CSEP 590A

Spring 2013

5 – Motifs: Representation & Discovery

Outline

Previously: Learning from data

- MLE: Max Likelihood Estimators
- EM: Expectation Maximization (MLE w/hidden data)

These Slides:

- Bio: Expression & regulation
  - Expression: creation of gene products
  - Regulation: when/where/how much of each gene product; complex and critical
- Comp: using MLE/EM to find regulatory motifs in biological sequence data

Gene Expression & Regulation

Gene Expression

Recall a *gene* is a DNA sequence for a protein

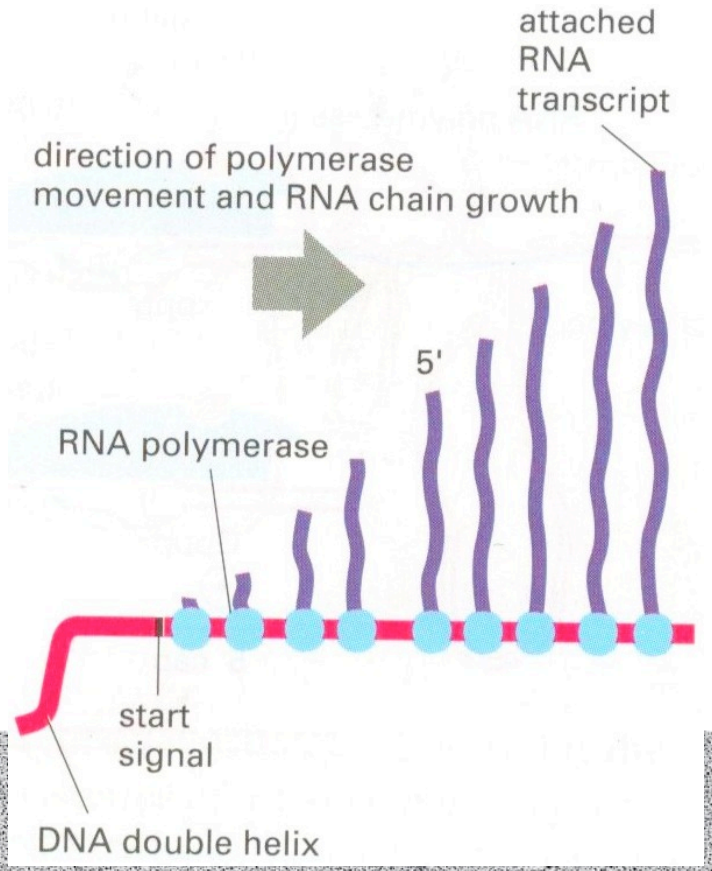
To say a gene is *expressed* means that it

- is *transcribed* from DNA to RNA
- the mRNA is *processed* in various ways
- is *exported* from the nucleus (eukaryotes)
- is *translated* into protein

A key point: not all genes are expressed all the time, in all cells, or at equal levels

RNA Transcription

Some genes heavily transcribed
(many are not)



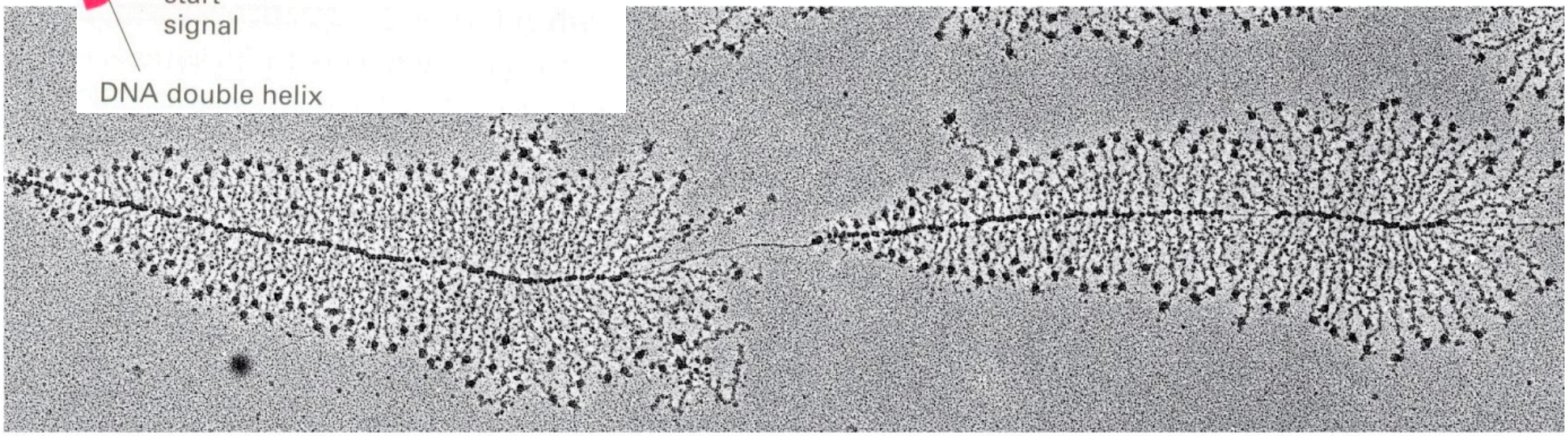


Figure 6-9 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Regulation

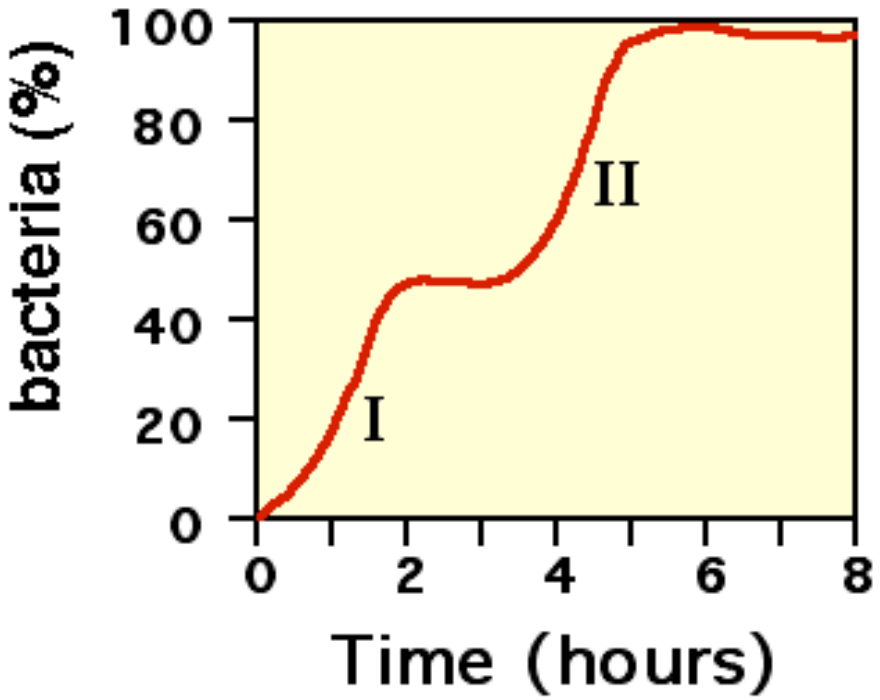
In most cells, pro- or eukaryote, easily a 10,000-fold difference between least- and most-highly expressed genes

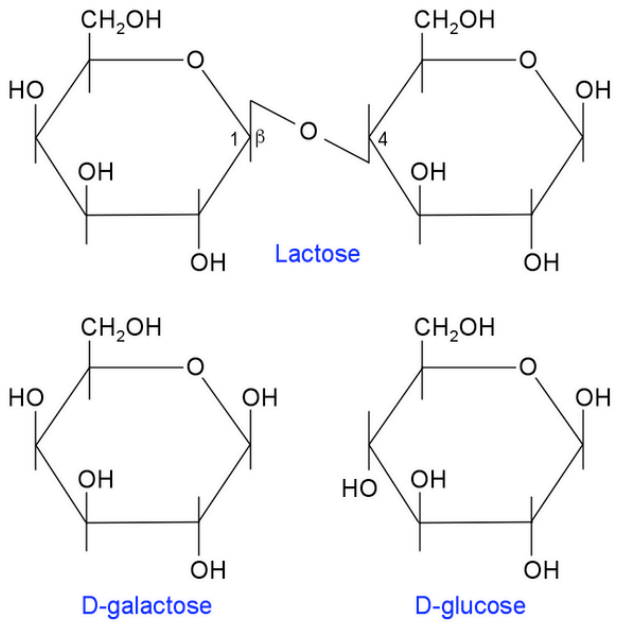
Regulation happens at all steps. E.g., some genes are highly transcribed, some are not transcribed at all, some transcripts can be sequestered then released, or rapidly degraded, some are weakly translated, some are very actively translated, ...

Below, focus on 1st step only:

