# TREE BASED MODELS

## Decision Trees

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# INTRODUCTION

- Decision Trees can be used for
  - Classification
  - Regression
- Decision Trees can be used as standalone algorithms (this is what we do here)
- Decision Trees can be used as components for other models such as:
  - Random Forest Models
  - Boosted Tree Models

# INTRODUCING THE IDEA OF DECISION TREES WITH THE TITANIC DATASET

- Code

| | Survived | Sex | Class | Age | Fare |
|---|---|---|---|---|---|
| 5 | 0 | male | 3 | 35 | 8.0500 |
| 7 | 0 | male | 1 | 54 | 51.8625 |
| 8 | 0 | male | 3 | 2 | 21.0750 |
| 13 | 0 | male | 3 | 20 | 8.0500 |
| 14 | 0 | male | 3 | 39 | 31.2750 |

# GENERATING A DECISION TREE WITH `tidymodels`

Note, `rpart` package needs to be installed. `tidymodels` loads the `rpart` package automatically. Therefore `library(rpart)` is not needed.

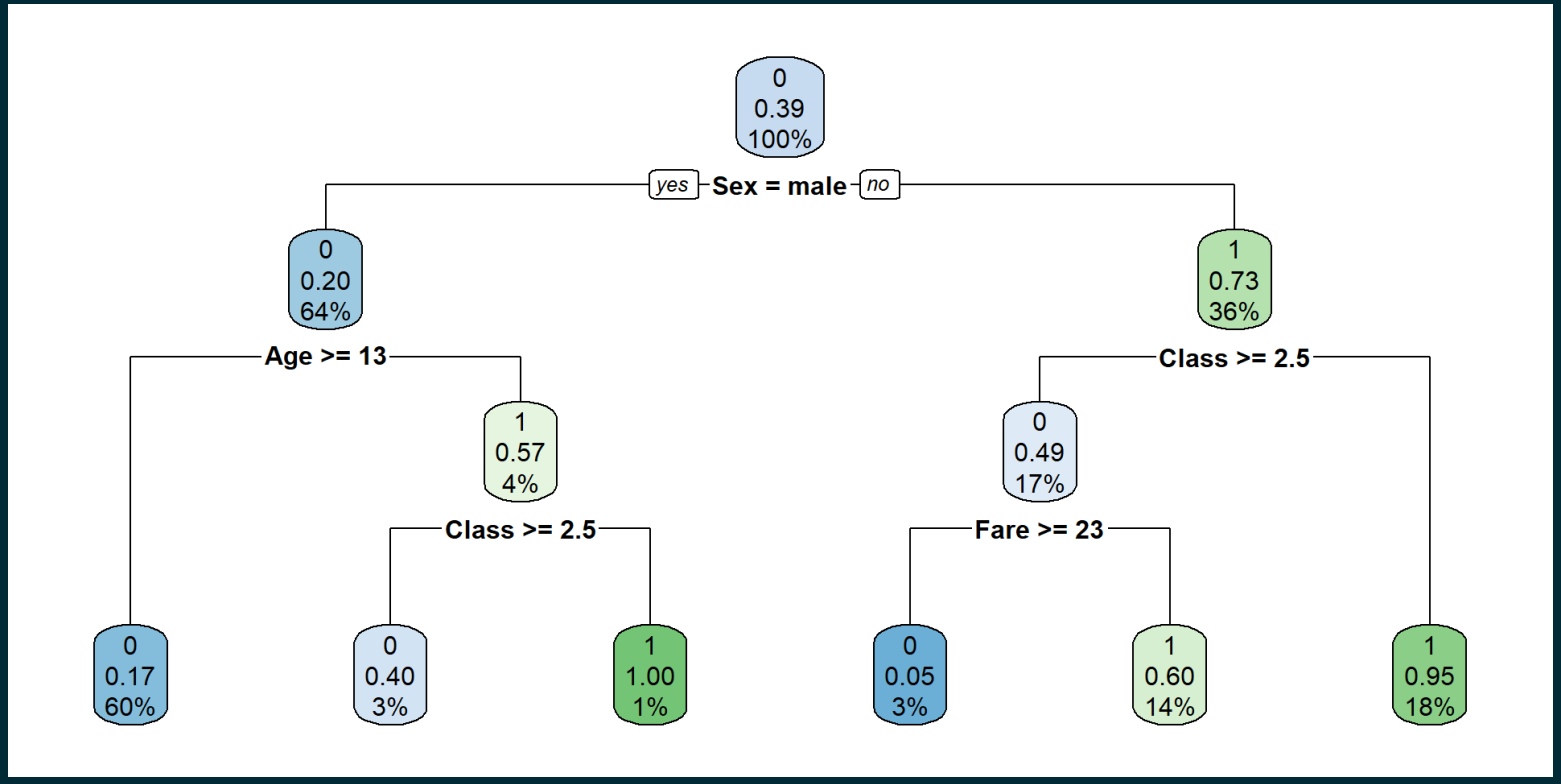
▶ Code

```
══ Workflow [trained] ══════════════════════════════════════════════════════════
Preprocessor: Recipe
Model: decision_tree()

── Preprocessor ────────────────────────────────────────────────────────────────
0 Recipe Steps

── Model ───────────────────────────────────────────────────────────────────────
n= 664

node), split, n, loss, yval, (yprob)
      * denotes terminal node

 1) root 664 256 0 (0.61445783 0.38554217)
   2) Sex=male 428  84 0 (0.80373832 0.19626168)
     4) Age>=13 400  68 0 (0.83000000 0.17000000) *
     5) Age< 13 28  12 1 (0.42857143 0.57142857)
      10) Class>=2 5 20   8 0 (0.60000000 0.40000000) *
```

