PROLONG

Penalized Regression on Longitudinal Omics Data with Network and Group Lasso Constraints

Steve Broll [1]

Advised by Sumanta Basu [1], Martin Wells [1], and Myung Hee Lee [2]

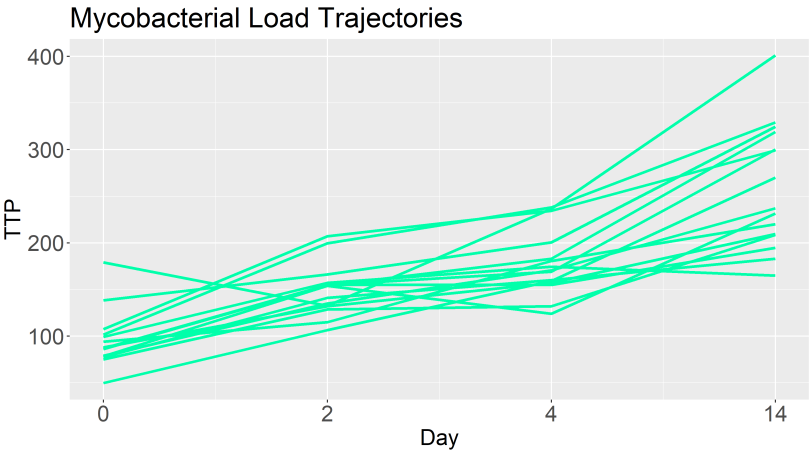
[1]Cornell Univeristy

[2]Weill Cornell Medicine

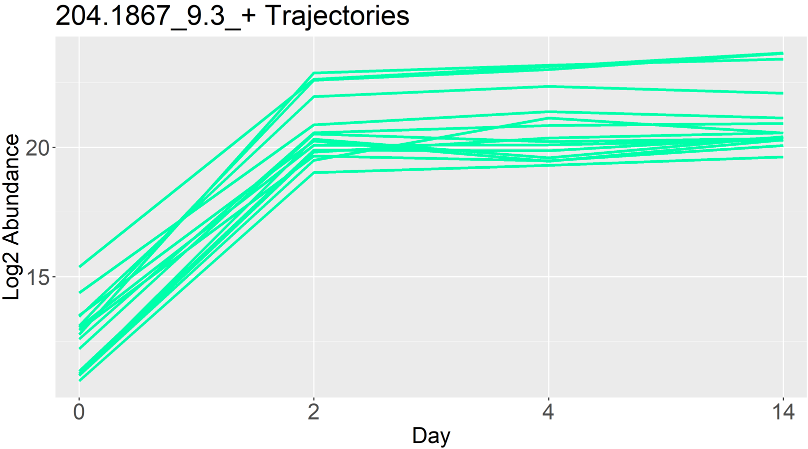
Motivation in Short

Clinician gives you a longitudinal clinical outcome, along with hundreds (or thousands) of longitudinal -omics variables, and asks which variables co-vary with the outcome?

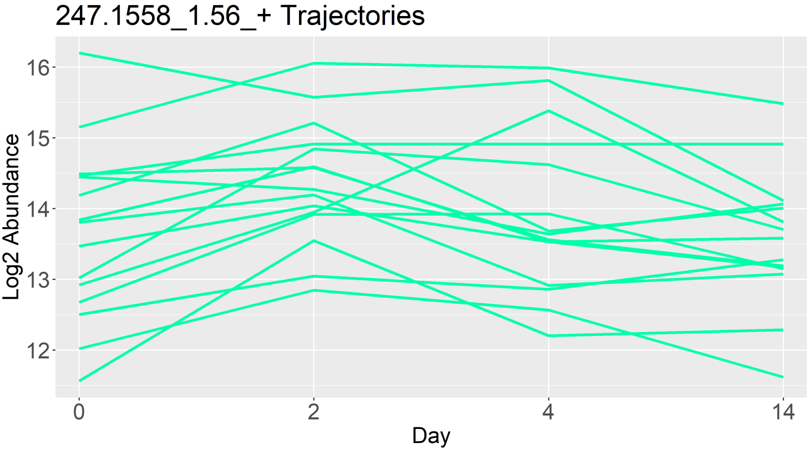
Motivation in Pictures - Outcome



Motivation in Pictures - Example Variable 1



Motivation in Pictures - Example Variable 2



Motivation in More Words

We have:

