

Lecture 008

Ensembles

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Admin

Today

Topic Ensembles (applied to decision trees)

Upcoming

Readings

- *Today* ISL Ch. 8.2
- *Next* ISL Ch. 9

Project Project topic and group due next week (Feb. 25th).

Decision trees

Review

Decision trees

Fundamentals

Decision trees

- split the *predictor space* (our \mathbf{X}) into regions
- then predict the most-common value within a region

Regression trees

- **Predict:** Region's mean
- **Split:** Minimize RSS
- **Prune:** Penalized RSS

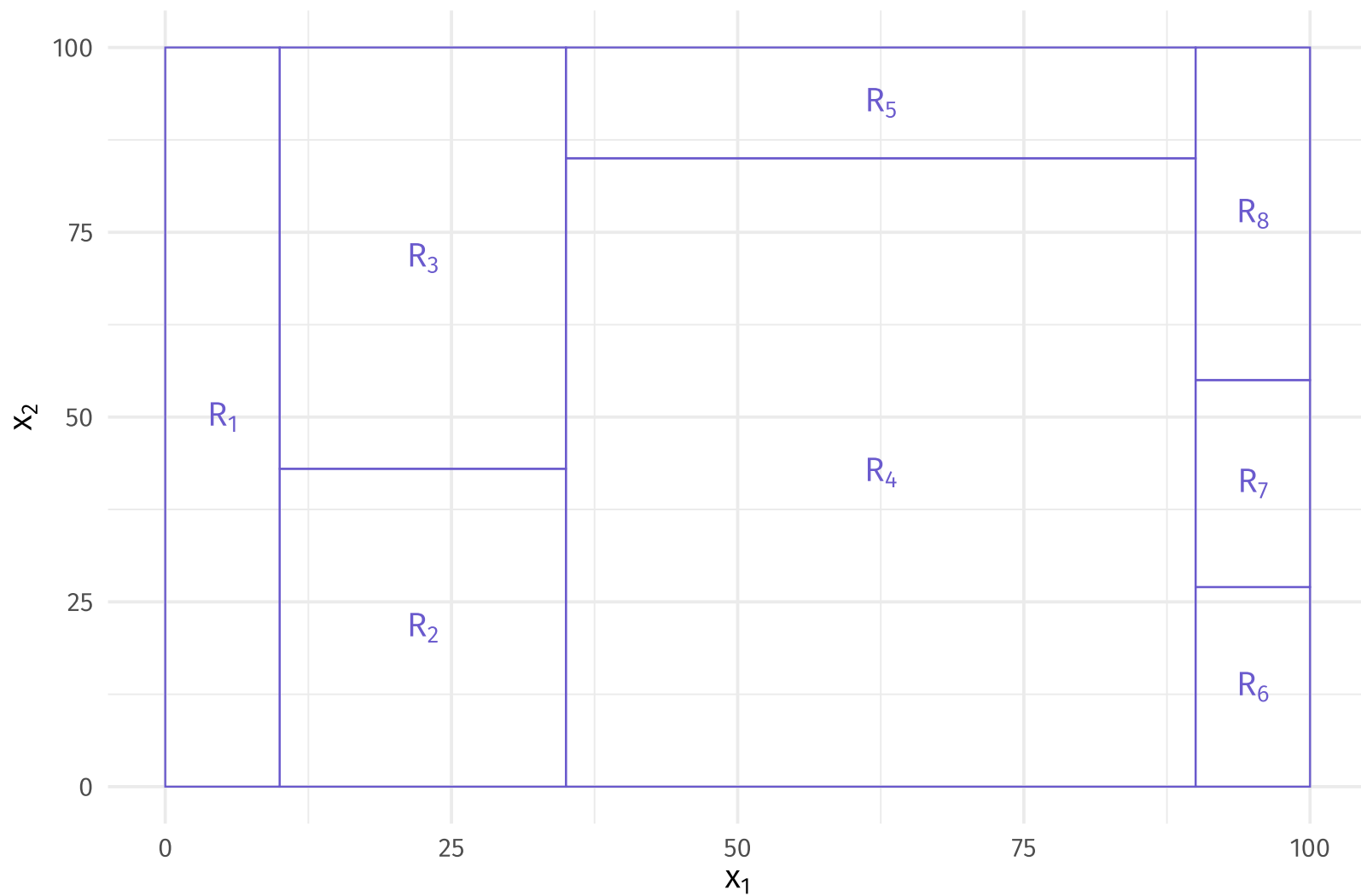
Classification trees

- **Predict:** Region's mode
- **Split:** Min. Gini or entropy.super
- **Prune:** Penalized error rate 🌴

