

CSE 549: Computational Biology

🗨 Substitution Matrices

How should we score alignments

So far, we've looked at “arbitrary” schemes for scoring mutations. How can we assign scores in a more meaningful way?

Are these scores

	A	C	G	T
A	5	-5	-3	-5
C	-5	5	-5	-3
G	-3	-5	5	-5
T	-5	-3	-5	5

better than these scores?

	A	C	G	T
A	4	-1	-1	-1
C	-1	4	-1	-1
G	-1	-1	4	-1
T	-1	-1	-1	4

How should we score alignments

So far, we've looked at “arbitrary” schemes for scoring mutations. How can we assign scores in a more meaningful way?

Are these scores

better than these scores?

	A	C	G	T
A	5	-5	-3	-5
C	-5	5	-3	-5
G	-3	-3	5	-5
T	-5	-3	-5	5

One option — “learn” the substitution / mutation rates from real data

	A	C	G	T
A	4	-1	-1	-1
C	-1	4	-1	-1
G	-1	-1	4	-1
T	-1	-1	-1	4

How should we score alignments

Main Idea: **Assume** we can obtain (through a potentially burdensome process) a collection of high quality, high confidence sequence alignments.

We have a collection of sequences which, presumably, originated from the same ancestor — differences are mutations due to divergence.

Learn the frequency of different mutations from these alignments, and use the frequencies to derive our scoring function.



BLOSUM62 matrix



A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	
5	-2	-2	-2	0	0	0	0	-2	-2	-3	-2	-1	-2	0	0	0	-2	-3	0	A
	5	-2	-3	-3	0	-1	-2	0	-3	-4	1	-3	-3	-2	-2	0	0	-3	-4	R
		5	0	0	0	-2	0	0	-4	-5	-2	-3	-3	-2	0	0	-2	-2	-5	N
			5	-4	0	1	-1	0	-5	-6	-3	-4	-4	0	-2	-2	-2	-2	-5	D
				8	-2	-3	-1	-1	0	-2	-3	0	-1	-1	1	0	0	-2	0	C
					5	2	0	0	-2	-4	0	-2	-3	0	0	0	0	-2	-3	Q
						5	0	0	-3	-4	0	-3	-3	0	0	0	-2	-3	-3	E
							6	0	-4	-5	-2	-3	-2	-2	0	0	0	-2	-3	G
								6	-3	-4	0	-2	0	0	0	0	0	2	-2	H
									4	0	-3	2	0	-2	-3	0	0	-3	2	I
										4	-4	0	0	-3	-4	-3	0	-4	0	L
											4	-2	-4	-1	-2	0	0	-3	-4	K
												6	0	-3	-3	-2	0	-3	2	M
													6	-3	-2	-2	2	2	0	F
														7	0	0	-2	-3	0	P
															4	2	-2	-2	-3	S
																5	-1	-3	0	T
																	9	2	-1	W
																		7	-3	Y
																			4	V

Brick, Kevin, and Elisabetta Pizzi. "A novel series of compositionally biased substitution matrices for comparing Plasmodium proteins." BMC bioinformatics 9.1 (2008): 236.

Probabilities to Scores

Assuming we have a reasonable process by which to compute **frequencies**, how can we use this to obtain a **score**?

Probabilities to Scores

Assuming we have a reasonable process by which to compute **frequencies**, how can we use this to obtain a **score**?

Hypothesis we wish to test; two amino acids are correlated because they are homologous.

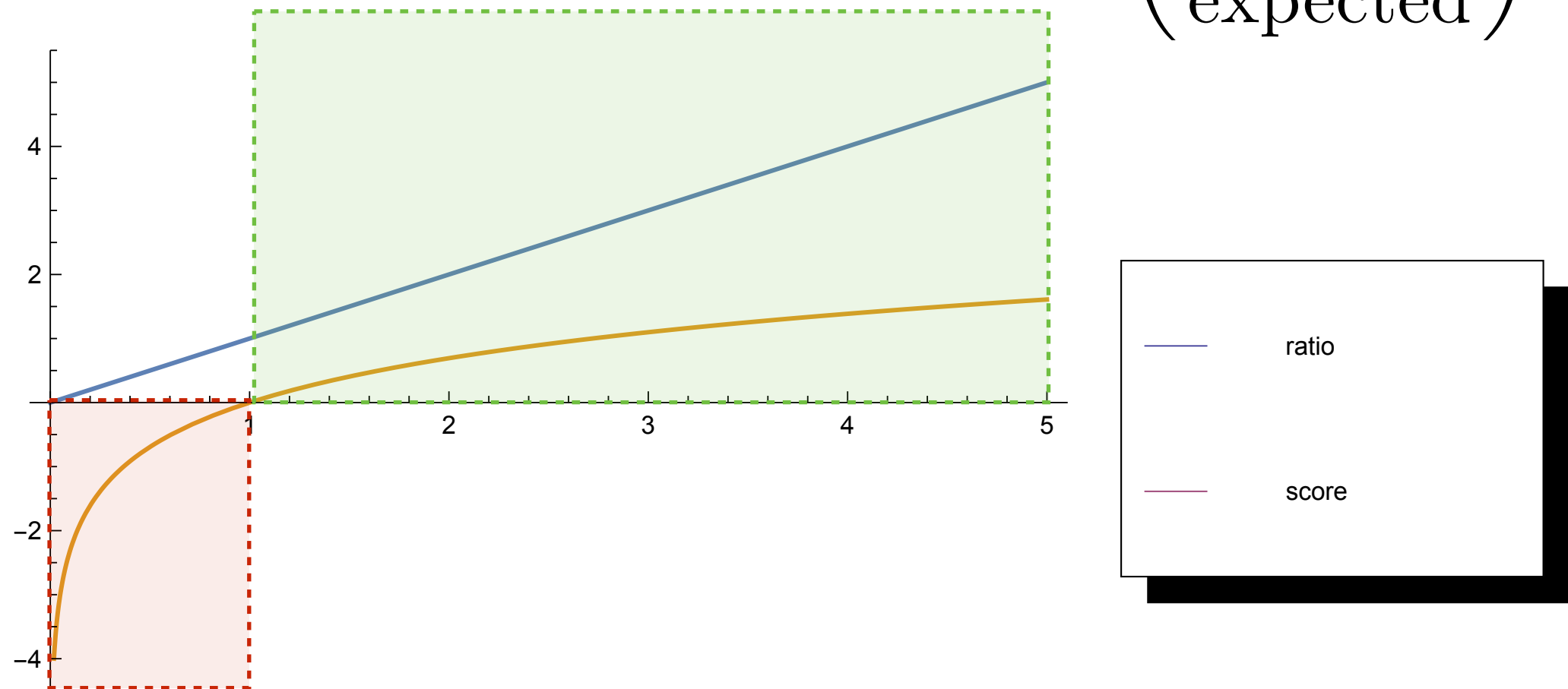
☐

$$\text{score} = \log \text{ odds ratio} = s_{AB} \propto \log \left(\frac{\text{observed}}{\text{expected}} \right)$$

Null hypothesis; two amino acids occur independently (and are uncorrelated and unrelated).

Probabilities to Scores

$$\text{score} = \log \text{ odds ratio} = s_{AB} \propto \log \left(\frac{\text{observed}}{\text{expected}} \right)$$



Positive scores mean we find “conservative substitutions”

Negative scores mean we find “nonconservative substitutions”

BLOSUM matrix

Introduced by Henikoff & Henikoff in 1992

Start with the BLOCKS database (H&H '91)

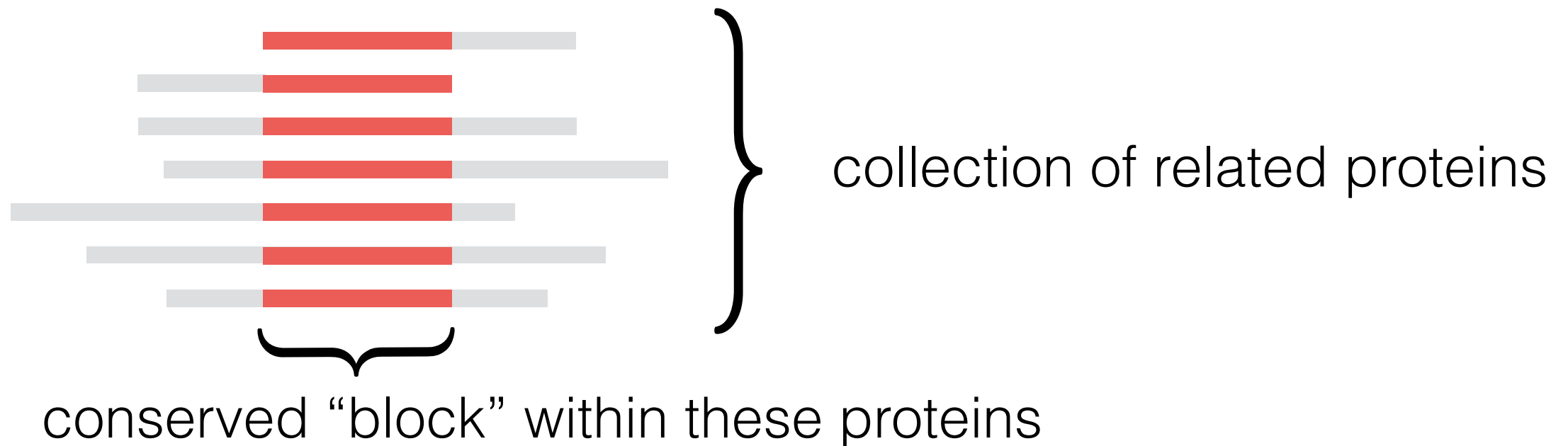
1. Look for conserved (gapless, $\geq 62\%$ identical) regions in alignments.
2. Count all pairs of amino acids in each column of the alignments.
3. Use amino acid pair frequencies to derive “score” for a mutation/replacement



BLOSUM matrix

Start with the BLOCKS database (H&H '91)

1. Look for conserved (gapless) regions in alignments.



sequences too similar are “clustered” & represented by either a single sequence, or a weighted combination of the cluster members