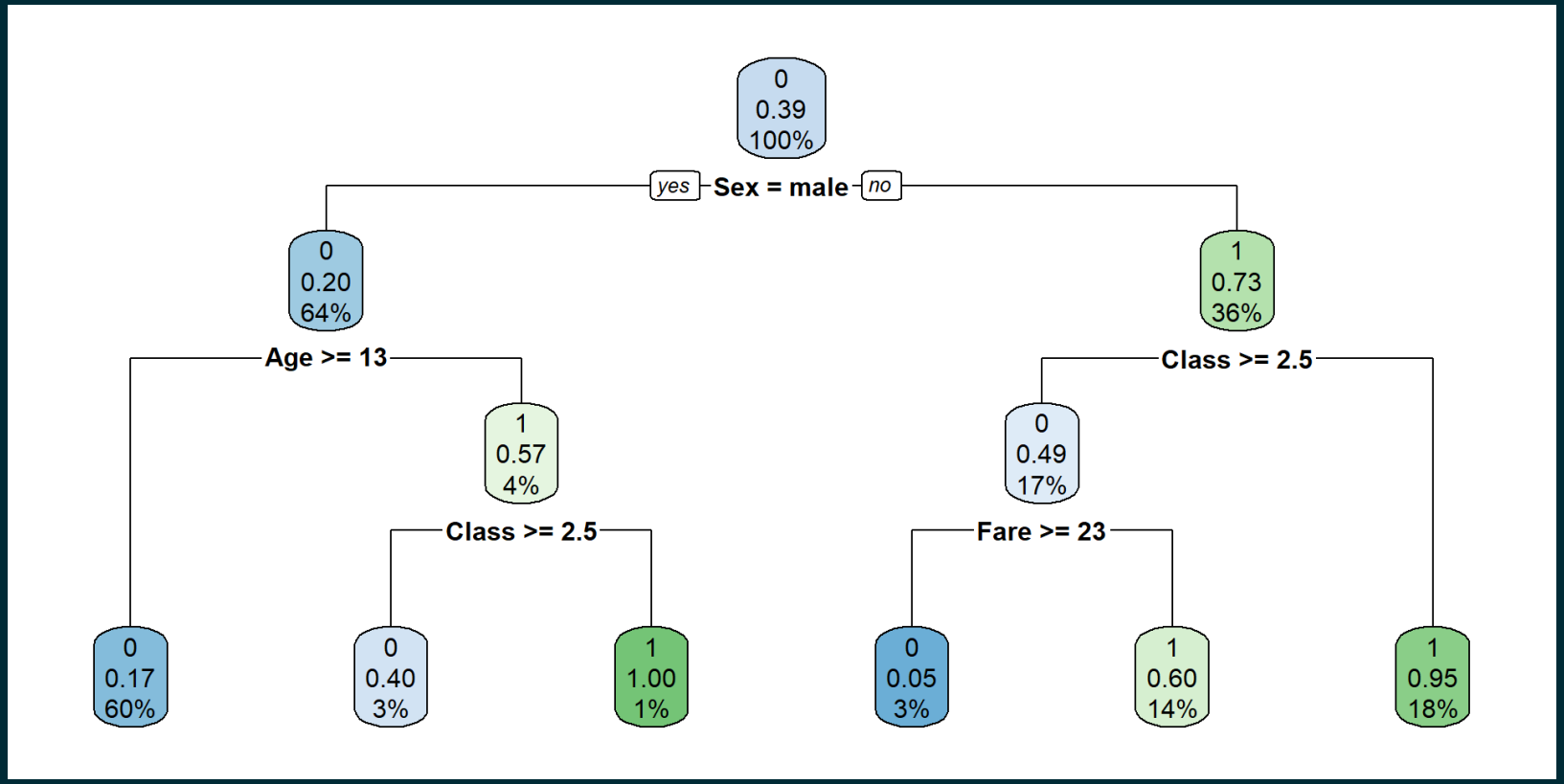
# DISPLAYING THE DECISION TREE WITH `rpart.plot`

Note, `rpart.plot` package needs to be installed and loaded with `library(rpart.plot)`.

- Code



# NODES IN THE DECISION TREE (IGNORE DECISION RULES FOR NOW)




- Nodes are like containers holding all or some of the training data
  - *root* node holds all training records.
  - moving down the tree *parent nodes* get split into *child nodes*
- `RPart` nodes show three types of information.»

