

# Covering Pairs in Directed Acyclic Graphs

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# Outline

- 1 Path Cover and *Constrained* Path Cover in Bioinformatics
- 2 *Max Required Pairs with a Single Path* problem
  - $W[1]$ -hardness  
(if parameterized by the optimum)
  - fixed-parameter algorithm  
(if parameterized by the overlapping pairs)
- 3 Conclusions

# Minimum Path Cover on DAGs

**Problem:** Min Path Cover on DAGs (MinPC)

**Instance:** a DAG  $D = (N, A)$

**Solution:** a set  $\Pi$  of paths that “cover”  $N$

**Measure:**  $|\Pi|$

It can be solved in time  $O(n^3)$

(Dilworth 1950, Fulkerson 1965, Hopcroft and Karp 1973)

Existence of fixed source and target vertices can be safely assumed

# Minimum Path Cover on DAGs

MinPC has been used to solve Bioinformatics problems:

- Viral haplotype assembly (Eriksson *et al.* 2008)
- Transcript reconstruction (Trapnell *et al.* 2010)

*Different applications, same problem:*

Reconstructing a set of complete sequences starting from their fragments

*Basic idea:*

- vertices=fragments
- paths=possible complete sequences

# Minimum Path Cover on DAGs

**Common issue:** how to choose among same-size covers?

*Paired-end reads could help!*

Two paired-end reads are extracted from the same sequence.

⇒ they must be covered by the same path

**Required pair**  $[u, v]$ :

There must exist a path in the solution that contains **both**  $u$  **and**  $v$

# Constrained MinPC

**Problem:** Min Path Cover with Required Pairs (MinPCRP)

**Instance:** a DAG  $D = (N, A)$  **and** a set  $R$  of required pairs

**Solution:** a set  $\Pi$  of paths that “cover”  $N$  **and**  $R$

**Measure:**  $|\Pi|$

## On Path Cover Problems in Digraphs and Applications to Program Testing

S. C. NTAFOU AND S. LOUIS HAKIMI, FELLOW, IEEE

*Abstract*—In this paper various path cover problems, arising in program testing, are discussed. Dilworth’s theorem for acyclic digraphs is generalized. Two methods for finding a minimum set of paths (minimum path cover) that covers the vertices (or the edges) of a digraph are given. To model interactions among code segments, the notions of required pairs and required paths are introduced. It is shown that finding a minimum path cover for a set of required pairs is NP-hard. An efficient algorithm is given for finding a minimum path cover for a set of required paths. Other constrained path problems are considered

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ON  
d in software validation  
of test paths that covers  
finding appropriate test  
may choose, for example,  
statement is executed at  
et that would exercise all  
represent a program as

# MaxRPSP

## Possible greedy heuristic approach:

Add at each step the path that covers the maximum number of required pairs.

**Problem:** Max Required Pairs with a Single Path (MaxRPSP)

**Instance:** a DAG  $D = (N, A)$  **and** a set  $R$  of required pairs

**Solution:** a path  $\pi$

**Measure:** no. of required pairs covered by  $\pi$

## Computational complexity?

# 1 – MaxRPSP parameterized by the optimum

## Theorem

*$k$ -RPSP is  $W[1]$ -hard when parameterized by the number  $k$  of covered required pairs.*

## Proof (idea):

By parameterized reduction from  $h$ -Clique  
(which is  $W[1]$ -hard, Downey and Fellows 1995)

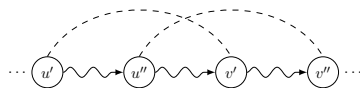
**Corollary:** no  $O(2^k P(n))$  exact algorithm exists (unless  $P = NP$ )



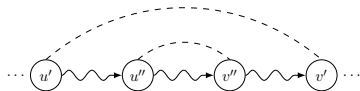
## 2 – Fixed-parameter algorithm

MaxRPSP has a fixed-parameter algorithm when parameterized by the *maximum number of overlapping required pairs*.