BLOSUM r : the matrix built from blocks with no more than $r\%$ of similarity – e.g., BLOSUM62 is the matrix built using sequences with no less than 62% similarity.*

BLOSUM matrix

Start with the BLOCKS database (H&H '91)

2. Count all pairs of amino acids in each column of the alignments.



FPTADAGGRS
FVTADALGRS
FPTPDAGLRN
FVTAEAGIRQ
FPTAEAGGRS

$$c_{AB}^{(i)} = \begin{cases} \binom{c_A^{(i)}}{2} & \text{if } A = B \\ c_A^{(i)} \times c_B^{(i)} & \text{otherwise} \end{cases}$$

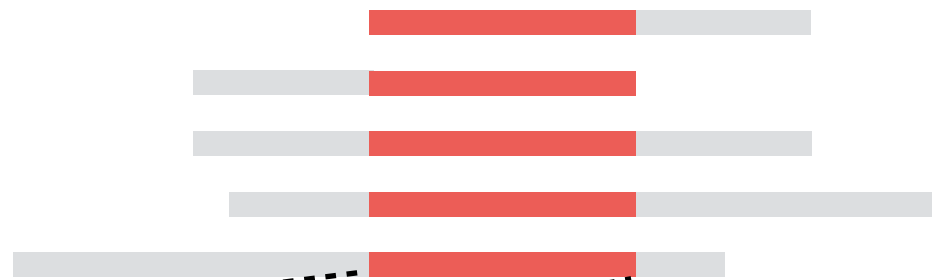
$c_A^{(i)}$ = num. of occurrences of A in column i

What is the intuition behind this expression?

BLOSUM matrix

Start with the BLOCKS database (H&H '91)

2. Count all pairs of amino acids in each column of the alignments.



FPTADAGGRS
FVTADALGRS
FPTPDAGLRN
FVTAEAGLRQ
FPTAEAGGRS

Example:

$$c_{GG}^{(i)} = \binom{3}{2} = 3$$

$$c_{GL}^{(i)} = 3 \times 2$$

$$c_{LL}^{(i)} = \binom{2}{2} = 1$$

In this column, there are 3 ways to pair G with G, 6 potential ways to pair G with L and 1 potential way to pair L with L.

Computing Scores

3. Use amino acid pair frequencies to derive “score” for a mutation/replacement

Total # of potential align. between A & B: $c_{AB} = \sum_i c_{AB}^{(i)}$

Total number of pairwise char. alignments: $T = \sum_{A \geq B} c_{AB}$

Normalized frequency of aligning A & B: $q_{AB} = \frac{c_{AB}}{T}$

BLOSUM matrix



FPTADAGGRS

FVTADALGRS

FPTPDAGLRN

FVTAEAGLRQ

FPTAEAGGRS

In our example, we get

$$q_{GL} = \frac{0 + 0 + 0 + 0 + 0 + 0 + 4 + 6 + 0 + 0}{10^{\frac{(5)(4)}{2}}} = \frac{10}{100}$$

BLOSUM matrix



FPTADAGGRS

FVTADALGRS

FPTPDAGLRN

FVTAEAGLRQ

FPTAEAGGRS

In our example, we get

$$q_{GL} = \frac{0 + 0 + 0 + 0 + 0 + 0 + 4 + 6 + 0 + 0}{10^{\frac{(5)(4)}{2}}} = \frac{10}{100}$$

why does this denominator work?

BLOSUM matrix



FPTADAGGRS

$$C_{VP} = 2 * 3 = 6$$

FVTADALGRS

$$C_{PP} = 3 \text{ choose } 2 = 3$$

FPTPDAGLRN

$$C_{VV} = 2 \text{ choose } 2 = 1$$

FVTAEAGLRQ

$$\text{So } C_{VP} + C_{PP} + C_{VV} = 10 = 5 \text{ choose } 2$$

FPTAEAGGRS

In our example, we get

$$q_{GL} = \frac{0 + 0 + 0 + 0 + 0 + 0 + 4 + 6 + 0 + 0}{10 \frac{(5)(4)}{2}} = \frac{10}{100}$$

why does this denominator work?

BLOSUM matrix



FPTADAGGRS

FVTADALGRS

FPTPDAGLRN

FVTAEAGLRQ

FPTAEAGGRS

In our example, we get

$$q_{GL} = \frac{0 + 0 + 0 + 0 + 0 + 0 + 4 + 6 + 0 + 0}{10^{\frac{(5)(4)}{2}}} = \frac{10}{100}$$

total column sum is always # rows choose 2

Computing Scores

3. Use amino acid pair frequencies to derive “score” for a mutation/replacement

Probability of occurrence of amino acid A in any {A,B} pair:

$$p_A = q_{AA} + \sum_{A \neq B} q_{AB}$$

Expected likelihood of each {A,B} pair, assuming independence:

$$e_{AB} = \begin{cases} (p_A)(p_B) = (p_A)^2 & \text{if } A = B \\ (p_A)(p_B) + (p_B)(p_A) = 2(p_A)(p_B) & \text{otherwise} \end{cases}$$

Computing Scores

Recall the original idea (likelihood \rightarrow scores)

$$\text{score} = \log \text{ odds ratio} = s_{AB} \propto \log \left(\frac{\text{observed}}{\text{expected}} \right)$$

$$\text{score} = \log \text{ odds ratio} = s_{AB} = \text{Round} \left(\left(\frac{1}{\lambda} \right) \log_2 \left(\frac{q_{AB}}{e_{AB}} \right) \right)$$

Scaling factor used to produce scores that can be rounded to integers; set to 0.5 in H&H '92.

Scores are data-dependent

distribution of amino acids across columns matters

GG

GA

WG

WA

NG

GA

GA

$$p_G = 0.5$$

$$e_{GG} = 0.25$$

$$q_{GG} = 0.214$$

$$\begin{aligned} s_{GG} &= \text{Round}[(2)\log_2(0.214 / 0.25)] \\ &= \text{Round}[(2)(-0.22)] = 0 \end{aligned}$$

GW

GA

GW

GA

GN

GA

GA

$$p_G = 0.5$$

$$e_{GG} = 0.25$$

$$q_{GG} = 0.5$$

$$\begin{aligned} s_{GG} &= \text{Round}[(2)\log_2(0.5 / 0.25)] \\ &= \text{Round}[(2)(1)] = 2 \end{aligned}$$

Scores are data-dependent

{G,W} observed a lot

GG

GA

WG

AW

NG

GA

GA

$$p_G = 0.5 \quad p_W = 0.143$$

$$e_{GW} = 0.143$$

$$q_{GW} = 0.167$$

$$\begin{aligned} s_{GW} &= \text{Round}[(2)\log_2(0.167 / 0.143)] \\ &= \text{Round}[(2)(0.224)] = 0 \end{aligned}$$

{G,W} observed rarely

GW

GA

GW

GA

GN

GA

AG

$$p_G = 0.5 \quad p_W = 0.143$$

$$e_{GW} = 0.143$$

$$q_{GW} = 0.048$$

$$\begin{aligned} s_{GW} &= \text{Round}[(2)\log_2(0.048 / 0.143)] \\ &= \text{Round}[(2)(-1.575)] = -3 \end{aligned}$$

Example

FPTADAGGRS

FVTADALGRS

FPTPDAGLRN

FVTAEAGLRQ

FPTAEAGGRS



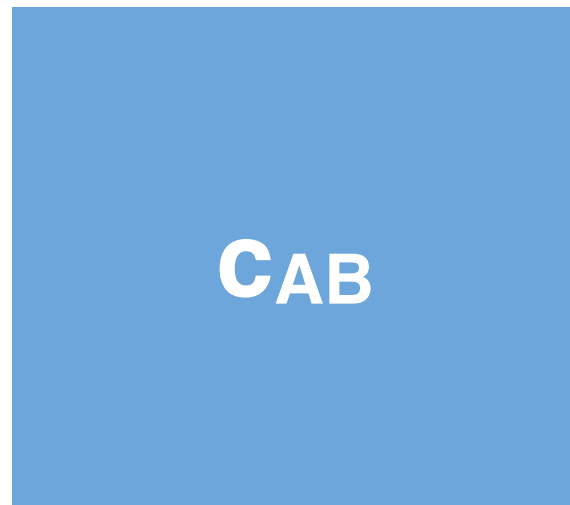
$$c_{AB} = \sum_i c_{AB}^{(i)} \longrightarrow$$

Matrix of c_{AB} values

	A	D	E	F	G	L	N	P	Q	R	S	T	V
A	16												
D		3											
E		6	1										
F				10									
G					9								
L					10	1							
N							0						
P	4							3					
Q							1		0				
R										10			
S							3		3		3		
T												10	
V								6					1

Example

Matrix of q_{AB} values

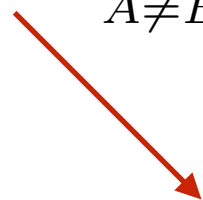


$$q_{AB} = \frac{C_{AB}}{T}$$



	A	D	E	F	G	L	N	P	Q	R	S	T	V
A	0.16												
D		0.03											
E		0.06	0.01										
F				0.1									
G					0.09								
L					0.1	0.01							
N							0						
P	0.04							0.03					
Q							0.01		0				
R										0.1			
S							0.03		0.03		0.03		
T												0.1	
V								0.06					0.01

$$p_A = q_{AA} + \sum_{A \neq B} q_{AB}$$



P _A	P _D	P _E	P _F	P _G	P _L	P _N	P _P	P _Q	P _R	P _S	P _T	P _V
0.18	0.06	0.04	0.1	0.14	0.06	0.02	0.08	0.02	0.1	0.06	0.1	0.04