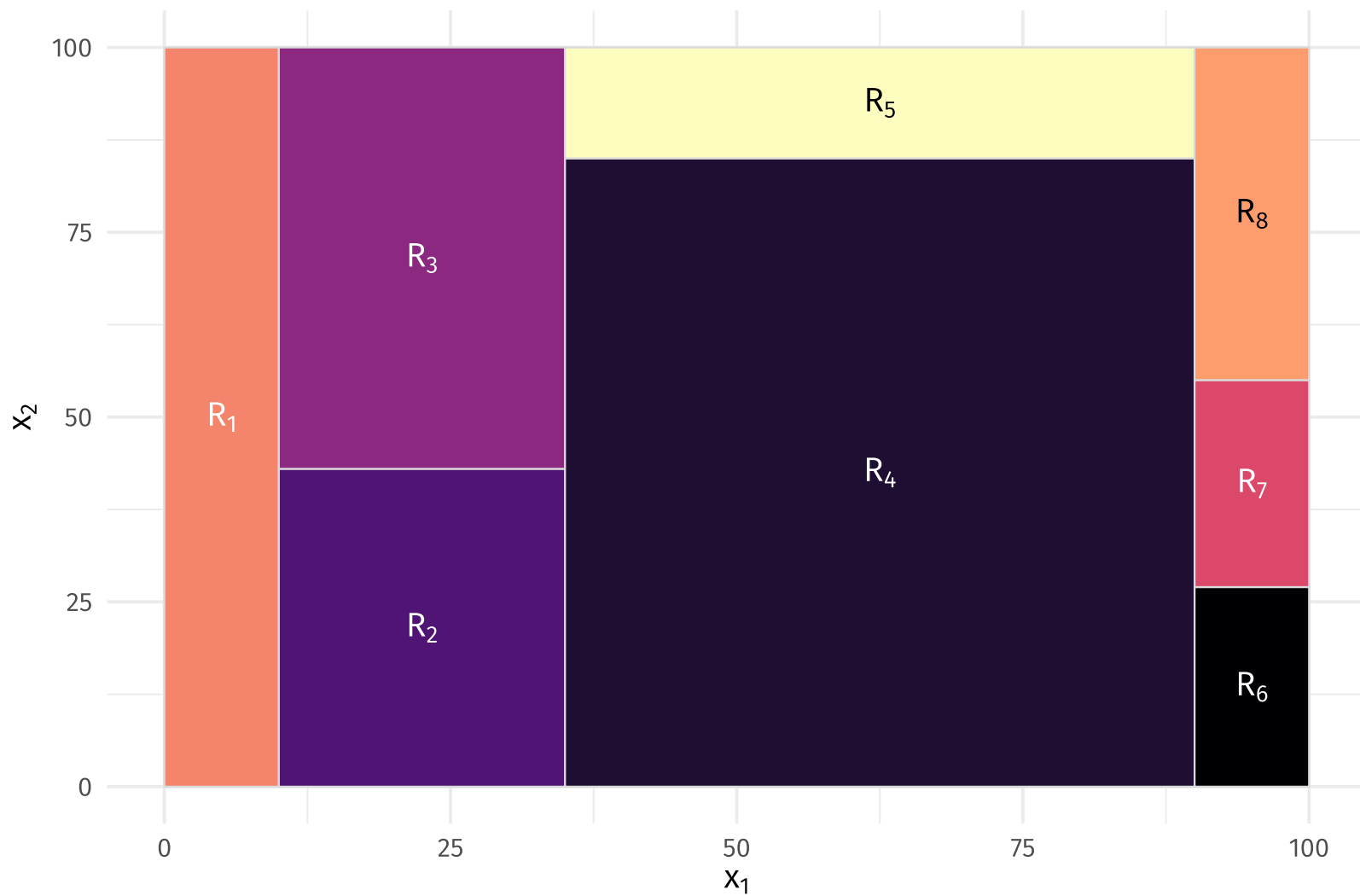
An additional nuance for **classification trees**: we typically care about the **proportions of classes in the leaves**—not just the final prediction.

