CSEP 590B

Fall 2014

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

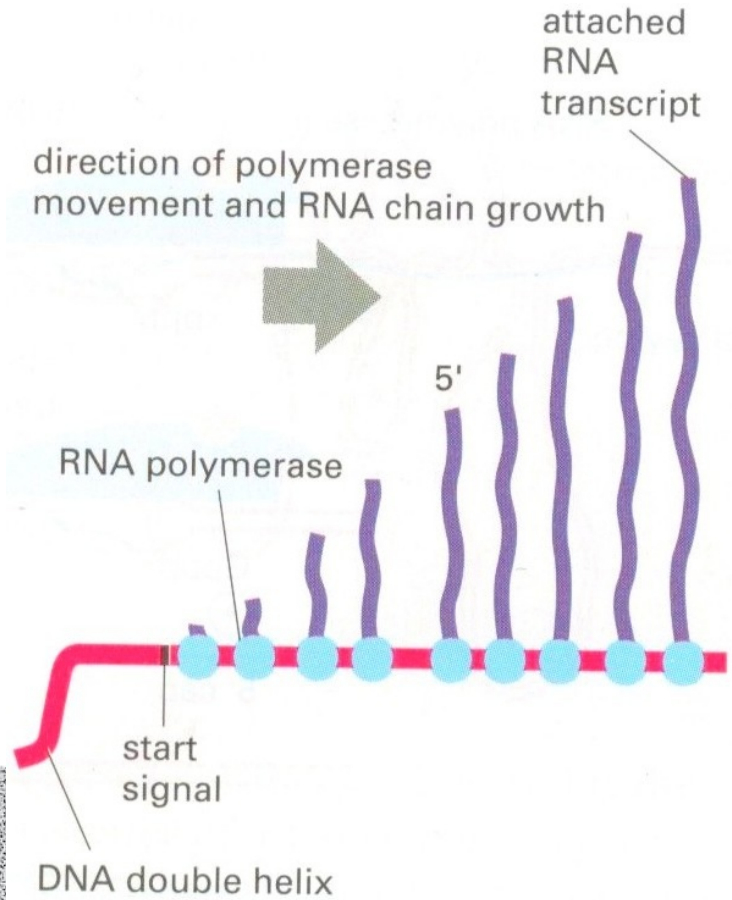
To say a gene is *expressed* means that it

- 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)



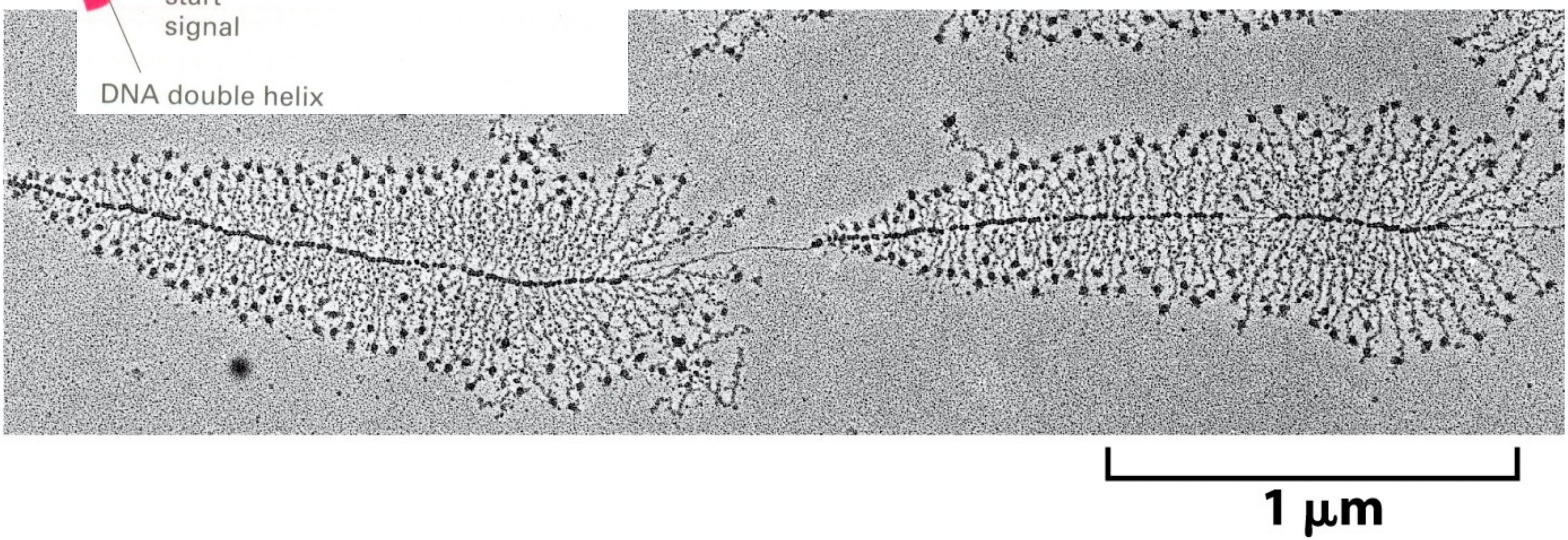


Figure 6-9 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Regulation

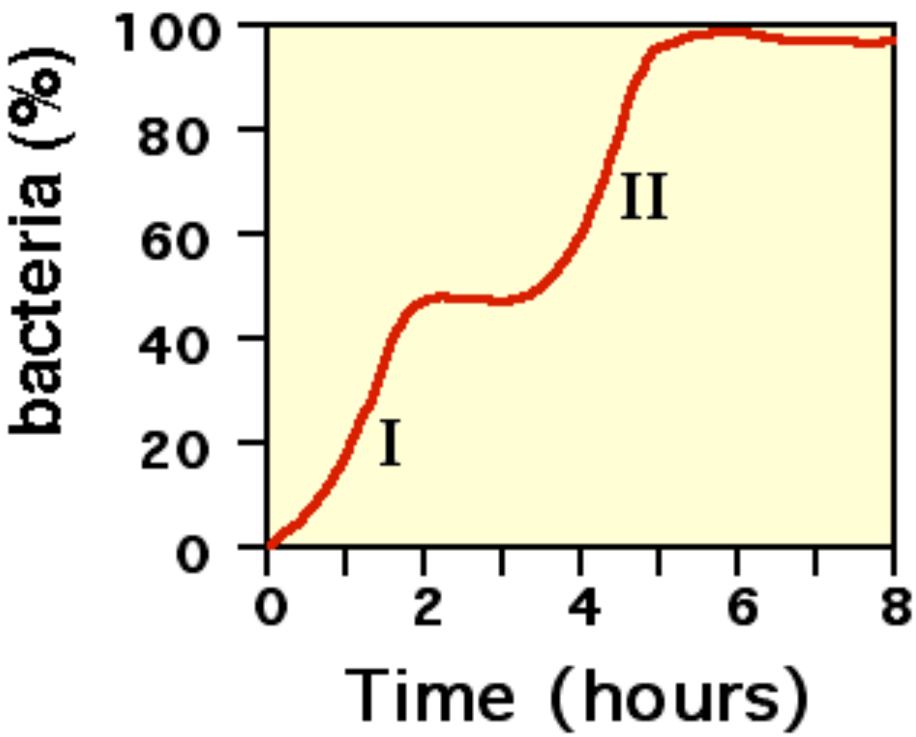
In most cells, pro- or eukaryote, easily a 10,000-fold difference between least- and most-highly expressed genes

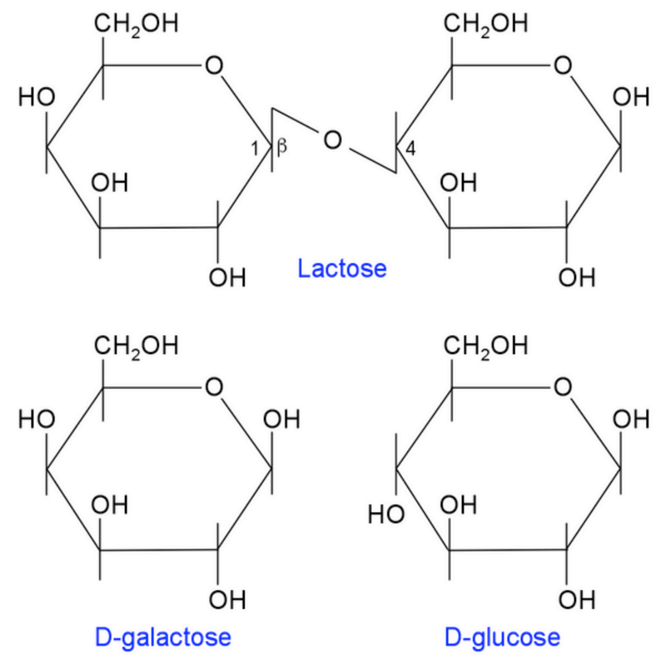
Regulation happens at all steps. E.g., some genes are highly transcribed, some are not transcribed at all, some transcripts can be sequestered then released, or rapidly degraded, some are weakly translated, some are very actively translated, ...

All are important, but below, focus on 1st step only:

