

# Tools

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Statistical Methods for Next Generation Sequencing  
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# Unix shell scripting

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(BASH)

`cut, uniq, wc, sed, awk, grep`

redirection

These tools are extremely fast.

# Software packages

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An aligner (Bowtie, BWA, Bowtie 2)

Samtools

Picard

Some browser (IGB?)

# R packages

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Rsamtools, ShortRead

IRanges, GenomicRanges

Biostrings, BSgenome

GenomicFeatures, VariantAnnotation

DESeq, baySeq, edgeR, cqn

Gviz (replacing GenomeGraphs)