Generating Random Number and Distributions as Models

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Today

- How *does* R get “random” numbers, anyway?
- It doesn’t, really – it uses a trick that should be indistinguishable from the real McCoy

These Cost Money and I'm Cheap

Pseudorandom generators produce a deterministic sequence that is indistiguishable from a true random sequence if you don't know how it started.

Example: `runif`, where we know where it started

```r
runif(1:10)
```

```
##  [1] 0.838859813 0.799813183 0.060404619 0.528704596 0.118761233
##  [6] 0.693799150 0.885252765 0.770147909 0.005823351 0.377979636
```

```r
set.seed(10)
runif(1:10)
```

```
##  [1] 0.50747820 0.30676851 0.42690767 0.69310208 0.08513597 0.22543662
##  [7] 0.27453052 0.27230507 0.61582931 0.42967153
```

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How does R get everything we need?

A few distributions of interest:

- Discret Uniform{1,. . . ,n}
- Uniform(0,1)
- Bernoulli(p)
- Binomial(n,p)
- normal(mu,sigma)
- Exponential(lambda)
- Gamma(n,lambda)

Use **sample** function to generate random number from a discret uniform distribution

```r
sample(1:10,size = 5,replace = T)
```

```
## [1] 7 6 2 6 4
```

```r
sample(10,size = 5,replace = T) # if the first argument is not vector
```

```
## [1] 5 1 3 4 9
```

Suppose we were working with the Exponential distribution.

- `rexp()` generates variates from the distribution.
- `dexp()` gives the probability density function.
- `pexp()` gives the cumulative distribution function.
- `qexp()` gives the quantiles.

- `d`*foo* = the probability *d* ensity (if continuous) or probability mass function of *foo* (pdf or pmf)
- `p`*foo* = the cumulative *p* robability function (CDF)
- `q`*foo* = the *q* uantile function (inverse to CDF)
- `r`*foo* = draw *r* andom numbers from `foo` (first argument always the number of draws)

`?Distributions` to see which distributions are built in

If you write your own, follow the conventions

```r
dnorm(x=c(-1,0,1),mean=1,sd=0.1)
```

```
## [1] 5.520948e-87 7.694599e-22 3.989423e+00
```

```r
pnorm(q=c(2,-2)) # defaults to mean=0,sd=1
```

```
## [1] 0.97724987 0.02275013
```

```r
dbinom(5,size=7,p=0.7,log=TRUE)
```

```
## [1] -1.146798
```

```r
qchisq(p=0.95,df=5)
```

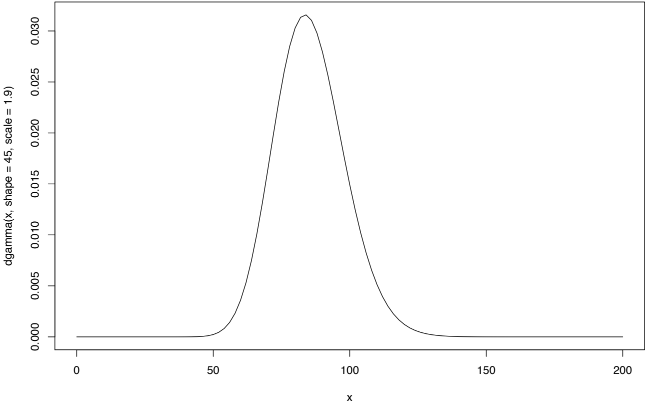
```
## [1] 11.0705
```

```r
rt(n=4,df=2)
```

```
## [1]  1.0154673 -0.1983909  0.9861791 -1.5666848
```

`curve` is very useful for the `d`, `p`, `q` functions:

```
curve(dgamma(x,shape=45,scale=1.9),from=0,to=200)
```



N.B.: the `r` functions aren't things it makes much sense to plot

How Do We Fit Distributional Models to the Data?

- Match moments (mean, variance, etc.)
- Match other summary statistics
- Maximize the likelihood

Method of Moments (MM), Closed Form

- Pick enough moments that they **identify** the parameters
  - At least 1 moment per parameter; algebraically independent
- Write equations for the moments in terms of the parameters
  e.g., for gamma

$$E(X) = \bar{x} \ , \ E(X^2) = \bar{x^2}$$

- Do the algebra by hand to solve the equations

$$shape = \bar{x}^2/s^2 \ , \ scale = s^2/\bar{x}$$

```
gamma.est_MM <- function(x) {
  m <- mean(x); v <- var(x)
  return(c(shape=m^2/v, scale=v/m))
}
```

- Usually we think of the parameters as fixed and consider the probability of different outcomes, $f(x;\theta)$ with θ constant and x changing **Likelihood** of a parameter
- With independent data points $x_1, x_2, \ldots, x_n$, likelihood is

$$L(\theta) = \prod_{i=1}^{n} f(x_i;\theta)$$

- Multiplying lots of small numbers is numerically bad; take the log:

$$\ell(\theta) = \sum_{i=1}^{n} \log f(x_i;\theta)$$

- In pseudo-code:

```
loglike.foo <- function(params, x) {
  sum(dfoo(x=x,params,log=TRUE))
}
```

What Do We Do with the Likelihood?

