Sampling distributions part 2 (means)

Thomas Scofield

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Pertinent R

The sample() command. You can make a containter of objects and make random draws from it:

```
die = c(1,2,3,4,5,6)
sample(die, size=3, replace=TRUE) # the optional 'replace' switch affects command's behavior
```

[1] 3 5 2

Or, you can sample (draw randomly) rows/cases from a data frame.

```
sample(iris, size=5, replace=TRUE)
```

##	Sepal.Length	Sepal.Width	Petal.Length	${\tt Petal.Width}$	Species	orig.id
## 31	4.8	3.1	1.6	0.2	setosa	31
## 47	5.1	3.8	1.6	0.2	setosa	47
## 42	4.5	2.3	1.3	0.3	setosa	42
## 54	5.5	2.3	4.0	1.3	versicolor	54
## 146	6.7	3.0	5.2	2.3	virginica	146

There is a related command, resample(), which assumes you want to sample with replacement, so it doesn't require the extra switch replace=TRUE to make that happen.

```
resample(iris, size=5) # automatically draws with replacement
```

##		Sepal.Length	Sepal.Width	Petal.Length	${\tt Petal.Width}$	Species	orig.id
##	19	5.7	3.8	1.7	0.3	setosa	19
##	106	7.6	3.0	6.6	2.1	virginica	106
##	38	4.9	3.6	1.4	0.1	setosa	38
##	42	4.5	2.3	1.3	0.3	setosa	42
##	2	4.9	3.0	1.4	0.2	setosa	2

Pertinent R Markdown

At times, you will want to insert math symbols into a report. One can write E=mc^2 as text, but it looks better if you enter the same thing in math mode. You indicate the start to math mode by including a dollar-sign \$ in your source file, and once your equation is finished, you indicate math mode is over with another dollar sign. So, placing \$E=mc^2\$ in your source (.Rmd) file results in $E=mc^2$. Greek letters require math mode, and what you put between the dollar signs is a backslash character \ followed by the name (spelled out in English) of the desired Greek letter. So, including \$\mu\$\$ in the source file produces μ in your document. See if you can guess what you to include in your .Rmd file in order to get the two versions of the Greek letter sigma—that is, Σ and σ . Math mode also allows you to add things like a "hat" to p, or a "bar" over an x.

- In .Rmd file: \hat{p} is rendered as \hat{p}
- In .Rmd file: $\$ verline x\$ is rendered as \overline{x}

Sampling distribution for sample mean \bar{x}

The textbook illustrates this same concept using the data set **StatisticsPhD**, the first few rows of which are head(StatisticsPhD)

##				University	Department	${\tt FTGradEnrollment}$
##	1		Baylo	r University	Statistics	26
##	2		Bosto	n University	Biostatistics	39
##	3		Brow	n University	Biostatistics	21
##	4		Carnegie Mello	n University	Statistics	39
##	5	Case	Western Reserv	e University	Statistics	11
##	6		Colorado Stat	e University	Statistics	14

We might calculate the mean (which can be viewed as a population mean μ , since this data is a *census* of all Ph.D. statistics programs in the country, not merely a sample of such programs) number of full-time students enrolled, using the mean() command and indicating column (variable name) and data frame name in the usual way:

```
mean(~FTGradEnrollment, data=StatisticsPhD)
```

```
## [1] 53.53659
```

If, however, we want to simulate the process of computing a mean from a random sample of 10 of these Ph.D. programs, we need only indicate a different data set on which to calculate the mean—not the full **StatisticsPhD** data frame, but a random sample of 10 cases selected from it:

```
mean(~FTGradEnrollment, data=resample(StatisticsPhD,size=10))
```

```
## [1] 47
```

This command

- draws a sample of 10 schools with replacement
- calculates \overline{x} , the mean number of FTGradEnrollment for the schools in the sample.

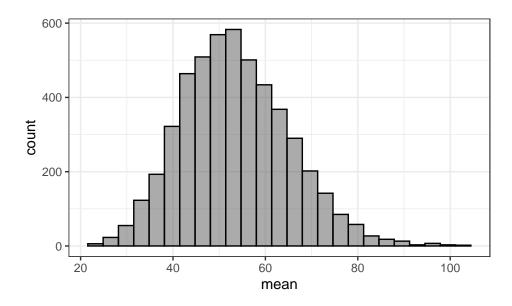
Doing it once gives you \overline{x} for a single random sample with n=10. Do it many times, and you'll start to see the sort of values \overline{x} can take, and which ones occur more frequently, in a random sample of 10 programs. In other words, you get an idea of the sampling distribution of \overline{x} for samples of size 10 taken from this population.

```
manyXbars <- do(5000) * mean(~FTGradEnrollment, data=resample(StatisticsPhD, size=10))
head(manyXbars)</pre>
```

```
## mean
## 1 51.6
## 2 51.6
## 3 73.6
## 4 65.1
## 5 39.3
## 6 34.8
```

Seeing that the results (stowed in the data frame manyXbars) have been given the column name mean, we will incorporate those names in a call to the gf_histogram() command:

```
gf_histogram(~mean, data=manyXbars, color="black")
```



Exercise 1:

- a) Find an approximate standard error of the mean, $SE_{\overline{x}}$, for samples of size 10 from this population.
- b) Does it appear that \bar{x} is an unbiased estimator of μ ? How can you tell?
- c) How often (give an answer in terms of relative frequency) is \overline{x} as large as 60?

Exercise 2:

Repeat the work done already to generate and view an approximate sampling distribution for \overline{x} , again with sample sizes n=10, but with the difference that you sample without replacement instead of with replacement. Are there noticeable differences between this sampling distribution and the one for samples of size n=10 taken with replacement? Does favstats() reveal any major differences in the two distributions?

Exercise 3:

Now that you have looked at sampling distributions for \overline{x} both with and without replacement for samples of size n = 10, try comparing the two for samples of size n = 20. Once again apply favstats() to see if there are notable differences. Are the differences you noted between the two distributions at n = 10 even more pronounced at n = 20?