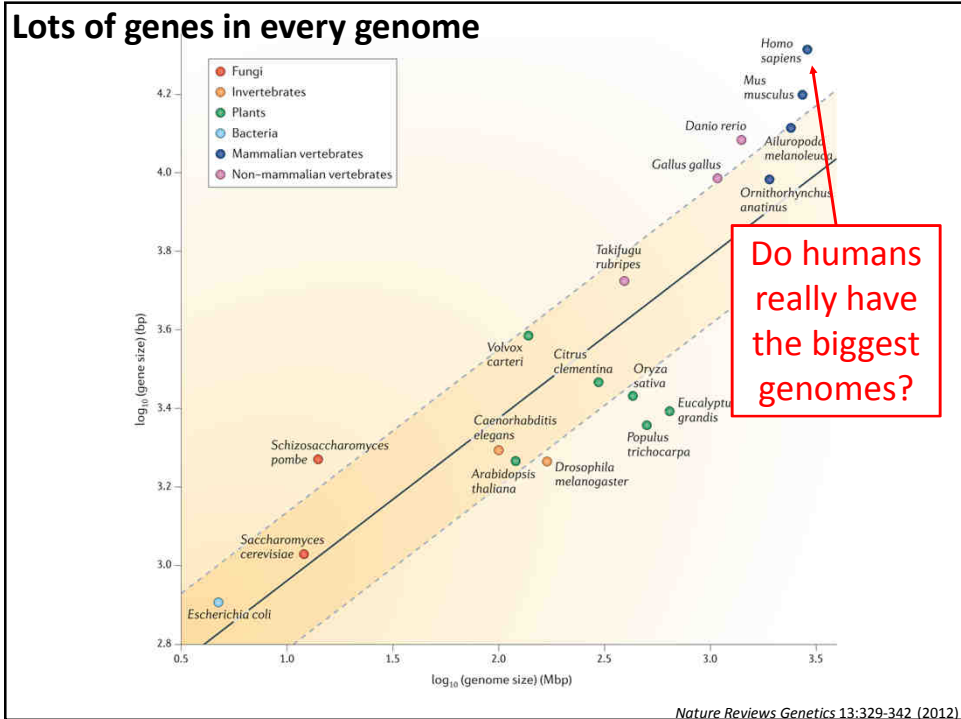


Gene Finding

BCH364C/394P Systems Biology / Bioinformatics

Edward Marcotte, Univ of Texas at Austin



Lots of genes in every genome

animal
Largest Genome Ever Sequenced Belongs To Locust Species
January 1, 2014



Image Credit: Thinkstock.com

April Flowers for redOrbit.com – Your Universe Online

The whole genome sequence of Locust (*Locusta migratoria*), the most widespread locust species, has been successfully decoded by researchers from the Institute of Zoology, Chinese Academy of Sciences, BGI and other institutes. The researchers were surprised by the remarkably large (6.5 gigabases) yielded genome, which is the largest animal genome sequenced so far.

6.5 Gb
(2X human)
17K genes

gigabases (not gigabytes)

The Telegraph

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World's largest genome belongs to slow-growing mountain flower

An unremarkable and slow-growing plant has stunned scientists after they found it had the world's largest genome – 50 times bigger than that of our own species.



The DNA contained within *Paris japonica* dwarves all other plant and animal genomes that have been analysed so far. Photo: CLIVE NICHOLS

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Science News

News » UK News »

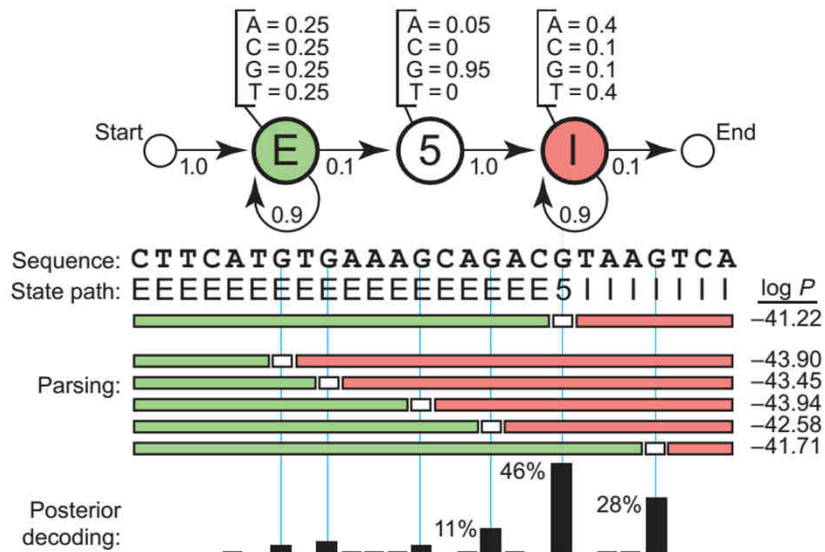
Science »

Earth News »

