A Simple Protocol for the Inference of RNA Global Pairwise Alignments

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Content

LocARNA

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- Extensive Caching (Dynamic Programming) + Pruning

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- **Runtime** $O(n^4)$
- **Space** $O(n^4)$
- Web Interface
- Developed at the University of Freiburg

LocARNA - Procedure

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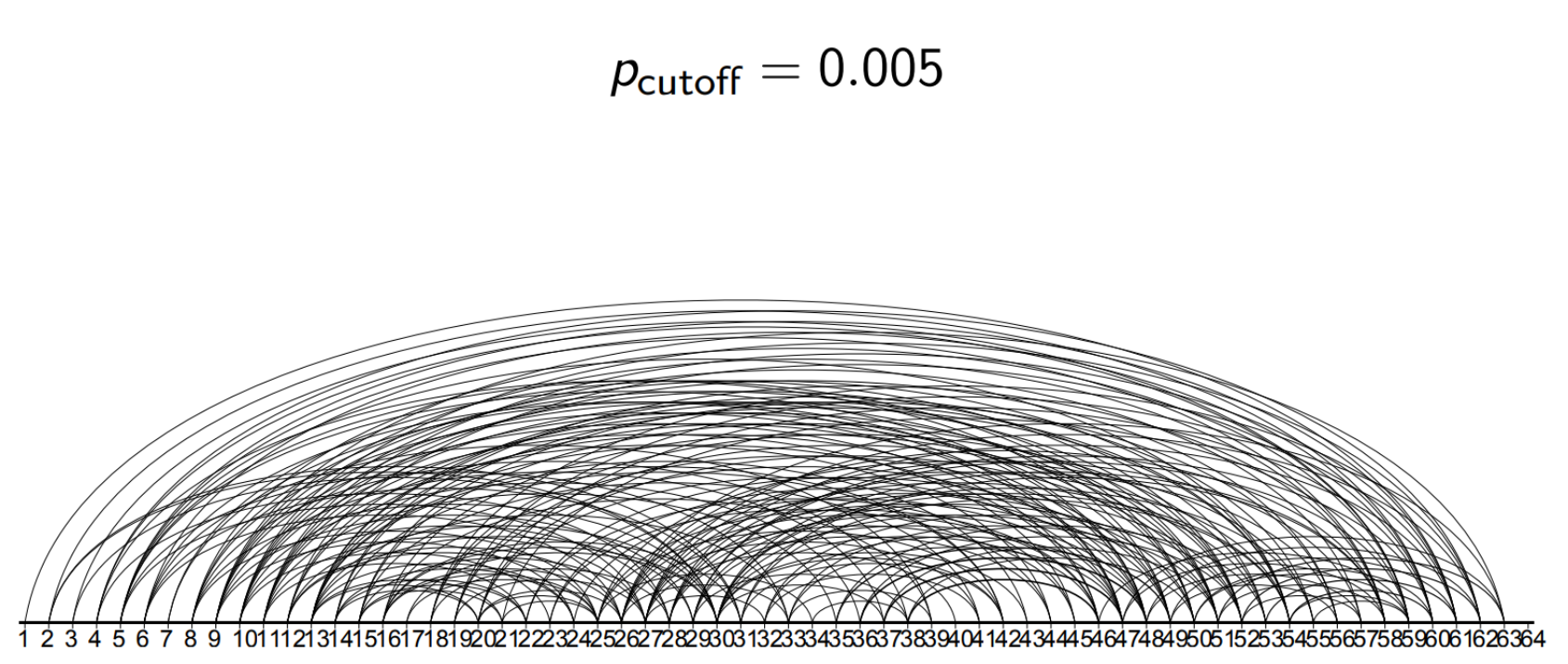
- Last: 'looking up' optimal alignment

LocARNA - Where can arcs happen? And how likely are they?



