Today's Lecture

• Algorithm generalities / complexity

• Directed graphs, WDAGs

Genomes are big but computers are fast!

- Typical laptop clock speed: ~ 1 Ghz
 Potentially billions of CPU instructions / sec
- Important practical consideration in dealing with genome-scale data sets: compared to CPU operations,
 - *non-cache memory accesses* are very slow (100s of cycles)
 - *disk accesses* are even slower (1000s of cycles)
 - for both, random (non-sequential) accesses are much slower than sequential accesses

Algorithms – Some General Remarks

- The most widely used algorithms are the oldest
 - e.g. sorting lists, traversing trees, dynamic programming.

The challenge in CMB is usually *not* finding *new* algorithms, but rather

- finding *biologically appropriate applications* of old ones.
- Often prefer
 - suboptimal but easy-to-program algorithm over more optimal one
 - or space-efficient algorithm over time-efficient one.
- *Probabilities* are important in
 - interpreting results
 - guiding search

The most powerful analyses generally involve probabilistic models, rather than deterministic ones.

Algorithmic Complexity

- Basic questions about an algorithm:
 - how long does it take to run?
 - how much space (RAM or disk space) does it require?
- Would like precise function f(N), e.g.

 $f(N) = .05 N^3 + 50.7 N^2 + 6.03 N$

for

- running time in secs, or
- space in kbytes,
- as function of the size N of input data set.
- But
 - tedious to derive &
 - depends on (often uninteresting though important!) hardware & software implementation details.

• Instead, more customary to give "the" *asymptotic complexity*, i.e. expression *g*(*N*) such that

 $C_1 g(N) < f(N) < C_2 g(N)$

for some constants C_1 and C_2 , and N large enough.

- This is written O(g(N)), where notation O() means "up to an unspecified multiplicative constant".
 - e.g. for the f(N) above, the dominating term for large N is .05 N^3 , so
 - can take $g(N) = N^3$
 - asymptotic complexity = $O(N^3)$.

- Can be misleading, since
 - for small N a different term may dominate
 - (e.g. 2^d term in above example much more important for *N* < 1000)
 - size of constant may be quite important
 - (big difference between .05 and 5,000,000!)
 - e.g. BLAST and Smith-Waterman both $O(N^2)$, but size of constant enormously different
 - *but* very useful as rough guide to performance.

• Cache misses (non-cache memory accesses) and disk accesses often dominate running time, yet are 'invisible' to complexity analysis (because affect constant factor only)

- Another limitation to complexity analysis:
 - time or space requirement may depend on specific characteristics of input data.
- Usually give "worst case" complexity

 applies to the worst data set of a given size,

but

- in biological situations the *average biologically* occurring case is
 - more relevant
 - often much easier than worst case (which may never arise in practice), or even "average case" in some idealized sense.

- Proof that a problem is *NP-hard*
 - (has complexity very likely greater than any polynomial function of *N* and therefore effectively unsolvable for large *N*)

can be useful in guiding search for more efficient algorithms

but can also be misleading, since

- we need *some* solution anyway, for data sets occurring in practice
- average *biologically relevant* case may be quite manageable

Directed Graphs

- A *directed graph* is a pair (V, E) where
 - *V* is a finite set of *vertices*, or *nodes*.
 - -E is a set of ordered pairs (called *edges*) of vertices in *V*.
- An edge (v_i, v_j) is said to *leave* v_i and to *enter* v_j . - $(v_i \text{ and } v_j \text{ are vertices})$
- *in-degree* of a vertex = # edges entering it;
- *out-degree* = # edges leaving it.

Example:

- $V = \{1, 2, 3, 4, 5, 6\},\$
- $E = \{(1,2), (1,3), (2,4), (4,1), (5,3), (3,1)\}$
- Vertex 3 has in-degree 2 and out-degree 1.



