SeqQual pipeline overview

Combining various tools for processing files automatically

Part 1
Sanger-based chromatogram sequences / many fragments, N / 2N data

Phred Phrap

ace
phd
fasta
poly

Polyphred

Polyphred.out
Updated *.ace

.phd /.ace
*.fasta

Core Bioperl scripts integrating quality at the nucleotide level

Part 2
Large ace assembly files < NGS data
fasta/fasta.qual

Ace-dealing Bioperl scripts

Fastq → bam → ace

Part 3
Batches of fasta alignments (low quality masked at chosen quality score)
IUPAC codes for heterozygotes in 2N data

Fasta batch post-treatment Tools
Trimming / filtering
Merging reads/sequences
Alignment optimization
SNP summary statistics
Haplotype data phase unknown...

Updated fasta alignments,
SNP alignments
Un-aligned fasta
Arlequin formatted files