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# Fst between haploids and diploids in species with discrete ploidal generations

Here we put supplementary information for our manuscript, “Fst between haploids and diploids in species with discrete ploidal generations”.

Note that, you might have to reset the variables as necessary because we reuse same variables in the different sections.

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## Appendix

### Appendix A

#### Equations

We define the probabilities of identities  $Q_{ij}$  of genes sampled in deme  $i$  and  $j$  ( $QHD=QDH$ ).

When we derive the recursions for  $Q$ , we assume that the number of haploid and diploid individuals are fixed as  $NH = N \rho_H$  and  $ND = N \rho_D$ . We also assume that the probability of identity from diploid population is independent of whether the two alleles are sampled from the same individual or different individuals (no inbreeding).

$$\begin{aligned} \text{NextQHH} &= (1 - \mu)^2 * \left( mHfromH^2 * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) + mHfromH * mHfromD * QHD + \right. \\ &\quad \left. mHfromD * mHfromH * QDH + mHfromD^2 * \left( \frac{1}{2 * Dip} + \left( 1 - \frac{1}{2 * Dip} \right) * QDD \right) \right); \\ \text{NextQHD} &= (1 - \mu)^2 * \left( mHfromH * mDfromH * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) + mHfromH * mDfromD * QHD + \right. \\ &\quad \left. mHfromD * mDfromH * QDH + mHfromD * mDfromD * \left( \frac{1}{2 * Dip} + \left( 1 - \frac{1}{2 * Dip} \right) * QDD \right) \right); \\ \text{NextQDH} &= (1 - \mu)^2 * \left( mDfromH * mHfromH * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) + mDfromH * mHfromD * QHD + \right. \\ &\quad \left. mDfromD * mHfromH * QDH + mDfromD * mHfromD * \left( \frac{1}{2 * Dip} + \left( 1 - \frac{1}{2 * Dip} \right) * QDD \right) \right); \\ \text{NextQDD} &= (1 - \mu)^2 * \left( mDfromD^2 * \left( \frac{1}{2 * Dip} + \left( 1 - \frac{1}{2 * Dip} \right) * QDD \right) + mDfromH * mDfromD * QHD + \right. \\ &\quad \left. mDfromD * mDfromH * QDH + mDfromH^2 * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) \right); \end{aligned}$$

The recursion equations for  $Q$  can be described as,  $(1 - \mu)^2 A (Q + c)$ ;  
(this equation corresponds to Eq. (9.30) in Rousset (2004))

$$\text{MatrixA} = \begin{pmatrix} mHfromH * mHfromH & mHfromH * mHfromD & mHfromD * mHfromH & mHfromD * mHfromD \\ mHfromH * mDfromH & mHfromH * mDfromD & mHfromD * mDfromH & mHfromD * mDfromD \\ mDfromH * mHfromH & mDfromH * mHfromD & mDfromD * mHfromH & mDfromD * mHfromD \\ mDfromH * mDfromH & mDfromH * mDfromD & mDfromD * mDfromH & mDfromD * mDfromD \end{pmatrix};$$

$$\text{VectC} = \begin{pmatrix} \frac{1}{Hap} * (1 - QHH) \\ 0 \\ 0 \\ \frac{1}{2*Dip} * (1 - QDD) \end{pmatrix};$$

$$\begin{pmatrix} \text{NextQHH} \\ \text{NextQHD} \\ \text{NextQDH} \\ \text{NextQDD} \end{pmatrix} - (1 - \mu)^2 * \text{MatrixA} \cdot \begin{pmatrix} QHH \\ QHD \\ QDH \\ QDD \end{pmatrix} + \text{VectC} // \text{Simplify}$$

$\{\{0\}, \{0\}, \{0\}, \{0\}\}$

Note that, we can write,  $A = \text{TensorProduct}[F, F]$

$$\text{MatrixF} = \begin{pmatrix} mHfromH & mHfromD \\ mDfromH & mDfromD \end{pmatrix};$$

$$\text{TensorProduct}[\text{MatrixF}, \text{MatrixF}] // \text{MatrixForm}$$

$$\text{MatrixA} // \text{MatrixForm}$$

$$\left( \begin{pmatrix} mHfromH^2 & mHfromD mHfromH \\ mDfromH mHfromH & mDfromD mHfromH \end{pmatrix} \begin{pmatrix} mHfromD mHfromH & mHfromD^2 \\ mDfromH mHfromD & mDfromD mHfromD \end{pmatrix} \begin{pmatrix} mDfromH mHfromH & mDfromH mHfromD \\ mDfromD mHfromH & mDfromD mHfromD \end{pmatrix} \begin{pmatrix} mDfromH^2 & mDfromD mDfromH \\ mDfromH mDfromH & mDfromD mDfromH \end{pmatrix} \begin{pmatrix} mHfromD^2 & mHfromD mHfromH & mHfromD mHfromD \\ mDfromD mHfromD & mDfromD mHfromH & mDfromD mHfromD \\ mDfromH mHfromD & mDfromH mHfromH & mDfromD mHfromD \\ mDfromH^2 & mDfromD mDfromH & mDfromD mDfromH \end{pmatrix} \right)$$

$$\left( \begin{pmatrix} mHfromH^2 & mHfromD mHfromH & mHfromD mHfromH & mHfromD^2 \\ mDfromH mHfromH & mDfromD mHfromH & mDfromH mHfromD & mDfromD mHfromD \\ mDfromH mHfromH & mDfromH mHfromH & mDfromD mHfromH & mDfromD mHfromD \\ mDfromH^2 & mDfromD mDfromH & mDfromD mDfromH & mDfromD^2 \end{pmatrix} \right)$$

Note that, the matrix A is a probability matrix;

$$\text{MatrixA} \cdot \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \end{pmatrix} /. mHfromD \rightarrow 1 - mHfromH /. mDfromH \rightarrow 1 - mDfromD // \text{Simplify}$$

