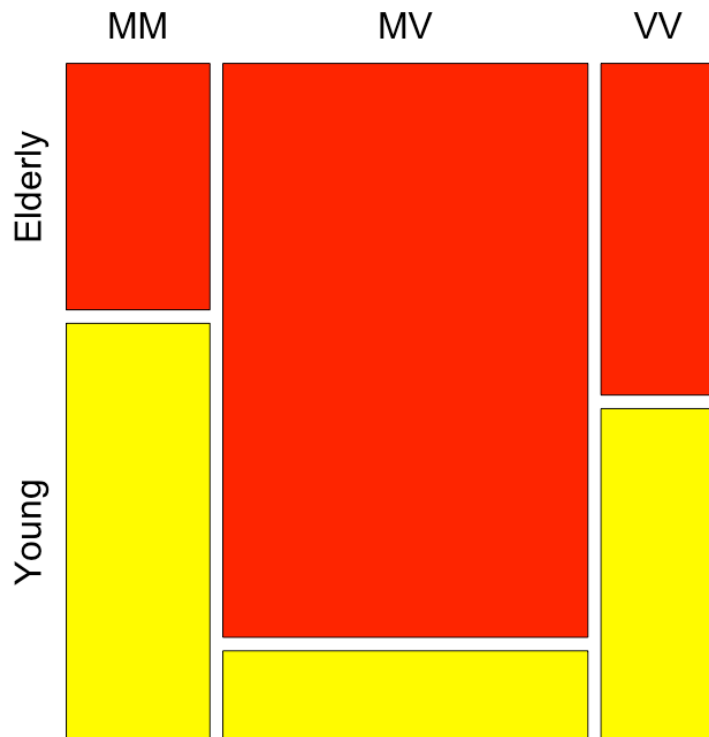


**** On analyzing Contingency Tables**

**** The normal distribution**

Week 08

Kuru dataset



```
kuru=  
matrix(data=c(13,77,14,22,12  
,14), nrow =2, ncol =3,  
byrow = T)  
rownames(kuru)=c("Elderly",  
"Young")  
colnames(kuru) = c("MM",  
"MV", "VV")  
mosaicplot(t(kuru), main="",  
col=c("red","yellow"),  
cex=2)
```

Test for contingency tables

Chi square test (9.4)

$$Df = (r - 1) * (c - 1)$$

Just another G o F test

G-test (9.6, see
likelihood)

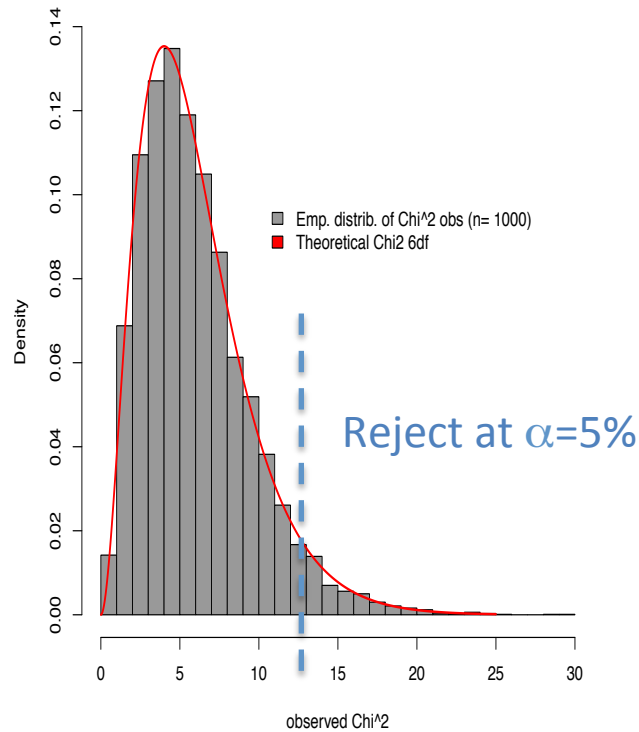
Fisher's exact test (9.5)

Enumerate all tables that
are more “extreme” and
sums up their
probabilities... actually
HARD to do ... works great
for small counts

Remember A well behaved test

Test statistic from Data under H_0 is well approximated by the **limiting distribution**

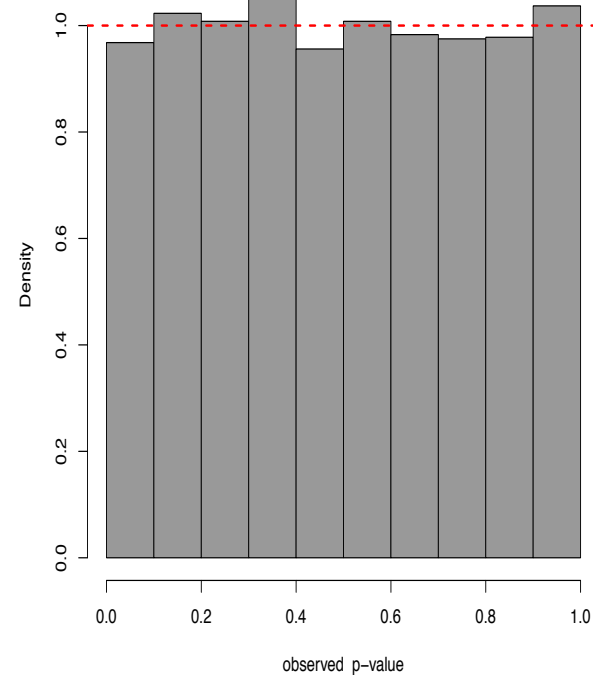
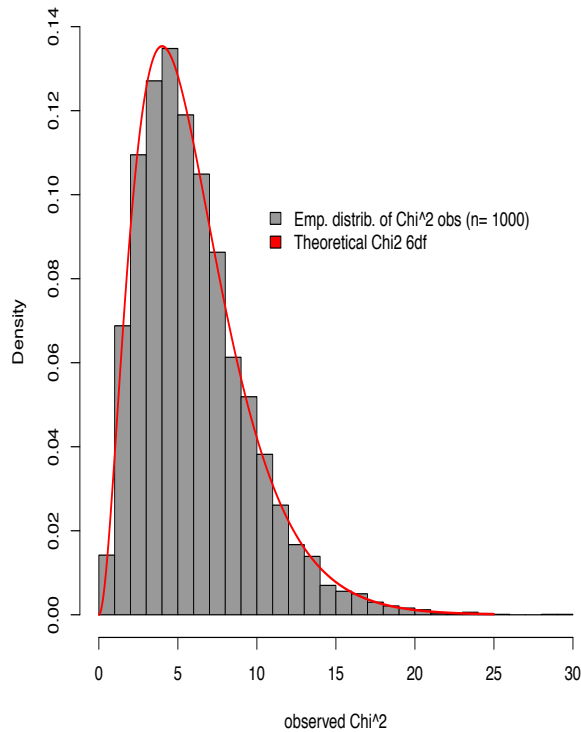
→ P-values are ...?



