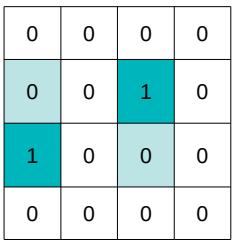
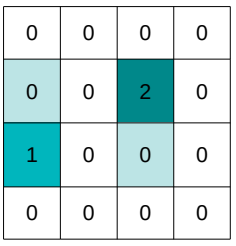
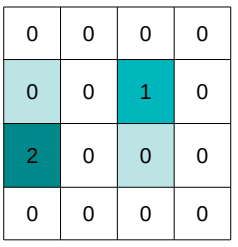
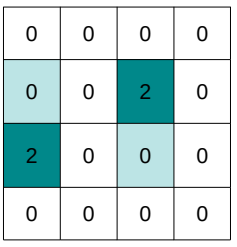
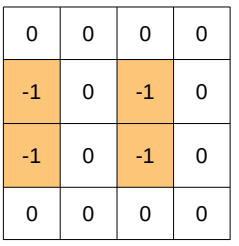
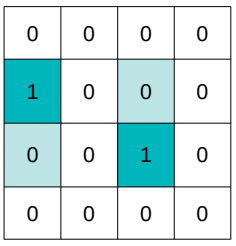
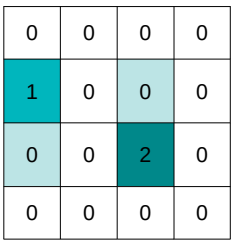
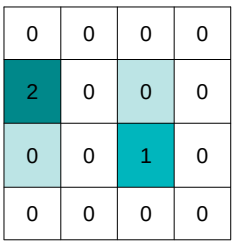
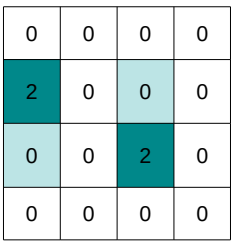
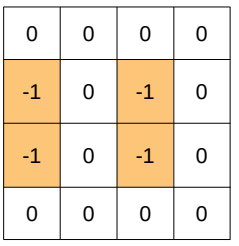
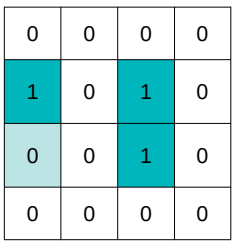
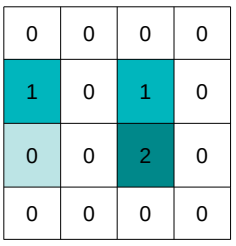
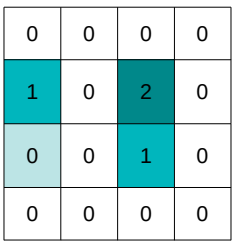
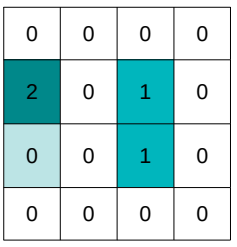
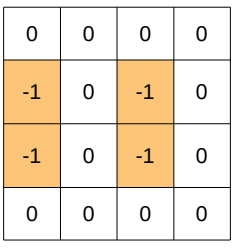
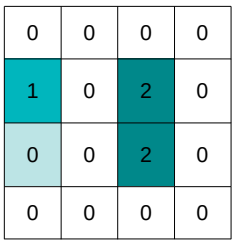
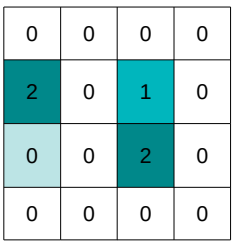
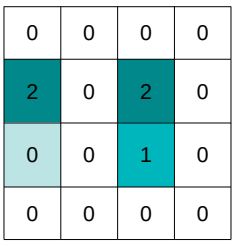
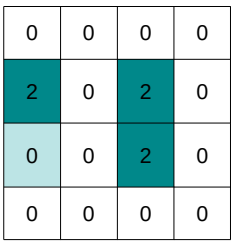
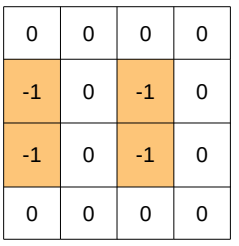
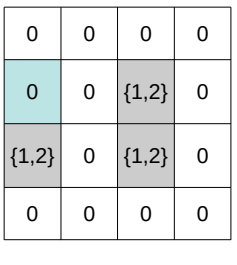
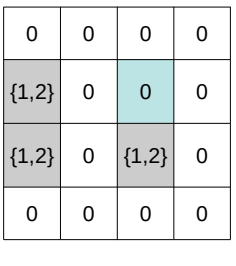
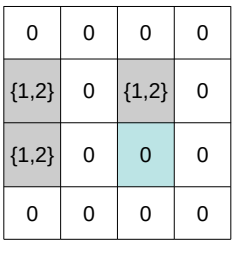
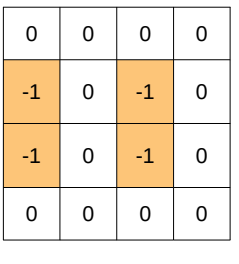
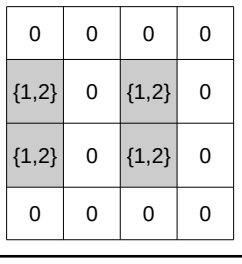
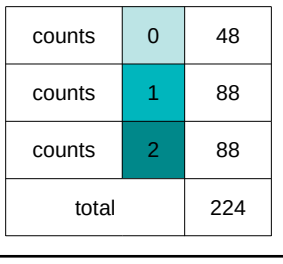
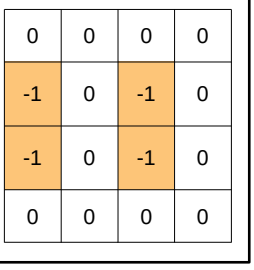
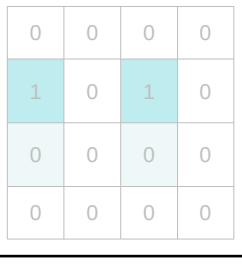
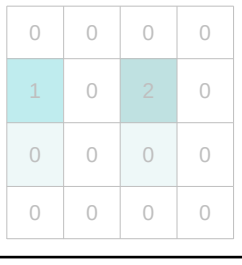
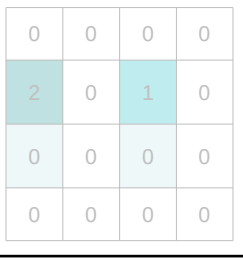
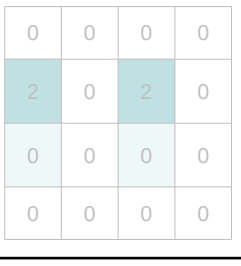
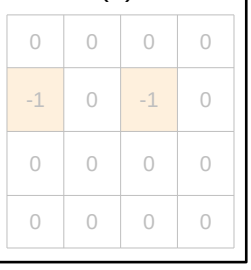
(I)

