DistributedFBA.jl: High-level, high-performance flux balance analysis in Julia

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Project Goals: Constraint-Based Reconstruction and Analysis (COBRA) [1] **is a widely used approach for modeling genome-scale biochemical networks and integrative analysis of omics data in a network context. For kilo-scale models, flux variability analysis (FVA) can currently be performed efficiently using existing methods** [2, 3, 4]**. However, these implementations perform best when using only one computing node with a few cores, which becomes a temporal limiting factor when exploring the steady state solution space of larger models. Here, we exploit Julia** [5]**, a high-level, high-performance dynamic programming language, to distribute sets of flux balance analysis problems and compare its performance to existing implementations.**

Flux balance analysis, and its variants, are widely used methods for predicting steady-state reaction rates in biochemical reaction networks. The exploration of high dimensional networks with such methods is currently hampered by software performance limitations. *DistributedFBA.jl* is a high-level, high-performance, open-source implementation of flux balance analysis in Julia. It is tailored to solve multiple flux balance analyses on a subset or all the reactions of large and huge-scale networks, on any number of threads or nodes. The code and benchmark data are freely available on *github.com/opencobra/COBRA.jl*. The documentation can be found at *opencobra.github.io/COBRA.jl*.

References

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[5] Bezanson J, Edelman A, Karpinski S, Shah VB (2014) Julia: A Fresh Approach to Numerical Computing. arXiv:14111607 [cs] .