Unit 1 Introduction to Clinical Bioinformatics # Cheat Sheet 1 SOP of AOV (Standard Operating procedure for Analysis of Variants)

Summary

Cosmic Track (gene name, specific base changes, forward or reverse strand, cDNA numbering, variant position, nearby variant, exon number)

dbSNP transcript an variant call in **HGVS** format e.g. NM_000435.2:c.743G>C and SNP ID, Chromosome coordinates and position

Minor allele, frequency of allele, count of alleles

Clinical significance

SIFT

Mutation taster

Polyphen 2

Conservation

Requires a screenshot of protein domains.

Nucleotide considerations

Orthologues

BAM Alignment

Calculation of a GVGD output

Grantham distance (GD- a measure of physiochemical differences between amino acids and Grantham variation GV – a measure of species conservation)

Screenshot of a GVGD output, Polyphen – 2 screenshot Hum/Var, SIFT output

Comparing amino acid screenshots

Splicing

Databases

gnomAD screenshot

dbSNP screenshot

Ensembl screenshots

Specific disease database screenshot

HGMD database screenshot

OMIM screenshot

UCSC screenshot

GEN ATLAS

UNIPROT screenshot

Written summary of each screenshot

Functional

Use Uniprot to identify the protein and domain regions that could be affected by the **variant**

When a missense variant **evaluate** the region where the variant is located and determine the level of local or regional constraint

Screenshot of uniport for **topology**, **family** and **domains** and amino acid modification

Write a summary of the VAF (variant allele frequency)

Use **decipher** for a screenshot of the gene, protein under view

Classification

Evaluate the **RED** evidence of **PATHOGENIC**

Evaluate the GREEN evidence of BENIGN

Final Classification

- Benign
- 2. Likely Benign
- 3. Uncertain Significance
- 4. Likely Pathogenic
- Pathogenic

Use ACMG reference criteria

References

Make a note of all relevant publications for this and related **variants**