Structure Fold II

Software to facilitate rapid analysis of genome-wide chemical probing data on RNA structure

(-)DMS   (+)DMS   A, B: Control   C, D: Experimental

Inputs:
- A.fastq
- B.fastq
- C.fastq
- D.fastq

Adapter Trimming / Quality Trimming

fastq_trimmer.py ①

- A_trimmed.fastq
- B_trimmed.fastq
- C_trimmed.fastq
- D_trimmed.fastq

Map to Reference Transcriptome

fastq_mapper.py ②

- A_trimmed_mapped.sam
- B_trimmed_mapped.sam
- C_trimmed_mapped.sam
- D_trimmed_mapped.sam

Filter <.sam>

sam_filter.py ③

- A_trimmed_mapped_filtered.sam
- B_trimmed_mapped_filtered.sam
- C_trimmed_mapped_filtered.sam
- D_trimmed_mapped_filtered.sam

Generate <.rtsc>

sam_to_rtsc.py ④

- A.rtsc
- B.rtsc
- C.rtsc
- D.rtsc

Generate <.react>

rtsc_to_react.py ⑤

- AB.react
- CD.react