Examples

These examples, which featured in the preprint medRxiv 2022.11.23.22282669, are used as tests in the Pv3Rs R package and thus described here as developer documentation. The only significant difference between this write-up and that of the preprint is reference to allelic assignments that are equivalent up to within-episode genotype permutations. The notation is taken from the preprint. In addition, Roman numerals are used to enumerate members of discrete spaces ($a \in \mathcal{A}, p \in \mathcal{P}, g \in \mathcal{G}$) over which we sum. Arabic numerals are used to index rows and columns etc.

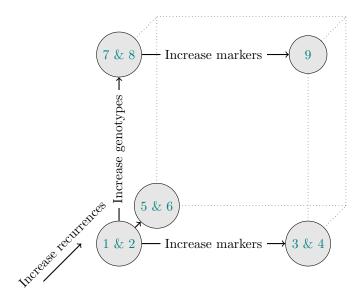


Figure 1: Visual summary of the examples. We start in the simplest setting (examples 0.1 & 0.2). We then add complexity in three separate directions: by increasing the number of markers (examples 0.3 & 0.4), by increasing the number of recurrences (example 0.5 & 0.6), and by increasing the number of genotypes per infection (examples 0.7 & 0.8), where the latter focuses on the computation of the probability of phased alleles given an IBD partition, to better illustrate how cells are multiplied over. Our final example addresses the need to phase, which can occur when there are multiple genotypes per infection and multiple markers typed (example 0.9).

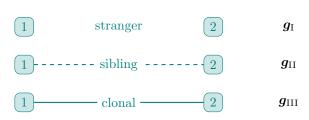
0.1 Single heterologous marker

Observed and phased alleles Suppose a single allele is observed at a single marker, indexed by j, genotyped in an enrolment infection, t=0, and single recurrent infection, t=1. Since we detect only one allele per infection we assume there is only one genotype per infection, indexed by i, and one way to phase the observed alleles, e.g.,

$$egin{aligned} oldsymbol{y} &= egin{pmatrix} \{A\} \\ \{T\} \end{pmatrix} egin{aligned} t &= 0 \\ t &= 1 \end{aligned} \end{array} , \qquad oldsymbol{a} &= egin{pmatrix} A \\ T \end{pmatrix} egin{pmatrix} i &= 1 \\ i &= 2. \end{aligned}$$

Relationship graphs To compute the posterior probability of the single recurrent state, s, being either a relapse, L, reinfection, I, or recrudescence C, we sum over three graphs ($g_{\rm I}$, $g_{\rm III}$) of relationships between parasite genotypes 1 and 2,

Incident infection, t = 0 Recurrence, t = 1



IBD partitions For each relationship graph, we sum over two IBD partitions of genotypes 1 and 2 at the single marker, $p_{\rm I} = \{\{1\}, \{2\}\}$ and $p_{\rm II} = \{\{1, 2\}\}$ that correspond to the following two IBD graphs.

Incident infection, t = 0 Recurrence, t = 1

Likelihood As there is one way to phase the observed alleles and m = 1, $\mathbb{P}(y|s) = \mathbb{P}(a|s) = \mathbb{P}(a, |s)$ where

$$\underbrace{\begin{array}{c} L & I & C \\ a & (^{1}\!/_{2}f(A)f(T) & f(A)f(T) & 0) \\ & & & \\$$

and

$$\mathbb{P}(\boldsymbol{a}_{\cdot 1}|\boldsymbol{p}_{\mathrm{I}}) = \mathbb{P}(\{A\}|\{1\}) \times \mathbb{P}(\{T\}|\{2\}) = f(A)f(T).$$

 $\mathbb{P}(\boldsymbol{a}_{\cdot 1}|\boldsymbol{p}_{\mathrm{II}}) = \mathbb{P}(\{A,T\}|\{1,2\}) = 0 \text{ because } |\{A,T\}| \neq 1.$

Posterior For a uniform prior on s, $\mathbb{P}(y) = 1/2 f(A) f(T)$, such that $\mathbb{P}(s = L|\boldsymbol{y}) = 1/3$, $\mathbb{P}(s = I|\boldsymbol{y}) = 2/3$ and $\mathbb{P}(s = C|\boldsymbol{y}) = 0$.

0.2 Single homologous marker

For ${\boldsymbol y}=(\{A\},\{A\})^T$ and a uniform prior on s, $\mathbb{P}(y)={}^1/{}_2f(A)^2+{}^1/{}_2f(A)$, such that $\mathbb{P}(s=L|{\boldsymbol y})={}^1/{}_3$, $\mathbb{P}(s=I|{\boldsymbol y})={}^2/{}_3f(A)(f(A)+1)^{-1}$ and $\mathbb{P}(s=C|{\boldsymbol y})={}^2/{}_3(f(A)+1)^{-1}$ following

0.3 Multiple partially heterologous markers

Observed and phased alleles In the simplest example a single allele is observed per marker genotyped in an incident and single recurrent infection. Since we detect only one allele per infection we assume there is only one genotype per infection and thus there is only one to phase the observed alleles, e.g.,

Relationship graphs and IBD partitions We sum over the same three graphs of relationships between genotypes and the same two IBD partitions as in example 0.1.

