

# Research Notes: Week 4

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Drawing from our previous work, we spent this week transitioning from fitting the simple Lotka-Volterra system to fitting the 12-equation Type 1 diabetes system described in Shtylla et al. 2019. Delayed Rejection Adaptive Metropolis (DRAM) was used to fit the model's 53 parameters to mean glucose data collected by Matthews et al. 2015 in NOD mice. Additionally, global optimization methods began to be explored. Such methods are widely used and act as a good benchmark for checking the accuracy of parameter fits suggested by DRAM. Specifically, Particle Swarm Optimization (PSO) was examined.

## 1 Data

The data consisted of the mean glucose measurements of 400 mice over a period of 24 days prior to the onset of diabetes, as characterized by the increase of blood glucose levels past 250 mg/dl for two measurements in a row. Measurements were taken irregularly; with samples being taken every two days for all mice, and samples every 24 hours for mice exceeding the 250 mg/dl threshold. Ideally, we would be able to fit parameters to glucose readings from individual mice, but the dataset is missing a large number of values, and this became a clearly daunting task. To avoid the inconsistencies in the data, we decided instead to examine the mean of the glucose readings for two groups of mice: those with progressive T1D, and those with acute T1D. According to research notes from Mathew et al.:

"After data was taken, mice were classified according to the characteristics of their onset. If the mouse had steady euglycemia (glucose levels in the healthy range) before having a sudden onset of hyperglycemia, the mouse was categorized as having an acute form of the disease. Conversely, if the mouse simply had an 'excursion' above 200 mg/dL (meaning there was a reading of 200 or above, and at least one subsequent reading before diagnosis with diabetes was below this number), the diagnosis of the disease was categorized to be progressive."

Additionally, these data points had to be time-adjusted. Originally collected on a time frame relative to diabetes onset (i.e. starting at day -24 and progressing to day 0), they had to be altered to exist on linear, consecutive time. As data collection began when the mice were 8-weeks old, we adjusted days -24 to 0 to be days 56 to 80. This left us with the data shown in Figure 1 and plotted in Figure 2.

Day	Progressive Mean	Acute Mean
56	147.0866	134.8056
57	148.4262	125.1818
58	152.7895	134.3529
59	142.7593	128.3333
60	157.8933	133.6072
61	157.5000	131.5556
62	163.0263	133.9677
63	164.6021	134.1964
64	167.7400	121.1818
65	166.0227	137.5652
66	165.5556	132.8333
67	178.1389	136.8219
68	170.0714	136.5429
69	176.4964	142.4889
70	186.1304	144.2787
71	184.1519	133.3750
72	189.6414	143.6000
73	183.8125	142
74	199.3645	149.1579
75	197.7468	155.2600
76	213.8244	162.5909
77	223.3852	159.8675
78	230.8983	129
79	350.0821	88.5480
80	380.9802	94.9865

Figure 1: Mean glucose data for progressive and acute mice populations

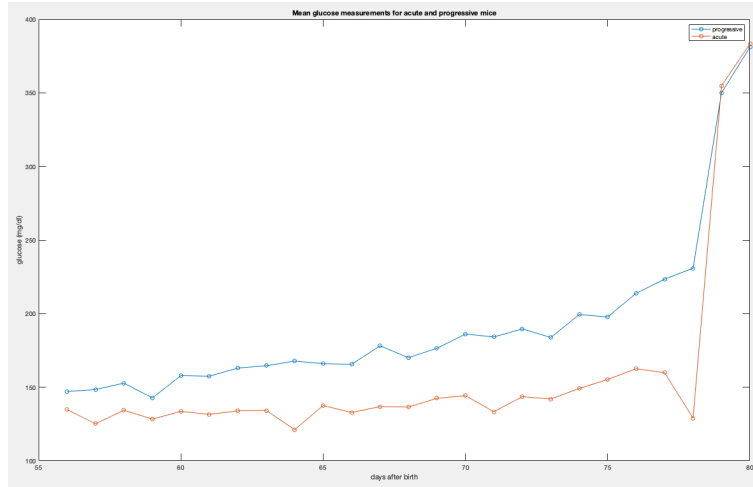


Figure 2: Mean glucose data for progressive and acute mice populations over days since birth.

## 2 Fitting with DRAM

As a refresher from last week, DRAM is an MCMC algorithm that combines the methods of the adaptive Metropolis and delayed rejection algorithms (outlined below).

### 2.1 Adaptive Metropolis

1. Sample parameter sets for a period of length  $k_0$  where values are computed using an initial covariance matrix  $V_0$

- $k_0$  is chosen to balance mixing with sufficient diversity of points to ensure a non-singular covariance matrix
  - Shorter adaptation intervals tend to produce better mixing and high acceptance ratios; thus the chain is more responsive to new data
  - In practice,  $k_0$  is often 100
2. At the  $k$ th step of the chain, adaptation commences: the initial  $V_0$  is updated to the covariance matrix,  $V_k$

$$V_k = s_p \text{cov}(q^0, q^0, \dots, q^{k-1}) + \epsilon I_p$$

- $s_p$  is a design parameter that depends on the dimension ( $p$ ) of the parameter space; a common choice is  $s_p = 2.38^2/p$
- The term  $\epsilon I_p$  refers to an ID matrix of dimension  $p$ . It simply exists to ensure that  $V_k$  is positive definite. Often,  $\epsilon = 0$

## 2.2 Delayed Rejection

In the standard Metropolis algorithm, when a candidate parameter set  $q^*$  is rejected (with its prescribed acceptance ratio), the current step parameter set,  $q^{k-1}$ , is retained and  $q^*$  is discarded before choosing the next sample. In the *delayed rejection* (DR) algorithm, when  $q^*$  is rejected, alternative candidates  $q^{*j}$  are constructed and considered instead of immediately reverting back to  $q^{k-1}$ . For example,  $q^{*2}$ , a second-stage candidate, is chosen using proposal function

$$J_2(q^{*2}|q^{k-1}, q^*) = N(q^{k-1}, \gamma_2^2 V_k)$$

- $V_k = R_k R_k^T$  is the covariance matrix produced in the adaptive algorithm
- $J_2(q^{*2}|q^{k-1}, q^*)$  indicates that we propose  $q^{*2}$  having started at  $q^{k-1}$  and rejected  $q^*$
- $\gamma_2 < 1$  narrows the second-stage function and increases mixing

The acceptance criteria for the second-stage candidate is

$$\alpha_2(q^{*2}|q^{k-1}, q^*) = \min(1, \frac{\pi(q^{*2}|v)J(q^*|q^{*2})[1-\alpha(q^*|q^{*2})]}{\pi(q^{k-1}|v)J(q^*|q^{k-1})[1-\alpha(q^*|q^{k-1})]})$$

The DRAM algorithm works as follows: Starting with parameter set  $q^{k-1}$ , we choose candidate sample  $q^*$ . If  $q^*$  is rejected, we propose candidate  $q^{*2}$ . If  $q^{*2}$  is rejected, we impose candidate  $q^{*3}$  and so on until we accept candidate  $q^{*j}$ . We begin sampling again with  $q^{k-1} = q^{*j}$  as our current parameter set. After taking  $k$  samples, we update our covariance matrix (and thus our proposal distribution and acceptance ratio).

In the DRAM algorithm, the adaptive Metropolis and delayed rejection work together: AM updates the proposal via previously accepted candidates and the covariance matrix DR alters the proposal function to improve mixing.

Last week we focused on adapting DRAM to the Lotka-Volterra model. This week we adapted DRAM to the Type 1 Diabetes model.

## 2.3 Fitting the Type 1 Diabetes Model with DRAM

The Type 1 Diabetes model consists of a system of 12 differential equations (variables) and 53 parameters. Our DRAM algorithm allows us to parameterize the entire system even though glucose measurements are our only source of data. We began with a parameterization of the entire system to get a feel for how our algorithm would react to the increase in number of parameters and variables. After our discussion during the weekly meeting, a better approach would be to only fit parameters that are associated with the Glucose equation (we will attempt this next week). For now, we focus on the whole system.

### 2.3.1 Implementing the algorithm

The basic framework of our algorithm came from Marko Laine (found *here*) who parameterized a 3 equation, 20 parameter ODE system of algae. populations. The algorithm runs as follows:

1. *Load data*: see description above (Section 2)
2. *Set initial parameter values*: These values were loaded from the preset definitions given in Shtylla et al. 2019.
3. *Determine likelihood function*: Our sum of squares function takes the difference between the ode-solved data and the original data. In other words, it defines the error in the model. In this (and many scenarios), we assume that this error has a normal distribution.

```
%% Calculating model sum of squares
model.ssfun = @(theta, data) T1Dss(theta, data);
-----
%% Sum-of-squares function
function ss = T1Dss(theta, data)
ydata=data(:,2); % original data

% Ynowave: no wave wild type (1)
% Ynowave: NOD no wave (2)
% Ywave: wild type + wave (3)
% Ynwave: NOD + wave (4)
[~,ymodel]= T1Dfun(2); % uses Matlab ODE solver

ss = sum((ymodel-ydata).^2);
end
```

4. *Define the prior distribution*: When we know little about our parameters and model, we will assume a noninformative (uniform distribution) prior. Because we are supplied with individual differential equations, we can use the Matlab *fminsearch* function to determine a guess for the variance of our prior distribution. In this way, we are supplying our algorithm with a little more information about the sampling space of our parameters.

```
function [mse, params] = T1D_fitInitialParams(params, data)
% Extract the initial guess for your parameters (must be in vector form)
for i = 1:length(params)
    initGuess(i) = params{i}{2}; % value of parameter
    lb(i) = params{i}{3}; % lower bound of uniform prior
    ub(i) = params{i}{4}; % upper bound of uniform prior
end

%Run a quick fminsearch to get initial parameter and s2 guesses for DRAM
if length(data(:,1)) > length(params)
    fun = @(params) T1Dss(params, data); % solve ODE
    opt = optimset('Display', 'off');
    % Find minimum of constrained function
    [theta, ss0] = fmincon(fun, initGuess, [], [], [], [], lb, ub, [], opt);
    mse = ss0/(length(data(:,1))-length(params));

    %Now replace params starting values with fminsearch output
    for i = 1:length(params)
        params{i}{2} = theta(i);
```

```

        end
    else
        mse = 1; % THIS MAY NEED TO BE CHANGED! Normal guess for mse breaks down! Need more
                % data pts than parameters
    end
end

```

5. *Generating samples:* In this algorithm we run 2 DRAM chains. The first chain acts as the burn-in period. After this chain is completed, we take the final chain sample and use it as the initial chain values for our second chain, from which we actually collect and store parameter values.

```

%% Burn-in iterations
% First generate an initial chain.
options.nsimu = 1000; % number of iterations
options.method = 'dram'; % sampling method is DRAM
[results, chain, s2chain]= mcmcrun(model,data,params,options);

%% Running MCMC chain
% Then re-run starting from the results of the previous run,
options.nsimu = 5000;
options.method = 'dram';
[results, chain, s2chain] = mcmcrun(model,data,params,options, results); % note that the
% results of the first chain are an input of the second mcmcrun

```

## 6. Results

- Plot parameter densities
  - Print mean parameter values
  - Check convergence via Geweke's diagnostic (convergence when mean of the first 10% = mean of the last 50% of the chain). Geweke value  $> 0.7$  signals convergence
7. *Model Prediction:* This algorithm is also designed to plot predicted values of the model system using the parameter values sampled in the chain. Plotting these predictions tells us how much variability in the system our sampled parameters create; ideally we would want small variability which would tell us that our samples fit our model well.

### 2.3.2 Data/Model Options and Assumptions

Due to the various options of mouse data and ODE solver assumptions, there are many combinations of the model that we can run our algorithm on. We define the following combinations:

- NOD mouse + no wave + *simulated data*
- NOD mouse + no wave + *acute mouse data*
- NOD mouse + no wave + *progressive mouse data*
- NOD mouse + wave + *simulated data*
- NOD mouse + wave + *acute mouse data*
- NOD mouse + wave + *progressive mouse data*

Underlined options determine specific ODE solving assumptions and italicized options determine the different classifications of mouse data (see Section 2). Wave refers to the presence of the apoptotic  $\beta$ -cell wave.

We also only run our algorithm on the NOD mouse option because Mathews et al. 2015 mentions that they collected data only from NOD mice. We recognize however that we cannot be certain that this is true, so eventually we do plan to run our algorithm using the "wild-type" options as well.

Simulated data was generated by solving the ODE model (with and without wave) and adding normally distributed noise:

```
% Simulate 100 data points
[tmodel, ymodel]=T1D_dataSim(4); % ex. NOD mouse + no wave
% add normal noise
noise=normrnd(0,1,[1,100]);
data=[tmodel ymodel+noise'];
```

## 2.4 Results and Analysis

We ran our algorithm a total of 6 times. In this section we will illustrate the results of 1 of the 6 combinations that we ran our DRAM algorithm with and provide analysis. The rest of the results should be analyzed in the same fashion. To view full result figures please see *Appendix*. Here we view and analyze the DRAM performance on NOD mice + no wave + simulated data as this appears to be the "best" (or more accurate with the least variation) run.

We look first at the density plots produced by the algorithm, Figure 3.

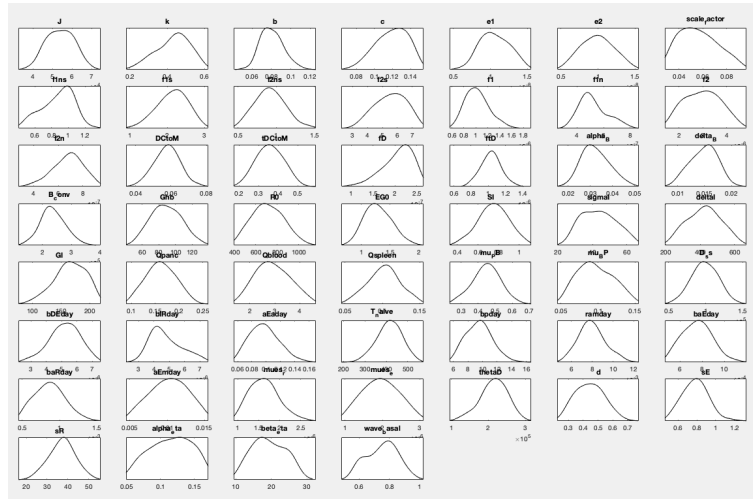


Figure 3: Parameter posterior density functions (pdfs) plots (53) for NOD mouse + no wave + simulated data.

From this figure we can see that the parameter pdfs look, for the most part, smooth with a single mode. This gives us a general indication that our algorithm is running correctly, as we would like our density functions to be smooth and continuous (although it may be that some parameters distributions are multi-modal).

Next we look at the information produced by our chain, namely the mean parameter values and Geweke's diagnostic for convergence, Figure 4.

	mean	std	MC_err	tau	geweke
J	53974	6875.2	984.93	159.19	0.95768
k	0.43252	0.087196	0.012956	360.98	0.75361
b	0.080428	0.011531	0.0017569	107.77	0.97863
c	0.11919	0.01726	0.0028018	157.93	0.76257
e1	1.0596e-08	1.9405e-09	2.5726e-10	89.372	0.86366
e2	9.92e-09	2.1401e-09	2.6791e-10	96.318	0.77692
scale_factor	0.056254	0.015691	0.0021661	334.56	0.61534
f1ns	0.87644	0.18558	0.032224	442.7	0.69247
f1s	2.1413	0.40046	0.066585	450.25	0.62309
f2ns	0.91731	0.1941	0.030707	165.74	0.92644
f2s	5.5436	1.022	0.13216	92.565	0.73459
f1	1.0251e-06	1.9666e-07	3.3966e-08	387.98	0.66286
f1n	5.206e-07	1.0308e-07	1.7121e-08	520.11	0.69036
f2	2.9834e-06	7.3557e-07	1.0798e-07	90.817	0.72121
f2n	6.7999e-07	1.1938e-07	1.963e-08	534.97	0.78478
DCtoM	0.057777	0.0070723	0.00090037	69.835	0.9955
DCtoM	0.35712	0.067113	0.012279	247.77	0.57448
fD	2.0636e-07	3.3832e-08	6.196e-09	407.04	0.75611
fTD	1.0315e-06	1.1404e-07	1.6376e-08	99.503	0.99915
alpha_B	0.03234	0.0061066	0.00068464	88.27	0.84909
delta_B	0.014847	0.0024632	0.00040747	173.21	0.86385
B_conv	2.3621e+05	41695	5337.6	98.105	0.8635
Ghb	88.889	17.878	3.158	332.32	0.69416
R0	713.62	142.58	19.786	108.77	0.83778
EG0	1.2912	0.22916	0.03281	109.23	0.80274
SI	0.75147	0.14375	0.023272	150.87	0.89388
sigmaI	43.714	9.7977	1.5876	322.32	0.54848
deltaI	424.15	95.237	15.273	145.49	0.91643
GI	165.63	26.9	3.3559	99.245	0.89439
Qpanc	0.16222	0.030309	0.0042573	110.85	0.98922
Qb1000	2.9195	0.67457	0.088611	83.52	0.99969
Qap1000	0.1018	0.020965	0.00336	148.9	0.99398
mu_PB	0.4484	0.079934	0.012118	169.31	0.97602
mu_BP	0.096583	0.023291	0.0034901	194.06	0.63319
D_ss	98944	17603	2749.3	174.8	0.79815
bDEday	5.2096e-06	9.6646e-07	1.6204e-07	147.37	0.93557
bIRday	4.7779e-06	1.0032e-06	1.8274e-07	375.42	0.64459
aEday	0.097293	0.01987	0.003207	121.83	0.6491
T_naive	414.01	56.898	8.5803	128.18	0.92217
bpday	9.5068	1.7484	0.28257	161.23	0.74832
randay	0.0079633	0.0012633	0.00018264	144.66	0.93441
baEday	0.00075473	0.00013031	1.7167e-05	92.687	0.85946
baRday	0.0008679	0.00019909	3.0296e-05	142.59	0.61097
aEday	0.010256	0.0024783	0.00035619	223.2	0.70533
mues_r	1.6314e-06	3.4026e-07	5.6353e-08	360.69	0.879
mues_e	1.9553e-06	4.7516e-07	7.1117e-08	110.95	0.73987
thetaD	2.1479e+05	35982	6470	399.95	0.74653
d	0.44464	0.095279	0.014334	117.23	0.63978
sE	0.78454	0.13593	0.019514	123.04	0.94578
sR	37.24	6.2038	0.96475	154.62	0.99113
alpha_eta	0.11535	0.029932	0.0045729	178.61	0.61593
beta_eta	19.301	4.5358	0.72709	142.28	0.61677
wave_basal	0.75219	0.10035	0.019658	537.96	0.61577

Figure 4: Table with details of the DRAM chain for NOD mouse + no wave + simulated data.

From this table, we can see that for a majority of the parameters our chain did converge with Geweke  $> 0.7$ . The best outcome would be for the chain to converge for all parameters, but given the number of parameters and the fact that we only have glucose measurement data, we are not sure how feasible this will be. The parameter means are useful for comparison of methods. For example, we plan to use the means produced by DRAM and PSO (Section 3) to compare the consistency and accuracy of each method.

Lastly, we can use our algorithm to predict what the model will do in the future given the parameter values sampled in the chain, Figure 5.

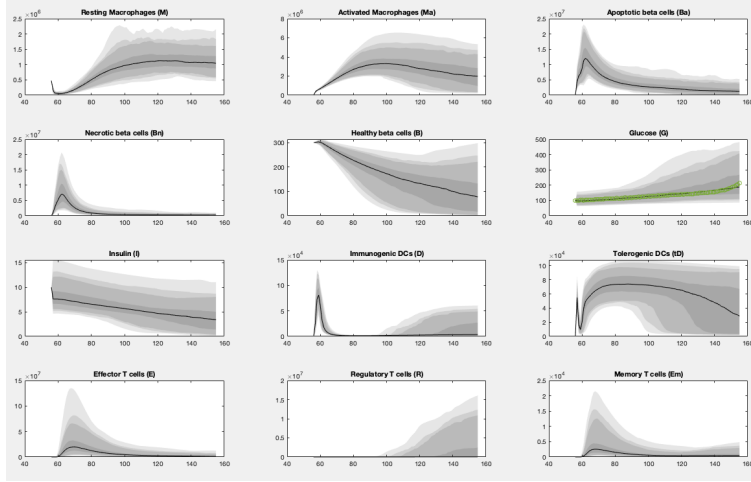


Figure 5: Predicted models for the NOD mouse + no wave + simulated data.

Here it is important to note that the overlapping gray shapes represent different predictions of the model based on individual parameter values that were taken from the results of our completed DRAM chain. Ideally we would like the range of these predictions to be small as that tells us our DRAM-ed parameter values fall in a smaller range, fit the model well, and produce little variation. It is easier to determine a "best" parameter value (for use in computations or other algorithms, models etc.) from a small rather than a large range of values.

#### 2.4.1 Comments on results

It is important to note that at the moment we are unable to produce the predicted model figure for the DRAM combinations *with wave* (see Appendix: Fig. 12-14).

We would also note that, in general, the model predictions for acute and progressive mouse data without wave, are highly variable. This tells us that our parameter values are creating a lot of variation between predictions (see Appendix: Fig. 10 and 11). We are planning to investigate this issue further.

### 2.5 Improvements

We would like to run all our combinations again (plus those that incorporate the "wild-type" mouse data) on a subset of parameters. Instead of trying to fit all 53 parameters, it would be more useful to parameterize those which are included in and associated with the equation for Glucose (as this is the data we have). We hope to see better convergence of parameters as well as smaller variation in our models prediction as a result.

## 3 Fitting with PSO

### 3.1 What is PSO?

Particle Swarm Optimization (PSO) is global optimization algorithm serving to locate the global minimum of a function, known as the objective function. Like MCMC, the algorithm works iteratively to propose candidate solutions, measure the quality of these proposals according to the objective function, and adjust future proposals based on the outcome. The algorithm's development was based on a flock of birds hunting for food. As the birds fly, each bird is looking for food. Each bird knows where the best food source it has seen is, and it can listen to the squawks of others to determine their findings. If another bird has found a better food source than this bird has ever seen, it will likely change its flight path to investigate what that other bird has found. Otherwise, it will continue to explore, but also move towards its best discovered food source. All in all, as this process progresses, this leads to the flock localizing to one area, the one with the optimum food. Putting this mathematically, the algorithm is as follows:



1. Initialize a particle swarm of size  $n$  by selecting points ('particles') according to  $i \sim \text{Uniform}(X_{min}, X_{max})$  where  $X_{min}, X_{max}$  represent the lower and upper bounds of the search space, respectively
  - (a) Assign each particle,  $i$ 's, initial position as its personal best at time  $t$ :  $P_{best,i}^t$
  - (b) Determine the global best with  $G_{best} = \min(P_{best,i}^t)$  for all  $i$
2. Initialize parameters  $c_1$  and  $c_2$ , acceleration parameters that determine a particle's attraction to its own findings and the findings of others, respectively
3. Begin the process of simulating the swarm by calculating the velocity vector for each particle  $i$  in each dimension  $j$ :

$$v_{ij}^{t+1} = v_{ij}^t + c_1 r_1^t [P_{best,i}^t - x_{ij}^t] + c_2 r_2^t [G_{best,i}^t - x_{ij}^t]$$

where  $r$  represents a uniform random values  $(0, 1)$

4. Update the location of each particle:

$$x_i^{t+1} = x_i^t + v_i^{t+1}$$

5. Recalculate  $P_{best}$  and  $G_{best}$  by evaluating the objective function for each  $x_i$ :
  - $P_{best}$  = best location found by particle  $i$
  - $G_{best}$  = best location found by all particles
6. Repeat velocity and position updates until either the maximum number of iterations is reached, or the spread of the swarm is negligible (minimum threshold set before PSO begins)

This process is well-summarized in the following flowchart.

## 3.2 PSO Implementation

PSO was used to fit the 53 parameters of the T1D system to the data in Figure 1. MATLAB includes a built-in implementation of PSO in the Global Optimization Toolbox, thus that was used.

