CSEP 590A
Computational Biology
Spring 2013

3: BLAST, Alignment score significance;
PCR and DNA sequencing

Outline

BLAST

Scoring

Weekly Bio Interlude: PCR & Sequencing

BLAST:
Basic Local Alignment Search Tool
Altschul, Gish, Miller, Myers, Lipman, J Mol Biol 1990

The most widely used comp bio tool

Which is better: long mediocre match or a few nearby, short, strong matches with the same total score?

- score-wise, exactly equivalent
- biologically, later may be more interesting, & is common
- at least, if must miss some, rather miss the former

BLAST is a heuristic emphasizing the later

- speed/sensitivity tradeoff: BLAST may miss former, but gains greatly in speed

BLAST: What

Input:

- A query sequence (say, 300 residues)
- A data base to search for other sequences similar to the query (say, 10^6 - 10^9 residues)
- A score matrix $\sigma(r,s)$, giving cost of substituting r for s (& perhaps gap costs)
- Various score thresholds & tuning parameters

Output:

- "All" matches in data base above threshold
- "E-value" of each

Blast: demo

E.g.

http://expasy.org/sprot
(or http://www.ncbi.nlm.nih.gov/blast/)
look up MyoD
go to blast tab
paste in ID or seq for human MyoD
set params (gapped=yes, blosum62,…)
get top 100 (or 1000) hits

BLAST: How

Idea: most interesting parts of DB are those with a good ungapped match to some short subword of the query

Break query into overlapping words w_i of small fixed length (e.g. 3 aa or 11 nt)

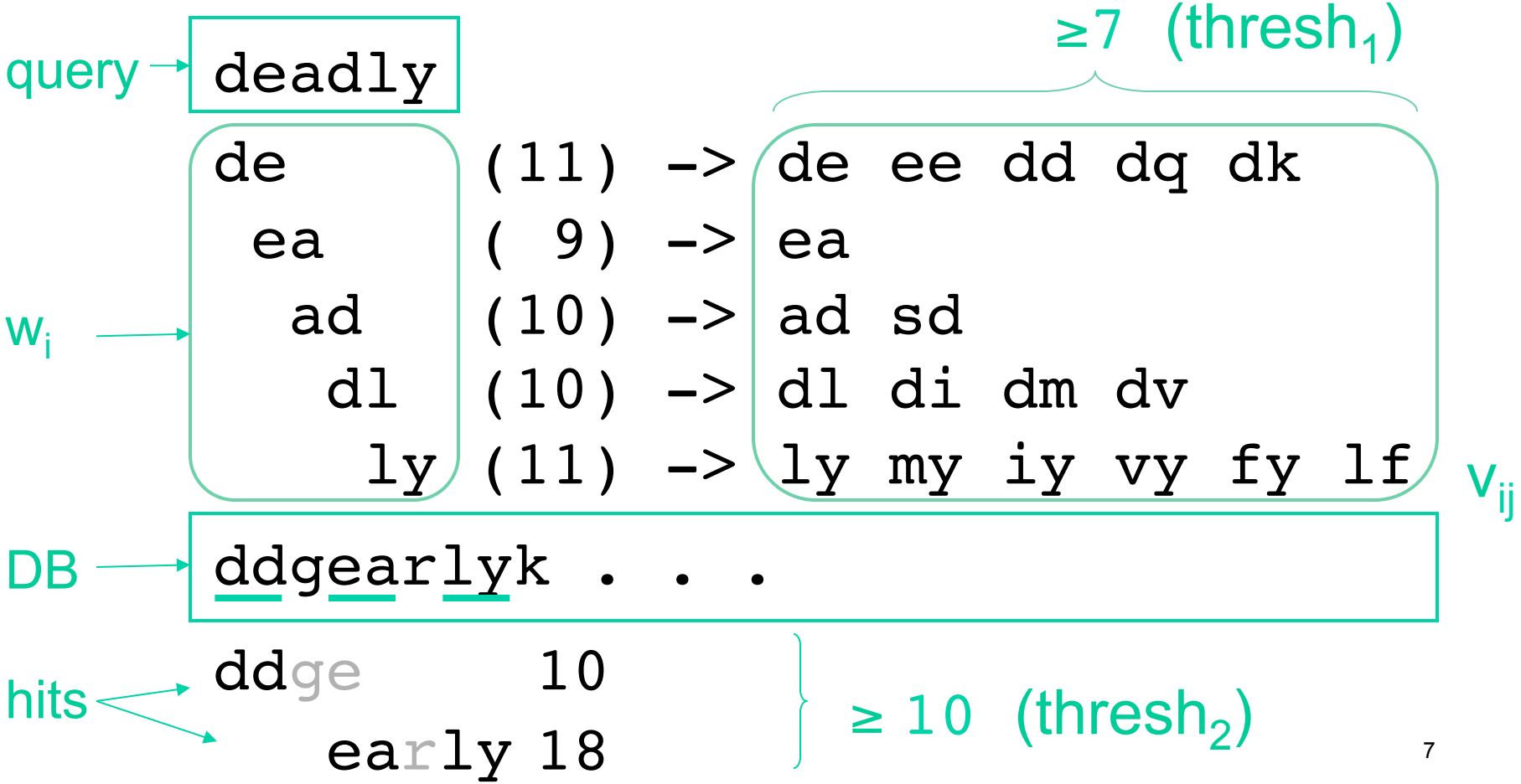
For each w_i, find (empirically, ~50) "similar" words v_{ij} with score $\sigma(w_i, v_{ij}) > \text{thresh}_1$ (say, 1, 2, … letters different)

Look up each v_{ij} in database (via prebuilt index) -- i.e., exact match to short, high-scoring word

Grow each such "seed match" bidirectionally

Report those scoring > thresh_2, calculate E-values

BLAST: Example



BLOSUM 62 (the "σ" scores)

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	**4**	-1	-2	-2	0	-1	-1	0	-2	-1	-1	-1	-1	-2	-1	1	0	-3	-2	0
R	-1	**5**	0	-2	-3	1	0	-2	0	-3	-2	2	-1	-3	-2	-1	-1	-3	-2	-3
N	-2	0	**6**	1	-3	0	0	0	1	-3	-3	0	-2	-3	-2	1	0	-4	-2	-3
D	-2	-2	1	**6**	-3	0	2	-1	-1	-3	-4	-1	-3	-3	-1	0	-1	-4	-3	-3
C	0	-3	-3	-3	**9**	-3	-4	-3	-3	-1	-1	-3	-1	-2	-3	-1	-1	-2	-2	-1
Q	-1	1	0	0	-3	**5**	2	-2	0	-3	-2	1	0	-3	-1	0	-1	-2	-1	-2
E	-1	0	0	2	-4	2	**5**	-2	0	-3	-3	1	-2	-3	-1	0	-1	-3	-2	-2
G	0	-2	0	-1	-3	-2	-2	**6**	-2	-4	-4	-2	-3	-3	-2	0	-2	-2	-3	-3
H	-2	0	1	-1	-3	0	0	-2	**8**	-3	-3	-1	-2	-1	-2	-1	-2	-2	2	-3
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	**4**	2	-3	1	0	-3	-2	-1	-3	-1	3
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	**4**	-2	2	0	-3	-2	-1	-2	-1	1
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	**5**	-1	-3	-1	0	-1	-3	-2	-2
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	**5**	0	-2	-1	-1	-1	-1	1
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	**6**	-4	-2	-2	1	3	-1
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	**7**	-1	-1	-4	-3	-2
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	**4**	1	-3	-2	-2
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	**5**	-2	-2	0
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	**11**	2	-3
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	**7**	-1
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	**4**

BLAST Refinements

“Two hit heuristic” -- need 2 nearby, nonoverlapping, gapless hits before trying to extend either

“Gapped BLAST” -- run heuristic version of Smith-Waterman, bi-directional from hit, until score drops by fixed amount below max

PSI-BLAST -- For proteins, iterated search, using “weight matrix” (next week?) pattern from initial pass to find weaker matches in subsequent passes

Many others

Significance of alignment scores

http://dericbownds.net/uploaded_images/god_face2.jpg

Significance of Alignments

Is “42” a good score?

Compared to what?

Usual approach: compared to a specific “null model”, such as “random sequences”

Brief Review of Probability

random variables

Discrete random variable: takes values in a finite or countable set, e.g.

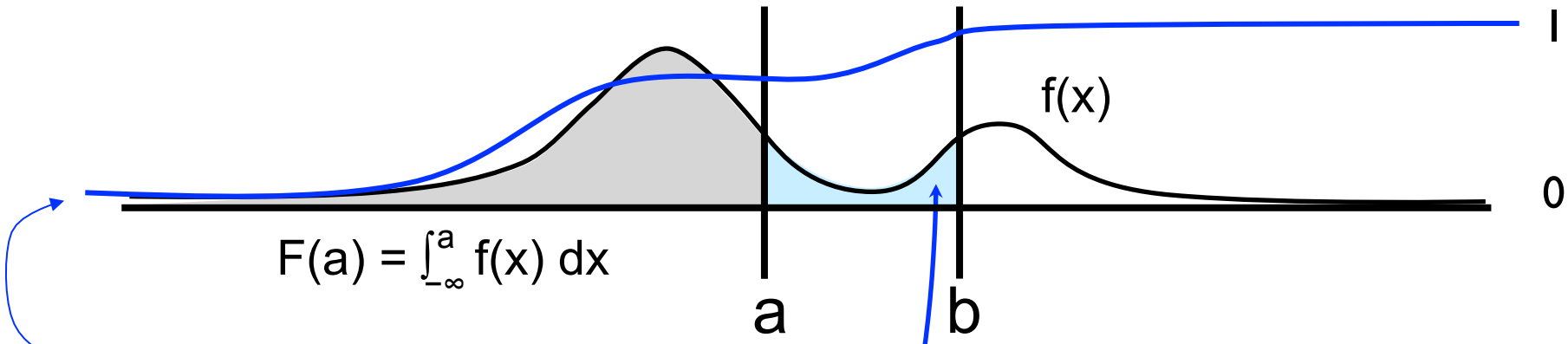
- $X \in \{1,2, ..., 6\}$ with equal probability
- X is positive integer i with probability 2^{-i}

Continuous random variable: takes values in an uncountable set, e.g.