Likelihood The likelihood computation is similar to examples 0.1 & 0.2, but because there are multiple markers, which are conditionally independent given the relationship graphs, a product over markers is taken before summing over relationship graphs. In addition, alleles are indexed by j, since a given allele at one locus might have a different frequency at another locus.

Posterior For a uniform prior on s,

$$\mathbb{P}(\boldsymbol{y}) = \frac{1}{3}f(A_1)f(T_1)f(T_2)f(G_3)\left(\frac{1}{3}(f(T_2)f(G_3) + \frac{1}{8}(f(T_2) + 1)(f(G_3) + 1)) + f(T_2)f(G_3)\right),$$

such that

$$\mathbb{P}(s=L|\boldsymbol{y}) = \frac{\frac{1}{3}(f(T_2)f(G_3) + \frac{1}{8}(f(T_2) + 1)(f(G_3) + 1))}{\frac{1}{3}(f(T_2)f(G_3) + \frac{1}{8}(f(T_2) + 1)(f(G_3) + 1)) + f(T_2)f(G_3)},$$

$$\mathbb{P}(s=I|\boldsymbol{y}) = \frac{f(T_2)f(G_3)}{\frac{1}{3}(f(T_2)f(G_3) + \frac{1}{8}(f(T_2) + 1)(f(G_3) + 1)) + f(T_2)f(G_3)},$$

$$\mathbb{P}(s=C|\boldsymbol{y}) = 0.$$

0.4 Multiple exclusively homologous markers

When markers are homologous over infections, $\mathbb{P}(s=C|\boldsymbol{y})>0$. For example, if

$$a = \begin{pmatrix} j=1 & j=2 & j=3 \\ A & T & G \\ A & T & G \end{pmatrix} \begin{array}{ccc} i=1 \\ i=2 \end{array},$$

$$\mathbb{P}(\boldsymbol{y}) = \frac{1}{9}f(A_1)f(T_2)f(G_3)\Big(\frac{1}{8}(f(A_1) + 1)(f(T_2) + 1)(f(G_3) + 1) + 4f(A_1)f(T_2)f(G_3) + 4\Big),$$

such that

$$\mathbb{P}(s=L|\boldsymbol{y}) = \frac{\frac{1}{8}(f(A_1)+1)(f(T_2)+1)(f(G_3)+1)+f(A_1)f(T_2)f(G_3)+1}{\frac{1}{8}(f(A_1)+1)(f(T_2)+1)(f(G_3)+1)+4f(A_1)f(T_2)f(G_3)+4},$$

$$\mathbb{P}(s=I|\boldsymbol{y}) = \frac{3f(A_1)f(T_2)f(G_3)}{\frac{1}{8}(f(A_1)+1)(f(T_2)+1)(f(G_3)+1)+4f(A_1)f(T_2)f(G_3)+4},$$

$$\mathbb{P}(s=C|\boldsymbol{y}) = \frac{3}{\frac{1}{8}(f(A_1)+1)(f(T_2)+1)(f(G_3)+1)+4f(A_1)f(T_2)f(G_3)+4}.$$

because

$$\begin{split} \mathbb{P}(y|s) &= \mathbb{P}(a|s) \forall s \in \{L, I, C\}, \\ &= \begin{cases} & a \\ & \left(\frac{1}{3}f(A_{1})f(T_{2})f(G_{3})\left(f(A_{1})f(T_{2})f(G_{3}) + \frac{1}{8}(f(A_{1}) + 1)(f(T_{2}) + 1)(f(G_{3}) + 1) + 1\right)}{f(A_{1})^{2}f(T_{2})^{2}f(G_{3})^{2}} \\ & f(A_{1})^{2}f(T_{2})^{2}f(G_{3}) \end{cases} & f(A_{1})f(T_{2})f(G_{3}) \\ &= \begin{cases} & a \\ & f(A_{1})^{2}f(T_{2})^{2}f(G_{3})^{2} \\ & f(A_{1})f(T_{2})f(G_{3}) \end{cases} & g_{\Pi} \\ & f(A_{1})f(T_{2})f(A_{1})^{2} + \frac{1}{2}f(A_{1}) & f(A_{1}) \\ & f(A_{2})^{2} & \frac{1}{2}f(A_{1})^{2} + \frac{1}{2}f(A_{1}) & f(A_{1}) \\ & f(A_{2})^{2} & \frac{1}{2}f(A_{2})^{2} + \frac{1}{2}f(A_{1}) & f(A_{1}) \\ & f(A_{2})^{2} & \frac{1}{2}f(A_{2})^{2} + \frac{1}{2}f(A_{2}) & f(A_{2}) \\ & f(A_{3})^{2} & \frac{1}{2}f(A_{3})^{2} + \frac{1}{2}f(A_{3}) & f(A_{3}) \\ & & f(A_{3})^{2} & \frac{1}{2}f(A_{3})^{2} + \frac{1}{2}f(A_{3}) & f(A_{3}) \\ & f(A_{3})^{2} & \frac{1}{2}f(A_{3})^{2} + \frac{1}{2}f(A_{3}) & f(A_{3}) \\ & f(A_{3})^{2} & \frac{1}{2}f(A_{3})^{2} & \frac{1}{2}f(A_{3}) & \frac{1}{2} \\ & f(A_{3})^{2} & \frac{1}{2}f(A_{3}) & \frac{1}{2} \\ & \frac{1}{2}f(A_{3})^{2} & \frac{1}{2}f(A_{3}) & \frac{1}{2}f(A_{3}) & \frac{1}{2}f(A_{3}) & \frac{1}{2}f(A_{3}) \\ & \frac{1}{2}f(A_{3})^{2} & \frac{1}{2}f(A_{3}) & \frac{1}{2}f(A_{3}) & \frac{1}{2}f(A_{3}) & \frac{1}{2}f(A_{3}) \\ & \frac{1}{2}f(A_{3})^{2} & \frac{1}{2}f(A_{3}) &$$