### Overlapping required pairs

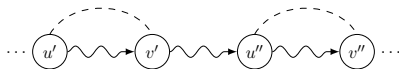


Alternated



Nested

### Non-overlapping required pairs



## 2 – Fixed-parameter algorithm – Idea

### Dynamic programming recurrence

$P\left[ [v_i^1, v_i^2], S \right]$  Maximum number of required pairs covered by a path ending in  $v_i^2$  and containing all the vertices in  $S$

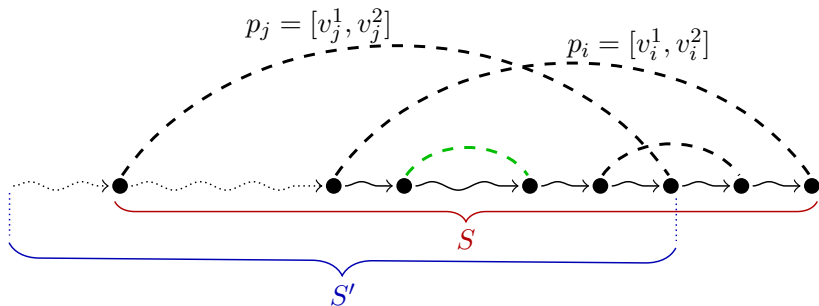
Let  $\pi$  be a path that:

- ends in vertex  $v_i^2$  and covers the required pair  $p_i = [v_i^1, v_i^2]$ ;
- contains the vertices of set  $S$ .

Suppose that  $p_j = [v_j^1, v_j^2]$  is the “rightmost” required pair covered by  $\pi$  which is not nested in  $p_i$ .

## 2 – Fixed-parameter algorithm – Recursive step

$p_j$  = “rightmost” required pair covered by  $\pi$  and not nested in  $p_i$



## 2 – Fixed-parameter algorithm – Idea

**Running time:**  $O(4^{2h} n^2)$

- $n$  no. of vertices
- $h$  maximum no. of overlapping pairs

**Why?** Cardinality of  $S$  is bounded by  $2h!$

# Conclusions

- Adding **constraints** to Min Path Cover could help finding “better” (=closer to the hidden truth) solutions
- Various constrained variants of Min Path Cover appear to be computationally **hard**
- We need “**good**” algorithms  
(=approximation/fixed-parameter/heuristics/...)



# Additional Content

# Minimum Path Cover on DAGs

**Problem:** Min Path Cover on DAGs (MinPC)

**Instance:** a DAG  $D = (N, A)$

**Solution:** a set  $\Pi$  of paths that “cover”  $N$

**Measure:**  $|\Pi|$

**Algorithm (idea):**

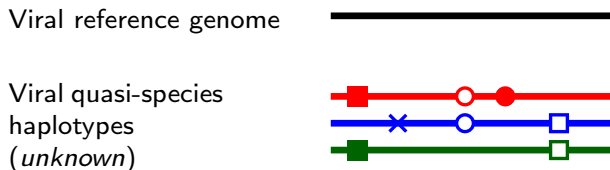
- The size of the cover is equal to the size of a maximum matching of a “corresponding” *bipartite* graph
- Maximum matching can be solved in time  $O(n^3)$

(Dilworth 1950, Fulkerson 1965, Hopcroft and Karp 1973)



# Applications of MinPC in Bioinformatics

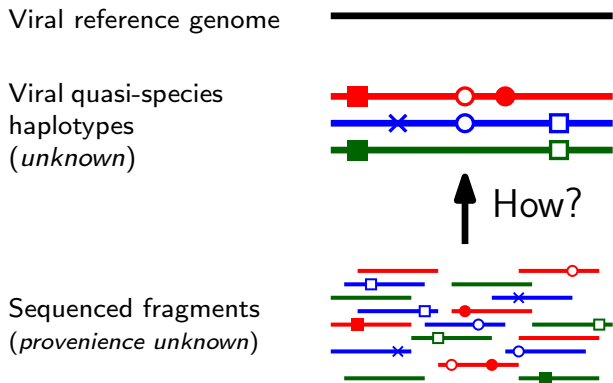
## Viral quasi-species assembly



(Eriksson *et al.* 2008)

