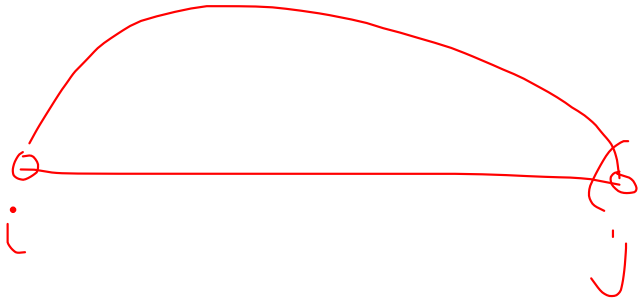
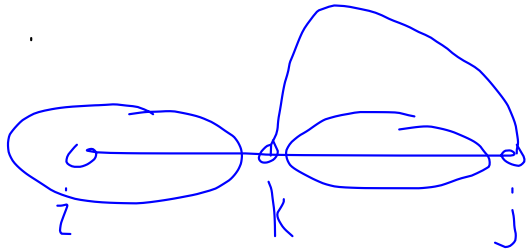
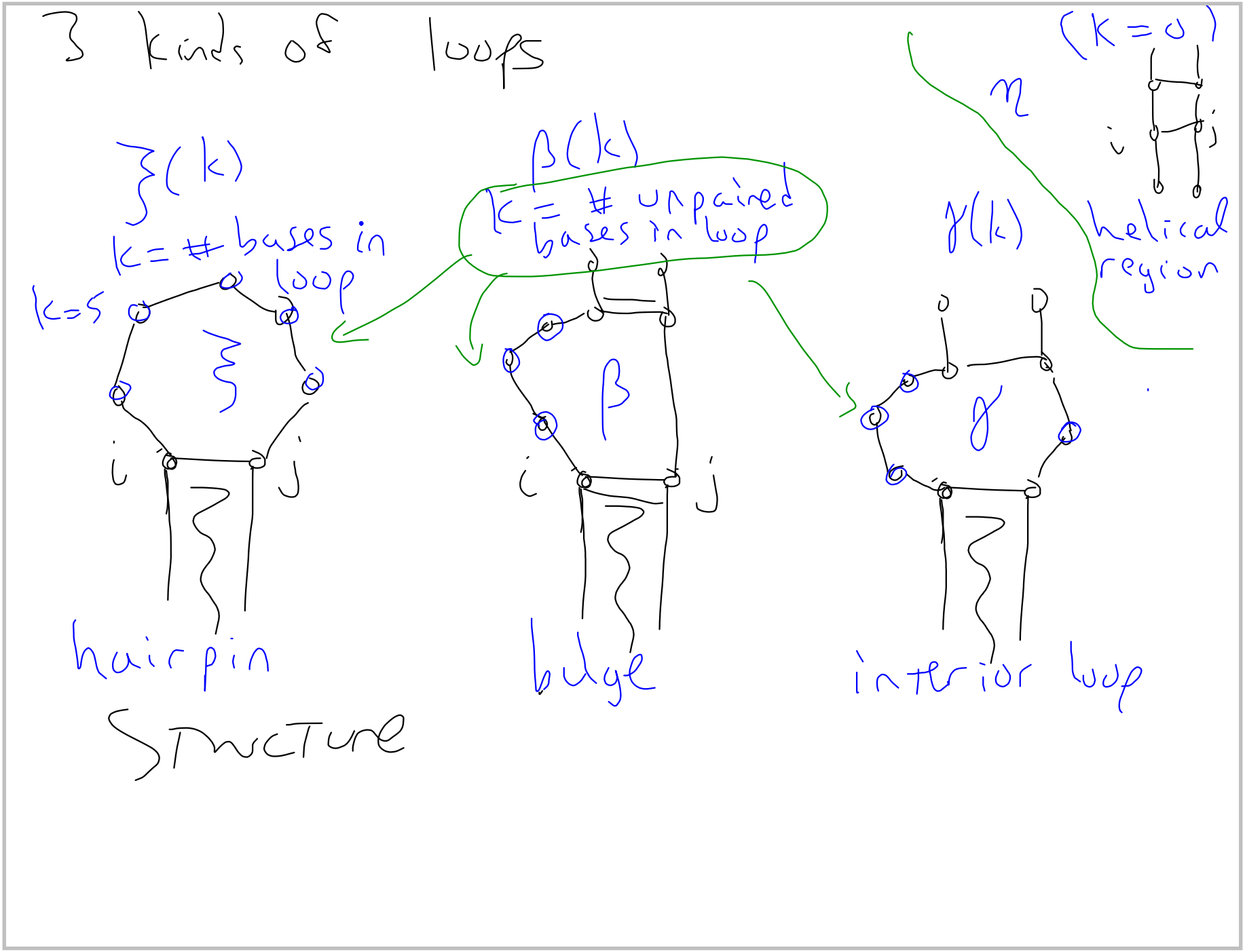
RNA Secondary Structure Prediction.

