# Multi-Assembly Problems for RNA Transcripts

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Multi-assembly	Assembly	Assembly and expression levels	Long, and paired-end reads	End
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#### CENTRAL DOGMA OF MOLECULAR BIOLOGY







Problem: assemble the RNA transcripts from the RNA-Seq reads and quantify their expression levels

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### Multi-Assembly

Assembly of fragments from different, but related, sequences

- transcriptomics (RNA-Seq)
- viral quasi-species
- metagenomics

Assumptions:

existing reference (genome-guided multi-assembly)

✗ no existing annotation



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### Splicing graphs





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#### Splicing graphs



Splicing graphs:

- exons  $\equiv$  nodes
- reads overlapping two exons  $\equiv$  arcs
- ► + coverage information

Existing reference  $\implies$  directed acyclic graphs (DAGs)



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#### **OVERLAP GRAPHS**



- reads  $\equiv$  nodes
- overlaps  $\equiv$  arcs
- ► + coverage information

Existing reference  $\implies$  directed acyclic graphs (DAGs)



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### OUTLINE OF THE TALK

Three problem formulations:

- 1. Assembly only
- 2. Simultaneous assembly and estimation of expression levels
- 3. Assembly only, with long reads, or paired-end reads



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# ASSEMBLY: MINIMUM PATH COVER (MPC)

What is the minimum number of paths required to cover all nodes of a DAG?

- ▶ RNA-Seq: Cufflinks 2010, CLASS 2012, BRANCH 2013
- ► Viral quasi-species: ShoRAH 2011



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# ASSEMBLY: MINIMUM PATH COVER (MPC)

In general it is NP-hard (one path iff *G* has a Hamiltonian path)

But it is solvable in polynomial-time on DAGs:

- Dilworth's theorem 1950 + Fulkerson's constructive proof 1956
- ► by a maximum matching algorithm, solvable in time  $O(t(G)\sqrt{n})$
- the weighted version can be solved in time  $O(n^2 \log n + t(G)n)$

where  $m \le t(G) \le n^2$  is #arcs in the transitive closure of *G*.

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MIN-COST MPC VIA MIN-COST FLOWS

- ► Unweighted case: MPC via min-flows, e.g. [*Pijls*, *Potharst*, 2013]
- ► Weighted case: MPC via min-cost flows



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## MPC VIA MIN-COST FLOWS

This min-cost flow problem

- ► can be solved in time  $O(n^2 \log n + nm)$  by [*Gabow and Tarjan, 1991*]
- ▶ observed in [*Rizzi*, *T.*, *Mäkinen*, 2014]

This is better than  $O(n^2 \log n + nt(G))$ , since  $m \le t(G) \le n^2$ 

► as soon as there is a path of length O(n), we have  $t(G) = O(n^2)$ 



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#### ASSEMBLY AND ESTIMATION OF EXPRESSION LEVELS

**INPUT:** An arc-weighted DAG G, and

• A superset *S* of the sources, and a superset *T* of the sinks

**TASK:** Find a collection of paths  $P_1, \ldots, P_k$  in *G*, and their expression levels  $e_1, \ldots, e_k$ , such that:

- every *P<sub>i</sub>* starts in *S*, and ends in *T*, and
- the following cost is minimized

$$\sum_{(x,y)\in E} \left| w(x,y) - \sum_{j : (x,y)\in P_j} e_j \right|.$$

Variants for RNA-Seq in: IsoInfer 2010, IsoLasso 2011, CLIIQ 2012, FlipFlop 2014

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#### ASSEMBLY AND ESTIMATION OF EXPRESSION LEVELS





Cost is |6 - 8| + |3 - 0| + |4 - 3|



### ASSEMBLY AND ESTIMATION OF EXPRESSION LEVELS

Previous solutions based on enumeration of all paths (+ILP)

Solvable in polynomial-time by min-cost flows

▶ [T., Kuosmanen, Rizzi, Mäkinen, 2013]

If number *k* of paths is given in input, then NP-hard But solvable in time  $O(W^k aw(G)^k n^2)$ 

▶ [T., Gagie, Popa, Rizzi, Kuosmanen, Mäkinen, 2015]



