$$c_{ij} = \frac{1}{2}\left(c_{i \to j} + c_{j \to i}\right) \qquad p_{ij} = \frac{c_{ij}}{100 f_i \sum_a \sum_{b \neq a} c_{ab}} \qquad p_{ii} = 1 - \sum_{j \neq i} p_{ij}$$

f = A = 0,2083 D = 0,25 N = 0,0278

C = 0,2083 G = 0,1528 R = 0,1528

	A	C	D	G	N	R
A	0.99	0	0	0	0	0
C	0	0.99	0	0	0	0
D	0	0	0.99	0	0	0
G	0	0	0	0.98	0	0
N	0	0.01	0.01	0.01	0.95	0
R	0	0	0	0	0	0.98

$\xrightarrow{\times 10000}$

	A	C	D	G	N	R
A	9918	21	21	7	7	[illegible]
C	21	9904	27	27	14	[illegible]
D	17	23	9931	6	11	[illegible]
G	9	37	9	9897	19	[illegible]
N	51	103	103	103	9337	[illegible]
R	37	9	19	28	19	[illegible]

$$S(i,j) = \log_2\left(\frac{p_{ij}}{f_i}\right) \Rightarrow$$

	A	C	D	G	N	R
A	2	-7	-7	-8	-5	-6
C	-7	2	-7	-6	-4	-8
D	-7	-7	2	-8	-5	-7
G	-8	-6	-8	3	-4	-6
N	-5	-4	-5	-4	5	-4
R	-6	-8	-7	-6	-4	3

PAM 250 dayoff 10 log10

	A	C	D	G	N	R
A	1	0	-1	-1	0	0
C	0	1	0	0	0	-1
D	-1	0	1	-1	0	-1
G	-1	0	-1	1	0	0
N	0	0	0	0	0	0
R	0	-1	-1	0	0	1

Is theorical solid?

IMO. Coherent under assumption, but the extrapolation over 250 magnifies estimation of error

How to get PAM 250 from PAM 1

- Consider PAM1 as a time-homogeneous Markov matrix P of one-step subs
- Compute P^{250} (matrix power)
- Convert to a scoring matrix via log odds against frequencies S_{ij} (base 2 or 10)

Rationale?

- Assume evolution is a first order, time homogeneous Markov process. 1 PAM = 1% accepted mutations
- Powers of P model "longer evolutionary time"