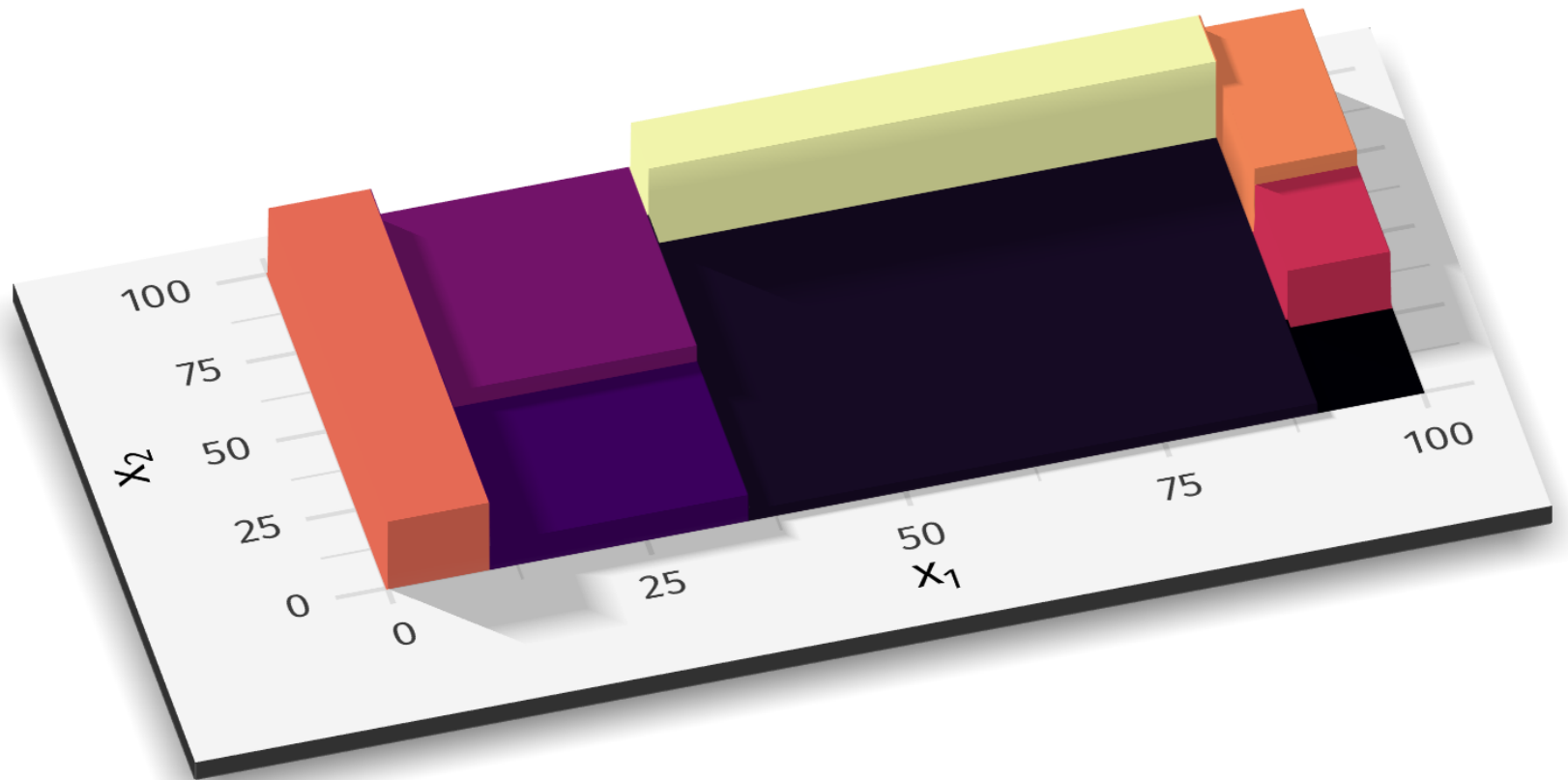
🌴 ... or Gini index or entropy

Example Each split in our tree creates **regions**.



Example Each region has its own **predicted value**.





Decision trees

Strengths and weaknesses

As with any method, decision trees have tradeoffs.

Strengths

- + Easily explained/interpreted
- + Include several graphical options
- + Mirror human decision making?
- + Handle num. or cat. on LHS/RHS 🌳

Weaknesses

- Outperformed by other methods
- Struggle with linearity
- Can be very "non-robust"

Non-robust: Small data changes can cause huge changes in our tree.

Next: Create ensembles of trees 🌲 to strengthen these weaknesses. 🌴

🌳 Without needing to create lots of dummy variables!

🌲 Forests! 🌴 Which will also weaken some of the strengths.

Ensemble methods

Ensemble methods

Intro

Rather than focusing on training a **single**, highly accurate model, **ensemble methods** combine **many** low-accuracy models into a *meta-model*.

Today: Three common methods for **combining individual trees**

1. **Bagging**
2. **Random forests**
3. **Boosting**

Why? While individual trees may be highly variable and inaccurate, a combination of trees is often quite stable and accurate. 🌲

🌲 We will lose interpretability.

Ensemble methods

Bagging

Bagging creates additional samples via **bootstrapping**.

Q How does bootstrapping help?

A *Recall*: Individual decision trees suffer from variability (*non-robust*).

This *non-robustness* means trees can change *a lot* based upon which observations are included/excluded.

We're essentially using many "draws" instead of a single one. 🌴

🌴 Recall that an estimator's variance typically decreases as the sample size increases.

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Bagging

Bootstrap aggregation (bagging) reduces this type of variability.

1. Create B bootstrapped samples
2. Train an estimator (tree) $\hat{f}^b(x)$ on each of the B samples
3. Aggregate across your B bootstrapped models:

$$\hat{f}_{\text{bag}}(x) = \frac{1}{B} \sum_{b=1}^B \hat{f}^b(x)$$

This aggregated model $\hat{f}_{\text{bag}}(x)$ is your final model.

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Bagging trees

When we apply bagging to decision trees,

- we typically **grow the trees deep and do not prune**
- for **regression**, we **average** across the B trees' regions
- for **classification**, we have more options—but often take **plurality**

Individual (unpruned) trees will be very **flexible** and **noisy**, but their **aggregate** will be quite **stable**.

The number of trees B is generally not critical with bagging. $B = 100$ often works fine.

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Out-of-bag error estimation

Bagging also offers a convenient method for evaluating performance.

For any bootstrapped sample, we omit $\sim n/3$ observations.

Out-of-bag (OOB) error estimation estimates the test error rate using observations **randomly omitted** from each bootstrapped sample.

For each observation i :

1. Find all samples S_i in which i was omitted from training.
2. Aggregate the $|S_i|$ predictions $\hat{f}^b(x_i)$, e.g., using their mean or mode
3. Calculate the error, e.g., $y_i - \hat{f}_{i,\text{OOB},i}(x_i)$

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Out-of-bag error estimation

When B is big enough, the OOB error rate will be very close to LOOCV.

Q Why use OOB error rate?

A When B and n are large, cross validation—with any number of folds—can become pretty computationally intensive.

Quick aside: Here is a tool to search `parsnip` models:

| <https://www.tidymodels.org/find/parsnip/>

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Bagging in R

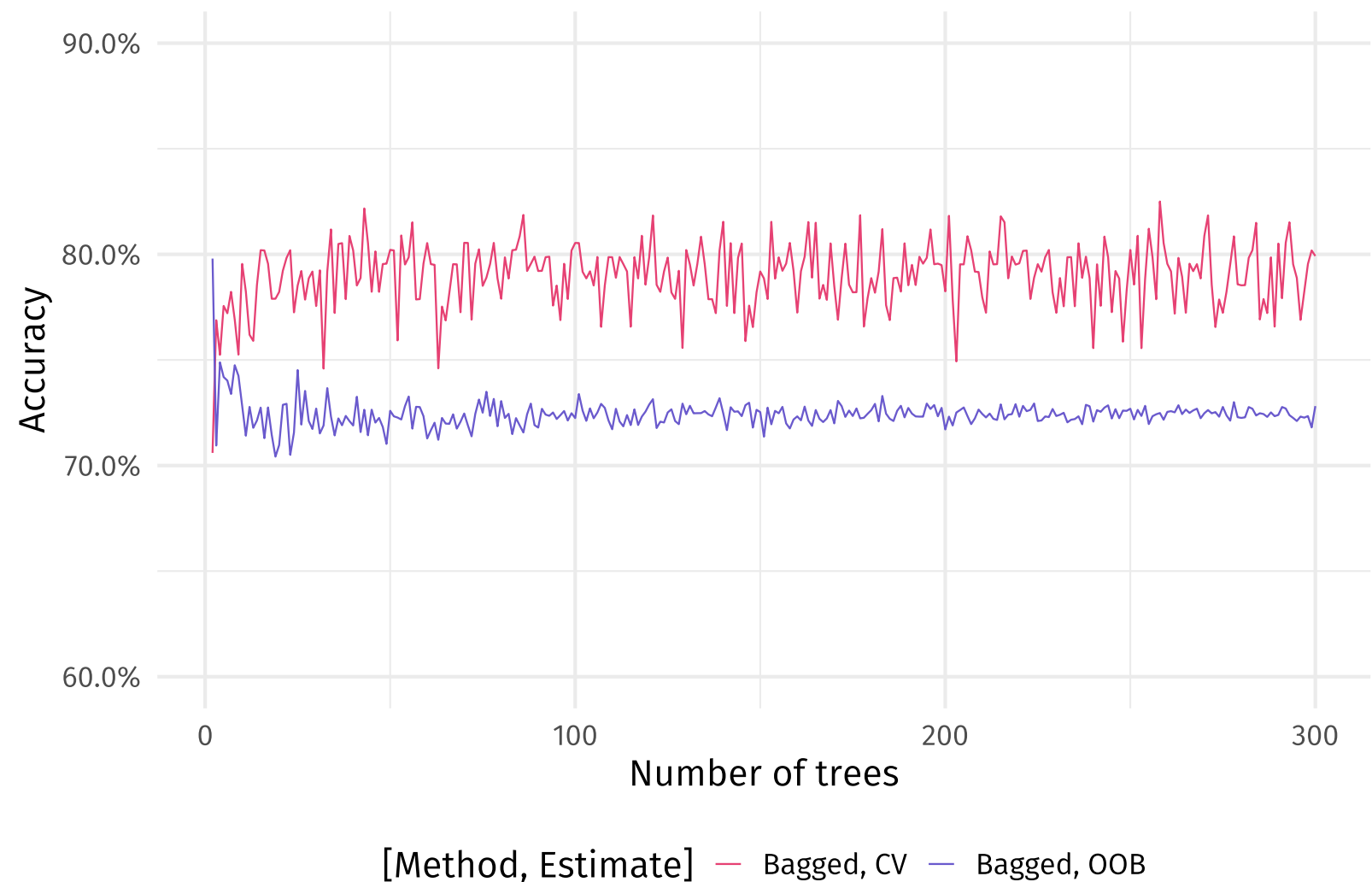
We can use `tidymodels` plus the `baguette` package to bag trees.

Function: `bag_treebag()`

- "Specifies" model for `parsnip`.
- `mode`: `class.`, `reg.`, or `unknown`
- `cost_complexity`: the penalty for model complexity (`cp`)
- `tree_depth`: max. tree depth
- `min_n`: min. # obs. to split
- `class_cost`: magnify *cost*
- `rpart` is the default engine
- `times`: the number of trees

```
# Train a bagged tree model
bag_tree(
  mode = "classification",
  cost_complexity = 0,
  tree_depth = NULL,
  min_n = 2,
  class_cost = NULL
) %>% set_engine(
  engine = "rpart",
  times = 100
)
```

Bagging and the number of trees



Unfortunately, this combination of `rpart` / `baguette` / `parsnip` / `yardstick` doesn't (**currently**) offer OOB-based metrics. 😞

We can "trick" random forests (`ranger`) into doing OOB for bagged trees.

But first, we need to learn about random forests...

... and before *that*, let's briefly talk about variable importance.

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Variable importance

While ensemble methods tend to **improve predictive performance**, they also tend **reduce interpretability**.

We can illustrate **variables' importance** by considering their splits' reductions in the model's performance metric (RSS, Gini, entropy, etc.). 🌳

Note By default, many variable-importance functions will scale importance.

🌳 This idea isn't exclusive to bagging/ensembles; it also works for a single tree.

In the case of "rpart" bagged trees...

```
# Recipe to clean data (impute NAs)
heart_recipe = recipe(heart_disease ~ ., data = heart_df) %>%
  step_medianimpute(all_predictors() & all_numeric()) %>%
  step_modeimpute(all_predictors() & all_nominal())
# Define the bagged tree model
heart_bag = bag_tree(
  mode = "classification",
  cost_complexity = 0,
  tree_depth = NULL,
  min_n = 2,
  class_cost = NULL
) %>% set_engine(
  engine = "rpart",
  times = 100
)
# Define workflow
heart_bag_wf = workflow() %>%
  add_model(heart_bag) %>%
  add_recipe(heart_recipe)
# Fit/assess with CV
heart_bag_fit = heart_bag_wf %>% fit(heart_df)
```

... the fitted object automatically includes variable importance.

```
#> Bagged CART (classification with 100 members)
```

```
#>
```

