

Appendix: Additional Numerical Results

Table 5: Simulation for a continuous response under the transformation model. AR(0.8) correlation structure and Error 1. In each cell, AUC based on 100 replicates (mean in the first row, standard deviation in the second row).

	$t^{1/3}$	t	t^3	t^5
SPRE	0.805	0.828	0.828	0.831
	0.057	0.049	0.041	0.054
Single Index	0.752	0.767	0.614	0.551
	0.102	0.063	0.077	0.053

Table 6: Analysis of the lung cancer data using PeAFT: identified main effects and interactions.

Gene name	main effects						interactions				
	age	gender	smoke	chemo	stage	gene	age	gender	smoke	chemo	stage
<i>CDC2</i>	0.0020	-0.0058	-0.0082	0.0367	-0.0511	-0.0004					
<i>CDK1</i>	0.0016	-0.0057	-0.0089	0.0370	-0.0505	-0.0027					
<i>UBE2C</i>	0.0016	-0.0061	-0.0085	0.0373	-0.0509	-0.0025					
<i>TIMP3</i>	0.0016	-0.0059	-0.0080	0.0364	-0.0517	0.0039					
<i>PFKP</i>	0.0020	-0.0058	-0.0081	0.0366	-0.0512	-0.0000					
<i>CDC2</i>	0.0013	-0.0057	-0.0090	0.0370	-0.0502	-0.0040					
<i>CCNB2</i>	0.0009	-0.0058	-0.0101	0.0368	-0.0491	-0.0070					
<i>CCNA2</i>	0.0018	-0.0060	-0.0086	0.0369	-0.0506	-0.0026					
<i>TXNIP</i>	0.0019	-0.0057	-0.0082	0.0367	-0.0510	0.0008					
<i>AFP</i>	0.0030	-0.0073	-0.0079	0.0341	-0.0516		0.0098				
<i>ANXA3</i>	0.0009	-0.0058	-0.0081	0.0364	-0.0510		-0.0033				
<i>KCTD12</i>	0.0018	-0.0060	-0.0079	0.0367	-0.0512		-0.0010				
<i>DPT</i>	0.0012	-0.0064	-0.0072	0.0363	-0.0510		-0.0052				0.0046
<i>HIST1H2AC</i>	0.0022	-0.0065	-0.0082	0.0377	-0.0516			0.0059			
<i>ETV1</i>	0.0014	-0.0054	-0.0091	0.0370	-0.0514						
<i>HIST1H2BC</i>	0.0024	-0.0058	-0.0082	0.0370	-0.0512						0.0044
<i>DPT</i>	0.0011	-0.0062	-0.0072	0.0360	-0.0512		-0.0061				
<i>MFAP4</i>	0.0017	-0.0055	-0.0078	0.0369	-0.0513		-0.0030				
<i>DPT</i>	0.0019	-0.0059	-0.0081	0.0366	-0.0512		-0.0008				
<i>SDC2</i>	0.0025	-0.0055	-0.0089	0.0362	-0.0501			0.0041			
<i>QKI</i>	0.0020	-0.0059	-0.0080	0.0368	-0.0511		-0.0008				
<i>TTRAP</i>	0.0019	-0.0060	-0.0081	0.0370	-0.0518			-0.0020			
<i>FRMD4B</i>	0.0000	-0.0072	-0.0080	0.0364	-0.0517		-0.0098				
<i>OSTM1</i>	0.0020	-0.0061	-0.0078	0.0367	-0.0510		-0.0012				
<i>HIST1H2BH</i>	0.0022	-0.0057	-0.0082	0.0369	-0.0512						0.0016
<i>HIST1H2BD</i>	0.0020	-0.0058	-0.0081	0.0366	-0.0512						0.0000
<i>RDX</i>	0.0016	-0.0053	-0.0081	0.0364	-0.0501		-0.0035				
<i>SMARCA2</i>	0.0028	-0.0066	-0.0077	0.0368	-0.0519		-0.0031				

Table 7: Analysis of the lung cancer data using PeCOX: identified main effects and interactions.