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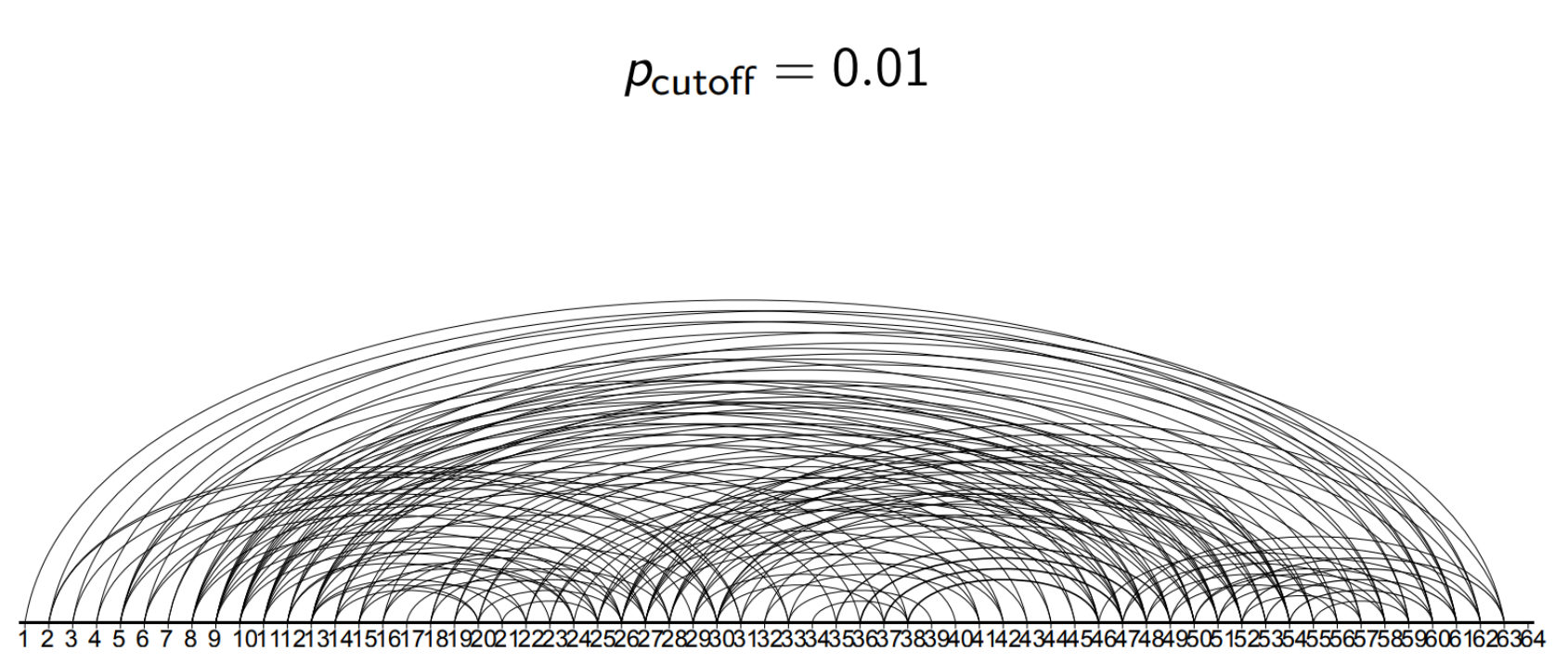

