RNA Search and Motif Discovery

Lecture 9
CSEP 590A
Summer 2006

Outline

Whirlwind tour of ncRNA search & discovery
- Covariance Model Review
- Algorithms for Training
  - "Mutual Information"
- Algorithms for searching
  - Rigorous & heuristic filtering
- Motif discovery

Wrap up

Course Evals

The Human Parts List, circa 2001

3 billion nucleotides, containing:

- 25,000 protein-coding genes (only ~1% of the DNA)
- Messenger RNAs made from each
- Plus a double-handful of other RNA genes

Noncoding RNAs

Dramatic discoveries in last 5 years
- *100s* of new families
- Many roles: Regulation, transport, stability, catalysis, …

1% of DNA codes for protein, but 30% of it is copied into RNA, i.e. ncRNA >> mRNA

"RNA sequence analysis using covariance models"

Eddy & Durbin

Nucleic Acids Research, 1994
vol 22 #11, 2079-2088
(see also, Ch 10 of Durbin *et al.*)

What

A probabilistic model for RNA families
- The "Covariance Model"
- ≈ A Stochastic Context-Free Grammar
- A generalization of a profile HMM

Algorithms for Training
- From aligned or unaligned sequences
- Automates "comparative analysis"
- Complements Nusinov/Zucker RNA folding

Algorithms for searching

Main Results

Very accurate search for tRNA
- (Precursor to tRNAscanSE - current favorite)

Given sufficient data, model construction comparable to, but not quite as good as, human experts

Some quantitative info on importance of pseudoknots and other tertiary features

Probabilistic Model Search

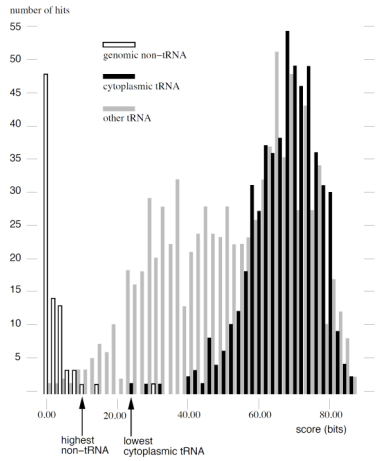
As with HMMs, given a sequence, you calculate likelihood ratio that the model could generate the sequence, vs a background model

You set a score threshold

Anything above threshold → a "hit"

Scoring:
- "Forward" / "Inside" algorithm - sum over all paths
- Viterbi approximation - find single best path
- (Bonus: alignment & structure prediction)

Example: searching for tRNAs



Alignment Quality

Trusted:

```
DF6280    GCGGAUUUAGCUCAGUU GGG AGAGCGCCAGACUGAAG                AUCUGGAG            GUCCUGUGUUCGAUCCACAGAAUUCGCACCA
DF6280G   GCGGAUUUAGCUCAGUU GGG AGAGCGCCAGACUGAAGAAAUACUUCGGUCAAGUUAUCUGGAG            GUCCUGUGUUCGAUCCACAGAAUUCGCA
DD6280    UCCGUGAUAGUUUAAU  GGUCAGAAUGGGCGCUUGUCG                CGUGCCAG            A UCGGGGUUCAAUUCCCCGUCGCGGAGCCA
DX1661    CGCGGGGUUGGAGCAGCCUGGU AGCUGCUUCGGGCUCAUA              ACCCGAAG            GUCGUCGGUUCAAAUCCGGCCCCGCGAACCA
DS6280    GGCAACUUGGCCGAGU  GGUUAAGGCGAAAGAUUAGAA                AUCUUUU  GGGCUUUGCCCG CGCAGGUUCGAGUCCUGCAGUUGUCGCCA
```

U100:

```
DF6280    GCGGAUUUAGCUCAG UUGGGAGAGCGCCAGACU          GA   AG    AUCUGGA          GGUCCUGUGUUCGAUCCACAGAAUUCGCAcca
DF6280G   GCGGAUUUAGCUCAG UUGGGAGAGCGCCAGACUgaagaaauacuUCgguCAaguuAUCUGGA          GGUCCUGUGUUCGAUCCACAGAAUUCGCA
DD6280    UCCGUGAUAGUUUAA UGGUCAGAAUGGGCGCUU          GU   CG    CGUGCCA          GAU CGGGGUUCAAUUCCCCGUCGCGGAGcca
DX1661    CGCGGGGUUGGAGCAGcCUGGUAGCUGCUUCGGGCU        CA   UA    ACCCGAA          GUCGUCGGUUCAAAUCCGGCCCCGCGAAcca
DS6280    GGCAACUUGGCCGAG UGGUUAAGGCGAAAGAUU          AG   AA    AUCUUUUgggcuuugcccG  CGCAGGUUCGAGUCCUGCAGUUGUCGcca
```

ClustalV:

```
DF6280    GCGGAUUUAGCUCAGUUGGGAGAGCGCCAGACUGAAGA                UCUGGAGGUCCUGUGUUCGAUCCACAGAAUUCGCACCA
DF6280G   GCGGAUUUAGCUCAGUUGGGAGAGCGCCAGACUGAAGAAAUACUUCGGUCAAGUUAUCUGGAGGUCCUGUGUUCGAUCCACAGAAUUCGCA
DD6280    UCCGUGAUAGUUUAAU        G GUCAGAAUGG GCG    CUUG  UCGCGUGCC   AGAUCGG GGUUCAAUUCCCCGUCGCGGAGCCA
DX1661    CGCGGGGUUGGAGCAGC       CUGGUAGCUCGUCGGG    CUCA  UAACCGA    AGGUCGUCGGUUCAAAUCCGGCCCCGCGAACCA
DS6280    GGCAACUUGGCCGAGUGGUUAAGGCGAAAGAUU  AGAAAUCUUUUGGGC  UUUGCCCG      CGCAGGUUCGAGUCCUGCAGUUGUCGCCA
```

