

Lecture Notes for INF281 Basics of Bioinformatics Sequence Analysis

Takaya Saito



This work is licensed under a Creative Commons Attribution 4.0 International License.

Contents

I	1	
1	Introduction	1
1.1	Introduction to Molecular Biology	1
1.2	Introduction to Biotechnology	5
1.3	Bioinformatics	6
II	8	
2	Global pairwise alignment	8
2.1	Pairwise alignment	8
2.2	Alignment by brute-force	9
2.3	Table representation of alignment	10
2.4	Global alignment with DP	12
2.5	Backtracking	14
2.6	Needleman-Wunsch algorithm	17
3	Extension of global alignment	18
3.1	Homology at the sequence level	18
3.2	Introduction of score matrix	19
3.3	Extension of gap penalties	23
3.4	Affine gap penalties with a single DP table	24
3.5	Affine gap penalties with three DP tables	26
3.6	Sequence distance	29
4	Local alignment	32
4.1	Local alignments	32
4.2	Local alignment with DP	32
4.3	Dot matrix	34
III	36	
5	Database search	36
5.1	Biological databases	36
5.2	Search in sequence databases	38
5.3	BLAST	39
5.4	N-gram based search	40
5.5	Lookup table of matching n-grams	41
5.6	Finite-state machine with n-grams	43
6	Evaluation of alignment scores	46
6.1	Statistical analysis	46
6.2	Evaluation of global alignment	47
6.3	Evaluation of local alignment	49
6.4	Evaluation of database search	51

6.5 Bit score and e-value	52
7 Model evaluation	54
7.1 Evaluation of binary classifiers	54
7.2 Confusion matrix	55
7.3 Basic evaluation measures	56
7.4 Measures with multiple thresholds	57
IV	59
8 Multiple sequence alignment	59
8.1 Multiple sequence alignment	59
8.2 Dynamic programming with m -dimensional array	61
9 Phylogenetic tree	63
9.1 Introduction to phylogenetic trees	63
9.2 Tree reconstruction methods	65
9.3 Distance-based methods	65
9.4 Maximum parsimony	68
9.5 Maximum likelihood	70
10 Progressive alignment	73
10.1 Introduction to progressive alignment	73
10.2 Alignment clustering	73
10.3 Aligning methods	75
10.4 CLUSTAL	78
V	79
11 Construction of scoring matrix	79
11.1 Scoring schemes for protein sequence alignment	79
11.2 PAM accepted mutations	81
11.3 PAM substitution matrix	83
11.4 BLOSUM	85
12 Sequence profiles	88
12.1 Sequence profiles and patterns	88
12.2 Position weight matrix	88
12.3 Sequence profiles	89
12.4 Profile search	91
12.5 PSI-BLAST	93
13 Hidden Markov model	94
13.1 Hidden Markov model	94
13.2 Viterbi algorithm	94
13.3 HMM profile	96

14 Sequence patterns	98
14.1 Sequence patterns	98
14.2 Pattern comparison	98
14.3 Pattern discovery	100

Part I

1 Introduction

1.1 Introduction to Molecular Biology

Molecular biology is the study of biology focusing on organisms and cells at the molecular level.

Five essential facts about cells

1. Two primary types of cells - eukaryotes and prokaryotes

- Eukaryote: animals & plants
- Prokaryote: bacteria & archaea

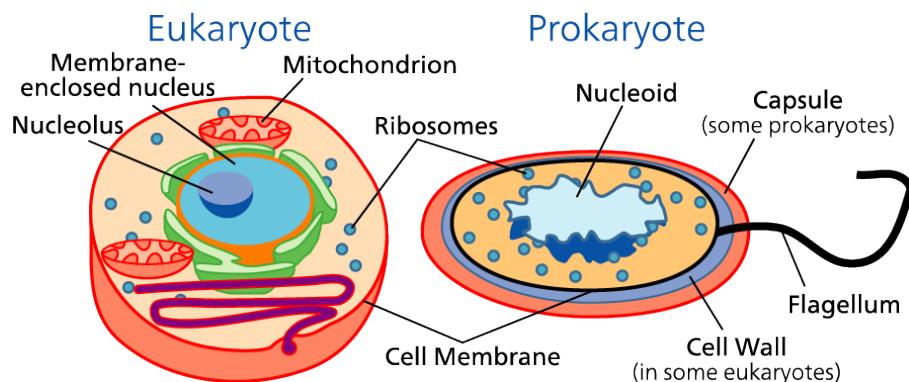


Figure 1.1: Eukaryotic and prokaryotic cells (source: Science Primer, Wikimedia Commons)

2. Cell size - around 1 to 100 micrometers

- Cell Size and Scale: <http://learn.genetics.utah.edu/content/cells/scale>

3. The number of cells

- Prokaryotes: 1 cell
- Human: Estimate of 15 trillion cells

4. An animal cell and cell organelles

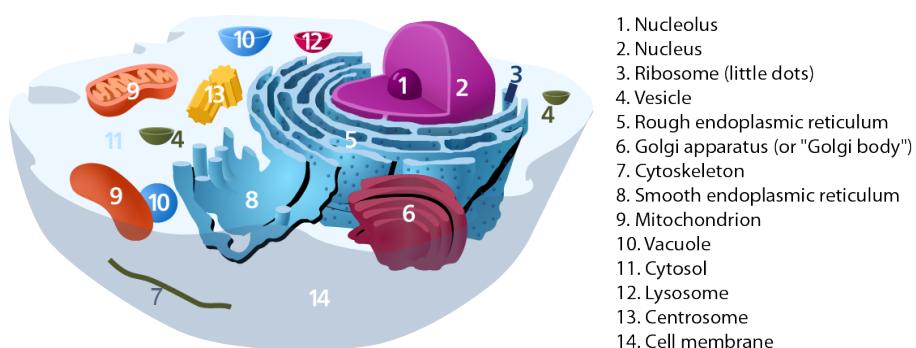


Figure 1.2: An animal cell and organelles (source: Kelvinsong, Wikimedia Commons)

5. Cellular processes

- Cell growth, cell development, cell signaling,
- Example: <http://www.nature.com/nrg/multimedia/rnai>

Central dogma of molecular biology

It describes the information flow within a cell.

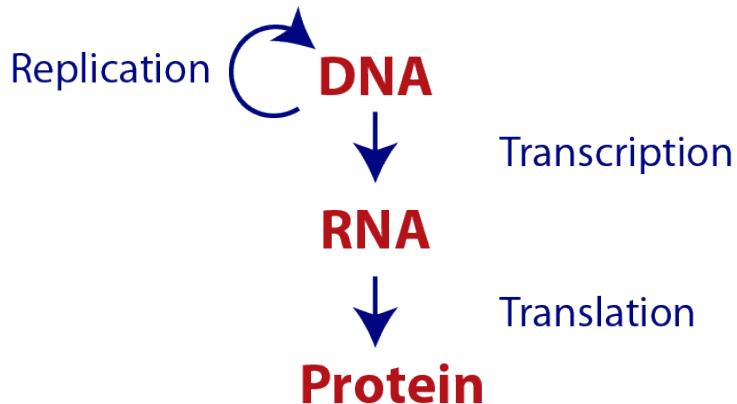


Figure 1.3: Central dogma of molecular biology

DNA (deoxyribonucleic acid)

DNA stores genetic information. It has four different bases: cytosine (C), guanine (G), adenine (A), and thymine (T).

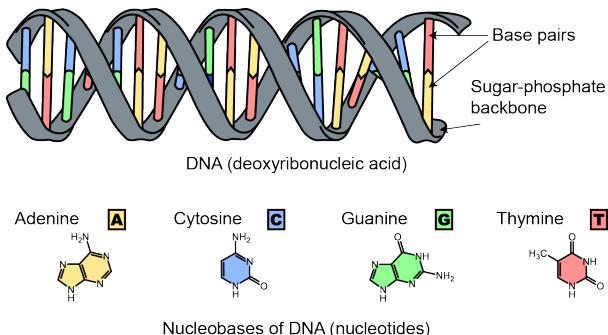


Figure 1.4: DNA double helix and base pairs
(modified from the original version by Sponk, Wikimedia Commons)

Base pair matching (Watson-Crick base pair)

Adenine (A) pairs with thymine (T), whereas cytosine (C) pairs with guanine (G).

DNA strand1: ACGT
||||
DNA strand2: TGCA

RNA (Ribonucleic acid)

RNA has various biological roles and several sub-classes. Messenger RNAs (mRNAs) convey genetic information. It has four different bases: cytosine (C), guanine (G), adenine (A), and uracil (U).

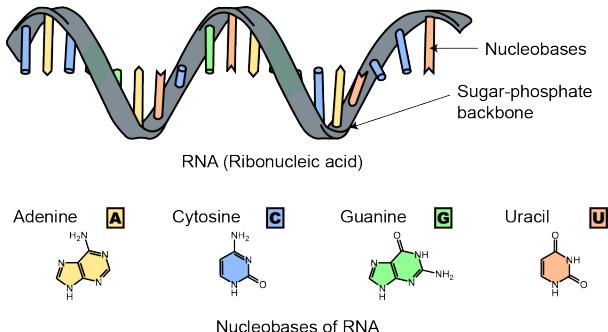


Figure 1.5: Single strand RNA
(modified from the original version by Sponk, Wikimedia Commons)

Transcription: mRNAs are transcribed from DNAs

DNA: ACGT -----> RNA: ACGU
Transcription

Protein

Proteins are large molecules consisting of amino acids. There are 20 common amino acids.

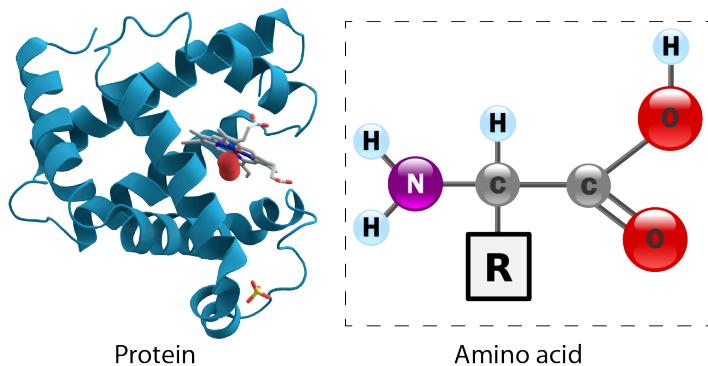


Figure 1.6: Protein 3D structure and amino acids
(sources: AzaToth, Wikimedia Commons, YassineMrabet, Wikimedia Commons)

Translation: Amino-acids are translated from mRNAs

mRNA: GUC -----> AA: Valine
Translation

Universal genetic code

A codon consists of three nucleic acids. Single-letter or three-letter names can be used for amino acids.

Gentic code				
2nd base				
	U	C	A	
3rd base in each row	U	UCU (Ser/S) Serine	UAU (Tyr/Y) Tyrosine	UGU (Cys/C) Cysteine
	UUC (Phe/F) Phenylalanine	UCC (Ser/S) Serine	UAC (Tyr/Y) Tyrosine	UGC (Cys/C) Cysteine
	UUA (Leu/L) Leucine	UCA (Ser/S) Serine	UAA Ochre (Stop)	UGA Opal (Stop)
	UUG (Leu/L) Leucine	UCG (Ser/S) Serine	UAG Amber (Stop)	UGG (Trp/W) Tryptophan
1st base	C	CUU (Leu/L) Leucine	CCU (Pro/P) Proline	CAU (His/H) Histidine
	CUC (Leu/L) Leucine	CCC (Pro/P) Proline	CAC (His/H) Histidine	CGU (Arg/R) Arginine
	CUA (Leu/L) Leucine	CCA (Pro/P) Proline	CAA (Gln/Q) Glutamine	GCG (Arg/R) Arginine
	CUG (Leu/L) Leucine	CCG (Pro/P) Proline	CAG (Gln/Q) Glutamine	CGA (Arg/R) Arginine
A	AUU (Ile/I) Isoleucine	ACU (Thr/T) Threonine	AAU (Asn/N) Asparagine	AGU (Ser/S) Serine
	AUC (Ile/I) Isoleucine	ACC (Thr/T) Threonine	AAC (Asn/N) Asparagine	AGC (Ser/S) Serine
	AUA (Ile/I) Isoleucine	ACA (Thr/T) Threonine	AAA (Lys/K) Lysine	AGA (Arg/R) Arginine
	AUG (Met/M) Methionine	ACG (Thr/T) Threonine	AAG (Lys/K) Lysine	AGG (Arg/R) Arginine
G	GUU (Val/V) Valine	GCU (Ala/A) Alanine	GAU (Asp/D) Aspartic acid	GGU (Gly/G) Glycine
	GUC (Val/V) Valine	GCC (Ala/A) Alanine	GAC (Asp/D) Aspartic acid	GGC (Gly/G) Glycine
	GUA (Val/V) Valine	GCA (Ala/A) Alanine	GAA (Glu/E) Glutamic acid	GGA (Gly/G) Glycine
	GUG (Val/V) Valine	GCG (Ala/A) Alanine	GAG (Glu/E) Glutamic acid	GGG (Gly/G) Glycine

Figure 1.7: Universal genetic code
(modified from the original version by Häggström, Wikimedia Commons)

Cellular functions of proteins

- Enzymes: catalyze chemical reaction
- Cell signaling: hormone (e.g. insulin), antibodies,
- Structural: collagen, cartilage, keratin,

Exercises 1.1

1. Draw a simple diagram of the central dogma of molecular biology and briefly explain the information flow of the molecules.

2. What are the DNA sequences of the opposite strand for the following DNA sequences?

Seq1 CCGATT
Seq2 TTACGC
Seq3 ACGCGC

3. What are the mRNA sequences transcribed from the following DNA sequences?

4. What are the polypeptide sequences translated from the following mRNA sequences?
Answer them with both one-letter and three letter names.

Seq1 AUGUUUUAA
Seq2 GCAGCAAAAA

1.2 Introduction to Biotechnology

Biotechnology is the use of laboratory techniques to study living organism and cells.

Applications of biotechnology

Branches of biotechnology can be explained with different colors.

- Red: medical processes
- Green: agricultural processes
- White: industrial processes
- Blue: marine and aquatic applications

Laboratory tools and equipment



Figure 1.8: Pipette, centrifuge, thermal cycler, and DNA sequencer
(sources: Domain, Manske, Rrror, RE73 via Wikimedia Commons)

Human genome project

It was a large-scale international research project to determine the whole DNA sequences of human.

- 1990 - 2003
- \$2.7 billion

Next generation sequencing

Sequence technologies have been rapidly advanced since the human genome project.

Example: sequence a whole human genome with Illumina HiSeq X Ten.

- One day
- \$1000

Protein sequencing

Proteins are generally more studied than DNAs and RNAs, but the whole proteome is generally harder to analyze than the whole genome. MS (mass-spectrometry) based technologies are widely used to sequence proteins.



Figure 1.9: Orbitrap mass spectrometer (source: Wiòrkiewicz, Wikimedia Commons)

1.3 Bioinformatics

Bioinformatics uses computational approaches to solve problems in life sciences. It is based on computer science.

Similar or almost equivalent disciplines

- Biostatistics
- Biophysics
- Systems biology
- Computational biology

Not much related with bioinformatics

- Health informatics
- Forensic science

Scope of INF281

We mainly cover the following fields of bioinformatics in this course.

- Pairwise alignment
- Database search
- Statistical evaluation
- Multiple alignment
- Phylogenetic tree
- Scoring scheme
- Sequence patterns

Popular bioinformatics programs

BLAST and ClustalW are popular tools for sequence analysis.

- BLAST: a program for database search
URL: <http://blast.ncbi.nlm.nih.gov>
- ClustalW: a program for multiple alignments
URL: <http://www.ch.embnet.org/software/ClustalW.html>

Rank	Title	Times cited
1	Protein measurement with the folin phenol reagent	305148
2	Cleavage of structural proteins during the assembly of the head of bacteriophage T4	213005
3	A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding	155530
4	DNA sequencing with chain-terminating inhibitors	65335
5	Single-step method of RNA isolation by acid guanidinium thiocyanate-phenol-chloroform extraction	60397
6	Electrophoretic transfer of proteins from polyacrylamide gels to nitrocellulose sheets: procedure and some applications	53349
7	Development of the Colle-Salvetti correlation-energy formula into a functional of the electron density	46702
8	Density-functional thermochemistry. III. The role of exact exchange	46145
9	A simple method for the isolation and purification of total lipides from animal tissues	45131
10	Clustal W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice	40289
11	Nonparametric estimation from incomplete observations	38600
12	Basic local alignment search tool	38380
13	A short history of SHELX	37978
14	Gapped BLAST and PSI-BLAST: A new generation of protein database search programs	36410
15	A revised medium for rapid growth and bio assays with tobacco tissue cultures	36132

Table 1.1: The 15 most cited papers of all time
(The top 100 papers, Van Noorden, Maher, and Nuzzo, *Nature*, 2014)

Part II

2 Global pairwise alignment

2.1 Pairwise alignment

A pairwise alignment is a basic sequence structure that consists of two sequences. A global alignment stretches to the whole part of two sequences, whereas a local alignment usually contains only part of the sequences.

Components of pairwise alignment

We name two sequences as database or d and query or q through this course. They may represent sequences from two different species or organisms.

Identical sequences.

q: ACGT
d: ACGT

One mismatch.

q: ACGT
d: ACGA

The '-' symbol represents a blank. A single or a set of multiple blanks further represents a gap, which is an indication of insertion or deletion in the course of evolution between two organisms.

q: ACGT
d: A-GT

N.B. A gap cannot be aligned with another gap.

Example of a simple scoring scheme

- Match: 1
- Mismatch: 0
- Gap penalty: 1 (use -1 for the actual calculation)

We may use the following notation.

- $R_{ab} = 1$ for $a = b$
- $R_{ab} = 0$ for $a \neq b$
- $g = 1$

Exercise 2.1

Use the simple scoring scheme above and calculate the scores of the following two alignments.

Alignment 1

q: GCA-GCA
d: GA-TG-A

Alignment 2

q: GCA-GCA
d: G-ATG-A

2.2 Alignment by brute-force

A brute-force approach finds the alignment with the highest score by simply considering all possible alignments and calculates the score for each of them.

An example of brute-force approach

We find the optimal alignment for the following sequences by using the scoring scheme below.

Sequences:

q: AG, d: ACG

Scoring scheme:

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

$$g = 1$$

1. The length of alignment

- Maximum length: $\text{length}(q) + \text{length}(d)$
- Minimum length: $\max(\text{length}(q), \text{length}(d))$

2. All possible alignments when length = 5

---AG	A---G	A--G-	AG---	--A-G
ACG--	-ACG-	-AC-G	--ACG	AC-G-
--AG-	-AG--	-A--G	-A-G-	A-G--
AC--G	A--CG	A-CG-	A-C-G	-A-CG

3. All possible alignments when length = 4

A--G	A-G-	AG--	A--G	-A-G	-AG-
ACG-	AC-G	A-CG	-ACG	ACG-	AC-G
-AG-	A-G-	--AG	--AG	-A-G	AG--
A-CG	-ACG	ACG-	AC-G	A-CG	-ACG

4. All possible alignments when length = 3

-AG	A-G	AG-
ACG	ACG	ACG

5. Alignment with the best score

ACG
A-G

Score: 1

Search space size of the brute-force approach

The search space size is the number of all possible alignments. It is 25 ($10 + 12 + 3$) for the example above.