### 3.2.1 Parameter fitting

In order to adapt PSO to fit parameters to the model, an appropriate objective function needed to be chosen. As the objective function is minimized in PSO, a function that would decrease when a better parameter set is proposed needed to be implemented. The most simple function to fit this requirement was a simple sum-of-squares functions measuring the difference of the model outputs of the glucose equation in the T1D system and the observed data at analogous time points. This technique is not a new one; a similar choice as made for the likelihood function in the Metropolis-Hastings implementation of the Lotka-Volterra system in Week 3. By using the parameters in this equation as the state variables, a potential parameter set can be evaluated for fit, meaning that as this sum-of-squares decreases, the fit becomes better.

### 3.2.2 Options

Many options exist in the MATLAB implementation of PSO itself: coefficients  $c_1$  and  $c_2$  can be specified, as well as swarm size, allowable neighborhood, and maximum number of iterations. In our implementation, coefficients were set to default values by MATLAB, the neighborhood was not restricted (global best), a swarm size of 40 was selected, and the maximum number of iterations were set to 400. From research, swarm sizes of 20-60 tend to give both accurate and efficient results (as runtime increases with swarm size), so a midpoint value of 40 was chosen. The choice of 400 iterations stemmed from example code parameterizing a similarly-sized system.

To address the different categories in the data, as well as different events allowable in the model, the PSO process as provided several other options. First, regarding the data, the model could be run on NOD

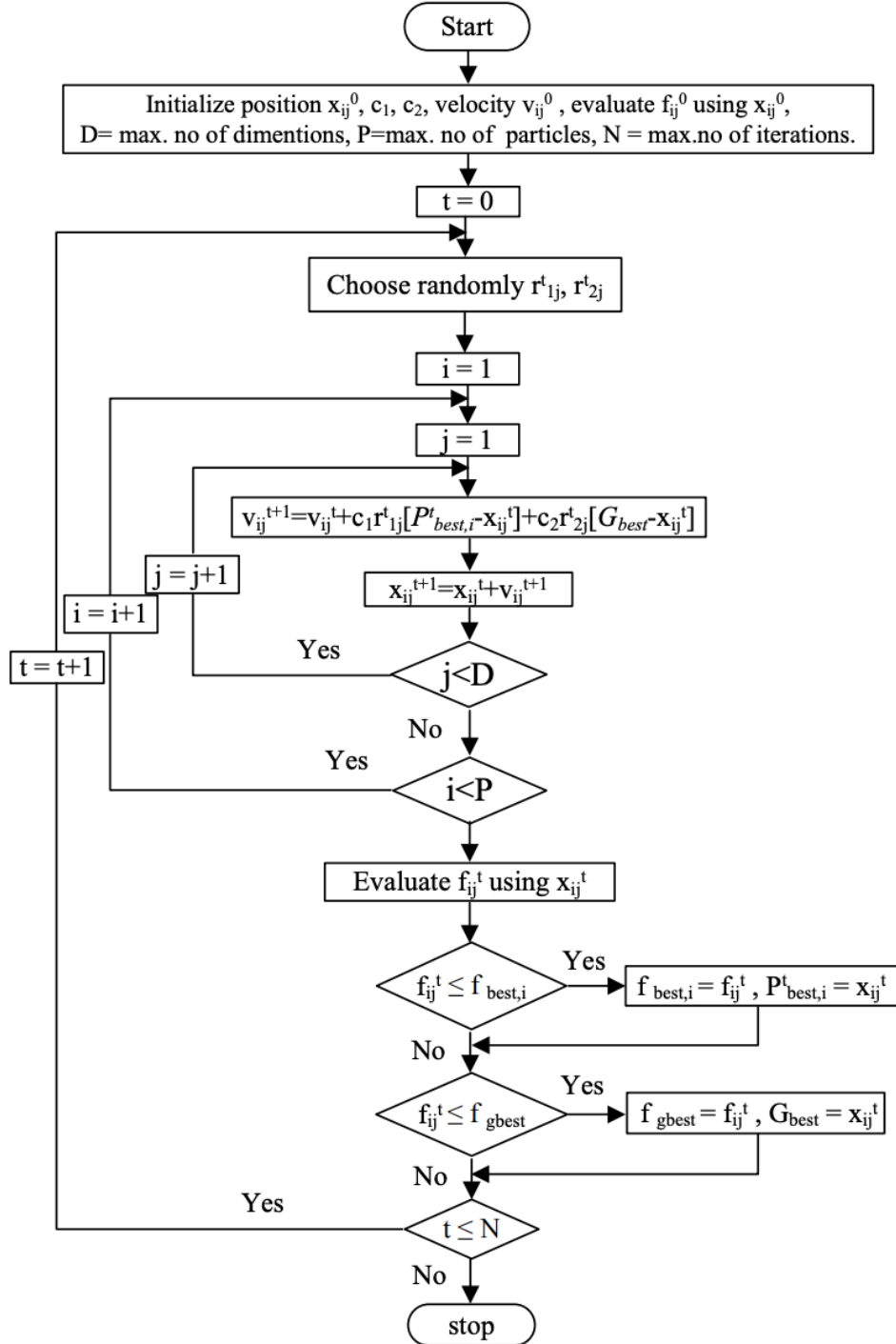


Figure 6: PSO Flowchart

or wild type mice. In this case, different versions of parameters are used based on mouse type, so the unused parameters were removed from optimization. Though this feature is included, it is not used as all the mice in the data set are of the NOD variety. In a similar fashion, the model could be parameterized with and without the apoptotic wave occurring. This would set the parameters regarding the wave to 0 for the entirety of the optimization process as well as run the model with the correct options provided to the ODE solver for the apoptotic wave. Additionally, the system provides a set of initial conditions to the ODE solver based on the Topp healthy rest state for beta cells, glucose, and insulin. To account for biological differences in mice, all non-zero elements within the initial conditions vector can be optionally treated as parameters for the model.

### 3.2.3 Assumptions

Besides baseline assumptions about the model being appropriate for the data, the largest assumption was in the allowable ranges for each of the parameters. Again based on example code for a similarly-sized system, the decision was made to allow guessing in an interval above and below an initial guess (the original parameters in the model). The size of this interval was determined to be  $\pm 50\%$  for system parameters and  $\pm 15\%$  for initial conditions. These numbers are fairly arbitrary, however, and were largely determined through trial and error. When run, if the optimal model parameters fell directly on upper/lower bounds, the spread of the interval was increased. The bounds on the initial conditions were tighter because it is assumed that the mouse is initially in a healthy state; we wanted our variation just to capture the natural biological different between mice, and a 50% interval would be much too large to remain within the healthy zone.

## 3.3 Results

During the run of the PSO function, three outputs are produced: a graph of the objective function's value at each iteration of the algorithm, a table printed in the command window containing information and the swarm at intermittent intervals, and a final set of optimized parameters. Below is an example of the graph and chart for the model run on the NOD progressive data. Additionally shown below are the optimal fits

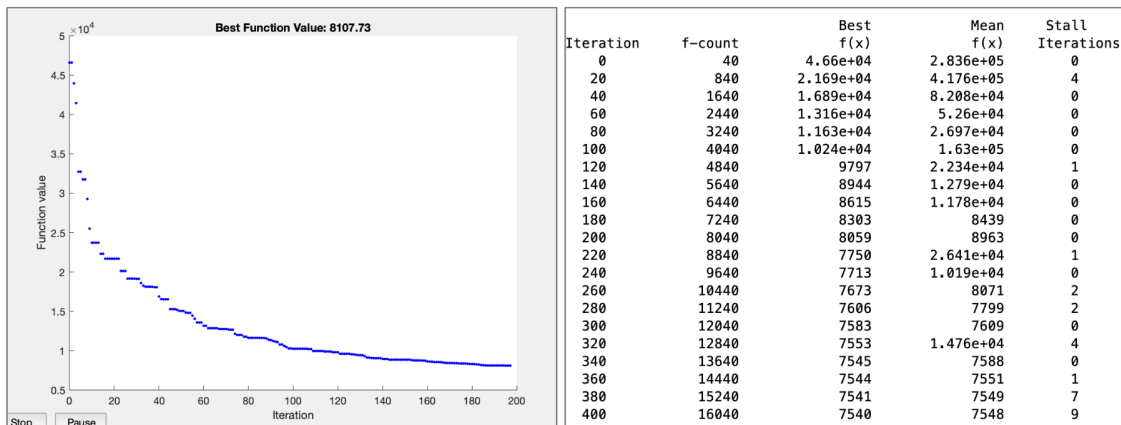


Figure 7: Output of MATLAB's PSO implementation

produced when running the model on the following combinations of data and model preferences (clockwise from top left):

