

## Transitions probability matrix for the aberration state HMM

Consistent with the model in hapLOH [1], all aberrant states are equal *a priori*, while different from the non-aberrant (normal) state. This is in contrast to GPHMM [2], which treats the normal and aberrant states equally. We use 3 parameters to describe the transition probability matrix (TPM). Let  $p_0$  be the probability that next state is any aberrant state given that the current state is the normal,  $p_1$  be the probability that next state is a different state (normal or another aberrant state) given that the current state is an aberrant state, and  $p_2$  be the probability that next state is another aberrant state, given that the current is aberrant state and a transition occurs. The probabilities  $(p_0, p_1, p_2)$  then induce the following TPM:

$$\begin{array}{c}
 \text{Normal} \\
 \text{Aberr}_1 \\
 \vdots \\
 \text{Aberr}_N
 \end{array}
 \begin{array}{cccc}
 \text{Normal} & \text{Aberr}_1 & \dots & \text{Aberr}_N \\
 \left( \begin{array}{cccc}
 1 - p_0 & \frac{p_0}{N} & \dots & \frac{p_0}{N} \\
 p_1(1 - p_2) & 1 - p_1 & \dots & \frac{p_1 p_2}{(N - 1)} \\
 \vdots & \vdots & \ddots & \vdots \\
 p_1(1 - p_2) & \frac{p_1 p_2}{(N - 1)} & \dots & 1 - p_1
 \end{array} \right),
 \end{array}$$

where  $N$  (up to 20 in our implementation; see main text) is the number of aberrant states. The three parameters  $(p_0, p_1, p_2)$  can be optionally estimated by keeping track of the probabilities  $p^{(i)}(l_m, l_{m+1}|g, b, r)$  at the  $i^{\text{th}}$  iteration in the usual way. We also use  $(p_0, p_1, p_2)$  to compute the stationary distributions for the starts of HMMs.

## References

- [1] Selina Vattathil and Paul Scheet. Haplotype-based profiling of subtle allelic imbalance with snp arrays. *Genome Research*, 23(1):152–158, 2013.
- [2] A. Li, Z. Liu, K. Lezon-Geyda, S. Sarkar, D. Lannin, V. Schulz, I. Krop, E. Winer, L. Harris, and D. Tuck. GPHMM: an integrated hidden markov model for identification of copy number alteration and loss of heterozygosity in complex tumor samples using whole genome snp arrays. *Nucleic Acids Research*, 39(12):4928–4941, 2011.