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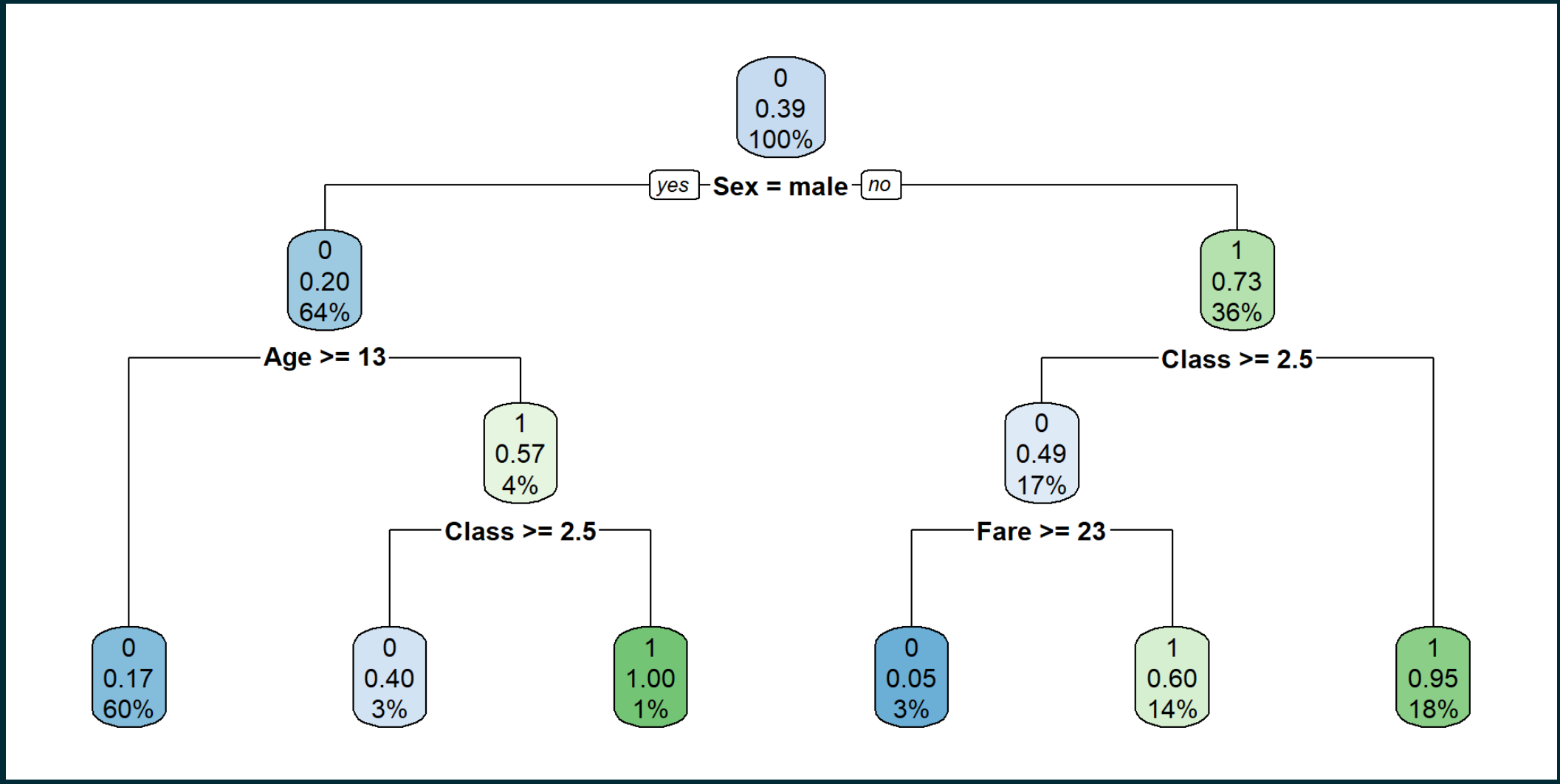
# NODES IN THE DECISION TREE — THE OPTIMIZER CREATED DECISION RULES

Let us follow the last observation in `DataTrain`

| | Survived | Sex | Class | Age | Fare |
|---|---|---|---|---|---|
| 886 | 1 | male | 1 | 26 | 30 |

# NODES IN THE DECISION TREE – INTERPRETING TERMINAL RULES

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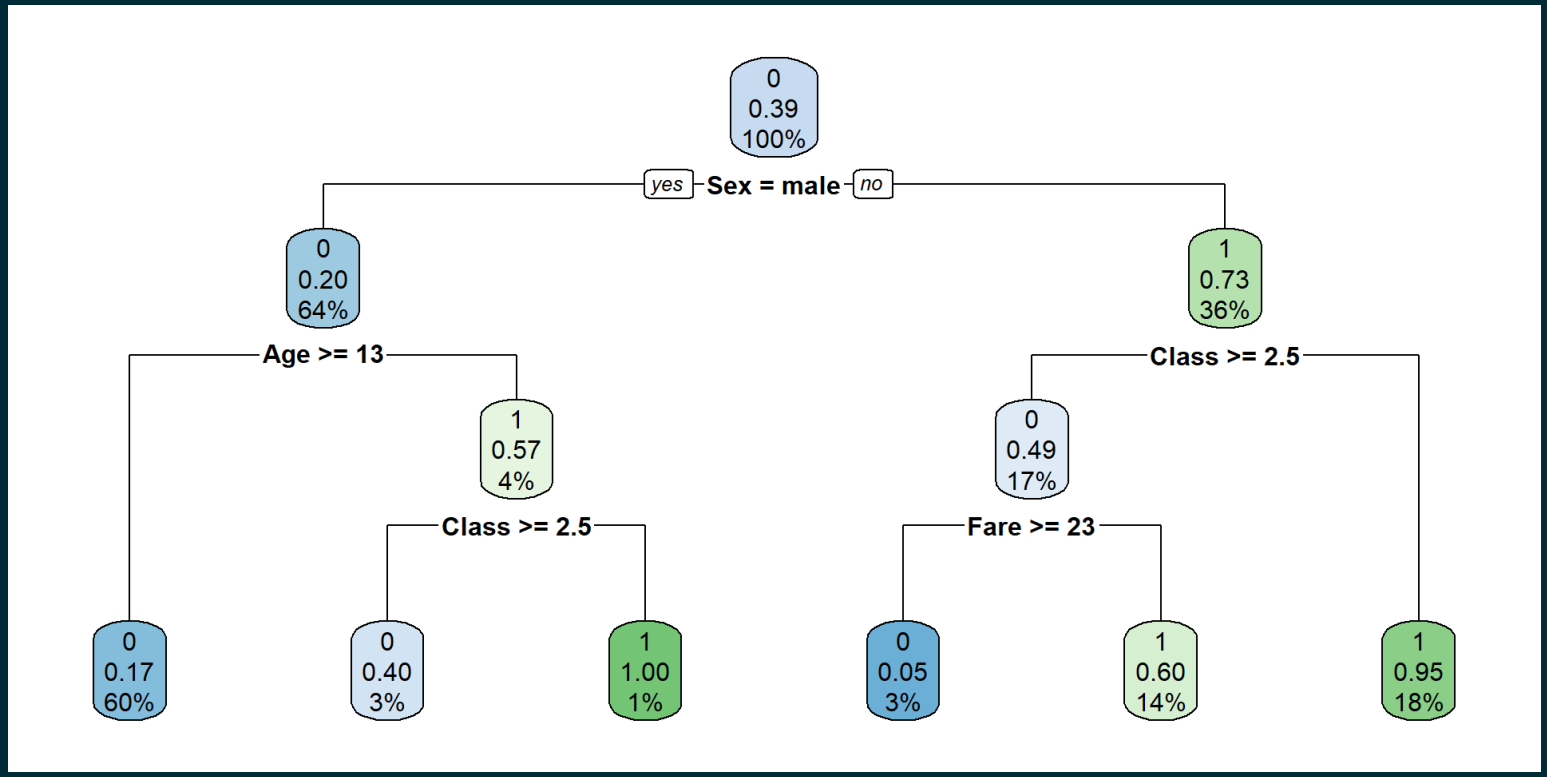
# NODES IN THE DECISION TREE – STYLIZED FACTS




