

# CSE 527

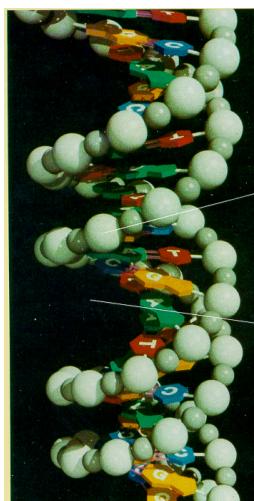
## Lecture 9

### The Gibbs Sampler

## The “Gibbs Sampler”

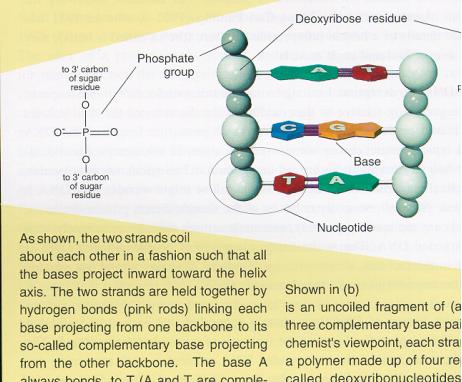
- Lawrence, et al.  
“Detecting Subtle Sequence Signals: A Gibbs Sampling Strategy for Multiple Sequence Alignment,”  
Science 1993

## The Double Helix



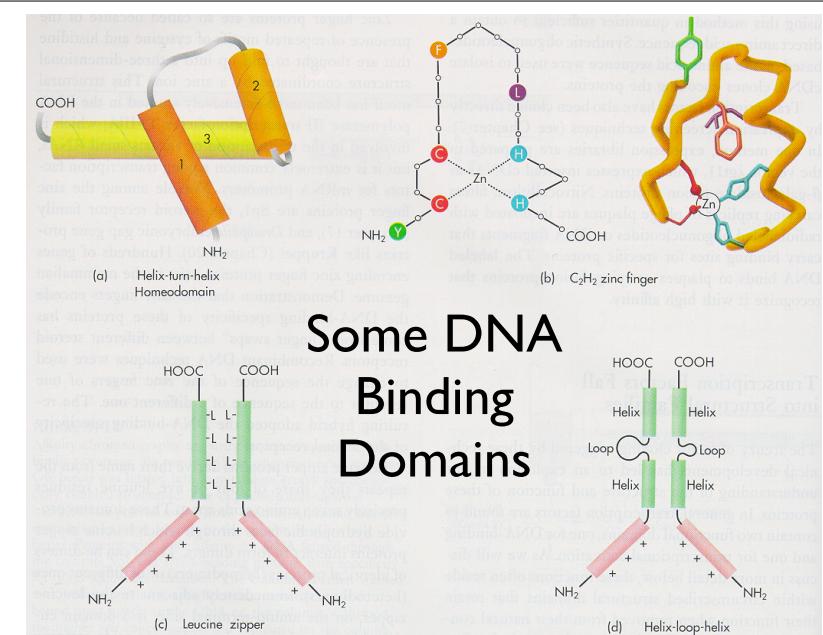
(a) Computer-generated Image of DNA  
(by Mel Pruett)

