Gene Finding

BCH394P/374C Systems Biology / Bioinformatics
Edward Marcotte, Univ of Texas at Austin

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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.

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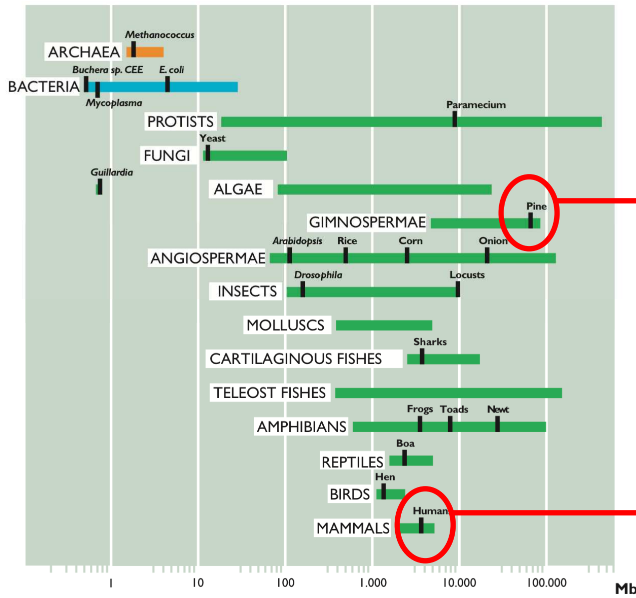
The DNA contained within Paris japonica dwarves all other plant and animal genomes that have been analysed so far Photo: CLIVE NICHOLS

2

Genome size ranges vary widely across organisms



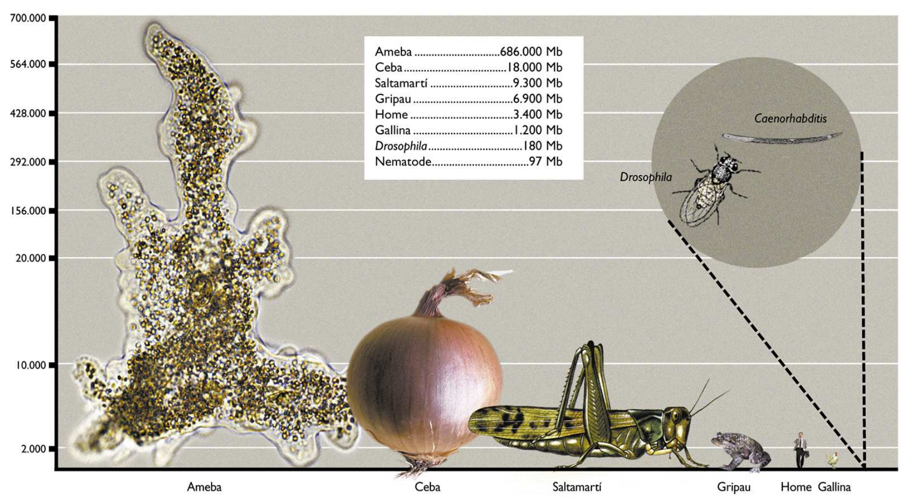
A pine tree

Us

https://metode.org/issues/monographs/the-size-of-the-genome-and-the-complexity-of-living-beings.html

3

Genome size ranges vary widely across organisms



Here, the height (i.e. vertical axis, not area) indicates genome size

https://metode.org/issues/monographs/the-size-of-the-genome-and-the-complexity-of-living-beings.html

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Where are the genes? How can we find them?

```
GATCACTTGATAAATGGGCTGAAGTAACTCGCCCAGATGAGGAGTGTGCTGCCTCCAGAAT
CCAAACAGGCCCACTAGGCCCGAGACACCTTGTCTCAGATGAAACTTTGGACTCGGAATT
TTGAGTTAATGCCGGAATGAGTTCAGACTTTGGGGGACTGTTGGGAAGGCATGATTGGTT
TCAAAATGTGAGAAGGACATGAGATTTGGGAGGGGCTGGGGGCAGAATGATATAGTTTG
GCTCTGCGTCCCCACCCAATCTCATGTCAAATTGTAATCCTCATGTGTCAGGGGAGAGGCCT
GGTGGGATGTGATTGGATCATGGGAGTGGATTTCCCTCTTGCAGTTCTCGTGATAGTGAGT
GAGTTCTCACGAGATCTGGTTGTTTGAAAGTGTGCAGCTCCTCCCCCTTCGCGCTCTCTCTC
TCCCCTGCTCCACCATGGTGAGACGTGCTTGCGTCCCCTTTGCCTTCTGCCATGATTGTAAG
CTTCCTCAGGCGTCCTAGCCACGCTTCCTGTACAGCCTGAGGAACTGGGAGTCAATGAAA
CCTCTTCTCTTCATAAATTACCCAGTTTCAGGTAGTTCTTTCTAGCAGTGTGATAATGGACGA
TACAAGTAGAGACTGAGATCAATAGCATTTGCACTGGGCCTGGAACACACTGTTAAGAAC
GTAAGAGCTATTGCTGTCATTAGTAATATTCTGTATTATTGGCAACATCATCACAATACACTGC
TGTGGGAGGGTCTGAGATACTTCTTTGCAGACTCCAATATTTGTCAAAACATAAAATCAGG
AGCCTCATGAATAGTGTTTAAATTTTTACATAATAATACATTGCACCATTTGGTATATGAGTCT
TTTTGAAATGGTATATGCAGGACGGTTTCCTAATATACAGAATCAGGTACACCTCCTCTTCCA
TCAGTGCGTGAGTGTGAGGGATTGAATTCCTCTGGTTAGGAGTTAGCTGGCTGGGGGTTC
TACTGCTGTTGTTACCCACAGTGCACCTCAGACTCACGTTTCTCCAGCAATGAGCTCCTGTT
CCCTGCACTTAGAGAAGTCAGCCCGGGGACCAGACGGTTCTCTCCTCTTGCCTGCTCCAG
CCTTGGCCTTCAGCAGTCTGGATGCCTATGACACAGAGGGCATCCTCCCCAAGCCCTGGTC
CTTCTGTGAGTGGTGAGTTGCTGTTAATCCAAAAGGACAGGTGAAAACATGAAAGCC...
```