1. Adult male passengers, regardless of the class and fare, had only a survival rate of 17%.
2. Female passengers, regardless of age and not considering the class or the fare, had a survival chance of 73%.
3. Considering the class female passengers traveled in (regardless of age), the survival rate was 95% for First or Second Class.

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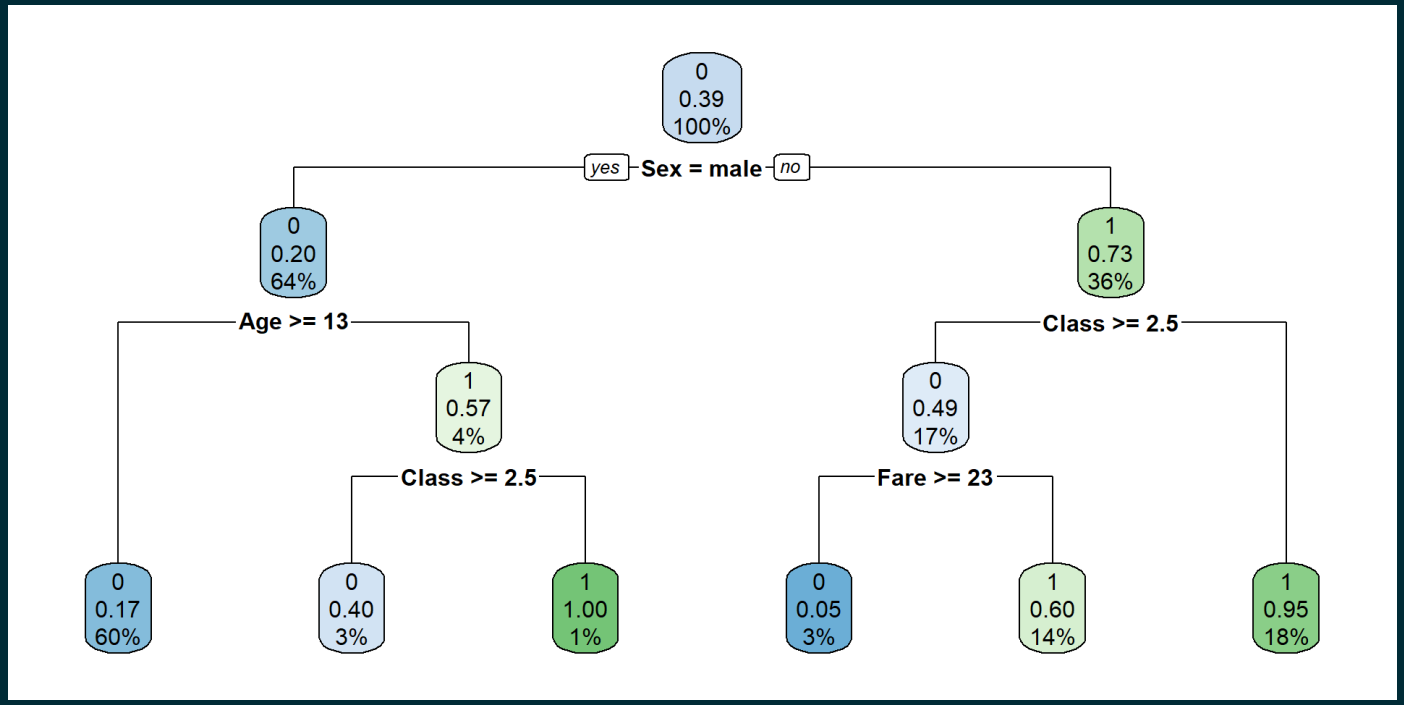
# NODES IN THE DECISION TREE – NOT ALL DECISION RULES MAKE SENSE




For example:

- Females traveling in Third Class have a survival rate of 49% (**this makes sense**)
- Next split **does not make much sense:**
  - Fare greater or equal to 23 British Pounds survival rate only 5%.
  - In contrast, lower fare had a survival rate of 60%.

