fastq fileを２分割

<https://github.com/shenwei356/seqkit/releases/tag/v0.15.0>

でseqkitをDLしてファイルを２分割できるようにした

[SeqKit v0.15.0](https://github.com/shenwei356/seqkit/releases/tag/v0.15.0)

* seqkit grep/locate: update help message.
* seqkit grep: **search on both strand when searching by sequence**.
* seqkit split2: fix redundant log when using -s.
* seqkit bam: new field RightSoftClipSeq. [#172](https://github.com/shenwei356/seqkit/pull/172)
* seqkit sample -2: remove extra \n. [#173](https://github.com/shenwei356/seqkit/issues/173)
* seqkit split2 -l: fix bug for splitting by accumulative length, this bug occurs when the first record is longer than -l, no sequences are lost.

例えば

$ seqkit split2 -p 2 SRR4423844.fastq.gz