Rapid growth of search space size

Example 1

q: ACGACG, d: AGAG

Search space size: 1289

Example 2

q: ACGACGACGACG, d: AGAGAGAG

Search space size: 4,673,345

Exercise 2.2

Find the alignment with the best score for the sequences. Use the simple scoring scheme below.

Sequences:

q: A, d: AC

Scoring scheme:

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

$$g = 1$$

1. What are the maximum and minimum lengths of the alignment?
2. Identify all possible alignments.
3. What is the best score?
4. What is the search space size when the brute-force approach is used?

2.3 Table representation of alignment

Several data structures can be used to represent an alignment. The table representation is frequently used and also makes the process clear when we combine it with dynamic programming (DP) later.

Data structures and algorithms

It is important to consider the following aspects before solving computational problems.

1. Identify and analyze the problem you want to solve
2. Pick up an algorithm that can efficiently solve the problem
3. Decide a data structure that works with the algorithm of your choice

We use a table format (2D array) to solve global alignments by dynamic programming.

Example of table format

Alignment:

q: -AG-
d: A-CG

1. Initial setup

1. Make a table with the size of $(1 + \text{length}(q))$ by $(1 + \text{length}(d))$
2. Add the database sequence as column labels
3. Add the query sequence as row labels

q/d		A	C	G
A	S			
G				E

2. Add arrows

We use three types of arrows to form an alignment.

- Move diagonally: add the letters from q and d to the alignment
- Move vertically: add - and the letter from d to the alignment
- Move horizontally: add the letter from q and - to the alignment

It should start from S and stop at E.

q/d		A	C	G
A	S →			
		↓	↘	→ E
G				

Exercise 2.3

Find the corresponding alignments for Table 1, 2 and 3.

Table 1

q/d		A	C	G
A	S ↘			
		↖	→ E	
G				

Table 2

q/d		A	C	G
A	S →	→	→	↓
				↓
G				

Table 3

q/d		A	C	G
A	S ↓			
		→	→	→ E
G				

2.4 Global alignment with DP

Dynamic programming (DP) provides a solution for a multi-stage decision process, in which larger decisions recursively nest smaller decisions.

Memorize the best score in a table cell

For global alignment, the core procedure of DP is updating a cell with the highest score from the three different scores calculated from its adjacent cells. DP ends when the entire table is updated.

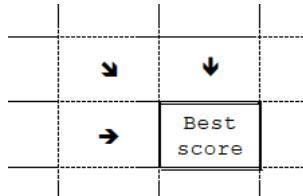
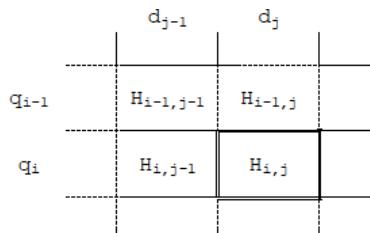


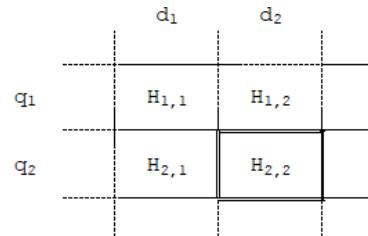
Table notation and indices

$H_{i,j}$ represents the score of the cell for the current update. $H_{i-1,j}$, $H_{i,j-1}$, and $H_{i-1,j-1}$ are the scores of the adjacent cells.

Cell $H_{i,j}$ and its adjacent cells



Example



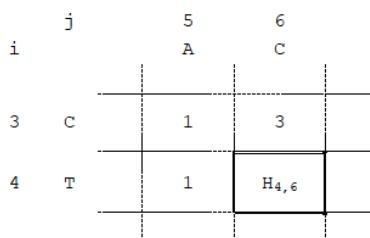
Calculation of three candidate scores

$H_{i,j}^{(0)}$, $H_{i,j}^{(1)}$, and $H_{i,j}^{(2)}$ represent the three candidate scores of $H_{i,j}$. They are respectively calculated as:

$$\begin{aligned} H_{i,j}^{(0)} &= H_{i-1,j} - g && \text{(vertical)} \\ H_{i,j}^{(1)} &= H_{i,j-1} - g && \text{(horizontal)} \\ H_{i,j}^{(2)} &= H_{i-1,j-1} + R_{a,b} && \text{(diagonal)} \end{aligned}$$

Exercise 2.4

Calculate the scores of $H_{4,6}^{(0)}$, $H_{4,6}^{(1)}$, and $H_{4,6}^{(2)}$ first and then update $H_{4,6}$.



Scoring scheme:

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

$$g = 1$$

Initialization

The first row and the first column can be calculated independently from the adjacent cells.

$$H_{0,j} : j * -1 * g$$

$$H_{i,0} : i * -1 * g$$

Example

		j	0	1	2
		i	A	C	
		0	0	-1	-2
0	G	-1			
1	T	-2			

Exercise 2.5

Update all cells of Table 1 and 2. Use the scoring scheme in Exercise 2.4.

Table 1

		A	C
G			

Table 2

		A
G		
T		

Sub-solutions

In DP, larger decisions recursively nest smaller decisions. For instance, Table S is included in Table L.

Table S

		A
A	H _{0,0}	H _{0,1}
	H _{1,0}	H _{1,1}

Table L

		A	G
A	H _{0,0}	H _{0,1}	H _{0,2}
	H _{1,0}	H _{1,1}	H _{1,2}
C	H _{2,0}	H _{2,1}	H _{2,2}

Pseudo-code of updating DP table for global alignment

Algorithm 2.1: Update dynamic programming table for global alignment

$H_{i,j}$: Dynamic programming table
 $R_{a,b}$: Match/mismatch scores
 g : Gap penalty

```
// Initialization
for i ← 0 to m do
    |  $H_{i,0} \leftarrow i * -1 * g;$ 
end
for j ← 1 to n do
    |  $H_{0,j} \leftarrow j * -1 * g;$ 
end

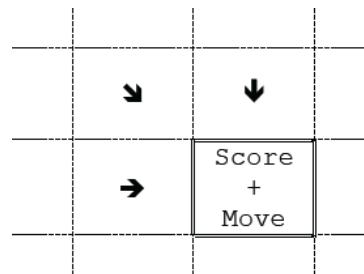
// Main loop for table update
for i ← 1 to m do
    for j ← 1 to n do
        |  $H_{i,j} \leftarrow \max(H_{i-1,j} - g, H_{i,j-1} - g, H_{i-1,j-1} + R_{a,b});$ 
    end
end
```

2.5 Backtracking

Backtracking is a post-processing procedure to find the alignments that have yielded the best score.

Store movement in cells

A table cell can be used for storing the movement.

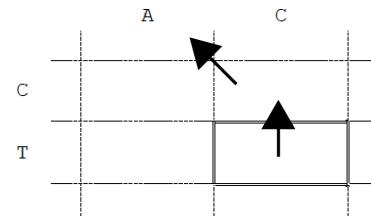


Example

Cells with scores and directions

	A	C
C	Score:1 Move:V	Score:3 Move:D
T	Score:0 Move:V	Score:2 Move:V

Use arrows to indicate backtracking



Exercise 2.6

Complete the DP table with scores and directions. What is the alignment with the best score?

	A	C
A		

Scoring scheme:

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

$$g = 1$$

Re-calculate candidate scores

Re-calculating the three candidate scores also reveals the movement.

$$H_{i,j}^{(0)} = H_{i-1,j} - g \quad (\text{vertical})$$

$$H_{i,j}^{(1)} = H_{i,j-1} - g \quad (\text{horizontal})$$

$$H_{i,j}^{(2)} = H_{i-1,j-1} + R_{a,b} \quad (\text{diagonal})$$

Example

	A	C
C	1	3
T	1	2

$$H_{i,j}^{(0)} = 3 - 1 = 2 = H_{i,j} \quad \checkmark \text{ (vertical)}$$

$$H_{i,j}^{(1)} = 1 - 1 = 0 \neq H_{i,j} \quad \text{(horizontal)}$$

$$H_{i,j}^{(2)} = 1 + 0 = 1 \neq H_{i,j} \quad \text{(diagonal)}$$

Common mistake with backtracking

For the re-calculation approach, it is not to find $\max(H_{i-1,j}, H_{i,j-1}, H_{i-1,j-1})$. You must re-calculate the candidates and then $\max(H_{i,j}^{(0)}, H_{i,j}^{(1)}, H_{i,j}^{(2)})$ to find the actual direction.

Implementation with recursive call

Recursive calls are usually used to implement DP backtracking.

Algorithm 2.2: DP backtracking

S_q : Sequence q
 S_d : Sequence d
 $H_{i,j}$: Dynamic programming table
 $R_{a,b}$: Match/mismatch scores
 g : Gap penalty

```

proc backTrack(i, j,  $A_q$ ,  $A_d$ , k)
  i : Index of sequence q
  j : Index of sequence d
   $A_q$  : q part of alignment (stored in reverse order)
   $A_d$  : d part of alignment (stored in reverse order)
  k : Index for  $A_q$  and  $A_d$ 

  //
  // Need to implement recursion termination here
  // ...
  //

  if  $H_{i,j} = H_{i-1,j} - g$  then                                // vertical
     $A_{q,k} \leftarrow S_{q,i};$ 
     $A_{d,k} \leftarrow '-';$ 
    backTrack(i - 1, j,  $A_q$ ,  $A_d$ , k + 1);
  end

  if  $H_{i,j} = H_{i,j-1} - g$  then                                // horizontal
     $A_{q,k} \leftarrow '-';$ 
     $A_{d,k} \leftarrow S_{d,i};$ 
    backTrack(i, j - 1,  $A_q$ ,  $A_d$ , k + 1);
  end

  if  $H_{i,j} = H_{i-1,j-1} + R_{S_{q,i},S_{d,i}}$  then          // diagonal
     $A_{q,k} \leftarrow S_{q,i};$ 
     $A_{d,k} \leftarrow S_{d,i};$ 
    backTrack(i - 1, j - 1,  $A_q$ ,  $A_d$ , k + 1);
  end
end
    
```

Exercise 2.7

Find the alignment with the best score.

	A	C
G		
T		

Scoring scheme:

$$\begin{aligned}
 R_{ab} &= 1 \text{ for } a = b \\
 R_{ab} &= 0 \text{ for } a \neq b \\
 g &= 1
 \end{aligned}$$

2.6 Needleman-Wunsch algorithm

The method of using DP to solve global pairwise alignment is called the Needleman-Wunsch algorithm in the field of bioinformatics.

Complexity

- Time: $O(nm)$
- Space: $O(nm)$

Comparisons with other algorithms

The Needleman-Wunsch algorithm is similar to several algorithms.

Divide and conquer algorithms

Sub-solutions must be independent with divide and conquer.

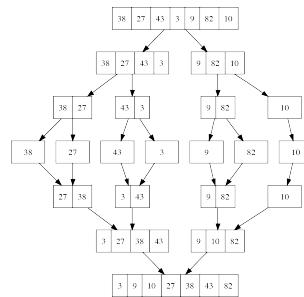


Figure 2.1: Merge sort (source: VineetKumar, Wikimedia Commons)

Dijkstra's algorithm

Worst-case performance of Dijkstra: $O(|E| + |V| \log |V|)$

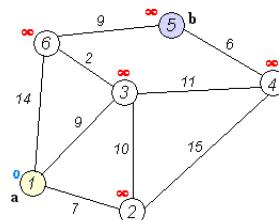


Figure 2.2: Dijkstra's algorithm (source: Ibmua, Wikimedia Commons)

3 Extension of global alignment

3.1 Homology at the sequence level

Constructing alignments can be useful to understand homology among different species. Finding homologies is important to reveal a common evolutionary ancestor.

Evolution and homology

All species are derived from a common ancestor at some point during the course of evolution.

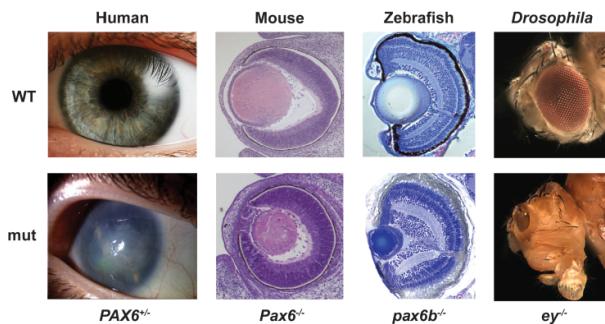


Figure 3.1: PAX6 alterations result in similar changes to eye morphology
(source: Washington et al, doi: 10.1371/journal.pbio.1000247 via Wikimedia Commons)

Homologous and analogous

It is useful to check similarity at the molecular level because there are cases that analogous structures may not indicate homologous.



Figure 3.2: Homologous and analogous structures
(source: John Romanes, 1892, Darwin and after Darwin via Wikimedia Commons)

Sequence homology

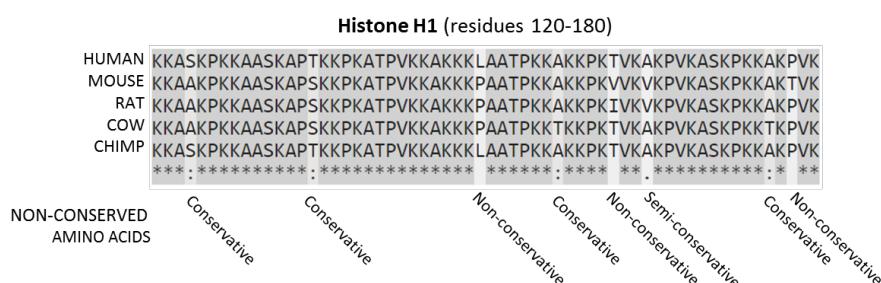


Figure 3.3: Multiple sequence alignment of histone sequences
(source: Shafee, Wikimedia Commons)

Evolution at the sequence level

Sequence differences in DNA

- Substitution (a mismatch in alignment)
- Insertion (a gap in alignment)
- Deletion (a gap in alignment)
- Inversion

Sources of variations

- Mutation
- Recombination
- Insertional mutagenesis
- ...

A mutation of the third nucleotide in a codon often does not affect which amino acid is synthesized.

- GCU → Ala (Alanine)
- GCC → Ala (Alanine)
- GCA → Ala (Alanine)
- GCG → Ala (Alanine)

An amino acid can be replaced by a different amino acid that has similar properties in some cases.

- AUU, AUC, AUA → Ile (Isoleucine)
- CUU, CUC, CUA → Leu (Leucine)

Extension of global alignment with DP

- Score matrix
DNA, RNA, and protein
- Gap penalty
Linear, affine, and constant

3.2 Introduction of score matrix

We will expand our simple scoring scheme to score matrices. This expansion allows us to solve general alignment problems with DNA, RNA, and protein sequences.

Extension of a scoring scheme to a score matrix

The matrix below is equivalent with match: 1 and mismatch: 0.

	a	b
a	1	0
b	0	1

Example of a DNA score matrix

The matrix below is equivalent with match: 5 and mismatch: -4.

	A	T	G	C
A	5	-4	-4	-4
T		5	-4	-4
G			5	-4
C				5

Applications of score matrix

Score matrices are more flexible than the simple scoring scheme. For instance, they can be used for the following cases.

- DNA pairs
- RNA pairs
- Similarity of protein sequences by amino acid properties

DNA pairs (Watson-Crick pairs)

A thymine pairs with an adenine, and a cytosine pairs with a guanine.

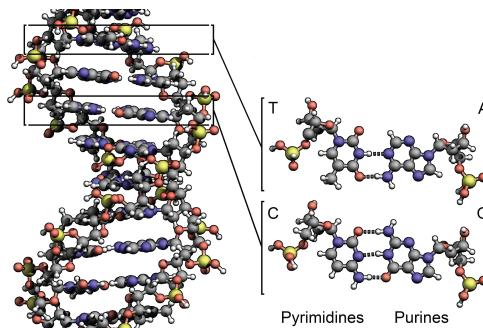


Figure 3.4: Watson-Crick pairs (source: Zephyris, Wikimedia Commons)

Example of score matrix for DNA pairs

The matrix reflects the differences of hydrogen bonds.

	A	T	G	C
A	-3	4	-3	-3
T		-3	-3	-3
G			-3	5
C				-3

Example of DP for DNA pairs

You can use DP to find a DNA alignment with Watson-Crick pairs. For instance, the DP table below is used to solve the optimal alignment for two DNA sequences: $q = AC$ and $d = GT$ with gap penalty $g = 4$.

DP table:

q/d		G	T
		0	-4
A	-4	-3	0
	C	-8	1

Alignment:

q: AC-
d: -GT

RNA pairs

A single stand of RNA can form a 3D structure that has a biological function. The secondary structure of RNA is a two-dimensional representation of the structure.

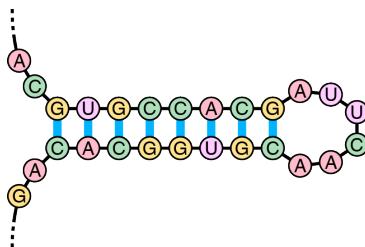


Figure 3.5: RNA stem-loop (source: Sakurambo, Wikimedia Commons)

Wobble pairs

Wobble pairs are not canonical Watson-Crick pairs, but they can still form hydrogen bonds.

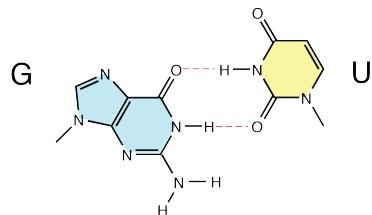


Figure 3.6: GU wobble pairs

(modified from the original version by Fdardel, Wikimedia Commons)

Example of score matrix for RNA pairs

The matrix takes GU wobbles into consideration.

	A	U	G	C
A	-3	5	-3	-3
U		-3	2	-3
G			-3	5
C				-3

Example of DP for RNA pairs

You can form the following DP table for two RNA sequences: q = AU and d = UGA with gap penalty g = 9.

DP table:

q/d	U	G	A
0	-9	-18	-27
A	-9	5	-4
U	-18	-4	7

Alignment:

q: A-U
d: UGA

Similarity of protein sequences

Amino acids can be categorized into several groups by their properties. Proteins alignments often need to take these properties into consideration.

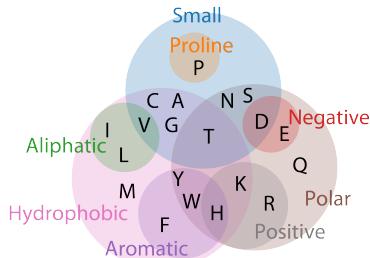


Figure 3.7: Venn diagram of amino acid properties

Example of a protein score matrix

It can be used to compare the similarity between two protein sequences.

