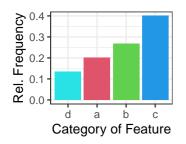
# **Introduction to Machine Learning**

# **CART Computational Aspects of Finding Splits**





#### Learning goals

- Know how monotone feature transformations affect the tree
- Understand how categorical features can be treated effectively while growing a CART
- Understand how missing values can be treated in a CART

#### MONOTONE FEATURE TRANSFORMATIONS

Monotone transformations of one or several features will neither change the value of the splitting criterion nor the structure of the tree, only the numerical value of the split point.



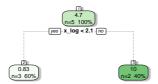
#### Original data

| Χ | 1.0 | 2.0 | 7.0 | 10.0 | 20.0 |  |
|---|-----|-----|-----|------|------|--|
| У | 1.0 | 1.0 | 0.5 | 9.0  | 11.0 |  |
|   |     |     |     |      |      |  |

### Data with log-transformed x

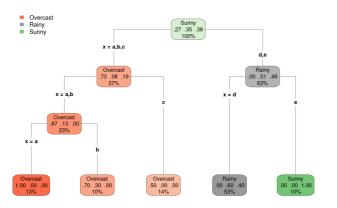
| log(x) | 0.0 | 0.7 | 1.9 | 2.3 | 3.0  |
|--------|-----|-----|-----|-----|------|
| У      | 1.0 | 1.0 | 0.5 | 9.0 | 11.0 |





• A split on a categorical feature partitions the feature levels:

$$x_j \in \{a, b, c\} \leftarrow \mathcal{N} \rightarrow x_j \in \{d, e\}$$





• A split on a categorical feature partitions the feature levels:

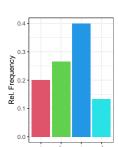
$$x_j \in \{a, b, c\} \leftarrow \mathcal{N} \rightarrow x_j \in \{d, e\}$$

- For a feature with m levels, there are about 2<sup>m</sup> different possible partitions of the m values into two groups
  (2<sup>m-1</sup> 1 because of symmetry and empty groups).
- Searching over all these becomes prohibitive for large values of *m*.
- For regression with L2 loss and for binary classification, we can define clever shortcuts.



For 0 - 1 responses, in each node:

• Calculate the proportion of 1-outcomes for each category of the feature in  $\mathcal{N}$ .

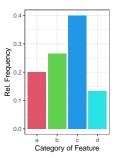


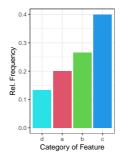
Category of Feature



For 0 - 1 responses, in each node:

- Calculate the proportion of 1-outcomes for each category of the feature in  $\mathcal{N}$ .
- Sort the categories according to these proportions.



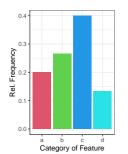


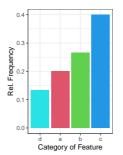


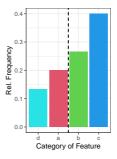
For 0 - 1 responses, in each node:

- Calculate the proportion of 1-outcomes for each category of the feature in  $\mathcal{N}$ .
- Sort the categories according to these proportions.
- The feature can then be treated as if it was ordinal, so we only have to investigate at most m-1 splits.







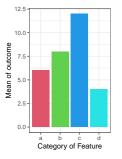


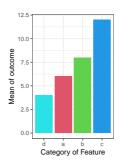
- This procedure finds the optimal split.
- This result also holds for regression trees (with L2 loss) if the levels of the feature are ordered by increasing mean of the target
- The proofs are not trivial and can be found here:
  - for 0-1 responses:
    - ▶ Breiman et al. 1984
    - ▶ Ripley 1996
  - for continuous responses:
    - ▶ Fisher 1958
- There are only heuristics for the multiclass case
  ▶ Wright and König 2019

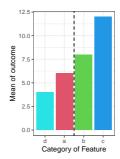


For continuous responses, in each node:

- Calculate the mean of the outcome in each category
- Sort the categories by increasing mean of the outcome









### MISSING FEATURE VALUES

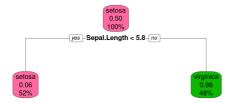
- When splits are evaluated, only observations for which the used feature is not missing are used. (This can actually bias splits towards using features with lots of missing values.)
- Surrogate splits can deal with missing values during prediction.
- Surrogate splits are created during training. They define replacement splitting rules, using a different feature, that result in almost the same child nodes as the original split.
- When observations are passed down the tree, and the feature value used in a split is missing, we use the surrogate split instead to decide to which child the data should be assigned.



#### **SURROGATE SPLITS**

- Each surrogate split is a decision stump that tries to learn the actual splitting rule
- Consider this tree with the primary split w.r.t. Sepal.Length where we perform binary classification (setosa vs. virginica):





Our surrogate split should optimize a splitting criterion w.r.t.
 Sepal.Length < 5.8</li>

#### **SURROGATE SPLITS**

• Consider this subsample of the data used to fit the tree:

|    | Sepal.Length | <br>Petal.Width | Species   | Sepal.Length < 5.8 |
|----|--------------|-----------------|-----------|--------------------|
| 1  | 5.10         | <br>0.20        | setosa    | TRUE               |
| 4  | 4.60         | <br>0.20        | setosa    | TRUE               |
| 9  | 4.40         | <br>0.20        | setosa    | TRUE               |
| 15 | 5.80         | <br>0.20        | setosa    | FALSE              |
| 18 | 5.10         | <br>0.30        | setosa    | TRUE               |
| 52 | 5.80         | <br>1.90        | virginica | FALSE              |
| 57 | 4.90         | <br>1.70        | virginica | TRUE               |
| 62 | 6.40         | <br>1.90        | virginica | FALSE              |
| 77 | 6.20         | <br>1.80        | virginica | FALSE              |
| 99 | 6.20         | <br>2.30        | virginica | FALSE              |

- Add column that indicates whether Sepal.Length < 5.8</li>
- Fit tree of depth 1 using all features but Sepal.Length to derive a split that explains Sepal.Length < 5.8 best ⇒ surrogate split</li>
- Typically, software stores the best and a few more surrogate splits

