Solving the model representation problem with broom

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Who am I?

Statistical models

The model representation problem

The broom package

Use cases

Open Questions & Hot Takes

tidymodels

These slides are available online!

https://tinyurl.com/broom-talk-sgsa

Who am I?



Just started the Ph.D. program here



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- Interned at RStudio over the summer



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- Active on #rstats Twitter and Github

Statistical models

What is a model?

Let x be values that live in some space \mathcal{X} , and let y be observations of interest that live in some space \mathcal{Y} . A **statistical model** is a *set* of probability distributions $\mathcal{P}(y|x)$ indexed by parameters $\theta \in \Theta^1$.

¹In some cases we treat θ as itself random, which means that our model is a class of probability distributions $\mathcal{P}(y,\theta|x)$.

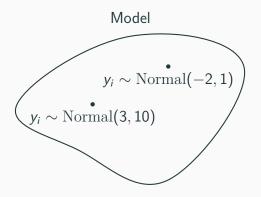
Example: the normal model

$$y_i \stackrel{\text{iid}}{\sim} \text{Normal}(\mu, \sigma^2)$$

Here $\theta = (\mu, \sigma^2)$ and the parameter space is $\mathbb{R} \times \mathbb{R}^+$.

Visualizing the normal model

Again: a model is a set.



We call a single element of a model a **fit**. The distribution with $\mu=-2,\sigma^2=1$ is a fit, for example.

Another (parametric) example: the linear model

Given response y and predictor variables x_1 and x_2 , the linear model looks like:

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \varepsilon_i$$
 $\varepsilon_i \stackrel{\text{iid}}{\sim} \text{Normal}(0, \sigma^2)$

This model says that y is i.i.d with a mean that depends on x and $\vec{\beta}$, and with fixed variance σ^2 .

Estimation

An **estimator** is a way to calculate the parameters of a model from data². They are many estimators for any given model, and which one we think is best depends on how we define "agrees best with the data."

²This is equivalent to selecting the best fit!

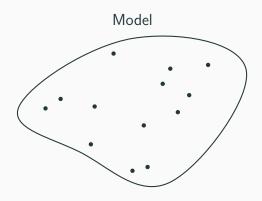
Some estimators for the normal model

•
$$\hat{\mu} = 1$$
 $\hat{\sigma}^2 = 10$

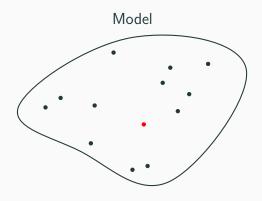
•
$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^{n} x_i$$
 $\hat{\sigma}^2 = \frac{1}{n} \sum_{i=1}^{n} (x_i - \bar{x})^2$

•
$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^{n} x_i$$
 $\hat{\sigma}^2 = \frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2$

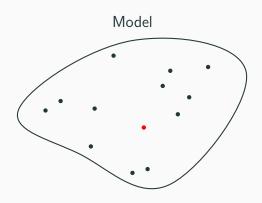
Visualizing estimation



Visualizing estimation

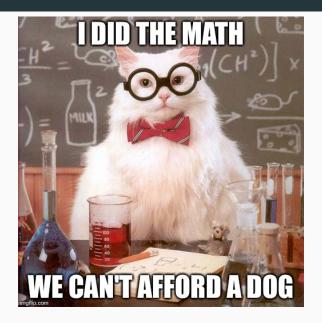


Estimates found!



Best fit: $y_i \sim \text{Normal}(-2,1)$. Finally we can do inference!

Do all the inference



Some intuition about models, estimators and fits

A **model** corresponds to a set of possible truths about the world. A **fit** is a single truth about the world. An **estimator** is a way to choose the truth most suggested by the data from a set of many possible truths.

The model representation

problem

Representing a fit in mathematical terms

Hopefully it feels natural to describe models mathematically

- Normal model: $y_i \sim \text{Normal}(\mu, \sigma^2)$
 - Fit from normal model: $y_i \sim \text{Normal}(-2, 1)$
 - Can also identify fits by parameter vectors: $\theta = (-2,1)$
 - Estimators for normal model:

$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^{n} x_i \qquad \hat{\sigma}^2 = \frac{1}{n} \sum_{i=1}^{n} (x_i - \bar{x})^2$$

Key: shared notation and community standards

How does R represent models, estimators and fits?