# Applications of MinPC in Bioinformatics

## Viral quasi-species assembly



(Eriksson *et al.* 2008)

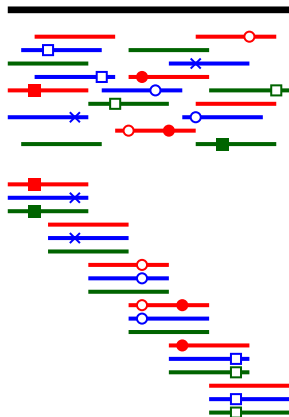
# Applications of MinPC in Bioinformatics

## Viral quasi-species assembly

Viral reference genome

Sequenced fragments  
(*provenience unknown*)

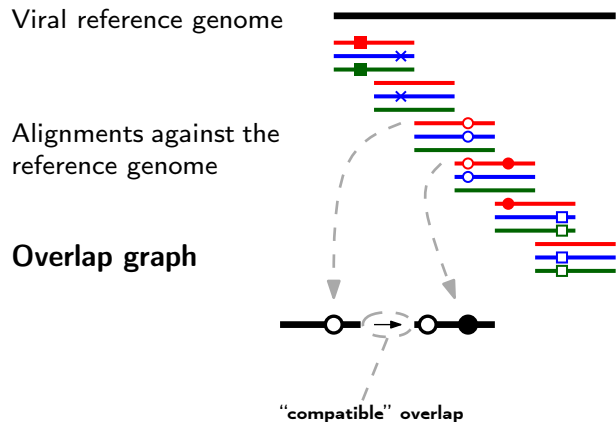
Alignments against the  
reference genome



(Eriksson *et al.* 2008)

# Viral quasi-species assembly – Overlap graph

## Overlap graph



(Eriksson *et al.* 2008)

# Viral quasi-species assembly – Overlap graph

## Overlap graph

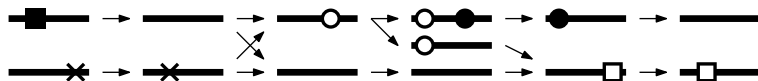
Viral reference genome



Alignments against the reference genome



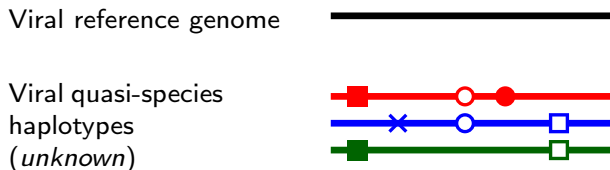
Overlap graph



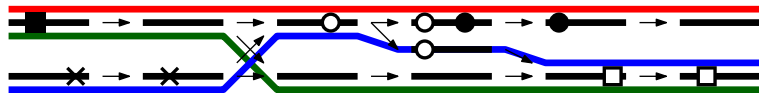
(Eriksson *et al.* 2008)

# Viral quasi-species assembly – Overlap graph

## Overlap graph



## Overlap graph



Paths are putative haplotypes

(Eriksson *et al.* 2008)

# Viral quasi-species assembly – Overlap graph

## Overlap graph

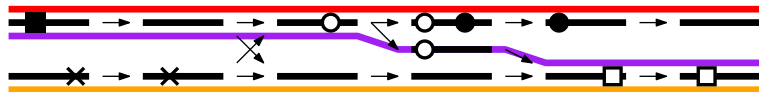
Viral reference genome



Viral quasi-species  
haplotypes  
(*unknown*)



Overlap graph



**Not all paths are correct!**

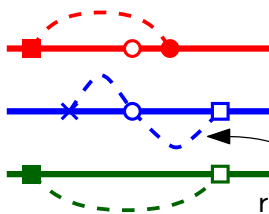
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# Constraining MinPC

