



IMMUNE DB: A Large Internet Framework for Collecting and Analysing Biological Immune Results

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Abstract

Data discovery is becoming increasingly dependent on bioinformatics analytic techniques and access to curated data repositories related to immune responses and particular pathogens. With the exponential growth of biological evidence, a growing number of biological databases have been created to assist human-immune system-related research. We present a list of human-immune system-related biological datasets and provided a mini-review by categorizing them into various data forms. This paper is largely aimed at computer scientists with only a rudimentary understanding of biology. Databases are replacing science literature as a means of disseminating this knowledge to the public immune disease database (https://venuparitala.shinyapps.io/immune_db/) apprehend the data cramped in figures, text, tables of the scientific literature promise it freely available and easily searchable to the public. Immune DB will assist biological researchers to explore about immune system categorized innate, autoimmune, and adaptive immune systems, each category has multiple disorders, each disorder has its own control and gene catalogue in summation with targets and networks. It discusses how to enhance immunity and which foods and medicines women and children can take. We covered which age individuals are suffering more, then after the information is provided about covid19 effects, symptoms, control, genes take place and collection of literature. It reflects the number of people of a certain age who have immune deficiency, as well as the percentage of people who can avoid and tolerate it. This index includes all facets of 14 autoimmune disorders, 1 adaptive immune disease, and 6 innate immune diseases, this database, which is accessible, compact, and open-source, should be useful to all.

Keywords:

Network; genes; Targets; Database; Covid19; Disease

Introduction

The immune system keeps track of any germ (microbe) it has ever overcome so it can easily recognize and eliminate the microbe if it re-enters the body. As the field of bioinformatics has developed and developed into an unused department of science, unused sub-disciplines have risen inside its immunoinformatics, the application of immunoinformatics to create a database and computational antibody plan [1-3]. The database is populated utilizing data captured or curated from peer-reviewed logical writing and from information submitted by

analysts. The immune system is a complex network of cells and proteins that fights infection in the body. The immune system classified into different types Adaptive immune diseases, innate immune disease, immunodeficiencies, and autoimmune disorders may also caused by immune system abnormalities [4-8]. List of diseases included in this database: (I) Innate immune diseases: 1. Chronic Granulomatous Phagocytic Disease, 2. Primary Immune Deficiency, 3. Complement Deficiencies, 4. Hyper IgE Syndrome, 5. Innate Immune Defects, 6. NEMO Deficiency Syndrome. (II) Autoimmune immune disorders: 1. Type 1 diabetes, 2. Rheumatoid arthritis, 3. Psoriasis/psoriatic arthritis, 4. Multiple sclerosis, 5. Systemic lupus erythematosus, 6. Inflammatory bowel disease, 7. Addison's disease, 8. Graves' disease, 9. Sjogren's syndrome, 10. Hashimoto's thyroiditis, 11. Myasthenia gravis, 12. Autoimmune vasculitis, 13. Pernicious anemia, 14. Celiac disease. (III) Adaptive immune disorders: 1. Rheumatic diseases.

Nearly 4% of the world's population is affected by one of more than 80 different autoimmune diseases, the most common of which include type 1 diabetes, multiple sclerosis, rheumatoid arthritis, lupus, Crohn's disease, psoriasis and scleroderma. Overall, 78% of people affected by autoimmune disease are female many people suffering from immunodeficiency in one million (Primary Immunodeficiency Disorders in India—A Situational Review.) COVID is estimated to affect 1 in 25,000 to 1 in 50,000 people worldwide, although the prevalence can vary across different populations (<https://medlineplus.gov/genetics/condition/common-variable-immune-deficiency/s>). The database contains the almost all literature related to immune disease, it consists of disease information about disease causing organism, disease type, how to control, genes and target of each disease and also found covid 19 data, genes, literature [9,10,11]. The purpose of database is to create awareness among the people, reduce the amount of time you spend managing data. Analyse data in a variety of ways. Promote a disciplined approach to data management. Turn disparate information into a valuable resource [12,13]. Genetic information or genetic test results can be used to prevent the onset of diseases, or to assure early detection and treatment, or to make reproductive decisions. This information can also be used for nonmedical purposes [14-16].

Target proteins are functional biomolecules that are addressed and controlled by biologically active compounds [17-19]. They are used in the processes of transduction, transformation and conjugation, target proteins controls the action and the kinetic behavior of drugs within the organism [20-22].