- ✦ transcriptional regulation

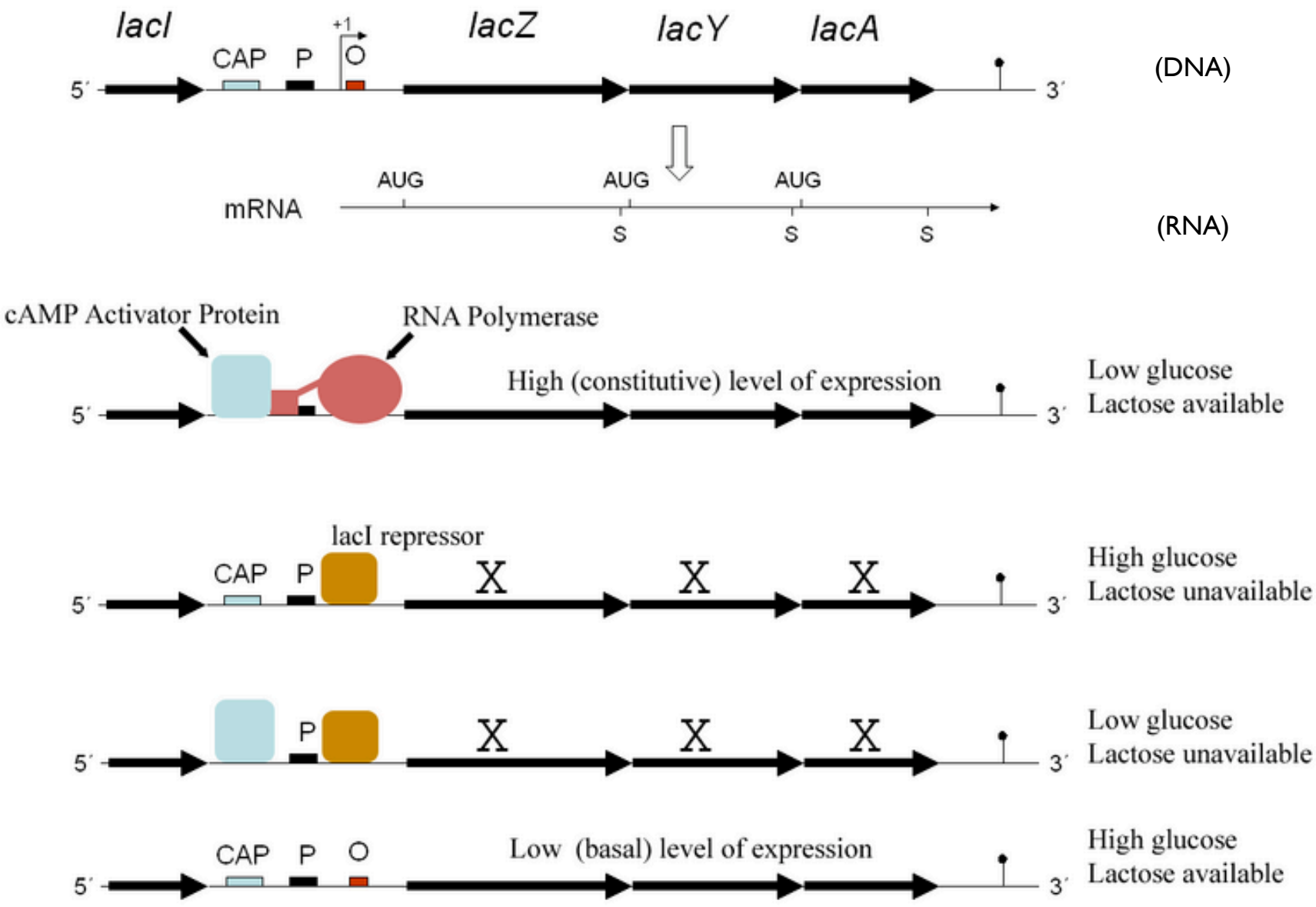
E. coli growth on glucose + lactose





http://en.wikipedia.org/wiki/Lac_operon

The *lac* Operon and its Control Elements



1965 Nobel Prize

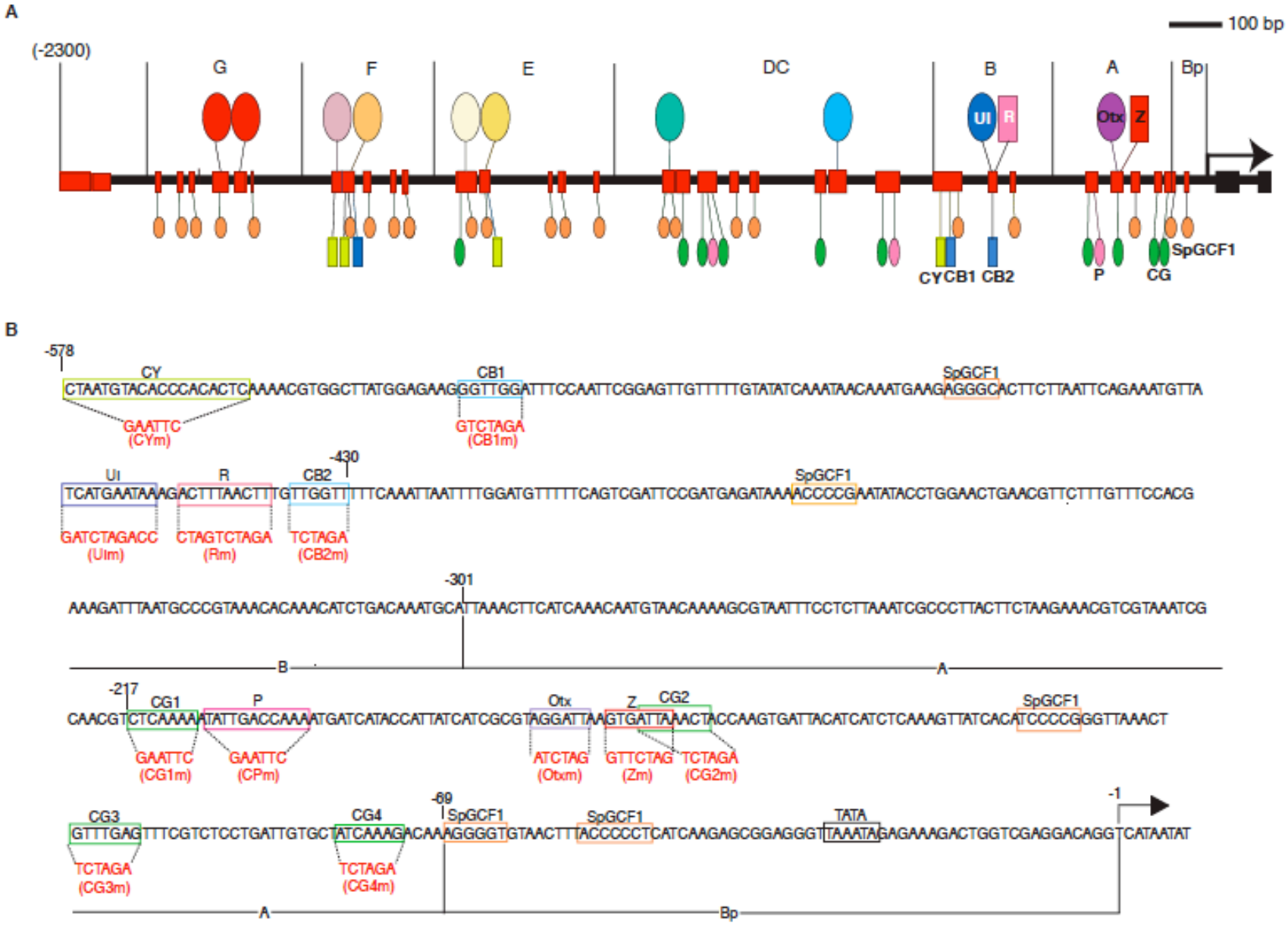
Physiology or Medicine

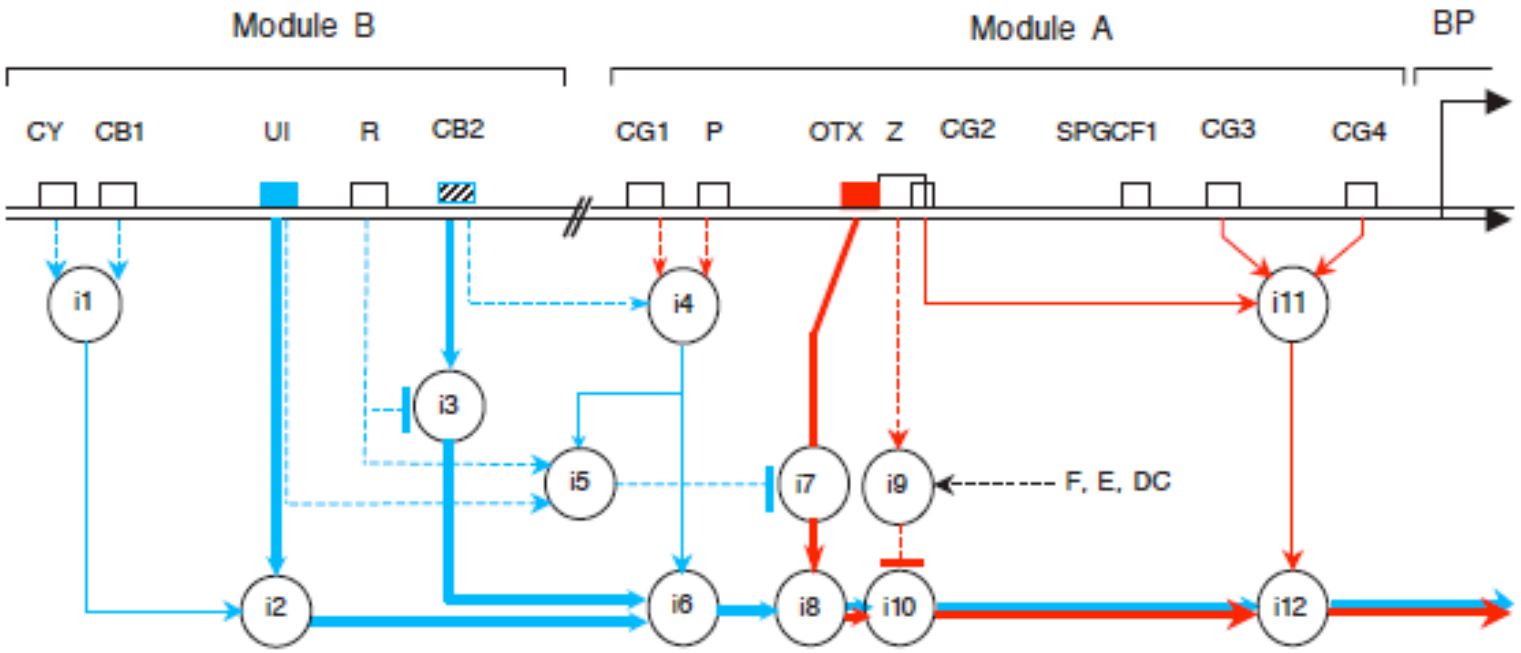
François Jacob, Jacques Monod, André Lwoff

1920-2013 1910-1976 1902-1994

The sea urchin *Strongylocentrotus purpuratus*

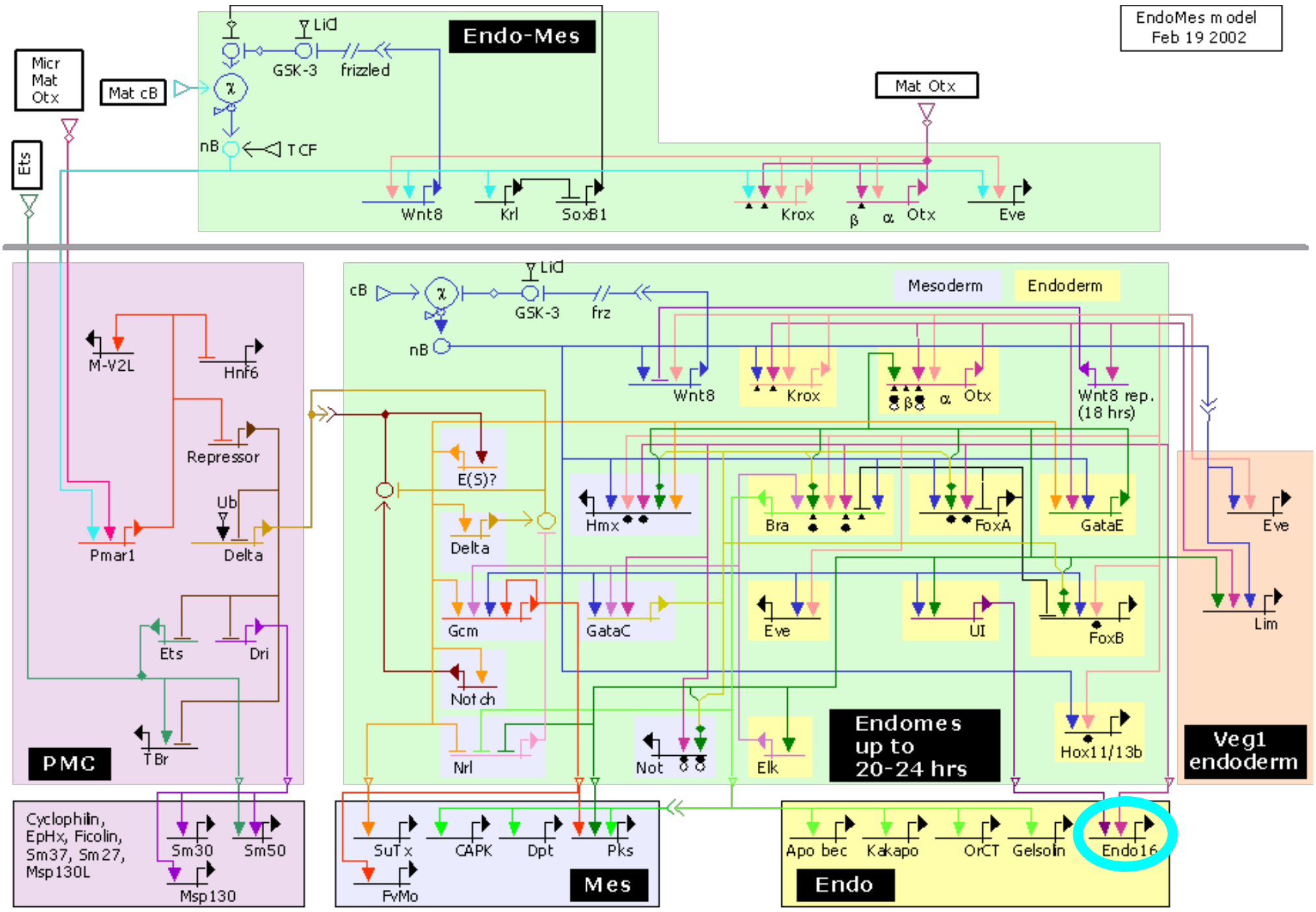
Sea Urchin - Endo16





if CY & CB1	i1 = 1
else	i1 = 0.5
	i2 = i1 · UI(t)
if R	i3 = CB2(t)
else	i3 = k · CB2(t) (1<k<2)
if P & CG1 & CB2	i4 = 2
else	i4 = 0
if UI(t)>threshold & R & i4≠0	i5 = 1
else	i5 = 0
	i6 = i4 · (i2+i3)

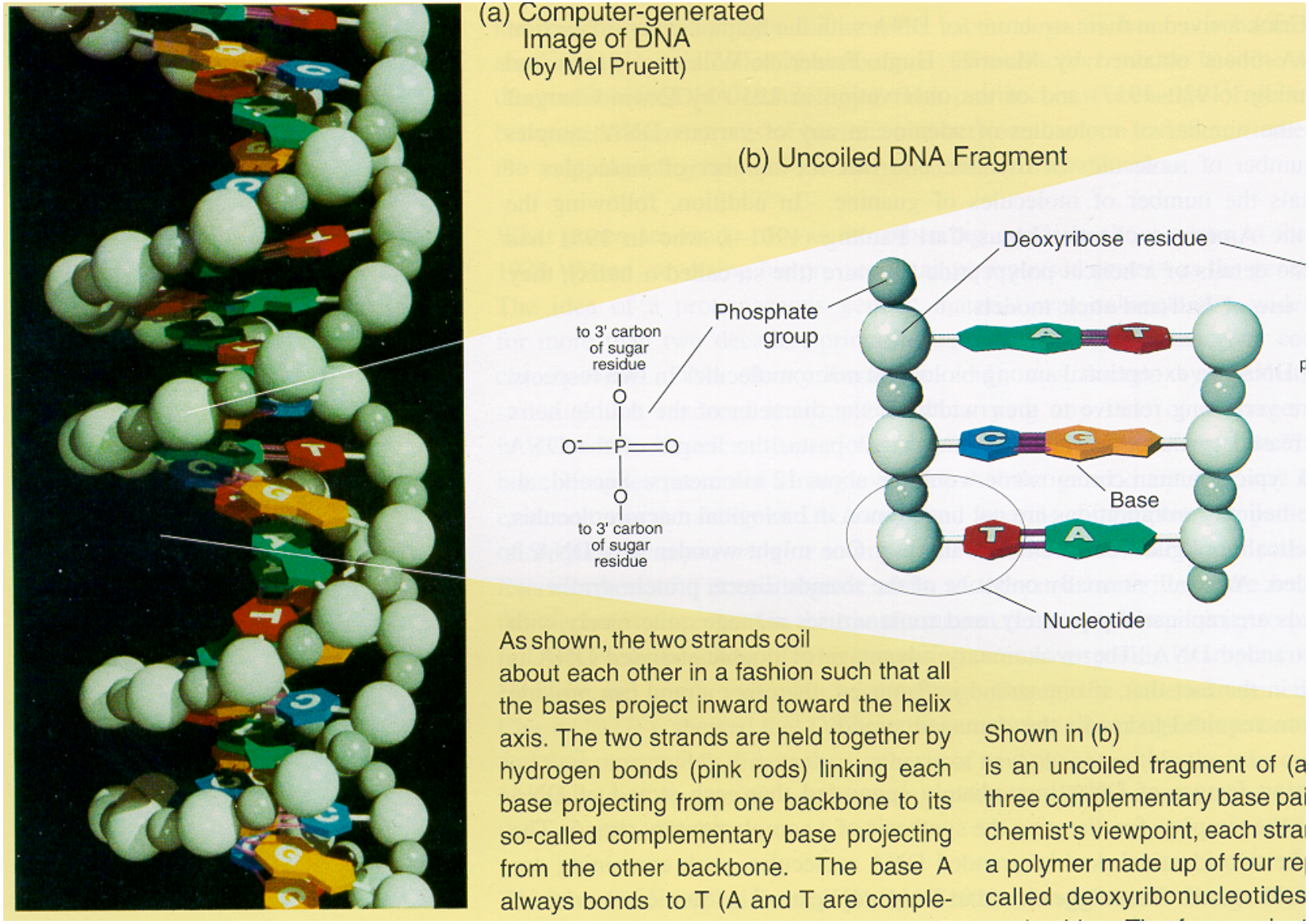
if i5=0	i7 = OTX(t)
else	i7 = 0
	i8 = i6 + i7
if (F or E or DC) & Z	i9 = 1
else	i9 = 0
if i9=1	i10 = 0
else	i10 = i8
if (CG2 & CG3 & CG4)	i11 = 2
else	i11 = 1
	i12 = i11 · i10


EndoMes model
Feb 19 2002
Endo-Mes
Micr
Mat
Otx
Mat cB
Ets
LiCl
GSK-3
frizzled
nB
TCF
Mat Otx
Wnt8
Krl
SoxB1
Krox
β
α
Otx
Eve
cB
LiCl
GSK-3
frz
nB
Mesoderm
Endoderm
Wnt8
Krox
β
α
Otx
Wnt8 rep.
(18 hrs)
M-V2L
Hnf6
Repressor
Ub
Pmar1
Delta
E(S)?
Delta
Hmx
Bra
FoxA
GataE
Eve
Lim
Gcm
GataC
Eve
UI
FoxB
Ets
Dri
Notch
TBr
Nrl
Not
Elk
Hox11/13b
PMC
Endomes
up to
20-24 hrs
Veg1
endoderm
Cyclophilin,
EpHx, Ficolin,
Sm37, Sm27,
Msp130L
Sm30
Sm50
Msp130
SuTx
CAPK
Dpt
Pks
FvMo
Mes
Apo bec
Kakapo
OrCT
Gelsolin
Endo16
Endo

DNA Binding Proteins

A variety of DNA binding proteins (so-called "transcription factors"; a significant fraction, perhaps 5-10%, of all human proteins) modulate transcription of protein coding genes

The Double Helix



Los Alamos Science

In the groove

Different patterns of potential H bonds at edges of different base pairs, accessible esp. in major groove

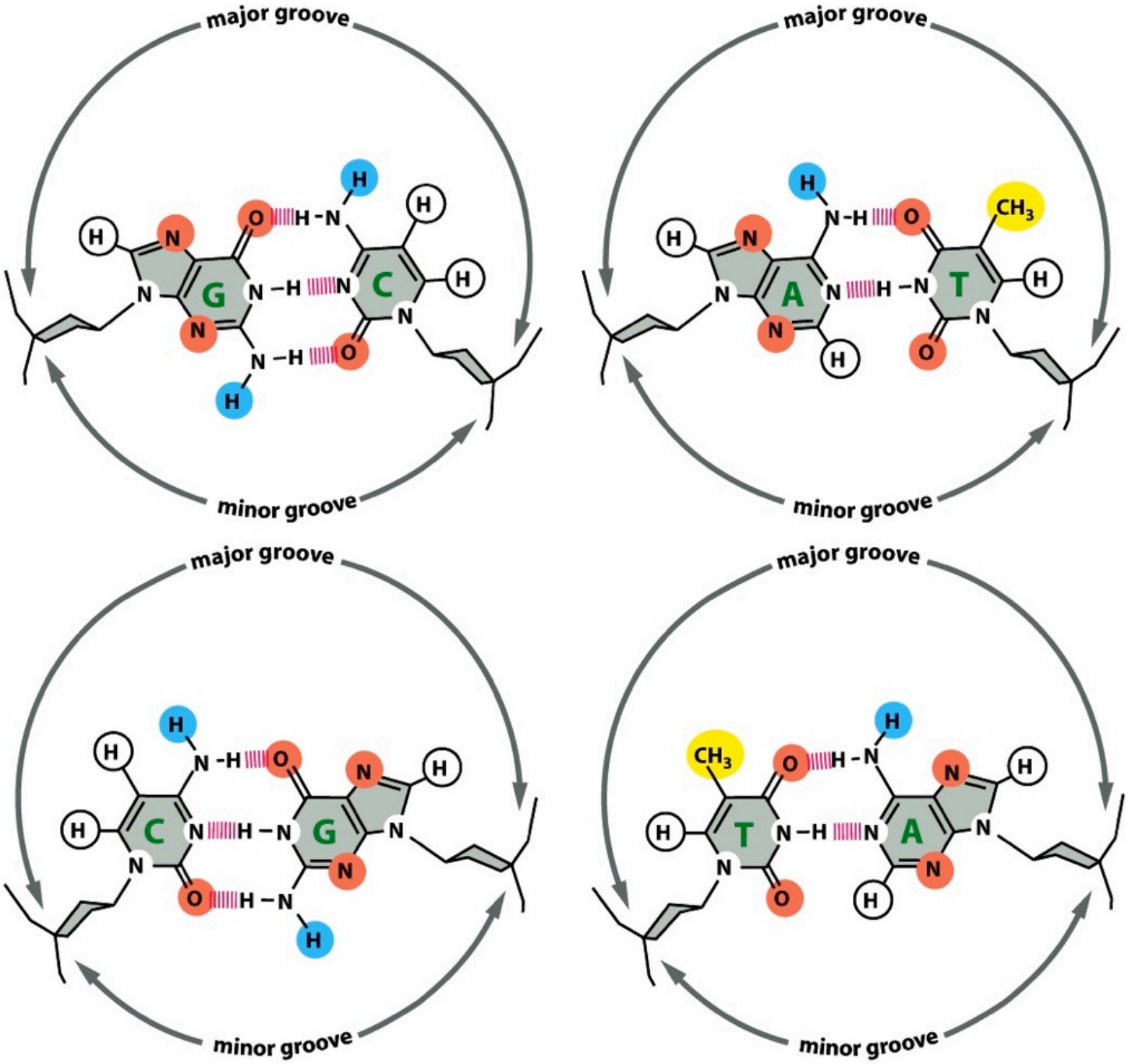


Figure 7-7 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Helix-Turn-Helix DNA Binding Motif

