**From GVCFs to VCF**

*Script name:* gvcfs\_to\_vcf.pl

What it does: it takes one or more gvcf files and call SNPs with HaplotypeCaller from GATK

*Synopsis:*

***perl gvcfs\_to\_vcf.pl -r musa.fasta -p output -x gvcf***

/!\ GVCF files have to be present in CWD.

*Parameters:*

-r (string): reference fasta filename

-p (string): VCF output prefix

-x (string): file extension (gvcf)

*All the steps in detail*

* Create a VCF file with GenotypeGVCFs from GATK

<https://software.broadinstitute.org/gatk/documentation/tooldocs/3.8-0/org_broadinstitute_gatk_tools_walkers_variantutils_GenotypeGVCFs.php>

* Prefiltering with VariantFiltration and SelectVariants from GATK. Annotating variants with:
  + SnpCluster: remove clusters of SNPs (more 2 SNPs in 10bp).
  + QualitybyDepth: remove SNPs with a QD < 1.5 (<https://software.broadinstitute.org/gatk/documentation/tooldocs/3.8-0/org_broadinstitute_gatk_tools_walkers_annotator_QualByDepth.php>)