

**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*