- transcriptional regulation

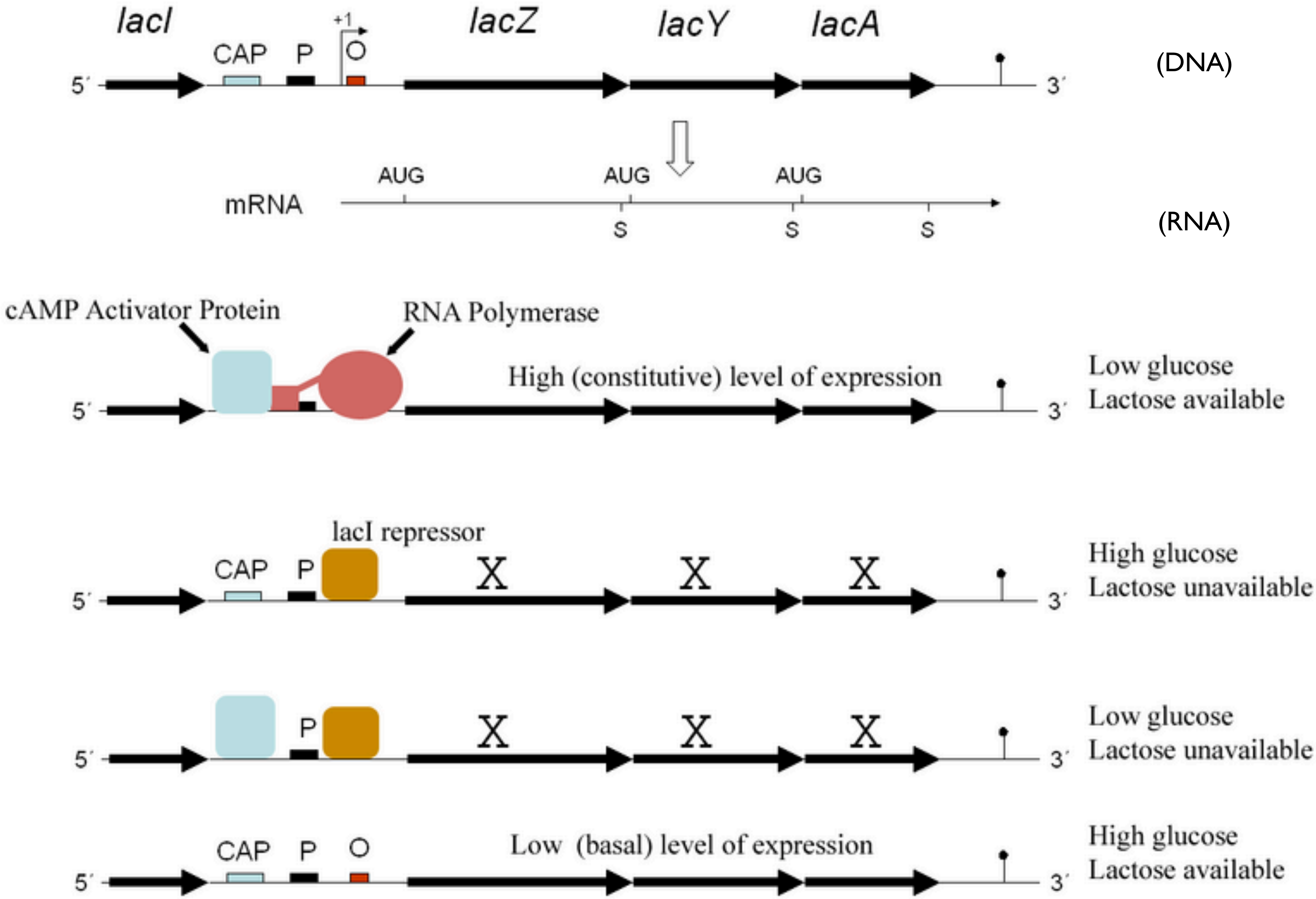
E. coli growth on glucose + lactose





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

The *lac* Operon and its Control Elements



1965 Nobel Prize

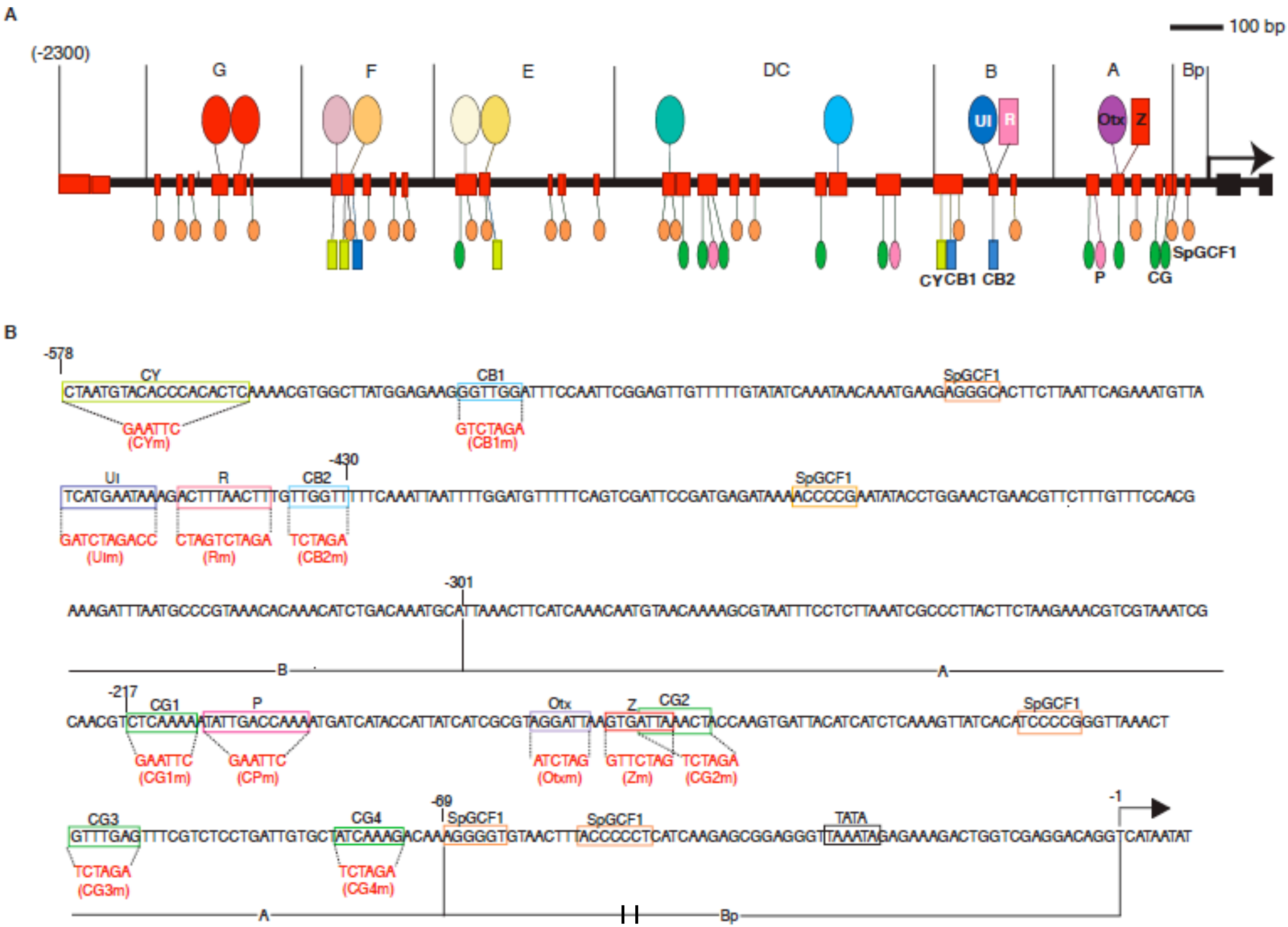
Physiology or Medicine

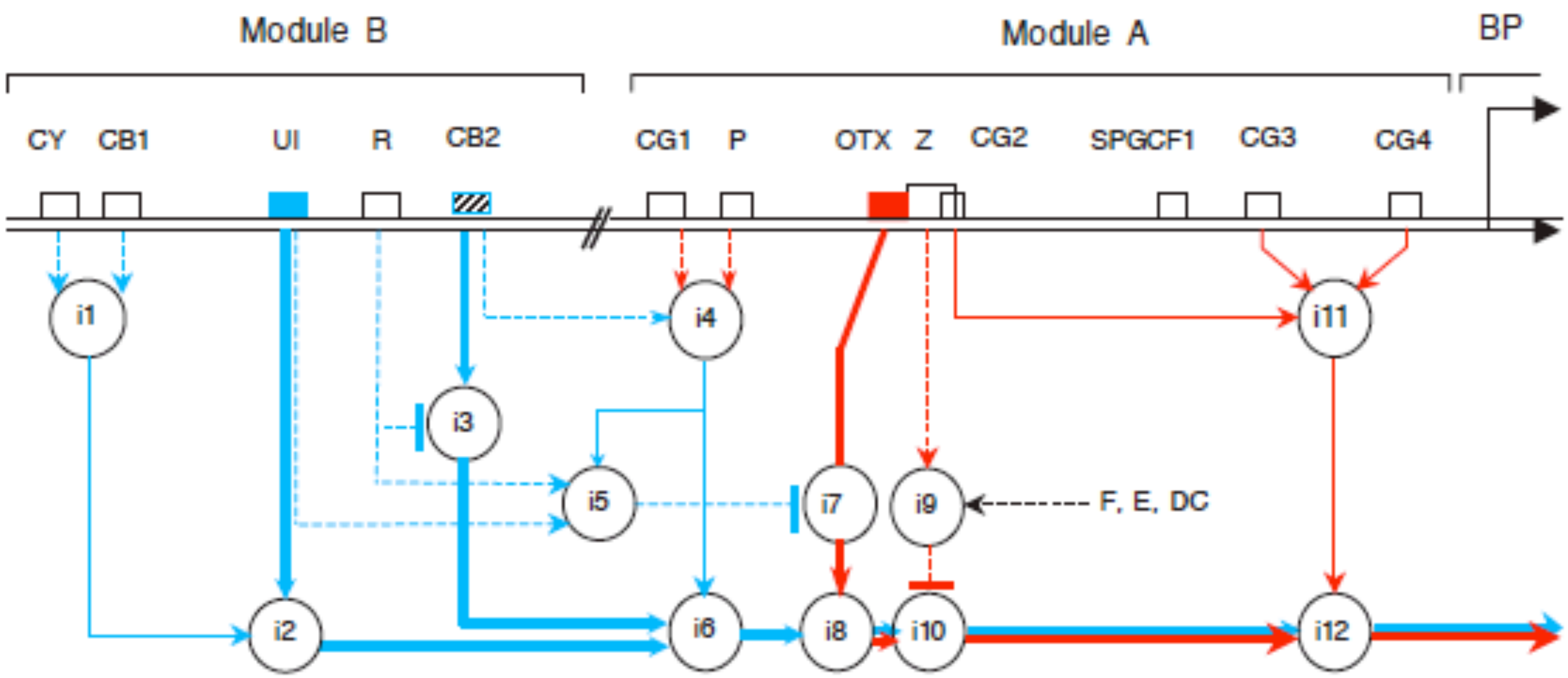
François Jacob, Jacques Monod, André Lwoff

1920-2013 1910-1976 1902-1994

The sea urchin *Strongylocentrotus purpuratus*

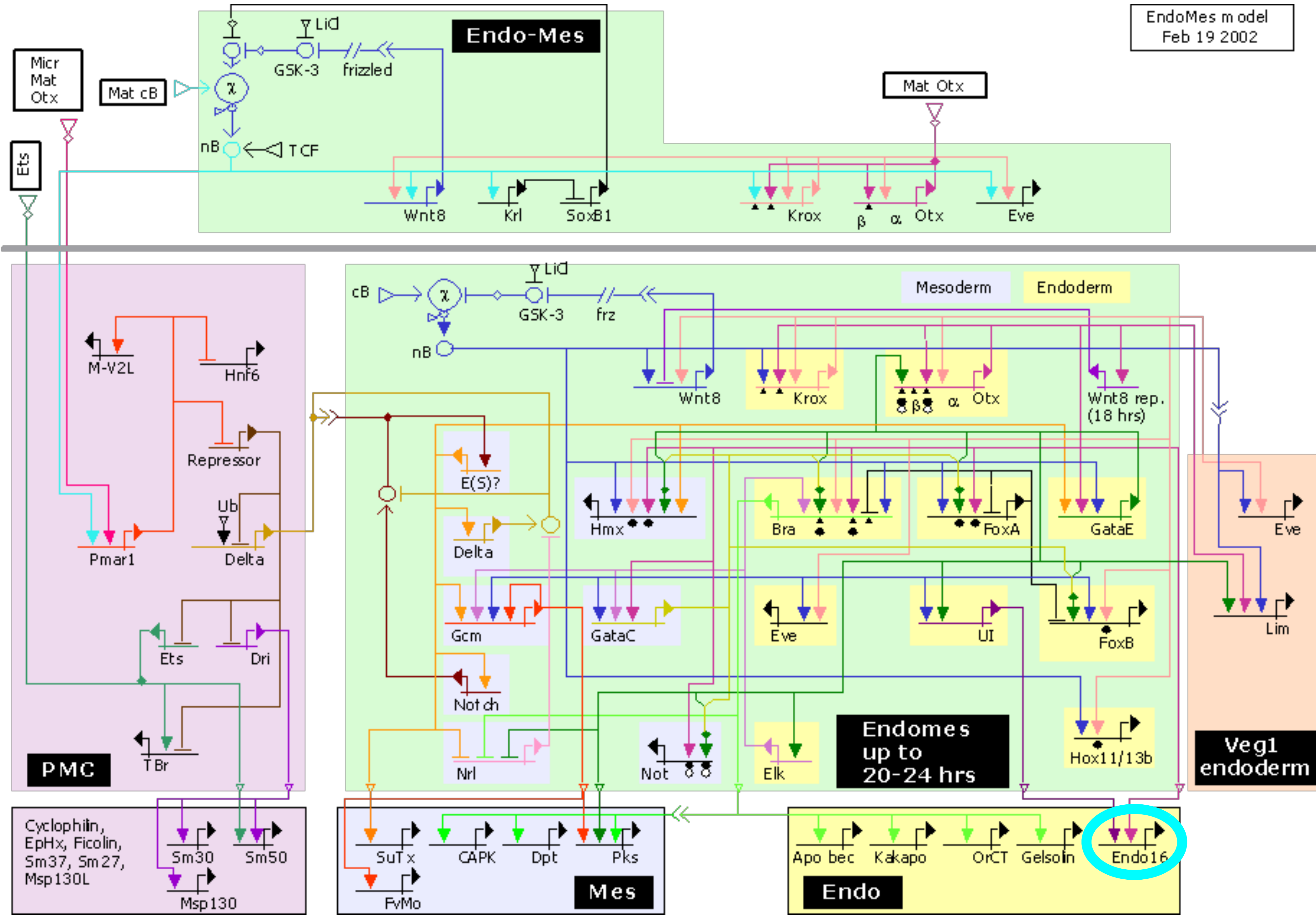
Sea Urchin - Endo16





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)

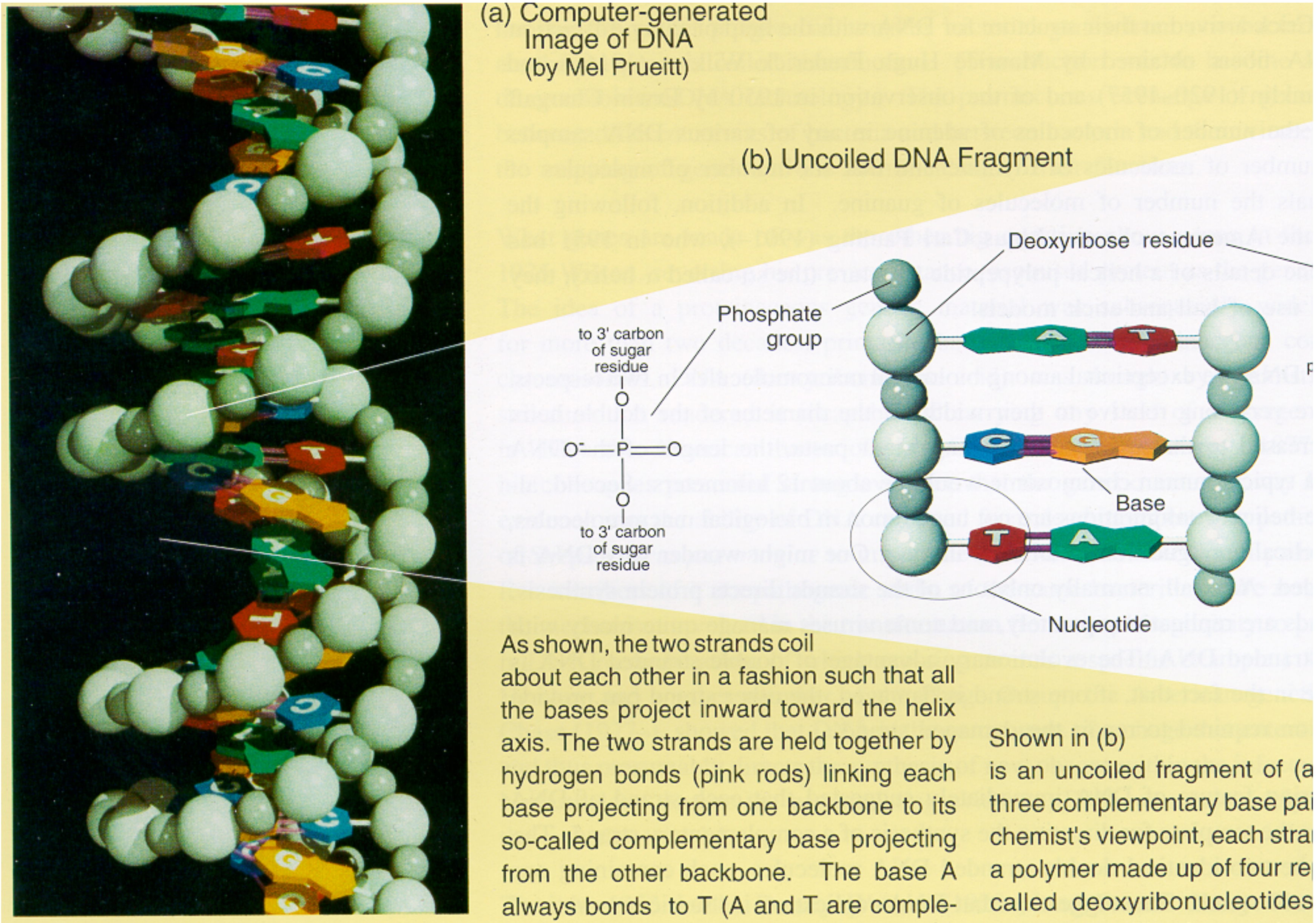
if i5=0	i7 = OTX(t)
else	i7 = 0
	i8 = i6 + i7
if (F or E or DC) & Z	i9 = 1
else	i9 = 0
if i9=1	i10 = 0
else	i10 = i8
if (CG2 & CG3 & CG4)	i11 = 2
else	i11 = 1
	i12 = i11 • i10


EndoMes model
Feb 19 2002
Micr
Mat
Otx
Mat cB
Ets
Endo-Mes
LiCl
GSK-3
frizzled
nB
TCF
Mat Otx
Wnt8
Krl
SoxB1
Krox
β
α
Otx
Eve
cB
GSK-3
frz
Mesoderm
Endoderm
M-V2L
Hnf6
Repressor
Ub
Pmar1
Delta
Ets
Dri
TBr
PMC
E(S)?
Delta
Gcm
Notch
Nrl
Hmx
GataC
Bra
FoxA
GataE
Eve
Ul
FoxB
Not
Elk
Hox11/13b
Wnt8 rep.
(18 hrs)
Eve
Lim
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

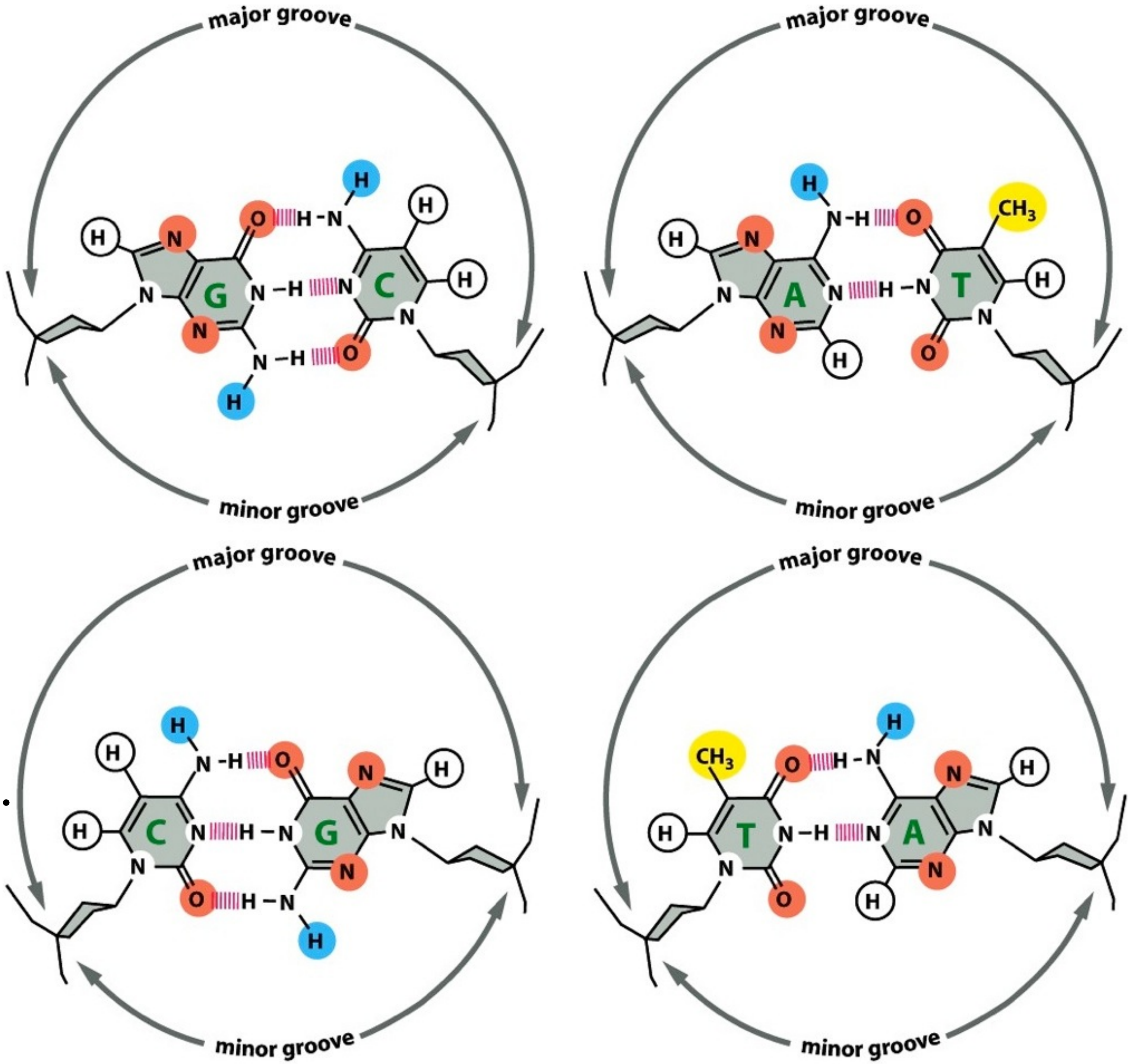


Figure 7-7 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Helix-Turn-Helix DNA Binding Motif