- Longitudinal measurements for some continuous outcome and for -omics variables with only a few time points
- Large amount of variables with relatively small number of subjects

We want to:

- Identify -omics variables that co-vary with the outcome
- Overcome time dependence, low signal, and high subject variability
- Incorporate correlation of the variables

Tuberculosis Data

- 15 subjects, TB patients treated with RHEZ [rifampin (R), isoniazid (H), ethambutol (E), and pyrazinamide (Z)]
- TB mycobacterial load measured by Time to Positivity (TTP) as our Y
- 352 urinary metabolites as our X
- 4 time points, days 0, 2, 4, 14

General Model Idea

- Take first-difference of the data to deal with observed temporal dependence
- Stack our $t - 1$ first-differenced value of X and Y so we have

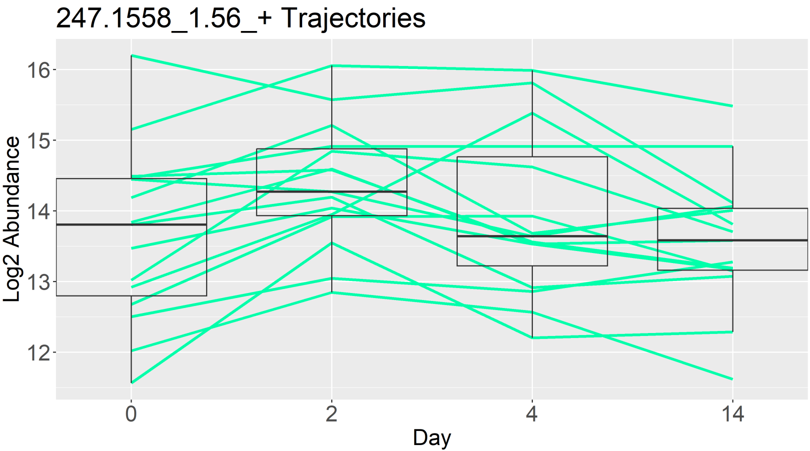
$$Y = [Y_4 - Y_3 \qquad Y_3 - Y_2 \qquad Y_2 - Y_1]^T$$

  And for each variable j we have

$$X_j = [X_{j4} - X_{j3} \qquad X_{j3} - X_{j2} \qquad X_{j2} - X_{j1}]^T$$

- Set up design matrix so that each first-differenced Y value is regressed on all prior first-differenced values of X to account for potential lags
- Apply network and group lasso penalties to induce sparsity while utilizing correlation and inherent group structure

First-Differencing



First-Differencing

- Analogous to paired test, increase in power compared to unpaired
- Remove any subject level (time invariant) fixed effects

Vectorized Y

$$\tilde{Y} = \begin{bmatrix} \tilde{Y}_{11} & \cdots & \tilde{Y}_{1T} \\ & \vdots & \\ \tilde{Y}_{n1} & \cdots & \tilde{Y}_{nT} \end{bmatrix}_{n \times T} \rightarrow \begin{bmatrix} \Delta \tilde{Y}_{11} & \cdots & \Delta \tilde{Y}_{1(T-1)} \\ & \vdots & \\ \Delta \tilde{Y}_{n1} & \cdots & \Delta \tilde{Y}_{n(T-1)} \end{bmatrix}_{n \times (t-1)}$$

$$\rightarrow Y = \begin{bmatrix} \Delta \tilde{Y}_{11} \\ \vdots \\ \Delta \tilde{Y}_{n1} \\ \Delta \tilde{Y}_{1(T-1)} \\ \vdots \\ \Delta \tilde{Y}_{n(T-1)} \end{bmatrix}_{n(T-1) \times 1}$$

Moving X from Tensor to Matrix

$$\tilde{X}^{[j]} = \begin{bmatrix} \tilde{X}^{[j]}_{11} & \cdots & \tilde{X}^{[j]}_{1T} \\ & \vdots & \\ \tilde{X}^{[j]}_{n1} & \cdots & \tilde{X}^{[j]}_{nT} \end{bmatrix}_{n\times T} \to \begin{bmatrix} \Delta\tilde{X}^{[j]}_{11} & \cdots & \Delta\tilde{X}^{[j]}_{1(T-1)} \\ & \vdots & \\ \Delta\tilde{X}^{[j]}_{n1} & \cdots & \Delta\tilde{X}^{[j]}_{n(T-1)} \end{bmatrix}_{n\times(T-1)}$$