$\{\{1\}, \{1\}, \{1\}, \{1\}\}$

Furthermore, this can be represented as,  $(1 - \mu)^2 (GQ + A\delta)$  and  $(1 - \mu)^2 (GQ + (I - G) 1)$ ;  
(this equation corresponds to Eq. (4.4) in Rousset (2004))

```
MatrixG =
```

$$\left( \begin{array}{cccc} mHfromH^2 * \left(1 - \frac{1}{Hap}\right) & mHfromH * mHfromD & mHfromD * mHfromH & mHfromD^2 * \left(1 - \frac{1}{2*D}\right) \\ mHfromH * mDfromH * \left(1 - \frac{1}{Hap}\right) & mHfromH * mDfromD & mHfromD * mDfromH & mHfromD * mDfromD * \left(1 - \frac{1}{2*D}\right) \\ mDfromH * mHfromH * \left(1 - \frac{1}{Hap}\right) & mDfromH * mHfromD & mDfromD * mHfromH & mDfromD * mHfromD * \left(1 - \frac{1}{2*D}\right) \\ mDfromH^2 * \left(1 - \frac{1}{Hap}\right) & mDfromH * mDfromD & mDfromD * mDfromH & mDfromD^2 * \left(1 - \frac{1}{2*D}\right) \end{array} \right);$$

$$Vect\delta = \begin{pmatrix} \frac{1}{Hap} \\ 0 \\ 0 \\ \frac{1}{2*Dip} \end{pmatrix};$$

$$\begin{pmatrix} NextQHH \\ NextQHD \\ NextQDH \\ NextQDD \end{pmatrix} - (1 - \mu)^2 * \left( MatrixG. \begin{pmatrix} QHH \\ QHD \\ QDH \\ QDD \end{pmatrix} + MatrixA.Vect\delta \right) // Simplify$$

$$\begin{pmatrix} NextQHH \\ NextQHD \\ NextQDH \\ NextQDD \end{pmatrix} - (1 - \mu)^2 * \left( MatrixG. \begin{pmatrix} QHH \\ QHD \\ QDH \\ QDD \end{pmatrix} + \left( \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} - MatrixG \right). \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \end{pmatrix} \right) /.$$

$mHfromD \rightarrow 1 - mHfromH / . mDfromH \rightarrow 1 - mDfromD // Simplify$

```
{ {0}, {0}, {0}, {0} }
```

```
{ {0}, {0}, {0}, {0} }
```

## Exact Fst

Recall that these are backwards rates so that mDD+mHD sum to one:

```
constraints = {mHfromH + mHfromD == 1, mDfromH + mDfromD == 1, pD + pH == 1};
subconstraints = {mHfromH \rightarrow 1 - mHfromD, mDfromD \rightarrow 1 - mDfromH};
```

At equilibrium, we have

```
sol = Simplify[Solve[(NextQHH == QHH && NextQDD == QDD && NextQHD == QHD && NextQDH == QDH), {QHH, QHD, QDH, QDD}], constraints];
```

When there is not mutation, because of a finite population size, Q must be 1.

```

sol /. μ → 0 // Simplify
{{QHH → 1, QHD → 1, QDH → 1, QDD → 1} }

EqQHH = Simplify[QHH /. sol[[1]], constraints]
EqQHD = Simplify[QHD /. sol[[1]], constraints]
EqQDH = Simplify[QDH /. sol[[1]], constraints]
EqQDD = Simplify[QDD /. sol[[1]], constraints]

```

Note that, we can show  $QHD = QDH$ , as expected:

```
EqQHD == EqQDH
```

```
True
```

Using  $Q$ , we define the  $F$ -like measures for the haploid-diploid population.

```

FaiHHstrict =
Simplify[Limit[(EqQHH - EqQHD)/(1 - EqQHD) /. Dip → ρD * Ntot /. Hap → ρH * Ntot, μ → 0], constraints]

FaiDDstrict = Simplify[
Limit[(EqQDD - EqQHD)/(1 - EqQHD) /. Dip → ρD * Ntot /. Hap → ρH * Ntot, μ → 0], constraints]

- (( (mDfromH - mHfromH) (mDfromH mHfromH (2 - 4 Ntot ρD) + mDfromH^2 (-1 + 2 Ntot ρD) +
mHfromH^2 (-1 + 2 Ntot ρD) + mHfromH Ntot (-2 + ρH) + Ntot ρH) ) /
(mDfromH^3 (-1 + 2 Ntot ρD) (-1 + Ntot ρH) + mDfromH^2 (1 + 2 Ntot (-1 + ρH)) +
(-Ntot ρH + 3 mHfromH (-1 + Ntot ρH)) -
(-2 Ntot ρD + mHfromH (-1 + 2 Ntot ρD)) (-Ntot ρH + mHfromH^2 (-1 + Ntot ρH)) +
mDfromH (Ntot (1 - 2 Ntot ρD) ρH + 3 mHfromH^2 (-1 + 2 Ntot ρD) (-1 + Ntot ρH) +
mHfromH Ntot (2 ρD + ρH - 4 Ntot ρD ρH)) ) )

- (( (mDfromH - mHfromH) (-Ntot ρH + mDfromH^2 (-1 + Ntot ρH) +
mHfromH^2 (-1 + Ntot ρH) + mDfromH (Ntot (2 ρD + ρH) + mHfromH (2 - 2 Ntot ρH))) ) /
(mDfromH^3 (-1 + 2 Ntot ρD) (-1 + Ntot ρH) + mDfromH^2 (1 + 2 Ntot (-1 + ρH)) +
(-Ntot ρH + 3 mHfromH (-1 + Ntot ρH)) -
(-2 Ntot ρD + mHfromH (-1 + 2 Ntot ρD)) (-Ntot ρH + mHfromH^2 (-1 + Ntot ρH)) +
mDfromH (Ntot (1 - 2 Ntot ρD) ρH + 3 mHfromH^2 (-1 + 2 Ntot ρD) (-1 + Ntot ρH) +
mHfromH Ntot (2 ρD + ρH - 4 Ntot ρD ρH)) ) )

```

Through a series of collecting factors, as in the following command, and gathering terms

```

Collect[Numerator[FaiHHstrict], {Ntot}, Factor]
(mDfromH - mHfromH)^3 - (mDfromH - mHfromH) Ntot
(-2 mHfromH + 2 mDfromH^2 ρD - 4 mDfromH mHfromH ρD + 2 mHfromH^2 ρD + ρH + mHfromH ρH)

