ML basics + classification

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Classical ML

- Can be broken down into two main categories

  - Supervised ML

    - Regression - Predict **value** based on past

    - Classification - Predict **group** based on past

  - Unsupervised ML

    - Clustering - Break into **groups**

    - Dimensionality Reduction - "Important" components

    - Anomaly Detection - "Weirdness"

The process

- Let there be some **feature(s)** x

- Let there be some **outcome** y

- Then, there exist some **hypothesis** h of the relationship between x and y

- This hypothesis relies on **parameters** K

- Using some **loss** L that we try to minimize, we estimate the best **parameters** for the given **hypothesis**

Parameters vs Hyperparameters

- **Parameters** - Parameters are the internal variables of a model that are learned from data during training.

- **Hyperparameters** - Hyperparameters are external settings chosen before training that control the learning process.
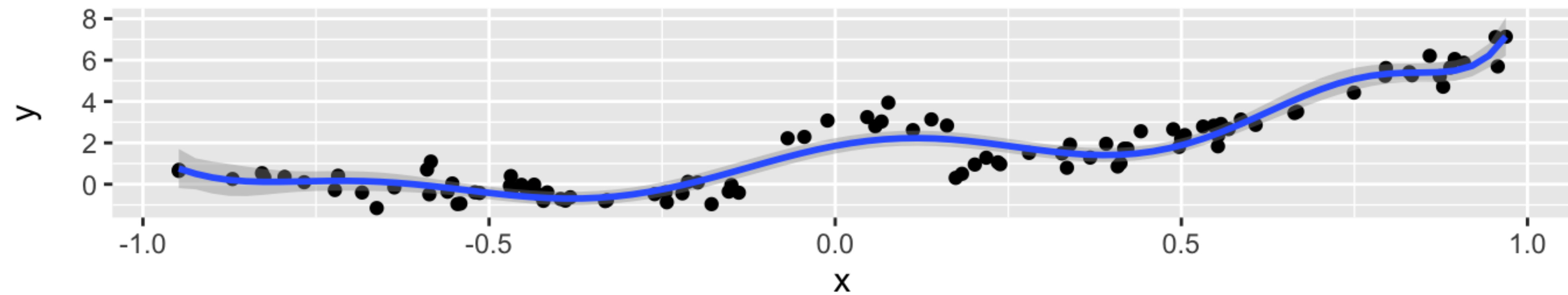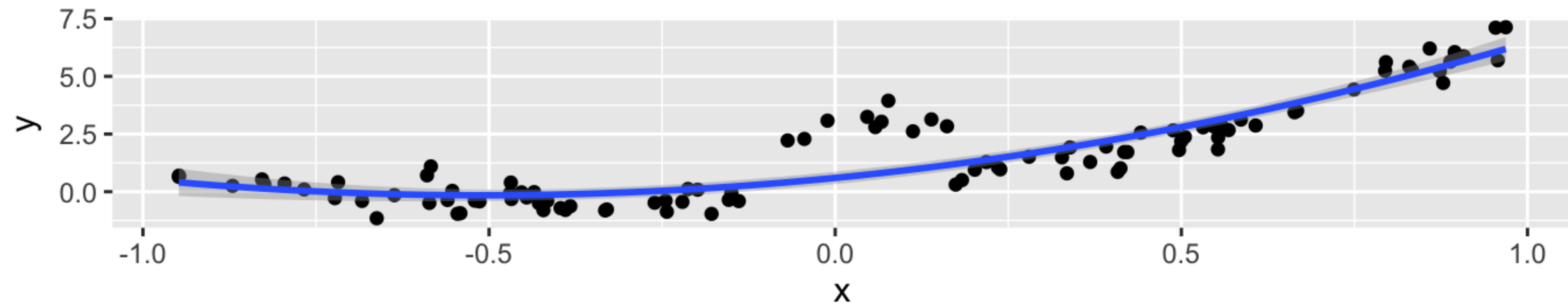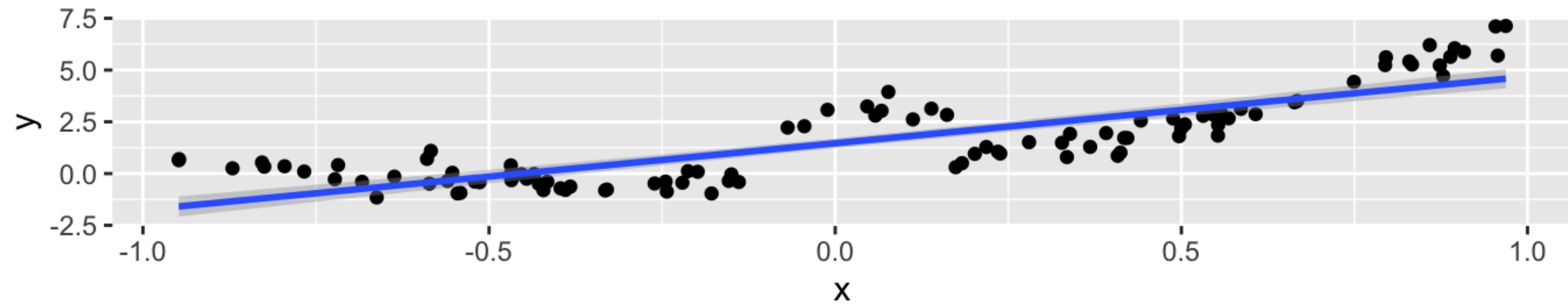
Underlying pattern vs sticking to points
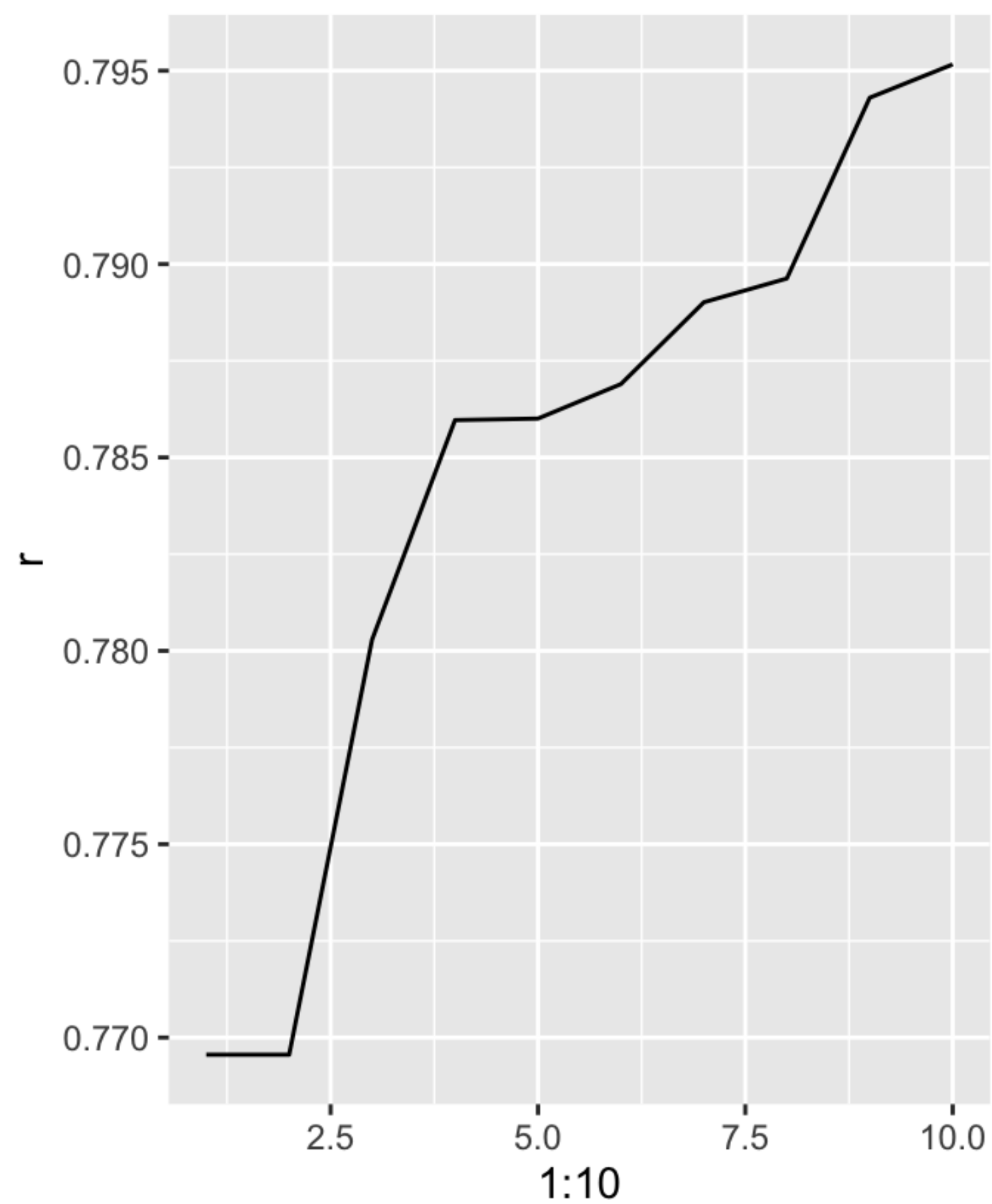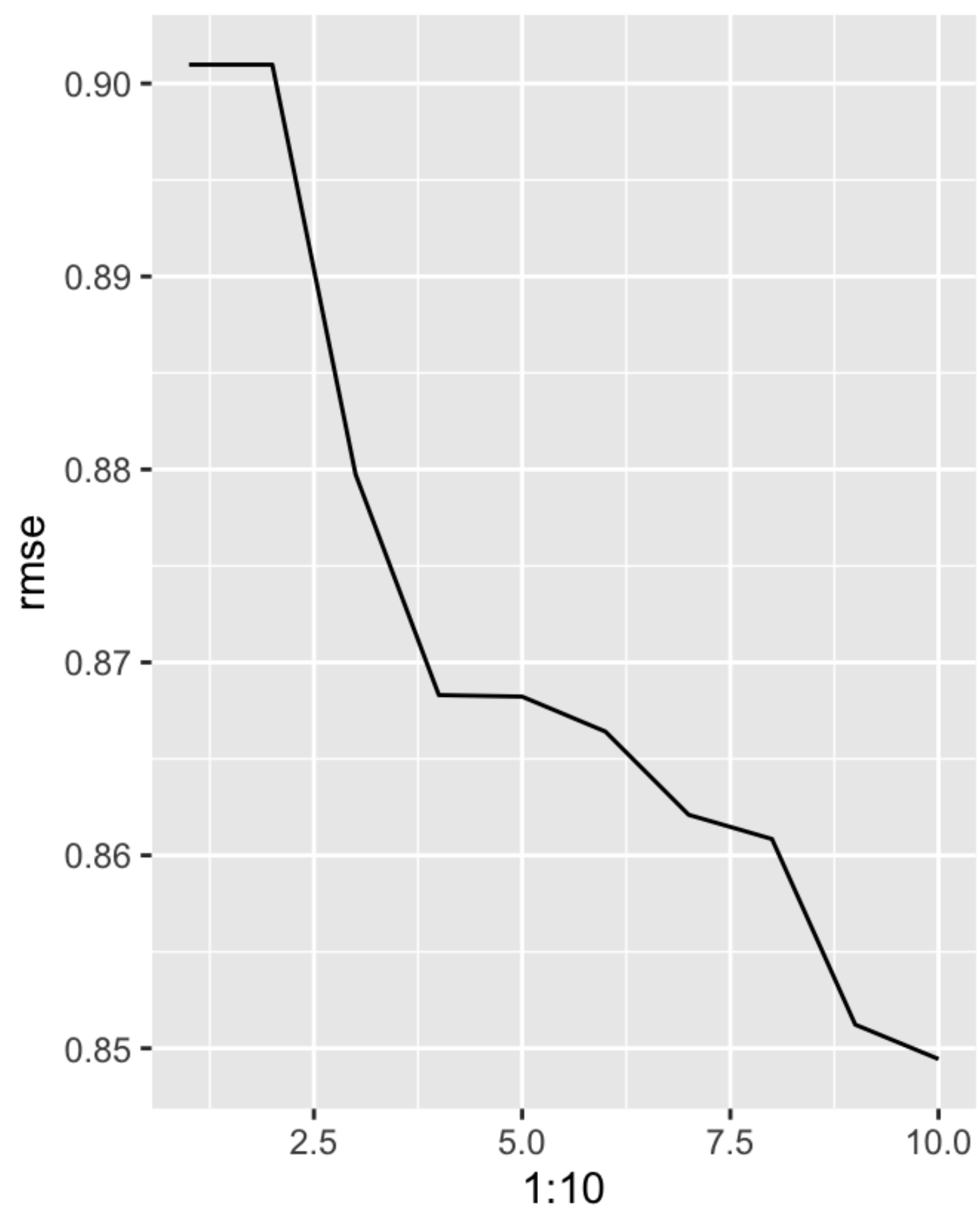
Bias Variance tradeoff

