**Split BAM files with specified regions**

*Script name:* samtools\_view\_region.pl

What it does: Takes a BAM file as input and output several BAMs of specified locus.

*Synopsis:*

***perl*** samtools\_view\_region.pl ***–x bam***

*Parameters:*

-x (string): file extension (bam)

/!\ BAM files have to be present in CWD.

/!\ The number of BAM files needs to be specify in the script (-t parameter 5th line)

/!\ The specified regions are in the array @regions in the script

*All the steps in detail*

* Samtools view to select reads in the specified locus

<http://www.htslib.org/doc/samtools-1.1.html>

* Samtools view to change SAM to BAM file
* Samtools flagstat to get basic statistics on the number of reads