$$\to X^{[j]} = \left[\begin{array}{c|c|c|c} \begin{matrix}\Delta\tilde{X}^{[j]}_{11}\\ \vdots \\ \Delta\tilde{X}^{[j]}_{n1}\end{matrix} & 0 & 0 & 0 \\ \hline 0 & \begin{array}{cc}\Delta\tilde{X}^{[j]}_{11} & \Delta\tilde{X}^{[j]}_{12} \\ \multicolumn{2}{c}{\vdots} \\ \Delta\tilde{X}^{[j]}_{n1} & \Delta\tilde{X}^{[j]}_{n2}\end{array} & 0 & 0 \\ \hline 0 & 0 & \ddots & 0 \\ \hline 0 & 0 & 0 & \begin{array}{ccc}\Delta\tilde{X}^{[j]}_{11} & \cdots & \Delta\tilde{X}^{[j]}_{1(T-1)} \\ & \vdots & \\ \Delta\tilde{X}^{[j]}_{n1} & \cdots & \Delta\tilde{X}^{[j]}_{n(T-1)}\end{array} \end{array}\right]_{n(T-1)\times T(T-1)/2}$$

Moving X from Tensor to Matrix

Now replace $\Delta\tilde{X}_{it}^{[j]}$ with row vector

$$\Delta\tilde{X}^{[j]} = |\Delta\tilde{X}_{ij}^{[1]}\Delta\tilde{X}_{ij}^{[2]} \dots \Delta\tilde{X}_{ij}^{[p]}|$$

$$\rightarrow X^{[j]} = \left[\begin{array}{c|c|c|c}
\begin{matrix}\Delta\tilde{X}_{11}^{[j]} \\ \vdots \\ \Delta\tilde{X}_{n1}^{[j]}\end{matrix} & 0 & 0 & 0 \\ \hline
0 & \begin{matrix}\Delta\tilde{X}_{11}^{[j]} & \Delta\tilde{X}_{12}^{[j]} \\ & \vdots & \\ \Delta\tilde{X}_{n1}^{[j]} & \Delta\tilde{X}_{n2}^{[j]}\end{matrix} & 0 & 0 \\ \hline
0 & 0 & \ddots & 0 \\ \hline
0 & 0 & 0 & \begin{matrix}\Delta\tilde{X}_{11}^{[j]} & \cdots & \Delta\tilde{X}_{1(T-1)}^{[j]} \\ & \vdots & \\ \Delta\tilde{X}_{n1}^{[j]} & \cdots & \Delta\tilde{X}_{n(T-1)}^{[j]}\end{matrix}
\end{array}\right]_{n(T-1)\times T(T-1)/2}$$

Group Lasso Laplacian Penalty

Given our first-differenced and stacked response vector Y, first-differenced and stacked design matrix X we seek to minimize

$$(Y - X\beta)^T(Y - X\beta) + \lambda_1 \sum_{j=1}^{p} \left\|\boldsymbol{\beta}_{(j)}\right\|_2 + \lambda_2 \beta^T L \beta,$$

- λ_1 is the tuning parameter for our group lasso penalty, where each group j corresponds to all of the representations in the design matrix of the jth variable
- λ_2 is the tuning parameter for the network penalty
- L is the Laplacian matrix for the weighted graph where the edge weights between each pair of variables are their absolute correlation

Models Compared

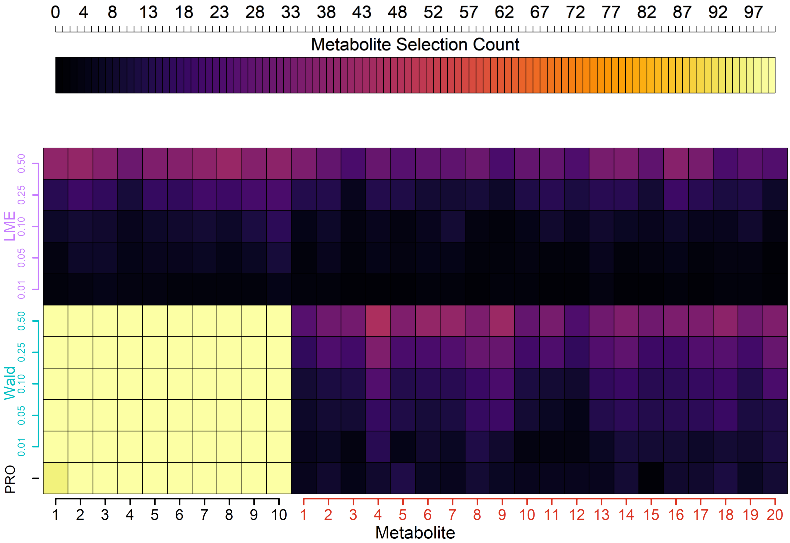
- Linear Mixed Effects Model, one variable at a time
- Wald test on the Δ scale, one variable at a time
- PROLONG