Materials and Methods

Implementation

IMMUNE DB web application is developed with R software. The server is hosted in a cloud platform. For the development of the analytical pipeline, used various R packages [23-25]. The packages are shiny themes, shinydashboard, shiny, bootstrap, shinycustomloader, htmltools, htmlwidgets, DT, ggplot2, slideview, shinycssloaders, shiny Widgets, leaflet, network, igraph, googleform, ggnetwork, shinyanimat. It contains both the user interface and server [26,27].

Shiny: These packages used in the same way as spreadsheets are "online," shiny apps are "live" as well. When users alter inputs, the outputs adjust immediately, without needing a window reload. For

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greater versatility, shiny user interfaces may be written entirely in R or in HTML, CSS, and JavaScript [28,29] , shiny themes: used to beautification of web page, shiny dashboard: With 'Shiny,' you can make dashboards. This kit applies a motif of 'Shiny,' making it easier to build visually enticing dashboards, Bootstrap: Bootstrap samples of virtually any statistic that can be calculated in R are conveniently produced using the R package boot. Estimates of bias, bootstrap confidence intervals, and plots of your bootstrap replicates can all be produced with these samples, shiny custom loader: In R's shiny, a custom CSS/html or gif/image format for the loading screen. The marquee can also be used to build a personalised text loading screen, Htmltools: htmltools is a R package designed to: Generate HTML tags from R. Handle web dependencies, Htmlwidgets: The package provides a framework for easily creating **Slideview**: With a Slider, you can match raster images side by side. Build a side-by-side view of raster(pixel)s with an interactive slider that allows you to switch between image regions. This is particularly helpful when comparing images of the same area taken at various times, Shinycssloaders: Add Loading Animations to a 'shiny' Production As It's Recalculating with shinycssloaders. When a 'Shiny' performance (such as a plot, table, map, or other visual representation) is recalculated, it stays apparent but becomes greyed out. Instead, you can use 'shinycssloaders' to apply a loading animation ("spinner") to outputs, shiny Widgets: This package offers custom widgets and other components to enhance your shiny applications. You can replace classical checkboxes with switch button, add colours to radio buttons and checkbox group, use buttons as radio or checkboxes. Each widget has an update method to change the value of an input from the server, Leaflet: is a popular open-source JavaScript library for creating interactive maps. This R package allows integrating and manipulating Leaflet maps in R simple. Network: The network package contains a class for encoding complex hierarchical structures made up of a vertex set and any combination of undirected/directed, valued/unvalued, dyadic/hyper, and single/multiple edges; storage requirements are proportional to the number of edges involved.igraph: Visualization and Network Analysis Routines for evaluating basic graphs and networks. It has functions for generating random and normal graphs, graph analysis, centrality processes, and many more, and it can handle big graphs well. Ggnetwork: ggnetwork is a small R package that emulates geomnet's behaviour by specifying several geoms to obtain similar effects. The ggnetwork software uses the method of aliasing any of

the ggplot2 package's native geoms. A geom that has been aliased is merely a subset of one that already exists, Shinyanimate: package is an R wrapper for animate. It allows user to easily add animations to any UI element in shiny app using the elements id [28,29].

Result and Discussion

Home: This tab panel contains the overall information about the database, which represents in textual and graphically.

Immune system: This item divided into three different categories innative immunity, autoimmune immunity and adaptive immunity, each category represents different types of diseases, each disease was explained with the information about disease and disease class. Filters are available to make job easy and user-friendly.

Immune Disease: Tab panel divided into three different categories, innative immunity, autoimmune immunity and adaptive immunity disease each category represents different types of diseases, each disease was explained with the information about disease symptoms and disease type. Filters are available to make job easy and user-friendly.

Control: The item was separated into three distinctive categories, to be specific natural insusceptibility, immune system resistance, and versatile resistance each category has a few disoredrs, each one clarifies the data malady control. Filters can be used to make the job simpler and more user- friendly.

Improve immunity: This tab panel segregate drugs into improve immunity, food to improve immunity and progeny colonize improve immunity. drugs to improve immunity subpanel consists of name of the drug and its uses, food to improve immunity subpanel consists name of the food, food category and vitamins, Filters can be used to make the job simpler and more user-friendly.

Genes: This genes tab panel represents all diseases when you select a disease it displays all possible gene names with gene symbol and frequency. On the left hand of the dashboard page click on the disease tab panel to explore about/gene information on another hand. it presents the top filters which easily search specify the gene name, it plots a graph between gene symbol and frequency which represents which disease is affecting more for eg: T code 30 times is more vital than others.

