

Biotechvana

The Online Platform on Bioinformatics
and Mobile Genetic Elements

THE COMPANY



Biotech Vana SL (Biotechvana) is an internet spin-off for research and science in Computational Biology and Bioinformatics. The company's headquarters are at the Science Park of the University of Valencia. Biotechvana strives to deliver know-how, IT infrastructure, and R&D products that are useful to the development of significant insight for researchers, enabling further advancement in research, health and education.

The enterprise is managed by researchers for researchers and covers a variety of business models. Our research team has excellence in the molecular diversity and evolution of viruses and mobile genetic elements. We cover a broad spectrum of activities ranging from fundamental research to industrial biotechnology. This includes internet services, creating databases, research projects, stand-alone software, and science publishing.

Our network of users spread across different areas of academia and industry, including governmental institutions, hospitals, universities, research centers, pharma- and bio-companies.



*“We believe that **innovation** through **R&D**
is the only feasible way for supporting the widest
possible dissemination of **scientific advance**
and **knowledge**”*

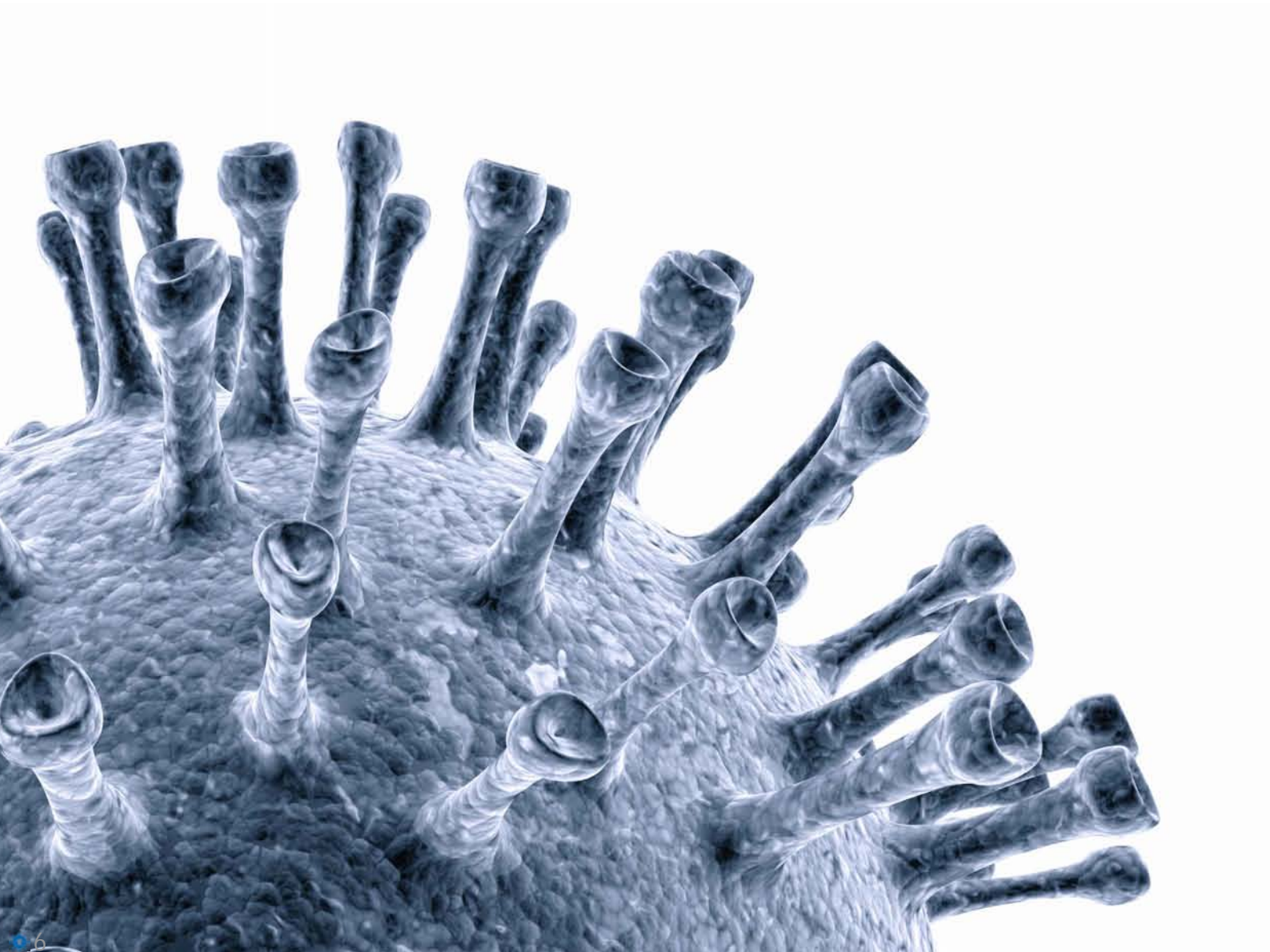
INTERNET PROJECTS

Biotechvana launches research projects concerned with the natural sciences and/or with the bio-research.
Our system is "work in progress" where we are open to accommodate new deals.

THE GYPSY DATABASE OF MOBILE GENETIC ELEMENTS

The Gypsy Database (GyDB) of mobile genetic elements is a long-term research project that furthers the scientific objective of excellence in research, services and education, by making available worldwide an open access in the field of viruses and mobile genetic elements. The GyDB is devoted to the evolutionary-based classification of Mobile Genetic Elements and related families of nonviral proteins.

"To predict the emergence of new viruses and infectious diseases it is essential to characterize the diversity of viruses and their related mobile genetic elements not only in humans, but in other organisms."