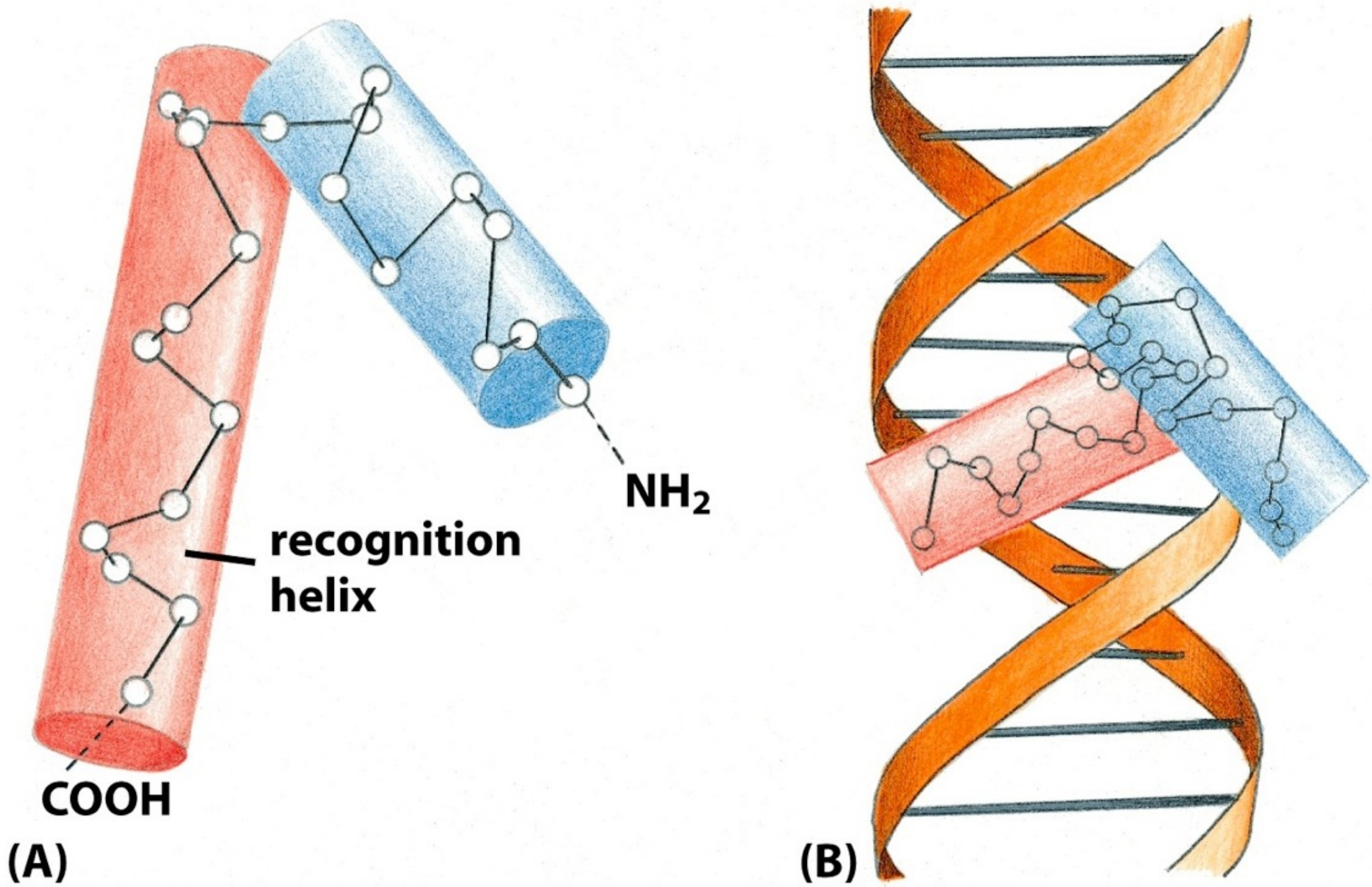


Figure 7-10 Molecular Biology of the Cell 5/e (© Garland Science 2008)

H-T-H Dimers

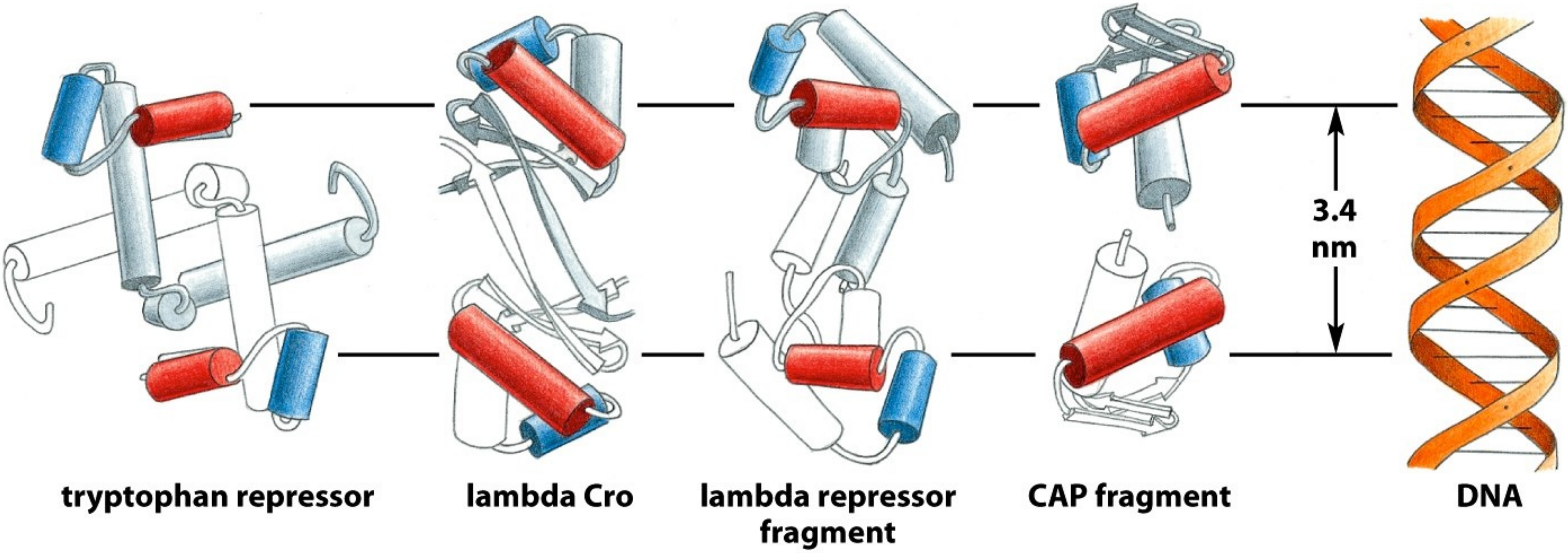
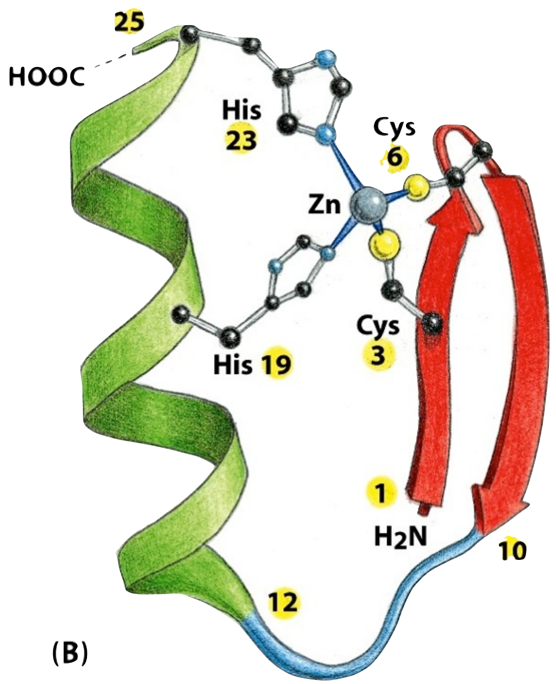


Figure 7-11 Molecular Biology of the Cell 5/e (© Garland Science 2008)

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

Zinc Finger Motif



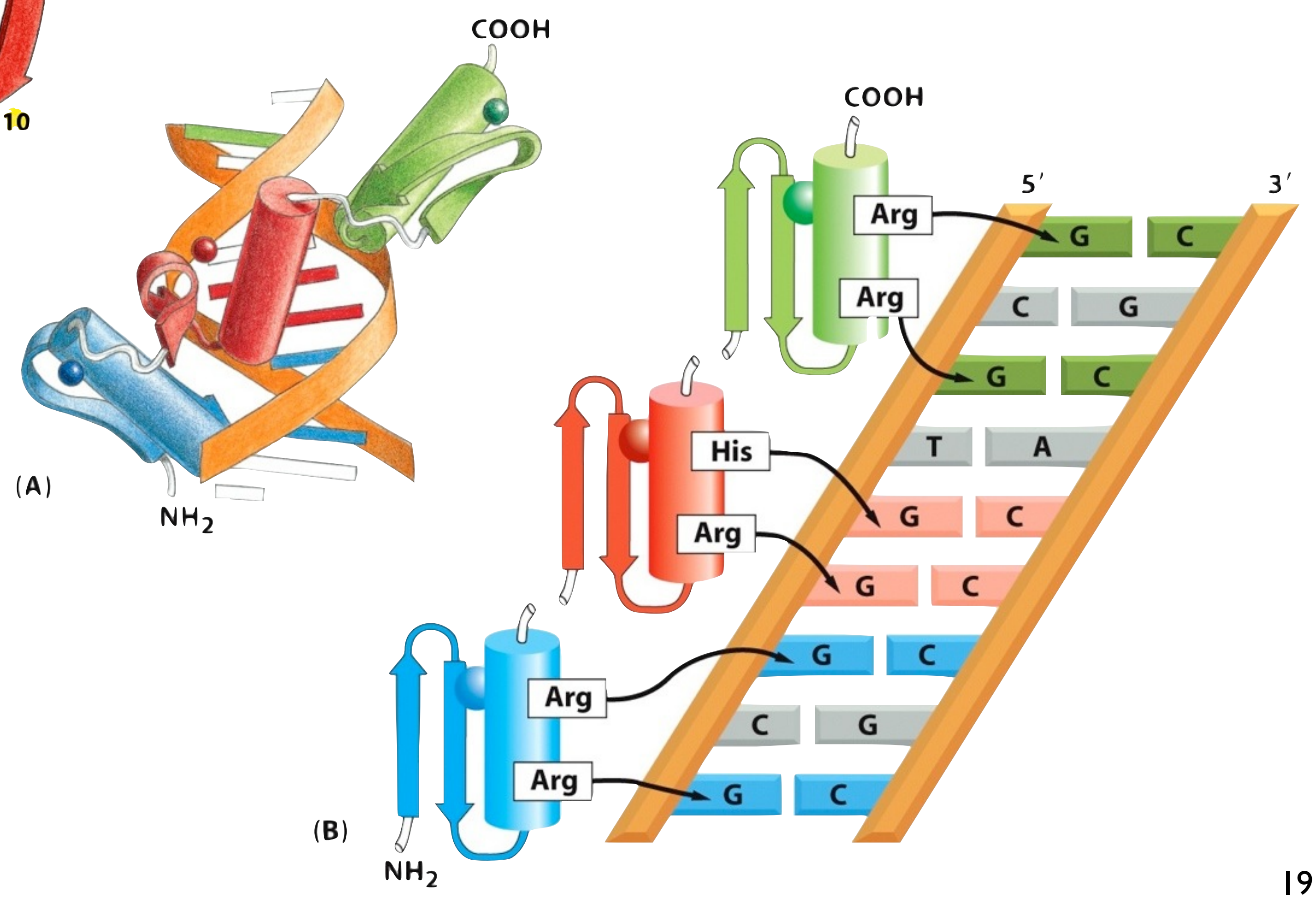


Figure 7-15 Molecular Biology of the Cell (5/e) (© Garland Science 2008)

Overheard at the Halloween Party

WWW.PHDCOMICS.COM
© Jorge Cham 10/29/2008

Leucine Zipper Motif

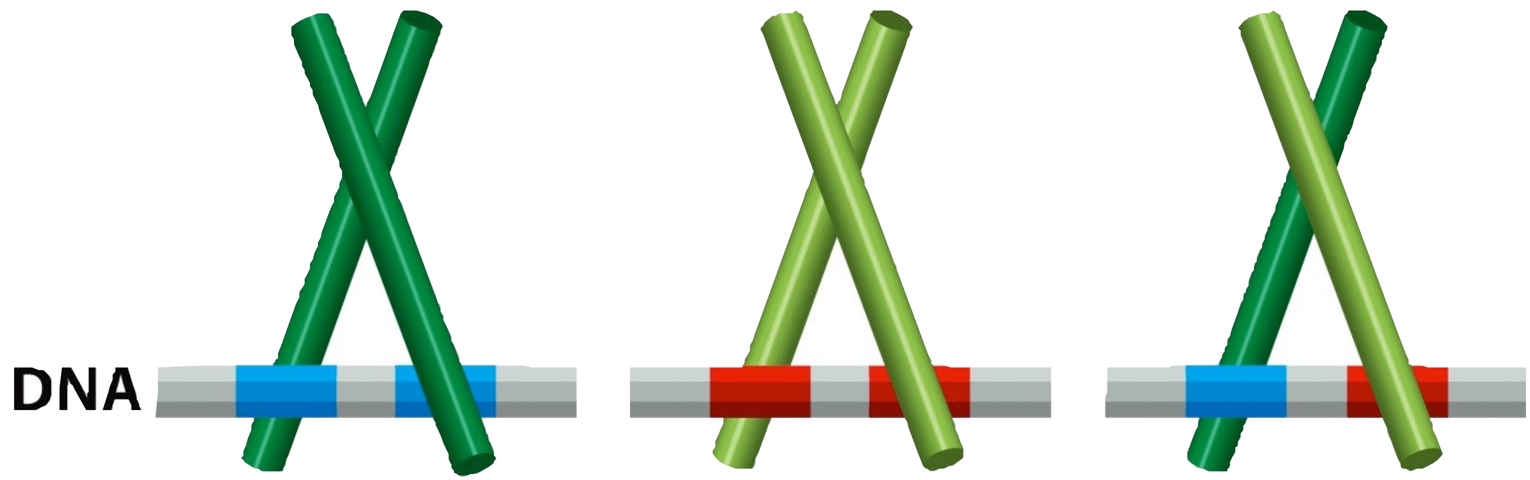


Figure 7-20 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Homo-/hetero-dimers and combinatorial control

