Supplementary Materials
# High Dimensional ODEs Coupled with Mixed-Effects Modeling Techniques for Dynamic Gene Regulatory Network Identification

Table S1: Notations and parameter definitions in the five-step CSIEF procedure.

Step	Parameter	Definition
I	n	total number of genes
	w_k	proportion of cluster k
	$\mu_k(.)$	mean curve of cluster k
	$\boldsymbol{T_i}$	vector of measurement times for gene i
	$\boldsymbol{b_i}$	random effect of gene i
	$\boldsymbol{\epsilon_i}$	measurement error of each gene in a cluster
II	n	total number of genes
	t_{ij}	design time points
	$g_{ki}(t_{ij})$	gene expression level at t_{ij} for gene i f the kth module
	$M_k(t)$	mean expression curve for the kth module
	$M_k'(t)$	first order derivative of $M_k(t)$
	$V_{ki}(t)$	random-effects functions for gene i in module k
III	$y_k(t)$	equivalent to $M_k'(t)$
	$x_j(t)$	equivalent to $M_k(t)$
	β_{kj}	coefficients of gene j within module k
	$\varepsilon_k(t)$	substitution error of module k
	λ	regularization parameter for SCAD penalty
IV	x_{ki}	gene expression level for the ith gene in the kth module
	n_k	number of genes in the kth module
	$M_{[kj]}(t)$	mean expression levels of the modules that have significant effects on the kth module
	m_k	number of modules that have significant effects on the kth module
	$g_{ki}(t)$	expression measurement of gene i at time t in module k
	$\boldsymbol{\beta}_k$	population parameters for the kth module
	$\boldsymbol{\beta}_{ki}$	individual parameters for gene i of the kth module
	$\varepsilon_{ki}(t)$	measurement error in the longitudinal measurement model
	$\mathbf{b}_{ki}$	random effects of mixed-effects ODE model
V	T	population size
	S	number of genes that share the same function in the population
	n_k	number of genes clustered in the kth module
	z	number of genes that share the same function in the module

Table S2: Parameter estimates of 41 ODEs for the module-based network from the yeast cell cycle data in Section 3.