```

we can rewrite  $FaiHHstrict$  and  $FaiDDstrict$  as:

```

Eq4a = ((1 - X)^3 + Ntot * (1 - X) * ((2 - X) * X * (2 * ρD) - mHfromD * (ρH + 2 * ρD)) ) /
((1 - X)^3 - Ntot * (1 - X) * ((1 - X)^2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) +
Ntot^2 * X^2 * (2 - X) * (2 * ρD) * ρH) ;
%- FaiHHstrict /. X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH // Factor
0

Eq4b = ((1 - X)^3 + Ntot * (1 - X) * ((2 - X) * X * ρH - mDfromH * (ρH + 2 * ρD)) ) /
((1 - X)^3 - Ntot * (1 - X) * ((1 - X)^2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) +
Ntot^2 * X^2 * (2 - X) * (2 * ρD) * ρH) ;
%- FaiDDstrict /. X → mDfromH + mHfromD /. subconstraints /. ρD → 1 - ρH // Factor
0

```

where  $X = mDH + mHD$ , the sum of the movement rates.

```

Fexact = { ((1 - X)^3 + Ntot * (1 - X) * ((2 - X) * X * (2 * ρD) - mHfromD * (ρH + 2 * ρD)) ) /
((1 - X)^3 - Ntot * (1 - X) * ((1 - X)^2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) +
Ntot^2 * X^2 * (2 - X) * (2 * ρD) * ρH),
((1 - X)^3 + Ntot * (1 - X) * ((2 - X) * X * ρH - mDfromH * (ρH + 2 * ρD)) ) /
((1 - X)^3 - Ntot * (1 - X) * ((1 - X)^2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) +
Ntot^2 * X^2 * (2 - X) * (2 * ρD) * ρH) };

```

If the movement rates are neither near zero nor near one and the population size is large

If  $N$  is large (total population size) relative to the migration rates (i.e., none of the migration rates is very rare) these reduce to [dropping terms not involving  $N_{tot}$ ] for {haploids, diploids}:

$$\begin{aligned}
& \text{Series}\left[F_{\text{exact}} / . N_{\text{tot}} \rightarrow \frac{N_{\text{tot}}}{\epsilon}, \{\epsilon, 0, 1\}\right] \\
& \text{Factor}\left[\text{Normal}\left[\text{Series}\left[F_{\text{exact}} / . N_{\text{tot}} \rightarrow \frac{N_{\text{tot}}}{\epsilon}, \{\epsilon, 0, 1\}\right]\right]\right] / . \epsilon \rightarrow 1 \\
& \left\{ -\frac{(-1 + X) (2 mHfromD \rho D - 4 X \rho D + 2 X^2 \rho D + mHfromD \rho H)}{2 (N_{\text{tot}} (-2 + X) X^2 \rho D \rho H)} + O[\epsilon]^2, \right. \\
& \quad \left. -\frac{(-1 + X) (2 mDfromH \rho D + mDfromH \rho H - 2 X \rho H + X^2 \rho H)}{2 (N_{\text{tot}} (-2 + X) X^2 \rho D \rho H)} + O[\epsilon]^2 \right\} \\
& \left\{ -\frac{(-1 + X) (2 mHfromD \rho D - 4 X \rho D + 2 X^2 \rho D + mHfromD \rho H)}{2 N_{\text{tot}} (-2 + X) X^2 \rho D \rho H}, \right. \\
& \quad \left. -\frac{(-1 + X) (2 mDfromH \rho D + mDfromH \rho H - 2 X \rho H + X^2 \rho H)}{2 N_{\text{tot}} (-2 + X) X^2 \rho D \rho H} \right\}
\end{aligned}$$

$$\text{FNlarge} = \left\{ \frac{(1 - X) * ((2 - X) * X * (2 * \rho D) - mHfromD (\rho H + 2 * \rho D))}{(2 - X) * X^2 * \rho H * (2 * \rho D) * Ntot}, \right.$$

$$\left. \frac{(1 - X) * ((2 - X) * X * \rho H - mDfromH (\rho H + 2 * \rho D))}{(2 - X) * X^2 * \rho H * (2 * \rho D) * Ntot} \right\};$$

**Simplify[% - %%, constraints]**

{0, 0}

We can use the above general Fst result when Ntot is large to estimate the degree of sexuality, although this is too complicated to present in the main paper:

$$\text{FNlarge} /. X \rightarrow mHfromD + mDfromH /. mHfromD \rightarrow 1 - mHfromH /. mDfromH \rightarrow 1 - mDfromD /.$$

$$mHfromH \rightarrow \frac{\theta HH}{Ntot} /. mDfromD \rightarrow \frac{\theta DD}{Ntot} // \text{Simplify};$$

**Simplify[Solve[{%[[1]] == \phi H, %[[2]] == \phi D}, {\theta HH, \theta DD}], constraints]**

$$\left\{ \begin{aligned} \theta HH &\rightarrow \left( 2 Ntot \rho H (1 + 2 Ntot \phi D) (\phi D + \phi H) + \right. \\ &4 Ntot^3 \rho H^4 \phi D (\phi D + \phi H)^2 - 2 Ntot^2 \rho H^3 (\phi D + \phi H) (\phi H + 4 Ntot \phi D (\phi D + \phi H)) + \\ &Ntot \rho H^2 (\phi D + \phi H) (-1 + 4 Ntot^2 \phi D (\phi D + \phi H) + Ntot (-4 \phi D + 2 \phi H)) - \\ &\sqrt{2} \sqrt{Ntot^3 \rho D \rho H \phi H^2 (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^3} \Big) / \\ &\left( (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^2 \right), \\ \theta DD &\rightarrow \left( 4 Ntot \phi D \phi H + 4 Ntot \phi H^2 + 4 Ntot^3 \rho H^4 \phi H^2 (\phi D + \phi H)^2 + \right. \\ &2 Ntot \rho H \phi H (\phi D + \phi H) (-3 + 2 Ntot (\phi D + 2 \phi H)) + \\ &2 Ntot \rho H^2 \phi H (\phi D + \phi H) (1 + 2 Ntot^2 \phi H (\phi D + \phi H) - Ntot (4 \phi D + 7 \phi H)) - \\ &2 Ntot^2 \rho H^3 \phi H (\phi D + \phi H) (\phi H (-3 + 4 Ntot \phi H) + \phi D (-2 + 4 Ntot \phi H)) - \\ &\sqrt{2} \phi D \sqrt{Ntot^3 \rho D \rho H \phi H^2 (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^3} \Big) / \\ &\left( \phi H (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^2 \right), \\ \theta HH &\rightarrow \left( 2 Ntot \rho H (1 + 2 Ntot \phi D) (\phi D + \phi H) + 4 Ntot^3 \rho H^4 \phi D (\phi D + \phi H)^2 - \right. \\ &2 Ntot^2 \rho H^3 (\phi D + \phi H) (\phi H + 4 Ntot \phi D (\phi D + \phi H)) + \\ &Ntot \rho H^2 (\phi D + \phi H) (-1 + 4 Ntot^2 \phi D (\phi D + \phi H) + Ntot (-4 \phi D + 2 \phi H)) + \\ &\sqrt{2} \sqrt{Ntot^3 \rho D \rho H \phi H^2 (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^3} \Big) / \\ &\left( (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^2 \right), \\ \theta DD &\rightarrow \left( 4 Ntot \phi D \phi H + 4 Ntot \phi H^2 + 4 Ntot^3 \rho H^4 \phi H^2 (\phi D + \phi H)^2 + \right. \\ &2 Ntot \rho H \phi H (\phi D + \phi H) (-3 + 2 Ntot (\phi D + 2 \phi H)) + \\ &2 Ntot \rho H^2 \phi H (\phi D + \phi H) (1 + 2 Ntot^2 \phi H (\phi D + \phi H) - Ntot (4 \phi D + 7 \phi H)) - \\ &2 Ntot^2 \rho H^3 \phi H (\phi D + \phi H) (\phi H (-3 + 4 Ntot \phi H) + \phi D (-2 + 4 Ntot \phi H)) + \\ &\sqrt{2} \phi D \sqrt{Ntot^3 \rho D \rho H \phi H^2 (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^3} \Big) / \\ &\left( \phi H (\phi D + \phi H) (\rho H + 2 \rho D (1 + Ntot \rho H (\phi D + \phi H)))^2 \right) \Big\} \end{aligned} \right.$$