- X is the weight of a random person (a real number)
- X is a randomly selected point inside a unit square
- X is the waiting time until the next packet arrives at the server

pdf and cdf

f(x) : the *probability density function* (or simply “density”)



P(X < a) = F(x): the *cumulative distribution function*

P(a < X < b) = F(b) - F(a)

Need $\int_{-\infty}^{+\infty} f(x)\,dx$ (= F(+∞)) = 1

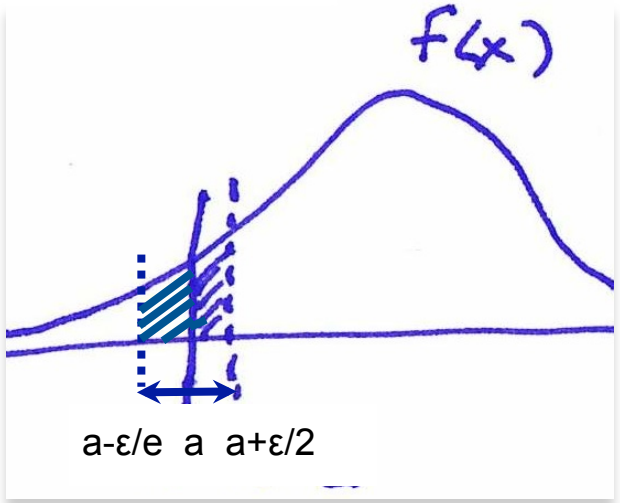
A key relationship:

$f(x) = \frac{d}{dx} F(x)$, since $F(a) = \int_{-\infty}^{a} f(x)\,dx$,

Densities are *not* probabilities; e.g. may be > 1

$P(x = a) = 0$

$P(a - \varepsilon/2 \le X \le a + \varepsilon/2) =$
$F(a + \varepsilon/2) - F(a - \varepsilon/2)$
$\approx \varepsilon \bullet f(a)$



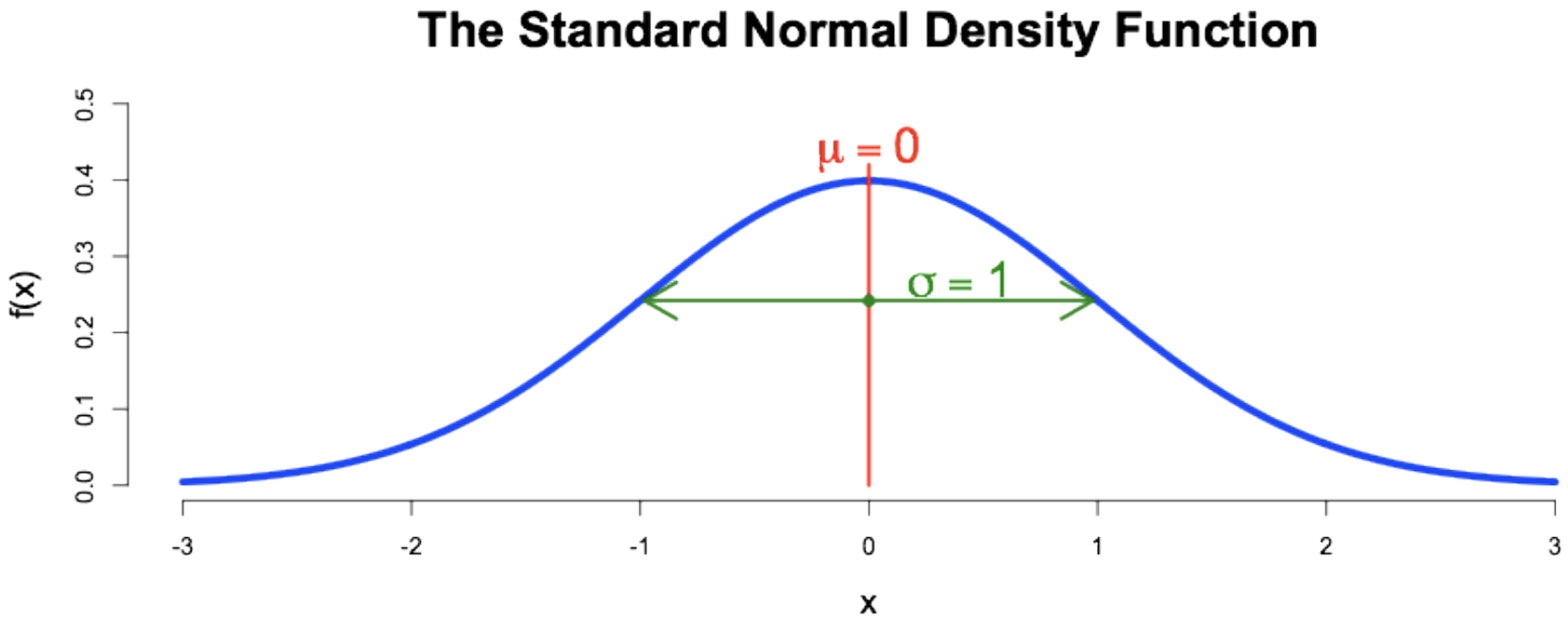
I.e., the probability that a continuous random variable falls *at* a specified point is *zero*

The probability that it falls *near* that point is proportional to the density; in a large random sample, expect more samples where density is higher (hence the name "density").

X is a normal (aka Gaussian) random variable $X \sim N(\mu, \sigma^2)$

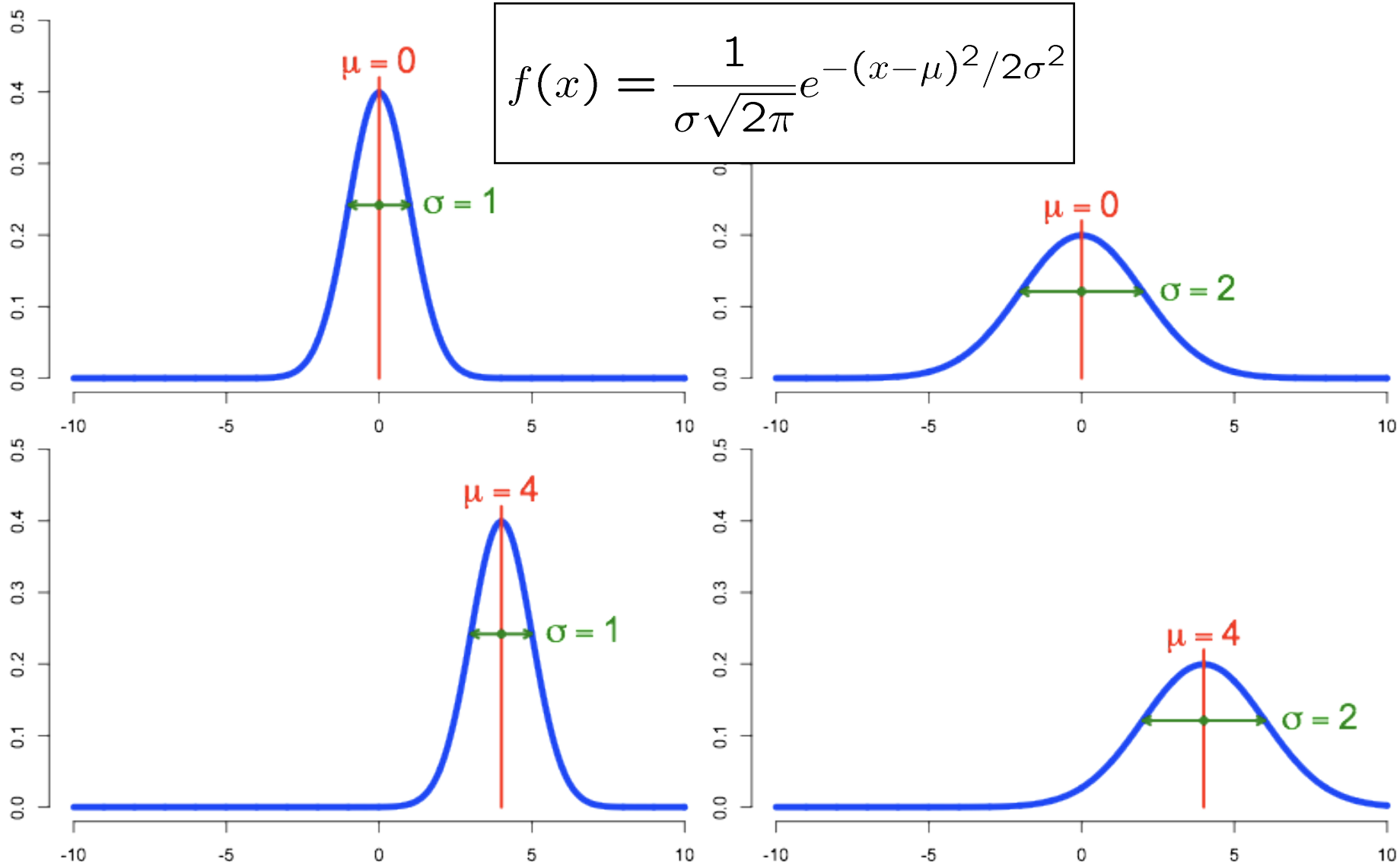
$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-(x-\mu)^2/2\sigma^2}$$

$$E[X] = \mu \qquad \mathrm{Var}[X] = \sigma^2$$



changing μ, σ

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-(x-\mu)^2/2\sigma^2}$$



density at μ is ≈ .399/σ

Z-scores

$Z = (X-\mu)/\sigma$ = (X - mean)/standard deviation

e.g.

Z = +3 means "3 standard deviations above the mean"

Applicable to *any* distribution, and gives a rough sense of how usual/unusual the datum is.

If X is normal(μ, σ^2) then Z is normal(0,1), and you can easily calculate (or look up in a table) how unusual

E.g., if normal, P(Z-score $\geq$ +3) $\approx$ 0.00135

Central Limit Theorem

If a random variable X is the sum of many independent random variables, then X will be approximately normally distributed.

Hypothesis Tests and P-values

Hypothesis Tests

Competing models might explain some data

E.g., you've flipped a coin 5 times, seeing HHHTH

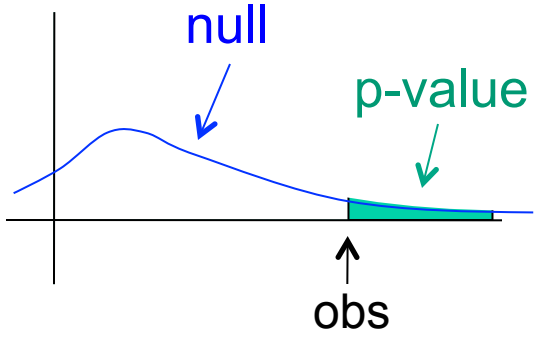
Model 0 (The "null" model): P(H) = 1/2

Model 1 (The "alternate" model): P(H) = 2/3

Which is right?

A possible decision rule: reject the null if you see 4 or more heads in 5 tries

p-values



The *p-value* of such a test is the probability, assuming that the null model is true, of seeing data as extreme or more extreme than what you actually observed

E.g., we observed 4 heads; p-value is prob of seeing 4 or 5 heads in 5 tosses of a fair coin

Why interesting? It measures *probability that we would be making a mistake in rejecting null*.