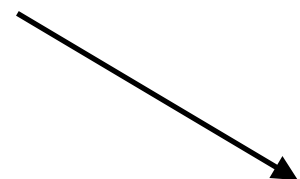
Example

Matrix of e_{AB} values

	A	D	E	F	G	L	N	P	Q	R	S	T	V
A	0.0324												
D	0.0216	0.0036											
E	0.0144	0.0048	0.0016										
F	0.0360	0.0120	0.0080	0.0100									
G	0.0504	0.0168	0.0112	0.0280	0.0196								
L	0.0216	0.0072	0.0048	0.0120	0.0168	0.0036							
N	0.0072	0.0024	0.0016	0.0040	0.0056	0.0024	0.0004						
P	0.0288	0.0096	0.0064	0.0160	0.0224	0.0096	0.0032	0.0064					
Q	0.0072	0.0024	0.0016	0.0040	0.0056	0.0024	0.0008	0.0032	0.0004				
R	0.0360	0.0120	0.0080	0.0200	0.0280	0.0120	0.0040	0.0160	0.0040	0.0100			
S	0.0216	0.0072	0.0048	0.0120	0.0168	0.0072	0.0024	0.0096	0.0024	0.0120	0.0036		
T	0.0360	0.0120	0.0080	0.0200	0.0280	0.0120	0.0040	0.0160	0.0040	0.0200	0.0120	0.0100	
V	0.0144	0.0048	0.0032	0.0080	0.0112	0.0048	0.0016	0.0064	0.0016	0.0080	0.0048	0.0080	0.0016

p_A

q_{AB}

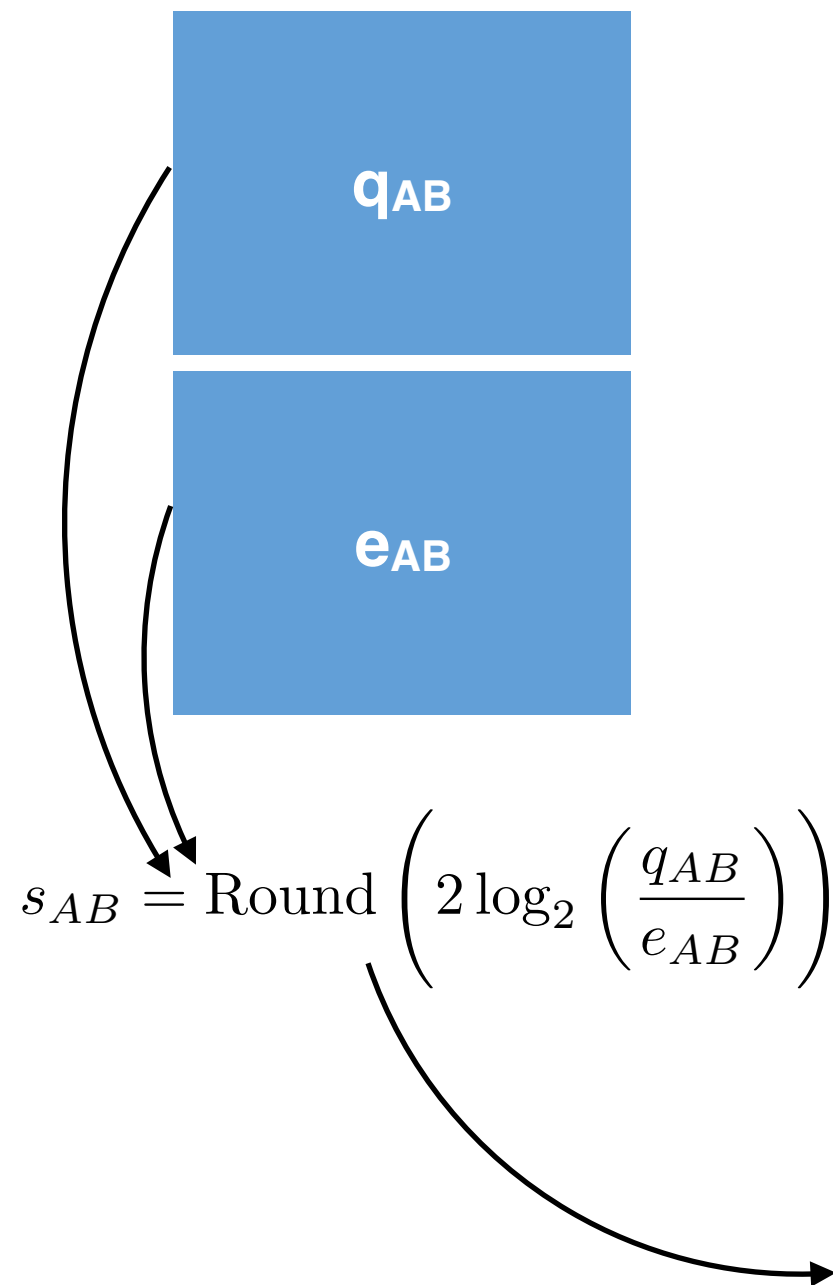


$$e_{AB} = \begin{cases} (p_A) (p_B) = (p_A)^2 & \text{if } A = B \\ (p_A) (p_B) + (p_B) (p_A) = 2 (p_A) (p_B) & \text{otherwise} \end{cases}$$



Example

Matrix of scores



	A	D	E	F	G	L	N	P	Q	R	S	T	V
A	5												
D		6											
E		7	5										
F				7									
G					4								
L					5	3							
N													
P	1							4					
Q							7						
R										7			
S							7		7		6		
T												7	
V								6					5

Blank cells are “missing data” (i.e. no observed values); wouldn’t happen with sufficient training data.

Dealing with sequence redundancy

E.g., for BLOSUM-80, group sequences that are >80% similar

TCMN_STRGA (331)	IADLGGGDGWFLAQILRRHPHATGLIMDLPRVA	74	
TCMO_STRGA (173)	FVDLGGARGNLAHLHRAHPHLRATCFDLPEME	81	
ZRP4_MAIZE (204)	LVDVGGGIGAAAQAISKAFPHVKCSVLDLAHV	68	
COMT_EUCGU (205)	VVDVGGGTGAVLSMIVAKYPSMKGINFDLPHVI	42	} 1 sequence (1/3 for each)
CHMT_POPTM (204)	LVDVGGGTGAVVNTIVSKYPSIKGINFDLPHVI	41	
COMT_MEDSA (204)	LVDVGGGTGAVINTIVSKYPTIKGINFDLPHVI	47	
CRTF_RHOSH (205)	IMDVGGGTGAFLAAVGRAYPLMELMLFDLPVVA	59	
OMTA_ASPPA (250)	VVDVGGGRGHLRVRVSQKHPHLRFIVQDLPAVI	47	

- Sequences are not independent because they are closely related, in this case COMT_EUCGU, CHMT_POPTM, and COMT_MEDSA are all >80 identical, and the others are more different
- BLOSUM approach accounts for this by treating the group of 3 as a count of 1
- One then gets a Weighted (BLOSUM 80) count of transitions for column 1:

$$\begin{array}{llll}
 c_{FF} = 0 & c_{FI} = 1 & c_{FL} = 2.67 & c_{FV} = 1.33 \\
 & c_{II} = 0 & c_{IL} = 2.67 & c_{IV} = 1.33 \\
 & & c_{LL} = 2.33 & c_{LV} = 3.33 \\
 & & & c_{VV} = 0.33
 \end{array}$$

(slide from Michael Gribskov)

Point Accepted Mutation Matrix

Introduced by Margaret Dayhoff in 1978

Observed mutation probabilities between amino acids over 71 families of closely related proteins (85% sequence identity within a family)



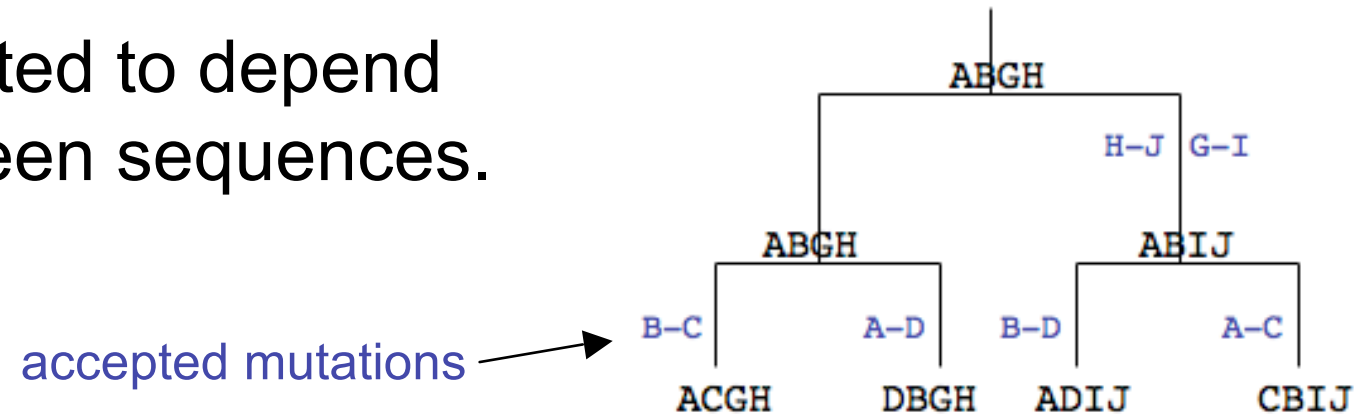
Based on a Markov mutation model; The PAM is a “unit of evolutionary mutation”. 1 PAM is the unit for which 1 mutation to occurs per 100 amino acids (this varies e.g. by species). The PAM₁ matrix express the log odds ratio of the likelihood of a point accepted mutation from one amino acid to another to the likelihood that these amino acids were aligned by chance.

PAM matrix slides below courtesy of Didier Gonze

(http://homepages.ulb.ac.be/~dgonze/TEACHING/pam_blosum.pdf)

PAM scoring matrices

The substitution score is expected to depend on the rate of divergence between sequences.



The **PAM matrices** derived by Dayhoff (1978):

- are based on evolutionary distances.
- have been obtained from carefully aligned closely related protein sequences (71 gapless alignments of sequences having at least 85% similarity).



M. Dayhoff

Reference: Dayhoff *et al.* (1978). A model of evolutionary change in proteins. In *Atlas of Protein Sequence and Structure*, vol. 5, suppl. 3, 345–352. National Biomedical Research Foundation, Silver Spring, MD, 1978.

