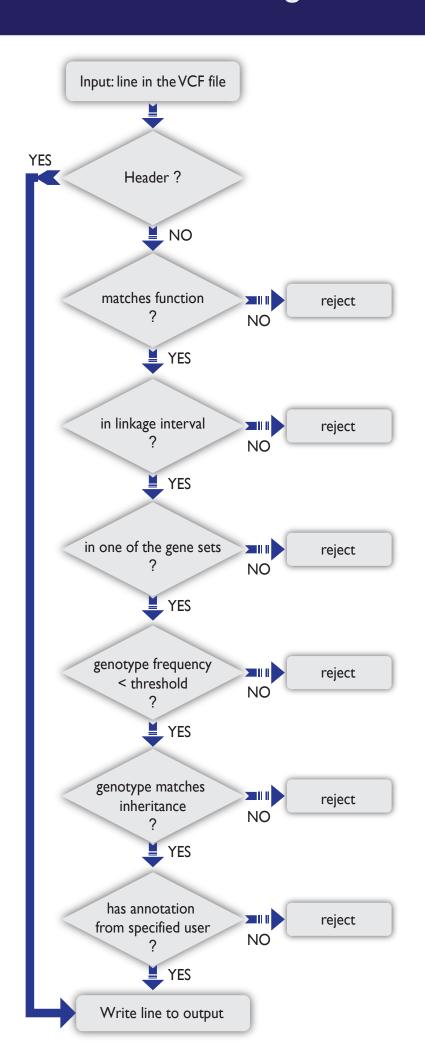
VCF-file filtering





Indels just pass the frequency filter.

The compound heterozygeous filter looks for two or more heterozygeous variants in one gene. Note that both variants have to pass the other filters (execpt the annotation filter). Custom regions specified in the gene sets count as one additional gene (i.e., if ≥2 heterozygeous variations are found in the custom regions of a gene set, they are reported as compound heterozygeous recessive).