Can analytically find p-value for simple problems like coins; often turn to simulation/permutation tests (introduced earlier) or to approximation (coming soon) for more complex situations

Usual scientific convention is to reject null only if p-value is < 0.05; sometimes demand $p \ll 0.05$ (esp. if estimates are inaccurate)

Alignment Scores

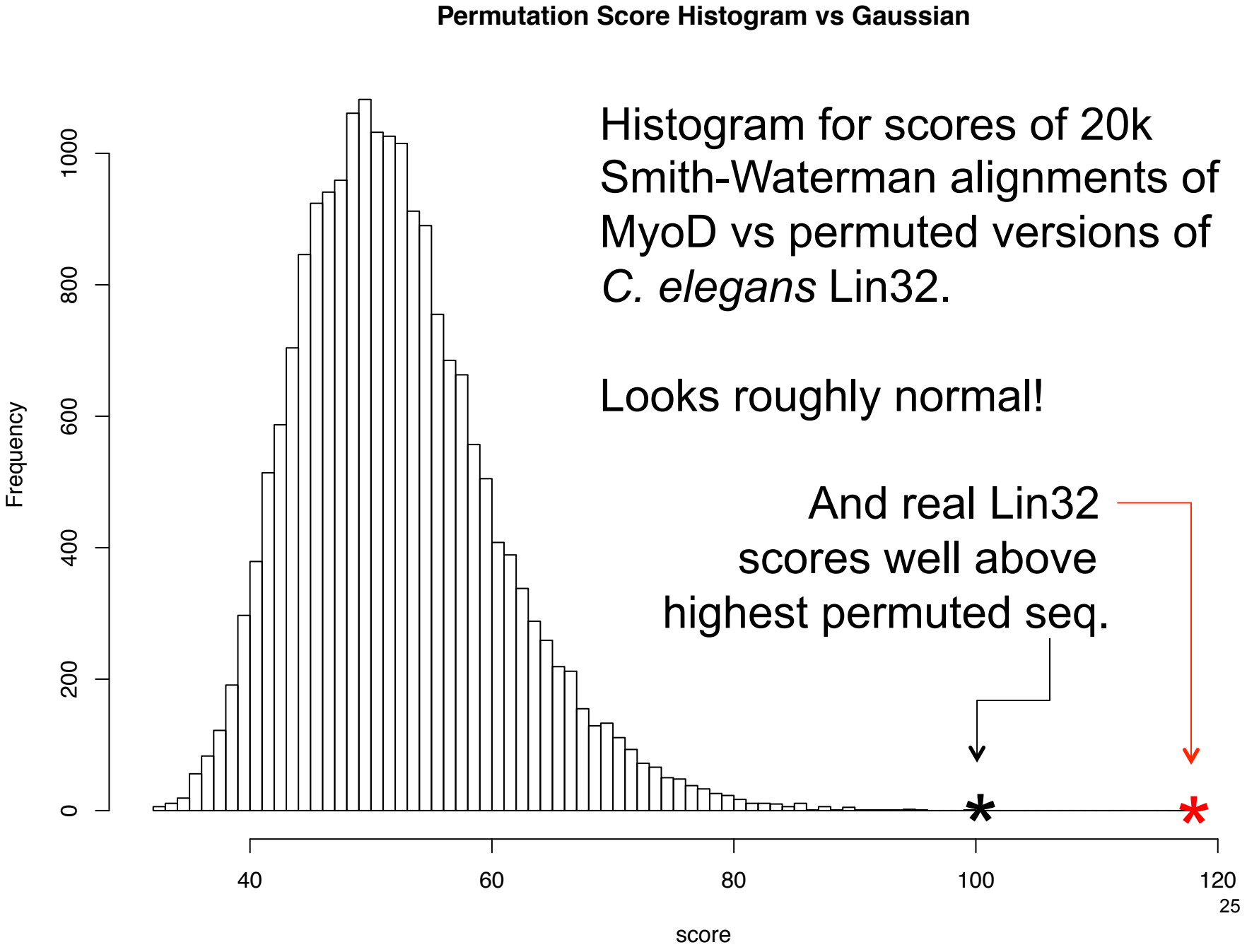
Distribution of alignment scores

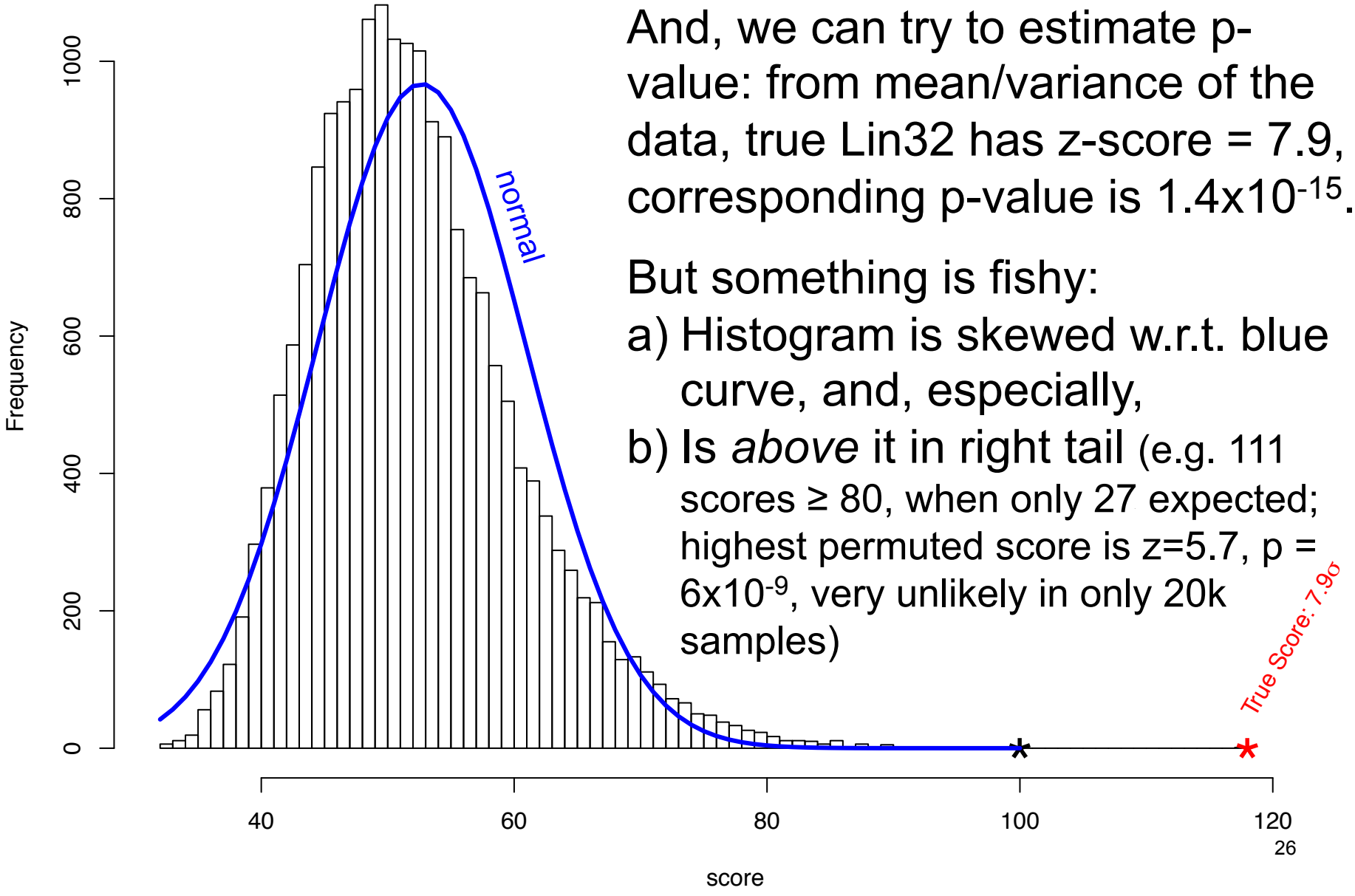
A straw man: suppose I want a simple null model for alignment scores of, say MyoD versus random proteins of similar lengths. Consider this: Write letters of MyoD in one row; make a random alignment by filling 2nd row with random permutation of other sequence plus gaps.

```
MELLSPPLR…
uv---wxyz…
```

Score for column 1 is a random number from the M row of BLOSUM 62 table, column 2 is random from E row, etc.

By central limit theorem, total score would be approximately normal


Permutation Score Histogram vs Gaussian
Histogram for scores of 20k Smith-Waterman alignments of MyoD vs permuted versions of *C. elegans* Lin32.
Looks roughly normal!
And real Lin32 scores well above highest permuted seq.
Frequency
0
200
400
600
800
1000
40
60
80
100
120
score
25



And, we can try to estimate p-value: from mean/variance of the data, true Lin32 has z-score = 7.9, corresponding p-value is 1.4×10^{-15}.

But something is fishy:

a) Histogram is skewed w.r.t. blue curve, and, especially,

b) Is *above* it in right tail (e.g. 111 scores ≥ 80, when only 27 expected; highest permuted score is z=5.7, p = 6×10^{-9}, very unlikely in only 20k samples)

Rethinking score distribution

Strawman above is ok: random permutation of letters & gaps *should* give normally distributed scores.

But S-W doesn't stop there; *it then slides the gaps around so as to maximize score, in effect taking the maximum over a huge number of alignments with same sequence but different gap placements.*

Overall Alignment Significance, I
A Theoretical Approach: EVD

Let X_i, $1 \le i \le N$, be indp. random variables drawn from some (non-pathological) distribution

Q. what can you say about distribution of $y = sum\{ X_i \}$?

A. y is approximately *normally* distributed (central limit theorem)

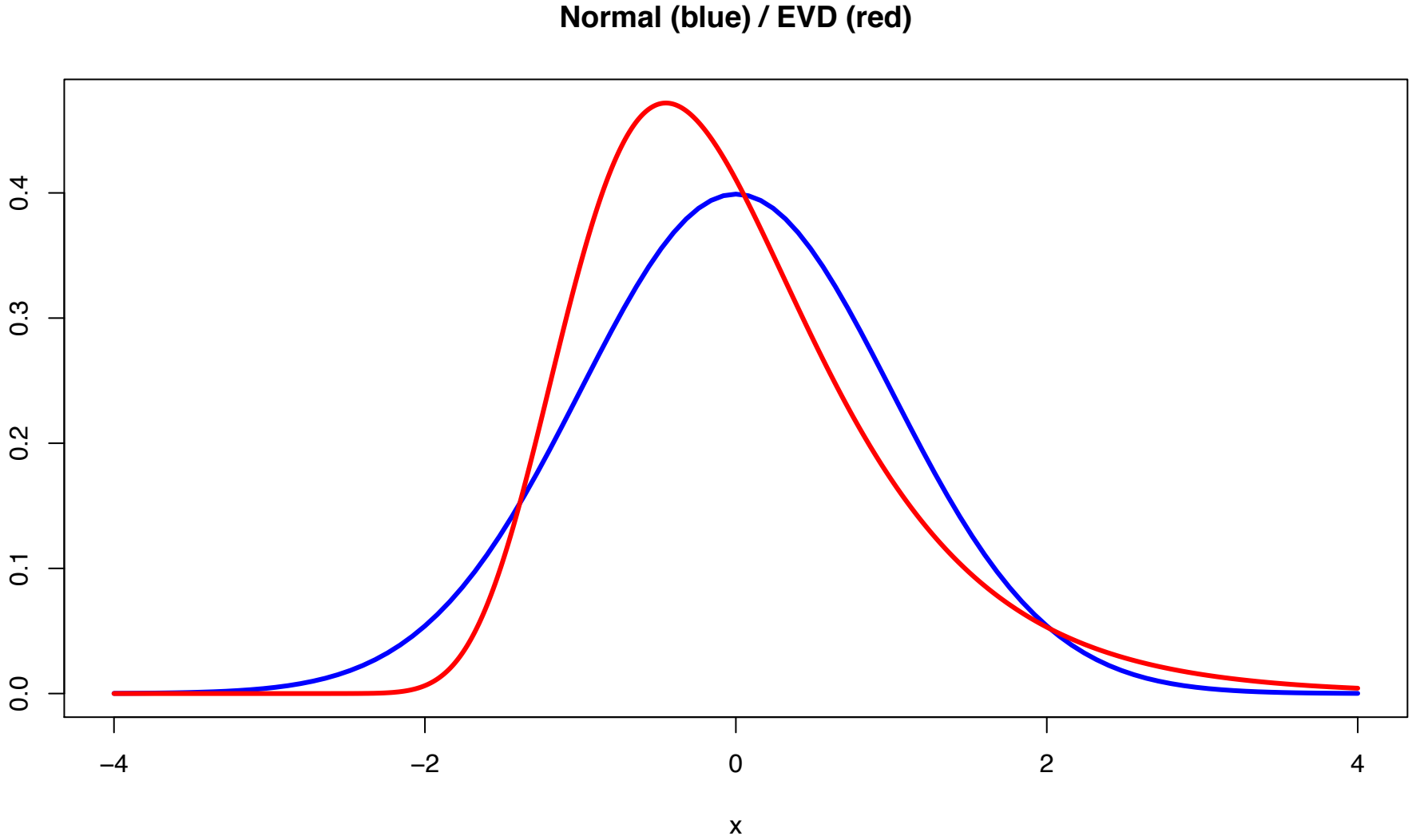
Q. what can you say about distribution of $y = max\{ X_i \}$?