PAM scoring matrices

PAM = Percent (or Point) Accepted Mutation

The PAM matrices are **series of scoring matrices**, each reflecting a certain level of divergence:

PAM = unit of evolution (1 PAM = 1 mutation/100 amino acid)

- **PAM1** proteins with an evolutionary distance of 1% mutation/position
- **PAM50** idem for 50% mutations/position
- **PAM250** 250% mutations/position (a position could mutate several times)

Reference: Dayhoff *et al.* (1978). A model of evolutionary change in proteins. In *Atlas of Protein Sequence and Structure*, vol. 5, suppl. 3, 345–352. National Biomedical Research Foundation, Silver Spring, MD, 1978.

Derivation of the PAM matrices

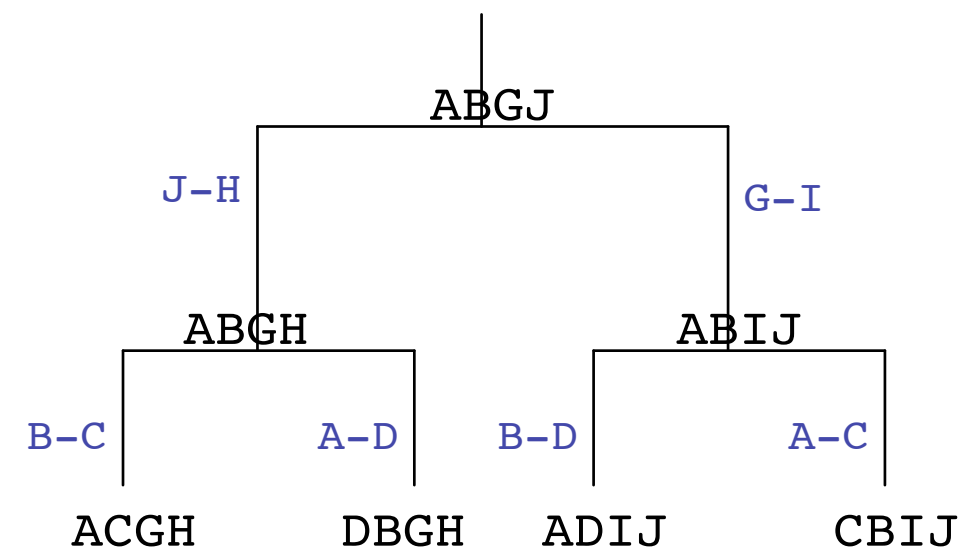
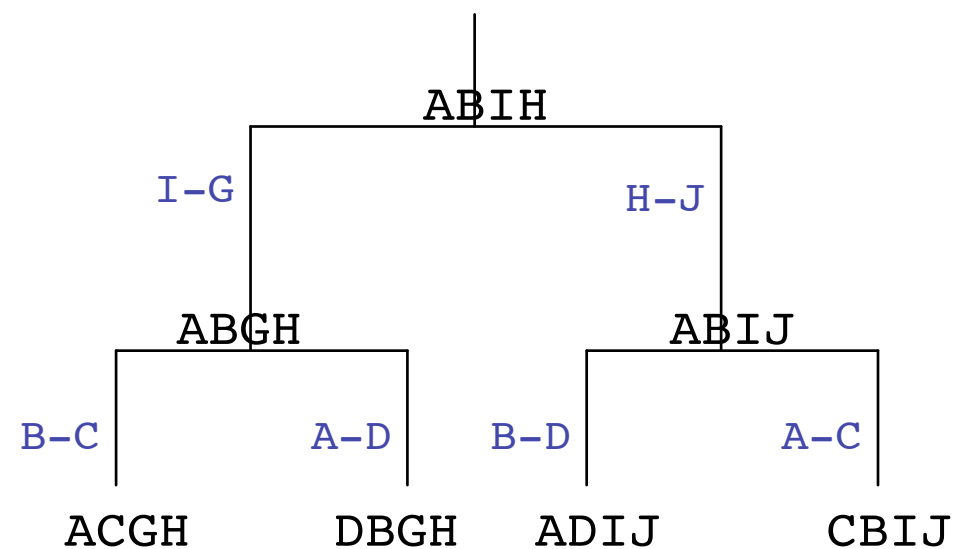
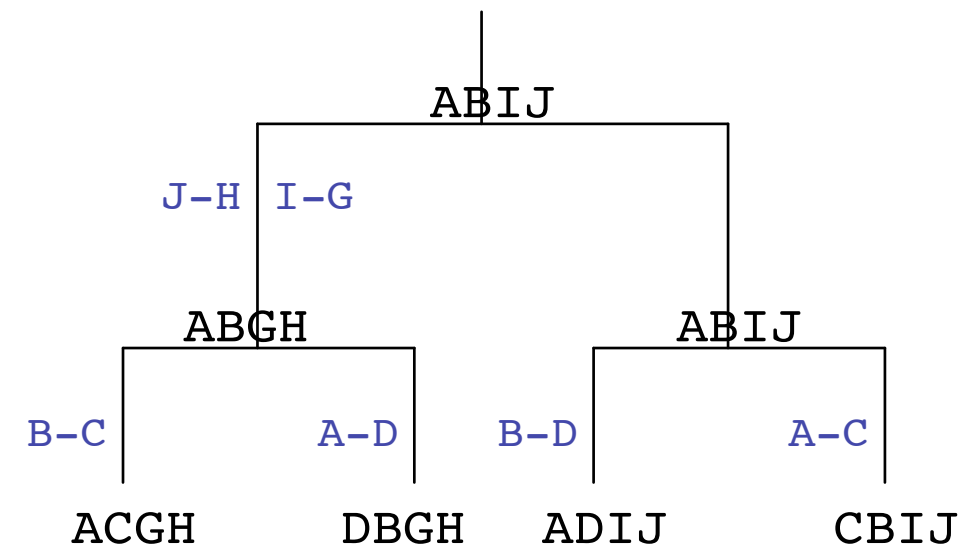
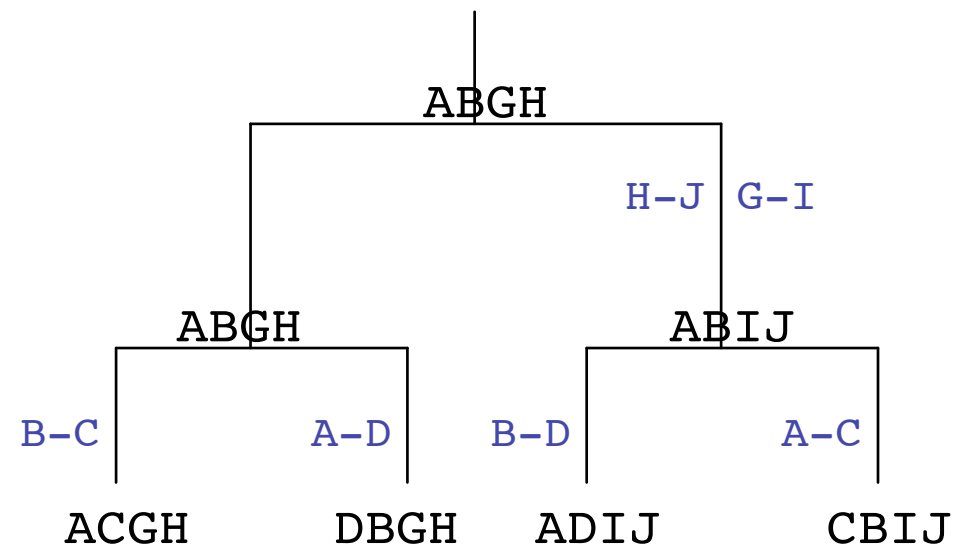
To illustrate how the PAM substitution matrices have been derived, we will consider the following artificial ungapped aligned sequences:

A	C	G	H
D	B	G	H
A	D	I	J
C	B	I	J

Reference: Borodovsky & Ekisheva (2007) Problems and Solutions in Biological sequence analysis. *Cambridge Univ Press*.

Derivation of the PAM matrices

Phylogenetic trees (maximum parsimony)



Here are represented the four more parsimonious (minimum of substitutions) phylogenetic trees for the alignment given above.

Derivation of the PAM matrices

Matrix of accepted point mutation counts (A)

	A	B	C	D	G	H	I	J
A		0	4	4	0	0	0	0
B	0		4	4	0	0	0	0
C	4	4		0	0	0	0	0
D	4	4	0		0	0	0	0
G	0	0	0	0		0	4	0
H	0	0	0	0	0		0	4
I	0	0	0	0	4	0		0
J	0	0	0	0	0	4	0	

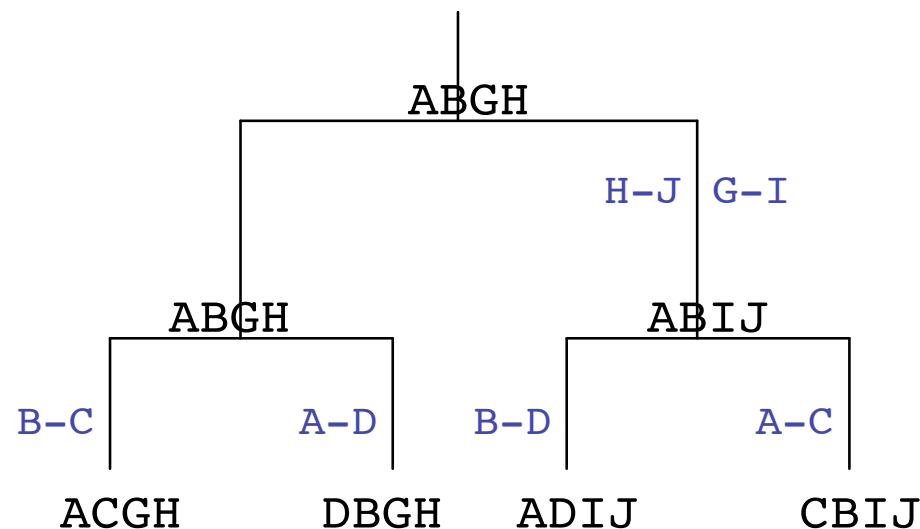
For each pair of different amino acids (i,j), the total number a_{ij} of substitutions from i to j along the edges of the phylogenetic tree is calculated.