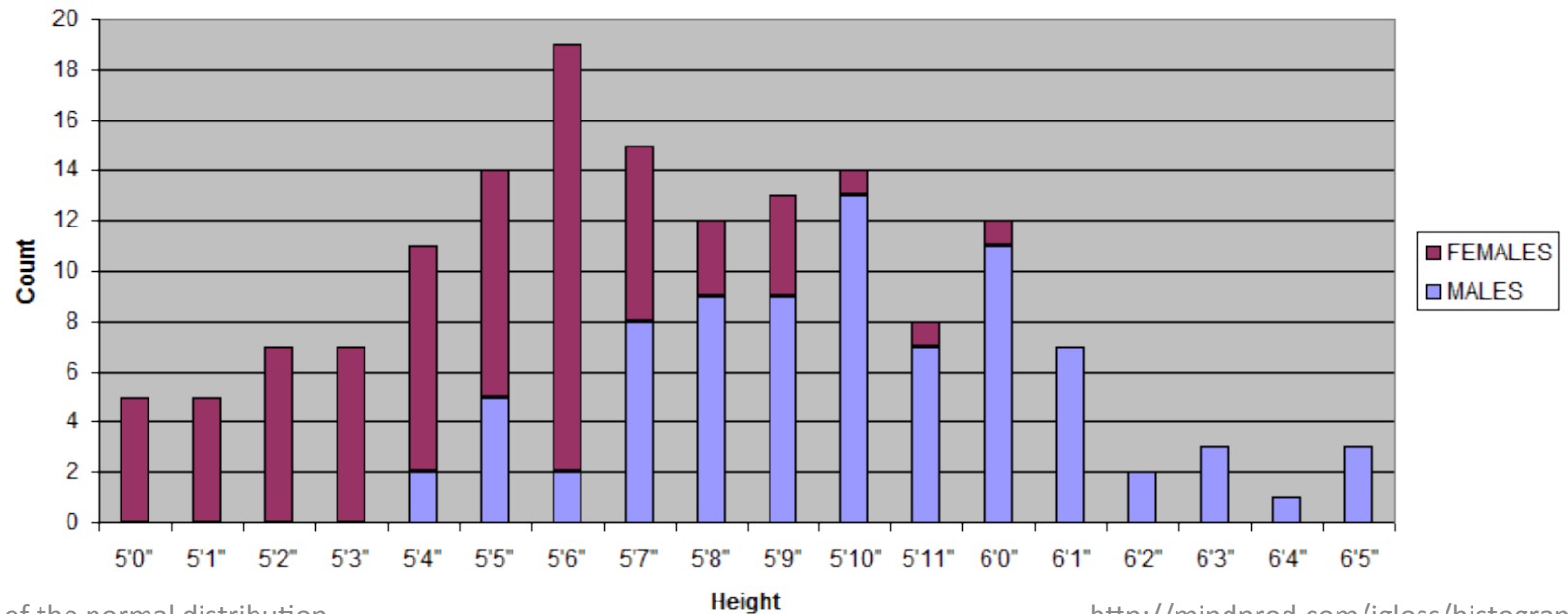
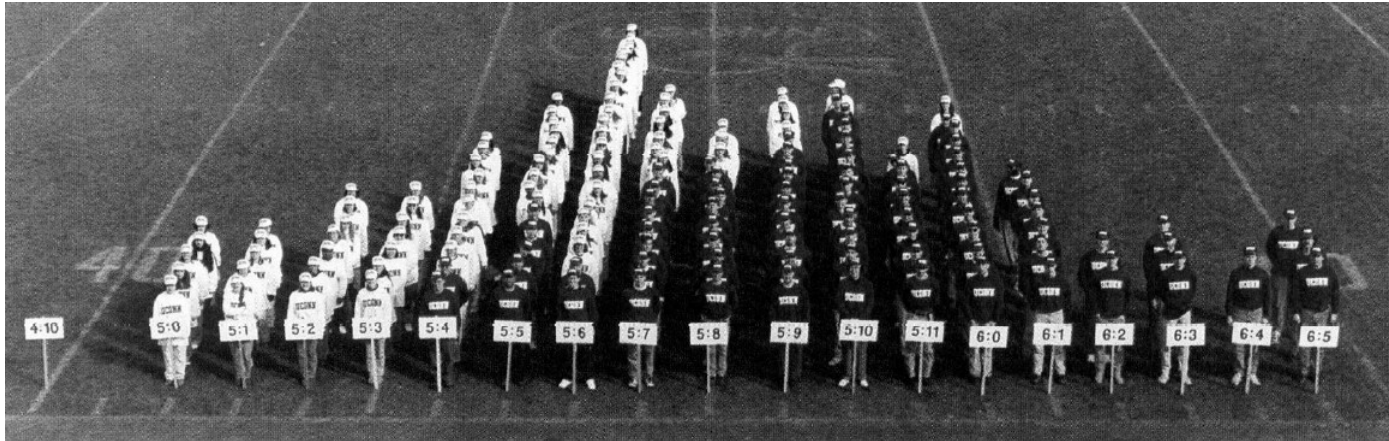
A well behaved test