(b) Uncoiled DNA Fragment



Los Alamos Science

## Some DNA Binding Domains



Sigma-37	223	IIDLTYIQNK	SQKETGDILGISQMHSVRS	LQRKAVKKLR	240	A25944
SpoIIIC	94	RFGFLDKKEK	TQREIAKELGIGRSYVSR	IEKRALMKMF	111	A28627
NahR	22	VVFNQLLVDR	RVSITAENLGLTQPAVSN	ALKRLRTSLQ	39	A32837
Antennapedia	326	FHFNRYLTRR	RRIEIAHALCLTERQIKI	WFONRRMKWK	343	A23450
NtrC (Brady.)	449	LTAALAAATRG	NQIRAADLGLNRNTRLK	KIRDLDIQQVY	466	B26499
DicA	22	IRYRRKNLKH	TQRSLAKALKIISHVSVSQ	WERGIDSEPTIG	39	B24328 (BVECDA)
MerD	5	MNAY	TVSRLALDAVGVSIVRDR	YLRLGLRPV	22	C29010
Fis	73	LDMVMQYTRG	NQTRAALMMGINRGTLRK	KLKKGGMN	90	A32142 (DNECFS)
MAT a1	99	FRRQSLNSK	EKEEVAKKCGITPLQVRV	WFINKRMRSK	116	A90983 (JEBY1)
Lambda cII	25	SALLNKIAML	GTEKTAEEAVGVDKSQISR	WKRDWIPKFS	42	A03579 (QCBP2L)
Crp (CAP)	169	THPDGMQIKI	TRQEIGQIVGCSRETIVGR	ILKMLEDPNL	186	A03553 (QRECC)
Lambda Cro	15	ITLKDYAMRF	GQTTAKADLGVYQSAINK	ATHAGRKIFL	32	A03577 (RCBPL)
P22 Cro	12	YKKDVIDHFG	TQRAVAKALGISDAAVSQ	WKEVIMEPKDA	29	A25867 (RGBP22)
AraC	196	ISDHLLADSNF	DIASVAQHVCLSPRSRLSH	LFRQQQLGIVS	213	A03554 (RGECA)
Fnr	196	FSPREFRLLTM	TRGDIGNYGLLTIVETISR	LLGRQFKSGM	213	A03552 (RGECF)
HtpR	252	ARWLDEDNKS	TLQELADRYGVSAERVRQ	LEKNAMKKLR	269	A00700 (RGECH)
NtrC (K.a.)	444	LITALRHQTQ	HKQEAARLLGWGRNITL	KLKELGME	461	A03564 (RGKBCP)
CytR	11	MKAKKQETAA	TMKDVALKAKVSTATVSR	ALMNPDKVSQ	28	A24963 (RPECCT)
DeoR	23	LQELKRSDSL	HLKDAAAALLGVSEMTIRR	DLNNHSAPVV	40	A24076 (RPECDO)
GalR	3	MA	TIKDVARLAGVSVATVSR	VINNQASHVSA	20	A03559 (RPECG)
LacI	5	MKPV	TLYDVAEYAGVSYQTCSR	VVNQASHVSA	22	A03558 (RPECL)
TetR	26	LLNEVGIEGL	TTRKLAQKLGVEQPTLYW	HVKNKRALLD	43	A03576 (RPECTN)
TrpR	67	IVEELLRGEM	SQRELKNELGAGIATIRR	GSNSLKAAPV	84	A03568 (RPECW)
NifA	495	LIAALEKAGW	VQAKAAARLLGMTPRQVAY	R1QIMDITMP	512	S02513
SpoIIG	205	RFGLVGEEEK	TQKDVADEMMGQISQSYISR	LEKRIIKRLL	222	S07337
Pin	160	QAGRLLIAAGT	PRQKVAAIYDVGVSTLYK	TFPGDK	177	S07958
PurR	3	MA	TIKDVAKRANVSTTVSH	VINKTRFAE	20	S08477
EbgR	3	MA	TLKDIADIAEGVSLATVSR	VLNDDPTLNV	20	S09205
LexA	27	DHISQTGMPP	TRAEIQLGRFSPNAAE	EHLKALARHG	44	S11945
P22 cI	25	SSILNRNIAIR	GQRKVADALGINESQISR	WKGDFIPKMG	42	B25867 (Z1BPC2)
*****						

