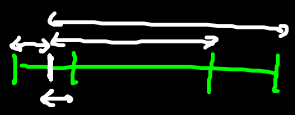
Theorem

For an input with $\binom{n}{2}$ elements the worst case running time of our algorithm is in $\mathcal{O}(2^n \cdot n \log(n))$.

Proof: Initialization possible in time $\mathcal{O}(n^2 \log(n))$ (note that $\binom{n}{2} = \frac{n(n-1)}{2}$ holds).

Worst-Case: Algorithm tries all possibilities to place the $n-1$ longest fragments at the left or right border.



$\Rightarrow$ Backtracking tree has height $n-1$ (edges) and $\sum_{0 \leq i \leq n-1} 2^i = 2^n - 1$ many nodes.
$\Rightarrow 2^n - 2$ many edges corresponding to a placement of an element and possibly a backtracking step.
For each placement we have to evaluate δ, possible in running time $\mathcal{O}(n)$ as $|\delta(X, y)|$ in $\mathcal{O}(n)$.
Proving these distances to be in A is done by repeated binary search, resulting in a running time in $\mathcal{O}(n \log(n))$.
By marking chosen distances (instead of deleting them) in A the backtracking step is possible in time $\mathcal{O}(n \log(n))$ analogous to placement.

Adding up all parts we get a total running time in $\mathcal{O}(n^2 \log(n) + 2^n \cdot n \log(n)) = \mathcal{O}(2^n \cdot n \log(n))$. □

Remark:

- Worst-Case still exponential but much faster than the brute-force search. $(n-1)! \cdot \binom{\binom{n}{2}}{n-1}$
- For real life inputs we have to expect a running time much smaller than the worst-case.
- For a set of n randomly chosen points on the real axis in each step one alternative (left or right placement) is discarded with probability 1 implying a running time in $\mathcal{O}(n^2 \log(n))$.

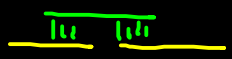
Mapping with unambiguous probes:

Situation: Many copies of the DNA molecule D to be sequenced are separated into overlapping pieces which are marked unambiguously.

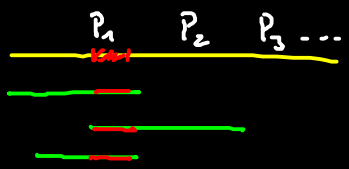
STS probes (sequence-tagged sites): Long parts of DNA sequences, occuring only once in the molecule to be sequenced due to their length. By radioactive markings the STS probes can be distinguished. Hybridization connects the STS probes to the fragments.

$\Rightarrow$ Ideally one gets a 0-1-matrix $A = (a_{i,j})$, where $a_{i,j} = 1$ if and only if STS probe j occurs in the i-th fragment.

(Experiments $\Rightarrow$ Errors, forming of chimeras)



Overlapping of fragments $\Rightarrow$ STS probes appear in several fragments.



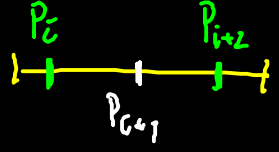
Unambiguousity of probes $\Rightarrow$ Probes mark places of fragments corresponding to the same position in D.

$\Rightarrow$ STS matrix: To reconstruct the molecule the columns have to be permuted so that all ones follow up each other without zeroes in between.

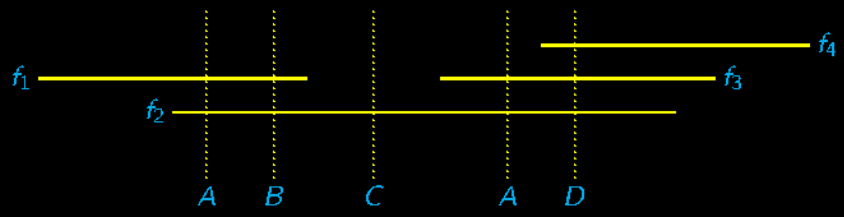
WHY ?

Let $p_1, p_2, \ldots, p_n$ be the correct order of the probes on D and assume there is a fragment containing p_i and p_{i+2} (two ones in one row) but not p_{i+1} (a zero in between). Then p_{i+1} can't be located between p_i and p_{i+2} in D, as the fragment is an identical copy of the respective part of D.