1. NOD mice + Progressive mice data + no wave + constant ICs
2. NOD mice + Progressive mice data + wave + constant ICs
3. NOD mice + Progressive mice data + no wave + variable ICs
4. NOD mice + Progressive mice data + wave + variable ICs

The fits, as anticipated, look very similar between the combinations. Even when plotted on the same graph, the results appear almost identical. Though this may appear to be the case, it is in fact not, as the sum-of-squares function evaluated for each optimal set is slightly different. It becomes clear that the inclusion of the initial conditions within the optimization process leads to a better fit, and that the inclusion of the wave does not impact the fit of the model in any recognizable way.

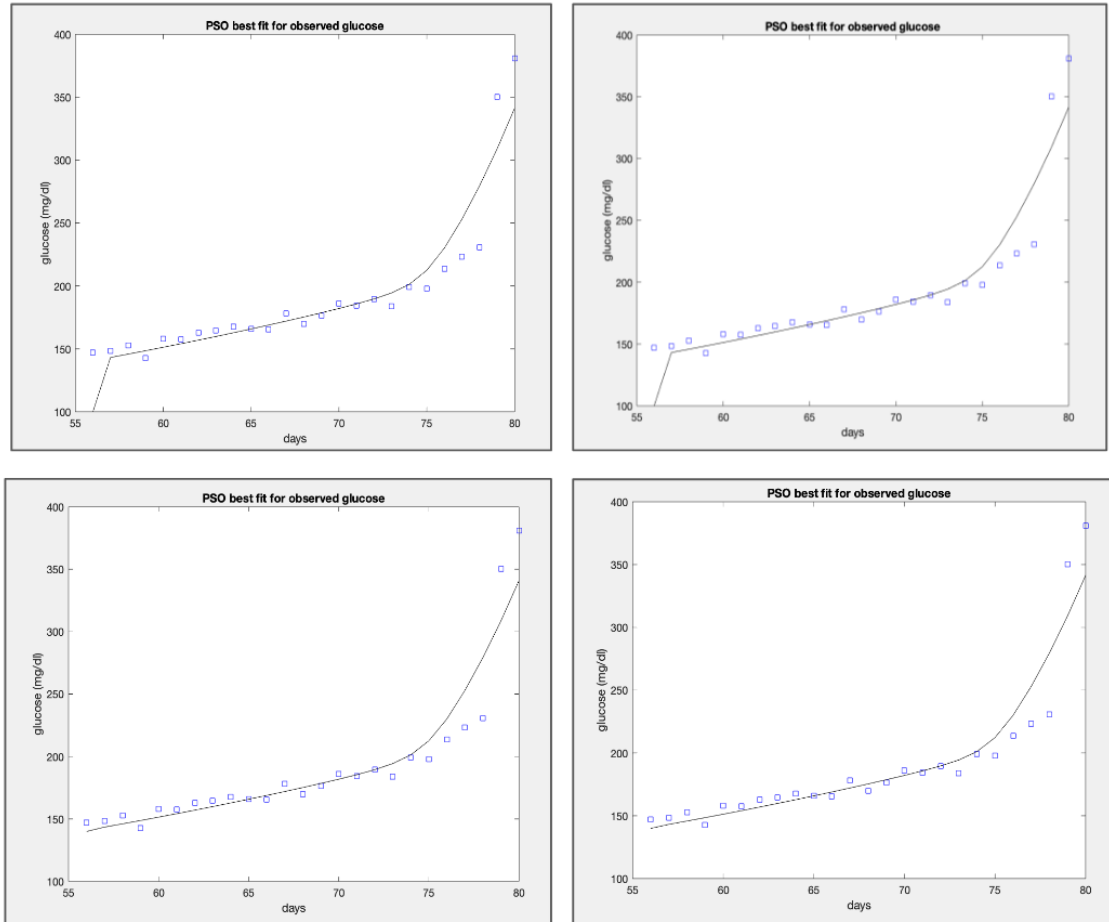


Figure 8: Best fit to model, data combinations for progressive mice

### 3.4 Improvements

To improve the biological applicability of this particular implementation of PSO, tightening the upper and lower bounds would be very helpful. The biological limits on certain parameters were not known, so the interval decided is not well-informed. Additionally, using more metrics to quantify how well the model fits the data would be beneficial over a visual inspection. Finally, all parameters were optimized in the work above. By incorporating more knowledge about the system by setting certain, non-sensitive parameters constant, the sensitive parameters can be optimized more carefully. From previous work done on the model with sensitivity analyses, these parameters can be identified.

## 4 Next Steps

Knowing that our methods are functional, we would like to work towards running both DRAM and PSO on the raw Mathews et al. data rather than the mean values. This requires extensive cleaning and organization

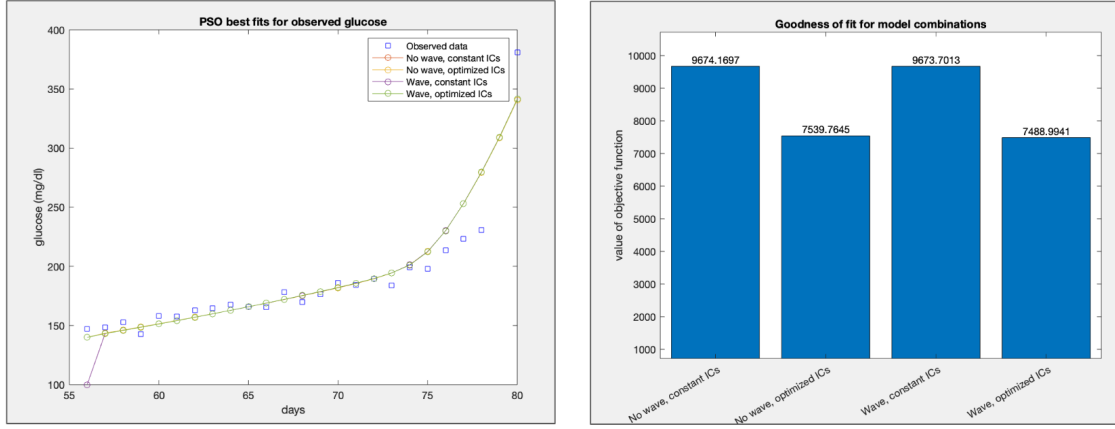
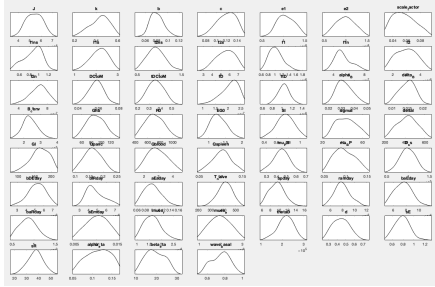


Figure 9: Comparison of fits

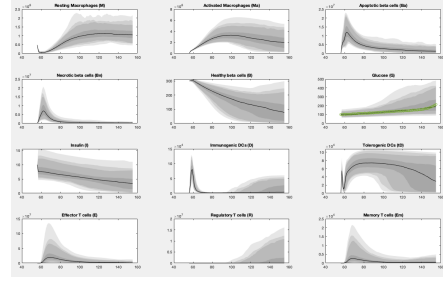
of the data, however, so we anticipate much time will need to be spent on this, and effective interpolation strategies developed. Also, we made certain assumptions regarding the timespan of the data, so it would be nice to figure out a systematic way to organize the data to match the collection procedures described by Mathews.

## 5 Appendix

The following figures are illustrate the results of the DRAM algorithm. For better view of these results visit our *GitHub repository*.