In the primarily sexual case (mDD and mHH small):

```

Factor[Normal[Series[
  Fexact /. X → mHfromD + mDfromH /. mHfromD → 1 - mHfromH /. mDfromH → 1 - mDfromD /.
    mHfromH → θHH / Ntot /. mDfromD → θDD / Ntot /. Ntot → ε, {ε, 0, 0} ]]]
{ 2 ρD + ρH
  2 ρD + ρH
  2 ρD + ρH
  2 ρD + ρH + 8 θDD ρD ρH + 8 θHH ρD ρH } ]
{ 2 ρD + ρH + 8 θDD ρD ρH + 8 θHH ρD ρH
  ρH + (2 * ρD)
  ρH + (2 * ρD) + 4 * ρH * (2 * ρD) * (θHH + θDD)
  0 // Simplify
}

```

Consistent with (B.1).

In the fully symmetric case with  $\rho H=2/3$ :

```

Factor[
  Fexact /. X → mHfromD + mDfromH /. mHfromH → 1 - m /. mDfromD → 1 - m /. mHfromD → m /.
    mDfromH → m /. ρD → 1 - ρH /. ρH → 2/3 // Simplify
{ - 3 (1 - 2 m)²
  3 (1 - 2 m)²
  - 3 + m (12 - 8 Ntot) + 4 m² (-3 + 2 Ntot) , - 3 + m (12 - 8 Ntot) + 4 m² (-3 + 2 Ntot) }

```

In agreement with equation (6):

```

(1 - 2 * m)²
────────────────────────────────────────────────────────;
2/3 * Ntot - (1 - 2 * m)² (2/3 * Ntot - 1)
%% - % // Factor
{0, 0}

```

## Extreme values of Fst

```

Simplify[FaiHHstrict /. subconstraints /. mHfromD → 0 /. mDfromH → 0, constraints]
Simplify[FaiDDstrict /. subconstraints /. mHfromD → 0 /. mDfromH → 0, constraints]
1
1
Simplify[FaiHHstrict /. subconstraints /. mHfromD → 1/2 /. mDfromH → 1/2, constraints]
Simplify[FaiDDstrict /. subconstraints /. mHfromD → 1/2 /. mDfromH → 1/2, constraints]
0
0

```

```

Simplify[FaiHHstrict /. subconstraints /. mHfromD → 1 /. mDfromH → 1, constraints]
Simplify[FaiDDstrict /. subconstraints /. mHfromD → 1 /. mDfromH → 1, constraints]
1
1

Simplify[FaiHHstrict /. subconstraints /. mHfromD → 0 /. mDfromH → 1, constraints]
Simplify[FaiDDstrict /. subconstraints /. mHfromD → 0 /. mDfromH → 1, constraints]
0
0

Simplify[FaiHHstrict /. subconstraints /. mHfromD → 1 /. mDfromH → 0, constraints]
Simplify[FaiDDstrict /. subconstraints /. mHfromD → 1 /. mDfromH → 0, constraints]
0
0

Simplify[FaiHHstrict /. subconstraints /. mHfromD → 1 - mDfromH, constraints]
Simplify[FaiDDstrict /. subconstraints /. mHfromD → 1 - mDfromH, constraints]
0
0

```

## Appendix B

### Equations

```

FaiHHstrict = ((1 - X)3 + Ntot * (1 - X) * ((2 - X) * X * (2 * ρD) - mHfromD * (ρH + 2 * ρD)) / 
((1 - X)3 - Ntot * (1 - X) * ((1 - X)2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) + 
Ntot2 * X2 * (2 - X) * (2 * ρD) * ρH) /. X → mHfromD + mDfromH // Simplify;
FaiDDstrict = ((1 - X)3 + Ntot * (1 - X) * ((2 - X) * X * ρH - mDfromH * (ρH + 2 * ρD)) / 
((1 - X)3 - Ntot * (1 - X) * ((1 - X)2 * (ρH + 2 ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) + 
Ntot2 * X2 * (2 - X) * (2 * ρD) * ρH) /. X → mHfromD + mDfromH // Simplify;

constraints = {mHfromH + mHfromD == 1, mDfromH + mDfromD == 1, ρD + ρH == 1};
subconstraints = {mHfromH → 1 - mHfromD, mDfromD → 1 - mDfromH};

```

## Complete symmetry case

**Simplify**[

FaiHHstrict /. subconstraints /. mHfromD → m /. mDfromH → m /. ρD → 1 - ρH /. ρH →  $\frac{2}{3}$ ,  
constraints]