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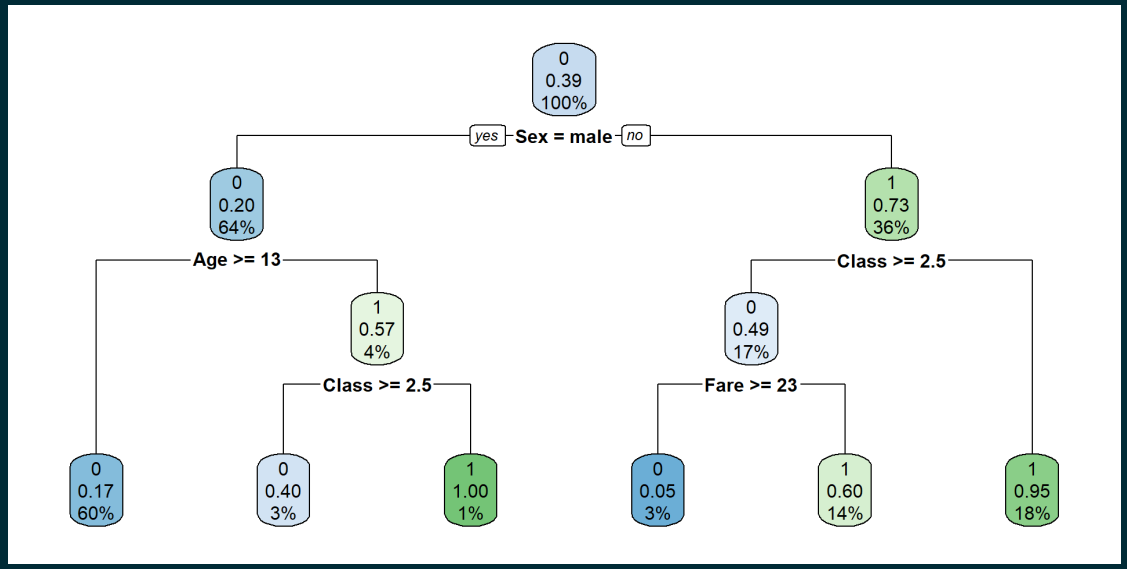
# PREDICTING TESTING DATA WITH A DECISION TREE




Predicting Survival (9-year Old Boy in Third Class)

| Survived | Sex | Class | Age | Fare |
|---|---|---|---|---|
| 1 | male | 3 | 9 | 15.9 |

Prediction: `Not Survived`

Observation is a `false positive` (0=:positive class)

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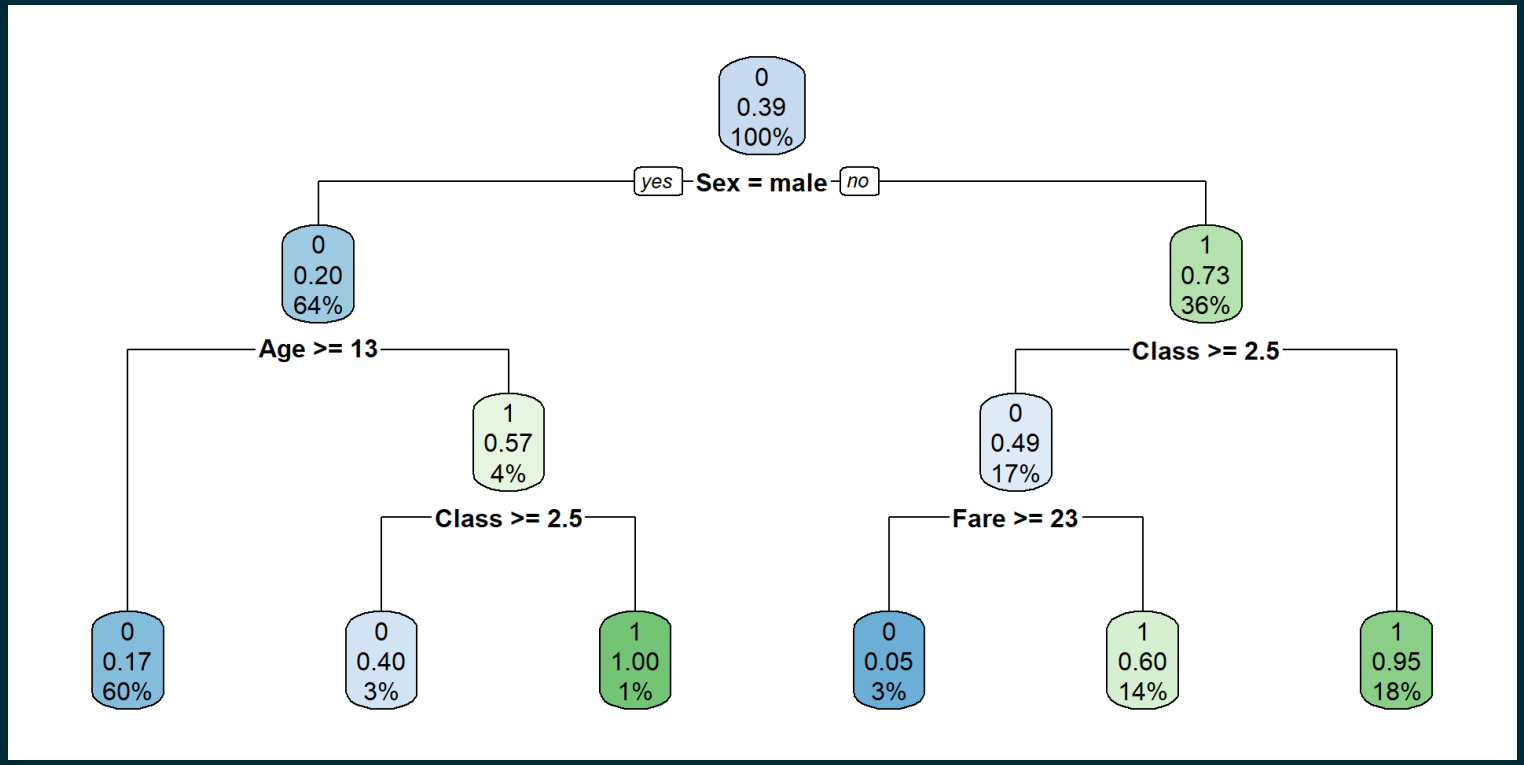
# PREDICTING ALL TESTING DATA WITH A DECISION TREE – PEDICTION