(a) Parameter density plots

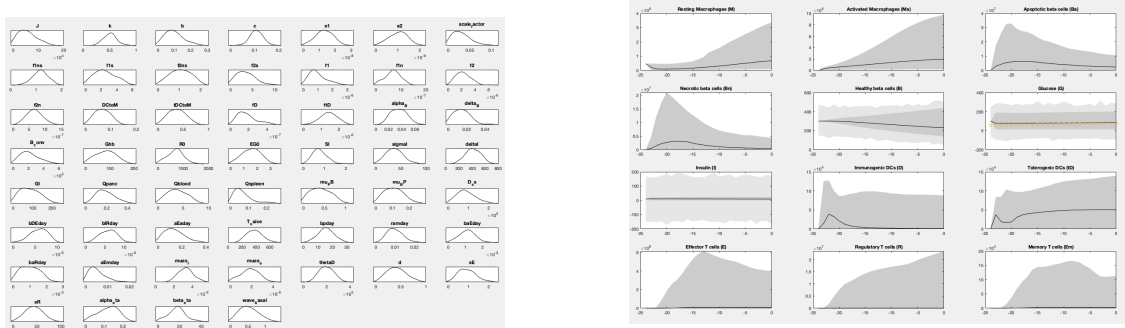


(b) Model prediction based on chain samples (per model variable). Original glucose data is overlaid in green.

	mean	std	MC_err	tau	<b>geweke</b>
J	53974	6875.2	984.93	159.19	0.95768
k	0.43252	0.087196	0.012956	308.98	0.75361
b	0.008428	0.011531	0.0017569	187.77	0.97863
c	0.11919	0.01726	0.0028018	157.93	0.76257
e1	1.0596e-08	1.9485e-09	2.5726e-10	89.372	0.86366
e2	9.92e-09	2.1401e-09	2.6791e-10	96.318	0.77692
scale_factor	0.056254	0.015691	0.0021661	334.56	0.61534
f1ns	0.87644	0.18558	0.032224	442.7	0.69247
f1s	2.1413	0.40846	0.065585	458.25	0.62309
f2ns	0.91731	0.1941	0.030707	165.74	0.92644
f2s	5.5436	1.022	0.13216	92.565	0.73459
f1	1.0251e-06	1.9666e-07	3.3966e-08	387.98	0.66286
f1n	5.206e-07	1.8308e-07	1.7121e-08	528.11	0.69036
f2	2.9834e-06	7.3557e-07	1.0798e-07	90.817	0.72121
f2n	6.7999e-07	1.1938e-07	1.963e-08	534.97	0.78478
DCtoM	0.057777	0.0070723	0.00090037	69.835	0.9955
DCtoM	0.35712	0.067113	0.012279	247.77	0.57448
fd	2.0636e-07	3.3832e-08	6.196e-09	407.04	0.75611
fd	1.0315e-06	1.1404e-07	1.6376e-08	99.583	0.99915
alpha_B	0.03234	0.0051066	0.00068464	88.27	0.84909
delta_B	0.014847	0.0024632	0.00040747	173.21	0.86385
R_conv	2.3621e+05	41695	5337.6	98.105	0.8635
glnb	88.889	17.878	3.158	332.32	0.60416
R0	713.62	142.58	19.786	108.77	0.83778
E0	1.2912	0.22916	0.03281	109.23	0.80274
SI	0.75147	0.14375	0.023272	158.67	0.89388
sigmaI	43.714	9.7977	1.5876	322.32	0.54848
deltaI	424.15	95.237	15.273	145.49	0.91643
GI	165.63	26.9	3.3559	99.245	0.89439
Qpnc	0.16222	0.030309	0.0042573	110.85	0.80022
Qload	2.9195	0.67457	0.088611	83.52	0.99969
Qslegh	0.1018	0.020965	0.00336	148.9	0.99398
mu_PB	0.4484	0.079934	0.012118	169.31	0.97682
mu_BP	0.09583	0.023291	0.0034901	194.06	0.63319
d_ss	98944	17603	2749.3	174.8	0.79815
hOCday	5.2096e-06	9.6646e-07	1.6204e-07	147.37	0.93557
bIRday	4.7779e-06	1.0032e-06	1.8274e-07	375.42	0.64459
aEday	0.097293	0.01987	0.003207	121.83	0.6491
T_naive	414.81	56.898	8.5883	128.18	0.92217
hnday	9.5868	1.7484	0.28257	161.23	0.74832
randay	0.0079633	0.0012633	0.00018264	144.66	0.93441
hEday	0.00075473	0.00013031	1.7167e-05	92.687	0.85946
hOCday	0.000679	0.00019909	3.0296e-05	142.59	0.61097
aEday	0.010256	0.0024783	0.00035619	223.2	0.78533
mues_r	1.6314e-06	3.4026e-07	5.6353e-08	368.69	0.879
mues_r	1.9553e-06	4.7516e-07	7.1171e-08	118.95	0.73987
thetaD	2.1479e+05	35982	6470	399.95	0.74653
d	0.44464	0.095279	0.014334	117.23	0.63978
se	0.78454	0.13593	0.019514	123.04	0.94578
sr	37.24	6.2838	0.96475	154.62	0.90113
alpha_eta	0.11535	0.029932	0.0045729	178.61	0.61593
beta_eta	19.381	4.5358	0.72709	142.28	0.61677
wave_basal	0.75219	0.10035	0.019658	537.96	0.61577

(c) Table showing mean parameter values and convergence criteria Geweke. We consider Geweke > 0.7 to have converged.

Figure 10: Results of DRAM on NOD mouse + no wave + simulated glucose data.



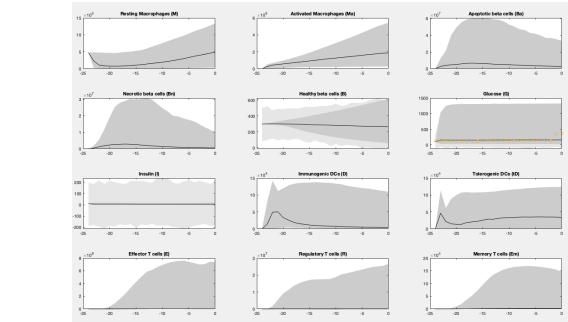
(a) Parameter density plots

(b) Model prediction based on chain samples (per model variable). Original glucose data is overlaid in yellow.