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	13	6	9	9	5	8	9	12	6	8	6	7	7	4	11	11	11	2	4	9
R	3	17	4	3	2	5	3	2	6	3	2	9	4	1	4	4	3	7	2	2
N	4	4	6	7	2	5	6	4	6	3	2	5	3	2	4	5	4	2	3	3
D	5	4	8	11	1	7	10	5	6	3	2	5	3	1	4	5	5	1	2	3
C	2	1	1	1	52	1	1	2	2	2	1	1	1	1	2	3	2	1	4	2
Q	3	5	5	6	1	10	7	3	7	2	3	5	3	1	4	3	3	1	2	3
E	5	4	7	11	1	9	12	5	6	3	2	5	3	1	4	5	5	1	2	3
G	12	5	10	10	4	7	9	27	5	5	4	6	5	3	8	11	9	2	3	7
H	2	5	5	4	2	7	4	2	15	2	2	3	2	2	3	3	2	2	3	2
I	3	2	2	2	2	2	2	2	2	10	6	2	6	5	2	3	4	1	3	9
L	6	4	4	3	2	6	4	3	5	15	34	4	20	13	5	4	6	6	7	13
K	6	18	10	8	2	10	8	5	8	5	4	24	9	2	6	8	8	4	3	5
M	1	1	1	0	1	1	1	1	2	3	2	6	2	1	1	1	1	1	2	
F	2	1	2	1	1	1	1	1	3	5	6	1	4	32	1	2	2	4	20	3
P	7	5	5	4	3	5	4	5	5	3	3	4	3	2	20	6	5	1	2	4
S	9	6	8	7	7	6	7	9	6	5	4	7	5	3	9	10	9	4	4	6
T	8	5	6	6	4	5	5	6	4	6	4	6	5	3	6	8	11	2	3	6
W	0	2	0	0	0	0	0	0	1	0	1	0	0	1	0	1	0	55	1	0
Y	1	1	2	1	3	1	1	1	3	2	2	1	2	15	1	2	2	3	31	2
V	7	4	4	4	4	4	4	5	4	15	10	4	10	5	5	5	72	4	17	

Table 3.1: Mutation probability matrix for the evolutionary distance of 250 PAMs (in percentage) (Chapter 22: A model of evolutionary change in proteins, Dayhoff and Schwartz, Atlas of Protein Sequence and Structure, 1978)

Exercise 3.1

1. Use the DNA score matrix below with $g = 10$ and find the optimal alignment for $q = \text{TG}$ and $d = \text{TCG}$.

	A	T	G	C
A	5	-4	-4	-4
T		5	-4	-4
G			5	-4
C				5

2. The 250 PAM mutation matrix above can not directly be used for global alignments. Explain what kind of matrix you need for calculating alignment scores.

3.3 Extension of gap penalties

Types of gap penalties

Three types of gap penalties can be considered when creating an alignment. They treat a gap penalty differently depending on the gap length.

- Linear
- Affine
- Constant

Gap penalty notation

- g : single gap penalty
- l : length of a gap
- g_l : gap penalty of length l
- g_{open} : initial gap penalty
- g_{extend} : extended gap penalty

Linear gap penalty

It is the same as our simple scoring scheme. It treats a gap with multiple blanks as a result of several mutations. A gap of length l can be calculated as: $g_l = g \times l$.

Example of a gap of length 2

q: ACCCGT
d: AC--GT

The score of the gap (only the gap part) is 10 when $g = 5$.

Affine gap penalty

It treats a gap with multiple blanks as a result of a single mutation. A gap with length l can be calculated as: $g_l = g_{open} + (l - 1) \times g_{extend}$.

Example of a gap of length 2

q: ACCCGT
d: AC--GT

The score of the gap (only the gap part) is 5.5 when g_{open} and g_{extend} are 5 and 0.5 respectively.

Constant gap penalty

It is similar to the affine gap penalty, but the score is independent from the gap length. A gap with length l can be calculated as: $g_l = g$

Example of a gap of length 2

q: ACCCGT
d: AC--GT

The score of the gap (only the gap part) for the alignment above is 5 when $g = 5$.

Exercise 3.2

Calculate all three types of gap penalties for the gap in alignment 1 & 2.

- $g: 5$
- $g_{open}: 5$
- $g_{extend}: 0.5$

Alignment 1

q: CCCGG
d: CC-CG

Alignment 2

q: CCCGG
d: C---G

3.4 Affine gap penalties with a single DP table

DP for general gap penalty

We need to modify DP so that extra cells are checked to find the optimal score of a cell.

Cell update rule of general gap penalty

$$H_{i,j} = \max \left[H_{i-1,j-1} + R_{q_i d_j}, \max_{1 \leq l \leq j} (H_{i,j-l} - g_l), \max_{1 \leq l \leq i} (H_{i-l,j} - g_l) \right]$$

Example of cell update

Sequences:

$q: AG$, $d: ACG$

Scoring scheme:

$$\begin{aligned}g_{open} &= 1 \\g_{extend} &= 0.1 \\R_{ab} &= 1 \text{ for } a = b \\R_{ab} &= 0 \text{ for } a \neq b\end{aligned}$$

Update $H_{2,1}$

		A	C	T	T	
		0	-1	-1.1	-1.2	-1.3
A	0	-1	1			
	-1	1				
T	-1.1	0				

- vertical: $\max(1 - 1, -1 - 1 - 0.1) = 0$
- horizontal: $-1.1 - 1 = -2.1$
- diagonal: $-1 - 0 = -1$

Update $H_{1,2}$

		A	C	T	T	
		0	-1	-1.1	-1.2	-1.3
A	0	-1	1	0		
	-1	1	0			
T	-1.1	0				

- vertical: $-1.1 - 1 = -2.1$
- horizontal: $\max(1 - 1, -1 - 1 - 0.1) = 0$
- diagonal: $-1 - 0 = -1$

Update $H_{1,3}$

		A	C	T	T	
		0	-1	-1.1	-1.2	-1.3
A	0	-1	1	0	-0.1	
	-1	1	0	-0.1		
T	-1.1	0	1			

- vertical: $-1.2 - 1 = -2.2$
- horizontal: $\max(0 - 1, 1 - 1 - 0.1, -1 - 1 - 0.1 - 0.1) = -0.1$
- diagonal: $-1.1 - 0 = -1.1$

Exercise 3.3

Complete the DP table below.

Sequences:

$q: AT, d: ACTT$

Scoring scheme:

$$\begin{aligned}g_{open} &= 1 \\g_{extend} &= 0.1 \\R_{ab} &= 1 \text{ for } a = b \\R_{ab} &= 0 \text{ for } a \neq b\end{aligned}$$

		A	C	T	T	
		0	-1	-1.1	-1.2	-1.3
A		-1	1	0	-0.1	
T		-1.1	0	1		

3.5 Affine gap penalties with three DP tables

DP can effectively solve affine gap penalties with three tables.

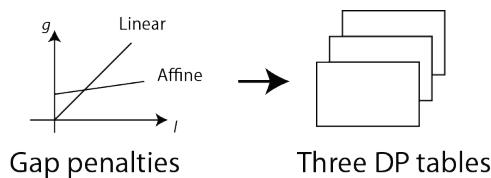


Figure 3.8: Affine gap penalties and three tables

Three DP tables

We need to modify DP so that extra cells are checked to find the optimal score of a cell.

- $E_{i,j}$: alignment ending with a gap extend (vertical)
- $F_{i,j}$: alignment ending with a gap extend (horizontal)
- $G_{i,j}$: alignment ending with a match/mismatch (diagonal)

Cell update rule of the three tables

$$\begin{aligned}E_{i,j} &= \max(E_{i-1,j} - g_{extend}, F_{i-1,j} - g_{open}, G_{i-1,j} - g_{open}) \\F_{i,j} &= \max(E_{i,j-1} - g_{open}, F_{i,j-1} - g_{extend}, G_{i,j-1} - g_{open}) \\G_{i,j} &= \max(E_{i-1,j-1} + R_{qid_j}, F_{i-1,j-1} + R_{qid_j}, G_{i-1,j-1} + R_{qid_j})\end{aligned}$$

You can calculate H only in the last cell.

$$H_{m,n} = \max(E_{m,n}, F_{m,n}, G_{m,n})$$

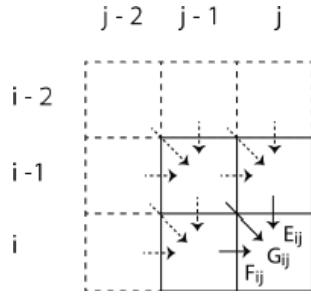


Figure 3.9: Update a cell with E, F, and G

Recurrence rules when $i = 0$ and $j = 0$

	$i > 1, j > 1$	$i = 1$	$j = 1$
$E_{i,j}$	$\max \begin{cases} E_{i-1,j} - g_{\text{extend}} \\ F_{i-1,j} - g_{\text{open}} \\ G_{i-1,j} - g_{\text{open}} \end{cases}$	$\max \begin{cases} E_{i-1,j} - g_{\text{open}} \\ F_{i-1,j} - g_{\text{open}} \\ G_{i-1,j} - g_{\text{open}} \end{cases}$	$\max \begin{cases} E_{i-1,j} - g_{\text{extend}} \\ F_{i-1,j} - g_{\text{open}} \\ G_{i-1,j} - g_{\text{open}} \end{cases}$
$F_{i,j}$	$\max \begin{cases} E_{i,j-1} - g_{\text{open}} \\ F_{i,j-1} - g_{\text{extend}} \\ G_{i,j-1} - g_{\text{open}} \end{cases}$	$\max \begin{cases} E_{i,j-1} - g_{\text{open}} \\ F_{i,j-1} - g_{\text{extend}} \\ G_{i,j-1} - g_{\text{open}} \end{cases}$	$\max \begin{cases} E_{i,j-1} - g_{\text{open}} \\ F_{i,j-1} - g_{\text{extend}} \\ G_{i,j-1} - g_{\text{open}} \end{cases}$
$G_{i,j}$	$\max \begin{cases} E_{i-1,j-1} + R_{q_id_j} \\ F_{i-1,j-1} + R_{q_id_j} \\ G_{i-1,j-1} + R_{q_id_j} \end{cases}$	$\max \begin{cases} E_{i-1,j-1} + R_{q_id_j} \\ F_{i-1,j-1} + R_{q_id_j} \\ G_{i-1,j-1} + R_{q_id_j} \end{cases}$	$\max \begin{cases} E_{i-1,j-1} + R_{q_id_j} \\ F_{i-1,j-1} + R_{q_id_j} \\ G_{i-1,j-1} + R_{q_id_j} \end{cases}$

Example of updating DP tables with affine gaps

Sequences:

q: AT, d: ACTT

Scoring scheme:

$$g_{\text{open}} = 1$$

$$g_{\text{extend}} = 0.1$$

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

Initialization

		E				F				
		A	C	T	T	A	C	T	T	
		0	-1	-1.1	-1.2	-1.3	0	-1	-1.1	-1.2
A	A	-1					-1			
T	T	-1.1					-1.1			

		G				
		A	C	T	T	
		0	-1	-1.1	-1.2	-1.3
A	A	-1				
T	T	-1.1				

Update the first row

		E				F			
		A	C	T	T	A	C	T	T
A	0	-1	-1.1	-1.2	-1.3	0	-1	-1.1	-1.2
	-1	-2	-2.1	-2.2	-2.3	-1	-2	0	-0.1
T	-1.1					-1.1			

		G			
		A	C	T	T
A	0	-1	-1.1	-1.2	-1.3
	-1	1	-1	-1.1	-1.2
T	-1.1	0	-1	-1.1	-1.2

Update the second row

		E				F			
		A	C	T	T	A	C	T	T
A	0	-1	-1.1	-1.2	-1.3	0	-1	-1.1	-1.2
	-1	-2	-2.1	-2.2	-2.3	-1	-2	0	-0.1
T	-1.1	0	-1	-1.1	-1.2	-1.1	-2.1	-1	0

		G				H			
		A	C	T	T	A	C	T	T
A	0	-1	-1.1	-1.2	-1.3				
	-1	1	-1	-1.1	-1.2				
T	-1.1	-1	1	1	0.9				0.9

Update H

		A				C			
		A	C	T	T	A	C	T	T
A	0	-1	-1.1	-1.2	-1.3	0	-1	-1.1	-1.2
	-1	-2	-2.1	-2.2	-2.3	-1	-2	0	-0.1
T	-1.1	0	-1	-1.1	-1.2	-1.1	-2.1	-1	0

		G				H			
		A	C	T	T	A	C	T	T
A	0	-1	-1.1	-1.2	-1.3				
	-1	1	-1	-1.1	-1.2				
T	-1.1	-1	1	1	0.9				0.9

Backtrack

	A	C	T	T	
A	0	-1	-1.1	-1.2	-1.3
	-1	-2	-2.1	-2.2	-2.3
T	-1.1	0	-1	-1.1	-1.2

	A	C	T	T	
A	0	-1	-1.1	-1.2	-1.3
	-1	-2	0	-0.1	-0.2
T	-1.1	-2.1	-1	0	0

	A	C	T	T	
A	0	-1	-1.1	-1.2	-1.3
	-1	1	-1	-1.1	-1.2
T	-1.1	-1	1	1	0.9

	A	C	T	T	
A					
T					0.9

Optimal alignment

q: A--T Score: 0.9
d: ACTT

Constant gap penalty

DP with constant gap penalty can be solved in the same way as the affine gap penalty.

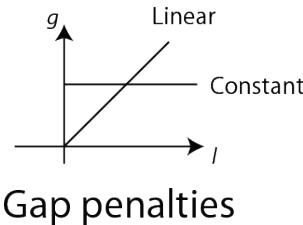


Figure 3.10: Constant gap penalty

3.6 Sequence distance

Distances can be also used to indicate the similarity of an alignment.

Edit distance

The Levenshtein distance is one of the most commonly used edit distances in computer science.

Insertion : $AC \rightarrow AGC$	$(\varepsilon \rightarrow G)$
Deletion : $ATC \rightarrow AC$	$(T \rightarrow \varepsilon)$
Substitution : $AAA \rightarrow ATA$	$(A \rightarrow T)$

Scoring scheme for Levenshtein distance

- $R_{ab} = 0$ for $a = b$
- $R_{ab} = -1$ for $a \neq b$
- $g = 1$

Distance from DP score

Given the best score T from DP, the edit distance d is $-T$.

Example of edit distance with DP

	A	T	C	
A	0	-1	-2	-3
	-1	0	-1	-2
C	-2	-1	-1	-1

$T = -1$

$d = 1$

Metric space

The edit distance constitutes a metric space.

- $d_{xy} = 0$ for $x = y$
- $d_{xy} > 0$ for $x \neq y$
- $d_{xy} = d_{yx}$
- $d_{xy} \leq d_{xz} + d_{zy}$ for any z (the triangle inequality)

Mutation and distance

Mutations may occur several times on the same position.

Example of single mutations

$ACGT \rightarrow AGT \rightarrow ACT \rightarrow AGT \rightarrow AGCT$

Four mutations have occurred, but the edit distance is 2.

Distance per column

It indicates the number of mutations per column (nucleotide/amino acid).

$$D = d / (\text{length of the longest sequence})$$

Correction of distance

The distance can be adjusted. Below is a simple correction approach for protein sequences.

$$K = -\ln(1 - D - 1/5D^2)$$

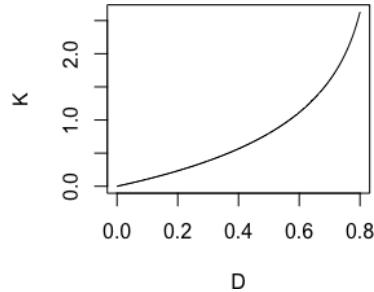


Figure 3.11: Correction of distance D

Example of distance correction

$$D = 0.5$$

$$K = -\ln(1 - 0.5 - 1/5 \times 0.25) = -\ln(0.45) \approx 0.8$$

4 Local alignment

4.1 Local alignments

Local pairwise alignments are aligned pairs of sub-sequences that have certain level of similarities.

Difference between global and local alignments

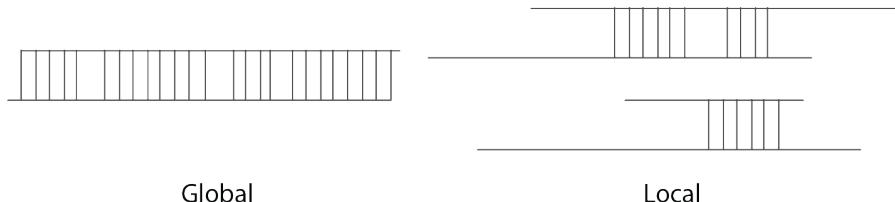


Figure 4.1: Global and local alignments

Elements of local alignment

- Segment: a substring of a sequence
- Segment pair: a pair of segments
- Local alignment: an alignment of a segment pair

Elements of local alignment

- Dynamic programming (Smith–Waterman)
- Dot matrix

Applications

- Sequence motifs
- Conserved regions
- Inverted repeats

4.2 Local alignment with DP

Dynamic programming can be used to find local alignments.

Requirements

- Find all local alignments between two sequences
- Assign scores to all local alignments

Modification of DP for local alignments

- The minimum alignment score must be 0
- Some entries of the score matrix should be negative
- Backtracking also needs to be modified

Update rule of DP cells

$$\begin{aligned}
 H_{i,j}^{(0)} &= H_{i-1,j} - g && (\text{vertical}) \\
 H_{i,j}^{(1)} &= H_{i,j-1} - g && (\text{horizontal}) \\
 H_{i,j}^{(2)} &= H_{i-1,j-1} + R_{a,b} && (\text{diagonal}) \\
 H_{i,j}^{(2)} &= 0 && (\text{minimum score})
 \end{aligned}$$

Example of cell update

	A	C	
C	0.1	0.4	
T	0.2	0	

Scoring scheme:
Match: 0.5
Mismatch: -0.3
Gap penalty: 0.5

$$\begin{aligned}
 H_{i,j}^{(0)} &= -0.1 && (\text{vertical}) \\
 H_{i,j}^{(1)} &= -0.3 && (\text{horizontal}) \\
 H_{i,j}^{(2)} &= -0.2 && (\text{diagonal}) \\
 H_{i,j}^{(2)} &= 0 && \checkmark (\text{minimum score})
 \end{aligned}$$

Backtracking for local alignments

It starts from the cells with the maximum score instead of the right bottom cell.

- Start cells: cells with the maximum score
- End cells: cells with 0

N.B. the end cell with score 0 should not be included in the alignment.

Example of backtracking

	A	C	G	C
C	0	0	0	0
G	0	0	0.5	0
A	0	0.5	0	0.5
			1	0.5
				0.7

Local alignment
q: 2 CG 3
d: 2 CG 3

Pseudo-code of updating DP table for local alignment

The cells in the first row and the first column are initialized with 0.

Algorithm 4.1: Update dynamic programming table for global alignment

$H_{i,j}$: Dynamic programming table
 $R_{a,b}$: Match/mismatch scores
 g : Gap penalty

```
// Initialization
for i ← 0 to m do
    |  $H_{i,0} \leftarrow 0$ ;
end
for j ← 1 to n do
    |  $H_{0,j} \leftarrow 0$ ;
end

// Main loop for table update
for i ← 1 to m do
    for j ← 1 to n do
        |  $H_{i,j} \leftarrow \max(0, H_{i-1,j} - g, H_{i,j-1} - g, H_{i-1,j-1} + R_{a,b})$ ;
    end
end
```

Exercise 4.1

Use DP to find a local alignment.

q/d	A	G	C	C
A				
G				
C				

Scoring scheme:
Match: 0.2
Mismatch: -0.2
Gap penalty: 0.2

4.3 Dot matrix

Using a dot matrix is an effective and easy way to find local similarities.

Basic concept

It uses an $m \times n$ binary matrix from two sequences.

- A dot: match
- Empty: mismatch

Example of dot matrix

q: ACATTAG, d: CATTAGG

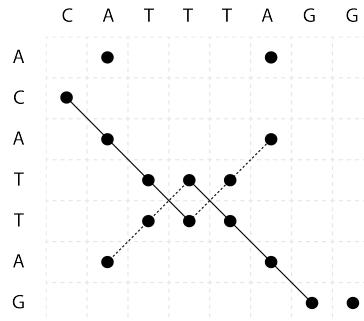


Figure 4.2: Dot matrix of 7×8

It is easy to find segment pairs with a dot matrix. Contiguous dots along diagonals indicate local alignments. It is also easy to find other similarities. For instance, contiguous dots along anti-diagonals indicate reversed substrings.