Comparison to TRNASCAN

Fichant & Burks - best heuristic then
- 97.5% true positive
- 0.37 false positives per MB

CM A1415 (trained on trusted alignment)
- > 99.98% true positives
- <0.2 false positives per MB

Current method-of-choice is "tRNAscanSE", a CM-based scan with heuristic pre-filtering (including TRNASCAN?) for performance reasons.

Slightly different evaluation criteria

Profile Hmm Structure

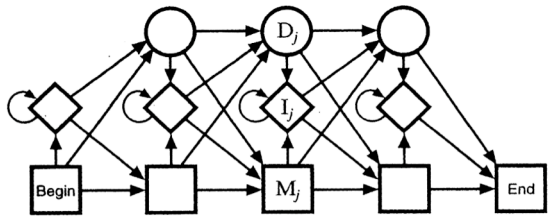


Figure 5.2 *The transition structure of a profile HMM.*

M_j: Match states (20 emission probabilities)
I_j: Insert states (Background emission probabilities)
D_j: Delete states (silent - no emission)

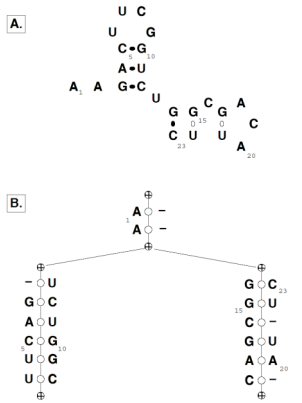
CM Structure

A: Sequence + structure

B: the CM "guide tree"

C: probabilities of letters/ pairs & of indels

Think of each branch being an HMM emitting both sides of a helix (but 3' side emitted in reverse order)

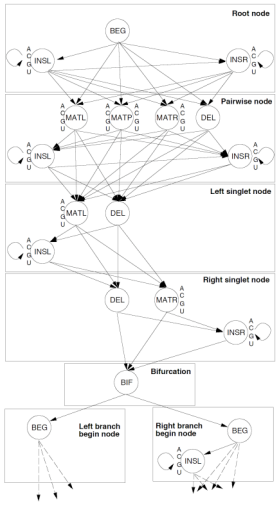


Overall CM Architecture

One box ("node") per node of guide tree

BEG/MATL/INS/DEL just like an HMM

MATP & BIF are the key additions: MATP emits *pairs* of symbols, modeling base-pairs; BIF allows multiple helices



CM Viterbi Alignment

x_i = i^{th} letter of input

x_{ij} = substring $i,...,j$ of input

T_{yz} = $P(\text{transition } y \rightarrow z)$

$E^y_{x_i,x_j}$ = $P(\text{emission of } x_i,x_j \text{ from state } y)$

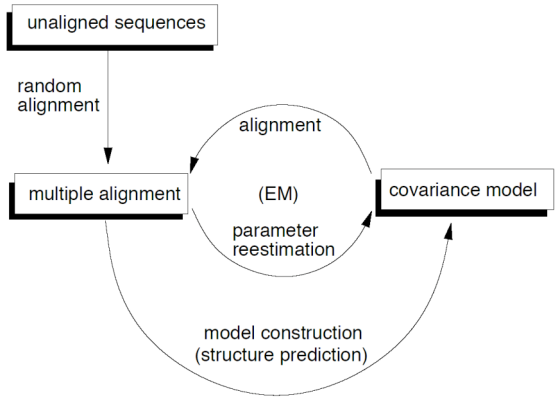
S^y_{ij} = $\max_\pi \log P(x_{ij} \text{ gen'd starting in state } y \text{ via path } \pi)$

$$S^y_{ij} = \max_\pi \log P(x_{ij} \text{ generated starting in state } y \text{ via path } \pi)$$

$$S^y_{ij} = \begin{cases} \max_z [S^z_{i+1,j-1} + \log T_{yz} + \log E^y_{x_i,x_j}] & \text{match pair} \\ \max_z [S^z_{i+1,j} + \log T_{yz} + \log E^y_{x_i}] & \text{match/insert left} \\ \max_z [S^z_{i,j-1} + \log T_{yz} + \log E^y_{x_j}] & \text{match/insert right} \\ \max_z [S^z_{i,j} + \log T_{yz}] & \text{delete} \\ \max_{i<k\le j} [S^{y_{left}}_{i,k} + S^{y_{right}}_{k+1,j}] & \text{bifurcation} \end{cases}$$

Time $O(qn^3)$, q states, seq len n

Model Training



Mutual Information

$$M_{ij} = \sum_{xi,xj} f_{xi,xj} \log_2 \frac{f_{xi,xj}}{f_{xi} f_{xj}}; \quad 0 \le M_{ij} \le 2$$

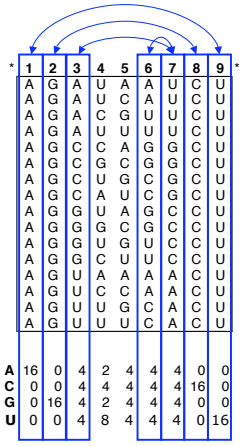
Max when *no* seq conservation but perfect pairing

MI = expected score gain from using a pair state

Finding optimal MI, (i.e. opt pairing of cols) is hard(?)