	mean	std	MC_err	tau	<b>geweke</b>
J	55675	35226	5335.2	453.01	0.9033
k	0.50644	0.12134	0.01976	328.26	0.9738
b	0.097982	0.055743	0.0098632	445.52	0.56074
c	0.10732	0.026769	0.0040792	153.07	0.79559
e1	1.3147e-08	5.3946e-09	8.0882e-10	84.701	0.78559
e2	1.0219e-08	4.0779e-09	6.3712e-10	87.874	0.77816
scale_factor	0.0306	0.020928	0.0033104	110.31	0.56366
f1ns	1.1655	0.29608	0.040394	122.54	0.9285
f1s	2.4714	1.3268	0.1969	96.85	0.60986
f2ns	1.0437	0.47899	0.081145	417.35	0.41469
f2s	3.4297	2.0549	0.29261	126.9	0.57782
f1	9.7658e-07	5.9588e-07	1.0068e-07	423.75	0.45542
f1n	6.7622e-07	3.0201e-07	5.3421e-08	218.42	0.81481
f2	2.2208e-06	1.0872e-06	1.6758e-07	98.126	0.55397
f2n	6.722e-07	2.3973e-07	4.071e-08	362.73	0.86388
DC10M	0.066144	0.030706	0.004236	86.301	0.88089
DC10M	0.36904	0.16856	0.027361	270.55	0.50501
FD	1.7672e-07	1.0299e-07	1.9074e-08	451.25	0.4581
ftD	1.411e-06	4.6008e-07	6.7109e-08	184.23	0.91297
alpha_B	0.035299	0.012138	0.0020495	404.47	0.68702
delta_B	0.014783	0.0090727	0.0013476	74.261	0.45092
B_gcnv	2.1375e+05	1.2098e+05	16560	191.29	0.48429
gbb	82.806	40.459	5.8416	115.79	0.99104
R0	680.52	307.91	54.699	155.43	0.92835
EG0	1.5582	0.66682	0.096668	71.257	0.94748
SI	0.7646	0.3288	0.057134	455.54	0.98127
sigmaI	36.927	16.316	2.566	139.66	0.61321
deltaI	418.53	112.94	15.483	124.62	0.68345
GI	86.182	49.912	6.1966	55.541	0.7271
Qpans	0.18721	0.084571	0.012577	210.23	0.69688
Qblood	3.7388	1.8774	0.32221	231.11	0.95824
Qspleen	0.0655	0.050285	0.0088138	255.2	0.55608
mu_PB	0.41144	0.23468	0.03143	231.96	0.92861
mu_BP	0.1073	0.055382	0.0077496	85.513	0.94881
D_ss	87414	43988	6102.3	96.724	0.58781
bDEday	5.7796e-06	1.9154e-06	2.8646e-07	233.47	0.65609
hRday	5.9014e-06	2.079e-06	2.969e-07	195.27	0.59239
aEday	0.1336	0.078958	0.011562	103.01	0.65826
T_naive	378.29	108.1	14.598	108.35	0.95252
hpdav	15.597	5.3874	0.74261	91.846	0.8428
ramdav	0.00977	0.0039451	0.00062858	225.32	0.82623
batdav	0.0010958	0.00045356	5.2118e-05	57.475	0.93471
hnrday	0.0010113	0.00056648	9.0907e-05	188.33	0.41718
aEndav	0.0051655	0.003754	0.00052506	166.66	0.39106
mues_r	3.2748e-06	7.93e-07	1.2077e-07	147.74	0.91148
mues_e	1.7968e-06	8.419e-07	1.2964e-07	215.51	0.81438
theta0	1.9652e+05	61154	8561.5	72.304	0.79099
d	0.41173	0.18592	0.03013	330.65	0.68347
sE	0.92956	0.42477	0.065108	153.26	0.79977
sR	43.427	18.175	2.4513	103.94	0.76246
alpha_eta	0.12116	0.053702	0.0082877	159.97	0.62273
beta_eta	17.379	7.8703	1.1315	235.71	0.9198
wave_basal	0.52359	0.26358	0.042652	189.18	0.44553

(c) Table showing mean parameter values and convergence criteria Geweke. We consider Geweke > 0.7 to have converged.

Figure 11: Results of DRAM on NOD mouse + no wave + acute mouse data.

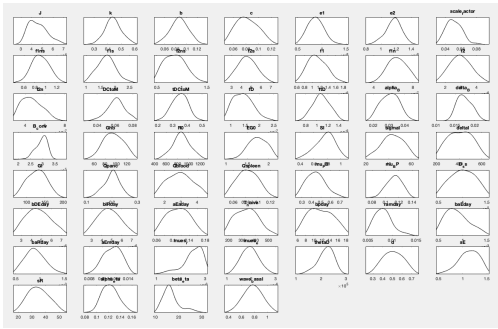


(b) Model prediction based on chain samples (per model variable). Original glucose data is overlaid in yellow.

	mean	std	MC_err	tau	gswks
J	52731	34336	6125.5	182.39	0.332
k	0.40874	0.18076	0.027698	294.08	0.26972
k	0.070446	0.027793	0.0034551	255.05	0.53466
c	0.11281	0.061556	0.0054866	34.827	0.34887
e1	1.2831e-08	7.3467e-07	1.0519e-09	180.29	0.78886
e2	6.3152e-09	3.1517e-09	4.3893e-10	88.341	0.86902
scale_factor	0.057081	0.029646	0.004222	125.52	0.62521
f1ns	1.225	0.35411	0.055089	180.29	0.61469
f1ns	1.2968	0.76809	0.1162	159.83	0.37949
f2ns	1.675	0.6814	0.10047	167.56	0.65421
f2s	6.0211	2.2777	0.34126	380.25	0.41985
f1	1.2355e-06	7.0479e-07	1.2199e-07	282.12	0.62867
f1n	6.0195e-07	2.6763e-07	4.3177e-08	199.48	0.38997
f2	3.9916e-06	1.7048e-06	2.442e-07	234.75	0.86789
f2	6.7265e-07	2.6956e-07	4.12e-08	187.56	0.75421
DC0m	0.054999	0.024288	0.0038234	286	0.27905
DC0m	0.29817	0.18552	0.031077	310.26	0.26781
fd	2.059e-07	5.5182e-08	7.8045e-09	112.97	0.78781
ftd	1.3856e-06	8.0911e-07	1.1706e-07	257.04	0.73946
alpha_B	0.032911	0.012532	0.0019635	171.29	0.85406
delta_B	0.015435	0.006131	0.0012611	264.61	0.75421
B_conv	2.4384e-05	1.5804e-05	23859	164.08	0.18479
Ghh	96.33	36.471	5.345	135.98	0.4842
R0	966.11	535.07	79.688	90.491	0.59679
SG	1.5735	0.57574	0.09893	282.19	0.9088
E1	0.73092	0.39892	0.063906	236.36	0.75753
sigma1	12.128	17.854	3.40035	284.6	0.58337
delta1	726.02	226.63	27.879	66.193	0.98995
GI	125.81	75.294	13.94	270.22	0.35903
Q0ans	0.23263	0.079577	0.013337	158.91	0.96419
Q0ans	3.6454	1.2257	0.21539	226.36	0.85346
Q0ans	0.18319	0.065319	0.007974	199.54	0.75421
mu_B	0.4244	0.17031	0.027435	123.11	0.99036
mu_BP	0.11163	0.055827	0.0080054	88.694	0.96168
D_ss	1.0284e-05	41427	5694.2	110.6	0.50437
b0day	4.7448e-06	1.8379e-06	3.81e-07	179.23	0.89108
b1day	7.3663e-06	1.9897e-06	3.1805e-07	242.85	0.74217
b2day	0.15206	0.70759	0.19199	197.01	0.66127
T_nave	395.08	201.2	27.805	102.24	0.77193
hday	14.323	4.7355	0.64099	143.62	0.9825
randay	0.0091878	0.0047796	0.00073176	110.8	0.34391
b0day	0.0006995	0.00047135	7.5444e-05	164.22	0.851705
b1day	0.00090772	0.0003955	0.0003955	149.91	0.851705
b2day	0.009481	0.0035647	0.00063672	34.76	0.46363
mues_r	1.041e-06	6.9941e-07	1.075e-07	303.6	0.12172
mues	1.6479e-06	9.7908e-07	1.1744e-07	76.041	0.83555
thetad	2.4772e-05	1.0397e-05	0.17898	306.58	0.34569
e	0.3245	0.16659	0.024125	101.44	0.92405
se	0.8945	0.45047	0.06893	157.06	0.95598
sR	39.589	15.199	2.5185	112.61	0.93348
alpha_e	0.12195	0.064021	0.011557	161.85	0.65082
beta_ea	25.321	12.902	1.5814	80.188	0.46734
wave_basal	0.86555	0.37247	0.047824	123.58	0.91442

Figure 12: Results of DRAM on NOD mouse + no wave + progressive mouse data.



