Bernoulli distribution

The simplest non-uniform distribution

p – probability of success (1)

1-p – probability of failure (0)

$$f(x) = P(X = x) = \begin{cases} p & \text{if } x = 1\\ 1 - p & \text{if } x = 0 \end{cases}$$

Jacob Bernoulli (1654-1705) Swiss mathematician (Basel)

- Law of large numbers
- Mathematical constant e=2.718...



Bernoulli distribution

$$f(x) = P(X = x) = \begin{cases} p & \text{if } x = 1\\ 1 - p & \text{if } x = 0 \end{cases}$$

$$E(X) = 0 \times P(X = 0) + 1 \times P(X = 1) = 0(1 - p) + 1(p) = p$$

$$Var(X) = E(X^{2}) - (EX)^{2} = [0^{2}(1 - p) + 1^{2}(p)] - p^{2} = p - p^{2} = p(1 - p)$$

Refresher: Binomial Coefficients

$$\binom{n}{k} = C_k^n = \frac{n!}{k!(n-k)!}, \text{ called } n \text{ choose } k$$

$$\binom{10}{3} = C_3^{10} = \frac{10!}{3!7!} = \frac{10 \cdot 9 \cdot 8 \cdot 7!}{3 \cdot 2 \cdot 1 \cdot 7!} = 120$$

Number of ways to choose k objects out of n without replacement and where the order does not matter. Called binomial coefficients because of the binomial formula

$$(p+q)^n = (p+q)\times(p+q)...\times(p+q) = \sum_{x=0}^n C_x^n p^x q^{n-x}$$

Binomial Distribution

- Binomially-distributed random variable X equals sum (number of successes) of n independent Bernoulli trials
- The probability mass function is:

$$f(x) = C_x^n p^x (1-p)^{n-x} \text{ for } x = 0,1,...n$$
 (3-7)

Based on the binomial expansion:

$$\int = \left(p + q \right)^{N} = \sum_{\chi = 0}^{N} \left(\frac{1}{\chi} p^{\chi} q^{N-\chi} \right)^{N}$$
Sec. 3-6 Ringmial Distribution

Binomial variance and standard deviation

Let *X* be a binomial random variable with parameters *p* and *n*

Variance:

$$\sigma^2 = V(X) = np(1-p)$$

Standard deviation:

$$\sigma = \sqrt{np(1-p)}$$

Poisson Distribution

- Limit of the binomial distribution when
 - -n, the number of attempts, is very large
 - p, the probability of success is very small
 - $-E(X)=np=\lambda$ is O(1)

The annual numbers of deaths from horse kicks in 14 Prussian army corps between 1875 and 1894

Number deaths	of Observed frequency	Expected frequency
O	144	139
1	91	97
2	32	34
3	11	8
4	2	1
5 and over	0	0
Total	280	280

From von Bortkiewicz 1898



Siméon Denis Poisson (1781–1840) French mathematician and physicist

Let
$$\lambda = np = E(x)$$
, so $p = \frac{\lambda}{n}$

$$P(X = x) = \binom{n}{x} p^{x} (1 - p)^{n - x}$$

$$= \frac{n(n - 1) \dots (n - x + 1)}{x!} \left(\frac{\lambda}{n}\right)^{x} \left(1 - \frac{\lambda}{n}\right)^{n - x} \sim \frac{n^{x}}{x!} \left(\frac{\lambda}{n}\right)^{x} = \frac{\lambda^{x}}{x!};$$

$$\sum_{x} \frac{\lambda^{x}}{x!} = e^{\lambda}.$$

Normalization requires $\sum_{x} P(X = x) = 1$.

Thus
$$P(X = x) = \frac{\lambda^x}{x!}e^{-\lambda}$$

Poisson Mean & Variance

If X is a Poisson random variable, then:

- Mean: $\mu = E(X) = \lambda = h \cdot p$ Variance: $\sigma^2 = V(X) = \lambda = h \cdot p \cdot (1 p) \approx M \cdot p$
- Standard deviation: $\sigma = \lambda^{1/2}$

