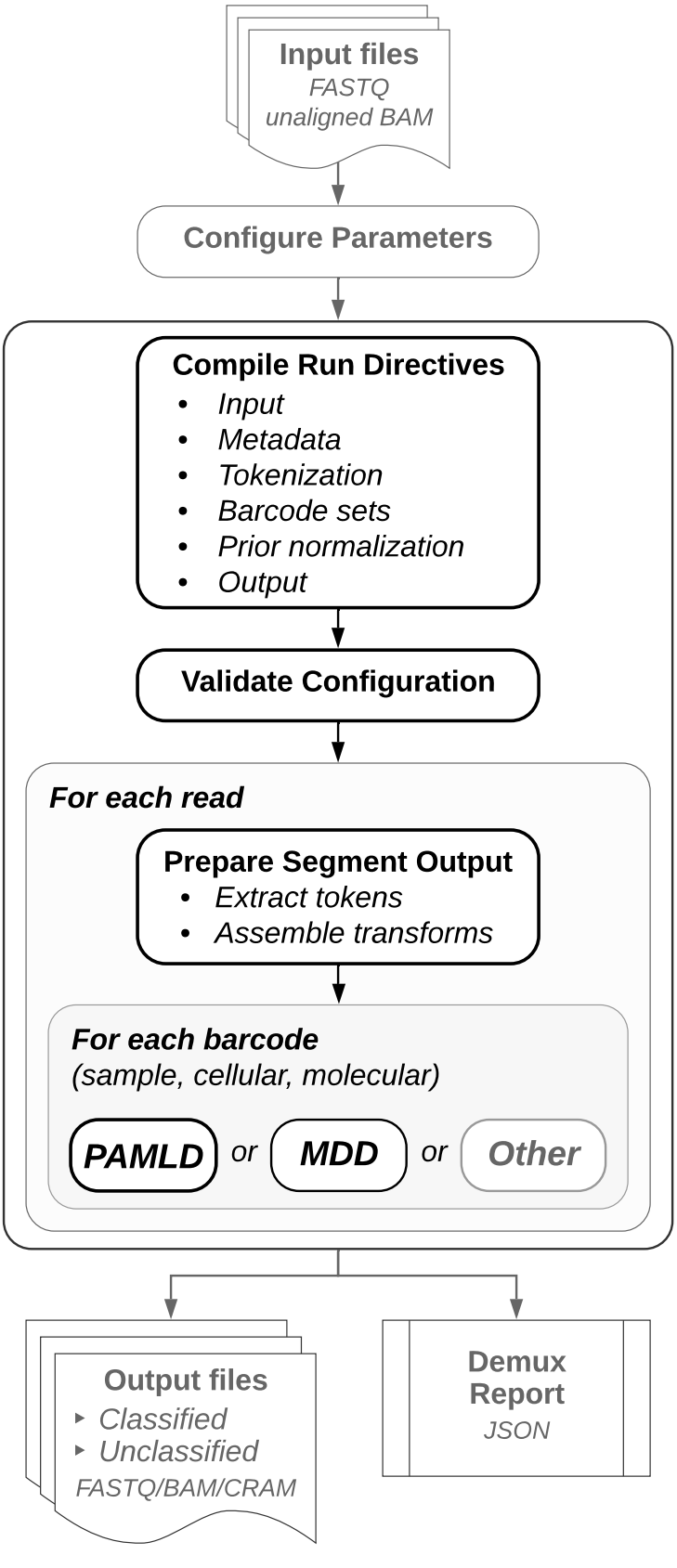
Input files
FASTQ
unaligned BAM
Configure Parameters
Compile Run Directives
Input
Metadata
Tokenization
Barcode sets
Prior normalization
Output
Validate Configuration
For each read
Prepare Segment Output
Extract tokens
Assemble transforms
For each barcode
(sample, cellular, molecular)
PAMLD
or
MDD
or
Other
Output files
Classified
Unclassified
FASTQ/BAM/CRAM
Demux Report
JSON