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	Sommario/riassunto	Network science has accelerated a deep and successful trend in research that influences a range of disciplines like mathematics, graph theory, physics, statistics, data science and computer science (just to name a few) and adapts the relevant techniques and insights to address relevant but disparate social, biological, technological questions. We are now in an era of 'big biological data' supported by cost-effective high-throughput genomic, transcriptomic, proteomic, metabolomic data collection techniques that allow one to take snapshots of the cells' molecular profiles in a systematic fashion. Moreover recently, also phenotypic data, data on diseases, symptoms, patients, etc. are being collected at nation-wide level thus giving us another source of highly related (causal) 'big data'. This wealth of data is usually modeled as networks (aka binary relations, graphs or webs) of interactions, (including protein–protein, metabolic, signaling and transcription-regulatory interactions). The network model is a key view point leading to the uncovering of mesoscale phenomena, thus providing an essential bridge between the observable phenotypes and 'omics' underlying mechanisms. Moreover, network analysis is a powerful 'hypothesis generation' tool guiding the scientific cycle of 'data gathering', 'data interpretation, 'hypothesis generation' and 'hypothesis testing'. A major challenge in contemporary research is the synthesis of deep insights coming from network science with the wealth of data (often noisy,

contradictory, incomplete and difficult to replicate) so to answer meaningful biological questions, in a quantifiable way using static and dynamic properties of biological networks.