Note: Variance = Mean

Note: Standard deviation/Mean = $\lambda^{-1/2}$ decreases with λ

> Sec 2-10

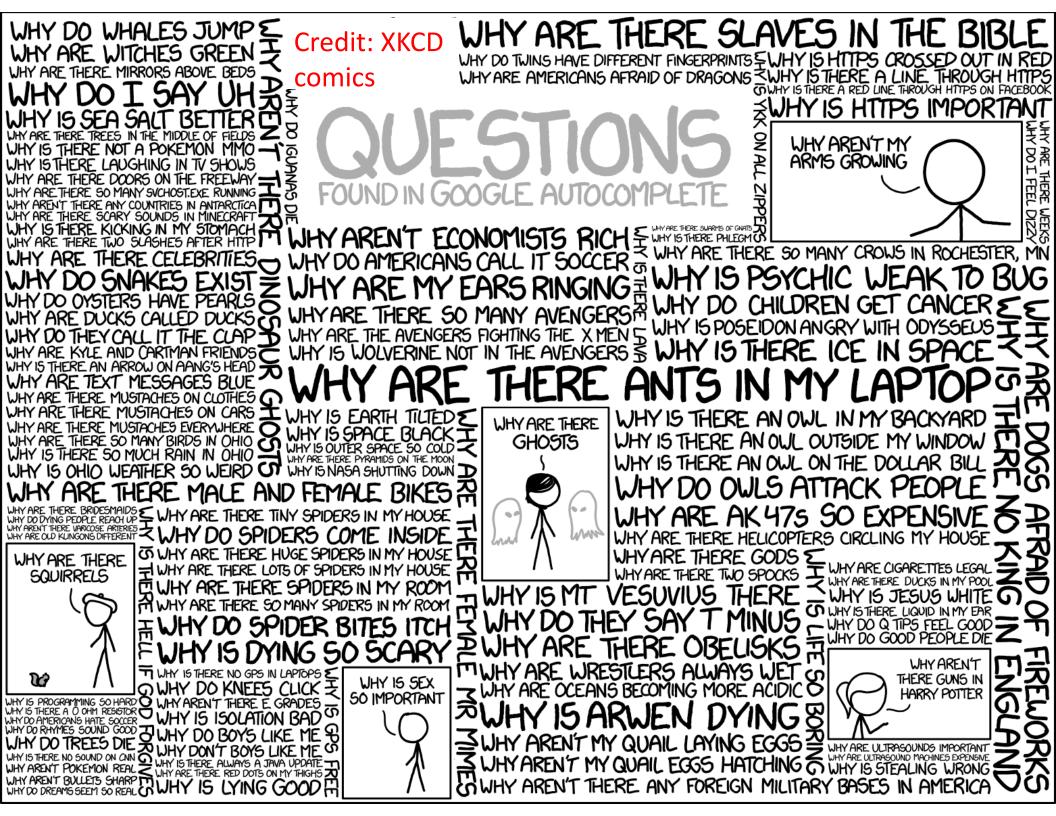
Matlab exercise: Poisson distribution

- Generate a sample of size 100,000 for Poissondistributed random variable X with $\lambda = 2$
- Plot the <u>approximation</u> to the Probability Mass Function based on <u>this sample</u>
- Calculate the mean and variance of <u>this</u> <u>sample</u> and compare it to theoretical calculations:

$$E[X] = \lambda$$
 and $V[X] = \lambda$

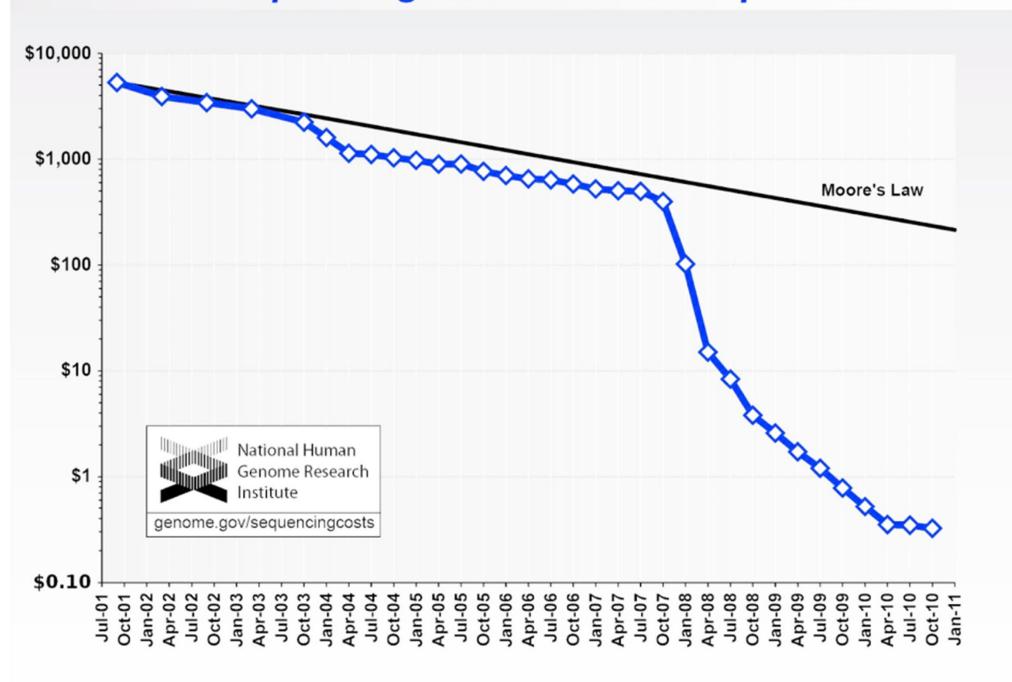
Matlab exercise: Poisson distribution

- Stats=100000; lambda=2;
- r2=random('Poisson',lambda,Stats,1);
- mean(r2)
- var(r2)
- [a,b]=hist(r2, 0:max(r2));
- p_p=a./sum(a);
- figure; stem(b,p_p);
- figure; semilogy(b,p_p,'ko-')



