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Sommario/riassunto	Mathematical and computational models play an essential role in understanding the cellular metabolism. They are used as platforms to integrate current knowledge on a biological system and to systematically test and predict the effect of manipulations to such systems. The recent advances in genome sequencing techniques have facilitated the reconstruction of genome-scale metabolic networks for a wide variety of organisms from microbes to human cells. These models have been successfully used in multiple biotechnological applications. Despite these advancements, modeling cellular metabolism still presents many challenges. The aim of this Research Topic is not only to expose and consolidate the state-of-the-art in metabolic modeling approaches, but also to push this frontier beyond the current edge through the introduction of innovative solutions. The articles presented in this e-book address some of the main challenges in the field, including the integration of different modeling formalisms, the integration of heterogeneous data sources into metabolic models, explicit representation of other biological processes during phenotype simulation, and standardization efforts in the representation of

