# Lab 2 - Alignments in R

# Let's align things!

Open R-studio

### Align Multiple Sequences

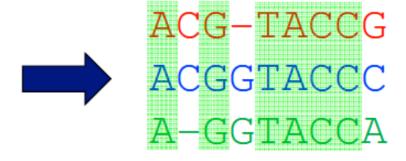
-TACCG

- Want a global alignment over all the sequences
- Different scoring functions possible

ACGTACCG ACGGTACCC ACGGTACCC AGGTACCA

#### Sum of Pairwise Scores

ACGTACCG ACGGTACCC AGGTACCA



ACG-TACCG
ACGGTACCC
mxmgmmmmx

ACG-TACCG

A-GGTACCA
mgmgmmmmx

ACGGTACCC A-GGTACCA mgmxmmmmx

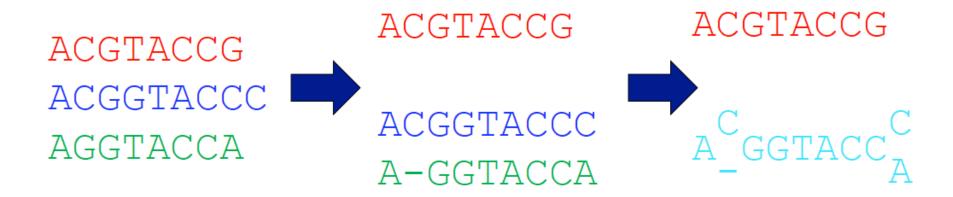
$$S = 18m + 5x + 4g = -12$$

match=+1, mismatch (x) = -2, gap = -5

## Algorithms for MSA

- Computational intractable
  - Time on the order of length of each sequence multiplied
  - For 100 sequence of 100 bp it would be  $100^{100}$
- Use heuristics to make more manageable
  - Not guaranteed to find highest scoring global alignments
  - Usually use progressive alignments

#### Progressive Alignments



Find the bestscoring pair and align Replace the pair with the consensus sequence

#### Progressive Alignments

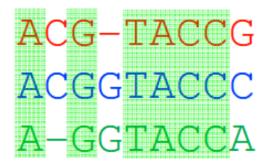
#### ACGTACCG



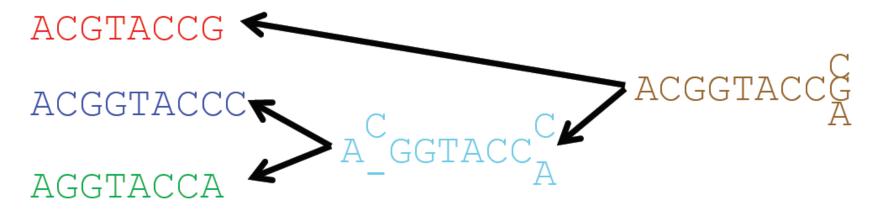
Find the bestscoring pair and align Replace the pair with the consensus sequence

#### **Progressive Alignments**

 Backtracking through the progressive alignment gives the MSA



We can also get a phylogenetic tree



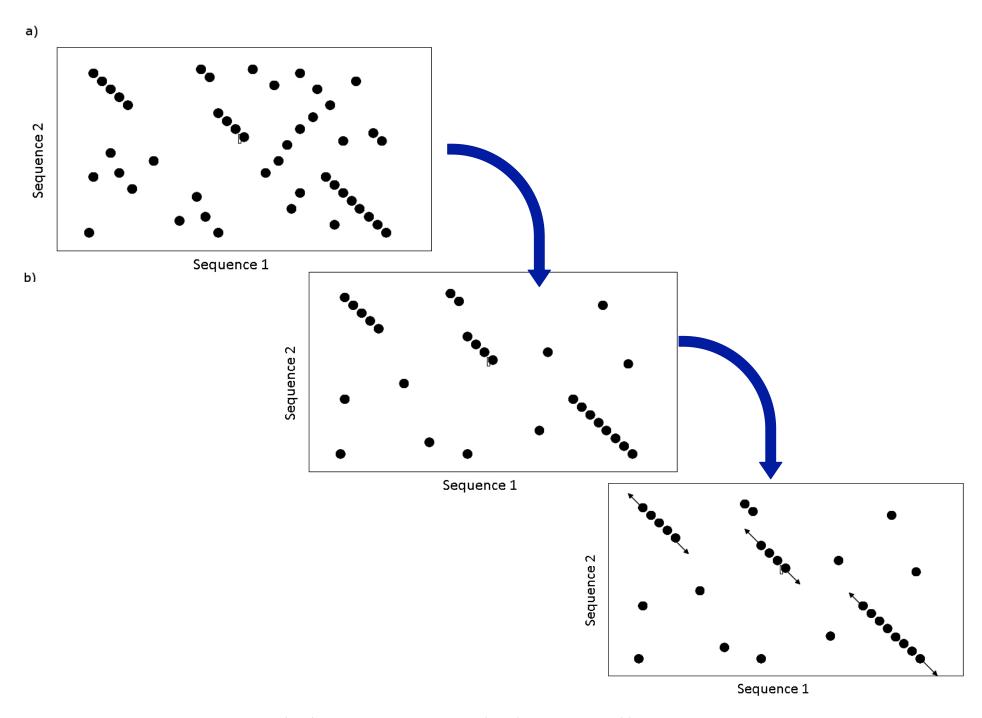
### Let's do some MSAs

### Basic Local Alignment Search Tool (BLAST)

- Fast search through database of sequences
- Uses heuristics to make it fast
  - Not always "best" alignment



- 1. Eleven letter "words" are made from the query sequence
- 2. List of neighborhood words are generated (small changes in sequence)
- 3. This list of actual and close words are compared to each sequence in data base looking for exact matches
- 4. When an exact match is found, it is extended both directions using a local alignment algorithm until the score reaches threshold
- 5. These local alignments are pooled and combined to make maximally extended alignments



Questions about alignments or BLAST?