Data simulated under H_0 is well approximated by limiting distribution

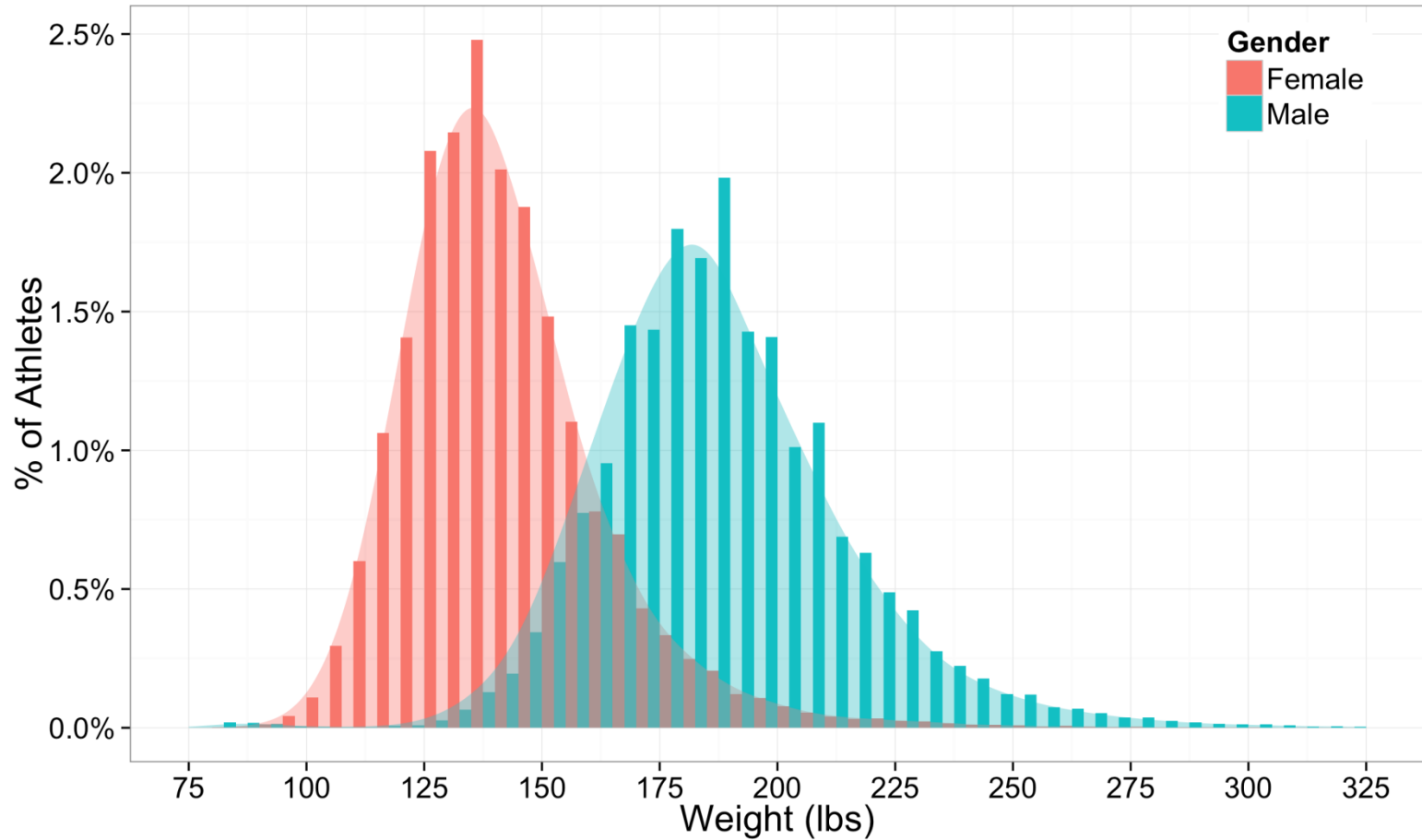
↔ **P-values are uniform in $[0,1]$**



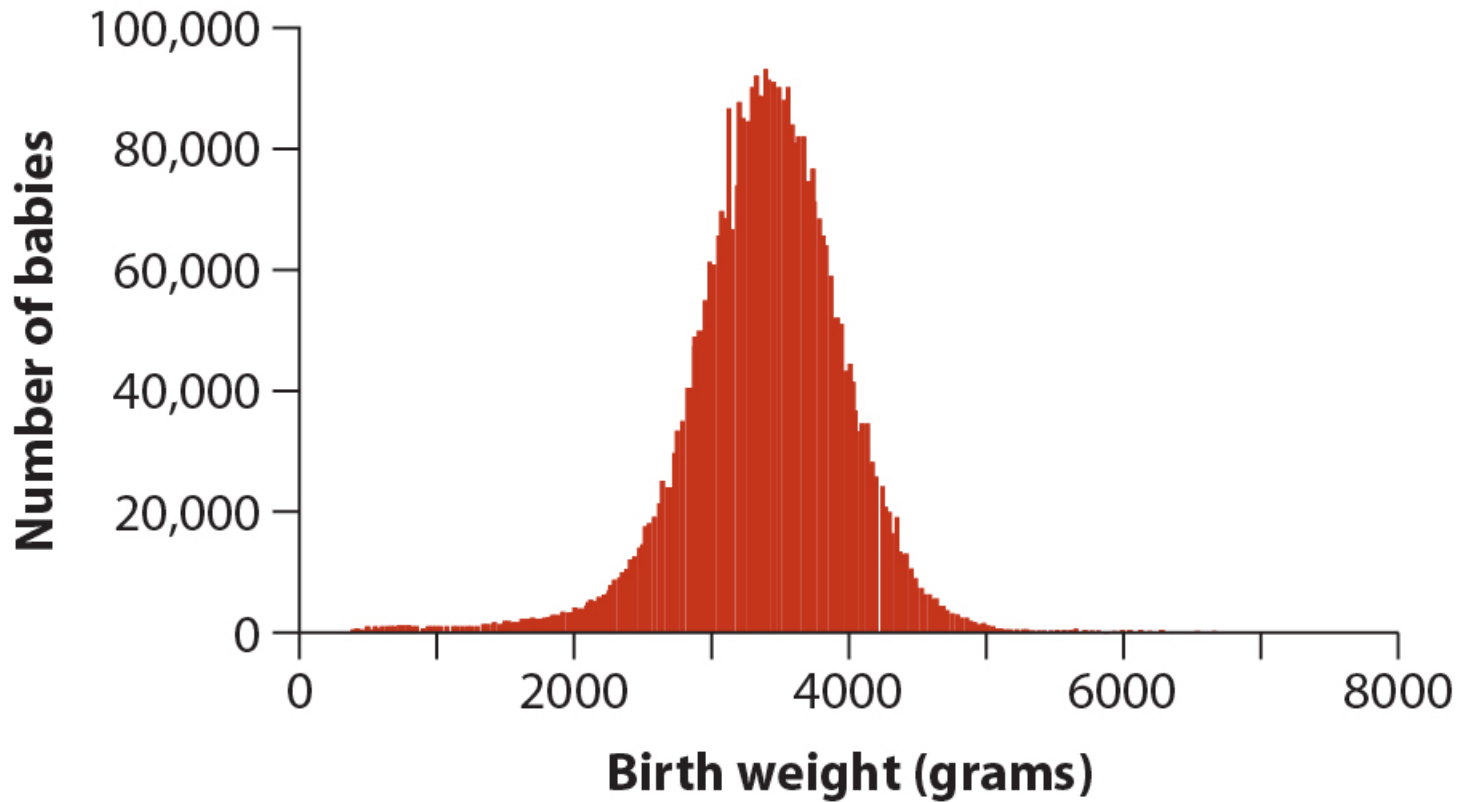
Height of college students



