

## Chapter 5 – Inferring Population History and Demography

### Inferring Demography Using Summary Statistics

Coalescence Simulations and Confidence Intervals

Estimating Evolutionary Trees

Gene Trees Versus Species Trees

Interpreting Estimated Trees from Population Genetic Data

### Likelihood and the Felsenstein Equation

MCMC and Bayesian Methods

The Effect of Recombination

Population Assignment, Clustering, and Admixture

## Sequence Divergence

- ❖ simple genetic distance,  $d$  = the proportion of sites that differ between two aligned, homologous sequences
- ❖ given a constant mutation/substitution rate,  $d$  should provide a measure of time since divergence
  - ❖ but this is greatly complicated by **multiple hits** (homoplasy)
- ❖ given that there are **not** an infinite number of sites in a sequence, how is  $d$  expected to change with time?

consider two recently diverged  
sequences...

```
ACGTACGTACGTACGTACGTACGTACGTACGT
ACGTACGTACGTACGTACGTACGTACGTACGT
```

consider two recently diverged  
sequences...

```
ACGTACGTACGTACGTACGTACGTACGTACGT
ACGTACGTACGTACGTAAAGTACGTACGT
```



what is the chance that the next  
substitution obscures the first?

consider two recently diverged sequences...

ACGTACGCACGTACGTACGTACGTACGT  
ACGTACGTACGTACGTACGTAAGTACGTACGT

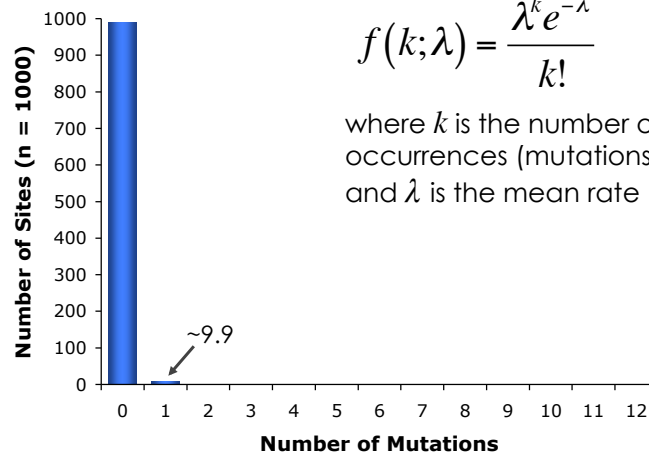
now, what is the chance that the next substitution obscures one of the first two?