overfitting and underfitting

Ways to Combat

- Testing training split

- Cross validation split
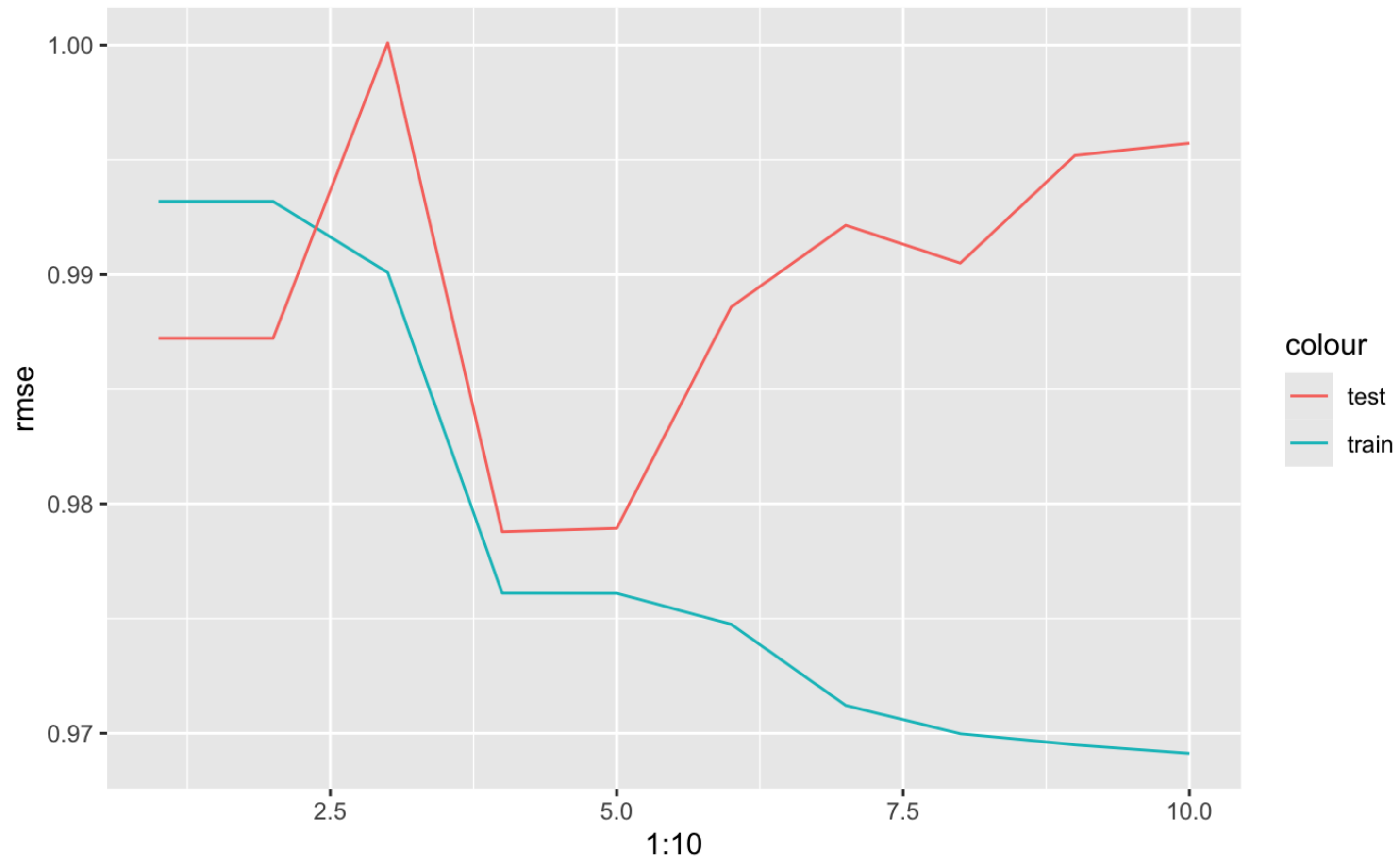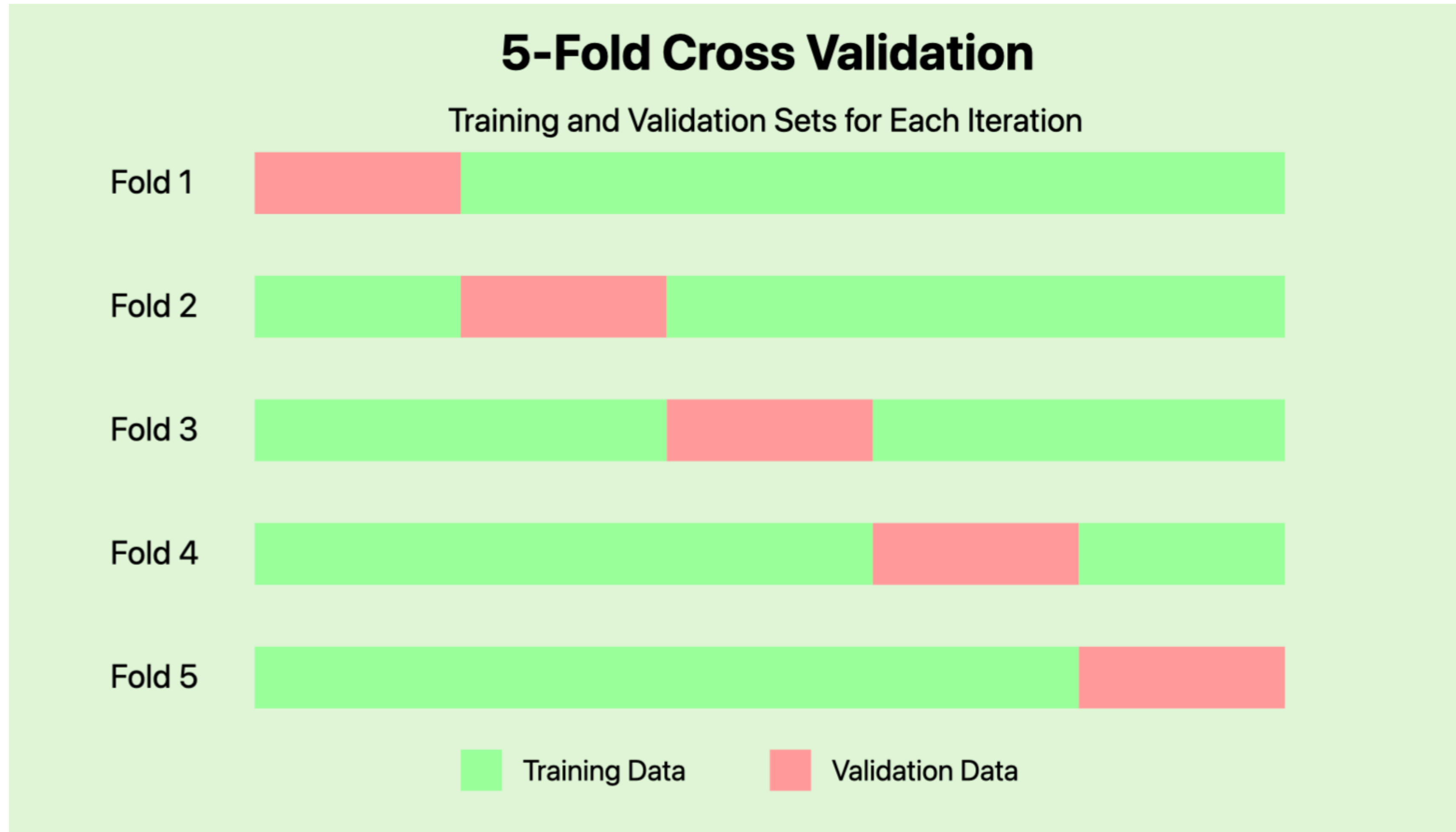
Training vs Test
Training on everything

Training vs Test
Training vs testing 80-20

Cross Validation
Training on everything

Classification!

