

## **XHSD**

This package contains the MATLAB implementation of the proposed xor-haplotyping algorithm.

Please see the script **textXHSD.m** to test XHSD algorithm on CFTR data with the desired parameters.

The main program is **sparsehaplotypeSPL.m**, which demands as input the genotype data. The genotypes should be located in the columns of the input matrix.

### **INSTRUCTIONS for `saprsehaplotypeSPL.m`:**

**Input Format:** L x N matrix corresponding to N individuals with L SNPs are typed as follows.

0: homozygous-common 00

2: homozygous-mutant 11

1: heterozygous 01/10

4: homozygous-hidden (XOR-site) 00/11

6: missing SNP

#### **Parameters:**

W= maximum block size in PL method

interest= which individuals to infer haplotypes. Use [1, 2, ..., N] as default.

Lmiss= L x N binary matrix where 1 means a missing site.

flagBlock= 1:PL method (default), 2:fixed-length partitioning, 0:no-partition

**Output Format:** L x N x 2 matrix.

Haplotypes are located in the corresponding columns in dimension 1 (L,N,1) and dimension 2 (L,N,2).