林木单地点半同胞子代测定

遗传模型分析软件 HalfsibSS 1.0 使用说明

林木单地点半同胞子代测定统计分析模型为

 $y_{ijk} = \mu + B_i + F_j + BF_{ij} + e_{ijk}$

其中, y_{ijk} 为第i个区组第j个家系第k个单株的数量性状值; μ 为总体均值; B_i 为第i个区组的固定效应, i = 1, 2, ..., b; F_j 为第j个家系的随机效应, j = 1, 2, ..., f, $E(F_j) = 0$, $Var(F_j) = \sigma_F^2$; BF_{ij} 为第i个区组第j个家系的随机效应, $E(BF_{ij}) = 0$, $Var(BF_{ij}) = \sigma_{BF}^2$; e_{ijk} 为第i个区组第j个家系第k个单株的随机误差, $k = 1, 2, ..., n_{ij}, E(e_{ijk}) = 0$, $Var(e_{ijk}) = \sigma_e^2$; 同时假定所有因子间的协方差为 0。

对于无论是平衡数据还是非平衡数据,HalfsibSS 可以对该模型的多个性状数据进行分析计算,可以计算每个性状的方差分量、方差分量的标准误、方差分量的假设检验统计量、 家系遗传力和单株遗传力及其标准误、性状间的遗传相关系数及其标准误。

1 数据格式

如下表所示,HalfsibSS的输入数据存放在文本文件里,第一行中的三个数字分别表示 区组数、区组中的家系数和数量性状的个数。第一行之后的第一列和第二列表示单株所在的 区组和家系记号,第三列、第四列等表示单株的第一个性状值、第二个性状值,等等。

bl	ock	5 fam	ily 20	trait	2
1	1	7.877	21.17		
1	1	10.13	19.65		
1	2	9.044	21.16		
1	2	4.947	17.27		
1	2	9.22	17.47		
2	1	12.97	21.76		
2	1	10.39	22.81		
2	2	8.658	20.54		
2	2	8.829	23.74		
2	2	9.571	19.82		

表 1 HalfsibSS 的输入数据格式

2 数据分析

运行软件HalfsibSS 1.0,选择菜单"File",选择"Open"选项。打开文本数据文件 (如本软件自带的模拟数据文件"simudata.txt"),按"OK"按钮,如果数据文件格式 正确的话,就打开了如图1所示的数据文件。

选择菜单"Analysis",点击"Computing"选项,一会儿屏幕上出现如图 2 的分析结 果。其中 Sigma_F、Sigma_BF和 Sigma_E 分别表示家系、区组×家系和环境的方差分量, Hf 和 Hi 表示家系遗传力和单株遗传力。选择菜单"File",点击"Save As"选项,可将计 算结果存为文本文件。

nalysis <u>H</u> elp				
Block 5	Family	20 Trait	2	
в	F	Τ1	T2	
1	1	7.8770	21.1700	
1	1	10.1300	19.6500	
1	1	8.4240	20.3500	
1	1	7.0340	20.1100	
1	1	6.5090	21.8700	
1	2	8.0800	19.3600	
1	2	9.0440	21.1600	
1	2	4.9470	17.2700	
1	2	9.2200	17.4700	
1	2	9.4450	16.6200	
1	3	6.3500	15.8900	
1	3	8.2530	18.8000	
1	3	5.7360	19.7600	
1	3	5.9110	19.7000	
1	3	10.2200	21.1400	
1	3	7.9630	20.2800	

图 1 HalfsibSS 打开数据后的窗口

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Sigma_E 1.9123 0.1216	Sigma BF	0.4994	0.1350	2.5480	0.0000	
	Sigma_E	1.9123	0.1216			
11+ D 5075 D 176D	uf	0 5075	0 1460			
ni 0.373 0.1400	ni Hi	0.3973	0.1400			
UT 0.2018 0.1201	пт	0.30/9	0.1901			
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图 2 HalfsibSS 数据分析结果窗口