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

MyoD

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

We understand some Protein/DNA interactions

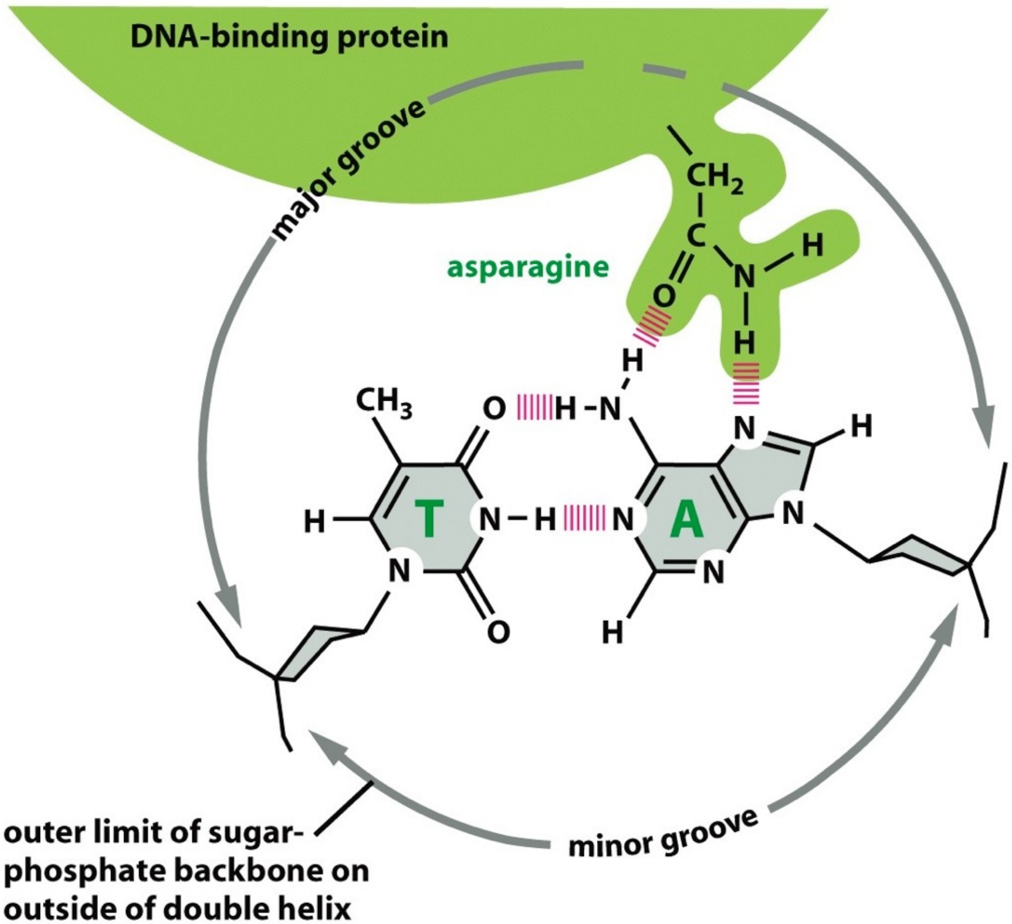


Figure 7-9 Molecular Biology of the Cell 5/e (© Garland Science 2008)

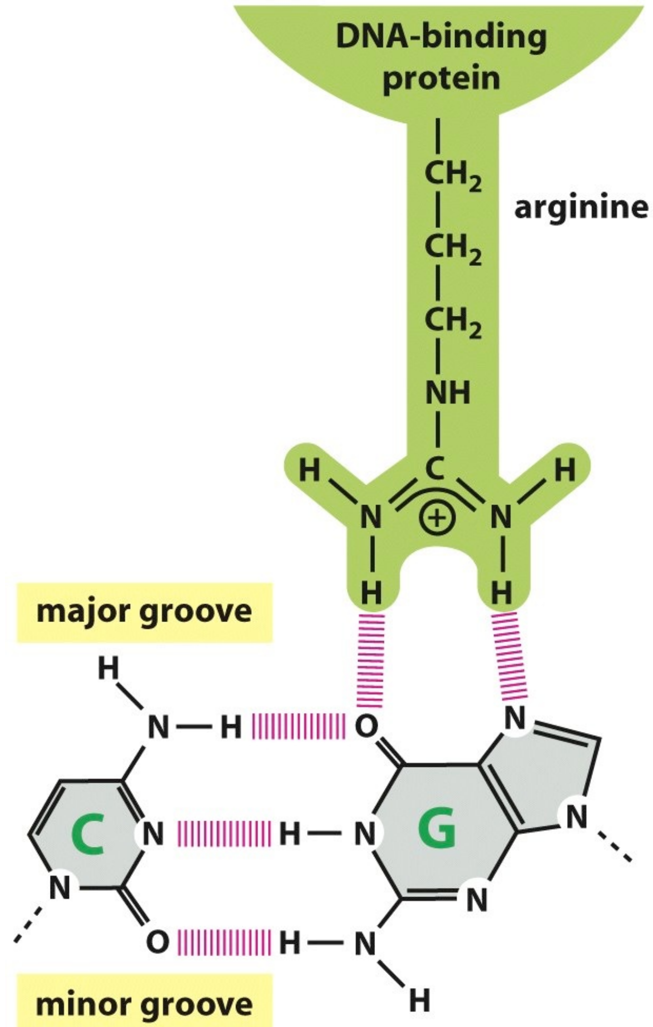


Figure 7-25 Molecular Biology of the Cell 5/e (© Garland Science 2008)

But the overall DNA binding “code” still defies prediction

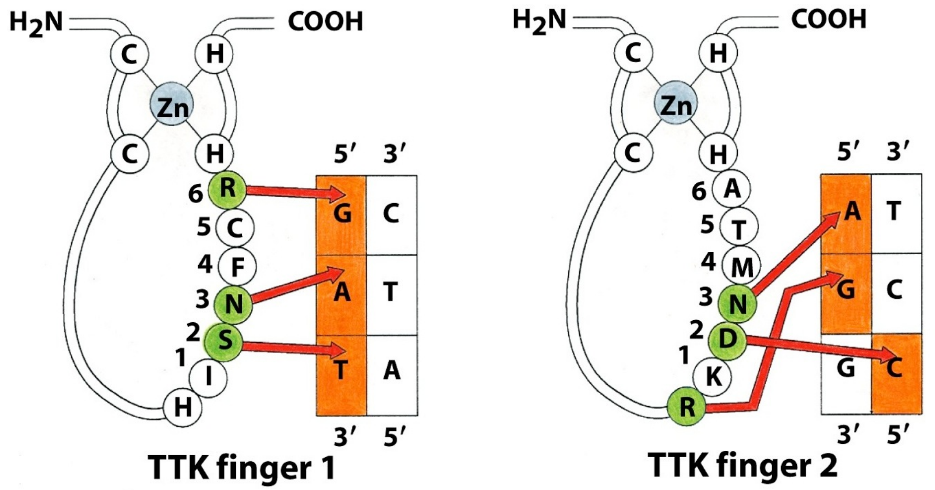


Figure 7-26 part 1 of 3 Molecular Biology of the Cell 5/e (© Garland Science 2008)

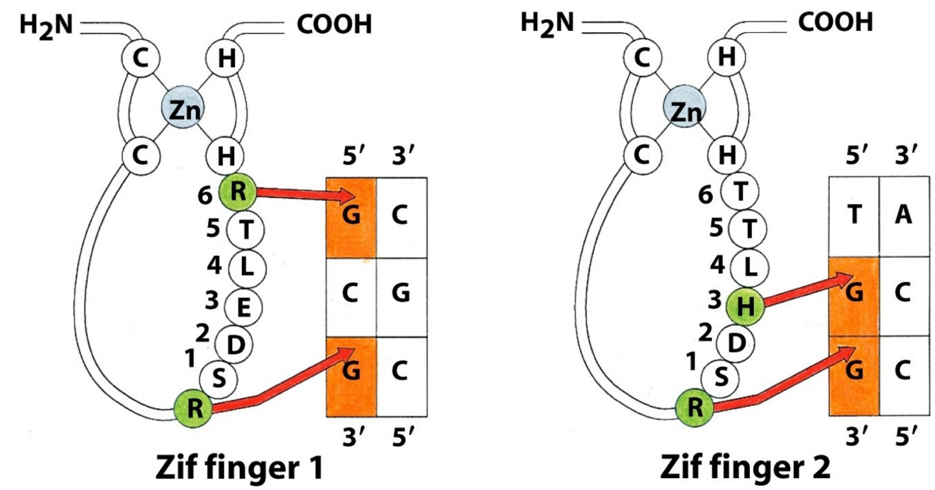


Figure 7-26 part 2 of 3 Molecular Biology of the Cell 5/e (© Garland Science 2008)

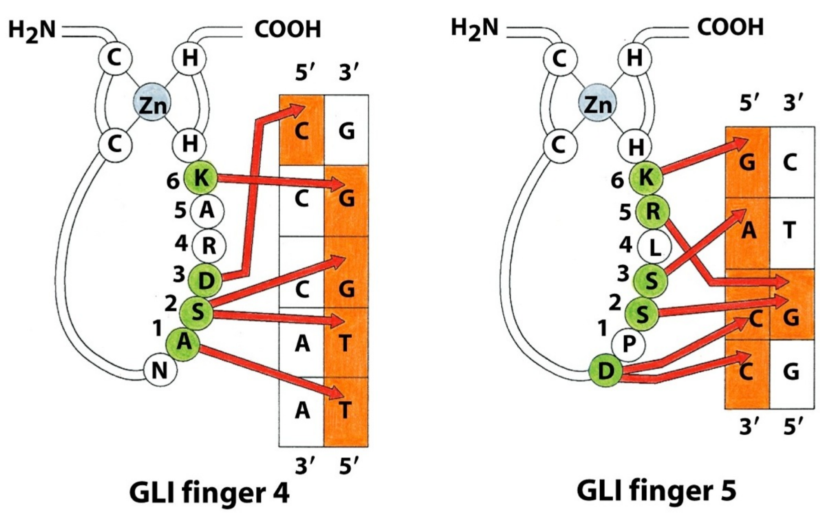
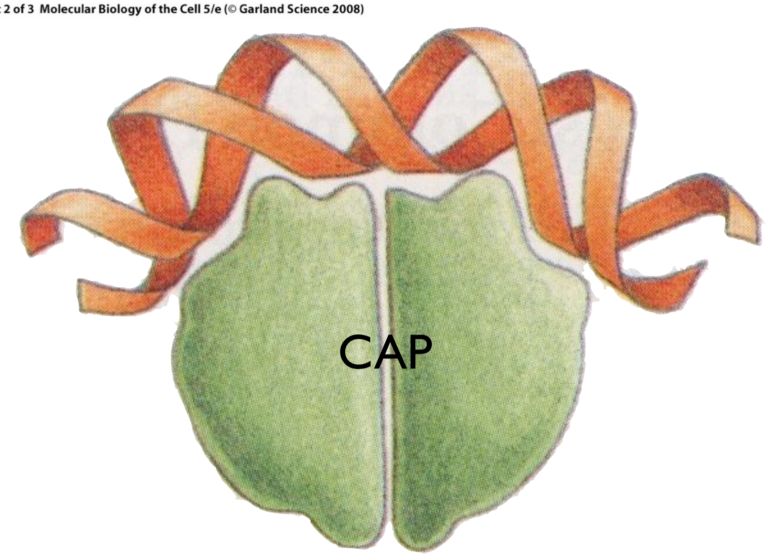


Figure 7-26 part 3 of 3 Molecular Biology of the Cell 5/e (© Garland Science 2008)



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"

base \ pos	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

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

A C T A T A A T C G

= -90

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

A C T A T A A T C G

= 85

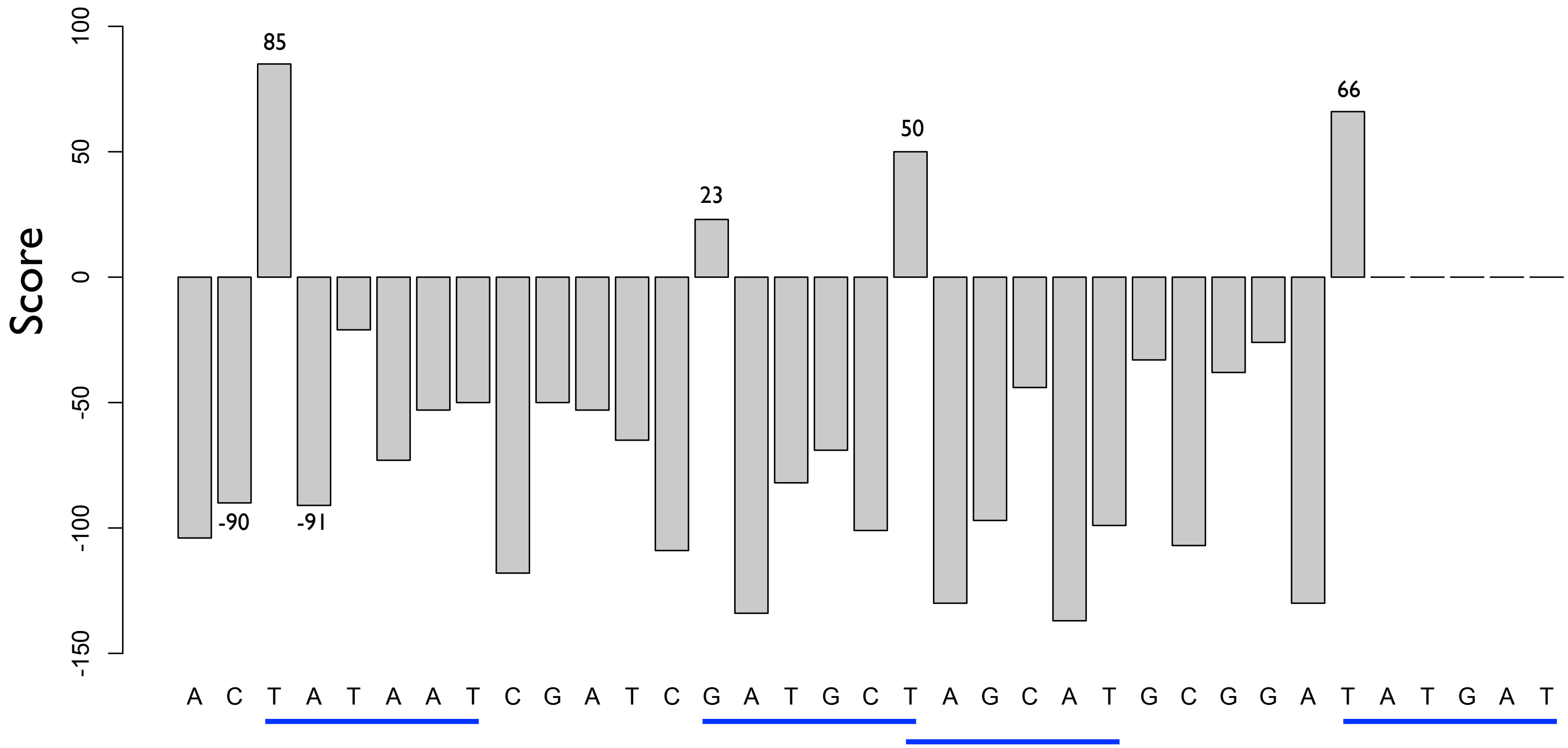
A	-36	19	1	12	10	-46
C	-15	-36	-8	-9	-3	-31
G	-13	-46	-6	-7	-9	-46
T	17	-31	8	-9	-6	19