gene name	main effects						interactions					
	age	gender	smoke	chemo	stage	gene	age	gender	smoke	chemo	stage	
<i>PDZK1IP1</i>	0.3718	-0.1070	-0.1224	0.1410	0.7556						-0.0384	
<i>GSTA1</i>	0.3782	-0.1362	-0.1051	0.1308	0.7582						-0.0501	
<i>IGFBP1</i>	0.3679	-0.1200	-0.1097	0.1371	0.7522						-0.0141	
<i>AFP</i>	0.3624	-0.1144	-0.1133	0.1449	0.7375						-0.0017	
<i>CPB2</i>	0.3630	-0.1155	-0.1128	0.1437	0.7385						-0.0031	
<i>AHCYL2</i>	0.3779	-0.1156	-0.1177	0.1482	0.7538						-0.0401	
<i>FST</i>	0.3663	-0.1165	-0.1130	0.1426	0.7422		0.0109				-0.0217	
<i>LEPREL1</i>	0.3686	-0.1244	-0.1073	0.1340	0.7491						-0.0955	
<i>RAB25</i>	0.3957	-0.1312	-0.1125	0.1200	0.7880						-0.0059	
<i>PAH</i>	0.3649	-0.1165	-0.1121	0.1426	0.7418						0.0064	
<i>IGF2BP2</i>	0.3648	-0.1140	-0.1145	0.1463	0.7395						0.0385	
<i>UGCG</i>	0.3698	-0.1243	-0.1063	0.1321	0.7591						-0.0180	
<i>SLC16A4</i>	0.3703	-0.1152	-0.1115	0.1418	0.7484						-0.0126	
<i>ACE2</i>	0.3689	-0.1189	-0.1124	0.1416	0.7477						0.0029	
<i>GPR183</i>	0.3630	-0.1149	-0.1129	0.1447	0.7383						0.0931	
<i>CSE1L</i>	0.3665	-0.1220	-0.1081	0.1281	0.7731						-0.0590	
<i>MAL</i>	0.3757	-0.1288	-0.1007	0.1202	0.7743						-0.0143	
<i>CBR3</i>	0.3687	-0.1196	-0.1117	0.1413	0.7494						-0.0554	
<i>CEACAM7</i>	0.3904	-0.1354	-0.0998	0.1153	0.7932						-0.0021	
<i>RIT1</i>	0.3629	-0.1149	-0.1128	0.1441	0.7382						-0.0161	
<i>SCUBE2</i>	0.3672	-0.1192	-0.1110	0.1428	0.7432						-0.0248	
<i>SPINK4</i>	0.3699	-0.1196	-0.1112	0.1368	0.7483						0.0073	
<i>PLAGL1</i>	0.3630	-0.1152	-0.1132	0.1436	0.7387						-0.0208	
<i>HSD17B2</i>	0.3693	-0.1209	-0.1121	0.1384	0.7464						-0.0317	
<i>ADHIC</i>	0.3754	-0.1315	-0.1077	0.1316	0.7655						-0.0070	
<i>FAT1</i>	0.3658	-0.1160	-0.1126	0.1433	0.7419							
<i>TDP2</i>	0.3803	-0.1189	-0.1117	0.1328	0.7686		0.0404					
<i>SCML1</i>	0.3865	-0.1331	-0.1076	0.1292	0.7597						0.0556	
<i>ACE2</i>	0.3634	-0.1151	-0.1132	0.1444	0.7385						-0.0027	
<i>UPK1B</i>	0.3640	-0.1164	-0.1122	0.1432	0.7407						-0.0044	
<i>PCNA</i>	0.3625	-0.1164	-0.1108	0.1413	0.7467						0.0381	
<i>CDH17</i>	0.3624	-0.1146	-0.1130	0.1443	0.7375						-0.0014	
<i>BMP6</i>	0.3850	-0.1320	-0.1057	0.1279	0.7695						-0.0420	

Table 8: Analysis of the lung cancer data using Sig (the significance level method): identified main effects and interactions.

Gene name	main effects						interactions				
	age	gender	smoke	chemo	stage	gene	age	gender	smoke	chemo	stage
<i>PRSS3</i>	-1.00	-0.06	1.79	-0.24	-3.13	-2.96					
<i>KLK6</i>	-1.00	-0.13	0.54	-0.32	-1.86	-1.69					
<i>KIAA1199</i>	-1.00	0.36	0.22	-0.29	-2.76	1.43					1.25
<i>TANK</i>	-1.00	0.16	0.51	-0.84	-2.52	1.88	-2.50				
<i>CPM</i>	-1.00	0.07	0.72	-0.44	-1.41	0.97				-1.41	
<i>SERPIND1</i>	-1.00	-0.20	0.38	-0.25	-0.81	1.72					
<i>RET</i>	-1.00	0.37	-0.06	-0.11	-2.15	-1.94					
<i>CLDN18</i>	-1.00	0.59	0.98	-0.40	-2.74	-1.49					
<i>MUC5AC</i>	-1.00	0.22	0.02	-0.97	-1.78	-1.74					
<i>ABAT</i>	-1.00	0.00	0.48	-0.58	-0.76	1.43					

