# Völundr single cell work flow.

Völundr.py

* Single cell = True
  + Single\_Cell.SingleCell(o) # instantiate the class object.
    - Fastq.Fastq\_Validate
      * Check for file existence, exit if False.
      * Set file type = FASTQ
      * Set dt = current date # %Y%M%D format
      * Set file\_path = base path of FASTQ file.
      * Set mime\_type of FASTQ file using pymajic
      * Define file object base on mime\_type.
      * Return all this as a named tuple converted to a dictionary.
    - IndexFileParser(o.index\_file).interval\_file. # parse the index file.
      * Check file existence.
      * Iterate file
        + Skip lines that are comments or spaces.
        + Skip end of line comments and spaces.
        + Stop if column count <3.
      * Reassemble data as a list of tuples.
      * Return list.
    - Build dictionary based on index object.
    - Define and initialize the output files
  + fastq\_analysis # if bam\_only = False
    - Iterate the FASTQ file one line at a time.
      * Add each line to a list that represents the current read. Each FASTQ read consists of four lines.
      * When the list contains 4 lines, pass all four to the FASTQ.Reader
        + Instantiate the list into 4 variables.
        + Make sure sequence length and quality strings are the same length.
        + Return sequence read object.
      * Iterate the index file object.