Where are the genes? How can we find them?

```
GATCACTTGATAAATGGGCTGAAGTAACTCGCCCAGATGAGGAGTGTGCTGCCTCCAGAAT
CCAAACAGGCCCACTAGGCCCGAGACACCTTGTCTCAGATGAACTTTGGACTCGGAATT
TTGAGTTAATGCCGAATGAGTTCAGACTTTGGGGGACTGTTGGGAAGGCATGATTGGTT
TCAAAATGTGAGAAGGACATGAGATTGGGAGGGGCTGGGGGCAGAATGATATAGTTTG
GCTCTGCGTCCCCACCAATCTCATGTCAAATTGTAATCCTCATGTGTCAGGGGAGAGGCCT
GGTGGGATGTGATTGGATCATGGGAGTGGATTCCCTCTTGCACTTCTCGTGATAGTGAGT
GAGTTCTCACGAGATCTGGTTGTTTGAAGTGTGCAGCTCCTCCCCCTTCGCGCTCTCTCTC
TCCCCTGTCCACCATGGTGAGACGTGCTTGCGTCCCCTTTGCCTTCTGCCATGATTGTAAG
CTTCCTCAGGCGTCCTAGCCACGCTTCCTGTACAGCCTGAGGAACTGGGAGTCAATGAAA
CCTCTTCTCTTCATAAATTACCCAGTTTCAGGTAGTTCTTTCTAGCAGTGTGATAATGGACGA
TACAAGTAGAGACTGAGATCAATAGCATTGCACTGGGCTGGAACACACTGTTAAGAAC
GTAAGAGCTATTGCTGTCATTAGTAATATTCTGTATTATTGGCAACATCATCACAAATACACTGC
TGTGGGAGGGTCTGAGATACTTCTTGCAGACTCCAATATTTGTCAAAACATAAAATCAGG
AGCCTCATGAATAGTGTAAATTTTACATAATAATACATTGCACCATTTGGTATATGAGTCT
TTTTGAAATGGTATATGCAGGACGGTTTCTAATATACAGAATCAGGTACACCTCCTCTTCCA
TCAGTGCGTGAGTGTGAGGGATTGAATTCCTCTGGTTAGGAGTTAGCTGGCTGGGGGTTTC
TACTGCTGTTGTTACCCACAGTGCACCTCAGACTCACGTTTCTCCAGCAATGAGCTCCTGTT
CCCTGCACTTAGAGAAGTCAGCCCAGGGGACCAGACGGTTCTCTCCTCTTGCTGCTCCAG
CCTTGGCCTTCAGCAGTCTGGATGCCTATGACACAGAGGGCATCCTCCCAAGCCCTGGTC
CTTCTGTGAGTGGTGAGTTGCTGTTAATCCAAAGGACAGGTGAAAACATGAAAGCC...
```

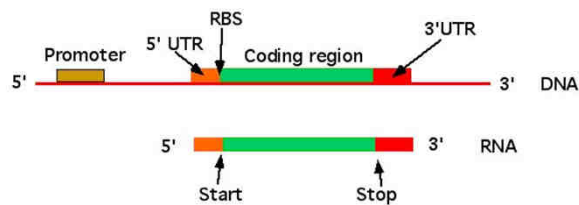
A toy HMM for 5' splice site recognition (from Remember this? linked on the course web page)



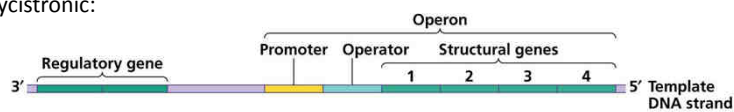
Let's start with prokaryotic genes

What elements should we build into an HMM to find bacterial genes?

Let's start with prokaryotic genes



Can be polycistronic:



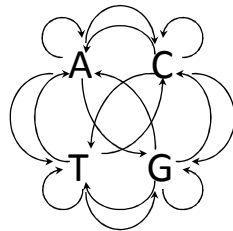
Copyright © 2006 Pearson Education, Inc., publishing as Benjamin Cummings.

<http://nitro.biosci.arizona.edu/courses/EEB600A-2003/lectures/lecture24/lecture24.html>

A CpG island model might look like:

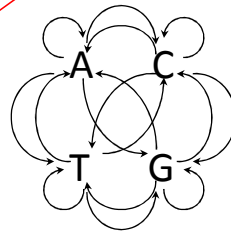
Remember this?

(of course, need the parameters, but maybe these are the most important....)



$p(C \rightarrow G)$ is higher

CpG island model



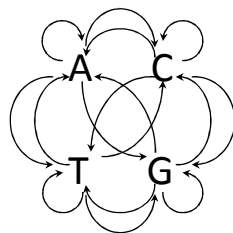
$p(C \rightarrow G)$ is lower

Not CpG island model

Could calculate
$$\frac{P(X \mid \text{CpG island})}{P(X \mid \text{not CpG island})}$$

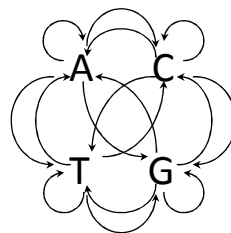
(or log ratio) along a sliding window, just like the fair/biased coin test

One way to build a minimal gene finding Markov model



Transition probabilities reflect codons

Coding DNA model



Transition probabilities reflect intergenic DNA

Intergenic DNA model

Could calculate
$$\frac{P(X \mid \text{coding})}{P(X \mid \text{not coding})}$$

(or log ratio) along a sliding window, just like the fair/biased coin test

Really, we'll want to detect codons.

The usual trick is to use a *higher-order Markov process*.

A standard Markov process only considers the current position in calculating transition probabilities.

An n^{th} -order Markov process takes into account the past n nucleotides, e.g. as for a 5th order:

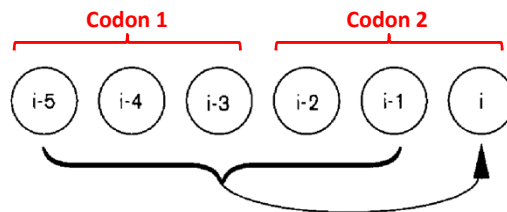
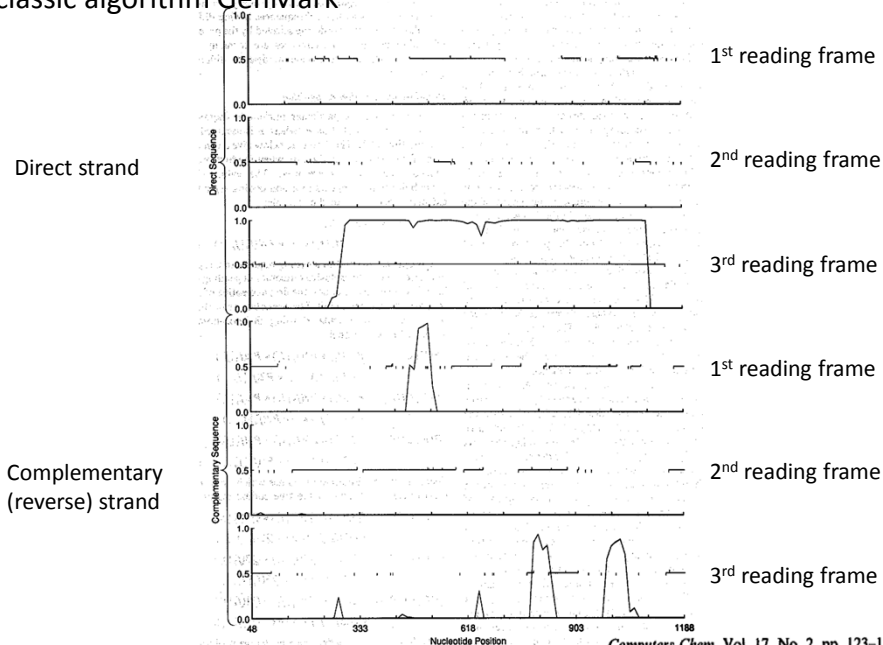


