# Exploring Cancer Pharmacogenomics January 18-21, 2016

LEARN TO EXPLORE PHARMACOGENOMICS DATASETS USING CELLMINER, PATHWAY COMMONS, AND CBIOPORTA

This "hands-on" workshop will teach participants how to integrate data, and perform simple and complex analysis within computational databases in pharmacogenomics. Focus will be on easy-to-use online tools and programmatic analysis using R language.

#### January 18

- Introduction to cancer pharmacogenomics and CellMiner
- Introduction to using R for statistical analysis

### January 19

- Data analysis using the CellMiner platform
- Exploration and visualization of CellMiner data using R
- Introduction to CBioPortal and Pathway Commons
  January 20
- Online tools and R packages for pharmacogenomic dataset exploration, visualization and analysis

#### January 21

- Integrative analyses using multiple datasets
- Turning analyses into interactive web applications

#### January 22

- A short presentation of various Computational Bioinformatics projects conducted by Professors and students at Institute of Biomedical Sciences
- Introduction of CEFAP core facility

**Speakers:** Augustin Luna (Danna Faber Cancer Institute, Boston, MA, USA), Fabricio Garmus Sousa (UFMS), Robson F. de Souza (ICB-USP), Arthur Gruber (ICB-USP), Elder Nakaya (FCF-USP), Adilson Kleber (ICB-USP), João Setubal (IQ-USP), Jonas Weissmann (CEFAP-USP), João Marcelo P Alves (ICB-USP).

Who should attend: Graduate and Post-graduate students with an interest in bioinformatics, cancer pharmacology; all computer programming knowledge levels welcomed.

## For questions and registration contact Jose Belizario (jebeliza@usp.br)



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