

Brief overview on how to start exploring **functionality**

Christian Werner

(Quantitative geneticist and biostatistician) **EiB, CIMMYT**, Texcoco (Mexico)

Filippo Biscarini

(Biostatistician, bioinformatician, and quantitative geneticist) **CNR-IBBA**, Milan (Italy)



HerrFalloppio

Oscar González-Recio

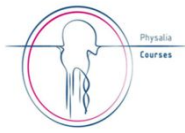
(Computer biologist, and quantitative geneticist) **INIA-UPM**, Madrid (Spain)



OscarGenomics



Functional analysis



- Examining the function of genes and their role in biological processes.
 - by looking at how changes in a gene's sequence affect its function
 - by studying how different genes interact with each other to carry out specific functions in the cell.
 - using bioinformatics tools to analyze large datasets of genomic information, such as the sequence of an entire genome or the expression levels of thousands of genes in different tissues or under different conditions. This can help identify patterns and connections between genes that may be involved in specific functions or processes, such as disease development or response to environmental stimuli.


Overall, a genomic functional analysis can provide valuable insights into the roles that genes play in biological processes, and can help researchers better understand the underlying causes of diseases and other biological phenomena




Work Flow in FUMA

- 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 from [here](#))



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DAVID Bioinformatics Resources
Laboratory of Human Electrodynamics and Immunoinformatics (LHRI)



LHRI

[Home](#)
[Start Analysis](#)
[Shortcuts to DAVID Tools](#)
[Technical Center](#)
[Downloads & APIs](#)
[Terms of Service](#)
[About DAVID](#)
[About LHRI](#)


Overview

The Database for Annotation, Visualization and Integrated Discovery (DAVID) is a freely available web-based tool that provides a comprehensive set of biological meaning behind large lists of genes. These tools are powered by the comprehensive DAVID Bioinformatics Resources (DBR) which are built upon the LINDA Gene concept which pulls together multiple sources of functional annotations.

DAVID tools are able to:

 - Identify enriched biological themes, particularly GO terms
 - Discover enriched functional-related gene groups
 - Cluster redundant annotation terms
 - Visualize genes on BioCarta & KEGG pathway maps
 - Display related many-to-many terms on 3-D view
 - Link for other functionally related genes not in the list
 - List Interacting proteins
 - Exploit gene names in both
 - Search gene-disease associations
 - Highlight protein functional domains and motifs
 - Redirect to related literature
 - Convert gene identifiers from one type to another
 - And more

Hot Links

Multiple positions available in LHRI 

The Laboratory of Human Electrodynamics and Immunoinformatics (LHRI) has collaborated with the National Institute on Aging and Infectious Diseases (NIAID) and supported NIAID clinical trials for patients infected with HIV mutants resisting anti-retroviral therapies (LHRI) has isolated the multiple-class drug-resistant (MDR) variants from HIV mutants and characterized each variant's drug sensitivity and infectivity. The study aims to define salvage therapy and develop novel therapy (chemotherapy and immunotherapy). During the investigation, LHRI has characterized the emergence of resistance mutations on drug susceptibility and viral replication. LHRI is a pioneer in researching the anti-viral cytokines, Interleukin-23, DNA-paI-receptor (KIR3)-mediated natural immune response against HIV and other virus co-infection and novel subsets of immune cells. LHRI maintains the Database for Annotation, Visualization and Integrated Discovery (DAVID).

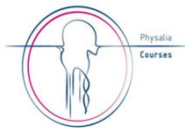
(1) **Scientists** - **Virology** position available to perform the defective proviral study in our **Basic Research Section**.

(2) **Scientists-cytokines** and **HIV** available in our **Basic Research Section**. We are looking for a cytotype immunologist who is interested in virus (HIV) and/or HIV pathogenesis. They may include for cell types (macrophages, dendritic cells, and monocyte cells).