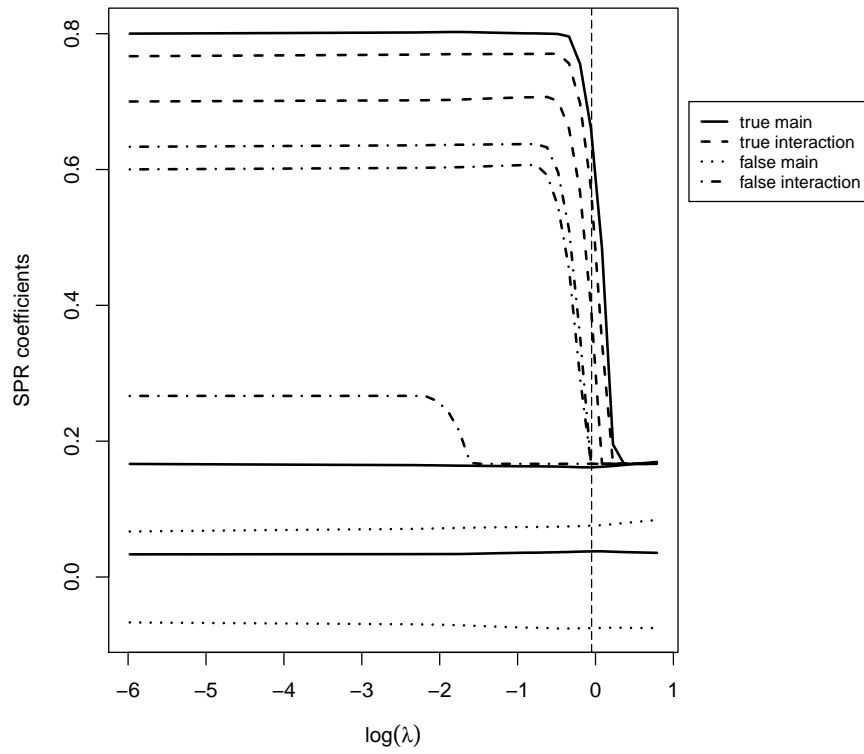


Figure 1: Parameter paths for a gene *with* important interactions. The vertical line corresponds to λ selected using 2-fold cross validation.

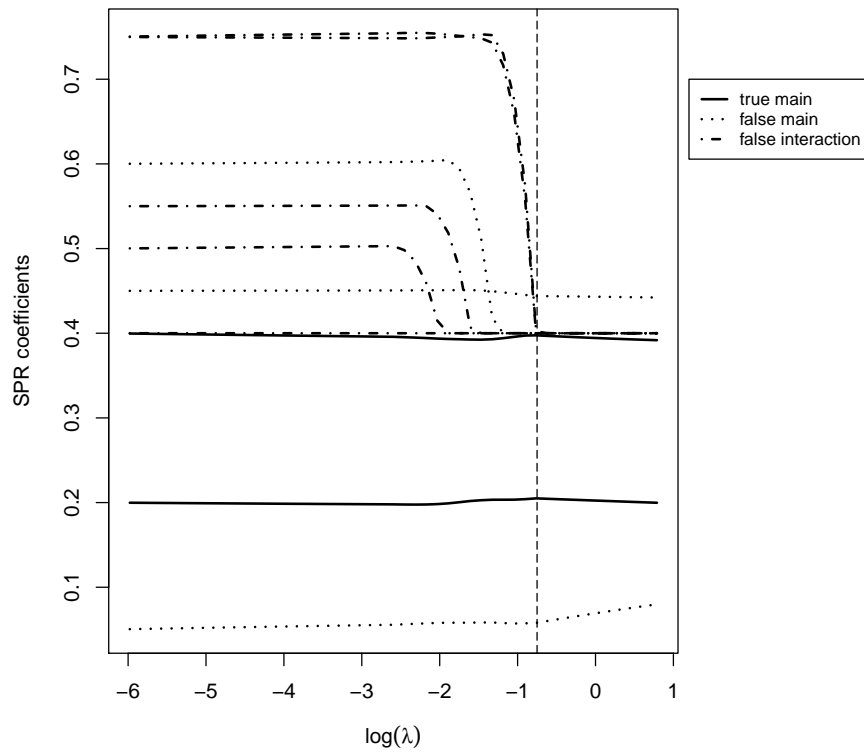


Figure 2: Parameter paths for a gene *without* important interaction. The vertical line corresponds to λ selected using 2-fold cross validation.