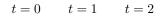
0.5 More than one recurrence: partially heterologous markers

Observed and phased alleles In the simplest example a single allele is observed at one marker genotyped in an incident infection t = 0 and in t = 1, 2 recurrent infections. Since we detect only one allele per infection we assume there is only one genotype per infection, s.t. y = a, e.g.,

$$egin{aligned} oldsymbol{y} = egin{pmatrix} \{A\} \\ \{T\} \\ \{T\} \end{pmatrix} egin{aligned} t = 0 \\ t = 1 \\ t = 2 \end{aligned} , \qquad oldsymbol{a} = egin{pmatrix} A \\ T \\ i = 2 \\ i = 3 \end{aligned} .$$

Relationship graphs and IBD partitions We sum over 12 relationship graphs, shown below in teal. For each graph, we sum over five IBD partitions $p_{\rm I}$ to $p_{\rm V}$ which can also be depicted as IBD graphs in grey.

$$egin{aligned} oldsymbol{p}_{\mathrm{I}} &= \{\{1\}, \{2\}, \{3\}\}, \ oldsymbol{p}_{\mathrm{III}} &= \{\{1, 2, 3\}\}, \ oldsymbol{p}_{\mathrm{III}} &= \{\{2, 3\}, \{2\}\}, \ oldsymbol{p}_{\mathrm{IV}} &= \{\{1, 2\}, \{3\}\}, \ oldsymbol{p}_{\mathrm{V}} &= \{\{1, 3\}, \{2\}\}. \end{aligned}$$



$$t=0$$
 $t=1$ $t=2$

$$t = 0$$
 $t = 1$ $t = 2$

$$1$$
 2 3 $g_{\rm I}$



$$1$$
 g_{VIII}



$$1$$
 $-- 2$ 3 g_{X}

$$1$$
 2 3 p_{IV}



$$\begin{array}{c} 1 \\ \hline \end{array}$$

Likelihood Remembering that in linear algebra $(CBA)^T = (A^TB^TC^T)$,

 $\mathbb{P}(\boldsymbol{y}|\boldsymbol{s})\forall \boldsymbol{s} \in \{L,I,C\} \times \{L,I,C\} = \mathbb{P}(\boldsymbol{a}|\boldsymbol{s})\forall \boldsymbol{s} \in \{L,I,C\} \times \{L,I,C\},$

 $\mathbb{P}(\boldsymbol{a}|\boldsymbol{s})\forall \boldsymbol{s} \in \{L, I, C\} \times \{L, I, C\}$

 $\mathbb{P}(\boldsymbol{g}|\boldsymbol{s})\forall \boldsymbol{g}\!\in\!\boldsymbol{\mathcal{G}}, \!\boldsymbol{s}\!\in\!\{L,\!I,\!C\}\!\times\!\{L,\!I,\!C\}$

 $\mathbb{P}(\boldsymbol{a}|\boldsymbol{s})\forall \boldsymbol{s}{\in}\{L,\!I,\!C\}{\times}\{L,\!I,\!C\}$

 \boldsymbol{a}

 $\mathbb{P}(\boldsymbol{g}|\boldsymbol{s})\forall \boldsymbol{g}\!\in\!\boldsymbol{\mathcal{G}}, \!\boldsymbol{s}\!\in\!\{L,\!I,\!C\}\!\times\!\{L,\!I,\!C\}$