Logistic Regression

Health insurance coverage

- Yes or No?

- What will we predict?

```r
health %>%
  pull(coverage) %>%
  table()
```

```
.
    0     1
13691 61114
```

Health insurance coverage

- Yes or No?

- Against Age
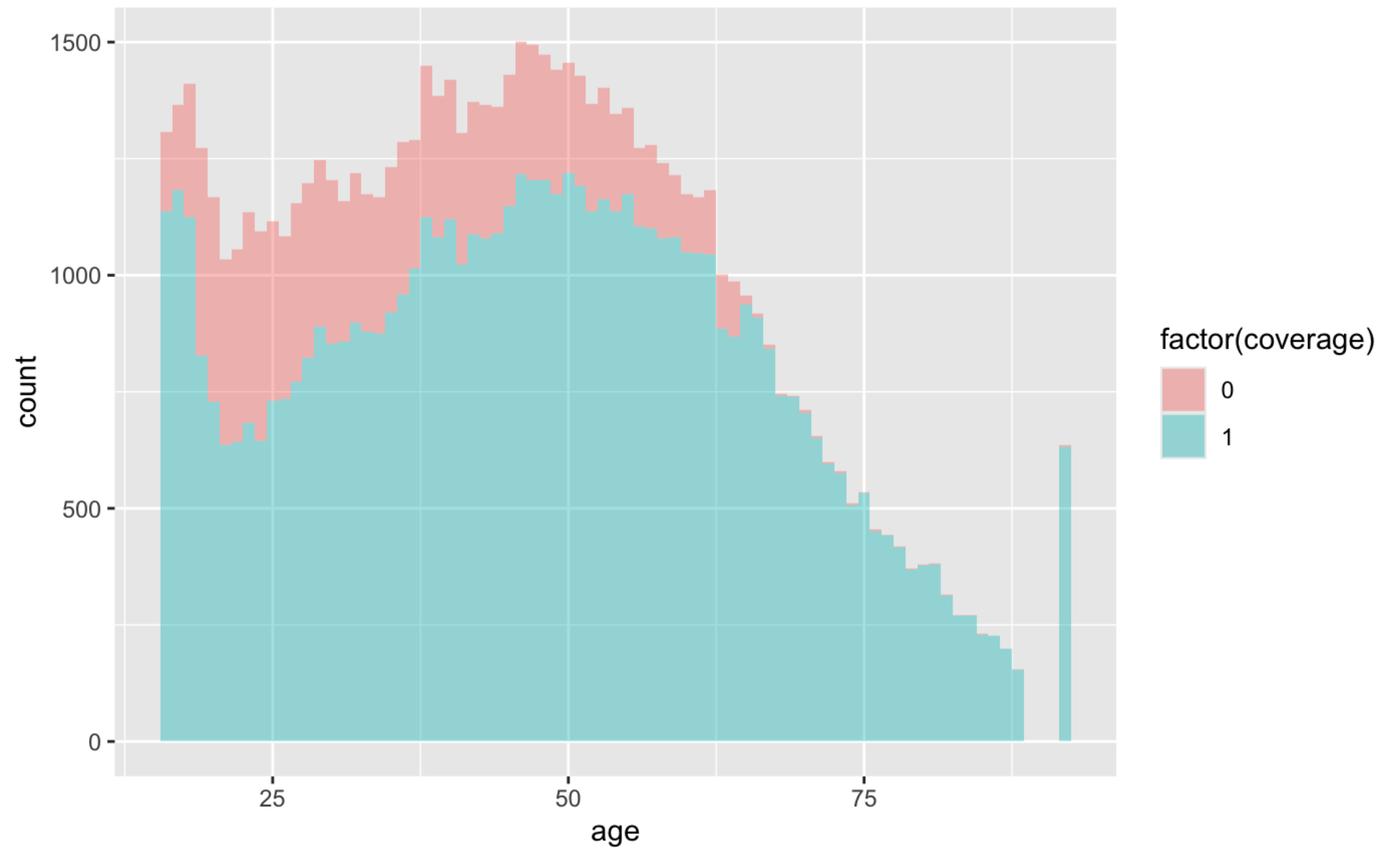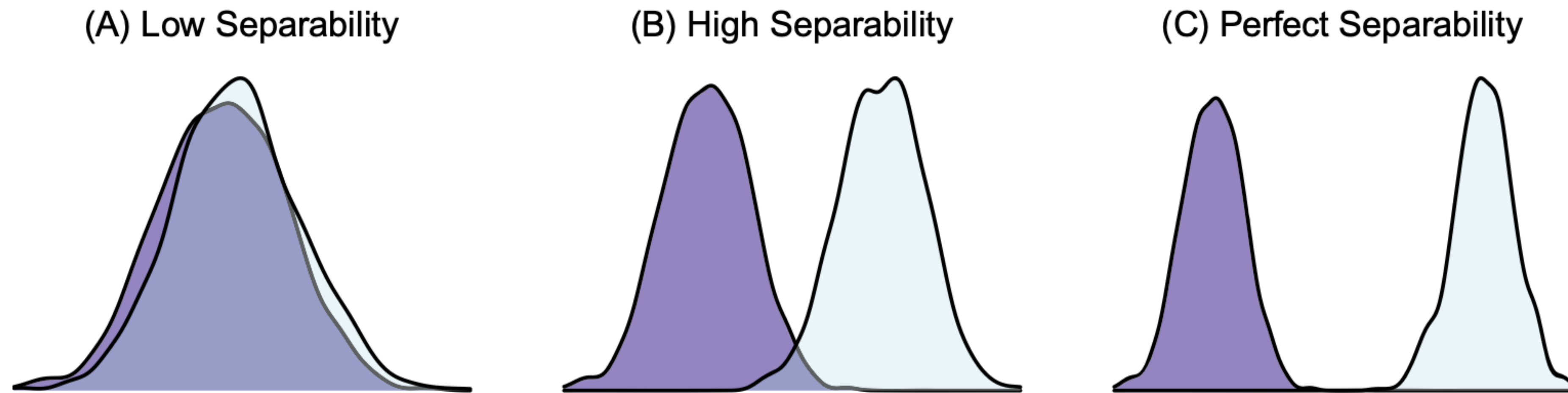
Figure 8.1: Separability can be easily seen in the distributions of a continuous variable when separated into two classes. These kernel density diagrams illustrate three scenarios: (A) Low Separability, (B) High Separability, (C) Perfect Separability.