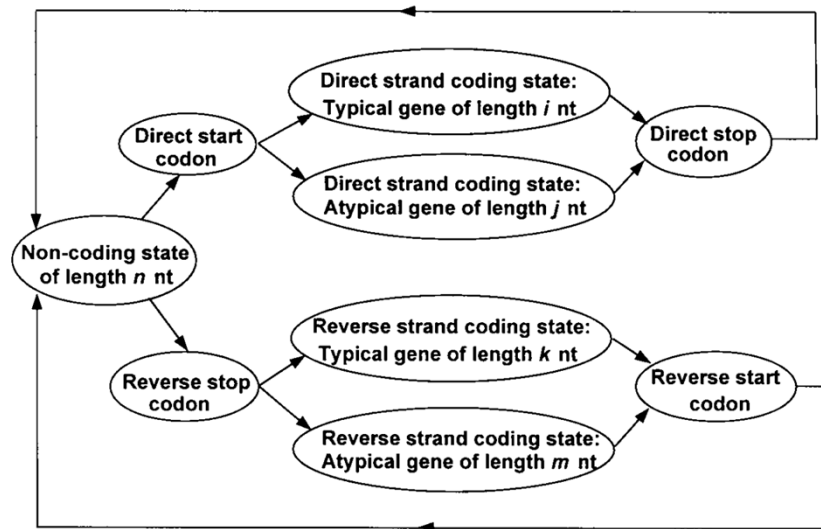
Image from Curr Opin Struct Biol 8:346-354 (1998)

5th order Markov chain, using models of coding vs. non-coding using the classic algorithm GenMark



Computers Chem. Vol. 17, No. 2, pp. 123-133, 1993

An HMM version of GenMark



GeneMark.hmm: new solutions for gene finding

Alexander V. Lukashin and Mark Borodovsky^{1,*}

Nucleic Acids Research, 1998, Vol. 26, No. 4 1107-1115

For example, accounting for variation in start codons...

The probabilities of the start codons were defined in agreement with the *E.coli* genome statistics: $P(\text{ATG}) = 0.905$, $P(\text{GTG}) = 0.090$, $P(\text{TTG}) = 0.005$. The probability of transition from a non-coding state to a Typical (Atypical) coding state was set to 0.85 (0.15).

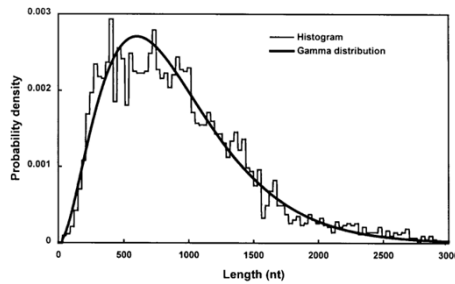
GeneMark.hmm: new solutions for gene finding

Alexander V. Lukashin and Mark Borodovsky^{1,*}

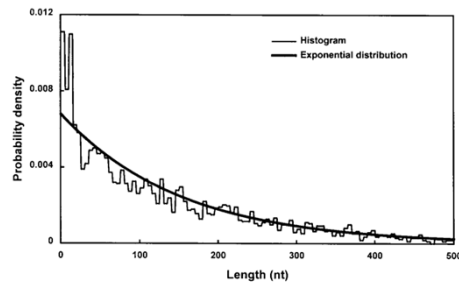
Nucleic Acids Research, 1998, Vol. 26, No. 4 1107-1115

... and variation in gene lengths

Length distributions (in # of nucleotides)



Coding (ORFs)



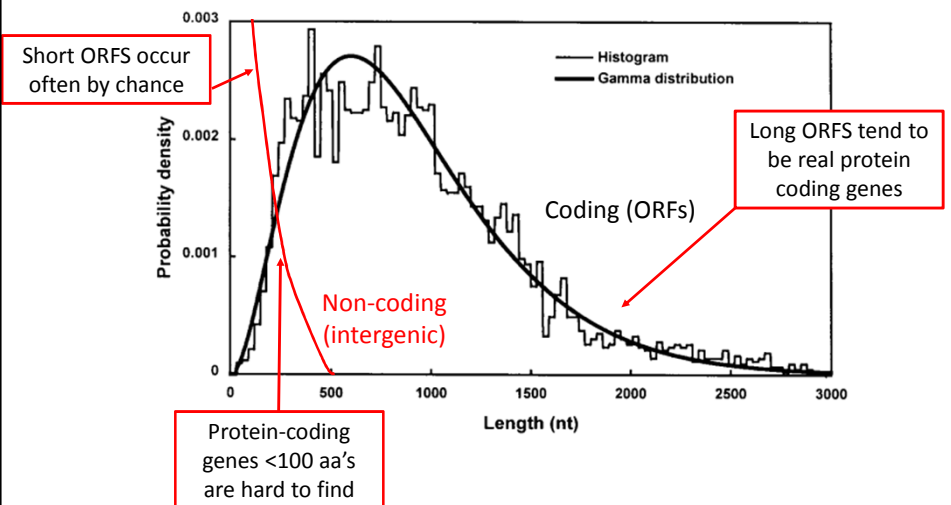
Non-coding (intergenic)

