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

Linkage phase:

1 2 3 4

1 2 3 4

1 2 3 4

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | True Value | Estimate (H2=0.2) | | |
| N=200 | N=400 | N=800 |
| Position (cM) | 32 | 32.171 (6.322) | 31.956 (5.553) | 31.435 (3.431) |
| *α* | 0.2 | 0.203 (0.025) | 0.201 (0.020) | 0.198 (0.013) |
| *β* | 0.2 | 0.204 (0.027) | 0.200 (0.018) | 0.200 (0.013) |
| *γ* | 0.2 | 0.211 (0.036) | 0.207 (0.031) | 0.205 (0.026) |
| *μ1* | 1.4 | 1.441 (0.877) | 1.422 (0.555) | 1.434 (0.385) |
| *μ2* | 1.5 | 1.530 (0.752) | 1.528 (0.564) | 1.490 (0.390) |
| *μ3* | 1.6 | 1.672 (0.825) | 1.605 (0.550) | 1.599 (0.369) |
| *μ4* | -0.5 | -0.603 (0.795) | -0.494 (0.565) | -0.524 (0.375) |
| *μ5* | 2.2 | 2.310 (0.440) | 2.250 (0.326) | 2.239 (0.210) |
| *μ6* | 2.4 | 2.376 (0.442) | 2.442 (0.316) | 2.445 (0.209) |
| *μ7* | 0.4 | 0.418 (0.437) | 0.414 (0.312) | 0.405 (0.218) |
| *μ8* | 2.5 | 2.494 (0.442) | 2.525 (0.316) | 2.535 (0.217) |
| *μ9* | 0.5 | 0.468 (0.455) | 0.508 (0.323) | 0.508 (0.219) |
| *μ10* | 0.6 | 0.627 (0.489) | 0.597 (0.316) | 0.632 (0.208) |
| *σ2* | 4.4341 | 4.149 (0.490) | 4.317 (0.322) | 4.380 (0.250) |
|  |  |  |  |  |
| *μ* | 1 | 1.010 (0.420) | 1.015 (0.287) | 0.999 (0.193) |
| *a1* | 0.4 | 0.431 (0.721) | 0.407 (0.485) | 0.434 (0.326) |
| *a2* | 0.5 | 0.520 (0.682) | 0.513 (0.489) | 0.490 (0.345) |
| *a3* | 0.6 | 0.662 (0.724) | 0.590 (0.472) | 0.599 (0.318) |
| *d12* | 0.3 | 0.349 (1.017) | 0.315 (0.729) | 0.315 (0.480) |
| *d13* | 0.4 | 0.273 (1.068) | 0.430 (0.712) | 0.412 (0.479) |
| *d14* | 0.5 | 0.590 (1.045) | 0.502 (0.681) | 0.495 (0.527) |
| *d23* | 0.4 | 0.302 (0.989) | 0.408 (0.689) | 0.447 (0.536) |
| *d24* | 0.5 | 0.550 (0.956) | 0.490 (0.740) | 0.542 (0.459) |
| *d34* | 0.5 | 0.568 (1.144) | 0.501 (0.724) | 0.557 (0.472) |

Table 1-1: 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 1-2: 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 | 32.051 (8.308) | 31.364 (7.000) | 31.017 (5.102) |
| *α* | 0.2 | 0.200(0.029) | 0.203 (0.021) | 0.201 (0.015) |
| *β* | 0.2 | 0.198 (0.031) | 0.203 (0.020) | 0.201 (0.013) |
| *γ* | 0.2 | 0.208 (0.041) | 0.209 (0.034) | 0.205 (0.029) |
| *μ1* | 1.4 | 1.457 (1.305) | 1.440 (0.762) | 1.433 (0.524) |
| *μ2* | 1.5 | 1.637 (1.267) | 1.481 (0.808) | 1.498 (0.546) |
| *μ3* | 1.6 | 1.497 (1.180) | 1.742 (0.776) | 1.604 (0.595) |
| *μ4* | -0.5 | -0.427 (1.180) | -0.583 (0.843) | -0.481 (0.589) |
| *μ5* | 2.2 | 2.126 (0.689) | 2.223 (0.417) | 2.243 (0.317) |
| *μ6* | 2.4 | 2.418 (0.652) | 2.440 (0.426) | 2.436 (0.323) |
| *μ7* | 0.4 | 0.433 (0.684) | 0.374 (0.445) | 0.411 (0.305) |
| *μ8* | 2.5 | 2.585 (0.631) | 2.550 (0.445) | 2.563 (0.295) |
| *μ9* | 0.5 | 0.427 (0.620) | 0.457 (0.462) | 0.544 (0.298) |
| *μ10* | 0.6 | 0.623 (0.613) | 0.626 (0.453) | 0.623 (0.333) |
| *σ2* | 8.8682 | 8.228 (0.889) | 8.617 (0.637) | 8.776 (0.487) |
|  |  |  |  |  |
| *μ* | 1 | 1.041 (0.626) | 1.020 (0.358) | 1.013 (0.287) |
| *a1* | 0.4 | 0.416 (1.111) | 0.420 (0.685) | 0.42 0(0.473) |
| *a2* | 0.5 | 0.596 (1.118) | 0.461 (0.753) | 0.484 (0.477) |
| *a3* | 0.6 | 0.456 (0.976) | 0.722 (0.674) | 0.591 (0.504) |
| *d12* | 0.3 | 0.072 (1.613) | 0.322 (1.009) | 0.326 (0.676) |
| *d13* | 0.4 | 0.505 (1.632) | 0.278 (1.032) | 0.413 (0.740) |
| *d14* | 0.5 | 0.444 (1.576) | 0.537 (1.023) | 0.472 (0.739) |
| *d23* | 0.4 | 0.491 (1.428) | 0.347 (1.035) | 0.475 (0.739) |
| *d24* | 0.5 | 0.258 (1.475) | 0.579 (1.090) | 0.540 (0.727) |
| *d34* | 0.5 | 0.594 (1.503) | 0.487 (1.099) | 0.514 (0.773) |

