

Figure 1. Solution paths under the homogeneity model for a simulated dataset for a gene associated with responses.

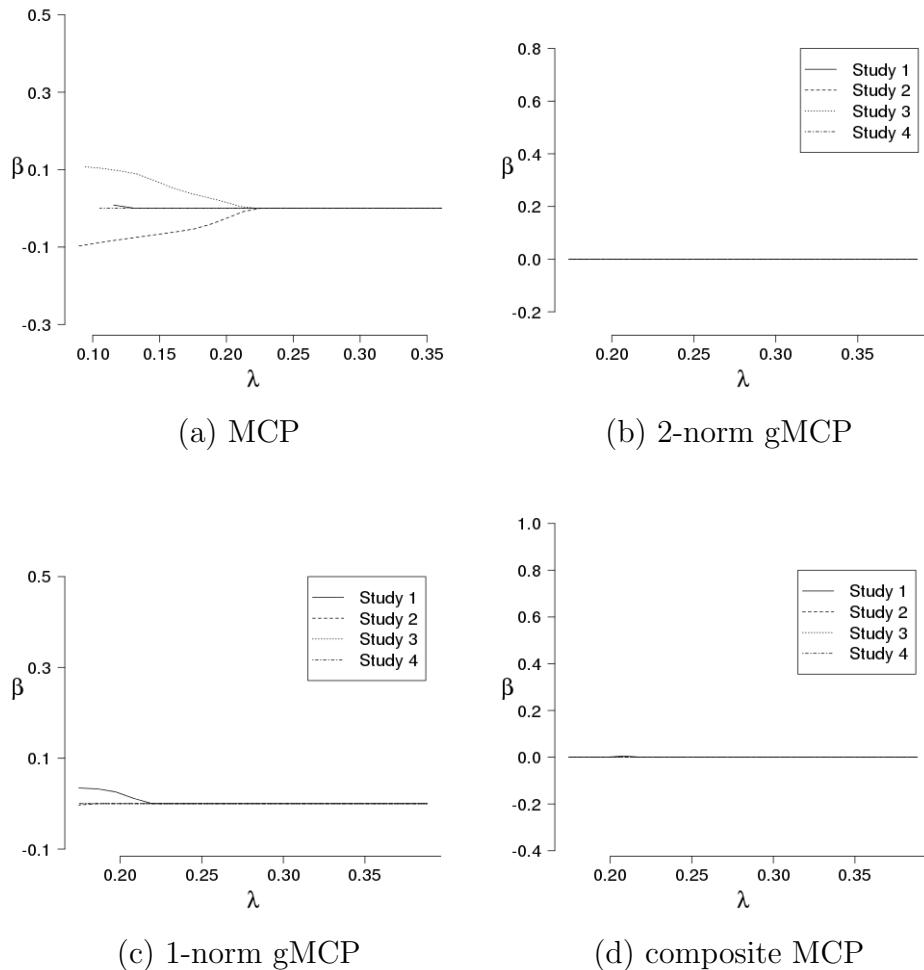


Figure 2. Solution paths under the homogeneity model for a simulated dataset for a gene not associated with responses.