- Code

```
# A tibble: 6 × 8
  Survived Sex    Class   Age  Fare .pred_class .pred_0 .pred_1
  <fct>    <chr>  <int> <dbl> <dbl> <fct>         <dbl>   <dbl>
1 0        male       3    22  7.25 0             0.83    0.17
2 1        female     1    35 53.1  1             0.0492  0.951
3 0        male       3    27  8.46 0             0.83    0.17
4 1        female     3    27 11.1  1             0.402   0.598
5 0        female     3    31 18    1             0.402   0.598
6 0        male       2    35 26    0             0.83    0.17
```

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# PREDICTING ALL TESTING DATA WITH A DECISION TREE – METRICS

```
1  DataTestWithPred=augment(WfModelTitanic, new_data =  DataTest)
```

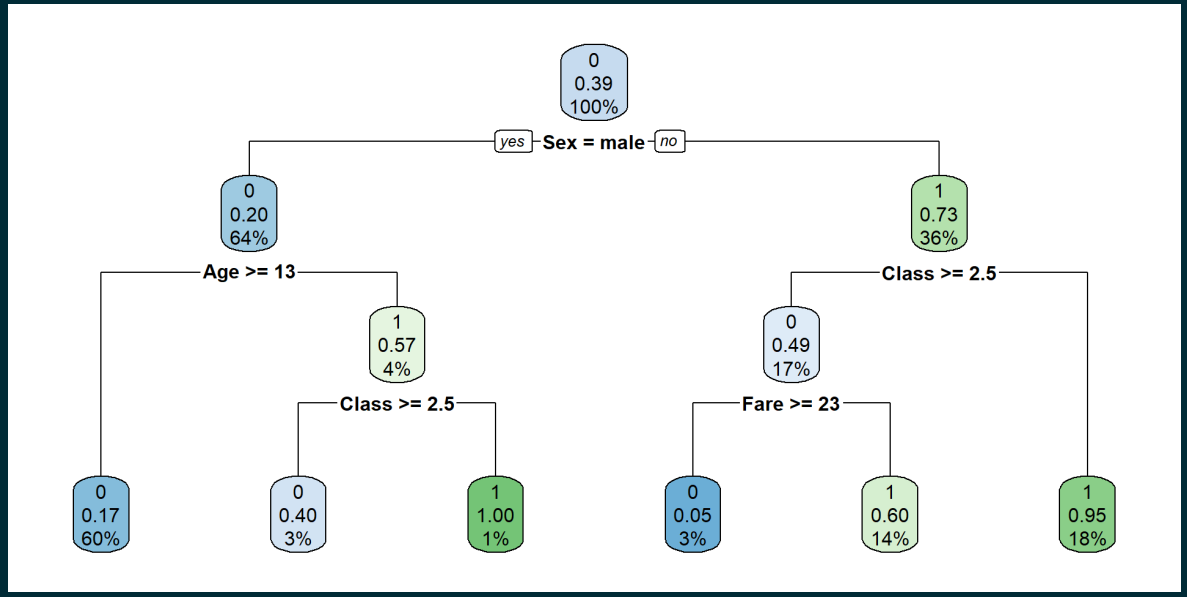
```
1  conf_mat(DataTestWithPred, truth = Survived, estimate = .pred_class)
```

```
          Truth
Prediction   0   1
         0 123  23
         1  14  63
```

```
1  metricSetTitanic=metric_set(accuracy, sensitivity, specificity)
2  metricSetTitanic(DataTestWithPred, truth = Survived, estimate = .pred_class)
```

```
# A tibble: 3 × 3
  .metric     .estimator .estimate
  <chr>       <chr>          <dbl>
1 accuracy    binary         0.834
2 sensitivity binary         0.898
3 specificity binary         0.733
```

# HOW ARE THE DECISION RULES DETERMINED?




The short answer: **by the *Optimizer*.**

- Decision rules are determined from the top down to the bottom.
- Regardless of decision rule on next level.
  - No turning back reversing decision rule on higher level.
  - *greedy algorithm*
- Decision rules consists of two components:
  i. the **splitting variable**,
  ii. the **splitting value** (e.g., `Age` for splitting (here: `Age>=13` for `yes`)

*Optimizer* compares all *splitting variables* and all possible *splitting values* to find **best decision rule**.

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# CRITERIA TO QUANTIFY QUALITY OF DECISION RULES

**How can we determine if a decision rule is good?**

Common criteria for categorical outcomes:

- *Information Gain*
- *Chi-Square*
- **Gini Impurity** used by `RPart` »

# HOW ARE THE DECISION RULES DETERMINED? — GINI IMPURITY CRITERIUM

**Gini Impurity** is calculated for an individual node and estimates ” (…) the probability that two entities taken at random from the dataset of interest (with replacement) represent (…) different types.” (Wikipedia contributors. 2022. “Diversity Index — Wikipedia, the Free Encyclopedia.”)

# CRITERIA TO ASSESS DECISION RULES – GINI IMPURITY

$$G^{Imp} = 1 - \overbrace{(P^2_{Surv.} + \underbrace{P^2_{NotSurv.}}_{(1-P_{Surv.})^2})}^{\text{Prob. for 2 identical outcomes}}$$

$P_{Surv.}$ := Proportion Surv.
and
$P_{NotSurv.}$ := Proportion Not Surv.