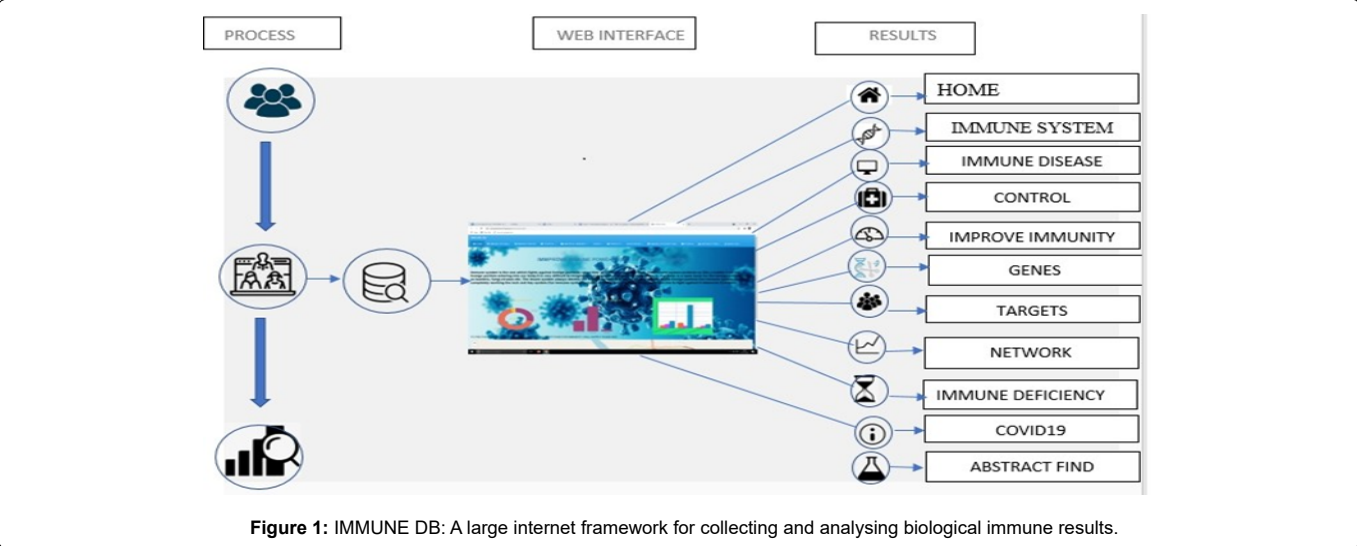


Figure 1: IMMUNE DB: A large internet framework for collecting and analysing biological immune results.

Targets: This targets tab panel represents all diseases when you select a disease its display's all possible targets with organism type, targets, compound, accession id and taxonomic id.

Immune deficiency age: The tab panel contains the overall information about the age of the person, immune deficiency occur, percentage of causing immune deficiency and percentage of cure immune deficiency it represented in tables and graphically (Figure 1).

Covid19: This tab panel contains the information about corona virus, symptoms, prevention, genes and literature, it presents the data graphically.

Abstract find: This tab panel contains the literature of the all immune diseases, each article contain the PMCID, first author, title and published book and publishing year. Filters can be used to make the job simpler and more user-friendly [30].

Availability and Implementations

IMMUNE DB available at: https://venuparitala.shinyapps.io/immune_db/

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Supplementary information: supplementary data available in bioinformatics online

