

Chapter 2: Sequence Alignment

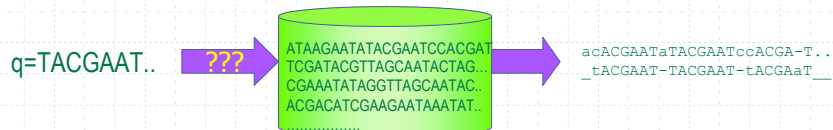
2.3 Searching Sequence Databases; FASTA, BLAST

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The Problem

- How to search a sequence database (DB) for local alignments of a query sequence?
 - E.g., Search a promoter sequence in a DB of 10^5 sequences



- Dynamic Programming is prohibitively complex
- Need techniques that are:
 - Fast: focus search on likely solutions (trade speed for completeness)
 - Tunable: retrieve meaningful alignments (ones with sufficiently high score)
- FASTA & BLAST

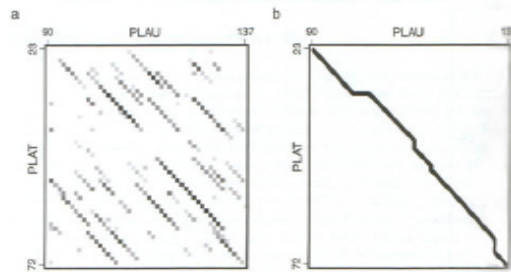
Tutorial: W.R. Pearson "Protein sequence comparison and Protein evolution Tutorial - ISMB2000" (October, 2001)
<http://www.people.virginia.edu/%7Ewrp/papers/ismb2000.pdf>

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Reconsider DP Geometry

- Diagonal matching segments provide the basis for alignments
- Alignment may be viewed as connecting matching diagonals
 - Using mismatched diagonals or horizontal/vertical gapped segments
- Scoring is additive contributions of matching diagonal and connectors
 - Mismatched diagonals or vertical/horizontal gapped segments may reduce the score
 - It is best to focus on high scoring diagonals and use connectors with positive score



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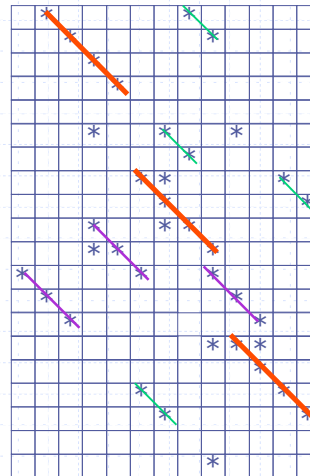
Dot Matrix Heuristics

Rule 1: Find high-scoring diagonals

- Search small diagonal segments
- Extend to max diagonal matches
- Connect diagonals to max score

Rule 2: Focus on meaningful alignments

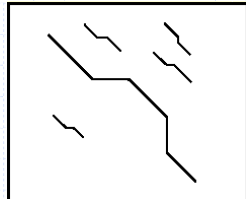
- Filter low-scoring diagonals



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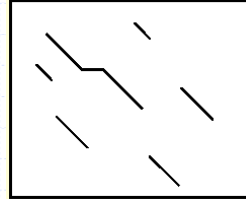
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Tradeoff: Time vs. Optimality



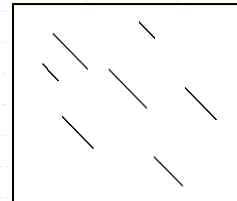
Smith-Waterman

10 min



FASTA

2 min



Blast

20 sec

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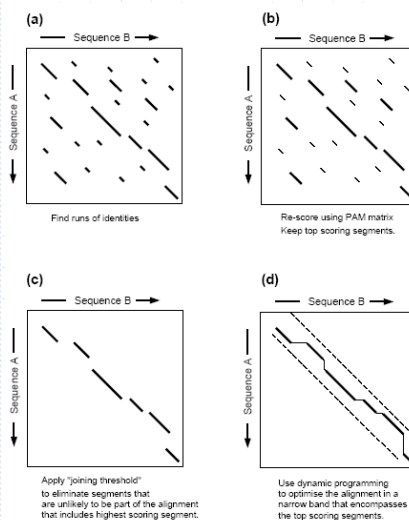
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FASTA

■ Key idea (Pearson & Lipman 88):

- Find short diagonals by indexing the DB
- Extend these to high scoring diagonals
- Use DP to connect them

■ A 4 steps process



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Step (a): Find Diagonal Matches by Indexing

- Key idea: create an index of k-tuples of the DB
 - Scan database to index k-tuples [$k=1..5$]
 - Scan query to index k-tuples
 - Find all diagonal matches of length k by comparing the hash tables
 - Merge these short diagonals into maximal diagonal matches

■ Example:

Database d: TATCGATCGA
Position: 1 2 3 4 5 6 7 8 9 10

Query q: GATCG
Position: 1 2 3 4 5

1. Extract index

TAT	1
ATC	2, 6
TCG	3, 7
CGA	4, 8
GAT	5

Ktup=3 d

GATCG	1
ATCGA	2
TCGAT	3
CGATC	4
GATCG	5

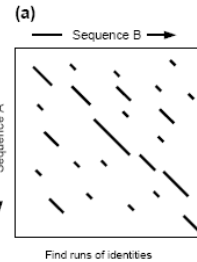
q

Offset=q-d

2. Find matches

GATCG	1
ATCGA	2
TCGAT	3
CGATC	4
GATCG	5

3. Merge diagonal matches



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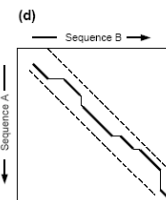
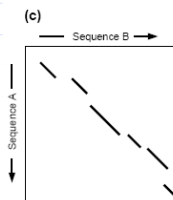
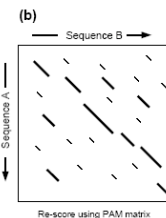
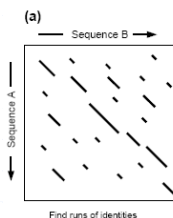
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FASTA Steps (b-d): Optimize Score

b) Filter low-score diagonals

c) Extend diagonals to max score; keep high-scoring segments

d) Use DP for a narrow band around the high scoring segments



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Example

YOUR EMAIL	SEARCH TITLE	RESULTS	PROGRAM	DATABASES
<input type="text"/>	Sequence	interactive	fast3	Protein
			fast3	UniProt
			fast3	UniRef100
				UniParc
GAP PENALTIES		SCORES & ALIGNMENTS	KTUP/HISTOGRAM	DNA STRAND
OPEN	-12	SCORES	10	KTUP
RESIDUE	2	ALIGN	50	HIST
			no	
EXPECTATION		EXPECTATION	SEQUENCE	DATABASE
UPPER VALUE	10.0	LOWER VALUE	default	RANGE
				START-END
				MOLECULE
				TYPE
				Protein

Enter or Paste a **PROTEIN** Sequence in any format:

```

>Mus musculus protein sequence
MSAIIKDDGK  LKIDKENVID  RAQAEAEQK  QAEERAKLE
DELATMGKKI  KGTDELDKY  SEALKDAQK  IELAEEKAD
AEAEVASINR  RIQIVVEELD  RAQERIALA  QLEAEAKAA
DEAEQGVKI  ERAIKDEEK  NELAQIKLE
AKHIAEADK  KYEEVACKIV  IEGIIERTE  ERAELAEKK
SELEELKNV  TANIKLEAQ  AEKYSQKED  YEEIKIILD
KIKAEETRAE  FAERAVAKLE  KTIIDIELI  YAQIKYKAI
SDELDHAIN  MTSI
//

```

Upload a file:

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BLAST: Basic Local Alignment Search

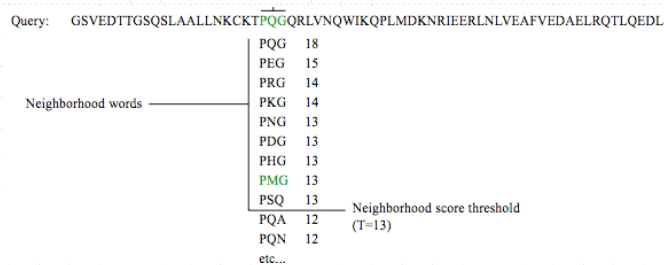
- Altschul & Karlin [1990]; a family of algorithms
- Idea: find matches with significant score statistics
 - Find maximal segment pairs (MSP): segments with significant score
 - Based on extensive statistical theory (summarized soon)
- Base Algorithm:
 - Step 1: index DB for words of size W (W-mers);
index query sequence for W-mers with score >Threshold
 - W= 3 for protein, 11 for nucleotides
 - Step 2: search for matches with high score (HSP=high scoring pairs)
 - Step 3: extend hits to maximal score segments
 - Step 4: report matches with score above S

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BLAST Step 1-3: Finding Short High-Scoring Pairs (HSP)

- Create an Index of W-mers for database & query
 - For proteins W=3 means a dictionary of $20^3=8000$ words
- Match W-mers that score above a threshold T
 - FASTA searches for exact matches of ktuples
 - BLAST, in contrast, searches for high scoring pairs (HSP)
 - Key idea: exploit the fast part of the search to max the score rather than push the maximization for later, slower, phases

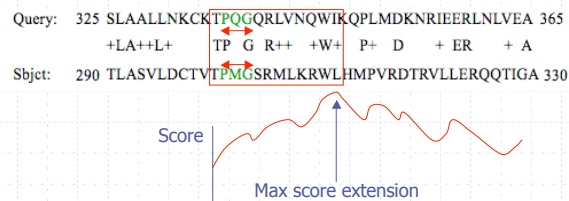


From A. Baxevanis: "Nucleotide and Protein Sequence Analysis I"
via Kellis & Indyk, MIT, "BLAST & Database Search, Lecture 2"
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Blast Steps 3-4: Extending Short HSPs