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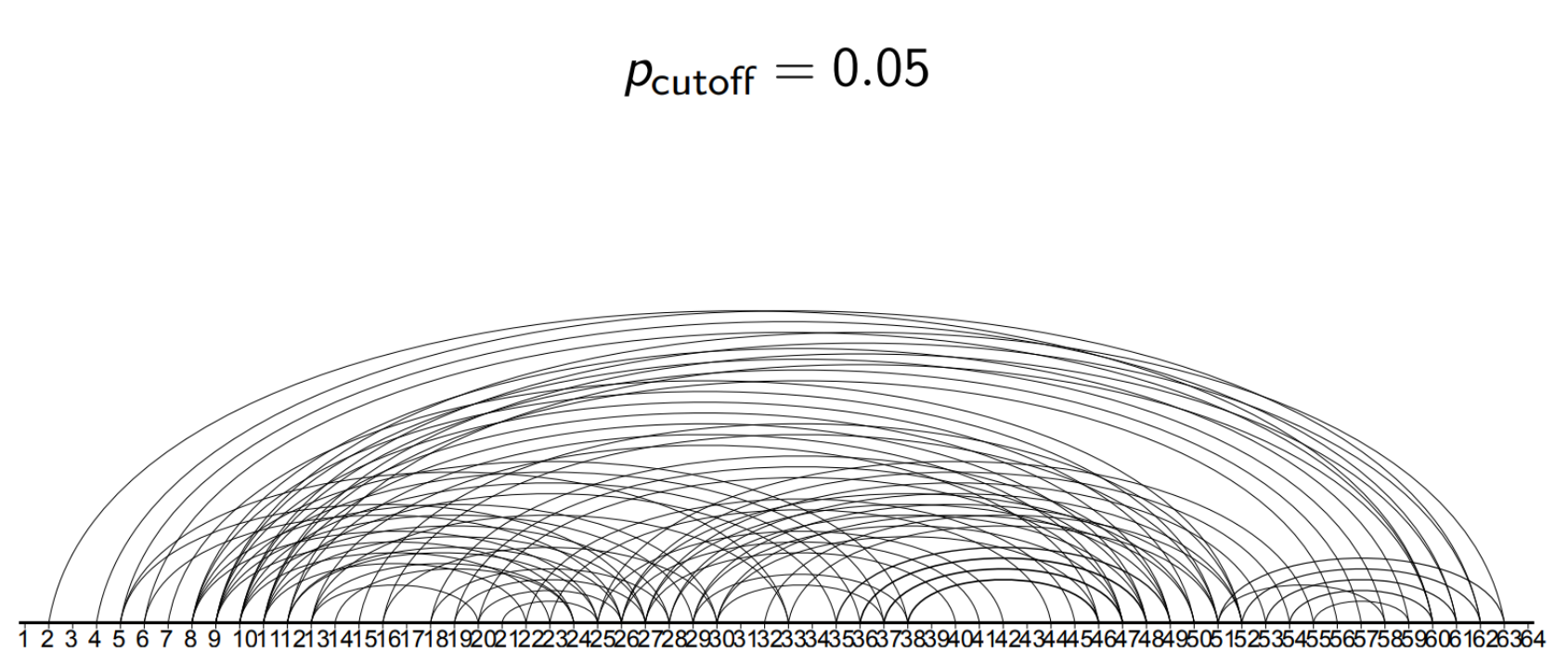
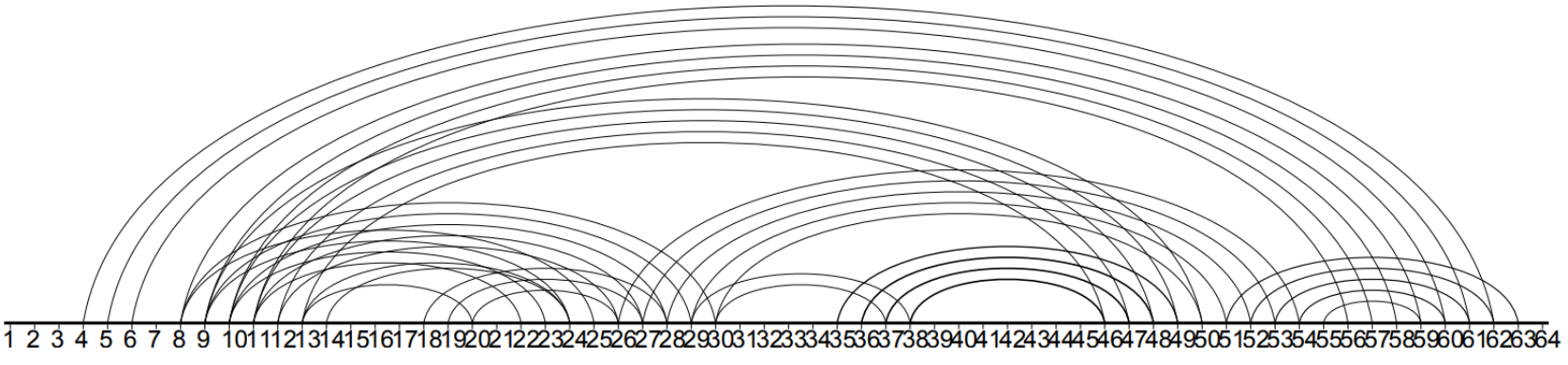
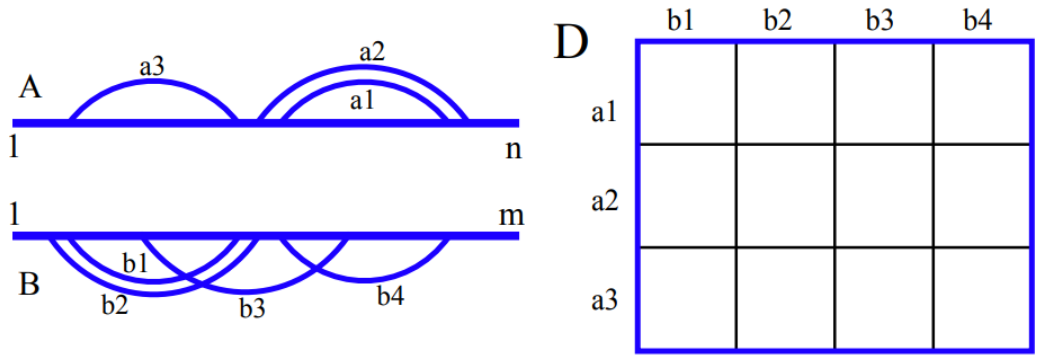


LocARNA - Where can arcs happen? And how likely are they?

