

# Solving the model representation problem with broom

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2018-01-17

These slides are available online!

<https://tinyurl.com/rstudioconf-broom>

# The model representation problem

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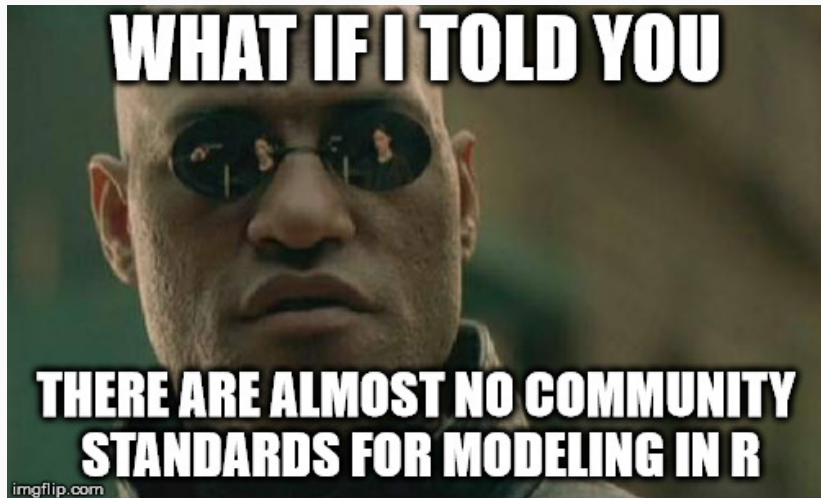


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- Key: shared notation and community standards

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

# The model representation problem

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

# The broom package

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## broom provides a standard way to represent fits

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1. `tidy()`: summarize information about fit components
2. `glance()`: report goodness of fit measures
3. `augment()`: add information about observations to a dataset



# The normal model: an example

```
# simulate Normal(-2, 1) data
x <- rnorm(5000, -2, 1)

# create a fit object using
# MLE estimator and normal model

normal_fit <- MASS::fitdistr(
  x,
  dnorm,
  start = list(mean = 0, sd = 1)
)
```

# What is normal\_fit?

```
## $estimate
##      mean      sd
## -2.034081  1.014121
##
## $sd
##      mean      sd
## 0.01434184 0.01014118
##
## $vcov
##      mean      sd
## mean  2.056884e-04 -4.617406e-13
## sd    -4.617406e-13  1.028435e-04
##
## $loglik
## [1] -7164.801
```

# What is the tidy representation of `normal_fit`?

```
library(tidyverse)
library(broom)

tidy(normal_fit)
## # A tibble: 2 x 3
##   term      estimate std.error
##   <chr>      <dbl>      <dbl>
## 1 mean      -2.03      0.0143
## 2 sd         1.01      0.0101
```

# What is the tidy representation of `normal_fit`?

```
glance(normal_fit)
## # A tibble: 1 x 4
##       n logLik    AIC    BIC
##   <int> <dbl> <dbl> <dbl>
## 1  5000 -7165. 14334. 14347.
```

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)
```

# The tidy representation of `lm` objects

```
tidy(ols_fit)
## # A tibble: 3 x 5
##   term          estimate std.error statistic p.value
##   <chr>          <dbl>    <dbl>    <dbl>   <dbl>
## 1 (Intercept)    54.1      86.1      0.628  0.535
## 2 mpg           -2.77      2.18     -1.27  0.213
## 3 cyl            24.0      7.35      3.26  0.00281
```

# The tidy representation of `lm` objects

```
glance(ols_fit)
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df
## *   <dbl>         <dbl> <dbl>    <dbl>    <dbl> <int>
## 1   0.709         0.689  38.2    35.4 1.66e-8     3
## # ... with 5 more variables: logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>, df.residual <int>
```

# The tidy representation of `lm` objects