**Simplify**[FaiDDstrict /. subconstraints /. mHfromD → m /. mDfromH → m /. ρD → 1 - ρH /.  
 $\rho H \rightarrow \frac{2}{3}$ , constraints]

$$-\frac{3 (1 - 2 m)^2}{-3 + m (12 - 8 N_{tot}) + 4 m^2 (-3 + 2 N_{tot})} \\ -\frac{3 (1 - 2 m)^2}{-3 + m (12 - 8 N_{tot}) + 4 m^2 (-3 + 2 N_{tot})}$$

$$\text{Eq6} = \frac{(1 - 2 * m)^2}{\frac{2}{3} * N_{tot} - (1 - 2 * m)^2 * \left(\frac{2}{3} * N_{tot} - 1\right)};$$

**Eq6 - %** // Simplify

0

If we assume N large and N m of order one, we get

$$\text{Simplify}\left[\text{Normal}\left[\text{Series}\left[\text{Eq6} /. m \rightarrow \frac{\theta}{N_{tot}} /. N_{tot} \rightarrow \frac{N_{tot}}{\epsilon}, \{\epsilon, 0, 0\}\right]\right]\right] \\ \frac{3}{3 + 8 \theta}$$

which reduces to the classic Fst prediction when expressing the total population size in terms of the effective number of diploids:

$$\text{Simplify}\left[\% /. \theta \rightarrow \frac{3}{2} * m * cN_{tot}\right] \\ \frac{1}{1 + 4 cN_{tot} m}$$

**Limit[Eq6, m → 0]**

$$\text{Limit}\left[\text{Eq6}, m \rightarrow \frac{1}{2}\right]$$

**Limit[Eq6, m → 1]**

1

0

1

## Rare sexuality in a large population

We consider the case when there is frequent asexual reproduction ( $\alpha \approx 1$ , and then  $mH_{fromD}$  and  $mD_{fromH}$  is small), and large population size. We assume;

- $mH_{fromD} = O(\epsilon)$
- $mD_{fromH} = O(\epsilon)$
- $N_{tot} = O(1/\epsilon)$

These assumptions indicates,  $\theta HD = mH_{fromD} N_{tot} = O(1)$  and  $\theta DH = mD_{fromH} N_{tot} = O(1)$ .

```
FNlarge[[1]] /. X → mHfromD + mDfromH
```

$$\frac{((1 - mD_{fromH} - mH_{fromD}) (2 (2 - mD_{fromH} - mH_{fromD}) (mD_{fromH} + mH_{fromD}) \rho D - mH_{fromD} (2 \rho D + \rho H)) / (2 (2 - mD_{fromH} - mH_{fromD}) (mD_{fromH} + mH_{fromD})^2 N_{tot} \rho D \rho H))}{(2 (2 - mD_{fromH} - mH_{fromD}) (mD_{fromH} + mH_{fromD})^2 N_{tot} \rho D \rho H)}$$

```
FaiHH♦RS = Simplify[
```

$$\begin{aligned} & \text{Normal}\left[\text{Series}\left[FaiHHstrict /. \text{subconstraints} /. \rho D \rightarrow 1 - \rho H /. mH_{fromD} \rightarrow \frac{\theta HD}{N_{tot}} /.\right.\right. \\ & \quad \left.\left.mD_{fromH} \rightarrow \frac{\theta DH}{N_{tot}} /.\ N_{tot} \rightarrow cN_{tot} * \frac{1}{\epsilon}, \{\epsilon, 0, 0\}\right]\right] \\ & - \frac{1 + \theta HD (2 - 3 \rho H) - 4 \theta DH (-1 + \rho H)}{-1 - 4 \theta DH - 2 \theta HD + 3 \theta DH \rho H + 4 (\theta DH + \theta HD)^2 (-1 + \rho H) \rho H} \end{aligned}$$

```
FaiDD♦RS = Simplify[
```

$$\begin{aligned} & \text{Normal}\left[\text{Series}\left[FaiDDstrict /. \text{subconstraints} /. \rho D \rightarrow 1 - \rho H /. mH_{fromD} \rightarrow \frac{\theta HD}{N_{tot}} /.\right.\right. \\ & \quad \left.\left.mD_{fromH} \rightarrow \frac{\theta DH}{N_{tot}} /.\ N_{tot} \rightarrow cN_{tot} * \frac{1}{\epsilon}, \{\epsilon, 0, 0\}\right]\right] \\ & - \frac{1 + 2 \theta HD \rho H + \theta DH (-2 + 3 \rho H)}{-1 - 4 \theta DH - 2 \theta HD + 3 \theta DH \rho H + 4 (\theta DH + \theta HD)^2 (-1 + \rho H) \rho H} \end{aligned}$$

$$Eq9a = \frac{1 + (2 * \rho D) * (\theta HD + \theta DH) - (\rho H * \theta HD - (2 * \rho D) * \theta DH)}{1 + 2 * (\theta HD + \theta DH) + 2 * \rho H * (2 * \rho D) * (\theta HD + \theta DH)^2 - (\rho H - (2 * \rho D)) * \theta DH};$$

$$Eq9b = \frac{1 + \rho H * (\theta HD + \theta DH) + (\rho H * \theta HD - (2 * \rho D) * \theta DH)}{1 + 2 * (\theta HD + \theta DH) + 2 * \rho H * (2 * \rho D) * (\theta HD + \theta DH)^2 - (\rho H - (2 * \rho D)) * \theta DH};$$

```
FaiHH♦RS - Eq9a /. \rho D \rightarrow 1 - \rho H // Simplify
```

```
FaiDD♦RS - Eq9b /. \rho D \rightarrow 1 - \rho H // Simplify
```

