**Computational Human Genomics Project**

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1. **Project Rationale**

(max 10 lines)

Computational Genomic analysis on samples obtained from a diseased patient. The aim of this project is to apply an example of human genomic workflow on a patient, characterizing both tumor and control samples.

Bla bla spiegare meglio!!

1. **Computational Workflow**

(including details to make it reproducible)

Starting from the two provided BAM files (tumor and control DNA sequences from the same individual) we first analysed the general and detailed statistics using *samtools flagstat* and *samtool stats.*

We then operated a process of realignment, to identify all the positions in which hidden deletions are present. Specifically, this was possible via the GATK tool, that base its functionality on the default CIGAR line. First, *RealignedTargetCreator* is applied to the BAM file to identify which regions need to be realigned. Then, *IndelRealigner* performs the actual realignment at the target intervals. To perform this analysis we used as a reference the *human\_g1k\_v37.fasta,* an Homo Sapiens genome reference file that was built starting from the GRCh37 reference. We also provided a set of target regions in which to limit this protocol, specifically, we limited the analysis to a set of regions in chromosomes 15, 16, 17, and 18 (information contained in the file *Captured\_Regions.bed*).

A process of base quality score recalibration was operated to assign accurate confidence scores to each sequence, specifically adjusting the PHRED quality scores. Specifically, this process requires four steps that include the use of the *BaseRecalibrator* tool, that model the errors and generates a *BaseRecalibrator Table* that tells us how much correction is needed. The recalibrated data is then written to a BAM file thanks to the *PrintReads* tool. The process is then repeated to build the after model to evaluate the remaining errors and finally, it is possible to obtain the before and after plots via the tool *AnalyzeCovariates*. The *hapmap\_3.3.b37.vcf* database, containing information on known polymorphic sites, was selected as the one to exclude regions around known polymorphisms from analysis. We also explicated the argument *–emit-original-qual* to emit original base qualities and obtain a faster process.

We marked the duplicates using the *MarkDuplicates* tool from Picard. This tool exploits the CIGARs to infer the presence of duplicates. Specifically, thanks to the argument *REMOVE\_DUPLICATES* set to true, it is possible to create a new .bam file without the duplicates found.

The process of variant calling was possible thanks to the tools *BCFTOOLS* and *GATK*.  
We combined (pipe |) *bcftool mpileup* with *bcftool call* to investigate the presence of variations. We explicated the parameters *-f*, needed for the human reference file in the FASTA format; the parameter *-v* (variants-only), to output variant sites only and finally the parameter *-c* (consensus-caller), to use the original samtools/bcftools calling method. We also operated the variant calling using GATK. We specifically used the tool *UnifiedGenotyper.* The obtained files where then analyzed using *vcftools*. We filtered the variants based on the quality, using a threshold for the minimum quality at 20 (--*minQ*) and a threshold for the minimum mean depth at 30 (*--min-meanDP)*.

We then proceeded the analysis operating a process of variant annotation, a crucial step in linking sequence variants with changes in phenotype. We specifically used SnpEff, a variant effect predictor program that is able to categorize each variant. We operated the annotation of both the *GATK* and the *BCF* .vcf files. Thanks to the tool *SnpSift* it was possible to add a layer of annotation to the variants. We specifically used two different files of annotations, *hapmap\_3.3.b37.vcf,* and *clinvar\_Pathogenic.vcf.* Specifically, the second file collects information on medical conditions with a genetic basis.

Thanks to a process of somatic variant calling we were able to identify SNPs and SNVs. This was possible by implementing in our workflow the tool *Varscan.v2.3.9*. We initially used the program *mpileup2snp* with a p-value threshold of 0.01.to generate a file containing SNPs found in the control sample. We then filtered this file using *vcftools,* applying the same thresholds as seen above.  
We then focused on the somatic point mutations, this was possible by specifying the setting *somatic* of the tool *Varscan.* For this passage it was necessary to input both the control and the tumor sample pileup files. We filtered again using *vcftools* and then we operated a process of annotation. This was possible via the tool *SnpEff*.

We operated a process of ancestry analysis to investigate the mixture of the genome of the patient. This analysis was possible thanks to the tool *EthSEQ*, specifically thanks to the package EthSEQ in R studio, via the command *ethseq.Analysis* and given in input the .vcf files obtained by *Varscan*, we were able to proceed with the analysis.

Applying an algorithm of *Circular Binary Segmentation (CBS)* we were able to obtain information on the somatic copy number abberations. In order to apply CBS we initially used an R script called RCode\_DNAcopy.R that was given us by the Professor Yari Ciani (mettiamo anche la demichelis??). This script works on .csv files obtained via the previous analysis. The information on the coverage was extracted using *samtool mpileup* combined with the *Varscan copynumber* tool. The obtained output can be used to transform the coverage into information on the copy number (amplifications, deletions and homozygous deletions). This was possible using the tool *copyCaller* of *Varscan*. We finally used the Rscript CBS.R, also given to us by Professor Ciani, to perform the Circular Segmantation. Specifically in this script the library *DNAcopy* is used and a process of segmentation is performed via the command *segment.*

We then estimated the purity and the ploidy of our sample. We decided to perform this analysis since it is important to understand if our sample is an admixture of clones and if the sample has ploidy greater than one. Thanks to the tool *CLONET,* which uses information on the log2R and the Beta value, it was possible to obtain information on the clonality of the tumor sample. Using the tool *TPES* it was possible to estimate the purity from SNVs data. We specifically used an RScript, given to us by Professor Ciani, called CLONET.R which use the packages *TPES* and *CLONETv2* to operate an estimation of the purity and ploidy. DA SPIEGARE I COMANDI USATI??

We finally decided to use the *SNP Panel Identification Assay (SPIA),* a Rstudio package that determines cell line identities starting from data from SNPs. Specifically, we used a Rscipt that was given to us by Professor Francesca Demichelis and called *esercitazione\_SPIA\_code\_to\_upload.R*.

1. **Relevant Results and Interpretation**

NB graphs need to have a goooddd description

Both the files were associated to high average quality (>30) and a percentage of mapping major than 99.75%.

1. **Pitfalls and Criticism**

(max 10 lines).

Un singolo paziente

Qualità super alta

Analisi piu semplice perché i dati iniziali sono ottimi