```
augment(ols_fit)
## # A tibble: 32 x 11
##   .rownames    hp   mpg   cyl .fitted .se.fit .resid
## * <chr>      <dbl> <dbl> <dbl>   <dbl>   <dbl>   <dbl>
## 1 Mazda RX4    110   21     6   140.     6.84 -29.7
## 2 Mazda RX~    110   21     6   140.     6.84 -29.7
## 3 Datsun 7~     93  22.8    4   86.7    13.3   6.28
## # ... with 29 more rows, and 4 more variables:
## #   .hat <dbl>, .sigma <dbl>, .cooks <dbl>,
## #   .std.resid <dbl>
```



# 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

# Comparing models by goodness of fit measures

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

# Comparing models by goodness of fit measures

```
gof
```

```
## # A tibble: 3 x 12
```

```
##   model r.squared adj.r.squared sigma statistic p.value
```

```
##   <chr>      <dbl>          <dbl> <dbl>      <dbl>    <dbl>
```

```
## 1 fit3      0.903          0.857  26.0      19.5 1.90e-8
```

```
## 2 fit1      0.693          0.683  38.6      67.7 3.48e-9
```

```
## 3 fit2      0.709          0.689  38.2      35.4 1.66e-8
```

```
## # ... with 6 more variables: df <int>, logLik <dbl>,
```

```
## #   AIC <dbl>, BIC <dbl>, deviance <dbl>,
```

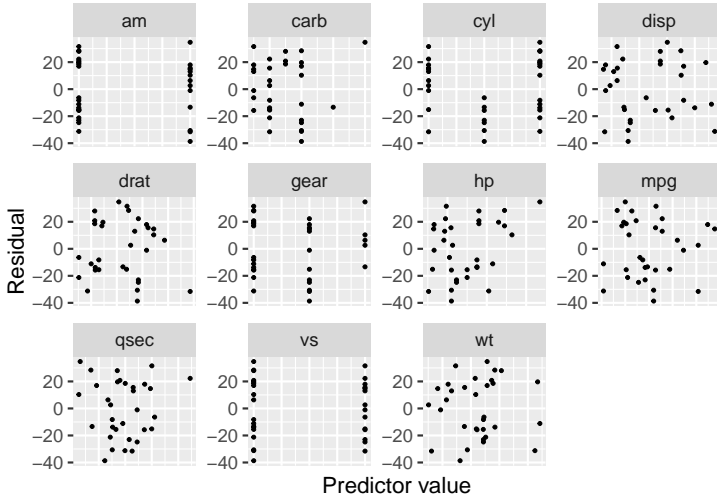
```
## #   df.residual <int>
```

# Inspecting residuals from multiple linear regression

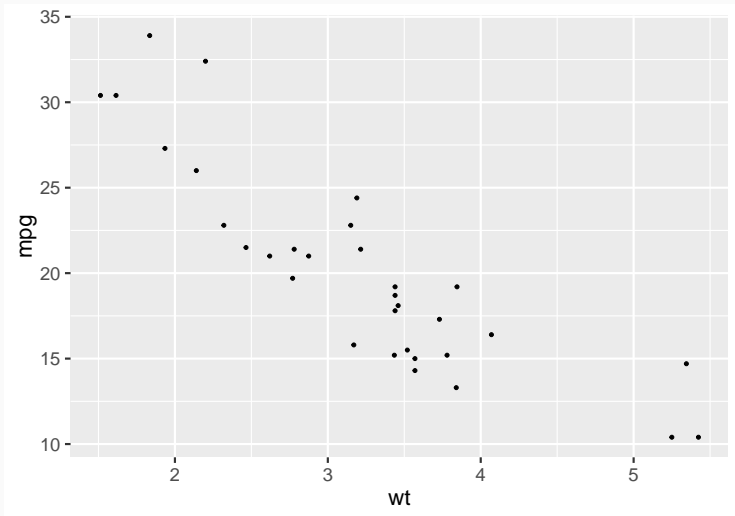
```
fit <- lm(hp ~ ., mtcars)
au <- broom::augment(fit)

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



# Bootstrapping



# Bootstrapping

Consider a model:

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

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



# Bootstrapping

```
library(rsample)

boots <- bootstraps(mtcars, times = 100)
boots
## # Bootstrap sampling
## # A tibble: 100 x 2
##   splits          id
##   <list>         <chr>
## 1 <split [32/10]> Bootstrap001
## 2 <split [32/7]>  Bootstrap002
## 3 <split [32/13]> Bootstrap003
## # ... with 97 more rows
```