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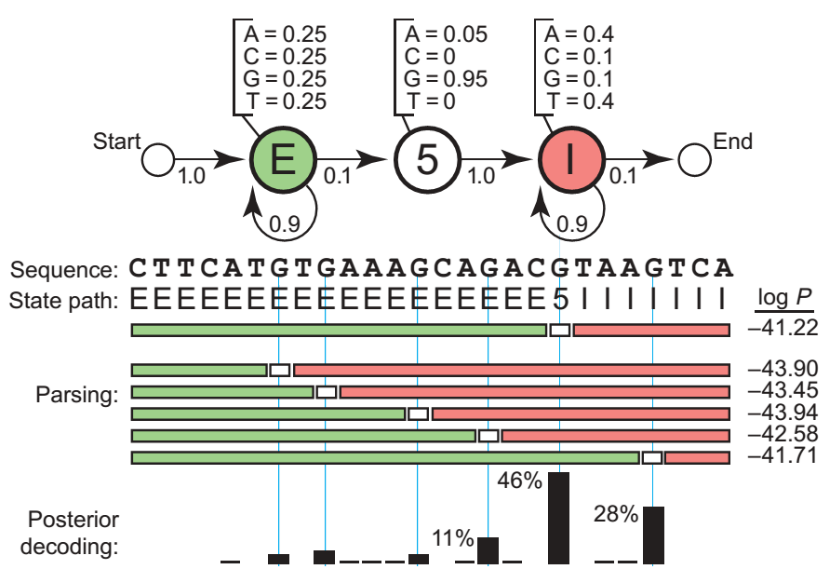
A toy HMM for 5′ splice site recognition (from linked on the course web page)

Remember this?



6

Let’s start with prokaryotic genes

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

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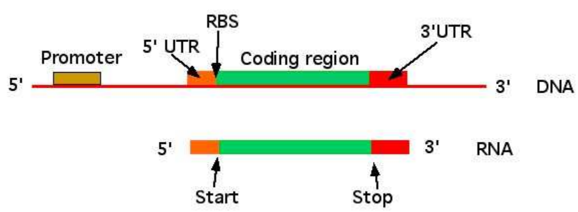
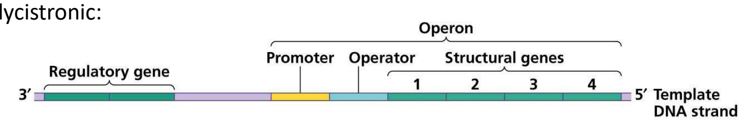
Let’s start with prokaryotic genes



Can be polycistronic:



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

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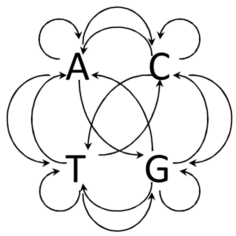
A CpG island model might look like:

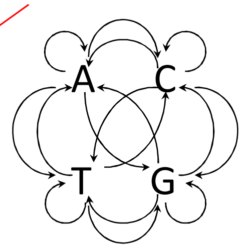
Remember this?

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



p(C→G) is higher

CpG island model



p(C→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

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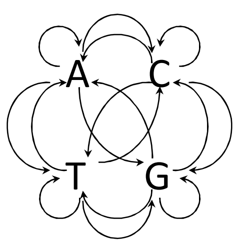
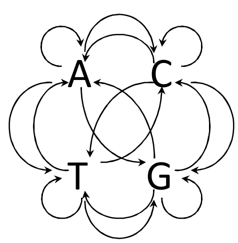
One way to build a minimal gene finding Markov model



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

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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 5^{th} order:

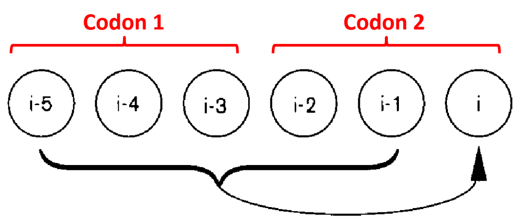

Image from *Curr Op Struct Biol* 8:346-354 (1998)

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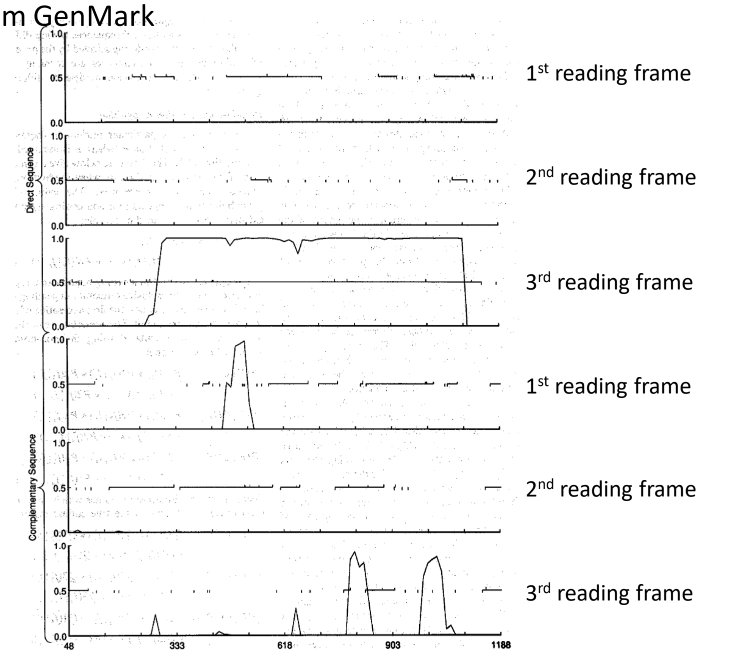
5^{th} order Markov chain, using models of coding vs. non-coding using the classic algorithm GenMark