Finding optimal MI *without pseudoknots* can be done by dynamic programming

M.I. Example (Artificial)



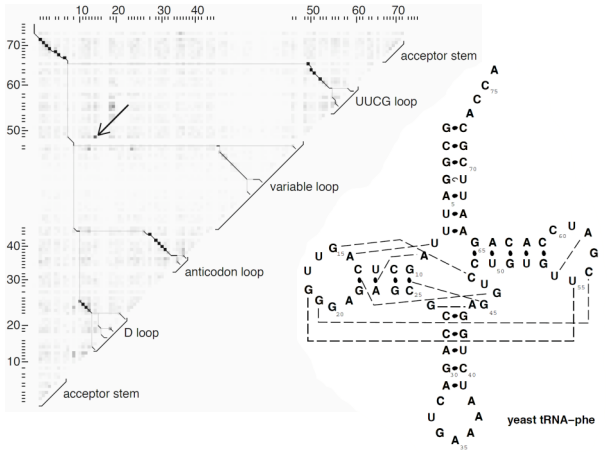
	1	2	3	4	5	6	7	8	9
	A	G	A	U	A	A	U	C	U
	A	G	A	U	C	A	U	C	U
	A	G	A	C	G	U	U	C	U
	A	G	A	U	U	U	U	C	U
	A	G	C	C	A	G	G	C	U
	A	G	C	G	C	G	G	C	U
	A	G	C	U	G	C	G	C	U
	A	G	C	A	U	C	G	C	U
	A	G	G	U	A	G	C	C	U
	A	G	G	G	G	U	C	C	U
	A	G	G	U	C	U	C	C	U
	A	G	U	A	A	A	C	C	U
	A	G	U	C	C	A	C	C	U
	A	G	U	U	G	A	C	C	U
	A	G	U	U	U	C	C	C	U
A	16	0	4	2	4	4	4	0	0
C	0	0	4	4	4	4	4	16	0
G	0	16	4	2	4	4	4	0	0
U	0	0	4	8	4	4	4	0	16

MI:	1	2	3	4	5	6	7	8	9
9	0	0	0	0	0	0	0	0	
8	0	0	0	0	0	0	0		
7	0	0	**2**	**0.30**	**0**	**1**			
6	0	0	**1**	**0.55**	**1**				
5	0	0	**0**	**0.42**					
4	0	0	**0.30**						
3	0	0							
2	0								
1									

Cols 1 & 9, 2 & 8: perfect conservation & *might* be base-paired, but unclear whether they are. M.I. = 0

Cols 3 & 7: *No* conservation, but always W-C pairs, so seems likely they do base-pair. M.I. = 2 bits.

Cols 7->6: unconserved, but each letter in 7 has only 2 possible mates in 6. M.I. = 1 bit.



MI-Based Structure-Learning

Find best (max total MI) subset of column pairs among i…j, subject to absence of pseudo-knots

$$S_{i,j} = \max \begin{cases} S_{i,j-1} \\ \max_{i \le k < j-4} S_{i,k-1} + M_{k,j} + S_{k+1,j-1} \end{cases}$$

"Just like Nussinov/Zucker folding"

BUT, need enough data---enough sequences at right phylogenetic distance

Pseudoknots disallowed allowed $\left(\sum_{i=1}^{n} \max_j M_{i,j}\right)/2$

Dataset	Avg. id	Min id	Max id	ClustalV accuracy	1° info (bits)	2° info (bits)
TEST	.402	.144	1.00	64%	43.7	30.0-32.3
SIM100	.396	.131	.986	54%	39.7	30.5-32.7
SIM65	.362	.111	.685	37%	31.8	28.6-30.7

Table 1: Statistics of the training and test sets of 100 tRNA sequences each. The average identity in an alignment is the average pairwise identity of all aligned symbol pairs, with gap/symbol alignments counted as mismatches. Primary sequence information content is calculated according to [48]. Calculating pairwise mutual information content is an NP-complete problem of finding an optimum partition of columns into pairs. A lower bound is calculated by using the model construction procedure to find an optimal partition subject to a non-pseudoknotting restriction. An upper bound is calculated as sum of the single best pairwise covariation for each position, divided by two; this includes all pairwise tertiary interactions but overcounts because it does not guarantee a disjoint set of pairs. For the meaning of multiple alignment accuracy of ClustalV, see the text.

Model	training set	iterations	score (bits)	alignment accuracy
A1415	all sequences (aligned)	3	58.7	95%
A100	SIM100 (aligned)	3	57.3	94%
A65	SIM65 (aligned)	3	46.7	93%
U100	SIM100 (degapped)	23	56.7	90%
U65	SIM65 (degapped)	29	47.2	91%

Table 2: Training and multiple alignment results from models trained from the trusted alignments (A models) and models trained from no prior knowledge of tRNA (U models).