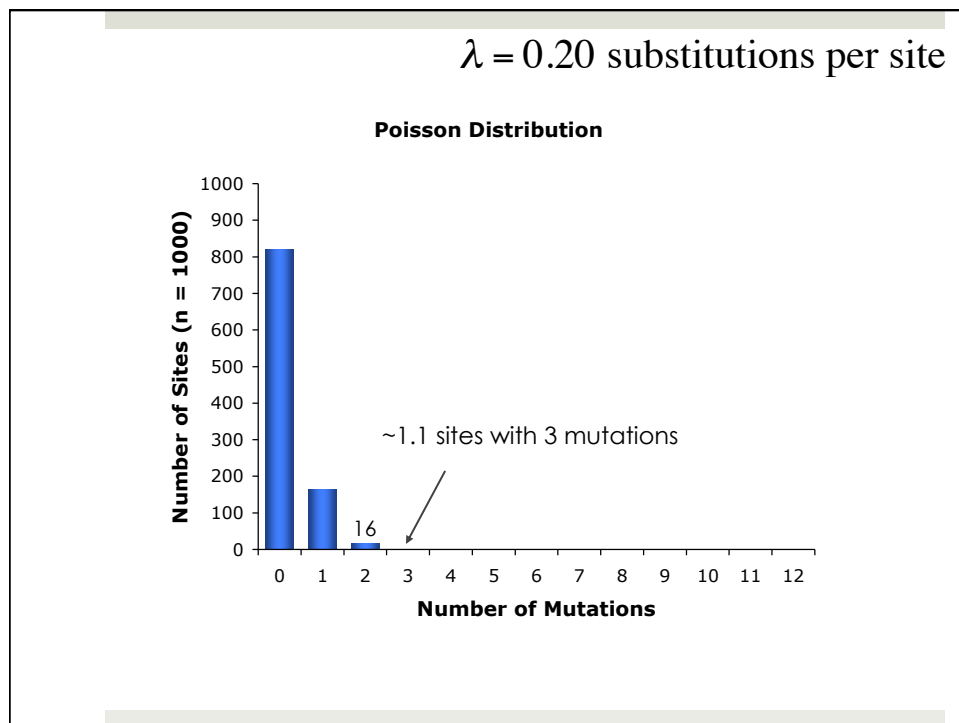
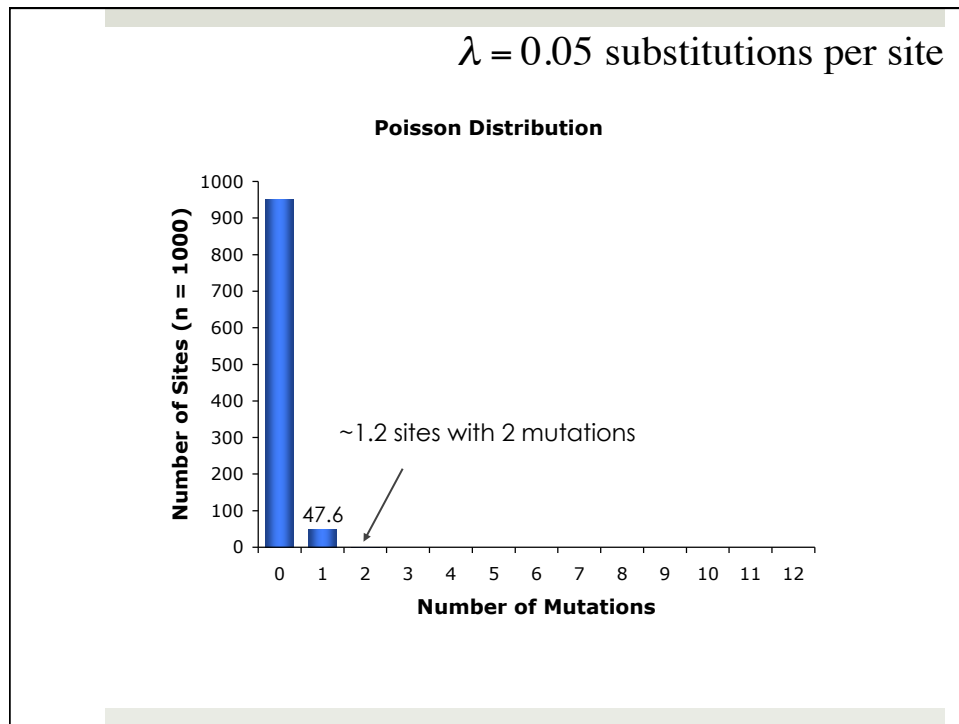
$\lambda = 0.01$  substitutions per site