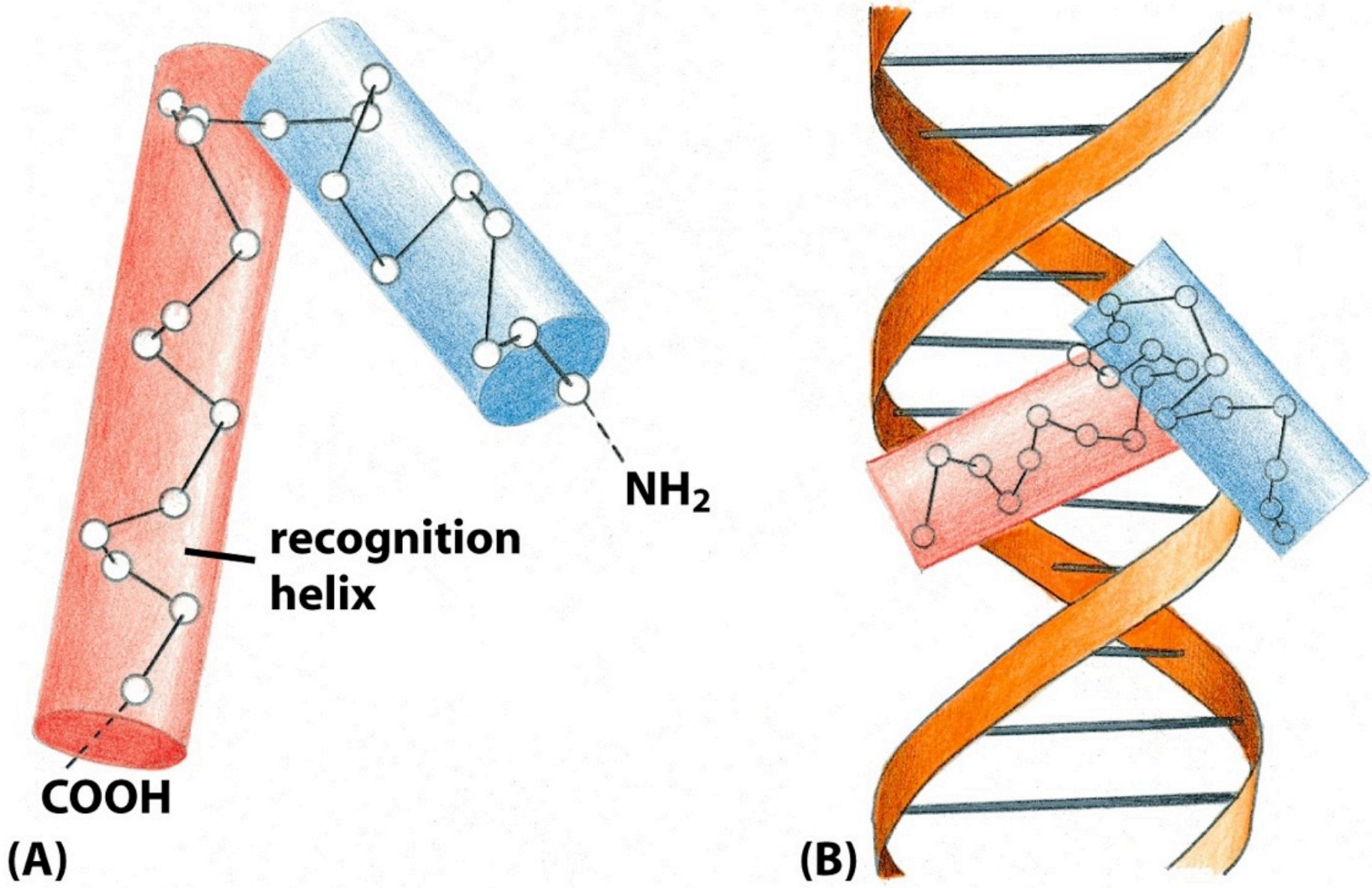


Figure 7-10 Molecular Biology of the Cell 5/e (© Garland Science 2008)

H-T-H Dimers

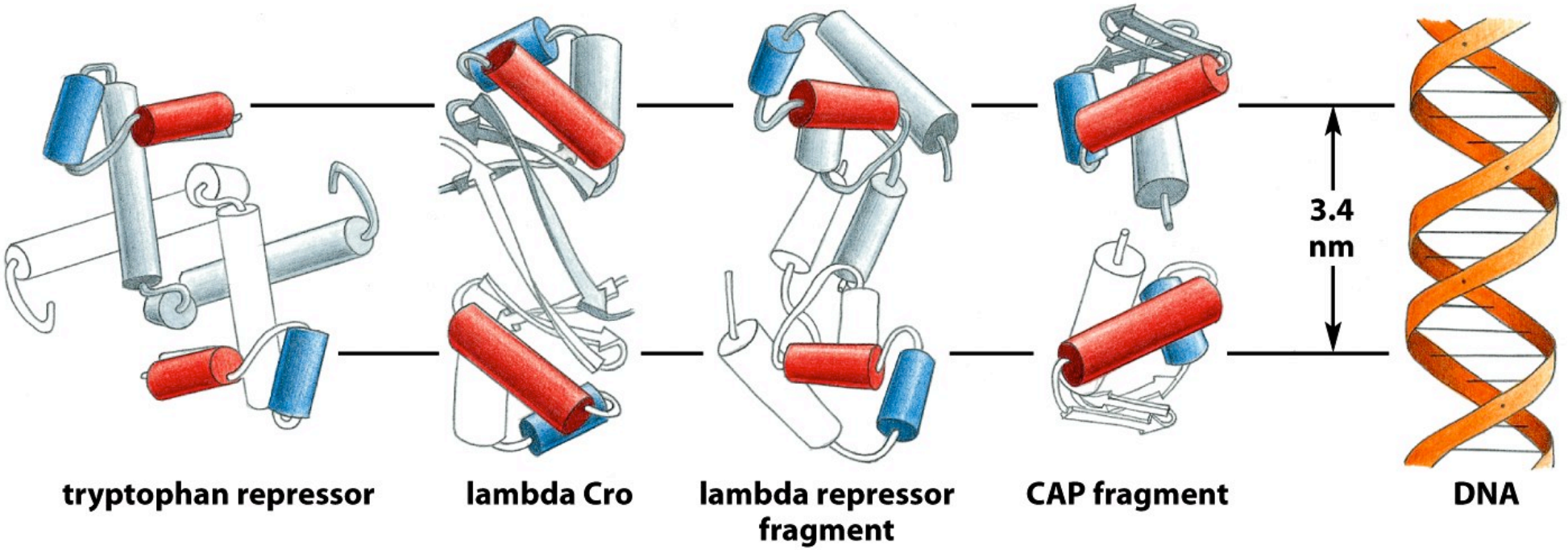


Figure 7-11 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Bind 2 DNA patches, ~ 1 turn apart
Increases both specificity and affinity

Zinc Finger Motif

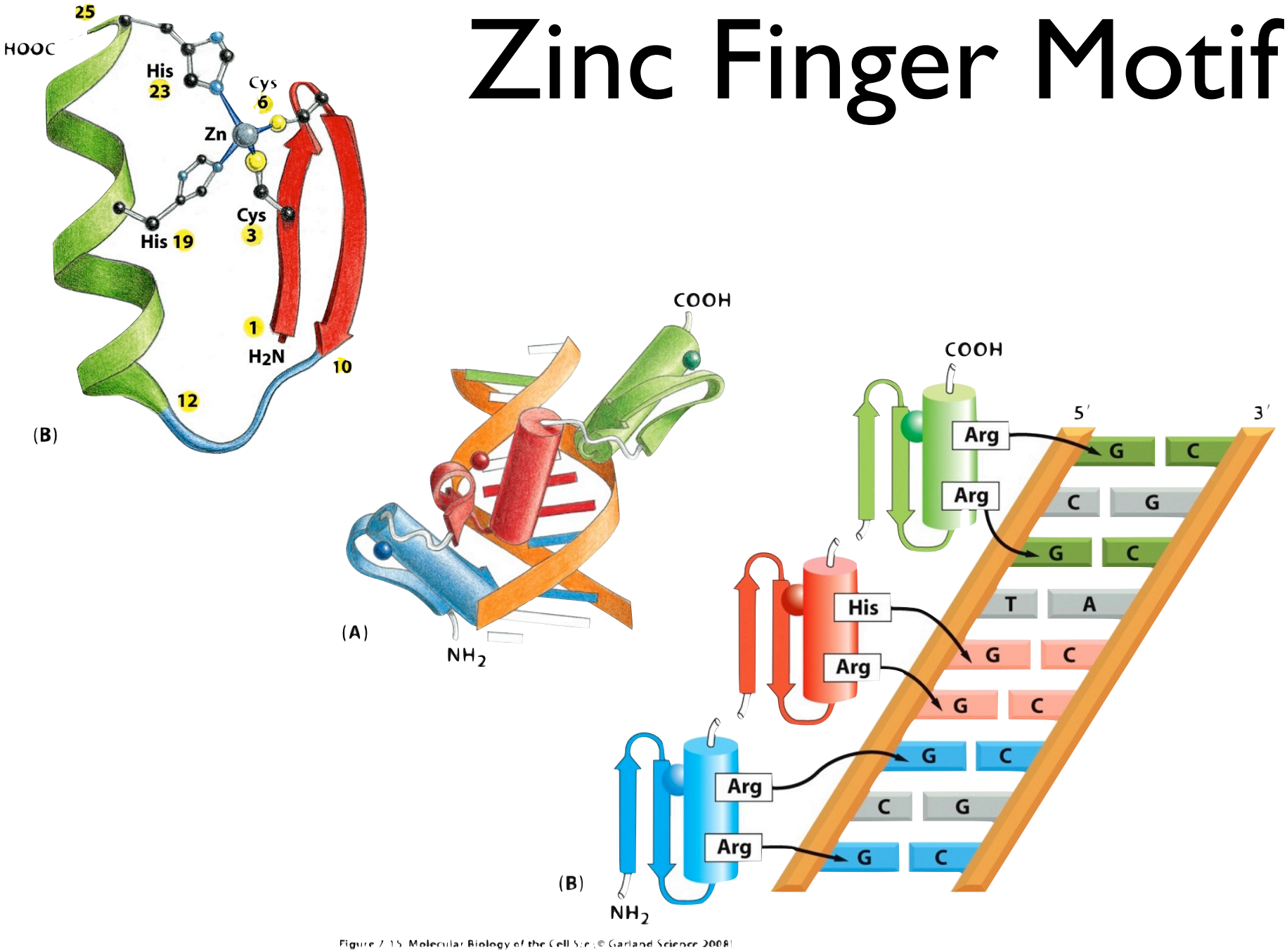


Figure 7.15 Molecular Biology of the Cell 5/e. © Garland Science 2008

Leucine Zipper Motif

Figure 7-19 Molecular Biology of the Cell 5/e (© Garland Science 2008)

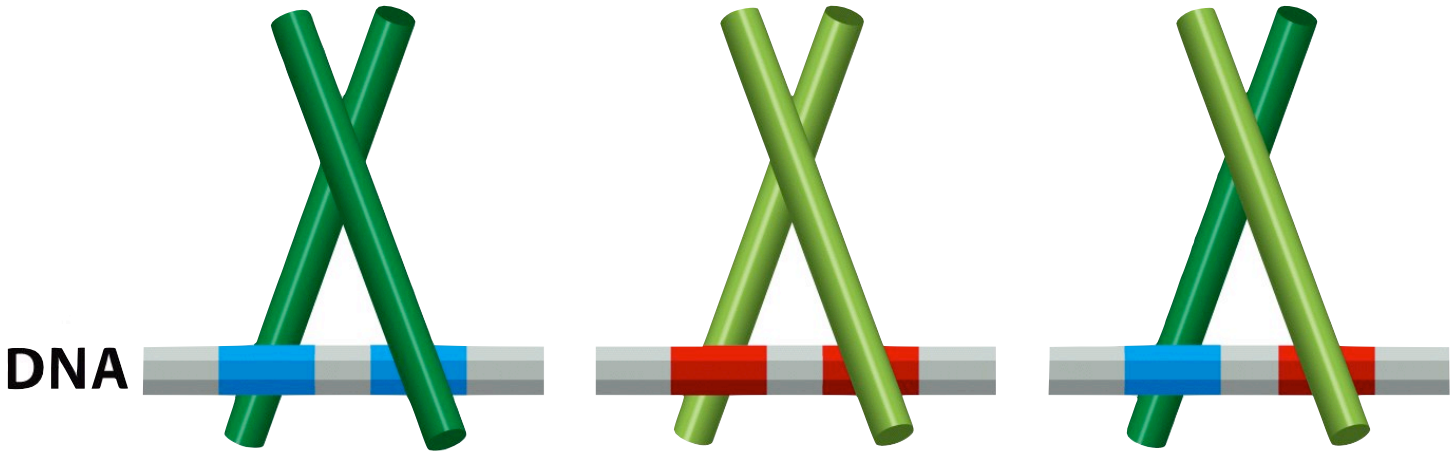


Figure 7-20 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Homo-/hetero-dimers and combinatorial control

MyoD

http://www.rcsb.org/pdb/explore/jmol.do?structureId=1MDY&bionumber=1

We understand some Protein/DNA interactions

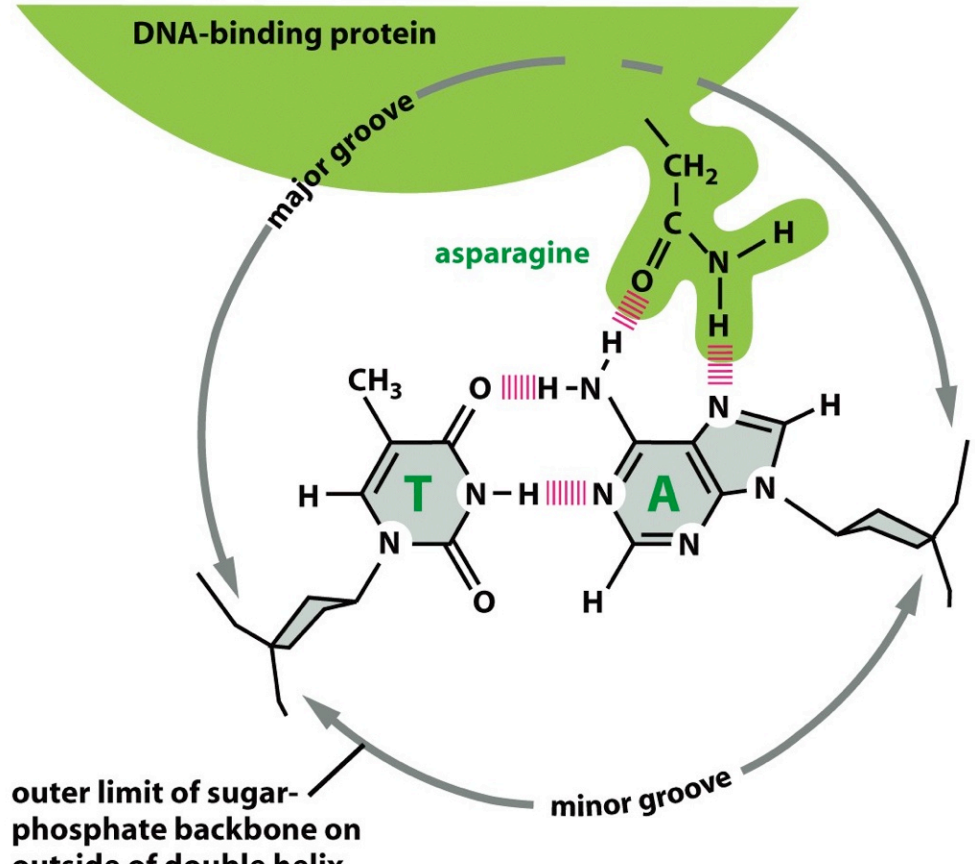


Figure 7-9 Molecular Biology of the Cell 5/e (© Garland Science 2008)