# CRITERIA TO ASSESS DECISION RULES – GINI IMPURITY

$$
\begin{aligned}
G^{Imp} &= 1 - \left(P^2_{Surv.} + (1 - P_{Surv.})^2\right) \\
G^{Imp} &= 1 - P^2_{Surv.} - 1 + 2P_{Surv.} - P^2_{Surv.} \\
G^{Imp} &= 2P_{Surv.} - 2P^2_{Surv.} \\
G^{Imp} &= 2P_{Surv.}(1 - P_{Surv.})
\end{aligned}
$$

# QUANTIFYING QUALITY OF DECISION RULES – GINI IMPURITY

$$G^{Imp} = 2P_{Surv.}(1 - P_{Surv.})$$

**Purest Possible Node:**

- Only *Survived* observations: $P_{Surv.} = 1$ and $(1 - P_{Surv.}) = 0$
- *or*
- only *Not Survived* observations: $P_{Surv.} = 0$ and $(1 - P_{Surv.}) = 1$
- **In any case:** $G^{Imp} = 0$
  (probability of drawing two different outcomes = 0)

# QUANTIFYING QUALITY OF DECISION RULES – GINI IMPURITY

$$G^{Imp} = 2P_{Surv.}(1 - P_{Surv.})$$

**Impurest Possible Node:**

- Equal amount of *Survived* and *Not Survived* observations:
  $P_{Surv.} = 0.5$ and $(1 - P_{Surv.}) = 0.5$
- $G^{Imp} = 2 \cdot 0.25 \cdot 0.25 = 0.5$
  (Note, $G^{Imp} = 0.5$ is maximum for Gini Impurity for 2 categories)

# DETERMINING IMPURITY FOR ROOT'S PARENT AND CHILD NODES

# REAL WORLD DATA WITH A DECISION TREE

Predicting vaccination rates in the U.S. based on data from September 2021.

- Outcome variable: Percentage of fully vaccinated (two shots) people ($PercVacFull$).
- Data from 2,630 continental U.S. counties.

# REAL WORLD DATA WITH A DECISION TREE – PREDICTOR VARIABLES

- Race/Ethnicity:
  - Counties' proportion African Americans ($PercBlack$),
  - Counties' proportion Asian Americans ($PercAsian$), and
  - Counties' proportion Hispanics ($PercHisp$)
- Political Affiliation (Presidential election 2020):
  - Counties' proportion Republican votes ($PercRep$)
- Age Groups in Counties:
  - Counties' proportion young adults (20-25 years); $PercYoung25$
  - Counties' proportion older adults (65 years and older); $PercOld65$)
- Income related:
  - Proportion of households receiving food stamps ($PercFoodSt$)

# LOADING THE DATA AND ASSIGNING TRAINING AND TESTING DATA

▶ Code

| County | State | PercVacFull | PercRep | PercAsian | PercBlack | PercHisp | PercYoung2 |
|---|---|---|---|---|---|---|---|
| Baldwin | AL | 0.504 | 0.7506689 | 0.0092 | 0.0917 | 0.0456 | 0.063418 |
| Barbour | AL | 0.416 | 0.4911710 | 0.0048 | 0.4744 | 0.0436 | 0.073464 |
| Chambers | AL | 0.315 | 0.7063935 | 0.0112 | 0.3956 | 0.0238 | 0.064653 |
| Cherokee | AL | 0.318 | 0.8319460 | 0.0025 | 0.0460 | 0.0159 | 0.052545 |
| Choctaw | AL | 0.648 | 0.7445596 | 0.0013 | 0.4255 | 0.0041 | 0.061241 |
| Cleburne | AL | 0.319 | 0.8402859 | 0.0002 | 0.0275 | 0.0246 | 0.059486 |

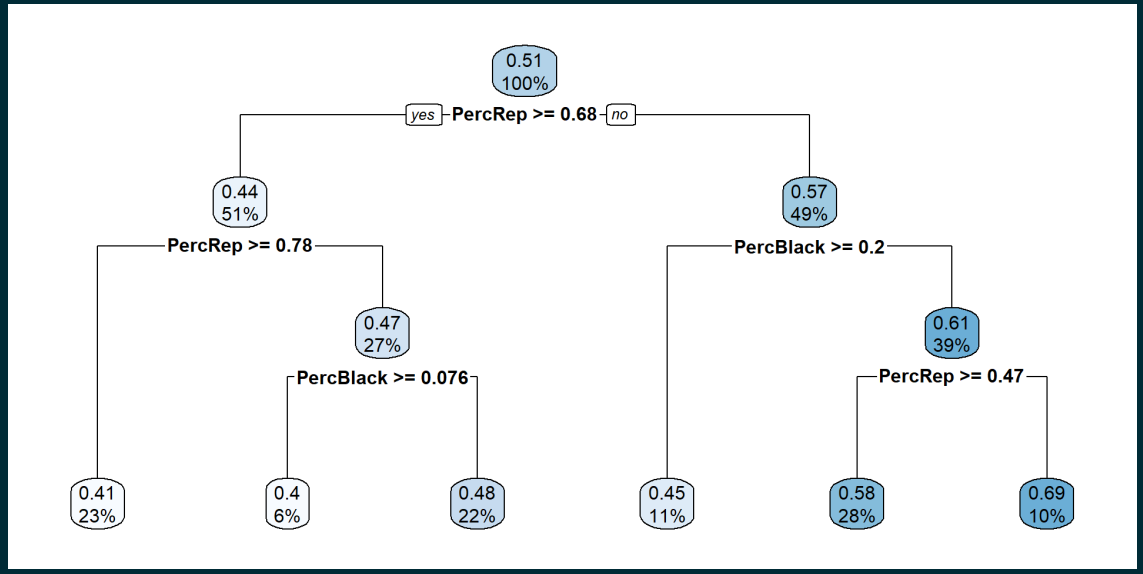
# CREATING MODEL DESIGN, RECIPE, AND FITTED WORKFLOW

- Code

```
══ Workflow [trained] ══════════════════════════════════════════════════════════
Preprocessor: Recipe
Model: decision_tree()

── Preprocessor ────────────────────────────────────────────────────────────────
0 Recipe Steps

── Model ───────────────────────────────────────────────────────────────────────
n= 2234

node), split, n, deviance, yval
      * denotes terminal node

 1) root 2234 47.539570 0.5068938
   2) PercRep>=0.683455 1132 14.614060 0.4410887
     4) PercRep>=0.7847773 522  5.763314 0.4119579 *
     5) PercRep< 0.7847773 610  8.028707 0.4660172
      10) PercBlack>=0.0755 129  2.231454 0.3983725 *
```