A. it's approximately an *Extreme Value Distribution (EVD)*

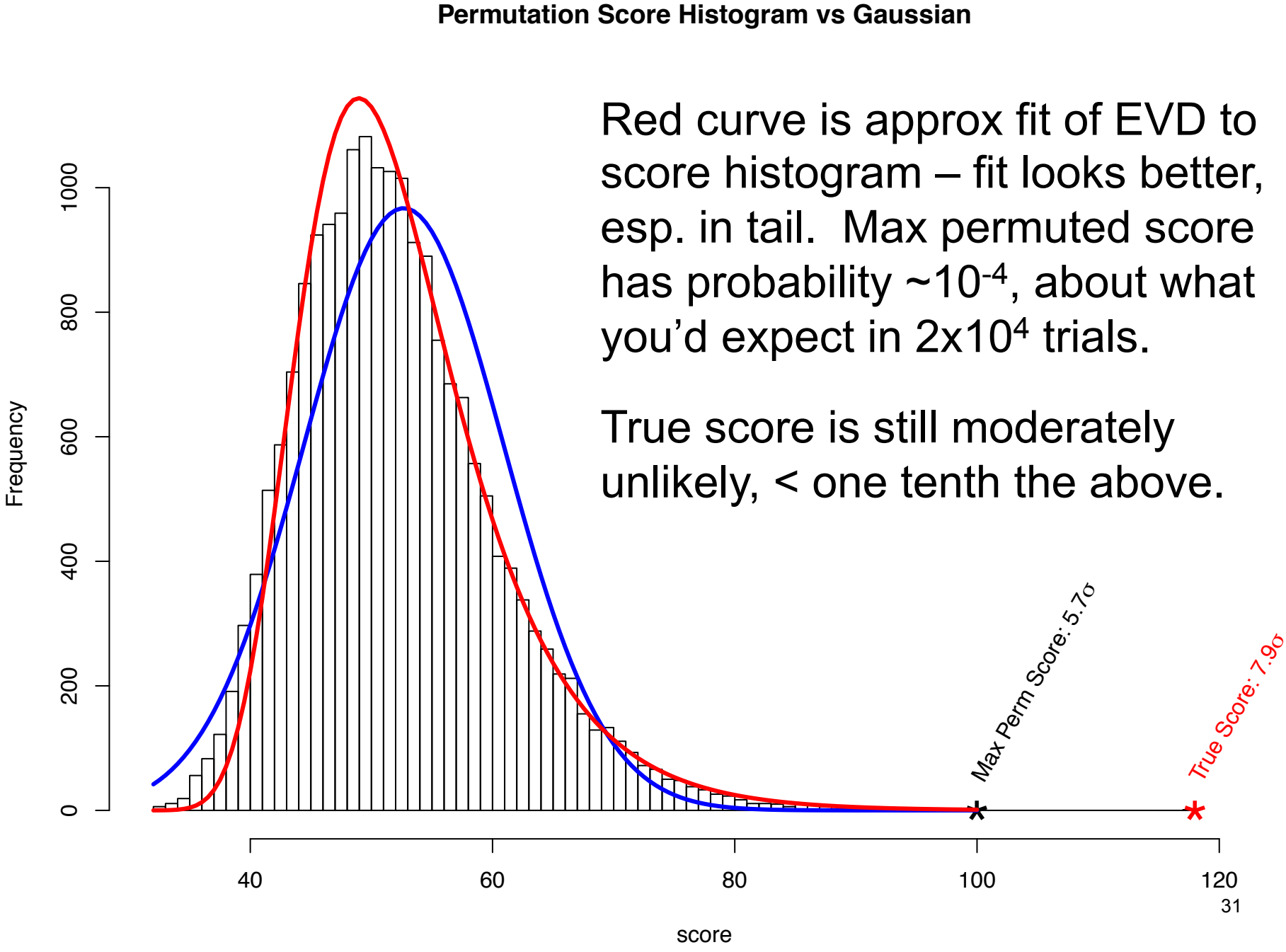
[one of only 3 kinds; for our purposes, the relevant one is:]

$$P(y \le z) \approx \exp(-KNe^{-\lambda(z-\mu)}) \qquad (*)$$

For ungapped local alignment of seqs x, y, N ~ |x|*|y|
λ, K depend on score table & gap costs, or can be estimated by curve-fitting random scores to (*). (cf. reading)



Both mean 0, variance 1; EVD has “fat tail”


Permutation Score Histogram vs Gaussian
Red curve is approx fit of EVD to score histogram – fit looks better, esp. in tail. Max permuted score has probability ~10-4, about what you'd expect in 2x104 trials.
True score is still moderately unlikely, < one tenth the above.
Max Perm Score: 5.7σ
True Score: 7.9σ
Frequency
0
200
400
600
800
1000
40
60
80
100
120
score
31

EVD Pro/Con

Pro:

- Gives p-values for alignment scores

Con:

- It's only approximate
- You must estimate parameters
- Theory may not apply. E.g., known to hold for ungapped local alignments (like BLAST seeds). It is NOT proven to hold for gapped alignments, although there is strong empirical support.

Overall Alignment Significance, II
Empirical (via randomization)

You just searched with x, found "good" score for x:y

Generate N random "y-like" sequences (say N = 10^3 - 10^6)

Align x to each & score

If k of them have better score than alignment of x to y, then the (empirical) probability of a chance alignment as good as observed x:y alignment is (k+1)/(N+1)

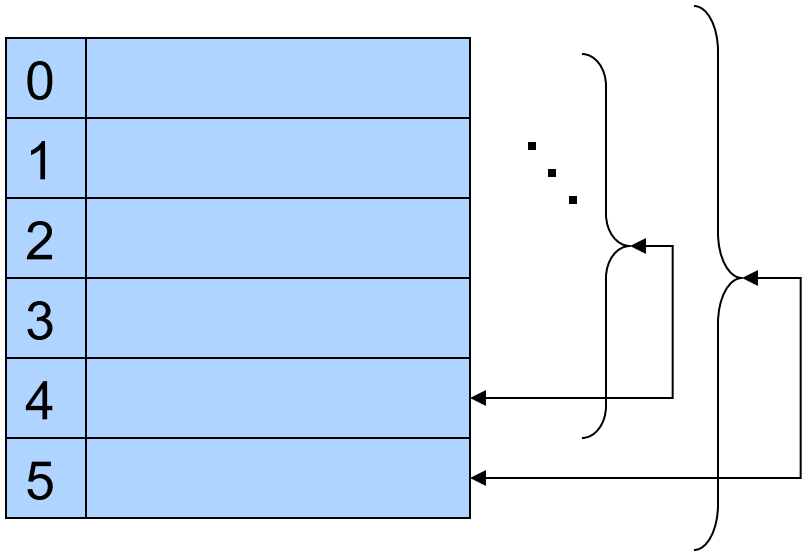
- e.g., if 0 of 99 are better, you can say "estimated p < .01"

How to generate "random y-like" seqs? Scores depend on:

- Length, so use same length as y
- Sequence composition, so uniform 1/20 or 1/4 is a bad idea; even background p_i can be dangerous
- Better idea: *permute* y N times

Generating Random Permutations

```
for (i = n-1; i > 0; i--){
    j = random(0..i);
    swap X[i] <-> X[j];
}
```



All n! permutations of the original data equally likely: A specific element will be last with prob 1/n; given that, a specific other element will be next-to-last with prob 1/(n-1), …; overall: 1/(n!)

C.f. http://en.wikipedia.org/wiki/Fisher–Yates_shuffle and (for subtle way to go wrong) http://www.codinghorror.com/blog/2007/12/the-danger-of-naivete.html

Permutation Pro/Con

Pro:

- Gives empirical p-values for alignments with characteristics like sequence of interest, e.g. residue frequencies
- Largely free of modeling assumptions (e.g., ok for gapped…)

Con:

- Can be inaccurate if your method of generating random sequences is unrepresentative
- E.g., probably better to preserve di-, tri-residue statistics and/or other higher-order characteristics, but increasingly hard to know exactly what to model & how
- Slow
- Especially if you want to assess low-probability p-values

Summary

BLAST is a highly successful search/alignment heuristic. It looks for alignments anchored by short, strong, ungapped “seed” alignments

Assessing statistical significance of alignment scores is crucial to practical applications

- Score matrices derived from “likelihood ratio” test of trusted alignments vs random “null” model
- For gapless alignments, Extreme Value Distribution (EVD) is theoretically justified for overall significance of alignment scores; empirically ok in other contexts, too, e.g., for gapped alignments
- Permutation tests are a simple (but brute force) alternative

