## **BLOSUM Matrices**

- Trusted data
  - 2000 blocks of conserved regions in ~500 groups of proteins
- Count amino acid pairs:  $A_{xy}^N$ 
  - Parameterize by evolutionary distance, N
  - Correct for sample bias
- Calculate amino acid frequencies:
  - Related pairs:  $q_{xy}^N$
  - Background pair frequencies:  $E_{xy}$
- Log likelihood scoring matrix

$$-S^N = 2 \log_2 \frac{q_{xy}^N}{E_{xy}}$$

## Count amino acid pairs: $A_{xy}^N$

## Parameterize by evolutionary distance, *N* Correct for sample bias

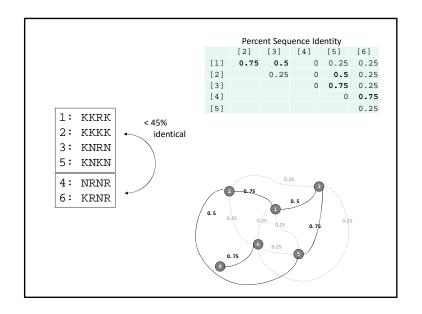
- Cluster sequences such that if s1 and s2 are in different clusters, then identity(s1, s2) < N%</li>
- Count amino acid pairs in s1 aligned with s2 only if s1 and s2 are in different clusters
- Normalize for cluster size

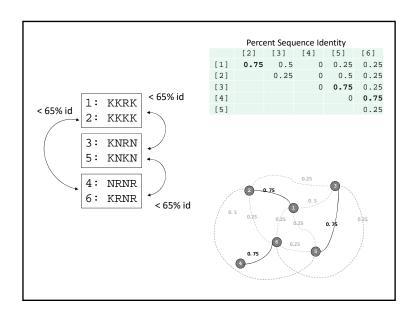
## **BLOSUM** clustering example

		Percent Sequence Identity						
1:	KKRK			[2]	[3]	[4]	[5]	[6]
2:	KKKK		[1]	0.75	0.5	0	0.25	0.2
2.	ZMDM		[2]		0.25	0	0.5	0.2
3: KNRN		[3]			0	0.75	0.2	
4:	NRNR		[4]				0	0.7
5:	KNKN		[5]					0.2

6: KRNR

Unclustered sequences: Every sequence is at least 25% identical





	PAM	BLOSUM		
Evolutionary model	Explicit evolutionary model	None		
Data	Full length MSAs of closely related sequences.	Conserved blocks. i.e., ungapped local MSAs		
Bias correction	Trees	Clustering		
Multiple substitutions	Markov model: $P^n = (P^1)^n$	Implicitly represented in data (clustering)		
Evolutionary distance	Markov model: $P^n = (P^1)^n$	Clustering		
Matrices	Transition and log odds scoring matrices	Log odds scoring matrix only.		
Parameter n	Distance increases with n	Distance decreases with n		
Biophysical properties	Derived indirectly from data	Derived indirectly from data		