Filtering of dot matrix

Dot matrices usually get noisy with too many dots. Overlapping windows are usually applied to reduce the noise.

Example of filtering

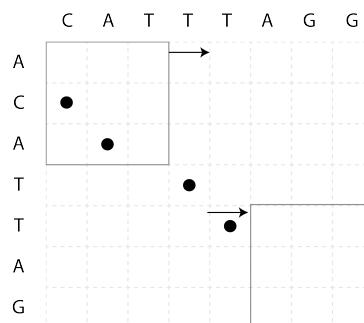


Figure 4.3: Filtered dot matrix with window size 3 and threshold 3.

Exercise 4.2

Find local similarities between two DNA sequences, q: GATTACA and d: GGATTTAC.

1. Create a dot matrix for the two sequences.
2. Filter dots with overlapping windows size 3 and threshold 3.

Part III

5 Database search

5.1 Biological databases

Biological databases contain biological information, mainly collected from molecular biology experiments, life science literature, and bioinformatics analyses.

Categories of databases

Annual Nucleic Acids Research database issue includes the following database categories.

- Nucleotide Sequence Databases
- RNA sequence databases
- Protein sequence databases
- Structure Databases
- Proteomics Resources
- Human and other Vertebrate Genomes
- Genomics Databases (non-vertebrate)
- Plant databases
- Human Genes and Diseases
- Metabolic and Signaling Pathways
- Immunological databases
- ...

GenBank

- A comprehensive database of publicly available nucleotide sequences
- Produced and maintained by NCBI (National Center for Biotechnology Information, URL: <http://www.ncbi.nlm.nih.gov>)

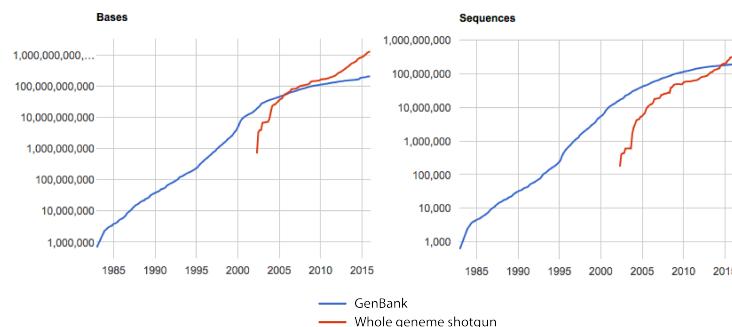


Figure 5.1: Growth of GenBank and WGS (source: NCBI)

UniProt

- A central repository of protein data from Swiss-Prot, TrEMBL, and PIR-PSD databases
- Maintained by the UniProt consortium

Sequence data

- Identifier
- Sequence

Data format of sequence data

FASTA is the most popular format for sequence data.

```
>gi|31563518|ref|NP_852610.1| microtubule-associated proteins 1A/1B light chain 3A isoform b
MKMRRFSSPCGKAAVDPADRCKEVQQIRDQHPSKIPVIIERYKGEKQLPVLDTKFLVPDHVNMSLVKI
IRRLQLNPTQAFFLLVNQHSMVSVSTPIADIYEQEKGDEDFLYMVYASQETFGFIRENE
```

Annotation data

Sequences databases usually contain annotations in addition to sequences.

- Notes and descriptions of important regions and components
- Meta data

Data format of annotation data

Annotation data can be downloaded in many different formats. GFF is one of the popular file formats for storing genomic features.

```
0 ##gff-version 3.2.1
1 ##sequence-region ctg123 1 1497228
2 ctg123 . gene      1000 9000  . + . ID=gene00001;Name=EDEN
3 ctg123 . TF_binding_site 1000 1012  . + . ID=tfbs00001;Parent=gene00001
4 ctg123 . mRNA     1050 9000  . + . ID=mRNA00001;Parent=gene00001;Name=EDEN.1
5 ctg123 . mRNA     1050 9000  . + . ID=mRNA00002;Parent=gene00001;Name=EDEN.2
6 ctg123 . exon     1050 1500  . + . ID=exon00002;Parent=mRNA00001,mRNA00002
7 ctg123 . CDS      1201 1500  . + 0 ID=cds00001;Parent=mRNA00001;Name=edenprotein.1
```

Tools

Many database tools are available for various purposes.

Search tools for sequence databases

- BLAST at NCBI (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>)
- BLAT/BLAST at Ensembl (<http://www.ensembl.org/Multi/Tools/Blast>)

Data browsing tools of annotation and sequence data

- UCSC Genome Browser (<https://genome.ucsc.edu>)
- Ensemble Genome Browser (<http://www.ensembl.org>)

Data download tools for annotation and sequence data

- UCSC Table Browser (<http://genome.ucsc.edu/cgi-bin/hgTables>)
- Ensemble BioMart (<http://www.ensembl.org/biomart>)

Tools for protein data

- UniProt (<https://www.uniprot.org>)

5.2 Search in sequence databases

Since biological databases contain a large number of sequences, heuristics search methods are usually applied to database search.

Aims of searching in sequence databases

- Find homologies
- Find segments with important functionality

Main procedures of sequence search

- Perform local pairwise alignments
- Evaluate the alignments statistically

Estimated computational time for dynamic programming (DP)

Table 5.1: Estimated computational time of DP for the three cases 1ms, 10ms, and 1sec

Time of one alignment	Database size		
	1000	1,000,000	1,000,000,000
1 ms	1 sec	16 min	2.6 h
10 ms	10 sec	2.6 h	11 days
1 sec	16 min	11 days	31 years

Heuristic approach

- Need to search billions of entries
- Tradeoff between accuracy/precision and speed
- Use n-gram based search
- BLAST (Basic Local Alignment Search Tool)
- BLAT (BLAST-like alignment tool)

5.3 BLAST

BLAST (Basic Local Alignment Search Tool) is the most popular tool to find homologous sequences in large-scale sequence databases.

Methods

- Generate n-grams from query sequence
- Find n-gram hits in database
- Expand n-gram hits to HSP
- Increase HSP scores
- Introducing gaps
- Give the expect values (E-values) to HSPs

N-gram hits to HSP

- Connect multiple n-gram hits
- Increase HSP score

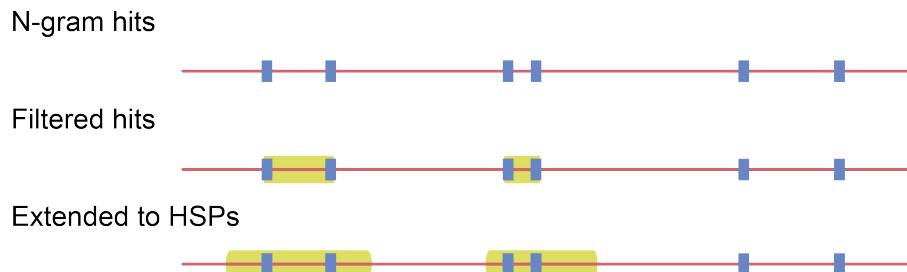


Figure 5.2: N-gram hits to HSPs

Increase HSP score

BLAST changes the length of HSP by shortening or extending in order to increase the score.

Example

Query sequence: R P P Q G L F
Database sequence: D P P E G V V
Score: -2 7 7 2 6 1 -1
Optimal accumulated score = 7+7+2+6+1 = 23

Exact match is scanned.
HSP

Figure 5.3: HSP extension process (source: DISP, Wikimedia Commons)

Introducing gaps

Banded dynamic programming is used to introduce gaps to an HSP.

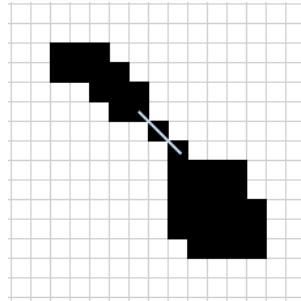


Figure 5.4: Banded DP with the starting seed pair

E-value

“The Expect value (E) is a parameter that describes the number of hits one can expect to see by chance when searching a database of a particular size”

– BLAST Frequently Asked questions (<http://blast.ncbi.nlm.nih.gov>)

5.4 N-gram based search

Using n-grams is a useful method to find segment pairs.

Equivalent or related concepts to n-gram

- q-gram
- n-letter word
- n-tuple
- n-mer

Create n-grams

Decomposing a given sequence into n-letter words creates a list of n-grams.

Example

q: ACGATT

Word size: 2
AC, CG, GA, AT, TT

Word size: 3
ACG, CGA, GAT, ATT

Find segment pairs in database sequences

N-grams can be used to find segment pairs.

Example

q: ACGATT

2-gram: AC, CG, GA, AT, TT

d1: CTAAG

0 hits

d2: CGTAT

2 hits

d3: ATAGA

2 hits

5.5 Lookup table of matching n-grams

A lookup table can be used for effectively finding n-gram matches.

Terminology

- Indices: positions in q
- Matching n-grams: Possible matching n-grams by threshold score T

Example of creating a lookup table

q: ACGTAC

2-gram: AC, CG, GT, TA, AC

T: 3

Score matrix:

	A	T	G	C
A	2	-2	1	-2
T		2	-2	1
G			2	-2
C				2

Step 1. Index of q

Add indices to all n-grams.

Index	N-gram
1	AC
2	CG
3	GT
4	TA
5	AC

Step 2. Scores of segment pairs and matching n-grams

Calculate scores between the first n-gram AC and all its matching n-grams.

N-gram	Matching n-gram	Score
AC	AA	$2 + (-2) = 0$
AC	AC	$2 + 2 = 4$
AC	AG	$2 + (-2) = 0$
AC	AT	$2 + 1 = 3$
AC	CA	$(-2) + (-2) = -4$
AC	CC	$(-2) + 2 = 0$
AC	CG	$(-2) + (-2) = -4$
AC	CT	$(-2) + 1 = -1$
AC	GA	$1 + (-2) = -1$
AC	GC	$1 + 2 = 3$
AC	GG	$1 + (-2) = -1$
AC	GT	$1 + 1 = 2$
AC	TA	$(-2) + (-2) = -4$
AC	TC	$(-2) + 2 = 0$
AC	TG	$(-2) + (-2) = -4$
AC	TT	$(-2) + 1 = -1$

Use threshold $T = 3$.

N-gram	Matching n-grams	Scores
AC	AC, AT, GC	4, 3, 3

Repeat the same procedure for all n-grams of q and add their indices.

Index	N-gram	Matching n-grams	Scores
1	AC	AC, AT, GC	4, 3, 3
2	CG	CG, TG, CA	4, 3, 3
3	GT	GT, AT, GC	4, 3, 3
4	TA	TA, CA, TG	4, 3, 3
5	AC	AC, GC, AT	4, 3, 3

Step 3. Lookup table of matching n-grams

Transform the table above to create a lookup table of matching n-grams.

Matching n-gram	Indices of q	Scores of segment pairs
AC	1, 5	4, 4
GC	1, 3, 5	3, 3, 3
AT	1, 3, 5	3, 3, 3
CG	2	4
TG	2, 4	3, 3
CA	2, 4	3, 3
GT	3	4
TA	4	4

Step 4. Search

d1: AAAGTG

```
2 hits
GT index: 3, score: 4
TG index: (2, 4), score: (3, 3)
```

Exercise 5.1

Create a lookup table of 2-grams with the indices of q and the scores of segment pairs. Use the threshold T and pre-calculated scores of 2-gram segment pairs.

q: CATG
T: 3

The table below shows pre-calculated scores of 2-gram segment pairs.

Matching n-gram	N-gram		
	CA	AT	TG
AA	0	0	-1
AC	-4	3	-4
AG	-1	0	0
AT	-4	4	-4
CA	4	-4	2
CC	0	-1	-1
CG	3	-4	3
CT	0	0	-1
GA	0	-1	-1
GC	-4	2	-4
GG	-1	-1	0
GT	4	3	-4
TA	3	-4	3
TC	-1	-1	0
TG	2	-4	4
TT	-1	0	0

5.6 Finite-state machine with n-grams

Finite-state machine enables efficient database search by expanding the basic n-gram based search.

Number of potential matching n-grams

The number of potential n-grams increases by the alphabet size and the word size.

DNA

$$C = \{A, C, G, T\}$$

$$\text{Word size } 2 \rightarrow 4^2 = 16$$

Word size 3 $\rightarrow 4^3 = 64$

Word size 12 $\rightarrow 4^{12} = 16,777,216$

Protein

C = {A, R, N, D, C, Q, E, G, H, I, L, M, F, P, S, T, W, Y, V}

Word size 2 $\rightarrow 20^2 = 400$

Word size 3 $\rightarrow 20^3 = 8000$

Finite-state machine

A finite-state machine can be used to scan database sequences instead of using a lookup table. Finite-state machines are usually faster than lookup tables.

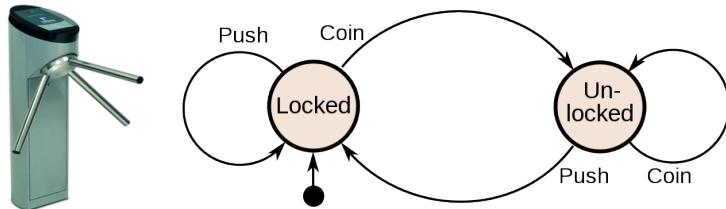


Figure 5.5: Finite-state machine for coin-operated turnstile
(sources: Chetvorno and Sebasgui via Wikimedia Commons)

Example of creating a finite-state machine

q: ACGTAC, Word size: 2, T: 3

Lookup table

Matching n-gram	Indices of q	Scores of segment pairs
AC	1, 5	4, 4
GC	1, 3, 5	3, 3, 3
AT	1, 3, 5	3, 3, 3
CG	2	4
TG	2, 4	3, 3
CA	2, 4	3, 3
GT	3	4
TA	4	4

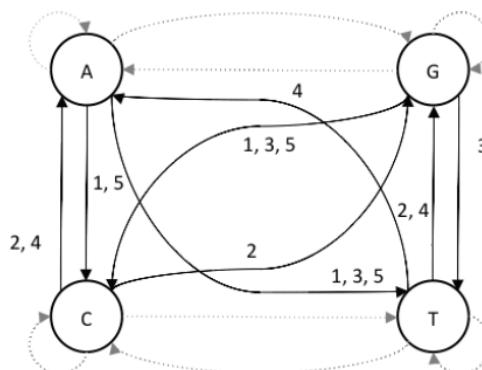


Figure 5.6: Finite-state machine to output the indices of 2-grams

d1: AAAGTG

```
2 hits
GT index: 3
TG index: (2, 4)
```

Exercise 5.2

Create a finite-state machine and use it to find a segment pair.

1. Create a finite-state machine for the lookup table for q: ACGTAC. Add both indices and scores to the edges.

Lookup table

Matching n-gram	Indices of q	Scores of segment pairs
AC	1, 5	2, 2
CG	2	4
GT	3	2
TA	4	0

2. Use the finite-state machine and find a segment pair between q and d: AAAGTG.

6 Evaluation of alignment scores

6.1 Statistical analysis

Statistical tests are performed to give an explanation to observed alignment scores.

Hypothesis testing

- Alternative hypothesis
- Null hypothesis

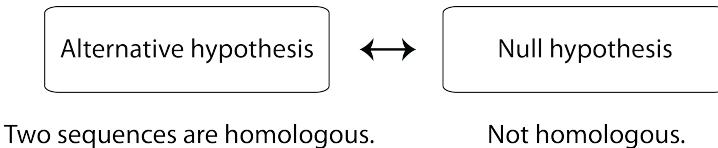


Figure 6.1: The null hypothesis and the alternative hypothesis

P-value

“The p-value is defined as the probability of obtaining a result equal to or more extreme than what was actually observed, assuming that the null hypothesis is true”

– the p-value page on Wikipedia (<https://en.wikipedia.org/wiki/P-value>)

Significance level (α)

The significance level should be chosen to indicate strong/weak evidence against the null hypothesis.

Significance levels 0.05 and 0.01 are often used in life sciences.

- Statistically significant: $\alpha = 0.05$
- Statistically highly significant: $\alpha = 0.01$

Common misunderstandings of p-value

“The p-value is not the probability that the null hypothesis is true or the probability that the alternative hypothesis is false.”

– the p-value page on Wikipedia (<https://en.wikipedia.org/wiki/P-value>)

Underlying (background) score distributions

Table 6.1: Alignment methods and distributions

Method	Underlying distribution
Global alignment	Unknown
Local alignment (ungapped)	Gumbel

6.2 Evaluation of global alignment

The underlying distribution of global alignment scores is unknown.

Random generation of sequences

One needs to consider using the appropriate length and compositions of amino acids or nucleotides needs when creating randomised sequences.

Example

Input sequences

q: ACGT
d: AGTACC

Frequencies: $f_A = 0.2$, $f_C = 0.4$, $f_G = 0.1$, $f_T = 0.3$

Length: 6

d1: CCAGTC
d2: TCACCG
d3: CTTGAA
...
...

Frequency distributions

- Universal (e.g. the whole protein database)
- Global (e.g. protein super families)
- Local (e.g. query and database sequences)

Additional constraints

Constraints on sequences generation are often considered.

- Di-amino acid frequencies
- Sub-region specific frequencies

Non-parametric test and p-value

The simplest non-parametric test is calculating the rank of the score for the original alignment as the p-value.

$$p = (b + 1)/(n + 1)$$

where b is the number of randomly generated scores above the score of the original alignment, and n is the sample size.

N.B. n should be sufficiently large (e.g. >1000) to estimate an accurate p-value.

Example

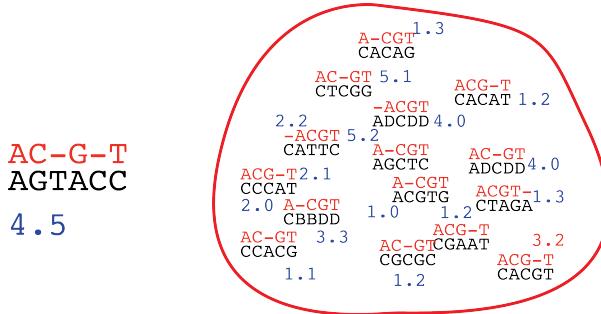


Figure 6.2: Randomly generated sequences and alignment scores

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	1.1	1.3	1.4	1.7	2.1	2.2	2.2	2.3	2.5	2.8	3	3.2	3.3	3.4	3.6	4.2	4.4	4.7	5.2

$$\text{p-value: } (2 + 1)/(20 + 1) = 0.1429$$

- Significance level $\alpha = 0.2$: reject the null hypothesis
- Significance level $\alpha = 0.05$: the null hypothesis is not rejected

Exercise 6.1

1. Calculate the frequencies of nucleotides from the four sequences below.

d1: CCAGC
d2: TCACG
d3: CTTAA
d4: AACAA

$$\text{Frequencies: } \{f_A = \quad, f_C = \quad, f_G = \quad, f_T = \quad\}$$

2. Calculate the p-value of the alignment below.

q: AACG
d: A-CG
Score: 40

Assume that the scores are pre-calculated for the alignments of the query sequence and nine randomly generated sequences as follows. Use them for the p-value calculation.

No.	1	2	3	4	5	6	7	8	9
Score	4	14	33	45	74	76	82	83	94

Using the normal distribution

The underlying distribution of global alignment scores is unknown, but the z-score is sometimes calculated.

The z-score is:

$$z = \frac{x - \mu}{\sigma}$$

where:

μ is the mean of the population.