Direct strand

Complementary (reverse) strand



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

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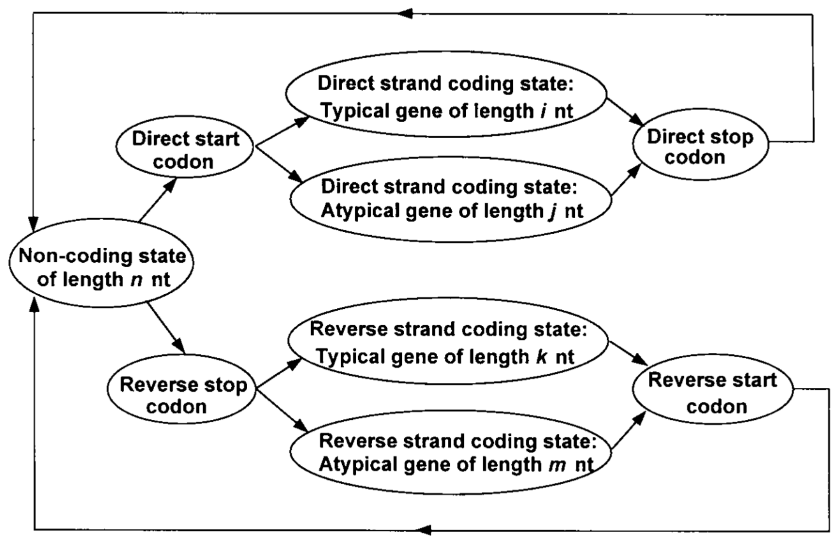
An HMM version of GenMark



GeneMark.hmm: new solutions for gene finding
Alexander V. Lukashin and Mark Borodovsky[1,*]
Nucleic Acids Research, 1998, Vol. 26, No. 4 ***1107–1115***

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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*(ATG) = 0.905, *P*(GTG) = 0.090, *P*(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***

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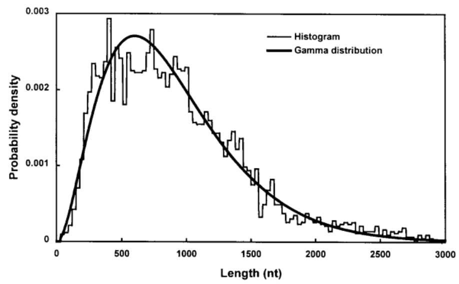
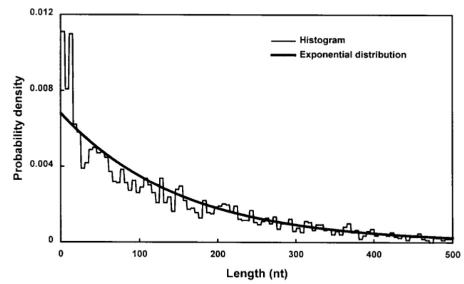
... and variation in gene lengths

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

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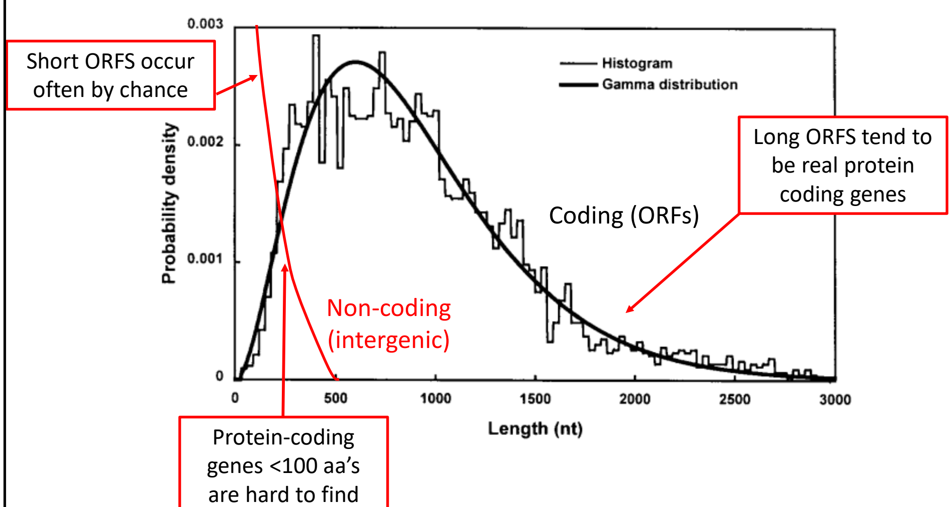
(Placing these curves on top of each other)



GeneMark.hmm: new solutions for gene finding
Alexander V. Lukashin and Mark Borodovsky[1,*]
Nucleic Acids Research, 1998, Vol. 26, No. 4 1107–1115

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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***

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How well does it do on well-characterized genomes?

Genome	Genes annotated	Genes predicted	Exact prediction (%)	Missing genes (%)	Wrong genes (%)
A.fulgidus	2407	2530	73.1	10.8 (2.0)	15.1
B.subtilis	4101	4384	77.5	3.6 (2.8)	9.8
E.coli	4288	4440	75.4	5.0 (2.7)	8.2
H.influenzae	1718	1840	86.7	3.8 (3.2)	10.2
H.pylori	1566	1612	79.7	6.0 (4.4)	8.7
M.genitalium	467	509	78.4	9.9 (1.7)	17.3
M.jannaschii	1680	1841	72.7	4.6 (0.8)	12.9
M.pneumoniae	678	734	70.1	7.8 (4.1)	13.6
M.thermoauthotrophicum	1869	1944	70.9	5.0 (3.5)	8.6
Synechocystis	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!

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Eukaryotic genes

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

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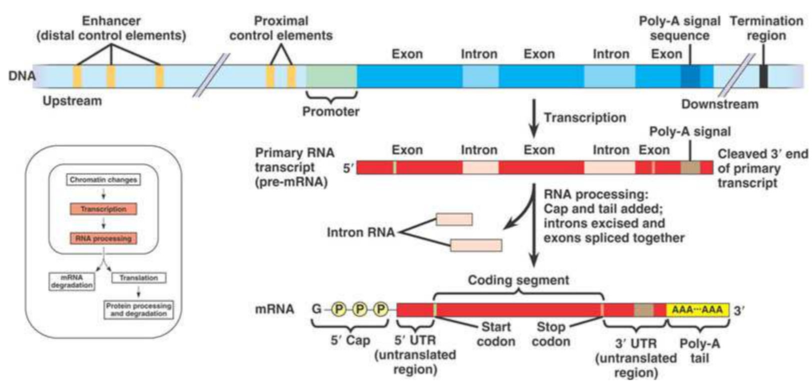
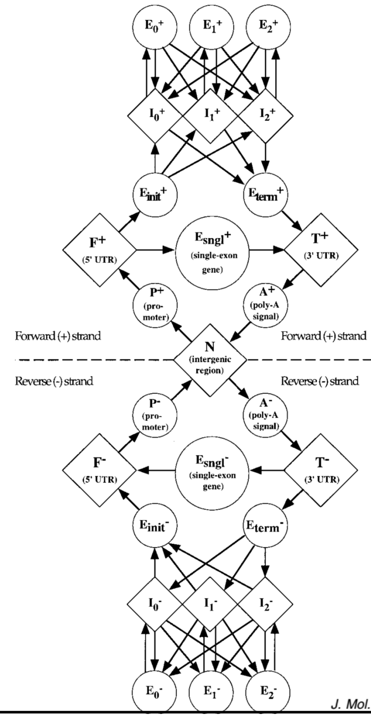
Eukaryotic genes



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

20

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



J. Mol. Biol. (1997) 268, 78–94

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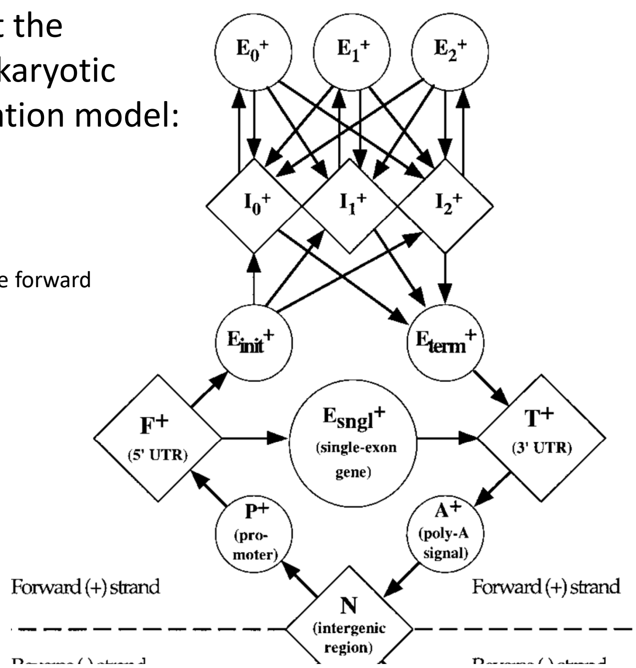
We'll look at the GenScan eukaryotic gene annotation model:

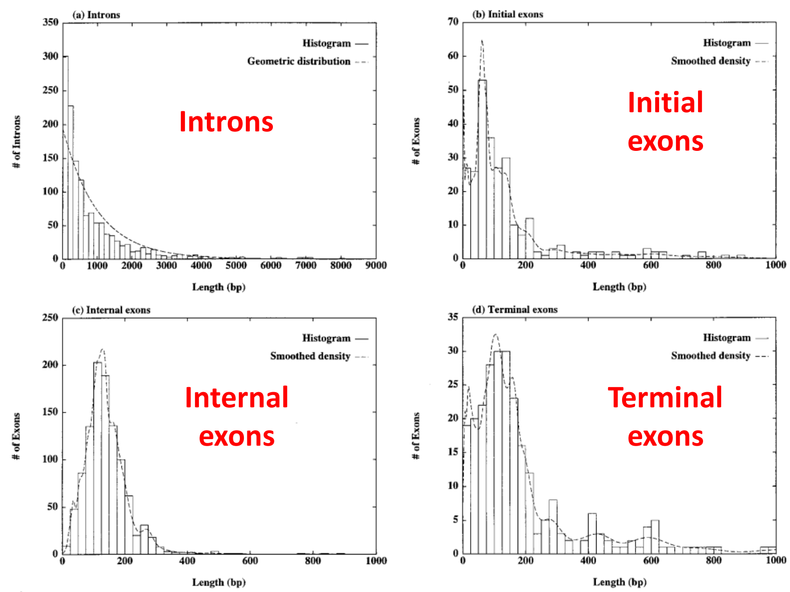
Zoomed in on the forward strand model…



J. Mol. Biol. (1997) 268, 78–94

22

Introns and different flavors of exons all have different typical lengths



J. Mol. Biol. (1997) **268**, 78–94

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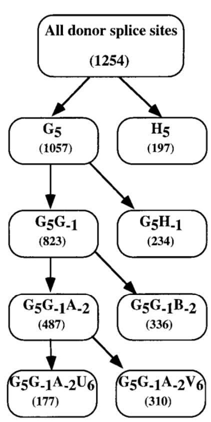
Taking into account donor splice sites

Pos	A%	C%	G%	U%
-3	33	36	19	13
-2	56	15	15	15
-1	9	4	78	9
+3	44	3	51	3
+4	75	4	13	9
+6	14	18	19	49
-3	34	37	18	11
-2	59	10	15	16
+3	40	4	53	3
+4	70	4	16	10
+6	17	21	21	42
-3	37	42	18	3
+3	39	5	51	5
+4	62	5	22	11
+6	19	20	25	36
-3	32	40	23	5
+3	27	4	59	10
+4	51	5	25	19



