



*Opinionated*  
Lessons  
in Statistics

*by Bill Press*

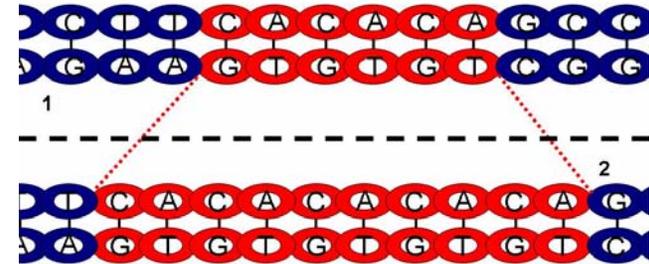
*#6 The Towne Family Tree*

## Neat example (with some biology):

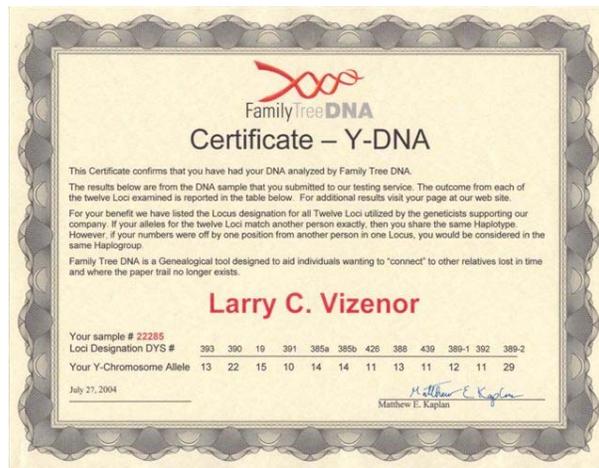
Individual identity, or ancestry, can be determined by “variable length short tandem repeats” (STRs) in the genome.

~0.5% mutation prob per STR per generation (though highly variable)

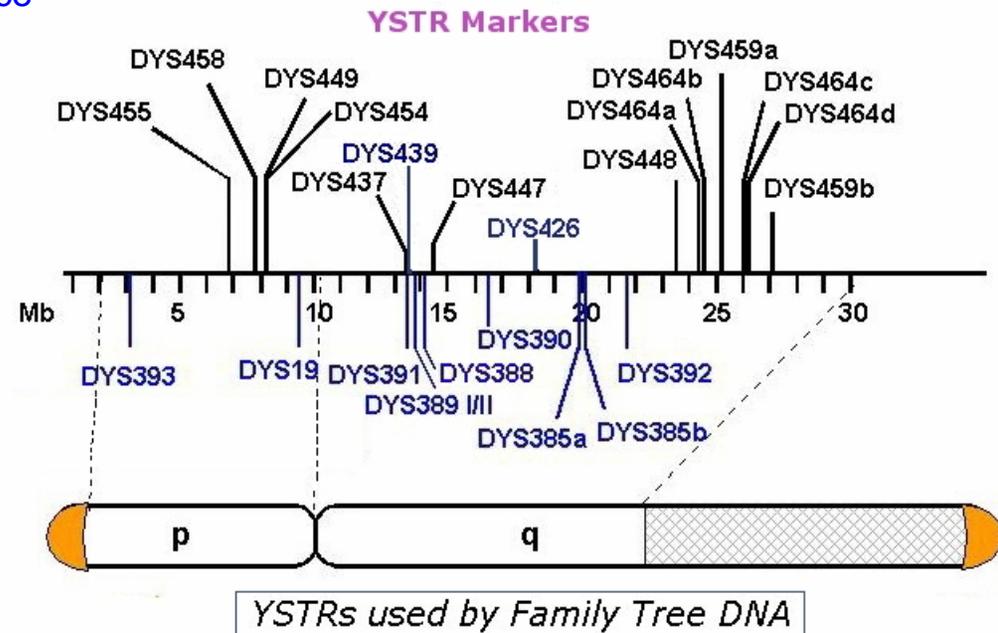
if use Y chromosome only, get paternal ancestry



There are companies that sell “certificates” with your genotype. A bit opportunistic, since in a few years your whole genome will be sequenced by your health plan.

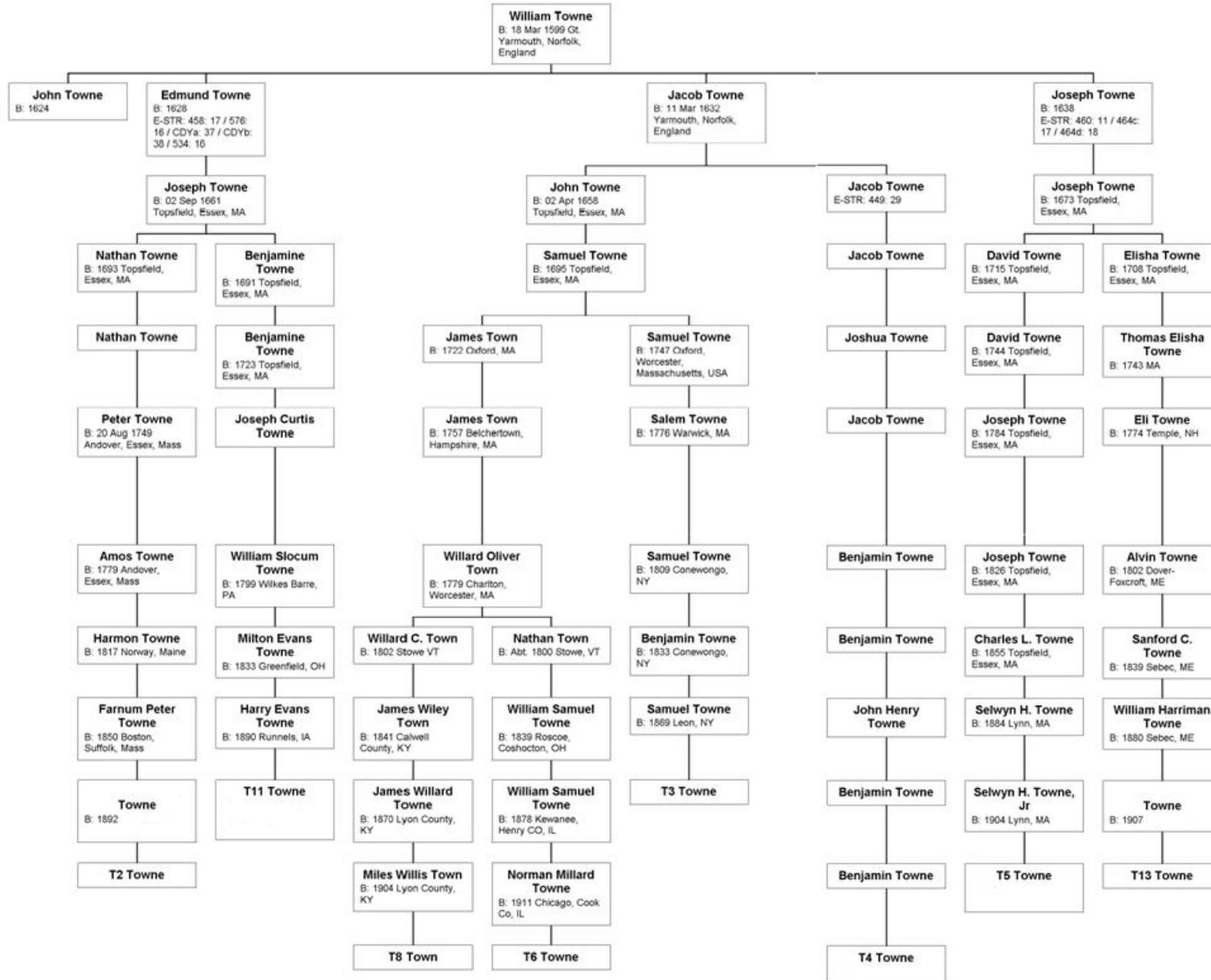


## YSTR Positions along Y Chromosome



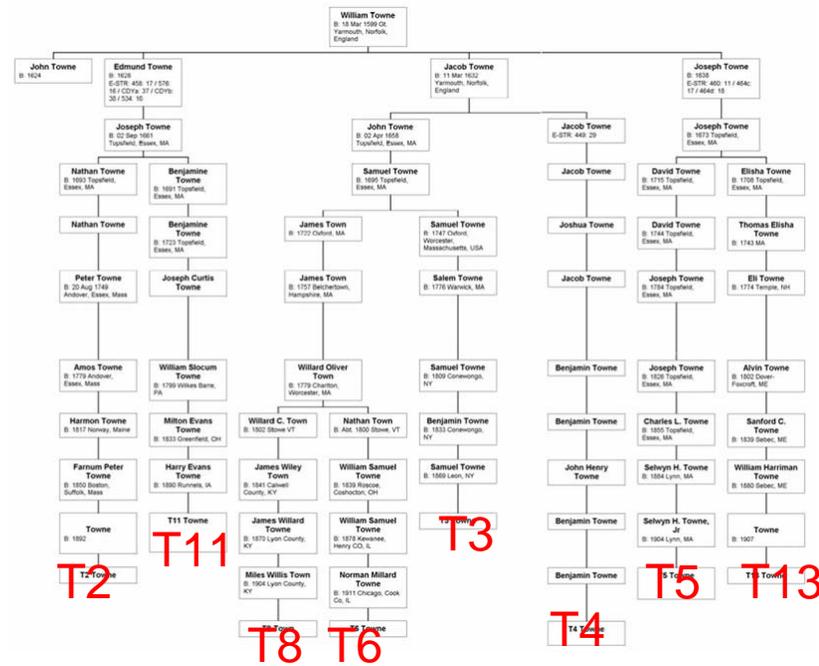
Descendant Chart for William Towne

Margaret, my ex-wife, is really into the Towne family.  
