A practical fpt algorithm for Flow Decomposition and transcript assembly

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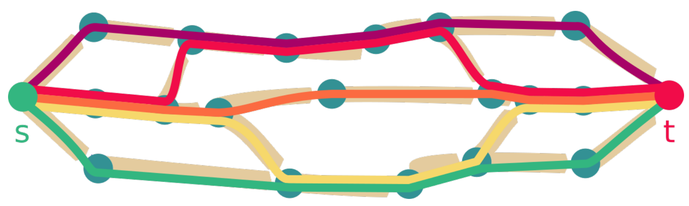
The Motivation

Shared segments between DNA/RNA strands create ambiguity in the assembly problem.

Connecting overlapping segments and counting their frequencies yields a DAG and a flow. The problem is to split the flow into the least amount of s-t-paths, to recover the original DNA/RNA strands.



The Problem

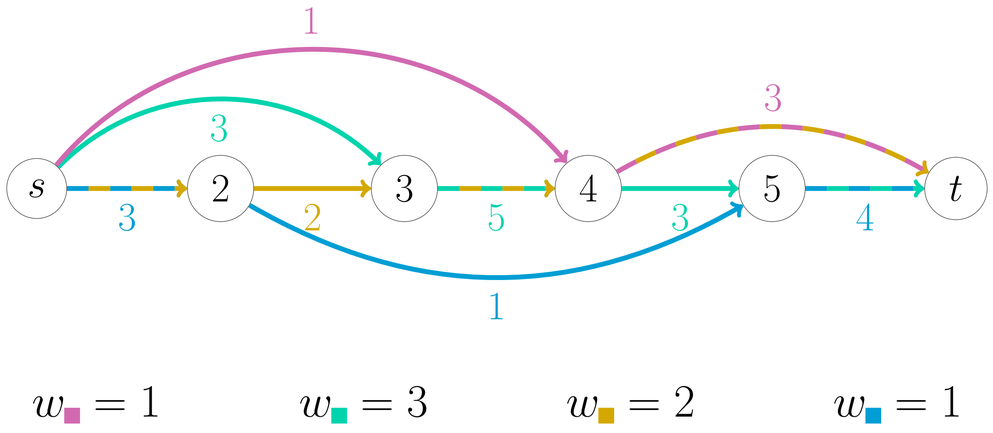
k-Flow Decomposition (*k*-FD)

Input: (G, f, k) with G an s-t–DAG, f a flow on G, and k a positive integer.

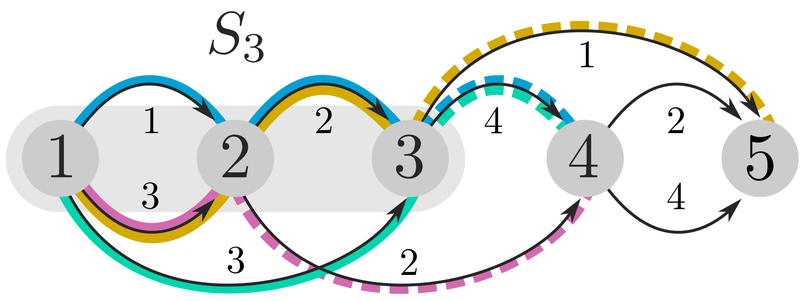
Problem: Is there an integral *flow decomposition* of (G, f) using at most k paths?

About ten years ago, some computer scientists came by and said they heard we have some really cool problems. They showed that the problems are NP-complete and went away!

-Joseph Felsenstein (Biologist)

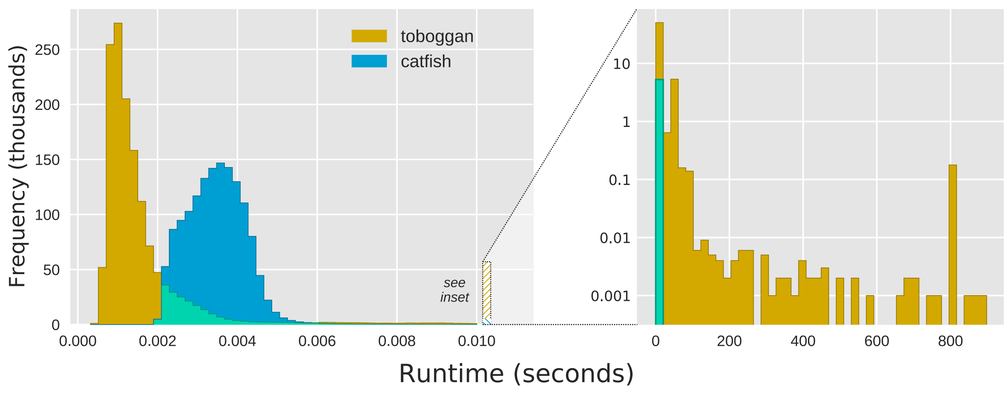


The Algorithm



The routing g out of S_3 (dashed lines) is an extension of the previous routings (solid paths). Each row in the constraint system L on the right corresponds to an arc; those shaded in gray are from arcs inside S_3, and those in white come from g.

The Results



Runtimes of Toboggan and Catfish on all non-trivial instances. The y-axes indicate the number of instances on which the algorithms terminate in the given time window.

dataset	instances	non-trivial	optimal	non-optimal
`zebrafish`	1,549,373	445,880	99.907%	0.053%
`mouse`	1,316,058	473,185	99.401%	0.074%
`human`	1,169,083	529,523	99.490%	0.043%
all	4,034,514	1,448,588	99.589%	0.056%

k	instances	Catfish	Toboggan
2	63.2791%	0.992	**0.995**
3	22.0775%	0.967	**0.969**
4	8.5237%	**0.931**	0.930
5	3.4920%	0.886	0.886
6	1.5375%	**0.830**	0.828
7	0.6698%	**0.788**	0.780
8	0.2889%	**0.767**	0.766
9	0.1241%	0.740	**0.743**
10	0.0070%	0.752	**0.802**
11	0.0004%	0.500	0.500
all	100%	0.973	**0.975**

Since Toboggan finds optimal decompositions we can investigate the Groundtruth for optimality.

All data.

Acknowledgments

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Resources

The implemented solver is available on Github: `/theoryinpractice/toboggan`