

# **Computational identification of structural RNA homologs using Infernal and Rfam**

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National Institutes of Health

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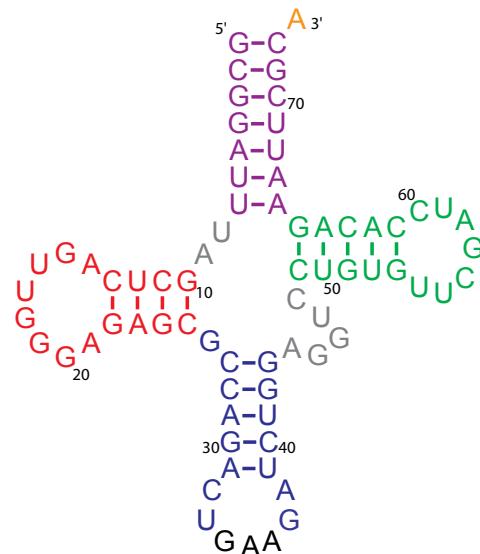
# Many functional RNAs adopt a conserved 3-dimensional structure

Three representations of a transfer RNA:

## Primary sequence

GC<sub>1</sub>GGAUUUAAGCUCAGUUGGG  
AGAGC<sub>2</sub>GCCAGACU<sub>3</sub>GAAGAUC  
UGGAGGUCC<sub>4</sub>UGUGUUCGAUC  
CACAGAAUUCGCA<sub>5</sub>

## Secondary structure



## 3-dimensional structure



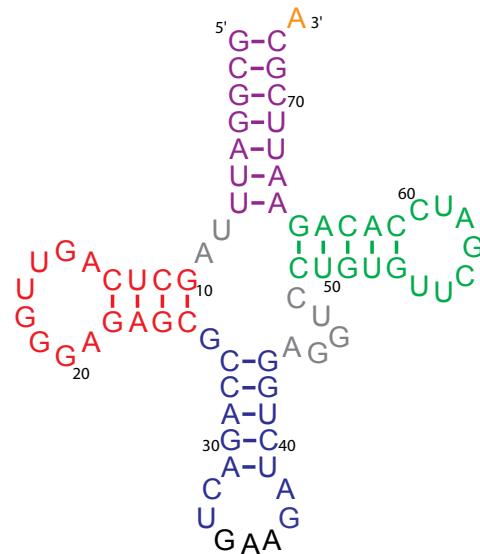
# Many functional RNAs adopt a conserved 3-dimensional structure

Three representations of a transfer RNA:

Primary sequence

GC<sub>1</sub>GGAUUUAGCUCAGUUGGG  
AGAGCGCCAGACUGAAGAUC  
UGGAGGUC<sub>2</sub>CUGUGUUCGAUC  
CACAGAAUUCGCA

Secondary structure



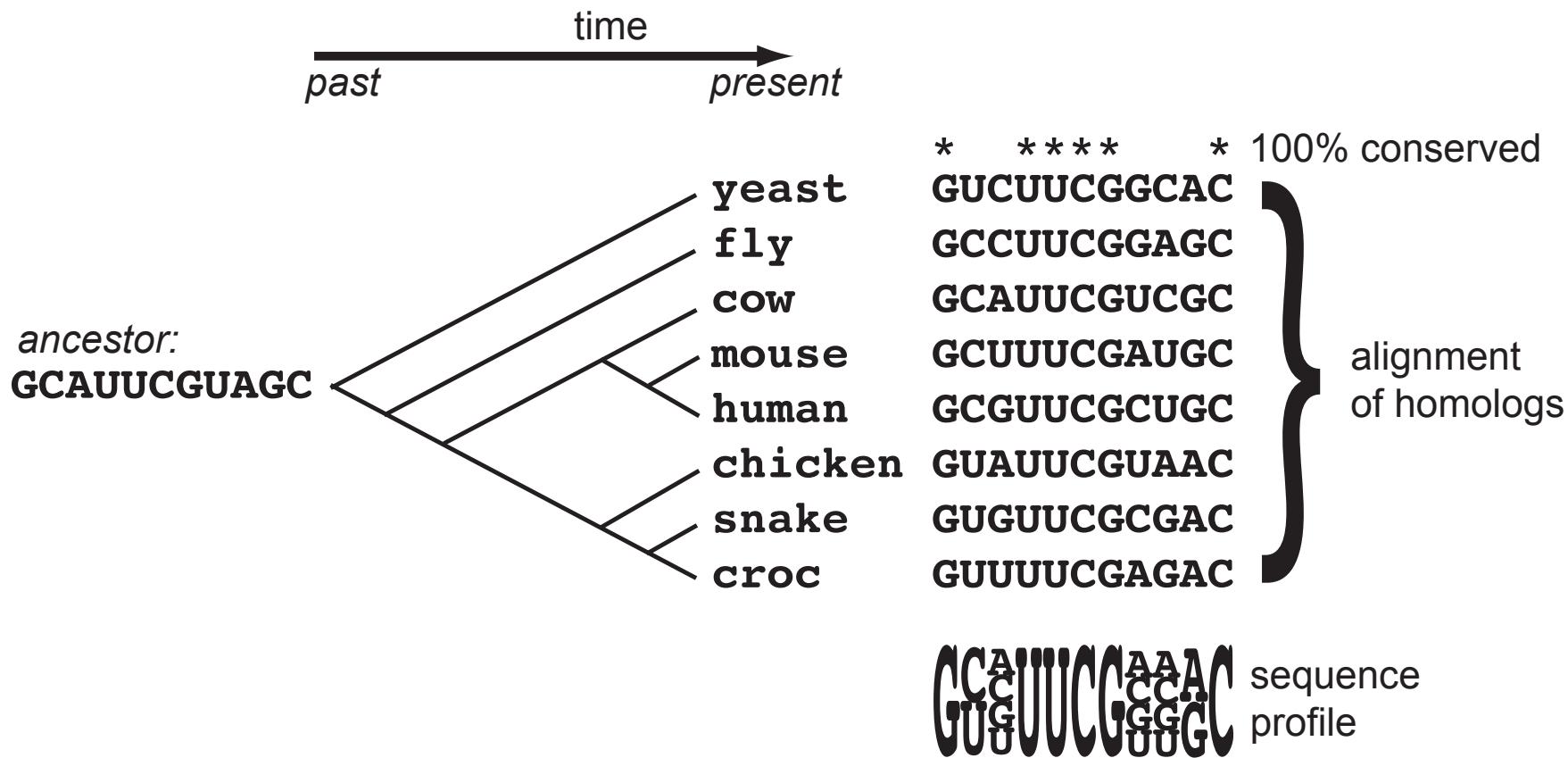
3-dimensional structure



- BLAST: given a single sequence, search genomes for similar sequences.
- BLAST cannot take advantage of:
  - sequence conservation, which varies across the gene
  - secondary structure

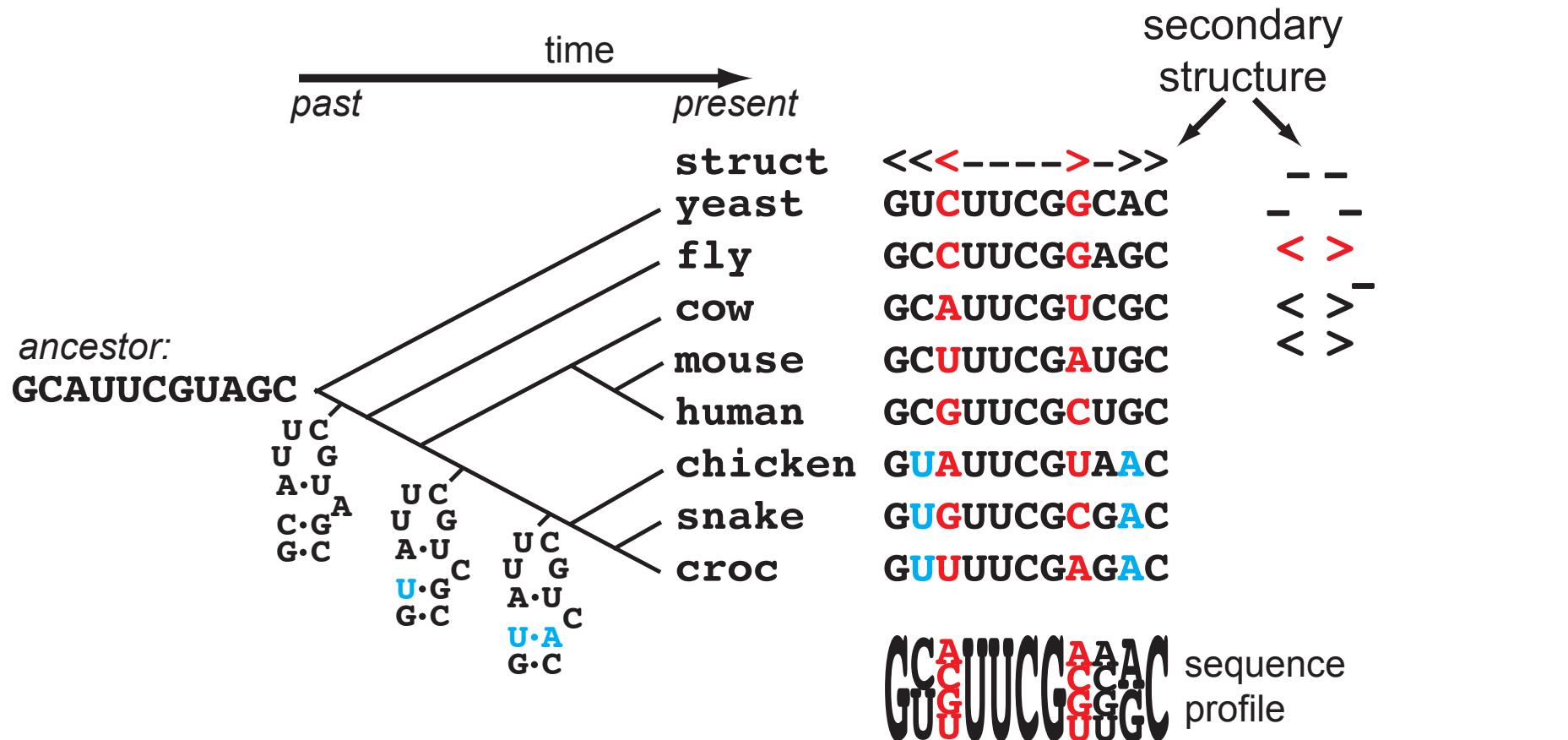
# Sequence conservation provides information for homology searches

Conservation levels vary across alignment columns.