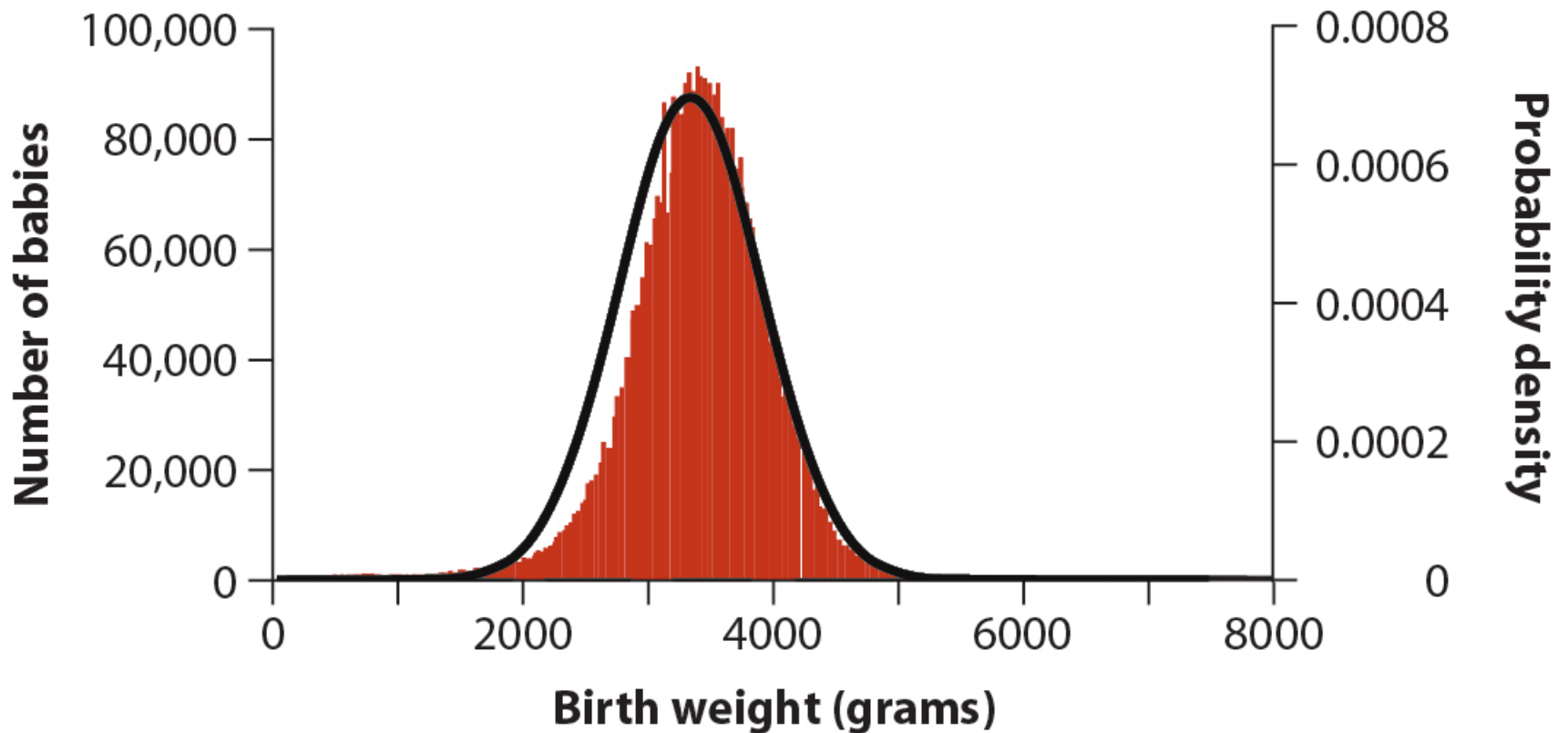
Weight of women vs men



Normal data



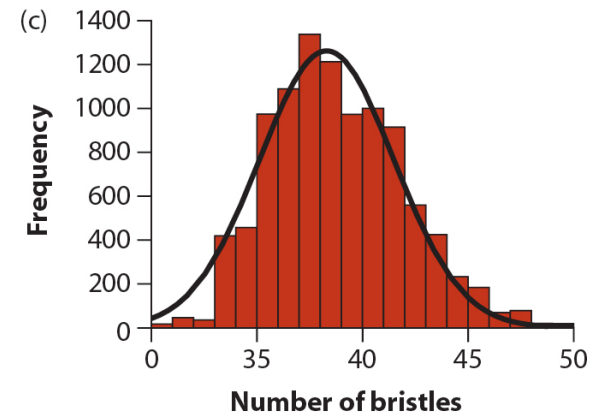
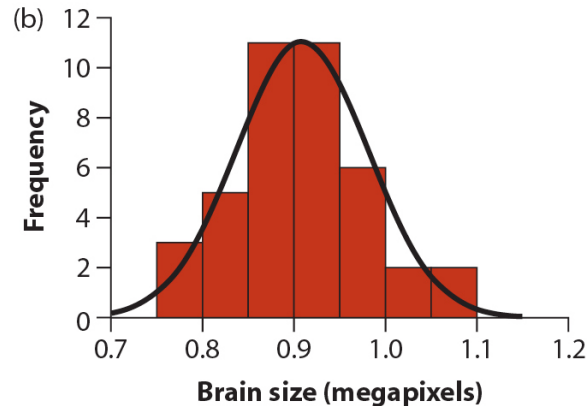
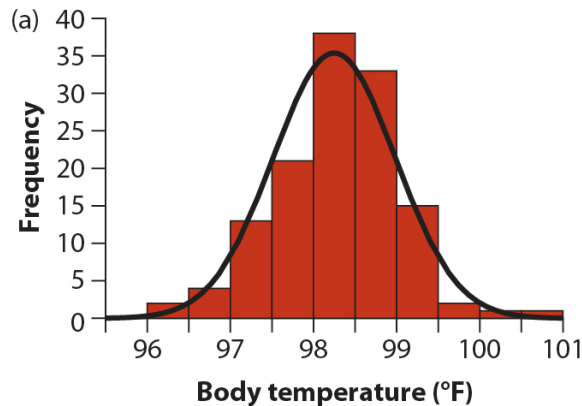
Normal distribution



