

Finite Adaptation and Multistep Moves in the Metropolis-Hastings Algorithm for Variable Selection in Genome-Wide Association Analysis

Supplementary Table S4

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Move size and rate statistics as averages over the 20 simulation datasets

Move size and rate statistics as averages over the 20 simulation datasets. Values are arithmetic means. RJD = Realized jump distance. PJD = Proposed jump distance. Move rate = proportion of moves with jump distance > 0 (acceptance rate for non-DR samplers). p is the parameter of the move size proposal distribution.

Setting / Sampler	RJD	PJD	RJD/PJD	Move rate	p
30 causal SNPs, $H^2 = 0.2$					
adaptive MS-DR	1.90	6.32	0.45	0.68	0.13
adaptive MS	1.02	4.36	0.39	0.39	0.24
adaptive SS	0.67	1.00	0.67	0.67	NA
non-adaptive MS-DR	1.26	5.86	0.32	0.60	0.15
non-adaptive MS	0.53	2.14	0.34	0.34	0.48
non-adaptive SS	0.47	1.00	0.47	0.47	NA
30 causal SNPs, $H^2 = 0.5$					
adaptive MS-DR	1.32	5.80	0.34	0.63	0.15
adaptive MS	0.57	1.73	0.42	0.42	0.61
adaptive SS	0.53	1.00	0.53	0.53	NA
non-adaptive MS-DR	0.82	5.86	0.21	0.48	0.15
non-adaptive MS	0.30	1.10	0.29	0.29	0.91
non-adaptive SS	0.30	1.00	0.30	0.30	NA
100 causal SNPs, $H^2 = 0.2$					
adaptive MS-DR	2.71	8.79	0.46	0.62	0.05
adaptive MS	1.97	9.73	0.31	0.31	0.02
adaptive SS	0.76	1.00	0.76	0.76	NA
non-adaptive MS-DR	1.90	6.68	0.43	0.66	0.12
non-adaptive MS	1.04	5.67	0.32	0.32	0.17
non-adaptive SS	0.63	1.00	0.63	0.63	NA
100 causal SNPs, $H^2 = 0.5$					
adaptive MS-DR	1.55	5.80	0.40	0.67	0.15
adaptive MS	0.72	2.66	0.40	0.40	0.39
adaptive SS	0.60	1.00	0.60	0.60	NA
non-adaptive MS-DR	1.20	5.86	0.31	0.59	0.15
non-adaptive MS	0.49	1.90	0.34	0.34	0.54
non-adaptive SS	0.45	1.00	0.45	0.45	NA