





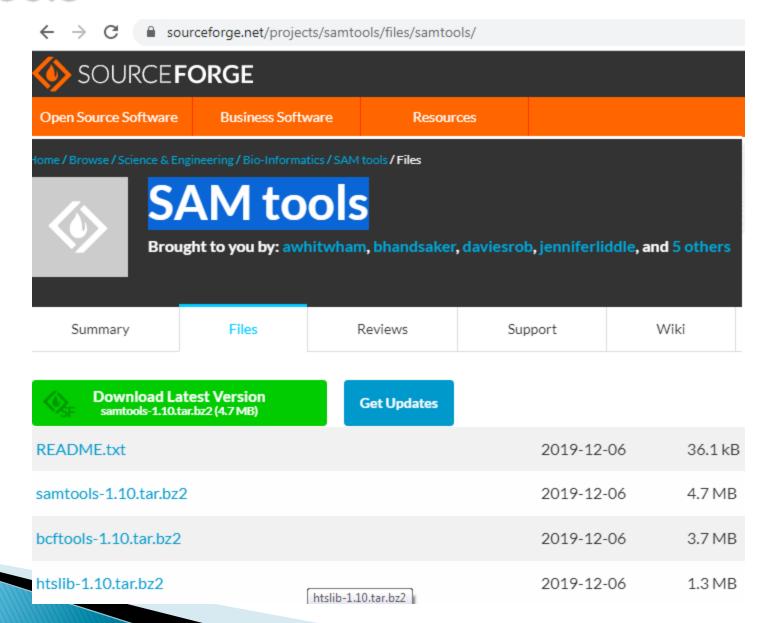
# Informatics on High-throughput Sequencing Data

(Summer Course 2020)

**Day 15** 



### **SAM tools**



## **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 Chr5:10000001900000 | 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! // |?