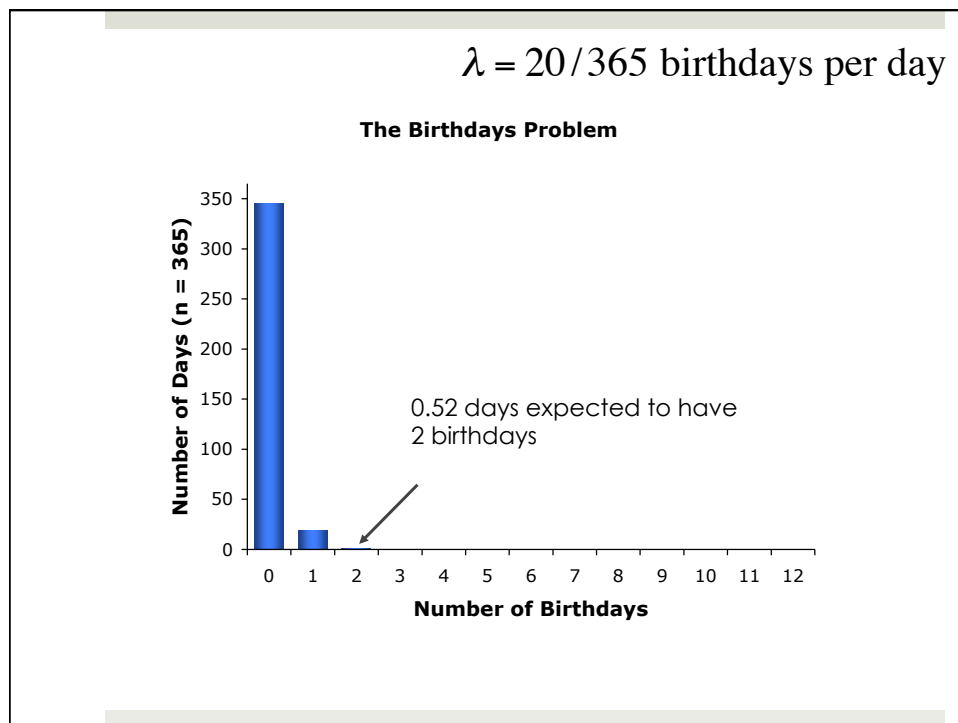
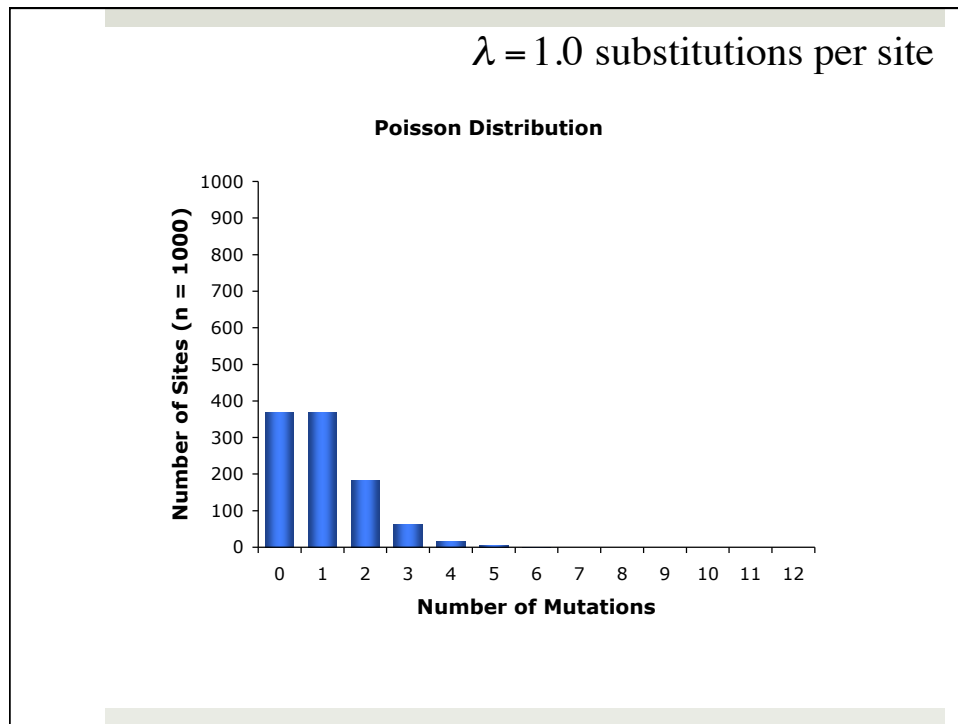
**Poisson Distribution**