σ is the standard deviation of the population.

Mean and variance

The sample mean (\bar{x}) and the sample variance (s^2) are calculated as follows.

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$$

$$s = \sqrt{\frac{\sum_{i=1}^n (x_i - \bar{x})^2}{n - 1}}$$

Example of z-score

- \bar{x} : 2.78
- s : 1.4964

$$z = \frac{4.5 - 2.78}{1.4964} = 1.1494$$

The p-value is 0.125196.

6.3 Evaluation of local alignment

The underlying distribution of local alignment scores is an extreme value distribution.

Gumbel distribution

The Gumbel distribution is a member of the extreme value distribution family.

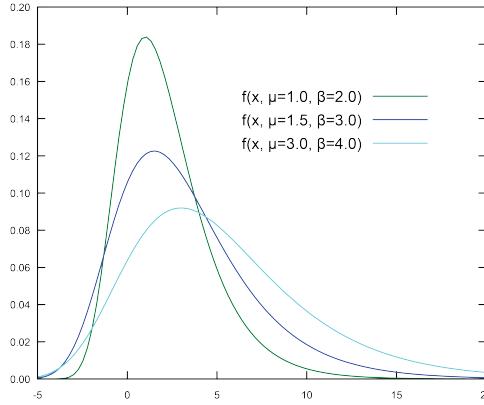


Figure 6.3: Gumbel distribution (source: Herr blaschke, Wikimedia Commons)

The cumulative distribution function (CDF) of the Gumbel distribution:

$$F_Y(y) = \exp[-e^{-\lambda(y-\mu)}]$$

Parameters

- μ : the modal value of the distribution, characteristic value
- λ : a measure of the variance, decay constant

Extreme value distribution

An extreme value distribution is a limiting distribution for the minimum or the maximum of a sufficiently large sample. Ungapped alignments with large sequence lengths are known to have this type of distribution.

Example (m and n are not large in this example)

	A	C	G	C	A	C	G
A	0	0	0	0	0	0	0
C	0	0	0.5	0	0.5	0	0.5
G	0	0	0	1	0.5	0.2	0
A	0	0.5	0	0.5	0.7	0.2	0

CG	CG	GC		AC		
CG	CG	GA	...	CG
1	1	0.2		-0.6		

Parameter estimation

The p-value of the Gumbel distribution can be calculated as:

$$P[Y > y] = 1 - F_Y(y) = 1 - \exp[-e^{-\lambda(y-\mu)}]$$

The parameters μ and λ can be estimated from the arithmetic mean m_Y and the variance σ_Y^2 of the observed sample.

$$\lambda \approx 1.282/\sigma_Y$$

$$\mu \approx m_Y - 0.577/\lambda$$

Example of parameter estimation

Below is the optimal local alignment with the score between q:ACAGACTACTA and d:TCAGACTGGAACCE.

```
CAGACT
CAGACT
Score: 6
```

The mean and the variance of the alignment scores are estimated as follows from randomly generated sequences.

$$m_Y: 1.7221$$

$$\sigma_Y: 1.6025$$

Then, λ and μ are estimated from m_Y and σ_Y .

$$\lambda \approx 1.282/1.6025 = 0.8$$

$$\mu \approx 1.7221 - 0.577/0.8 \approx 1$$

The p-value is approximately 0.0181 when $\lambda = 0.8$ and $\mu = 1$. The test result is statistically significant ($\alpha = 0.05$), and therefore, the null hypothesis is rejected.

Conclusion: The query and the database sequences are homologous (p-value: 0.0181).

6.4 Evaluation of database search

BLAST reports bit scores and e-values as search result. Bit score are calculated from raw scores, and e-values represent the expected numbers of database hits.

Example of BLAST output

- q: HSBGPG Human gene for bone gla protein (BGP)
- d: osteocalcin [Felis catus]
- Sequence ID: XP_003999760.1

	Score	Expect	Identities	Positives	Gaps
	38.5 bits (88)	3.5	19/25 (76%)	20/25 (80%)	0/25 (0%)
Query	677	TAFVSKQEGSEVVKRPRRYLYQWLG AFVSKQEGSEVV+R RRYL LG		751	
Sbjct	36	AAFVSKQEGSEVVRLRRYLAPGLG		60	

Karlin-Altschul statistics

- λ is a scalar parameter for score matrix
- K is a scalar parameter for search space size

BLAST pre-calculates both parameters in a search space independent manner.

Example of Karlin-Altschul statistics

- Matrix: BLOSUM62
- Lambda: 0.267
- K: 0.041

Sequence databases

The NCBI site provides several databases for BLAST search.

- Nucleotide collection (nr/nt)
- Non-redundant protein sequences (nr)

Example of database statistics

- Database: nr
- Number of letters: 41,667,927,126
- Number of sequences: 113,671,629

6.5 Bit score and e-value

BLAST reports bit-scores and e-values that can be used for evaluation on search results.

Bit score

Bit scores are normalized scores that have the same unit (bit). The scores can be comparable even when different scoring schemes are used.

$$S' = \frac{(\lambda S - \ln K)}{\ln 2}$$

$2^{S'}$ indicates the expected search space size that one would find one alignment with score at least S by chance alone.

Example of bit score calculation

- Lambda (λ): 0.267
- K: 0.041
- Score: 88

$$S' = \frac{(\lambda S - \ln K)}{\ln 2} = \frac{(0.267 \times 88 - \ln 0.041)}{\ln 2} = 38.506$$

$$2^{S'} = 2^{38.506} = 390,300,663,957$$

E-value

“The Expect value (E) is a parameter that describes the number of hits one can expect to see by chance when searching a database of a particular size”

- BLAST Frequently Asked questions (<http://blast.ncbi.nlm.nih.gov>)

$$E(S) = Kmne^{-S} = \frac{mn}{2^{S'}}$$

Example of E-value calculation

- n: 25
- m: 41,667,927,126
- Lambda (λ): 0.267
- K: 0.041
- Score: 88

$$E(88) = \frac{41,667,927,126 \times 25}{2^{38.506}} = 2.669$$

Exercise 6.2

- λ : 1.28
- K: 0.5
- m: 1000
- n: 100

Calculate $\exp(-1.28)$ as 0.28.

1. What is the e-value of the score 1?
2. Is the alignment with score 1 likely homologous?

7 Model evaluation

7.1 Evaluation of binary classifiers

Binary classifiers are mathematical or computational models that classify an input data set and produce the output with two labels.

Evaluation of models

The performance of different models can be evaluated under the same test dataset.

- Algorithms
- Scoring schemes
- Statistical analysis

Test data

It should contain both homologous and non-homologous alignments.

- Positive: homologous
- Negative: non-homologous

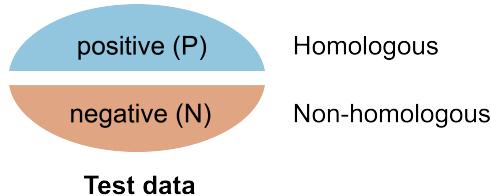


Figure 7.1: Test dataset for homologous and non-homologous

Model output

Different models often output different formats of scores.

- Raw scores, bit scores, z-scores
- P-values, e-values

Threshold values are used to separate the result into positives and negatives.

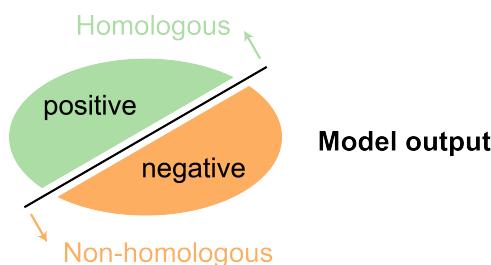


Figure 7.2: Model output for homologous and non-homologous

7.2 Confusion matrix

The output of a model produces two false and two correct classifications.

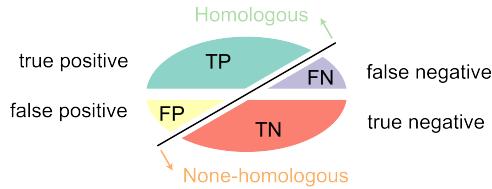


Figure 7.3: Four outcomes of model classification

Example of model output

A test dataset contains 10 positives and 10 negative.

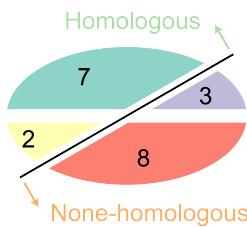


Figure 7.4: An example of the four outcomes

- 7 true positives
- 8 true negatives
- 2 false positives
- 3 false negatives

Confusion matrix

The classification result can be formed into a matrix format.

Table 7.1: Confusion matrix

		Test data	
		Homologous	Non-homologous
Model classification	Homologous	TP	FP
	Non-homologous	FN	TN

Example of confusion matrix

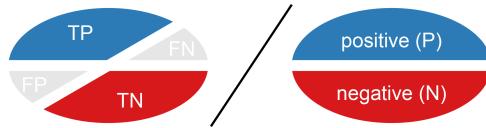
7 TPs	2 FPs
3 FNs	8 TNs

7.3 Basic evaluation measures

Various measures can be derived from the confusion matrix.

Accuracy

$$\frac{TP + TN}{TP + FP + TN + FN} = \frac{TP + TN}{P + N}$$



Error rate

$$\frac{FP + FN}{TP + FP + TN + FN} = \frac{FP + FN}{P + N}$$



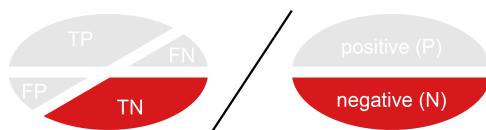
Sensitivity, True positive rate, Recall

$$\frac{TP}{TP + FN} = \frac{TP}{P}$$



Specificity, True negative rate

$$\frac{TN}{FP + TN} = \frac{TN}{N}$$



Precision, Positive predictive value

$$\frac{TP}{TP + FP}$$



7.4 Measures with multiple thresholds

The test data set needs to be sorted by scores, and then confusion matrices can be calculated for multiple threshold values.

Example of making confusion matrices with multiple thresholds

Test data set

Label	N	P	P	N	N	N	P	P	P	N	P	N	P	P	N	N	P	P	N	N
Score	27	4	17	9	11	2	15	19	22	3	23	7	10	25	11	1	26	28	24	3

Sorted test data set

1st threshold (score = 25.5)

2 TPs	1 FPs
8 FNs	9 TNs

2nd threshold (score = 16)

7 TPs	2 FPs
3 FNs	8 TNs

3rd threshold (score = 3.5)

10 TPs	6 FPs
0 FNs	4 TNs

ROC and precision-recall

These measures are based on the confusion matrices of all possible threshold values.

- ROC (Receiver operating characteristic) plot
 - Precision-recall plot

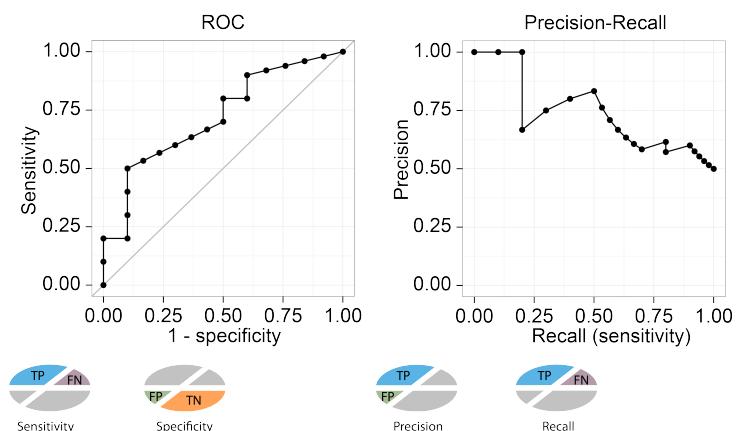
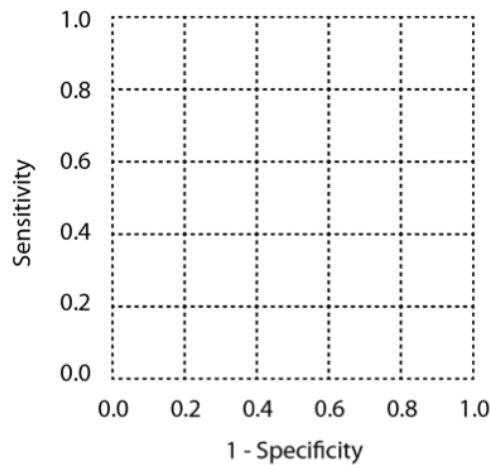


Figure 7.5: ROC and precision-recall plots

Exercise 7.1

Draw an ROC curve for the following specificity and sensitivity values.

Threshold	Specificity	1 - Specificity	Sensitivity
10	1	0	0
9	0.8	0.2	0.8
8	0.6	0.4	0.8
7	0.6	0.4	1
6	0.4	0.6	1
5	0.2	0.8	1
4	0	1	1



Part IV

8 Multiple sequence alignment

8.1 Multiple sequence alignment

A multiple sequence alignment is an effective tool to understand the characteristics of genes by comparing multiple sequences of different species at the same time.

Multiple Sequence Alignment (MSA) for protein sequences



Figure 8.1: An MSA of insulin proteins of seven sequences

Notation of MSA

- \mathcal{A} : Alignment
- m : Number of sequences in \mathcal{A}
- s_j^i : An amino acid or a nucleotide of sequence i and position j (without gaps)
- \bar{s}_j^i : An amino acid or a nucleotide of sequence i and column j (with gaps)

Example of MSA notation

HUMAN: TP-K
MOUSE: TLSK
RAT : TPSK

- m : 3
- s_1^1 : T (1st position of HUMAN)
- s_2^2 : L (2nd position of MOUSE)
- s_4^3 : K (4th position of RAT)
- \bar{s}_3^1 : - (3rd position of HUMAN)

Making an optimal MSA

- Insert gaps to the sequences in \mathcal{A}
- Maximize the score of \mathcal{A}

All combinations of elements per column

The number of all possible combinations of elements per column can be calculated as follows.

$$\sum_{i=0}^{m-1} \binom{m}{i} = 2^m - 1$$

Example of the number of combinations

s_1^1	-	s_3^1	s_4^1	-	-	s_7^1
s_1^2	s_2^2	-	s_4^2	-	s_6^2	-
s_1^3	s_2^3	s_3^3	-	s_5^3	-	-

- $m: 3$
- $2 \times 2 \times 2 - 1 = 7$

Alignment methods

- Dynamic programming with m -dimensional array (deterministic)
- Progressive alignment (heuristics)

SP score

One of the common methods to calculate the score of an alignment is using SP (sum-of-pairs) scores. SP uses pair-wise scores on all possible paired sequences to obtain the final score for the alignment. SP is defined as below.

$$S(\mathcal{A}) = \sum_{i=1}^{m-1} \sum_{j=i+1}^m S(\bar{s}^i, \bar{s}^j)$$

N.B. The score of $S(\bar{s}^i, \bar{s}^j)$ is 0 when both elements are gaps.

Example of SP score

Use the simple scoring scheme and calculate the SP score. Simple scoring scheme: Match: 1, Mismatch: 0, and Gap penalty: 1

Seq1 A-GC
 Seq2 ACG-
 Seq3 A-TC

$$S(\bar{s}^1, \bar{s}^2) = 1 - 1 + 1 - 1 = 0$$

$$S(\bar{s}^1, \bar{s}^3) = 1 + 0 + 0 + 1 = 2$$

$$S(\bar{s}^2, \bar{s}^3) = 1 - 1 + 0 - 1 = -1$$

$$S(\mathcal{A}) = S(\bar{s}^1, \bar{s}^2) + S(\bar{s}^1, \bar{s}^3) + S(\bar{s}^2, \bar{s}^3) = 0 + 2 - 1 = 1$$

Exercise 8.1

Use the simple scoring scheme and calculate the SP score.

Seq1 A-CC

Seq2 C-TC

Seq3 CAG-

8.2 Dynamic programming with m -dimensional array

Dynamic programming (DP) can be extended to handle multiple alignments.

Multi-dimensional array for dynamic programming

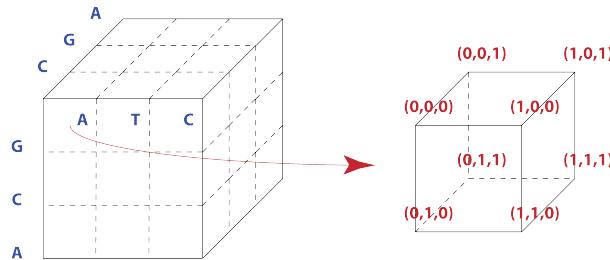


Figure 8.2: A three-dimensional DP array

Example of alignment representation

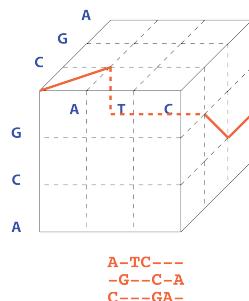


Figure 8.3: An alignment with a three-dimensional DP array

The number of candidate scores for a vertex

The number of the inbound neighboring vertices is defined as follows.

$$\sum_{i=0}^{m-1} \binom{m}{i} = 2^m - 1$$

Example of edges of 3-dimensional cell

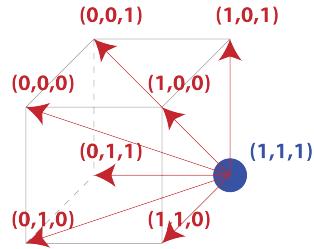


Figure 8.4: An example of seven different edges to one vertex when $m = 3$

A pruning method

- K : a score of an MSA (it does not need to be the optimal)
- ν : current vertex
- S_ν : best score from the start vertex to ν (by DP)
- F_ν : best score from the end vertex to ν (by non-DP)
- if $S_\nu + F_\nu < K$ then ν does not lie on the optimal path

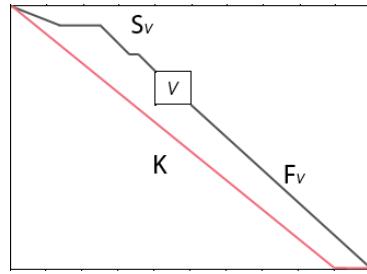


Figure 8.5: Score estimation

Forward-recursion DP for MSA

Instead of looking up inbound neighboring vertices, the forward recursion DP sends the calculated score to all outbound neighboring vertices.

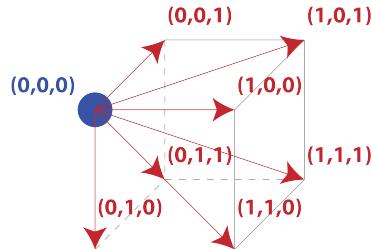


Figure 8.6: Values are forwarded to all outgoing neighbors

9 Phylogenetic tree

9.1 Introduction to phylogenetic trees

A phylogenetic provides additional views on the analysis of multiple sequences.