GeneMark.hmm: new solutions for gene finding

Alexander V. Lukashin and Mark Borodovsky^{1,*}

Nucleic Acids Research, 1998, Vol. 26, No. 4 1107-1115

(Placing these curves on top of each other)



GeneMark.hmm: new solutions for gene finding

Alexander V. Lukashin and Mark Borodovsky^{1,*}

Nucleic Acids Research, 1998, Vol. 26, No. 4 1107-1115

Model for a ribosome binding site (based on ~300 known RBS's)

Nucleotide	Position 1	2	3	4	5
T	0.161	0.050	0.012	0.071	0.115
C	0.077	0.037	0.012	0.025	0.046
A	0.681	0.105	0.015	0.861	0.164
G	0.077	0.808	0.960	0.043	0.659

GeneMark.hmm: new solutions for gene finding

Alexander V. Lukashin and Mark Borodovsky^{1,*}

Nucleic Acids Research, 1998, Vol. 26, No. 4 1107-1115

How well does it do on well-characterized genomes?

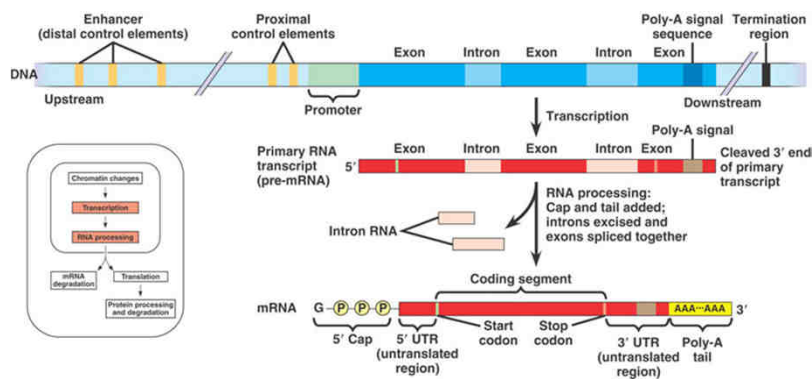
Genome	Genes annotated	Genes predicted	Exact prediction (%)	Missing genes (%)	Wrong genes (%)
<i>A.fulgidus</i>	2407	2530	73.1	10.8 (2.0)	15.1
<i>B.subtilis</i>	4101	4384	77.5	3.6 (2.8)	9.8
<i>E.coli</i>	4288	4440	75.4	5.0 (2.7)	8.2
<i>H.influenzae</i>	1718	1840	86.7	3.8 (3.2)	10.2
<i>H.pylori</i>	1566	1612	79.7	6.0 (4.4)	8.7
<i>M.genitalium</i>	467	509	78.4	9.9 (1.7)	17.3
<i>M.jannaschii</i>	1680	1841	72.7	4.6 (0.8)	12.9
<i>M.pneumoniae</i>	678	734	70.1	7.8 (4.1)	13.6
<i>M.thermoautotrophicum</i>	1869	1944	70.9	5.0 (3.5)	8.6
<i>Synechocystis</i>	3169	3360	89.6	4.0 (1.5)	9.4
Averaged	21 943	23 194	78.1	5.4 (2.7)	10.4

But this was a long time ago!

Eukaryotic genes

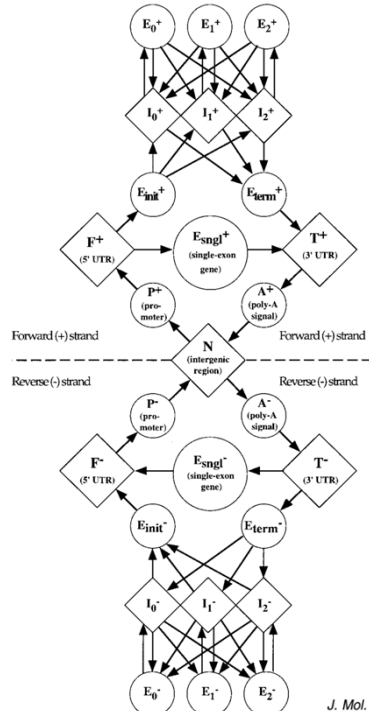
What elements should we build into an HMM to find eukaryotic genes?

Eukaryotic genes



http://greatneck.k12.ny.us/GNPS/SHS/dept/science/krauz/bio_tv/Biology_Handouts_Diagrams_Videos.htm

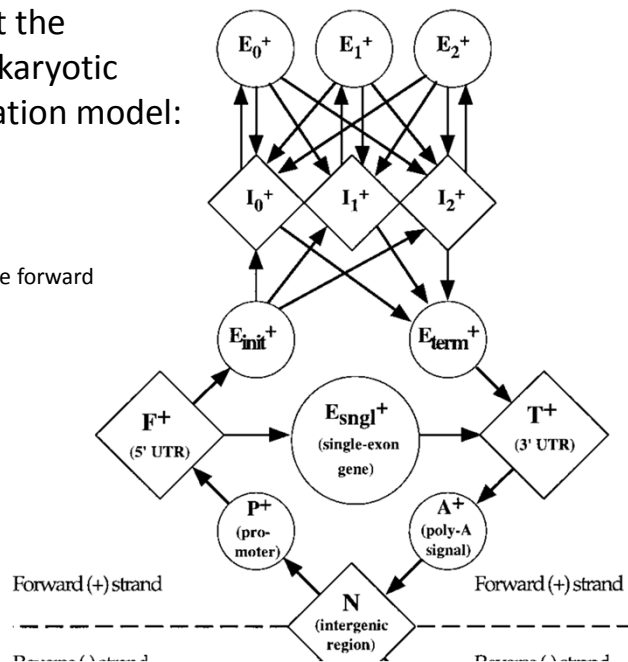
We'll look at the
GenScan eukaryotic
gene annotation model:



J. Mol. Biol. (1997) 268, 78–94

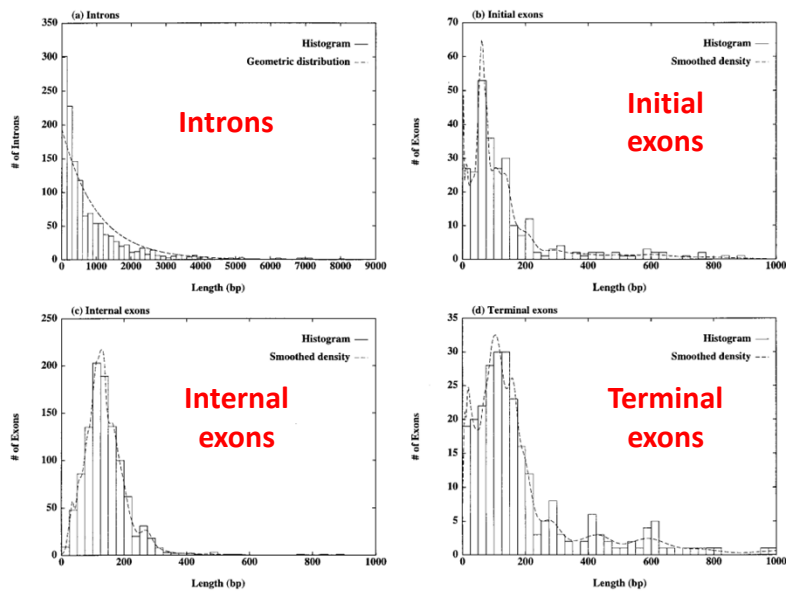
We'll look at the
GenScan eukaryotic
gene annotation model:

Zoomed in on the forward
strand model...



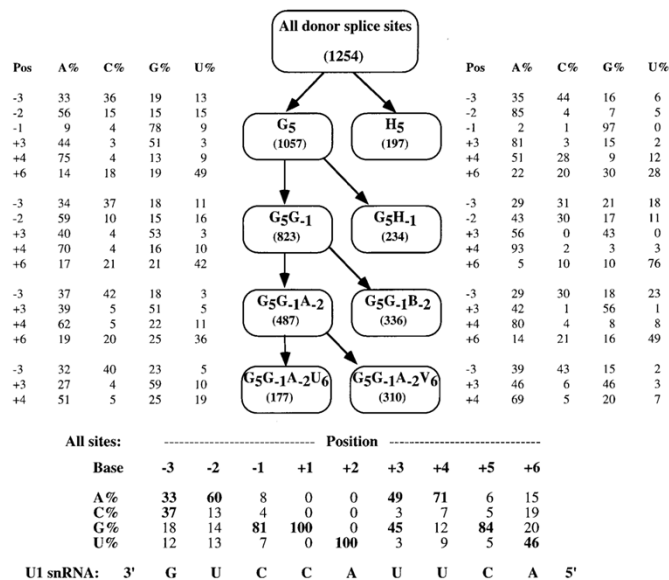
J. Mol. Biol. (1997) 268, 78–94

Introns and different flavors of exons all have different typical lengths



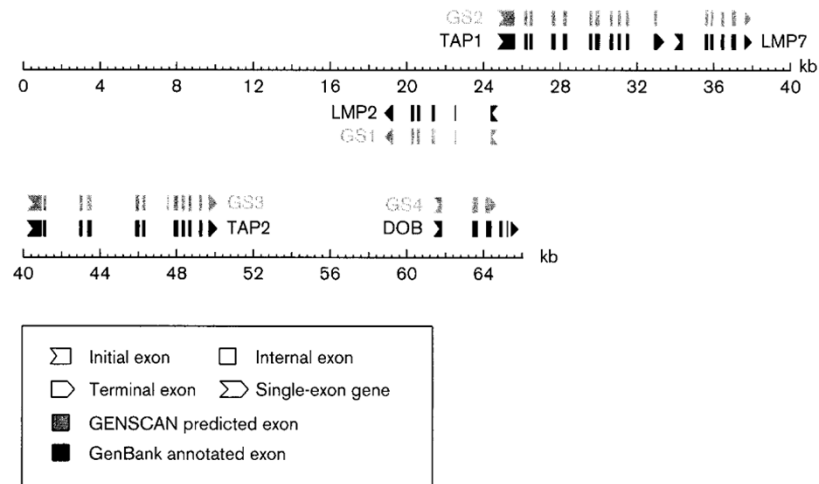
J. Mol. Biol. (1997) 268, 78–94

Taking into account donor splice sites



J. Mol. Biol. (1997) 268, 78–94

An example of an annotated gene...



Current Opinion in Structural Biology 1998, 8:346-354

How well do these programs work?

We can measure how well an algorithm works using these:

True answer:

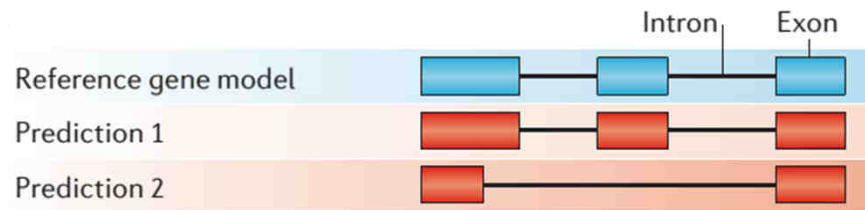
		Positive	Negative
Algorithm predicts:	Positive	True positive	False positive
	Negative	False negative	True negative

$$\text{Specificity} = \text{TP} / (\text{TP} + \text{FP})$$

$$\text{Sensitivity} = \text{TP} / (\text{TP} + \text{FN})$$

Nature Reviews Genetics 13:329-342 (2012)

How well do these programs work?
How good are our current gene models?