 $\mathbb{P}(p|g) \forall p \in \mathcal{P}, g \in \mathcal{G}$

Posterior For a uniform prior on $s \in \{L, I, C\}$, $\mathbb{P}(a) = \frac{253}{360} f(A) f(T)^2 + \frac{53}{80} f(A) f(T)$ and

$$\mathbb{P}(s_{1}|\boldsymbol{y})\forall s_{1} \in \{L, I, C\} = \underbrace{\left(\frac{253}{360}f(A)f(T)^{2} + \frac{53}{80}f(A)f(T)\right)^{-1}}_{\mathbb{P}(\boldsymbol{y})} \times \frac{1}{3} \times \underbrace{\left(\frac{17/24f(A)f(T)^{2} + \frac{11/16f(A)f(T)}{7/5f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{7/5f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{\mathbb{P}(\boldsymbol{y}|s_{1})\forall s_{1} \in \{L, I, C\}} \right) \cdot \underbrace{\left(\frac{17/24f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{7/5f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{\mathbb{P}(\boldsymbol{y})}\right) \cdot \underbrace{\left(\frac{17/24f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{7/5f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{1}\right) \cdot \underbrace{\left(\frac{17/24f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}}_{1}\right) \cdot \underbrace{\left(\frac{17/24f(A)f(T)^{2} + \frac{13/10f(A)f(T)}{1}\right) \cdot \underbrace{\left(\frac{$$

0.6 More than one recurrence: exclusively homologous markers

If instead $y = (\{A\}, \{A\}, \{A\})^T$, $\mathbb{P}(y|s) = \mathbb{P}(a|s)$, which for s = II and s = CC

$$= \begin{pmatrix} f(A)^3 \\ f(A) \end{pmatrix} II \\ CC ,$$

$$\mathbb{P}(a|s) \text{ for } II \text{ and } CC$$

$$= \mathbb{P}(\boldsymbol{g}|\boldsymbol{s}) \text{ for } \boldsymbol{II} \text{ and } \boldsymbol{CC} \times \begin{pmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 1/2 & 1/2 & 0 & 0 & 0 \\ 0 & 1/2 & 0 & 0 & 1/2 & 0 \\ 0 & 1/2 & 0 & 0 & 1/2 & 0 \\ 0 & 1/4 & 1/4 & 1/4 & 1/4 & 0 \\ 1/2 & 0 & 1/2 & 0 & 0 & 0 \\ 1/2 & 0 & 0 & 1/2 & 0 & 0 \\ 1/2 & 0 & 0 & 0 & 1/2 & 0 \\ 0 & 1/2 & 0 & 0 & 1/2 & 0 & 0 \\ 1/2 & 0 & 0 & 0 & 1/2 & 0 & 0 \\ 1/2 & 0 & 0 & 0 & 1/2 & 0 & 0 \\ 1/2 & 0 & 0 & 0 & 1/2 & 0 & 0 \\ 1/2 & 0 & 0 & 0 & 1/2 & 0 & 0 \\ 0 & 1/2 & 0 & 1/2 & 0 & 0 & 0 \end{pmatrix} \underbrace{ \begin{array}{c} \boldsymbol{g}_{\text{III}} \\ \boldsymbol{g}_{\text{VIII}} \\ \boldsymbol{g}_{\text{IX}} \\ \boldsymbol{g}_{\text{XI}} \\ \boldsymbol{g}_{\text{XI}} \\ \boldsymbol{g}_{\text{XI}} \\ \boldsymbol{g}_{\text{XII}} \\ \end{pmatrix}_{\boldsymbol{p}_{\text{IV}} = \{\{1, 2\}, \{3\}\} \\ \boldsymbol{p}_{\text{V}} = \{\{1, 2\}, \{3\}\} \\ \boldsymbol{p}_{\text{V}} = \{\{1, 3\}, \{2\}\} \\ \boldsymbol{p}_{\text{V}} = \{\{1, 3\}, \{2\}, \{2\}, \{2\}, \{2\}, \{2\}, \{2\}, \{2$$

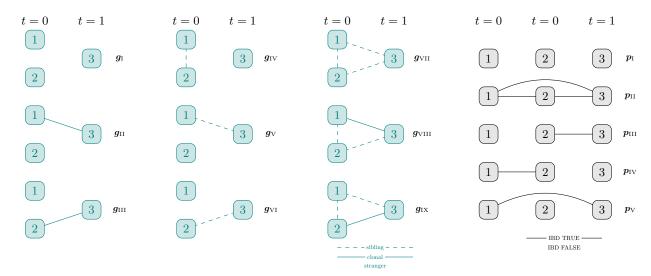
0.7 Simple example for more than one genotype per infection

