Advanced ODE Modeling and Simulation at Bristol Myers Squibb

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Bristol Myers Squibb / Spectraforce (Contract)

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Project Overview

- Contract role as Algorithm Developer Scientist from Aug 2019 to Jul 2021.
- Focused on performance optimization and simulation of large-scale biological models.
- Worked closely with pharmacology and discovery teams.

757-Equation Model Optimization

- Ported a complex 757-ODE model from MATLAB to Julia.
- Achieved 5x performance improvement using Julia's native solvers.
- Validated numerical accuracy across solvers (e.g., LSODA, SUNDIALS).

Steady-State Adaptive Modeling Tools

- Refactored MATLAB steady-state solution algorithms.
- Implemented adaptive model reduction to improve computational efficiency.
- Automated generation of analytical Jacobians to support solver accuracy and stiffness detection.

PBPK App Development

- Built a Physiologically-Based Pharmacokinetic (PBPK) app around the ODE model.
- Allowed scientists to simulate drug exposure and pharmacokinetics under multiple scenarios.
- App supported solver switching, sensitivity toggles, and parameter editing.

Sensitivity Analysis Calibration

- Applied global sensitivity analysis to guide model refinement.
- Calibrated biological models to experimental data using cost function minimization.
- Explored parameter identifiability and robustness of predictions.

Summary

- Delivered highly optimized modeling workflows using Julia for performance-critical tasks.
- Enabled model-driven pharmacology through interactive PBPK tools.
- Advanced robustness and interpretability via automation and global sensitivity methods.

Thank You

Questions or technical discussion welcome! christian.daniel.basile@gmail.com