New algorithms to represent complex pseudoknotted RNA structures in dot-bracket notation

– Supplementary material –

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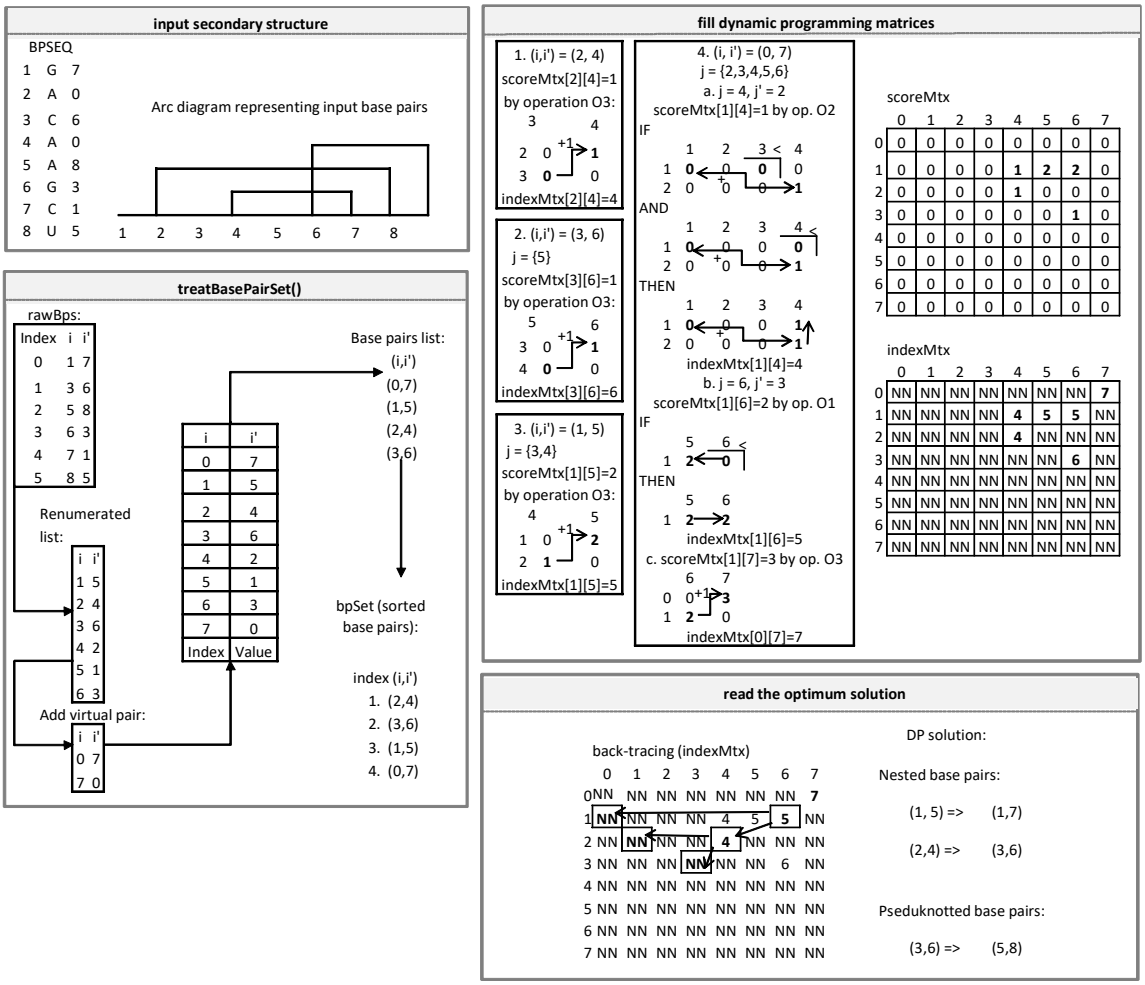

Figure S1: Example execution of DP algorithm.