# Bootstrapping

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

# Bootstrapping

```
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>        <list>    <list>
```

```
## 1 <split [32/10]> Bootstrap001 <S3: nl~ <tibble [2 x 5~
```

```
## 2 <split [32/7]>  Bootstrap002 <S3: nl~ <tibble [2 x 5~
```

```
## 3 <split [32/13]> Bootstrap003 <S3: nl~ <tibble [2 x 5~
```

```
## # ... with 97 more rows
```

# Bootstrapping

```
boot_coefs <- boot_fits %>%  
  unnest(coef_info)
```

```
boot_coefs
```

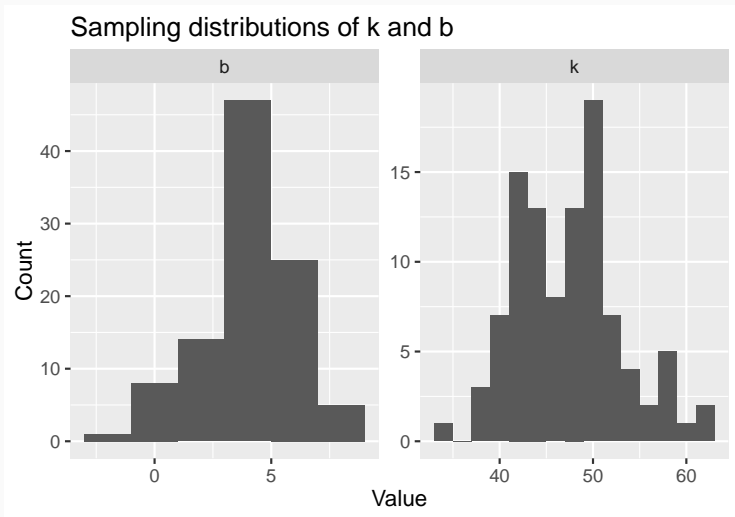
```
## # A tibble: 200 x 6
```

```
##   id          term estimate std.error statistic p.value  
##   <chr>      <chr>   <dbl>    <dbl>    <dbl>    <dbl>  
## 1 Bootstra~ k      41.8      4.05     10.3 2.18e-11  
## 2 Bootstra~ b       5.96      1.64      3.64 1.01e- 3  
## 3 Bootstra~ k      50.6      3.96     12.8 1.16e-13  
## # ... with 197 more rows
```

# Bootstrapping

```
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"  
  )
```

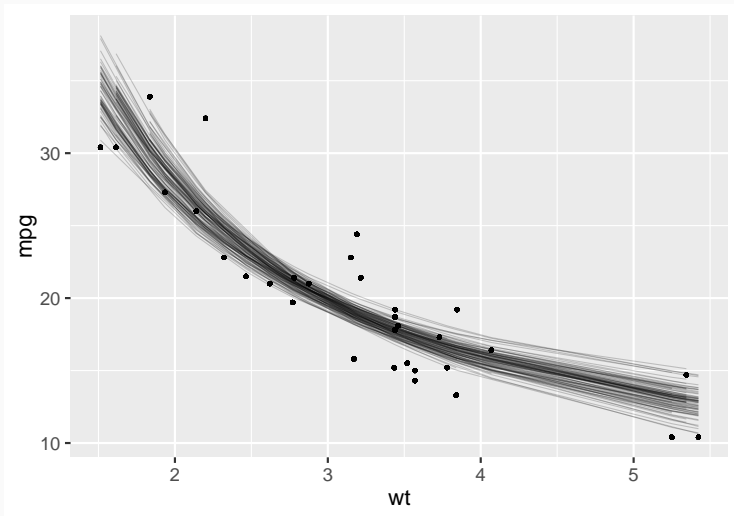
# Bootstrapping



# Bootstrapping

```
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)
```

# Bootstrapping





# Thank you! Questions?

Read about the [broom 0.5.0 release](#) or [how to implement new tidiers!](#)



<https://broom.tidyverse.org>



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