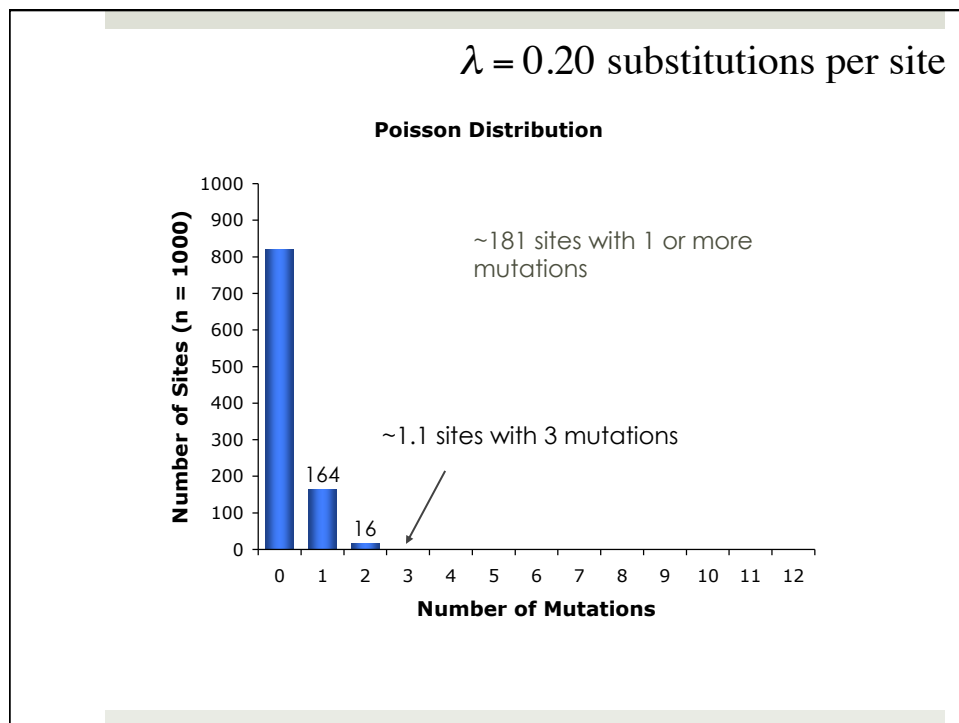
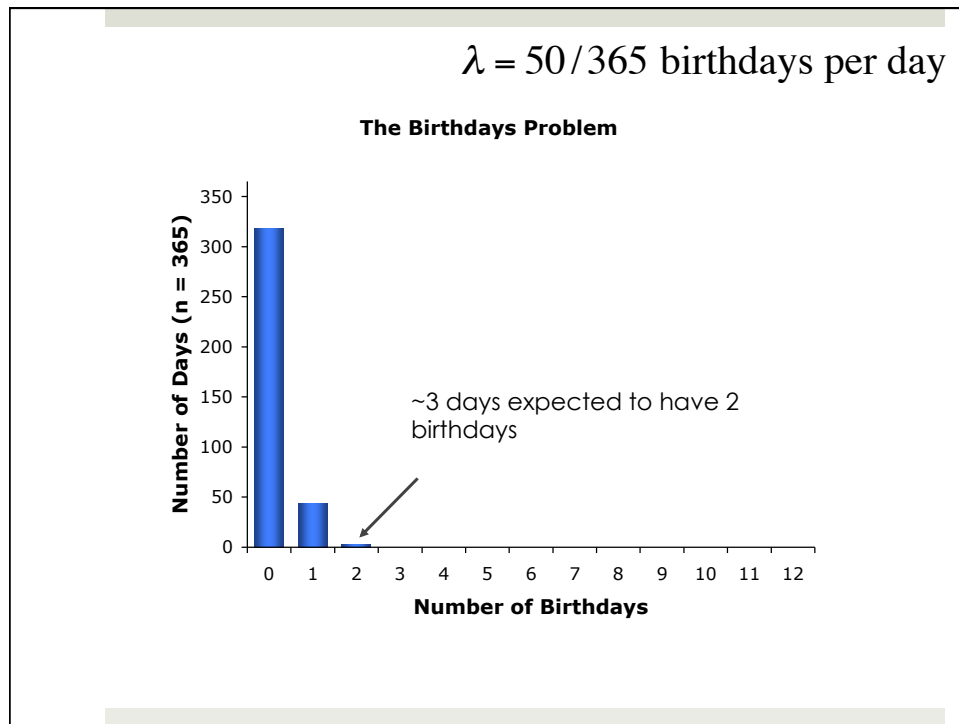
$$f(k; \lambda) = \frac{\lambda^k e^{-\lambda}}{k!}$$

where  $k$  is the number of occurrences (mutations)  
and  $\lambda$  is the mean rate



