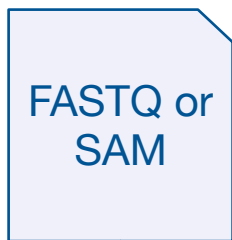


Single file with
sequencing error
information

Multiple files with
sequencing error
information

Single file **without**
sequencing error
information



Phred / quality
scores

Average of Phred /
quality scores

Assume error
distribution, e.g., Beta

Probabilistic sequence
using **nucleotide-level**
uncertainty

0.93	0.02	0.03	...	0.03	0.05	0.82
0.02	0.93	0.01	...	0.01	0.91	0.05
0.03	0.03	0.94	...	0.95	0.02	0.03
0.02	0.02	0.02	...	0.01	0.02	0.10

For example, selecting the m
most probable sequences

Probabilistic sequences	0.000051	ACGT...TGCA
using sequence-level	0.000047	ACGA...TGCA
uncertainty	0.000034	ACGT...CGCA