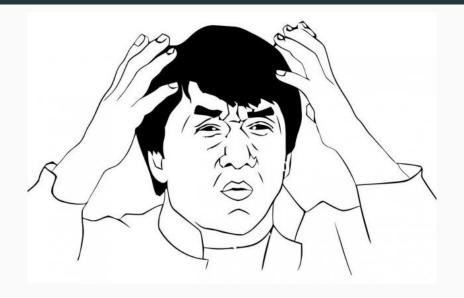


A taste of the pain

Suppose you want class probabilities from a fit called obj:

Object	Code
lda	predict(obj)
glm	<pre>predict(obj, type = "response")</pre>
gbm	<pre>predict(obj, type = "response", n.trees)</pre>
mda	<pre>predict(obj, type = "posterior")</pre>
rpart	<pre>predict(obj, type = "prob")</pre>
Weka	<pre>predict(obj, type = "probability")</pre>
logitboost	<pre>predict(obj, type = "raw", nIter)</pre>
pamr.train	<pre>pamr.predict(obj, type = "posterior")</pre>

How am I supposed to keep track of all this!?



The model representation problem

We have no shared framework or understanding of how to represent statistical models, estimation methods and fits with R objects.

Aside

- People who write and share code to enable data analysis are awesome
- This isn't anyone's fault
- Trying to get things done can still be frustrating

The broom package

The scene

Say we:

- 1. pick a model,
- 2. pick an estimator for that model, and then
- 3. get an R object fit using that estimator.
- The fit object is different for every model.
- The fit object could be great to work with, or awful.

broom provides a standard way to represent fits

broom treats fits as having three parts:

- 1. A table of information about fit parameters
- 2. A table of information about each observation used to estimate the fit
- 3. A table of overall goodness-of-fit measures
- Each of table reported as a tidy tibble.
- Together these constitute a tidy representation of a fit.

Aside: What is a tibble

A tibble is a more consistent data.frame. tibbles are used widely throughout the tidyverse.

Aside: What does it mean to be tidy?

I highly recommend reading Hadley Wickham's Tidy Data paper! The short version: a **tidy dataset** is one where:

- 1. Each variable forms a column.
- 2. Each observation forms a row.
- 3. Differents kinds of data live in different tables.

The broom generics

So how do we turn fits into tidy tibbles?

- tidy() summarizes information about fit components
- glance() reports information about the entire fit
- augment() adds information about observations to a dataset

Continuing with the normal model example

```
# simulate Normal(-2, 1) data
x \leftarrow rnorm(5000, -2, 1)
# create a fit object using
# MLE estimator and normal model
normal fit <- MASS::fitdistr(</pre>
  х,
  dnorm, # use the normal model!
  start = list(mean = 0, sd = 1)
```

What is normal fit?

```
str(normal fit)
## List of 5
## $ estimate: Named num [1:2] -2.03 1.01
## ..- attr(*, "names")= chr [1:2] "mean" "sd"
## $ sd : Named num [1:2] 0.0143 0.0101
## ..- attr(*, "names")= chr [1:2] "mean" "sd"
  $ vcov : num [1:2, 1:2] 2.06e-04 -4.62e-13 -4.
##
## ..- attr(*, "dimnames")=List of 2
## ....$ : chr [1:2] "mean" "sd"
  ....$ : chr [1:2] "mean" "sd"
##
## $ loglik : num -7165
##
  \$ n : int 5000
## - attr(*, "class")= chr "fitdistr"
```

What is the tidy representation of normal_fit?

```
library(tidyverse)
library(broom)
tidy(normal fit)
## # A tibble: 2 x 3
## term estimate std.error
## \langle chr \rangle \langle dbl \rangle
## 1 mean -2.03 0.0143
## 2 sd 1.01 0.0101
```

What is the tidy representation of normal_fit?