Health insurance coverage
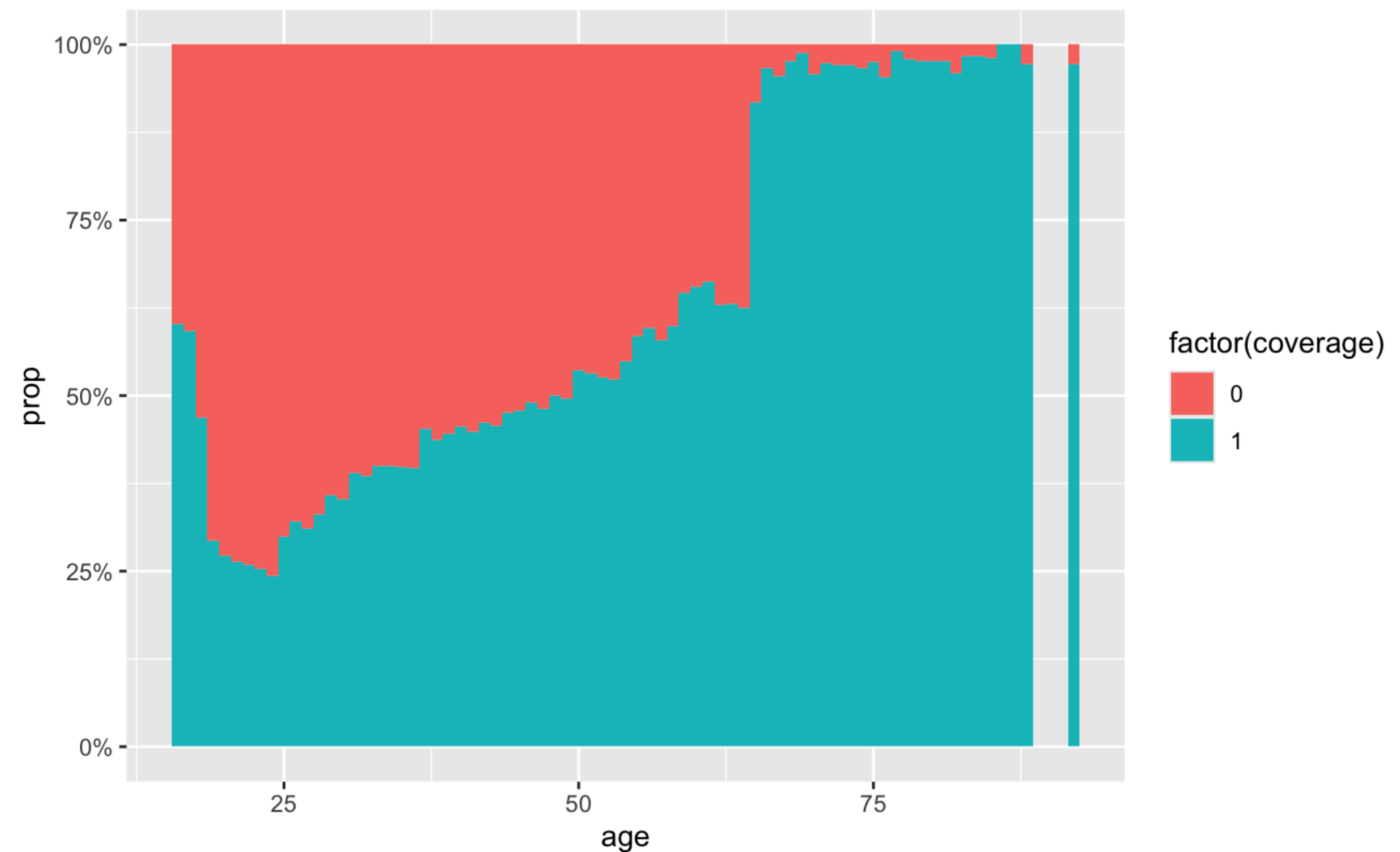
- Yes or No?

- Against Age

Health insurance coverage

- Yes or No?

- Against Age

```r
linear_reg() %>%
  fit(formula = coverage ~ age, data = health) %>%
  tidy()
```

A tibble: 2 × 5

term <chr>	estimate <dbl>	std.error <dbl>	statistic <dbl>	p.value <dbl>
(Intercept)	0.576725845	3.729793e-03	154.62678	0
age	0.005225987	7.545483e-05	69.25981	0