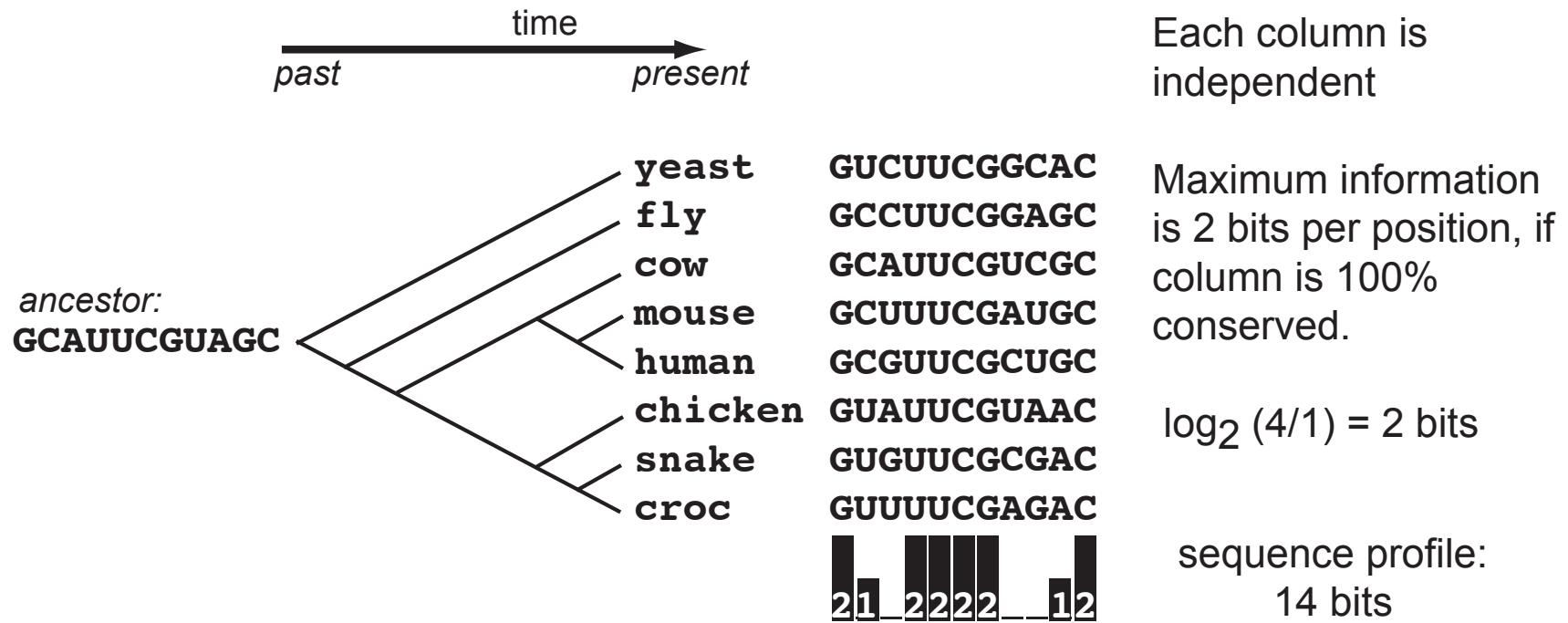


**Structure conservation provides additional information**

Base-paired positions covary  
to maintain Watson-Crick complementarity.