Rfam – an RNA family DB

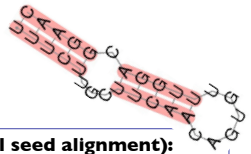
Griffiths-Jones, et al., NAR '03,'05

Biggest scientific computing user in Europe - 1000 cpu cluster for a month per release

Rapidly growing:

- Rel 1.0, 1/03: 25 families, 55k instances
- Rel 7.0, 3/05: 503 families, >300k instances

Rfam



Input (hand-curated):
- MSA "seed alignment"
- SS_cons
- Score Thresh T
- Window Len W

Output:
- CM
- scan results & "full alignment"

IRE (partial seed alignment):

```
Hom.sap.   GUUCCUGCUUCAACAGUGUUUGGAUGGAAC
Hom.sap.   UUUCUUC.UUCAACAGUGUUUGGAUGGAAC
Hom.sap.   UUUCCUGUUUCAACAGUGCUUGGA.GGAAC
Hom.sap.   UUUAUC..AGUGACAGAGUUCACU.AUAAA
Hom.sap.   UCUCUUGCUUCAACAGUGUUUGGAUGGAAC
Hom.sap.   AUUAUC..GGGAACAGUGUUUCCC.AUAAU
Hom.sap.   UCUUGC..UUCAACAGUGUUUGGACGGAAG
Hom.sap.   UGUAUC..GGAGACAGUGAUCUCC.AUAUG
Hom.sap.   AUUAUC..GGAAGCAGUGCCUUCC.AUAAU
Cav.por.   UCUCCUGCUUCAACAGUGCUUGGACGGAGC
Mus.mus.   UAUAUC..GGAGACAGUGAUCUCC.AUAUG
Mus.mus.   UUUCCUGCUUCAACAGUGCUUGAACGGAAC
Mus.mus.   GUACUUGCUUCAACAGUGUUUGAACGGAAC
Rat.nor.   UAUAUC..GGAGACAGUGACCUCC.AUAUG
Rat.nor.   UAUCUUGCUUCAACAGUGUUUGGACGGAAC
SS_cons    <<<<<...<<<<<.....>>>>>.>>>>>
```

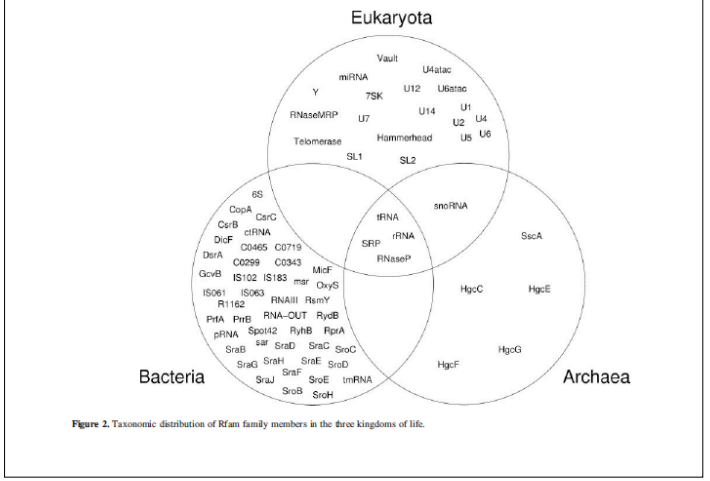


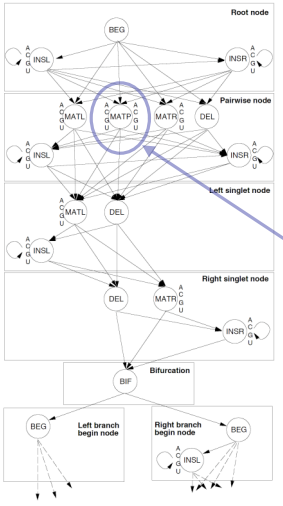
Figure 2. Taxonomic distribution of Rfam family members in the three kingdoms of life.

Faster Genome Annotation of Non-coding RNAs Without Loss of Accuracy

Zasha Weinberg

& W.L. Ruzzo

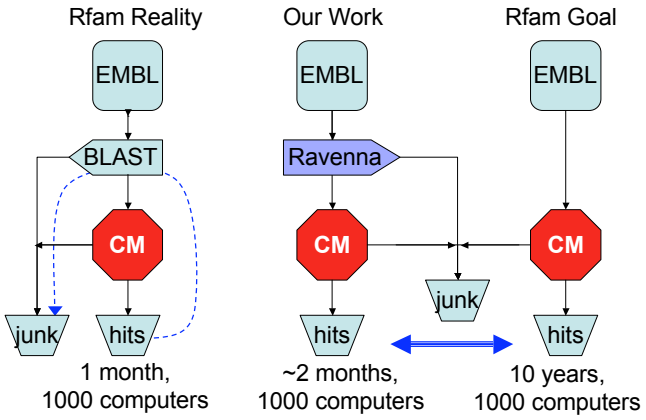
Recomb '04, ISMB '04, Bioinfo '06



Covariance Model

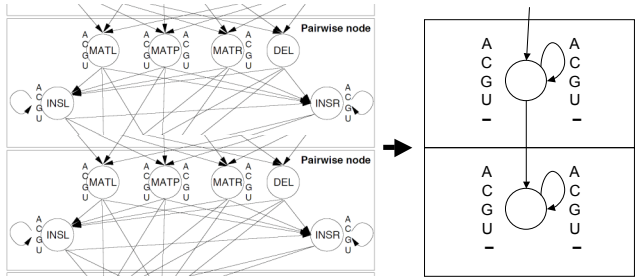
Key difference of CM vs HMM: Pair states emit paired symbols, corresponding to base-paired nucleotides; 16 emission probabilities here.

