

BLAST (Basic Local Alignment Search Tool) [Altschul et al., 1990].



```
Query: 325 SLAALLNKCKTPQGQRLVNQWIKQPLMDKNRIEERLNLVEA      365
          +LA++L+   TP G R++ +W+  P+ D    + ER    + A
Sbjct: 290 TLASVLDCTVTPMGSRMLKRWLHMPVRDTRVLLERQQTIGA      330
```

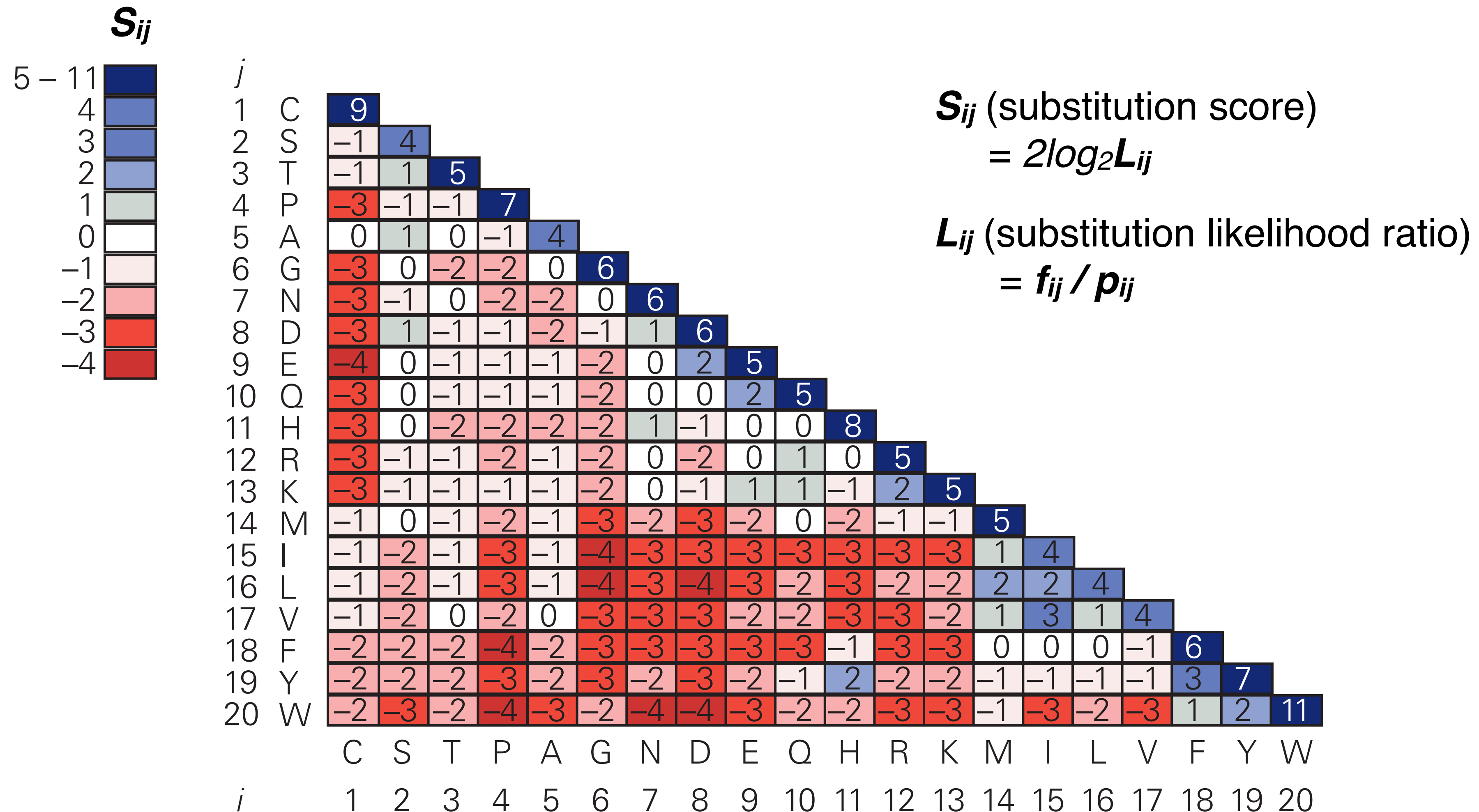
- E-value < 10e-100 Identical sequences.
- 10e-50 < E-value < 10e-100 Almost identical sequences.
- 10e-10 < E-value < 10e-50 Closely related sequences, domain match or similar.
- 1 < E-value < 10e-6 Could be a true homologue but it is a gray area.
- E-value > 1 Proteins are most likely not related
- E-value > 10 Hits are most likely junk

Additional material:

https://www.ccg.unam.mx/~vinuesa/tlem/pdfs/Bioinformatics_explained_BLAST.pdf

BLOSUM-62 matrix for sequence alignment

“block substitution matrix”



BLOSUM-62 : based on sequence alignments in which no pair of sequences have greater than 62% sequence identity
- in order to remove biases

read chapter 5.6-5.11 BLOSUM-62 matrix in preparation of practical of week 4