**AutoQTL: an autoML approach to QTL analysis and epistasis detection**

Supplementary File S2

XOR Penetrance Function

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **SNP 2** | | | | **Marginal penetrance** |
|  | **Genotype** | **BB (0)** | **Bb (1)** | **bb (2)** |
| **SNP 1** | **AA (0)** | 0 | 1 | 0 | 0.5 |
| **Aa (1)** | 1 | 0 | 1 | 0.5 |
| **aa (2)** | 0 | 1 | 0 | 0.5 |
|  | **Marginal Penetrance** | 0.5 | 0.5 | 0.5 | K = 0.5 |

The table above describes the XOR penetrance function. XOR is both a strict and pure penetrance function. Strict in that all the loci (in this case, 2) are predictive of the phenotype and pure in that the interaction does not display main effects [1]. XOR is a fully penetrant and purely epistatic model in which each two-locus genotype results in a marginal penetrance of exactly 0.5.

**References**

1. Urbanowicz RJ, Kiralis J, Sinnott-Armstrong NA, Heberling T, Fisher JM, Moore JH. GAMETES: a fast, direct algorithm for generating pure, strict, epistatic models with random architectures. BioData Min. 2012;5:16.