



# Kalman Filters

## Week 5

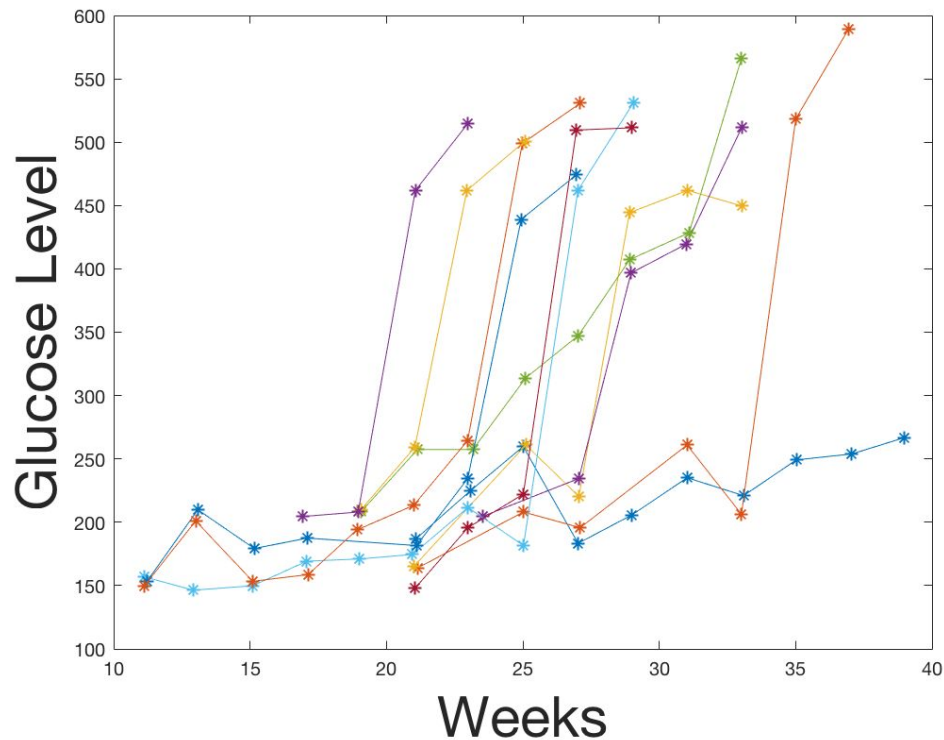
Subteam 2



# Li et al Data

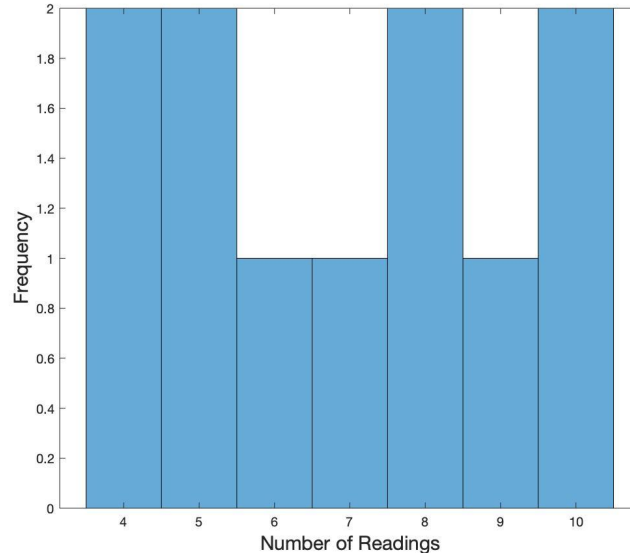
- Glucose readings from 11 mice
- All NOD mice
- Taken at time points given in weeks

# Li et al Data Visualization (from git repo)



# Li et al Data Info

- Average number of readings: **6.91**
- Average time between readings: **2.15 weeks**



# Parameters

- 7 parameters chosen based off Sensitivity Analysis
- $D_{ss}$  - dendritic cells in pancreas
- $GI$  - insulin saturation point with respect to glucose
- $SI$  - rate glucose taken up with respect to insulin
- $Q_{panc}$  - pancreas volume
- $\alpha_B$  - beta cell production rate
- $\mu_r$  - effector and regulatory cell interaction
- $\mu_e$  - effector and regulatory cell interaction

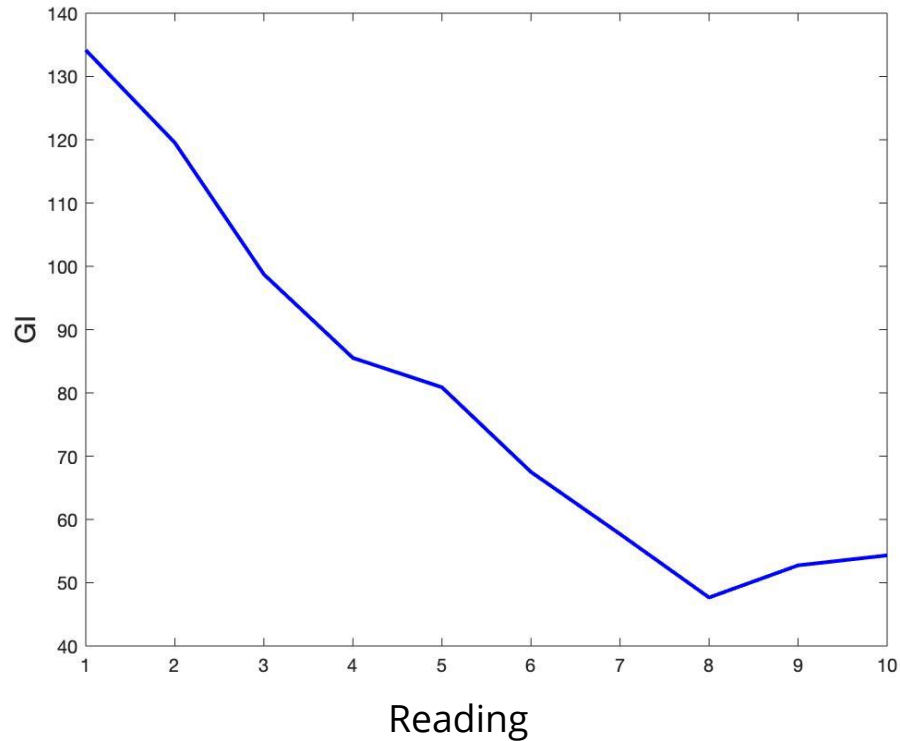
# Big Picture Goal

- Fit mouse individually using UKF
  - Dual
  - Joint
- Understand distribution of estimated parameters
- Apply process to Li
  - Connect with MCMC

# This Week

- Run Dual and Joint on single mouse
  - This is where the tuning took place
- Run Dual and Joint on all mice to produce distributions
- Single mouse, multiple iterations to analyze parameter convergence - Dual only

# Single Mouse Dual - Example of Parameter Mvt





# Estimation Workflow

For all mice:

- Simulate with ODE's until first available reading

- Use current states as Initial Conditions

- Run UKF on this individual mouse

  - Run Dual

  - Run Joint

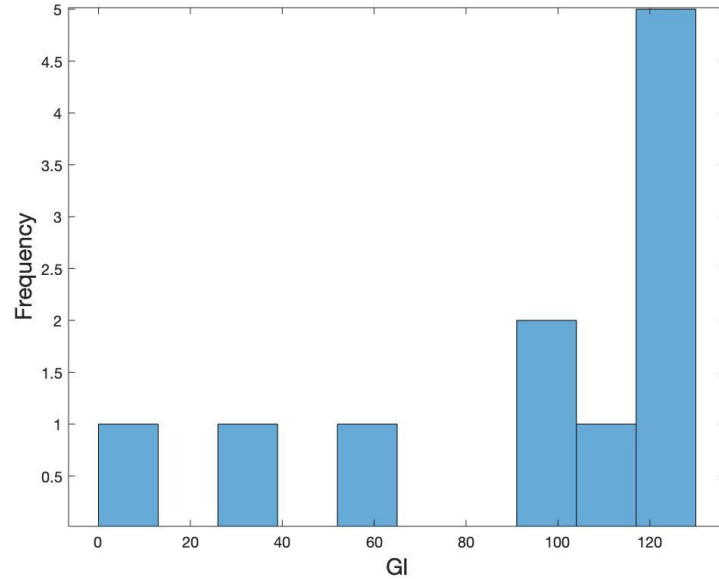
# Difference in Dual versus Joint Setup

- Initial Conditions for Parameters
  - Dual - slight deviation from baseline
  - Joint - taken from baseline parameter values
- Covariance matrices
  - Dual - large variance/covariances for parameters
  - Joint - small variance/covariances for parameters

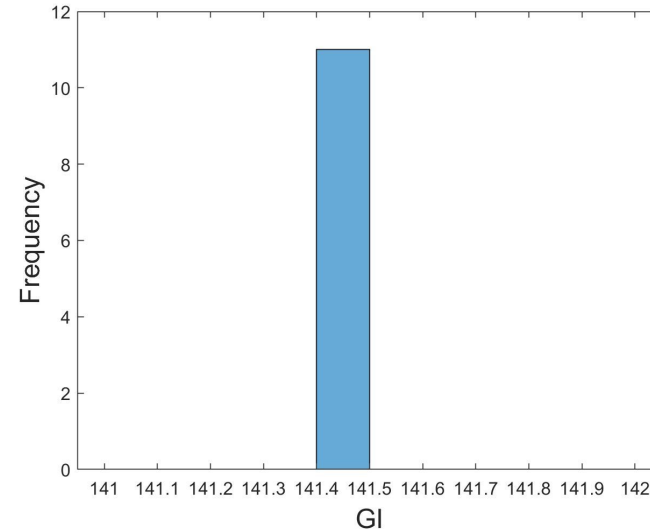
```
P0_params = [10^5 1 1 1 1 1 1;  
             1 10 1 1 1 1 1;  
             1 1 10000 1 1 1 1;  
             1 1 1 10 1 1 1;  
             1 1 1 1 10 1 1;  
             1 1 1 1 1 10^-2 1;  
             1 1 1 1 1 1 10^-2];
```

Dual Parameter Covariance

# Results - Parameter Distributions Single Run - GI

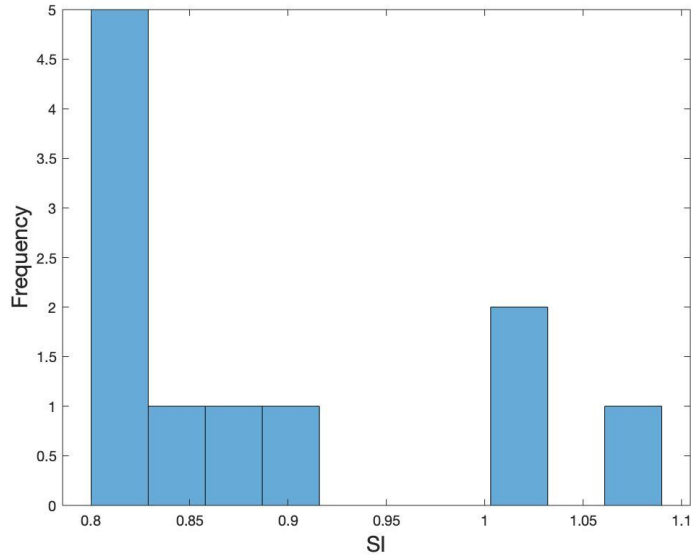


Dual (IC - 134)

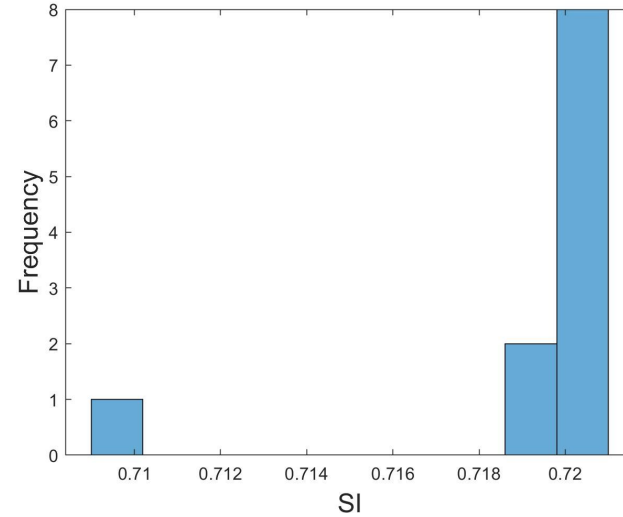


Joint (IC - 141.4)

# Results - Parameter Distributions Single Run - SI

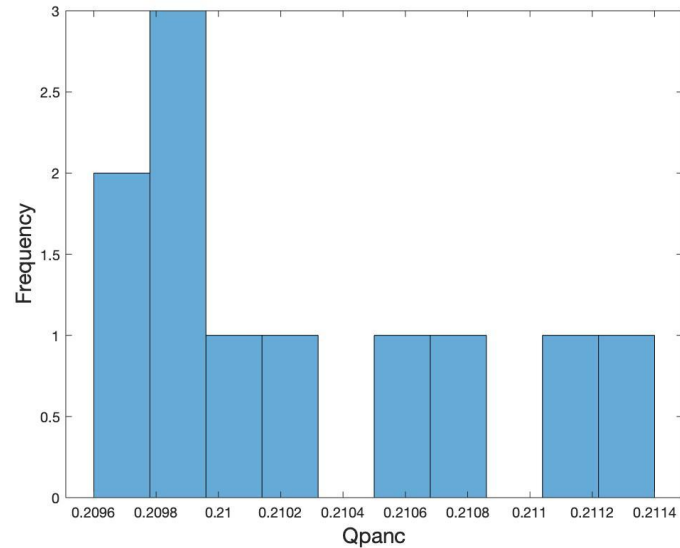


Dual (IC - 0.8)

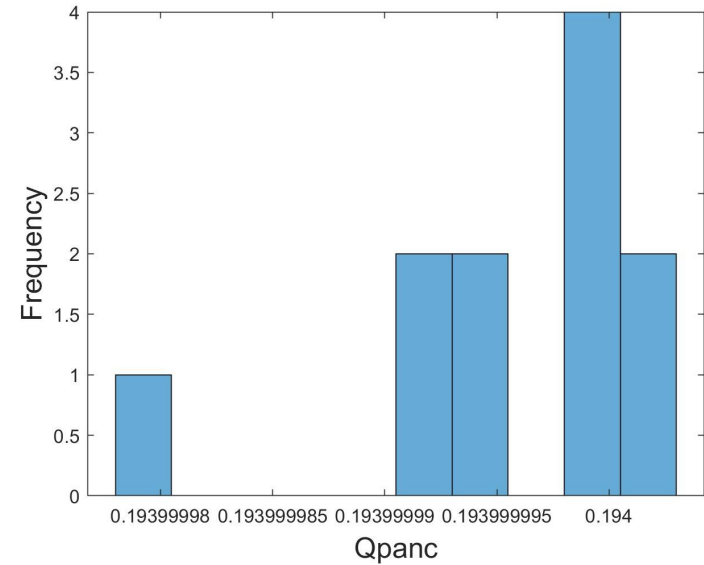


Joint (IC - 0.72)

# Results - Parameter Distributions Single Run - $Q_{\text{panc}}$

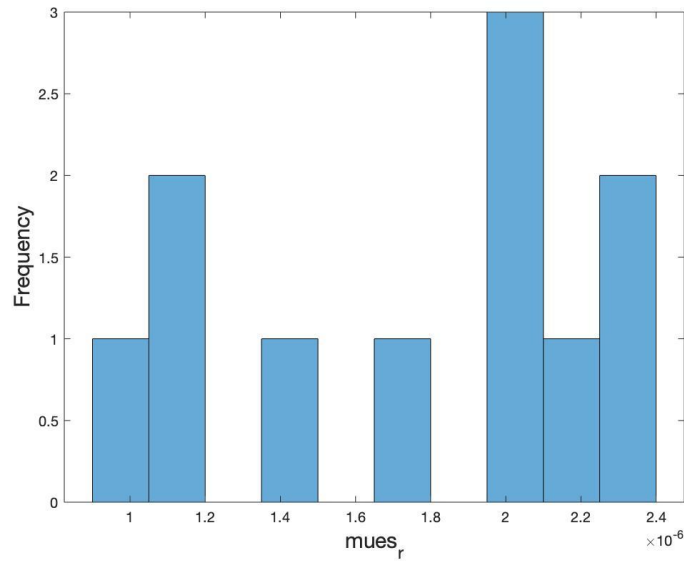


Dual (IC - 0.210)

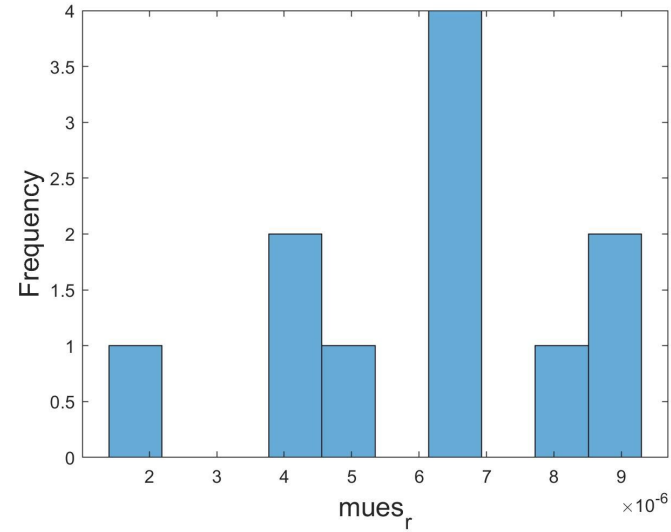


Joint (IC - 0.194)

# Results - Parameter Distributions Single Run - $\mu_r$

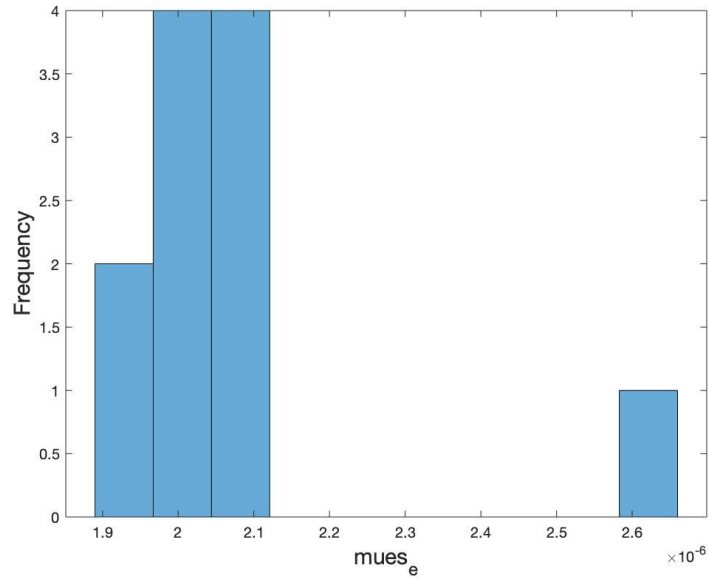


Dual (IC - 2e-6)