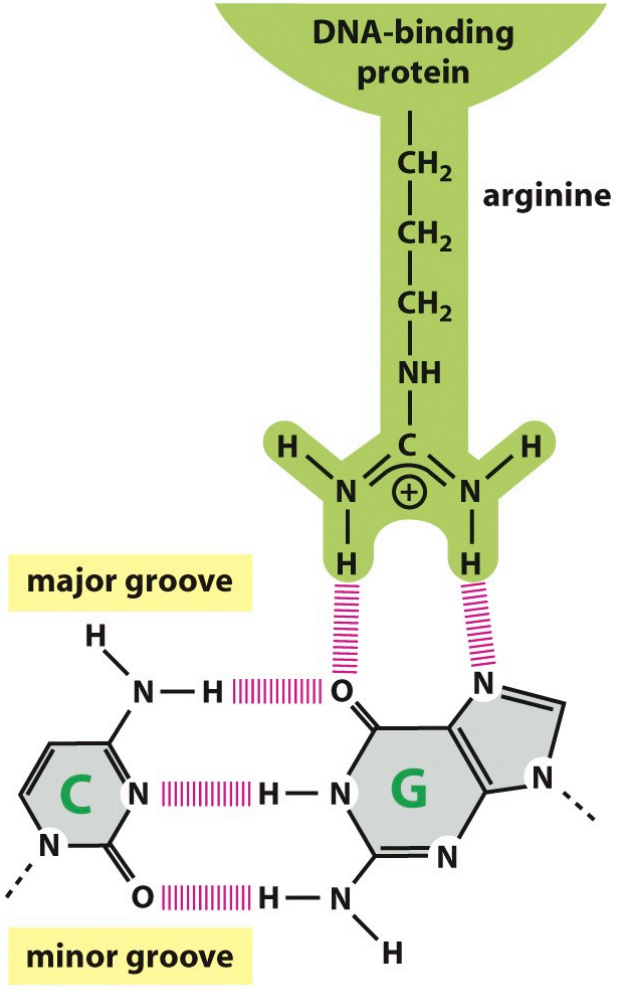


Figure 7-25 Molecular Biology of the Cell 5/e (© Garland Science 2008)

But the overall DNA binding "code" still defies prediction

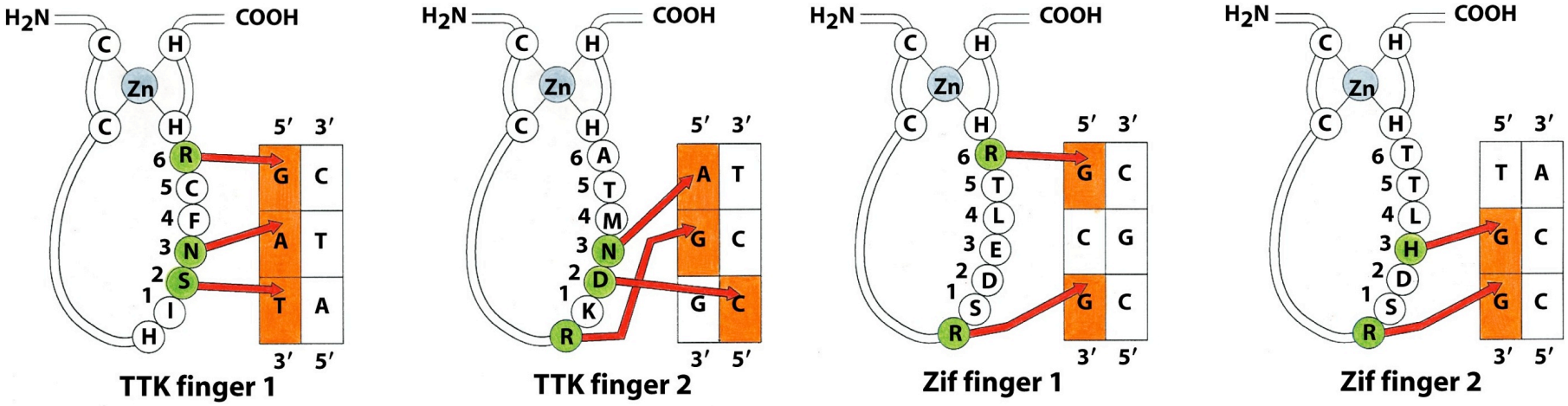


Figure 7-26 part 1 of 3 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Figure 7-26 part 2 of 3 Molecular Biology of the Cell 5/e (© Garland Science 2008)

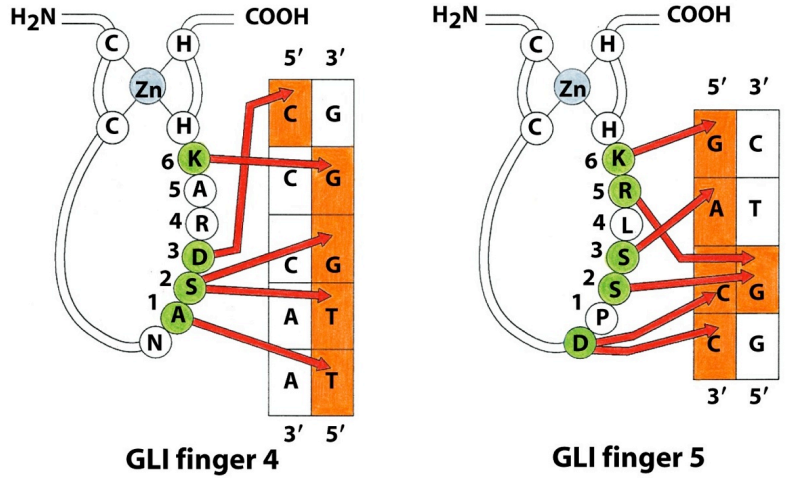
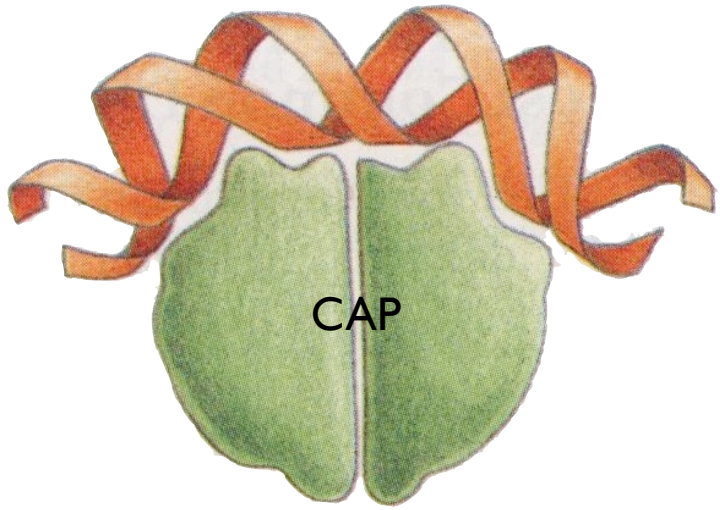


Figure 7-26 part 3 of 3 Molecular Biology of the Cell 5/e (© Garland Science 2008)



Summary

Proteins can bind DNA to regulate gene expression (i.e., production of other proteins & themselves)

This is widespread

Complex combinatorial control is possible

Sequence Motifs

Motif: "a recurring salient thematic element"

Last few slides described *structural* motifs in *proteins*

Equally interesting are the *sequence* motifs in *DNA* to which these proteins bind - e.g. , one leucine zipper dimer might bind (with varying affinities) to dozens or hundreds of similar sequences

DNA binding site summary

Complex "code"

Short patches (4-8 bp)

Often near each other (1 turn = 10 bp)

Often reverse-complements (dimer symmetry)

Not perfect matches

E. coli Promoters

"TATA Box" ~ 10bp upstream of transcription start

How to define it?

- *Consensus* is TATAAT
- BUT all differ from it
- Allow k mismatches?
- Equally weighted?
- Wildcards like R, Y? ({A,G}, {C,T}, resp.)

```
TACGAT
TAAAAT
TATACT
GATAAT
TATGAT
TATGTT
```

E. coli Promoters

"TATA Box" - consensus TATAAT

~10bp upstream of transcription start

Not exact: of 168 studied (mid 80's)

- nearly all had 2/3 of TAxyzT
- 80-90% had all 3
- 50% agreed in each of x,y,z
- no perfect match

Other common features at -35, etc.

TATA Box Frequencies

pos / base	1	2	3	4	5	6
A	2	95	26	59	51	1
C	9	2	14	13	20	3
G	10	1	16	15	13	0
T	79	3	44	13	17	96

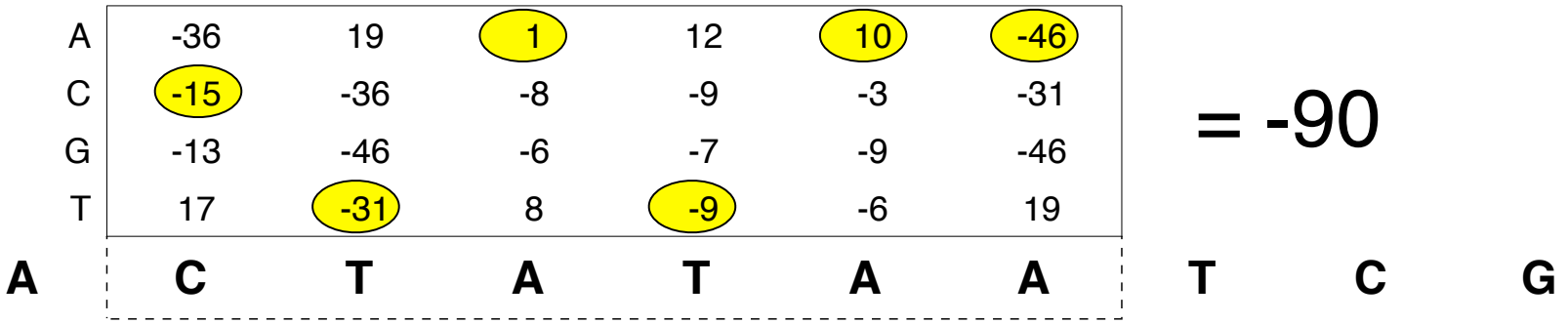
TATA Scores

A "Weight Matrix Model" or "WMM"

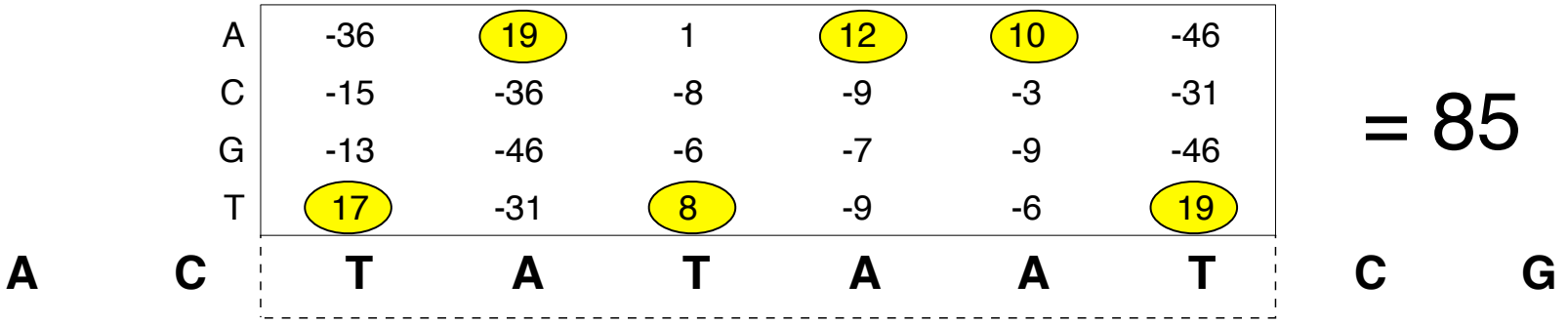
pos / base	1	2	3	4	5	6
A	-36	19	1	12	10	-46
C	-15	-36	-8	-9	-3	-31
G	-13	-46	-6	-7	-9	$-46_{(?)}$
T	17	-31	8	-9	-6	19