2 rows

Health insurance coverage

- Yes or No?
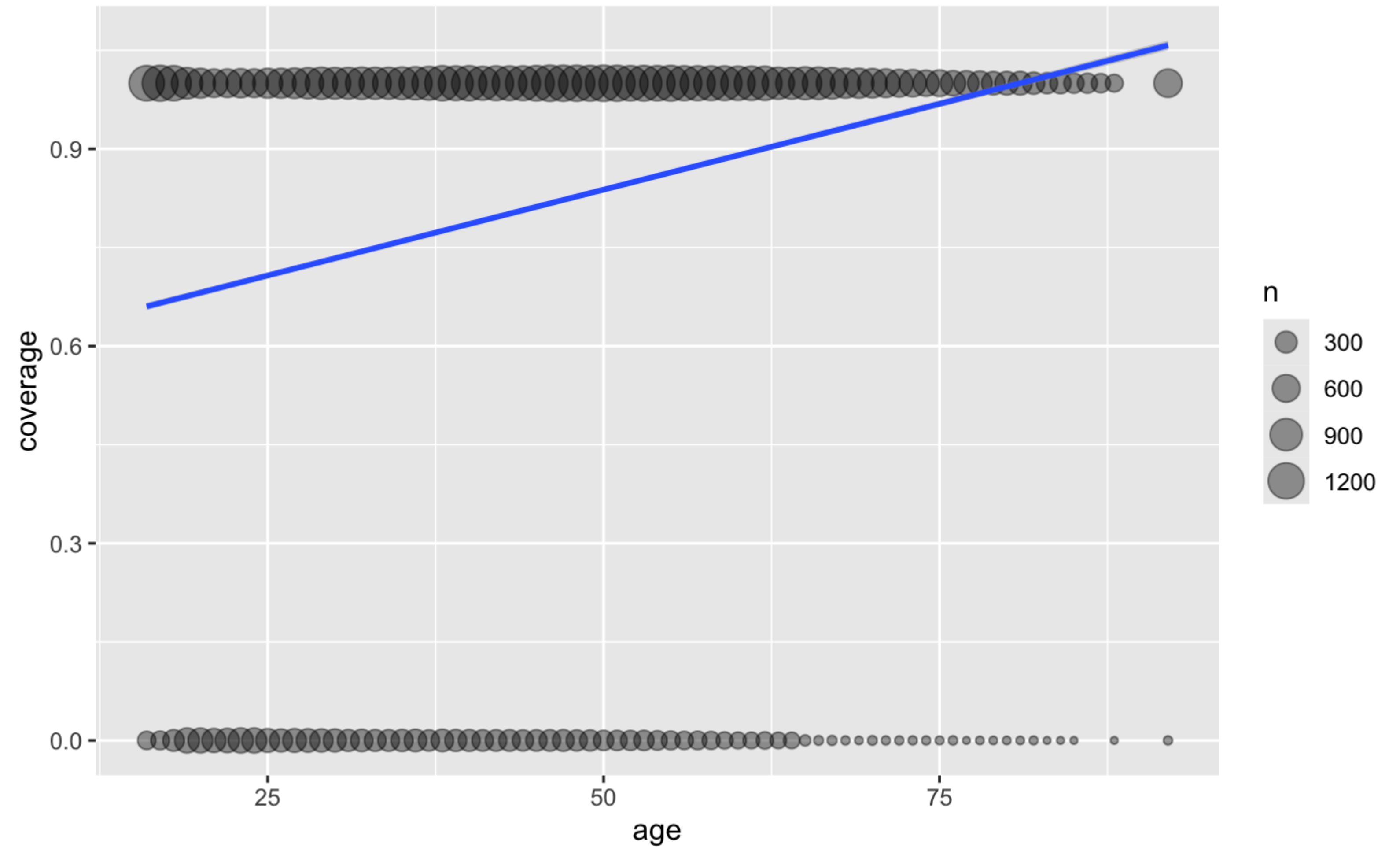
- Against Age

Logistic Regression!

```r
57
58  ```{r}
59
60  log_reg_fit <- logistic_reg() %>%
61    fit(formula = coverage ~ age, data = health)
62
63  log_reg_fit %>%
64    tidy()
65  ```
```

A tibble: 2 × 5

term <chr>	estimate <dbl>	std.error <dbl>	statistic <dbl>	p.value <dbl>
(Intercept)	−0.17773347	0.0255674024	−6.951565	3.612551e−12
age	0.03981371	0.0006140727	64.835498	0.000000e+00

2 rows

- Coefficient - "Average Change in Log Odds"

- e^coef - "Average Change in Odds"

- Probability of event -

  - Find y

  - p = e^y / (1 + e^y)

```{r}
health %>% mutate(pred_y = (age * 0.03981371) - 0.17773347) %>%
  ggplot(data = .) + geom_point(aes(x = age, y = pred_y))
```
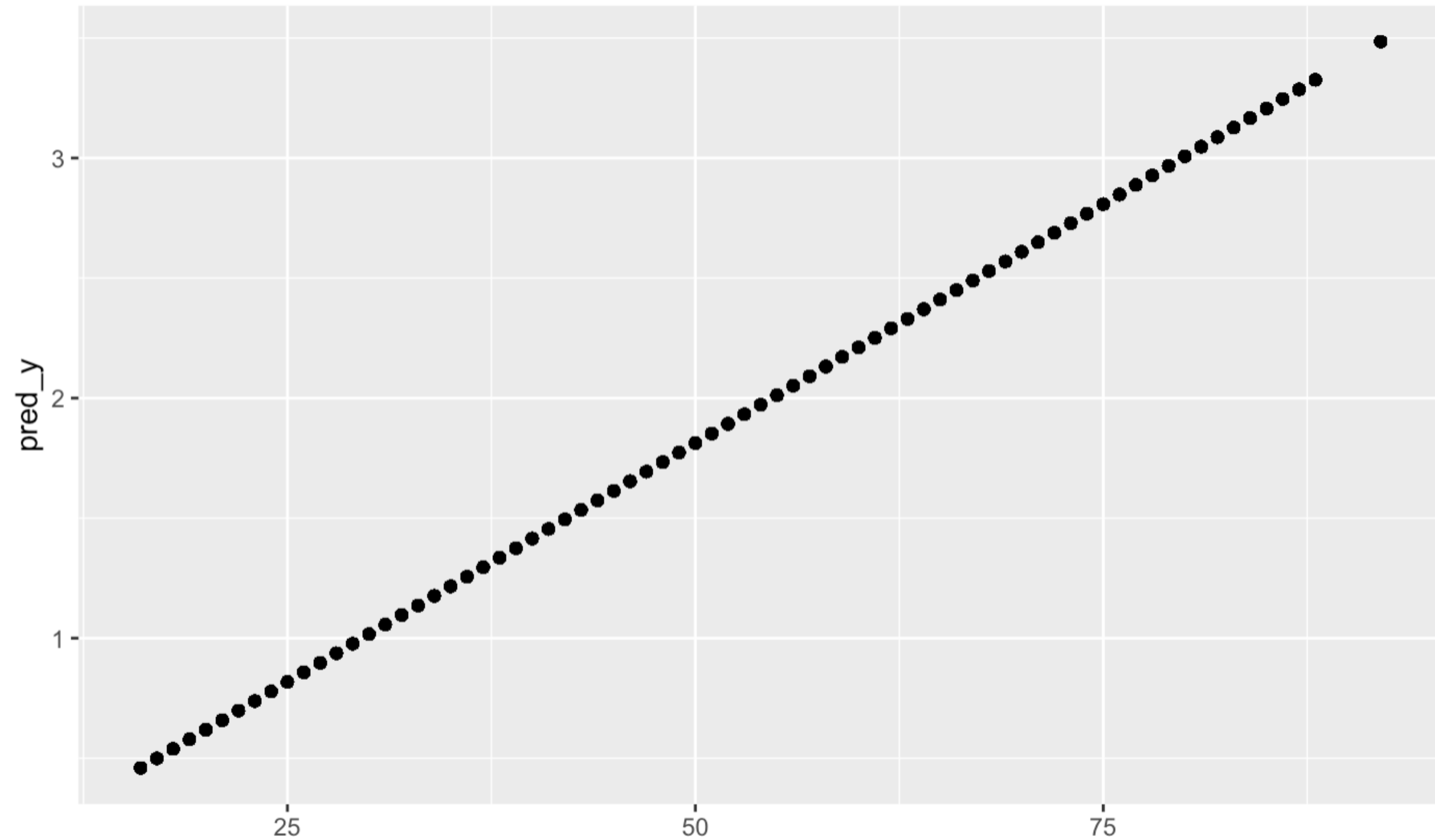
```{r}
health %>% mutate(pred_y = (age * 0.03981371) - 0.17773347) %>%
  mutate(pred_p = exp(pred_y) / (1 + exp(pred_y))) %>%
  ggplot(data = .) + geom_point(aes(x = age, y = pred_p))
```
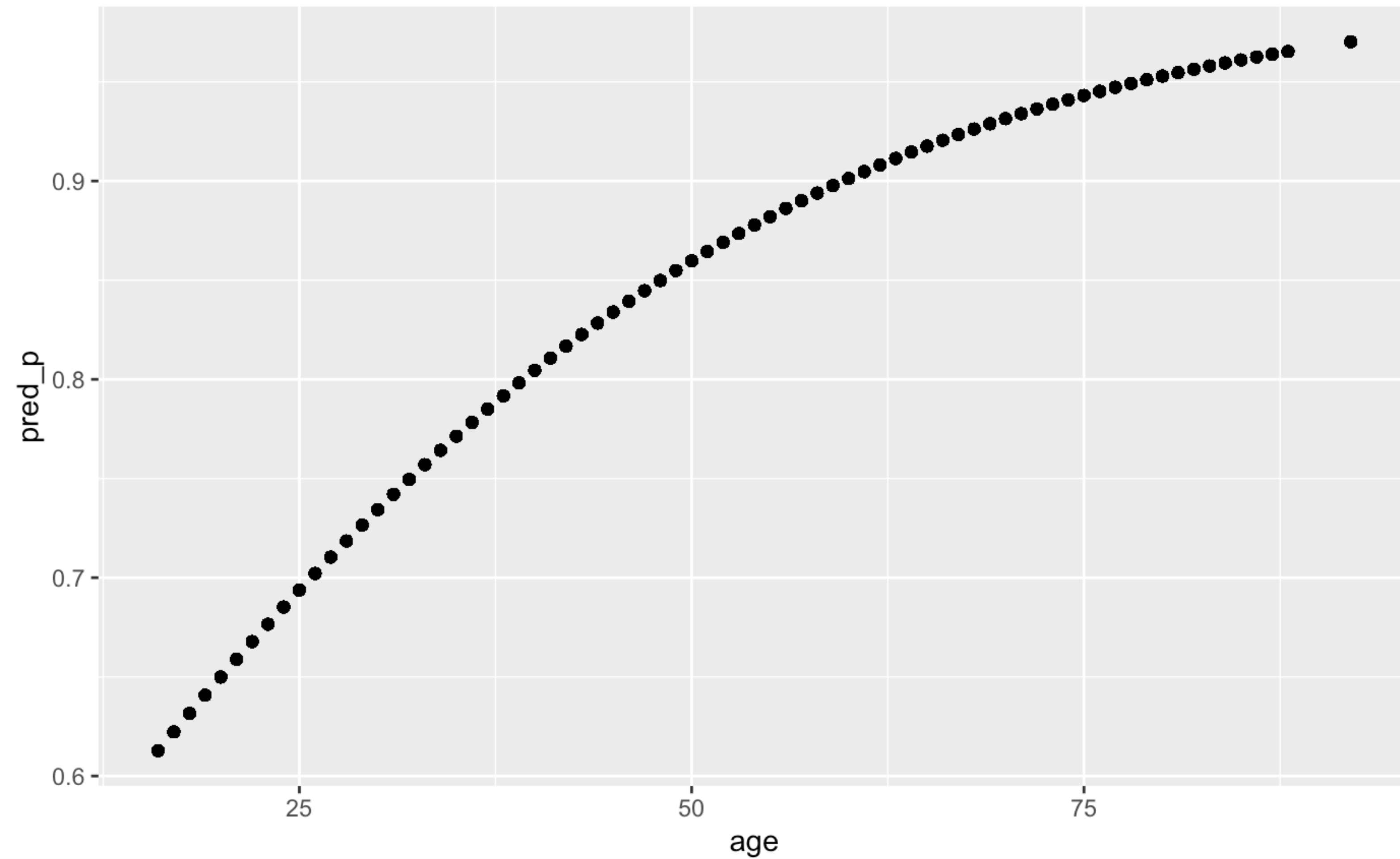
What is this logistic?