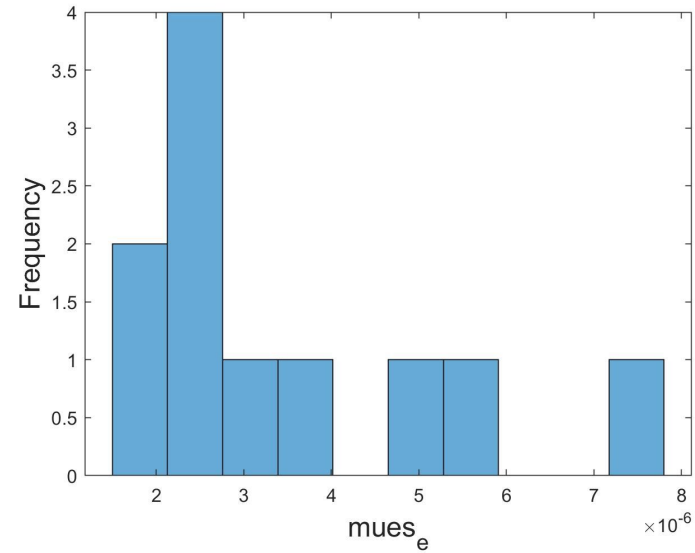


Joint (IC - 2e-6)

# Results - Parameter Distributions Single Run - $\mu_e$

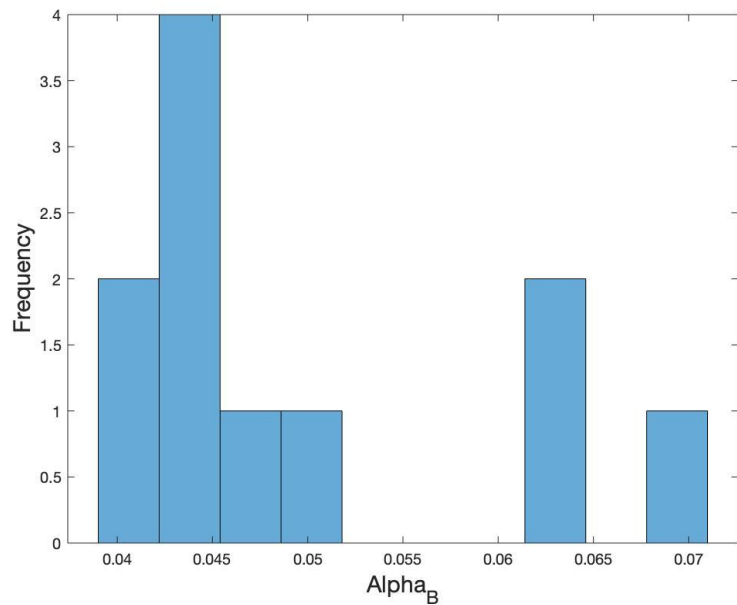


Dual (IC - 2e-6)

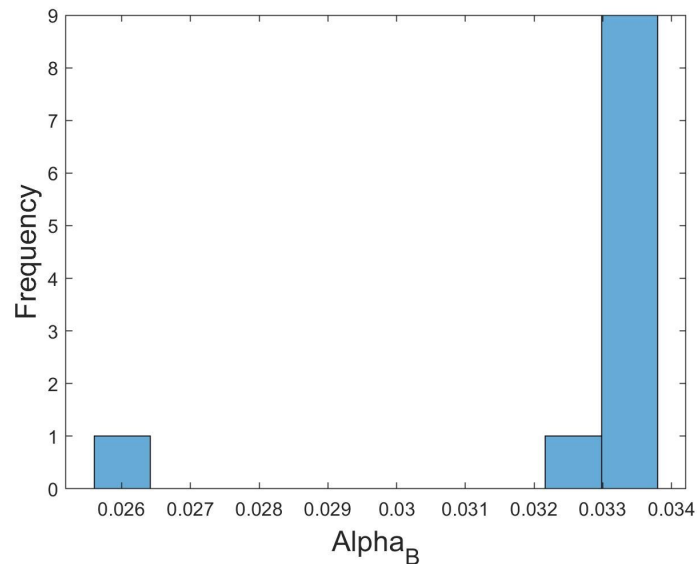


Joint (IC - 2e-6)

# Results - Parameter Distributions Single Run - $\text{Alpha}_B$



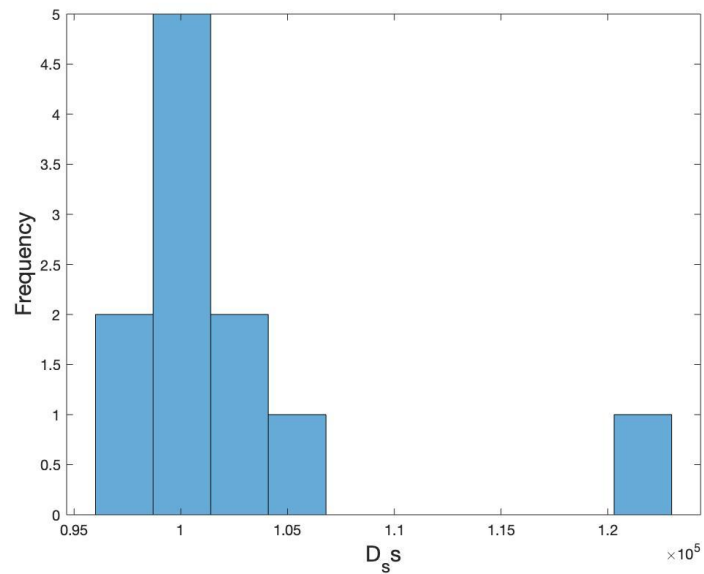
Dual (IC - 0.0334)



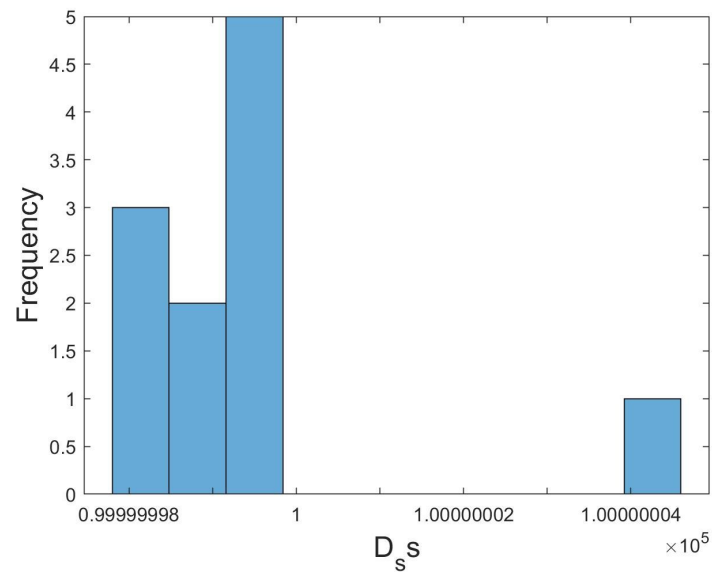
Joint (IC - 0.0334)



