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)
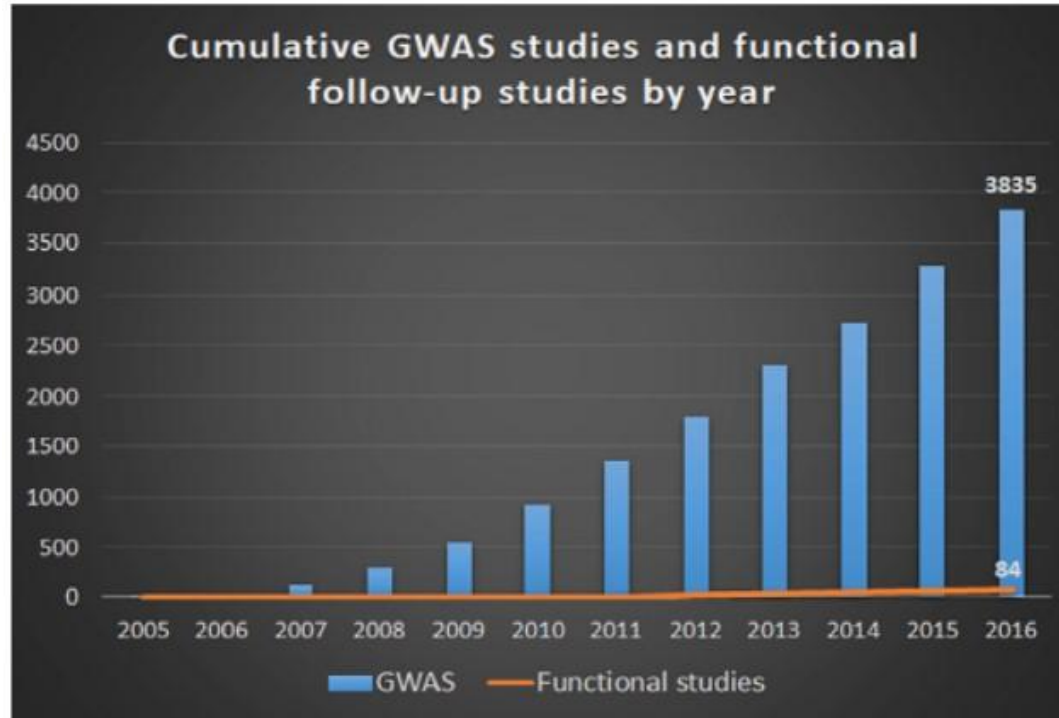   Background genes from the specie (Canis_familiaris.bkg_genes)

Figure 1. Mechanistic Understanding of Disease Risk Loci Identified by GWASs Lags Far Behind the Discovery of New SNP-Trait Associations