(they are indicated in blue on the previous slide)

Derivation of the PAM matrices

Each edge of a given tree is associated with the ungapped alignment of the two sequences connected by this edge.

Thus, any tree shown above generates 6 alignments. For example the first phylogenetic tree generates the following alignments:



A B G H

A B G H

A B G H

D B G H

A B G H

A B I J

A B I J

A D I J

A B G H

A C G H

A B I J

C B I J

Those alignments can be used to assess the "relative mutability" of each amino acid.

Derivation of the PAM matrices

Relative mutability (m_j)

The relative mutability is defined by the ratio of the total number of times that amino acid j has changed in all the pair-wise alignments (in our case $6 \times 4 = 24$ alignments) to the number of times that j has occurred in these alignments, i.e.

alns / tree

of trees

$$m_j = \frac{\text{number of changes of } j}{\text{number of occurrences of } j}$$

Relative amino acid mutability values m_j for our example

Amino acid	A	B	I	H	G	J	C	D
Changes (substitutions)	8	8	4	4	4	4	8	8
Frequency of occurrence	40	40	24	24	24	24	8	8
Relative mutability m_j	0.2	0.2	0.167	0.167	0.167	0.167	1	1

The relative mutability accounts for the fact that the different amino acids have different mutation rates. This is thus the probability to mutate.

Derivation of the PAM matrices

Relative mutability of the 20 amino acids

aa	m_i	aa	m_i
Asn	134	His	66
Ser	120	Arg	65
Asp	106	Lys	56
Glu	102	Pro	56
Ala	100	Gly	49
Thr	97	Tyr	41
Ile	96	Phe	41
Met	94	Leu	40
Gln	93	Cys	20
Val	74	Trp	18

Values according Dayhoff (1978)

The value for Ala has been arbitrarily set at 100.

Trp and Cys are less mutable

Cys is known to have several unique, indispensable function (attachment site of heme group in cytochrome and of FeS clusters in ferredoxin). It also forms cross-links such as in chymotrypsin or ribonuclease.

Big groups like Trp or Phe are less mutable due to their particular chemistry. On the other extreme, the low mutability of Cys must be due to its unique smallness that is advantageous in many places.

Asn, Ser, Asp and Glu are most mutable

Although Ser sometimes functions in the active center, it more often performs a function of lesser importance, easily mimicked by several other amino acids of similar physical and chemical properties.

Derivation of the PAM matrices

Effective frequency (f_i)

The notion of effective frequency f_i takes into account the difference in variability of the primary structure conservation in proteins with different functional roles. Two alignment blocks corresponding to 2 different families may contribute differently to f_i even if the number of occurrence of amino acid j in these blocks is the same.

$$\left(\begin{array}{l} \text{relative frequency of} \\ \text{exposure to mutation} \end{array} \right) = \left(\begin{array}{l} \text{average composition} \\ \text{of each group} \end{array} \right) \times \left(\begin{array}{l} \text{number of mutations in} \\ \text{the corresponding tree} \end{array} \right)$$

Derivation of the PAM matrices

Effective frequency (f_i)

The effective frequency is defined as

$$f_j = k \sum_b q_j^{(b)} N^{(b)}$$

where the sum is taken over all alignment blocks b

$q_j^{(b)}$ is the observed frequency of amino acid j in block b ,

$N^{(b)}$ is the number of substitutions in a tree built for b

and the coefficient k is chosen to ensure that the sum of the frequencies $f_j = 1$.

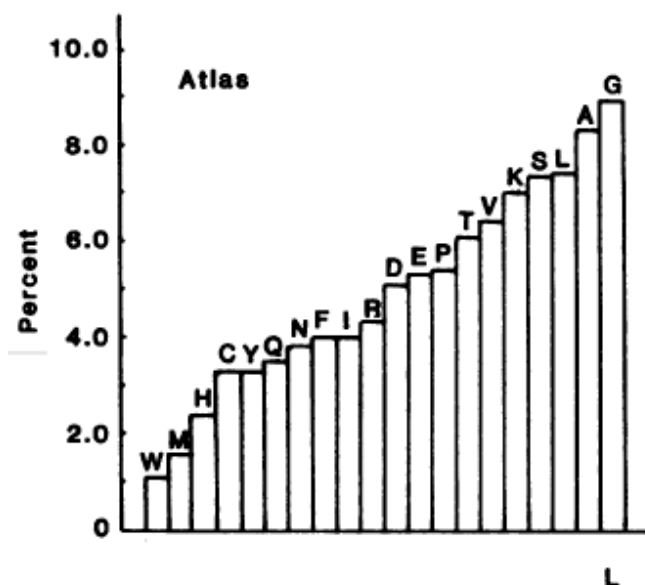
In our example, there is only one block, therefore the effective frequencies are equal to the compositional frequencies ($f_i = q_j$)

Derivation of the PAM matrices

Effective frequency of the 20 amino acids determined for the original alignment data (Dayhoff *et al.*, 1978)

Amino acid	Gly	Ala	Leu	Lys	Ser	Val	Thr
Frequency f	0.089	0.087	0.085	0.081	0.070	0.065	0.058
Amino acid	Pro	Glu	Asp	Arg	Asn	Phe	Gln
Frequency f	0.051	0.050	0.047	0.041	0.040	0.040	0.038
Amino acid	Ile	His	Cys	Tyr	Met	Trp	
Frequency f	0.037	0.034	0.033	0.030	0.015	0.010	

Source: Dayhoff, 1978



Distribution of amino acids found in 1081 peptides and proteins listed in the *Atlas of Protein Sequence and Structure* (1981).

Doolittle RF (1981) Similar amino acid sequences: chance or common ancestry? *Science*. 214:149-59.

Derivation of the PAM matrices

Mutational probability matrix (M)

Let's define M_{ij} the probability of the amino acid in column j having been substituted by an amino acid in row i over a given evolutionary time unit.

Non-diagonal elements of M :

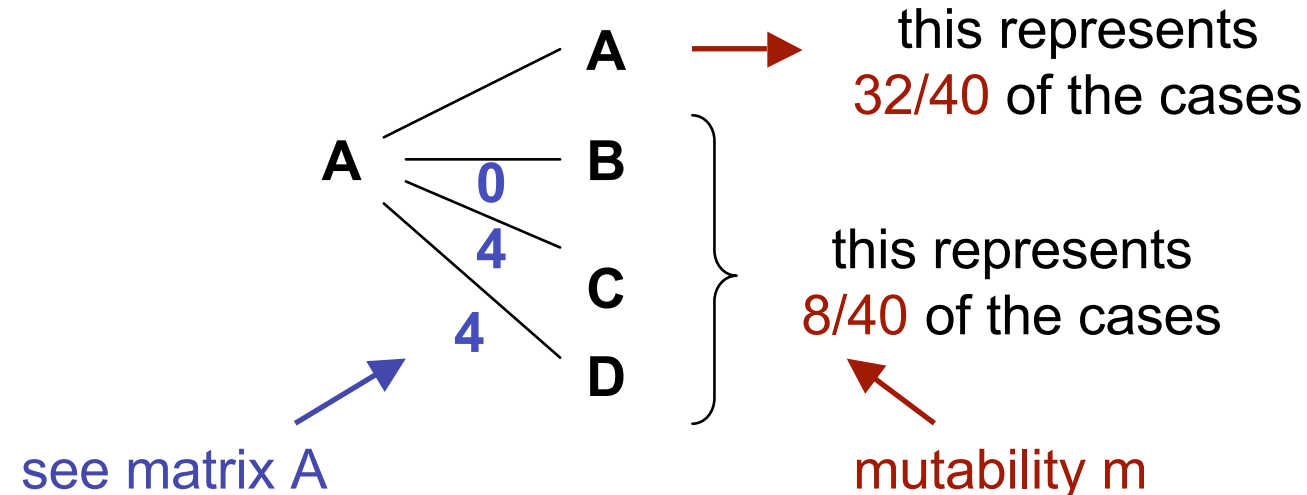
$$M_{ij} = \frac{\lambda m_j A_{ij}}{\sum_k A_{kj}}$$

Diagonal elements of M :

$$M_{ii} = 1 - \lambda m_i$$

In these equations, m is the relative mutability and A is the matrix of accepted point mutations. The constant λ represents a degree of freedom that could be used to connect the matrix M with an evolutionary time scale.

In our example:



If A is mutated, the probability that it is mutated into D is

$$A_{DA} / (A_{BA} + A_{CA} + A_{DA}) = 4/8$$

Thus the probability that A is mutated into D is:

$$M_{DA} = 4/8 * 8/40 = 4/40$$

and the probability that A is not mutated is:

$$M_{AA} = 1 - 8/40 = 32/40$$

Derivation of the PAM matrices

Mutational probability matrix (M)

Let's define M_{ij} the probability of the amino acid in column j having been substituted by an amino acid in row i over a given evolutionary time unit.

Non-diagonal elements of M :

$$M_{ij} = \frac{\lambda m_j A_{ij}}{\sum_k A_{kj}}$$

Diagonal elements of M :

$$M_{ii} = 1 - \lambda m_i$$

In these equations, m is the relative mutability and A is the matrix of accepted point mutations. The constant λ represents a degree of freedom that could be used to connect the matrix M with an evolutionary time scale.