SN	SP
1 (1)	1 (1)
0.63 (0.33)	1 (0.5)

Nature Reviews Genetics 13:329-342 (2012)

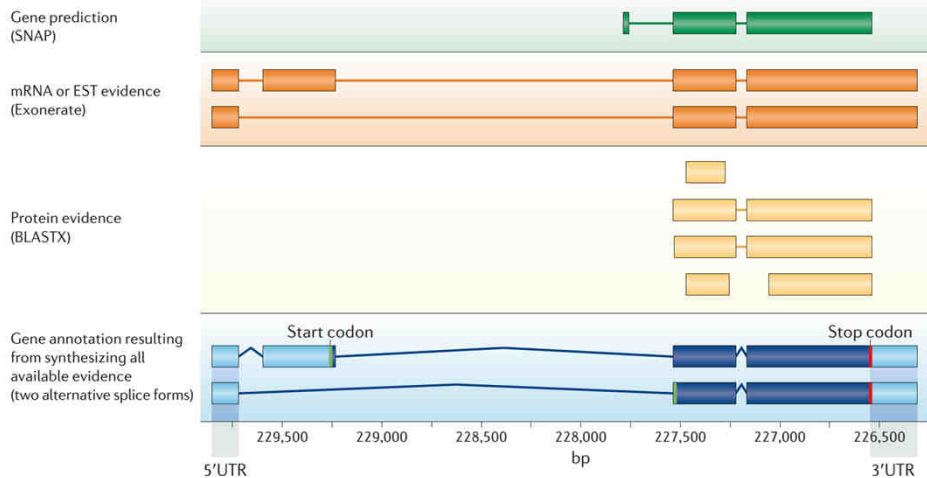
GENSCAN, when it was first developed....

Program	Sequences	Accuracy per base		Accuracy per exon	
		Sn	Sp	Sn	Sp
GENSCAN	570 (8)	0.93	0.93	0.78	0.81
FGENEH	569 (22)	0.77	0.88	0.61	0.64
GeneID	570 (2)	0.63	0.81	0.44	0.46
Genie	570 (0)	0.76	0.77	0.55	0.48
GenLang	570 (30)	0.72	0.79	0.51	0.52
GeneParser2	562 (0)	0.66	0.79	0.35	0.40
GRAIL2	570 (23)	0.72	0.87	0.36	0.43
SORFIND	561 (0)	0.71	0.85	0.42	0.47
Xpound	570 (28)	0.61	0.87	0.15	0.18
GeneID+	478 (1)	0.91	0.91	0.73	0.70
GeneParser3	478 (1)	0.86	0.91	0.56	0.58

J. Mol. Biol. (1997) 268, 78-94

In general, we can do better with more data, such as mRNA and conservation

Box 2 | Gene prediction versus gene annotation



Nature Reviews Genetics 13:329-342 (2012)

How well do we know the genes now?

In the year 2000

Genome Annotation Assessment in *Drosophila melanogaster*

= scientists from around the world held a contest (“GASP”) to predict genes in part of the fly genome, then compare them to experimentally determined “truth”

	Program name	Gene finding	Promoter recognition	EST/c DNA alignment	Protein similarity	Repeat	Gene function
Mural et al., Oakridge, US	GRAIL	X		X			X
Panra et al., Barcelona, ES	GeneID	X					
Krogh, Copenhagen, DK	RMGene	X					
Henikoff et al., Seattle, US	BLOCKS				X		X
Solovyev et al., Sanger, UK	FGenes	X					
Gaasterland et al., Rockefeller, US	MAGE	X	X	X		X	X
Benson et al., Mount Sinai, US	TRF					X	
Werner et al., Munich, GER	CoreInspector		X				
Ohler et al., Nuremberg, GER	MCPromoter		X				
Birney, Sanger, UK	GeneWise				X		X
Reese et al., Berkeley/Santa Cruz, US	Gene	X	X				

Genome Research 10:483-501 (2000)

How well do we know the genes now?

In the year 2000

“Over 95% of the coding nucleotides ... were correctly identified by the majority of the gene finders.”

“...the correct intron/exon structures were predicted for >40% of the genes.”

Most promoters were missed; many were wrong.

“Integrating gene finding and cDNA/EST alignments with promoter predictions decreases the number of false-positive classifications but discovers less than one-third of the promoters in the region.”

Genome Research 10:483–501 (2000)

How well do we know the genes now?

In the year 2006

EGASP: the Project

= scientists from
predict gene
experimental

18 groups
36 programs

Table 3
Summary of programs used to determine predictions submitted for each EGASP category