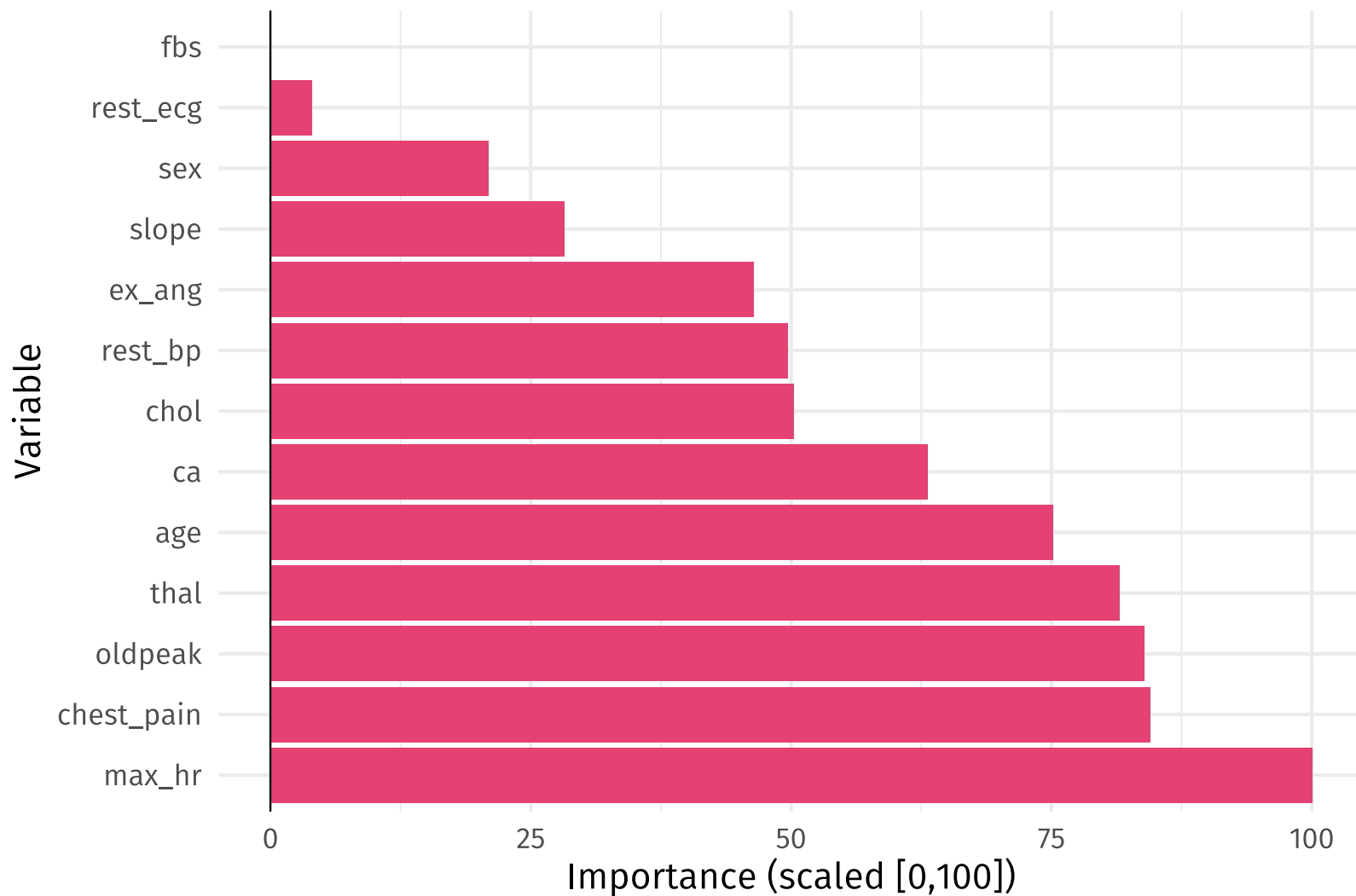
```
#> Variable importance scores include:
```

```
#>
```

```
#> # A tibble: 13 x 4
```

#>	term	value	std.error	used
#>	<chr>	<dbl>	<dbl>	<int>
#> 1	max_hr	42.0	0.856	100
#> 2	chest_pain	35.9	1.29	100
#> 3	oldpeak	35.7	0.704	100
#> 4	thal	34.7	1.21	100
#> 5	age	32.3	0.804	100
#> 6	ca	27.6	1.25	100
#> 7	chol	22.5	0.698	100
#> 8	rest_bp	22.3	0.632	100
#> 9	ex_ang	21.1	0.844	100
#> 10	slope	13.9	0.744	100
#> 11	sex	11.1	0.601	100
#> 12	rest_ecg	4.51	0.283	93
#> 13	fbs	2.95	0.227	91

Variable importance from our bagged tree model.



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Bagging

Bagging has one additional shortcoming...

If one variable dominates other variables, the **trees will be very correlated**.

If the trees are very correlated, then bagging loses its advantage.

Solution We should make the trees less correlated.

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Random forests

Random forests improve upon bagged trees by *decorrelating* the trees.

In order to decorrelate its trees, a **random forest** only **considers a random subset of m ($\approx \sqrt{p}$) predictors** when making each split (for each tree).

Restricting the variables our tree sees at a given split

- nudges trees away from always using the same variables,
- increasing the variation across trees in our forest,
- which potentially reduces the variance of our estimates.

If our predictors are very correlated, we may want to shrink m .

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Random forests

Random forests thus introduce **two dimensions of random variation**

1. the **bootstrapped sample**
2. the m **randomly selected predictors** (for the split)

Everything else about random forests works just as it did with bagging. 🌲

🌲 And just as it did with plain, old decision trees.

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Random forests in R

You have several **options** for training random forests with `tidymodels`. 🌲
E.g., `ranger`, `randomForest`, `spark`.

`rand_forest()` accesses each of these packages via their *engines*.

- The default engine is `"ranger"` (**ranger** package).
- The argument `mtry` gives *m*, the # of predictors at each split.

You've already seen the other hyperparameters for `ranger`:

- `trees` the number of trees in your (random) forest
- `min_n` min. # of observations

🌲 And even more if you look outside of `tidymodels`.