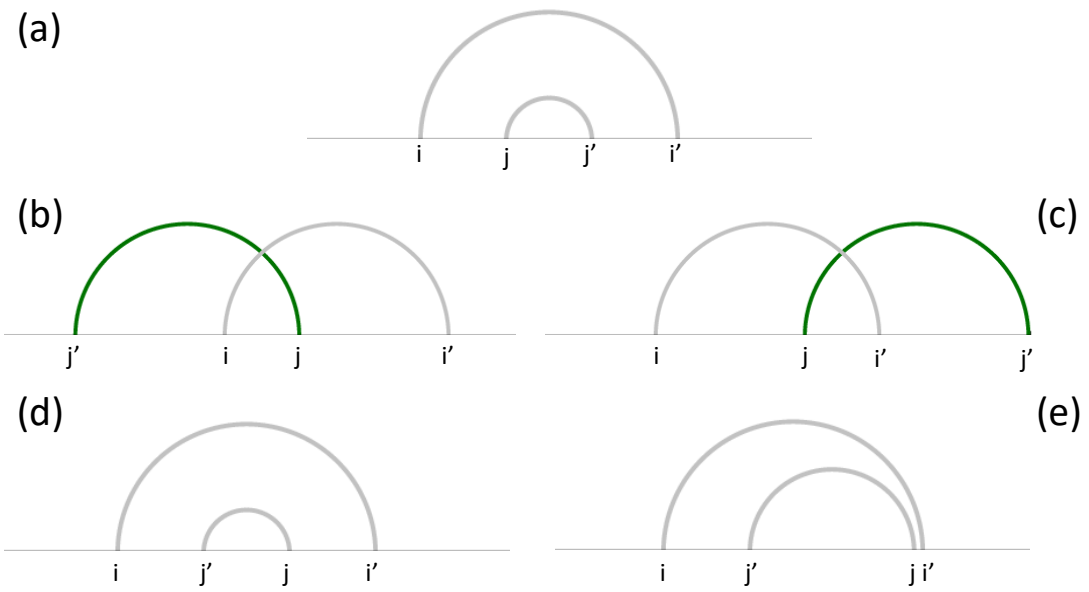

Figure S2: Relationships between two base pairs differentiated by DP algorithm.

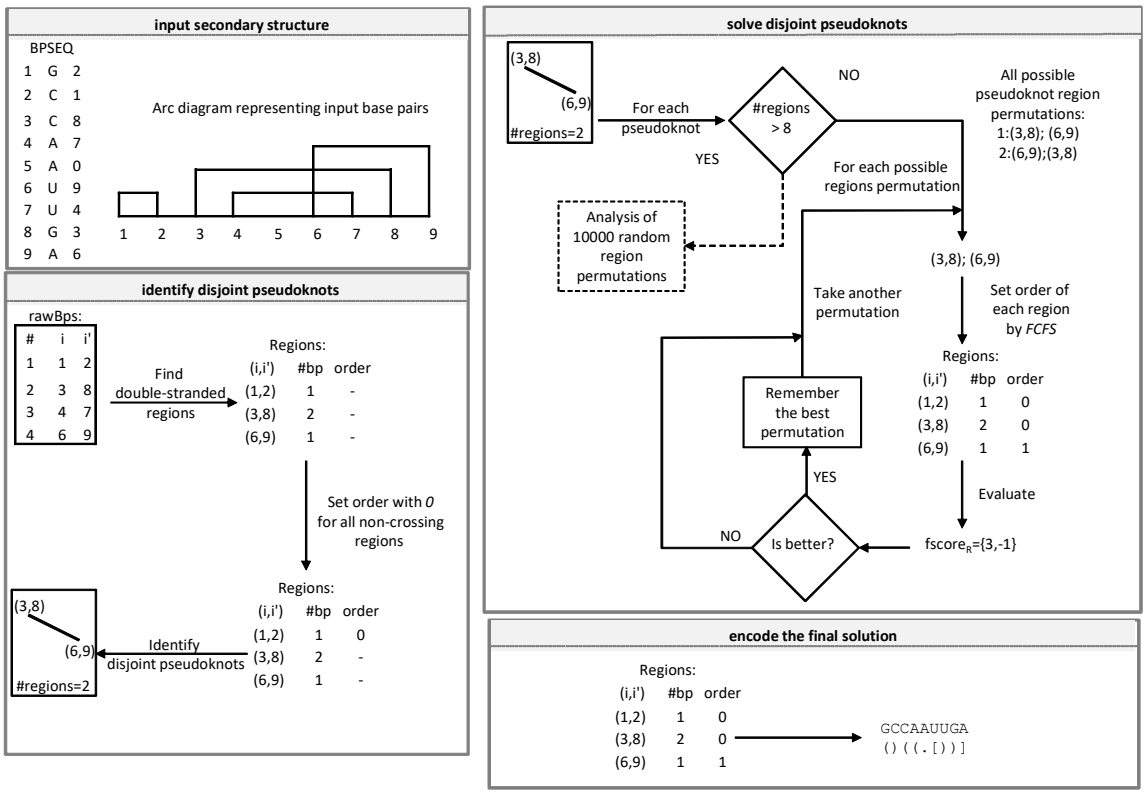

Figure S3: Example execution of HYB algorithm.

Table S1: All-against-all algorithm comparison for $DS1'$ dataset upon $fscoreI$.