References

- Martin K, Alistair G R, Vesteinn T, Christophe B, Bin Li, et al. (2008) "The Innate Immune Database (IIDB)." *BMC Immunol* 5:7.
- Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, et al. (2015) "The immune epitope database (IEDB) 3.0." *Nucleic Acids Res* 43: 405–412.
- Vita R, Peters B, Sette A (2008) "The curation guidelines of the immune epitope database and analysis resource." *Cytometry A* 73: 1066–1070.
- UniProt Consortium T (2018) "UniProt: the universal protein knowledgebase." *Nucleic Acids Res* 46: 2699.
- Aoki-Kinoshita K, Agravat S, Aoki NP, Arpinar S, Cummings RD et al. (2016) "GlyTouCan 1.0—The international glycan structure repository." *Nucleic Acids Res* 44: 1237–1242.
- Resource Coordinators, N.C.B.I. (2018) "Database resources of the national center for biotechnology information." *Nucleic Acids Res* 46: 8–13.
- Rose PW, Prlic A, Altunkaya A, Bi C., Bradley AR, et al. (2017) "The RCSB protein data bank: integrative view of protein, gene and 3D structural information." *Nucleic Acids Res* 45: 271–281.
- Vita R, Overton JA, Sette A, Peters B (2017) "Better living through ontologies at the Immune Epitope Database". *Database (Oxford)* 2017.
- Hastings J, Owen G Dekker A, Ennis M, Kale N (2016) "ChEBI in 2016: Improved services and an expanding collection of metabolites". *Nucleic Acids Res* 44: 1214–1219.
- Sigrist CJA, Cerutti L, Hulo N, Gattiker A, Falquet L et al. (2002) "PROSITE: a documented database using patterns and profiles as motif descriptors". *Brief. Bioinform* 3: 265–274.
- Hulo N, Sigrist CJA, Le Saux V, Langendijk-Genevaux PS, et al. (2004) "Recent improvements to the PROSITE database." *Nucleic Acids Res* 32:134–137.
- Sigrist CJA, Castro E (2005) "ProRule: a new database containing functional and structural information on PROSITE profiles". *Bioinformatics* 21: 4060–4066.
- Gattiker A, Michoud K, Rivoire C, Auchincloss AH, Coudert E, et al. (2003) "50 Automated annotation of microbial proteomes in SWISS-PROT". *Comput. Biol. Chem* 27: 49–58.
- Kullander K, Klein R (2002) "Mechanisms and functions of Eph and ephrin signalling". *Nature Rev. Mol. Cell. Biol* 7: 475–486.
- Matsuoka H, Iwata N, Ito M (1997) "Expression of a kinase-defective Eph-like receptor in the normal human brain *Biochem. Biophys. Res. Commun* 235: 487–492.
- Golovin A, Dimitropoulos D, Oldfield T, Rachedi A, Henrick K (2005) "MSDsite: a database search and retrieval system for the analysis and viewing of bound ligands and active sites." *Proteins* 58: 190–199.
- Hofmann K (2000) "Sensitive protein comparisons with profiles and hidden Markov models." *Brief. Bioinform* 2:167–178.
- Kyrpides NC (1999) "Genomes OnLine Database (GOLD 1.0): a monitor of complete and ongoing genome projects world-wide". *Bioinformatics* 15: 773–774.
- Bernal A, Ear U, Kyrpides N (2001) "Genomes OnLine Database (GOLD): a monitor of genome projects world-wide." *Nucleic Acids Res* 29:126–127.
- Pagani K, Liolios J, Jansson IM, Chen T, Smirnova B Kyrpides (2012) "The Genomes OnLine Database (GOLD) v. 4: status of genomic and metagenomic projects and their associated metadata." *Nucleic Acids Res.* 40: 571–579.
- Jorda J, Baudrand T, Kajava AV (2012) "PRDB: Protein Repeat DataBase". *Proteomics* 12:1333–1336.
- Baxeavanis AD (2001) "The Molecular Biology Database Collection: an updated compilation of biological database resources." *Nucleic Acids Res* 29: 1–10.
- Baxeavanis AD (2006) "The importance of biological databases in biological discovery." *Curr. Protoc. Bioinformatics* 1:1.
- Baxeavanis AD (2009) "The importance of biological databases in biological discovery." *Curr. Protoc. Bioinformatics* 1 1.1.
- Galperin MY, Fernandez-Suarez XM (2012) "The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection." *Nucleic Acids Res* 40: 1-8.
- Galperin MY, Cochrane GR (2009) "Nucleic Acids Research annual Database Issue and the NAR online Molecular Biology Database Collection in 2009." *Nucleic Acids Res* 37: 1–4.
- Islamaj R, Dogan GC, Murray A (2009) "Understanding PubMed user search behavior through log analysis." *2009 Database (Oxford)*.
- Z. Lu, PubMed and beyond: a survey of web tools for searching biomedical literature, 2011 Database (Oxford) (2011 Jan 18) baq036
- Sayers EW, Barrett T, Benson DA, Bolton E, Bryant K, et al. (2012) "Database resources of the National Center for Biotechnology Information." *Nucleic Acids Res* 40: 13–25.
- Ding J, Hughes LM, Berleant D, Fulmer AW, Wurtele ES (2006) "PubMed Assistant: a biologist- friendly interface for enhanced PubMed search." *Bioinformatics* 22: 378–380.

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