- Sigmoid function - "S curve"

- Bounds the values between 0 and 1

$$\phi(z) = \frac{1}{1 + e^{-z}}$$

A tibble: 17 × 5

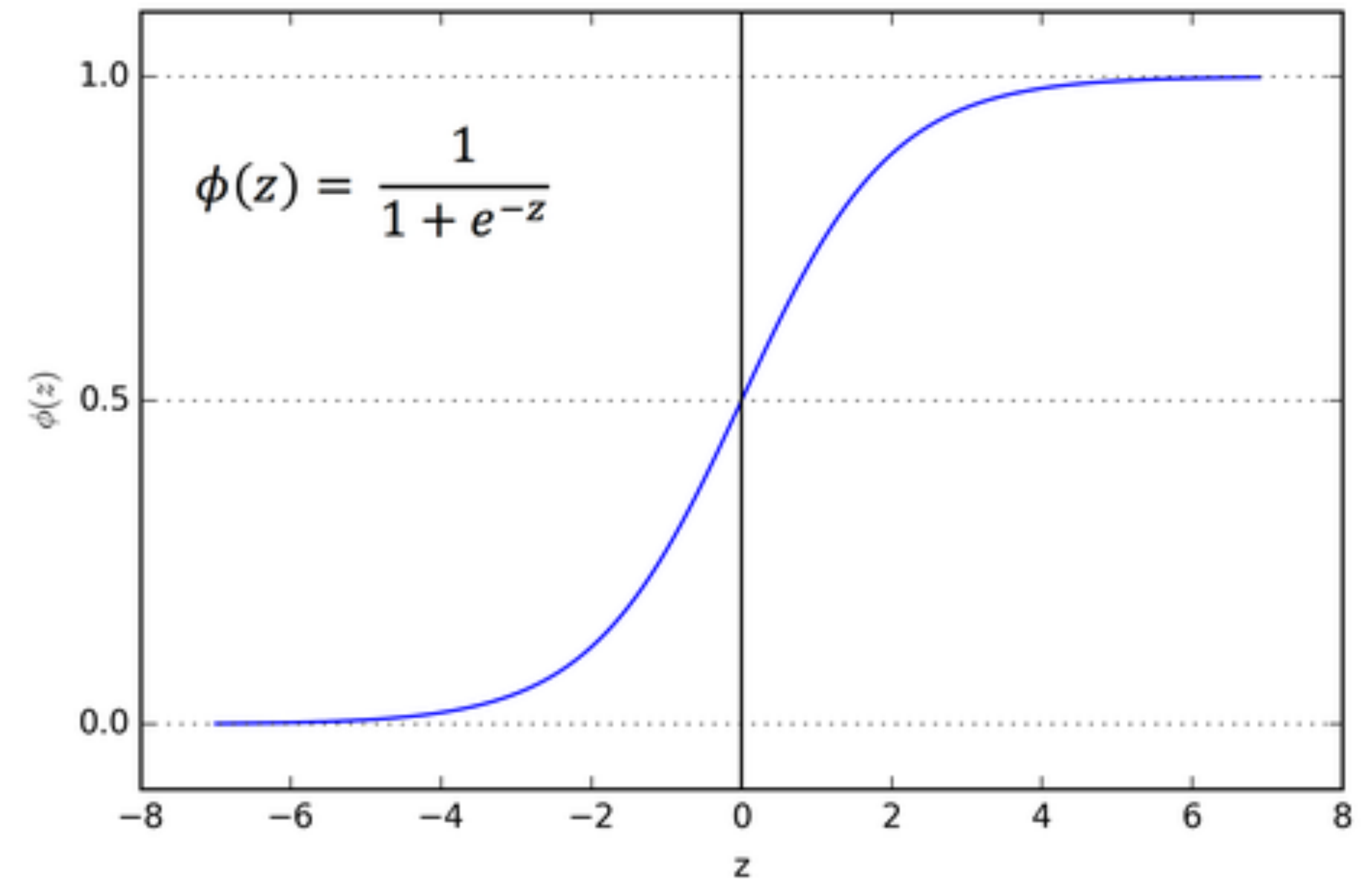| term <chr>	estimate <dbl>	std.error <dbl>	statistic <dbl>	p.value <dbl>
(Intercept)	1.17292366	0.2037067703	5.7579022	8.516568e-09
age	0.02987467	0.0008197871	36.4419831	9.215897e-291
raceAsian	0.22997884	0.1966444685	1.1695160	2.421958e-01
raceBlack	-0.07784148	0.1885716443	-0.4127952	6.797566e-01
raceNat. Hawaiian/Pac. Isl.	0.74787580	0.5266612659	1.4200319	1.555984e-01
raceOther	-0.72486863	0.1986325033	-3.6492951	2.629609e-04
raceTwo or More	0.26995172	0.2072153424	1.3027593	1.926569e-01
raceWhite	0.27370557	0.1881632136	1.4546179	1.457751e-01
sexMale	-0.30052090	0.0210534758	-14.2741703	3.170386e-46
citNon-citizen	-1.73990375	0.0416013990	-41.8232030	0.000000e+00