Observed and phased alleles In a simple example two and one alleles are observed at a single marker genotyped in an incident and single recurrent infection, respectively. We assume the most parsimonious explanation of the data: the number of genotypes in the first and second infections are two and one, respectively. There is no-longer a one-to-one mapping between genotypes and infections over time. Instead, there are two possible allele assignments:

$$\mathbf{y} = \begin{pmatrix} j = 1 \\ \{A, T\} \\ \{T\} \end{pmatrix} \begin{tabular}{l} $t = 0$ \\ $t = 1$ \end{tabular} , & & & & & & & \\ $a_{\rm I} = \begin{pmatrix} A \\ T \\ T \end{pmatrix} \begin{tabular}{l} $i = 1, \ t = 0 \\ $i = 2, \ t = 0$ \end{tabular} , & & & & & \\ $a_{\rm II} = \begin{pmatrix} T \\ A \\ T \end{pmatrix} \begin{tabular}{l} $i = 1, \ t = 0 \\ $i = 2, \ t = 0$ \end{tabular} . \\ $i = 3, \ t = 1$ \end{tabular}$$

Since $a_{\rm I}$ and $a_{\rm II}$ are equivalent up to a swap between the two genotypes in the first episode, we have $s \in \{L, I, C\}$ that $\mathbb{P}(y|s) = 2\mathbb{P}(a_{\rm I}|s)$.

Relationship graphs and IBD partitions There are nine relationship graphs (a subset of those in example 0.5 because clonal relationships within infections are disallowed) to sum over and five IBD partitions (the same as those in example 0.5), corresponding to the same five IBD graphs as follows.



Likelihood Remembering that in linear algebra $(CBA)^T = (A^TB^TC^T)$,

$$\mathbb{P}(\boldsymbol{y}|s)\forall s \in \{L,I,C\} = 2 \underbrace{\begin{pmatrix} 5/18f(A)f(T)^2 + 1/4f(A)f(T) \\ 3/4f(A)f(T)^2 \\ 3/8f(A)f(T) \end{pmatrix} \begin{pmatrix} L \\ I \\ C \end{pmatrix}}_{\mathbb{P}(\boldsymbol{a_I}|s)\forall s \in \{L,I,C\}} \boldsymbol{b_I}$$

$$=2\underbrace{\begin{pmatrix} g_{\mathrm{I}} & g_{\mathrm{II}} & g_{\mathrm{II}} & g_{\mathrm{IV}} & g_{\mathrm{V}} & g_{\mathrm{VI}} & g_{\mathrm{VII}} & g_{\mathrm{IX}} \\ \frac{1}{9} & \frac{1}{9} \\ \frac{1}{2} & 0 & 0 & \frac{1}{2} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{4} & \frac{1}{4} & 0 & 0 & 0 & 0 & \frac{1}{4} & \frac{1}{4} \end{pmatrix} \underbrace{L}_{C}}_{\mathbb{P}(g|s) \forall g \in \mathcal{G}, s \in \{L, I, C\}} \underbrace{\begin{pmatrix} f(A)f(T)^{2} \\ 0 \\ f(A)f(T) \\ \frac{1}{2}f(A)f(T)^{2} \\ \frac{1}{2}f(A)f(T)^{2} \\ \frac{1}{2}f(A)f(T)^{2} \\ \frac{1}{2}f(A)f(T)(f(T)+1) \\ 0 \\ \frac{1}{2}f(A)f(T) \end{pmatrix}}_{g_{\mathrm{VII}}} \underbrace{g_{\mathrm{VII}}}_{g_{\mathrm{VIII}}}$$

$$=2\begin{pmatrix} g_{\rm I} & g_{\rm II} & g_{\rm IV} & g_{\rm V} & g_{\rm VI} & g_{\rm VII} & g_{\rm IXI} & g_{\rm IX} \\ 1/9 & 1/9 & 1/9 & 1/9 & 1/9 & 1/9 & 1/9 & 1/9 & 1/9 & 1/9 & 1/9 \\ 1/2 & 0 & 0 & 1/2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1/4 & 1/4 & 0 & 0 & 0 & 0 & 1/4 & 1/4 \end{pmatrix} \begin{matrix} L \\ I \\ C \end{matrix}$$

 $\mathbb{P}(p|g) \forall p \in \mathcal{P}, g \in \mathcal{G}$

The prefactor of 2 corresponds to \mathcal{A} consisting of an equivalence class of 2 allele assignments. Note that if the data for the incident infection and the recurrence were reversed, e.g. if $y_{t=0} = \{T\}$ and $y_{t=1} = \{A, T\}$, the posterior probability of recrudescence would be zero because recrudescences must have the same or fewer genotypes than the directly preceding infection

Posterior For a uniform prior on $s \in \{L, I, C\}$, $\mathbb{P}(y) = \frac{1}{3} \left(\frac{37}{36} f(A) f(T)^2 + \frac{5}{8} f(A) f(T) \right)$ and

$$\mathbb{P}(s_{1}|\boldsymbol{y})\forall s_{1} \in \{L, I, C\} = \underbrace{\left(\frac{37}{108}f(A)f(T)^{2} + \frac{5}{24}f(A)f(T)\right)^{-1}}_{\mathbb{P}(\boldsymbol{y})} \times \underbrace{\frac{1}{3} \times \left(\frac{\frac{5}{18}f(A)f(T)^{2} + \frac{1}{4}f(A)f(T)}{\frac{3}{4}f(A)f(T)^{2}}\right) \frac{L}{3}}_{\mathbb{P}(\boldsymbol{y}|\boldsymbol{s})\forall \boldsymbol{s} \in \{L, I, C\}}$$