$p_{\text{cutoff}} = 0.1$



LocARNA - Matrices



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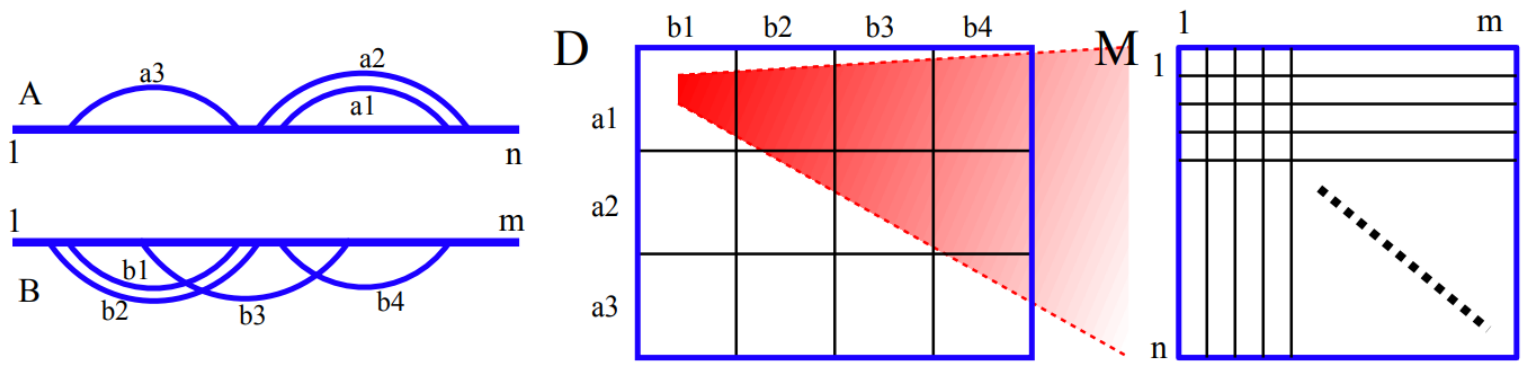

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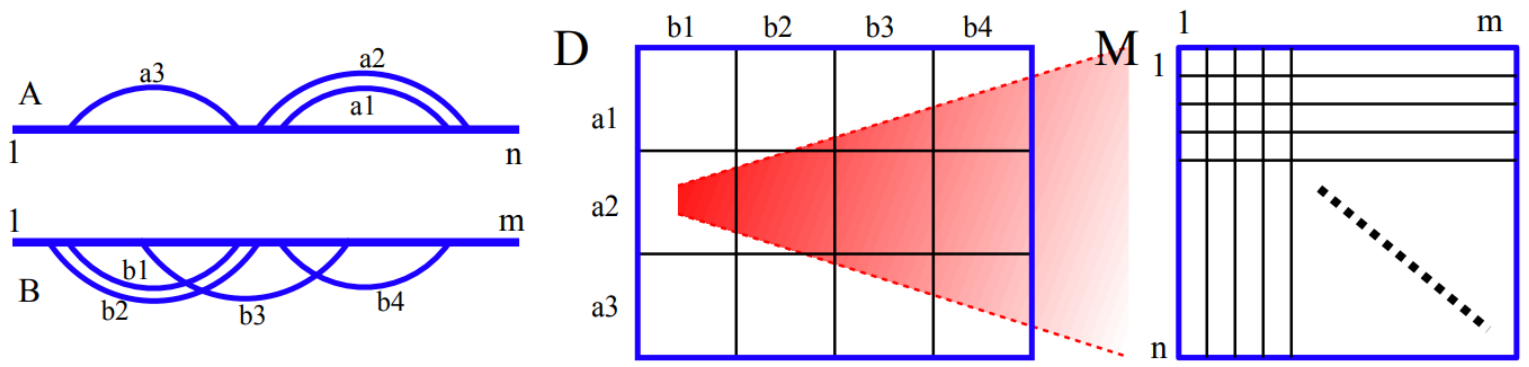

LocARNA - Aligning between secondary structures

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Cases:

- Base match
- Base insertion
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- Base **pair** match

