Sequence Alignment

Sequence alignment is a way of finding the similar regions between two DNA or protein sequences. This is an indicator of the genetic relatedness between different organisms.

- **Sequence Alignment**
  - **Alignment:**
    - AAGGCCT
    - AAGGCCT
  - **Score:** +4 -1 +1 +4 = 2 -1 -2 -1 -1 = 3
  - Why *fast* Sequence Alignment

**Current Popular Methods**

- **Candidate**
  - **BLAST did not report**
  - **BLAST predicted**

**Prediction of Candidate d**

- **Candidate d = BLAST predicted best d**
- **Candidate d ≠ BLAST predicted d**
- For some q, BLAST did not report

**Case I:** Database >> Query

- **Sequence Alignment**
  - **Sequence 1:** AAGGCCT
  - **Sequence 2:** AAGGCCT
  - **Gap opening = -1**
  - **Gap extension = 0**
  - **Mismatch = -2**

**Materials and Methods**

- **Tools for Fast Sequence Alignment**