(And, she's neither a biologist nor a Towne.)



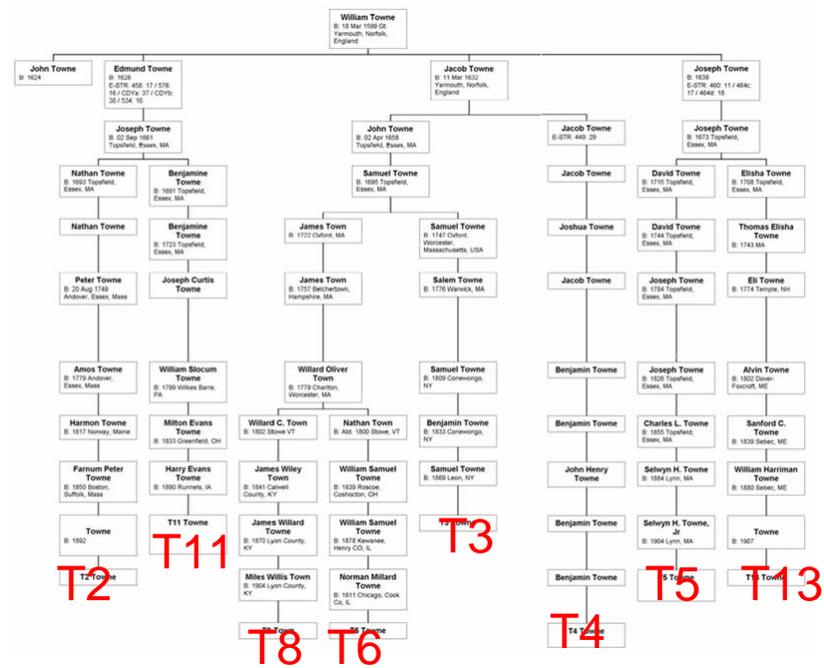
Here's data from Margaret on 8 recent Townes (identified only by T code).  
 (We'll use this data several times in the next few of lectures.)