Table 1-3: 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 | 32.581 (10.007) | 31.176 (9.032) | 31.952 (7.237) |
| *α* | 0.2 | 0.198 (0.031) | 0.199 (0.017) | 0.201 (0.014) |
| *β* | 0.2 | 0.197 (0.031) | 0.198 (0.018) | 0.201 (0.014) |
| *γ* | 0.2 | 0.210(0.044) | 0.203 (0.036) | 0.207 (0.029) |
| *μ1* | 1.4 | 1.487 (1.823) | 1.348 (1.204) | 1.513 (0.724) |
| *μ2* | 1.5 | 1.691 (1.965) | 1.628 (1.190) | 1.464 (0.721) |
| *μ3* | 1.6 | 1.897 (2.105) | 1.610 (1.168) | 1.622 (0.748) |
| *μ4* | -0.5 | -0.452 (1.912) | -0.529 (1.236) | -0.543 (0.861) |
| *μ5* | 2.2 | 2.313 (0.974) | 2.242 (0.675) | 2.248 (0.416) |
| *μ6* | 2.4 | 2.250 (0.977) | 2.423 (0.666) | 2.425 (0.427) |
| *μ7* | 0.4 | 0.390 (1.016) | 0.425 (0.658) | 0.419 (0.452) |
| *μ8* | 2.5 | 2.570 (0.879) | 2.551 (0.635) | 2.597 (0.440) |
| *μ9* | 0.5 | 0.446 (0.990) | 0.507 (0.625) | 0.530 (0.446) |
| *μ10* | 0.6 | 0.589 (0.926) | 0.594 (0.633) | 0.684 (0.464) |
| *σ2* | 17.7364 | 16.447 (1.811) | 17.208 (1.332) | 17.571 (0.970) |
|  |  |  |  |  |
| *μ* | 1 | 1.156 (1.005) | 1.014 (0.569) | 1.014 (0.368) |
| *a1* | 0.4 | 0.331 (1.549) | 0.334 (1.060) | 0.499 (0.669) |
| *a2* | 0.5 | 0.535 (1.621) | 0.614 (1.017) | 0.450 (0.603) |
| *a3* | 0.6 | 0.741 (1.709) | 0.596 (1.044) | 0.608 (0.669) |
| *d12* | 0.3 | 0.291 (2.381) | 0.28 0(1.597) | 0.285 (0.959) |
| *d13* | 0.4 | 0.021 (2.681) | 0.479 (1.428) | 0.304 (0.970) |
| *d14* | 0.5 | 0.511 (2.355) | 0.621 (1.571) | 0.463 (0.991) |
| *d23* | 0.4 | 0.137 (2.683) | 0.327 (1.587) | 0.525 (0.990) |
| *d24* | 0.5 | 0.363 (2.520) | 0.422 (1.534) | 0.622 (1.060) |
| *d34* | 0.5 | 0.299 (2.147) | 0.527 (1.544) | 0.619 (1.071) |

Table 1-4: The power of correctly ﬁnding the QTL at three fully informative markers.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample size** | **Heritability** | | |
| 0.05 | 0.1 | 0.2 |
| **200** | 0.13 | 0.46 | 0.82 |
| **400** | 0.51 | 0.78 | 0.82 |
| **800** | 0.85 | 0.91 | 0.96 |

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

Table 1-5: The FPR of ﬁnding the QTL at three fully informative markers.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample size** | **Significance** | | |
| 0.005 | 0.01 | 0.05 |
| **200** | 0.01 | 0.01 | 0.05 |
| **400** | 0.00 | 0.01 | 0.04 |
| **800** | 0.00 | 0.00 | 0.04 |

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