



Informatics on High-throughput Sequencing Data


(Summer Course 2020)

Day 15




SAM tools

← → ↻ sourceforge.net/projects/samtools/files/samtools/

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 **SAM tools**

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README.txt	2019-12-06	36.1 kB
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htslib-1.10.tar.bz2	2019-12-06	1.3 MB

[htslib-1.10.tar.bz2](#)

SAM tools

Installing samtools

Follow these steps:

```
cd ~  
# optional. you may already have a src directory  
mkdir src  
cd ~/src  
git clone https://github.com/samtools/htslib  
git clone https://github.com/samtools/samtools  
cd samtools  
make  
cp samtools ~/bin
```

SAM tools

- ▶ `./samtools view -S -b sample.sam > sample.bam`
- ▶ `./samtools view sample.bam | head` (i.e. without header info)
- ▶ `./samtools view -h sample.bam > sample.sam`
- ▶ `./samtools flagstat sample.bam`
- ▶ `./samtools sort sample.bam -o sample.sorted.bam`
- ▶ `./samtools view sample.sorted.bam | head`
- ▶ `./samtools index sample.sorted.bam` (i.e. sample.sorted.bam.bai)
(IGV viewer and easy to access alignment regions)
- ▶ `./samtools view sample.sorted.bam Chr5:1000000-1900000 | wc -l` (i.e. files must be sorted then indexed)
- ▶ `./samtools view -L example.bed sample.sorted.bam`
(i.e. combine with head shows the lower range / tail for upper range)

Thanks!

// | ?