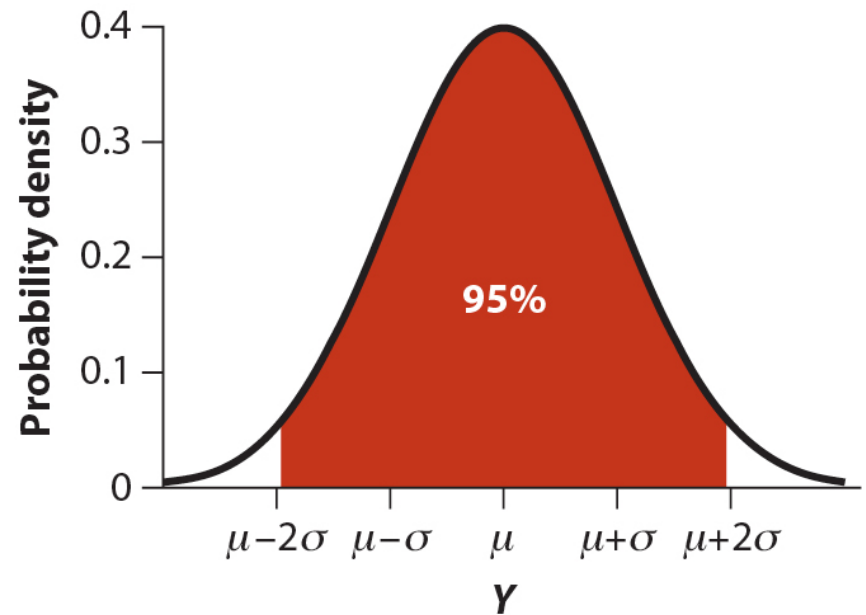
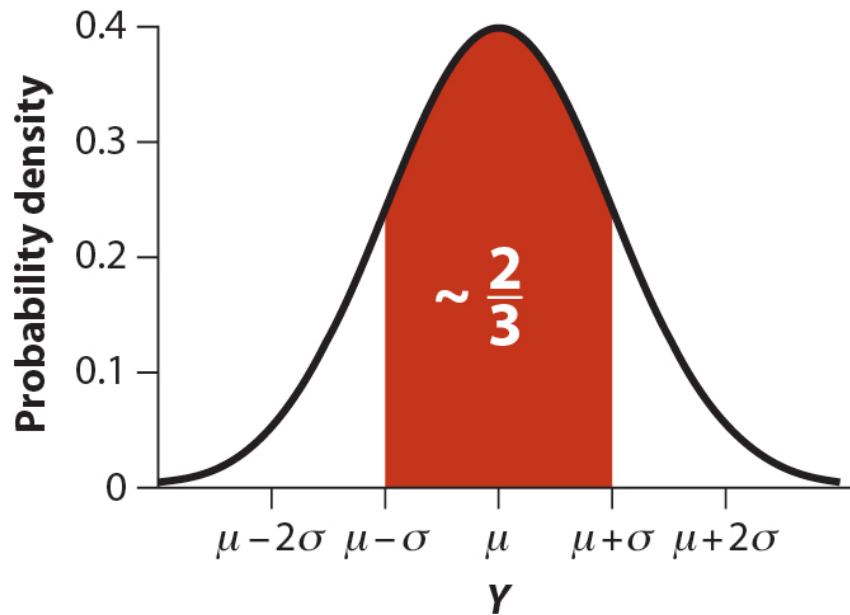
$$f(Y|\mu, \sigma) = \frac{1}{\sigma \sqrt{2\pi}} e^{-\frac{(Y - \mu)^2}{2\sigma^2}}$$

Common in nature

- Many biological measures are (almost) normally distributed
 - body temperature
 - brain size
 - height
 - brain size
 - weight
 - number of bristles (discrete)
 - BMI



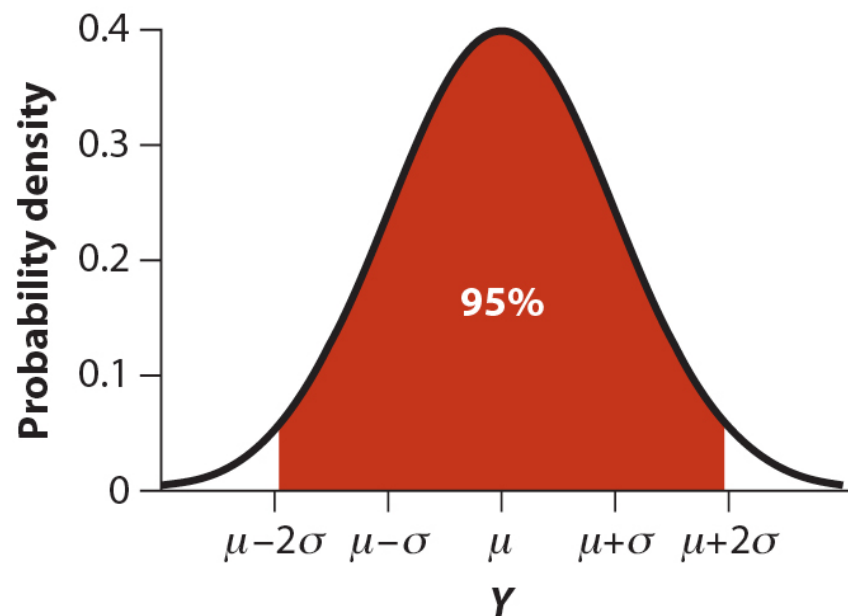
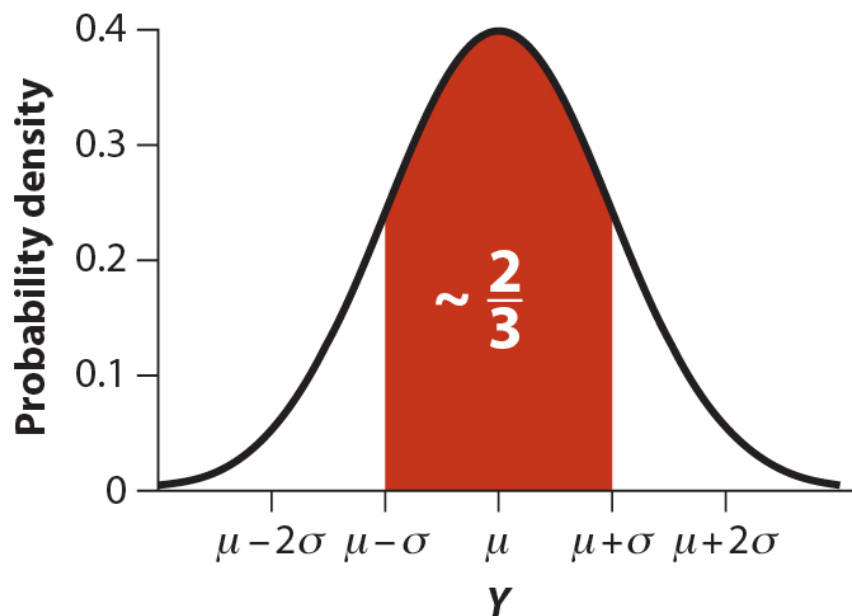
Properties