(3) **Postdoctoral fellow** available in our **Basic Research Section**. This position is an excellent opportunity for a young Ph.D. who has no experience in virus research and seeks a career in a new research field. You will learn



Work Flow in DAVID

The screenshot shows the DAVID Gene Name Batch Viewer interface. It has a top navigation bar with links like Home, Start Analysis, and About DAVID. The main content area is titled "Gene Name Batch Viewer" and includes a "Submit your gene list to start!" button. Below this, there's a section "What does this tool do?" with bullet points. The left sidebar contains four steps: Step 1: Enter Gene List (with a text input and a "Clear" button), Step 2: Select Identifier (with a dropdown menu), Step 2a: Select species (with a text input), and Step 3: List Type (with radio buttons for "Gene List" and "Background"). A "Submit List" button is at the bottom. Red arrows point from the text on the right to specific elements: the first arrow points to the text input in Step 1, the second to the dropdown in Step 2, the third to the text input in Step 2a, and the fourth to the "Submit List" button.

Paste the list of genes (output from the getGenes.R)

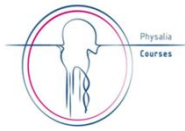
Select OFFICIAL_GENE_SYMBOL

Type the species

Submit analysis

Use the results of your functional analysis to gain insights into the biological processes and functions that are represented in your data. You can use the information from DAVID to help identify potential pathways and mechanisms involved in the development of diseases, for example, or to investigate how different genes or proteins interact to perform specific functions in the cell.

Work Flow in DAVID



The screenshot shows the DAVID Functional Annotation Tool interface. The top navigation bar includes links for Home, Start Analysis, Shortcut to DAVID Tools, Technical Center, Downloads & APIs, Term of Service, About DAVID, and About LHRI. The main content area is titled 'Annotation Summary Results' and displays various annotation categories and their corresponding counts and percentages. The left sidebar contains the 'Gene List Manager' and 'List Manager' sections.

Functional Annotation Tool
DAVID Bioinformatics Resources, NIAID/NIH

Home Start Analysis Shortcut to DAVID Tools Technical Center Downloads & APIs Term of Service About DAVID About LHRI

Upload List Background

Gene List Manager

Select to limit annotations by one or more species [Help](#)

- Use All Species -
Canis lupus familiaris(7)

Select Species

List Manager [Help](#)

List_1

Select List to:
Use Rename
Remove Combine
Show Gene List

Annotation Summary Results [Help and Tool Manual](#)

Current Gene List: List_1
Current Background: Canis lupus familiaris
7 DAVID IDs
Check Defaults ☒ Clear All

☒ Functional_Annotations (6 selected)

Annotation	Percentage	Count	Chart
<input checked="" type="checkbox"/> COG_ONTOLOGY	28.6%	2	
<input checked="" type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS	42.9%	3	
<input checked="" type="checkbox"/> UP_KW_CELLULAR_COMPONENT	42.9%	3	
<input checked="" type="checkbox"/> UP_KW_MOLECULAR_FUNCTION	28.6%	2	
<input checked="" type="checkbox"/> UP_KW_PTM	28.6%	2	
<input checked="" type="checkbox"/> UP_SEQ_FEATURE	100.0%	7	

☒ General_Annotations (0 selected)

☒ Interactions (1 selected)

☒ Pathways (1 selected)

Annotation	Percentage	Count	Chart
<input checked="" type="checkbox"/> KEGG_PATHWAY	42.9%	3	
<input type="checkbox"/> WIKIPATHWAYS	28.6%	2	

☒ Protein_Domains (0 selected)

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

Functional Annotation Clustering

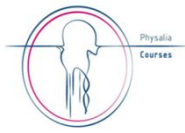
Functional Annotation Chart

Functional Annotation Table

Go again to the Shortcut to **David Tools** and select '**Functional Annotation**'

You can select the different options to gain insights into the biological processes and functions that are represented in your data. You can use the information from DAVID to help identify potential pathways and mechanisms involved in the expression of the phenotype. For example, to investigate how different genes or proteins interact to perform specific functions in the cell.

Limitations



- FA relies on algorithms and methods that make assumptions and simplifications about the data being analyzed. These assumptions may not always hold true in all cases, and they can affect the accuracy and reliability of the results.
- FA are often based on large datasets that may not be representative of all possible scenarios. This can lead to bias in the results, and can make it difficult to generalize the findings to other situations or organisms.
- FA can provide valuable insights, but it is important to carefully consider the limitations and uncertainties of the methods and algorithms used, and to interpret the results with caution.