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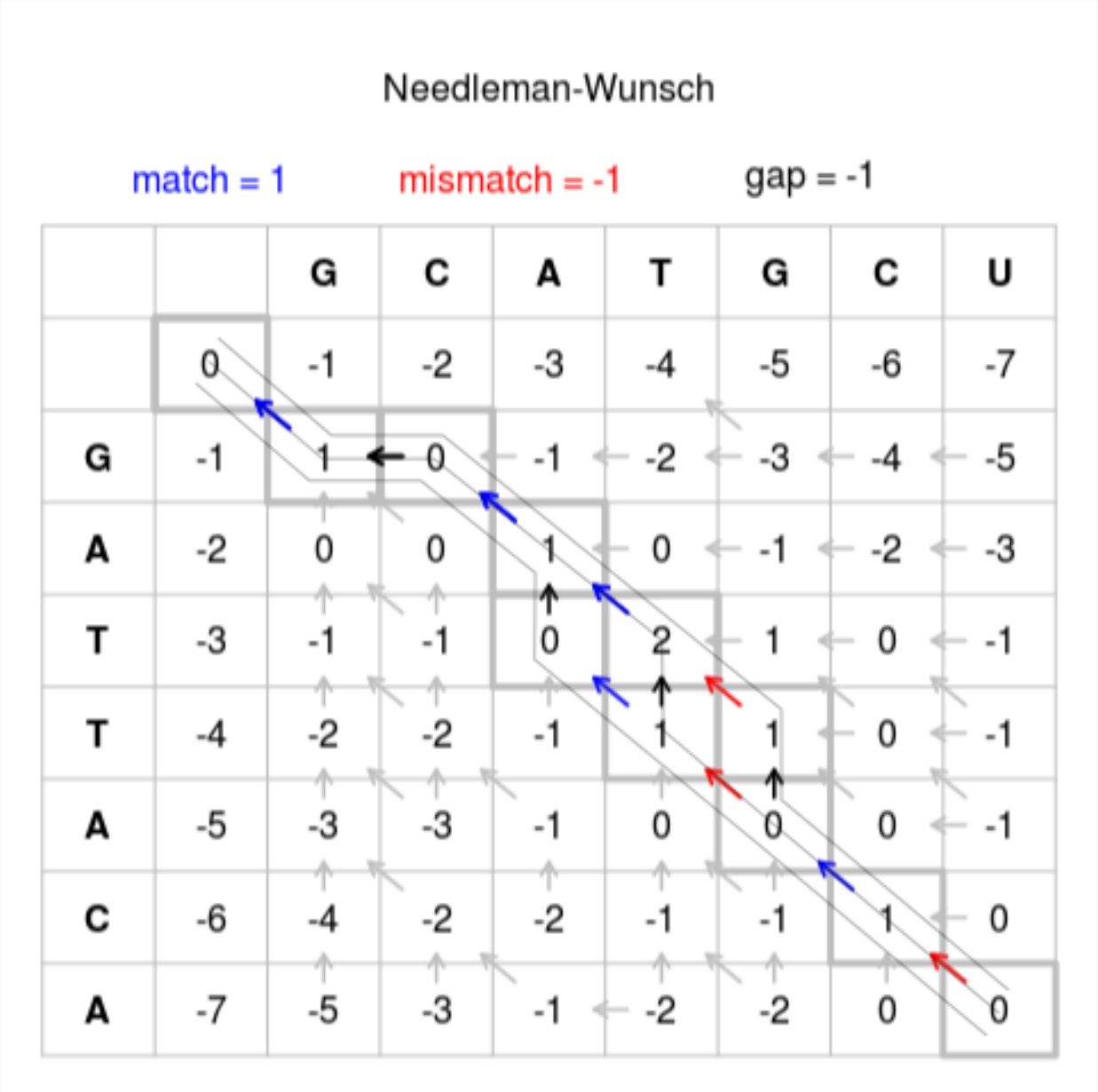

		G	C	A	T	G	C	U
	0	-1	-2	-3	-4	-5	-6	-7
G	-1	1	0	-1	-2	-3	-4	-5
A	-2	0	0	1	0	-1	-2	-3
T	-3	-1	-1	0	2	1	0	-1
T	-4	-2	-2	-1	1	1	0	-1
A	-5	-3	-3	-1	0	0	0	-1
C	-6	-4	-2	-2	-1	-1	1	0
A	-7	-5	-3	-1	-2	-2	0	0

LocARNA - Example