Module	Influence Module(Parameter Estimates)	Module	Influence Module(Parameter Estimates)
1	9(-0.017), 15(-0.021), 18(-0.063), 30(-0.032)	22	14(-0.01), 18(0.109), 20(-0.622), 32(-0.158), 41(-0.065)
2	8(-0.019), 25(-0.042), 30(-0.052), 32(0.069), 41(0.028)	23	25(-0.186), 30(-0.117), 38(0.014), 41(-0.065)
3	7(0.048), 9(-0.012), 14(-0.063), 18(-0.005), 25(0.015)	24	8(0.098), 9(0.087), 14(0.017), 25(-0.031), 32(0.024), 41(-0.085)
4	9(0.024), 14(0.017), 32(0.015), 39(0.019), 41(-0.157)	25	9(-0.086), 20(-0.35), 32(0.04), 41(0.049)
5	8(1.45), 9(0.184), 14(0.212), 18(-1.47), 32(0.395), 41(0.525)	26	8(0.016), 9(-0.014), 14(-0.004), 30(-0.022), 32(0.019), 41(0.03)
6	18(-0.045), 25(0.003), 30(0.037), 32(-0.055), 41(-0.047)	27	8(0.014), 9(-0.05), 15(0.16), 25(-0.033), 41(0.132)
7	18(0.109), 25(-0.146), 30(-0.078), 32(0.159), 41(0.007)	28	8(0.036), 9(-0.02), 32(0.024), 38(0.02), 41(-0.075)
8	18(-0.328), 32(0.007), 41(-0.31)	29	14(0.067), 15(0.086), 18(-0.269), 30(0.19), 32(0.04)
9	14(0.204), 18(-0.484), 20(1.41), 32(-0.09), 41(0.46)	30	14(0.052), 32(-0.38), 38(-0.089)
10	9(0.039), 14(0.019), 18(0.052), 25(-0.063), 32(0.056), 41(0.044)	31	9(0.136), 14(0.031), 15(-0.089), 18(-0.05), 30(-0.034), 41(0.038)
11	9(0.055), 14(0.003), 18(-0.055), 41(-0.148)	32	8(0.086), 9(-0.029), 14(0.249), 18(0.109), 30(0.79)
12	14(-0.063), 15(0.025), 41(-0.086)	33	14(-0.023), 15(0.015), 18(0.085), 30(-0.031), 32(-0.083), 41(0.093)
13	9(-0.031), 14(-0.012), 25(0.047), 32(0.005), 41(-0.026)	34	9(-0.03), 15(0.062), 18(-0.167), 32(0.136), 38(0.026)
14	14(-0.139), 15(0.066), 25(-0.072), 30(-0.128), 38(0.0154), 41(-0.044)	35	9(0.253), 14(0.121), 15(-0.12), 18(0.054), 30(0.012), 41(0.038)
15	14(0.021), 15(-0.227), 30(0.22), 32(-0.263), 41(0.115)	36	14(-0.013), 20(-0.027), 30(-0.11), 32(0.09), 38(0.024)
16	14(0.002), 30(-0.143), 32(-0.053), 38(-0.023), 41(0.024)	37	9(-0.028), 14(-0.051), 15(-0.016), 18(0.15), 30(-0.162), 41(0.027)
17	14(-0.029), 15(0.008), 25(-0.019), 30(-0.043), 41(-0.013)	38	14(0.276), 15(-0.293), 25(0.262), 30(0.747), 41(0.103)
18	8(0.326), 9(0.015), 38(0.013), 41(-0.518)	39	8(0.708), 14(0.086), 18(-0.448), 30(-0.074), 38(0.194)
19	8(0.082), 9(0.066), 14(0.031), 25(-0.102), 32(0.03), 41(-0.017)	40	8(-0.057), 9(-0.111), 14(-0.033), 25(-0.071), 32(-0.024), 41(-0.01)
20	9(-0.152), 18(-0.167), 25(0.262), 41(-0.071)	41	9(0.109), 14(0.041), 18(0.635), 25(-0.192), 41(-0.225)
21	9(0.047), 14(-0.026), 18(-0.193), 25(0.052), 34(0.422), 41(-0.237)		
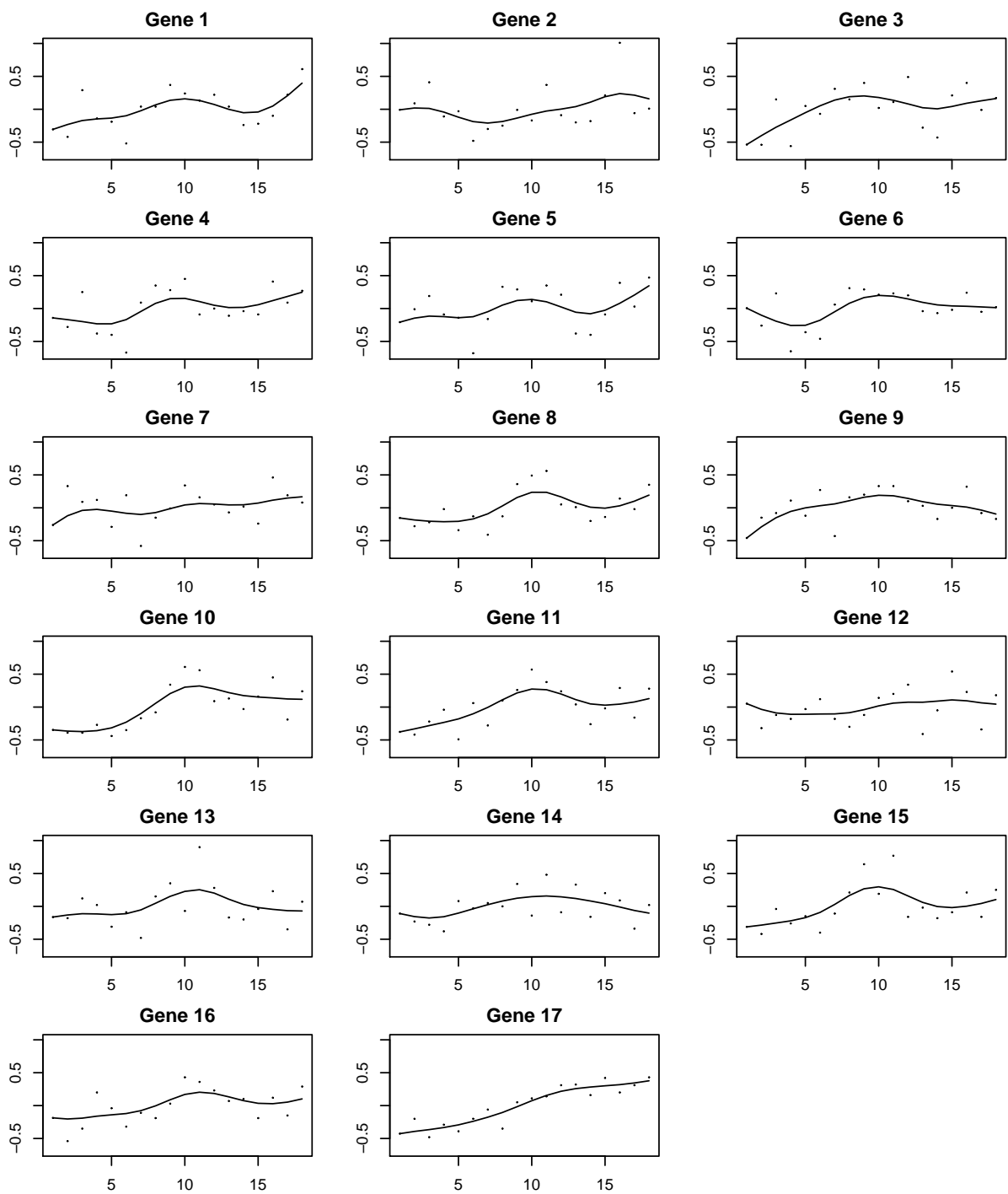
Figure S1. Illustration of individual gene fitting based on model (2.11): fitted curves (solid lines) of 17 genes from Module 1 overlayed with gene expression data (dots).