Weekly Bio(tech) Interlude

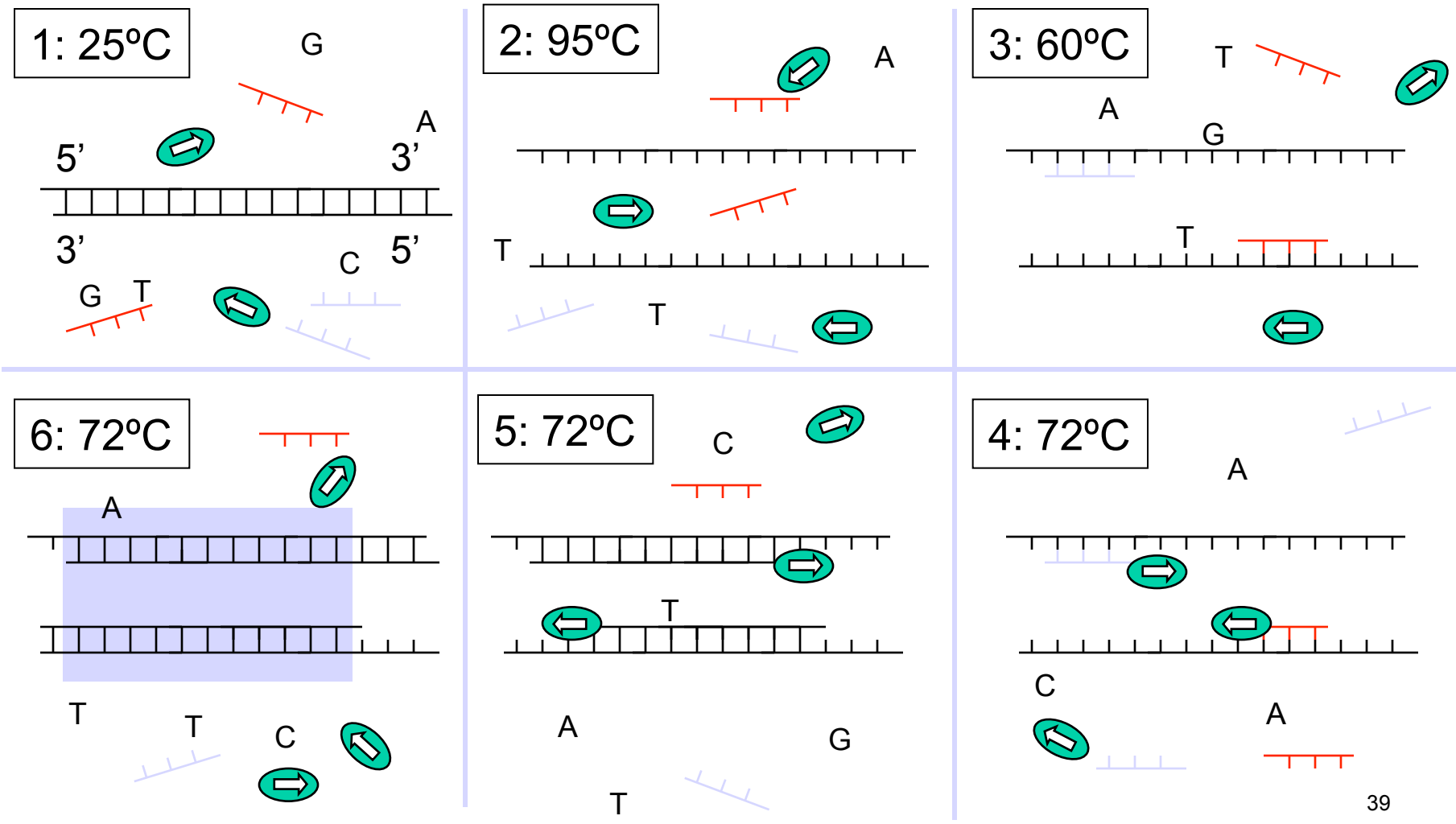
3 Nobel Prizes:

PCR: Kary Mullis, 1993

Electrophoresis: A.W.K. Tiselius, 1948

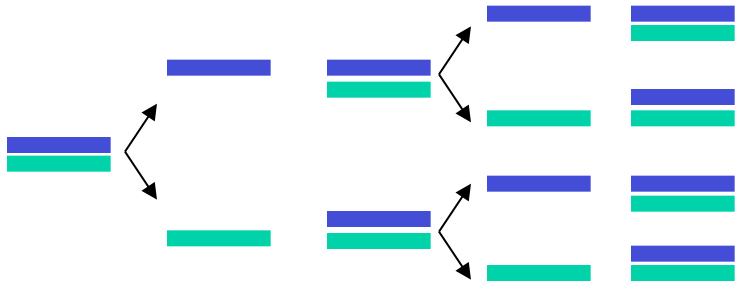
DNA Sequencing: Frederick Sanger, 1980

PCR


1: 25ºC
G
A
5'
3'
3'
5'
C
G
T
2: 95ºC
A
T
T
3: 60ºC
T
A
G
T
6: 72ºC
A
T
T
C
5: 72ºC
C
T
A
G
T
4: 72ºC
A
C
A

Hot spring, near Great Fountain Geyser, Yellowstone National Park

PCR



Ingredients:

- many copies of deoxy nucleotide triphosphates
- many copies of two primer sequences (~20 nt each)
  - readily synthesized
- many copies of Taq polymerase (*Thermus aquaticus*),
  - readily available commercialy
- as little as 1 strand of template DNA
- a programmable “thermal cycler”

Amplification: million to billion fold

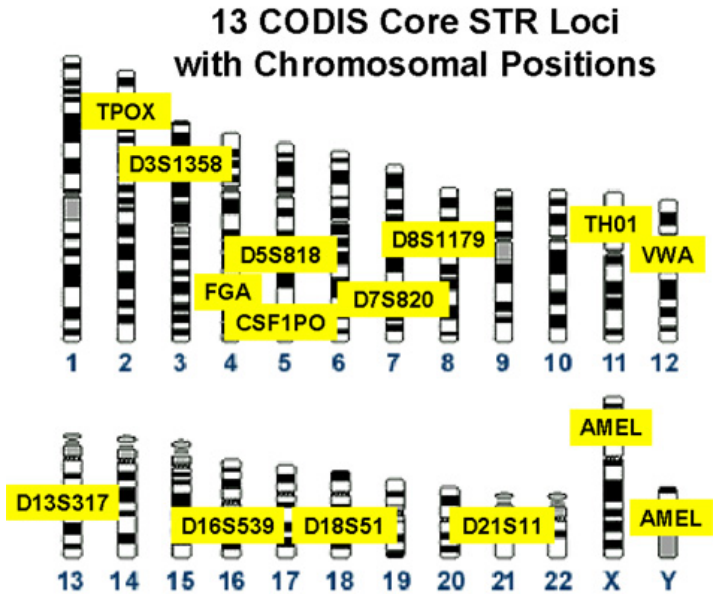
Range: up to 2k bp routinely; 50k with other enzymes & care

Why PCR?

PCR is important for all the reasons that filters and amplifiers are important in electronics, e.g., sample size is reduced from grams of tissue to a few cells, can pull out small signal amidst “noisy” background

Very widely used; forensics, archeology, cloning, sequencing, …

DNA Forensics



E.g. FBI "CODIS" (combined DNA indexing system) data base

As of 1/2013, over 10,142,600 offender profiles

Picked 13 "short tandem repeats", i.e., variable-length regions of human genome flanked by (essentially) invariant sequences (primer targets), several alleles common at each locus, of which you have 2

Amplify each from, e.g., small spot of dried blood

Measure product lengths (next slides)

http://www.fbi.gov/about-us/lab/biometric-analysis/codis

http://www.dna.gov/solving-crimes/cold-cases/howdatabasesaid/codis/

Gel Electrophoresis

DNA/RNA backbone is negatively charged (they're acids)

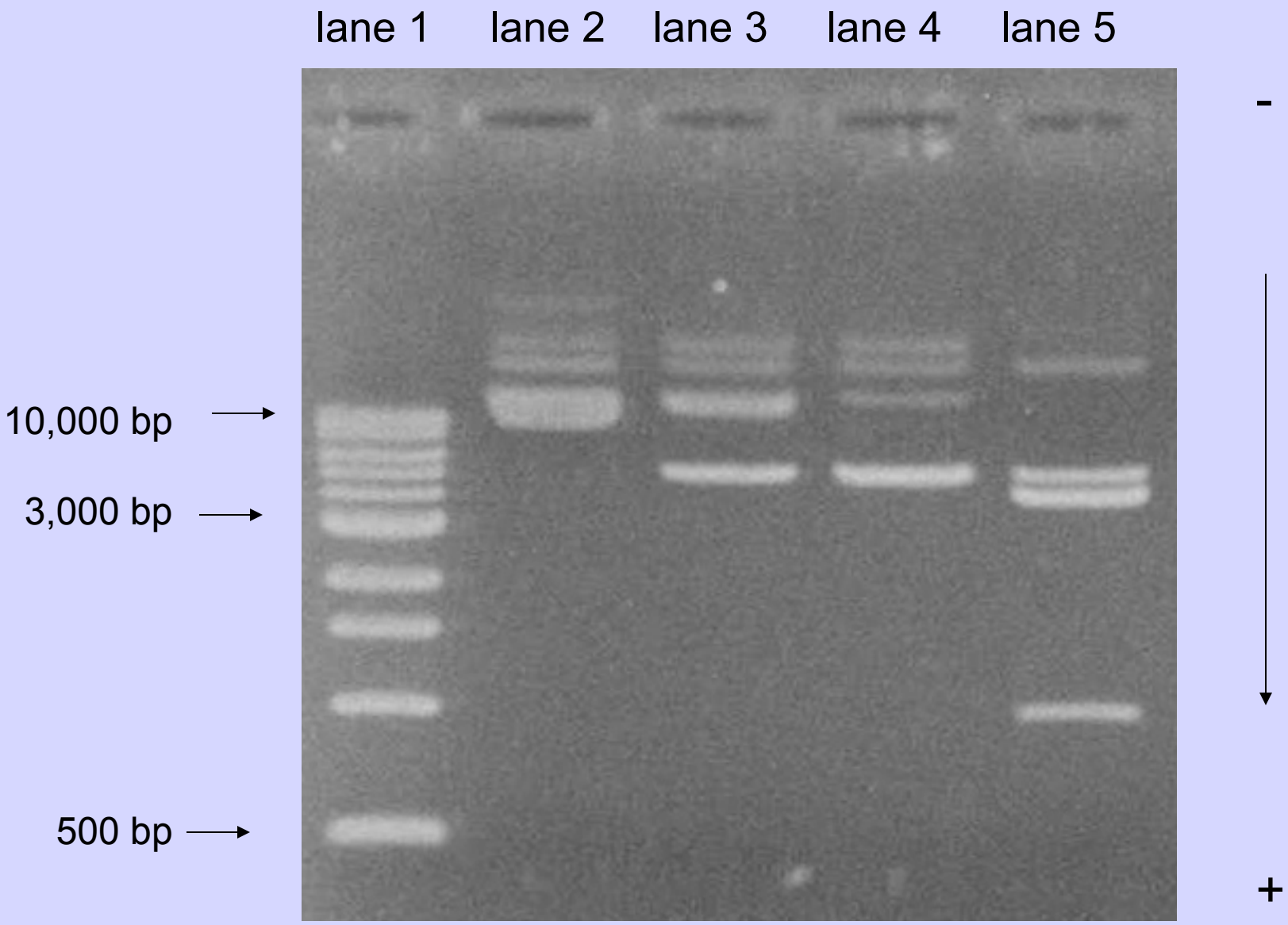
Molecules moves slowly in gels under an electric field

- agarose gels for large molecules
- polyacrylamide gels for smaller ones

Smaller molecules move faster

So, you can *separate DNAs & RNAs by size*

Nobel Chem prize, 1948 Arne Wilhelm Kaurin Tiselius

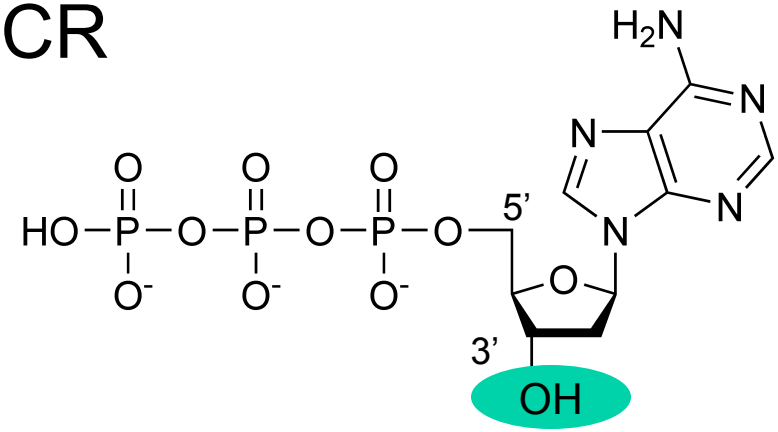

lane 1
lane 2
lane 3
lane 4
lane 5
10,000 bp
3,000 bp
500 bp
-
+

DNA Sequencing – Sanger Method

Like one-cycle, one-primer PCR

Suppose 0.1% of A's:

- are *di*-deoxy adenosine's; backbone can't extend
- carry a green florescent dye



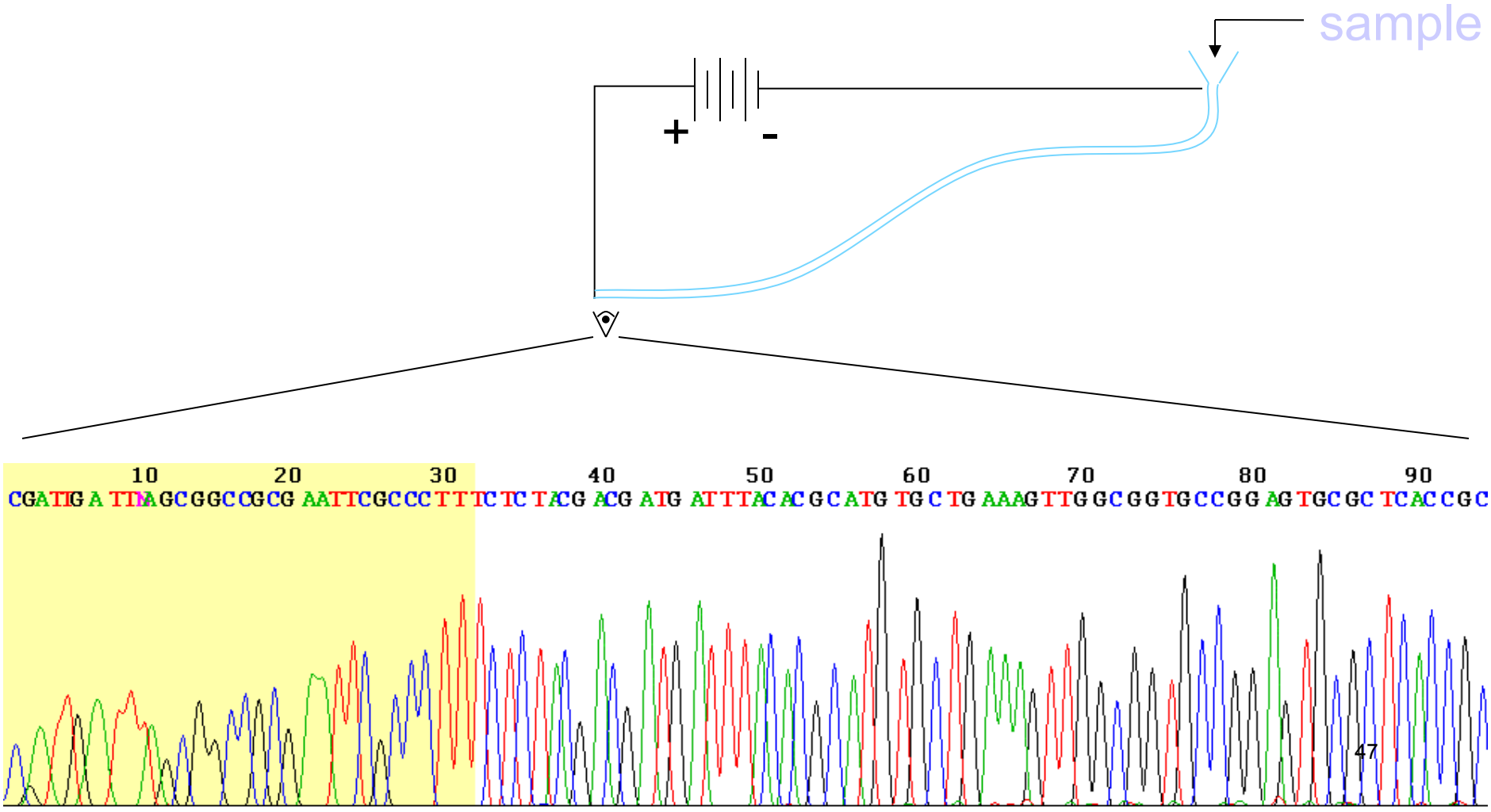
Separate by capillary gel electrophoresis

If frags of length 42, 49, 50, 55 … glow green, those positions are A's

Ditto C's (blue), G's (yellow), T's (red)

DNA Sequencing

Sanger with capillary electrophoresis



Sequencing A Genome

Highly automated

Typical Sanger "read" about 600 nt

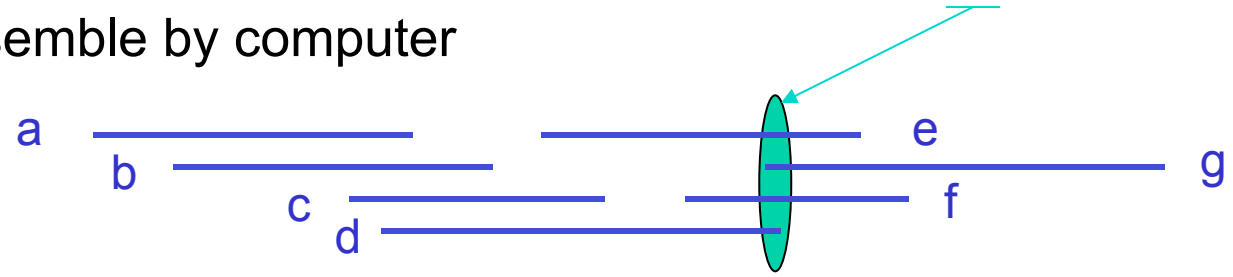
"Whole Genome Shotgun" approach:

randomly fragment (many copies of) genome

sequence many, enough to cover each base 10x or more times

reassemble by computer

E.g., human genome project:
≈ 30Gbases and
≈ $3 \times 10^9 / 600 \times 10$
= 5×10^7 reads



Complications: repeated region, missed regions, sequencing errors, chimeric DNA fragments, …

But overall accuracy ~10^{-4}, if careful

“Next Generation” Sequencing

Many technical improvements to Sanger approach over many years, culminating in highly automated machines used for the HGP

Since then, many innovative new ideas/products:

- Helicos: single molecule flourescence tethered to flow cell
- Illumina: colony PCR; reversible dye terminator
- Ion Torrent: semiconductor detection of ions released by polymerase
- Roche 454: emulsion PCR; pyro sequencing
- Oxford Nanopore
- Pacific Biosciences: single tethered polymerases in “zero mode waveguide” nano-wells, circularized DNA, “real time”
- ABI SOLiD: emulsion PCR, sequence by ligation, “color-space”
- Complete Genomics: rolling circle replication/DNA nanoballs

Technology is changing rapidly!

Illumina Sequencing

~1 billion microscopic PCR “colonies” on 1x2” slide

“Read” ~50-150bp of sequence from (1 or 2) ends of each

Reversible dye terminators

Automated: takes a few days; ~ 100 G bases/day

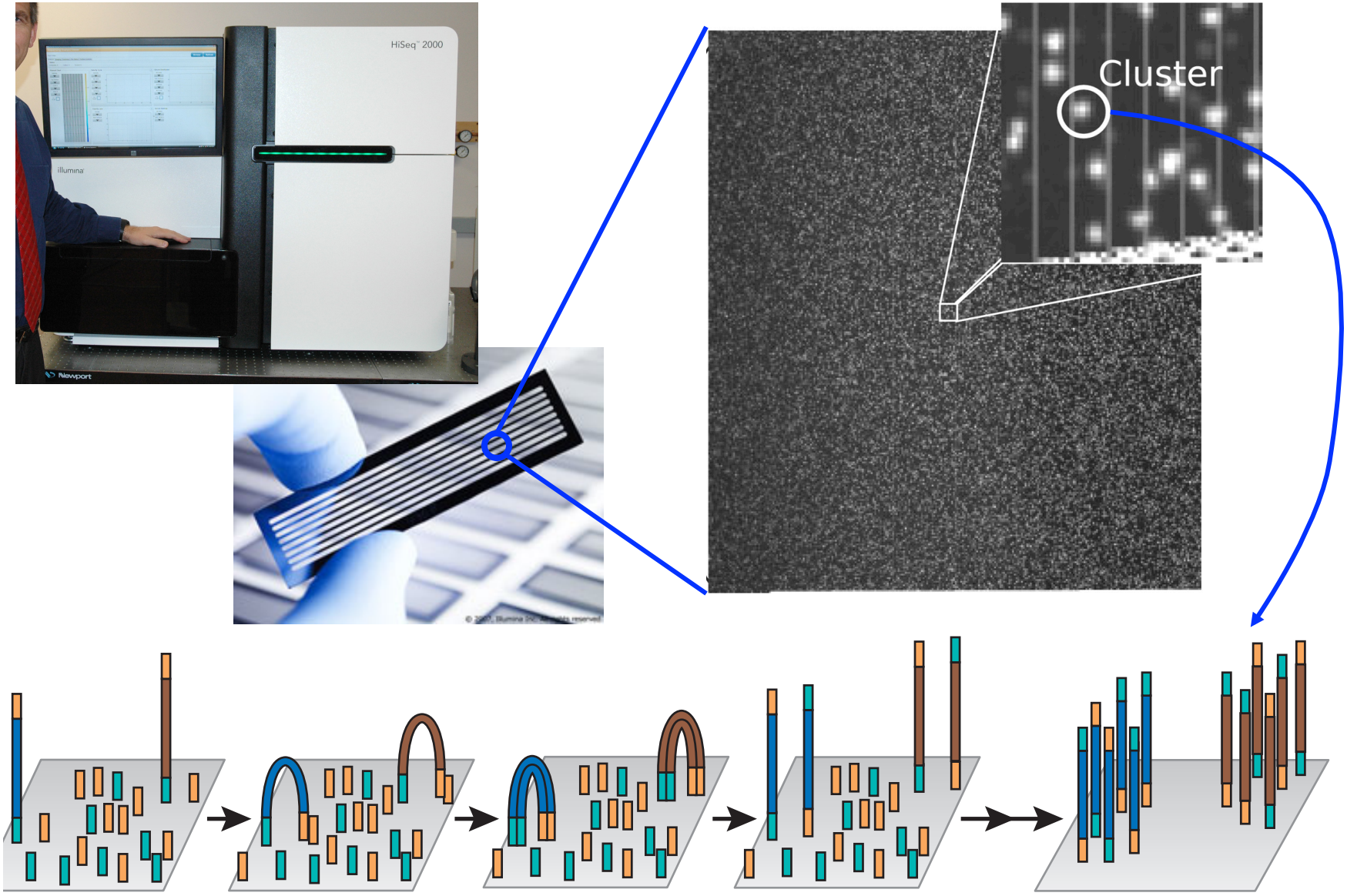
Costs a few thousand dollars

Generates terabytes of data (mostly images)

I,e., ~ 30x human genome/day

(you need 25x-50x to assemble)

(equal to all of pre-2008 Genbank)



http://www.technologyreview.com/sites/default/files/legacy/pgenome_x220.jpghttp://bioinformatics.oxfordjournals.org/content/25/17/2194/F1.large.jpg

http://bioinformatics.oxfordjournals.org/content/25/17/2194/F1.large.jpg

Fig from: Shendure and Ji 2008. “Next-Generation DNA Sequencing..” *Nature Biotechnol* 26 (10) (October): 1135–1145. doi:10.1038/nbt1486.