# DECISION TREE FOR THE VACCIANTION MODEL

- Code




What is difference compared to a classigication model?

- Terminal node stimates now continous variable.
- Variance instead of Gini Impurity

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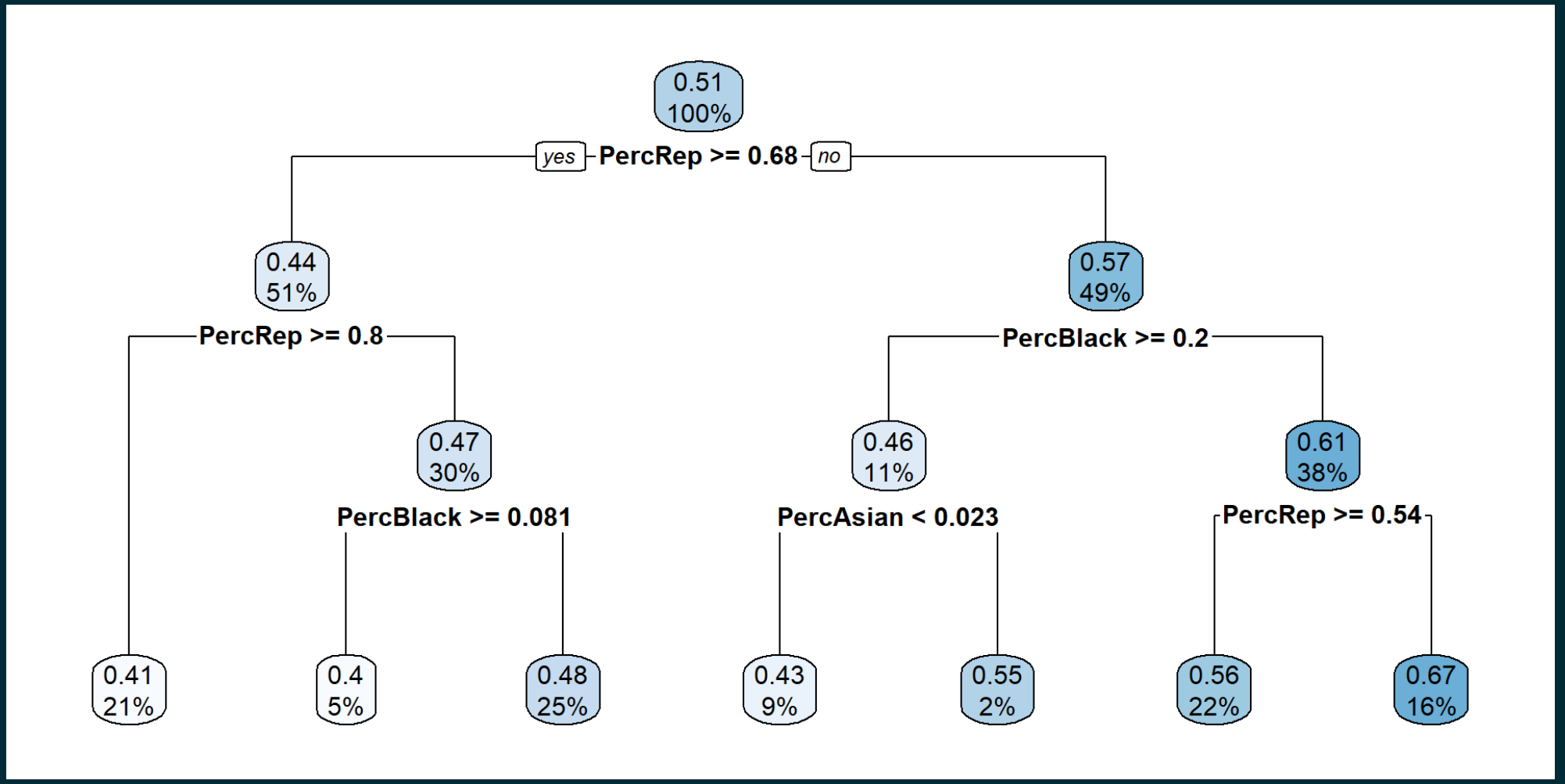
# METRICS FOR THE DECISION TREE VACCINATION MODEL

▶ Code

```
# A tibble: 3 × 3
  .metric .estimator .estimate
  <chr>   <chr>          <dbl>
1 rmse    standard       0.120
2 rsq     standard       0.341
3 mae     standard       0.0852
```

# INSTABILITY OF DECISION TREES

- Code

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# METRICS FOR THE (SLIGHTLY) CHANGED DECISION TREE VACCINATION MODEL

- Code

```
# A tibble: 3 × 3
  .metric .estimator .estimate
  <chr>   <chr>          <dbl>
1 rmse    standard       0.129
2 rsq     standard       0.323
3 mae     standard       0.0918
```

# WHEN AND WHEN NOT TO USE DECISION TREES