$$\Pr[\mu - \sigma \leq x \leq \mu + \sigma] \approx 0.683$$

$$\Pr[\mu - 2\sigma \leq x \leq \mu + 2\sigma] \approx 0.955$$

Properties

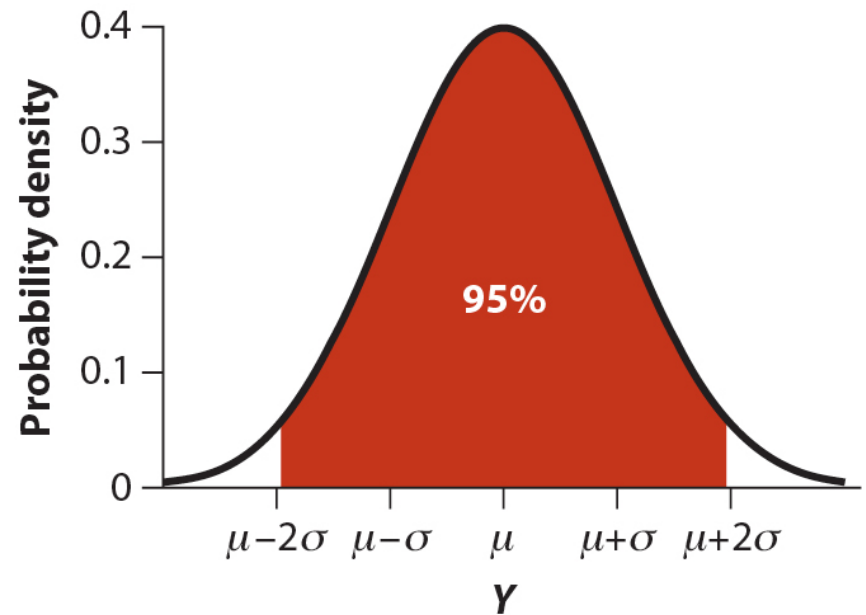
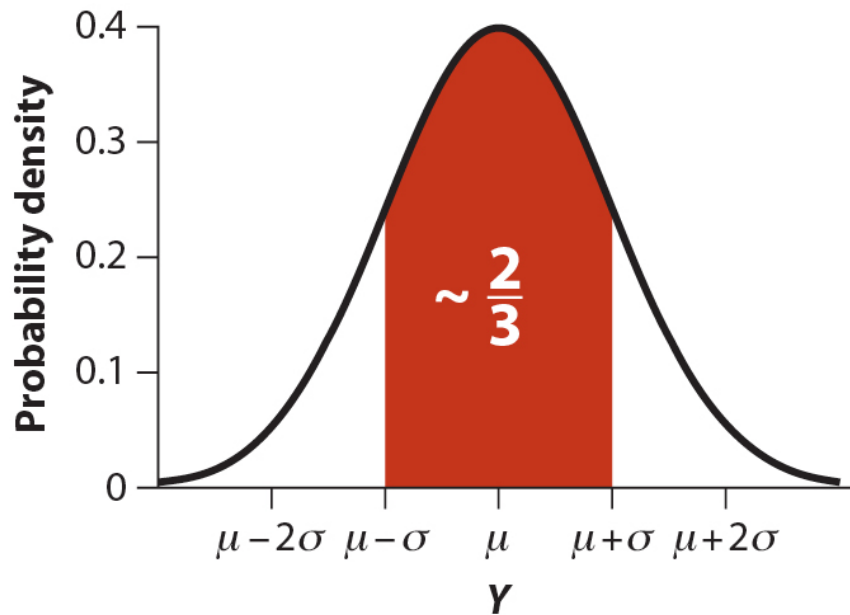


$$\Pr[\mu - \sigma \leq x \leq \mu + \sigma] \approx 0.683$$

$$\Pr[\mu - 2\sigma \leq x \leq \mu + 2\sigma] \approx 0.955$$

Approximate 95% CI (chapter 4): $[Y - 2SE\downarrow Y, Y + 2SE\downarrow Y]$

Properties



$$\Pr[\mu - \sigma \leq x \leq \mu + \sigma] \approx 0.683$$

$$\Pr[\mu - 2\sigma \leq x \leq \mu + 2\sigma] \approx 0.955$$

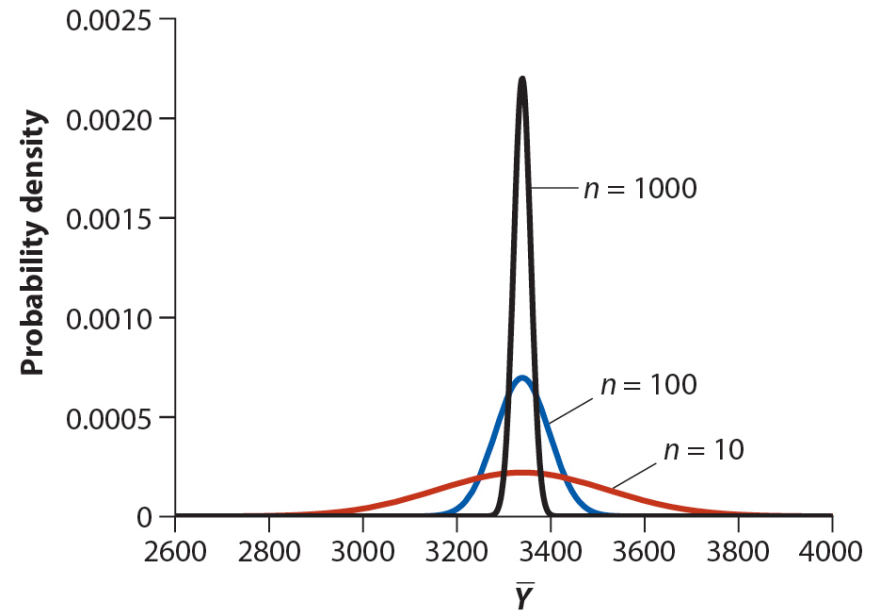
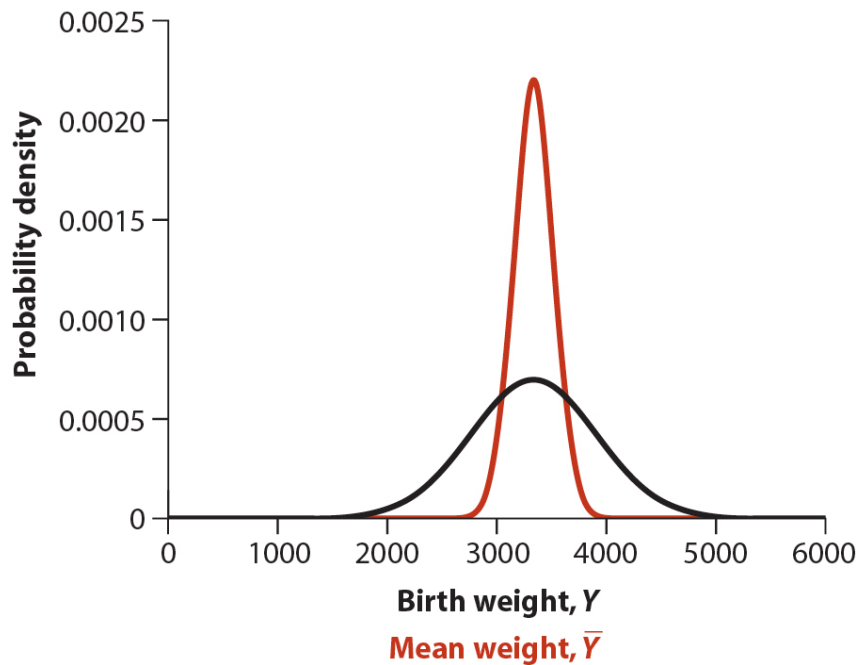
Approximate 95% CI (chapter 4): $[Y - 2SE\downarrow Y, Y + 2SE\downarrow Y]$