Elements of phylogenetic tree

- Terminal nodes: sequences, groups of genes, species, operational taxonomic units
- Internal nodes: hypothetical ancestral units
- Edges: often represent distances

Types of trees

- Cladogram or phylogram
- Bifurcating or multifurcating
- Rooted or unrooted

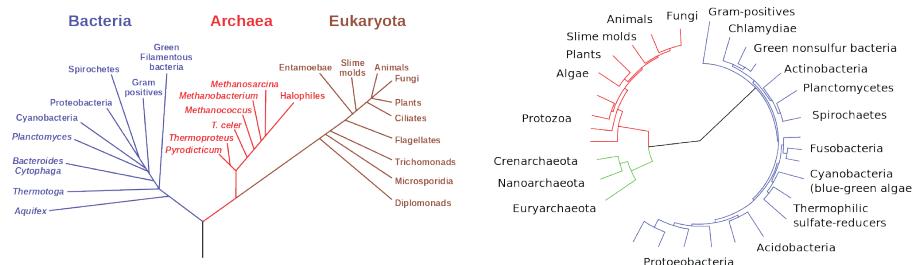


Figure 9.1: Phylogenetic trees (sources: TimVickers, Wikimedia Commons, NASA Astrobiology Institute, Wikimedia Commons))

Rooted and unrooted trees

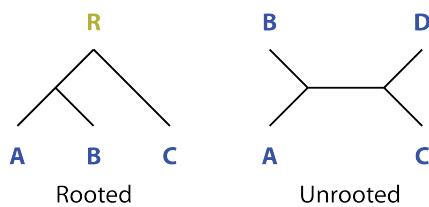


Figure 9.2: A rooted tree with three nodes and an unrooted tree with four nodes

Additive and ultrametric trees

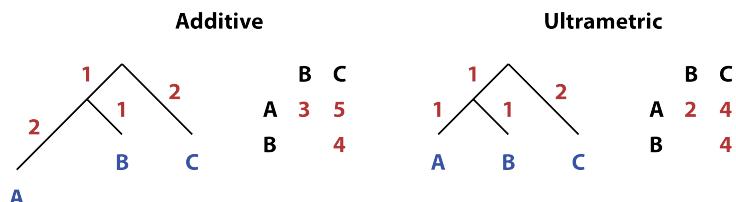


Figure 9.3: Additive and ultrametric trees

An ultrrrametic tree is a special version of additive tree. It assumes that the distances from two sequences to their common ancestor are always equal.

Number of topologically different trees

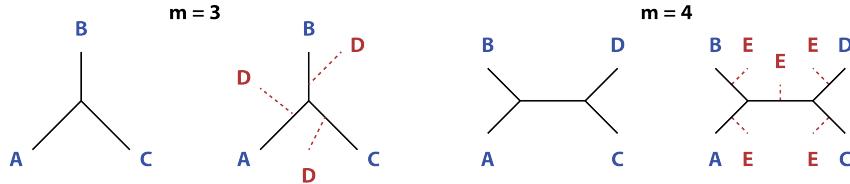


Figure 9.4: Adding one external node to unrooted trees

The number of all possible topologically different unrooted trees $T_{\text{unroot}}(m)$ can be obtained by the double factorial of $2m - 5$.

$$T_{\text{unroot}}(m) = (2m - 5)!! \equiv \frac{(2m - 5)!}{2^{m-3}(m - 3)!}$$

$T_{\text{root}}(m)$ can be calculated from $T_{\text{unroot}}(m)$.

$$T_{\text{root}}(m) = (m - 1) \times T_{\text{unroot}}(m)$$

Example of the number of unrooted trees

What is the number of all possible topologically different unrooted trees when $m = 7$?

$$T_{\text{unroot}}(7) = (2 \times 7 - 5)!! = 9!! = 1 \times 3 \times 5 \times 7 \times 9 = 945$$

or

$$T_{\text{unroot}}(7) = \frac{(2 \times 7 - 5)!}{2^{7-3}(7 - 3)!} = \frac{9!}{2^4(4)!} = 945$$

Exercise 9.1

1. Calculate the number of all possible topologically different unrooted trees when $m = 5$.
2. Construct an additive rooted tree for the distance matrix below. Estimate the edge values by trial and error.

	B	C
A	4	7
B		5

9.2 Tree reconstruction methods

A number of methods have been proposed to reconstruct a phylogenetic tree.

Two types of reconstruction methods

- Distance-based methods
- Character-based methods

Distance-based methods

A distance is a positive value with larger values indicating that two sequences are separated further.

- PGMA (pair-group method using arithmetic mean)
- Neighbor-joining (NJ)

Character-based methods

Character based methods rely on characters (amino acid/nucleotide letters) to reconstruct a tree.

- Maximum parsimony
- Maximum likelihood

Evaluation of reconstructed trees

Bootstrapping is one of the methods to test the robustness of a reconstruct tree by adding noises and comparing the results.

1. Randomly generate a pseudo MSA from the original MSA
2. Reconstruct a tree
3. Repeat the process
4. Compare the trees

9.3 Distance-based methods

PGMA (pair-group method using arithmetic mean) and neighbor-joining are two popular distance-based methods to reconstruct a phylogenetic tree.

UPGMA

UPGMA is an unweighted version of PGMA. It requires the evolutionary rate should be constant (ultrametric). Pairwise distances need to be pre-calculated, for instance, by DP.

- w : A new node
- u, v : Child nodes of w
- m_A The number of original sequences in subtree A
- $D_{A,B}$: Distance between sequences/subtrees A and B

$$D_{w,x} = \frac{m_u D_{u,x} + m_v D_{v,x}}{m_u + m_v}$$

Example of UPGMA

Reconstruct a phylogenetic tree from the pre-calculated distances below.

	B	C	D
A	4	2	5
B		4	8
C			5

Step 1a. Find a pair with the closest distance



Step 1b. Recalculate the distances

$$d_{B,(AC)} = \frac{d_{B,A} + d_{B,C}}{2} = 4, \quad d_{D,(AC)} = \frac{d_{D,A} + d_{D,C}}{2} = 5$$

Step 1c. Update the distance matrix with a new node (AC)

	B	D
(AC)	4	5
B		8

Step 2a. Find a pair with the closest distance



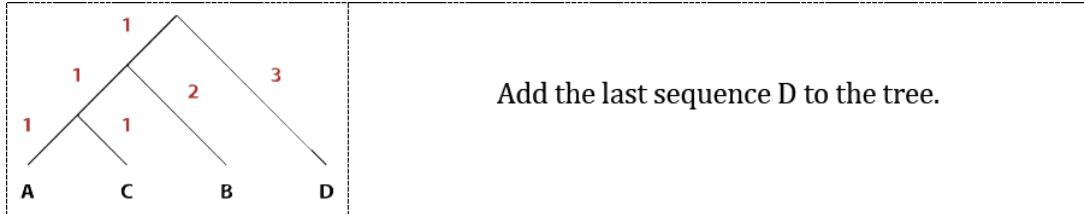
Step 2b. Recalculate the distance

$$d_{((AC)B),D} = \frac{2 \times d_{(AC),D} + d_{B,D}}{3} = 6$$

Step 2c. Update the distance matrix with a new node ((AC)B)

	D
((AC)B)	6

Step 3. Complete the tree



Evaluation on how well fitted to the original distances

Several criteria are available to find the best-fitted tree for a given distance matrix, such as the Cavalli-Sforza and Edwards criterion:

$$\sum_{i,j} (M_{i,j} - d_{i,j})^2$$

where $M_{i,j}$ and $d_{i,j}$ are respectively the original and the calculated pairwise distances.

Example of the Cavalli-Sforza and Edwards criterion

		Original			Reconstructed		
		B	C	D	B	C	D
A	4	2	5	4	2	6	
B		4	8		4	6	
C			5			6	

$$\sum_{i,j} (M_{i,j} - d_{i,j})^2 = 2((5 - 6)^2 + (8 - 6)^2 + (5 - 6)^2) = 12$$

WPGMA

WPGMA is a weighted version of PGMA.

$$D_{w,x} = \frac{D_{u,x} + D_{v,x}}{2}$$

Neighbor-joining (NJ) method

It starts with the initial tree and then select two sequences which results in the smallest sum of edge lengths. It continues until there are no sequences to join. Unlike UPGMA, it does not require a constant evolutionary rate.

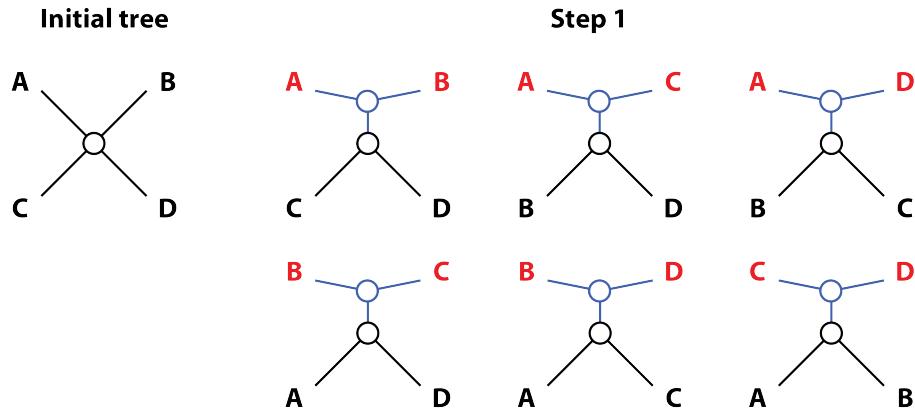


Figure 9.5: All possible combinations of adding one node to the four sequences

Exercise 9.2

1. Reconstruct a phylogenetic tree by using UPGMA and the following pre-calculated distances.

	B	C
A	2	3
B		5

2. Create the distance matrix of the reconstructed tree.

	B	C
A		
B		

3. Calculated the Cavalli-Sforza and Edwards criterion.

9.4 Maximum parsimony

Maximum parsimony is a character-based method to reconstruct a phylogenetic tree.

Definition of parsimony

Definition of parsimony (source: <http://www.merriam-webster.com>)
noun | par·si·mo·ny | \pär-sə-,mō-nē

a : the quality of being careful with money or resources : **thrift**
b : the quality or state of being stingy

Tree search method of maximum parsimony

The maximum parsimony method uses a tree search to find the tree with the minimum number of mutations.

Algorithm 9.1: Maximum parsimony with the minimum union operations

Construct an MSA;

```
foreach column  $c \in MSA$  do
    foreach tree  $t \in$  all possible topologically different trees do
        | Count the number of union operations in  $c$  for tree  $t$ ;
    end
    Add one point to the tree with the minimum union operations;
end
```

Report the tree with the maximum point;

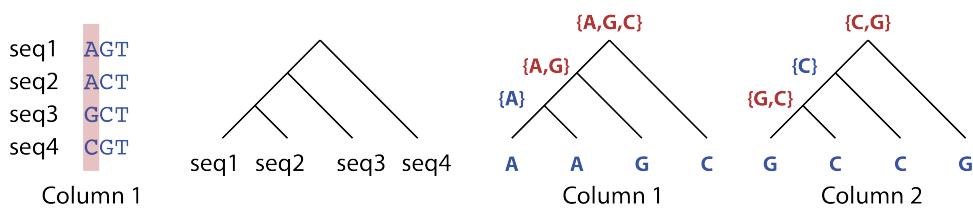
Count the number of union operations

Either intersection or union operation is performed for each internal node.

- $s_i = s_j \cap s_k$ If there is at least one element in s_j and s_k
- $s_i = s_j \cup s_k$ Otherwise

Example of counting the number of union operations

Count the number of union operations for the first and the second columns.



Column 1

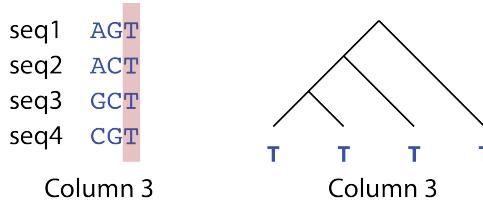
- $A \cap A \rightarrow \{A\}$
 - $\{A\} \cup G \rightarrow \{A, G\}$
 - $\{A, G\} \cup C \rightarrow \{A, G, C\}$
- # of union operations: 2

Column 2

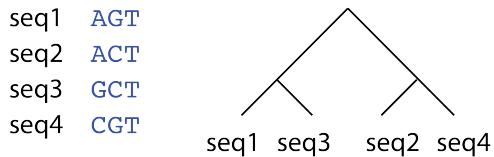
- $G \cup C \rightarrow \{G, C\}$
 - $\{G, C\} \cap C \rightarrow \{C\}$
 - $\{C\} \cup G \rightarrow \{C, G\}$
- # of union operations: 2

Exercise 9.3

- What is the number of union operations for the third column?



- What is the number of union operations for each column?



- Column 1:
- Column 2:
- Column 3:

9.5 Maximum likelihood

The maximum likelihood can be used to reconstruct a phylogenetic tree.

Conditional probabilities

- $P(H|D)$ where D is observed data and H is a hypothesis
- $P(M|D)$ where D is observed data and M is a model

Not easy to solve $P(H|D)$ or $P(M|D)$ directly

Bayes' theorem

$$P(H|D) = \frac{P(D|H)P(H)}{P(D)}$$

- $P(H|D)$, $P(M|D)$: conditional probabilities
- $P(H)$, $P(D)$: marginal probabilities
- $P(H|D)$: posterior probability
- $P(H)$: prior probability
- $P(D|H)$: likelihood
- $L(H|D)$: likelihood function (equivalent with $P(D|H)$)

Maximum likelihood estimate (MLE)

We assume a uniform prior distribution for $P(H)$. Then, we can find the hypothesis that achieves the maximum likelihood $L(H|D)$.

$$\hat{\theta} \in \arg \max_{\theta \in \Theta} L(\theta|D)$$

Example of fair and unfair dice

Roll a die three times, and a 6 comes up three times in a row.

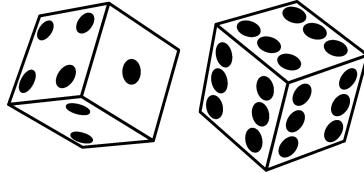


Figure 9.6: Two dice - a fair die and a die with three 6s

Probabilities:

- Three die roles with a fair die $P(D|H = \text{fair}) = (1/6)^3 \simeq 0.028$
- Three die roles with the unfair die: $P(D|H = \text{unfair}) = (3/6)^3 = 0.125$

Maximum likelihood estimate:

- $\arg \max_{\theta \in (\text{fair}, \text{unfair})} L(\theta|D) = \text{unfair}$

Tree search method of maximum likelihood

The maximum likelihood method is also based on tree search. It tries to find the tree with the highest likelihood for a given MSA.

Example of tree search method

Calculate the likelihood $L(T = \text{tree1}|D)$.

Tree: tree1

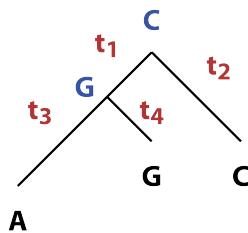


Figure 9.7: Two dice - a fair die and a die with three 6s

Likelihood: $L(T = \text{tree1}|D) = P(D|T = \text{tree1}) = P_{CG}(t1)P_{CC}(t2)P_{GA}(t3)P_{GG}(t4)$

Log-likelihood

- Logarithm is a monotonically increasing function
- $\log(ab) = \log(a) + \log(b)$

Time complexity of tree search

Since it needs to search all possible trees, both the maximum parsimony and the maximum likelihood methods are NP hard problems.

- Exhaustive search: up to 8-10 sequences
- Branch and bound or pruning: up to 15-20 sequences
- Heuristics: 100+ sequences

10 Progressive alignment

10.1 Introduction to progressive alignment

Several heuristic solutions to compute MSAs have been developed to avoid the multi-dimensional DP approach that requires heavy computational power.

Three cases of aligning multiple sequences

- Two sequences, e.g. s^1 and s^2
- One alignment and one sequence, e.g. \mathcal{A}^1 and s^1
- Two alignments, e.g. \mathcal{A}^1 and \mathcal{A}^2

Guiding methods

- Clustering
- Phylogenetic tree

Aligning methods

- Complete alignment
- Pair-guided alignment

Once a gap always a gap

Many progressive alignment procedures use the once a gap always a gap policy, hence it is difficult to fix the errors that are made in early steps.

10.2 Alignment clustering

Alignment clustering can be used even when accurate phylogenetic trees are not available.

Clustering methods

- Linear clustering
- Linkage clustering

Linear clustering

1. Start with an alignment with a single sequence
2. Add a single sequence to the alignment
3. Repeat until no sequence is left

Selection of the next sequence

- Most similar to the one already in the alignment
- Most similar to the average sequence in the alignment

Pseudo-code of linear progressive alignment (general progressive alignment)

Algorithm 10.1: General progressive alignment

U : Set of sequences not aligned

\mathcal{A} : Current alignment

```

 $U \leftarrow \{s_1, s_2, \dots, s_n\};$ 
Choose two sequences  $s$  and  $t$  from  $U$ ;
 $U \leftarrow U - \{s, t\};$ 
 $\mathcal{A} \leftarrow Align(s, t);$ 

```

```

for  $i \leftarrow 1$  to  $n - 2$  do
| Choose a sequence  $s$  from  $U$ ;
|  $U \leftarrow U - \{s\};$ 
|  $\mathcal{A} \leftarrow Align(\mathcal{A}, s);$ 
end

```

Linkage methods

It requires the pair-wise alignment scores of all possible combinations.

- Average linkage
- Maximum linkage
- Minimum linkage

Example of linkage methods

It requires the pair-wise alignment scores of all possible combinations.

Decide two alignments from the three alignments, $\mathcal{A}^1 = \{s^1\}$, $\mathcal{A}^2 = \{s^2\}$, and $\mathcal{A}^3 = \{s^3, s^4\}$, for clustering.

Pair-wise scores

	s1	s2	s3	s4
s1	0	7	5	3
s2		0	4	8
s3			0	2
s4				0

Linkage selection

Average linkage	$S(\mathcal{A}_1, \mathcal{A}_2) = 7$	\checkmark
	$S(\mathcal{A}_1, \mathcal{A}_3) = (5 + 3)/2 = 4$	
	$S(\mathcal{A}_2, \mathcal{A}_3) = (4 + 8)/2 = 6$	

Maximum linkage	$S(\mathcal{A}_1, \mathcal{A}_2) = 7$	
	$S(\mathcal{A}_1, \mathcal{A}_3) = \max(5, 3) = 5$	
	$S(\mathcal{A}_2, \mathcal{A}_3) = \max(4, 8) = 8$	\checkmark

Minimum linkage	$S(\mathcal{A}_1, \mathcal{A}_2) = 7$	\checkmark
	$S(\mathcal{A}_1, \mathcal{A}_3) = \min(5, 3) = 3$	
	$S(\mathcal{A}_2, \mathcal{A}_3) = \min(4, 8) = 4$	

Exercise 10.1

Select two alignments from the three alignments: $\mathcal{A}^1 = \{s^1\}$, $\mathcal{A}^2 = \{s^2\}$, and $\mathcal{A}^3 = \{s^3, s^4\}$ for clustering.

	s1	s2	s3	s4
s1	0	2	2	5
s2		0	4	5
s3			0	1
s4				0

1. Use the average linkage.
2. Use the maximum linkage.
3. Use the minimum linkage.

10.3 Aligning methods

The progressive alignment method keeps combining two alignments until it produces the final alignment.

Aligning methods for progressive alignment

- Complete alignment
- Pair-guided alignment
- Conesus alignment
- Profile alignment

Complete alignment

It uses DP with a two-dimensional array to find gap positions between two alignments.

The score of a cell at column j and row i can be calculated as:

$$S(i, j) = \frac{1}{nm} \sum_{p \in \{p_1 \dots p_n\}} \sum_{q \in \{q_1 \dots q_m\}} R(\bar{s}_i^p, \bar{s}_j^q).$$

where n and m are the size of alignments, and $R(\cdot, \cdot)$ is a score function.

N.B. Notice $R(-, -)$ is always 0.

Example of complete alignment

Combine two alignments, \mathcal{A}^p and \mathcal{A}^q with a simple scoring scheme: Match: 1, Mismatch: -1, and Gap penalty: 1.