0

0

```

FaiHH♦RS /. ρH → 2 / . θHD → m * Ntot /. θDH → m * Ntot /. Ntot → 3 / 2 * Nlocal // Factor
3
2
FaiDD♦RS /. ρH → 2 / . θHD → m * Ntot /. θDH → m * Ntot /. Ntot → 3 / 2 * Nlocal // Factor
3
1
1 + 4 m Nlocal
1
1 + 4 m Nlocal

sol = Simplify[
  Solve[(Eq9a /. ρD → 1 - ρH) == φH && (Eq9b /. ρD → 1 - ρH) == φD, {θHD, θDH}], 0 < ρH < 1]
{θHD → (φD (-4 + 4 ρH + 4 φH - 5 ρH φH) + φH (-2 + 3 ρH + 2 φH - 2 ρH φH)) / (4 (-1 + ρH) ρH (φD + φH)^2),
  θDH → (ρH φD^2 - 2 ρH φH + φD (2 - 2 φH + ρH (-3 + 4 φH))) / (4 (-1 + ρH) ρH (φD + φH)^2)}
Eq10a = (2 * ρD) * (1 - φH) * (φH + 2 * φD) - ρH * φH * (1 - φD) / (2 * ρH * (2 * ρD) * (φH + φD)^2);
Eq10b = (ρH * (1 - φD) * (2 * φH + φD) - (2 ρD) * φD * (1 - φH)) / (2 * ρH * (2 * ρD) * (φH + φD)^2);
(θHD /. sol[[1]]) - Eq10a /. ρD → 1 - ρH // Simplify
(θDH /. sol[[1]]) - Eq10b /. ρD → 1 - ρH // Simplify

```

0

0

This matches equation 10.

### Common sexuality in a large population

We consider the case when the species has frequent sexual reproduction ( $a \approx 0$ , and then  $m_{HH}$  and  $m_{DD}$  is small), large population size.

We assume  $m_{HH} = O(\epsilon)$ ,  $m_{DD} = O(\epsilon)$ ,  $N = O(1/\epsilon)$ ,  $m_{HH} N = O(1)$ , and  $m_{DD} N = O(1)$ .

```

FaiHH♦RA =
Simplify[Normal[Series[FaiHHstrict /. mHfromD → 1 - mHfromH /. mDfromH → 1 - mDfromD /.
  mHfromH → θHH / Ntot /. mDfromD → θDD / Ntot /. Ntot → cNtot * 1 / ε, {ε, 0, 0}]]]
2 ρD + ρH
ρH + ρD (2 + 8 θDD ρH + 8 θHH ρH)

```

$$\text{Faidd}\blacklozenge\text{RA} = \text{Simplify}\left[\text{Normal}\left[\text{Series}\left[\text{Faiddstrict} /. \text{mHfromD} \rightarrow 1 - \text{mHfromH} /. \text{mDfromH} \rightarrow 1 - \text{mDfromD} /. \text{mHfromH} \rightarrow \frac{\theta\text{HH}}{\text{Ntot}} /. \text{mDfromD} \rightarrow \frac{\theta\text{DD}}{\text{Ntot}} /. \text{Ntot} \rightarrow \text{cNtot} * \frac{1}{\epsilon}, \{\epsilon, 0, 0\}\right]\right]\right]$$

$$\frac{2 \rho D + \rho H}{\rho H + \rho D (2 + 8 \theta DD \rho H + 8 \theta HH \rho H)}$$

These are equal to one another.

$$\text{EqB1} = \frac{\rho H + (2 * \rho D)}{\rho H + (2 * \rho D) + 4 * \rho H * (2 * \rho D) * (\theta HH + \theta DD)};$$

$$\text{FaHH}\blacklozenge\text{RA} - \text{EqB1} /. \rho D \rightarrow 1 - \rho H // \text{Simplify}$$

$$\text{Faidd}\blacklozenge\text{RA} - \text{EqB1} /. \rho D \rightarrow 1 - \rho H // \text{Simplify}$$

$$0$$

$$0$$

$$\text{sol} = \text{Simplify}\left[\text{Solve}\left[\frac{\rho H + (2 * \rho D)}{\rho H + (2 * \rho D) + 4 * \rho H * (2 * \rho D) * \text{sum}} = \varphi, \{\text{sum}\}\right], 0 < \rho H < 1\right]$$

$$\left\{\left\{\text{sum} \rightarrow -\frac{(2 \rho D + \rho H) (-1 + \varphi)}{8 \rho D \rho H \varphi}\right\}\right\}$$

$$(\text{sum} /. \text{sol}[[1]]) - \frac{(1 - \varphi) * (\rho H + (2 * \rho D))}{4 * \varphi * \rho H * (2 * \rho D)} /. \rho D \rightarrow 1 - \rho H // \text{Simplify}$$

$$0$$

which matches equation (B.2).

## Rare sexuality in a very large population

We consider the case when the specie represents frequent asexual reproduction ( $a \leq 1$ , and then  $m_{DtoH}$  and  $m_{HtoD}$  is small), large population size.

We assume  $m_{DtoH} = O(\epsilon)$ ,  $m_{HtoD} = O(\epsilon)$ ,  $N = O(1/\epsilon^2)$ ,  $m_{DtoH} N = O(1/\epsilon)$ , and  $m_{HtoD} N = O(1/\epsilon)$ .

```

Series[FaiHHstrict /. X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH /.
mHfromD → cmHfromD * ε /. mDfromH → cmDfromH * ε /.
Ntot → cNtot *  $\frac{1}{\epsilon^2}$ , {ε, 0, 1}] // FullSimplify

FaiHH♦RSlargemN = Normal[%] /. cmDfromH →  $\frac{mDfromH}{\epsilon}$  /. cmHfromD →  $\frac{mHfromD}{\epsilon}$  /.
cNtot → Ntot * ε2 /. mHfromD →  $\frac{\theta HD}{Ntot}$  /. mDfromH →  $\frac{\theta DH}{Ntot}$  // FullSimplify


$$\frac{(4 \text{cmDfromH} (-1 + \rho H) + \text{cmHfromD} (-2 + 3 \rho H)) \epsilon}{4 (\text{cmDfromH} + \text{cmHfromD})^2 \text{cNtot} (-1 + \rho H) \rho H} + O[\epsilon]^2$$



$$\frac{4 \theta DH (-1 + \rho H) + \theta HD (-2 + 3 \rho H)}{4 (\theta DH + \theta HD)^2 (-1 + \rho H) \rho H}$$


Series[FaiDDstrict /. X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH /.
mHfromD → cmHfromD * ε /. mDfromH → cmDfromH * ε /.
Ntot → cNtot *  $\frac{1}{\epsilon^2}$ , {ε, 0, 1}] // FullSimplify

FaiDD♦RSlargemN = Normal[%] /. cmDfromH →  $\frac{mDfromH}{\epsilon}$  /. cmHfromD →  $\frac{mHfromD}{\epsilon}$  /.
cNtot → Ntot * ε2 /. mHfromD →  $\frac{\theta HD}{Ntot}$  /. mDfromH →  $\frac{\theta DH}{Ntot}$  // FullSimplify


$$\frac{(\text{cmDfromH} (2 - 3 \rho H) - 2 \text{cmHfromD} \rho H) \epsilon}{4 (\text{cmDfromH} + \text{cmHfromD})^2 \text{cNtot} (-1 + \rho H) \rho H} + O[\epsilon]^2$$



$$\frac{\theta DH (2 - 3 \rho H) - 2 \theta HD \rho H}{4 (\theta DH + \theta HD)^2 (-1 + \rho H) \rho H}$$


FaiHH♦RSlargemN - 
$$\frac{(2 * \theta DH + \theta HD) * (2 * \rho D) - \theta HD * \rho H}{4 * (\theta DH + \theta HD)^2 * \rho H * \rho D} // Simplify$$

FaiDD♦RSlargemN - 
$$\frac{(2 * \theta HD + \theta DH) * \rho H - \theta DH * (2 * \rho D)}{4 * (\theta DH + \theta HD)^2 * \rho H * \rho D} // Simplify$$

0
0

sol = Simplify[Solve[(FaiHH♦RSlargemN /. ρD → 1 - ρH) == φH & &
(FaiDD♦RSlargemN /. ρD → 1 - ρH) == φD, {θHD, θDH}], 0 < ρH < 1]
{θHD → 
$$\frac{4 (-1 + \rho H) \varphi D + (-2 + 3 \rho H) \varphi H}{4 (-1 + \rho H) \rho H (\varphi D + \varphi H)^2}$$
, θDH → 
$$\frac{(2 - 3 \rho H) \varphi D - 2 \rho H \varphi H}{4 (-1 + \rho H) \rho H (\varphi D + \varphi H)^2}}$$
}

