

## Appendix

Below is a pseudo-code for the score-limited DP algorithm.

**Input** : Genotype likelihood vectors for n individuals,  $L_1, \dots, L_n$

**Output**: Site likelihood vector, h

```
epsilon=10(-9);
h=array(0, length=2n+1);
h[0]=L1[0]; h[1]=L1[1]; h[2]=L1[2];
left=0; right=2;

for j in 2 to n {
  nChr=2*j;
  L0=Lj[0]; L1=Lj[1]; L2=Lj[2];
  if(L0 >=L1 and L0 >= L2)
    bestGuessGT=0;
  else if(L1 > L2)
    bestGuessGT=1;
  else
    bestGuessGT=2;

  /* Set a left boundary and update it accordingly */
  left= left+ bestGuessGT;
  checkVal=(nChr-left)*(nChr-left-1)*L0*h[left]
    +2*left*(nChr-left)*L1*h[left-1]
    +left*(left-1)*L2*h[left-2];
  while(checkVal > epsilon) {
    left=left-1;
    checkVal=(nChr-left)*(nChr-left-1)*L0*h[left]
      +2*left*(nChr-left)*L1*h[left-1]
      +left*(left-1)*L2*h[left-2];
  }
  /* Set a right boundary and update it accordingly */
  right = right+ bestGuessGT;
  checkVal=(nChr-right)*(nChr-right-1)*Lj[0]*h[right]
    +2*right*(nChr-right)*Lj[1]*h[right-1]
    +right*(right-1)*Lj[2]*h[right-2];
  while(checkVal > epsilon) {
    right=right+1;
    checkVal=(nChr-right)*(nChr-right-1)*Lj[0]*h[right]
      +2*right*(nChr-right)*Lj[1]*h[right-1]
      +right*(right-1)*Lj[2]*h[right-2];
  }
  /* Update the site likelihood vector */
  for x in right to left {
    h[x]=(nChr-x)*(nChr-x-1)*Lj[0]*h[x]
      +2*x*(nChr-x)*Lj[1]*h[x-1]
      +x*(x-1)*Lj[2]*h[x-2];
  }
  /* Normalization */
  mymax=max(h);
  for k in left to right
    h[x] = h[x]/mymax;
}
```