\mathcal{A}^p		\mathcal{A}^q
s^{p1} : GAT		s^{q1} : GT
s^{p2} : G-T		s^{q2} : A-

		s^{q1}	G	T
		s^{q2}	A	-
		s^{q3}	A	T
s^{p1}	s^{p2}	0		
G	G			
A	-			
T	T			

DP table

		s^{q1}	G	T
		s^{q2}	A	-
		s^{q3}	A	T
s^{p1}	s^{p2}	0		
G	G			
A	-			
T	T			

Initialization

$$S(0, 1) = \frac{1}{6}(-1 \times 6) = -1$$

$$S(0, 2) = -1 + \frac{1}{6}(-1 \times 4) = -1.67$$

$$S(1, 0) = \frac{1}{6}(-1 \times 6) = -1$$

$$S(2, 0) = -1 + \frac{1}{6}(-1 \times 3) = -1.5$$

$$S(3, 0) = -1.5 + \frac{1}{6}(-1 \times 6) = -2.5$$

Cell update: $S(1, 1)$

$$S(1, 1)^{(1)} = -1 - 1 = -2$$

$$S(1, 1)^{(2)} = -1 - 1 = -2$$

$$\begin{aligned} S(1, 1)^{(3)} &= \frac{1}{2 \times 3} ((R(G, G) + R(G, A) + R(G, A)) + (R(G, G) + R(G, A) + R(G, A))) \\ &= \frac{1}{6} ((1 - 1 - 1) + (1 - 1 - 1)) = -0.33 \end{aligned}$$

DP table after $S(1, 1)$ update

		s^{q1}	G	T
		s^{q2}	A	-
		s^{q3}	A	T
s^{p1}	s^{p2}	0	-1	-1.67
G	G	-1	-0.33	
A	-	-1.5		
T	T	-2.5		

Pair-guided alignment

Pair-guide alignment uses two sequences from two different alignments.

Example of pair-guided alignment

Combine two alignments, \mathcal{A}^p and \mathcal{A}^q .

\mathcal{A}^p

$s^{p1}:$	ACGG
$s^{p2}:$	A-GG
$s^{p3}:$	-CGG

\mathcal{A}^q

$s^{q1}:$	A-GTG
$s^{q2}:$	ACGT-

$s^{p1} \& s^{q1}$		$s^{p1} \& s^{q2}$	
Pairwise	Combined MSA	Pairwise	Combined MSA
ACG-G	ACG-G	ACGG-	ACGG-
A-GTG	A-G-G	ACGT-	A-GG-
	-CG-G		-CGG-
	A-GTG		A-GTG
	ACGT-		ACGT-

Exercise 10.2

Combine two alignments \mathcal{A}^p and \mathcal{A}^q by using the pair-guided approach.

\mathcal{A}^p	\mathcal{A}^q
s^{p1} : TCG	s^{q1} : T-G
s^{p2} : -CG	s^{q2} : ACG
s^{p3} : T-C	

1. Use the alignment between s^{p3} and s^{q2} .

s^{p3} :	T-C-
s^{q2} :	-ACG

10.4 CLUSTAL

CLUSTAL W is the most widely used progressive alignment program.

Original version (CLUSTAL)

- Pairwise alignment between all sequence pairs
- Phylogenetic tree by UPGMA
- Guided by phylogenetic tree
- Align by consensus sequences

CLUSTAL W

- Phylogenetic tree by Neighbor-joining
- Align by profiles

Gap penalty

- Open
- Extend
- End
- Separation

Web version

- <http://www.ch.embnet.org/software/ClustalW.html>

Part V

11 Construction of scoring matrix

11.1 Scoring schemes for protein sequence alignment

Applying an appropriate scoring scheme is critical to create biologically accurate alignments and phylogenetic trees.

Different types of scoring schemes for proteins

- Use of identity
- Use of the genetic code
- Use of a classification of amino acids
- Scoring matrix

Use of identity

The score is calculated by counting identical amino acids. It is equivalent with a simple scoring scheme with match: 1, mismatch: 0, and gap penalty: 0.

Example of “use of identity”

Calculate the SP score by counting identical amino acids.

Seq1 F-NV
Seq2 FPN-
Seq3 FC-V

$$S(\bar{s}^1, \bar{s}^2) = 2$$

$$S(\bar{s}^1, \bar{s}^3) = 2$$

$$S(\bar{s}^2, \bar{s}^3) = 1$$

$$S(\mathcal{A}) = S(\bar{s}^1, \bar{s}^2) + S(\bar{s}^1, \bar{s}^3) + S(\bar{s}^2, \bar{s}^3) = 2 + 2 + 1 = 5$$

Score: 5

Use of the genetic code

The score is based on the distance between two amino acids at the codon level.

Example of “use of the genetic code”

Seq1 FFFF
Seq2 FCNG

Phe (UUU, UUC) & Phe (UUU, UUC): 3
 Phe (UUU, UUC) & Cys (UGU, UGC): 2
 Phe (UUU, UUC) & Asn (AAU, AAC): 1
 Phe (UUU, UUC) & Glu (GAA, GAG): 0

Score: 6

Use of a classification of amino acids

The score is based on the physio-chemical properties. For example, AACH (amino acid class hierarchy) can be used as a scoring scheme.

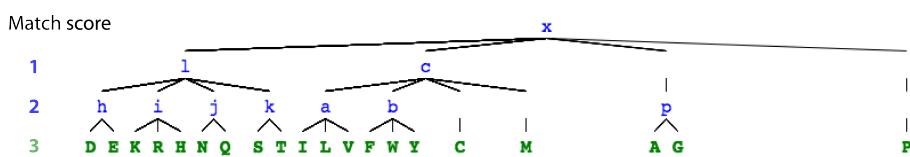


Figure 11.1: Example of amino acid class hierarchy (AACH)

Example of “Use of a classification of amino acids”

Calculate the score by using AACH.

Seq1 DDDP
 Seq2 DEKD

D & D: 3, D & E: 2, D & K: 1, P & D: 0
 Score: 6

Scoring matrix

- DNA/RNA: 4×4
- Protein: 20×20

PAM and BLOSUM

BLAST parameters

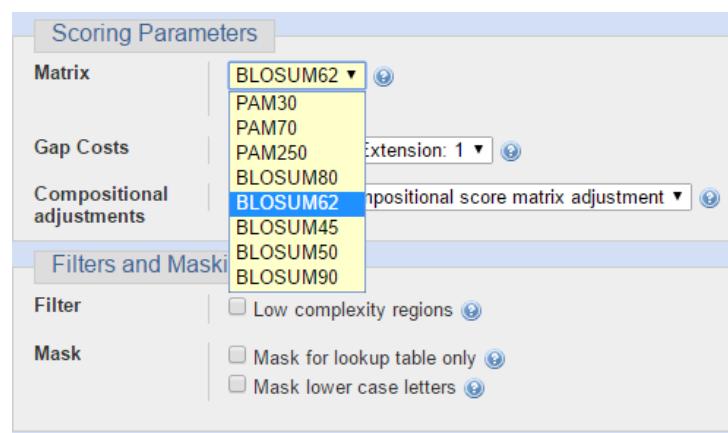


Figure 11.2: BLAST score parameters (source: <http://blast.ncbi.nlm.nih.gov>)

Correspondence between PAM and BLOSUM

PAM 120	PAM 160	PAM 250
BLOSUM 80	BLOSUM 62	BLOSUM 45

Types of substitutions

There are several types of substitutions between two sequences from the common ancestor.

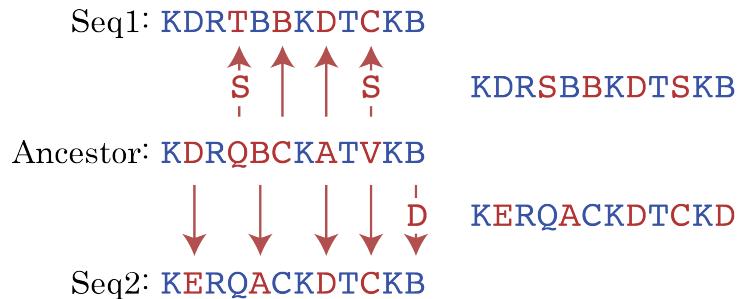


Figure 11.3: Different types of substitutions

Exercise 11.1

Calculate the score of the alignment by using different scoring schemes.

Seq1 K-RI
Seq2 KDCC

- Use the identity.
- Use the genetic code.

K	Lys	AAA, AAG
D	Asp	GAU, GAC
R	Arg	CGU, CGC, CGA
I	Ile	AUU, AUC AUA
C	Cys	UGU, UGC

- Use AACH.

11.2 PAM accepted mutations

PAM is a popular scoring scheme for protein sequence alignments. It is based on substitution matrices created from experiment data.

Accepted point mutations

- Independent of positions and neighbor residues
- Independent from previous mutations at the same position
- Biological clock is assumed (the rate of mutations is constant)

PAM (point accepted mutation)

One PAM means one accepted point mutation per 100 residues.

Resources of constructing a PAM score

- 34 super-families
- 71 groups of homologous sequences (85% identity)

Preparations for constructing a PAM score

Counting the number of mutations is the first step to make a PAM score. Several sub-steps are involved.

- Create a phylogenetic tree
- Estimate ancestor sequences
- Count all occurrences of mutations

Frequencies of estimated mutations

Frequencies of estimated mutations are counted in internal nodes of the reconstructed tree.

f_{ab} : The number of mutations from a to b or from b to a

f_a : The total number of mutations in which a takes part

f : Twice the total number of mutations

Example of frequency calculation

Calculate f_{CA} , f_C , and f from the phylogenetic tree and the table below.

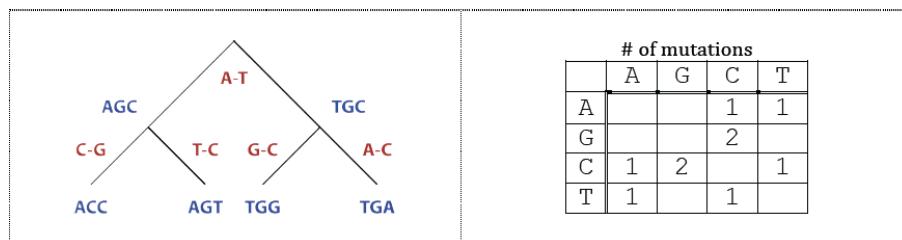


Figure 11.4: Phylogenetic tree and a table of the number of mutations

$$f_{CA} = 1$$

$$f_C = 1 + 2 + 1 = 4$$

$$f = 10$$

Background frequencies

The background probabilities are calculated from the data source.

p_a : The relative occurrence of a in the observed sequences

Example of background frequencies

Calculate p_G from the sequences below.

Seq1 ACC
Seq2 AGT
Seq3 TGG
Seq4 TGA

$$p_G = \frac{4}{12} \approx 0.333$$

11.3 PAM substitution matrix

PAM is based on a substitution matrix created from experimental data.

Relative mutability

The probabilities of amino acid mutations are calculated based on relative mutability.

$$m_a : \frac{1}{100p_a} \times \frac{f_a}{f}$$

Example of relative mutability calculation

- Frequencies of estimated mutations

$f_A: 2$	$f_G: 2$	$f_C: 4$	$f_T: 2$
$f : 10$			

- Background frequencies

$p_A: 3/12$	$p_G: 4/12$	$p_C: 2/12$	$p_T: 3/12$
$100p_A: 23$	$100p_G: 33.33$	$100p_C: 16.67$	$100p_T: 25$

- Relative mutability (1 PAM)

$m_A: 0.008$	$m_G: 0.006$	$m_C: 0.024$	$m_T: 0.008$
--------------	--------------	--------------	--------------

Mutation probability

Mutation probabilities are summarized in a matrix format called substitution matrix.

$$M_{ab} : m_a \times \frac{f_{ab}}{f_a} \quad M_{aa} : 1 - m_a$$

Example of substitution matrix

- Frequencies of estimated mutations

f_{AC} :	1	f_{AT} :	1	f_{GC} :	2	f_{CT} :	1
f_{CA} :	1	f_{TA} :	1	f_{CG} :	2	f_{TC} :	1
f_A :	2	f_G :	2	f_C :	4	f_T :	2

- Relative mutability (1 PAM)

m_A :	0.008	m_G :	0.006	m_C :	0.024	m_T :	0.008
---------	-------	---------	-------	---------	-------	---------	-------

- Mutation probabilities

m_{AC} :	0.004	m_{AT} :	0.004		
m_{GC} :	0.006				
m_{CA} :	0.006	m_{GC} :	0.012	m_{CT} :	0.006
m_{TA} :	0.004	m_{TC} :	0.004		
m_{AA} :	0.992	m_{GC} :	0.994	m_{CC} :	0.976
				m_{TT} :	0.992

- Substitution matrix

	A	G	C	T
A	0.992		0.004	0.004
G		0.994	0.006	
C	0.006	0.012	0.976	0.006
T	0.004		0.004	0.992

Matrices for general evolutionary time

Markov chains can be used to generalize PAM with arbitrary values. For instance, the substitution value for 2 PAM (=2) for amino acids a to b can be calculated as:

$$M_{ab}^2 = M_{ab}M_{bb} + M_{aa}M_{ab} + \sum_{c \notin \{a,b\}} M_{ac}M_{cb} = \sum_{c \in M} M_{ac}M_{cb}$$

Odds matrix

Substitution scores can be transformed to odds values. Odds values O_{ab} are equal to O_{ba} , and therefore an odds matrix is symmetrical.

$$O_{ab} = \frac{M_{ab}}{p_b}$$

when $a \neq b$:

$$O_{ab} = \frac{M_{ab}}{p_b} = m_a \times \frac{f_{ab}}{f_a} \times \frac{1}{p_b} = \frac{1}{100p_a} \times \frac{f_a}{f} \times \frac{f_{ab}}{f_a} \times \frac{1}{p_b} = \frac{f_{ab}}{100fp_ap_b}$$

Transformation of an odds matrix to a score matrix

Odds values can be further transformed to log-odds values.

$$R_{ab} = \log O_{ab} = \log \frac{M_{ab}}{p_b}$$

11.4 BLOSUM

BLOSUM is another popular method of constructing a scoring matrix. It is more useful for diverse sequences than PAM.

Resources of constructing a BLOSUM score

- Scanned very conserved regions of protein families on the BLOCKS database
- Identified 2000 blocks
- A block contains multiple sequences that are highly conserved

Observed mutations

T : The total number of pairs from all blocks.

The number of amino acid pairs of a block with length w and m sequences can be calculated as $1/2wm(m - 1)$.

f_{ab} : The frequencies of an observed pair a and b .

Example of observed mutations

Block1	Block2
AGCC	AGA
TAGC	TAC
AGCC	

$$T = 1/2 \cdot 4 \cdot 3 \cdot 2 + 1/2 \cdot 3 \cdot 2 \cdot 1 = 12 + 3 = 15$$

f_{AA} : 1/15	f_{AC} : 1/15	f_{AG} : 3/15	f_{AT} : 3/15
f_{GG} : 1/15	f_{GC} : 2/15	f_{CC} : 4/15	

Example of observed mutations

- Frequencies of estimated mutations

f_A : 2	f_G : 2	f_C : 4	f_T : 2
f : 10			

Background frequencies

$$p_a = f_{aa} + \sum_{e \neq a} \frac{f_{ae}}{2}$$

$$e_{aa} = p_a \cdot p_a$$

$$e_{ab} = p_a \cdot p_b + p_b \cdot p_a = 2 \cdot p_a \cdot p_b$$

Example of background frequencies

$$p_A = \frac{1}{15} + \frac{1}{2} \times \left(\frac{3}{15} + \frac{1}{15} + \frac{3}{15} \right) = \frac{1}{15} + \frac{7}{30} = \frac{9}{30}$$

$$p_G = \frac{1}{15} + \frac{1}{2} \times \left(\frac{3}{15} + \frac{2}{15} \right) = \frac{1}{15} + \frac{5}{30} = \frac{7}{30}$$

$$p_C = \frac{4}{15} + \frac{1}{2} \times \left(\frac{2}{15} + \frac{1}{15} \right) = \frac{4}{15} + \frac{3}{30} = \frac{11}{30}$$

$$p_T = \frac{0}{15} + \frac{1}{2} \times \left(\frac{3}{15} \right) = \frac{0}{15} + \frac{3}{30} = \frac{3}{30}$$

$$e_{AA} = p_A \cdot p_A = \frac{9}{30} \times \frac{9}{30} = \frac{81}{900}$$

$$e_{AG} = p_A \cdot p_G = 2 \times \frac{9}{30} \times \frac{7}{30} = \frac{126}{900}$$

Scoring matrix

BLOSUM scores are calculated as log ratios of observed and background probabilities.

$$R_{ab} = \log \frac{f_{ab}}{e_{ab}}$$

BLOSUM scores of different distances

One can categorize segments by an identify x to create BLOSUM x.

Example of BLOSUM x

1	AGCC
2	TAGC
3	AGTC
4	AGTT

100% identity

1	AGCC
2	TAGC
3	AGTC
4	AGTT

Number of mutations in the first column:
6 (3 ATs & 3 AAs)

75% identity

	C
1,3	AG C
	T
2	TAGC
4	AGTT

Number of mutations in the first column:
3 (2 ATs & 1 AA)

50% identity

	CC
1,3,4	AGTC
	TT
2	TAGC

Number of mutations in the first column:
1 (1 AT)

12 Sequence profiles

12.1 Sequence profiles and patterns

Protein secondary structures

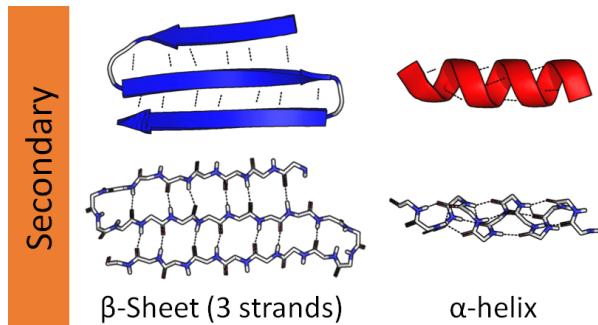


Figure 12.1: Protein secondary structures (source: Shafee, Wikimedia Commons)

Functional regions found in MSA

- <http://www.bioinformatics.org/strap/>
- <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0070843>

Applications of MSAs

- Position weight matrix
- Sequence profile
- HMM profile
- Motifs

12.2 Position weight matrix

A position weight matrix (PWM) is a two-dimensional array that contains position-specific scores. PWMs usually contain no gaps.

Creating a position probability matrix (PPM)

It requires an MSA without gaps.

Example of PPM

Make a PPM from the alignment below.

Seq1 AGT
Seq2 CAG
Seq3 AAT
Seq4 ATT

Position-specific frequencies

	1	2	3
A	3	2	0
G	0	1	1
C	1	0	0
T	0	1	3

PPM

	1	2	3
A	0.75	0.5	0
G	0	0.25	0.25
C	0.25	0	0
T	0	0.25	0.75

From PPM to PWM

Similar to pair-wise scores, log-odds scores can be used for profiles.

$$\text{PWM}_{ar} = \log \frac{\text{PPM}_{ar}}{q_a}$$

q_a : Background probability of a

r : Position in MSA

12.3 Sequence profiles

A protein sequence profile is a two-dimensional array that contains position-specific scores.

Profile values

A profile is based on position-specific weights and a score matrix.