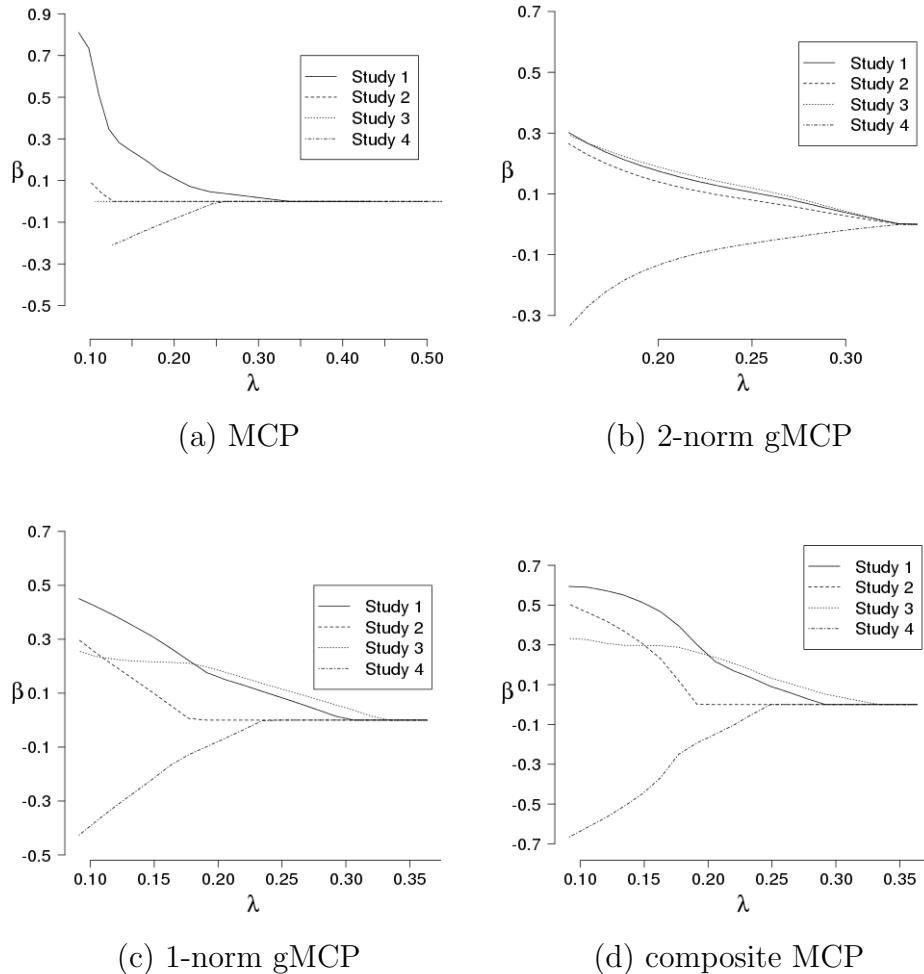


Figure 3. Solution paths under the heterogeneity model for a simulated dataset for a gene associated with responses in all four studies.

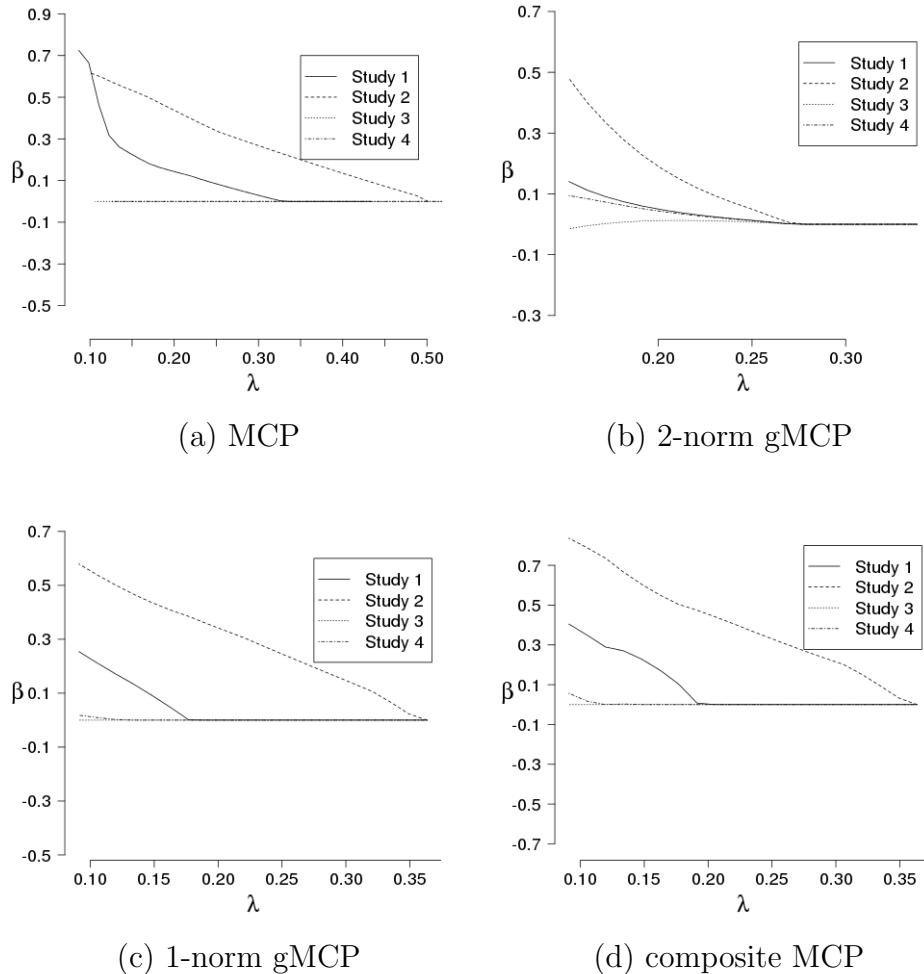


Figure 4. Solution paths under the heterogeneity model for a simulated dataset for a gene associated with responses in studies 1 and 2.