Paths and Cycles

- A *path* of *length k* in *G* from *u* to *u*' (vertices) is
 - a sequence *P* of vertices (v_0, v_1, \ldots, v_k) such that
 - $v_0 = u$,
 - $v_k = u$ ', and
 - (v_{i-1}, v_i) is an edge for i = 1, 2, ..., k.
- A path can have length 0.
- We write |P| = k.
- A *cycle* is a path of length ≥ 1 from a vertex to itself.
- In example at right,
 - -(1,2,4) is a path,
 - -(1,3,5) is not, and
 - -(1,2,4,1) and (1,3,1) are cycles.



Paths and Cycles (cont'd)

- Can join
 - any path (u, ..., v) from u to v, to
 - any path (v, ..., w) from v to w
 - to get a path (u, ..., v, ..., w) from u to w.

DAGs

- A *directed acyclic graph* (DAG) is a directed graph with no cycles.
- In a DAG, for distinct nodes v_i and v_j , we say
 - $-v_i$ is a *parent* of v_j , and v_j is a *child* of v_i , if
 - there is an edge (v_i, v_j)
 - $-v_i$ is an *ancestor* of v_i , and v_i is a *descendant* of v_i , if
 - there is a path from v_i to v_j
- In a DAG the length of a path cannot exceed |V| 1,
 (where |V| = total # vertices in graph)

because

- in a path of length $\geq |V|$,
 - at least one vertex *v* would have to appear twice in the path;
- but then there would be a path from *v* to *v*, i.e. a cycle.

Structure of DAGs

- Define the *depth* of a node v in V as:
 the length of the longest path ending at v;
 by above, the depth is well-defined and ≤ |V| 1.
- Every descendant w of a node v has higher depth than v: If
 - -(u, ..., v) is path of length n = depth(v) ending at v, and

$$-(v, ..., w)$$
 is path from v to w,

then (u, ..., v, ..., w) is a path of length > n ending at w, so depth(w) > n.

Structure of DAGs (cont'd)

- Every node v of positive depth has a parent of depth exactly one less:
 - Let (u, ..., v', v) be path of length n = depth(v) ending at v.
 - Then v' is a parent of v.
 - Since (u, ..., v') has length n 1, depth $(v') \ge n 1$.
 - Since also depth(v') < n (because v is a descendant of v'), depth(v') is exactly n - 1.
- The nodes on any path are of increasing depth.

Structure of DAGs (cont'd)



Important special cases:

- A (rooted) tree is a DAG which
 - has unique depth 0 node (the root), and
 - every other node has in-degree 1
 - (i.e. has a unique parent, of depth one less than that of the node).
- A *binary tree* is a tree in which
 - every node has out-degree at most 2.
- A *linked list* is a tree in which
 - every node has out-degree at most 1
 - or equivalently, a DAG in which \exists at most one node of each depth

binary tree

linked list





Remarks on Depth Structure

- For *dynamic programming* algorithm
 - we need an order $v_1, v_2, ..., v_n$ for the vertices
 - (not a path!)

in which parents appear before children.

– From the above, *depth order*

• (in which depth 0 nodes are listed first, then depth 1 nodes, etc.) is such an order.

- In general there are many other such orders.
- We haven't given constructive procedure for finding the depths of all vertices.
 - For an arbitrary DAG, can be done in O(|V| + |E|) time;
 - we omit algorithm, since for DAGs related to sequence analysis, the depth structure is obvious.

Weighted Directed Graphs

- A weighted directed graph is
 - a directed graph (V, E) together with
 - a function w from E to the real numbers,
 - i.e. with a numerical *weight* w(e) (which may be positive, negative, or 0) associated to each edge e.
 - A weighted DAG is called a WDAG.
- The (*sum*) *weight of a path* is defined to be the sum of the weights on the edges of the path.
- Similarly, the *product weight of a path* is the product of the edge weights
 - usually only consider this when all weights are non-negative.
- weight of a path P is written w(P)
- For a path of length 0 (i.e. consisting of a single vertex):
 - the sum weight is 0
 - the product weight is 1