A C T A T A A T C G

= -91

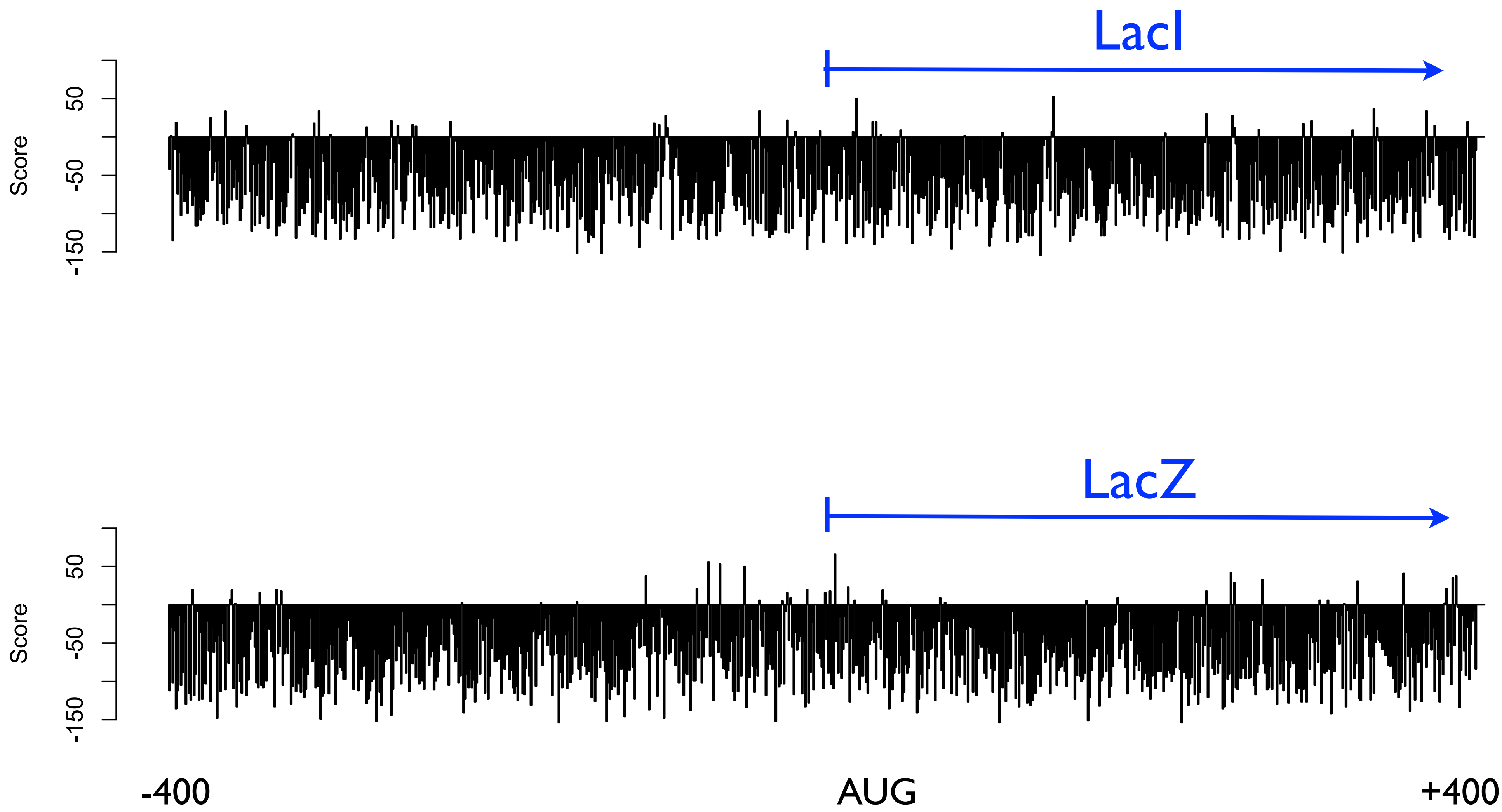
Stormo, Ann. Rev. Biophys. Biophys Chem, 17, 1988, 241-263

Scanning for TATA



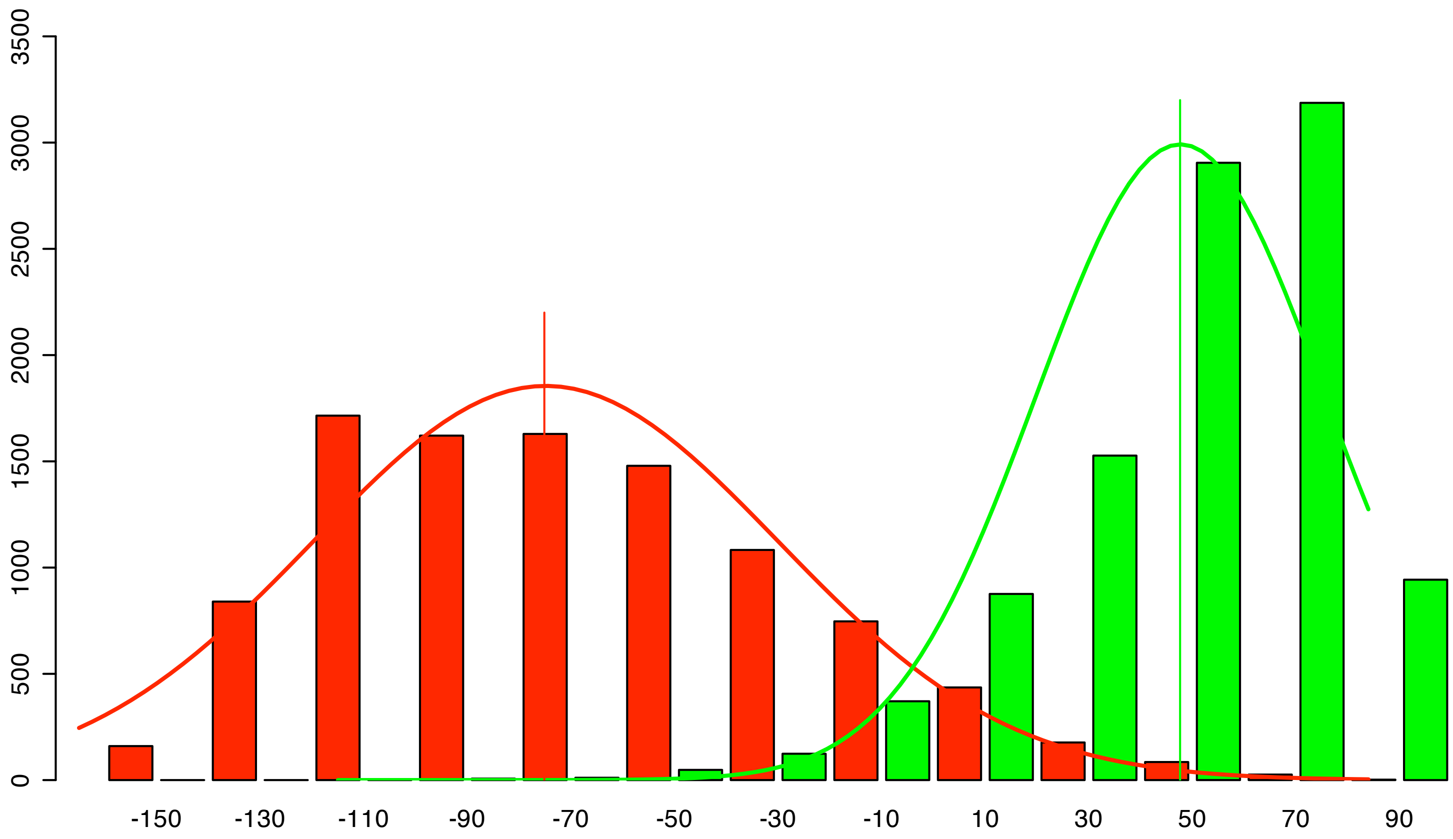
See also slide 60

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 $S = B_1 B_2 \ldots B_6$:

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

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 $\Theta = \theta_2$.

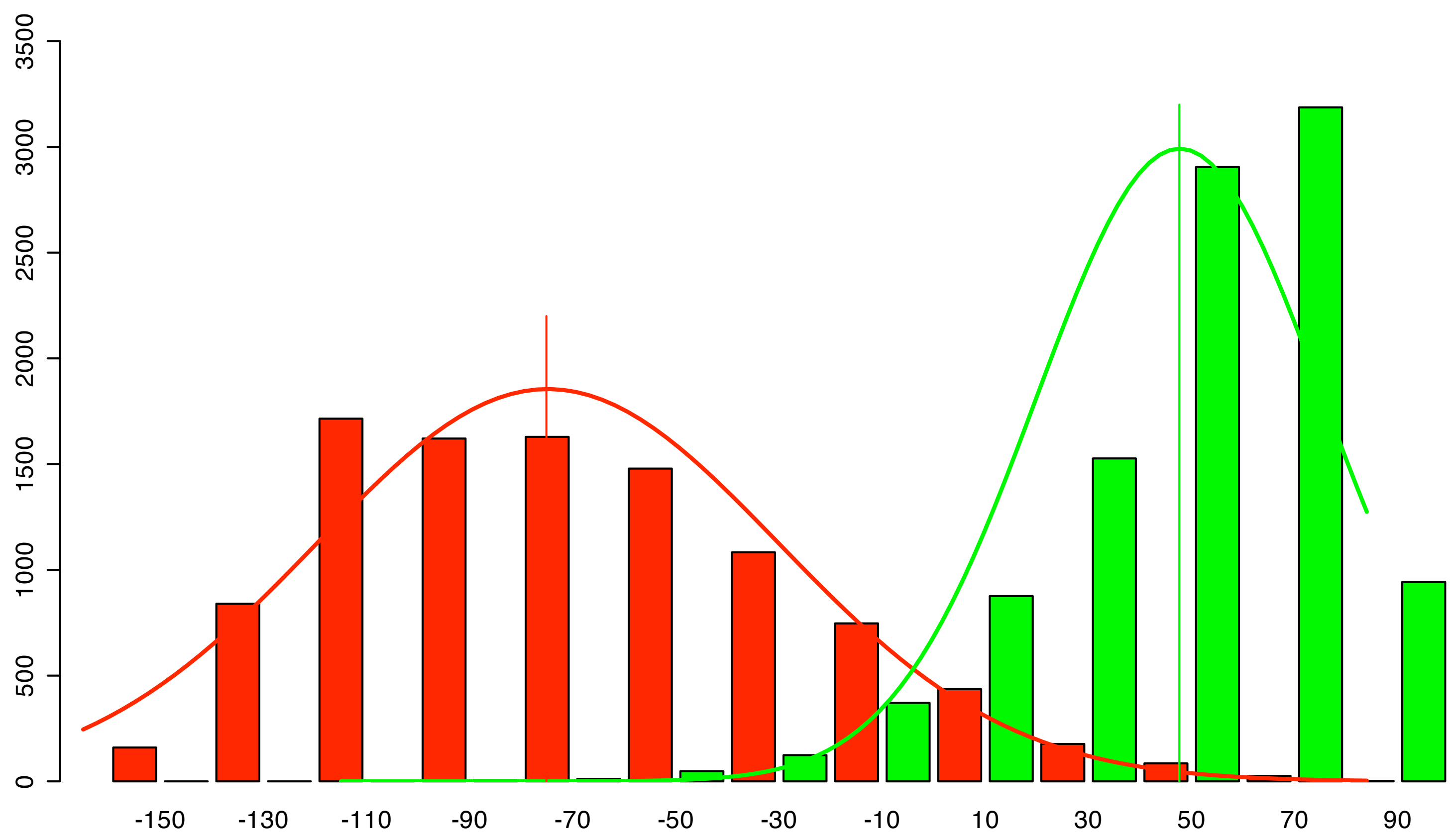
Might as well look at *likelihood ratio:*

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

(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) unknown 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. (Possible HW?)

Weight Matrices: Biophysics

Experiments show ~80% correlation of log likelihood weight matrix scores to measured binding energies
[Fields & Stormo, 1994]

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	0.25	0	1
T	0.125	1	0

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

Log-Likelihood Ratio:

$$\log_2 \frac{f_{x_i,i}}{f_{x_i}}, \;\; f_{x_i} = \frac{1}{4}$$ (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	-∞	3
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?

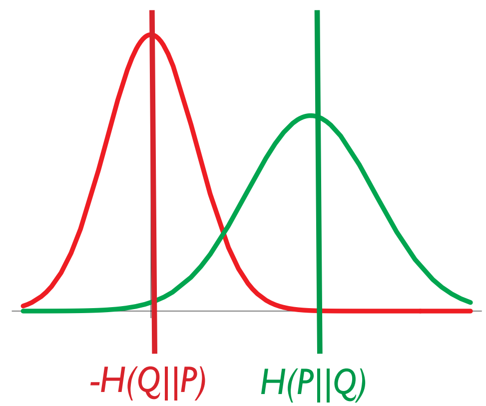
For any fixed length sequence *x*, let

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

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

Relative Entropy:

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

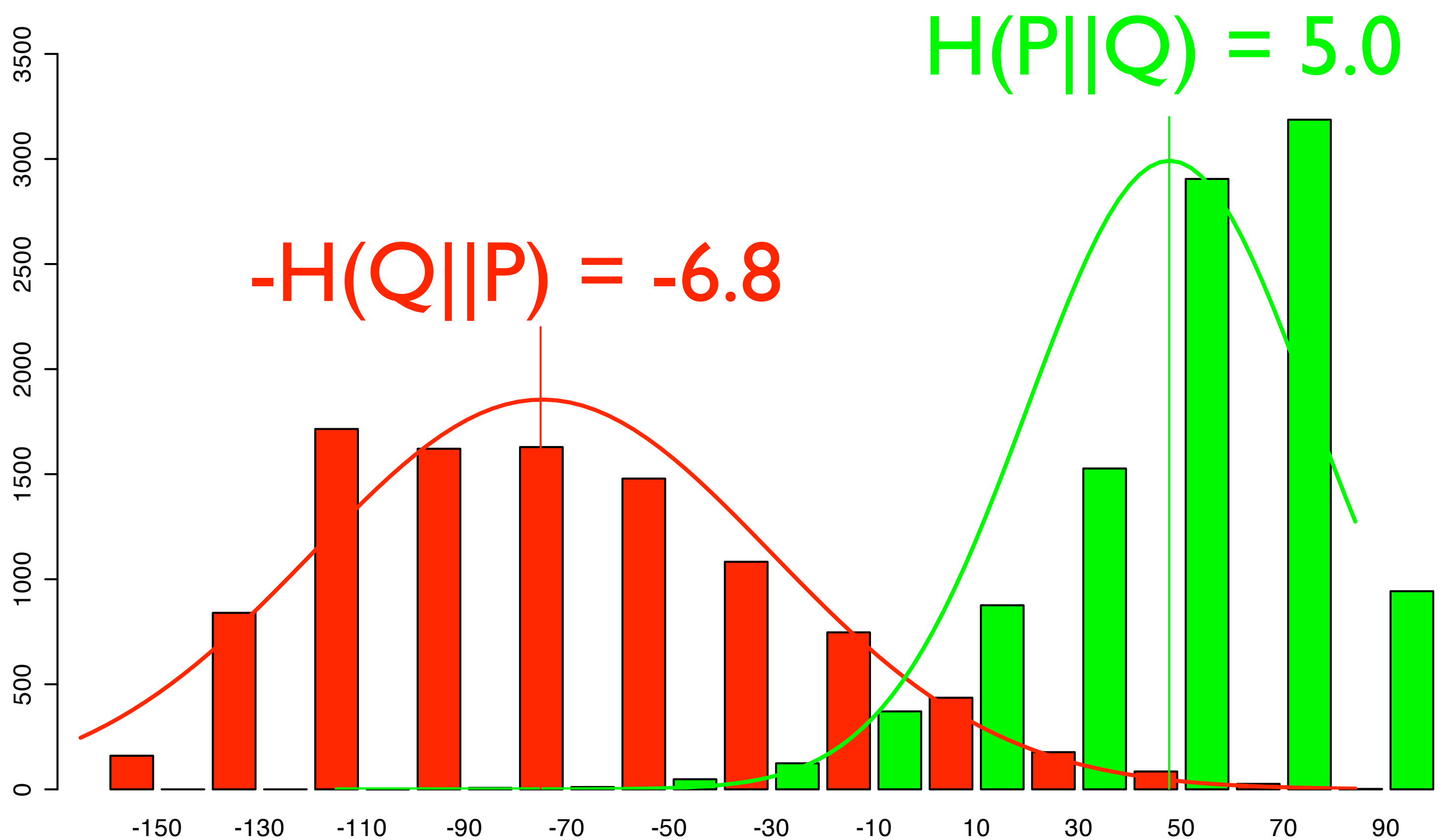


H(P||Q) is *expected log likelihood score* of a sequence randomly chosen from *WMM* *(wrt background)*;

-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	0.25	0	1
T	0.125	1	0

Uniform

LLR	Col 1	Col 2	Col 3	
A	1.32	$-\infty$	$-\infty$	
C	$-\infty$	$-\infty$	$-\infty$	
G	0	$-\infty$	2	
T	-1	2	$-\infty$	
RelEnt	0.7	2	2	4.7

Non-uniform

LLR	Col 1	Col 2	Col 3	
A	0.74	$-\infty$	$-\infty$	
C	$-\infty$	$-\infty$	$-\infty$	
G	1	$-\infty$	3	
T	-1.58	1.42	$-\infty$	
RelEnt	0.51	1.42	3	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 (k^{th} order MM)

