

SOAP-HLA

The usage of SOAP-HLA:

Description

MHC typing pipeline ; V1.2

Contact

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Analysis steps

HLA typing steps as follows:

- 1 collect reads from each exons
- 2 realignment by blast
- 3 assemble reads to haps and filter haps
- 5 combination all exons' haps to select the best two types

usage

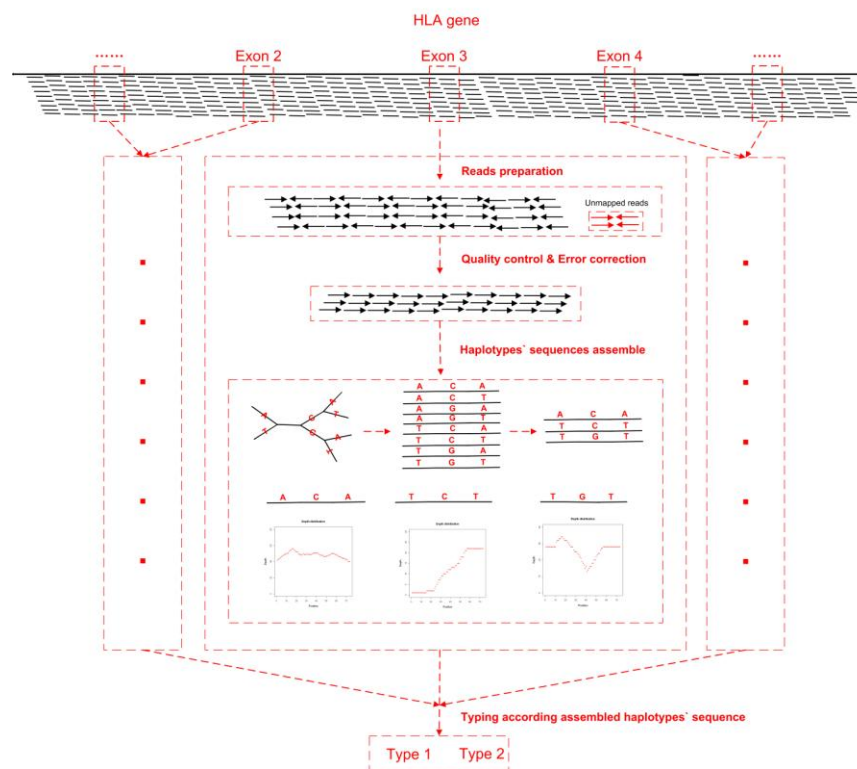
Options:

- i input bam file(Alignment by bwa)
- od output dir
- v ref version(Hg19)

sample

perl MHC_autopipeline_total.pl -i bam -od outdir -v version

The pipeline of SOAP-HLA:



For the first step, we select reads from each gene, and do realignment with the reference that contains all genes' types. Then we assemble the reads into haplotypes and combination all haplotypes from all exons to choose the best two types as the genes' types.