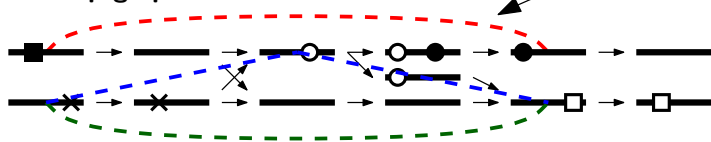
**Required pair**  $[u, v]$ :

There must exist a path in the solution that contains  $u$  **and**  $v$

Viral quasi-species  
haplotypes  
(*unknown*)



Overlap graph



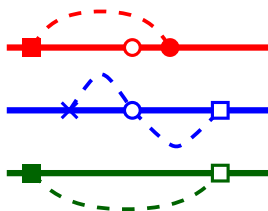


# Constraining MinPC

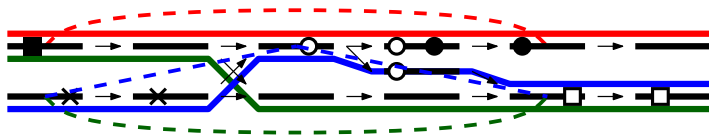
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Viral quasi-species  
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Overlap graph



## 2 – Fixed-parameter algorithm – DP recurrence

### Dynamic programming recurrence

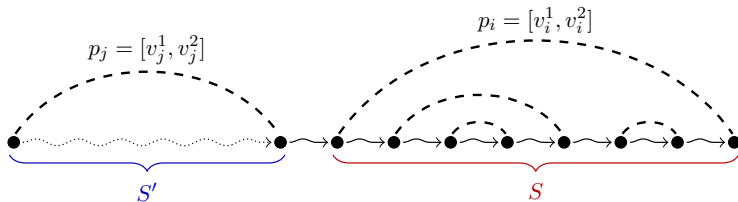
$$P[[v_i^1, v_i^2], S] = \max \left\{ P[[v_j^1, v_j^2], S'] + |Ov([v_i^1, v_i^2], S \setminus S')| \right\}$$

where:

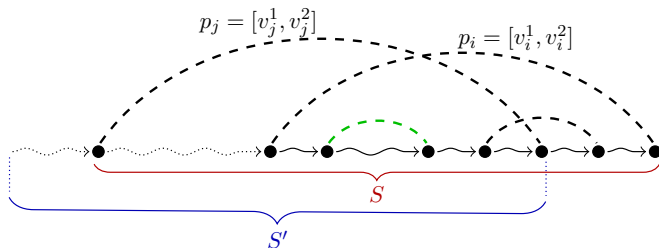
- $[v_j^1, v_j^2]$  is not nested in  $[v_i^1, v_i^2]$  and  $j < i$
- $S'$  in agreement with  $S$
- there exists a path from  $v_j^2$  to  $v_i^2$  containing all vertices in  $S \setminus S'$
- $Ov([v_i^1, v_i^2], S \setminus S') = \{[v_h^1, v_h^2] \mid [v_h^1, v_h^2] \text{ nested in } [v_i^1, v_i^2] \wedge v_h^1 \in S \wedge v_h^2 \in S \setminus S'\}$

## 2 – Fixed-parameter algorithm – Recursive step

Case 1)  $p_j$  and  $p_i$  do not overlap:



Case 2)  $p_j$  and  $p_i$  overlap:



## 2 – Fixed-parameter algorithm – Idea

**Running time:**  $O(4^{2h}n^2)$

- $n$  no. of vertices
- $h$  maximum no. of overlapping pairs

Cardinality of  $S$  is bounded!

**Observation:** for each req. pair  $[v_i^1, v_i^2]$ , only the vertices of required pairs overlapping  $[v_i^1, v_i^2]$  really matter.

$OP([v_i^1, v_i^2]) =$  vertices of required pairs overlapping  $[v_i^1, v_i^2]$

$$\Rightarrow |S| = O\left(|OP([v_i^1, v_i^2])|\right) = O(h)$$