- The short HSPs are extended to increase the score



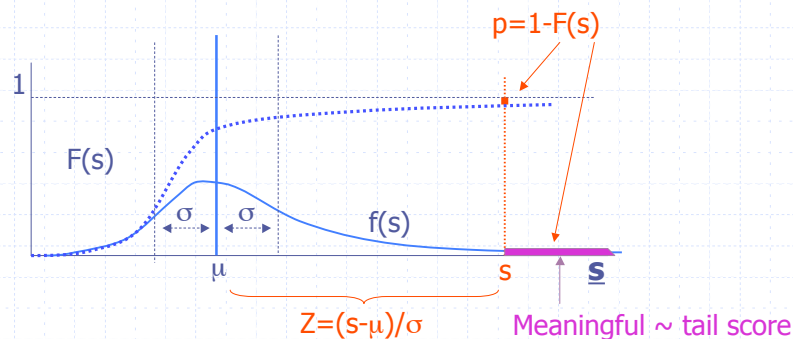
- Report above threshold HSPs and their scores

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Distinguishing Meaningful From Random

- “meaningful” ~ score is at the tail of the distribution
- Z-Score: $Z(s) = (s - \mu) / \sigma$ $[z(s) \geq 7 \rightarrow d \text{ is meaningful}]$
- P-Score: $p = p[\underline{S} > s] = 1 - F(s)$ $[p \leq 0.02 \rightarrow d \text{ is meaningful}]$



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How Significant is An Alignment?

- Key idea: Consider the highest matching score \underline{S} as a random variable and use Z-score to determine whether an alignment is meaningful
- Strategy:
 - Define the highest matching score \underline{S} as a random variable
 - Let q be a query and d a sequence from a database D
 - Define $\underline{S}(q, d) = \text{Max} \{ s(q, q') \}$ where $s(q, q')$ is the score of an alignment of q and a subsequence q' of d
 - \underline{S} is a random variable defined over the space of local alignments $\{(q, d)\}$
 - Suppose \underline{S} has mean μ and standard deviation σ
 - Use Z-score, $Z(s) = (s - \mu) / \sigma$ to determine significance of a local alignment scoring s
 - For protein sequences $Z(s) > 7$ is considered significant
- Key challenge: how do we determine the distribution of \underline{S} ?

Karlin, S., and Altschul, S. F. (1990) "Method for assessing the statistical significance of molecular sequence features by using general scoring schemes," *Proceedings of the National Academy of Science, USA* 87, 2264-2268.

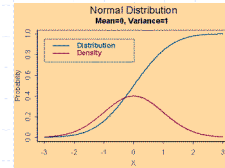
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What Is The Distribution of S ?

- Consider the scores $\mathbf{S}'(q, q')$ for N random sequences q'
 - The score $\mathbf{S}'(q, q') = \sum_k s(q_k, q'_k)$ is the sum of independent random variables
 - For sufficiently long sequences $\underline{\mathbf{S}}(q, q')$ is normally distributed

$$f(x; \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left(-\frac{(x - \mu)^2}{2\sigma^2}\right).$$



- BLAST maximizes the score: $\underline{\mathbf{S}}(q, d) = \text{Max}\{\mathbf{S}'(q, q') : q' \text{ is sub of } d\}$
 - $\underline{\mathbf{S}}$ has extreme order distribution: $F(x) = P[\underline{\mathbf{S}} < x] = P[\mathbf{S}'(q, q') < x \text{ for all } q' \text{ sub of } d]$
 - Extreme order theory: $F(x)$ is exponentially distributed
- Karlin-Altschul Statistics: $F(x) = P[\underline{\mathbf{S}}(q, d) < x] \sim 1 - \exp[-(Kmn)\exp(-\lambda x)]$
 - Here $m=|q|$, $n=|d|$, λ and K may be computed from the scoring statistics
 - A good approximation for aligning sequences of length m, n is: $\lambda \sim \log(mn)$, $\sigma \sim 1$

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Application Example

- Consider local alignment of protein sequences (q, d)
 - Suppose the best local alignment is:
 $X' = \text{FWLEVEGNSMTAPTG}$
 $Y' = \text{FWLDVQGDSMTAPAG}$
- Compute the score of this local alignment:
 - Using PAM250, the score is $s=73$; normalized to log2 scale this gives $s' = \log(s) = 24.3$
- Compute the parameters of a random scoring normal distribution:
 - Suppose $|q|=|d|=256$
 - The normal distribution for random scoring: $\mu = \log(mn) = \log(256 \cdot 256) = 16$, $\sigma = 1$;
- Compute
 - $Z(s') = (24.3 - 16)/1 = 8.3 \text{ bits} > 7 \rightarrow \text{alignment is significant}$

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Conclusions

- Indexing the sequence DB can accelerate alignment
 - FASTA: accelerate search for diagonal matches, then optimize alignment
 - BLAST: accelerate both, search for matches and optimizing the alignment
- FASTA innovations:
 - Exploit the geometry of diagonals
 - Grow alignments from seeds
- BLAST innovation: recast alignment as a pure search
 - Use scoring statistics as a mere guideline for the search
 - Contrast with DP use of (inexact) scoring to solve an exact optimization problem