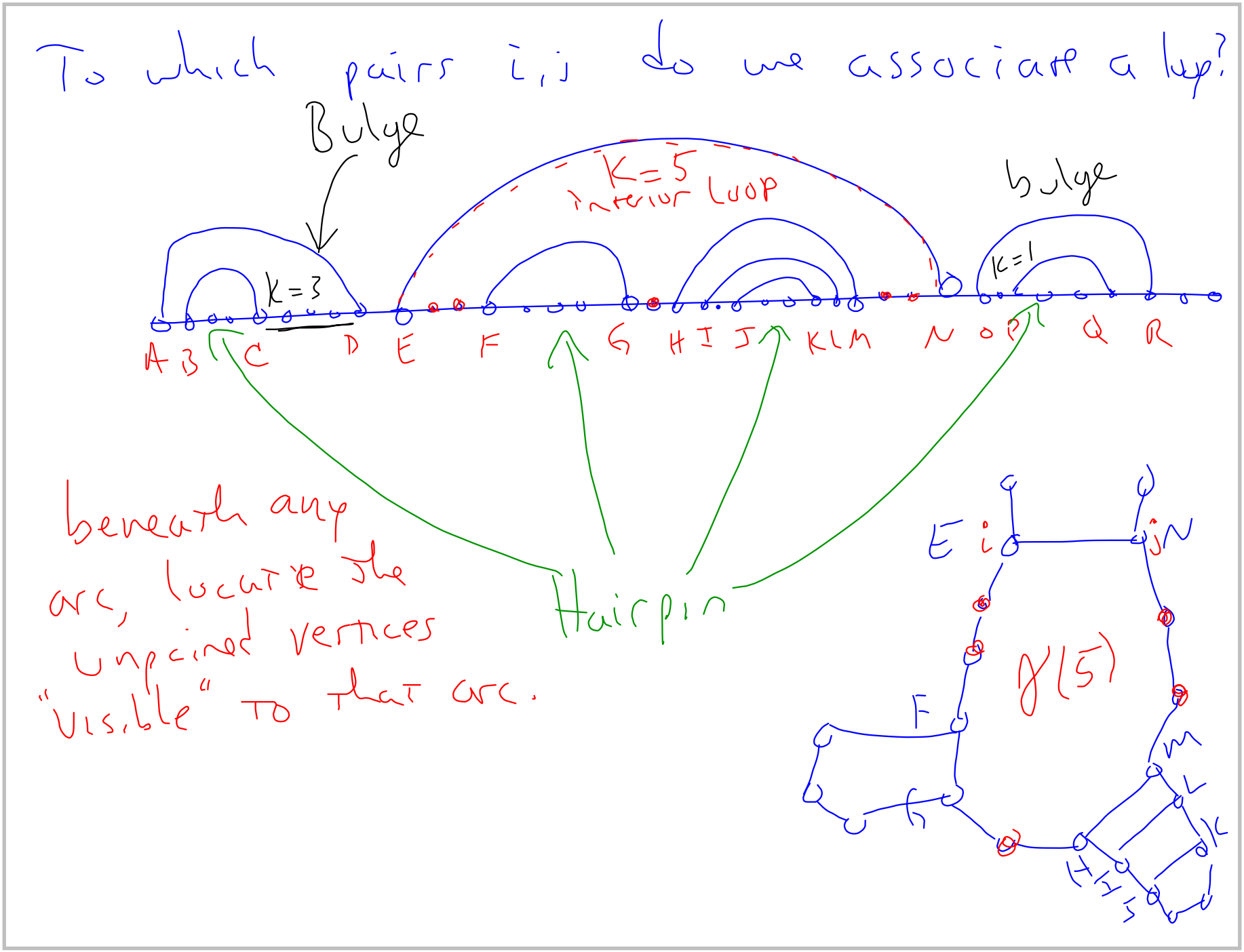
$$S_{i,j} = \min \begin{cases} S_{i,j-1} \\ \alpha(i,j) + S_{i+1,j-1} \\ \min_k \left[\alpha(k,j) + S_{i,k-1} + S_{k+1,j-1} \right] \end{cases}$$