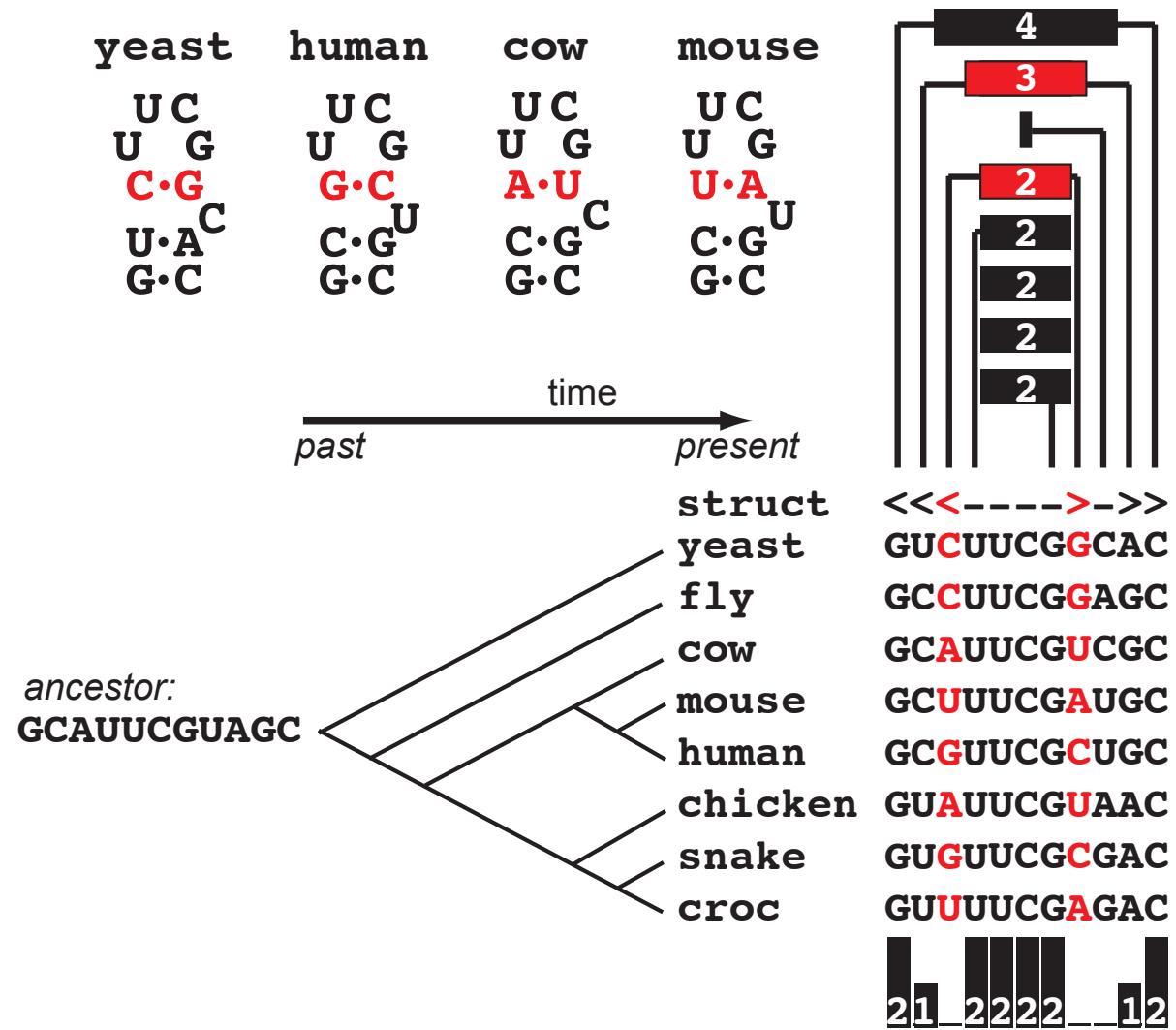


# Amount of information in a profile can be measured in bits



expect a match by chance: 1 in  $2^{14}$  nt  $= \sim 16$  Kb

# Structure contributes additional information from covariation



sequence + **structure**  
profile: 17 bits

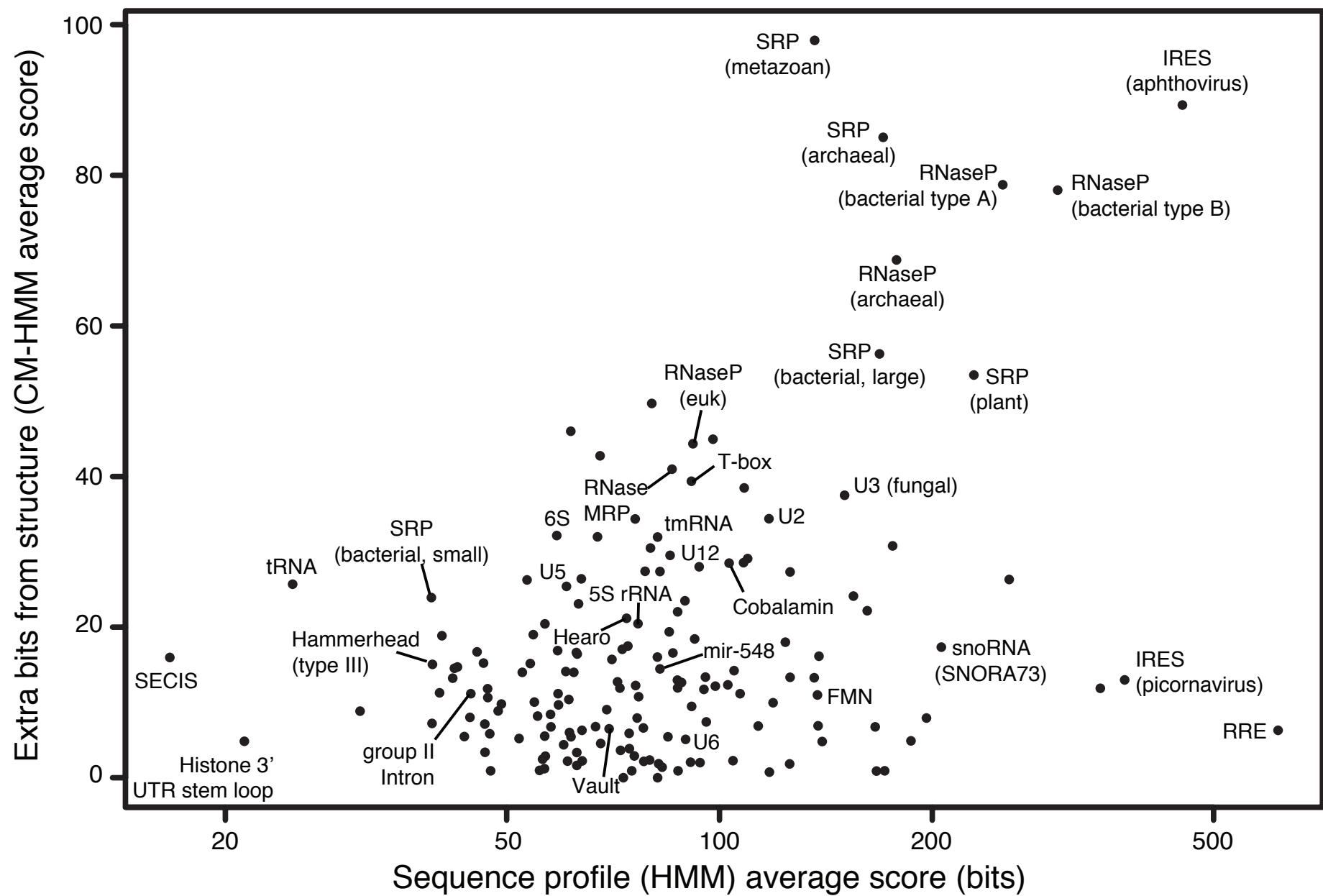
Base-paired columns  
are not independent

Maximum **extra** info:  
2 bits per base pair

$\log_2 (16/4) = 2$  bits

expect a match by chance:  $1 \text{ in } 2^{17} \text{ nt} = \sim 130 \text{ Kb}$   
 reducing expected false positives by  $2^3 = 8\text{-fold}$

# Levels of sequence and structure conservation in RNA families



# Eddy lab software for profile probabilistic models (since 1994)

	sequence profiles	sequence and structure profiles
models	profile HMMs	covariance models (CMs)
software	HMMER	Infernal
main use	proteins, repetitive DNA elements	structural RNAs
databases	Pfam and Dfam (14831 and 1132 entries)	Rfam (2450 families)
performance for RNAs	faster but less accurate	slower but more accurate



<http://hmmer.janelia.org>  
Eddy, SR. PLoS Comp. Biol.,  
7:e1002195, 2011.  
Eddy, SR. PLoS Comp. Biol.,  
4:e1000069, 2008.  
Eddy, SR. Bioinformatics,  
14:755-763, 1998.

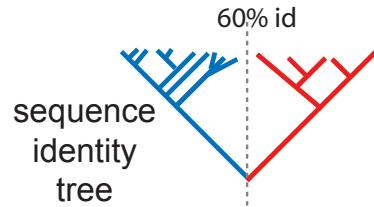
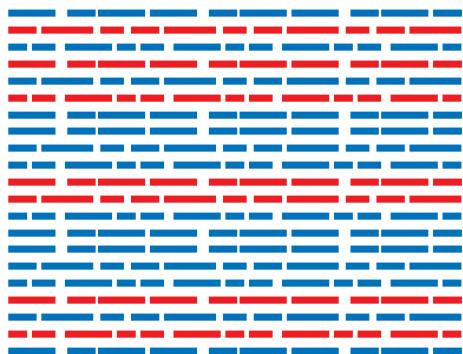


<http://infernal.janelia.org>  
Nawrocki EP, Eddy SR.  
Bioinformatics, 29:  
2487-2489, 2013.  
Eddy SR, Durbin R.  
Nucleic Acids Research,  
22:2079-2088, 1994.

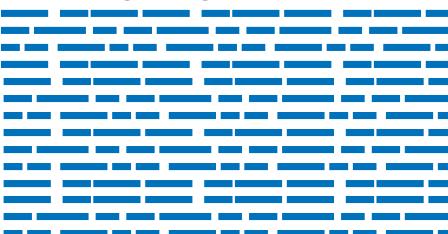
# Is the added complexity worth it?

## RMARK: a challenging internal RNA homology search benchmark

Rfam seed alignment:

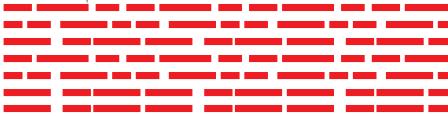


training alignment

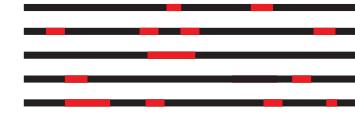


no train/test sequence pair is > 60% identical

test sequences



embed in  
pseudo-genome

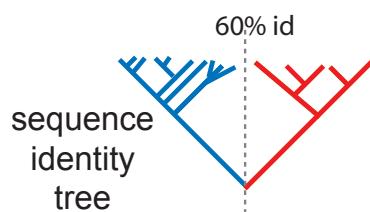
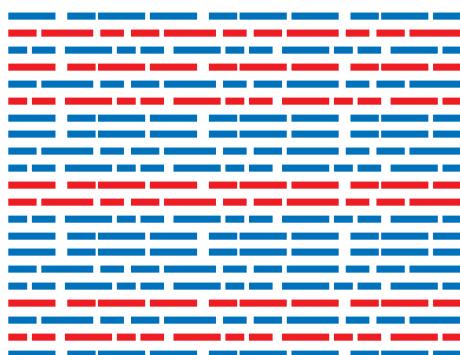


10 1Mb sequences  
with 780 embedded  
test seqs from 106 families

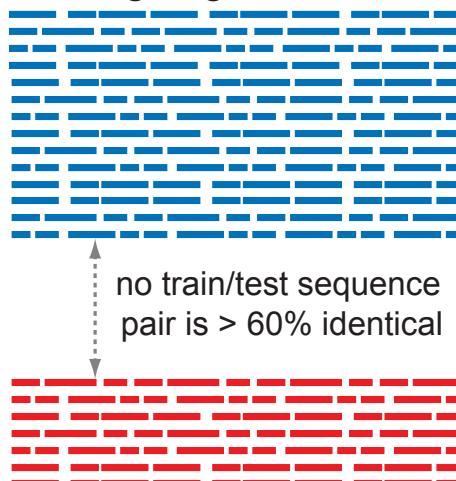
# Is the added complexity worth it?

## RMARK: a challenging internal RNA homology search benchmark

Rfam seed alignment:



training alignment



test sequences

no train/test sequence pair is > 60% identical

embed in  
pseudo-genome



profile  
(CM or HMM)

BLAST

search

E=1E-40 132.53 bits rmark7 OLE 340023 339402 +

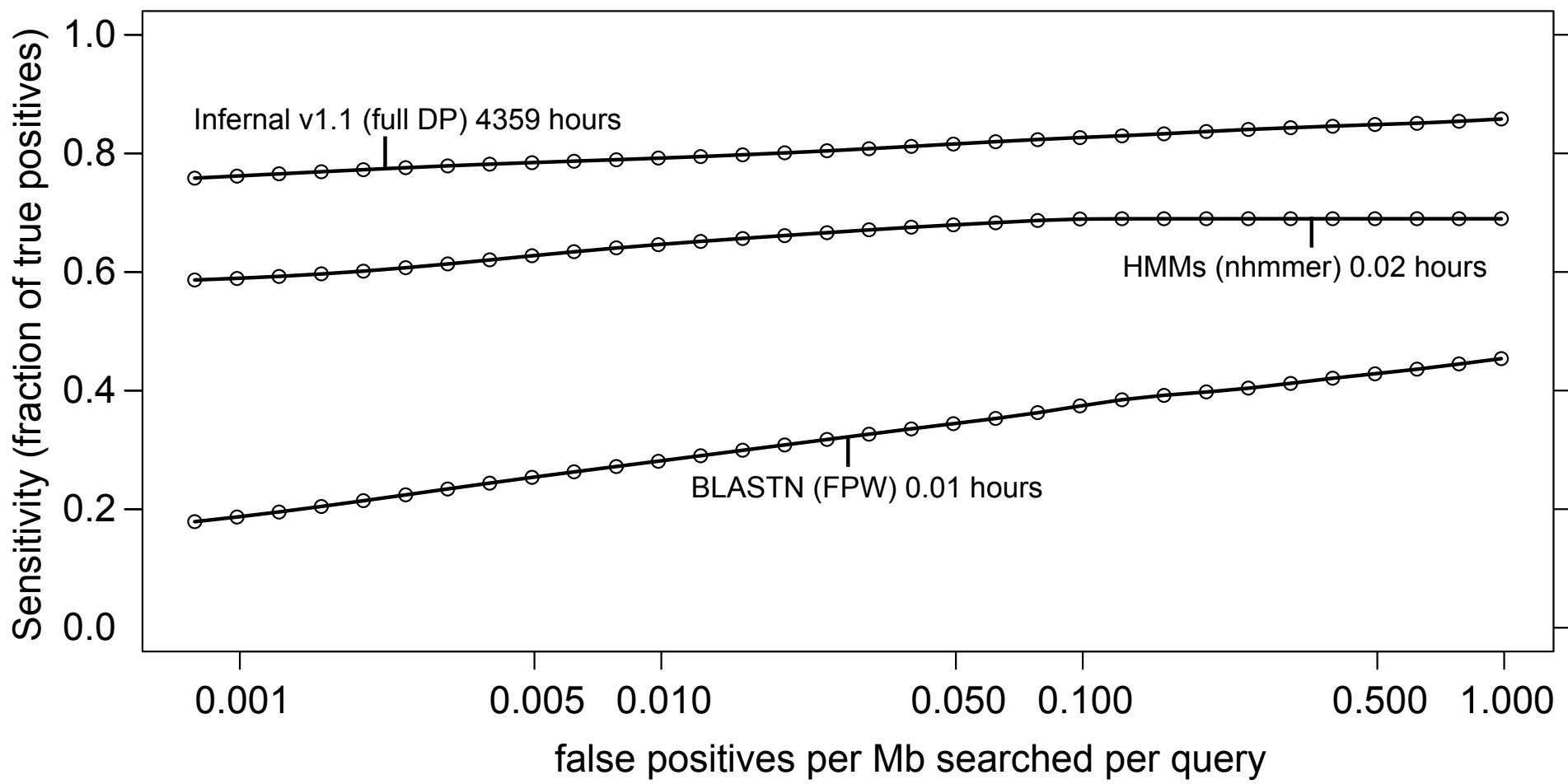
...

