

How to calculate deviation from Mendelian inheritance expectations (transmission ratio distortion) by using haplotypes. It is shown here how to do it starting from genotypes, making phased data, create haplotypes and then calculate all possible matings.

Assume we have this pedigree for 4 animals:

Animal	Sire	Dam
1	0	0
2	1	0
3	1	2
4	3	2

And their genotypes for 5 SNPs in format 012 are:

	SNP1	SNP2	SNP3	SNP4	SNP5
Animal 1	1	0	2	2	1
Animal 2	2	1	1	0	2
Animal 3	1	0	1	1	2
Animal 4	1	0	2	1	2

This genotyped can be phased using any software such that 0 is AA, 1 is AB or BA and 2 is BB. We can give these phased genotypes different values:

0 (AA): 0
 1 (AB): 3
 1 (BA): 4
 2 (BB): 2

The data above will be:

	SNP1	SNP2	SNP3	SNP4	SNP5
Animal 1	3	0	2	2	4
Animal 2	2	4	4	0	2
Animal 3	4	0	3	3	2
Animal 4	3	0	2	3	2

To create haplotypes, we need to consider at 2 SNPs in each window. In this example will use a 3-SNP window:

First window (SNPs 1 to 3):

	SNP1	SNP2	SNP3
Animal 1	3	0	2
Animal 2	2	4	4
Animal 3	4	0	3
Animal 4	3	0	2

So, now we need to create first and second haplotype for each animal. To distinguish the differences between these genotypes, we can assign each genotype to a different numeric value:

0	1 1
2	2 2
3	1 2
4	2 1

Animal 1	Haplotype 1	1	1	2
	Haplotype 2	2	1	2
Animal 2	Haplotype 1	2	2	2
	Haplotype 2	2	1	1
Animal 3	Haplotype 1	2	1	1
	Haplotype 2	1	1	2
Animal 4	Haplotype 1	1	1	2
	Haplotype 2	2	1	2

Now, we need to get the unique haplotypes among all these obtained haplotypes. So, we need to remove all duplicated haplotypes (Highlighted are unique):

112

212

222

211

211

112

112

212

Now, these haplotypes will be the genotypes. For example, haplotype 112: animals that carry two copies of 112 will be AA, one copy will be AB and BB if do not carry this haplotype.

The following are all possible matings:

Parent 1		Parent 2	Offspring
AA	x	AA	AA
AA	x	AB	AA
AA	x	AB	AB
AA	x	BB	AB
AB	x	AA	AA
AB	x	AA	AB
AB	x	AB	AA
AB	x	AB	AB
AB	x	AB	BB
AB	x	BB	AB
AB	x	BB	BB
BB	x	AA	AB
BB	x	AB	AB
BB	x	AB	BB
BB	x	BB	BB

Since we have four unique haplotypes, then we need to use them to obtain all possible matings. Animals 1 and 2 (from the pedigree) had at least one parent missing, so they would not be involved in this calculation. We start from animal 3. The parents for animal 3 are 1 and 2:

Haplotype	Sire(1)		Dam(2)	Offspring
112	AB	X	BB	AB
212	AB	X	BB	BB
222	BB	X	AB	BB
211	BB	X	AB	BB

The same could be done for animal 4 (its parents are 3 and 2):

Haplotype	Sire (3)		Dam(2)	Offspring
112	AB	X	BB	AB
212	BB	X	BB	AB
222	BB	X	AB	BB
211	AB	X	AB	BB

The same steps can be followed for other haplotypes windows. The summary for the haplotypes in the first window is shown in the next table:

[illegible]