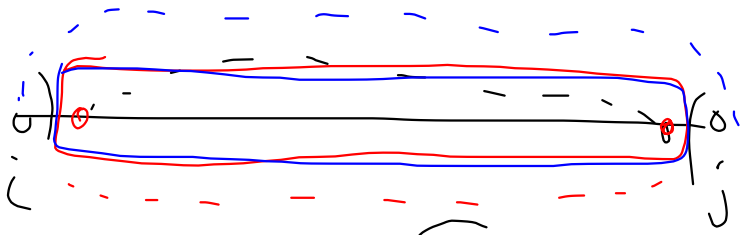




Now we want to account for loops


3 kinds of loops
ζ(k)
k = # bases in loop
k=5
i
j
hairpin
β(k)
k = # unpaired bases in loop
β
i
j
bulge
γ(k)
γ
interior loop
η
(k = 0)
i
j
helical region
structure

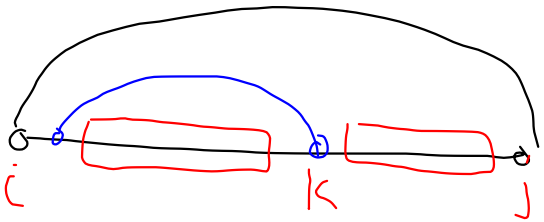

To which pairs i,j do we associate a hyp?
Bulge
K=5
Interior Loop
bulge
K=3
K=1
A B C D E F G H I J K L M N O P Q R
beneath any arc, locate the unpaired vertices "visible" to that arc.
Hairpin
E i j N
F
M
L
K
H I J

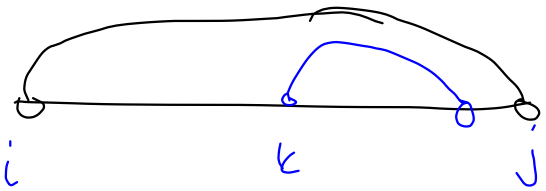


$S_{i,j} = E(S_{i,j})$ (bool)

(U, S)