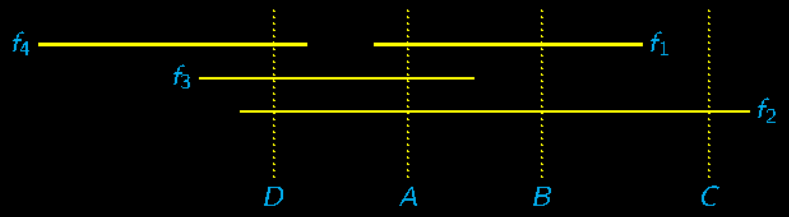
It is still possible to form a molecule D' from a matrix with non-consecutive ones. In this case, however, D' will contain at least one STS probe twice.



	A	B	C	D
f_1	1	1	0	0
f_2	1	1	1	1
f_3	1	0	0	1
f_4	0	0	0	1



	D	A	B	C
f_1	0	1	1	0
f_2	1	1	1	1
f_3	1	1	0	0
f_4	1	0	0	0



Definition

Let A be a $n \times m$-matrix over $\{0,1\}$. A has the consecutive ones property, *if there is a permutation π of the columns of A, satisfying*

$$(a_{i,\pi^{-1}(k)} = 1 \wedge a_{i,\pi^{-1}(l)} = 1) \rightarrow (\forall j \in [k{+}1 : l{-}1]) : (a_{i,\pi^{-1}(j)} = 1),$$

for all $1 \leq i \leq n$ and all $1 \leq k < l \leq m$. If this condition holds for π the identical permutation, we say, A has consecutive ones form.

Matrix results from (error free) experiment $\Rightarrow$ consecutive ones property.
Reconstruction of the molecule $\Leftrightarrow$ find permutation π, arranging the columns of the matrix as needed.

So: Decide if a given matrix has consecutive ones property and if so find a witnessing permutation (consecutive ones problem).

Brute force: For realistic m too many alternatives.:-(

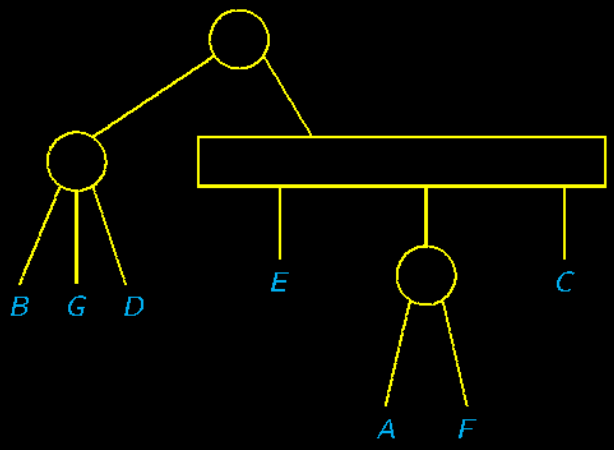
Solution: Use a data structure, allowing the efficient maintenance of permutations.

Definition

Let $U = \{u_1, \ldots, u_m\}$ a finite set. A PQ tree T over U is a 6-tuple $T = (V, E, r, B, l, t)$ satisfying

1. *(V, E) is an ordered tree,*
2. *$r \in V$ is the root of (V, E),*
3. *$B \subseteq U$ is the set of leaves of (V, E),*
4. *$l : B \to U$ is a* **bijective** *mapping from the leaves to U, and*
5. *$t : V \setminus B \to \{P, Q\}$ is a* **total** *function, assigning type P or Q to each internal node.*

$\{A, B, C, D, E, F, G\}$, $\bigcirc = P$-node, $\square = Q$-node.



We define $Front(T) := (l(v_1), l(v_2), \ldots, l(v_n))$ for $v_1, v_2, \ldots, v_n$ the sequence of leaves from left to right.

Definition

Let T a PQ tree over $U = \{u_1, \ldots, u_m\}$. The following operations on T are feasible:

- *Arbitrary variation of the order of children of a P-node in T;*
- *inverting the order of the children of a Q-node in T.*

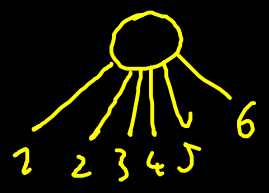
The set $Perm(T)$ of permutations represented by T is then given by

$$Perm(T) := \{Front(T') \mid T \rightsquigarrow T' \text{ by sequence of feasible operations}\}$$

where the empty sequence is allowed as a sequence of feasible

operations.

