Tutorial: BASH one-liners for subsampling reads

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In the following one-liners, k=10000 subsamples the files to 10000 reads using reservoir sampling:

Subsampling paired-end reads (FASTQ):

```
paste forward.fastq reverse.fastq | awk '{ printf("%s",$0); n++;
if(n%4==0) { printf("\n");} else { printf("\t");} }' |
awk -v k=10000 'BEGIN{srand(systime() + PROCINFO["pid"]);}{s=x++<k?x-1:int(rand()*x);if(s<k)R[s]=$0}END{for(i in R)print R[i]}' |
awk -F"\t" '{print $1"\n"$3"\n"$5"\n"$7 > "forward_sub.fastq";print
$2"\n"$4"\n"$6"\n"$8 > "reverse_sub.fastq"}'
```

Subsampling paired-end reads (FASTA):

Subsampling single reads (FASTQ):

```
cat single.fastq | awk '{ printf("%s",$0); n++; if(n%4==0) {
printf("\n");} else { printf("\t");} }' |
awk -v k=10000 'BEGIN{srand(systime() + PROCINFO["pid"]);}{s=x++<k?x-1:int(rand()*x);if(s<k)R[s]=$0}END{for(i in R)print R[i]}' |
awk -F"\t" '{print $1"\n"$2"\n"$3"\n"$4 > "single_sub.fastq"}'
```

Subsampling single reads (FASTA):

```
awk '/^>/ {printf("\n%s\n",$0);next; } { printf("%s",$0);} END
{printf("\n");}' < single.fasta | awk 'NR>1{ printf("%s",$0); n++;
if(n%2==0) { printf("\n");} else { printf("\t");} }' |
awk -v k=10000 'BEGIN{srand(systime() + PROCINFO["pid"]);}{s=x++<k?x-1:int(rand()*x);if(s<k)R[s]=$0}END{for(i in R)print R[i]}' |
awk -F"\t" '{print $1"\n"$2 > "single_sub.fasta"}'
```

Reservoir sampling:

A simple random sampling strategy to produce a sample without replacement from a stream of data - that is, in one pass: O(N)

Want to sample s instances - uniformly at random without replacement - from a population size of n records, where n is not known.

Figuring out n would require 2 passes. Reservoir sampling achieves this in 1 pass. A reservoir R here is simply an array of size s. Let D be data stream of size n

Algorithm:

Store first s elements into R.
for each element in position k = s+1 to n,
accept it with probability s/k
if accepted, choose a random element from R to replace.

Partial analysis:

Base case is trivial. For the k+1st case, the probability a given element i with position $\le k$ is in R is s/k. The prob. i is replaced is the probability k+1st element is chosen multiplied by i being chosen to be replaced, which is: s/(k+1) * 1/s = 1/(k+1), and prob that i is not replaced is k/k+1.

So any given element's probability of lasting after k+1 rounds is: (chosen in k steps, and not removed in k steps)

```
= s/k * k/(k+1), which is s/(k+1).
```

So, when k+1 = n, any element is present with probability s/n.

Reference: http://blogs.msdn.com/b/spt/archive/2008/02/05/reservoir-sampling.aspx