E=0.0013 32.3 bits rmark3 6S 10135 10261 +  
E=0.0026 27.6 bits rmark6 tRNA 789278 789466 +  
E= 0.0061 28.3 bits rmark2 Cobalamin 32032 31787 -  
E=0.0231 25.4 bits rmark 6 FALSE 673200 673340 +  
E=0.0670 25.3 bits rmark6 tRNA 789278 789116 -

...

E=103.3 16.4 bits rmark 4 FALSE 783222 782803 -

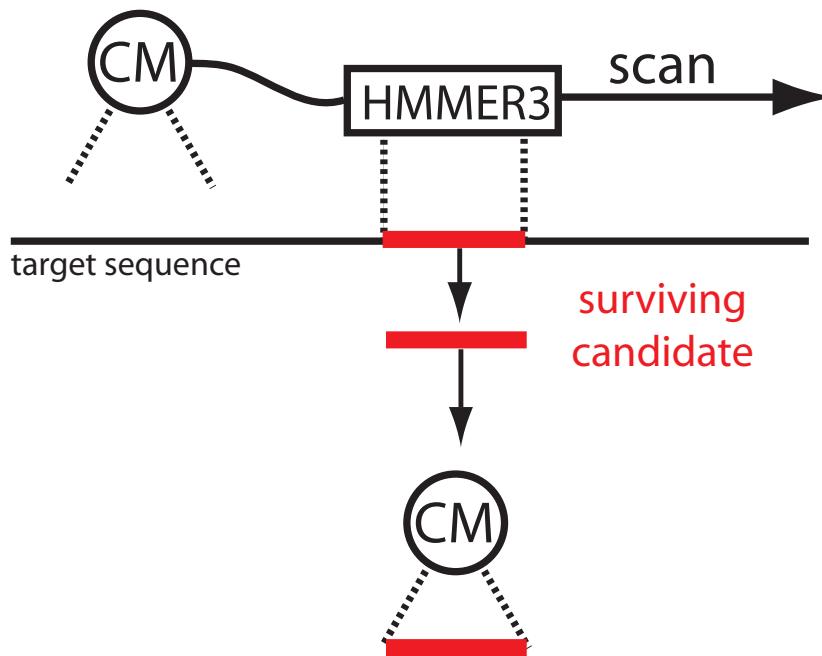
# Infernal outperforms primary-sequence based methods on our benchmark (and others\*, not shown)



Nawrocki EP, Eddy SR. Bioinformatics, 29:2487-2489, 2013.

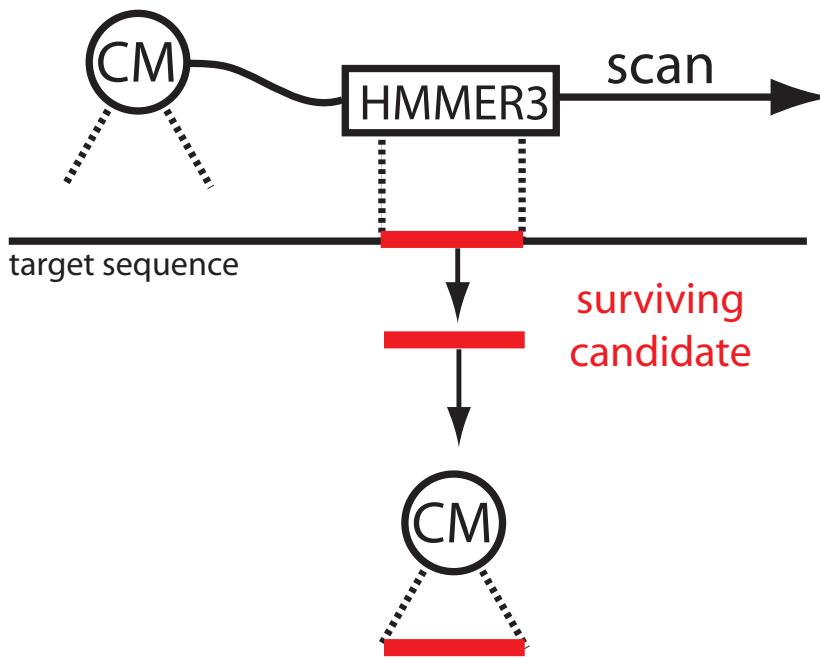
# Filter target database using profile HMMs\*

HMM filter first pass



# Filter target database using profile HMMs\*

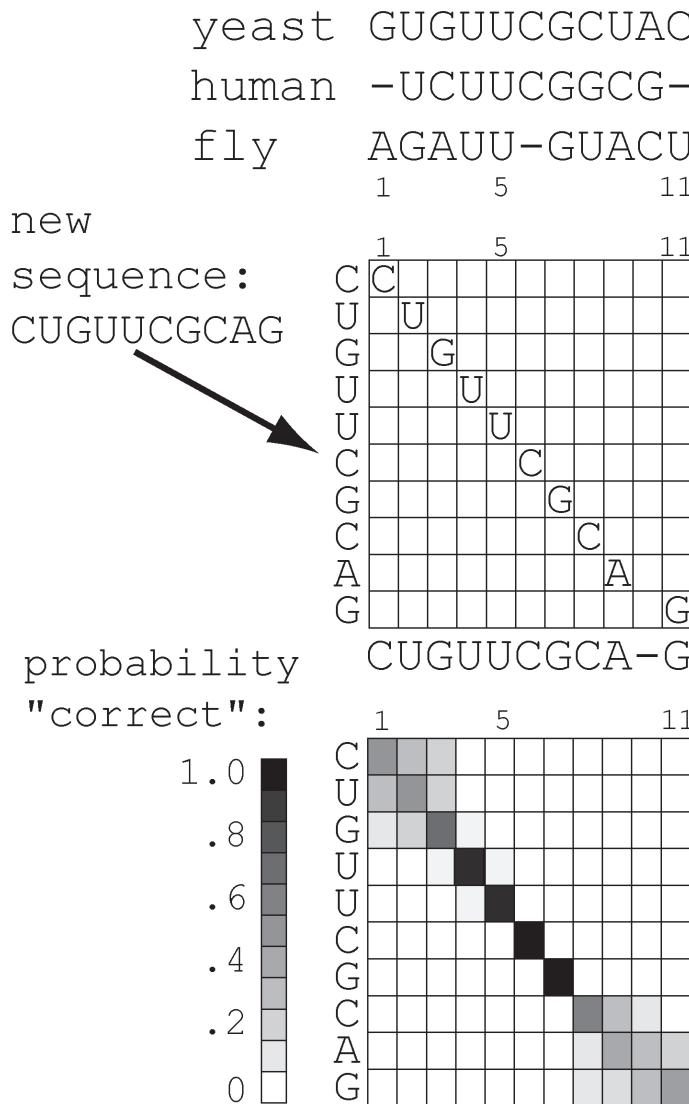
HMM filter first pass



- Even if we filter out 99% of the database (for up to 100X acceleration), searches will still be too slow.
- CM step needs to be accelerated.

\*Weinberg, Ruzzo, RECOMB, 243-251, 2004; Weinberg, Ruzzo, Bioinformatics, 22(1) 35-39 2006.

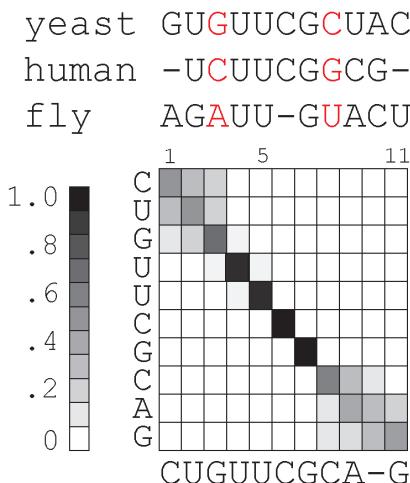
# Accelerating CM alignment step 1: HMM posterior decoding to get confidence estimates



# Accelerating CM alignment step 2: use HMM alignment confidence to constrain CM alignment\*

**HMMs -**

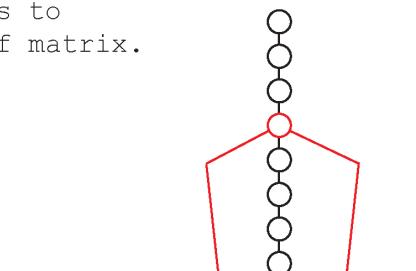
Each column of seed alignment corresponds to a column of matrix.