```

$$\frac{\theta HD + \theta DH / . sol[[1]] // Simplify}{\frac{-2 + \rho H}{4 (-1 + \rho H) \rho H (\varphi D + \varphi H)}}$$

We note, this approximation can be derived from the approximation of large N limit.

$$\begin{aligned} & \text{Simplify} \\ & \text{Normal}\left[\text{Series}\left[FNlarge /. X \rightarrow mHfromD + mDfromH /. \text{subconstraints} /. \rho D \rightarrow 1 - \rho H /. \right.\right. \\ & \quad \left.mHfromD \rightarrow \frac{\theta HD}{Ntot} /. mDfromH \rightarrow \frac{\theta DH}{Ntot} /. Ntot \rightarrow cNtot * \frac{1}{\epsilon}, \{\epsilon, 0, 0\}\right]\left.\right] \\ & \% - \{FaiHH \diamond RSLargemN, FaiDD \diamond RSLargemN\} \\ & \left\{ \frac{4 \theta DH (-1 + \rho H) + \theta HD (-2 + 3 \rho H)}{4 (\theta DH + \theta HD)^2 (-1 + \rho H) \rho H}, \frac{\theta DH (2 - 3 \rho H) - 2 \theta HD \rho H}{4 (\theta DH + \theta HD)^2 (-1 + \rho H) \rho H} \right\} \\ & \{0, 0\} \end{aligned}$$

## Appendix C

### Definition of Fst in Whitlock and Barton (1997)

The generalized Wright's Fst coefficient can be defined as;

$$\text{Corr}[ij] = \frac{F_{ij} - F_{ave}}{1 - F_{ave}}$$

Because  $F_{ij}$  could be approximated as;

$$F_{ij}(t) = 1 - r_{ij} \lambda^t$$

$$F_{ave} = \frac{H^2}{(H+2D)^2} F_{HH} + \frac{H(2D)}{(H+2D)^2} F_{HD} + \frac{(2D)H}{(H+2D)^2} F_{DH} + \frac{(2D)^2}{(H+2D)^2} F_{HH}$$

using leading eigenvalue  $\lambda$  and right eigenvector  $u$  for matrix  $G$ , the Fst becomes

$$\begin{aligned} \text{Corrijave}[ij] &= \frac{F_{ij} - F_{ave}}{1 - F_{ave}} = \\ & \frac{\left( \frac{H^2}{(H+2D)^2} r_{HH} + \frac{H(2D)}{(H+2D)^2} r_{HD} + \frac{(2D)H}{(H+2D)^2} r_{DH} + \frac{(2D)^2}{(H+2D)^2} r_{HH} - r_{ij} \right) \lambda^t}{\left( \frac{H^2}{(H+2D)^2} r_{HH} + \frac{H(2D)}{(H+2D)^2} r_{HD} + \frac{(2D)H}{(H+2D)^2} r_{DH} + \frac{(2D)^2}{(H+2D)^2} r_{HH} \right) \lambda^t} = 1 - \frac{r_{ij}}{\frac{H^2}{(H+2D)^2} r_{HH} + \frac{H(2D)}{(H+2D)^2} r_{HD} + \frac{(2D)H}{(H+2D)^2} r_{DH} + \frac{(2D)^2}{(H+2D)^2} r_{HH}} \end{aligned}$$

Hence, we will need the leading right eigenvector for the matrix  $G$ .

```
MatrixG =
```

$$\left( \begin{array}{cccc} mHfromH^2 * \left( 1 - \frac{1}{Hap} \right) & mHfromH * mHfromD & mHfromD * mHfromH & mHfromD^2 * \left( 1 - \frac{1}{2*D} \right) \\ mHfromH * mDfromH * \left( 1 - \frac{1}{Hap} \right) & mHfromH * mDfromD & mHfromD * mDfromH & mHfromD * mDfromD * \left( 1 - \frac{1}{2*D} \right) \\ mDfromH * mHfromH * \left( 1 - \frac{1}{Hap} \right) & mDfromH * mHfromD & mDfromD * mHfromH & mDfromD * mHfromD * \left( 1 - \frac{1}{2*D} \right) \\ mDfromH^2 * \left( 1 - \frac{1}{Hap} \right) & mDfromH * mDfromD & mDfromD * mDfromH & mDfromD^2 * \left( 1 - \frac{1}{2*D} \right) \end{array} \right);$$