score = 10 $\log_2$ foreground:background odds ratio, rounded

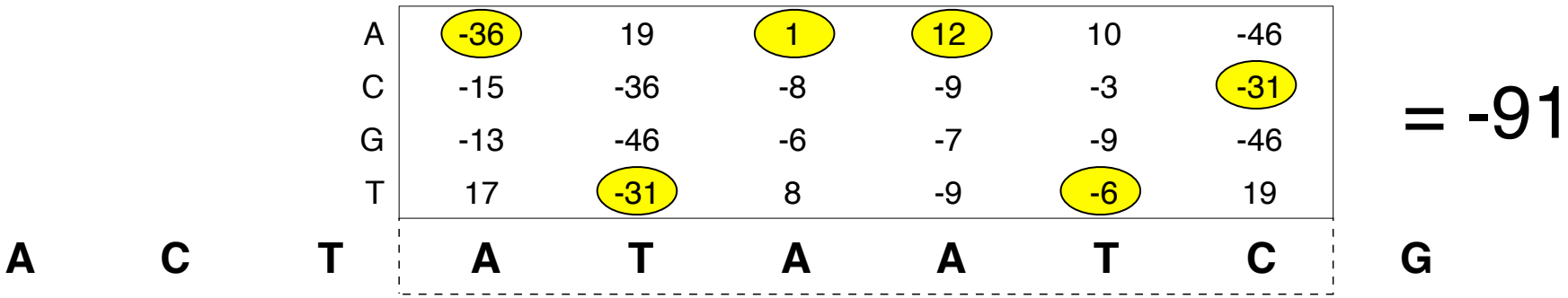
Scanning for TATA



= -90



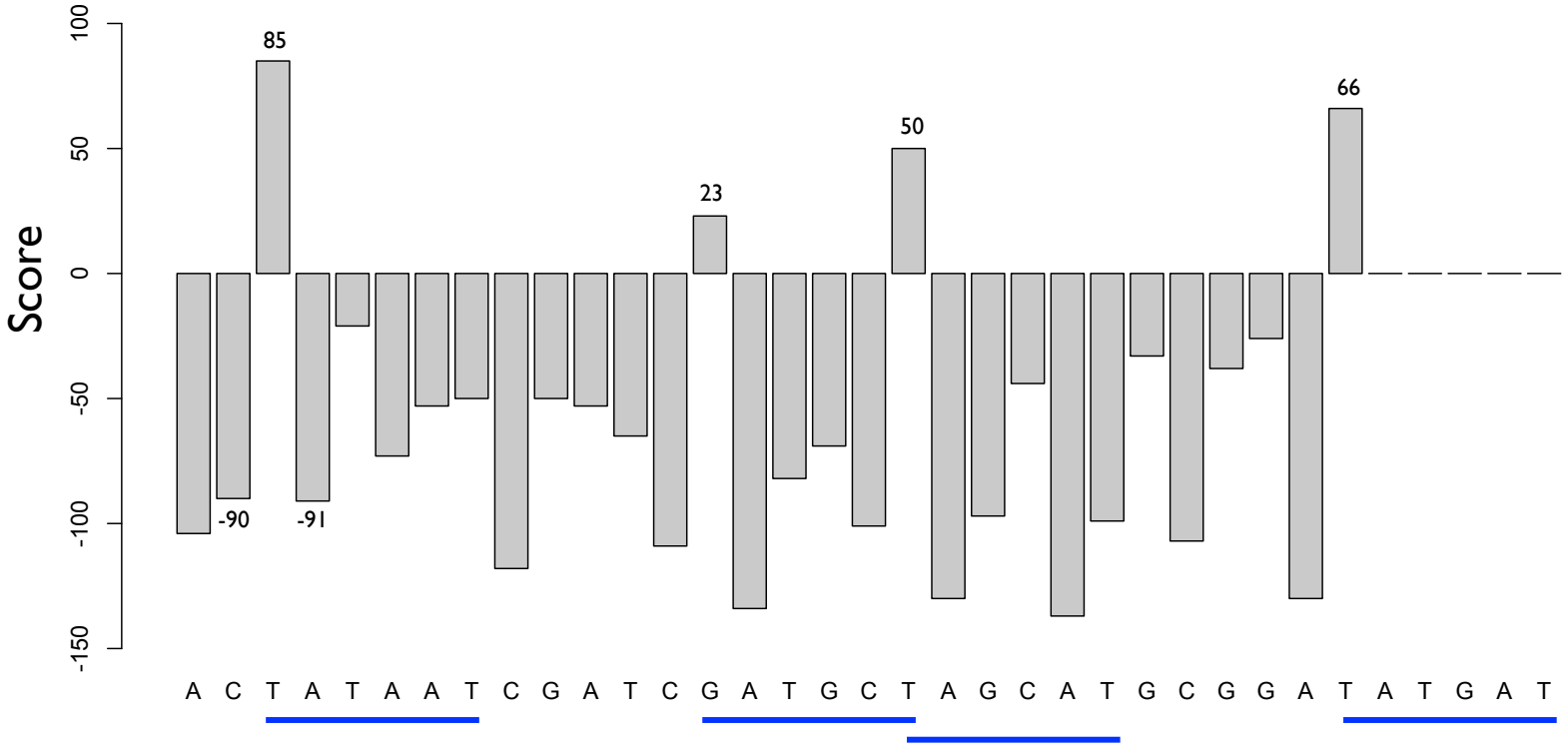
= 85



= -91

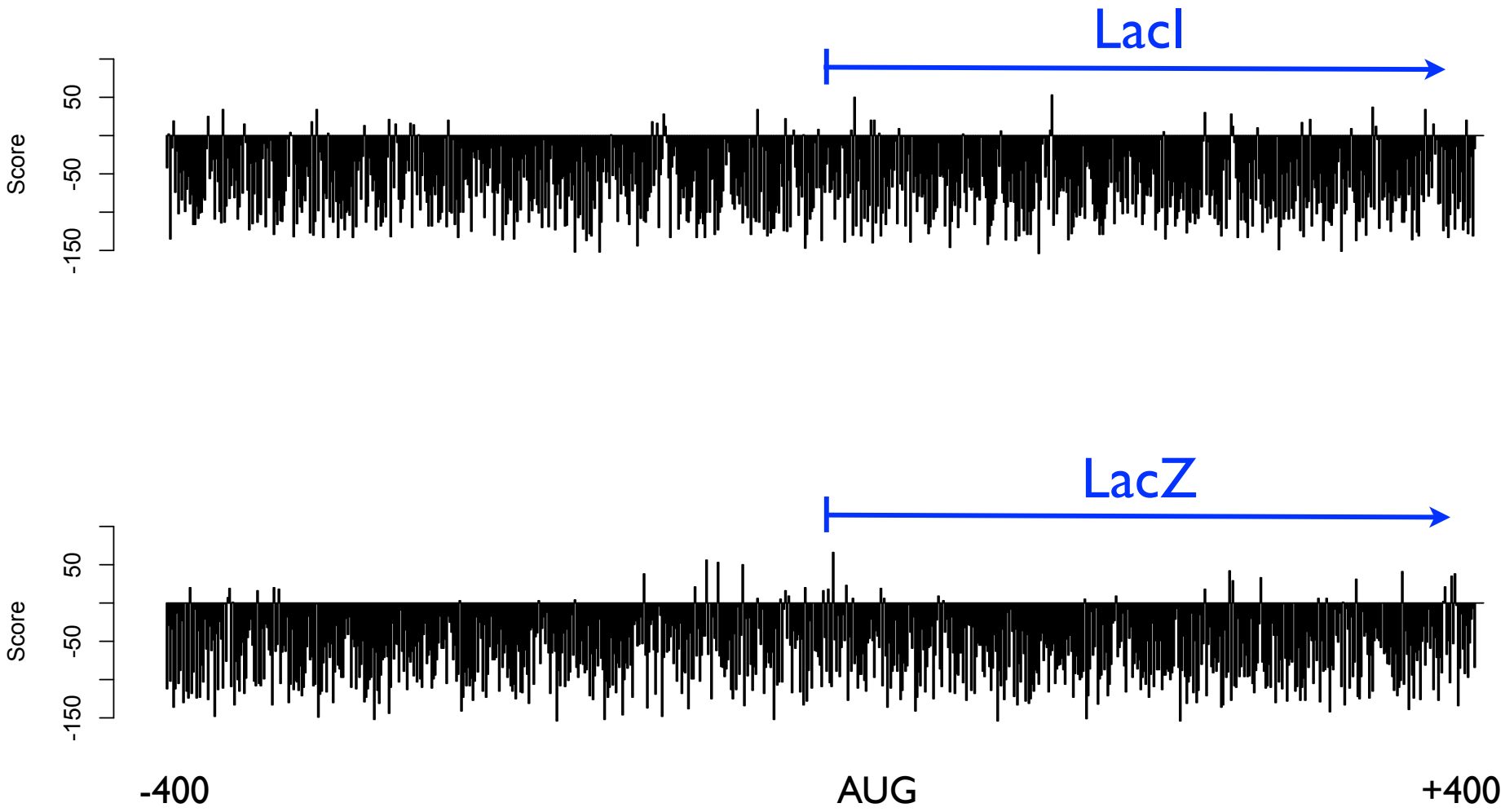
Stormo, Ann. Rev. Biophys. Biophys Chem, 17, 1988, 241-263

Scanning for TATA



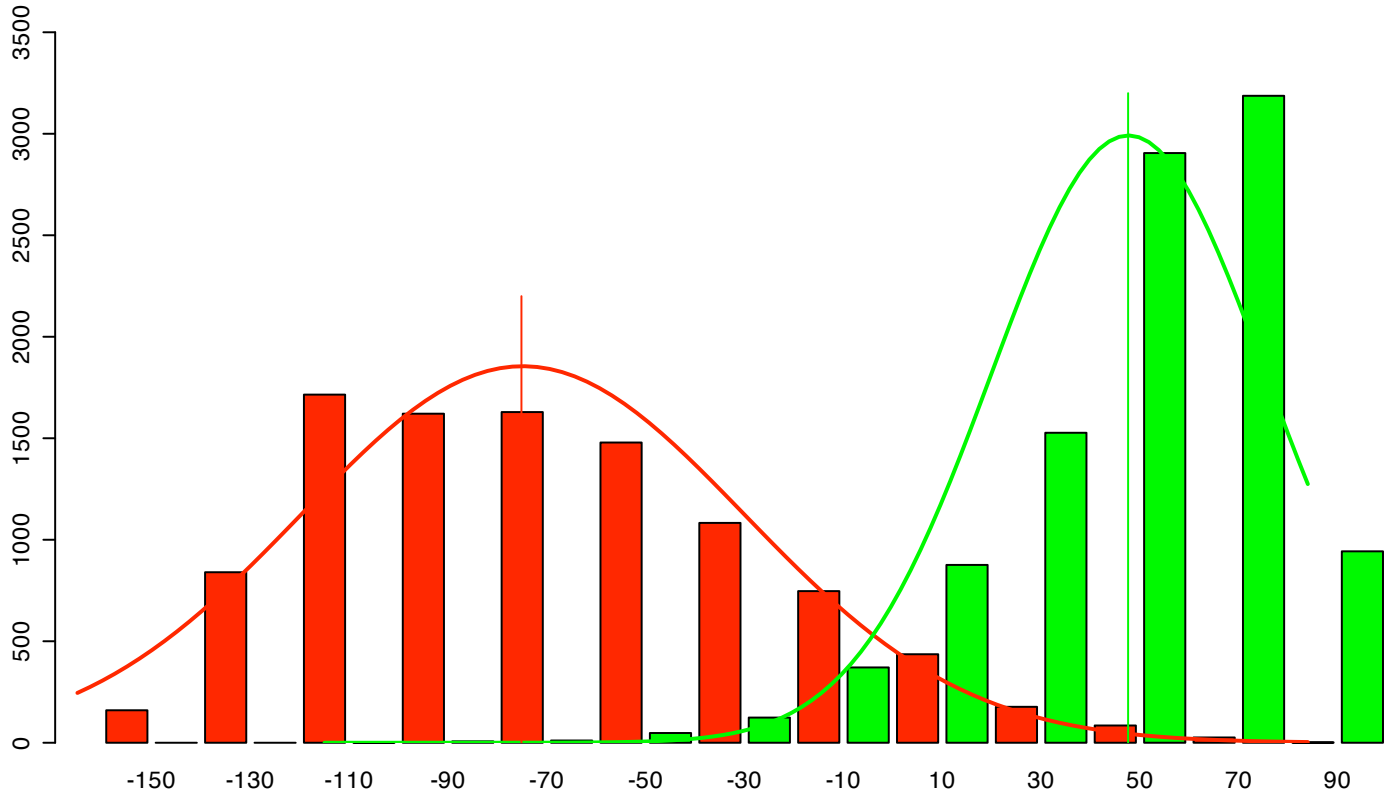
See also slide 58

TATA Scan at 2 genes



Score Distribution

(Simulated)



10^4 random 6-mers from foreground (green) or uniform background (red)

Weight Matrices: Statistics

Assume:

$f_{b,i}$ = frequency of base *b* in position *i in TATA*

f_b = frequency of base *b* in all sequences

Log likelihood ratio, given $S = B_1 B_2 ... B_6$:

$$\log \left(\frac{P(S|\text{“tata”})}{P(S|\text{“non-tata”})} \right) = \log \frac{\prod_{i=1}^{6} f_{B_i,i}}{\prod_{i=1}^{6} f_{B_i}} = \sum_{i=1}^{6} \log \frac{f_{B_i,i}}{f_{B_i}}$$

Assumes *independence*

Neyman-Pearson

Given a sample $x_1, x_2, ..., x_n$, from a distribution $f(...|\Theta)$ with parameter Θ, want to test hypothesis $\Theta = \theta_1$ vs $\Theta = \theta_2$.

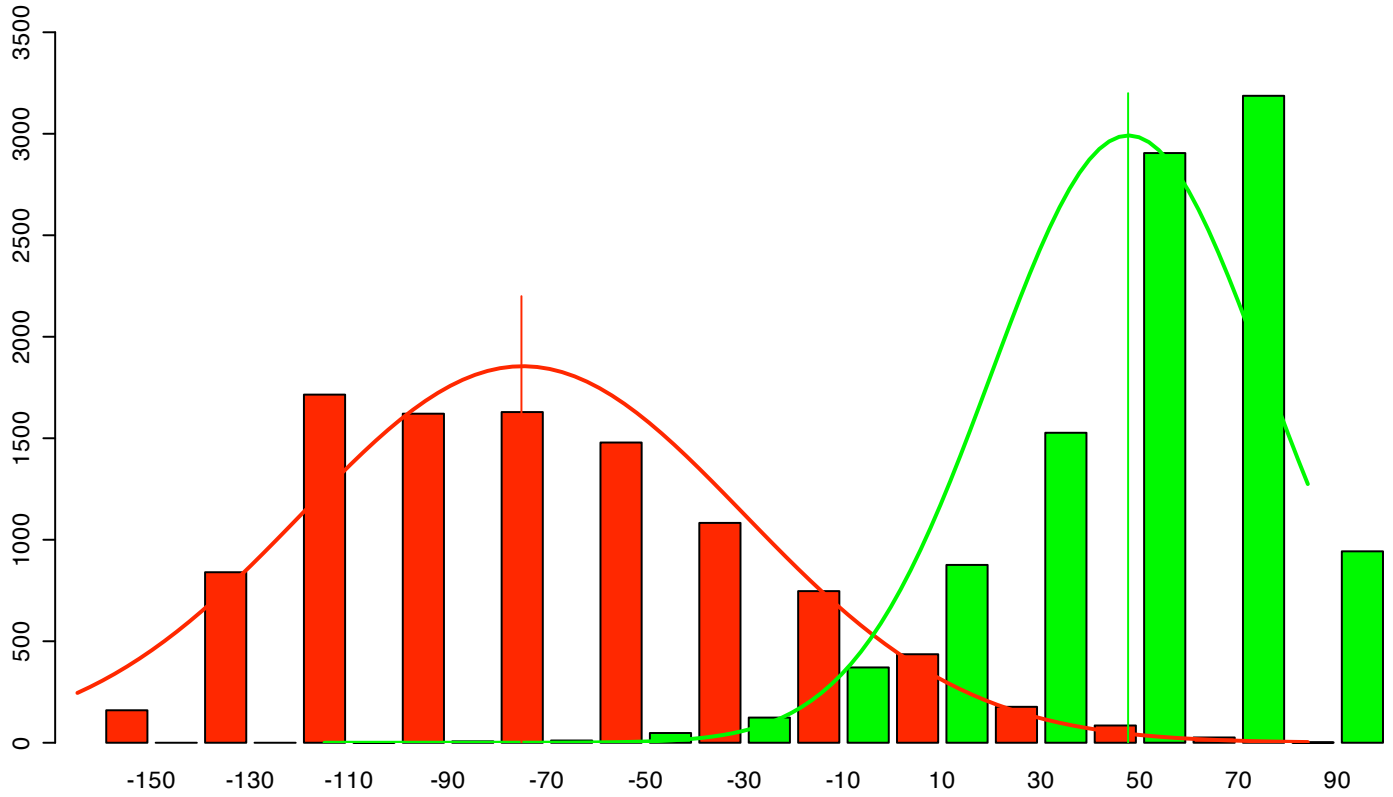
Might as well look at *likelihood ratio:*

$$\frac{f(x_1, x_2, ..., x_n|\theta_1)}{f(x_1, x_2, ..., x_n|\theta_2)} > \tau$$

(or *log likelihood ratio*)

Score Distribution

(Simulated)



10^4 random 6-mers from foreground (green) or uniform background (red)

What's best WMM?

Given, say, 168 sequences $s_1, s_2, ..., s_k$ of length 6, assumed to be generated at random according to a WMM defined by 6 x (4-1) parameters θ, what's the best θ?

E.g., what's MLE for θ given data $s_1, s_2, ..., s_k$?

Answer: like coin flips or dice rolls, count frequencies per position (see HW?)

Weight Matrices: Chemistry

Experiments show ~80% correlation of log likelihood weight matrix scores to measured binding energy of RNA polymerase to variations on TATAAT consensus
[Stormo & Fields]

Another WMM example

8 Sequences:

ATG
ATG
ATG
ATG
ATG
GTG
GTG
TTG

Freq.	Col 1	Col 2	Col 3
A	0.625	0	0
C	0	0	0
G	0.250	0	1
T	0.125	1	0

LLR	Col 1	Col 2	Col 3
A	1.32	-∞	-∞
C	-∞	-∞	-∞
G	0	-∞	2.00
T	-1.00	2.00	-∞

Log-Likelihood Ratio:

$$\log_2 \frac{f_{x_i,i}}{f_{x_i}}, \quad f_{x_i} = \frac{1}{4}$$ (uniform background)

Non-uniform Background

- *E. coli* - DNA approximately 25% A, C, G, T
- *M. jannaschi* - 68% A-T, 32% G-C

LLR from previous example, assuming

$$f_A = f_T = 3/8$$
$$f_C = f_G = 1/8$$

LLR	Col 1	Col 2	Col 3
A	0.74	-∞	-∞
C	-∞	-∞	-∞
G	1.00	-∞	3.00
T	-1.58	1.42	-∞

e.g., G in col 3 is 8 x more likely via WMM than background, so ($\log_2$) score = 3 (bits).

Relative Entropy

AKA Kullback-Liebler Divergence,
AKA Information Content

Intuitively "distance", but technically not, since it's asymmetric

Given distributions P, Q

$$H(P||Q) = \sum_{x \in \Omega} P(x) \log \frac{P(x)}{Q(x)} \quad \geq 0$$

Notes:

$$\text{Let } P(x) \log \frac{P(x)}{Q(x)} = 0 \text{ if } P(x) = 0 \text{ [since } \lim_{y \to 0} y \log y = 0]$$

$$\text{Undefined if } 0 = Q(x) < P(x)$$

WMM: How "Informative"? Mean score of site vs bkg?

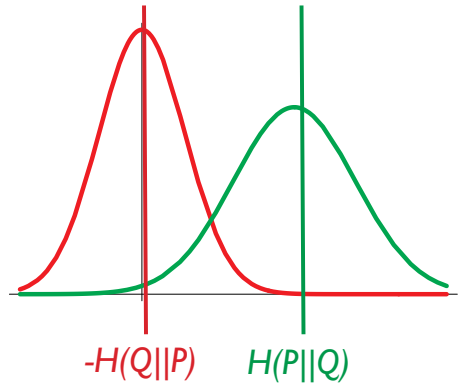
For any fixed length sequence *x*, let

P(x) = Prob. of *x* according to WMM

Q(x) = Prob. of *x* according to background

Relative Entropy:

$$H(P||Q) = \sum_{x \in \Omega} P(x) \log_2 \frac{P(x)}{Q(x)}$$

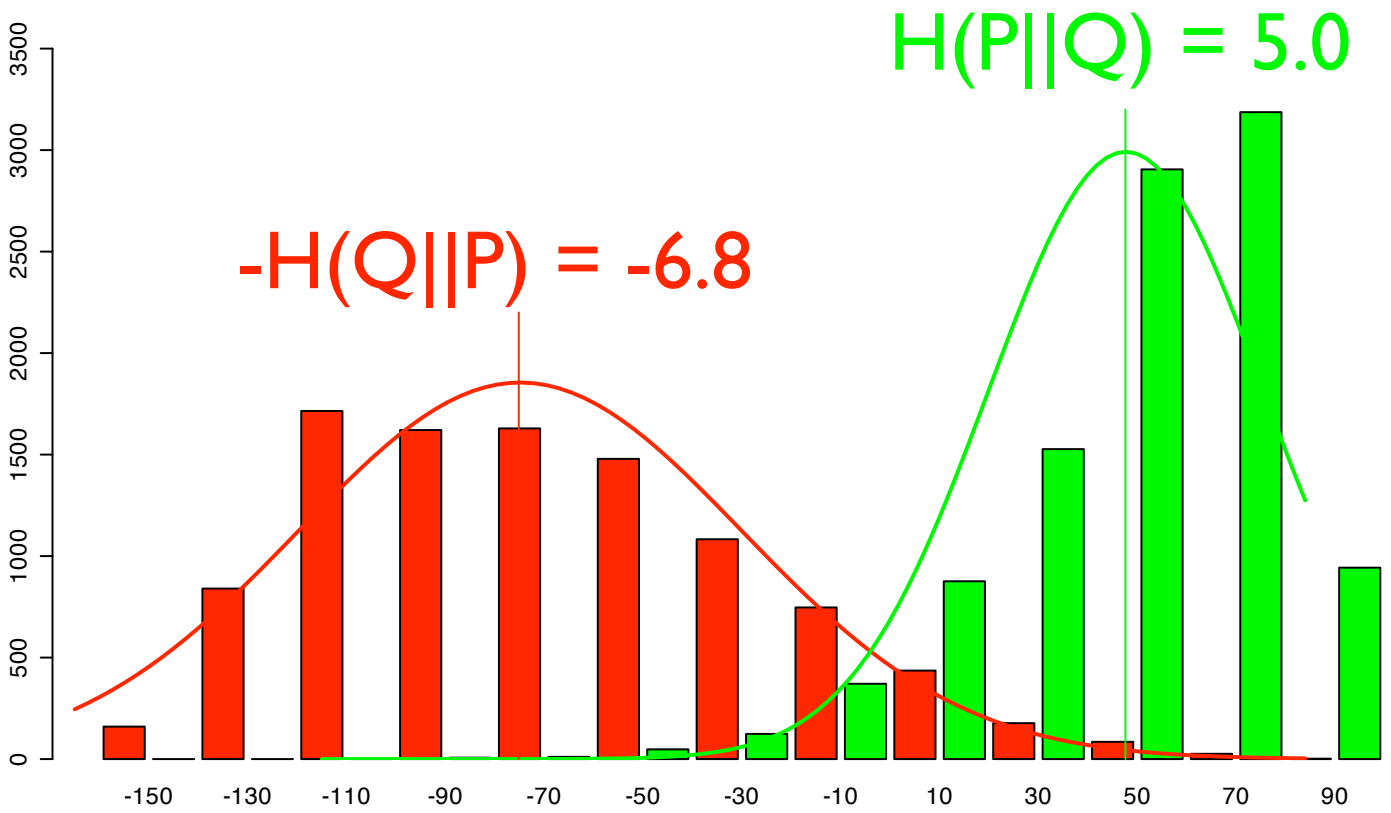


H(P||Q) is *expected log likelihood score* of a sequence randomly chosen from *WMM* *(wrt background);*

-H(Q||P) is expected score of *Background* *(wrt WMM)*

Expected score difference: *H(P||Q)* + *H(Q||P)*

WMM Scores vs Relative Entropy



On average, foreground model scores > background by 11.8 bits
(score difference of 118 on 10x scale used in examples above).