Pos	A%	C%	G%	U%
-3	35	44	16	6
-2	85	4	7	5
-1	2	1	97	0
+3	81	3	15	2
+4	51	28	9	12
+6	22	20	30	28
-3	29	31	21	18
-2	43	30	17	11
+3	56	0	43	0
+4	93	2	3	3
+6	5	10	10	76
-3	29	30	18	23
+3	42	1	56	1
+4	80	4	8	8
+6	14	21	16	49
-3	39	43	15	2
+3	46	6	46	3
+4	69	5	20	7

All sites: ---------- **Position** ----------

	Base	**-3**	**-2**	**-1**	**+1**	**+2**	**+3**	**+4**	**+5**	**+6**	
	A%	**33**	**60**	8	0	0	**49**	**71**	6	15	
	C%	**37**	13	4	0	0	3	7	5	19	
	G%	18	14	**81**	**100**	0	**45**	12	**84**	20	
	U%	12	13	7	0	**100**	3	9	5	**46**	
U1 snRNA:	**3'**	**G**	**U**	**C**	**C**	**A**	**U**	**U**	**C**	**A**	**5'**

J. Mol. Biol. (1997) **268**, 78–94

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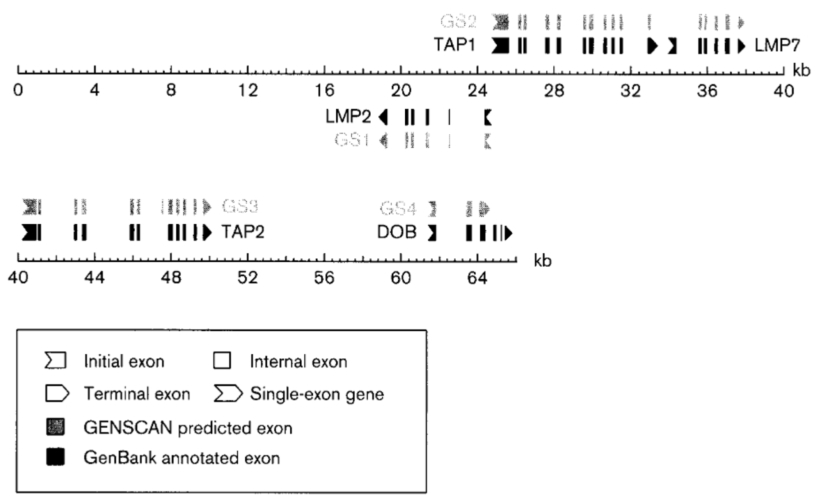
An example of an annotated gene…



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

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How well do these programs work?
We can measure how well an algorithm works using these:

True answer:

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

Specificity = TP / (TP + FP)

Sensitivity = TP / (TP + FN)

Nature Reviews Genetics 13:329-342 (2012)

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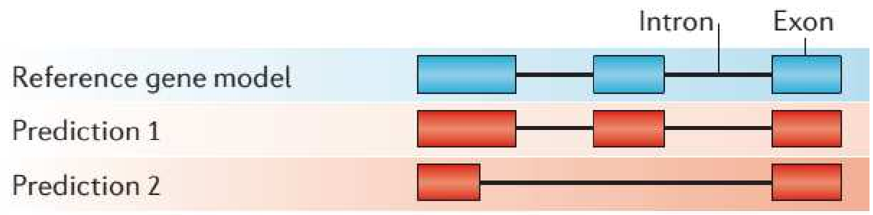
How well do these programs work?
How good are our current gene models?



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

Nature Reviews Genetics 13:329-342 (2012)

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GENSCAN, when it was first developed….

		Accuracy per base		Accuracy per exon	
Program	Sequences	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

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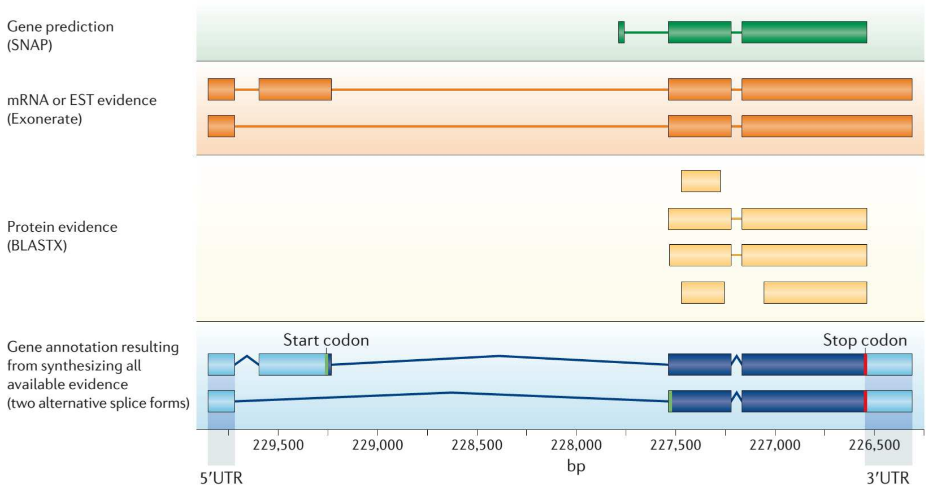
In general, we can do better with more data, such as mRNA and conservation

Box 2 | **Gene prediction versus gene annotation**



Nature Reviews Genetics 13:329-342 (2012)

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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"

Table 1. Participating Groups and Associated Annotation Categories

	Program name	Gene finding	Promoter recognition	EST/c DNA alignment	Protein similarity	Repeat	Gene function
Mural et al. Oakridge, US	GRAIL	X		X			X
Parra et al. Barcelona, ES	GeneID	X					
Krogh Copenhagen, DK	HMMGene	X					
Henikoff et al. Seattle, US	BLOCKS				X		X
Solovyev et al. Sanger, UK	FGenes	X					
Gaasterland et al. Rockefeller, US	MAGPIE	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	Genie	X	X				

Genome Research 10:483–501 (2000)

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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 **Assessment**
Project