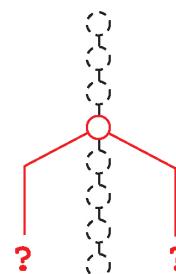
**CMs -**

Each column of seed alignment corresponds to a state.

yeast	human	fly
U C	U C	U
U G	U G	U G
<b>G•C</b>	<b>C•G</b>	<b>A•U</b>
U•A U	U•G C	G•C A
G•C		A•U



struct << <-----> ->>  
 yeast GUGUUCG**C**UAC  
 human -UCUUCGG**G**CG-  
 fly AGAUU-G**U**ACU

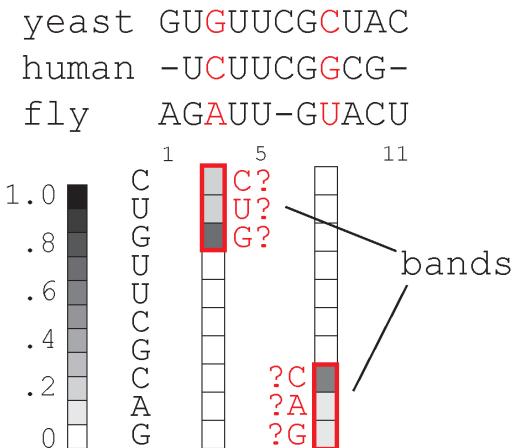


CUGUUCGCAG  
 45 possibilities

# Accelerating CM alignment step 2: use HMM alignment confidence to constrain CM alignment\*

**HMMs -**

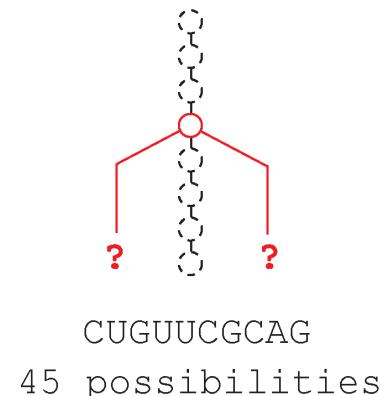
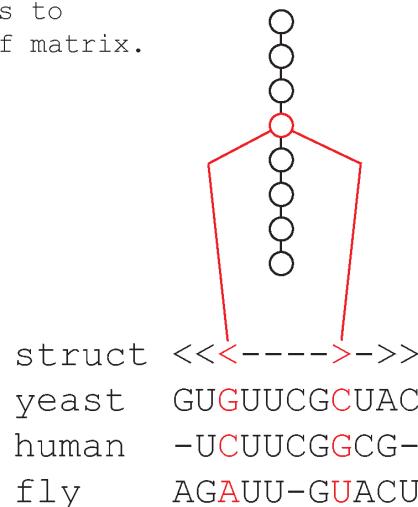
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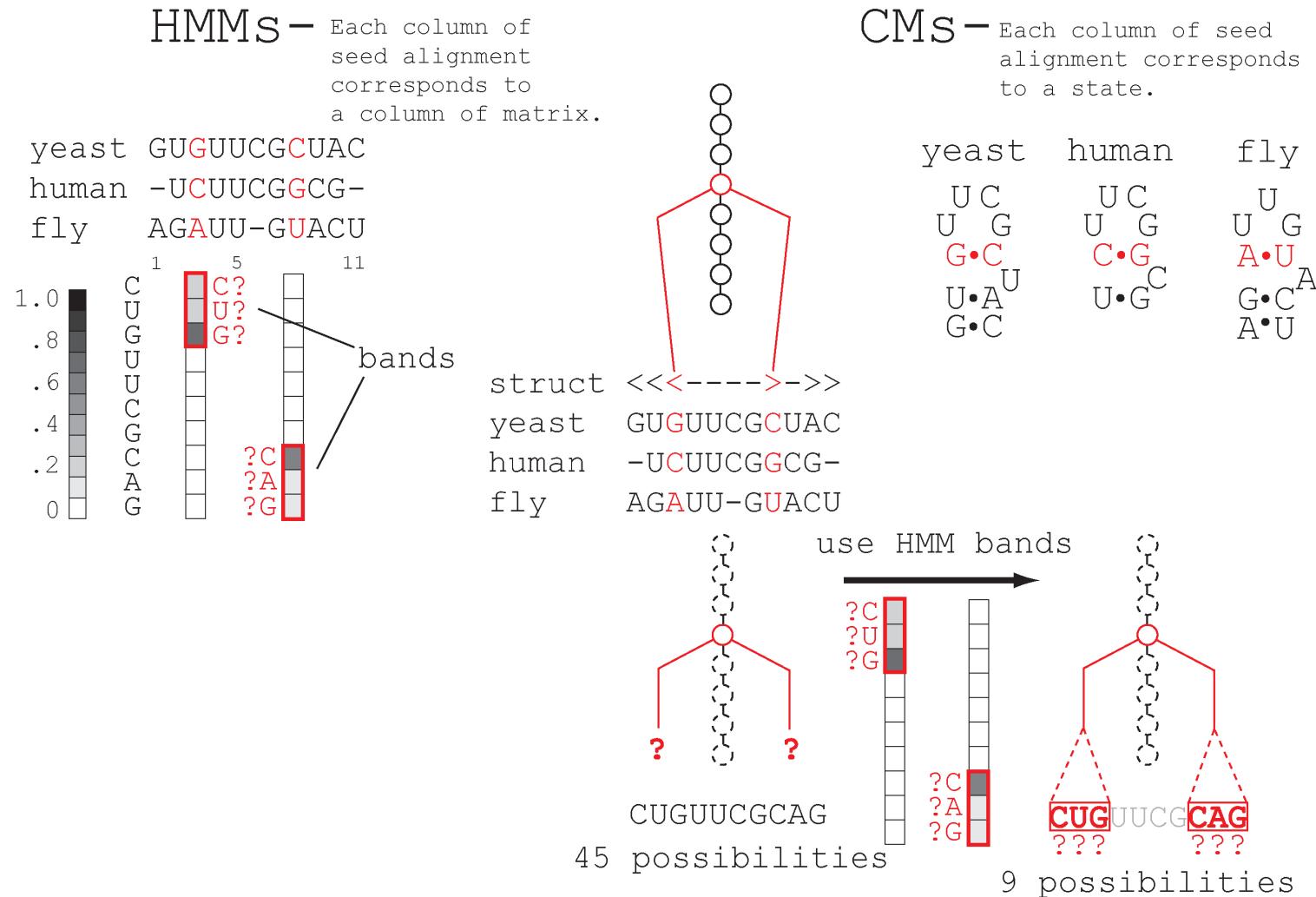
**CMs -**

Each column of seed alignment corresponds to a state.

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U C	U C	U
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<b>G•C</b>	<b>C•G</b>	<b>A•U</b>
U•A U	U•G C	G•C A
G•C		A•U