CM's are good, but slow

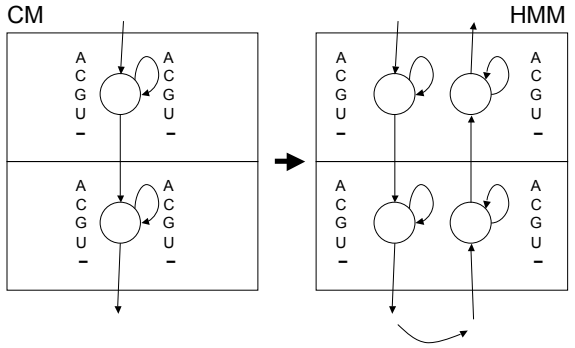


Oversimplified CM

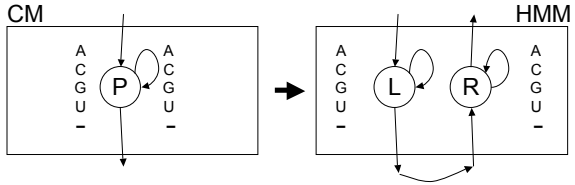
(for pedagogical purposes only)



CM to HMM



Key Issue: 25 scores → 10



Need: log Viterbi scores CM ≤ HMM

Viterbi/Forward Scoring

Path π defines transitions/emissions

Score(π) = product of "probabilities" on π

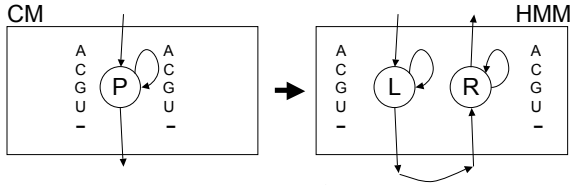
NB: ok if "probs" aren't, e.g. $\Sigma \neq 1$
(e.g. in CM, emissions are odds ratios vs 0th-order background)

For any nucleotide sequence x:

Viterbi-score(x) = max{ score(π) | π emits x}

Forward-score(x) = Σ[score(π) | π emits x}

Key Issue: 25 scores → 10



Need: log Viterbi scores CM ≤ HMM

$P_{AA} \le L_A + R_A$	$P_{CA} \le L_C + R_A$	…
$P_{AC} \le L_A + R_C$	$P_{CC} \le L_C + R_C$	…
$P_{AG} \le L_A + R_G$	$P_{CG} \le L_C + R_G$	…
$P_{AU} \le L_A + R_U$	$P_{CU} \le L_C + R_U$	…
$P_{A-} \le L_A + R_-$	$P_{C-} \le L_C + R_-$	…

NB: HMM not a prob. model

Rigorous Filtering

$P_{AA} \le L_A + R_A$
$P_{AC} \le L_A + R_C$
$P_{AG} \le L_A + R_G$
$P_{AU} \le L_A + R_U$
$P_{A-} \le L_A + R_-$
…

Any scores satisfying the linear inequalities give rigorous filtering

Proof:

CM Viterbi path score
≤ "corresponding" HMM path score
≤ Viterbi HMM path score
(even if it does not correspond to *any* CM path)

Some scores filter better

$P_{UA} = 1 \le L_U + R_A$
$P_{UG} = 4 \le L_U + R_G$

Option 1:
$L_U = R_A = R_G = 2$

Option 2:
$L_U = 0, R_A = 1, R_G = 4$

Assuming ACGU ≈ 25%
Opt 1: $L_U + (R_A + R_G)/2 = 4$
Opt 2: $L_U + (R_A + R_G)/2 = 2.5$

Optimizing filtering

For any nucleotide sequence x:

Viterbi-score(x) = max{ score(π) | π emits x }

Forward-score(x) = Σ{ score(π) | π emits x }

Expected Forward Score

$E(L_i, R_i) = \Sigma_{\text{all sequences } x}$ Forward-score(x)*Pr(x)

NB: E is a function of L_i, R_i only

Under 0th-order background model

Optimization:

Minimize $E(L_i, R_i)$ subject to score Lin.Ineq.s

This is heuristic ("forward↓ ⇒ Viterbi↓ ⇒ filter↓")

But still rigorous because "subject to score Lin.Ineq.s"

Calculating $E(L_i, R_i)$

$E(L_i, R_i) = \Sigma_x$ Forward-score(x)*Pr(x)

Forward-like: for every state, calculate expected score for all paths ending there, easily calculated from expected scores of predecessors & transition/emission probabilities/scores

Minimizing $E(L_i, R_i)$

Calculate $E(L_i, R_i)$ *symbolically*, in terms of emission scores, so we can do partial derivatives for numerical convex optimization algorithm

$$\frac{\partial E(L_1, L_2, \ldots)}{\partial L_i}$$

Estimated Filtering Efficiency

(139 Rfam 4.0 families)

Filtering fraction	# families (compact)	# families (expanded)
$< 10^{-4}$	105	110
10^{-4} - 10^{-2}	8	17
.01 - .10	11	3
.10 - .25	2	2
.25 - .99	6	4
.99 - 1.0	7	3

~100x speedup

Results: New ncRNA's?