Ensemble methods

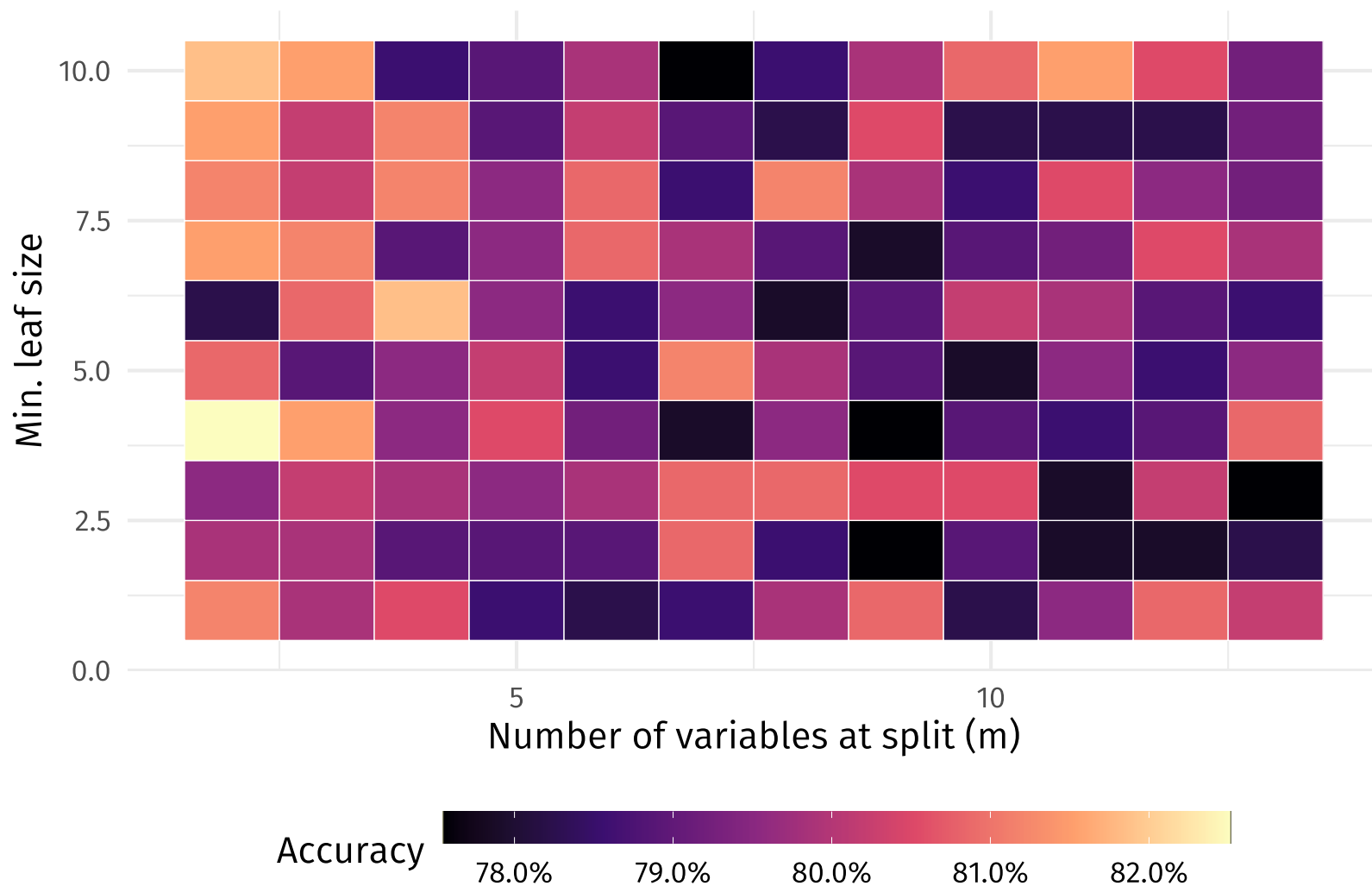
Training a random forest in R using `tidymodels`...

... and `ranger`

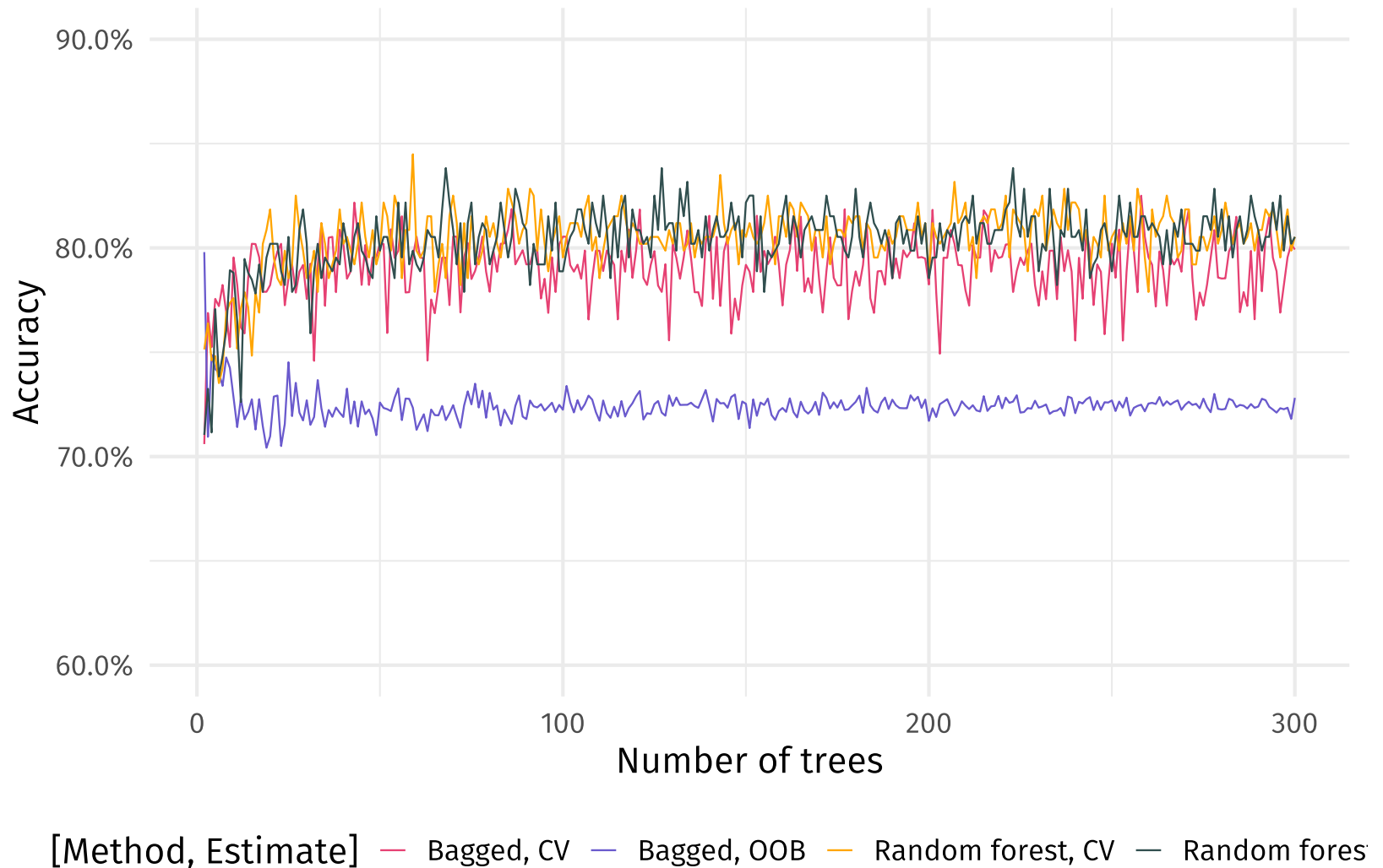
- Goal: Classification
- Three variables per split
- 100 trees in the forest
- At least 2 obs. to split
- Choose the `ranger` engine
- Set a **splitting rule**

```
# Define the random forest
heart_rf = rand_forest(
  mode = "classification",
  mtry = 3,
  trees = 100,
  min_n = 2
) %>% set_engine(
  engine = "ranger",
  splitrule = "gini"
)
```