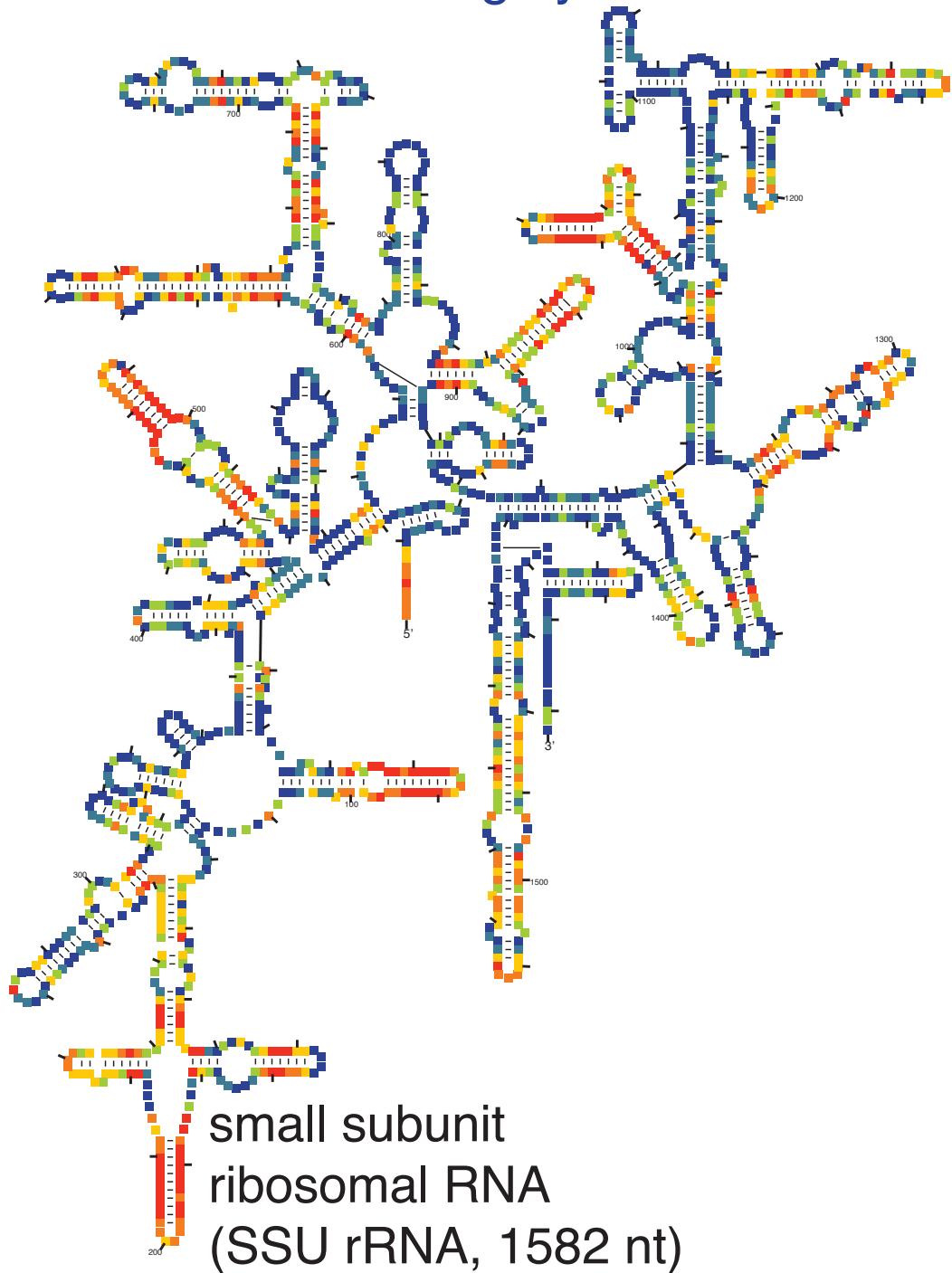


# Accelerating CM alignment step 3: use HMM alignment confidence to constrain CM alignment\*



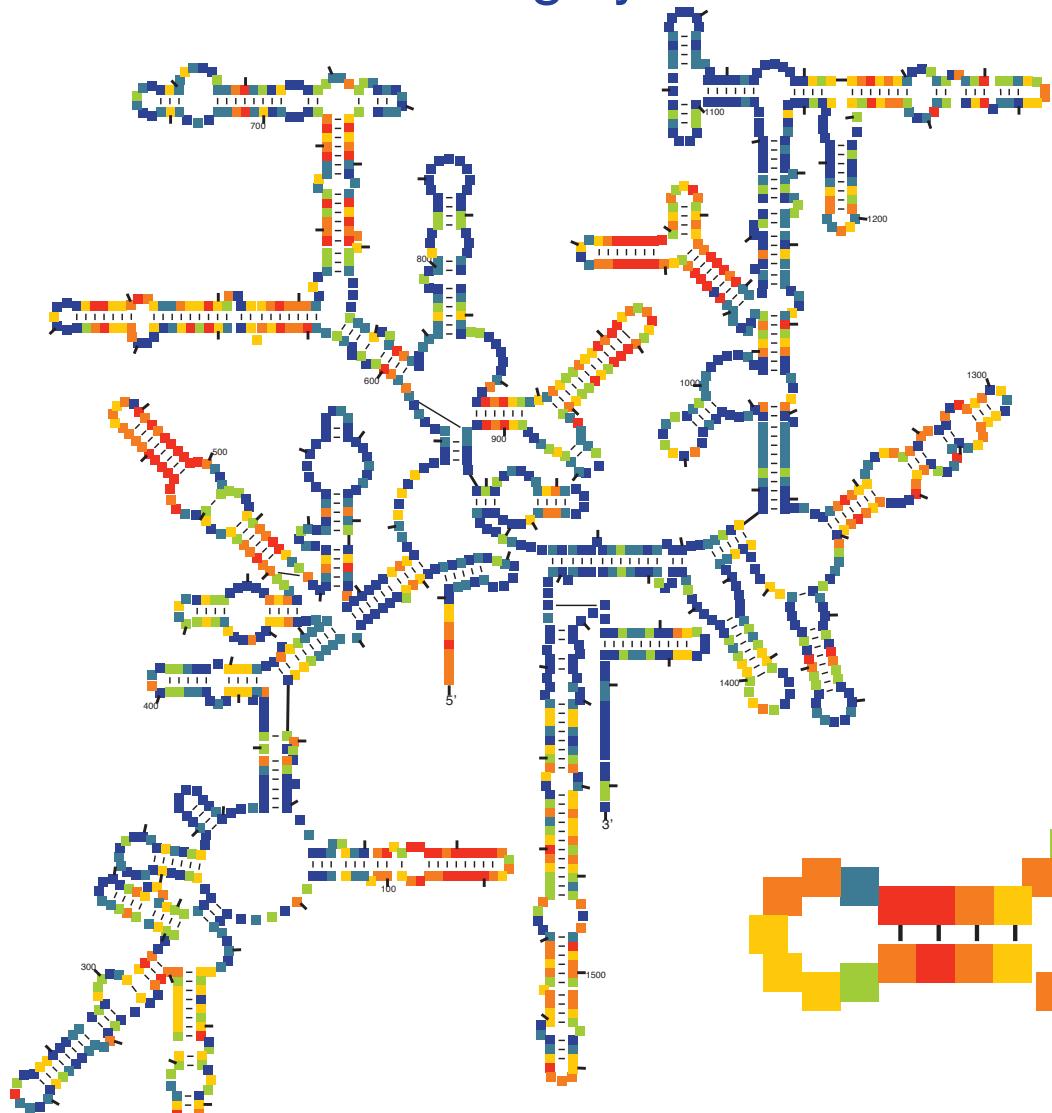
# Sequence conservation per position

blue:highly conserved ..... red: highly variable

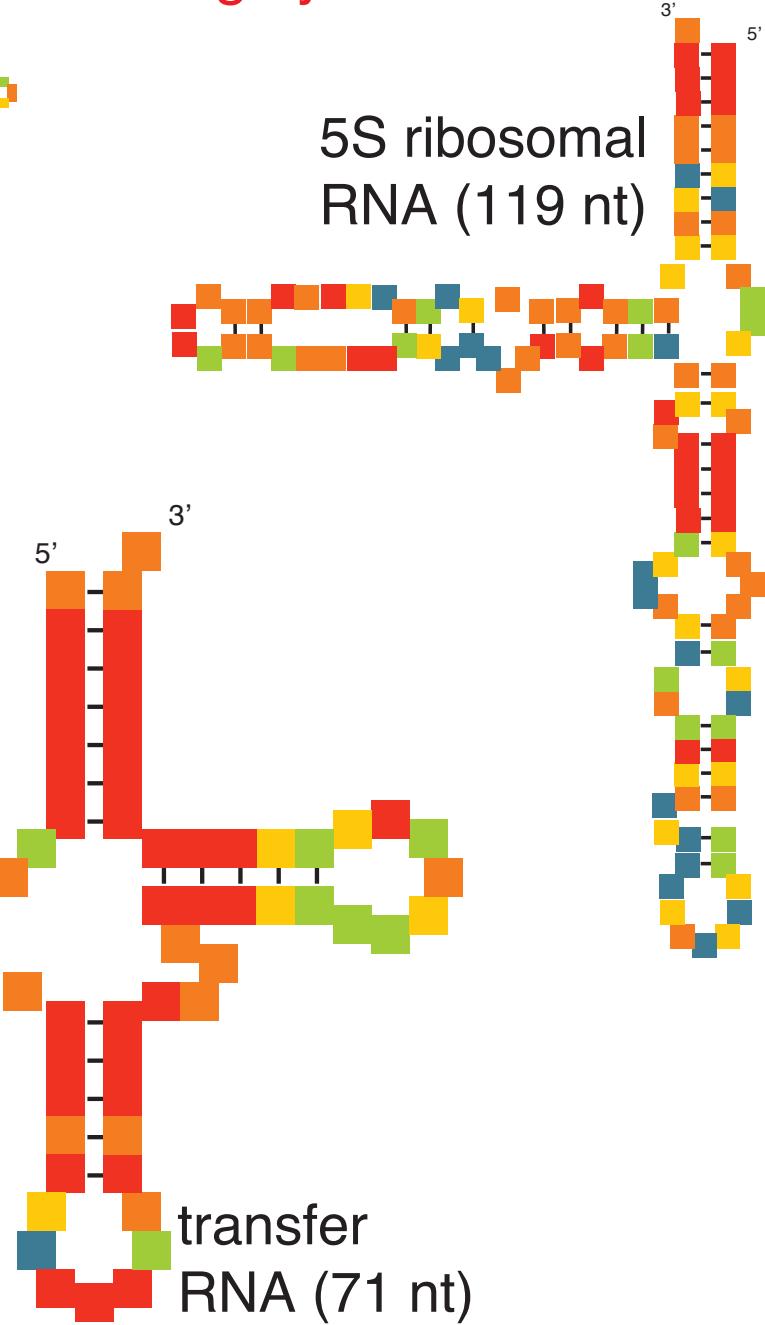


# Sequence conservation per position

blue:highly conserved ..... red: highly variable



small subunit  
ribosomal RNA  
(SSU rRNA, 1582 nt)