$$\Pr[\mu - 1.96\sigma \leq x \leq \mu + 1.96\sigma] \approx 0.950$$

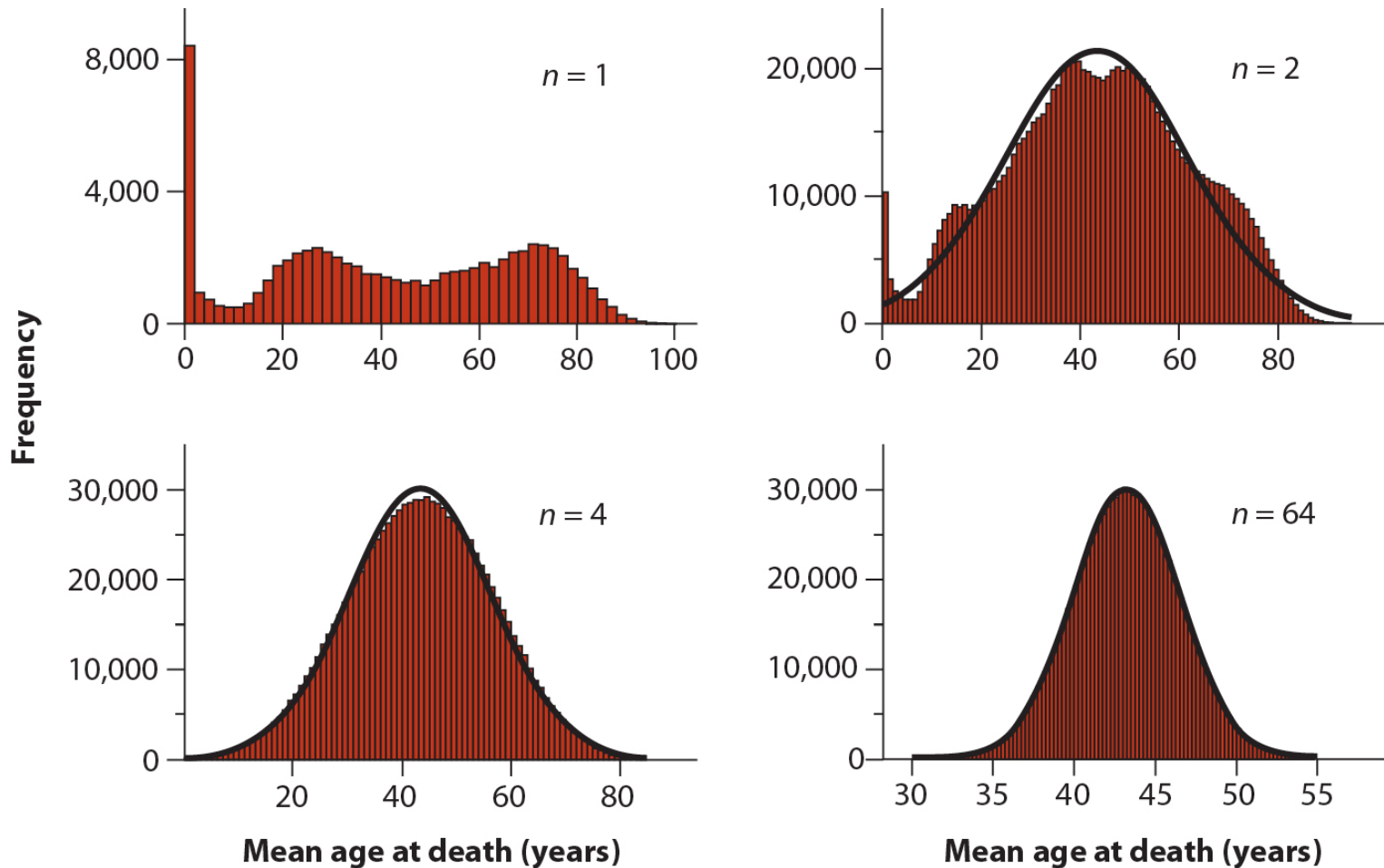
Normal distribution in R

- `rnorm` `pnorm` `dnorm`

The distribution of sample means

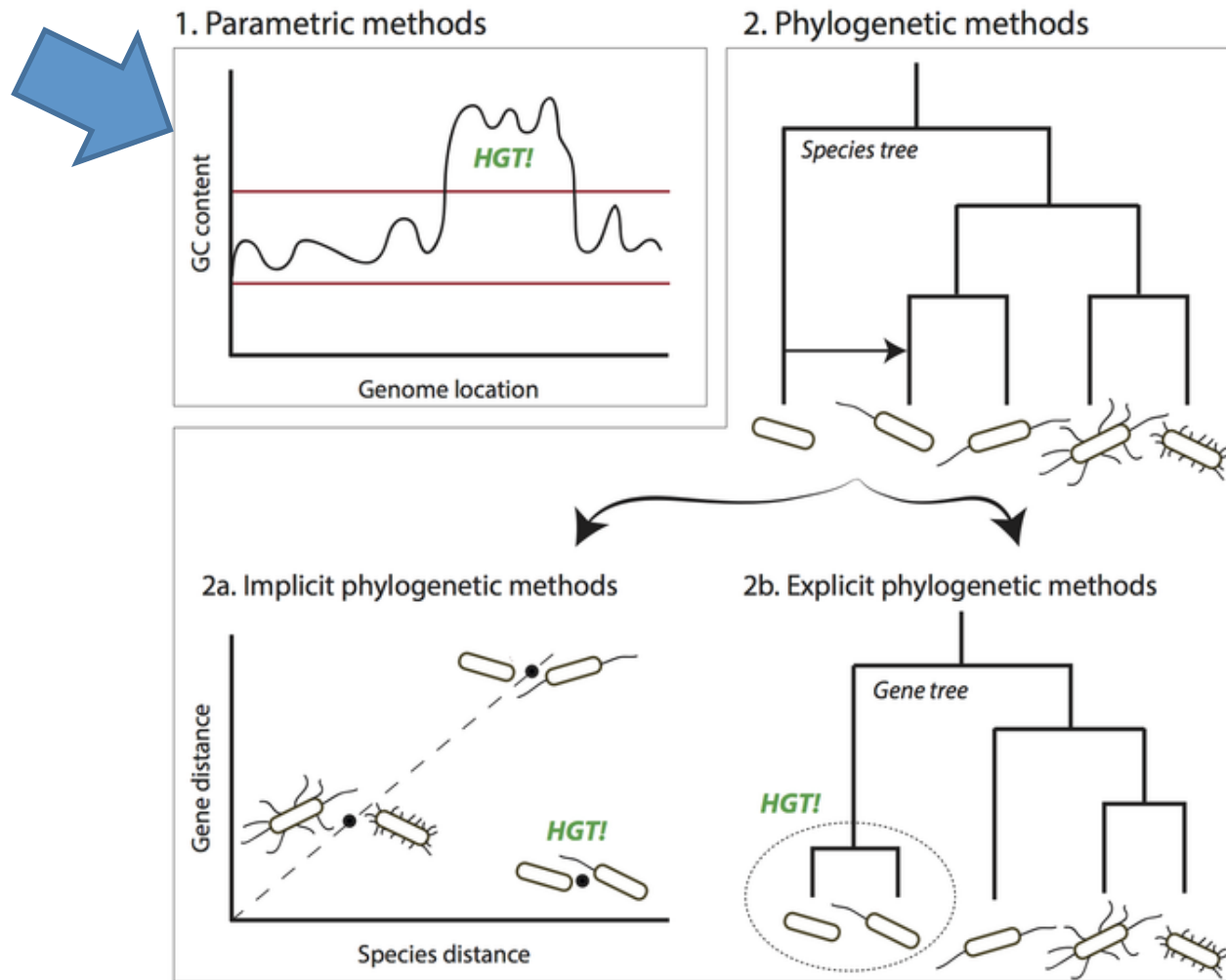


The CLT: central limit theorem



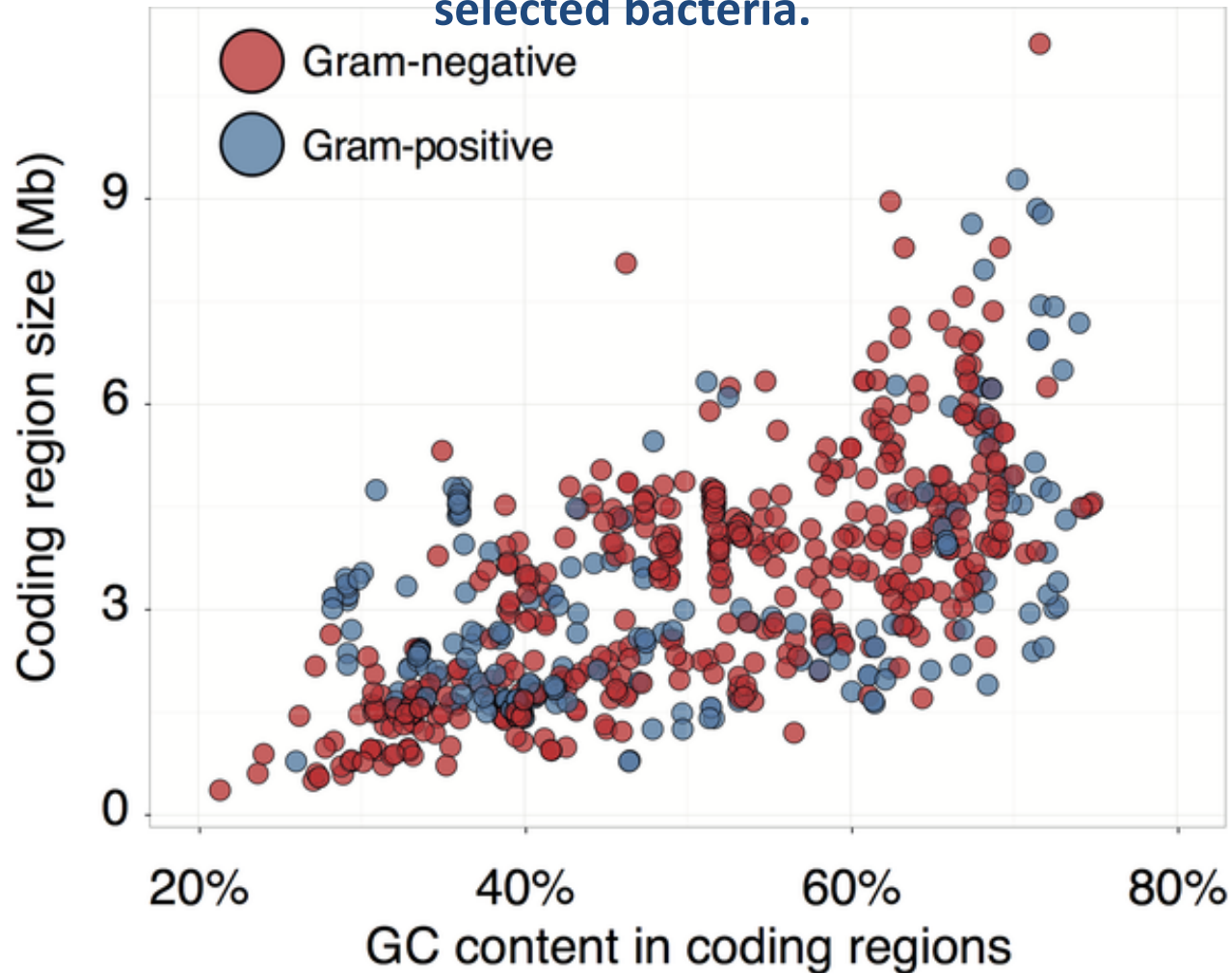
Draw a distribution that can “cheat”
CLT

Conceptual overview of HGT inference methods.



Ravenhall M, Škunca N, Lassalle F, Dessimoz C (2015) Inferring Horizontal Gene Transfer. PLOS Computational Biology 11(5): e1004095. <https://doi.org/10.1371/journal.pcbi.1004095>
<http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004095>

Average GC content of coding regions compared to the genome size for selected bacteria.



Ravenhall M, Škunca N, Lassalle F, Dessimoz C (2015) Inferring Horizontal Gene Transfer. PLOS Computational Biology 11(5): e1004095. <https://doi.org/10.1371/journal.pcbi.1004095>
<http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004095>

