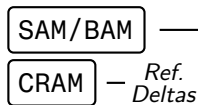


Alignment Input



Condensed Repr. ($\times n$ threads)



Process 3' to 5'

Estimated
RNA Mod.
Location

Alignment
Operation

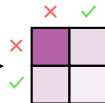
PHRED Score
Quality Filter



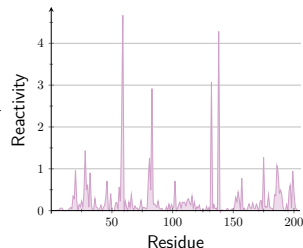
Per-Base Statistics

	A	C	G	T	del	ins	trm
A							
C							
G							
T							

Pairwise Statistics



Normalized Profiles



Mutual Information