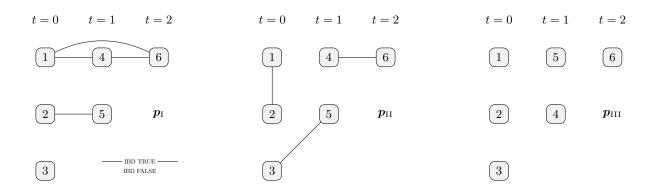
0.8 Simple zoomed-in example for six genotypes

Observed and phased alleles Suppose the observed alleles suggest there are n > 3 genotypes, e.g.,

$$\mathbf{y} = \begin{pmatrix} j = 1 \\ \{A, T, C\} \\ \{A, T\} \\ \{A\} \end{pmatrix} \begin{array}{c} t = 0 \\ t = 1 \\ t = 2 \\ t = 2 \\ \end{array} , \qquad \mathbf{a} = \begin{pmatrix} A \\ T \\ C \\ A \\ i = 3 \\ i = 4 \\ T \\ A \\ i = 5 \\ i = 6 \\ \end{cases} .$$

IBD partitions For n = 6, there are 203 IBD partitions in \mathcal{P} . Three examples, depicted below as graphs, are:

$$\begin{aligned} & \boldsymbol{p}_{\mathrm{I}} = \{ \{\{1,4,6\},\{2,5\},\{3\}\}, \\ & \boldsymbol{p}_{\mathrm{II}} = \{\{1,2\},\{3,5\},\{4,6\}\}, \\ & \boldsymbol{p}_{\mathrm{III}} = \{\{1\},\{2\},\{3\},\{4\},\{5\},\{6\}\}. \end{aligned}$$



$$\mathbb{P}(\boldsymbol{a}_{\cdot 1}|\boldsymbol{p}_{1}) = \mathbb{P}(\boldsymbol{a}_{\{1,4,6\}1}|\{1,4,6\}) \times \mathbb{P}(\boldsymbol{a}_{\{2,5\}1}|\{2,5\}) \times \mathbb{P}(a_{31}|\{3\}),
= f(A_{1}) \times f(T_{1}) \times f(C_{1}).
\mathbb{P}(\boldsymbol{a}_{\cdot 1}|\boldsymbol{p}_{11}) = \mathbb{P}(\boldsymbol{a}_{\{12\}1}|\{1,2\}) \times \mathbb{P}(\boldsymbol{a}_{\{3,5\}1}|\{3,5\}) \times \mathbb{P}(\boldsymbol{a}_{\{4,6\}1}|\{4,6\}),
= 0 \times 0 \times f(A_{1}).
\mathbb{P}(\boldsymbol{a}_{\cdot 1}|\boldsymbol{p}_{111}) = \mathbb{P}(a_{11}|\{1\}) \times \mathbb{P}(a_{21}|\{2\}) \times \mathbb{P}(a_{31}|\{3\}) \times \mathbb{P}(a_{41}|\{4\}) \times \mathbb{P}(a_{51}|\{5\}) \times \mathbb{P}(a_{61}|\{6\}),
= f(A)^{3} \times f(T)^{2} \times f(C).$$

0.9 Simple example involving phasing

Observed and phased alleles In a simple example two alleles are observed at two of three markers genotyped in an incident infection, while one allele is observed per marker genotyped in a single recurrent infection. As in example 0.7, we assume the most parsimonious explanation of the data: the number of genotypes in the first and second infections are

two and one, respectively. However, there are now two non-equivalent ways to phase allelic data into n=3 genotypes,

$$\begin{aligned} y &= \begin{pmatrix} j=1 & j=2 & j=3 \\ \{A,T\} & \{T\} & \{C,G\} \\ \{T\} & \{T\} & \{C\} \end{pmatrix} \, t = 0 \\ \{C\} & \{C\} \end{pmatrix} \, t = 1 \ , \end{aligned}$$

$$\begin{aligned} j &= 1 & j=2 & j=3 \\ a_{\rm I} &= \begin{pmatrix} A & T & C \\ T & T & G \\ T & T & C \end{pmatrix} \, j = 1, \, t = 0 \\ j &= 2, \, t = 0 \\ j &= 3, \, t = 1 \end{aligned}$$

$$\begin{aligned} a_{\rm II} &= \begin{pmatrix} A & T & G \\ T & T & C \\ T & T & C \end{pmatrix} \, j = 1, \, t = 0 \\ j &= 2, \, t = 0 \\ j &= 3, \, t = 1 \end{aligned}$$

The total number of allele assignments is in fact $|\mathcal{A}| = 4$, which can be partitioned into two equivalence classes of two allele assignments each; a_{I} and a_{II} are representatives of the two equivalence classes.