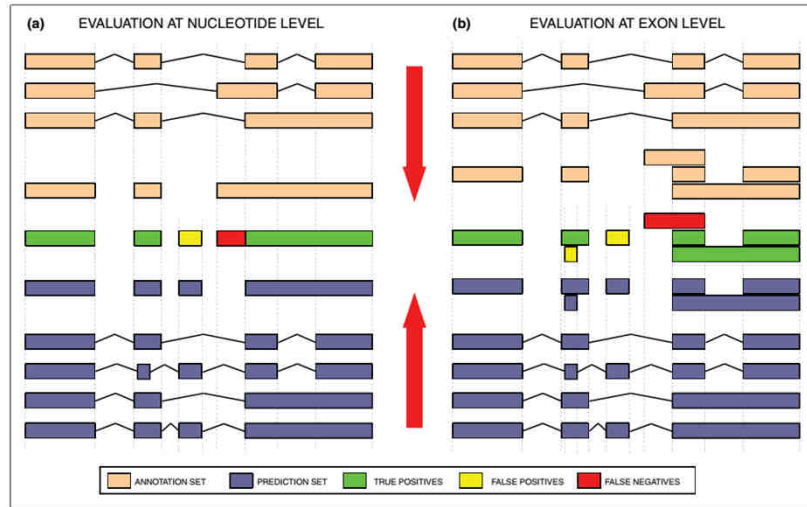
Submission category	Program	Affiliation	Reference
1 (AUGUSTUS-any)	AUGUSTUS	Georg-August-Universität, Göttingen	[58]
2 (AUGUSTUS-align)			
3 (AUGUSTUS-EST)			
4 (AUGUSTUS-dual)			
1	GENES4++	Solberry Inc.	[56]
2	JIGSAW	The Institute for Genomic Research (TIGR)	[59]
3 (PAIRAGON-any)	PAIRAGON and NSCAN_EST	Washington University, Saint Louis (WUSTL)	[57]
3 (PAIRAGON+NSCAN_EST)			
2	GENEMARK-ES	Georgia Institute of Technology	[60]
2	GENEZEAL	TIGR	[61]
2	ACEVIEW	National Center for Biotechnology Information (NCBI)	[52]
2	ENSEMBL	The Wellcome Trust Sanger Institute (WTSI) and European Bioinformatics Institute (EBI)	[64]
3	EXONSCAN	Ecole Normale Supérieure, Paris	[62]
3	EXONHUNTER	University of Waterloo	[63]
4	ACESCAN	Salk Institute	[82]
4	DOORISH-C	WTSI	[67]
4	NSCAN	WUSTL	[57]
4	SAGA	University of California at Berkeley	[66]
4	MARS	WUSTL - EBI	[65]
5	GENEID-U12	Institut Municipal d'Investigació	-
5	SGP2-U12	Medica, Barcelona	
6	ASPICT	Università degli Studi di Milano	[83]
6 (AUGUSTUS-exon)	AUGUSTUS	Georg-August-Universität, Göttingen	[58]
6	CSTMNER	Università degli Studi di Milano	[84]
6	DOORISH-C-E	WTSI	[67]
6	SPICA	EBI	[65]
6	UNCOVER	Duke University	[66]
1	CCDSGene	UCSC tracks [7]	[55]
1	KNOWNGene		[54]
1	REFSEQ (REFGene)		[5]
2	GENEID		[19]
2	GENSCAN		[18]
3	NCBI-EST		[52]
3	ECGene		[53]
3	ENSEMBL (ENSGene)		[5]
3	MGCGene		[5]
4	SGP2		[9]
4	TWINSCAN		[12,13]
-	COORDING 20050607	GENCODE annotation	[33]
-	GENES 20050607		

We
discussed
these
earlier

Assessment

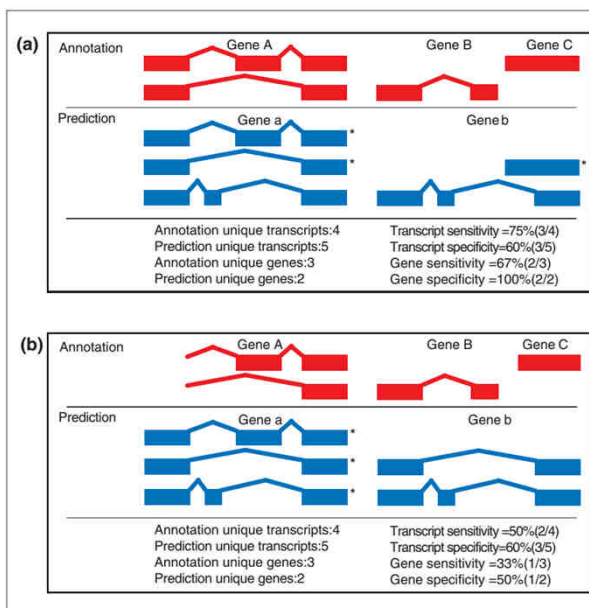
SP”) to
are them to

Genome Biology 2006, 7(Suppl 1):S2



Genome Biology 2006, 7(Suppl 1):S2

Transcripts vs. genes



Genome Biology 2006, 7(Suppl 1):S2

In the year 2006

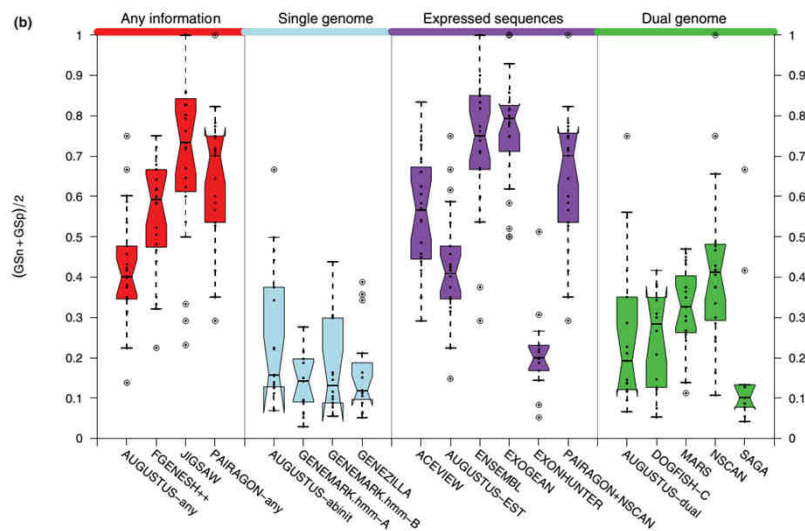
So how did they do?

- “The best methods had at least one gene transcript correctly predicted for close to **70%** of the annotated genes.”
- “...taking into account alternative splicing, ... only approximately **40% to 50%** accuracy.”
- At the coding nucleotide level, the best programs reached an accuracy of **90%** in both sensitivity and specificity.”

Genome Biology 2006, 7(Suppl 1):S2

In the year 2006

At the gene level, most genes have errors



Genome Biology 2006, 7(Suppl 1):S2

How well do we know the genes now?

