

## Universität Bielefeld

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VANESA is a software solution for visualizing and examining biomedical networks in system biology applications. It addresses biomedical case studies and is used to create and to model individual network systems and their details. The aim of VANESA is to provide a set of powerful features to examine essential questions for research in natural science. With the use of VANESA a scientist can be supported in answering important questions posed by research activities such as:

"Does the flap of a butterfly's wings in Brazil set off a tornado in Texas?" Philip Merilees, 1972

## What is VANESA?

Biological networks have always been of wide interest. Discovering the secrets of many biological phenomena has motivated research activities. Over the course of time, natural science and its studies on living organisms has answered many essential questions. But still, a lot of biochemical processes have yet to be understood.

During research, enormous amounts of biological data are produced daily. Information from different fields of studies are brought together to examine and analyze quantities and relationships. The approach of extracting, analyzing and modeling meaningful biological data of heterogeneous data sets as a biomedical network is one of the big strengths of the software application VANESA.

## What does VANESA offer?

This outstanding software solution makes an accurate representation of research data. Information is visualized in a clear and understandable manner to meet the purposes of underlying research activities. With an intuitive graphical user interface, the user is able to record in writing research results and thoughts in form of a digital network model. The user is not limited to any kind of biological model, moreover it is possible to create an individual system that most suits the wishes and requirements of each research activity (see figure 1).

Another important feature is access to external biomedical data sources. The software solution consults different kind of databases to support the user with useful information. The user can access the biological data sources KEGG and BRENDA, as well as the data warehouse DAWIS. VANESA provides the user with 11 different databases (see figure 2). Communication between VANESA and the biomedical data sources is realized by a web service. The user merely needs an internet connection to access the information of interest. There is no need for a local data repository (see figure 3).

The aforementioned data sources provide an established basis for the modeling and characterization of biomedical systems. Moreover, the information from these data sources can aid in finding missing links in a system. The data integration is a powerful feature of VANESA which provides a variety of possibilities.

Furthermore, graph comparison and graph theory functions support the user in a better understanding of biological circumstances. Highlighting and comparison functions point out important facts in a set of different models. In order to make the graphical representation and analysis on the networks more legible, graph layout transformations and animation algorithms are also considered.

In addition to the previously mentioned features, an interface for experimental data like PCR (Polymerase Chain Reaction) and microarray is considered as well. Export formats such as SBML, CSML and GraphML are provided by the software solution.

In summary, VANESA with its various useful functions aids users in reaching goals in biomedical network modeling. It is free, platform-independent and user-friendly.

Convince yourself by trying out VANESA at:

## www.vanesa.sf.net

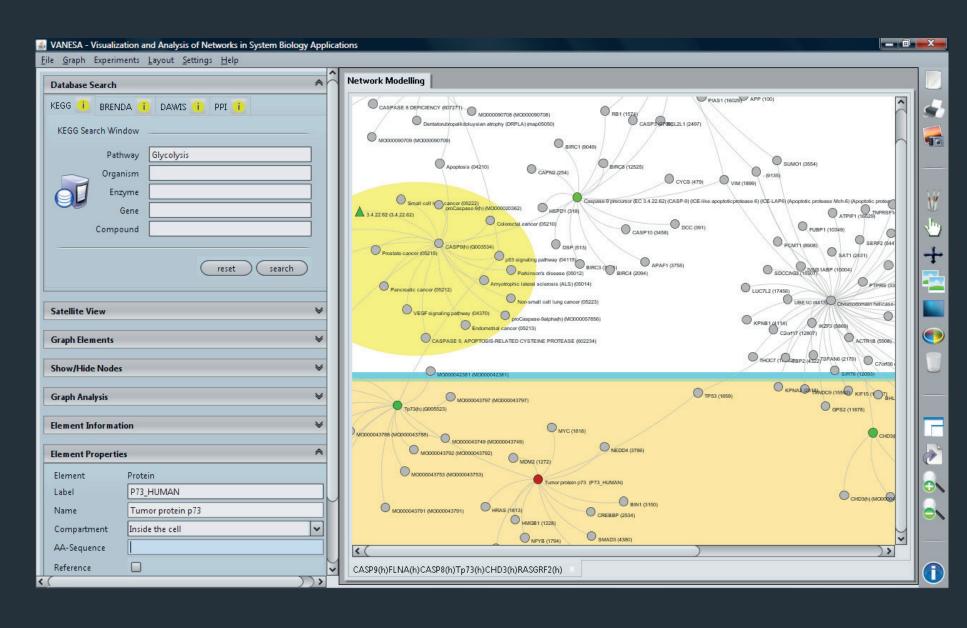


Figure 1: Illustration of a biomedical network realized by VANESA

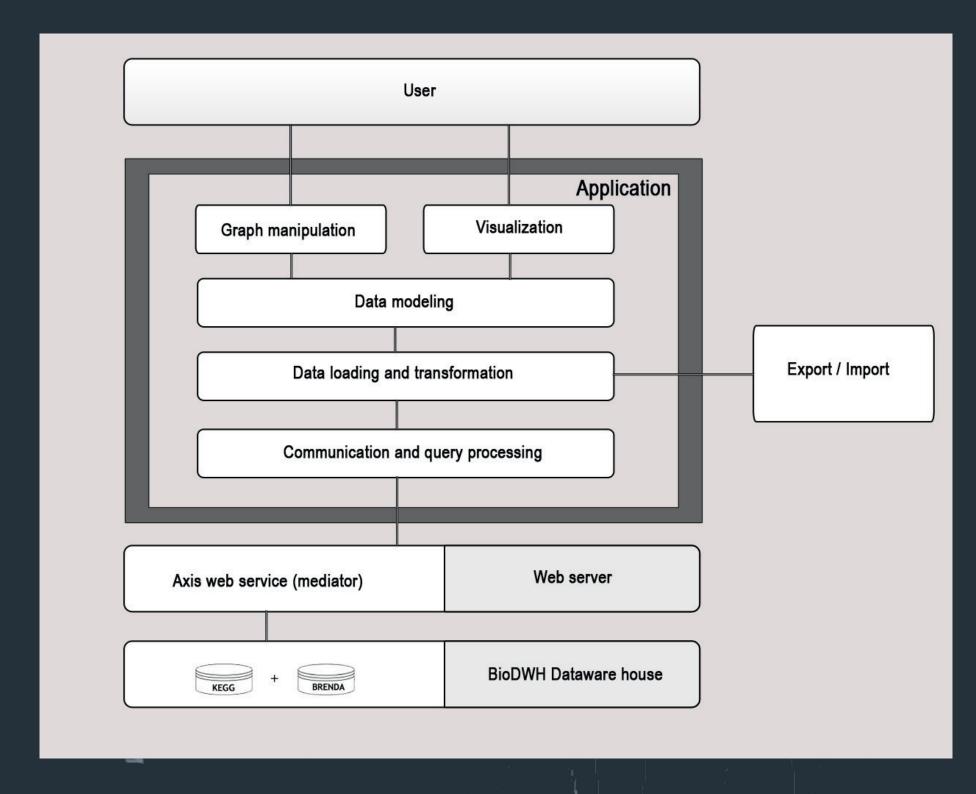


Figure 2: System architecture of VANESA

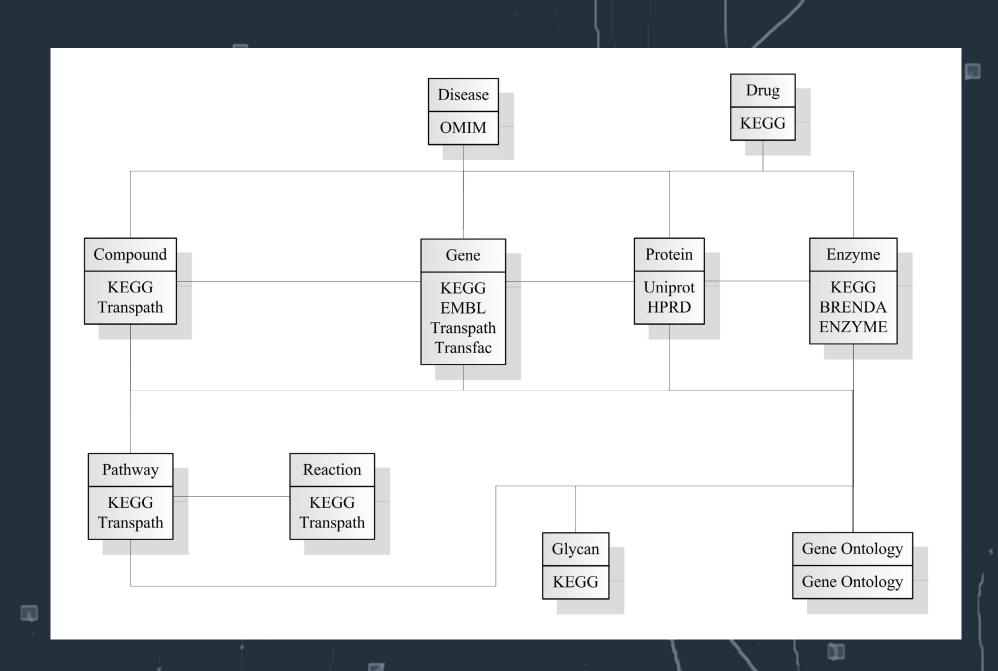


Figure 3: Graphical representation of the integrated data sources among different domains in VANESA