Prof_{ra} : Position-specific score of a at position r

R_{ab} : Pair-wise score of a and b

r : Position in MSA

a, b : Nucleotide/amino acid element

M : All nucleotides/amino acids

W_{rb} : Weight value of b at position r

Profile with linear weights

$$\text{Prof}_{ra} = \frac{1}{m_r} \sum_{b \in M} R_{ba} F_{rb}$$

$$W_{rb} = \frac{F_{rb}}{m_r}$$

F_{rb} : The number of occurrences of b at position r

m_r : The number of residues without gaps at position r

Example of profile with linear weights

Make a profile with linear weights.

Alignment

```
Seq1 AGC
Seq2 -AC
Seq3 AAT
```

Scoring matrix

	A	G	C	T
A	2	1	-3	-2
G	1	3	-2	-1
C	-3	-2	4	1
T	-2	-1	1	2

Scores can be calculated as follows.

$$A1 : 1/2 \times (2 \times 2 + 1 \times 0 + (-3) \times 0 + (-2) \times 0) = 1/2 \times 4 = 2$$

$$G1 : 1/2 \times (1 \times 2 + 3 \times 0 + (-2) \times 0 + (-1) \times 0) = 1/2 \times 2 = 1$$

$$C1 : 1/2 \times ((-3) \times 2 + (-2) \times 0 + 4 \times 0 + 1 \times 0) = 1/2 \times (-6) = -3$$

$$T1 : 1/2 \times ((-2) \times 2 + (-1) \times 0 + 1 \times 0 + 2 \times 0) = 1/2 \times (-4) = -2$$

$$A2 : 1/3 \times (2 \times 2 + 1 \times 1 + (-3) \times 0 + (-2) \times 0) = 1/3 \times 5 = 1.67$$

$$G2 : 1/3 \times (1 \times 2 + 3 \times 1 + (-2) \times 0 + (-1) \times 0) = 1/3 \times 5 = 1.67$$

$$C2 : 1/3 \times ((-3) \times 2 + (-2) \times 1 + 4 \times 0 + 1 \times 0) = 1/3 \times (-8) = -2.67$$

$$T2 : 1/3 \times ((-2) \times 2 + (-1) \times 1 + 1 \times 0 + 2 \times 0) = 1/3 \times (-5) = -1.67$$

$$A3 : 1/3 \times (2 \times 0 + 1 \times 0 + (-3) \times 2 + (-2) \times 1) = 1/3 \times (-8) = -2.67$$

$$G3 : 1/3 \times (1 \times 0 + 3 \times 0 + (-2) \times 2 + (-1) \times 1) = 1/3 \times (-5) = -1.67$$

$$C3 : 1/3 \times ((-3) \times 0 + (-2) \times 0 + 4 \times 2 + 1 \times 1) = 1/3 \times (9) = 3$$

$$T3 : 1/3 \times ((-2) \times 0 + (-1) \times 0 + 1 \times 2 + 2 \times 1) = 1/3 \times (4) = 1.33$$

Calculated profile with linear weights.

	A	G	C	T
1	2	1	-3	-2
2	1.67	1.67	-2.67	-1.67
3	-2.67	-1.67	3	1.33

Non-linear weights

Amino acids/nucleotides occurring many times are “favored”.

$$W_{rb} = \frac{\ln((1 - F_b)/(1 + m_r))}{\ln(1/(1 + m_r))}$$

Amino acids/nucleotides occurring many times are “punished”.

$$W_{rb} = \frac{1 + \ln(1 - F_b)}{1 + \ln m_r}$$

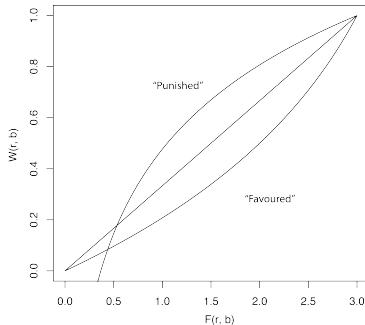


Figure 12.2: Two different weight functions)

Treating gaps

Position-specific gap penalties are usually added to profiles.

12.4 Profile search

A constructed profile can be used to find sequence patterns.

Profile score of a query sequence

The score of a query sequence can be calculated by adding all corresponding position-specific scores.

Example of profile score

Find the best score for $q = AGCT$.

Profile:

	A	G	C	T	Gap	Len
1	5	-5	-2	-1	10	10
2	-2	3	4	-7	10	10
3	1	2	1	-1	5	7
4	-3	3	-2	7	10	10

Score: $5 + 3 + 1 + 7 = 16$

Searching databases with a profile

A dynamic programming method can be used for a profile search.

$$H_{i,j} = \max \left\{ 0, \text{Prof}_{jd_i} + \max \left\{ \begin{array}{l} H_{i-1,j-1} \\ \max_{2 \ll k \ll j-1} H_{i-1,j-k} - g_k^d \\ \max_{2 \ll l \ll i-1} H_{i-l,j-1} - g_l^d \end{array} \right\} \right\}$$

where g_k^d and g_l^P are database and profile gap penalties.

Example of database search with profile

d1 = ACT

Gap penalty: $5 + 2(l - 1)$

Profile:

	A	G	C	T	Gap	Len
1	5	-5	-2	-1	10	10
2	-2	3	4	-7	10	10
3	1	2	1	-1	5	7
4	-3	3	-2	7	10	10

DP table:

	1	2	3	4
A	0	0	0	0
C	0	5	0	1
T	0	0	9	5
	0	0	8	12

H _{1,1} : 5 Prof _{1A} : 5 Diagonal: 5 + 0 Vertical: 5 + (0 - 10) Horizontal: 5 + (0 - 5)	H _{1,2} : 0 Prof _{2A} : -2 Diagonal: -2 + 0 Vertical: -2 + (0 - 10) Horizontal: -2 + (5 - 5)	H _{1,3} : 1 Prof _{3A} : 1 Diagonal: 1 + 0 Vertical: 1 + (0 - 10) Horizontal: 1 + (5 - 7)	H _{1,4} : 0 Prof _{4A} : -3 Diagonal: -3 + 0 Vertical: -3 + (0 - 10) Horizontal: -3 + (1 - 5)
H _{2,1} : 0 Prof _{1C} : -2 Diagonal: -2 + 0 Vertical: -2 + (5 - 10) Horizontal: -2 + (0 - 5)	H _{2,2} : 9 Prof _{2C} : 4 Diagonal: 4 + 5 Vertical: 4 + (0 - 10) Horizontal: 4 + (0 - 5)	H _{2,3} : 5 Prof _{3C} : 1 Diagonal: 1 + 0 Vertical: 1 + (1 - 10) Horizontal: 1 + (9 - 5)	H _{2,4} : 0 Prof _{4C} : -2 Diagonal: -2 + 1 Vertical: -2 + (0 - 10) Horizontal: -2 + (9 - 7)
H _{3,3} : 0 Prof _{1T} : -1 Diagonal: -1 + 0 Vertical: -1 + (0 - 10) Horizontal: -1 + (0 - 5)	H _{3,2} : 0 Prof _{2T} : -7 Diagonal: -7 + 0 Vertical: -7 + (9 - 10) Horizontal: -7 + (0 - 5)	H _{3,3} : 8 Prof _{3T} : -1 Diagonal: -1 + 9 Vertical: -1 + (5 - 10) Horizontal: -1 + (0 - 5)	H _{3,4} : 12 Prof _{4T} : 7 Diagonal: 7 + 5 Vertical: 7 + (0 - 10) Horizontal: 7 + (8 - 5)

Alignment:

```
profile: 1234
d1: AC-T
```

12.5 PSI-BLAST

Position-specific iterated BLAST (PSI-BLAST) is an extension of BLAST. It is much more sensitive than BLAST. It can be used to find distantly related proteins.

Pseudo-code of linear progressive alignment (general progressive alignment)

Algorithm 12.1: Simplified procedure of PSI-BLAST

q: query sequence
t: threshold for significance

```
Q = BLAST(q, t);
do
    Q1 = Reduce(Q);                                // Remove identical segments
    M = MultipleAlignment(Q1);
    P = Profile(M);
    Q = ProfileSearch(P);
    while convergence(Reduce(Q) = Q1) or maximum number of cycles;
```

13 Hidden Markov model

13.1 Hidden Markov model

An HMM (hidden Markov model) is a probabilistic graphical model that assumes a Markov property. It contains two different types of probabilities: transition and emission probabilities.

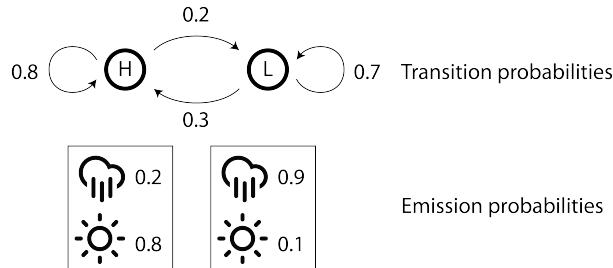


Figure 13.1: HMM for weather conditions

Example of HMM probability calculation

Calculate the probability when the observed weather conditions are (Sunny, Sunny, Sunny) and the corresponding states are (L, H, H). Assume no particular prior distribution for the initial states.

$$\begin{aligned} & p(L) \cdot p(\text{Sunny}|L) \times p(H|L) \cdot p(\text{Sunny}|H) \times p(H|H) \cdot p(\text{Sunny}|H) \\ &= 0.5 \cdot 0.1 \times 0.3 \cdot 0.8 \times 0.8 \cdot 0.8 \\ &= 0.00768 \end{aligned}$$

Search and training of HMM

A dynamic programming is commonly used to search the most probable path, and an EM (Expectation-Maximization) algorithm is often used for training.

- Viterbi algorithm: A dynamic programming for searching HMM
- BaumWelch algorithm: An EM algorithm for training HMM

Exercise 13.1

Use the transition and emission probabilities in the HMM above and calculate the probability when the observed weather conditions are (Rain, Rain, Sunny) and the corresponding states are (H, L, L).

13.2 Viterbi algorithm

The Viterbi algorithm is used to find the most probable path of HMM.

Probabilities of possible paths when the states are unknown

All possible paths need to be considered for an observed instance when the states are unknown.

Example of all possible paths

How many possible paths can one find when there are two states $\{S1, S2\}$ and three observation $\{O1, O2, O3\}$?

The number of all possible paths: 8

$(S1, S1, S1), (S1, S1, S2), (S1, S2, S1), (S1, S2, S2),$
 $(S2, S1, S1), (S2, S1, S2), (S2, S2, S1), (S2, S2, S2)$

Dynamic programming

The Viterbi algorithm is a dynamic programming that can be used to find the most probable path and its probability of an HMM.

Example of dynamic programming

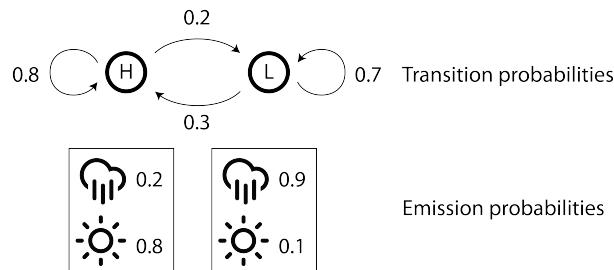


Figure 13.2: HMM for weather conditions

Find the most probable path in the HMM above when the observed weather conditions are (Sunny, Sunny, Sunny). Assume no particular prior distribution for the initial states.

Table 13.1: DP table for the Viterbi algorithm

	H	L
Sunny	$0.5 \times 0.8 = \mathbf{0.4}$	$0.5 \times 0.4 = 0.2$
Sunny	$(H)0.4 \times 0.8 \times 0.8 = \mathbf{0.256}$ $(L)0.2 \times 0.3 \times 0.8 = 0.048$	$(H)0.4 \times 0.2 \times 0.1 = 0.008$ $(L)0.2 \times 0.7 \times 0.1 = 0.014$
Sunny	$(H)0.256 \times 0.8 \times 0.8 = \mathbf{0.16384}$ $(L)0.014 \times 0.3 \times 0.8 = 0.00336$	$(H)0.256 \times 0.2 \times 0.1 = 0.00512$ $(L)0.014 \times 0.7 \times 0.1 = 0.00098$

Exercise 13.2

Use the HMM above and find the most probable path for the following weather conditions. Assume no particular prior distribution for the initial states.

1. (Sunny, Rain).

	H	L
Sunny		
Rain		

2. (Rain, Rain).

	H	L
Rain		
Rain		

13.3 HMM profile

An HMM (Hidden Markov model) profile is similar to a regular profile, but it is based on a probabilistic graphical model.

HMM profile to find sub-strings

An HMM profile represents position-specific probabilities of amino acids.

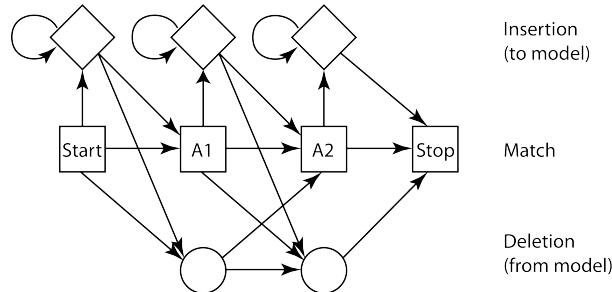


Figure 13.3: An HMM for an alignment of two columns A1 and A2

Example of HMM profile for finding sub-strings

Assume Seq1 = q1 q2 q3 q4 and its path is indicated with solid lines. Create the alignment of Seq1 and the profile.

	Start	Insertion	Match	Deletion	Stop
	-1				
q1		(2 start)			
q2			(4 deletion)	(3 insertion)	
q3		(5 match)			
q4		(6 Insertion)			
					(7 insertion)

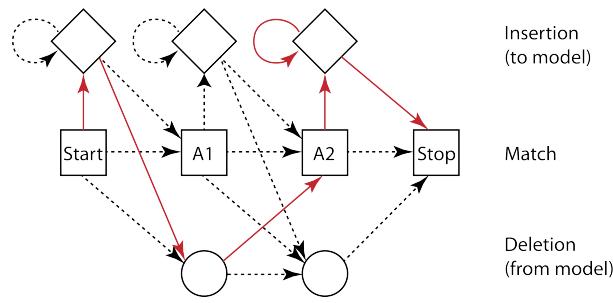


Figure 13.4: An HMM profile to find the optimal alignment

Local alignment:

q1	-	q2	q3	q4
-	A1	A2	-	-

14 Sequence patterns

14.1 Sequence patterns

A sequence pattern can be used to find protein family members. The concept of finding patterns is similar to creating regular expressions.

The PROSITE language

- x: An arbitrary amino acid
- -: Separating elements
- []: A list of amino acids
- {}: A list of not accepted amino acids
- (): A range of en element

Example of PROSITE

Find all matched sequences for the patterns. Assume the alphabet $M = \{A, G, C, T\}$.

Pattern 1: A - [GC] - {AGC}

AGT
ACT

Pattern 2: A - x(1,3) - G

AxG
AxxG
AxG

Exercise 14.1

Find all matched sequences for the pattern. Assume the alphabet $M = \{A, G, C, T\}$.

Pattern: [AC] - {GCT} - x(1, 2) - T

14.2 Pattern comparison

Information theory is used to score a pattern. Calculated scores indicate the specificity of patterns.

Information theory for amino acid distribution

$I(a)$ represents the information content of amino acid a when the probability of a is p_a .

$$I(a) = -\log p_a$$

$H(M)$ represents the entropy of all amino acids.

$$H(M) = - \sum_{a \in M} p_a \log p_a$$

Example of entropy calculation

Calculate the information content of an amino acid A when $p(A) = 0.25$. Use base 2.

$$I(a) = -\log p_a = -1 \times -2 = 2$$

Calculate the entropy of M that contains three pseudo amino acids A, B, C with the probabilities $p(A) = 1/2$, $p(B) = 1/4$, and $p(C) = 1/4$.

$$\begin{aligned} H(M) &= -p(A) \cdot \log p(A) - p(B) \cdot \log p(B) - p(C) \cdot \log p(C) \\ &= (-0.5) \times (-1) + (-0.25) \times (-2) + (-0.25) \times (-2) = 1.5 \end{aligned}$$

Scores of patterns

Patterns can be scored for their specificity.

p'_{ai} represents an adjusted probability of a at position i .

$$p'_{ai} = \frac{p_a}{\sum_{b \in K_i} p_b}$$

I'_{K_i} represents the information content of a set of amino acids K_i at position i .

$$I'(K_i) = H(M) - \left(- \sum_{a_i \in K_i} p'_{a_i} \log p'_{a_i} \right)$$

The information content of a pattern P can be the sum of I'_{K_i} for all i .

$$I(P) = \sum_i I'(K_i) - c \sum_k (j_k - i_k)$$

where c is a constant value for a wildcard region $x(j_k - i_k)$.

Example of pattern specificity scores

Calculate the information content of the following patterns when the probabilities of the pseudo amino acids are $p(A) = 1/2$, $p(B) = 1/4$, and $p(C) = 1/4$. Use $c = 0.1$.

P₁ : A - B

$$I'(K_1) = 1.5 - (-1 \log 1) = 1.5$$

$$I'(K_2) = 1.5 - (-1 \log 1) = 1.5$$

$$I(P_1) = 1.5 + 1.5 = 3$$

P₂ : [AC] - B

$$p'_{A1} = \frac{1/2}{(1/2 + 1/4)} = \frac{1/2}{3/4} = \frac{2}{3}$$

$$p'_{C1} = \frac{1/4}{(1/2 + 1/4)} = \frac{1/4}{3/4} = \frac{1}{3}$$

$$\begin{aligned} I'(K_1) &= 1.5 - \left(-\frac{2}{3} \log \frac{2}{3}\right) - \left(-\frac{1}{3} \log \frac{1}{3}\right) \\ &= 1.5 + \frac{2}{3}(1 - \log 3) - \frac{2}{3} \log 3 \\ &= \frac{13}{6} - \log 3 \end{aligned}$$

$$I'(K_2) = 1.5 - (-1 \log 1) = 1.5$$

$$I(P_2) = 1.5 + \frac{13}{6} - \log 3 = \frac{22}{6} - \log 3 = 2.817$$

P₃ : A - B - x(1, 2)

$$I(P_3) = 3 - 0.1 \times (2 - 1) = 2.9$$

14.3 Pattern discovery

Sequence patterns can be created from MSAs.

Pattern discovery methods

- Comparison-based methods
- Pattern-driven methods

Pivot-based methods

The pivot-based method is one of the comparison-based methods. One sequence is used as pivot, and all the rest of the sequences are compared with this pivot to find similar segments.

Example of pivot-based methods

Find similar segments of size 3 with one edit distance without insertion/deletion for the following sequences. The first sequence should be used as pivot.

Seq1 GATC
Seq2 GGACCG
Seq3 GAG
Seq4 GGGT

Select segments for GAT.

Seq2 GAC
Seq3 GAG
Seq4 GGT

Construct a pattern for the segment of GAT.

G - [AG] - [CGT]

Select segments for ATC.

Seq2 ACC

Construct a pattern for the segment of ATC.

A - [TC] - C

Pratt

Pratt is one of the pattern-driven methods.

$$C_1 - x(i_1, j_1) - C_2 - x(i_2, j_2) - \dots - C_{p-1} - x(i_{p-1}, j_{p-1}) - C_p$$

Example of Pratt

Find a matched pattern for the following three sequences.

Seq1 ACTG
Seq2 ACGT
Seq3 ACT

$$A - x(0, 0) - C - x(1, 2)$$

Pratt procedure

Pratt uses the following three main steps to find the best matched pattern.

- Preprocessing
- Searching
- Specialization