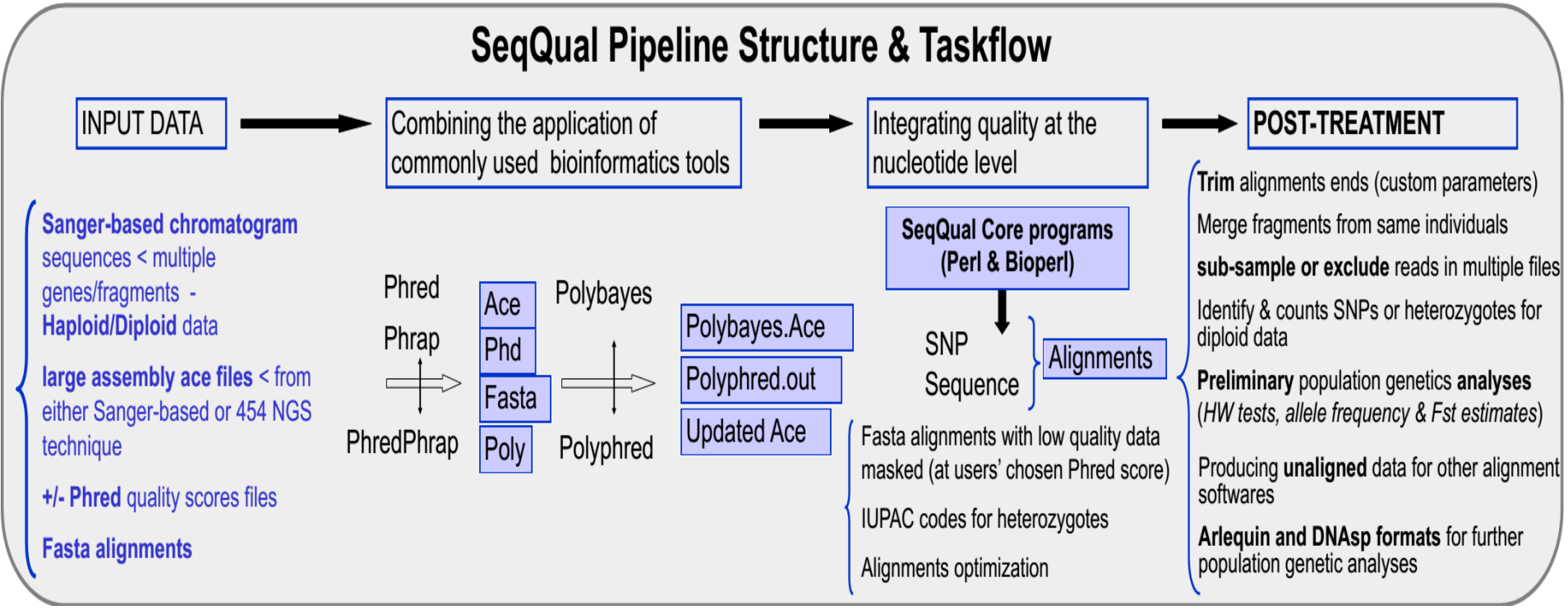
SeqQual Pipeline Structure & Taskflow
INPUT DATA
Combining the application of commonly used bioinformatics tools
Integrating quality at the nucleotide level
POST-TREATMENT
Sanger-based chromatogram sequences < multiple genes/fragments - Haploid/Diploid data
large assembly ace files < from either Sanger-based or 454 NGS technique
+/- Phred quality scores files
Fasta alignments
Phred
Phrap
PhredPhrap
Ace
Phd
Fasta
Poly
Polybayes
Polyphred
Polybayes.Ace
Polyphred.out
Updated Ace
SeqQual Core programs (Perl & Bioperl)
SNP
Sequence
Alignments
Fasta alignments with low quality data masked (at users' chosen Phred score)
IUPAC codes for heterozygotes
Alignments optimization
Trim alignments ends (custom parameters)
Merge fragments from same individuals
sub-sample or exclude reads in multiple files
Identify & counts SNPs or heterozygotes for diploid data
Preliminary population genetics analyses (HW tests, allele frequency & Fst estimates)
Producing unaligned data for other alignment softwares
Arlequin and DNAsp formats for further population genetic analyses