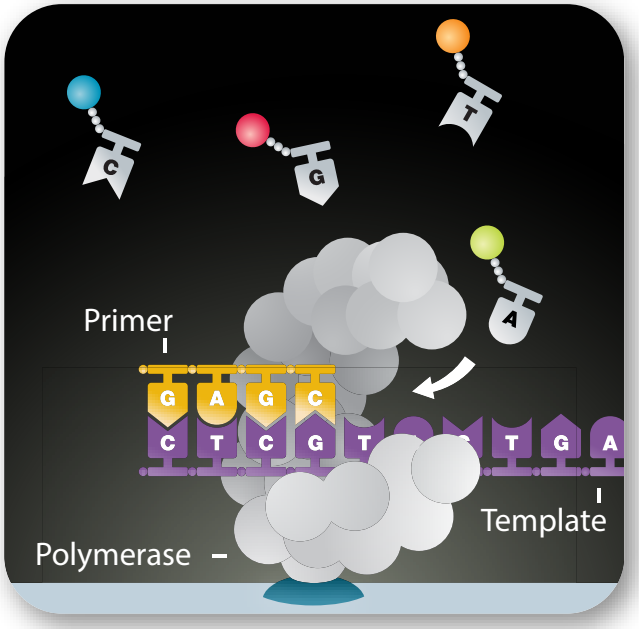
Illumina HiSeq (1500/2500, as of Spring 2013)

	HIGH OUTPUT RUN MODE*			RAPID RUN MODE*		
Read Length	Dual Flow Cell (2500 only)	Single Flow Cell (1500 or 2500)	Dual Flow Cell Run Time	Dual Flow Cell (2500 only)	Single Flow Cell (1500 or 2500)	Dual Flow Cell Run Time
1 x 36	95-105 Gb	47-52 Gb	2 days	18-22 Gb	9-11 Gb	7 hr
2 × 50	270-300 Gb	135-150 Gb	5.5 days	50-60 Gb	25-30 Gb	16 hr
2 x 100	540-600 Gb	270-300 Gb	11 days	100-120 Gb	50-60 Gb	27 hr
2 x 150	N/A	N/A	N/A	150-180 Gb	75-90 Gb	40 hr
Reads Passing Filter	Up to 3 billion single reads or 6 billion paired-end reads	Up to 1.5 billion single reads or 3 billion paired-end reads		Up to 600 million single reads or 1.2 billion paired-end reads	Up to 300 million single reads or 600 million paired-end reads	
Quality	> 85% of bases above Q30 at 2 × 50 bp > 80% of bases above Q30 at 2 × 100 bp			> 85% of bases above Q30 at 2 × 50 bp > 80% of bases above Q30 at 2 × 100 bp > 75% of bases above Q30 at 2 × 150 bp		

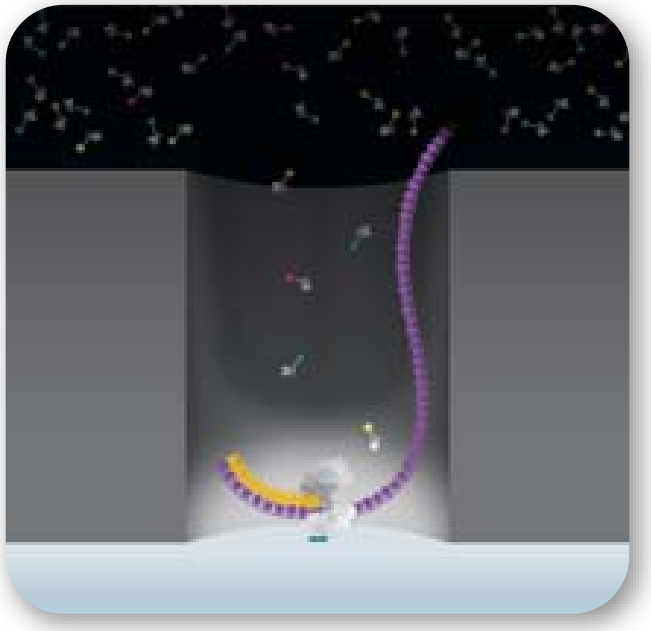
*Install specifications based on Illumina PhiX control library at supported cluster densities (between 610-678 K clusters/mm2 passing filter using TruSeq v3 Kits or 700-820 clusters/mm2 passing filter using TruSeq Rapid Kits. Run times for rapid run mode correspond to on-board cluster generation (1.5 hr) and sequencing; for high output mode, run times correspond to sequencing only. Performance may vary based on sample quality, cluster density, and other experimental factors. Early HiSeq 2000 instruments will run slightly slower when upgraded to a HiSeq 2500.

Source: http://www.illumina.com/systems/hiseq_2500_1500/performance_specifications.ilmn (downloaded 5/9/13)

Pacific Biosciences



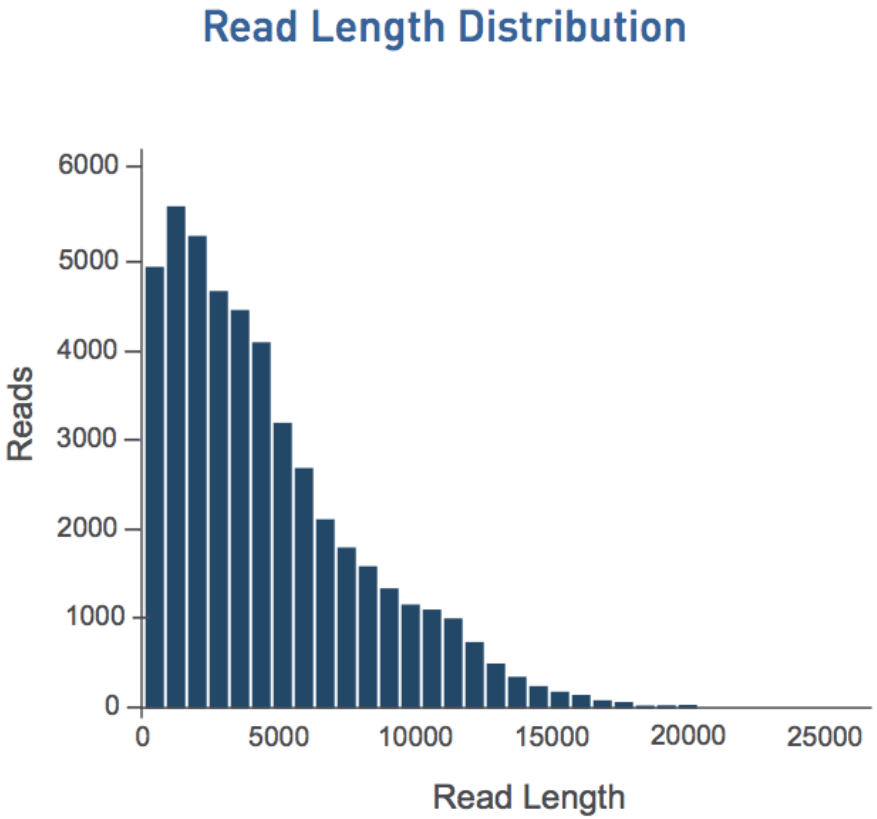
Phospholinked nucleotides



Zero-Mode Waveguides

http://files.pacb.com/pdf/PacBio_RS_II_Brochure.pdf http://www.globenewswire.com/NewsRoom/Attachment/18068

Pacific Biosciences



Advantages:
- single molecules
- long reads
- direct CH_3 detection

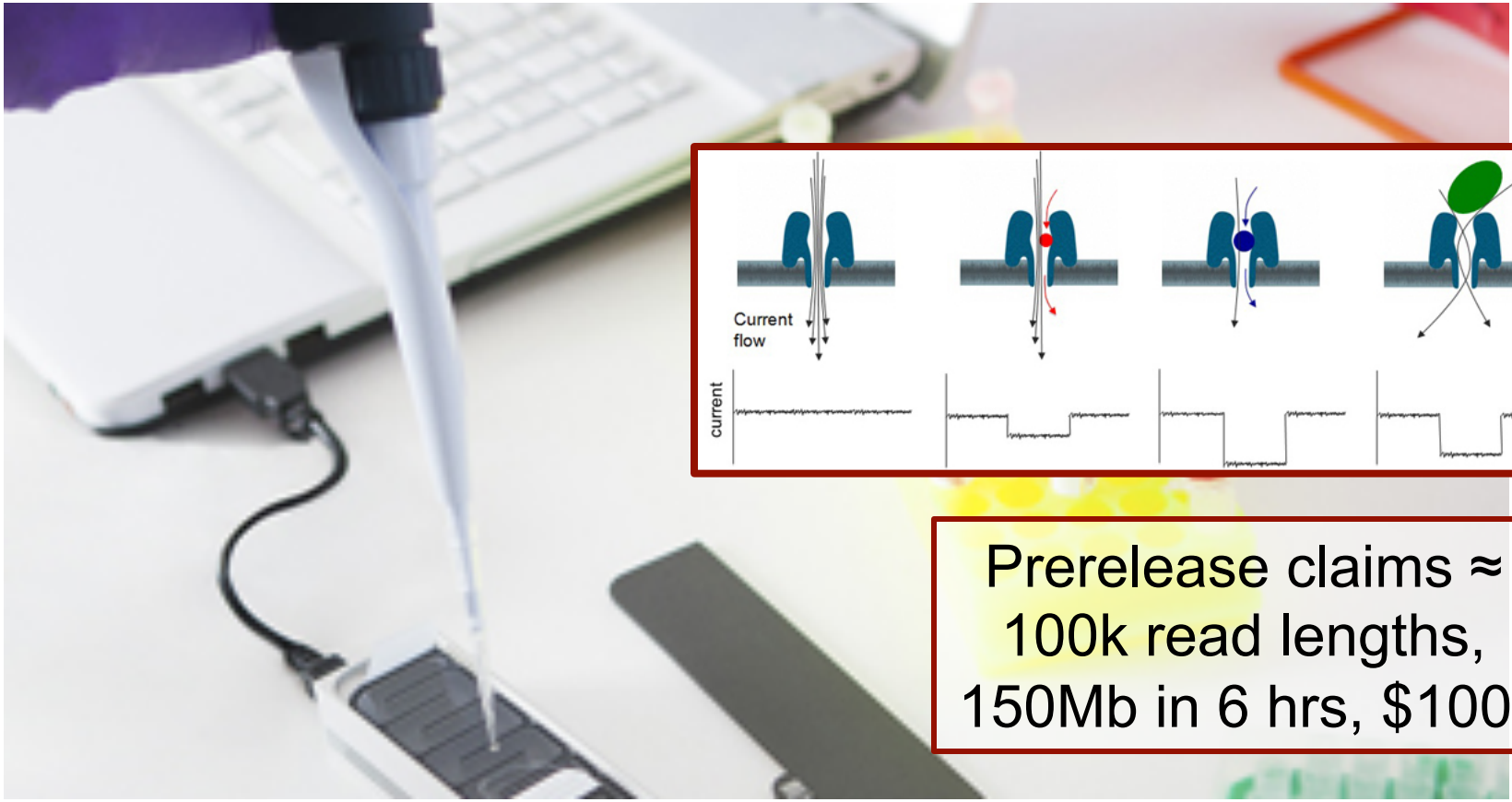
Disadvantages:
- throughput
- error rate; (circularize?)

