Suppose for a trait of interest, we have strains and the mean treat values for strains are , respectively.

First, we will consider the best possible p value for any two-haplotype block. By definition, such a two-haplotype block will divide the strains into 2 groups. We can always reorder the treat values such that:

Therefore, there are possible candidate groupings that have the potential to generate the best p values.

1. vs
2. vs

…

n-1): vs

Therefore, we will obtain the corresponding p values for each of these groupings and find the minimum one, which is the best possible p values for two-haplotype blocks.

NOTE: since we ultimately use an F-test to evaluate the association, we should always use equal-variance assumption if t-test is used to evaluate the p values for these groupings. Alternatively, we can just use F-test which naturally impose the equal-variance assumption.

Similarly, for three-haplotype blocks, there are possible candidate groupings for the best p value. We just evaluate them one-by-one to find the best p values.