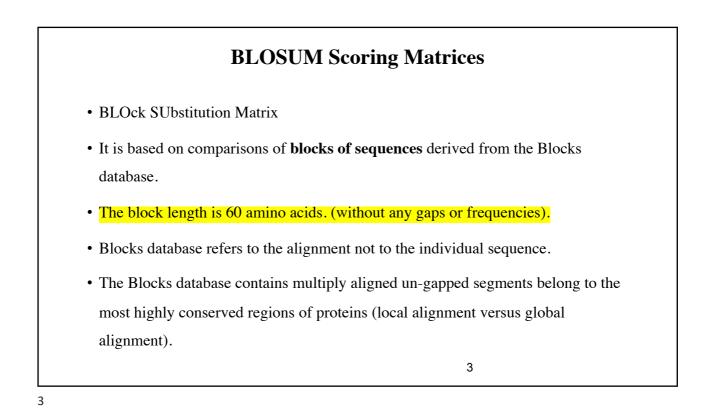
Bioinformatics II: BLOSUM Matrices

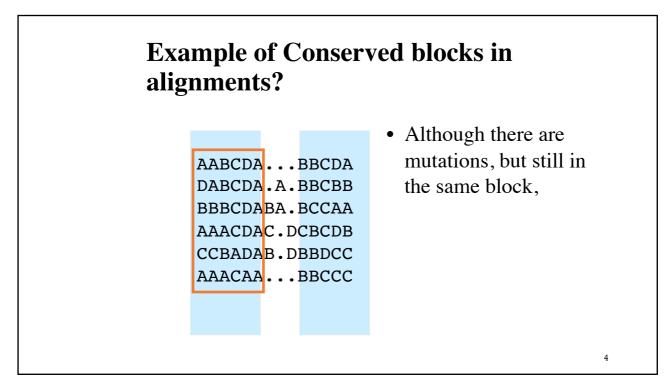
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1

What are BLOSUM matrices? Example?

- 1. <u>Blo</u>cks <u>Substitution</u> <u>Matrix</u>.
- It is a matrix that calculates scores for each position which are obtained frequencies of substitutions in blocks of local alignments of protein sequences.
- 3. For example BLOSUM62 is derived from sequence alignments with no more than 62% identity.





What do matrices usually seek for?

- It seeks for measuring the score of the alignment.
- Why?
- Score measures the conservation.(what does that mean?)
- Which is the any substation of amino acids in the nature.

What is identical sequence?

- It tells the % of matching.
- It can be 100% even if there is a substitution.
- It tells how much the sequence is conserved!
- As mentioned before, the score measures the % of alignment of the sequence to construct matrices.

5

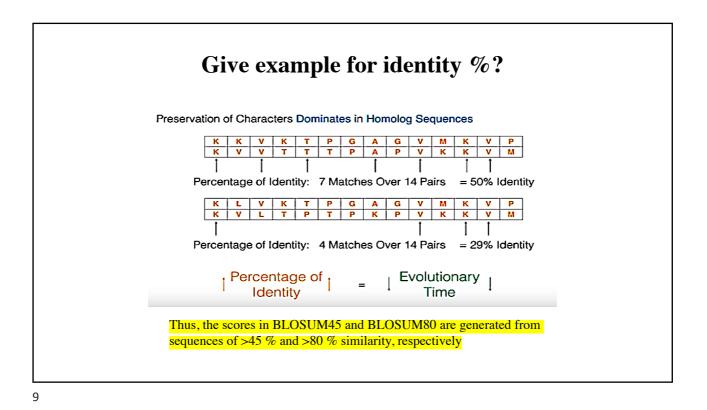
What is the relation between?

- What is the relation between the identity and the revolution time?
- The highest the % of identity, the shorter the evolutionary time to separate the sequences.

7

How many?

- In the construction of the BLOSUM family of matrices, ~ 2000 block segments were analyzed for mare than 500 groups of related proteins.
- These blocks were clustered according to their % of identity.



Range 1: 127 to 501 GenPept				🔻 Next Match 🔺 Previous Match	
Score	Expect	Method	Identities	Positives	Gaps Fram
431 bits(108) 3e-147()	Compositional matrix adjust.	203/375(54%)	278/375(74%)) 8/375(2%)
Sbjct 12 Query 92 Sbjct 18 Query 15 Sbjct 24	 7 KQRERERLERG TYYVEGAHQQY Y ++G HQ 7 IYKIDGPHQLA 2 CNSVNFPEPPY CNS+ FP+PPY 	IEFVRRNTWFFVYWLGLGVLSSVGLGT PDQIICPEEEGAEGAISLWSIISKVRI	TRLLQORLLLATEIUI GLHTFLLYLGPHIASV GLHTFLLYLGPHIASV GLHTFLLYLGPHIASV EACMWGIGTAIGELPI EA +WG GTA+GELPI	SIVFSV 186 TTLAAYE 151 TTLAAYE 246 PYFMARA 211 PYFMARA 211	The positives (+) in the alignment indicate good high scoring mismatches. Matrix scores >0.

