All simulations were run in Matlab R2021a.

**Folder: MATLAB**

batch\_mcmc.m – runs the file mcmc.m in parallel on a local machine (set to 5 cores).

batch\_mcmc\_activity.m – runs the file mcmc\_activity.m in parallel on a local machine (set to 5 cores).

batch\_mcmc\_1OHMid3.m – runs the file mcmc\_1OHMid3.m in parallel on a local machine (set to 5 cores).  
  
mcmc.m – MCMC routine that fits Equations (6)-(10) and Equation (23) to gene expression data and produces metadata folders chains\_1, chains\_2, chains\_3, chains\_4, and chains\_5.

mcmc\_activity.m - MCMC routine that fits Equation (18) to CYP-specific activity data from the substrate mixture experiment and produces metadata folders chains\_activity\_cyp3a4, chains\_activity\_cyp2c9, and chains\_activity\_cyp2b6.

mcmc\_1OHMid3.m - MCMC routine that fits Equation (18) to CYP3A4 activity data from the single substrate experiment and produces metadata folders chains\_1OHMid3.

plot\_mcmc\_kinetics.m – plots solutions of Equations (6)-(10) using MCMC-accepted parameter sets (generates Figure 2).

plot\_mcmc\_kinetics\_activity.m - plots CYP-specific activity data (substrate mixture experiments), plots solutions of Equations (14) and (18) using MCMC-accepted parameter sets. Plots sensitivity of the solution to changes in the input rifampicin concentration (generates Figures S4, S5, and S6 in S1 Text).

plot\_mcmc\_kinetics\_1OHMid3.m - plots CYP3A4 activity data (single substrate experiment), plots solutions of Equations (14) and (18) using MCMC-accepted parameter sets. Plots sensitivity of the solution to changes in the input rifampicin concentration (generates Figure 4).

posterior\_values\_ci.m – generates files maxLikValues.txt with the best-fit parameter values (Equations (6)-(10)), and posteriorValues.txt with mean, median, lower, and upper value of the 95% credible interval for each parameter.

posterior\_values\_ci\_activity.m - generates files maxLikValues\_activity.txt with the best-fit parameter values (Equation (18)), and posteriorValues\_activity.txt with mean, median, lower, and upper value of the 95% credible interval for each parameter.

posterior\_values\_ci\_1OHMid3.m - generates files maxLikValues\_1OHMid3.txt with the best-fit parameter values (Equation (18)), and posteriorValues\_1OHMid3.txt with mean, median, lower, and upper value of the 95% credible interval for each parameter.

plot\_mcmc\_posteriors.m – plots posterior distributions for parameters from Equations (6)-(10) (generates Figure 3 and Figure S2 in S1 Text).

plot\_mcmc\_posteriors\_activity.m - plots posterior distributions for CYP-specific metabolic rates from Equation (18) (generates Figure S7 in S1 Text).

plot\_data.m – plots gene expression and degradation data (generates Figure 1).

plot\_data\_fold\_activity.m – plots CYP-specific metabolic activity data (generates Figure S3 in S1 Text).

plot\_data\_MDR1deg.m – plots MDR1 mRNA degradation data (generates Figure S1 in S1 Text).

peaks\_enzymes.m – plots, for each variable from Equations (6)-(10), the time at which the best-fit solution reached the highest value with respect to varying rifampicin concentration (generates Figure S8 in S1 Text).

plot\_CYP3A4\_validation.m – plots Donor 4 data against the prediction bands for CYP3A4 mRNA fold time course kinetics.

plot\_mcmc\_posterior\_BIC.m – plots Bayesian information criterion for Equations (6)-(10) assuming kr = 0 and kr > 0 (generates Figure S10 in S1 text).

sensitivity.m – plots the best-fit solutions of Equations (6)-(10) as it varies with varying input rifampicin concentration (generates Figure 5).

**Folder: MATLAB\_no\_resouce\_depletion**

batch\_mcmc.m – runs the file mcmc.m in parallel on a local machine (set to 5 cores).

mcmc.m - MCMC routine that fits Equations (6)-(10) and Equation (23) assuming kr = 0 to gene expression data and produces metadata folders chains\_1, chains\_2, chains\_3, and chains\_4.

plot\_mcmc\_kinetics.m – plots solutions of Equations (6)-(10) assuming kr = 0 using MCMC-accepted parameter sets (generates Figure S9 in S1 text).

posterior\_values\_ci.m – generates files maxLikValues.txt with the best-fit parameter values (Equations (6)-(10) assuming kr = 0), and posteriorValues.txt with mean, median, lower, and upper value of the 95% credible interval for each parameter.