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In September 2011, scientists announced new experimental findings that would not only threaten the conduct and publication of influenza research, but would have significant policy and intelligence implications. The findings presented a modified variant of the H5N1 avian influenza virus (hereafter referred

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to as the H5N1 virus) that was transmissible via aerosol between ferrets. These results suggested a worrisome possibility: the existence of a new airborne and highly lethal H5N1 virus that could cause a deadly global pandemic. In response, a series of international discussions on the nature of dual-use life science arose. These discussions addressed the complex social, technical, political, security, and ethical issues related to dual-use research. This Research Topic will be devoted to contributions that explore this matrix of issues from a variety of case study and international perspectives.

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Journey through time, across the globe and through multiple disciplines. Indeed, we need to be thinking about these concepts and applying them every day to do our jobs better.” Farah Magrabi, Macquarie University, Australia “The reader will find intriguing not only the title but also the content of the book. I’m also pleased that public health, and even more specifically epidemiology has an important place in this ambitious discussion.” Elena Andresen, Oregon Health & Science University, USA “This book is very well written and addresses an important topic. It presents many reasons why basic scientists/researchers should establish collaborations and

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major contribution to the research ethics literature.” David Fleming, University of Missouri, USA A comprehensive review of the research phase of life sciences from design to discovery with suggestions to improve innovation This vital resource explores the creative processes leading to biomedical innovation, identifies the obstacles and best practices of innovative laboratories, and supports the production of effective science. Innovative Research in Life Sciences draws on lessons from 400 award-winning scientists and research from leading universities. The book explores the innovative process in life sciences and puts the focus on how great ideas are born and

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become landmark scientific discoveries. The text provides a unique resource for developing professional competencies and applied skills of life sciences researchers. The book examines what happens before the scientific paper is submitted for publication or the innovation becomes legally protected. This phase is the most neglected but most exciting in the process of scientific creativity and innovation. The author identifies twelve competencies of innovative biomedical researchers that described and analyzed. This important resource: Highlights the research phase from design to discovery that precedes innovation disclosure Offers a step by step

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**Crabtree** explanation of how to improve innovation Offers solutions for improving research and innovation productivity in the life sciences Contains a variety of statistical databases and a vast number of stories about individual discoveries Includes a process of published studies and national statistics of biomedical research and reviews the performance of research labs and academic institutions Written for academics and researchers in biomedicine, pharmaceutical science, life sciences, drug discovery, pharmacology, Innovative Research in Life Sciences offers a guide to the creative processes leading to biomedical innovation and identifies the best practices of innovative scientists and



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From 1814, linked to their educational work, Jesuits made significant contributions to the natural sciences, especially in the

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fields of astronomy, meteorology, seismology, terrestrial magnetism, mathematics, and biology in a worldwide network of universities, secondary schools and observatories.

The six-volume set LNCS 8579-8584 constitutes the refereed proceedings of the 14th International Conference on Computational Science and Its Applications, ICCSA 2014, held in Guimarães, Portugal, in June/July 2014. The 347 revised papers presented in 30 workshops and a special track were carefully reviewed and selected from 1167. The 289 papers presented in the workshops cover various areas in

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Computational science ranging from computational science technologies to specific areas of computational science such as computational geometry and security.

Stable, predictive biomarkers and interpretable disease signatures are seen as a significant step towards personalized medicine. In this perspective, integration of multi-omic data coming from genomics, transcriptomics, glycomics, proteomics, metabolomics is a powerful strategy to reconstruct and analyse complex multi-dimensional interactions, enabling deeper mechanistic and medical insight. At the same time, there is a rising concern that

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much of such different omic data –although often publicly and freely available- lie in databases and repositories underutilised or not used at all. Issues coming from lack of standardisation and shared biological identities are also well-known. From these considerations, a novel, pressing request arises from the life sciences to design methodologies and approaches that allow for these data to be interpreted as a whole, i.e. as intertwined molecular signatures containing genes, proteins, mRNAs and miRNAs, able to capture inter-layers connections and complexity. Papers discuss data integration approaches and methods of several types and extents, their application in

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Understanding the pathogenesis of specific diseases or in identifying candidate biomarkers to exploit the full benefit of multi-omic datasets and their intrinsic information content. Topics of interest include, but are not limited to: • Methods for the integration of layered data, including, but not limited to, genomics, transcriptomics, glycomics, proteomics, metabolomics; • Application of multi-omic data integration approaches for diagnostic biomarker discovery in any field of the life sciences; • Innovative approaches for the analysis and the visualization of multi-omic datasets; • Methods and applications for systematic measurements from

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single/undivided samples (comprising genomic, transcriptomic, proteomic, metabolomic measurements, among others); • Multi-scale approaches for integrated dynamic modelling and simulation; • Implementation of applications, computational resources and repositories devoted to data integration including, but not limited to, data warehousing, database federation, semantic integration, service-oriented and/or wiki integration; • Issues related to the definition and implementation of standards, shared identities and semantics, with particular focus on the integration problem. Research papers, reviews and short communications on all

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