The GyDB welcomes the contribution of other researchers interested in shedding light on the molecular biology, diversity and evolution of mobile genetic elements; the emergence of, and role played by, mobile genetic elements and viruses in the evolution and complexity of prokaryotes and eukaryotes; and all the different aspects of mobile genetic elements involving the molecular changes responsible for various characteristics in humans and other eukaryotic organisms related with infection and disease.

Subscribing researchers are free to open new research lines and create new servers in the database, which can be published as standard in international journals and specialized open access. The project infrastructure consists of an ongoing database freely accessible at <http://gydb.uv.es>. The database includes a Wiki that is only accessible for subscribers, which can edit and/or revise contents and submit material.

Authors retain the copyright of their work and can use the database as a repository for material attached to electronic publications by unique identifiers. Subscribers can also activate and receive the benefit of other services such as newsletters, article alerts and/or RSS feeds.



GyDB
Gypsy Database

Main | Blast | Data Submission | HMM Server | Literature | Gydb Map | Contact

page | discussion | edit | history | delete | move | protect | watch

A database devoted to the evolutionary-based classification of Mobile Genetic Elements and related families of nonviral proteins.

GyDB
Gypsy Database

Due to the impressive molecular diversity of Mobile Genetic Elements, the Gypsy Database (GyDB) is in continuous progress. We welcome your collaboration in improving this project. You may report new data, errors, and omissions, via our data submission form. Please see the Section below "Terms of use and policy" for further information.

Cite this Project:

- Llorens, C., Futami, R., Bezemer, D., and A. Moya. (2008) The Gypsy Database (GyDB) of mobile genetic elements.
- Llorens C., Farell, M.A., and A. Moya. Gag-pol Relationships between Ty3/Gypsy and Retroviral LTR retroelements and the Three Kings Hypothesis (Submitted).
- Llorens, C. and A. Moya. The Phylogenetic Retroviral Recurrence into the Ty3/Gypsy Bio-distribution within the LTR retroelement Big Bang (Submitted).
- Llorens, C., Futami, R. and A. Moya. Bioinformatic Pipeline and Database to Investigate the Origins and Diversity of Clan AA Peptidases (Submitted).