For a WMM:

$$H(P||Q) \quad = \quad \sum_i H(P_i||Q_i)$$

where P_i and Q_i are the WMM/background distributions for column i.

Proof: exercise

Hint: Use the assumption of independence between WMM columns

WMM Example, cont.

Freq.	Col 1	Col 2	Col 3
A	0.625	0	0
C	0	0	0
G	0.250	0	1
T	0.125	1	0

Uniform

LLR	Col 1	Col 2	Col 3	
A	1.32	-∞	-∞	
C	-∞	-∞	-∞	
G	0	-∞	2.00	
T	-1.00	2.00	-∞	
RelEnt	0.70	2.00	2.00	4.70

Non-uniform

LLR	Col 1	Col 2	Col 3	
A	0.74	-∞	-∞	
C	-∞	-∞	-∞	
G	1.00	-∞	3.00	
T	-1.58	1.42	-∞	
RelEnt	0.51	1.42	3.00	4.93

Pseudocounts

Are the $-\infty$'s a problem?

- Certain that a given residue *never* occurs in a given position? Then $-\infty$ just right.
- Else, it may be a small-sample artifact

Typical fix: add a *pseudocount* to each observed count—small constant (e.g., .5, 1)

Sounds *ad hoc*; there is a Bayesian justification

WMM Summary

Weight Matrix Model (aka Position Weight Matrix, PWM, Position Specific Scoring Matrix, PSSM, "possum", 0th order Markov model)

Simple statistical model assuming independence between adjacent positions

To build: count (+ pseudocount) letter frequency per position, log likelihood ratio to background

To scan: add LLRs per position, compare to threshold

Generalizations to higher order models (i.e., letter frequency per position, conditional on neighbor) also possible, with enough training data

How-to Questions

Given aligned motif instances, build model?

- Frequency counts (above, maybe w/ pseudocounts)

Given a model, find (probable) instances

- Scanning, as above

Given unaligned strings thought to contain a motif, find it? (e.g., upstream regions of co-expressed genes)

- Hard ... rest of lecture.

Motif Discovery

Unfortunately, finding a site of max relative entropy in a set of unaligned sequences is NP-hard [Akutsu]

Motif Discovery: 4 example approaches

Brute Force

Greedy search

Expectation Maximization

Gibbs sampler

Brute Force

Input:

Motif length L, plus sequences $s_1, s_2, ..., s_k$ (all of length $n+L-1$, say), each with one instance of an unknown motif

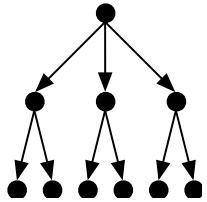
Algorithm:

Build all k-tuples of length L subsequences, one from each of $s_1, s_2, ..., s_k$ (n^k such tuples)

Compute relative entropy of each

Pick best

Brute Force, II



Input:

Motif length L, plus seqs $s_1, s_2, ..., s_k$ (all of length n+L-1, say), each with one instance of an unknown motif

Algorithm in more detail:

Build singletons: each len L subseq of each $s_1, s_2, ..., s_k$ (nk sets)

Extend to pairs: len L subseqs of each pair of seqs ($n^2\binom{k}{2}$ sets)

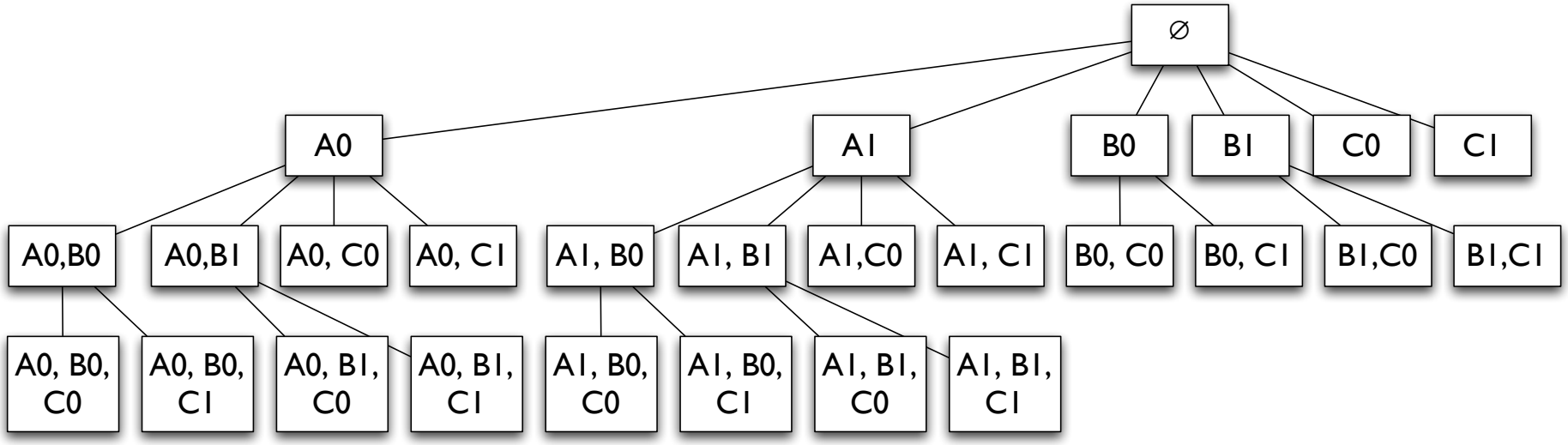
Then triples: len L subseqs of each triple of seqs ($n^3\binom{k}{3}$ sets)

Repeat until all have k sequences ($n^k\binom{k}{k}$ sets)

$(n+1)^k$ in total; compute relative entropy of each; pick best

problem: astronomically slooooow

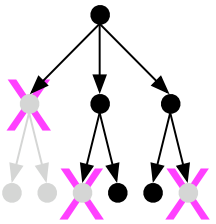
Example



Three sequences (A, B, C), each with two possible motif positions (0,1)

Greedy Best-First

[Hertz, Hartzell & Stormo, 1989, 1990]



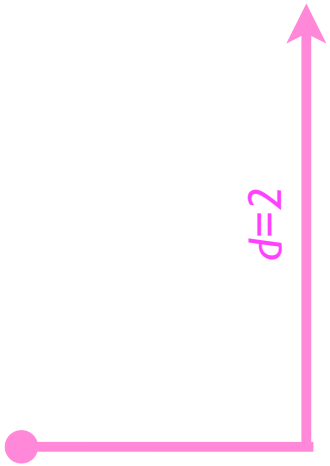
Input:

Sequences $s_1, s_2, ..., s_k$; motif length L;

"breadth" d, say $d = 1000$

Algorithm:

As in brute, but discard all but best d relative entropies at each stage



usual "greedy" problems

Expectation Maximization
[MEME, Bailey & Elkan, 1995]

Input (as above):

- Sequence s_1, s_2, ..., s_k; motif length l; background model; again assume one instance per sequence (variants possible)

Algorithm: EM

- Visible data: the sequences
- Hidden data: where's the motif

$$Y_{i,j} = \begin{cases} 1 & \text{if motif in sequence } i \text{ begins at position } j \\ 0 & \text{otherwise} \end{cases}$$

- Parameters θ: The WMM

MEME Outline

Typical EM algorithm:

Parameters θ^t at t^{th} iteration, used to estimate where the motif instances are (the hidden variables)

Use those estimates to re-estimate the parameters θ to maximize likelihood of observed data, giving θ^{t+1}

Repeat

Key: given a few good matches to best motif, expect to pick more

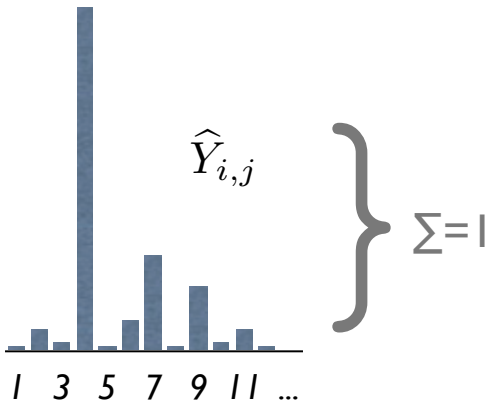
Expectation Step

(where are the motif instances?)

$$
\begin{aligned}
\widehat{Y}_{i,j} &= E(Y_{i,j} \mid s_i, \theta^t) \\
&= P(Y_{i,j} = 1 \mid s_i, \theta^t) \\
&= P(s_i \mid Y_{i,j} = 1, \theta^t) \frac{P(Y_{i,j}=1|\theta^t)}{P(s_i|\theta^t)} \\
&= cP(s_i \mid Y_{i,j} = 1, \theta^t) \\
&= c' \prod_{k=1}^{l} P(s_{i,j+k-1} \mid \theta^t)
\end{aligned}
$$

$E = 0 \cdot P(0) + 1 \cdot P(1)$

Bayes



where c' is chosen so that $\sum_j \widehat{Y}_{i,j} = 1$.

Recall slide 32

Maximization Step

(what is the motif?)

Find θ maximizing expected log likelihood:

$$
\begin{aligned}
Q(\theta \mid \theta^t) &= E_{Y \sim \theta^t}[\log P(s, Y \mid \theta)] \\
&= E_{Y \sim \theta^t}[\log \textstyle\prod_{i=1}^{k} P(s_i, Y_i \mid \theta)] \\
&= E_{Y \sim \theta^t}[\textstyle\sum_{i=1}^{k} \log P(s_i, Y_i \mid \theta)] \\
&= E_{Y \sim \theta^t}[\textstyle\sum_{i=1}^{k} \sum_{j=1}^{|s_i|-l+1} Y_{i,j} \log P(s_i, Y_{i,j} = 1 \mid \theta)] \\
&= E_{Y \sim \theta^t}[\textstyle\sum_{i=1}^{k} \sum_{j=1}^{|s_i|-l+1} Y_{i,j} \log(P(s_i \mid Y_{i,j} = 1, \theta) P(Y_{i,j} = 1 \mid \theta))] \\
&= \textstyle\sum_{i=1}^{k} \sum_{j=1}^{|s_i|-l+1} E_{Y \sim \theta^t}[Y_{i,j}] \log P(s_i \mid Y_{i,j} = 1, \theta) + C \\
&= \textstyle\sum_{i=1}^{k} \sum_{j=1}^{|s_i|-l+1} \widehat{Y}_{i,j} \log P(s_i \mid Y_{i,j} = 1, \theta) + C
\end{aligned}
$$

M-Step (cont.)

$$Q(\theta \mid \theta^t) \quad = \quad \sum_{i=1}^{k} \sum_{j=1}^{|s_i|-l+1} \widehat{Y}_{i,j} \log P(s_i \mid Y_{i,j} = 1, \theta) + C$$

Exercise: Show this is maximized by "counting" letter frequencies over all possible motif instances, with counts weighted by $\widehat{Y}_{i,j}$, again the "obvious" thing.

s_1 : ACGGATT...

...

s_k : GC...TCGGAC

$\widehat{Y}_{1,1}$	ACGG
$\widehat{Y}_{1,2}$	CGGA
$\widehat{Y}_{1,3}$	GGAT
⋮	⋮
$\widehat{Y}_{k,l-1}$	CGGA
$\widehat{Y}_{k,l}$	GGAC

Initialization

1. Try *every* motif-length substring, and use as initial θ a WMM with, say, 80% of weight on that sequence, rest uniform
2. Run a few iterations of each
3. Run best few to convergence

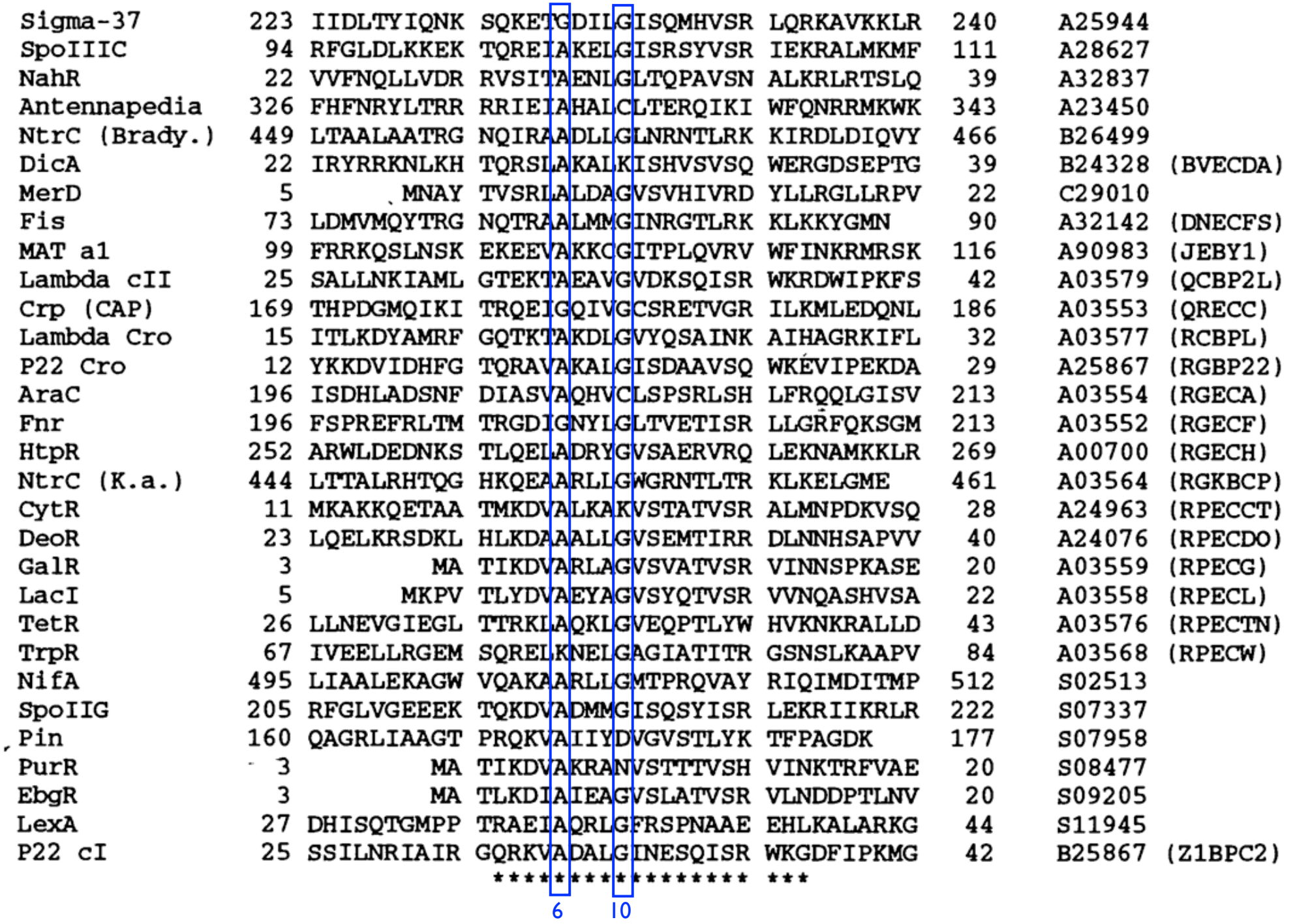
(Having a supercomputer helps):

http://meme.sdsc.edu/

Another Motif Discovery Approach

The Gibbs Sampler

Lawrence, *et al.* "Detecting Subtle Sequence Signals: A Gibbs Sampling Strategy for Multiple Sequence Alignment," *Science* 1993


