**Title:** Conservation analysis of genome-scale biochemical networks

**Author:** Nick Henderson, Ding Ma, Yuekai Sun, and Michael Saunders

Conservation analysis is a crucial preliminary step in the analysis of biochemical networks. Emerging genome-scale models of biochemical networks capture the multiscale nature of biological systems and require specialized algorithms. We propose a method for conservation analysis of genome-scale biochemical networks based on rank-revealing LU factorization and describe an implementation powered by LUSOL, asparse LU factorization and update package.