

# CeTICSdb Database resources and functionalities for the integration of -omics data and mathematical models of signaling networks

Milton Y. Nishiyama-Jr<sup>1</sup>, Marcelo S. Reis<sup>1</sup>, Bruno Ferreira de Souza<sup>2</sup>, Henrique Cursino Vieira<sup>3</sup>, Daniel F. Silva<sup>4</sup>, Inácio L.M. Junqueira-De-Azevedo<sup>5</sup>, Julia P.C. da Cunha<sup>1</sup>, Junior Barrera<sup>6</sup>, Leo K. Iwai<sup>7</sup>, Solange M.T. Serrano<sup>8</sup>, Hugo A. Armelin<sup>1</sup>,

*1 Instituto Butantan*

*2 ECC-CeTICS, Instituto Butantan*

*3 LECC-CeTICS, Instituto Butantan*

*4 Escola Politécnica, USP São Paulo*

*5 LETA-CeTICS, Instituto Butantan, São Paulo, Brazil*

*6 Instituto de Matemática e Estatística, Universidade de São Paulo*

*7 LETA-CeTICS, Instituto Butantan*

*8 LETA-CeTICS, Instituto Butantan, São Paulo*

## Abstract

The understanding of biological systems and signaling networks processes constitutes not only a conceptual challenge but a multi-factorial problem if based on different experimental conditions, treatments, time points, etc. The Center of Toxins, Immune-response and Cell Signaling (CeTICS) aims to understand the behavior of biological systems in specific treatments and conditions, using the -omics data and signaling networks analysis; The studies and research in CeTICS project are intrinsically interdisciplinary, which is coupled to the -omics data and heterogeneous knowledge and implies a necessity of data organization and integration to carry out scientific investigations for the generation of new insights and meaningful results. The CeTICSdb aims to provide a dynamic, user-friendly integrated system, for fully support research management, data management, perform customized on the fly analysis, simulations and apply pattern recognition methods for integration of multiple -omics data. CeTICSdb is the core of ARTISiN, an amalgam of repositories and tools, both public and in-house built ones for analysis of signaling networks. ARTISiN will allow a communication between CeTICSdb and SigNetSim, a tool for generation of dynamical models. Moreover, it has been designed for the integration of multi-omic data and mathematical modeling of signaling network. The CeTICSdb has been built with Django (Python web framework) and is composed of multiple components, which will allow to efficiently evolving it into a data management framework, requiring fewer manual changes, especially in the development of new applications. The platform will integrate the data between multiple platforms such as Galaxy and GBrowse, and public components such as Biocompare database, Cytoscape plugin and Mascot. To evaluate and test the platform, we integrated transcriptome and protein expression profiles with Metabolic Pathways to: i) estimate the pathways relative abundance between different conditions; ii) define and compare the functional activity for the pathways in each condition; iii) infer networks based on STRING information. Finally, our mid-term objective is to make the CeTICSdb platform available as a dry lab to the scientific community and the core for ARTISiN. It has already been

used as reference in the projects Biota/FAPESP and Tityus Scorpions species. CeTICSdb is free software licensed under GNU Affero General Public License (AGPL) and is available at <http://cetics.butantan.gov.br/ceticsdb>.

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