In the following simulations, the univariate models are evaluated at different FDR thresholds and compared to PROLONG

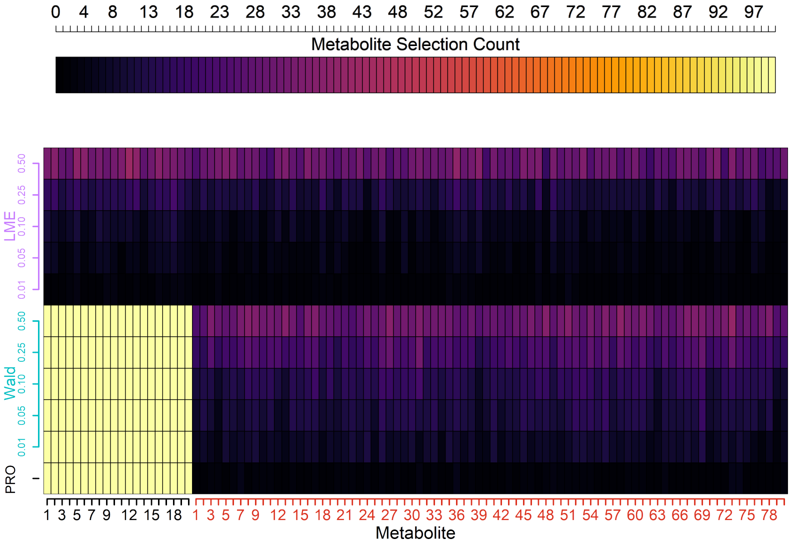
Simulation Scenarios

- Simulated data mimics real TB data in means, variances etc. but with specified relationships between X's and Y
  - Y is generated both on first-difference scale and levels scale in our paper
- Outcome is generated by simulated, correlated target variables at varying dimensions with a SNR ranging from 1 to 2
  - 10, 20, and 50 target variables
  - 20, 80, and 300 noise variables
- Each scenario is run 100 times, and the models are evaluated by selection rate of target and noise variables