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

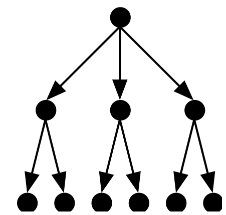
Input:

- 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)

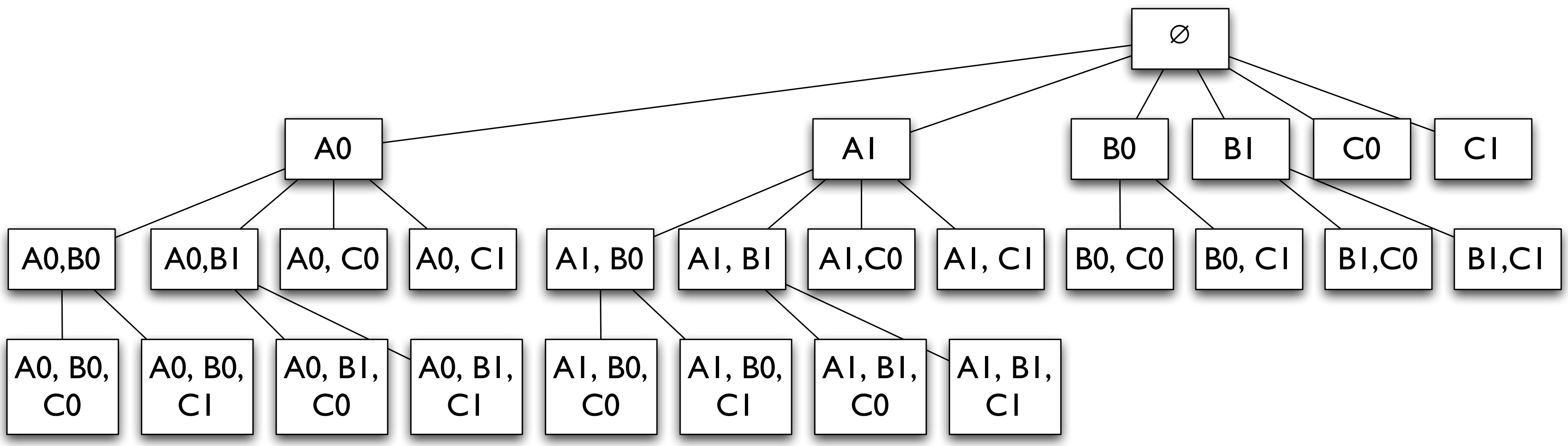
Then triples: len L subseqs of each triple of seqs ($n^3\binom{k}{3}$ sets)

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 slooow

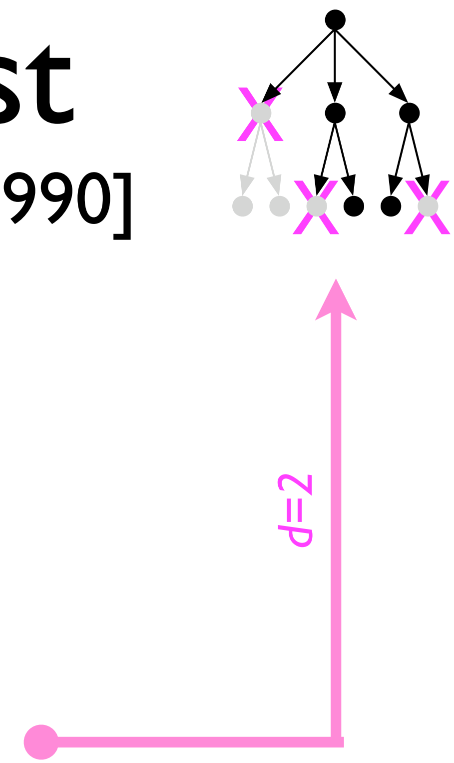
Example



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

Greedy Best-First

[Hertz, Hartzell & Stormo, 1989, 1990]



Input:

Sequences $s_1, s_2, \ldots, s_k$; 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):

Sequences $s_1, s_2, ..., s_k$; 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

Cartoon Example

xATAyz

```
CATGACTAGCATAATCCGAT
TATAATTTCCCAGGGATAGCA
TACAATAGGACCATAGAATGCGC
```

xATAAz

```
CATGACTAGCATAATCCGAT
TATAATTTCCCAGGGATAGCA
TACAATAGGACCATAGAATGCGC
```

TAtAAT

```
         CATGACTAGCATAATCCGAT
                  TATAATTTCCCAGGGATAGCA
TACAATAGGACCATAGAATGCGC
```

Expectation Step

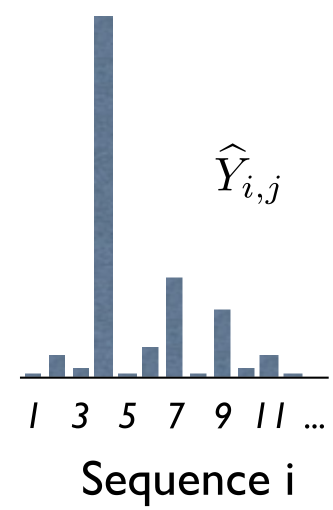
(where are the motif instances?)

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

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

Bayes

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



$\Sigma=1$

Recall slide 33

Maximization Step

(what is the motif?)

Find θ maximizing expected log likelihood:

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

From E-Step

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.

$$\begin{array}{ll} s_1: & \text{ACGGATT}\ldots \\ & \ldots \\ s_k: & \text{GC}\ldots\text{TCGGAC} \end{array}$$

$$\begin{array}{ll} \widehat{Y}_{1,1} & \text{ACGG} \\ \widehat{Y}_{1,2} & \text{CGGA} \\ \widehat{Y}_{1,3} & \text{GGAT} \\ \vdots & \vdots \\ \widehat{Y}_{k,l-1} & \text{CGGA} \\ \widehat{Y}_{k,l} & \text{GGAC} \end{array}$$

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

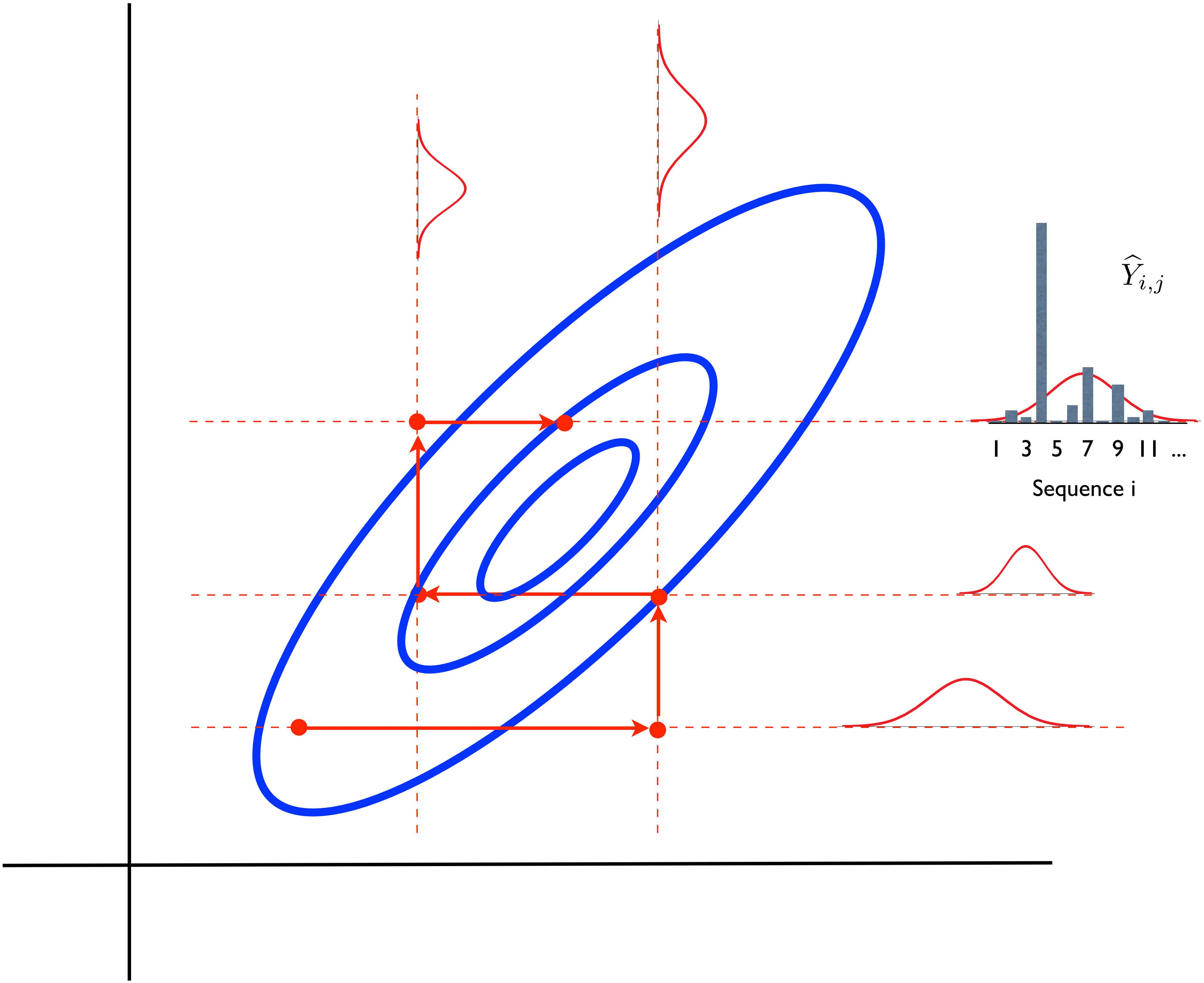
  $$P(x_i \mid x_1, x_2, \ldots, x_{i-1}, x_{i+1}, \ldots, x_k)$$

- Algorithm

  for t = 1 to ∞

  for i = 1 to k do :

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



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

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

Motif model: WMM

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

"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

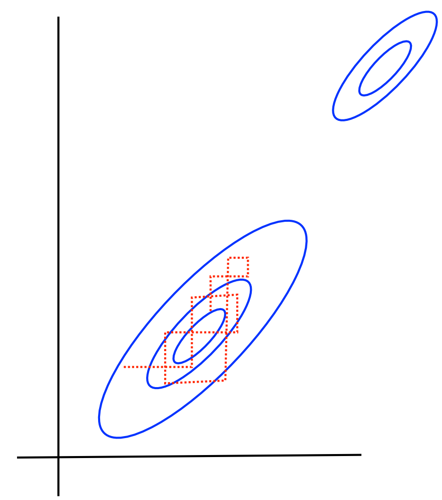
Similar to MEME, but it would *average* over, rather than *sample* from

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

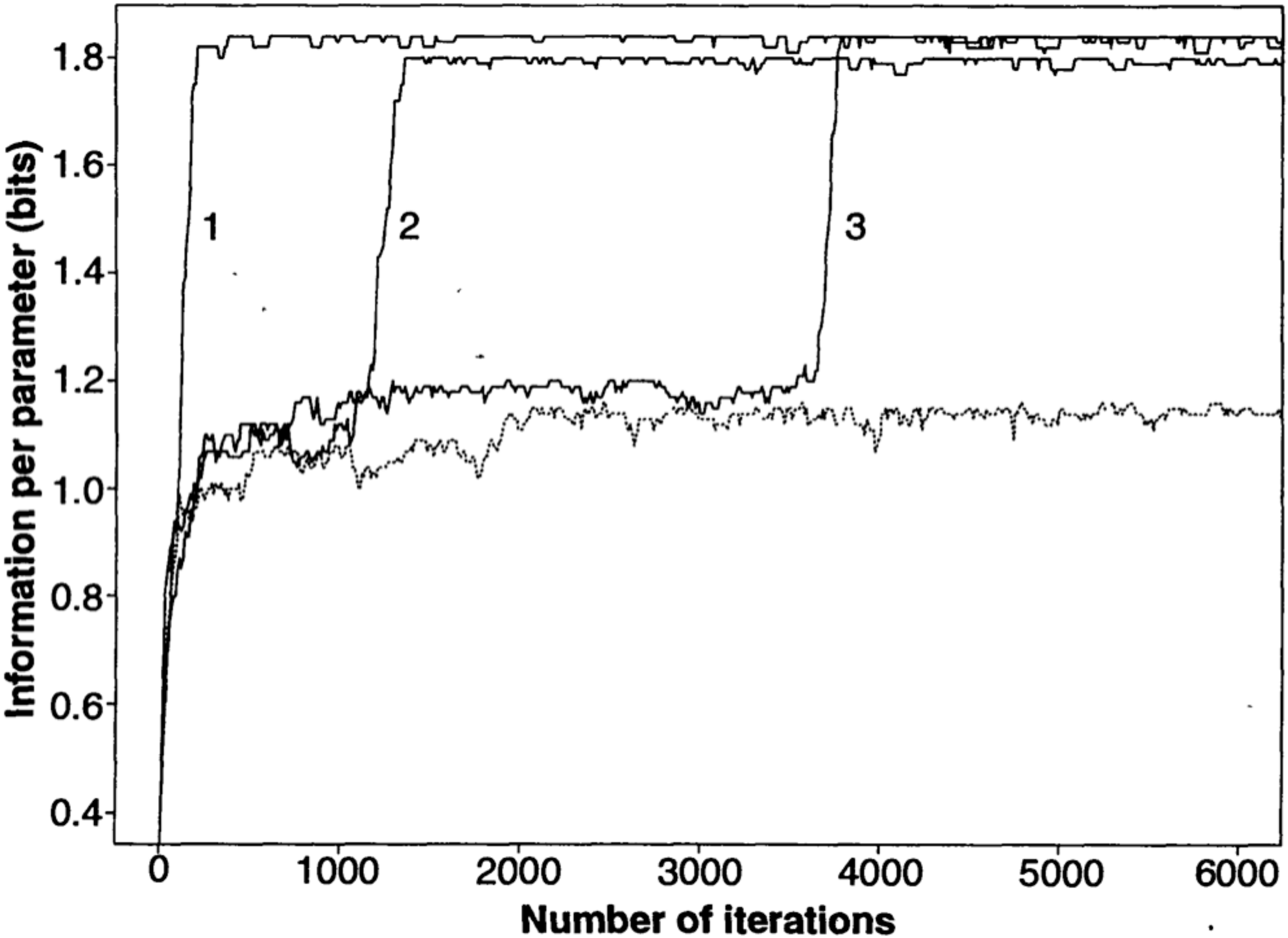


Variants & Extensions

"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

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

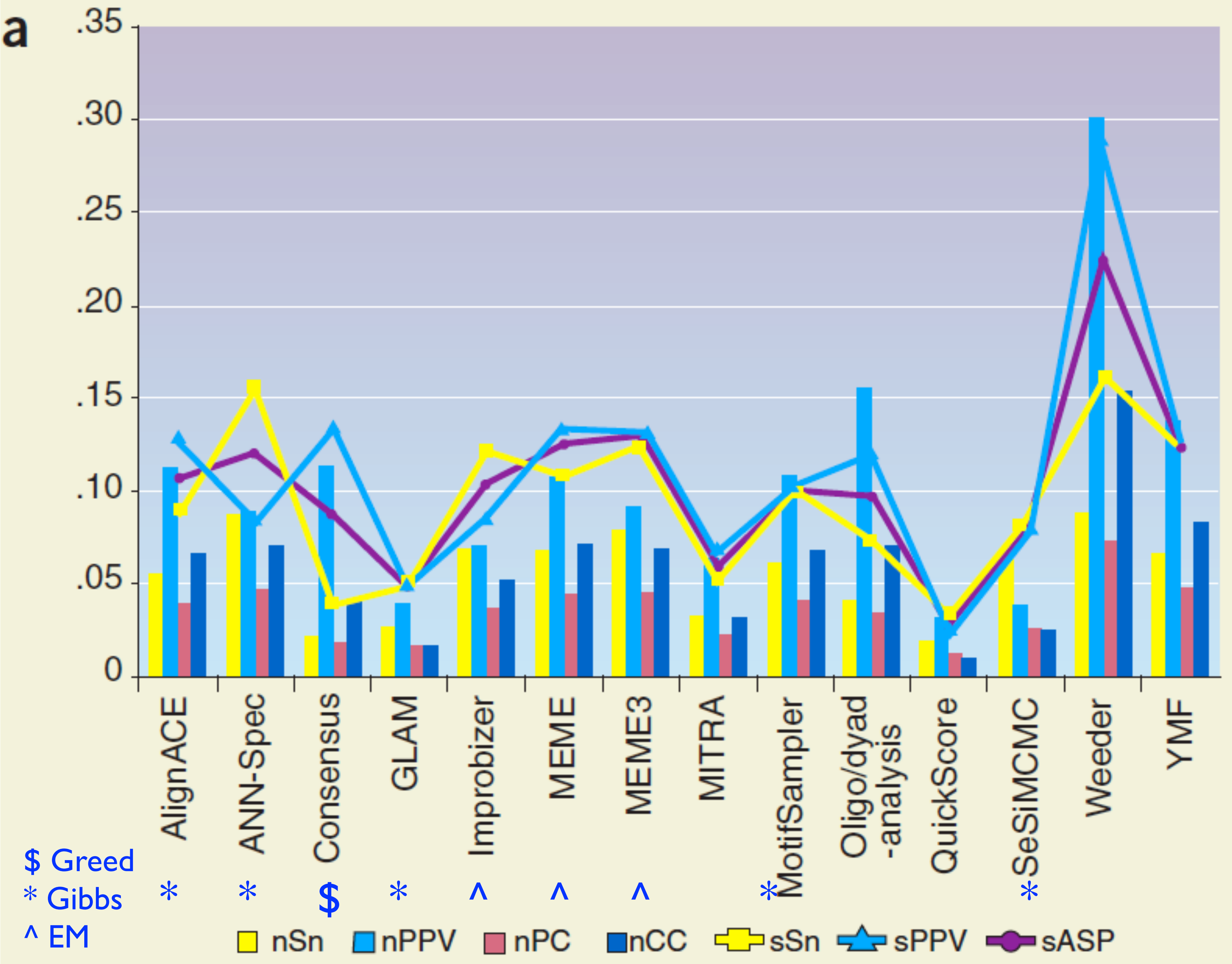
Real ‘motifs’ (Transfac)

