# MINER: UNCOVERING NEXT-GENERATION SYSTEMS BIOLOGY MODELS THROUGH TEXT MINING

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**ABSTRACT**

MINER is a cutting-edge computational tool that has revolutionized text mining applications. One particular application of MINER is its ability to aid in the development of Next-Generation Systems Biology models (NGSB models). These models are built on a large scale, incorporating hundreds of differential equations with millions of interactions and metabolic transformations, and aim to approximate real-life biological processes as closely as possible. MINER achieves this by taking metabolic pathways in KGML format as input data and converting them into systems of differential equations by applying text classification methodologies. This process allows for the identification of all endogenous metabolites involved in a biological process, as well as those that increase or decrease their concentration simultaneously and may be indirectly affected by a disruptor or other biological events. The development is comprised of five different levels of models, depending on the data availability. The application fields for NGSB models are vast and include the construction of comprehensive biological models, estimation of dose response curves, identification of new relationships and interactions between biological entities as well as systems biology-based AOPs and quantitative AOPS (qAOPs). In addition, they can also be used for the quantitative determination of the impact that a disruptor may have on human health, providing decision makers with a valuable tool for the evaluation of a possible disruption. By leveraging the power of MINER, researchers are now able to develop more comprehensive and accurate models of biological systems. It will soon be available as an online Shiny application.

**KEYWORDS:** Computational Systems Biology, Text Classification, KEGG pathway, Mechanistic Models

**REFERENCES**