The coefficient λ could be adjusted to ensure that a specific (small) number of substitutions would occur on average per hundred residues. This adjustment was done by Dayhoff *et al* in the following way. The expected number of amino acids that will remain **unchanged** in a protein sequence 100 amino acid long is given by:

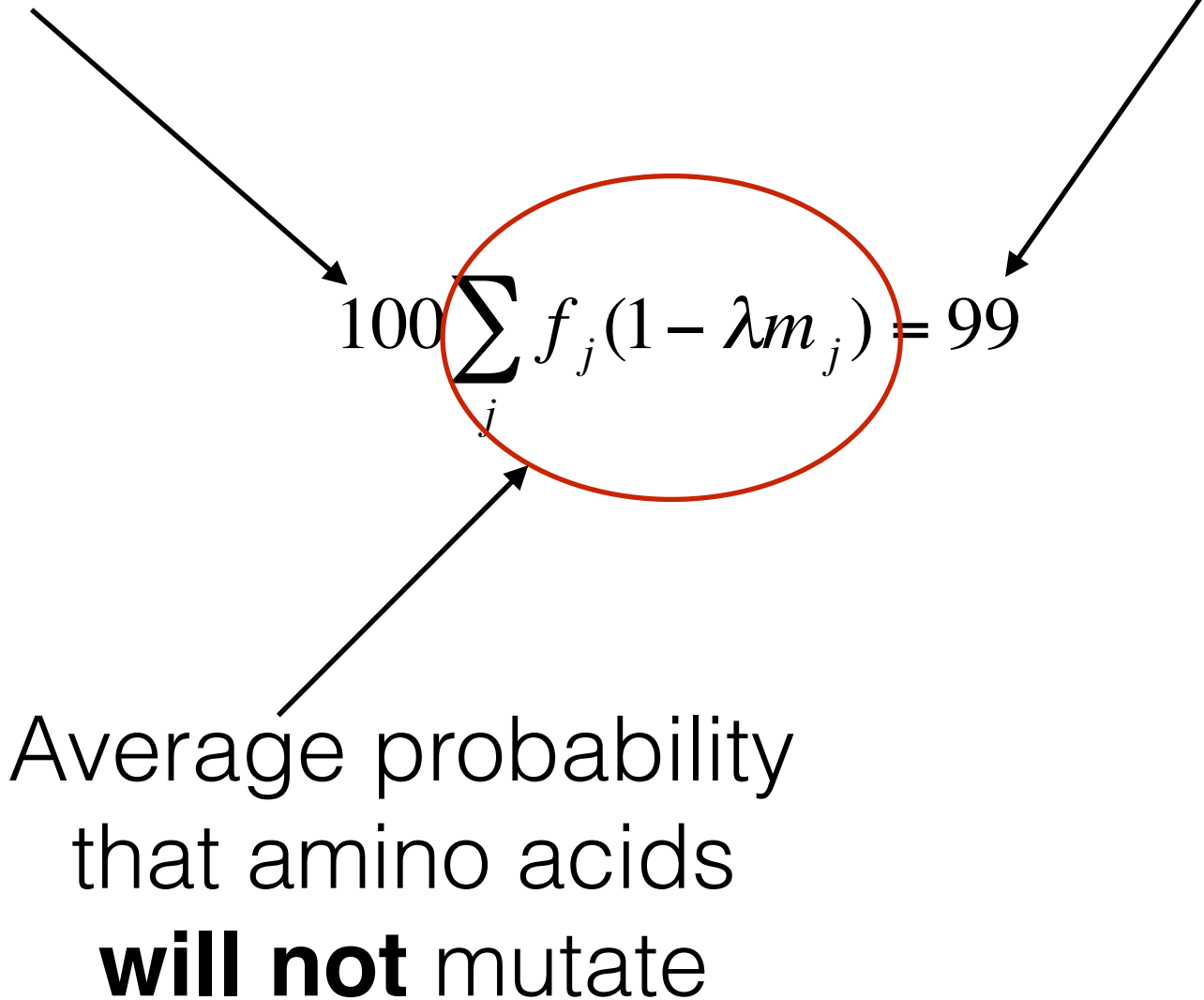
$$100 \sum_j f_j M_{jj} = 100 \sum_j f_j (1 - \lambda m_j)$$

If only one substitution per residue is allowed, then λ is calculated from the equation:

$$100 \sum_j f_j (1 - \lambda m_j) = 99$$

For every 100
amino acids

We want 99 of them to
remain unchanged.


$$100 \sum_j f_j (1 - \lambda m_j) = 99$$

Average probability
that amino acids
will not mutate

Derivation of the PAM matrices

Mutational probability matrix

In our example, $\lambda = 0.0261$ and the mutation probability matrix (PAM1) is:

	A	B	C	D	G	H	I	J
A	0.9948	0	0.0131	0.0131	0	0	0	0
B	0	0.9948	0.0131	0.0131	0	0	0	0
C	0.0026	0.0026	0.9740	0	0	0	0	0
D	0.0026	0.0026	0	0.9740	0	0	0	0
G	0	0	0	0	0.9957	0	0.0043	0
H	0	0	0	0	0	0.9957	0	0.0043
I	0	0	0	0	0.0043	0	0.9957	0
J	0	0	0	0	0	0.0043	0	0.9957

Note that M is a non-symmetric matrix.

Derivation of the PAM matrices

Mutational probability matrix derived by Dayhoff for the 20 amino acids

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	9867	2	9	10	3	8	17	21	2	6	4	2	6	2	22	35	32	0	2	18
R	1	9913	1	0	1	10	0	0	10	3	1	19	4	1	4	6	1	8	0	1
N	4	1	9822	36	0	4	6	6	21	3	1	13	0	1	2	20	9	1	4	1
D	6	0	42	9859	0	6	53	6	4	1	0	3	0	0	1	5	3	0	0	1
C	1	1	0	0	9973	0	0	0	1	1	0	0	0	0	1	5	1	0	3	2
Q	3	9	4	5	0	9876	27	1	23	1	3	6	4	0	6	2	2	0	0	1
E	10	0	7	56	0	35	9865	4	2	3	1	4	1	0	3	4	2	0	1	2
G	21	1	12	11	1	3	7	9935	1	0	1	2	1	1	3	21	3	0	0	5
H	1	8	18	3	1	20	1	0	9912	0	1	1	0	2	3	1	1	1	4	1
I	2	2	3	1	2	1	2	0	0	9872	9	2	12	7	0	1	7	0	1	33
L	3	1	3	0	0	6	1	1	4	22	9947	2	45	13	3	1	3	4	2	15
K	2	37	25	6	0	12	7	2	2	4	1	9926	20	0	3	8	11	0	1	1
M	1	1	0	0	0	2	0	0	0	5	8	4	9874	1	0	1	2	0	0	4
F	1	1	1	0	0	0	0	1	2	8	6	0	4	9946	0	2	1	3	28	0
P	13	5	2	1	1	8	3	2	5	1	2	2	1	1	9926	12	4	0	0	2
S	28	11	34	7	11	4	6	16	2	2	1	7	4	3	17	9840	38	5	2	2
T	22	2	13	4	1	3	2	2	1	11	2	8	6	1	5	32	9871	0	2	9
W	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	9976	1	0
Y	1	0	3	0	3	0	1	0	4	1	1	0	0	21	0	1	1	2	9945	1
V	13	2	1	1	3	2	2	3	3	57	11	1	17	1	3	2	10	0	2	9901

For clarity, the values have been multiplied by 10000

This matrix corresponds to an evolution time period giving 1 mutation/100 amino acids, and is referred to as the **PAM1 matrix**.

Source: Dayhoff, 1978

Derivation of the PAM matrices

Mutational probability matrix derived by Dayhoff for the 20 amino acids

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	9867	2	9	10	3	8	17	21	2	6	4	2	6	2	22	35	32	0	2	18
R	1	9913	1	0	1	10	0	0	10	3	1	19	4	1	4	6	1	8	0	1
N	4	1	9822	36	0	4	6	6	21	3	1	13	0	1	2	20	9	1	4	1
D	6	0	42	9859	0	6	53	6	4	1	0	3	0	0	1	5	3	0	0	1
C	1	1	0	0	9973	0	0	0	1	1	0	0	0	0	1	5	1	0	3	2
Q	3	9	4	5	0	9876	27	1	23	1	3	6	4	0	6	2	2	0	0	1
E	10	0	7	56	0	35	9865	4	2	3	1	4	1	0	3	4	2	0	1	2
G	21	1	12	11	1	3	7	9935	1	0	1	2	1	1	3	21	3	0	0	5
H	1	8	18	3	1	20	1	0	9912	0	1	1	0	2	3	1	1	1	4	1
I	2	2	3	1	2	1	2	0	0	9872	9	2	12	7	0	1	7	0	1	33
L	3	1	3	0	0	6	1	1	4	22	9947	2	45	13	3	1	3	4	2	15
K	2	37	25	6	0	12	7	2	2	4	1	9926	20	0	3	8	11	0	1	1
M	1	1	0	0	0	2	0	0	0	5	8	4	9874	1	0	1	2	0	0	4
F	1	1	1	0	0	0	0	1	2	8	6	0	4	9946	0	2	1	3	28	0
P	13	5	2	1	1	8	3	2	5	1	2	2	1	1	9926	12	4	0	0	2
S	28	11	34	7	11	4	6	16	2	2	1	7	4	3	17	9840	38	5	2	2
T	22	2	13	4	1	3	2	2	1	11	2	8	6	1	5	32	9871	0	2	9
W	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	9976	1	0
Y	1	0	3	0	3	0	1	0	4	1	1	0	0	21	0	1	1	2	9945	1
V	13	2	1	1	3	2	2	3	3	57	11	1	17	1	3	2	10	0	2	9901

