Web-based Supplementary Materials for:

Estimating Time-Varying Directed Gene Regulation Networks by Yunlong Nie, Liangliang Wang, Jiguo Cao

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1 Web Figures

Figure 1 shows the raw time-course gene expression data for the target gene Myo31DF and the selected three regulatory genes Myo61DF, Prm and tim. Figure 2 shows the raw pairwise time-course gene expression data for the selected three regulatory genes Myo61DF, Prm and tim against the target gene Myo31DF.

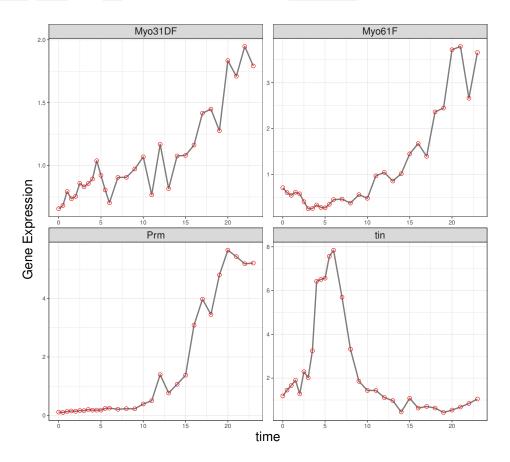


Figure 1: The raw time-course gene expression data for the target gene $\underline{\text{Myo31DF}}$ and the selected three regulatory genes $\underline{\text{Myo61DF}}$, $\underline{\text{Prm}}$ and $\underline{\text{tin}}$. The red circles represent the observed gene expression data at the corresponding time point.

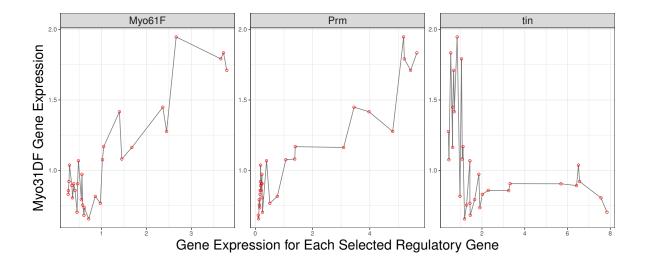


Figure 2: The raw pairwise time-course gene expression data for the selected three regulatory genes <u>Myo61DF</u>, <u>Prm</u> and <u>tin</u> against the target gene <u>Myo31DF</u>. The red circles represent the observed time points.

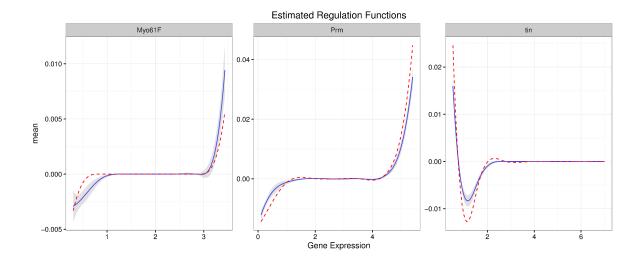


Figure 3: Estimated regulation functions from the simulated data with the noise-to-signal ratio of the simulated data $\rho=1\%$ using the locally sparse method. The dashed red and solid blue lines represent the true regulation functions and the mean of the estimated regulation functions in 100 simulation replicates. The grey bands denote the pointwise 95% confidence interval of the estimated regulation functions.

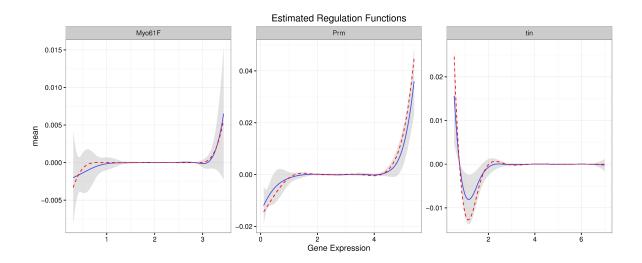


Figure 4: Estimated regulation functions from the simulated data with the noise-to-signal ratio of the simulated data $\rho=5\%$ using the locally sparse method. The dashed red and solid blue lines represent the true regulation functions and the mean of the estimated regulation functions in 100 simulation replicates. The grey bands denote the pointwise 95% confidence interval of the estimated regulation functions.

2 Web Tables

Method	Observed Value	Predicted Value
AR1	1.86	0.82
Constant Expression	1.86	1.11
Group Lasso	1.86	1.82
Locally Sparse	1.86	1.86

Table 1: The prediction for the expression of the target gene Myo31DF at the last time point using four methods in the real data application.

Method	ρ	Mean	Standard Deviation
Locally sparse	1%	7%	1%
	5%	8%	3%
Smoothing spline	1%	100%	0%
	5%	100%	0%
Linear fSCAD	1%	24%	3%
	5%	31%	5%
Group Lasso	1%	18%	13%
	5%	16%	5%

Table 2: The mean and standard deviation of the false positive rates using four methods in 100 simulation replicates. Here ρ represents the noise-to-signal ratio in the simulated data.

Method	ρ	Mean	Standard Deviation
Locally Sparse	1%	0.23	0.15
	5%	0.96	1.27
Group Lasso	1%	6.72	0.60
	5%	6.80	2.97
AR1	1%	8.66	0.62
	5%	8.70	3.00
Constant Expression	1%	568.80	1.07
	5%	568.45	5.37

Table 3: The mean and standard deviation of squared prediction errors using four methods in 100 simulation replicates. Here ρ represents the noise-to-signal ratio in the simulated data.