Example: Universal PQ tree for U is given by a single P-node to which all elements of U are attached as a child.



Consecutive ones problem:

Input: An finite set $U = \{u_1, \ldots, u_m\}$ and a set of restrictions $\mathcal{R} \subseteq 2^U$. (A restriction $R \in \mathcal{R}$ thus is a subset of U).
Output: All permutations π of elements in U, such that for all $R \in \mathcal{R}$ the elements of R are successors in π.

Method:
1. Create universal PQ tree for U.
2. Subsequently process all restrictions R from $\mathcal{R}$ and transform the PQ tree such that its set $Perm(T)$ satisfies the current and all previous restrictions.

As the satisfaction of an additional restriction generally reduces the size of set $Perm(T)$ we call these transformations *reductions*.

The following implements the reduction of tree T to satisfy restriction R:

1. $Q :=$ Queue with all leaves of T.
2. **while** Q is not empty **do**
   - 2.1 $x := Dequeue(Q)$;
   - 2.2 **if** x is a leaf **then**
     - **if** $x \in R$ **then**
       - mark x as *full*
     - **else**
       - mark x as *empty*;
   - 2.3 **else if** a rule can be applied to the subtree with root x **then**
     - apply this rule

2. (Continued)

2.4 **else** **return**(Λ) (empty tree, there is no fitting permutation);

2.5 **if** $R \subseteq \{y \mid y \text{ is a descendant of } x\}$ **then** **return**(T);

2.6 **if** all siblings of x were considered **then**
y:=Father(x);
Enqueue(y,Q);

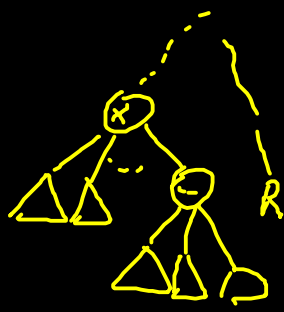
Essential are the rules mentioned in 2.3, which we will now consider in detail.

Notations: A node x of the PQ tree considered for reduction R is called

- *partial*, if only some of its descendants belong to R;
- *empty*, if neither x nor any of its descendants belong to R;
- *full*, if x or all of its descendants belong to R.

Rule P0: If all children of P-node x are empty, T remains unchanged.

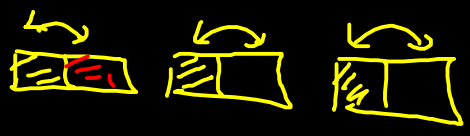
Rule P1: If all children of P-node x are full, x is marked as full.



Rule P2: Only some children of P-node x are full and x is the root of the smallest subtree of T containing all of R.
Then full and empty children of x are separated by inserting a new (full) P-node as child of x getting all full children of x as direct successors.

Rule P3: Only some children of P-node x are full and x is not the root of the smallest subtree of T containing all of R.
Then x is replaced by a partial Q-node containing two P-nodes as children, one having all full children of x as direct successors, the other having the empty children of x as direct successors.

P-nodes with k partial children:
$k = 1$: Rule P4 or P5, depending if x is the root of the smallest subtree containing all of R (P4) or not (P5).
$k = 2$: Rule P6.
$k > 2$: Impossible!



Why?