		Family Tree DNA 37 Marker Test																																					
		gens	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37
	William	0	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	28	15	15	16	17	10	10	23	23	16	15	17	17	35	39	12	12
T-3	by Jacob	9	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	28	15	15	16	17	10	10	23	23	16	15	17	17	35	39	12	12
T-4	by Jacob	11	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	29	15	15	16	17	10	10	23	23	16	15	17	17	35	39	12	12
T-6	by Jacob	11	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	28	15	15	16	17	10	10	23	23	16	15	17	17	35	39	12	12
T-8	by Jacob	11	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	28	15	15	16	17	10	10	23	23	16	15	17	17	34	39	12	12
T-5	by Joseph	10	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	28	15	15	17	18	11	10	23	23	16	15	17	17	35	39	12	12
T-13	by Joseph	10	13	24	14	11	11	13	12	12	13	14	13	29																									
T-11	by Edmund	9	13	24	14	11	11	14	12	12	11	14	13	30	17	9	10	11	11	24	14	19	28	15	15	16	17	10	10	23	23	16	15	16	17	37	38	12	12
T-2	by Edmund	10	13	25	14	11	11	13	12	12	12	13	14	29	18	9	10	11	11	24	15	18	28	15	16	16	17	11	11	19	23	17	16	18	17	37	38	12	12

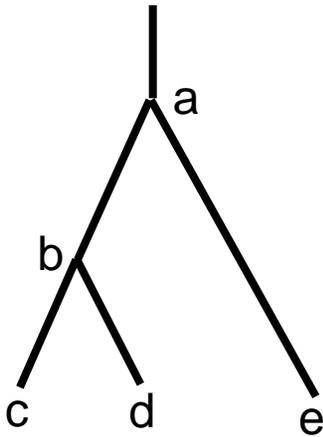


Or, just showing the changes from what we impute for William:

			Family Tree DNA 37 Marker Test																																							
			gens	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37		
William		0	13	24	14	11	11	14	12	12	11	14	13	30	16	9	10	11	11	24	14	19	28	15	15	16	17	10	10	23	23	16	15	17	17	35	12	12				
T-3	by Jacob	9																																								
T-4	by Jacob	11																						1																		
T-6	by Jacob	11																																								
T-8	by Jacob	11																																								
T-5	by Joseph	10																										1	1	1												
T-13	by Joseph	10					-1				2				-1																											
T-11	by Edmund	9														1																										
T-2	by Edmund	10		1																																						



# Unraveling dependencies



$$\begin{aligned} P(abcde) &= P(e|\cancel{abcd})P(abcd) \\ &= P(e|a)P(c|\cancel{abd})P(abd) \\ &= P(e|a)P(c|b)P(d|\cancel{ab})P(ab) \\ &= P(e|a)P(c|b)P(d|b)P(b|a)P(a) \end{aligned}$$

Another important idea is “conditional independence”

Example: b and e are “conditionally independent given a”

$$\begin{aligned} P(be|a) &= P(b|\cancel{e}a)P(e|a) \\ &= P(b|a)P(e|a) \end{aligned}$$

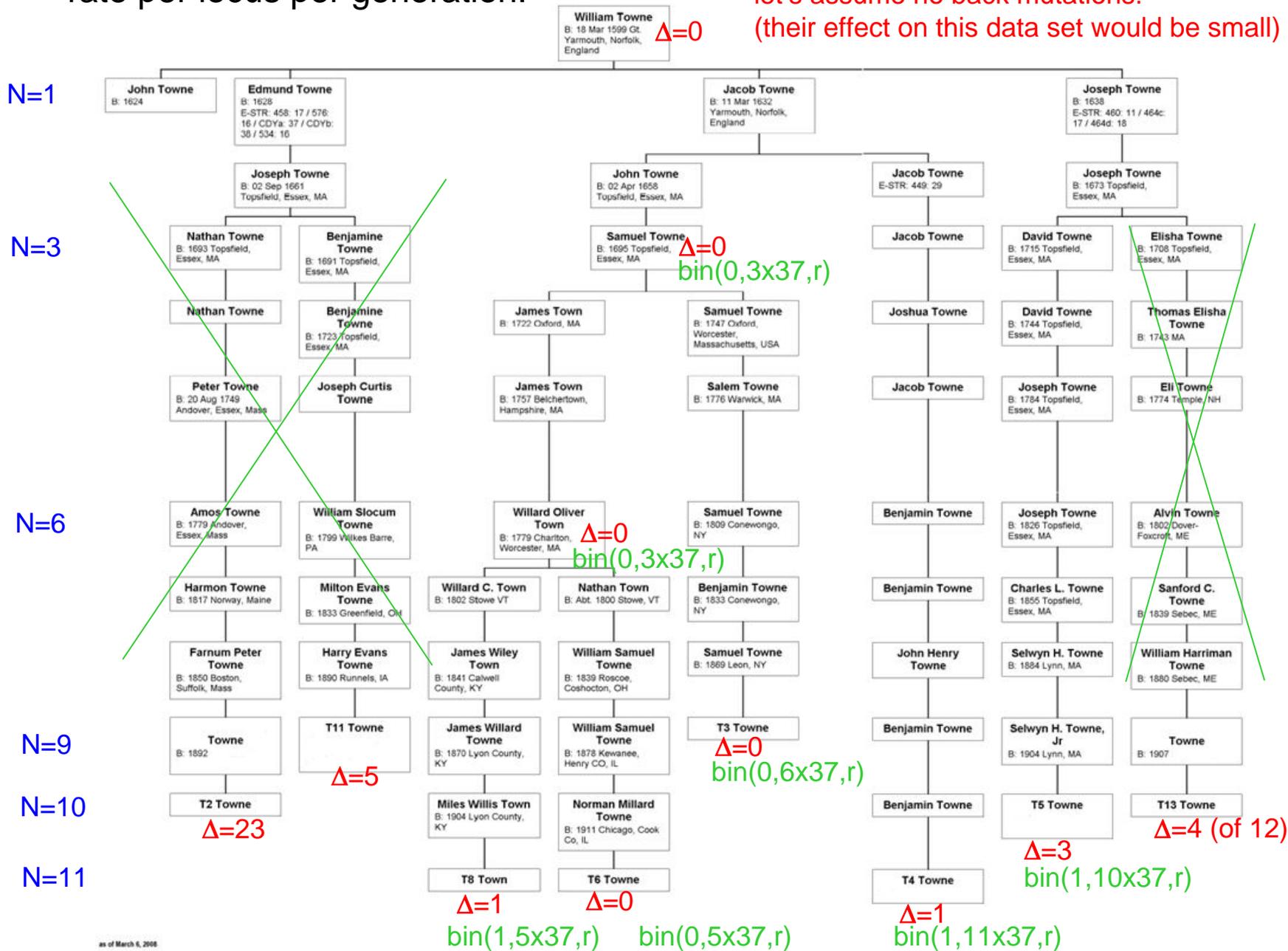
while b and d are not conditionally independent given a:

$$P(bd|a) = P(b|da)P(d|a)$$

?

Let's do a Bayesian estimation of the parameter  $r$ , the mutation rate per locus per generation.

let's assume no back mutations!  
(their effect on this data set would be small)



So we have a **statistical model** for the data!

Any **statistical model** is just a way to compute  $P(\text{data}|\text{parameters})$

Our model is not “exact”, but statistical models rarely (never?) are.

neglects backmutations

assumes single probability for all loci

etc.

