



Colorado Science and Engineering Fair

2024 Individual Project Abstract Form

Please print 2 copies of the completed form. Sign both copies, keep 1 for your notebook and submit 1 copy to your Regional Fair Director with your other paperwork.

Title of Project: A Novel Disaggregated Approach for Enhanced Flux Balance Analysis in Genome-Scale Metabolic Modeling Using Dual Anderson-ADMM

Finalist's Name: Michael Gao

School and City: Fairview High School, Boulder

Sponsor's Name: Stephen Thomas

Category: Mathematics & Computer Sciences (MACS)

Division: Senior (9th - 12th grades)

Abstract (250 words or less):

Flux balance analysis (FBA) is a linear-programming-based computational approach used in systems biology that allows for the quantification of reaction fluxes in metabolic networks and is crucial for understanding cellular metabolism, metabolic engineering strategies, and disease mechanisms. However, as metabolic networks expand and redundant fluxes increase, memory usage grows, forcing direct FBA to use excessive over-relaxation which introduces significant error. Furthermore, inaccuracies in reconstructions or gene-protein-reaction associations result in erroneous FBA predictions, and there is a lack of integration for alternative optimal flux distributions. FBA derivatives require analyses that introduce nonlinearities.

I developed a novel disaggregated approach for FBA using partitioning by reaction of the S-Matrix, Ruiz Scaling, Incomplete LU Factorization (ILU), and topological analysis. I wrapped the Alternating Direction Method of Multipliers (ADMM) into an Anderson Acceleration (AA) framework, using the Generalized Minimal Residual Method (GMRES) to solve for local convergence.

My approach converged on expansive networks such as the human genome whereas COBRA could not. ADMM achieved an average Euclidean norm of $< 4.5\%$ due to linearities (alternative flux distributions), producing an almost identical Escher Map with only substantial error in 2/95 reactions and reasonable time loss (200%). ADMM generated a congruent phenotypic phase plane and performed accurate flux variability analysis. The ADMM process traced the edge of the solution space, which revealed alternative flux distributions. My novel approach mitigates issues of computational demand, accuracy, and alternative solutions in FBA, providing a step forward for analyzing more complex metabolic networks, enhancing future metabolic engineering and disease modeling.

I hereby certify that the above statements are correct and the information provided in the Abstract is the result of one year's research. I also attest that the above properly reflects my own work.

Finalist's Signature:

Date: 02/27/2024

In addition, all students must complete the ISEF Student Checklist (1A), Research Plan, Approval Form (1B), and Checklist for Adult Sponsor (1), and any other ISEF forms required for this type of project. See the International Rules and Guidelines for form requirements. Return COPIES of all of these forms to your Regional Fair Director with you Finalist Verification/Permission Form. A signed copy of this form must be included in your notebook.