Simulation with partially informative markers. (H2=0.2, 0.1, 0.05)

Linkage phase:

1 2 3 3

1 2 3 4

1 2 2 2

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | True Value | Estimate (H2=0.2) | | |
| N=200 | N=400 | N=800 |
| Position (cM) | 32 | 32.13 (5.913) | 31.355 (4.567) | 31.254 (3.708) |
| *α* | 0.2 | 0.200 (0.033) | 0.2 00(0.022) | 0.200 (0.016) |
| *β* | 0.2 | 0.197 (0.034) | 0.201 (0.023) | 0.201 (0.017) |
| *γ* | 0.2 | 0.212 (0.043) | 0.208 (0.037) | 0.203 (0.028) |
| *μ1* | 1.4 | 1.456 (0.915) | 1.484 (0.548) | 1.418 (0.383) |
| *μ2* | 1.5 | 1.55 0(0.832) | 1.584 (0.631) | 1.503 (0.407) |
| *μ3* | 1.6 | 1.701 (0.835) | 1.720 (0.538) | 1.591 (0.385) |
| *μ4* | -0.5 | -0.648 (0.935) | -0.632 (0.632) | -0.576 (0.377) |
| *μ5* | 2.2 | 2.237 (0.466) | 2.220 (0.299) | 2.237 (0.223) |
| *μ6* | 2.4 | 2.440 (0.476) | 2.480 (0.316) | 2.43 0(0.225) |
| *μ7* | 0.4 | 0.311 (0.437) | 0.350 (0.320) | 0.395 (0.234) |
| *μ8* | 2.5 | 2.609 (0.457) | 2.515 (0.304) | 2.568 (0.221) |
| *μ9* | 0.5 | 0.469 (0.462) | 0.467 (0.307) | 0.508 (0.216) |
| *μ10* | 0.6 | 0.578 (0.476) | 0.603 (0.312) | 0.606 (0.218) |
| *σ2* | 4.4341 | 4.065 (0.496) | 4.232 (0.353) | 4.320(0.250) |
|  |  |  |  |  |
| *μ* | 1 | 1.015 (0.443) | 1.039 (0.272) | 0.984 (0.192) |
| *a1* | 0.4 | 0.441 (0.794) | 0.445 (0.518) | 0.434 (0.328) |
| *a2* | 0.5 | 0.535 (0.718) | 0.545 (0.559) | 0.519 (0.343) |
| *a3* | 0.6 | 0.686 (0.740) | 0.681 (0.451) | 0.607 (0.333) |
| *d12* | 0.3 | 0.245 (1.148) | 0.191 (0.703) | 0.300 (0.534) |
| *d13* | 0.4 | 0.298 (1.165) | 0.316 (0.705) | 0.404 (0.480) |
| *d14* | 0.5 | 0.517 (1.075) | 0.538 (0.755) | 0.538 (0.491) |
| *d23* | 0.4 | 0.372 (1.049) | 0.250 (0.813) | 0.457 (0.508) |
| *d24* | 0.5 | 0.581 (1.182) | 0.554 (0.729) | 0.566 (0.446) |
| *d34* | 0.5 | 0.539 (1.116) | 0.554 (0.789) | 0.576 (0.487) |

Table 2-1: Average parameter estimates and their standard errors of the QTL mapping model for a pseudo-test backcross population in a multivalent tetraploid based on 1000 repeat simulations. One QTL with the heritability of 0.2 is set.

Table 2-2: Average parameter estimates and their standard errors of the QTL mapping model for a pseudo-test backcross population in a multivalent tetraploid based on 1000 repeat simulations. One QTL with the heritability of 0.1 is set.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | True Value | Estimate (H2=0.1) | | |
| N=200 | N=400 | N=800 |
| Position (cM) | 32 | 32.162 (7.715) | 31.448 (6.115) | 31.968 (4.565) |
| *α* | 0.2 | 0.201 (0.031) | 0.200 (0.022) | 0.200 (0.016) |
| *β* | 0.2 | 0.200 (0.035) | 0.198 (0.024) | 0.201 (0.018) |
| *γ* | 0.2 | 0.213 (0.044) | 0.207 (0.039) | 0.205 (0.031) |
| *μ1* | 1.4 | 1.479 (1.253) | 1.413 (0.836) | 1.387 (0.545) |
| *μ2* | 1.5 | 1.486 (1.196) | 1.570 (0.788) | 1.577 (0.636) |
| *μ3* | 1.6 | 1.616 (1.262) | 1.697 (0.854) | 1.640 (0.529) |
| *μ4* | -0.5 | -0.570 (1.490) | -0.646 (1.038) | -0.599 (0.562) |
| *μ5* | 2.2 | 2.232 (0.653) | 2.262 (0.438) | 2.255 (0.297) |
| *μ6* | 2.4 | 2.490 (0.632) | 2.455 (0.453) | 2.458 (0.309) |
| *μ7* | 0.4 | 0.341 (0.683) | 0.384 (0.460) | 0.387 (0.297) |
| *μ8* | 2.5 | 2.620 (0.648) | 2.544 (0.458) | 2.588 (0.310) |
| *μ9* | 0.5 | 0.451 (0.630) | 0.479 (0.478) | 0.506 (0.320) |
| *μ10* | 0.6 | 0.589 (0.675) | 0.615 (0.453) | 0.603 (0.336) |
| *σ2* | 8.8682 | 8.212 (0.988) | 8.558 (0.653) | 8.695 (0.490) |
|  |  |  |  |  |
| *μ* | 1 | 1.003 (0.610) | 1.008 (0.400) | 1.001 (0.278) |
| *a1* | 0.4 | 0.477 (1.146) | 0.405 (0.732) | 0.386 (0.474) |
| *a2* | 0.5 | 0.483 (1.075) | 0.561 (0.720) | 0.576 (0.536) |
| *a3* | 0.6 | 0.613 (1.099) | 0.688 (0.757) | 0.639 (0.471) |
| *d12* | 0.3 | 0.269 (1.526) | 0.288 (1.063) | 0.292 (0.737) |
| *d13* | 0.4 | 0.398 (1.652) | 0.354 (1.157) | 0.432 (0.694) |
| *d14* | 0.5 | 0.434 (1.628) | 0.625 (1.110) | 0.600 (0.683) |
| *d23* | 0.4 | 0.521 (1.625) | 0.286 (1.094) | 0.372 (0.744) |
| *d24* | 0.5 | 0.538 (1.678) | 0.564 (1.204) | 0.529 (0.737) |
| *d34* | 0.5 | 0.546 (1.721) | 0.573 (1.106) | 0.564 (0.720) |