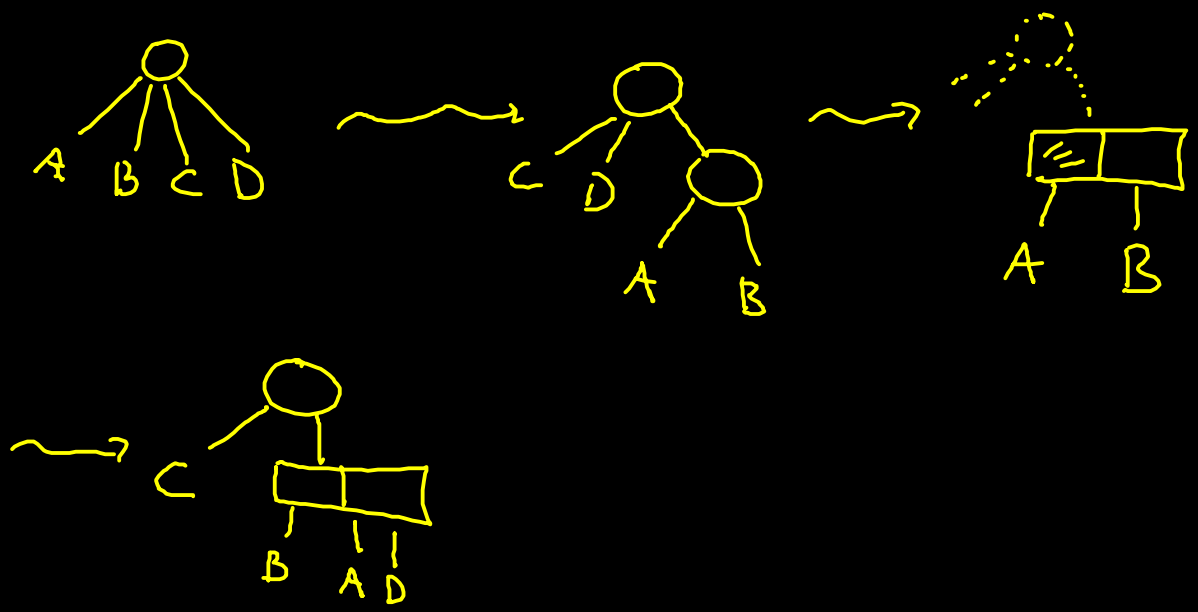
For $k > 2$ restriction R can not be satisfied as partial nodes are always Q-nodes whose front may only be inverted. So the resulting permutation would contain empty (do not belong to R) in between full nodes (belong to R). This contradicts our definition of a restriction forcing all elements in R to be neighbored.

In all other possible cases for P-nodes full and empty nodes would be nested making satisfaction impossible for the same reasons as above.

Q-nodes:
Rules Q0 to Q3, with the restriction on Q3 that x has to be the root of the smallest subtree of T containing all of R.
For the same reasons as before we only have to consider Q-nodes with at most two partial children.

Consecutive ones problem: Create $\mathcal{R} := \{R_1, \ldots, R_n\}$, where R_i contains exactly those column numbers where the STS matrix has entry 1 in row i.
Satisfying $R_i \Rightarrow$ all ones in row i are consecutive.
Starting with the universal PQ tree for $\{1, 2, \ldots, m\}$ (column numbers) and reducing to satisfy restrictions R_i, $i = 1, 2, \ldots, m$, one after another we get the empty tree, if the matrix does **not** have the consecutive ones property. Else we get a PQ tree T whose permutation set $Perm(T)$ represents exactly those permutations that transform the given matrix into consecutive ones form.

Example: $\mathcal{R} = \{\{A, B\}, \{A, B, C, D\}, \{A, D\}, \{D\}\}$.



Stochastic modeling: How good do randomly chosen fragments cover a molecule?

Definition

Let $A : \mathbb{R}_0 \to \mathbb{N}$ a nondecreasing function satisfying $A(0) = 0$, where $A(t)$ describes the number of events until time t. Then we have a poisson process with rate λ, if

(1) $\Pr[A(s + t) - A(s) = n] = \exp(-\lambda \cdot t)\frac{(\lambda \cdot t)^n}{n!}$ *and*

(2) *the distribution of the number of events is stationary, i.e. it depends only on the length but not on the position of a given interval.*

Theorem

Let A be a poisson process.

a) *The expected number $\mathbb{E}[A(t)]$ of events in an interval of length t satisfies $\mathbb{E}[A(t)] = \lambda \cdot t$.*

b) *Let T_n be the time between the $(n-1)$-th and the n-th event. Then*

$$\Pr[T_1 > t] = \Pr[T_n > t] = \exp(-\lambda \cdot t).$$

Model: Assuming fragments of length L are cut from multiple copies of a DNA molecule of length C randomly and independently. Then for i any position of the molecule

$$\Pr[i \text{ is covered by randomly chosen fragment}] = \frac{L}{C}$$

holds and thus

$$\left(1 - \frac{L}{C}\right)^N \approx \exp\left(-\frac{L \cdot N}{C}\right) \tag{1}$$

is the probability that i is not covered by any of the N fragments.

Poisson process?