Sigma-37 223 IIDLTYIQNK SQKETGDILGISQMHVSR LQRKAVKKLR 240 A25944
SpoIIIC 94 RFGLDLKKEK TQREIAKELGISRSYVSR IEKRALMKMF 111 A28627
NahR 22 VVFNQLLVDR RVSITAENLGLTQPAVSN ALKRLRTSLQ 39 A32837
Antennapedia 326 FHFNRYLTRR RRIEIAHALCLTERQIKI WFQNRRMKWK 343 A23450
NtrC (Brady.) 449 LTAALAATRG NQIRAADLLGLNRNTLRK KIRDLDIQVY 466 B26499
DicA 22 IRYRRKNLKH TQRSLAKALKISHVSVSQ WERGDSEPTG 39 B24328 (BVECDA)
MerD 5 MNAY TVSRLALDAGVSVHIVRD YLLRGLLRPV 22 C29010
Fis 73 LDMVMQYTRG NQTRAALMMGINRGTLRK KLKKYGMN 90 A32142 (DNECFS)
MAT a1 99 FRRKQSLNSK EKEEVAKKCGITPLQVRV WFINKRMRSK 116 A90983 (JEBY1)
Lambda cII 25 SALLNKIAML GTEKTAEAVGVDKSQISR WKRDWIPKFS 42 A03579 (QCBP2L)
Crp (CAP) 169 THPDGMQIKI TRQEIGQIVGCSRETVGR ILKMLEDQNL 186 A03553 (QRECC)
Lambda Cro 15 ITLKDYAMRF GQTKTAKDLGVYQSAINK AIHAGRKIFL 32 A03577 (RCBPL)
P22 Cro 12 YKKDVIDHFG TQRAVAKALGISDAAVSQ WKEVIPEKDA 29 A25867 (RGBP22)
AraC 196 ISDHLADSNF DIASVAQHVCLSPSRLSH LFRQQLGISV 213 A03554 (RGECA)
Fnr 196 FSPREFRLTM TRGDIGNYLGLTVETISR LLGRFQKSGM 213 A03552 (RGECF)
HtpR 252 ARWLDEDNKS TLQELADRYGVSAERVRQ LEKNAMKKLR 269 A00700 (RGECH)
NtrC (K.a.) 444 LTTALRHTQG HKQEAARLLGWGRNTLTR KLKELGME 461 A03564 (RGKBCP)
CytR 11 MKAKKQETAA TMKDVALKAKVSTATVSR ALMNPDKVSQ 28 A24963 (RPECCT)
DeoR 23 LQELKRSDKL HLKDAAALLGVSEMTIRR DLNNHSAPVV 40 A24076 (RPECDO)
GalR 3 MA TIKDVARLAGVSVATVSR VINNSPKASE 20 A03559 (RPECG)
LacI 5 MKPV TLYDVAEYAGVSYQTVSR VVNQASHVSA 22 A03558 (RPECL)
TetR 26 LLNEVGIEGL TTRKLAQKLGVEQPTLYW HVKNKRALLD 43 A03576 (RPECTN)
TrpR 67 IVEELLRGEM SQRELKNELGAGIATITR GSNSLKAAPV 84 A03568 (RPECW)
NifA 495 LIAALEKAGW VQAKAARLLGMTPRQVAY RIQIMDITMP 512 S02513
SpoIIG 205 RFGLVGEEEK TQKDVADMMGISQSYISR LEKRIIKRLR 222 S07337
Pin 160 QAGRLIAAGT PRQKVAIIYDVGVSTLYK TFPAGDK 177 S07958
PurR 3 MA TIKDVAKRANVSTTTVSH VINKTRFVAE 20 S08477
EbgR 3 MA TLKDIAIEAGVSLATVSR VLNDDPTLNV 20 S09205
LexA 27 DHISQTGMPP TRAEIAQRLGFRSPNAAE EHLKALARKG 44 S11945
P22 cI 25 SSILNRIAIR GQRKVADALGINESQISR WKGDFIPKMG 42 B25867 (Z1BPC2)
********** ********* ***
6
10

B

	Position in site																	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Arg	94	222	265	137	9	9	137	137	9	9	9	52	222	94	94	9	265	606
Lys	9	133	442	380	9	71	380	194	9	133	9	9	71	9	9	9	71	256
Glu	53	9	96	401	9	9	140	140	9	9	9	53	140	140	9	9	9	53
Asp	67	9	9	473	9	9	299	125	9	67	9	67	67	9	9	9	9	67
Gln	9	600	224	9	9	9	224	9	9	9	9	9	278	63	278	9	9	170
His	240	9	9	9	9	9	125	125	9	9	9	9	125	125	125	9	9	240
Asn	168	9	9	9	9	9	168	89	9	89	9	248	9	168	89	9	89	89
Ser	117	9	117	117	9	9	9	9	9	9	9	819	63	387	63	9	819	9
Gly	151	9	56	9	9	151	9	9	9	1141	9	151	9	56	9	9	56	9
Ala	9	9	112	43	181	901	43	181	215	9	43	9	43	181	112	43	78	9
Thr	915	130	130	9	251	9	9	9	9	9	9	311	130	70	855	9	130	9
Pro	76	9	9	9	9	9	9	9	9	9	9	9	210	210	9	9	9	9
Cys	9	9	9	9	9	9	9	9	295	581	295	9	9	9	9	9	9	9
Val	58	107	9	9	500	9	9	9	156	9	598	9	205	58	9	746	9	58
Leu	9	121	9	9	149	9	93	149	458	9	149	9	37	37	9	177	9	9
Ile	9	166	114	61	323	9	114	166	9	9	427	9	61	9	61	427	9	61
Met	9	104	9	9	9	9	9	198	198	9	104	9	9	198	9	9	9	9
Tyr	9	9	136	9	9	9	9	262	262	9	9	136	136	9	262	9	262	136
Phe	9	9	9	9	9	9	9	9	9	9	108	9	9	9	9	9	9	9
Trp	9	9	9	9	9	9	9	9	9	9	366	9	9	9	9	9	9	366

6 10

Some History

Geman & Geman, IEEE PAMI 1984

Hastings, Biometrika, 1970

Metropolis, Rosenbluth, Rosenbluth, Teller & Teller, "Equations of State Calculations by Fast Computing Machines," J. Chem. Phys. 1953

Josiah Williard Gibbs, 1839-1903, American physicist, a pioneer of thermodynamics

How to Average

An old problem:

n random variables:	$x_1, x_2, \ldots, x_k$
Joint distribution (p.d.f.):	$P(x_1, x_2, \ldots, x_k)$
Some function:	$f(x_1, x_2, \ldots, x_k)$
Want Expected Value:	$E(f(x_1, x_2, \ldots, x_k))$

How to Average

$$E(f(x_1, x_2, \ldots, x_k)) = \int_{x_1} \int_{x_2} \cdots \int_{x_k} f(x_1, x_2, \ldots, x_k) \cdot P(x_1, x_2, \ldots, x_k) dx_1 dx_2 \ldots dx_k$$

Approach 1: direct integration
(rarely solvable analytically, esp. in high dim)

Approach 2: numerical integration
(often difficult, e.g., unstable, esp. in high dim)

Approach 3: Monte Carlo integration
sample $\vec{x}^{(1)}, \vec{x}^{(2)}, \ldots \vec{x}^{(n)} \sim P(\vec{x})$ and average:

$$E(f(\vec{x})) \approx \frac{1}{n} \sum_{i=1}^{n} f(\vec{x}^{(i)})$$

Markov Chain Monte Carlo (MCMC)

- *Independent* sampling also often hard, but *not required* for expectation
- MCMC $\vec{X}_{t+1} \sim P(\vec{X}_{t+1} \mid \vec{X}_t)$ w/ stationary dist = *P*
- Simplest & most common: Gibbs Sampling

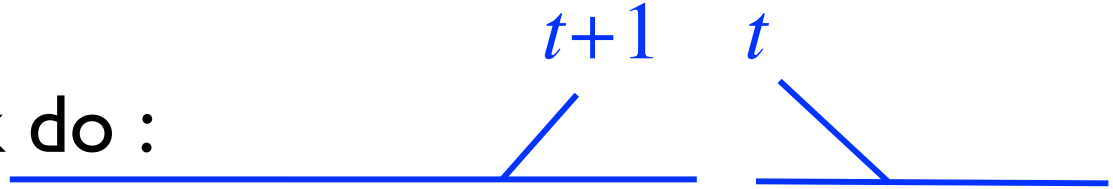
$$P(x_i \mid x_1, x_2, \ldots, x_{i-1}, x_{i+1}, \ldots, x_k)$$

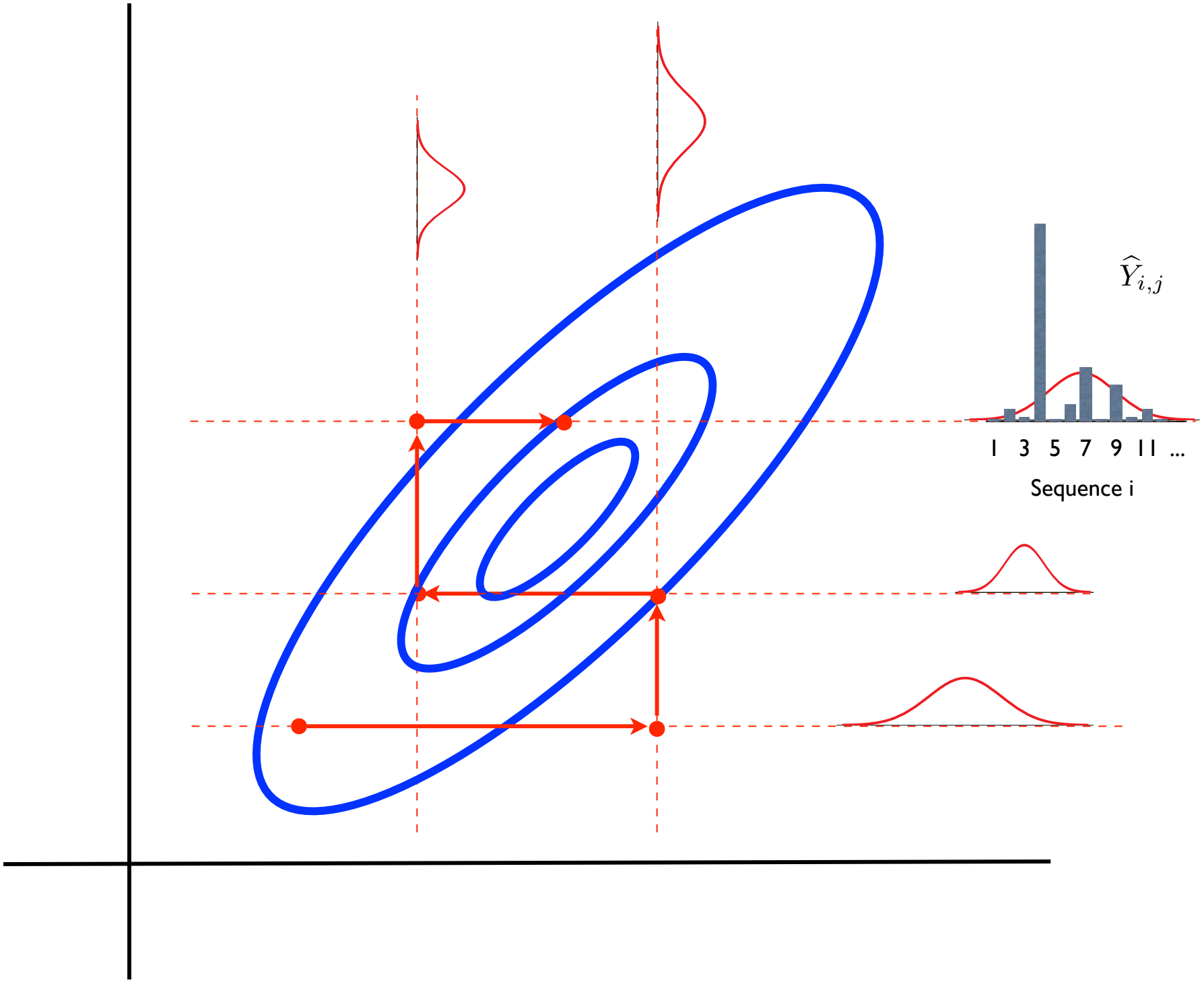
- Algorithm

  for t = 1 to ∞

    for i = 1 to k do :

$$x_{t+1,i} \sim P(x_{t+1,i} \mid x_{t+1,1}, x_{t+1,2}, \ldots, x_{t+1,i-1}, x_{t,i+1}, \ldots, x_{t,k})$$




$\widehat{Y}_{i,j}$
1 3 5 7 9 11 ...
Sequence i

Input: again assume sequences $s_1, s_2, ..., s_k$ with one length w motif per sequence

Motif model: WMM

Parameters: Where are the motifs? for $1 \leq i \leq k$, have $1 \leq x_i \leq |s_i|$-w+1

"Full conditional": to calc

$$P(x_i = j \mid x_1, x_2, \ldots, x_{i-1}, x_{i+1}, \ldots, x_k)$$

build WMM from motifs in all sequences except *i*, then calc prob that motif in i^{th} seq occurs at *j* by usual "scanning" alg.

Overall Gibbs Alg

Randomly initialize x_i's

for t = 1 to ∞

  for i = 1 to k

    discard motif instance from s_i;

    recalc WMM from rest

    for j = 1 ... $|s_i|$-w+1

      calculate prob that i^{th} motif is at j:

      $$P(x_i = j \mid x_1, x_2, \ldots, x_{i-1}, x_{i+1}, \ldots, x_k)$$

      pick new x_i according to that distribution

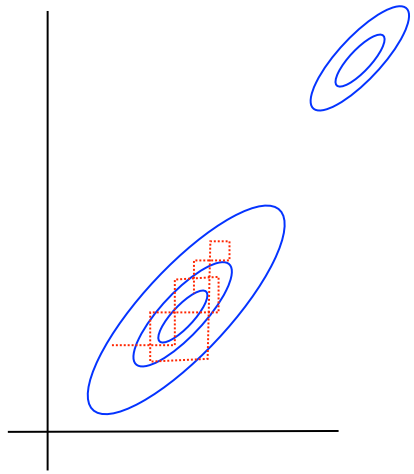
Similar to MEME, but it would *average* over, rather than *sample* from

Issues

Burnin - how long must we run the chain to reach stationarity?