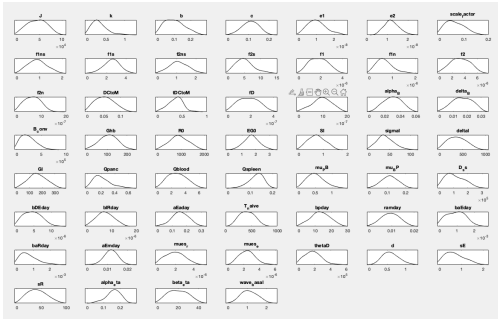


(a) Parameter density plots

	mean	std	MC_err	tau	geweke
J	45644	8469.1	1534.1	312.27	0.66995
k	0.44038	0.05924	0.0070522	85.081	0.97768
b	0.007097	0.015999	0.0021576	132.56	0.72904
c	0.00168	0.016823	0.0026792	277.13	0.02253
e1	8.7117e-09	1.6194e-09	2.3603e-10	82.467	0.81494
e2	1.163e-08	1.024e-09	1.5764e-10	94.565	0.97456
scale_factor	0.051046	0.0098416	0.0015665	246.11	0.84446
f1ns	0.89955	0.15674	0.025436	122.97	0.97951
f1s	1.6956	0.30647	0.040844	140.3	0.9025
f2ns	0.86135	0.20842	0.038285	360.68	0.45927
f2s	4.5825	0.94575	0.14338	179.23	0.80421
f1	1.1244e-06	2.3791e-07	3.2602e-08	98.668	0.74439
f1n	6.3744e-07	9.4322e-08	1.3546e-08	152.28	0.95954
f2	2.9679e-06	6.6536e-07	9.0267e-08	103.66	0.82721
f2n	4.6712e-07	1.0005e-07	1.3398e-08	101.55	0.80587
DcToM	0.061063	0.0096864	0.0015296	153.1	0.98427
fDcToM	0.34889	0.053337	0.0085796	164.75	0.92321
fd	1.4246e-07	3.3475e-08	5.4858e-09	469.36	0.77298
alpha_B	1.0018e-06	1.4770e-07	2.1539e-08	119.78	0.94548
alpha_B	0.030549	0.0056097	0.00086633	224.18	0.66837
delta_B	0.017344	0.0018486	0.00028648	128.4	0.91394
B_cony	2.9384e+05	23298	4127.6	495.77	0.87406
Ghb	95.246	17.765	2.6741	246.74	0.7994
R0	873.61	151.94	22.001	126.88	0.90738
EG0	1.7391	0.21341	0.036728	265.42	0.81123
SI	0.76682	0.14282	0.023665	202.97	0.96824
sigmaI	43.472	9.5943	1.5542	109.34	0.99959
deltaI	411.16	104.72	14.673	203.92	0.60833
GI	128.27	25.708	3.5205	135.84	0.7172
Qpans	0.19901	0.030984	0.0045666	120.68	0.94447
Qbload	2.9458	0.75334	0.12602	217.97	0.84724
QspLeen	0.083042	0.016306	0.001917	88.508	0.81699
mu_PB	0.44531	0.096883	0.012881	176.12	0.76086
mu_BP	0.11306	0.011242	0.0018089	247.22	0.83452
D_ss	1.0015e+05	25090	4029.4	334.57	0.53767
h0Eday	4.674e-06	1.1675e-06	1.6458e-07	157.6	0.97819
h1Eday	4.7113e-06	1.0845e-06	1.7752e-07	249.32	0.82196
aEday	0.11346	0.027569	0.0039698	266.9	0.58679
T_naive	335.57	84.309	12.28	103.03	0.97737
hEday	11.693	2.9992	0.41874	134.19	0.79964
randay	0.0081524	0.0017955	0.00029797	166.27	0.94959
haEday	0.0008848	0.0002378	4.1345e-05	515.28	0.88686
baEday	0.00089844	0.00020313	2.9558e-05	169.52	0.81486
aEday	0.011537	0.0013624	0.00021036	209.79	0.976
mues_r	2.4831e-06	4.1123e-07	7.9357e-08	435.19	0.69674
mues_e	1.9438e-06	3.4631e-07	4.9128e-08	206.13	0.96668
thetaD	2.1836e+05	30848	5461.8	333.91	0.79485
d	0.50881	0.10147	0.015256	152.28	0.73113
sE	1.1278	0.20508	0.033693	107.53	0.83913
sR	34.683	7.4952	1.1782	187.77	0.78019
alpha_eta	0.12287	0.013729	0.001951	127.5	0.86612
beta_eta	16.876	3.727	0.69985	215.63	0.74981
wave_basal	0.7725	0.14213	0.01988	126.51	0.97134

(b) Table showing mean parameter values and convergence criteria Geweke. We consider Geweke > 0.7 to have converged.

Figure 13: Results of DRAM on NOD mouse + wave + simulated mouse data.



(a) Parameter density plots

	mean	std	MC_err	tau	<b>Geweke</b>
J	44416	20882	2278.7	68.346	0.49525
k	0.31234	0.20523	0.036059	146.14	0.37978
b	0.10093	0.057858	0.01011	240.54	0.14883
c	0.10904	0.038945	0.0063701	353.26	0.65924
e1	1.0133e-08	5.0686e-09	7.2235e-10	136.67	0.96843
e2	1.2032e-08	3.4627e-09	5.937e-10	444.1	0.82188
scale_factor	0.061873	0.037462	0.0045067	101.93	0.92154
f1ns	0.09546	0.39421	0.04386	79.683	0.84238
f1s	2.53	0.81444	0.13053	314.1	0.63338
f2ns	1.0983	0.47046	0.068344	115.31	0.97182
f2s	5.0609	2.6989	0.43879	128.74	0.36715
f1	1.8055e-06	8.1474e-07	1.0916e-07	105.81	0.5451
f1n	6.5163e-07	3.549e-07	5.0729e-08	129.88	0.90574
f2	3.237e-06	1.4933e-06	2.2003e-07	425.88	0.81732
f2n	6.2916e-07	3.2402e-07	4.0703e-08	109.92	0.9149
DctoM	0.051934	0.02734	0.0031485	87.637	0.65319
fDctoM	0.36128	0.14515	0.023961	137.4	0.69181
fD	1.7844e-07	8.8134e-08	1.1609e-08	100.8	0.56976
alpha_B	9.4642e-07	3.0735e-07	5.5659e-08	129.93	0.85292
delta_B	0.029858	0.01126	0.0015704	388.54	0.6157
B_cony	0.016316	0.0069814	0.00091447	182.62	0.53902
Ghh	2.3109e+05	1.5455e+05	18424	112.54	0.64197
R0	106.31	45.163	7.563	346.79	0.95247
EG0	906.34	385.44	65.14	526.32	0.47042
SI	1.6875	0.5386	0.10083	459.5	0.62726
sigmaI	0.72627	0.33426	0.048765	281.21	0.29541
deltaI	39.107	20.092	3.6654	557.48	0.66956
GI	381.06	196.5	25.63	84.664	0.5493
Qpnc	161.43	68.88	8.6529	111.44	0.77853
Qbleed	0.21378	0.12537	0.021765	144	0.16811
Qapleed	2.7913	1.3291	0.15739	84.195	0.95495
mu_PB	0.1257	0.032759	0.0054556	198.91	0.89295
mu_BP	0.50404	0.25871	0.029535	72.388	0.9798
D_ss	0.11267	0.044521	0.0062249	145.58	0.68107
hDeday	1.0776e+05	66387	11090	136.45	0.26052
hIeday	4.4993e-06	2.5317e-06	3.1119e-07	94.873	0.4493
hAeday	7.209e-06	3.2981e-06	4.3692e-07	109	0.98611
hBeday	0.15581	0.056041	0.0092456	229.27	0.58145
aEnday	413.82	143.39	14.727	68.096	0.75815
mues_r	13.159	5.5801	0.85945	252.33	0.74494
mues_e	0.0094069	0.0038764	0.00045029	92.559	0.86816
thetaD	0.00093258	0.00052548	7.4912e-05	104.42	0.47109
sE	0.00071333	0.00052042	7.9434e-05	210.67	0.71858
sR	0.011719	0.0033175	0.00049001	129.29	0.8265
alpha_eta	1.9124e-06	1.0162e-06	1.2536e-07	115.1	0.96604
beta_eta	2.4218e-06	9.7888e-07	1.4066e-07	103.22	0.90941
wave_basal	1.7636e+05	1.0313e+05	13688	135.98	0.52317
	0.69063	0.21802	0.031293	100.23	0.88965
	40.589	18.868	2.673	91.307	0.47922
	0.15817	0.043207	0.0067333	158.07	0.81184
	19.605	9.4936	1.3923	136.48	0.72054
	1.1036	0.41974	0.06363	216.31	0.65559

(b) Table showing mean parameter values and convergence criteria Geweke. We consider Geweke > 0.7 to have converged.

Figure 14: Results of DRAM on NOD mouse + wave + acute mouse data.

(a) Parameter density plots

(b) Table showing mean parameter values and convergence criteria Geweke. We consider Geweke  $> 0.7$  to have converged.

Figure 15: Results of DRAM on NOD mouse + wave + progressive mouse data.