- We maximize it!
- Sometimes we can do the maximization by hand with some calculus
  - For Gaussian, MLE = just match the mean and variance
  - For Pareto, MLE $\widehat{a} = 1 + 1/\overline{\log\left(x/x_{\min}\right)}$
- Doing numerical optimization
  - Stick in a minus sign if we're using a minimization function

MLE for one-dimensional distributions can be done through `fitdistr` in the `MASS` package

It knows about most the standard distributions, but you can also give it arbitrary probability density functions and it will try to maximize them
A starting value for the optimization is optional for some distributions, required for others (including user-defined densities)

Returns the parameter estimates and standard errors
SEs come from large-n approximations so use cautiously

Fit the gamma distribution to the cats' hearts:

```
require(MASS)
```

```
## Loading required package: MASS
```

```
fitdistr(cats$Hwt, densfun="gamma")
```

```
##       shape          rate
##   20.2998092    1.9095724
##  ( 2.3729250) ( 0.2259942)
```

Returns: estimates above, standard errors below

Checking Your Estimator

- simulate, then estimate; estimates should converge as the sample grows

```
gamma.est_MM(rgamma(100,shape=19,scale=45))
```

```
##    shape    scale
## 20.03284 43.16644
```

```
gamma.est_MM(rgamma(1e5,shape=19,scale=45))
```

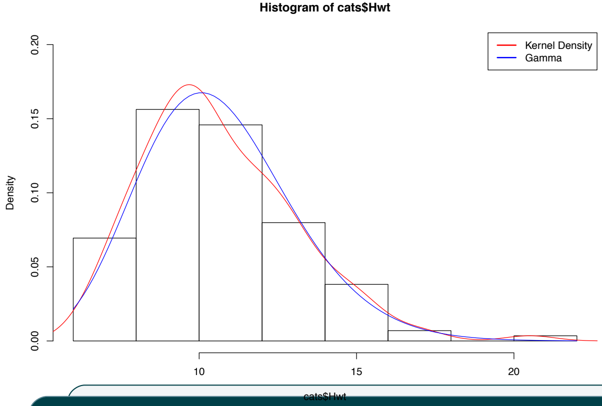
```
##    shape    scale
## 19.00715 44.88471
```

```
gamma.est_MM(rgamma(1e6,shape=19,scale=45))
```

```
##    shape    scale
## 18.99766 45.01638
```

Use your eyes: Graphic overlays of theory vs. data

```
hist(cats$Hwt,prob=T,ylim=c(0,.2))
lines(density(cats$Hwt),col=2)
cats.gamma <- gamma.est_MM(cats$Hwt)
curve(dgamma(x,shape=cats.gamma["shape"],scale=cats.gamma["scale"]),add=TRUE,co
legend("topright",c("Kernel Density","Gamma"),col=c(2,4),lty=1,lwd=2)
```



Kolmogorov-Smirnov Test

- How much should the QQ plot wiggle around the diagonal?
- Answer a different question...
- Biggest gap between theoretical and empirical CDF:

$$D_{KS} = \max_x \left| F(x) - \widehat{F}(x) \right|$$

- Useful because D_{KS} always has the same distribution *if* the theoretical CDF is fixed and correct
- Also works for comparing the empirical CDFs of two samples, to see if they came from the same distribution

KS Test, Data vs. Theory

```r
test.data <- rnorm(100,.5,.1)
ks.test(test.data,pnorm,mean=.1,sd=0.1)
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  test.data
## D = 0.97792, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

Ex: How does it works for other distributions?

Compare an actual table of counts to a hypothesized probability distribution:

```
coin <- rbinom(100,1,.45); chisq.test(table(coin),p=c(1/2,1/2))
```

```
##
##  Chi-squared test for given probabilities
##
## data:  table(coin)
## X-squared = 0.04, df = 1, p-value = 0.8415
```

```
coin <- rbinom(1000,1,.45) ; chisq.test(table(coin),p=c(1/2,1/2))
```

```
##
##  Chi-squared test for given probabilities
##
## data:  table(coin)
## X-squared = 29.584, df = 1, p-value = 5.355e-08
```

Chi-Squared Test: Degrees of Freedom

- The df is the number of cells in the table -1
- If we estimate q parameters, we need to subtract q degrees of freedom

- Divide the range into bins and count the number of observations in each bin; this will be `x` in `chisq.test()`
- Use the CDF function `p` *foo* to calculate the theoretical probability of each bin; this is `p`
- Plug in to `chisq.test`
- If parameters are estimated, adjust

- `hist()` gives us break points and counts:

```
cats.hist <- hist(cats$Hwt,plot=FALSE)
cats.hist$breaks
```

```
## [1]  6  8 10 12 14 16 18 20 22
```

```
cats.hist$counts
```

```
## [1] 20 45 42 23 11  2  0  1
```

Chi-Squared for Continuous Data (cont'd.)

Use these for a χ^2 test:

```
# Why the padding by -Inf and Inf?
p <- diff(pgamma(c(-Inf,cats.hist$breaks,Inf),shape=cats.gamma["shape"],
                 scale=cats.gamma["scale"]))
# Why the padding by 0 and 0?
 chisq.test(c(0,cats.hist$counts,0),p=p)
```

```
##
##  Chi-squared test for given probabilities
##
## data:  c(0, cats.hist$counts, 0)
## X-squared = 12.133, df = 9, p-value = 0.2059
```

Don't need to run `hist` first; can also use `cut` to discretize (see `?cut`)

Summary

- Visualizing and computing empirical distribution
- Parametric distributions are models
- Methods of fitting: moments and likelihood
- Methods of checking: visual comparisons, other statistics, tests, calibration