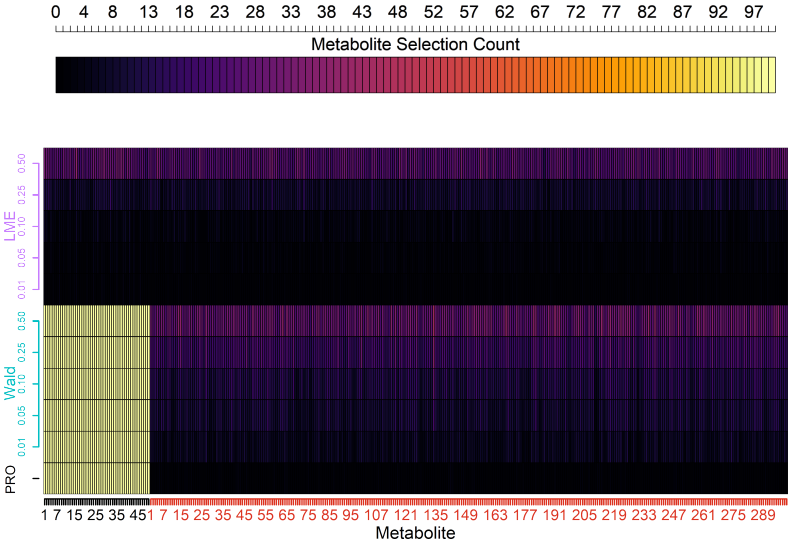
Performance in Simulations



Performance in Simulations



Performance in Simulations



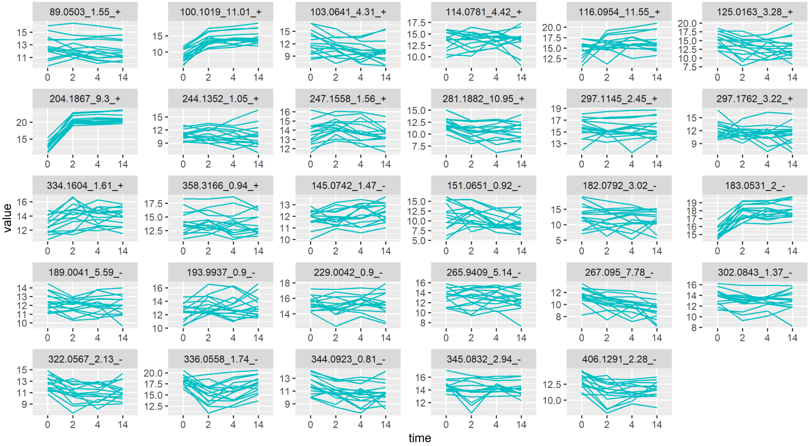
Performance with Real Data

- Univariate mixed effect models do not pick up a single metabolite from our 352 at an FDR of 0.05
- Univariate Delta Wald tests pick 116 metabolites at an FDR of 0.05
- PROLONG selects $\sim$ 30 metabolites, including targets identified by our clinician collaborators and during our EDA

Applying PROLONG

- R package ‘prolong‘, available on Github currently, takes in raw time-scale data and
    - First-differences and shapes the data into the block design structure
    - Automatically selects hyper-parameters and fits the model
    - Provides visualizations for the full data and for selected variables
- Shiny app is in development and will be included within the ‘prolong‘ package, providing a point-and-click interface for users with less familiarity with R

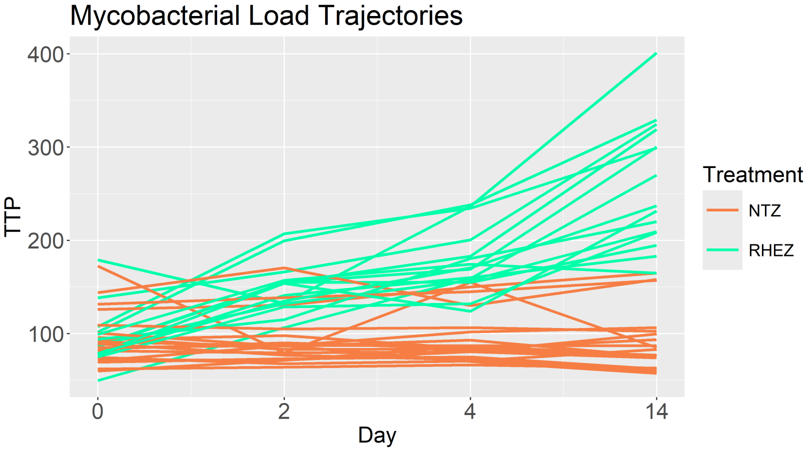
R Package Selected Variable Trajectories



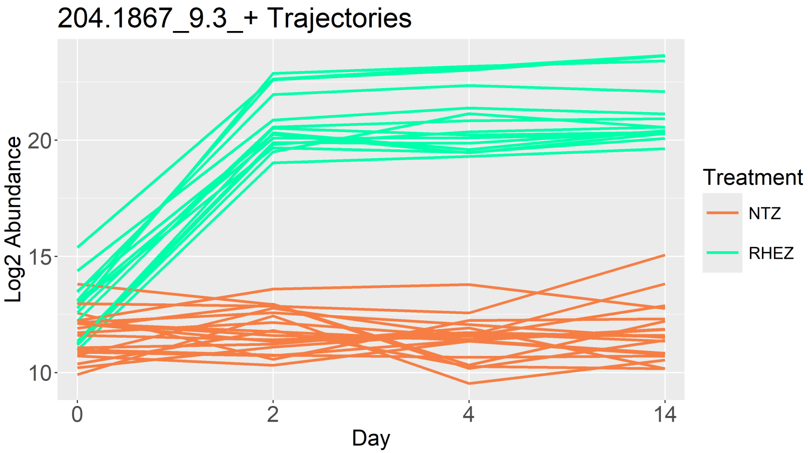
Pooled Data

- Same RHEZ subjects as before
- Additional 19 subjects, TB patients treated with NTZ (Nitazoxanide)
- Same 4 time points, 352 metabolites