Name	# found BLAST + CM	# found rigorous filter + CM	# new
Pyrococcus snoRNA	57	180	123
Iron response element	201	322	121
Histone 3' element	1004	1106	102
Purine riboswitch	69	123	54
Retron msr	11	59	48
Hammerhead I	167	193	26
Hammerhead III	251	264	13
U4 snRNA	283	290	7
S-box	128	131	3
U6 snRNA	1462	1464	2
U5 snRNA	199	200	1
U7 snRNA	312	313	1

Results: With additional work

	# with BLAST+CM	# with rigorous filter series + CM	# new
Rfam tRNA	58609	63767	5158
Group II intron	5708	6039	331
tRNAscan-SE (human)	608	729	121
tmRNA	226	247	21
Lysine riboswitch	60	71	11
And more…			

"Additional work"

Profile HMM filters use *no* 2[ary] structure info

- They work well because, tho structure can be critical to function, there is (usually) enough primary sequence conservation to exclude most of DB
- But not on all families (and may get worse?)

Can we exploit *some* structure (quickly)?

- Idea 1: "sub-CM"
- Idea 2: extra HMM states remember mate

} for some hairpins

- Idea 3: try lots of combinations of "some hairpins"
- Idea 4: chain together several filters (select via Dijkstra)

Filter Chains

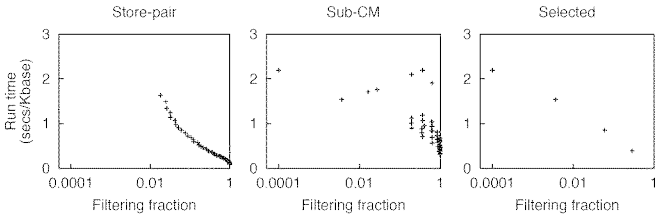


Fig. 2. Filter creation and selection. Filters for Rfam tRNA (RF00005) generated by the store-pair and sub-CM techniques and those selected for actual filtering are plotted by filtering fraction and run time. The CM runs at 3.5 secs/kbase. The four selected filters are run one after another, from highest to lowest fraction.

Heuristic Filters

Rigorous filters optimized for worst case

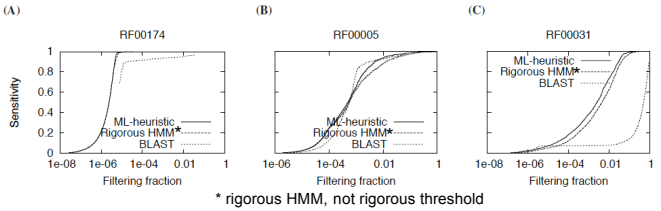
Possible to trade improved speed for small loss in sensitivity?

Yes – profile HMMs as before, but optimized for average case

"ML heuristic": train HMM from the infinite alignment generated by the CM

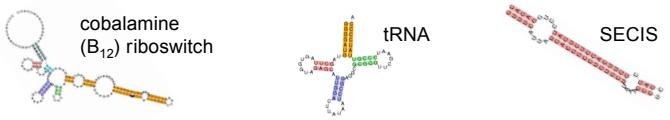
Often 10x faster, modest loss in sensitivity

Heuristic Filters



* rigorous HMM, not rigorous threshold

Fig. 1. Selected ROC-like curves. All plot sensitivity against filtering fraction, with filtering fraction in log scale. (A) RF00174 is typical of the other families; the ML-heuristic is slightly better than the rigorous profile HMM, and both often dramatically exceed BLAST. (B) Atypically, in RF00005, BLAST is superior, although only in one region. (C) BLAST performs especially poorly for RF00031. (Recall that rigorous scans were not possible for RF00031, so only ~90% of hits are known; see text.) The supplement includes all ROC-like curves, and the inferior ignore-SS.



Cmfinder--A Covariance Model Based RNA Motif Finding Algorithm

Bioinformatics, 2006, 22(4): 445-452

Zizhen Yao
Zasha Weinberg
Walter L. Ruzzo
University of Washington, Seattle

Searching for noncoding RNAs

CM's are great, but where do they come from?

An approach: comparative genomics

- Search for motifs with common secondary structure in a set of functionally related sequences.

Challenges

- Three related tasks
  - Locate the motif regions.
  - Align the motif instances.
  - Predict the consensus secondary structure.
- Motif search space is huge!
  - Motif location space, alignment space, structure space.

Approaches

Align sequences, then look for common structure

Predict structures, then try to align them

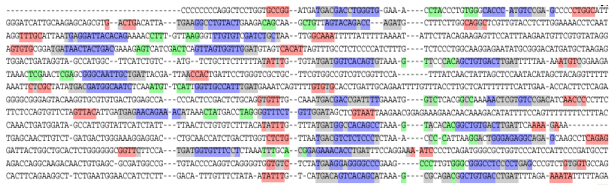
Do both together

Pitfall for sequence-alignment-first approach

Structural conservation ≠ Sequence conservation

Alignment without structure information is unreliable

CLUSTALW alignment of SECIS elements with flanking regions



same-colored boxes *should* be aligned

Approaches

Align sequences, then look for common structure

Predict structures, then try to align them

- single-seq struct prediction only ~ 60% accurate; exacerbated by flanking seq; no biologically-validated model for structural alignment

Do both together

- Sankoff – good but slow
- Heuristic

Design Goals

Find RNA motifs in unaligned sequences

Seq conservation exploited, but not required

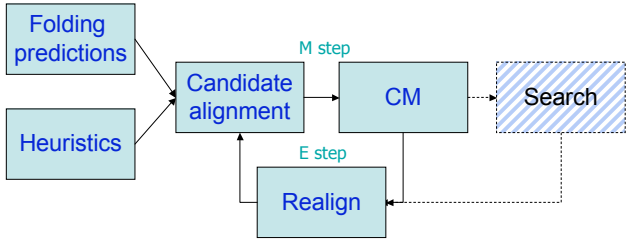
Robust to inclusion of unrelated sequences

