

# Series 4

Genomics and bioinformatics - Week 4

October 10, 2011

## 1 Sequence alignment

The Needleman-Wunsch algorithm uses a method called “dynamic programming”. This is a very general programming technique. It involves three main steps,

1. Initialization
2. Scoring (matrix fill)
3. Alignment (backtracking)

In the first exercise of this session you will manually perform a global alignment of two sequences based on the following scoring scheme,

*Match: +1, Mismatch: -1, Gap: -2*

Sequence 1: GAATTCAGA

Sequence 2: GGATCGA.


Solution: