

2021 Virutal Conferences

Checkout upcoming meetings:

Rare Disease Day at NIH March 1, 2021 Virtual Conference

Genomics of Rare Disease (Registration deadline 15 March) Virtual Conference 22-24 March 2021

14TH ANNUAL BIOCURATION CONFERENCE (VIRTUAL)
April 13, 2021

Curating the Clinical Genome Abstract deadline 16 March Virtual Conference Latest News: Checkout the latest data and website updates !

- Expanded DO's 'coronavirus infectious disease' classification, addition of COVID-19 (DOID:0080600) and Middle East respiratory syndrome (DOID:0080642)
- ♦ View OBO tree diplaying doid.obo enabling viewing of inferred, multi-parentage
- DO cancf slim updated glioma classification, additional molecular subtypes
- UMLS update 35,679 cross mappings to GARD, ICD9CM, ICD10CM, MESH, NCIt, OMIM, Orphanet, SNOMEDCT US and UMLS CUI
- ♦ DO's latest YouTube video Mining disease information via Imports



Publication Highlight: Tools

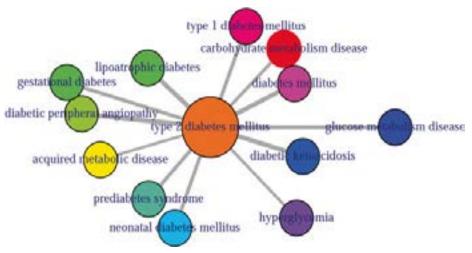
<u>UFO</u>: Cytoscape app - a tool for unifying biomedical ontology-based semantic similarity calculation, enrichment analysis and visualization. **PubMed ID:**32645039

HGPEC: Cytoscape app, predict novel disease-gene and disease-disease associations, and support network and rank-based visualization. Utilized protein complexes from CORUM (comprehensive resource of mammalian protein complexes. Project home page PubMed ID:28619054

<u>ChiPseeker:</u> Bioconductor package - annotating ChIP-seq peak annotation, comparison and visualization. Provides covplot to visualize the peak locations and intensities over the whole genome. **PubMed ID:**25765347

comoR: R package to analyze comorbidities from clinical data. PubMed ID: 25045465

disease comorbidity for type 2 diabetes mellitus



DOSE Bioconductor package, Disease Ontology Semantic and Enrichment analysis. Providing seman tic similarity computations among DO terms and genes which allows biologists to explore the similarities of diseases and of gene functions in disease perspective. **PubMed ID:25677125**



Latest Release Notes:

DO Data Release: Available in DO's GitHub repository: (previous release notes)

Release # 94: February 24, 2021 Release Notes

This release includes 10,671 disease terms, the addition of 23 new diseases, 41 definitions and 211 SubClassOf statements. Updates: glioma molecular subtypes and Bainbridge-Ropers syndrome, axioms defining transmission methods for bacterial infectious diseases and UMLS update.

Release # 93: January 28, 2021 Release Notes

This months Disease Ontology release of 10,347 DO disease terms (73%, 7654 defined) in This release of 10,648 human diseases, includes 50 new diseases, including Parkinsonism and vascular Parkinsonism, a revised glioma classification, new subtypes for pemphigus, developmental and epileptic encephalopathy, and hypocalcemia.

Looking Ahead ...

February 2021 Website Updates:

Community >> Collaborators

• Updated to include DO's expanded utility as a disease term resource, standardized terminology for annotating and analysis of biomedical data; for the development of biomedical and clinical resources; and for building novel computational tools and biomedical ontologies

DO Users:

 New users added - Check out DO's users at 275+ databases, discovery tools, knowledbases, variant assessment, reporting resources.** INCLUDING 52 ontologies utilzing the DO **

Disease Ontology Citations:

The DO team has identified > 700 DO project citations (as of January 2021).

This set of citations has been compiled as a public PubMed MyNCBI collection (DO citing papers).

This collection represents the growing number of instances of integration of DO in databases, research studies, and bioinformatics tools. The DO Citations are identified through PubMed data mining (direct DO paper citations, inclusions of 'Disease Ontology', DO URL or DOID).

DO's YouTube Video Tutorials

Checkout DO's latest YouTube tutorial:
 Mining disease information via imports:
 Connecting disease-related information



DO's Playlist at the



YouTube Channel

and Biomedical Ontology World YouTube Channel

Mining disease information via imports: Connecting disease-related information