Mixing - how long a post-burnin sample must we take to get a good sample of the stationary distribution? In particular:

- Samples are not independent; may not "move" freely through the sample space
- Many isolated modes

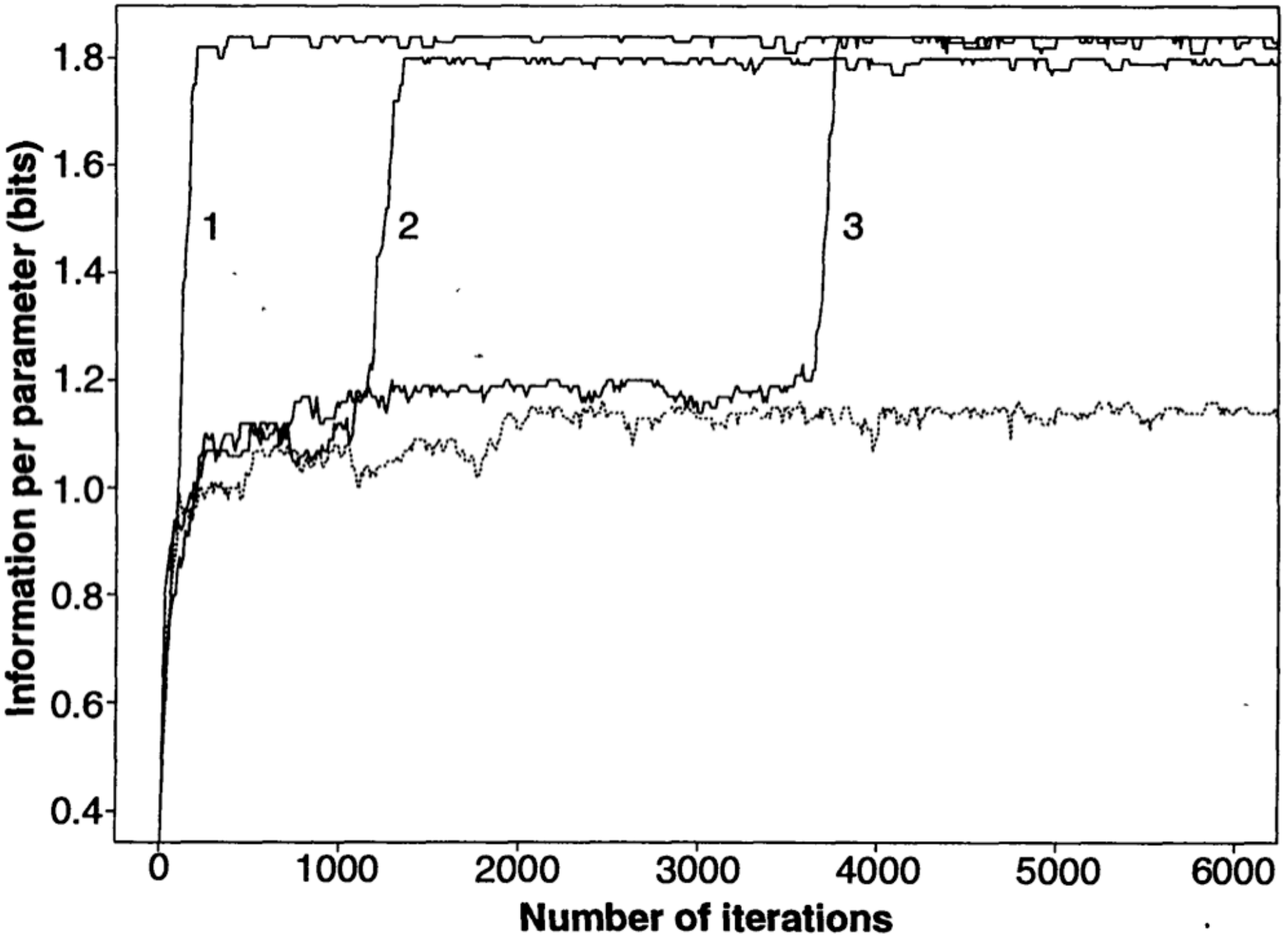


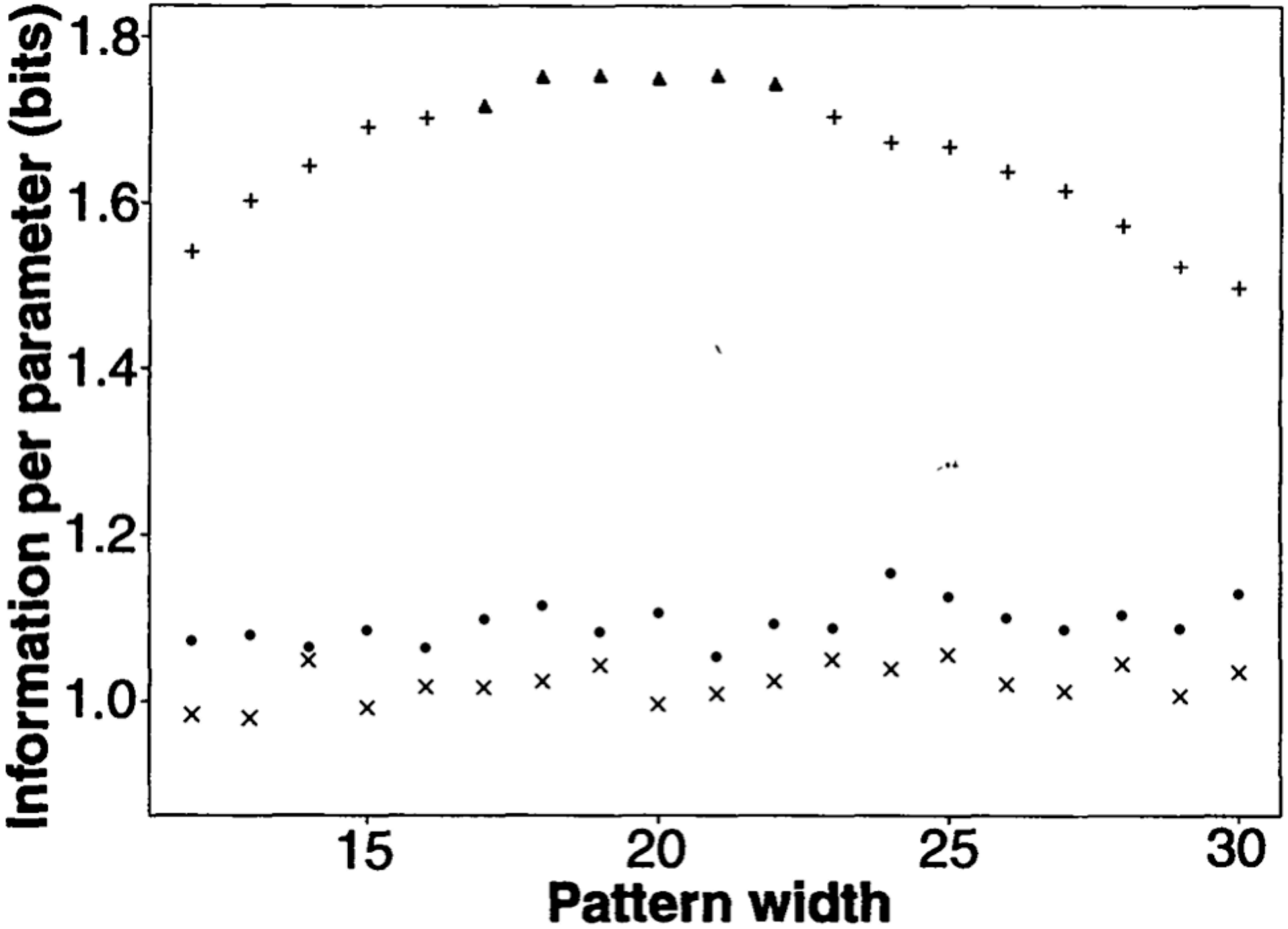
Variants & Extensions

"Phase Shift" - may settle on suboptimal solution that overlaps part of motif. Periodically try moving all motif instances a few spaces left or right.

Algorithmic adjustment of pattern width: Periodically add/remove flanking positions to maximize (roughly) average relative entropy per position

Multiple patterns per string


Information per parameter (bits)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
1
2
3
0
1000
2000
3000
4000
5000
6000
Number of iterations


Information per parameter (bits)
1.8
1.6
1.4
1.2
1.0
15
20
25
30
Pattern width

NATURE BIOTECHNOLOGY VOLUME 23 NUMBER 1 JANUARY 2005

Assessing computational tools for the discovery of transcription factor binding sites

Martin Tompa[1,2], Nan Li[1], Timothy L Bailey[3], George M Church[4], Bart De Moor[5], Eleazar Eskin[6], Alexander V Favorov[7,8], Martin C Frith[9], Yutao Fu[9], W James Kent[10], Vsevolod J Makeev[7,8], Andrei A Mironov[7,11], William Stafford Noble[1,2], Giulio Pavesi[12], Graziano Pesole[13], Mireille Régnier[14], Nicolas Simonis[15], Saurabh Sinha[16], Gert Thijs[5], Jacques van Helden[15], Mathias Vandenbogaert[14], Zhiping Weng[9], Christopher Workman[17], Chun Ye[18] & Zhou Zhu[4]

Methodology

13 tools

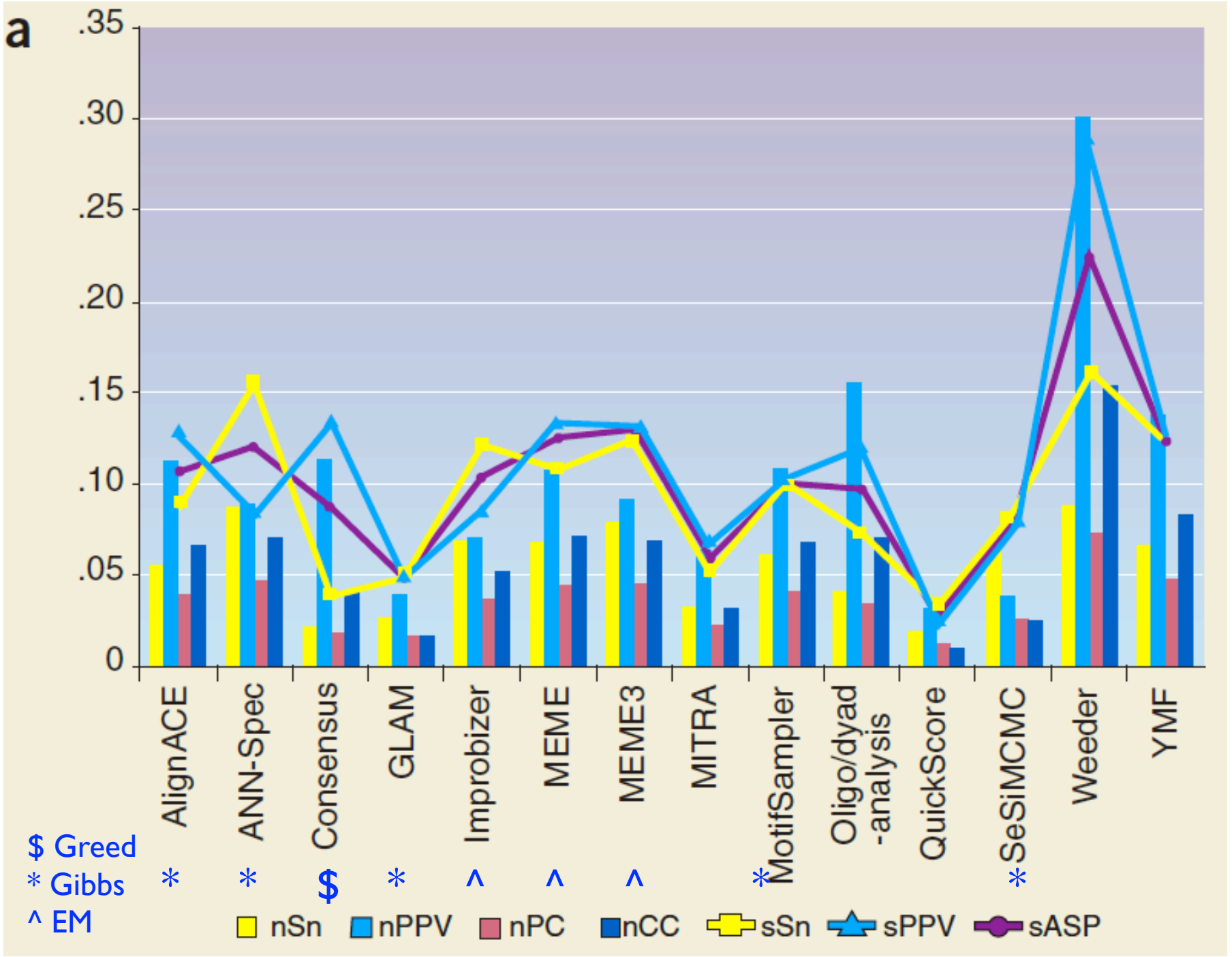
Real ‘motifs’ (Transfac)

56 data sets (human, mouse, fly, yeast)

‘Real’, ‘generic’, ‘Markov’

Expert users, top prediction only

“Blind” – sort of


a
.35
.30
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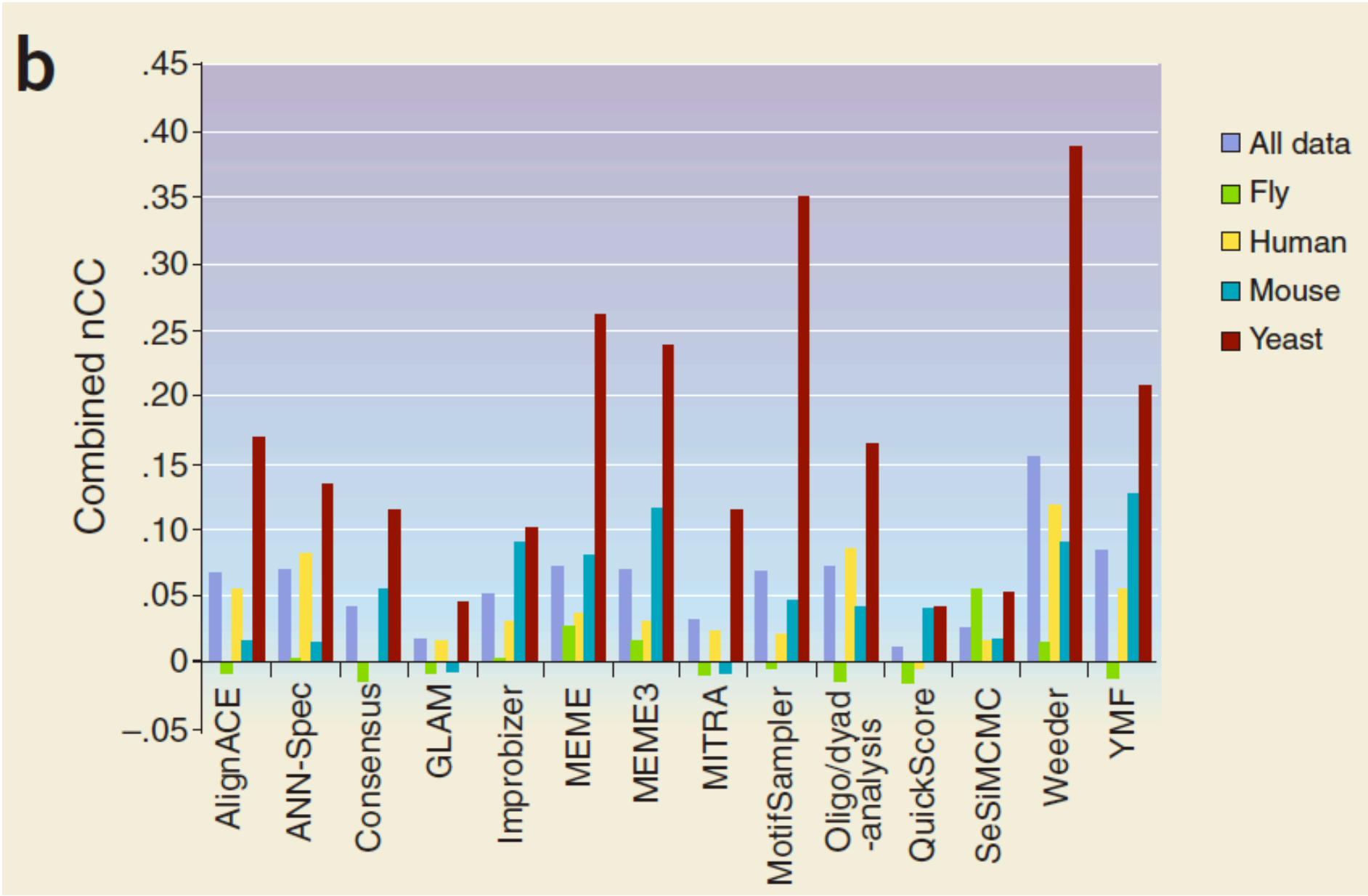
0
AlignACE
ANN-Spec
Consensus
GLAM
Improbizer
MEME
MEME3
MITRA
MotifSampler
Oligo/dyad -analysis
QuickScore
SeSiMCMC
Weeder
YMF
$ Greed
* Gibbs
^ EM
nSn
nPPV
nPC
nCC
sSn
sPPV
sASP


b
Combined nCC
.45
.40
.35
.30
.25
.20
.15
.10
.05
0
–.05
All data
Fly
Human
Mouse
Yeast
AlignACE
ANN-Spec
Consensus
GLAM
Improbizer
MEME
MEME3
MITRA
MotifSampler
Oligo/dyad -analysis
QuickScore
SeSiMCMC
Weeder
YMF

Lessons

Evaluation is hard (esp. when "truth" is unknown)

Accuracy low

- partly reflects limitations in evaluation methodology (e.g. ≤ 1 prediction per data set; results better in synth data)
- partly reflects difficult task, limited knowledge (e.g. yeast > others)

No clear winner re methods or models

Motif Discovery Summary

Important problem: a key to understanding gene regulation

Hard problem: short, degenerate signals amidst much noise

Many variants have been tried, for representation, search, and discovery. We looked at only a few:

Weight matrix models for representation & search

Greedy, MEME and Gibbs for discovery

Still much room for improvement. *Comparative genomics*, i.e. cross-species comparison is very promising