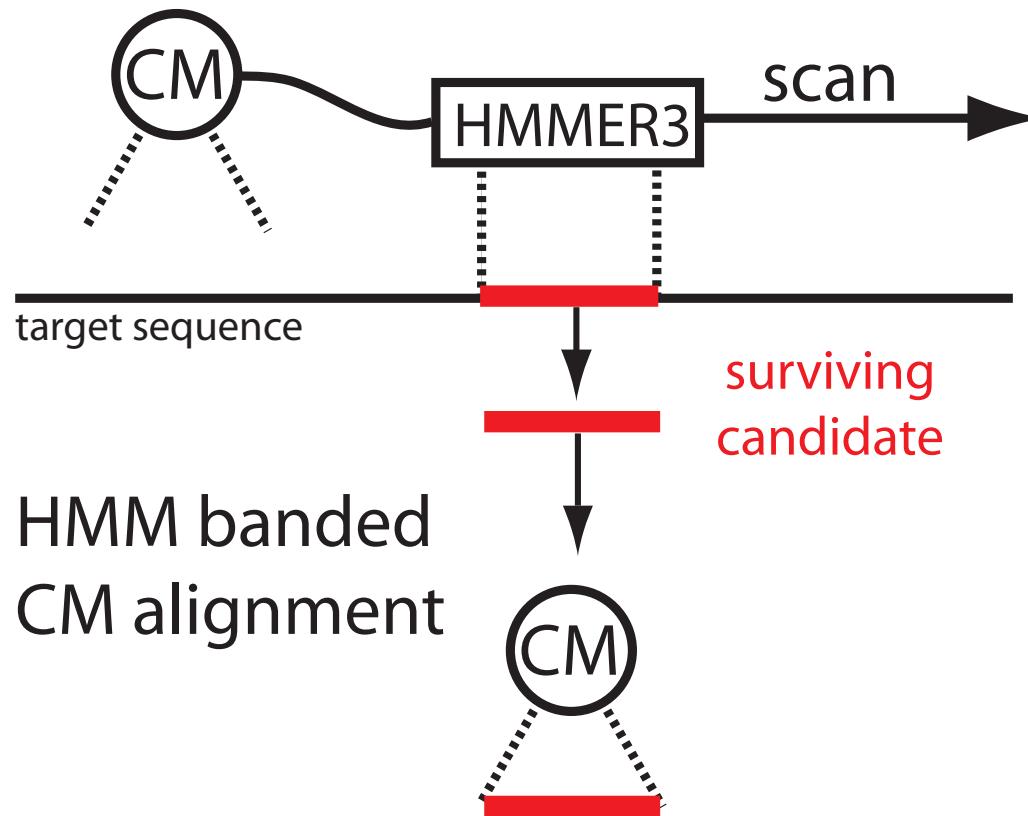


5S ribosomal  
RNA (119 nt)

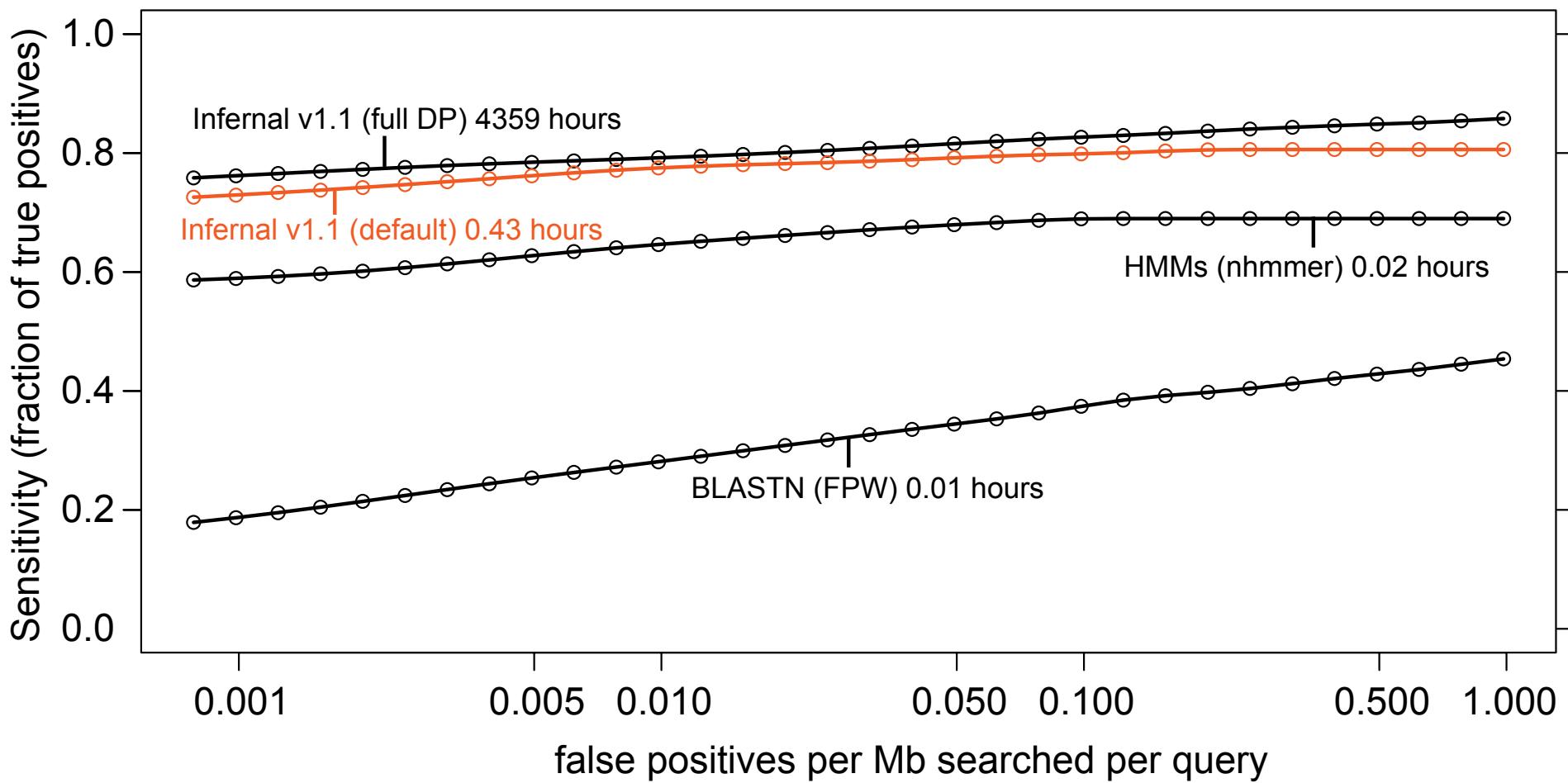
transfer  
RNA (71 nt)

# Use HMMs as filters and to constrain CM alignment

## HMM filter first pass



# HMM-based acceleration makes Infernal 10,000 times faster

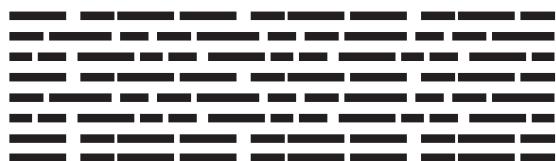


Nawrocki EP, Eddy SR. Bioinformatics, 29:2487-2489, 2013.

## Rfam used BLAST filters from 2003 to 2012

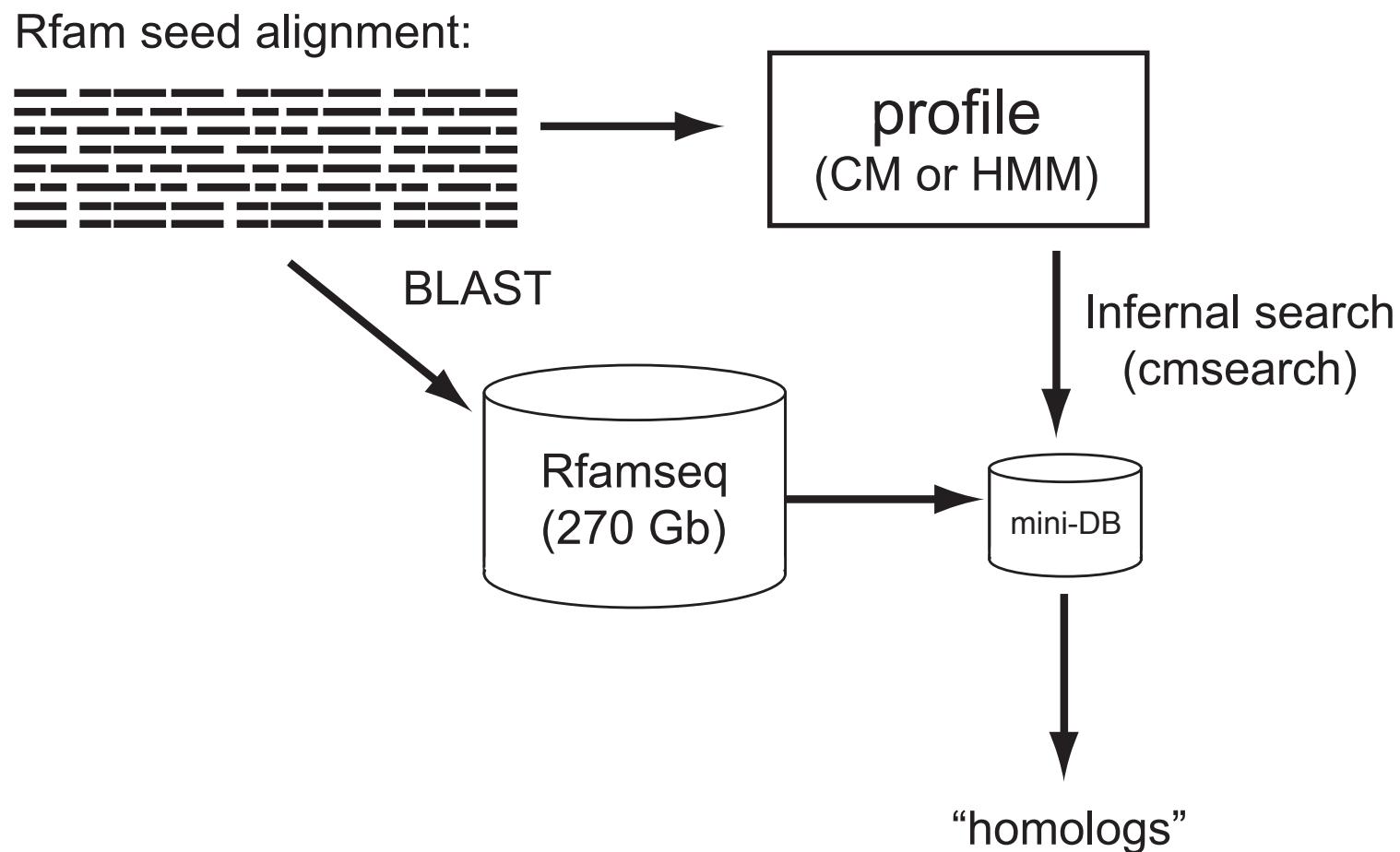
- Rfam includes > 2000 RNA families, each represented by an alignment, CM and set of predicted homologs in a large database (Rfamseq).