PHYLOGENIES FAMILIES

- Ty3/Gypsy
- Retroviral

DOMAINS

- LTRs
- Gag
- Probes
- Reverse Transcriptase
- Ribonuclease H
- Integrase
- Protease
- Chromidomains
- dUTPase
- Accessory genes

RELATED FAMILIES

- Clan AA
- Gypsy
- Chromidomains

CLAN AA META-SCENARIO

GyDB COLLECTION

SERVERS

SOFTWARE

ALGORITHMS

DATABASE UTILITIES

MULTIPLE ALIGNMENTS

HMM PROFILES

SUPERCOMPUTING

OTHERS



A screenshot of the Biotechvana Bioinformatics website. The page features a navigation menu at the top with links for Main, GyDB collection, Subscribe, Servers, Map, Support, Contact, Beta versions, and GyDB. The main content area is titled 'Biotechvana Bioinformatics' and 'The collection of Bioinformatics Software and Computational Resources in Molecular Biology and Evolution'. It lists various software tools and resources, each with a brief description and links for 'Abstract' and 'Access resource'. The tools listed include: Biotechvana Bioinformatics: Collection 2008, The CheckAlign logo-maker application, Phylograph: A multifunction java editor for handling phylogenetic trees, GyDB Package 1.0, Biotechvana Search Engine 1.0, Biotechvana Queue Manager 1.0, The Alignment Format Converter Server 1.0, The Join Alignments Server version 1.0, RMXS server 1.0, and Computational resources. The page also includes logos for IMPIVA, GENERALITAT VALENCIANA, ENISA, FEDER, and PARC CIENTIFIC.

For the most part, navigation of the contents at Biotechvana Bioinformatics is free. We make public sections where manuals, several servers and computational resources attached to publications are freely available to the academic community and industrial researchers. However, full-access to Biotechvana Bioinformatics requires payment of an annual subscription.

Subscribers can log on to the Biotechvana Bioinformatics infrastructure to download the different software and tools. We have a permanent support service to users' feedback, peer-review criticism helping us to improve the tools. The technical support service includes a forum for the sharing of ideas and algorithms with our users.

Subscription also includes space in the system to run analyses and servers in private mode as well as a supercomputing network for resolving complexity problems that are difficult to resolve with ordinary computers, such computational models, large phylogenies, molecular studies, drug design and more.

Should you are interested in subscribing to Biotechvana Bioinformatics, you can find detailed information on how to proceed at:

<http://biotechvana.com/loader.php?section=contents&page=policybv>

*"Our goal is to understand
the business and research of our clients
to free them to investigate the data
rather than constantly maintaining their projects"*



OMIC SERVICES

Biotechvana has excellence in computational engineering for genomics, proteomics and drug discovery. Our board is dedicated to responding to the needs of researchers and supporting the generation of multidisciplinary research in Biomedicine, Genetics, and Molecular Biology.

"Our expertise in molecular biology and genetics propels our condition of full-service research hub providing diagnostic application of -omic technologies."

Our team supports research in the following fields:

*Genomics and Proteomics
Metagenomics and Metabolomics
Transcriptomics and Phylogenomics
Genomic medicine
Molecular taxonomy
Drug and protein design*

*Structure and function prediction
Macro- and Microarray technology
Gene/protein families and profiling
Epidemiology and infectious diseases
Contig assembly and genome annotation
Viral and mobile genetic element diversity*



PROGRAMMING SOFTWARE

Using state-of-the-art technology, Biotechvana supplies integral programming solutions to strengthen and accelerate specific and large research projects. We design customized software solutions to work more effectively, shifting time spent from manual and mechanical tasks to reducing the time-to-market for our clients' research.

"We are open to new deals, products and tools, applying to them easy automatization and versatile management of biological data."



DATABASE DEVELOPMENT AND SOFTWARE SOLUTIONS

We deliver both academic and industrial bio-databases, performing the data mining and programming the integrated database software according to the client's requirements and standards.

We develop web infrastructure that can give our client's projects more effective corporate presence on the internet. This includes web and graphical design, hosting and housing, technical support, backups, maintenance and updates, data restoration, and other functions not available to the general public, such as security, assessment in legal requirements, disclaimers, and more.

We also facilitate conversion and movement of data between databases comparing, synchronizing, replicating and converting both data and database structure, among other tasks.

*“In the post-genomic era,
databases are essential to managing
the biological informatics.”*



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