Relationship graphs and IBD partitions We sum over relationship graphs and IBD partitions in example 0.7.

Likelihood

$$\mathbb{P}(\boldsymbol{y}|\boldsymbol{s}=L) = 2c \times \frac{1}{9} \Big(2f(T_1)f(T_2)^2 f(C_3) + \frac{3}{8}f(T_1)(f(T_2)^2 + f(T_2))f(C_3) + \frac{1}{8}f(T_1)(f(T_2)^2 + f(T_2))(f(C_3) + 1) + \frac{1}{8}(f(T_1) + 1)(f(T_1)^2 + f(T_1))f(C_3) + \frac{1}{8}(f(T_1) + 1)(f(T_1)^2 + f(T_1))(f(C_3) + 1) + \frac{1}{32}(3f(T_2) + 1) + \frac{1}{8}(9f(T_2) + 1) \Big),$$

$$\mathbb{P}(\boldsymbol{y}|\boldsymbol{s}=I) = 2c \times \frac{1}{8}f(T_1)f(T_2)f(C_3) \Big(9f(T_2) + 1 \Big),$$

$$\mathbb{P}(\boldsymbol{y}|\boldsymbol{s}=C) = 2c \times \frac{1}{32} \Big(9f(T_2) + 1 \Big),$$

where $c = f(A_1)f(T_1)f(T_2)f(C_3)f(G_3)$. Note that the prefactor of 2 corresponds to the fact that each equivalence class consists of two allele assignments.

The likelihood can be written as a summation over $a_{\rm I}$ and $a_{\rm II}$:

$$\mathbb{P}(\boldsymbol{y}|s)\forall s \in \{L, I, C\} = 2\left(\mathbb{P}(\boldsymbol{a}_{\mathrm{I}}|s)\forall s \in \{L, I, C\} + \mathbb{P}(\boldsymbol{a}_{\mathrm{II}}|s)\forall s \in \{L, I, C\}\right)$$

where, with differences between $a_{\rm I}$ and $a_{\rm II}$ highlighted in blue,

$$\mathbb{P}(\boldsymbol{a}_{\mathrm{I}}|s)\forall s\in\{L,I,C\}=$$

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and where

$$c \times \begin{pmatrix} f(T_1)f(T_2)^2f(C_3) \\ 0 \\ 0 \\ 1/8f(T_1)\left(f(T_2)^2 + f(T_2)\right)f(C_3) \\ 1/8f(A_1)f(T_1)^2\left(f(T_2)^3 + f(T_2)^2\right)f(C_3)^2f(G_3) \\ g_{VI} \\ g_{VI} \\ g_{VII} \\ 0 \\ 0 \end{pmatrix} g_{VII} \\ g_{VII} \\$$

