CARMEN - Comparative Analysis and *in silico* Reconstruction of organism-specific MEtabolic Networks

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ABSTRACT. New sequencing technologies provide ultra-fast access to novel microbial genome data. For their interpretation, an efficient bioinformatics pipeline that facilitates *in silico* reconstruction of metabolic networks is highly desirable. The software tool CARMEN performs *in silico* reconstruction of metabolic networks to interpret genome data in a functional context. CARMEN supports the visualization of automatically derived metabolic networks based on pathway information from the KEGG database or from user-defined SBML templates; this software also enables comparative genomics. The reconstructed networks are stored in standardized SBML format. We demonstrated the functionality of CARMEN with a major application

example focusing on the reconstruction of glycolysis and related metabolic reactions of *Xanthomonas campestris* pv. campestris B100. The curation of such pathways facilitates enhanced visualization of experimental results, simulations and comparative genomics. A second application of this software was performed on a set of corynebacteria to compare and to visualize their carbohydrate metabolism. In conclusion, using CARMEN, we developed highly automated data analysis software that rapidly converts sequence data into new knowledge, replacing the time-consuming manual reconstruction of metabolic networks. This tool is particularly useful for obtaining an overview of newly sequenced genomes and their metabolic blueprints and for comparative genome analysis. The generated pathways provide automated access to modeling and simulation tools that are compliant with the SBML standard. A user-friendly web interface of CARMEN is available at http://carmen.cebitec.uni-bielefeld.de.

Key words: Systems biology; Metabolic networks; *Xanthomonas*; Genome annotation; *Corynebacterium*