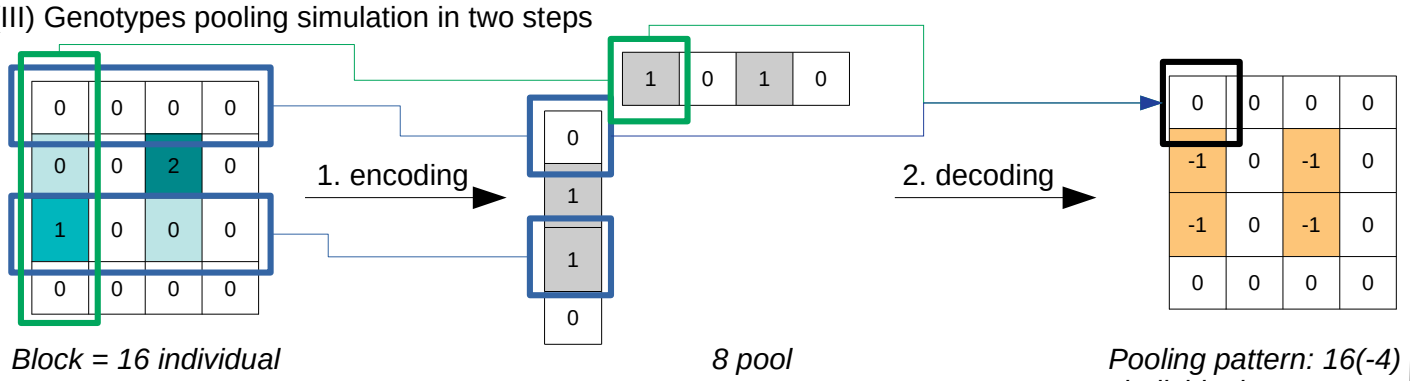
	(a)	(b)	(c)	(d)	(e)
(1)					
(2)					
(3)					
(4)					
(5) Permutations, repeat lines (4) and (5)					
(6)		Most likely marginal counts for the pattern ((2,2,0), (2,2,0))			

