BamBam
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http://sourceforge.net/projects/bambam/

Bam2Consensus
- Generate consensus for each contig
  - `bam2consensus A2.demo.bam`
- Generate consensus for each region
  - `bam2consensus -g sub.bed A2.demo.bam`
- Generate FASTA for each contig/region
  - `bam2consensus A2.demo.bam D5.demo.bam`
- Aligned unless also using indel detection
- Also extract reads with Bam2Fastq
- Support for paired end reads

Counter
- With or without RPKM normalization
  - `counter -g sub.bed A2.demo.bam D5.demo.bam`
  - `counter -g sub.bed A2.demo.bam D5.demo.bam -n1`
- Pass to EdgeR for differential expression
- Also look at coverage with
  - Effen – read coverage
  - Giraf – base coverage

Counter - results

InterSnp
- Straightforward SNP caller
  - `interSnp -m5 A2.demo.bam D5.demo.bam`
- Minimum allele coverage
- Minimum allele frequency
- Pebbles to impute missing data
- `pebbles --m3 --k3 demo.snp`
- Run snp2dist.pl and pass to PHYLIP
  - `snp2dist.pl demo.snp2 > infile`
- `neighbor`
- Lots of scripts to modify SNP files
InterSnp - results

SubBam
- Subset sorted BAM
- subBam -g sub.bed A2.demo.bam
- Quicker than SAMtools view in some cases
- Modify coordinates of a BAM to sub-reference
- subBam -g sub.bed A2.demo.bam -m 1
- Only genes or small regions of interest

HapHunt
- K-means clustering
- Short amplicons
- Continuous coverage

MetHead
- Summarize BS-seq
- Corrects for non-stranded protocols
- Binomial significance test
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