Read Length:	
Average:	4,606 bp
95th Percentile:	11,792 bp
Maximum:	23,297 bp
Throughput per SMRT® Cell:	216 Mb
	47,197 reads

Based on data from 11 kb plasmid library using a 120 minute movie

http://www.pacificbiosciences.com/img/assets/smrt_sequencing_advantage_readlength_lg.png

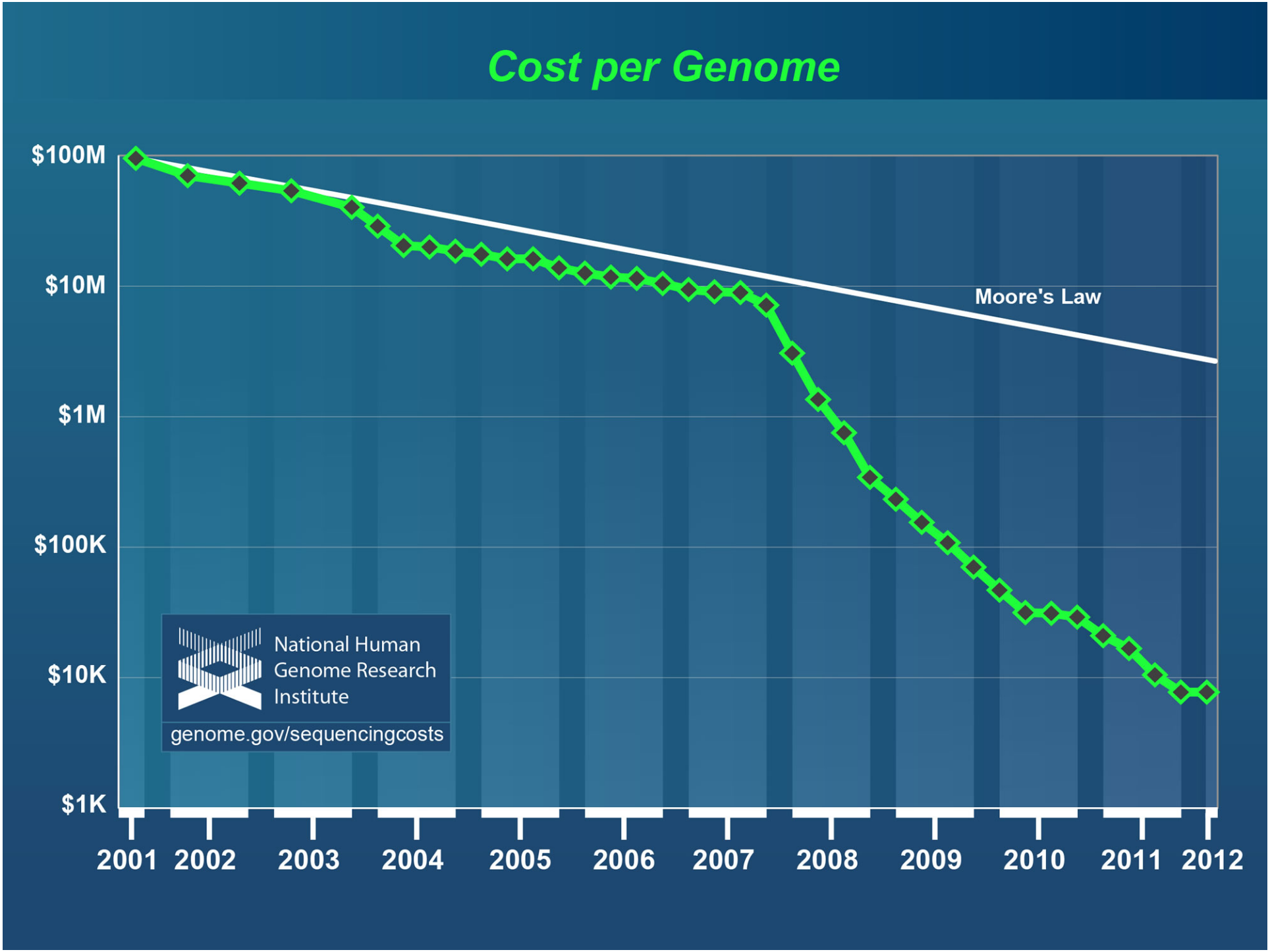
Oxford Nanopore



Prerelease claims ≈
100k read lengths,
150Mb in 6 hrs, $1000

http://www.nanoporetech.com/uploads/Technology_New/MinION/MinION_117.jpg

http://www.nanoporetech.com/uploads/Technology_New/Introduction_To_Nanopore_Sensing/Nanopore_sensing_101_0_rs.jpg


Cost per Genome
$100M
$10M
$1M
$100K
$10K
$1K
Moore's Law
National Human Genome Research Institute
genome.gov/sequencingcosts
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012

Summary

PCR allows simple *in vitro* amplification of minute quantities of DNA (having pre-specified boundaries)

Sanger sequencing uses

- a PCR-like setup with modified chemistry to generate varying length prefixes of a DNA template with the last nucleotide of each color-coded
- gel electrophoresis to separate DNA by size, giving sequence

Sequencing random overlapping fragments allows genome sequencing (and many other applications)

"Next Gen" sequencing: many innovations

- throughput up, cost down (lots!)

More on p-values and hypothesis testing

P-values & E-values

p-value: P(s,n) = *probability* of a score more extreme than s in a random target data base of size n

E-value: E(s,n) = *expected number* of such matches

They Are Related:

E(s,n) = pn (where p = P(s,1))

$P(s,n) = 1-(1-p)^n = 1-(1-1/(1/p))^{(1/p)(pn)} \approx 1-\exp(-pn) = 1-\exp(-E(s,n))$

E big ⇔ P big

E = 5 ⇔ P ≈ .993

E = 10 ⇔ P ≈ .99995

E small ⇔ P small

$E = .01 \Leftrightarrow P \approx E - E^2/2 + E^3/3! \ldots \approx E$

Both equally valid; E-value is perhaps more intuitively interpretable

Hypothesis Testing: A Very Simple Example

Given: A coin, either fair (p(H)=1/2) or biased (p(H)=2/3)

Decide: which

How? Flip it 5 times. Suppose outcome D = HHHTH

Null Model/Null Hypothesis M_0: p(H)=1/2

Alternative Model/Alt Hypothesis M_1: p(H)=2/3

Likelihoods:

$P(D \mid M_0) = (1/2)\,(1/2)\,(1/2)\,(1/2)\,(1/2) = 1/32$

$P(D \mid M_1) = (2/3)\,(2/3)\,(2/3)\,(1/3)\,(2/3) = 16/243$

Likelihood Ratio: $$\frac{p(D \mid M_1)}{p(D \mid M_0)} = \frac{16/243}{1/32} = \frac{512}{243} \approx 2.1$$

I.e., given data is ≈ 2.1x more likely under alt model than null model

Hypothesis Testing, II

Log of likelihood ratio is equivalent, often more convenient

- add logs instead of multiplying…

"Likelihood Ratio Tests": reject null if LLR > threshold

- LLR > 0 disfavors null, but higher threshold gives stronger evidence against

Neyman-Pearson Theorem: For a given error rate, LRT is as good a test as any (subject to some fine print).

A Likelihood Ratio

Defn: two proteins are *homologous* if they are alike because of shared ancestry; similarity by descent

Suppose among proteins overall, residue x occurs with frequency p_x

Then in a random alignment of 2 random proteins, you would expect to find x aligned to y with prob $p_x p_y$

Suppose among *homologs*, x & y align with prob p_{xy}

Are seqs X & Y homologous? Which is more likely, that the alignment reflects chance or homology? Use a *likelihood ratio test.*

$$\sum_i \log \frac{p_{x_i y_i}}{p_{x_i} p_{y_i}}$$

Non-*ad hoc* Alignment Scores

Take alignments of homologs and look at frequency of *x*-*y* alignments *vs* freq of *x, y* overall

Issues

- biased samples
- evolutionary distance

BLOSUM approach

- Large collection of trusted alignments
  (the BLOCKS DB)
- Subset by similarity
  BLOSUM62 ⇒ ≥ 62% identity
- e.g. http://blocks.fhcrc.org/blocks-bin/getblock.pl?IPB002546

$$\frac{1}{\lambda}\log_2\frac{p_{x\ y}}{p_x p_y}$$

Scores: formula above, rounded

BLOSUM 62

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	**4**	-1	-2	-2	0	-1	-1	0	-2	-1	-1	-1	-1	-2	-1	1	0	-3	-2	0
R	-1	**5**	0	-2	-3	1	0	-2	0	-3	-2	2	-1	-3	-2	-1	-1	-3	-2	-3
N	-2	0	**6**	1	-3	0	0	0	1	-3	-3	0	-2	-3	-2	1	0	-4	-2	-3
D	-2	-2	1	**6**	-3	0	2	-1	-1	-3	-4	-1	-3	-3	-1	0	-1	-4	-3	-3
C	0	-3	-3	-3	**9**	-3	-4	-3	-3	-1	-1	-3	-1	-2	-3	-1	-1	-2	-2	-1
Q	-1	1	0	0	-3	**5**	2	-2	0	-3	-2	1	0	-3	-1	0	-1	-2	-1	-2
E	-1	0	0	2	-4	2	**5**	-2	0	-3	-3	1	-2	-3	-1	0	-1	-3	-2	-2
G	0	-2	0	-1	-3	-2	-2	**6**	-2	-4	-4	-2	-3	-3	-2	0	-2	-2	-3	-3
H	-2	0	1	-1	-3	0	0	-2	**8**	-3	-3	-1	-2	-1	-2	-1	-2	-2	2	-3
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	**4**	2	-3	1	0	-3	-2	-1	-3	-1	3
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	**4**	-2	2	0	-3	-2	-1	-2	-1	1
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	**5**	-1	-3	-1	0	-1	-3	-2	-2
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	**5**	0	-2	-1	-1	-1	-1	1
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	**6**	-4	-2	-2	1	3	-1
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	**7**	-1	-1	-4	-3	-2
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	**4**	1	-3	-2	-2
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	**5**	-2	-2	0
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	**11**	2	-3
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	**7**	-1
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	**4**

ad hoc Alignment Scores?

Make up any scoring matrix you like

Somewhat surprisingly, under pretty general assumptions**, it is *equivalent* to the scores constructed as above from some set of probabilities p_{xy}, so you might as well understand what they are

NCBI-BLAST:	+1/-2	tuned for ~ 95% sequence identity
WU-BLAST:	+5/-4	tuned for ~ 66% identity ("twilight zone")

** e.g., average scores should be negative, but you probably want that anyway, otherwise local alignments turn into global ones, and some score must be > 0, else best match is empty