	FCFS	EG	EC	DP	HYB	# Duels won	# Battles won
FCFS	–	0	1	0	0	1	0
EG	69	–	17	0	1	87	0
EC	70	5	–	0	0	75	0
DP	74	5	17	–	1	97	0
HYB	73	5	16	0	–	94	0
# Duels lost	286	15	51	0	2	–	–
# Battles lost	65	0	1	0	0	–	–

Table S2: All-against-all algorithm comparison for $DS2'$ dataset upon $fscoreI$.

	FCFS	EG	EC	DP	HYB	# Duels won	# Battles won
FCFS	–	0	4	0	0	4	0
EG	159	–	85	0	4	248	0
EC	99	5	–	0	1	105	0
DP	162	5	85	–	4	256	0
HYB	159	5	82	0	–	246	0
# Duels lost	579	15	256	0	9	–	–
# Battles lost	96	0	4	0	0	–	–

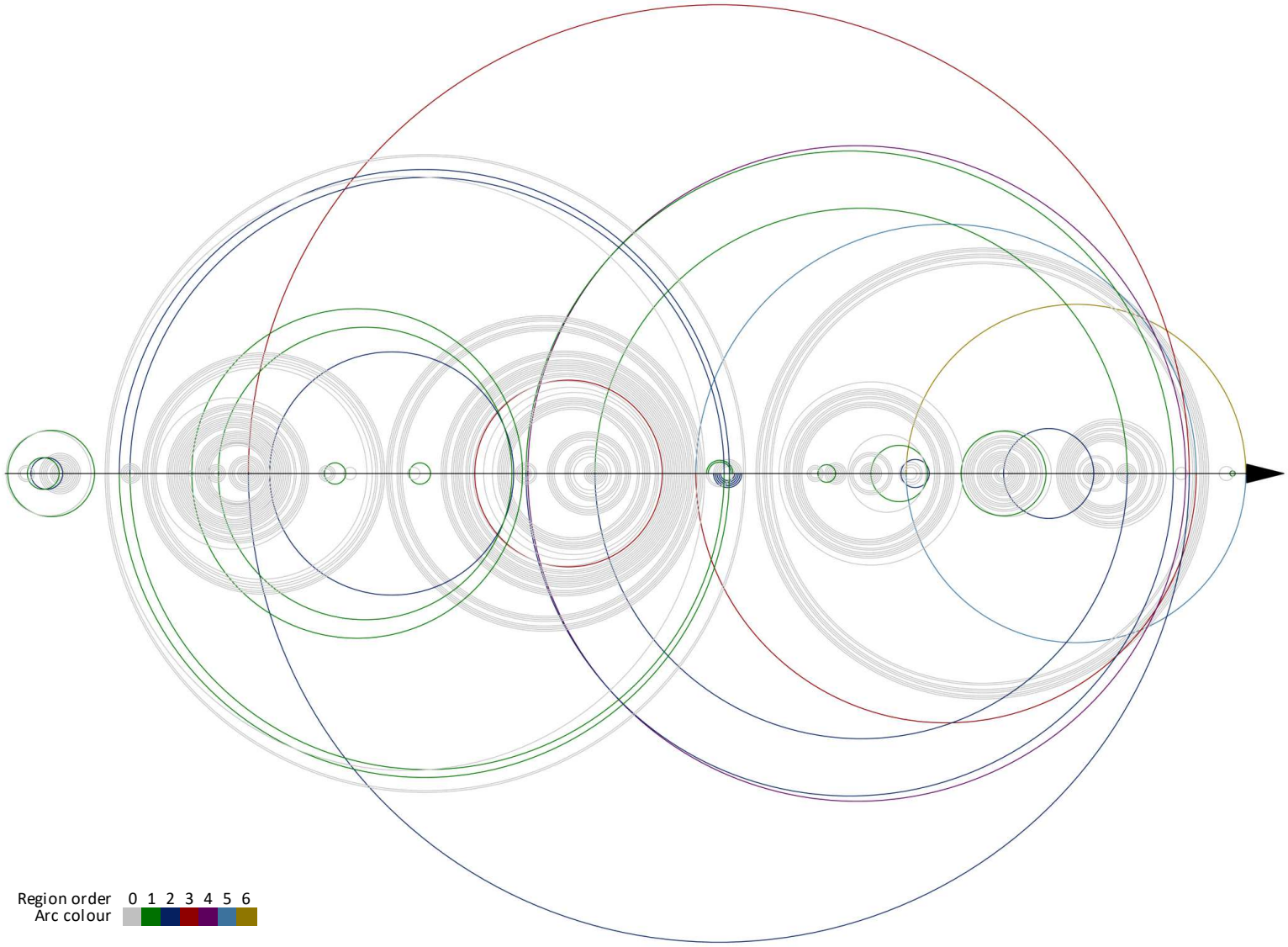

Figure S4: Arc diagrams of pseudoknot-involved regions in RNA from ribosomal subunit from human mitochondria (3J7Y, chain A) corresponding to EG/EC/DP (top) and FCFS (bottom) results.