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

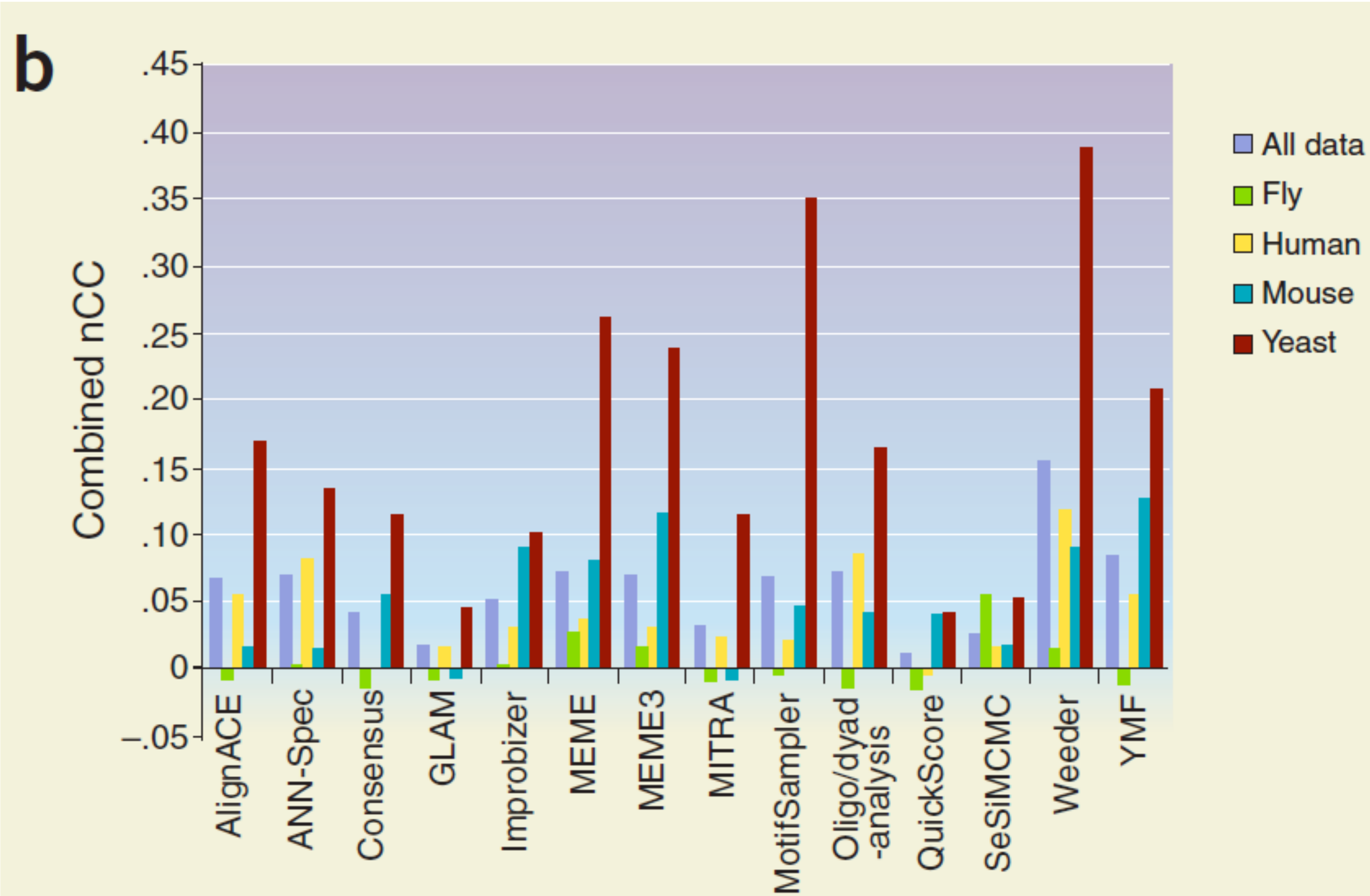
‘Real’, ‘generic’, ‘Markov’

Expert users, top prediction only

“Blind” – sort of



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

Lessons

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

Accuracy low

partly reflects limitations in evaluation methodology (e.g. $\leq$ 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

Bioinformatics Advance Access published November 26, 2013

BIOINFORMATICS **ORIGINAL PAPER**

2013, pages 1–9
doi:10.1093/bioinformatics/btt615

Sequence analysis

Advance Access publication October 25, 2013

Discriminative motif analysis of high-throughput dataset

Zizhen Yao[1,*], Kyle L. MacQuarrie[1,2], Abraham P. Fong[3,4], Stephen J. Tapscott[1,3,5], Walter L. Ruzzo[6,7,8] and Robert C. Gentleman[9]

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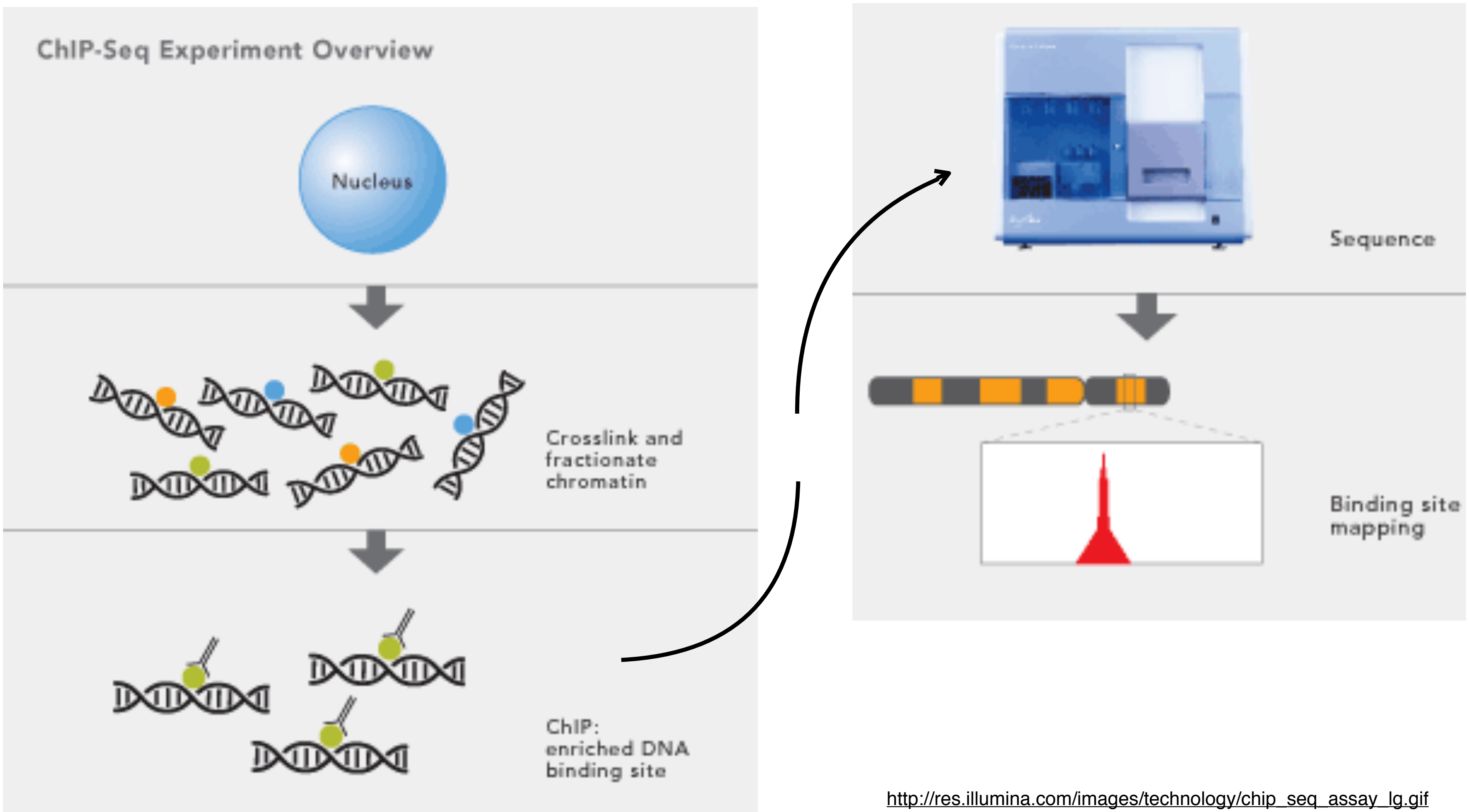
ChIP-seq



http://res.illumina.com/images/technology/chip_seq_assay_lg.gif

TF Binding Site Motifs From ChIPseq

LOTS of data

- E.g. 10^3–10^5 sites, hundreds of reads each (plus perhaps even more nonspecific)