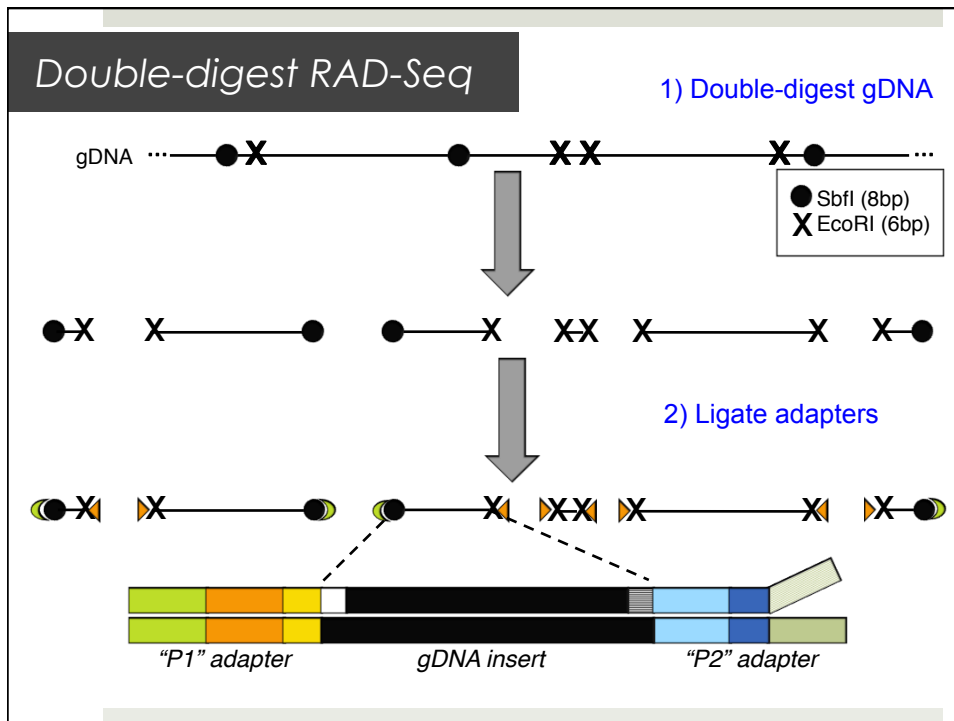






## Divergence of DNA Sequences

- ❖ even if mutation occurs by a random Poisson process...
  - ❖ **divergence** (genetic distance) depends on changes in both sequences, not just one
  - ❖ mutations yield one of four different nucleotides (A, C, G, T)
  - ❖ parallel and reverse mutations may result in sequences being identical at a particular position



# ddRAD-Seq output

Cluster #	Cluster depth	BLAST result	Bases at SNPs	Allele #			
Clstr: 576	912	one chr5 4388283					
Variable sites: 26, 31, 37							
MDS001		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT...	GGT 0	40	40	40.40.40	
MDS001		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0				
CNB253		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	45	82	40.40.40	
CNB253		CCTGCAGGTGAGCAGTGC...TATAATGTGACAGGAACAATTT	AAC 1	37		40.40.40	
CNB276		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	44	44	40.40.40	
CNB276		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0				
MDS014		CCTGCAGGTGAGCAGTGC...TATAATGTGACAGGAATAATTT	AAT 2	16	30	40.40.40	
MDS014		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	12		40.40.40	
MDS005		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	40	40	40.40.40	
MDS005		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0				
MDS006		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	38	38	40.40.40	
MDS006		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0				
MDS010		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	55	55	40.40.40	
MDS010		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0				
MDS011		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	22	43	40.40.40	
MDS011		CCTGCAGGTGAGCAGTGC...TATAATGTGACAGGAATAATTT	AAT 2	21		40.40.40	
MDS016		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	32	60	40.40.40	
MDS016		CCTGCAGGTGAGCAGTGC...TATAATGTGACAGGAACAATTT	AAC 1	28		40.40.40	
MDS019		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0	43	44	40.40.40	
MDS019		CCTGCAGGTGAGCAGTGC...TATAATGTGACGAGGAATAATTT	GGT 0				
.		.					
.		.					
.		.					

Annotations:

- Red arrows point from "Bases at SNPs" to the first column of the data table.
- Red arrows point from "Allele #" to the second and third columns of the data table.
- Red arrows point from "# reads per allele" to the fourth column of the data table.
- Red arrows point from "# total reads" to the fifth column of the data table.
- Red arrows point from "highest quality at SNPs" to the sixth and seventh columns of the data table.