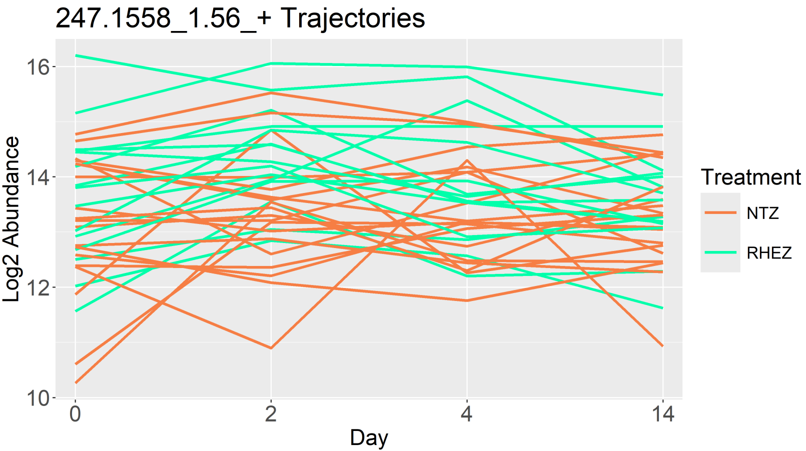
Pooled Data - Outcome



Pooled Data - Example Variable 1



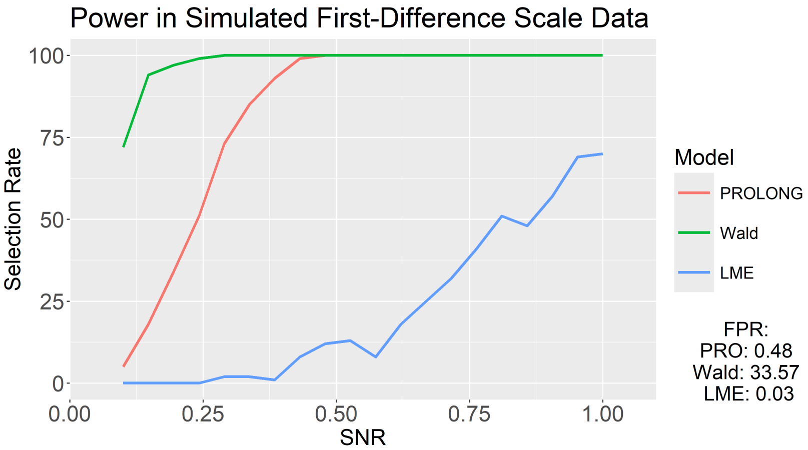
Pooled Data - Example Variable 2



Preliminary Results - Simulation Setup

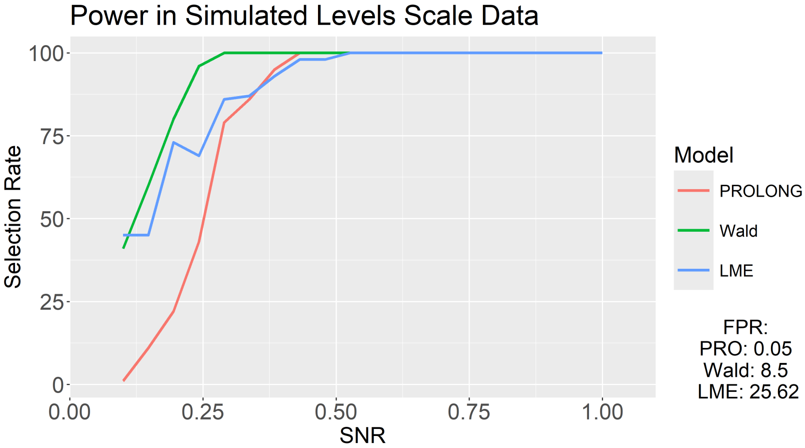
- Simulated data is similar to previous setup, but with a second group with no differential change and no effect on Y
- Much smaller SNR range to produce power curves
- 20 targets with varying SNR, 80 noise variables
- Each scenario is run 100 times, and the models are evaluated by power and false positive rate (FPR)

Preliminary Results - Delta Scale Sim



FPR:
PRO: 0.48
Wald: 33.57
LME: 0.03

Preliminary Results - Levels Scale Sim



Contact and Manuscript

Thank You!

R package available via Github:

https://github.com/stevebroll/prolong

Manuscript available via Biorxiv:

Steve Broll, Sumanta Basu, Myung Hee Lee, and Martin T. Wells.
PROLONG: Penalized regression for outcome guided longitudinal omics analysis with network and group constraints.
bioRxiv, 2023.

Email me at sb2643@cornell.edu

https://stevebroll.github.io