In the year **2008**

nGASP – the nematode genome annotation assessment project

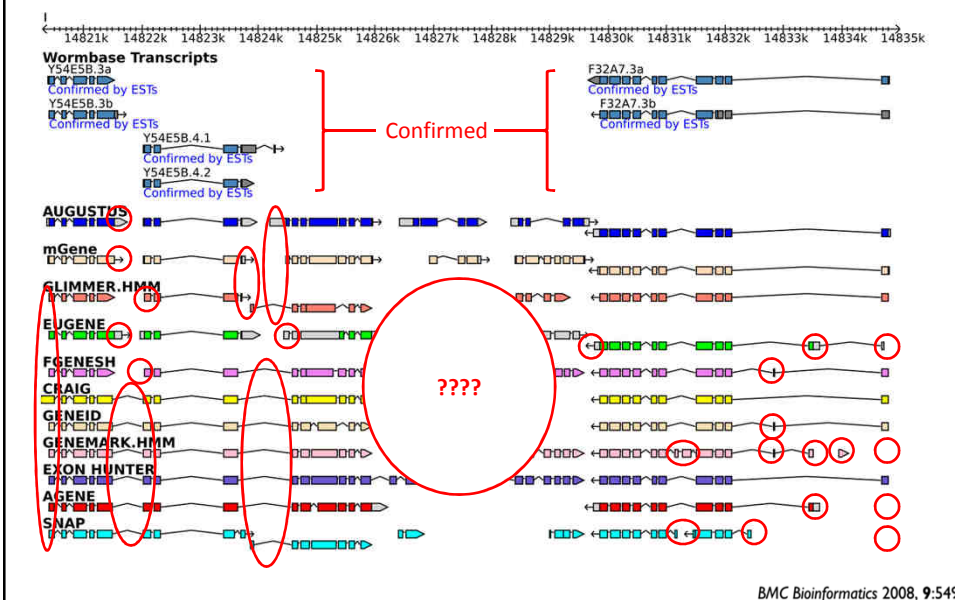
= scientists from around the world held a contest (“NGASP”) to predict genes in part of the worm genome, then compare them to experimentally determined “truth”

- 17 groups from around the world competed
- “Median gene level sensitivity ... was **78%**”
- “their specificity was **42%**”, comparable to human

BMC Bioinformatics 2008, 9:549

For example:

In the year **2008**



BMC Bioinformatics 2008, 9:549

How well do we know the genes now?

In the year **2012**

GENCODE: The reference human genome annotation for The ENCODE Project

= a large consortium of scientists trying to annotate the human genome using a combination of experiment and prediction.

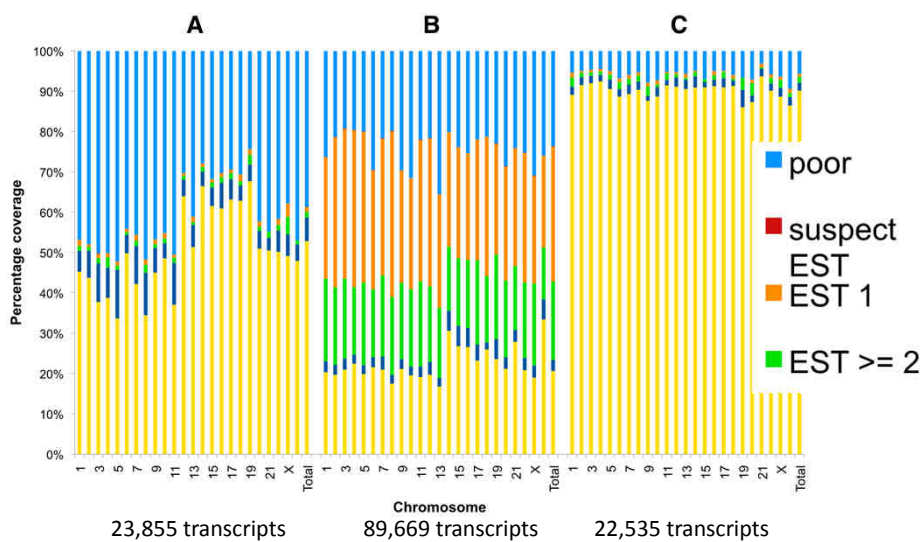
Best estimate of the current state of human genes.

Genome Res. 2012 22: 1760-1774

How well do we know the genes now?

In the year **2012**

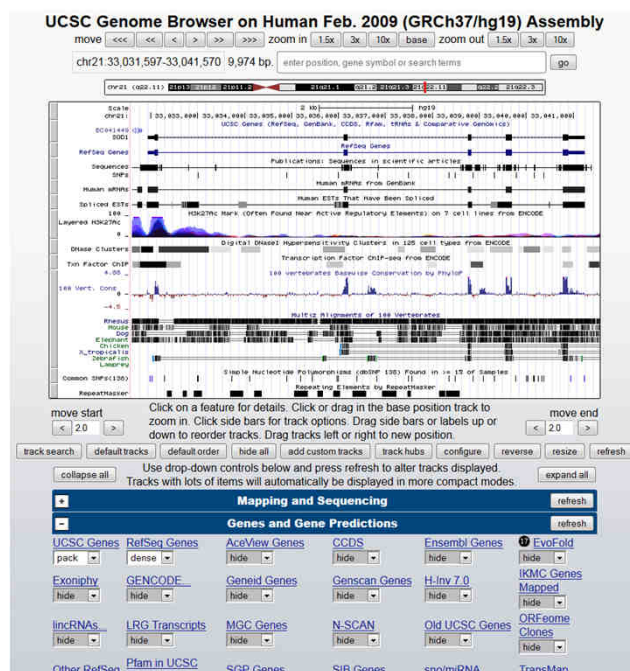
Quality of evidence used to support automatic, manually, and merged annotated transcripts (probably reflective of transcript quality)



Genome Res. 2012 22: 1760-1774

In the year 2015

- **Gene prediction and annotation are hard**
- **Annotations for all organisms are still buggy**
- **Few genes are 100% correct; expect multiple errors per gene**
- **Most organisms' gene annotations are probably much worse than for humans**



The Univ of California Santa Cruz genome browser