There's no augment() method defined for univariate distributions at the moment.

Another example: the linear model

```
# create a fit object using the
# OLS estimator for the linear model
ols_fit <- lm(hp ~ mpg + cyl, mtcars)
# try the following for yourself:
str(ols_fit)</pre>
```

The tidy representation of 1m objects

The tidy representation of 1m objects

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Notes about the tidy representation

- Always get a tibble back
- Column names in returned tibbles are consistent
- Some information in the original R object is lost

Use cases

Report model coefficients with tidy()

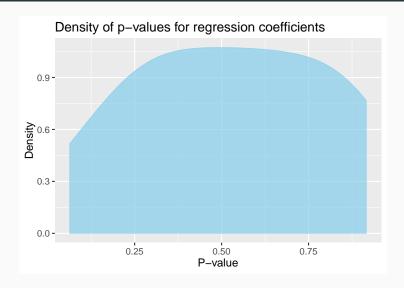
```
kable2 <- function(data)
knitr::kable(mutate_if(data, is.numeric, round, 2))
tidy(ols_fit) %>%
kable2()
```

term	estimate	std.error	statistic	p.value
(Intercept)	54.07	86.09	0.63	0.53
mpg	-2.77	2.18	-1.27	0.21
cyl	23.98	7.35	3.26	0.00

Plot histograms/densities of p-values

```
fit <- lm(mpg ~ ., mtcars)</pre>
td <- tidy(fit)
p <- ggplot(td, aes(p.value)) +
  geom density(
    fill = "skyblue", color = "skyblue", alpha = 0.7
  ) +
  labs(
    title = "Density of p-values for regression coeffice
    x = "P-value"
    y = "Density"
```

Plot histograms/densities of p-values



Comparing models by goodness of fit measures

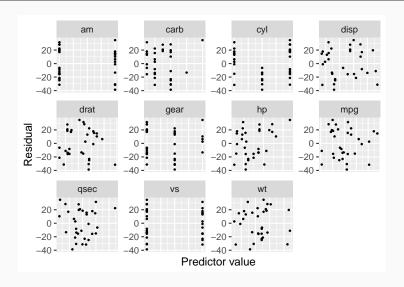
```
fits <- list(
  fit1 = lm(hp \sim cyl, mtcars),
  fit2 = lm(hp \sim cyl + mpg, mtcars),
  fit3 = lm(hp - ., mtcars)
gof <- map_df(fits, glance, .id = "model") %>%
  arrange(AIC)
```

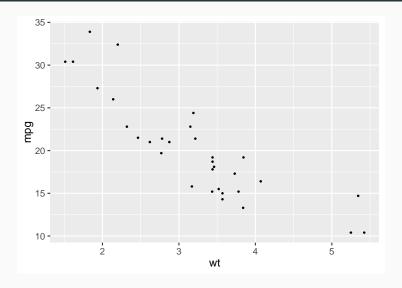
Comparing models by goodness of fit measures

Inspecting residuals from multiple linear regression

```
fit <- lm(hp ~ ., mtcars)
au <- broom::augment(fit)</pre>
p <- au %>%
  gather(x, val, -contains(".")) %>%
  ggplot(aes(val, .resid)) +
  geom point() +
  facet_wrap(~x, scales = "free") +
  labs(x = "Predictor value", y = "Residual") +
  theme(axis.text.x = element blank(),
        axis.ticks.x = element blank())
```

Inspecting residuals from multiple linear regression





Consider a model:

$$mpg = \frac{k}{wt} + b + \varepsilon, \quad \varepsilon \sim Normal(0, \sigma^2)$$