Table 2-3: Average parameter estimates and their standard errors of the QTL mapping model for a pseudo-test backcross population in a multivalent tetraploid based on 1000 repeat simulations. One QTL with the heritability of 0.05 is set.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | True Value | Estimate (H2=0.05) | | |
| N=200 | N=400 | N=800 |
| Position (cM) | 32 | 32.419 (9.023) | 32.181 (7.307) | 31.751 (6.149) |
| *α* | 0.2 | 0.198 (0.033) | 0.200 (0.024) | 0.2 00(0.016) |
| *β* | 0.2 | 0.195 (0.037) | 0.197 (0.025) | 0.200 (0.015) |
| *γ* | 0.2 | 0.208 (0.047) | 0.208 (0.043) | 0.203 (0.032) |
| *μ1* | 1.4 | 1.477 (1.939) | 1.539 (1.226) | 1.396 (0.854) |
| *μ2* | 1.5 | 1.453 (2.201) | 1.500 (1.250) | 1.484 (0.792) |
| *μ3* | 1.6 | 1.880 (1.922) | 1.596 (1.314) | 1.738 (0.829) |
| *μ4* | -0.5 | -0.544 (2.317) | -0.796 (1.387) | -0.606 (0.861) |
| *μ5* | 2.2 | 2.306 (0.910) | 2.256 (0.671) | 2.261 (0.467) |
| *μ6* | 2.4 | 2.327 (1.016) | 2.467 (0.692) | 2.456 (0.499) |
| *μ7* | 0.4 | 0.396 (0.955) | 0.406 (0.628) | 0.427 (0.461) |
| *μ8* | 2.5 | 2.538 (1.043) | 2.599 (0.664) | 2.584 (0.439) |
| *μ9* | 0.5 | 0.499 (0.887) | 0.467 (0.641) | 0.546 (0.457) |
| *μ10* | 0.6 | 0.659 (0.981) | 0.526 (0.647) | 0.623 (0.471) |
| *σ2* | 17.7364 | 16.394 (2.066) | 17.133 (1.358) | 17.441 (0.976) |
|  |  |  |  |  |
| *μ* | 1 | 1.066 (1.024) | 0.960 (0.627) | 1.003 (0.425) |
| *a1* | 0.4 | 0.410 (1.750) | 0.579 (1.085) | 0.393 (0.736) |
| *a2* | 0.5 | 0.386 (1.941) | 0.540 (1.154) | 0.481 (0.669) |
| *a3* | 0.6 | 0.814 (1.709) | 0.637 (1.088) | 0.735 (0.704) |
| *d12* | 0.3 | 0.443 (2.578) | 0.177 (1.598) | 0.383 (1.108) |
| *d13* | 0.4 | 0.037 (2.530) | 0.292 (1.637) | 0.325 (1.120) |
| *d14* | 0.5 | 0.530 (2.689) | 0.623 (1.628) | 0.640 (1.082) |
| *d23* | 0.4 | 0.271 (2.526) | 0.463 (1.655) | 0.365 (1.030) |
| *d24* | 0.5 | 0.657 (2.793) | 0.722 (1.603) | 0.671 (1.080) |
| *d34* | 0.5 | 0.390 (2.739) | 0.685 (1.763) | 0.495 (1.079) |

Table 2-4: The power of correctly ﬁnding the QTL at three partially informative markers.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample size** | **Heritability** | | |
| 0.05 | 0.1 | 0.2 |
| **200** | 0.15 | 0.48 | 0.87 |
| **400** | 0.48 | 0.79 | 0.93 |
| **800** | 0.81 | 0.94 | 0.94 |

The parameters of design are same to the partially informative markers simulation.

Table 2-5: The FPR of ﬁnding the QTL at three partially informative markers.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample size** | **Significance** | | |
| 0.005 | 0.01 | 0.05 |
| **200** | 0.01 | 0.01 | 0.06 |
| **400** | 0.00 | 0.00 | 0.06 |
| **800** | 0.00 | 0.01 | 0.05 |

The parameters of design are same to the partially informative markers simulation.