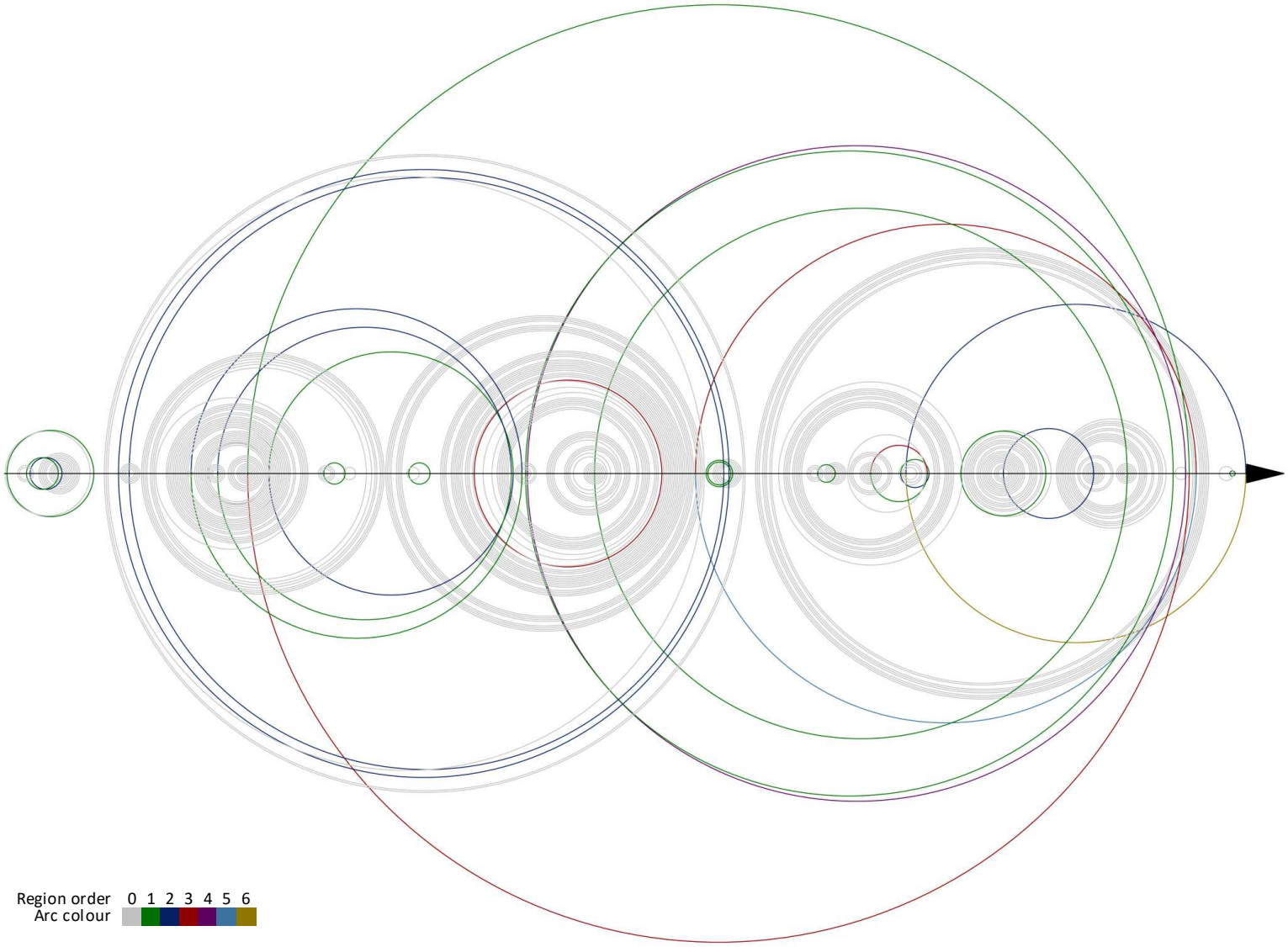

Figure S5: Arc diagrams of pseudoknot-involved regions in RNA from ribosomal subunit from human mitochondria (3J7Y, chain A) corresponding to HYB (top) and EG/EC/DP (bottom) results.