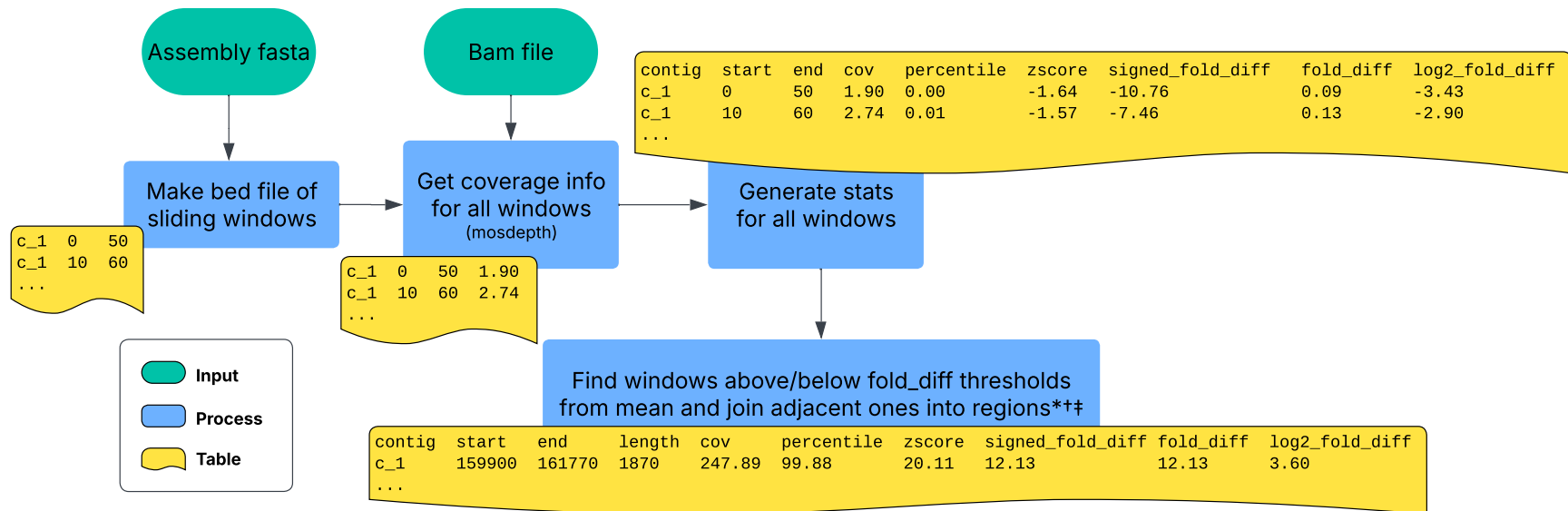


CovAnalyzer



Primary outputs:

- table of regions of relative high/low coverage
- fasta of regions of relative high/low coverage
- all window coverages stats and histogram

* ignores regions of low coverage within 200 bp of start/end of a contig

† default uses mean of whole assembly as baseline, but --per-contig can be set to use the mean of each contig for that contig as the baseline

‡ can pass contigs we want to ignore to the --exclude-contigs parameter (e.g., mitochondria/chloroplast)