counts	0	48
counts	1	88
counts	2	88
total		224

(II)

(a)	(b)	(c)	(d)	(e)
				

(III) Genotypes pooling simulation in two steps



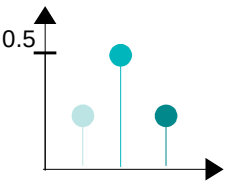
Block = 16 individual genotypes

8 pool genotypes

Pooling pattern: 16(-4) individual genotypes

(I) Initialization

Prior genotypes distribution **(0.25, 0.5, 0.25)**



(II) E step

(1)

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	2	0	0	0	1	0	0	0	2	0
1	0	0	0	1	0	0	0	2	0	0	0	2	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x 0.01932				x 0.00966				x 0.00966				x 0.00483			

(2)

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	2	0	0	0	2	0	0	0
0	0	1	0	0	0	2	0	0	0	1	0	0	0	2	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x 0.01932				x 0.00966				x 0.00966				x 0.00483			

(3)

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	1	0	1	0	1	0	2	0	2	0	1	0
0	0	1	0	0	0	2	0	0	0	1	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x 0.03864				x 0.01932				x 0.01932				x 0.01932			

(4)

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	2	0	2	0	1	0	2	0	2	0	2	0	2	0
0	0	2	0	0	0	2	0	0	0	1	0	0	0	2	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x 0.00966				x 0.00966				x 0.00966				x 0.00483			

(5)

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	{1,2}	0	{1,2}	0	0	0	{1,2}	0	{1,2}	0	{1,2}	0	{1,2}	0
{1,2}	0	{1,2}	0	{1,2}	0	{1,2}	0	{1,2}	0	0	0	{1,2}	0	{1,2}	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x …				x …				x …				x …			

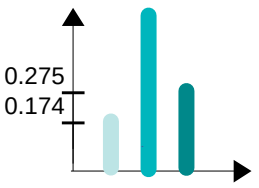
(6) $\sum$ (*proportion x*

0	0	0	0
...	0	...	0
...	0	...	0
0	0	0	0

) =

0	0	0	0
-1	0	-1	0
-1	0	-1	0
0	0	0	0

Expected-Maximized-Rescaled frequencies from conditional proportions



(III) Maximization

$\sum$ =

counts	0	0.69565
counts	1	2.20290
counts	2	1.10145
total		4

Most likely counts for the pattern ((2,2,0), (2,2,0)) assuming the prior is the true distribution

(IV) Rescaling (het. degeneracy)

alleles	GT	weights
00	0	1
01	1	2
10	1	
11	2	1

(a) Prior updating

$\sum$ / prior x (1,2,1)
= **(0.174, 0.551, 0.275)**
after 1 iteration

(b) Termination – Posterior computation

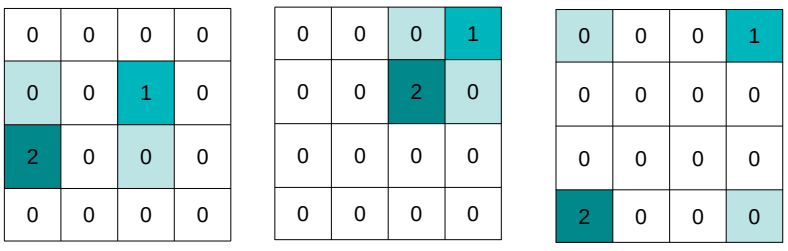
$\sum$ x (1,0.5,1)
= (0.240, 0.380, 0.380) after 1 iteration

