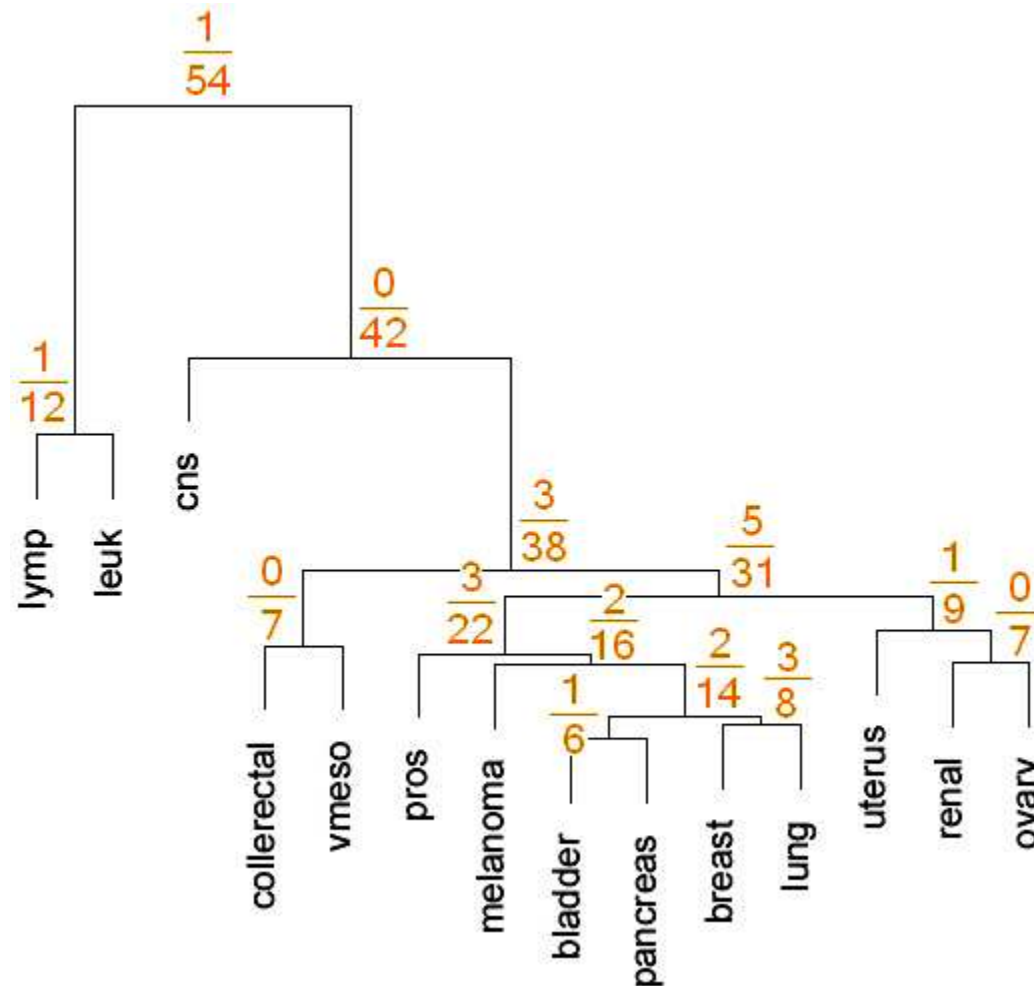
- Similar error rates **20**, 18, 18 and 35 (for nearest centroids)

		Margin Trees	
		Greedy	Complete
SVM		10	10
Greedy		0	2

- Table shows the number of times each classifier disagreed on the test set
- 90% overlap in true-positives and disagreement almost only on false-positives

# Experiment

- It emerges that the error rate increases close to the leafs



# Feature selection

- Nodes at the top seem to be less arbitratve
- Some features might have no effect on classification
- Reducing features would be beneficial, because
  - groups would be more interpretable
  - classification could become faster

# Hard thresholding

- Sort coefficients of weight vector which defines orientation of a margin in descending order
- Choose a number  $n_k$  for the  $k$ -th split
- Set first  $n_k$  coefficients to zero
- Adjust only position of reduced margin
- How to choose  $n_k$ ?