Robust to inclusion of flanking sequence

Reasonably fast and scalable

Produce a probabilistic model of the motif that can be directly used for homolog search

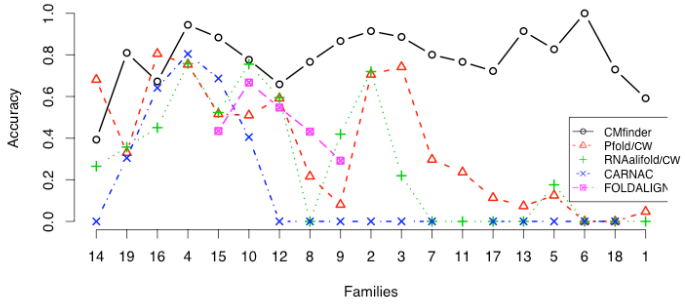
CMfinder Outline



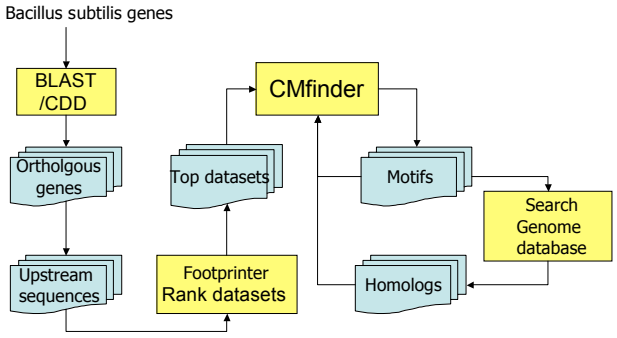
M-step uses M.I. + folding energy for structure prediction

CMfinder Accuracy

(on Rfam families *with* flanking sequence)

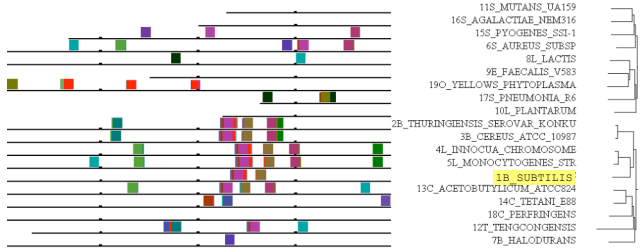


A pipeline for RNA motif genome scans



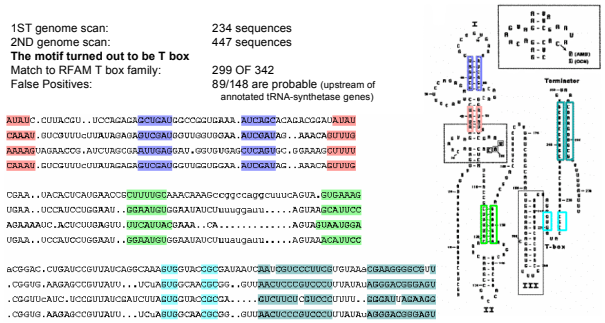
Footprinter finds patterns of conservation

Upstream of folC

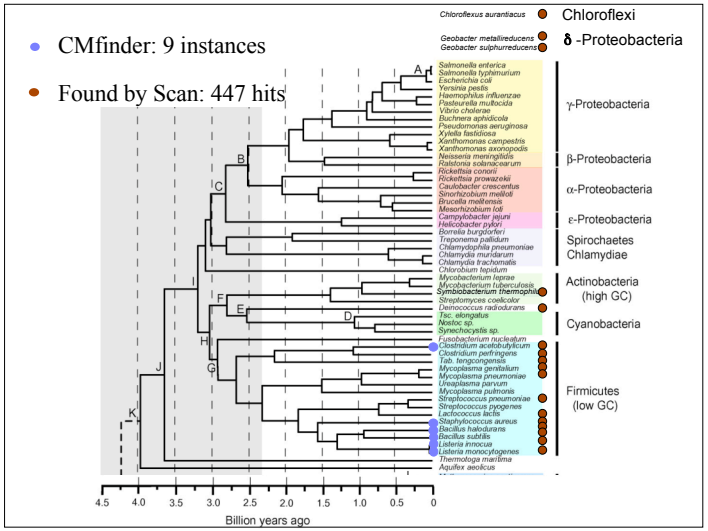


A blind test

1ST genome scan: 234 sequences
2ND genome scan: 447 sequences
The motif turned out to be T box
Match to RFAM T box family: 299 OF 342
False Positives: 89/148 are probable (upstream of annotated tRNA-synthetase genes)



tyrS T box structure



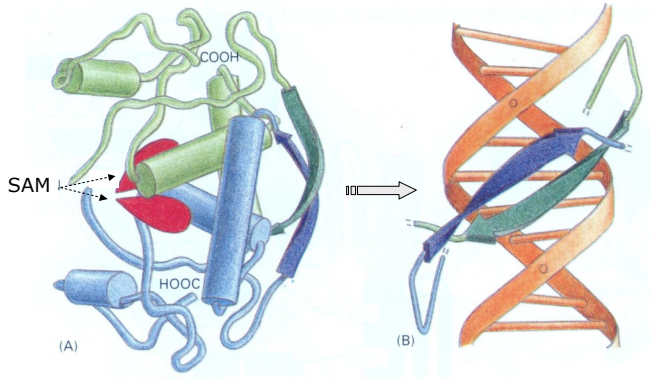
- CMfinder: 9 instances
- Found by Scan: 447 hits