1–10 of 17 rows   Previous 1   2   Next

.
       0   1
   3162 71643

Confusion Matrix

Table 8.3: Structure of confusion matrix.

	Predicted (F)	Predicted (T)
Actual (F)	True Negative (TN)	False Positive (FP)
Actual (T)	False Negative (FN)	True Positive (TP)

Table 8.4: A selection of classifier accuracy metrics derived from a confusion matrix.

Measure	Formula	Significance
True Positive Rate (TPR), Sensitivity, or Recall	$TPR = \frac{TP}{TP+FN}$	What proportion positive cases are correctly identified?
True Negative Rate (TNR) or Specificity	$TNR = \frac{TN}{TN+FP}$	What proportion negative cases are correctly identified?
False Positive Rate (FPR)	$FPR = \frac{FP}{FP+TN}$	What proportion of negative cases are incorrectly predicted as positive? Also known as Type I error rate.
False Negative Rate (FNR)	$FNR = \frac{FN}{TP+FN}$	Proportion of positive cases that are incorrectly predicted negative. Also known as the false alarm rate or Type II error rate.
Positive Predictive Value (PPV) or Precision	$PPV = \frac{TP}{TP+FP}$	The proportion of predicted positives will actually be positive? This measure is influenced by the prevalence of the outcome.

```{r}
log_reg_fit %>% predict(health) %>%
  cbind(health) %>%
  select(.pred_class, coverage) %>%
  table()
```

```
            coverage
 .pred_class      0      1
           0   1926   1236
           1  11765  59878
```

```r
log_reg_fit %>% predict(health) %>%
  cbind(health) %>%
  select(.pred_class, coverage) %>%
  sensitivity(truth = coverage, estimate = .pred_class, event_level = "second")
```

A tibble: 1 × 3

.metric <chr>	.estimator <chr>	.estimate <dbl>
sensitivity	binary	0.9797755

1 row

```r
log_reg_fit %>% predict(health) %>%
  cbind(health) %>%
  select(.pred_class, coverage) %>%
  specificity(truth = coverage, estimate = .pred_class, event_level = "second")
```

A tibble: 1 × 3

.metric <chr>	.estimator <chr>	.estimate <dbl>
specificity	binary	0.1406764

1 row

```{r}
log_reg_fit %>% predict(health) %>%
  cbind(health) %>%
  select(.pred_class, coverage) %>%
  precision(truth = coverage, estimate = .pred_class, event_level = "second")
```

A tibble: 1 × 3

.metric	.estimator	.estimate
<chr>	<chr>	<dbl>
precision	binary	0.835783

1 row

```{r}
log_reg_fit %>% predict(health) %>%
  cbind(health) %>%
  select(.pred_class, coverage) %>%
  recall(truth = coverage, estimate = .pred_class, event_level = "second")
```

A tibble: 1 × 3

.metric	.estimator	.estimate
<chr>	<chr>	<dbl>
recall	binary	0.9797755

Measure	Formula	Significance
Accuracy (ACC)	$ACC = \frac{TP+TN}{n}$	The proportion of that records are correctly classified.
F1-Score (F1)	$F1 = \frac{2}{\frac{1}{TPR} \times \frac{1}{PPV}}$	Alternative method of calculating accuracy using a harmonic mean. It balances the TPR with the PPV.

```r
131
132 ```{r}
133 log_reg_fit %>% predict(health) %>%
134   cbind(health) %>%
135   select(.pred_class, coverage) %>%
136   accuracy(truth = coverage, estimate = .pred_class, event_level = "second")
137 ```
```

A tibble: 1 × 3

.metric <chr>	.estimator <chr>	.estimate <dbl>
accuracy	binary	0.8262015

1 row

```r
126 log_reg_fit %>% predict(health) %>%
127   cbind(health) %>%
128   select(.pred_class, coverage) %>%
129   f_meas(truth = coverage, estimate = .pred_class, event_level = "second")
130 ```
```

A tibble: 1 × 3

.metric <chr>	.estimator <chr>	.estimate <dbl>
f_meas	binary	0.9020692

1 row

What do we generally do in the ML process?

- Preprocess (clean, transform etc.) data, select features

- Choose a model

- Check quality of model fit based on error metrics, cross-validation, and generalization checks

- Iterate by tuning hyperparameters, adjusting features, and trying different models

- Can be made easier by tuning hyper-parameters automatically
  - Next class

Two more models

- Random forest

- K nearest neighbors