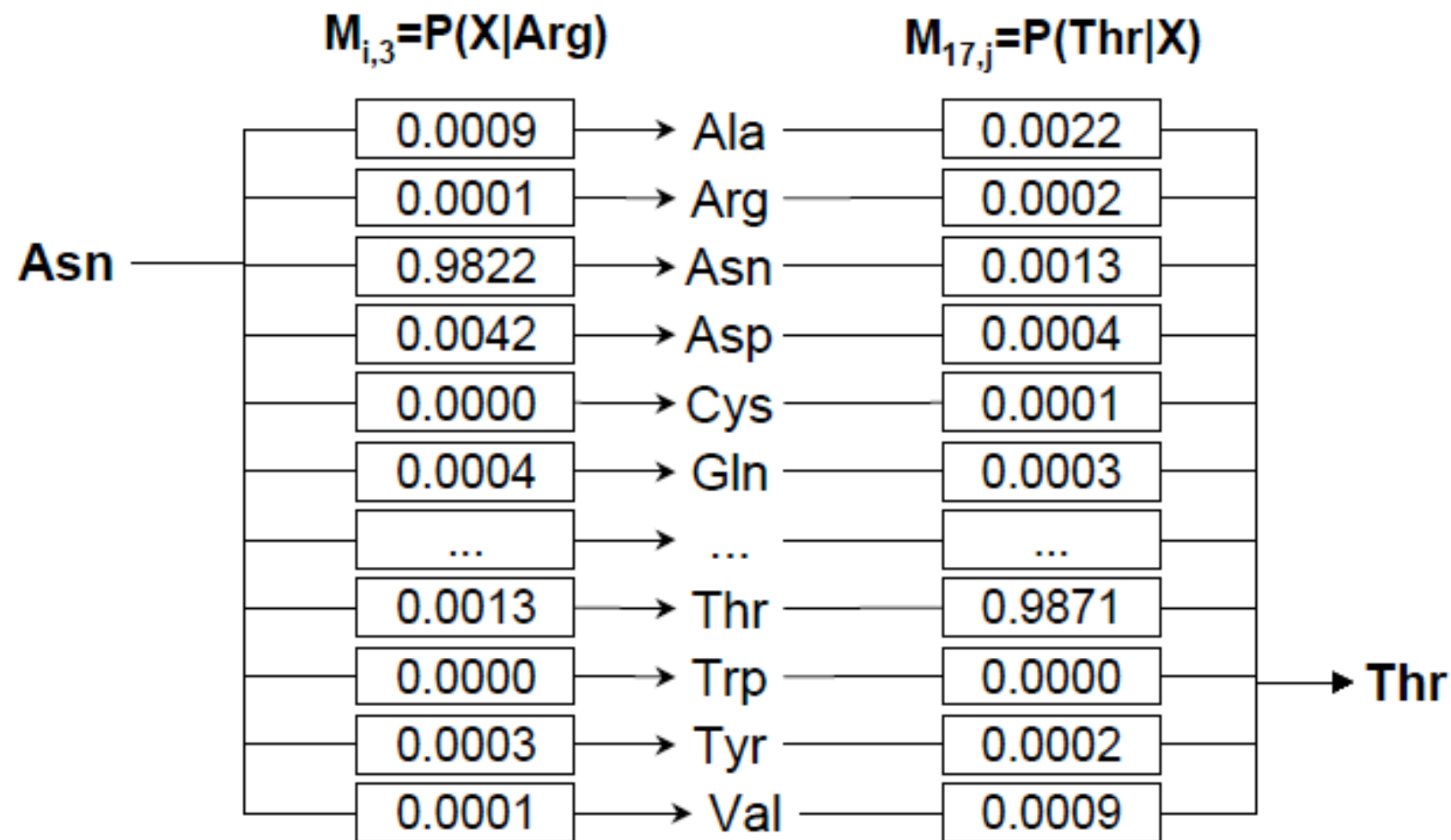
This matrix is the mutation probability matrix for an evolution time of **1 PAM**.

The **diagonal** represents the probability to still observe the same residue after 1 PAM. Therefore the diagonal represents the **99% of the case of non-mutation**.

Note that this does not mean that there was no mutation during this time interval. Indeed, the conservation of a residue could reflect either a conservation during the whole period, or a succession of two or more mutations ending at the initial residue

Derivation of the PAM matrices

From PAM1 to PAM2



$$P(\text{Asn} \rightarrow \text{Thr}) = P(\text{Asn} \rightarrow \text{Ala} \rightarrow \text{Thr}) + P(\text{Asn} \rightarrow \text{Arg} \rightarrow \text{Thr}) + \dots + P(\text{Asn} \rightarrow \text{Val} \rightarrow \text{Thr})$$

$$= (0.0009)(0.0001) + (0.0001)(0.0002) + \dots + (0.0001)(0.0009)$$

line 3 of PAM1

column 17 of PAM1

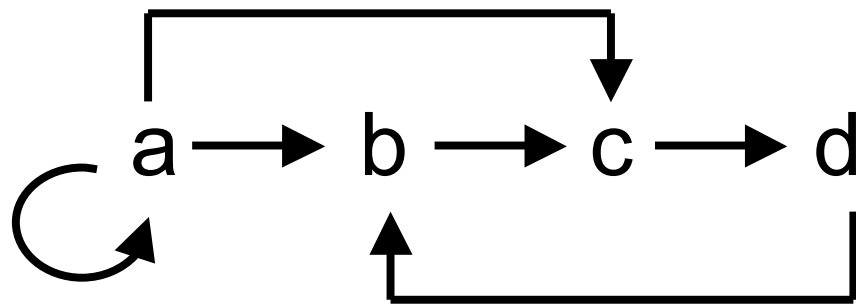
=> Matrix product: $PAM2 = PAM1 \times PAM1$

Source: J. van Helden

Derivation of the PAM matrices

From PAM1 to PAM2, PAM100, PAM250, etc...

Remark (from graph theory)



	a	b	c	d
a	1	1	1	0
b	0	0	1	0
c	0	0	0	1
d	0	1	0	0

Matrix **Q** indicates the number of paths going from one node to another in 1 step

	a	b	c	d
a	1	1	2	1
b	0	0	0	1
c	0	1	0	1
d	0	1	1	1

Matrix **Q²** indicates the number of paths going from one node to another in 2 steps

	a	b	c	d
a
b
c
d

Matrix **Qⁿ** indicates the number of paths going from one node to another in *n* steps

Derivation of the PAM matrices

From PAM1 to PAM2, PAM100, PAM250, etc...

Similarly:

PAM1	gives the probability to observe the changes $i \rightarrow j$ per 100 mutations
PAM2 = PAM1 ²	gives the probability to observe the changes $i \rightarrow j$ per 200 mutations
PAM100 = PAM1 ¹⁰⁰	gives the probability to observe the changes $i \rightarrow j$ per 10 000 mutations
PAM250 = PAM1 ²⁵⁰	gives the probability to observe the changes $i \rightarrow j$ per 25 000 mutations
PAM _n = PAM1 ⁿ	gives the probability to observe the changes $i \rightarrow j$ per 100× <i>n</i> mutations.

Convergence: it can be verified that

PAM_∞ = PAM1[∞] converges to the observed frequencies: $\lim_{n \rightarrow \infty} M^n = \begin{pmatrix} f_A & f_A & \dots & f_A \\ f_R & f_R & \dots & f_R \\ \dots & \dots & & \dots \\ f_V & f_V & \dots & f_V \end{pmatrix}$

Dayhoff *et al.* (1978) checked this convergence by computing M²⁰³⁴.

Derivation of the PAM matrices

PAM250 derived by Dayhoff for the 20 amino acids

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	13	6	9	9	5	8	9	12	6	8	6	7	7	4	11	11	11	2	4	9
R	3	17	4	3	2	5	3	2	6	3	2	9	4	1	4	4	3	7	2	2
N	4	4	6	7	2	5	6	4	6	3	2	5	3	2	4	5	4	2	3	3
D	5	4	8	11	1	7	10	5	6	3	2	5	3	1	4	5	5	1	2	3
C	2	1	1	1	52	1	1	2	2	2	1	1	1	1	2	3	2	1	4	2
Q	3	5	5	6	1	10	7	3	7	2	3	5	3	1	4	3	3	1	2	3
E	5	4	7	11	1	9	12	5	6	3	2	5	3	1	4	5	5	1	2	3
G	12	5	10	10	4	7	9	27	5	5	4	6	5	3	8	11	9	2	3	7
H	2	5	5	4	2	7	4	2	15	2	2	3	2	2	3	3	2	2	3	2
I	3	2	2	2	2	2	2	2	2	10	6	2	6	5	2	3	4	1	3	9
L	6	4	4	3	2	6	4	3	5	15	34	4	20	13	5	4	6	6	7	13
K	6	18	10	8	2	10	8	5	8	5	4	24	9	2	6	8	8	4	3	5
M	1	1	1	1	0	1	1	1	1	2	3	2	6	2	1	1	1	1	1	2
F	2	1	2	1	1	1	1	1	3	5	6	1	4	32	1	2	2	4	20	3
P	7	5	5	4	3	5	4	5	5	3	3	4	3	2	20	6	5	1	2	4
S	9	6	8	7	7	6	7	9	6	5	4	7	5	3	9	10	9	4	4	6
T	8	5	6	6	4	5	5	6	4	6	4	6	5	3	6	8	11	2	3	6
W	0	2	0	0	0	0	0	0	1	0	1	0	0	1	0	1	0	55	1	0
Y	1	1	2	1	3	1	1	1	3	2	2	1	2	15	1	2	2	3	31	2
V	7	4	4	4	4	4	4	4	5	4	15	10	4	10	5	5	5	72	4	17

For clarity, the values have been multiplied by 100

This matrix corresponds to an evolution time period giving 250 mutation/100 amino acids (i.e. an evolutionary distance of 250 PAM), and is referred to as the **PAM250 matrix**.

Source: Dayhoff, 1978

Derivation of the PAM matrices

Interpretation of the PAM250 matrix

	A	R	N	D	...
A	13	6	9	9	...
R	3	17	4	3	...
N	4	4	6	7	...
D	5	4	8	11	...
C	2	1	1	1	...
Q	3	5	5	6	...
E	5	4	7	11	...
G	12	5	10	10	...
H	2	5	5	4	...
I	3	2	2	2	...
L	6	4	4	3	...
K	6	18	10	8	...
M	1	1	1	1	...
F	2	1	2	1	...
P	7	5	5	4	...
S	9	6	8	7	...
T	8	5	6	6	...
W	0	2	0	0	...
Y	1	1	2	1	...
V	7	4	4	4	...

In comparing 2 sequences at this evolutionary distance (250 PAM), there is:

* * * * **A** * * * * *

250 PAM

* * * * **A** * * * * *

* * * * **R** * * * * *

* * * * **N** * * * * *

* * * * **W** * * * * *

...

probability of 13%

probability of 3%

probability of 4%

probability of 0%

Derivation of the PAM matrices

From probabilities to scores

So far, we have obtained a **probability matrix**, but we would like a **scoring matrix**.

A **score** should reflect the significance of an alignment occurring as a result of an evolutionary process with respect to what we could expect by chance.

