Supplemental Data

Using Principal Components of Genetic Variation

for Robust and Powerful Detection of Gene-Gene

Interactions in Case-Control and Case-Only Studies

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Table S1. List of allele frequencies of causal SNPs and baseline disease risks for the simulation study of type I error and power (Table 1 and Figure 5).

Stratum	Tertile along PC-s				Common MAF	Baseline Disease Risk	
No.	PC1	PC2	PC3	PC4	of Causal SNPs	Correlated**	Uncorrelated*
1	1	1	1	1	0.1500	0.0050	0.0118
2	1	1	1	2	0.1525	0.0054	0.0121
3	1	1	1	3	0.1544	0.0057	0.0124
4	1	1	2	1	0.1562	0.0057	0.0156
5	1	1	2	2	0.1638	0.0061	0.0159
6	1	1	2	3	0.1694	0.0065	0.0104
7	1	1	3	1	0.1626	0.0065	0.0110
8	1	1	3	2	0.1757	0.0070	0.0171
9	1	1	3	3	0.1856	0.0074	0.0126
10	1	2	1	1	0.1630	0.0070	0.0099
11	1	2	1	2	0.1731	0.0075	0.0103
12	1	2	1	3	0.1806	0.0079	0.0103
13	1	2	2	1	0.1831	0.0079	0.0147
14	1	2	2	2	0.2000	0.0085	0.0141
15	1	2	2	3	0.2127	0.0090	0.0158
16	1	2	3	1	0.2051	0.0090	0.0119
17	1	2	3	2	0.2299	0.0097	0.0122
18	1	2	3	3	0.2487	0.0102	0.0138
19	1	3	1	1	0.1687	0.0080	0.0115
20	1	3	1	2	0.1823	0.0086	0.0139
21	1	3	1	3	0.1924	0.0090	0.0116
22	1	3	2	1	0.1953	0.0091	0.0115
23	1	3	2	2	0.2166	0.0098	0.0134
24	1	3	2	3	0.2328	0.0103	0.0097
25	1	3	3	1	0.2249	0.0103	0.0123
26	1	3	3	2	0.2555	0.0111	0.0104
27	1	3	3	3	0.2788	0.0117	0.0120
28	2	1	1	1	0.1584	0.0061	0.0097
29	2	1	1	2	0.1629	0.0066	0.0134
30	2	1	1	3	0.1662	0.0070	0.0153
31	2	1	2	1	0.1713	0.0070	0.0102
32	2	1	2	2	0.1816	0.0075	0.0120
33	2	1	2	3	0.1891	0.0079	0.0084
34	2	1	3	1	0.1851	0.0080	0.0121
35	2	1	3	2	0.2019	0.0086	0.0213
36	2	1	3	3	0.2144	0.0090	0.0114
37	2	2	1	1	0.1816	0.0086	0.0107
38	2	2	1	2	0.1947	0.0092	0.0144
39	2	2	1	3	0.2044	0.0097	0.0109
40	2	2	2	1	0.2110	0.0097	0.0115
41	2	2	2	2	0.2321	0.0105	0.0095
42	2	2	2	3	0.2480	0.0110	0.0074
43	2	2	3	1	0.2438	0.0111	0.0108
44	2	2	3	2	0.2744	0.0119	0.0119
45	2	2	3	3	0.2975	0.0126	0.0130
46	2	3	1	1	0.1919	0.0098	0.0133

47	2	3	1	2	0.2091	0.0105	0.0150
48	2	3	1	3	0.2220	0.0111	0.0087
49	2	3	2	1	0.2293	0.0112	0.0133
50	2	3	2	2	0.2558	0.0120	0.0087
51	2	3	2	3	0.2757	0.0126	0.0104
52	2	3	3	1	0.2715	0.0127	0.0123
53	2	3	3	2	0.3088	0.0137	0.0123
54	2	3	3	3	0.3369	0.0144	0.0162
55	3	1	1	1	0.1748	0.0090	0.0111
56	3	1	1	2	0.1833	0.0096	0.0145
57	3	1	1	3	0.1896	0.0102	0.0098
58	3	1	2	1	0.2021	0.0102	0.0092
59	3	1	2	2	0.2179	0.0110	0.0148
60	3	1	2	3	0.2296	0.0116	0.0179
61	3	1	3	1	0.2324	0.0116	0.0155
62	3	1	3	2	0.2569	0.0125	0.0099
63	3	1	3	3	0.2752	0.0132	0.0084
64	3	2	1	1	0.2196	0.0125	0.0162
65	3	2	1	2	0.2392	0.0134	0.0124
66	3	2	1	3	0.2538	0.0141	0.0146
67	3	2	2	1	0.2697	0.0142	0.0146
68	3	2	2	2	0.2997	0.0152	0.0117
69	3	2	2	3	0.3222	0.0161	0.0139
70	3	2	3	1	0.3264	0.0161	0.0102
71	3	2	3	2	0.3682	0.0173	0.0135
72	3	2	3	3	0.3991	0.0183	0.0173
73	3	3	1	1	0.2405	0.0143	0.0145
74	3	3	1	2	0.2655	0.0153	0.0103
75	3	3	1	3	0.2842	0.0162	0.0123
76	3	3	2	1	0.3015	0.0162	0.0110
77	3	3	2	2	0.3383	0.0175	0.0145
78	3	3	2	3	0.3657	0.0184	0.0173
79	3	3	3	1	0.3705	0.0185	0.0135
80	3	3	3	2	0.4197	0.0199	0.0180
81	3	3	3	3	0.4557	0.0209	0.0116

** Disease risk (α_S) varies along the same direction as common MAF (p_S) of the two causal SNPs (i.e. monotonically along tertiles of each PC). The following two models were used (here i_1, i_2, i_3 and i_4 denote tertiles of the 4 significant PC-s for the Sth stratum).

$$\log(p_S/p_0) = \sum_{j=1}^{4} a_j \psi_j(i_j - 1) + \sum_{j}\sum_{k<j} a_{jk} \psi_j(i_j - 1)\psi_k(i_k - 1) \text{ and}$$

$$\log(\alpha_S/\alpha_0) = \sum_{j=1}^{4} A_j \psi_j(i_j - 1), \text{ where } a_j > 0,\ a_{jk} > 0, A_j > 0,\ \forall j,k$$

with $\psi_1(x) = x\sqrt{x},\ \psi_2(x) = \sqrt{x},\ \psi_3(x) = x,\ \psi_4(x) = \log(1+x)$

* Disease risk varies randomly independent of the principal components,
$\text{logit}(\alpha_S) \sim iid\ N(\mu,\sigma^2)$, for S = 1, …, 81