

A prior on **Functional Analysis**

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Work Flow

- Download bkg genes: <https://www.ensembl.org/info/data/ftp/index.html>
- Results overview in FUMA
 - <https://fuma.ctglab.nl/snp2gene>
 - Input file: GWASresults.txt
- Variant Effect Prediction in Ensembl
 - <https://www.ensembl.org/Multi/Tools/VEP>
 - Input file (significant SNPs): Map.selected.rs
 - Output file (Functional Info): Select 'Gene' column
- Enrichment analysis
 - <https://fuma.ctglab.nl/gene2func>
 - Input files: GENES from significant SNPs ('Gene' column from VEP)
Background genes from the specie (Canis_familiaris.bkg_genes)