Poisson Distribution in Genome Assembly

Cost per Megabase of DNA Sequence



Poisson Example: Genome Assembly

- Goal: figure out the sequence of DNA nucleotides (ACTG) along the entire genome
- Problem: Sequencers generate random short reads

TABLE 9.1 Next-generation sequencing technologies compared to Sanger sequencing. Adapted from the companies' websites, # http://en.wikipedia.org/wiki/DNA_sequencer, and literature cited for each technology.

Technology	Read length (bp)	Reads per run	Time per run	Cost per megabase (US\$)	Accuracy (%)
Roche 454	700	1 million	1 day	10	99.90
Illumina	50–250	<3 billion	1-10 days	~0.10	98
SOLiD	50	~1.4 billion	7–14 days	0.13	99.90
Ion Torrent	200	<5 million	2 hours	1	98
Pacific Biosciences	2900	<75,000	<2 hours	2	99
Sanger	400–900	N/A	<3 hours	2400	99.90

 Solution: assemble genome from short reads using computers. Whole Genome Shotgun Assembly.



MinION, a palm-sized gene sequencer made by UK-based Oxford Nanopore Technologies

Short Reads assemble into Contigs

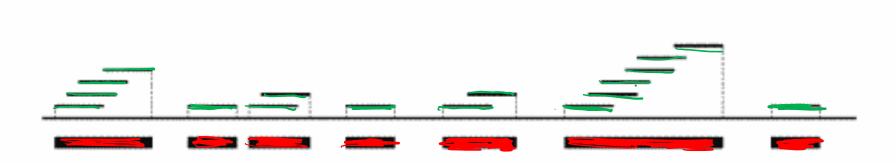
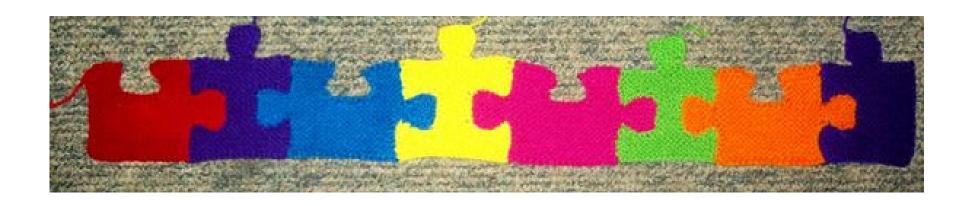


Figure 5.1.



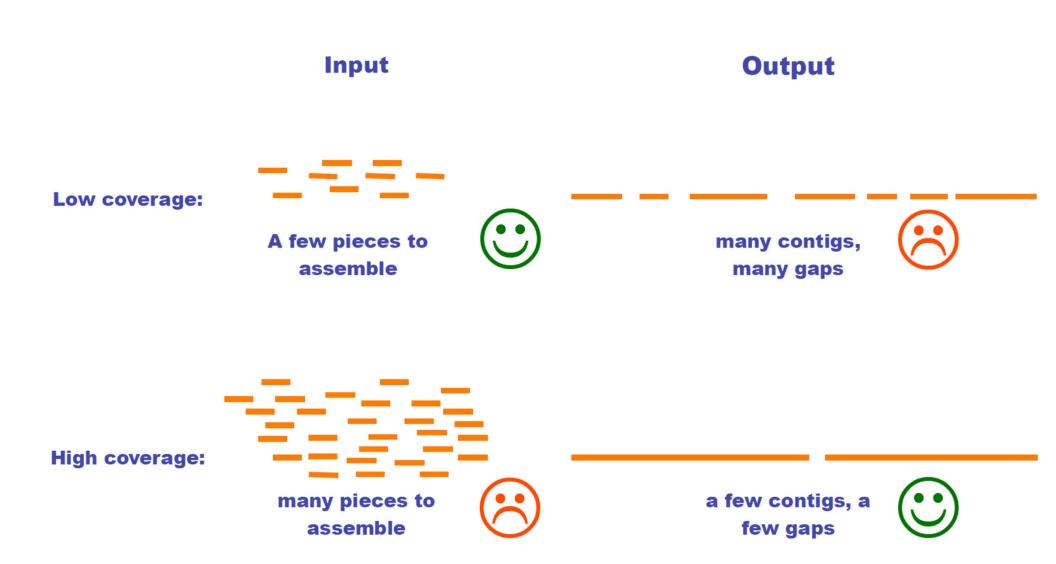
Promise of Genomics



Drew Sheneman, New Jersey -- The Newark Star Ledger, E-mail Drew.