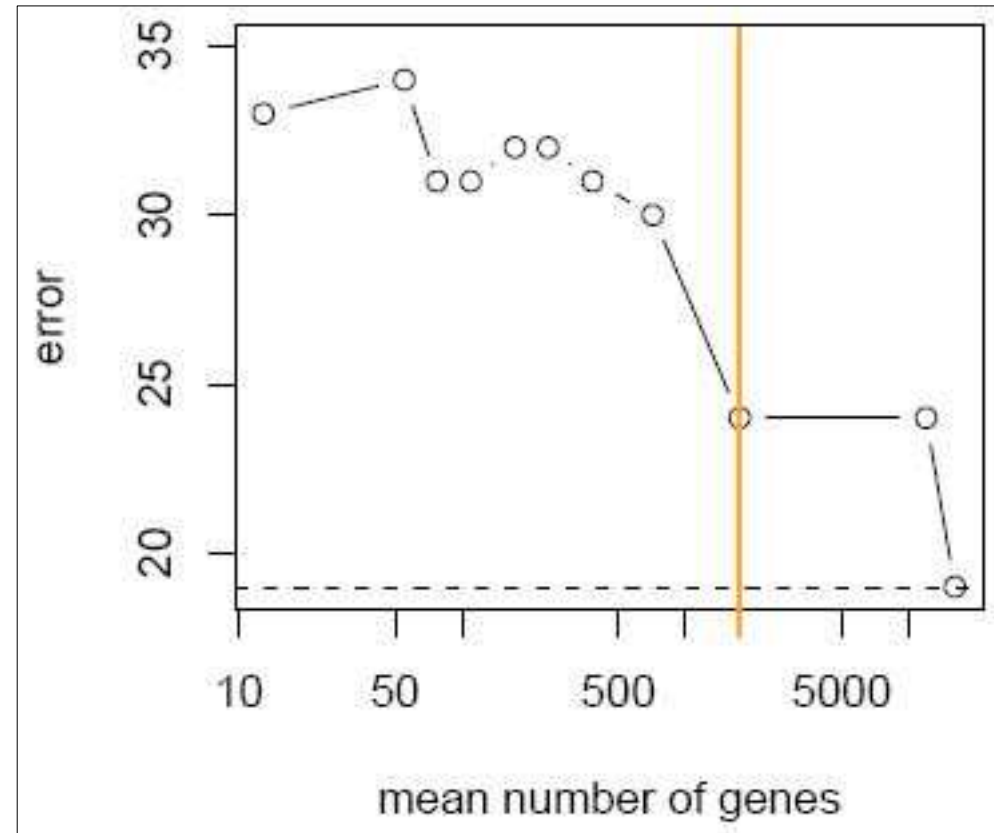
# Limit of deviation

- Introduce a new variable  $\alpha$
- $\alpha$  is limit of deviation between unmodified and trimmed weight vector
- At each level  $n_k$  is chosen individually
  - Fewer features at the top
  - More features close to the leafs
- Use tenfold cross-validation to estimate  $\alpha$



# Quality of hard thresholding

- Experiments point out that features can be reduced to  $< 12.5\%$  without too much loss of accuracy
- Recursive feature elimination only small advantage for already little number of features



# Quality of hard thresholding

- Preserves interpretability
  - Remaining coefficients are subset of total featurevector
  - Usually reduced coefficients not easily predictable with common methods

# Discussion

- Experiments show that margin trees are competitive to accurate methods like
  - Multiclass support vector machine
  - Nearest centroid methods
- Provide meaningful hierarchy and interpretable feature reduction
- Leave the door open for other classification strategies

# Discussion

- Nonlinear separable class distribution impede feature reduction
- Number of training samples is supposed to be less than number of features. Else:
  - Not linearly separable
  - One class might be splitted in to leaves
- There are several related methods to their work with asserts and drawbacks

# Further reading

- **Sources of paper:**

[stat.stanford.edu/~hastie/Papers/margintree.pdf](http://stat.stanford.edu/~hastie/Papers/margintree.pdf)

- **Agglomerative clustering:**

[fconyx.ncifcrf.gov/~lukeb/agclust.html](http://fconyx.ncifcrf.gov/~lukeb/agclust.html)

- **Nonlinear support vector machines:**

[www2.tuebingen.mpg.de/agbs/sc06/wiki/slides\\_nonlinear\\_svms.pdf](http://www2.tuebingen.mpg.de/agbs/sc06/wiki/slides_nonlinear_svms.pdf)

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**Presentation:** Marian Wiecek