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### Assembly with long reads







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# ASSEMBLY WITH LONG READS (2)



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### Assembly with long reads



**INPUT:** An arc-weighted DAG G, and

- 1. A superset S of the sources, and a superset T of the sinks
- 2. A family  $\mathcal{P}^{in} = \{P_1^{in}, \dots, P_c^{in}\}$  of directed paths in *G*

**TASK:** Find a minimum number *k* of directed paths  $P_1^{sol}, \ldots, P_k^{sol}$  in *G* such that

- 1. Every node in V(G) occurs in some  $P_i^{sol}$
- 2. Every path  $P^{in} \in \mathcal{P}^{in}$  is a subpath of some  $P_i^{sol}$
- 3. Every path  $P_i^{sol}$  starts in *S* and ends in *T*

4.  $\sum_{i=1}^{n} \sum_{e \in P_i^{sol}} w(e) \text{ is minimum among all such } k \text{ paths}$ 

 introduced by [Bao, Jiang, Girke, 2013, BRANCH], but the case of overlapping constraints not solved

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Subpath constraints as arc demands:







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### MIN-COST MPC WITH SUBPATH CONSTRAINTS **Problem 1:** a constraint *P* included in another constraint *Q*



- ► Remove P
- Can be implemented in time O(N) with a suffix tree for large alphabets, [Farach, 1997]
  - ► *N* = sum of lengths of Subpath Constraints

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#### MIN-COST MPC WITH SUBPATH CONSTRAINTS **Problem 2:** Suffix-prefix overlaps



- Iteratively merge constraints with longest suffix-prefix overlap
- ► All suffix-prefix overlaps can be found in optimal time O(N + |overlaps|) by [Gusfield, Landau and Schieber, 1992]
- Our iterative merging also takes O(N + |overlaps|) time

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Pre-processing phase

• O(N + |overlaps|)

The flow network has size:

• O(n) nodes and O(m + c) arcs

Min-cost MPC with Subpath Constraints can be solved in time  $O(N + |overlaps| + n^2 \log n + n(m + c))$  using [*Gabow and Tarjan*, 1991]

▶ [*Rizzi*, *T.*, *Mäkinen*, 2014]

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## MPC WITH PAIRED SUBPATH CONSTRAINTS

#### INPUT: A DAG G and

1. A family  $\mathcal{P}^{in} = \{(P_{1,1}^{in}, P_{1,2}^{in}), \dots, (P_{t,1}^{in}, P_{t,2}^{in})\}$  of pairs of directed paths in *G* 

**TASK:** Find a minimum number *k* of directed paths  $P_1^{sol}, \ldots, P_k^{sol}$  in *G* such that

1. Every node in V(G) occurs in some  $P_i^{sol}$ 

2. For every pair  $(P_{j,1}^{in}, P_{j,2}^{in}) \in \mathcal{P}^{in}$ , there exists  $P_i^{sol}$  such that both  $P_{j,1}^{in}$  and  $P_{j,2}^{in}$  are subpaths of  $P_i^{sol}$ 

- ▶ introduced by [Song and Florea, 2013, CLASS]
- NP-hard
  - ▶ [*Rizzi*, *T.*, *Mäkinen*, 2014]
  - ▶ [Beerenwinkel, Beretta, Bonizzoni, Dondi and Pirola, 2014]



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### CONCLUSIONS

Min-cost Minimum Path Cover

 $O(n^2 \log n + nm)$ 

Simultaneous assembly and expression estimation

polynomial-time, but NP-hard for given k

► Min-cost Minimum Path Cover with Subpath Constraints

 $O(N + |overlaps| + n^2 \log n + n(m + c))$ 

- ► *c* = number of Subpath Constraints
- ► *N* = sum of lengths of Subpath Constraints
- Minimum Path Cover with Pairs of Subpaths Constraints

NP-hard

Multi-assembly

Assembly 00000000 Assembly and expression levels

Long, and paired-end reads

End ○●○

#### Advertisement

Veli Mäkinen, Djamal Belazzougui, Fabio Cunial and Alexandru I. Tomescu

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