I think I found the corner piece!

How many short reads do we need?



Genome Assembly

Whole-genome "shotgun" sequencing starts by copying and fragmenting the DNA

("Shotgun" refers to the random fragmentation of the whole genome; like it was fired from a shotgun)

Input: GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

35bp

Copy GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

by GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

PCR: GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

Fragment: GGCGTCTA TATCTCGG CTCTAGGCCCTC ATTTTTT

GGC GTCTATAT CTCGGCTCTAGGCCCTCA TTTTTT

GGCGTC TATATCT CGGCTCTAGGCCCT CATTTTTT

GGCGTCTAT ATCTCGGCTCTAG GCCCTCA TTTTTT

Assembly

Assume sequencing produces such a large # fragments that almost all genome positions are *covered* by manyfragments...

...but we don't know what came from where

CTAGGCCCTCAATTTTT

GGCGTCTATATCT

CTCTAGGCCCTCAATTTTT

CTCTAGGCCCTCAATTTTT

TCTATATCTCGGCTCTAGG

this

GGCTCTAGGCCCTCATTTTT

TATCTCGACTCTAGGCCCTCA

GGCGTCGATATCT

TATCTCGACTCTAGGCC

GGCGTCTATATCTCG

GGCGTCTATATCTCG

Courtesy of **Ben Langmead**. Used with permission.

Assembly

Overlaps between short reads help to put them together

CTAGGCCCTCAATTTTT CTCTAGGCCCTCAATTTTT

GGCTCTAGGCCCTCATTTTTT

CTCGGCTCTAGCCCCTCATTTT

TATCTCGACTCTAGGCCCTCA

TATCTCGACTCTAGGCC

TCTATATCTCGGCTCTAGG

GGCGTCTATATCTCG

GGCGTCGATATCT

GGCGTCTATATCT

GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

177 nucleotides

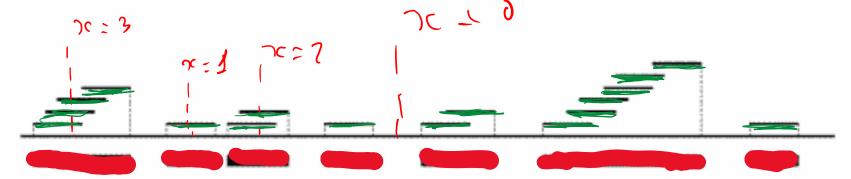
35 nucleotides

Where is the Poisson?

- G genome length (in bp)
- L short read average length
- N number of short read sequenced
- λ sequencing coverage redundancy = LN/G
- x- number of short reads covering a given site on the genome

$$P(x) = \frac{\lambda^x e^{-\lambda}}{x!}$$

Poisson as a limit of Binomial: For a given site on the genome for each short read Prob(site covered): p=L/G is very small. Number of attempts (short reads): N is very large. Their product (sequencing redundancy): $\lambda = NL/G$ is O(1).



What fraction of the genome is missing?

What fraction of genome is covered?

Coverage: λ=NL/G,
 X – random variable equal to the number of times a given site is covered by short reads.
 Poisson: P(X=x)= λ*exp(- λ)/x!
 P(X=0)=exp(- λ), P(X>0)=1- exp(- λ)

• Total length covered: $G^*[1-exp(-\lambda)]$

λ	2	4	6	8	10	12
Mean proportion of genome covered	.864665	.981684	.997521	.999665	.999955	.999994

Table 5.1. The mean proportion of the genome covered for different values of λ

How many contigs?

How many contigs?

- A given short read is the right end of a contig if and only if no left ends of other short reads fall within it.
- The left end of another short read has the probability p=(L-1)/G to fall within a given read. There are N-1 other reads. Hence the expected number of left ends inside a given shot read is $p \cdot (N-1) = (N-1) \cdot (L-1)/G \approx \lambda$
- If significant overlap required to merge two short reads is L_{ov} , modified λ is given by $(N-1) \cdot (L-L_{ov})/G$
- Probability that no left ends fall inside a short read is $exp(-\lambda)$. Thus the Number of contigs is $N_{contigs} = Ne^{-\lambda}$:

λ	0.5	0.75	1	1.5	2	3	4	5	6	7
Mean number of contigs	60.7	70.8	73.6	66.9	54.1	29.9	14.7	6.7	3.0	1.3

Table 5.2. The mean number of contigs for different levels of coverage, with G = 100,000 and L = 500.