Special Issue

Statistical Approaches to Omics Data: Searching for Biological Truth

Message from the Guest Editor

Omics approaches are very powerful tools for generating new knowledge about molecular processes, especially those from shotgun analyses. However, the information obtained must be reliable. To achieve this, it is essential to implement correct analyzes and statistical treatments for each stage of an omics workflow, without forgetting that the results must represent, in the best possible way, a biological reality. Thus, in addition to justifying one type of analysis or another (transcriptome based on reference vs. de novo, choice between quantification and sequence normalization methods, protein quantification methods, etc.), or performing a hypothesis contrast test or an alternative (t-test, ANOVA, Limma, DEqMS, negative binomial models, etc.), it is essential to know if the omics results fit those obtained through other methodologies within the context of functional validation. Additionally, differences between statistical and biological significance should be considered.

Guest Editor

Dr. Alfonso Olaya Abril
Departamento de Bioquímica y Biología Molecular, Edificio Severo Ochoa, Campus de Rabanales, Universidad de Córdoba, 14071 Córdoba, Spain

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Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
ijms@mdpi.com

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Department of Physiology, Institute of Nutrition and Food Technology
“Jose Mataix”, Biomedical Research Center, University of Granada,
Avda. Conocimiento s/n, 18100 Armilla, Granada, Spain

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