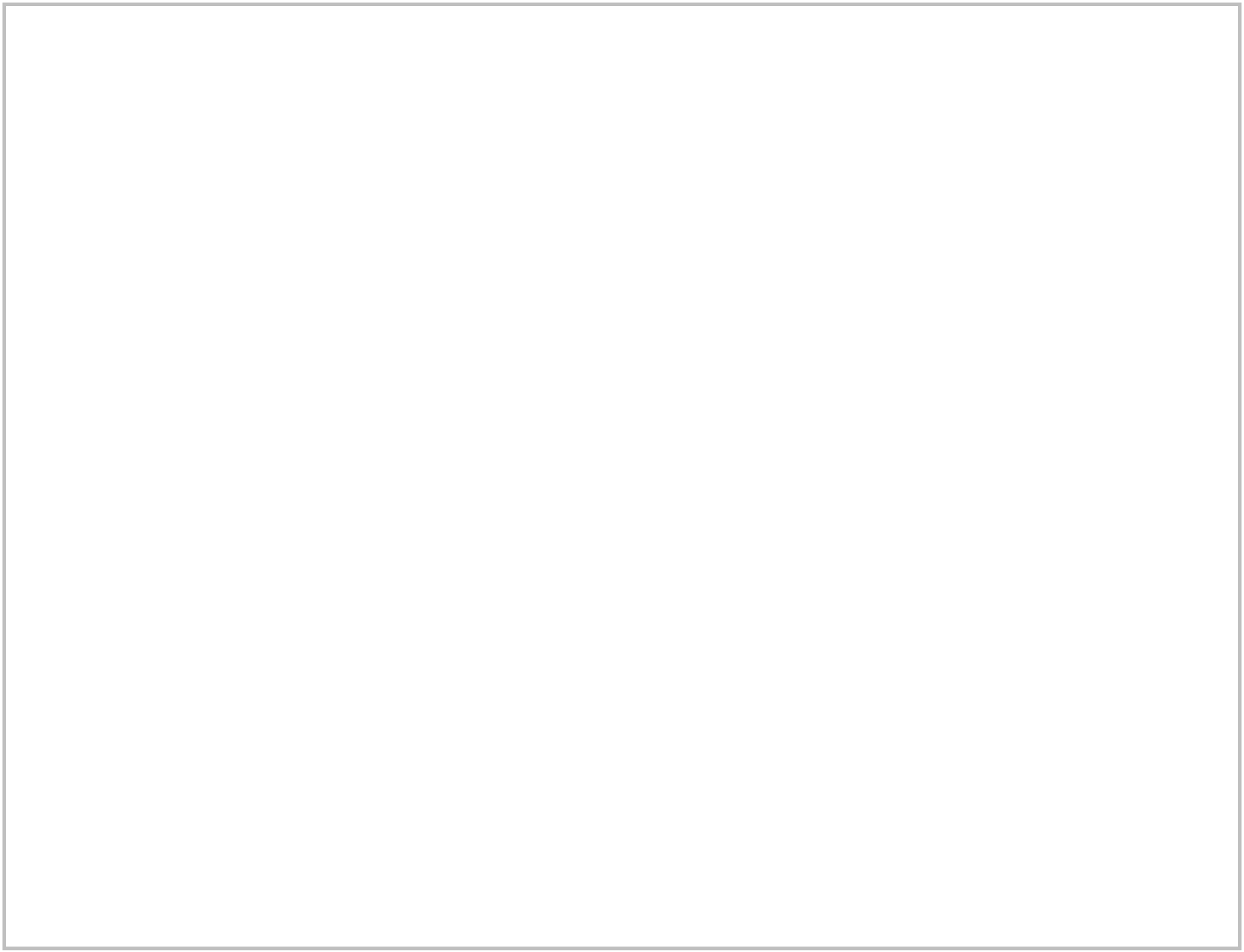
$$S_{i,j} = \min \begin{cases} \alpha(i,j) + \eta + L_{i+1,j-1} & \text{i paired with j helical loop} \\ \alpha(i,j) + \xi(j-i-1) & \text{i paired with j hairpin loop} \\ \alpha(i,j) + \alpha(i+1,k) + L_{i+1,k} + S_{k+1,j-1} & \text{i paired with j bulge} \\ \alpha(i,j) + \alpha(k,j-1) + L_{k,j-1} + S_{i+1,k-1} & \end{cases}$$





$L_{i,j}$ (analogous to $S_{i,j}$)

$L_{i,j}$ = best possible score or a structure ~~better~~ on substring $R_{i,j}$, assuming i and j are paired.



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