Accuracy (OOB) across the grid of our parameters.



Tree ensembles and the number of trees



Ensemble methods

Boosting

So far, the elements of our ensembles have been acting independently: any single tree knows nothing about the rest of the forest.

Boosting allows trees to pass on information to each other.

Specifically, **boosting** trains its trees  *sequentially*—each new tree trains on the residuals (mistakes) from its predecessors.

- We add each new tree to our model \hat{f} (and update our residuals).
- Trees are typically small—slowly improving \hat{f} *where it struggles*.

 As with bagging, boosting can be applied to many methods (in addition to trees).

Ensemble methods

Boosting

Boosting has three **tuning parameters**.

1. The **number of trees** B can be important to prevent overfitting.
2. The **shrinkage parameter** λ , which controls boosting's *learning rate* (often 0.01 or 0.001).
3. The **number of splits** d in each tree (trees' complexity).
 - Individual trees are typically short—often $d = 1$ ("stumps").
 - *Remember* Trees learn from predecessors' mistakes, so no single tree needs to offer a perfect model.

Ensemble methods

How to boost

Step 1: Set $\hat{f}(x) = 0$, which yields residuals $r_i = y_i$ for all i .

Step 2: For $b = 1, 2 \dots, B$ do:

A. Fit a tree \hat{f}^b with d splits.

B. Update the model \hat{f} with "shrunk version" of new tree \hat{f}^b

$$\hat{f}(x) \leftarrow \hat{f}(x) + \lambda \hat{f}^b(x)$$

C. Update the residuals: $r_i \leftarrow r_i - \lambda \hat{f}^b(x)$.

Step 3: Output the boosted model: $\hat{f}(x) = \sum_b \lambda \hat{f}^b(x)$.

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Boosting in R

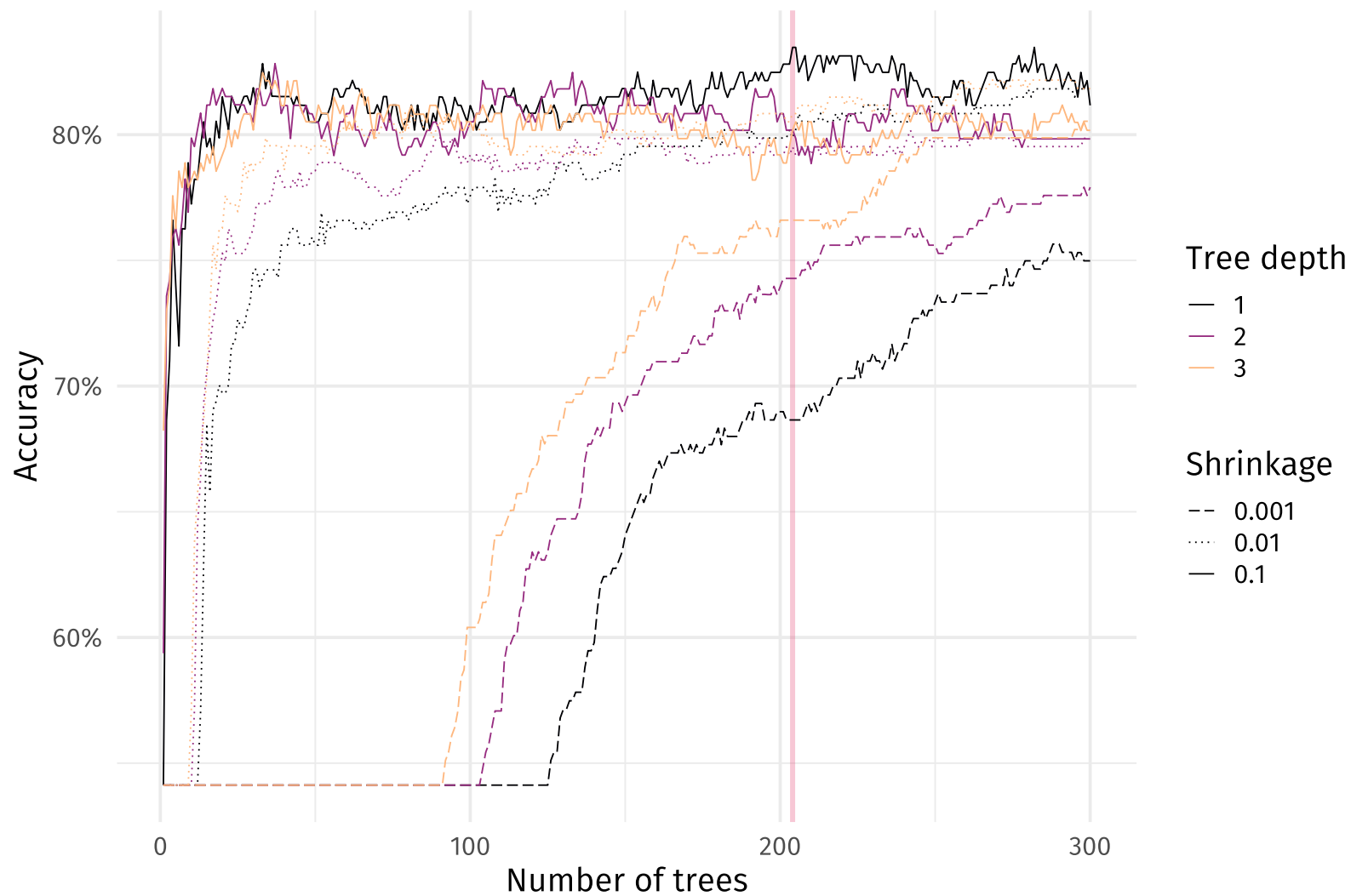
We will use `parsnips`'s `boost_tree()` to train boosted trees. 🌴

