Human Data

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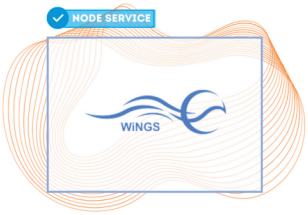

WiNGS

A federated genomics data sharing platform allowing users to query genomic and phenotypic information

WiNGS is a federated and web-based platform tackling the complexity of analysing genome sequencing data. By storing sensitive information, including extensive phenotypic data and variant information, in client-hosted hubs, WiNGS optimises ICT requirements of whole genome sequencing interpretation. Finally, it allows anonymized analyses of pan-client data, while fully preserving the privacy of patient information.

Currently, WiNGS is installed at four centres in Belgium (UZ Leuven, UZ Antwerp, UZ Liège and University of Antwerp), and is listed as the platform of choice to host a cross-institutional whole-genome sequencing project in Belgium (BeSolveRD).

WiNGS is based on both NGS-Logistics, the genomics data sharing platform established at KULeuven, and VariantDB, the interactive annotation and filtering platform developed at UAntwerp.

Federated MSDA infrastructure

A platform to support collaborative real-world Multiple Sclerosis data efforts

The Federated MSDA Infrastructure is a combination of software, data science pipelines and hardware aiming to support and speed-up large-scale collaborative real-world Multiple Sclerosis (MS) data efforts. It allows to collect and share patient and aggregated data, and to perform data quality assessment, error detection and analysis in a secure GDPR compliant private research environment.

The infrastructure was used successfully to support the COVID-19 &MS Global Data Sharing Initiative and is co-developed by UHasselt as one of the core partners in the international Multiple Sclerosis Data Alliance (MSDA).

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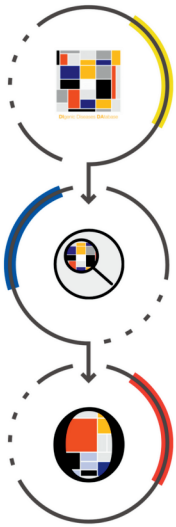
IBsquare Toolbox

A suite of three tools (OLIDA, VarCoPP, ORVAL) to assist in the identification of genetic diseases

The IBsquare Toolbox for Oligogenic Analysis comprises three tools that assist researchers and doctors in the identification of genetic diseases. These tools are closely intertwined as the data contained in the DIDA database was used to train the VarCopp predictor, which in turn is part of the pipeline for ORVAL. The tools are developed by the Interuniversity Institute of Bioinformatics in Brussels (IBsquare) which groups bioinformaticians and computational biologists from the VUB and ULB.



OLIDA

DIDA (Digenic Diseases Database) is a database that provides detailed information on genes and associated genetic variants involved in digenic diseases. The original DIDA database is transferred to a new repository named OLIDA (Oligogenic Diseases Database), which offers new features and adds support for new types of variants and combinations (from digenic to oligogenic) to the database.

VarCoPP

VarCoPP (Variant Combination Pathogenicity Predictor) predicts the potential pathogenicity of variant combinations in gene pairs. It is based on digenic data present in DIDA and it was trained against variants from the 1000 Genomes Project. VarCoPP consists of an ensemble of 500 individual Random Forest predictors.

ORVAL

ORVAL (Oligogenic Resource for Variant Analysis) is a platform which allows users to upload the genetic information of a patient and explore the potential oligogenic causes of rare diseases.

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TCRex

A web tool for the prediction of T-cell receptor epitope recognition

TCRex is a webtool for the functional interpretation of full human T-cell repertoire data derived from next generation sequencing. The tool is able to link T-cell receptor sequences to important immunogenic cancer, autoimmune disorder and viral epitopes, TCRex can calculate enrichment statistics and baseline prediction rates to evaluate full repertoires. It also brings together the largest database on TCR-epitope data to train the underlying machine learning models. TCRex is developed at the University of Antwerp.

ELIXIR Belgium is the national node of ELIXIR, the intergovernmental organization that brings together life science resources from across Europe, supporting life science research and its translation to medicine, environment, the bio-industries, and society. The research infrastructure provides platforms and guidance for research data management and reproducible data analysis, and offers domain specific services for Plant and Biodiversity, Human health and COVID-19 research. ELIXIR Belgium also provides data related training and workshops.

Funders

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