The model is:

$$P(\text{data}|r) = \text{bin}(0, 3 \times 37, r) \text{bin}(0, 3 \times 37, r) \text{bin}(1, 5 \times 37, r) \text{bin}(0, 5 \times 37, r) \\ \times \text{bin}(0, 6 \times 37, r) \text{bin}(1, 11 \times 37, r) \text{bin}(3, 10 \times 37, r)$$

Bayes estimation of the parameter:

$$P(r|\text{data}) \propto P(\text{data}|r) \times P(r) \propto P(\text{data}|r) \times \frac{1}{r}$$

What kind of prior is this???  
It is called “log-uniform”

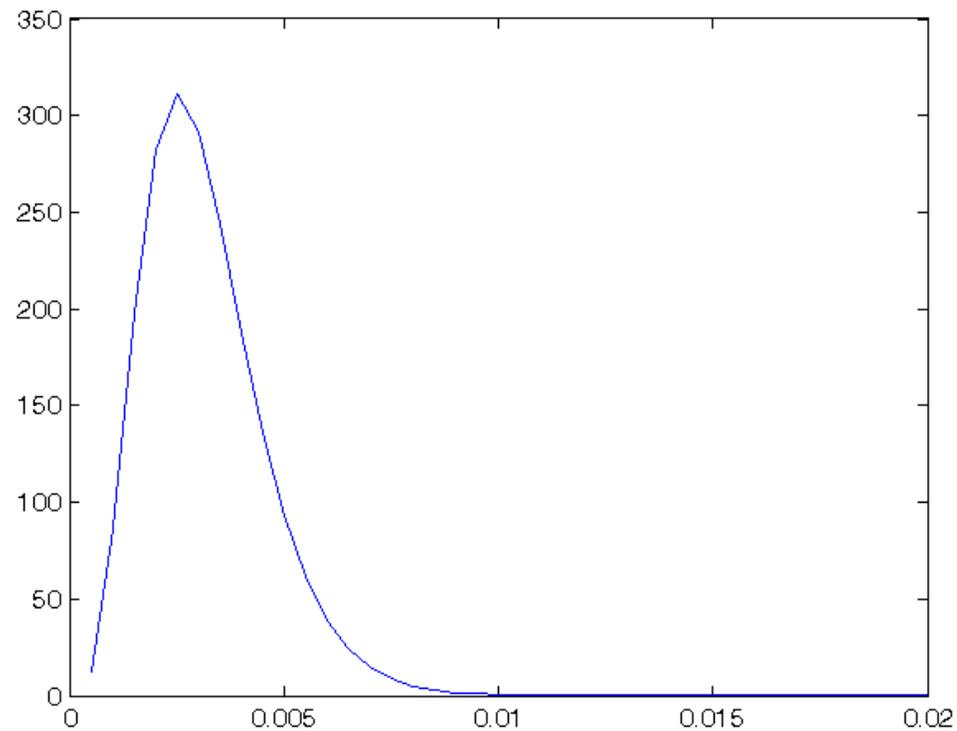
The log-uniform prior has equal probability in each order of magnitude.  $\int_r^{10r} P(r)dr = \int_r^{10r} \frac{1}{r} dr = \log 10$

It is often taken as the non-informative prior when you don't even know the order of magnitude of the (positive) quantity.

It is an “improper prior” since its integral is infinite.

This is almost always ok, but it is possible to construct paradoxes with improper priors (e.g., the “marginalization paradox”)