 $\mathbb{P}(a_{\mathrm{I}}|g) \forall g \in \mathcal{G}$ $\mathbb{P}(a_{\mathrm{I}}|g) \forall g \in \mathcal{G}$ $oldsymbol{a}_{ ext{I}\cdot 1}$ $\boldsymbol{a}_{\mathrm{I}\cdot 2}$ $a_{1\cdot 3}$ $f(A_1)f(T_1)^2$ $f(T_2)^3$ $f(C_3)^2 f(G_3)$ $oldsymbol{g}_{ ext{I}}$ $f(T_2)^2$ $f(C_3)f(G_3)$ 0 $oldsymbol{g}_{ ext{II}}$ $f(T_2)^2$ $f(A_1)f(T_1)$ 0 $oldsymbol{g}_{ ext{III}}$ $1/2f(C_3)^2f(G_3)$ $^{1}/_{2}f(A_{1})f(T_{1})^{2}$ $1/2(f(T_2)^3 + f(T_2)^2)$ $m{g}_{ ext{IV}}$ $1/2 (f(T_2)^3 + f(T_2)^2)$ = column product $1/2f(A_1)f(T_1)^2$ $1/2f(C_3)f(G_3)(f(C_3)+1)$ $oldsymbol{g}_{
m V}$ $1/2 (f(T_2)^3 + f(T_2)^2)$ $1/2f(A_1)f(T_1)(f(T_1)+1)$ $1/2f(C_3)^2f(G_3)$ $oldsymbol{g}_{ ext{VI}}$ $^{1}/_{4}f(A_{1})f(T_{1})$ $^{1}/_{4}f(T_{2})(3f(T_{2})+1)$ $^{1}/_{4}f(C_{3})f(G_{3})$ $oldsymbol{g}_{ ext{VII}}$ 0 $1/2f(T_2)(f(T_2)+1)$ $1/2f(C_3)f(G_3)$ $oldsymbol{g}_{ ext{VIII}}$ $1/2f(A_1)f(T_1)$ $1/2f(T_2)(f(T_2)+1)$ 0 $oldsymbol{g}_{ ext{IX}}$ $\mathbb{P}(a_{\mathrm{I} \cdot j}|g) \forall a_{\mathrm{I} \cdot j} \in a_{\mathrm{I}}, g \in \mathcal{G}$ $oldsymbol{p}_{ ext{II}}$ $p_{
m III}$ $p_{
m IV}$ $p_{
m V}$ p_{I} 0 0 0 0 $oldsymbol{g}_{ ext{I}}$ 0 0 0 0 1 $oldsymbol{g}_{ ext{II}}$ $oldsymbol{a}_{\mathrm{I}\cdot 1}$ $a_{1.2}$ $a_{1.3}$ $f(T_2)^3$ $f(A_1)f(T_1)^2$ $f(C_3)^2 f(G_3)$ 0 0 0 0 1 $oldsymbol{g}_{ ext{III}}$ $oldsymbol{p}_{ ext{I}}$ 0 0 1/20 0 $f(T_2)$ 0 $oldsymbol{g}_{ ext{IV}}$ $oldsymbol{p}_{ ext{II}}$ $1/_{2}$ 0 = column product 0 0 1/2 $f(A_1)f(T_1)$ $f(T_2)^2$ 0 $oldsymbol{g}_{ ext{V}}$ $oldsymbol{p}_{ ext{III}}$ $f(T_2)^2$ $^{1}/_{2}$ 0 $^{1}/_{2}$ 0 0 0 0 $m{g}_{
m VI}$ $oldsymbol{p}_{ ext{IV}}$ $f(T_2)^2$ 0 $1/_{4}$ $^{1/_{4}}$ $^{1}/_{4}$ $^{1}/_{4}$ 0 $f(C_3)f(G_3)$ $p_{
m V}$ $oldsymbol{g}_{ ext{VII}}$ 0 $1/_{2}$ 0 0 $1/_{2}$ $oldsymbol{g}_{ ext{VIII}}$ 0 $1/_{2}$ $1/_{2}$ $oldsymbol{g}_{ ext{IX}}$ $\mathbb{P}(\boldsymbol{a}_{\mathrm{I}\cdot j}|\boldsymbol{p})\forall \boldsymbol{a}_{\mathrm{I}\cdot j}\!\in\!\boldsymbol{a}_{\mathrm{I}}, \boldsymbol{p}\!\in\!\boldsymbol{\mathcal{P}}$ $\mathbb{P}(p|g) \forall p \in \mathcal{P}, g \in \mathcal{G}$

and

$$c \times \begin{pmatrix} f(T_1)f(T_2)^2 f(C_3) & g_1 \\ f(T_1)f(T_2)^2 + f(T_2)f(C_3) & g_{11} \\ f(S_1)f(T_1)(f(T_2)^2 + f(T_2))f(C_3) & g_{12} \\ f(S_1)f(T_1) f(T_2)^2 + f(T_2))f(C_3) & g_{13} \\ f(S_1)f(T_1) f(T_2)^2 + f(T_2))f(C_3) & g_{13} \\ f(S_1)f(T_1) f(T_2)^2 f(T_2)^3 f(C_3) & g_{13} \\ f(A_1)f(T_1)^2 f(T_2)^3 f(C_3)^2 f(C_3) & g_{13} \\ f(A_1)f(T_1)^2 f(T_2)^3 f(T_2)^2 f(C_3)^2 f(C_3) & g_{14} \\ f(A_1)f(T_1)^2 f(T_2)^3 f(T_2)^2 f(C_3)^2 f(C_3) & g_{14} \\ f(A_1)f(T_1)f(T_2)^2 f(T_2)^3 f(C_3)^2 f(C_3) & g_{14} \\ f(A_1)f(T_1)f(T_2)^2 f(T_2)^2 f(C_3)f(C_3) & g_{14} \\ f(A_1)f(T_1)f(T_2)(f(T_2) + 1)f(C_3)f(C_3) & g_{14} \\ f(A_1)f(T_1)f(T_2)(f(T_2) + 1)f(C_3)f(C_3) & g_{14} \\ f(A_1)f(T_1) f(T_2)(f(T_2) + 1)f(C_3)f(C_3) & g_{14} \\ f(A_1)f(T_1) f(T_2)^2 f(T_2)^2 f(T_2)^2 f(C_3)f(C_3) & g_{14} \\ f(A_1)f(T_1) f(T_2)^2 f(T_2)^2 f(T_2)^2 f(T_2)^2 f(C_3)f(C_3) \\ f(A_1)f(T_1) f(T_2)^2 f(T_2)^2 f(T_2)^2 f(T_2)^2 f(C_3)f(C_3) \\ f(A_1)f(T_1) f(T_2)^2 f(T_2$$

 $\mathbb{P}(\boldsymbol{p}|\boldsymbol{g}) \forall \boldsymbol{p} \in \mathcal{P}, \boldsymbol{g} \in \mathcal{G}$