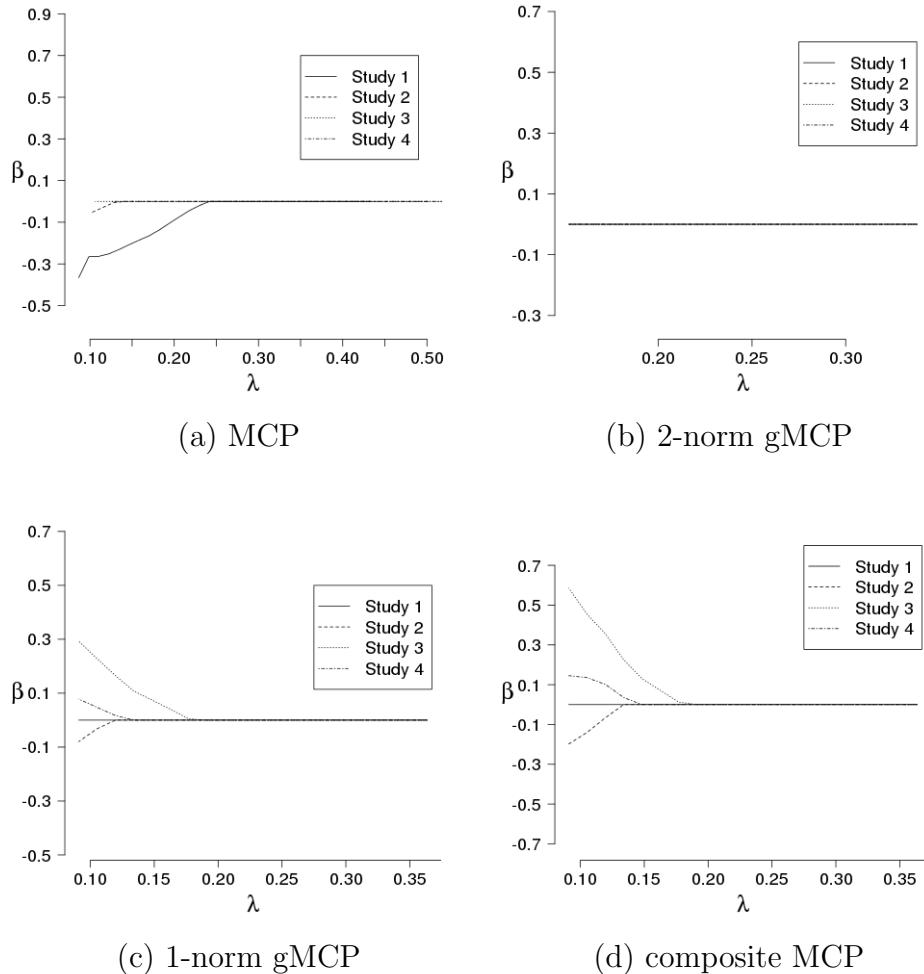


Figure 5. Solution paths under the heterogeneity model for a simulated dataset for a gene not associated with responses in all four studies.

Table 1
Parameter estimates for liver cancer studies.

Method	Gene #	D1	D2	D3	D4
MCP	287	-0.25			
	442	-0.02			
	921	-0.04			
	122		-0.48		
	942		-0.04		
	942				-1.37
2-norm gMCP	439	-0.19	-0.13	-0.36	0.10
	942	-0.31	-0.74	-0.91	-0.71
1-norm gMCP	122		-0.35		
	255	-0.02			
	287	-0.14			
	332		0.02		
	379				0.02
	442	-0.11			
	497			-0.05	
	498		0.11		
	523			-0.20	
	679	-0.06			
	713	-0.07			
	735	-0.10			
	774		-0.10		
	849		0.03		
	914				0.04
	921	-0.13			
	942		-0.27	-0.05	-0.32
	992			-0.01	
composite MCP	122		-0.48		
	287	-0.18			
	442	-0.02			
	921	-0.02			
	942				-0.17

Table 2*Parameter estimates for analysis of multiple cancer data.*

Method	Gene #	Kidney	Liver	Prostate	Stomach
MCP	525				-9.03
	824			-7.72	
	1145		12.41		
	2573	3.91			
2-norm gMCP	317	-2.11	-1.42	-5.11	-2.92
	1145	-2.30	10.33	0.96	3.81
	2211	11.51	0.62	-5.00	1.21
1-norm gMCP	530				-0.94
	672	-0.99			
	1145		2.65		0.22
	2211	1.64		-0.52	
	2991			1.18	
	3031	0.01			
composite MCP	40	-8.62			
	110				-4.01
	220			9.93	
	703	6.31			
	1145		12.15		