Rfam seed alignment:



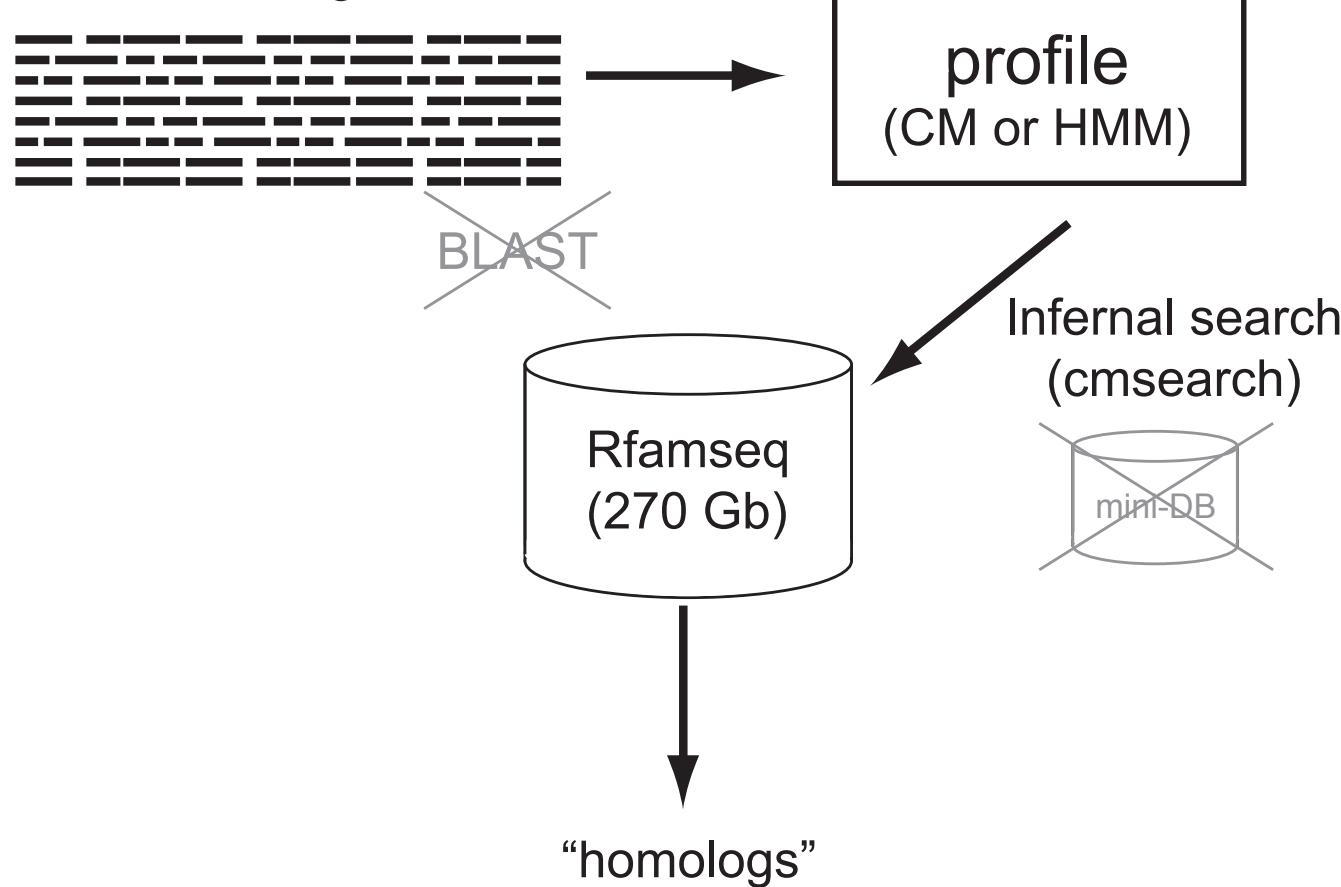
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# Rfam 12.0 (2014)\*, first release without BLAST filtering

Rfam seed alignment:



## Rfam 12.0 (2014)\*, first release without BLAST filtering

Search results against Rfamseq for 200 random families:

strategy	time (h)	# hits	# unique hits
Old (BLAST + Infernal 1.0)	4069.8	179,681	53
New (Infernal 1.1)	4222.2	201,814	22,312

# Infernal 1.1 finds 11,000 new group I intron candidates

**Table 1.** Comparison of the old Rfam 11.0 BLAST and Infernal 1.0 search strategy versus the new Rfam 12.0 Infernal 1.1 search strategy for 15 of 200 randomly chosen families

Accession	Family ID	Length (nt)	#of seed seqs	Time new (h)	Time old (h)	Time (old/new)	New total hits	Old total hits	New unique hits	Old unique hits
Top five families										
RF00028	Intron-gpI	251	12	125.0	357.2	2.8	71 433	60 264	11 175	1
RF00026	U6	104	188	31.2	181.1	5.8	66 517	62 174	4367	14
RF00003	U1	166	100	11.6	64.0	5.5	15 770	14 867	904	1
RF00162	SAM	108	433	8.3	590.0	70.8	4905	4797	108	0
RF00050	FMN	140	144	17.1	169.9	23.9	4381	4306	76	1

# It is now easier to use Rfam/Infernal to annotate your own datasets.

- A bacterial genome takes about 30 minutes for all 2450 models.
- Michael DiCuccio's group is working on adding Rfam/Infernal to the GPIPE pipeline.

**Table 2.** Summary statistics for Rfam-based annotation of RNAs in various genomes and metagenomics data sets

Genome/data set	Size (Mb)	# of hits	# of fams	CPU time (hours)	Mb/hour
<i>Homo sapiens</i>	3099.7	14 508	796	650	4.8
<i>Sus scrofa (pig)</i>	2808.5	6177	625	460	6.1
<i>Drosophila melanogaster</i>	168.7	4321	156	30	5.7
<i>Caenorhabditis elegans</i>	100.3	1022	175	20	5.2
<i>Saccharomyces cerevisiae</i>	12.2	376	96	1.7	7.3
<i>Escherichia coli</i>	4.6	256	112	0.46	10.2
<i>Bacillus subtilis</i>	4.1	211	52	0.57	7.2
<i>Methanocaldococcus jannaschii</i>	1.7	257	18	0.31	5.6
<i>Aquifex aeolicus</i>	1.6	52	7	0.22	7.3
<i>Borrelia burgdorferi</i>	0.9	44	7	0.22	4.1
Human immunodeficiency virus (HIV)	0.01	12	10	0.016	0.63
Human gut microbiome sample (sample ERS167139, 454 sequencing)	166.1	4342	54	22	7.7
Human gut microbiome sample (sample ERS235581, Illumina HiSeq sequencing) (28)	52.9	3159	47	8.5	6.2
Ocean metagenome (sample SRS580499, Illumina genome analyzer)	44.3	6692	59	13	3.5

# Acknowledgements

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Seolkyoung Jung	Jen Daub
Rob Finn	
Jody Clements	
Fred Davis	
Lee Henry	
Michael Farrar	

# Applications of CMs

- homology search/alignment: Infernal, COVE, Rfam\*, Alternal<sup>†</sup>, RNATOPS<sup>‡</sup>
- RNA discovery: CMfinder<sup>§</sup>, Zasha's pipeline(s)<sup>¶</sup>
- structure comparison: CMCompare<sup>||</sup>
- family-specific programs:
  - tRNAscan-SE\*\*,
  - 16S/18S rRNA alignment: SSU-ALIGN<sup>††</sup>
  - bacterial terminator identification: RNIE<sup>‡‡</sup>

\*E. P. Nawrocki, S. W. Burge et. al. NAR, 43:D130-D137, 2015.

†S. Janssen and R. Giegerich. BMC Bioinformatics 2015, 16:178

‡Z. Huang et. al, Bioinformatics, 24(20), 2281-2287, 2008.

§Z. Yao, Z. Weinberg, W. L. Ruzzo, Bioinformatics 2006, 22(4), 445-452.

¶Z. Weinberg, Z et. al. Nucleic acids research, 2007. 35(14), 4809-4819, Z. Weinberg et. al. Genome Biol, 2010. 11(3), R31.

||C. H. zu Siederdissen, and I. L. Hofacker Bioinformatics, 2010. 26(18), i453-i459.

\*\*T. M. Lowe, S. R. Eddy. NAR, 25:955-964, 1997.

††E. P. Nawrocki. PhD Thesis: 2009, Washington University School of Medicine

‡‡P.P. Gardner et. al. Nucleic acids research, 2011, 39(14), 5845-5852.