= scientists f SP") to
predict gene are them to
experimenta

18 groups
36 programs

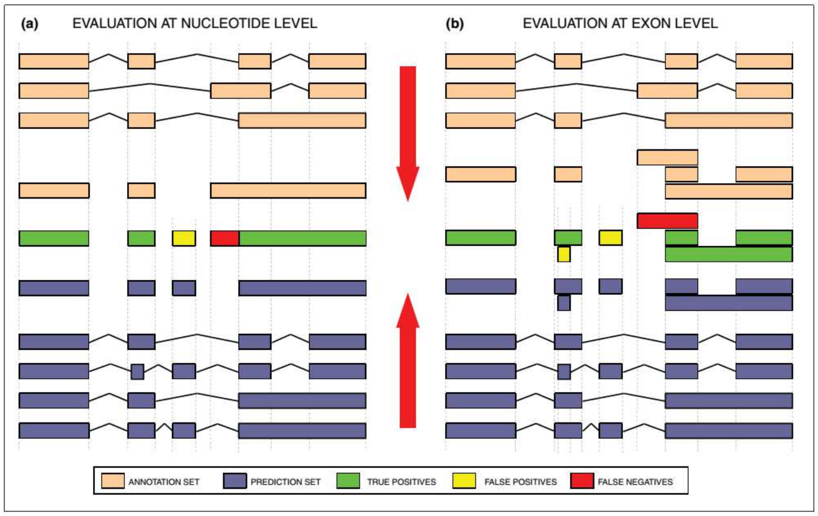
We discussed these earlier

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-abinit)			
3 (AUGUSTUS-EST)			
4 (AUGUSTUS-dual)			
1	FGENESH++	Softberry Inc.	[56]
1	JIGSAW	The Institute for Genomic Research (TIGR)	[59]
1 (PAIRAGON-any)	PAIRAGON and NSCAN_EST	Washington University, Saint Louis (WUSTL)	[57]
3 (PAIRAGON+NSCAN_EST)			
2	GENEMARK.hmm	Georgia Institute of Technology	[60]
2	GENEZILLA	TIGR	[81]
3	ACEVIEW	National Center for Biotechnology Information (NCBI)	[52]
3	ENSEMBL	The Wellcome Trust Sanger Institute (WTSI) and European Bioinformatics Institute (EBI)	[64]
3	EXOGEAN	Ecole Normale Superieure, Paris	[62]
3	EXONHUNTER	University of Waterloo	[63]
4	ACESCAN*	Salk Institute	[82]
4	DOGFISH-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	Mèdica, Barcelona	
6	ASPIC†	Università degli Studi di Milano	[83]
6 (AUGUSTUS-exon)	AUGUSTUS	Georg-August-Universität, Göttingen	[58]
6	CSTMINER‡	Università degli Studi di Milano	[84]
6	DOGFISH-C-E§	WTSI	[67]
6	SPIDA	EBI	[85]
6	UNCOVER§	Duke University	[86]
1	CCDSGene	UCSC tracks [7]	[55]
1	KNOWNGene		[54]
1	REFSEQ (REFGene)		[4]
2	GENEID		[19]
2	GENSCAN		[18]
3	ACEMBLY		[52]
3	ECGene		[53]
3	ENSEMBL (ENSGene)		[6]
3	MGCGene		[5]
4	SGP2		[9]
4	TWINSCAN		[12,13]
-	CODING 20050607	GENCODE annotation	[33]
-	GENES 20050607		

Genome **Biology** 2006, **7(Suppl 1):S2**



Genome Biology 2006, 7(Suppl 1):S2

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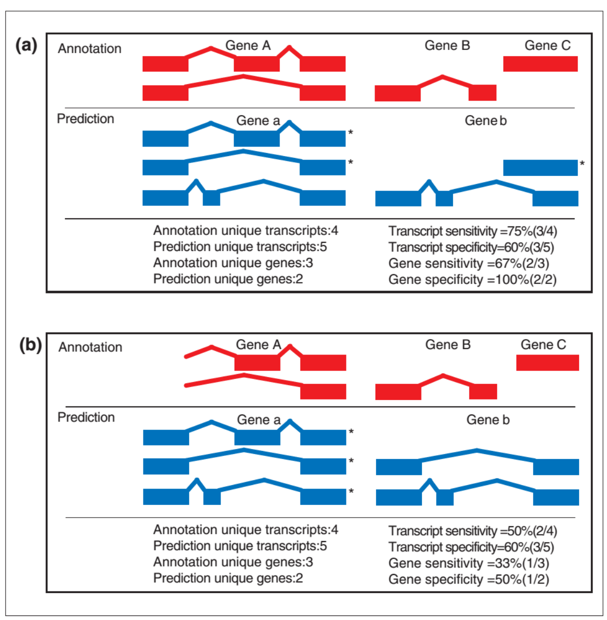
Transcripts vs. genes



Genome Biology 2006, 7(Suppl 1):S2

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In the year *2006*

So how did they do?

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

Genome **Biology** 2006, **7(Suppl 1):**S2

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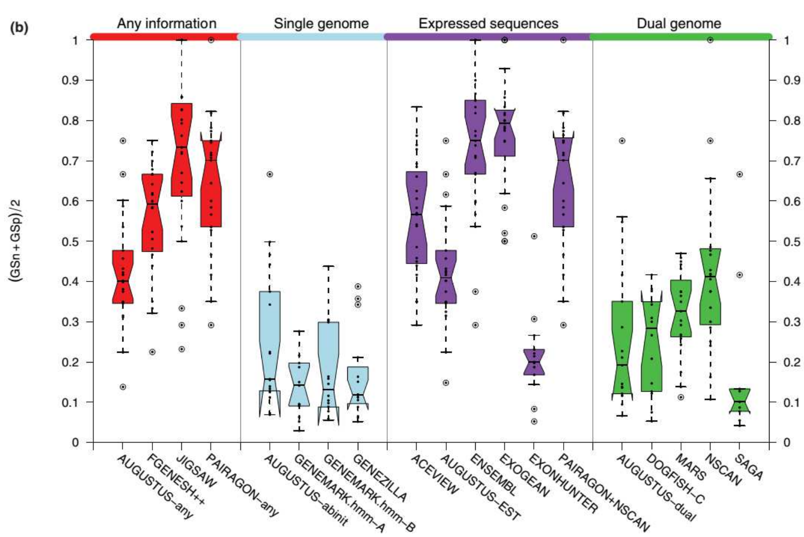
In the year *2006*