Suppose we want to know the sampling distributions of k and b via bootstrapping

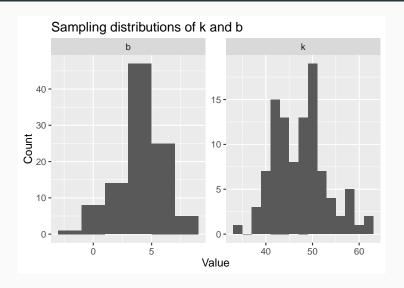
```
library(rsample)
boots <- bootstraps(mtcars, times = 100)</pre>
boots
## # Bootstrap sampling
## # A tibble: 100 x 2
             id
## splits
## \langle l.i.s.t \rangle \langle c.h.r \rangle
## 1 <split [32/10] > Bootstrap001
## 2 <split [32/7]> Bootstrap002
## 3 <split [32/13] > Bootstrap003
## # ... with 97 more rows
```

```
fit_nls_on_bootstrap <- function(split) {
   nls(
      mpg ~ k / wt + b,
      analysis(split),
      start = list(k = 1, b = 0)
   )
}</pre>
```

```
boot fits <- boots %>%
 mutate(fit = map(splits, fit nls on bootstrap),
        coef info = map(fit, tidy))
boot fits
## # Bootstrap sampling
## # A tibble: 100 x 4
## splits id
                        fit coef\_info
## * <list> <chr> chr> <list> <list> 
## 1 <split [32/10] > Bootstrap001 <S3: nls > <tibble [
## 2 <split [32/7] > Bootstrap002 <S3: nls > <tibble [
## 3 <split [32/13] > Bootstrap003 <S3: nls > <tibble [
## # ... with 97 more rows
```

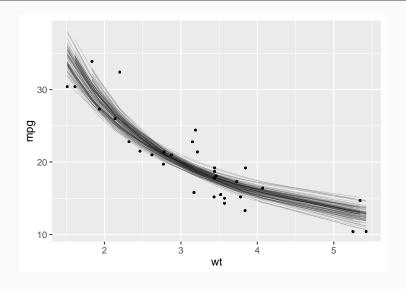
```
boot coefs <- boot fits %>%
 unnest(coef info)
boot coefs
## # A tibble: 200 x 6
## id term estimate std.error statistic
\#\# \langle chr \rangle \langle chr \rangle \langle dbl \rangle
                                  <db1>
                                            \langle db l \rangle
## 1 Bootstrap001 k 41.8 4.05
                                            10.3
## 2 Bootstrap001 b 5.96 1.64 3.64
## 3 Bootstrap002 k 50.6
                                3.96 12.8
## # ... with 197 more rows
```

```
p <- ggplot(boot_coefs, aes(estimate)) +
  geom_histogram(binwidth = 2) +
  facet_wrap(~ term, scales = "free") +
  labs(
    title = "Sampling distributions of k and b",
    y = "Count",
    x = "Value"
)</pre>
```



```
boot_aug <- boot_fits %>%
  mutate(augmented = map(fit, augment)) %>%
  unnest(augmented)

p <- ggplot(boot_aug, aes(wt, mpg)) +
  geom_point() +
  geom_line(aes(y = .fitted, group = id), alpha = 0.2)</pre>
```



General strategy

broom provides tidying methods for 100+ classes!

- 1. Put fits in a list, or a list-column of a tibble
- 2. Use purrr::map() to apply tidy(), glance() or augment() to each fit
- 3. Use tidyverse tools to manipulate and visualize resulting data!

Open Questions & Hot Takes

Sets of fits are particularly interesting to think about:

Path algorithms (i.e. LASSO fits)

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 - Can do inference from a single fit
 - Can do inference from the entire LASSO path
- Ensembles (i.e. random forests)

Generics should operate on *fits*, not models

Consider the following methods, all for the linear model:

- plot lasso path() for OLS vs LASSO fits
- coef standard errors() for OLS vs LASSO fits
- interpret_coefficients() for OLS vs GEE fits

Things pretty much everybody agrees on:

• fit(model, estimator, data)

Actions that are begging for S3 generics:

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- best practices for developing modeling packages
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- recipes: data pre-processing



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A general attempt to make modeling in R more consistent and tidy. Lots of big projects. Highlights:

- best practices for developing modeling packages
- parnsip: standardized modeling interfaces (now on CRAN!!)
- recipes: data pre-processing
- rsample: infrastructure for resampling

Questions?

Read about the recent broom release on the tidyverse blog.



https://broom.tidyverse.org



 ${\tt https://github.com/tidymodels/broom/}$





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