A computer algorithm for identifying compatible genetic backgrounds: For two given genetic backgrounds, \(G^{(1)} = \{x^{(1)}, y^{(1)}\}\) and \(G^{(2)} = \{x^{(2)}, y^{(2)}\}\), the algorithm described by the pseudo-codes below can simultaneously determine whether they are compatible and, if they are, the genetic background \(G^{(A)}\) of their parental haplotype:

INPUT \(x^{(1)} = (x_0^{(1)}, x_1^{(1)}, ..., x_{B1}^{(1)})\) and \(y^{(1)} = (y_1^{(1)}, ..., y_{B1}^{(1)})\)

INPUT \(x^{(2)} = (x_0^{(2)}, x_1^{(2)}, ..., x_{B2}^{(2)})\) and \(y^{(2)} = (y_1^{(2)}, ..., y_{B2}^{(2)})\)

CREATE ARRAY \(x^{(A)}\) (with no element initially)

CREATE ARRAY \(y^{(A)}\) (with no element initially)

SET \(p1\) to 1

SET \(p2\) to 1

SET isCompatible to true

WHILE \((p1 \leq B1 \text{ OR } p2 \leq B2)\)

CREATE VARIABLE \(x_{\text{temp}}\) and \(y_{\text{temp}}\)

IF \(x_1^{(1)} > x_2^{(2)}\)

SET \(x_{\text{temp}}\) to \(x_2^{(2)}\)

SET \(y_{\text{temp}}\) to \(y_2^{(2)}\)

SET \(y_{p1}^{(1)}\) to \((y_{p2}^{(1)} - y_{\text{temp}})\)

SET \(p2\) to \(p2 + 1\)

ELSE IF \(x_1^{(1)} = x_2^{(2)}\)

SET \(x_{\text{temp}}\) to \(x_2^{(2)}\)

SET \(y_{\text{temp}}\) to \(y_2^{(2)}\)

IF \(y_1^{(1)} = y_2^{(2)}\)

ELSE
SET $y_{tmp}$ to $y_{p2}$

ELSE

SET $y_{tmp}$ to -1

ENDIF

SET $p1$ to $p1 + 1$

SET $p2$ to $p2 + 1$

ELSE

SET $x_{tmp}$ to $x_{p1}$

SET $y_{tmp}$ to $y_{p1}$

SET $y_{p2}$ to $(y_{p2} - y_{tmp})$

SET $p1$ to $p1 + 1$

ENDIF

IF ($y_{tmp} < 0$)

SET isCompatible to false

ENDIF

IF ($x^A$ is empty)

APPEND 0 to $x^A$

ENDIF

APPEND $x_{tmp}$ to $x^A$

APPEND $y_{tmp}$ to $y^A$

ENDWHILE
and $G^2$ are compatible only if the Boolean variable \textit{isCompatible} is true after execution of the algorithm. The genetic background of the parental haplotype is given by $G^{(A)} = \{x^{(A)}, y^{(A)}\}$. 