Here is the plot of the (normalized)  $P(r|\text{data})$



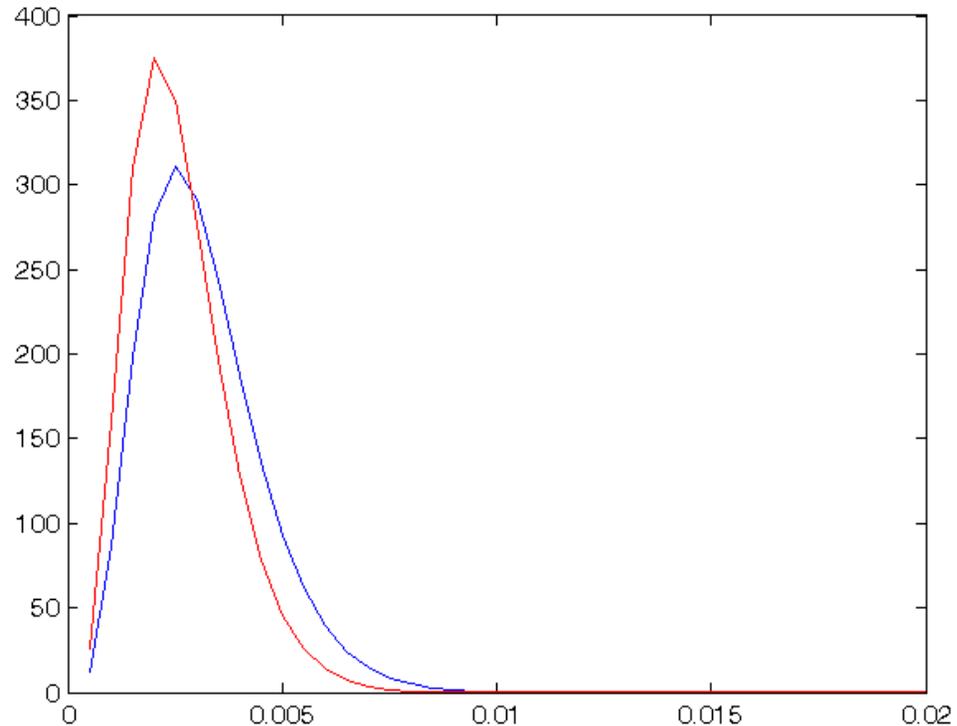
This is (almost) real biology. We've measured the mutation probability, per locus per generation of Y chromosome STRs. This tells us something about the actual DNA replication machinery!

It really did matter (a bit) that we sorted out the conditional dependencies correctly.

Here's a comparison to doing it **wrong by assuming all data independent:**

The true dependencies allow somewhat larger values of  $r$ , because we don't wrongly count the  $\Delta=0$  branches multiple times

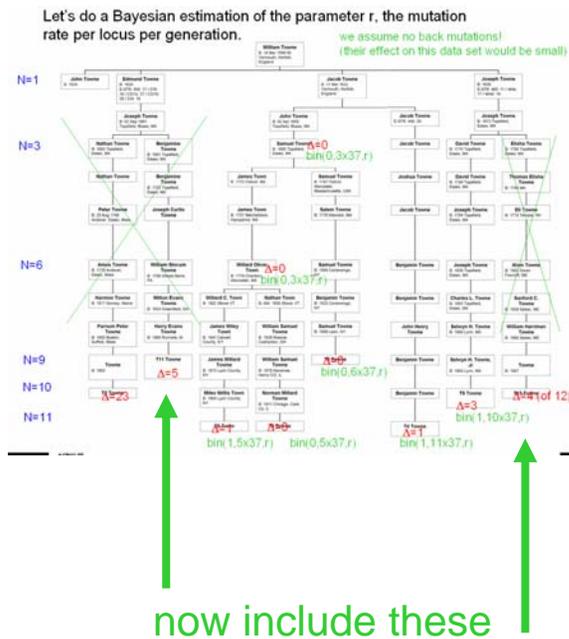
We'll come back to the Towne family for some fancier stuff later!



Ignoring conditional dependencies and just multiplying the probabilities of the data as if they were independent is called **naïve Bayes**. People often do this. It is mathematically incorrect, but sometimes it is all you can do!

A small cloud: The way we “trimmed” the data mattered. (And should trouble us a bit!) Here’s the effect of including T11 and T13, both of which seemed to be outliers:

$$P(\text{data}|r) = [\text{old model}] \times \text{bin}(5, 9 \times 37, r) \text{bin}(4, 10 \times 12, r)$$



Editing outliers is a tricky issue that we will return to when we learn about mixture models.

