Security

Various new security measures have been introduced in LOVD 2.0, protecting the sensitive patient data. LOVD 2.0 implements techniques to prevent brute force attacks, SQL injection and XSS attacks. When desired, access of authorized users can be limited to specific IP addresses making access to LOVD, even with the right password, impossible from other computers or from outside your institution.

Brute force attacks are prevented by locking submitter, curator and manager accounts after three failed login attempts. In addition LOVD 2.0 has a system log allowing the tracking of attempts to break security by authorized as well as external users.

To protect the data consistency in the MySQL database, the InnoDB table type has been chosen to be the default table type.

Did you know:
· The single largest known LOVD installation contains 70,376 variants in 54 genes.
· LOVD 2.0 has been tested to function properly when containing 5,000 genes, 1,000,000 mutations, 500,000 patients and 100,000 submitters.
· We offer LSDB curators the possibility to set up, with or without our help, their databases on our LOVD server free of charge. For more information see www.LOVD.nl.
· A CD is available to install LOVD and all necessary software on a Windows desktop computer in a few minutes with virtually no effort. This CD can be downloaded from our LOVD website and runs on Windows 98, NT, 2000, 2003, XP and Vista.
· LOVD collaborates with the UCSC and dbSNP to support display and access to DNA variants stored in LOVD-databases through genome browsers (see the UCSC for dystrophy LSDBs and dbSNP for TSC1 and 2).

Some LOVD installations (also see www.lovd.nl):
· Leiden Muscular Dystrophy pages (DMD, Sarcoglycans, LMNA, CAPN3, DYSF, ...)
 · http://www.dmd.nl/nmdb/

· Osteogenesis Imperfecta (COL1A1, COL1A2, LEPRE1, ...)
 · http://oi.gene.le.ac.uk/

· InSiGHT Colon Cancer (MLH1, MSH6, MUTYH, ...)
 · http://chromium.liacs.nl/LOVD2/colon_cancer/

· dbPEX (Peroxisome Biogenesis Factor)
 · http://www.dbpex.org/

· X-linked Mental Retardation
 · http://grenada.lumc.nl/LOVD2/MR/

· Monogenic Diabetes (GCK, HNF1A, HNF4A)
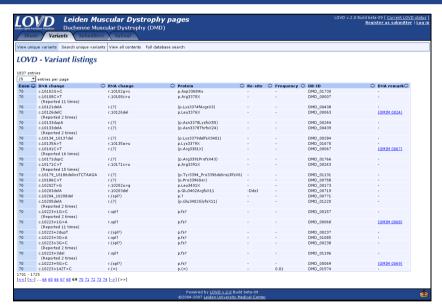 · http://grenada.lumc.nl/LOVD2/diabetes/

www.LOVD.nl

LOVD
Leiden Open Variation Database

A flexible, free tool for gene-centered collection, curation and display of DNA variation

LSDB-in-a-Box

www.LOVD.nl

Leiden University Medical Center, Leiden, Netherlands
Ing. Ivo F.A.C. Fokkema, Dr. Johan T. den Dunnen

LUMC

Main features

LOVD 2.0 is an "LSDB-in-a-Box", i.e. all functionalities to establish, manage and curate a web-based gene specific DNA variant database (LSDB) are included.

Sequence variant data and patient data are stored separately. This allows users to link large numbers of DNA variants in several genes to one patient, for example in the case of multi-gene disorders or large scale next-generation sequencing. The pathogenicity of each variant can be set by the submitter and the curator separately, allowing easy separation of disease causing from non-pathogenic variants.

Web submission of new data is done per patient per gene, but adding additional variants to patients or adding already existing variants to other patients is very easy.

For curators, LOVD 2.0 has enhanced possibilities to import new data through text files containing variant and patient data. Importing is independent of the order of the columns and optional columns can be left out. During import the data are checked for internal consistency and uniqueness (accidental import of duplicate data is blocked).

LOVD 2.0 introduces powerful new search functionality. Searching variant and patient records can be performed per column and allows the use of boolean search terms (AND, OR and NOT). Curators can also perform special "find and replace" actions on all variants or copy or move data from one column to the other in large sets of records at the same time.

Access levels

LOVD 2.0 features five access levels, all with different rights.

The _Database Administrator_ has full access to LOVD. There is only one account of this type and it is created during LOVD installation. The DB administrator has all rights.

An _LOVD Manager_ has access to the LOVD Setup, with rights closely similar to the Database Administrator but a Manager cannot uninstall LOVD and is not allowed to create or edit other Manager accounts. The LOVD DB Manager creates gene databases (LSDBs), structures the data to be collected and displayed and manages the curators (per gene).

A _Curator_ has access to specific genes, but no access to the LOVD Setup. The Curator has control over the sequence variants, performs gene-specific configuration tasks (setting up gene custom columns), decides which data are public and curates incoming submissions.

Through registration, a _Submitter_ creates an account which allows the submission of new variant and patient data to the database. Depending on the LOVD system settings, submitters may edit their previously submitted data too. Other than this a Submitter has only access to the public part of the LOVD gene databases.

A website _Visitor_ can view all the data that has been labeled to be public.

Flexibility

LOVD 2.0 has many settings that can be configured by DB managers and curators, given ample possibilities to customize an LSDB as desired. The custom column feature includes functionality to, on a per gene basis, add new columns, specify their content (e.g. text, numerical) and determine their collection (e.g. checkbox, drop-down menu, free text field). Custom columns are connected directly to the submission form and support explanation and examples to guide submitters. LOVD 2.0 comes with a set of HGVS recommended pre-configured variant and patient columns, which can be added by curators and managers in a click.

Modules

Extension of LOVD 2.0 functionality can be achieved in a very simple way using modules. Without requiring extensive programming, a module can directly affect LOVD forms by adding, editing or removing fields or buttons. Modules can store their own database settings. Managers and the DB administrator can install, enable, disable or uninstall modules.

An available module is Mutalyzer, which allows submitters and curators to check the correct description of variant data (according to HGVS standards) in relation to the reference sequence or Genbank file used and to predict the effect of the variant on the RNA and protein level.

Publish your work

By enabling the "Include in the global LOVD listing" setting in LOVD, the database name and location will be published on the LOVD website, therefore effectively getting immediate peer recognition. Also, by being included in this list, you are included in a LOVD querying service which allows users to search LOVD installations world-wide for the existence of a certain variant in one go.

Required software

LOVD is an "LSDB-in-a-Box" completely based on Open Source software. Besides LOVD all additional software required is common, freely available and usually already installed on the server of a hosting provider. Please note that some hosting providers may not always include a MySQL database, but obtaining all software for an LOVD installation on an own webserver is simple.

- _Apache HTTP webserver_
  (other webservers can be used, we encourage Apache 1.3 or up)
- _PHP scripting language_ (version 4.2.0 and up)
- _MySQL database_ (version 3.23.33 and up)

The software required to run LOVD works on Linux, Macintosh and Windows, amongst others. LOVD is also available on a CD for your Windows desktop computer. From our website you can download the install CD to install LOVD and all other necessary software on a Windows desktop computer in just a few minutes. It requires 150MB free space on your C: drive.