At the gene level, most genes have errors



Genome **Biology** 2006, **7(Suppl 1):**S2

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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

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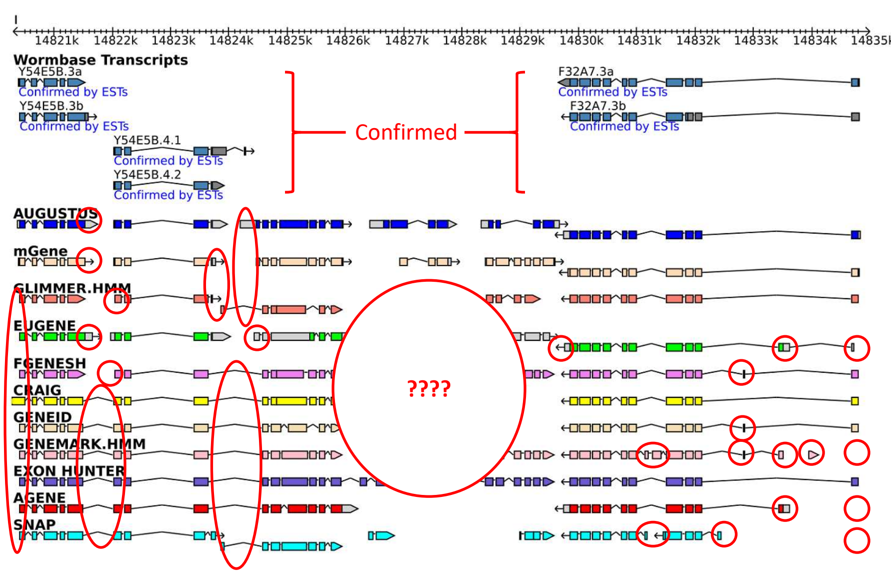
For example:

In the year *2008*



BMC Bioinformatics 2008, **9**:549

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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

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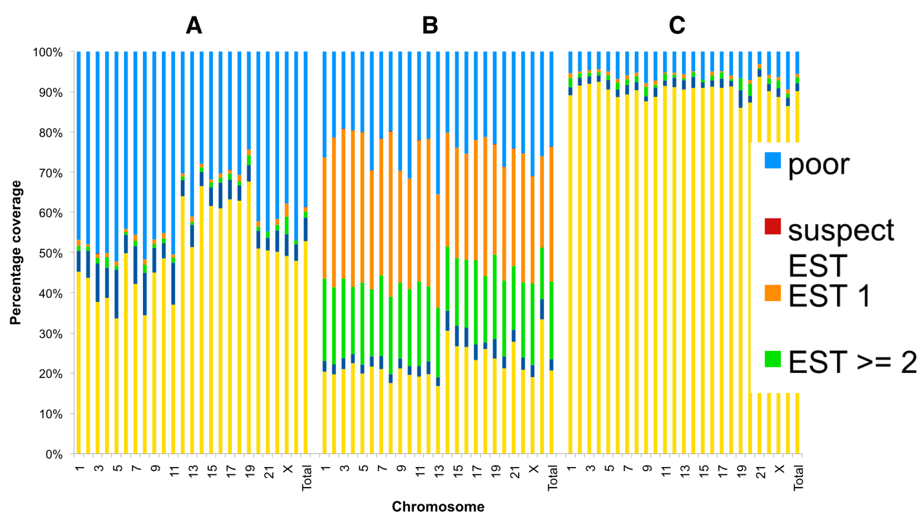
How well do we know the genes now?

In the year *2012*

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



23,855 transcripts 89,669 transcripts 22,535 transcripts

Genome Res. 2012 22: 1760-1774

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How well do we know the genes now?

In the year *2015*

The bottom line:

- **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**

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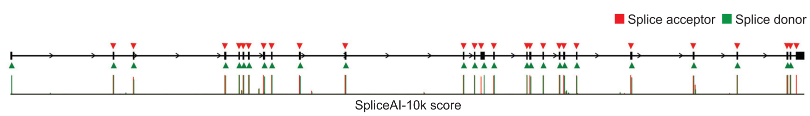
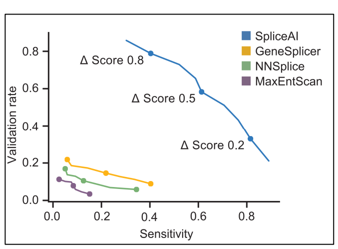
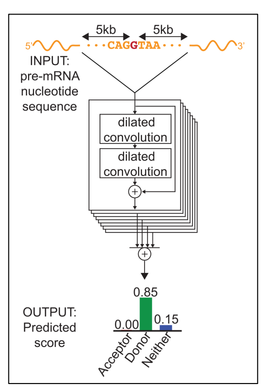
But the algorithms are nonetheless getting better, e.g. new advances (at last!) in predicting splice sites using deep learning

In the year *2019*







Predicting Splicing from Primary Sequence with Deep Learning

Kishore Jaganathan,[1,6] Sofia Kyriazopoulou Panagiotopoulou,[1,6] Jeremy F. McRae,[1,6] Siavash Fazel Darbandi,[2] David Knowles,[3] Yang I. Li,[3] Jack A. Kosmicki,[1,4] Juan Arbelaez,[2] Wenwu Cui,[1] Grace B. Schwartz,[2] Eric D. Chow,[5] Efstathios Kanterakis,[1] Hong Gao,[1] Amirali Kia,[1] Serafim Batzoglou,[1] Stephan J. Sanders,[2] and Kyle Kai-How Farh[1,7,*]
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https://doi.org/10.1016/j.cell.2018.12.015

