A Generalized Family-Based Association Test
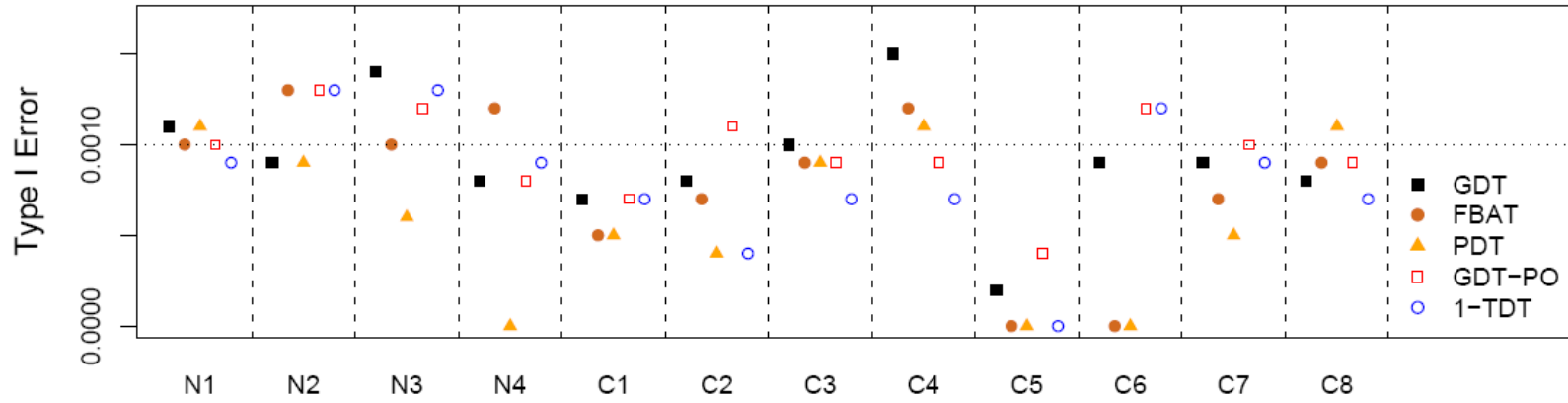
for Dichotomous Traits

Wei-Min Chen, Ani Manichaikul, and Stephen S. Rich

Type I Error Rate at Significance Level .01
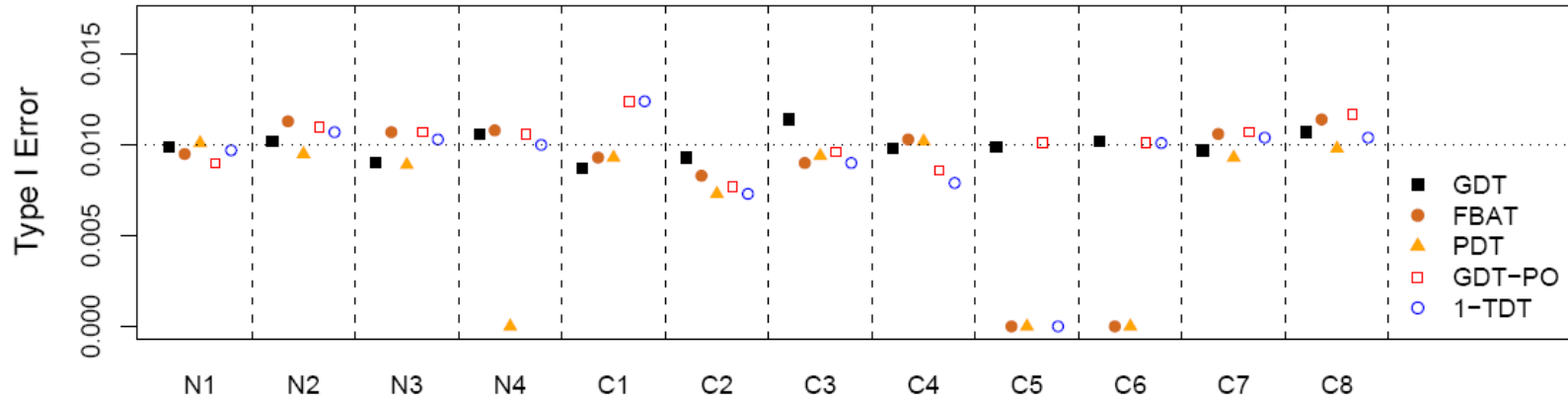
Type I Error Rate at Significance Level .001

Figure S1. Type I Error Rates for Five Association Tests in the Presence of Linkage

The prevalence of the disease is set at 0.3. The SNP under test is at the disease locus with no LD with the disease. Either 200 nuclear families or 100 cousin families were simulated 10,000 times.

Table S1. Power Comparison between PBAT, FBAT, and GDT for a Common Disease with Prevalence 0.3

	N1	N2	N3	N4	C1	C2	C3	C4	C7	C8
α=0.01										
PBAT	46.38	88.77	91.68	47.22	0.25	7.48	2.35	1.26	3.90	21.30
FBAT	46.71	88.77	91.68	47.22	23.38	56.52	56.87	29.56	81.04	47.34
GDT	67.04	94.90	96.77	91.88	68.28	96.40	74.32	68.65	93.83	60.82
α=0.001										
PBAT	20.34	69.42	74.19	21.36	0.01	1.14	0.16	0.07	0.27	6.55
FBAT	20.48	69.42	74.19	21.35	6.15	28.28	27.32	10.22	55.58	21.77
GDT	37.87	82.51	86.66	75.05	37.36	85.32	46.34	40.13	78.06	32.04

Note: Scenarios C5 and C6 are not included since methods PBAT and FBAT do not apply to these two pedigree scenarios (i.e., they have statistical power zero). Simulations for this table are identical to those for Figure 3.