A score should involve the ratio between the probability derived from non-random (evolutionary) to random models:

$$r_n(i, j) = \frac{M_{ji}^n}{f_j} = \frac{P_{ji,n}}{f_i f_j}$$

← probability to see a pair (i,j) due to evolution

← probability to see a pair (i,j) by chance

The matrix M_{ji}^n is the mutational probability matrices at PAM distance n .
Matrices M^1 and M^{250} have been shown before.

$P_{ji,n} = f_i M_{ji}^n$ is the probability that two aligned amino acids have diverged from a common ancestor $n/2$ PAM unit ago, assuming that the substitutions follow a Markov process (for details, see Borodovsky & Ekisheva, 2007).

Note that R (the odd-score or relatedness matrix) is a symmetric matrix.

Derivation of the PAM matrices

Log-odd scores

In practice, we often use the log-odd scores defined by

$$s_n(i, j) = \log \frac{M_{ji}^n}{f_j} = \log \frac{P_{ji,n}}{f_i f_j}$$

This definition has convenient practical consequences:

A **positive score** ($s_n > 0$) characterizes the accepted mutations

A **negative score** ($s_n < 0$) characterizes the unfavourable mutations

Another property of the log-odd scores is that they can be added to produce the score of an alignment:

T	A	H	G	K
Y	S	D	G	D

$$S_{\text{alignment}} = s(\text{T}, \text{Y}) + s(\text{A}, \text{S}) + s(\text{H}, \text{D}) + s(\text{G}, \text{G}) + s(\text{K}, \text{D})$$

Derivation of the PAM matrices

PAM250 matrix (log-odds)

[illegible]

Source: J. van Helden

PAM matrices: exercise

The original PAM250 substitution matrix scores a substitution of *Gly* by *Arg* by a negative score -3 (decimal logarithm and scaling factor 10 are used, with rounding to the nearest neighbour). The average frequency of *Arg* in the protein sequence database is 0.041. Use this information as well as the method described above to estimate the probability that *Gly* will be substituted by *Arg* after a PAM250 time period.

PAM matrices: exercise

The original PAM250 substitution matrix scores a substitution of *Gly* by *Arg* by a negative score -3 (decimal logarithm and scaling factor 10 are used, with rounding to the nearest neighbour). The average frequency of *Arg* in the protein sequence database is 0.041. Use this information as well as the method described above to estimate the probability that *Gly* will be substituted by *Arg* after a PAM250 time period.

The element s_{ij} of the PAM250 substitution matrix and the frequency of amino acid j (f_j) in a protein sequence database are connected by the following formula:

$$s_{ij} = \left(10 \log \frac{P(i \rightarrow j \text{ in } 250 \text{ PAM})}{f_j} \right)$$

Therefore, the probability of substitution of *Gly* by *Arg* is:

$$P(\text{Gly} \rightarrow \text{Arg in } 250 \text{ PAM}) = 0.041 \times 10^{-0.3} = 0.0205$$

Derivation of the PAM matrices

Scoring an alignment

C	12																			
S	0	2																		
T	-2	1	3																	
P	-1	1	0	6																
A	-2	1	1	1	2															
G	-3	1	0	-1	1	5														
N	-4	1	0	-1	0	0	2													
D	-5	0	0	-1	0	1	2	4												
E	-5	0	0	-1	0	0	1	3	4											
Q	-5	-1	-1	0	0	-1	1	2	2	4										
H	-3	-1	-1	0	-1	-2	2	1	1	3	6									
R	-4	0	-1	0	-2	-3	0	-1	-1	1	2	6								
K	-5	0	0	-1	-1	-2	1	0	0	1	0	3	5							
M	-5	-2	-1	-2	-1	-3	-2	-3	-2	-1	-2	0	0	6						
I	-2	-1	0	-2	-1	-3	-2	-2	-2	-2	-2	-2	-2	2	5					
L	-6	-3	-2	-3	-2	-4	-3	-4	-3	-2	-2	-3	-3	4	2	6				
V	-2	-1	0	-1	0	-1	-2	-2	-2	-2	-2	-2	-2	2	4	2	4			
F	-4	-3	-3	-5	-4	-5	-4	-6	-5	-5	-2	-4	-5	0	1	2	-1	9		
Y	0	-3	-3	-5	-3	-5	-2	-4	-4	-4	0	-4	-4	-2	-1	-1	-2	7	10	
W	-8	-2	-5	-6	-6	-7	-4	-7	-7	-5	-3	2	-3	-4	-5	-2	-6	0	0	17
	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W

A scoring matrix like PAM250 can be used to score an alignment

T A H G K
Y S D G D

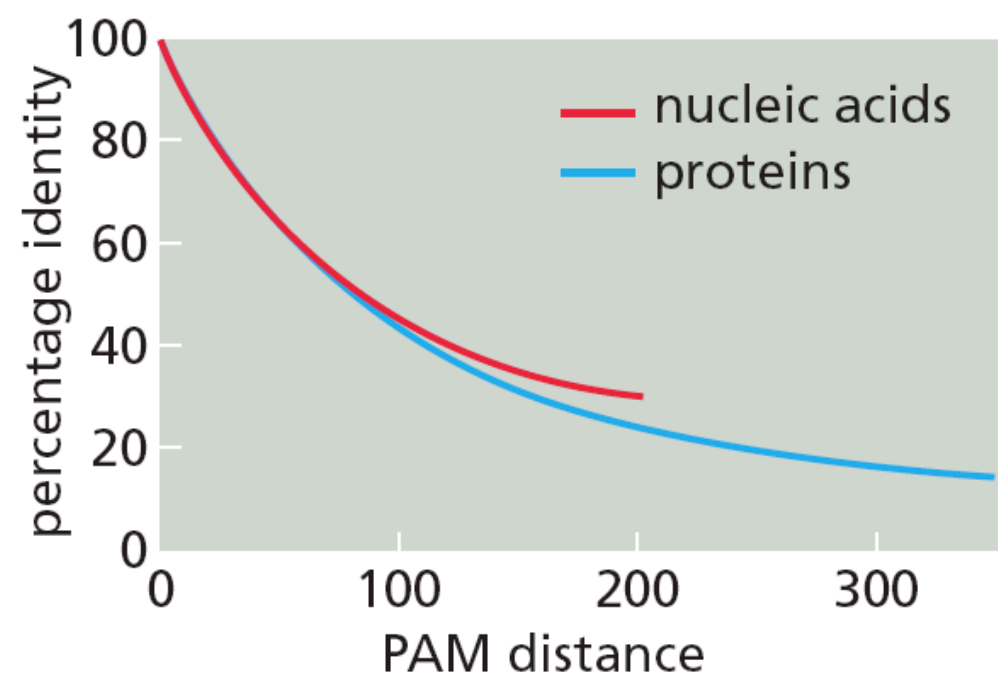
$$\begin{aligned}
 S_{\text{alignment}} &= s(\text{T}, \text{Y}) + s(\text{A}, \text{S}) + s(\text{H}, \text{D}) + s(\text{G}, \text{G}) + s(\text{K}, \text{D}) \\
 &= -3 + 1 + 1 + 5 + 0 \\
 &= 4
 \end{aligned}$$

Choosing the appropriate PAM matrix

How to choose the appropriate PAM matrix?

Correspondance between the observed percent of amino acid difference d between the evolutionary distance n (in PAM) between them:

$$100 \sum_j f_j M^n_{jj} = 100 - d$$



twilight zone
(detection limit)



identity (%)	difference d (%)	PAM index n
99	1	1
95	5	5
90	10	11
85	15	17
80	20	23
75	25	30
70	30	38
60	40	56
50	50	80
40	60	112
30	70	159
20	80	246
14	86	350

Choosing the appropriate PAM matrix

How to choose the appropriate PAM matrix?

Altschul SF(1991) Amino acid substitution matrices from an information theoretic perspective. *J Mol Biol.* 219:555-65.

- PAM120 matrix is the most appropriate for database searches
- PAM200 matrix is the most appropriate for comparing two specific proteins with suspected homology

Remark:

In the PAM matrices, the **index** indicates the percentage of substitution per position.

Higher indexes are more appropriate for **more distant** proteins (PAM250 better than PAM100 for distant proteins).

Other Scoring Matrices

PAM vs. BLOSUM

PAM	BLOSUM
To compare the closely related sequences, PAM matrices with lower numbers are created.	To compare the closely related sequences, BLOSUM matrices with higher numbers are created.
To compare the distantly related proteins, PAM matrices with high numbers are created.	To compare the distantly related proteins, BLOSUM matrices with low numbers are created.

PAM	BLOSUM
PAM100	BLOSUM90
PAM120	BLOSUM80
PAM160	BLOSUM60
PAM200	BLOSUM52
PAM250	BLOSUM45

Other Scoring Matrices

PAM vs. BLOSUM

PAM

Based on global alignments of closely related proteins.

PAM1 is the matrix calculated from comparisons of sequences with no more than 1% divergent

Other PAM matrices are extrapolated from PAM1

Larger numbers in name denote larger evolutionary distance

Based on explicit, Markovian, model of evolution

BLOSUM

Based on local alignments of protein segments.

BLOSUM 62 is calculated from comparisons of sequences no less than 62% identical

Other BLOSUM matrices are not extrapolated, but computed based on observed alignments at different identity percentage

Larger numbers in name denote higher sequence similarity (& therefore smaller evolutionary distance)

Not based on any explicit model of evolution, but learned empirically from alignments

What about gap penalties?

Despite some work⁺, the setting of gap penalties is still much more arbitrary than the selection of a substitution matrix.

- ★ Gap penalty values are designed to reduce the score when an alignment has been disturbed by indels. The value should be small enough to allow a previously accumulated alignment to continue with an insertion of one of the sequences, but should not be so large that this previous alignment score is removed completely.

Changing the gap function can have significant effects on reported alignments. People often resort to “defaults” to avoid having to justify a choice.

⁺Reese, J. T., and William R. Pearson. "Empirical determination of effective gap penalties for sequence comparison." *Bioinformatics* 18.11 (2002): 1500-1507.

★ http://en.wikipedia.org/wiki/Gap_penalty