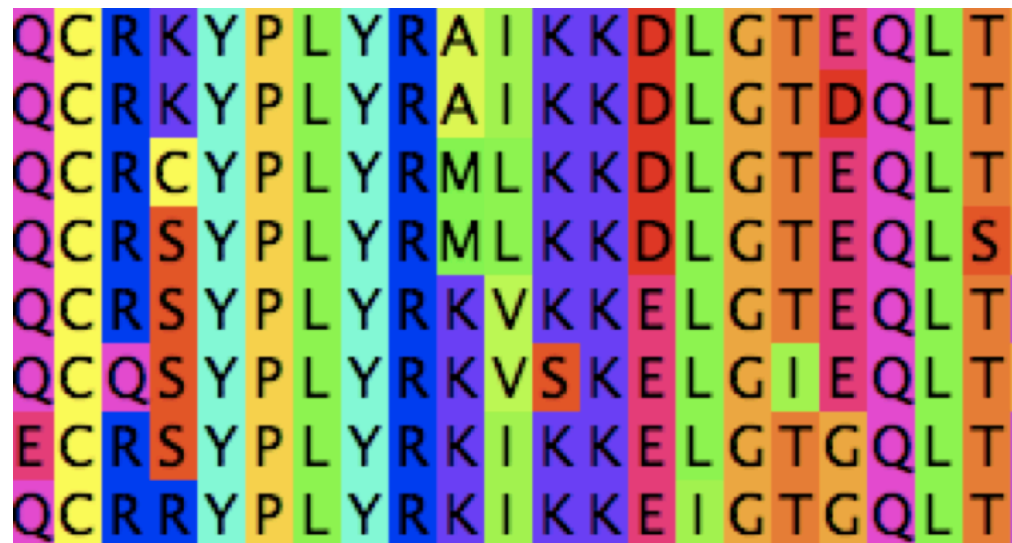
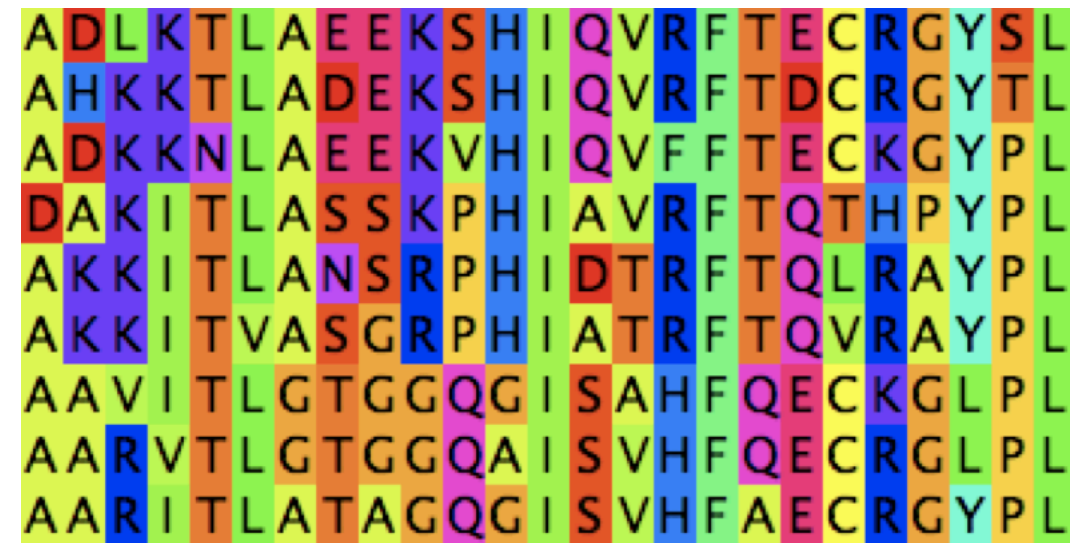