After m iterations

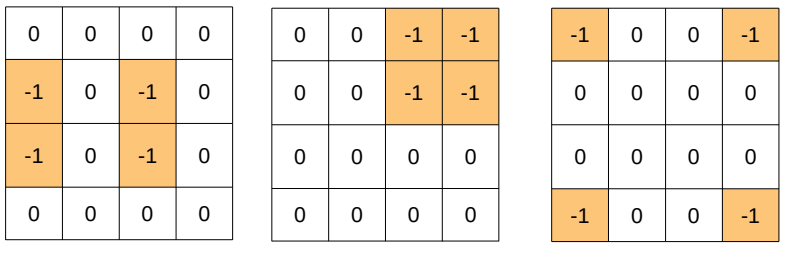
counts	0	**0.791**
counts	1	**1.604**
counts	2	**1.604**
total		4

(a)

λ = (0, 1, 2, 0)

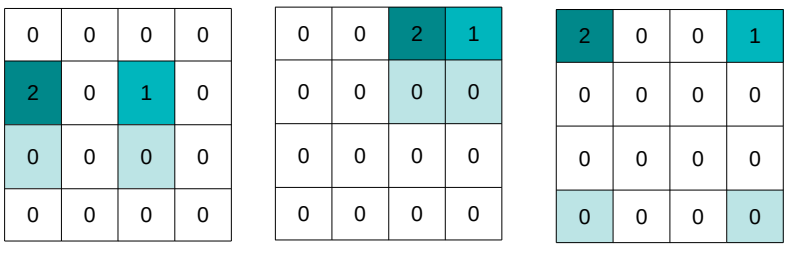


Ψ = ((2, 2, 0), (2, 2, 0))

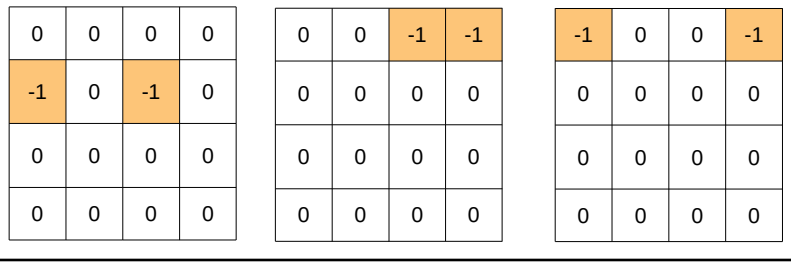


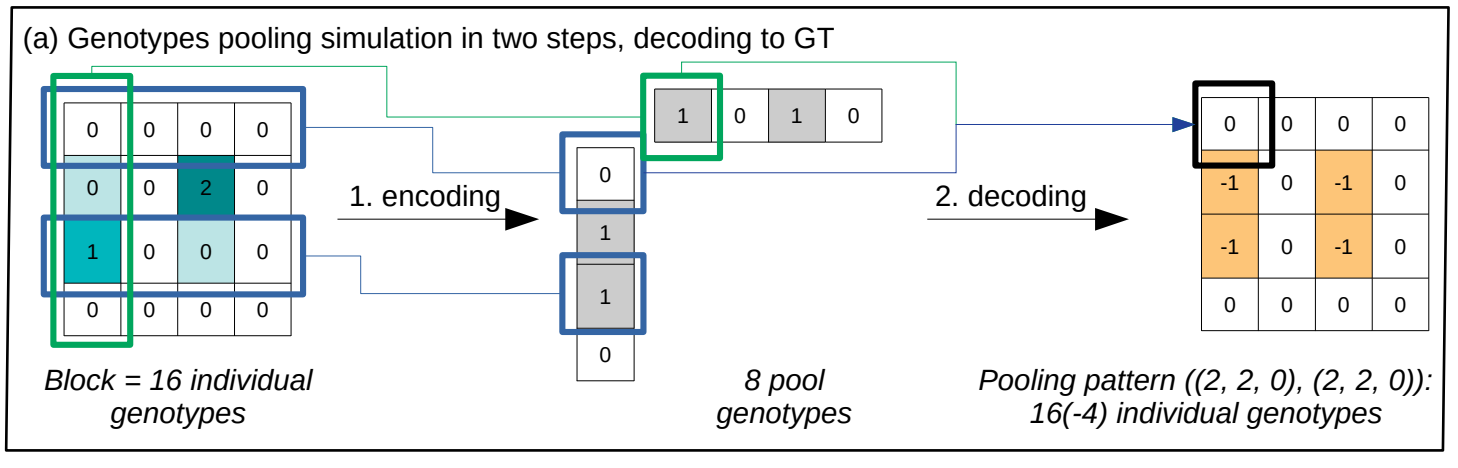
(b)