Some Preliminary Actino Results

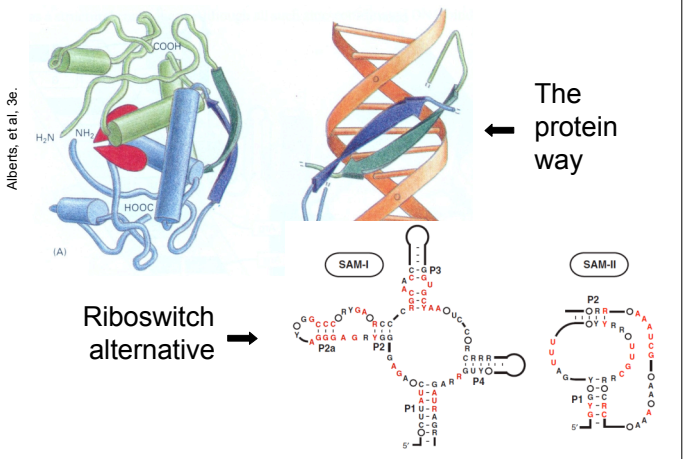
8 of 10 Rfam families found

Rfam Family	Type (metabolite)	Rank	
THI	riboswitch (thiamine)	4	
ydaO-yuaA	riboswitch (unknown)	19	
Cobalamin	riboswitch (cobalamin)	21	
SRP_bact	gene	28	not cis-regulatory (got one anyway)
RFN	riboswitch (FMN)	39	
yybP-ykoY	riboswitch (unknown)	48	
gcvT	riboswitch (glycine)	53	
S_box	riboswitch (SAM)	401	
tmRNA	gene	Not found	
RNaseP	gene	Not found	

Gene Regulation: The MET Repressor



Protein Alberts, et al, 3e. DNA



Corbino et al., Genome Biol. 2005

More Prelim Actino Results

Many others (not in Rfam) are likely real of top 50:

known (Rfam, 23S)	10
probable (Tbox, CIRCE, LexA, parP, pyrR)	7
probable (ribosomal genes)	9
potentially interesting	12
unknown or poor	12

One bench-verified, 2 more in progress

Preliminary results of genome scan

Top 115 datasets (some are redundant)
13 T box, 22 riboswitches, 30 ribosomal genes
RNase P, tRNA, CIRCE elements and other DNA binding sites

Gene	#motif	hits	RFAM	#seed	#full	#TP	specificity	sensitivity
metK	13	150	S_box	71	151	145	0.967	0.960
ribB	9	106	RFN	48	114	97	0.915	0.851
folC	9	447	T_box	67	342	299	0.669	0.874
xpt	14	106	Purine	37	100	97	0.915	0.970
glmS	16	33	glmS	14	37	33	1.000	0.892
thiA	16	305	THI	237	366	305	1.000	0.833
ykoY	10	34	yybP-ykoY	74	127	33	0.971	0.260

Summary

ncRNA - apparently widespread, much interest

Covariance Models - powerful but expensive tool for ncRNA motif representation, search, discovery

Rigorous/Heuristic filtering - typically 100x speedup in search with no/little loss in accuracy

CMfinder - CM-based motif discovery in unaligned sequences

Course Wrap Up

What is DNA? RNA?

How many Amino Acids are there?

Did human beings, as we know them, develop from earlier species of animals?

What are stem cells?

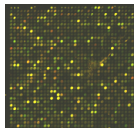
What did Viterbi invent?

What is dynamic programming?

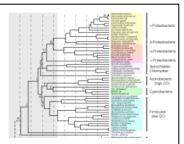
What is a likelihood ratio test?

What is the EM algorithm?

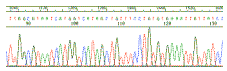
How would you find the maximum of $f(x) = ax^3 + bx^2 + cx + d$ in the interval $-10<x<25$?

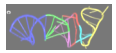


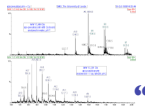
"High-Throughput BioTech"



- Sensors
  - DNA sequencing
  - Microarrays/Gene expression
  - Mass Spectrometry/Proteomics
  - Protein/protein & DNA/protein interaction
- Controls
  - Cloning
  - Gene knock out/knock in
  - RNAi







***Floods* of data**

"Grand Challenge" problems

CS Points of Contact

- Scientific visualization
  - Gene expression patterns
- Databases
  - Integration of disparate, overlapping data sources
  - Distributed genome annotation in face of shifting underlying coordinates
- AI/NLP/Text Mining
  - Information extraction from journal texts with inconsistent nomenclature, indirect interactions, incomplete/inaccurate models,…
- Machine learning
  - System level synthesis of cell behavior from low-level heterogeneous data (DNA sequence, gene expression, protein interaction, mass spec,
- Algorithms
- …

Frontiers & Opportunities

New data:

- Proteomics, SNP, arrays CGH, comparative sequence information, methylation, chromatin structure, ncRNA, interactome

New methods:

- graphical models? rigorous filtering?

Data integration

- many, complex, noisy sources

Frontiers & Opportunities

Open Problems:

- splicing, alternative splicing
- multiple sequence alignment (genome scale, w/ RNA etc.)
- protein & RNA structure
- interaction modeling
- network models
- RNA trafficing
- ncRNA discovery
- …

Exciting Times

Lots to do

Various skills needed

I hope I've given you a taste of it

Thanks!