Bioinformatics algorithms

Renew of algorithmic techniques A first problem

Recap of 1st time: · T did battle with (+ lost). technology · Syllabus review · Correctness

· Some runtimes



Efficiency (2.7 ~ 2.8 in book) · Exact speed can depend on many variables besides the algorithm.

Issues at play:

- machine

-language - actual algorithm

Alternative approach: Count primitive operations, which are smallest operations. In addition: generally only examine worst case running time. Why? more do able or more pessimistic

Now: How to actually compare? - Remember small difference may be due to processor, language, or any number of things that laren't dependent on the algorithm. - Also: need a way to account for inputs changing eg searching a list Big-O



Common run fres $(\mathbf{D} \alpha \mathbf{D})$ $() \circ (\log n)$ $(3) \circ (n)$ $\begin{array}{c} (4) O(n \log n) \\ (5) O(n^2) \end{array}$ (polynomial) And: $O(2^n)$ O(n!)O(nⁿ) $O(n^2)$ O(n) O(√n) Time O(log n) O(1) Input (number)

When these appear: • For loop: often O(h) = 1=1+++1 • Nested for loops; 1e: =1 =1 for $i \neq 1$ to nfor $i \neq 1$ to ifor $j \neq 1$ to i i = 1 total +j oci $\sum_{i=1}^{n} (\sum_{j=1}^{n})^{-1} = \sum_{i=1}^{n} (\sum_{j=1}^{n})^{-1} = \frac{n(n-1)}{n} = O(n)$ Both of these are examples of Heration. (ie using loops). Common ~ useful!

Example: Sorting.

Sorting: Input: n distinct integers AEL. n] Carray Contput: reordering of A Into BEL. n] s.t. ti, BELI < BELI Vi SELECTION SORT (A, n): return A Lto n A ETMIN (A E n) return A A[i] + A[j] TGETMIN (A, first, last): Offinder first Officer Konfirst to last If A[K] < A[index] Index K return index Correctness? At the end of iteration i of Runtime? My loop, the ith element is $\sum_{i=1}^{n} (n-i) = \sum_{i=1}^{n} (-\alpha_i)$

Recursion: an algorithm that calls itself





But stop for a minute:







The Tower of Hanoi algorithm; ignore everything but the bottom disk

Recersive algorithm:

 $\frac{\text{HANOI}(n, src, dst, tmp):}{\text{if } n > 0}$ HANOI(n - 1, src, tmp, dst) move disk n from src to dst HANOI(n - 1, tmp, dst, src)

Runtime? (# moves) H(1)=1 H(n) = H(n-1) + 1 + H(n-1)=2H(n-1)+12-> 2n-1 exponentia)

Sometimes both recursion and iteration make sense: Fibonacci numbers: to=0 $F_{n} = I$ $F_{n} = F_{n-1} + F_{n-2}$ 0,1,1,z,3,5,8,13,... 2 ways to compute: Rectib (n): ection (n) if n=0 or n=1 return n else return RecFib(n-1) + RecFib(n-2) Iterative Fib(n): Create a blank array Holon] F[i]= F[i]= F[i]= F[i]= F[i]]= F[i-1]+F[i-2] 2+2-2

Compare: -Both are correct -Efficiency? $\frac{\text{RecFib:}}{R(n) = R(n-1) + 1}$ R(n-2) + 1= R(n-2) + R(n-3) + 1'+ R(n-2) + 1= 2R(n-2) + R(n-3) + 2 $=O(p^n)$ exponential Iterative Fib: O(n)

Rest of Ch 2:

· More big-O examples Brief overview of types of algorithmic approaches:
exhaustive search - branch + bound = 3 pargraphs - gready - dynamic programing - divide + conquer - ML - Randomized (Useful to read, but I'll discuss these as we see bioinformatics examples in more detail.)

Ch 3: Molecular Biology Primer Biology

(This was super useful for me-but I suspect you all know it. Please skim, just so you know the terms I'll be using.)

Also: Ch2+3 are background for your first essay. (due in 1 week)



Figure 4.1 Different methods of digesting a DNA molecule. A complete digest produces only fragments between consecutive restriction sites, while a partial digest yields fragments between any two restriction sites. Each of the dots represents a restriction site.

Turning this into a concrecte problem: Partial digest problem (PDP): Dh. A muttet: ex: {2,2,2,3,3,4,5} <u>Dfn</u>: <u>Tf</u> X is a set of n points on a line segment, $\Delta X = \{ x_i - x_j : | = i < j \le n \}$ Asido: How big is ΔX ? (n) - n(n-1) - n. (2) - 21(n2)! Ex: Let X = 20, 2, 4, 7, 105. $\Delta \chi = \{2, 2, 3, 3, 4, 5, 6, 7, 8, 10\}$ $= \{2, 32, 4, 5, 1, 7, 8, 10\}$ PDP: Given ΔX , reconstruct X

Partial Digest Problem: Given all pairwise distances between points on a line, reconstruct the positions of those points. **Input:** The multiset of pairwise distances L, containing $\binom{n}{2}$ integers. **Output:** A set X, of n integers, such that $\Delta X = L$ Aside: CS people also (We called it the Turnpike problem.) Note: These aren't unique! Given a set A + value V, let A @ Ev] = {a+v: a EA? Then $\Delta(A + \epsilon v_1) = \Delta A$ Ex: A= 20, 2, 4, 7, 103 A @ 100 = ~ 100, 102, 104, 107, 1105

In general 2 sets A+B are called homometric if DA=DB Can show that if U+V are two sets of numbers, $U \oplus V = \sum u + v : u \in U, v \in V$ $+ U \Theta V = \{u - V : u \in U, v \in V\}$ are alweys homometric. Ex: U= 26,7,93 V = E-6,2,-65 $\begin{array}{c|cccc} U \oplus V & -6 & 2 & 6 \\ \hline 6 & 0 & 8 & 12 \\ \hline 7 & 1 & 9 & 13 \\ 9 & 3 & 11 & 15 \end{array}$ $\begin{array}{c|cccc} U \ominus V & -6 & 2 & 6 \\ \hline 6 & 12 & 4 & 0 \\ \hline 7 & 13 & 5 & 1 \\ 9 & 15 & 7 & 3 \end{array}$ Both have $\Delta(U \oplus V) = \Delta(U \oplus V)$ $= 2 1_{4}, 2_{4}, 3_{4}, 4_{5}, 5_{2}, 6_{2}, 7_{2},$ 8_3 , 9_2 , 10_2 , 11_2 , 12_3 , 13, 14, 15PDP asks for one X, but biologists often want all X. We'll always include 0. Note:



Improved brute force: Do we really read all items = M? Observation: If L obes not contain the value (), then y can't be in X, Why? Spps it were: Result: ANOTHERBRUTEFORCEPDP(L, n) $M \leftarrow$ maximum element in L 1 for every set of n-2 integers $0 < x_2 < \cdots < x_{n-1} < M$ from L 2 3 $X \leftarrow \{0, x_2, \dots, x_{n-1}, M\}$ Form ΔX from X 4 5 if $\Delta X = L$ return X7 output "No Solution" Runtire: (L) & LCCM Correctness: trying everything

Next time: A more practical approach of then on to moth f finding