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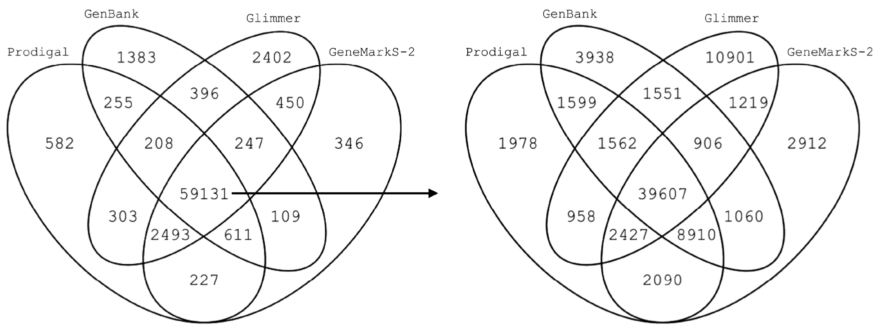
What about the current state of prokaryote gene models?

Here's the overlap in gene predictions from 4 algs on 20 test strains:



Coding regions agree (shared stop)

Starts and stops agree

AssessORF: combining evolutionary conservation and proteomics to assess prokaryotic gene predictions

Deepank R. Korandla [1,2,3], Jacob M. Wozniak[4,5], Anaamika Campeau[4,5], David J. Gonzalez[4,5] and Erik S. Wright [3,*]

Bioinformatics, 36(4), 2020, 1022–1029

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What about the current state of prokaryote gene models?

- **"We applied AssessORF to compare gene predictions offered by GenBank, GeneMarkS-2, Glimmer and Prodigal on genomes spanning the prokaryotic tree of life.**
- **Gene predictions were 88–95% in agreement with the available evidence, with Glimmer performing the worst but no clear winner.**
- ***All programs were biased towards selecting start codons that were upstream of the actual start."***

Bioinformatics, 36(4), 2020, 1022–1029

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In practice, gene finding and genome annotation combines all lines of evidence, e.g. as for the frog genome:

Align frog RNA sequencing data (ESTs and cDNA) & BLAST genes from other animals vs. frog assembly → **Define gene segments**

Integrate *ab initio* gene predictions & BLAST hits using Fgenesh and GenomeScan (= GenScan successor, *Genome Research* 11:803 (2001))

↓

Refine with RNA-seq and H3K4me3 data

↓

Refine vs final genome assembly

↓

Manually curate 412 gene models
→ Estimate 96% accuracy overall

Session *et al.*, *Nature* 2016
Supplementary Info, pg. 22

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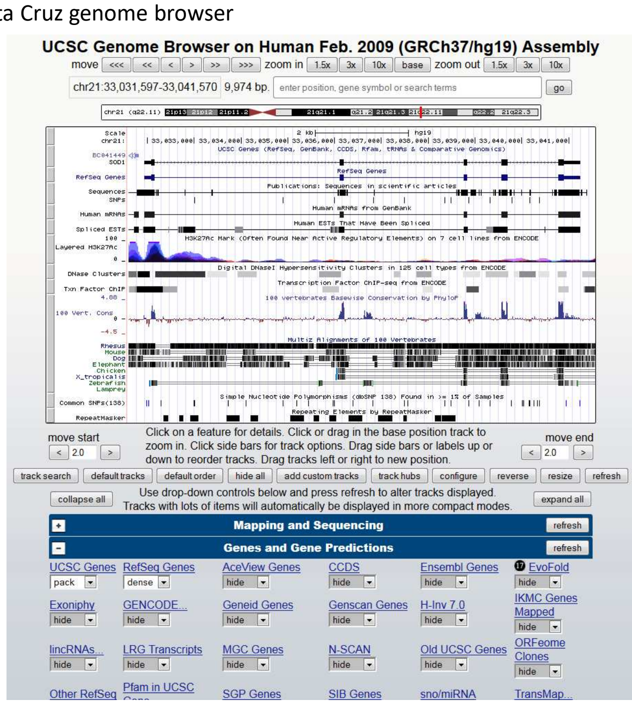
The Univ of California Santa Cruz genome browser



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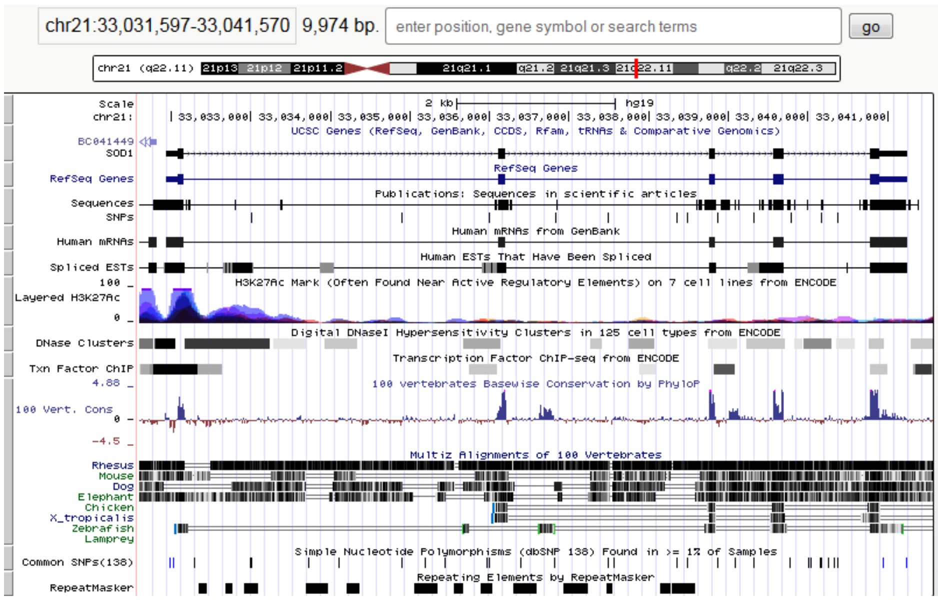
The Univ of California Santa Cruz genome browser



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