# Results - Parameter Distributions Single Run - $D_{ss}$



Dual (IC - 99700)



Joint (IC - 10e5)

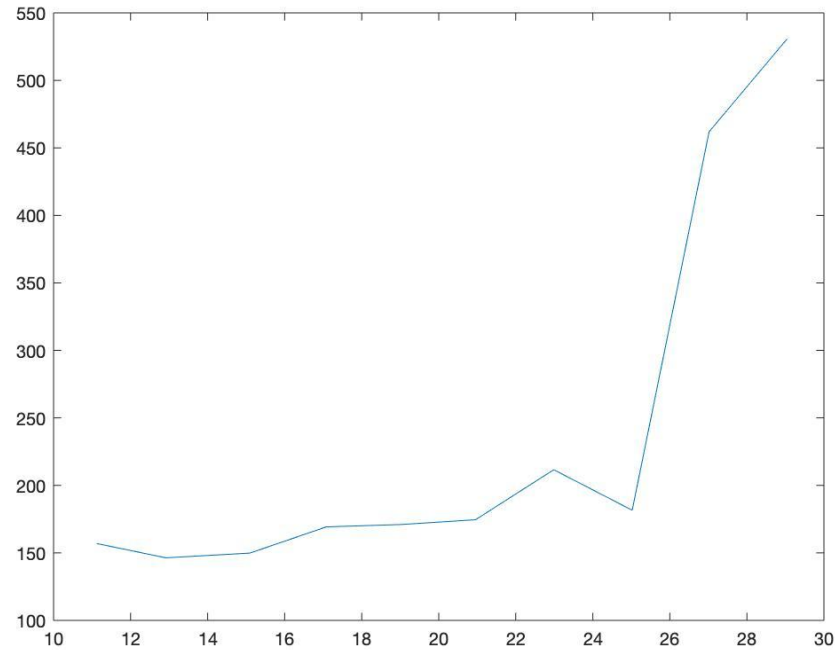
# Takeaways and Next Steps

- Initial conditions matter, but it seems like covariance matrices matter more, especially in terms of how much the parameter will move
- We should run the joint with the same initial covariance matrix as the dual and see what happens
- It's hard to know for sure what the differences are in the performance of the joint and the dual without an all else equal comparison (hopefully we will have this by the time we send out the summary)

# Multiple Runs on Same Mouse (DUAL UKF ONLY)

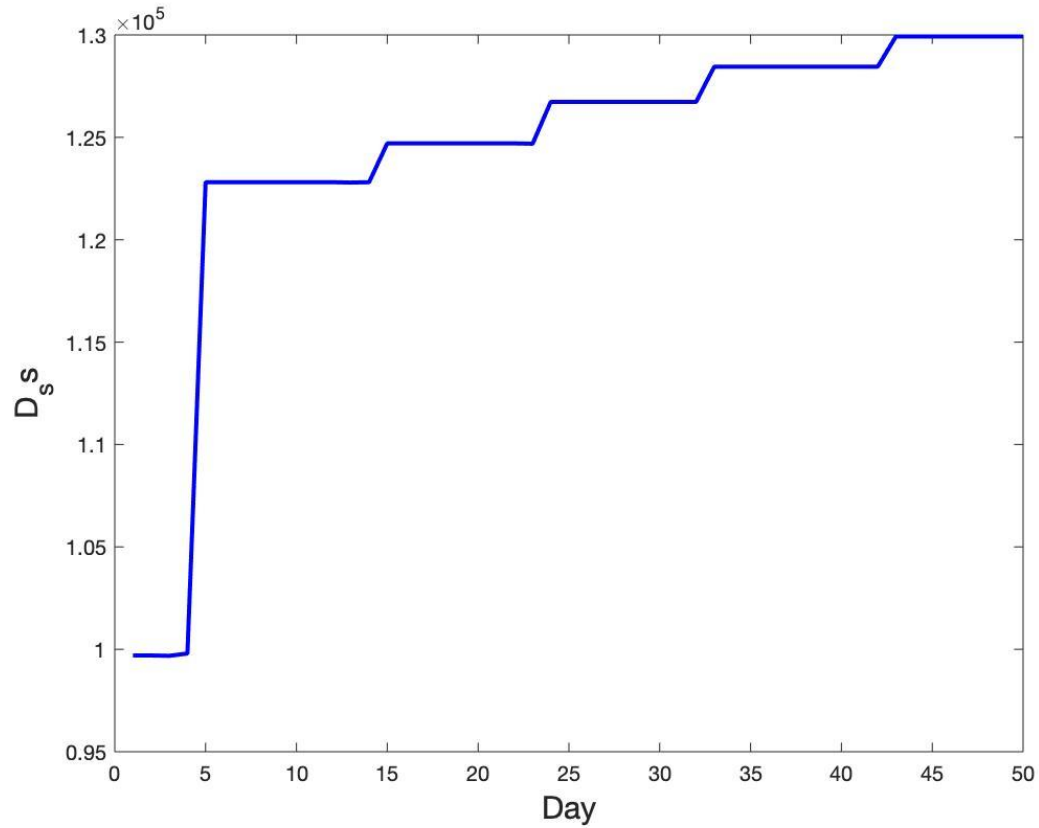
- Parameters want to “keep moving” as more number of readings
- Pick an “average” mouse
  - Mouse 6
- Run 5 iterations
  - Initial parameters for run (t) uses final parameters from (t-1)

# Mouse 6 Glucose



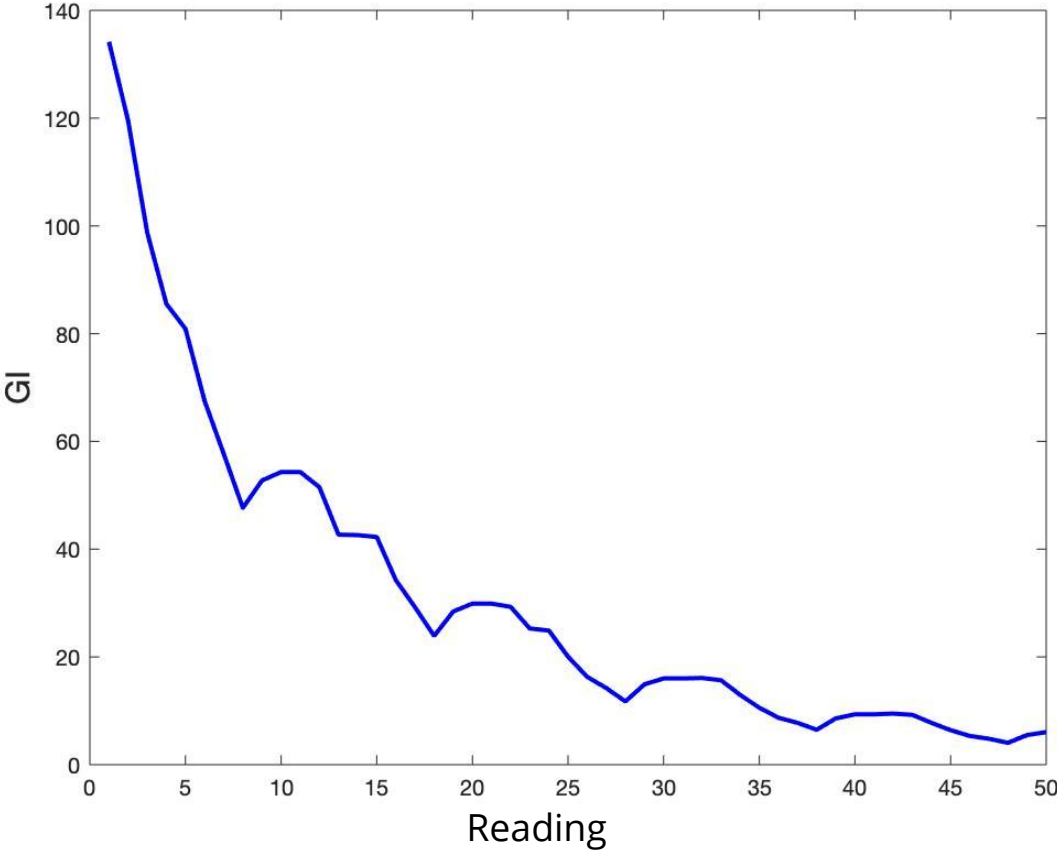
# D\_SS

\*\*Each run is 10 Readings\*\*



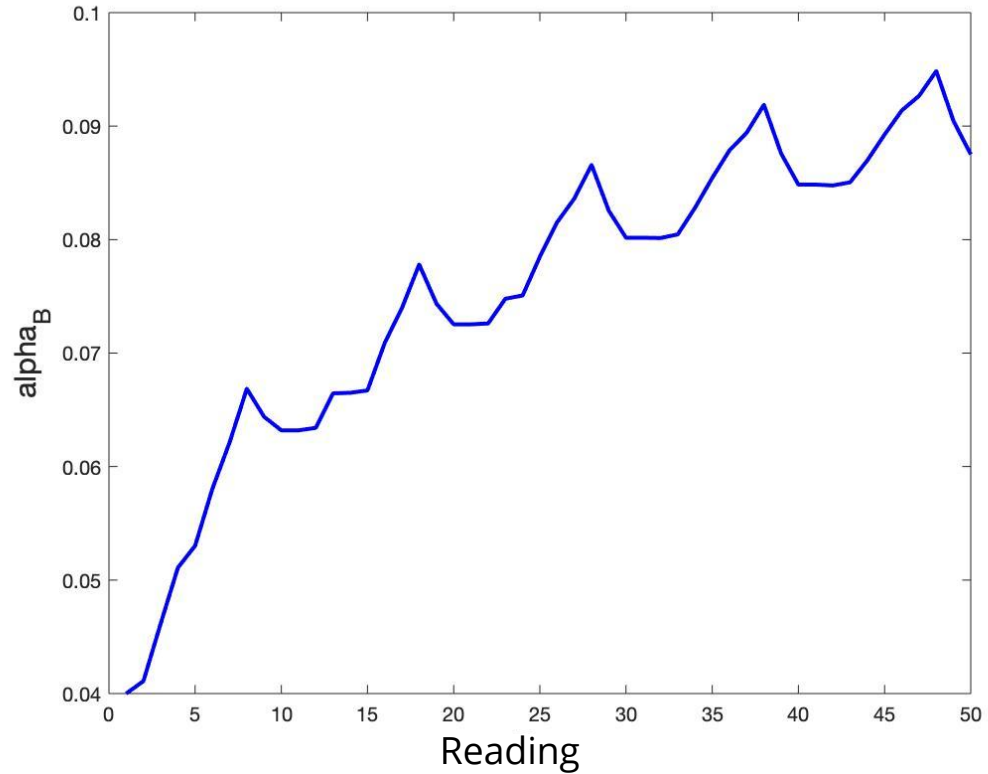
# GI

**\*\*Each run is 10 Readings\*\***



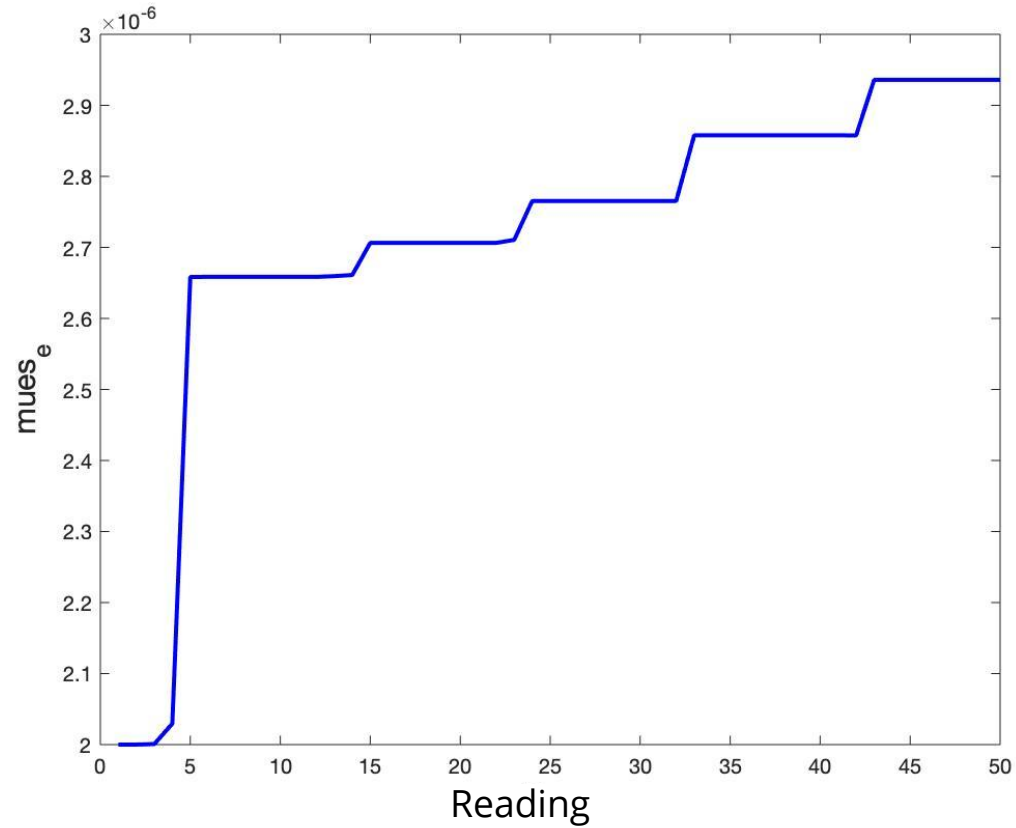
# Alpha\_B

\*\*Each run is 10  
Readings\*\*



# Mu\_e

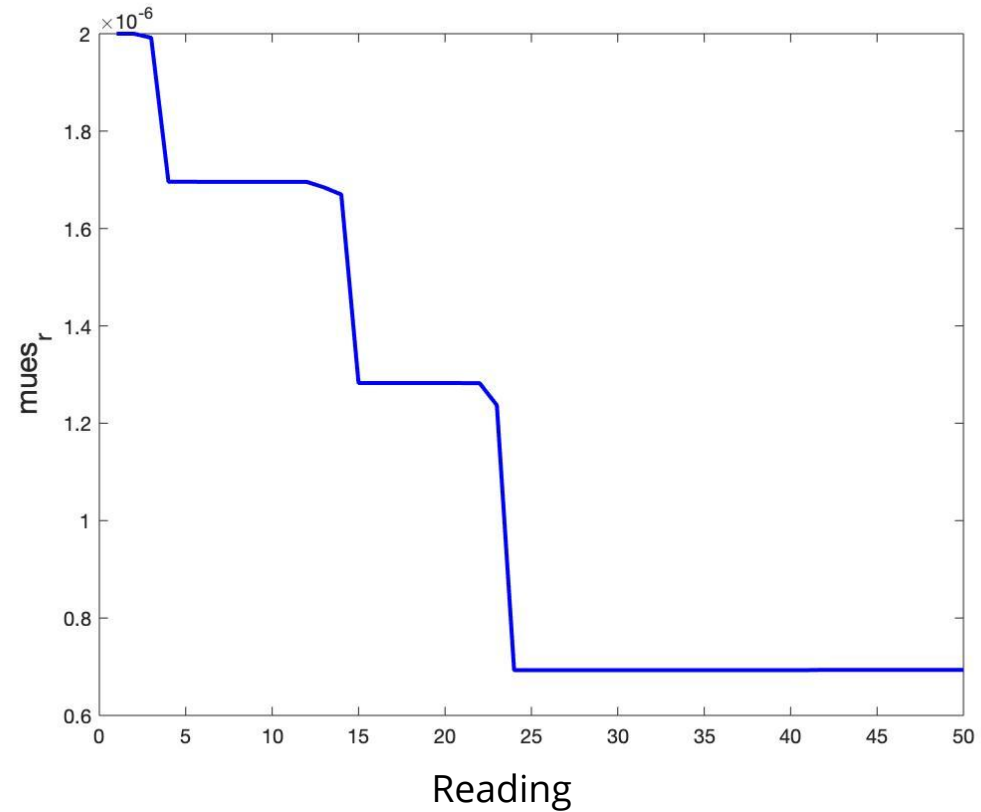
\*\*Each run is 10  
Readings\*\*





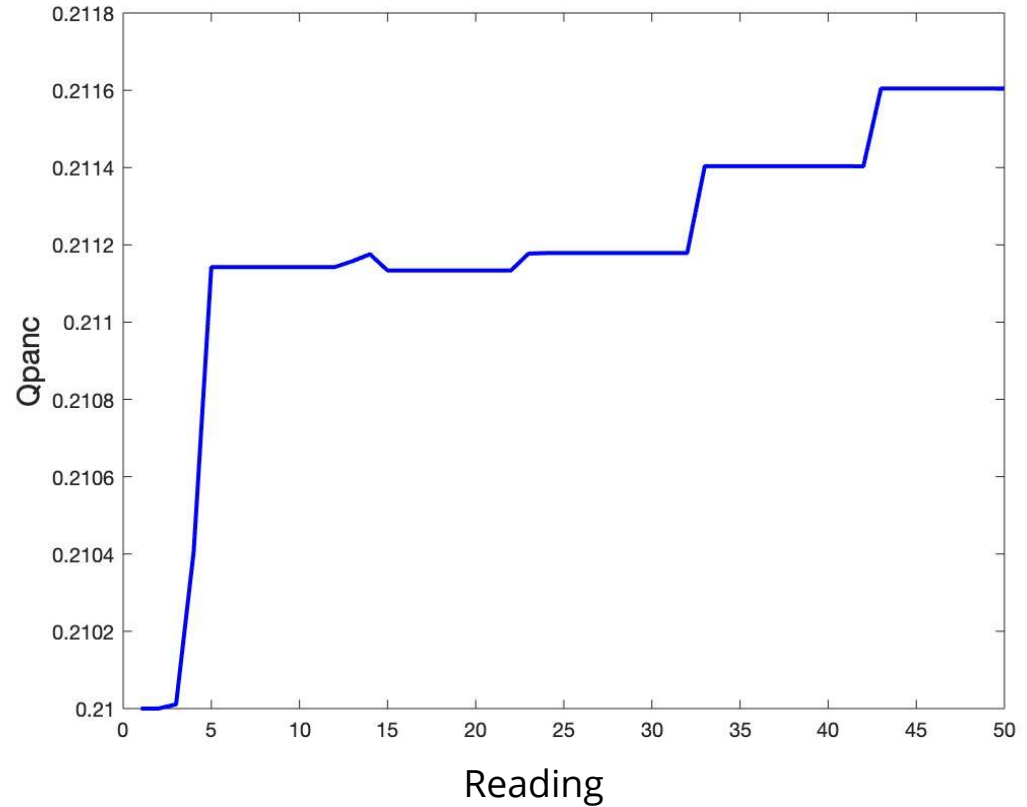
# Mu\_R

\*\*Each run is 10  
Readings\*\*



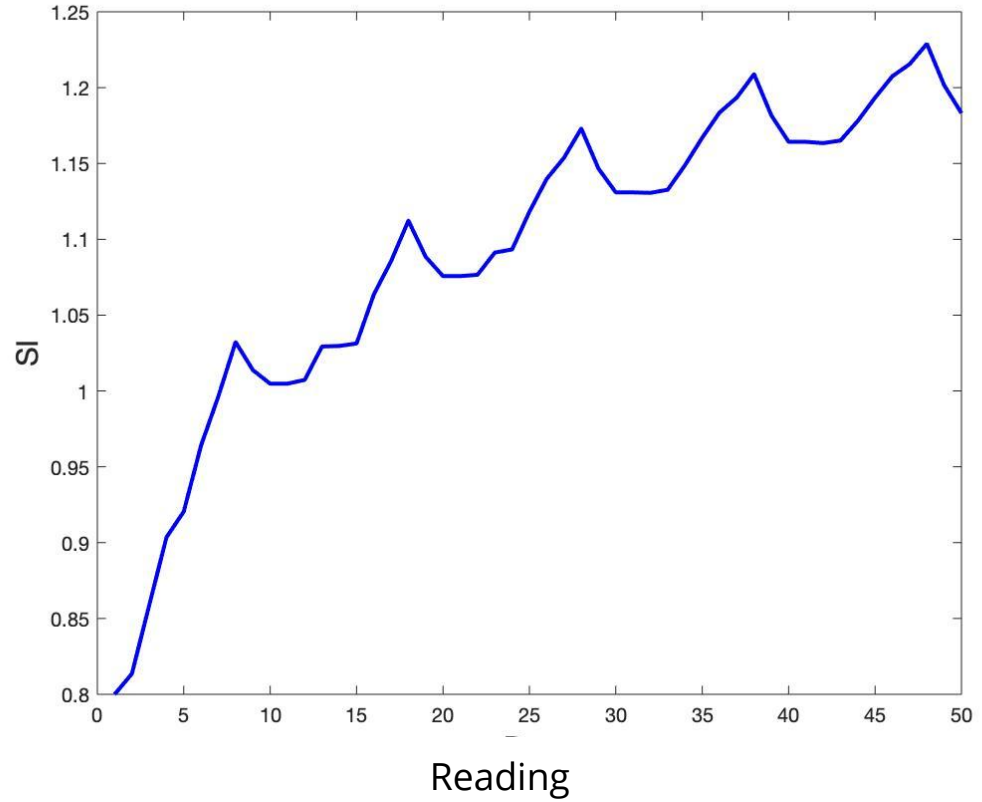
# Q\_panc

\*\*Each run is 10 Readings\*\*



# SI

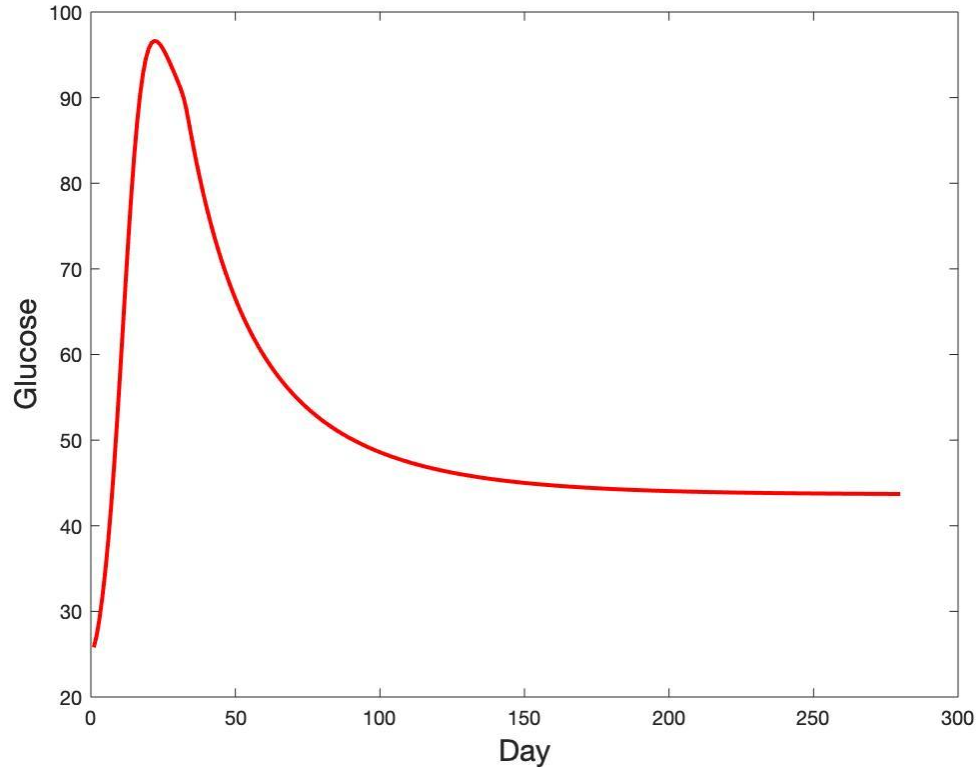
