L3 Bioinformatics - Eeo Jun

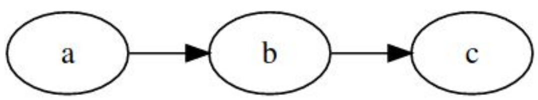
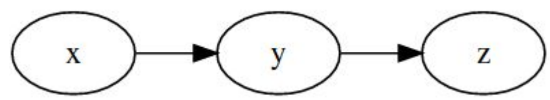
The setup is as follows. There are two (di)graphs, X and Y which may or may not be isomorphic that both have the same number of vertices. Graph X has vertices $x_1, x_2, ...x_n$, and Y has vertices $y_1, y_{2,}, ...y_n$. The input sequences are $x_1 x_2 ... x_n$ and all permutations of $y_1 y_2 ... y_n$ (there are $n!$ many of them).

The scoring function $\sigma : (V(X) \cup \{-\})^* \times (V(Y) \cup \{-\})^* \to \{-1, 0, 1\}$ is as follows:

- $\sigma(s, t) = -1$ iff any of s or t has length $\neq n$, has repeats, or contains indels. This enforces that any alignment must have all nodes from X and Y exactly once.
- $\sigma(s, t) = 1$ if the following holds - the function $f(s_i) = t_i$ for all $1 \leq i \leq n$ satisfies:
$$uv \in E(X) \Rightarrow f(u)f(v) \in E(Y) \quad \forall u, v \in V(X)$$
- $\sigma(s, t) = 0$ otherwise.

Note that since the scoring function doesn't care about the order of the sequences, we can relax our restrictions on the input sequences.

Example

Graph X	Graph Y
	

Then:

- $\sigma(abc, xyz) = 1$ (it is a valid 'proof' of isomorphism)
- $\sigma(abc, x-z) = -1$ (contains indels)
- $\sigma(abc, xzz) = -1$ (contains repeats)
- $\sigma(acb, xyz) = 0$ (contains all vertices, but is not a valid proof)