Motif variability

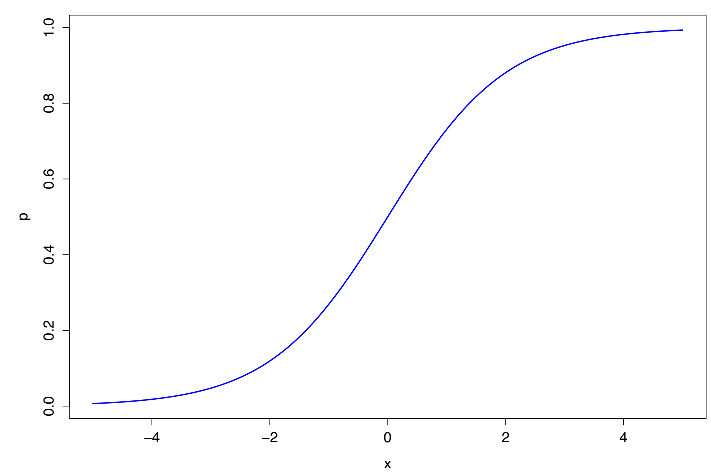
Co-factor binding sites

Method Outline

Discriminative model – foreground/background

Logistic regression – x = motif count

$$log \frac{p}{1-p} = \beta_0 + \beta_1 x$$

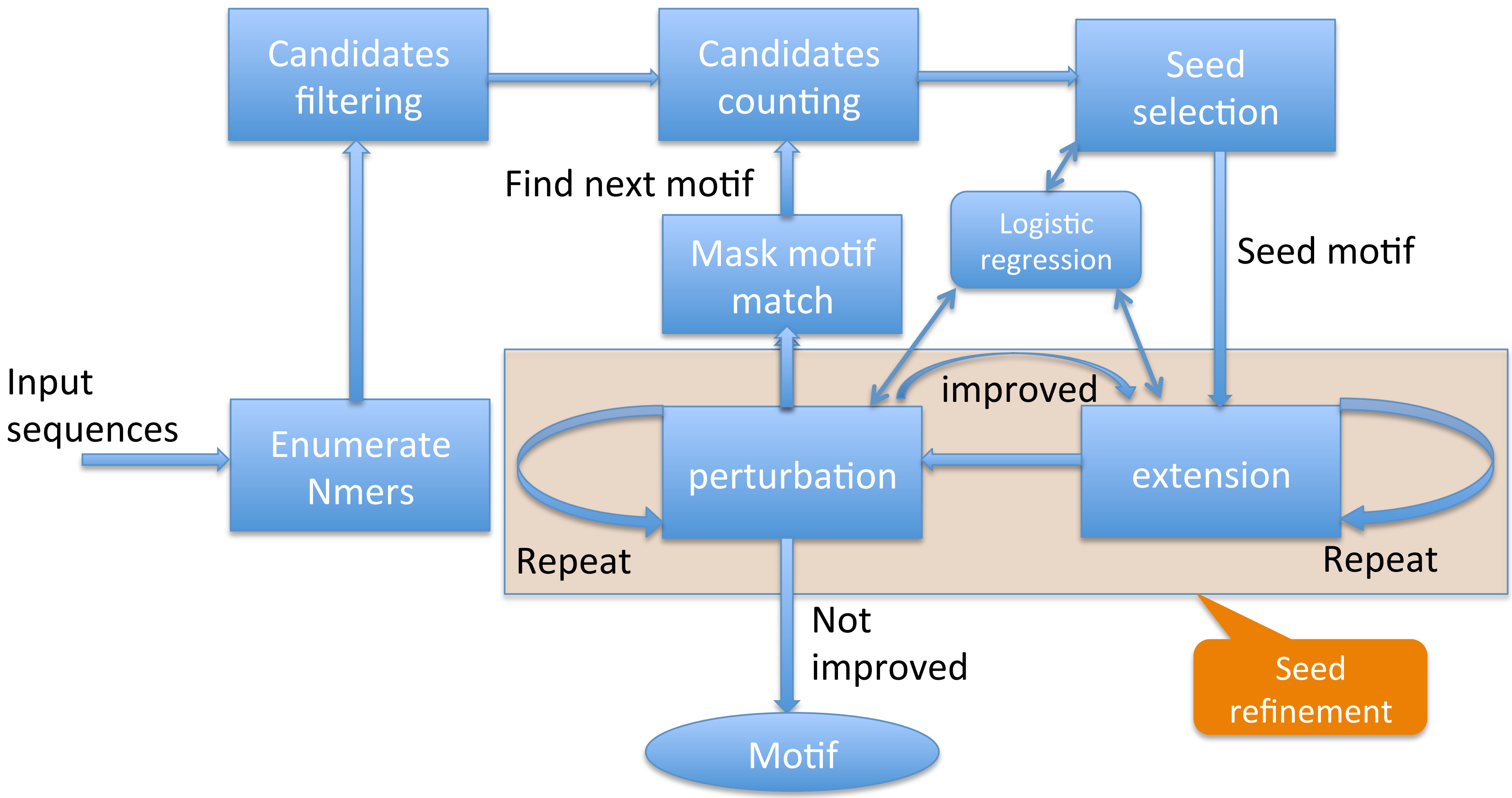


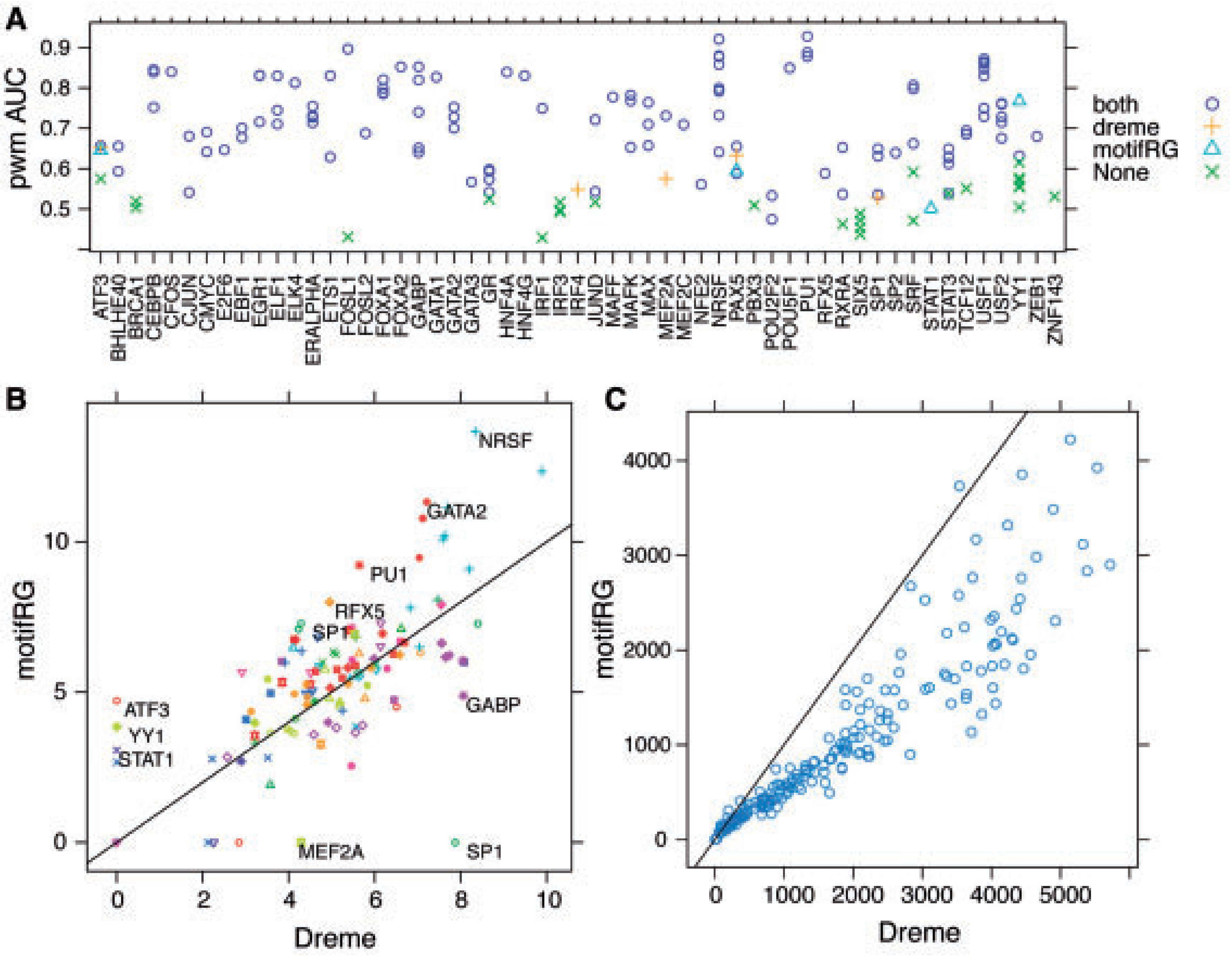
IUPAC patterns – e.g., “R” = A or G

seed/extend/perturb

Z-scores

Method Outline



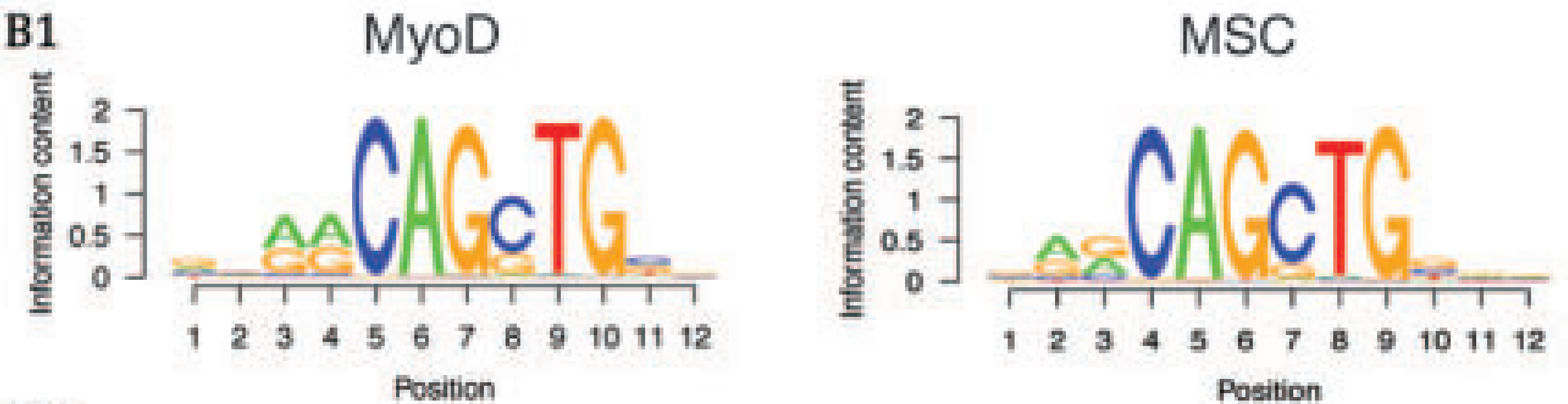

A
pwm AUC
0.9
0.8
0.7
0.6
0.5
both
dreme
motifRG
None
ATF3 BHLHE40 BRCA1 CEBPB CFOS CJUN CMYC E2F6 EBF1 EGR1 ELF1 ELK4 ERALPHA ETS1 FOSL1 FOSL2 FOXA1 FOXA2 GABP GATA1 GATA2 GATA3 GR HNF4A HNF4G IRF1 IRF3 IRF4 JUND MAFF MAFK MAX MEF2A MEF2C NFE2 NRSF PAX5 PBX3 POU2F2 POU5F1 PU1 RFX5 RXRA SIX5 SP1 SP2 SRF STAT1 STAT3 TCF12 USF1 USF2 YY1 ZEB1 ZNF143
B
motifRG
Dreme
NRSF
GATA2
PU1
RFX5
SP1
ATF3
YY1
STAT1
GABP
MEF2A
SP1
C
motifRG
Dreme

A1

A2

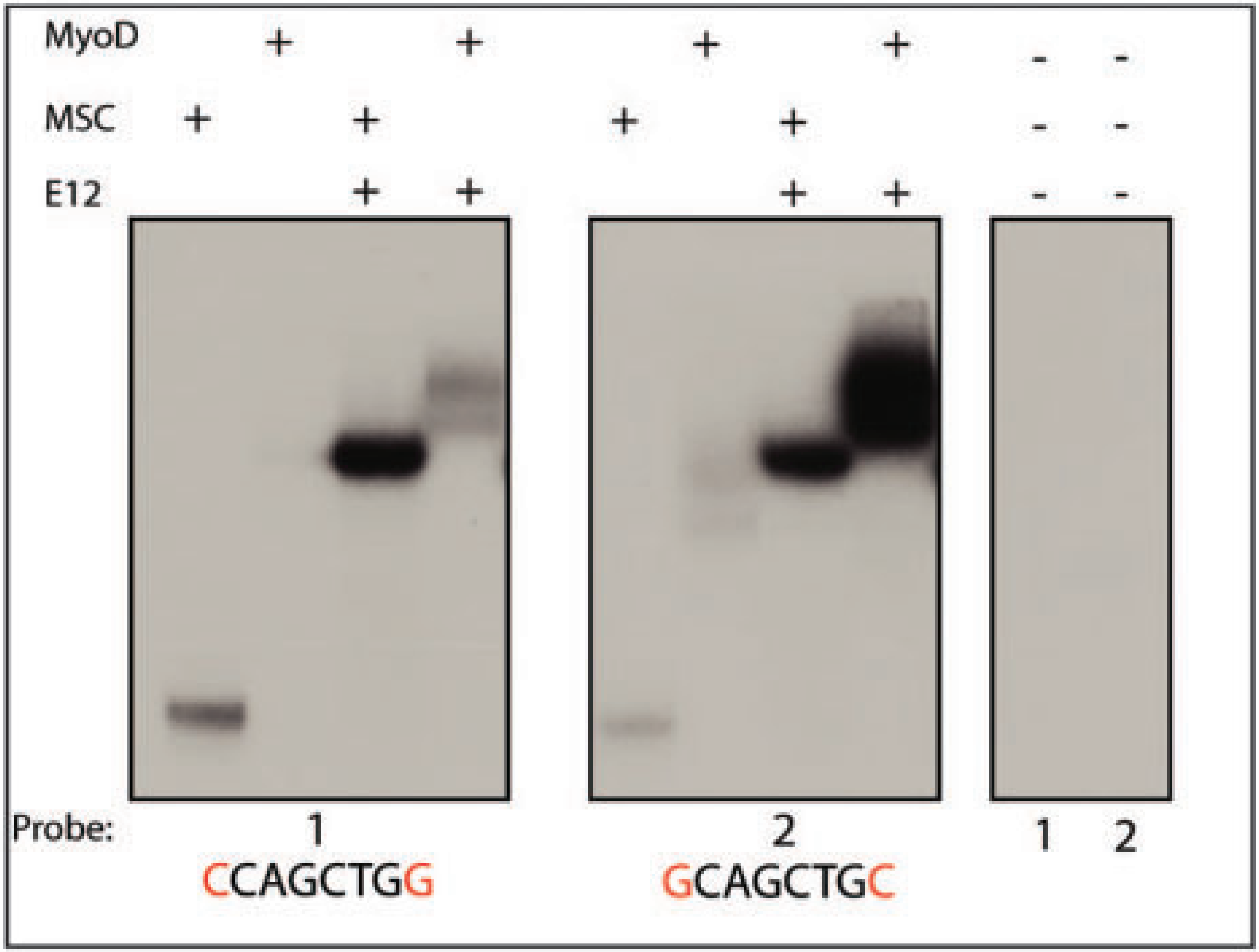
Consensus	scores	ratio	fg.frac	bg.frac	logo	DB match	DB Evalue	DB logo	
NNVCAGATGGNN	69	5.12	0.68	0.14		Tcfe2a	1.5e-09		NeuroD
NNCAGCTGSNN	42	1.57	0.92	0.73		Ascl2	9.2e-08		NeuroD
NNATCAATNN	22	3.34	0.13	0.04		Pbx1	9.1e-05		NeuroD
NNRCAGCTGNN	-68	0.35	0.47	0.90		Ascl2	2.4e-08		MyoD
NNTNASTCANN	-21	0.51	0.17	0.27		AP1	1.4e-05		MyoD
NNRCCACANN	-19	0.66	0.29	0.41		RUNX1	7.1e-07		MyoD
NNHNAAATADNN	-18	0.53	0.12	0.21					MyoD

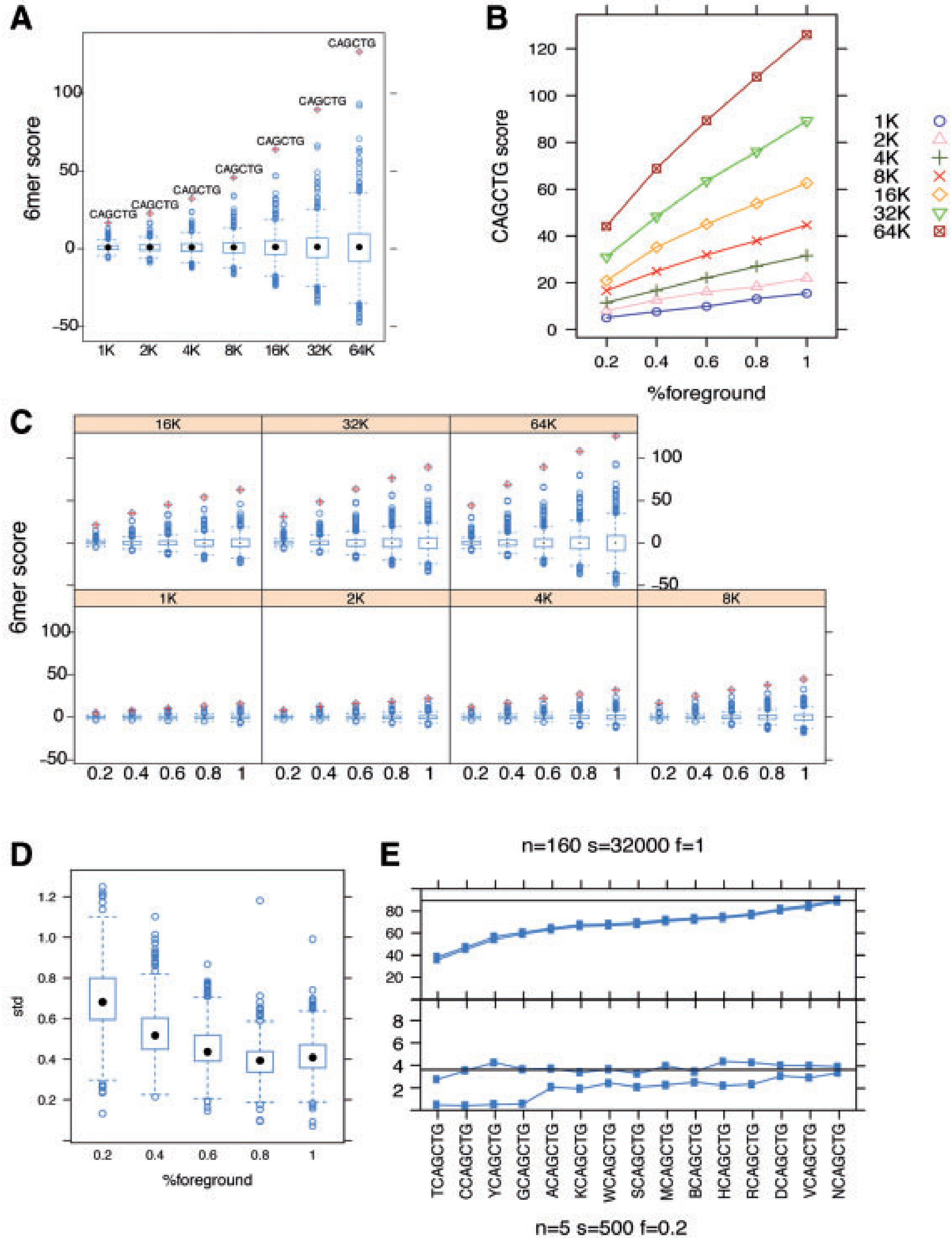
B1



B2

Consensus	scores	ratio	fg.frac	bg.frac	logo	
NRRCAGGTGNN	20.5	4.90	0.521	0.12		MyoD
NNCAGCTGGNN	-25.6	0.21	0.211	0.76		MSC
NNBCCAGCHN	-20.1	0.43	0.488	0.83		


MyoD + + + + - -
MSC + + + + - -
E12 + + + + - -
Probe: 1 2 1 2
CCAGCTGG
GCAGCTGC



A
6mer score
CAGCTG
1K 2K 4K 8K 16K 32K 64K
B
CAGCTG score
%foreground
1K
2K
4K
8K
16K
32K
64K
C
6mer score
16K 32K 64K
1K 2K 4K 8K
D
std
%foreground
E
n=160 s=32000 f=1
TCAGCTG CCAGCTG YCAGCTG GCAGCTG ACAGCTG KCAGCTG WCAGCTG SCAGCTG MCAGCTG BCAGCTG HCAGCTG RCAGCTG DCAGCTG VCAGCTG NCAGCTG
n=5 s=500 f=0.2

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 room for improvement. E.g., *ChIP-seq* and *Comparative genomics* (cross-species comparison) are very promising.