	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	52	222	94	94	9	265	606	
Lys	9	133	442	380	9	71	380	194	9	133	9	71	9	9	9	71	256	
Glu	53	9	96	401	9	9	140	140	9	9	53	140	140	9	9	9	53	
Asp	67	9	9	473	9	9	299	125	9	67	9	67	9	9	9	9	67	
Gln	9	600	224	9	9	9	224	9	9	9	9	278	63	278	9	9	170	
His	240	9	9	9	9	9	125	125	9	9	9	125	125	9	9	9	240	
Asn	168	9	9	9	9	9	168	89	9	89	9	248	9	168	89	9	89	
Ser	117	9	117	117	9	9	9	9	9	9	9	819	63	387	63	9	819	
Gly	151	9	56	9	9	151	9	9	9	1141	9	151	9	56	9	9	56	
Ala	9	9	112	43	181	901	43	181	215	9	43	43	181	112	43	78	9	
Thr	915	130	130	9	251	9	9	9	9	9	9	311	130	70	855	9	130	
Pro	76	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	9	295	581	295	9	9	9	9	9	
Val	58	107	9	9	500	9	9	9	156	9	598	9	205	58	9	746	58	
Leu	9	121	9	9	149	9	93	149	458	9	149	9	37	37	9	177	9	
Ile	9	166	114	61	323	9	114	166	9	9	427	9	61	9	61	427	9	
Met	9	104	9	9	9	9	9	198	198	9	104	9	9	198	9	9	9	
Tyr	9	9	136	9	9	9	9	262	262	9	9	136	9	262	9	262	136	
Phe	9	9	9	9	9	9	9	9	9	9	108	9	9	9	9	9	9	
Trp	9	9	9	9	9	9	9	9	9	9	366	9	9	9	9	9	366	

## 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:  $x_1, x_2, \dots, x_k$
- Joint distribution (p.d.f.):  $P(x_1, x_2, \dots, x_k)$
- Some function:  $f(x_1, x_2, \dots, x_k)$
- Want Expected Value:  $E(f(x_1, x_2, \dots, x_k))$

# How to Average

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

- 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  $\vec{x}^{(1)}, \vec{x}^{(2)}, \dots, \vec{x}^{(n)} \sim P(\vec{x})$  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  $\vec{X}_{t+1} \sim P(\vec{X}_{t+1} | \vec{X}_t)$  w/ stationary dist =  $P$

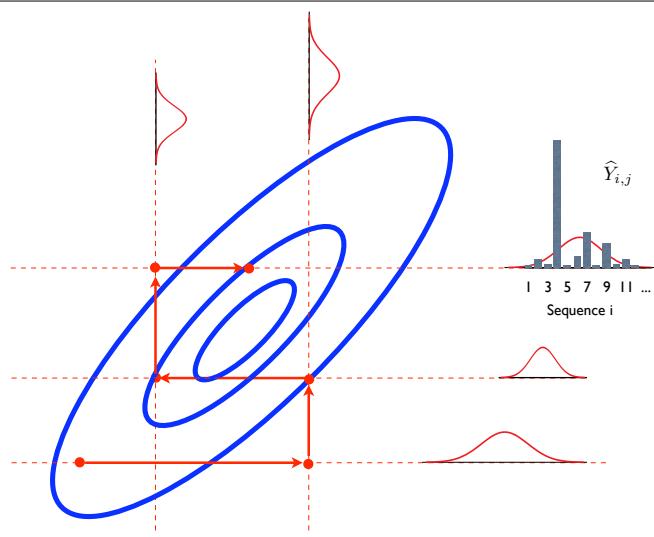
• Simplest & most common: Gibbs Sampling  
 $P(x_i | x_1, x_2, \dots, x_{i-1}, x_{i+1}, \dots, x_k)$

- Algorithm

for  $t = 1$  to  $\infty$

for  $i = 1$  to  $k$  do :

$\begin{array}{c} t+1 \quad t \\ / \quad \backslash \\ x_{t+1,i} \sim P(x_{t+1,i} | \underbrace{x_{t+1,1}, x_{t+1,2}, \dots, x_{t+1,i-1}}_{\diagdown}, \underbrace{x_{t,i+1}, \dots, x_{t,k}}_{\diagup}) \end{array}$



- Input: again assume sequences  $s_1, s_2, \dots, s_k$  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  
 $P(x_i = j | x_1, x_2, \dots, x_{i-1}, x_{i+1}, \dots, x_k)$   
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.

Randomly initialize  $x_i$ 's

for  $t = 1$  to  $\infty$

  for  $i = 1$  to  $k$

    discard motif instance from  $s_i$ ;

    recalc WMM from rest

    for  $j = 1 \dots |s_i|-w+1$

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

      →  $P(x_i = j | x_1, x_2, \dots, x_{i-1}, x_{i+1}, \dots, x_k)$

      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? (Recall that individual samples are not independent, and may not “move” freely through the sample space. Also, 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