**\*\*Each run is 10  
Readings\*\***



# The System with Final Parameters

- Need to test feasibility of these new parameters
  - Take final estimates (from run 5) and plot all states
- Goal is to see something that looks biologically plausible

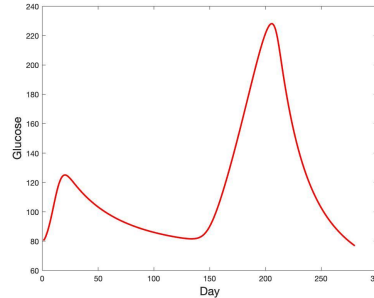
# Glucose Under New Parameters



**\*\*We expect much different behavior!\*\***

# What Went Wrong

- Parameters are changing too much
- Seems to matter which parameters
  - When utilize estimates for all parameter *except*  $\mu_r$  system looks slightly more reasonable



- However, all the final parameters were within “allowable” range
  - Does fixing the other parameters have drawbacks?

# A New Future and Ideal Framework (Once Parameters In Reasonable Range)

- Run **each** mouse “x” times to attempt to reach parameter convergence
- Make distributions using final parameters from run “x” for each mouse

# Data Limitations

- Final parameters dependent on initial conditions
- Only have parameter distributions off single run
- Limited avg number of readings
- Sample size of 11 mice
- Large average time between readings
  - A lot can happen in 2 weeks!