`boost_tree()` takes several parameters you've seen—plus one more:

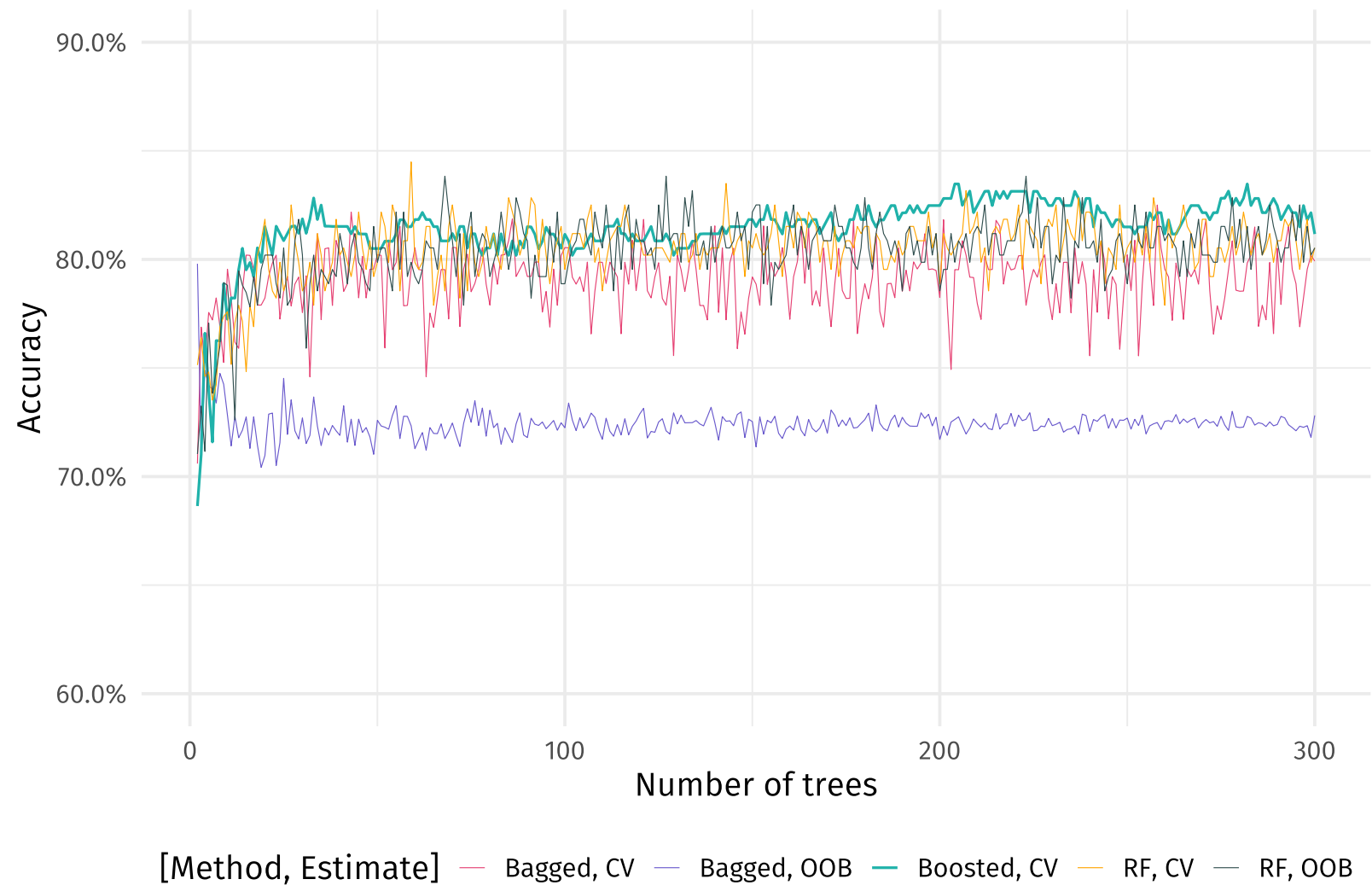
1. `mtry` number of predictors to try at each split
2. `trees`, the number of trees (B)
3. `min_n`, minimum observations to split
4. `tree_depth`, max. tree depth (max. splits from top)
5. `learn_rate`, the learning rate (λ)

🌴 This method uses the `xgboost` package.

Comparing boosting parameters—notice the rates of learning



Tree ensembles and the number of trees



Sources

These notes draw upon

- [An Introduction to Statistical Learning \(ISL\)](#)
James, Witten, Hastie, and Tibshirani

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