homologous sequences, high sequence similarity



$$s(a, b) = \log \left(\frac{p_{ab}}{q_a \times q_b} \right) \downarrow$$

homologous sequences, greater divergence



$$s(a, b) = \log \left(\frac{p_{ab}}{q_a \times q_b} \right) \downarrow$$

| | A | R | N | D | C | Q | E | G | H | I | L | K | M | F | P | S | T | W | Y | V | |
|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|---|--|
| A | 5 | | | | | | | | | | | | | | | | | | | | |
| R | -2 | 6 | | | | | | | | | | | | | | | | | | | |
| N | -2 | -1 | 7 | | | | | | | | | | | | | | | | | | |
| D | -3 | -3 | 1 | 7 | | | | | | | | | | | | | | | | | |
| C | -1 | -5 | -4 | -5 | 9 | | | | | | | | | | | | | | | | |
| Q | -1 | 1 | 0 | -1 | -4 | 7 | | | | | | | | | | | | | | | |
| E | -1 | -1 | -1 | 1 | -6 | 2 | 6 | | | | | | | | | | | | | | |
| G | 0 | -3 | -1 | -2 | -4 | -3 | -3 | 6 | | | | | | | | | | | | | |
| H | -2 | 0 | 0 | -2 | -5 | 1 | -1 | -3 | 8 | | | | | | | | | | | | |
| I | -2 | -4 | -4 | -5 | -2 | -4 | -4 | -5 | -4 | 5 | | | | | | | | | | | |
| L | -2 | -3 | -4 | -5 | -2 | -3 | -4 | -5 | -4 | 1 | 5 | | | | | | | | | | |
| K | -1 | 2 | 0 | -1 | -4 | 1 | 0 | -2 | -1 | -4 | -3 | 6 | | | | | | | | | |
| M | -2 | -2 | -3 | -4 | -2 | 0 | -3 | -4 | -3 | 1 | 2 | -2 | 7 | | | | | | | | |
| F | -3 | -4 | -4 | -5 | -3 | -4 | -5 | -5 | -2 | -1 | 0 | -4 | -1 | 7 | | | | | | | |
| P | -1 | -3 | -3 | -3 | -4 | -2 | -2 | -3 | -3 | -4 | -4 | -2 | -3 | -4 | 8 | | | | | | |
| S | 1 | -1 | 0 | -1 | -2 | -1 | -1 | -1 | -2 | -3 | -3 | -1 | -2 | -3 | -2 | 5 | | | | | |
| T | 0 | -2 | 0 | -2 | -2 | -1 | -1 | -3 | -2 | -1 | -2 | -1 | -1 | -3 | -2 | 1 | 6 | | | | |
| W | -4 | -4 | -5 | -6 | -4 | -3 | -5 | -4 | -3 | -4 | -3 | -5 | -2 | 0 | -5 | -4 | -4 | 11 | | | |
| Y | -3 | -3 | -3 | -4 | -4 | -3 | -4 | -5 | 1 | -2 | -2 | -3 | -2 | 3 | -4 | -3 | -2 | 2 | 8 | | |
| V | -1 | -3 | -4 | -5 | -2 | -3 | -3 | -5 | -4 | 3 | 0 | -3 | 0 | -2 | -3 | -2 | -1 | -3 | -3 | 5 | |

| | A | R | N | D | C | Q | E | G | H | I | L | K | M | F | P | S | T | W | Y | V | |
|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|---|---|--|
| A | 4 | | 0 | | | | | | | | | | | | | | | | | | |
| R | -1 | 8 | | | | | | | | | | | | | | | | | | | |
| N | 0 | -2 | 8 | | | | | | | | | | | | | | | | | | |
| D | 0 | -1 | 1 | 9 | | | | | | | | | | | | | | | | | |
| C | -3 | -2 | -1 | -3 | 17 | | | | | | | | | | | | | | | | |
| Q | 1 | 3 | -1 | -1 | -2 | 8 | | | | | | | | | | | | | | | |
| E | 0 | -1 | -1 | 1 | 1 | 2 | 6 | | | | | | | | | | | | | | |
| G | 0 | -2 | 0 | -1 | -4 | -2 | -2 | 8 | | | | | | | | | | | | | |
| H | -2 | -1 | -1 | -2 | -5 | 0 | 0 | -3 | 14 | | | | | | | | | | | | |
| I | 0 | -3 | 0 | -4 | -2 | -2 | -3 | -1 | -2 | 6 | | | | | | | | | | | |
| L | -1 | -2 | -2 | -1 | 0 | -2 | -1 | -2 | -1 | 2 | 4 | | | | | | | | | | |
| K | 0 | 1 | 0 | 0 | -3 | 0 | 2 | -1 | -2 | -2 | -2 | 4 | | | | | | | | | |
| M | 1 | 0 | 0 | -3 | -2 | -1 | -1 | -2 | 2 | 1 | 2 | 2 | 6 | | | | | | | | |
| F | -2 | -1 | -1 | -5 | -3 | -3 | -4 | -3 | -3 | 0 | 2 | -1 | -2 | 10 | | | | | | | |
| P | -1 | -1 | -3 | -1 | -3 | 0 | 1 | -1 | 1 | -3 | -3 | 1 | -4 | -4 | 11 | | | | | | |
| S | 1 | -1 | 0 | 0 | -2 | -1 | 0 | 0 | -1 | -1 | -2 | 0 | -2 | -1 | -1 | 4 | | | | | |
| T | 1 | -3 | 1 | -1 | -2 | 0 | -2 | -2 | -2 | 0 | 0 | -1 | 0 | -2 | 0 | 2 | 5 | | | | |
| W | -5 | 0 | -7 | -4 | -2 | -1 | -1 | 1 | -5 | -3 | -2 | -3 | 1 | -3 | -3 | -5 | 20 | | | | |
| Y | -4 | 0 | -4 | -1 | -6 | -1 | -2 | -3 | 0 | -1 | 3 | -1 | -1 | 3 | -2 | -2 | -1 | 5 | 9 | | |
| V | 1 | -1 | -2 | -2 | -2 | -3 | -3 | -3 | -3 | 4 | 1 | -2 | 0 | 1 | -4 | -1 | 1 | -3 | 1 | 5 | |

use to score new (pairwise or multiple) sequence alignments