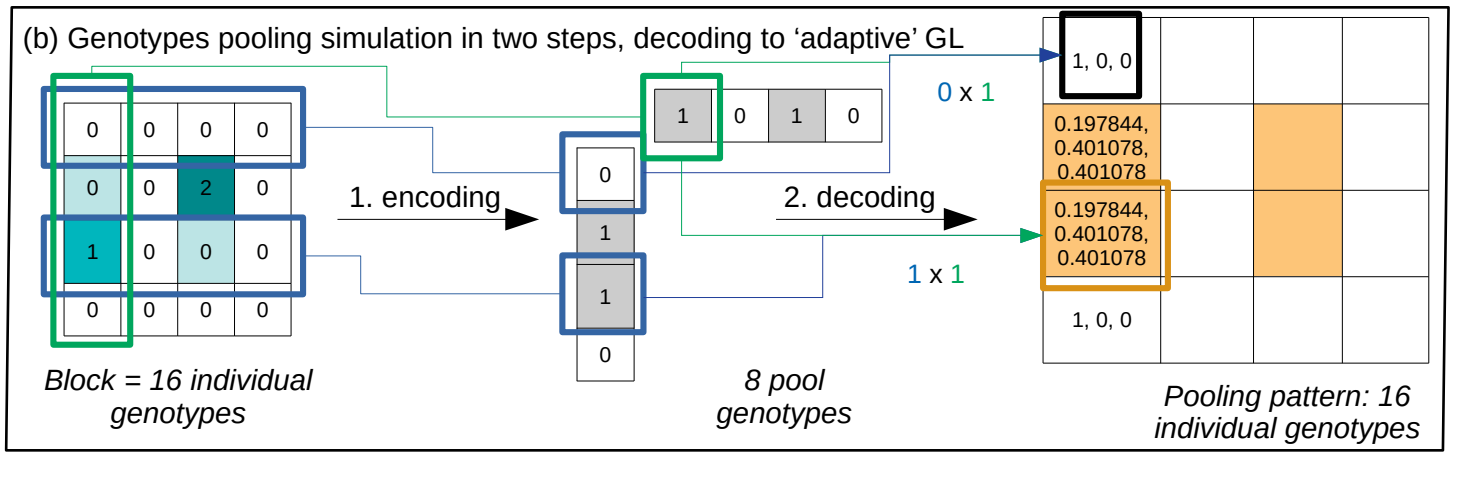
λ = (2, 1,0, 0)



Ψ = ((3, 1, 0), (2, 2, 0))




(a) Genotypes pooling simulation in two steps, decoding to GT
1. encoding
2. decoding
Block = 16 individual genotypes
8 pool genotypes
Pooling pattern ((2, 2, 0), (2, 2, 0)): 16(-4) individual genotypes


(b) Genotypes pooling simulation in two steps, decoding to 'adaptive' GL
1. encoding
2. decoding
0 x 1
1 x 1
1, 0, 0
0.197844, 0.401078, 0.401078
0.197844, 0.401078, 0.401078
1, 0, 0
Block = 16 individual genotypes
8 pool genotypes
Pooling pattern: 16 individual genotypes