We first consider the right leading eigenvalue of matrix G.

```
MatrixG /. subconstraints /. Hap → ρH * Ntot /. Dip → (1 - ρH) * Ntot /. Ntot → cNtot * 1/ε;
Limit[% , ε → 0];
% // MatrixForm
Eigenvalues[%]
Eigenvectors[%]

$$\begin{pmatrix} (-1 + mHfromD)^2 & -(-1 + mHfromD) mHfromD & -(-1 + mHfromD) mHfromD \\ mDfromH - mDfromH mHfromD & (-1 + mDfromH) (-1 + mHfromD) & mDfromH mHfromD \\ mDfromH - mDfromH mHfromD & mDfromH mHfromD & (-1 + mDfromH) (-1 + mHfromD) \\ mDfromH^2 & -(-1 + mDfromH) mDfromH & -(-1 + mDfromH) mDfromH \end{pmatrix}$$


$$\{1, 1 - mDfromH - mHfromD, 1 - mDfromH - mHfromD, (-1 + mDfromH + mHfromD)^2\}$$


$$\left\{ \{1, 1, 1, 1\}, \left\{ -\frac{mHfromD}{mDfromH}, -\frac{-mDfromH + mHfromD}{mDfromH}, 0, 1 \right\}, \right.$$


$$\left. \{0, -1, 1, 0\}, \left\{ \frac{mHfromD^2}{mDfromH^2}, -\frac{mHfromD}{mDfromH}, -\frac{mHfromD}{mDfromH}, 1 \right\} \right\}$$

CharEq = Det[MatrixG - λ * IdentityMatrix[4]] /. subconstraints /. Hap → ρH * Ntot /.
Dip → (1 - ρH) * Ntot // Simplify;
```

```

CharEqlargeN =
  CharEq /. Ntot → cNtot *  $\frac{1}{\epsilon}$  /. λ → λ0 + λ1 * ε + λ2 * ε2 + λ3 * ε3 + λ4 * ε4 + λ5 * ε5 +
    λ6 * ε6 + λ7 * ε7 + λ8 * ε8 + λ9 * ε9 + λ10 * ε10 // Simplify;
Limit[% , ε → 0]
Solve[% == 0 , λ0]
- (1 + mDfromH2 + 2 mDfromH (-1 + mHfromD) - 2 mHfromD + mHfromD2 - λ0)
(-1 + λ0) (-1 + mDfromH + mHfromD + λ0)2
{ {λ0 → 1} , {λ0 → 1 - mDfromH - mHfromD} ,
  {λ0 → 1 - mDfromH - mHfromD} , {λ0 → (-1 + mDfromH + mHfromD)2} }

Series[CharEqlargeN, {ε, 0, 1}];
% /. λ0 → 1 // Simplify
-  $\frac{1}{2(cNtot(-1 + \rho H)\rho H)} ((-2 + mDfromH + mHfromD)(mDfromH + mHfromD)$ 
 $(mHfromD^2(-1 + 2cNtot\lambda1(-1 + \rho H))\rho H + 4cNtotmDfromHmHfromD\lambda1(-1 + \rho H)\rho H +$ 
 $2mDfromH^2(-1 + \rho H)(1 + cNtot\lambda1\rho H)) \in + O[\epsilon]^2$ 

solλ1 = Simplify[Solve[(Normal[%]) == 0, λ1], 0 < cNtot]
{ {λ1 →  $\frac{-2mDfromH^2(-1 + \rho H) + mHfromD^2\rho H}{2cNtot(mDfromH + mHfromD)^2(-1 + \rho H)\rho H}$  } }

Order0λ = 1;
Order1λ = λ1 /. solλ1[[1]];

λGapprox = Order0λ + Order1λ * ε /. cNtot → Ntot * ε // Simplify
1 +  $\frac{-2mDfromH^2(-1 + \rho H) + mHfromD^2\rho H}{2(mDfromH + mHfromD)^2Ntot(-1 + \rho H)\rho H}$ 

```

We next derive the right leading eigenvector of matrix G.

$$\text{RightVapprox} = \begin{pmatrix} rHHorder0 + rHHorder1 * \epsilon + rHHorder2 * \epsilon^2 \\ rHDorder0 + rHDorder1 * \epsilon + rHDorder2 * \epsilon^2 \\ rDHorder0 + rDHorder1 * \epsilon + rDHorder2 * \epsilon^2 \\ rDDorder0 + rDDorder1 * \epsilon + rDDorder2 * \epsilon^2 \end{pmatrix};$$

$$\text{condRightV} = (\text{MatrixG.RightVapprox}) - (\lambda * \text{RightVapprox}) /. \lambda \rightarrow \lambdaGapprox + \lambda2 * \epsilon^2 / .$$
 $\text{subconstraints} /. \text{Hap} \rightarrow \rho H * \text{Ntot} / .$ 
 $\text{Dip} \rightarrow (1 - \rho H) * \text{Ntot} / . \text{Ntot} \rightarrow cNtot * \frac{1}{\epsilon} // \text{Simplify};$

We consider order 0, we have

```

Series[condRightV, {ε, 0, 0}];
Normal[%] // Simplify

{{mHfromD (rDHorder0 + rHDorder0 - 2 rHHorder0 +
    mHfromD (rDDorder0 - rDHorder0 - rHDorder0 + rHHorder0))},
 {mHfromD (rDDorder0 - mDfromH rDDorder0 - rHDorder0 +
    mDfromH (rDHorder0 + rHDorder0 - rHHorder0)) + mDfromH (-rHDorder0 + rHHorder0)},
 {mHfromD (rDDorder0 - mDfromH rDDorder0 + (-1 + mDfromH) rDHorder0 +
    mDfromH (rHDorder0 - rHHorder0)) + mDfromH (-rDHorder0 + rHHorder0)},
 {mDfromH ((-2 + mDfromH) rDDorder0 + rDHorder0 - mDfromH rDHorder0 +
    rHDorder0 - mDfromH rHDorder0 + mDfromH rHHorder0)}}

sol0 = Solve[% == {{0, 0, 0, 0}} && rHHorder0 + rHDorder0 + rDHorder0 + rDDorder0 == const,
 {rHHorder0, rHDorder0, rDHorder0, rDDorder0}]

{{rHHorder0 → const/4, rHDorder0 → const/4, rDHorder0 → const/4, rDDorder0 → const/4}}

```

First order term

```

Series[condRightV, {e, 0, 1}];
Normal[%] /. sol0[[1]] // Simplify

{ \in \left( \begin{aligned} & mHfromD^2 rDDorder1 + mHfromD rDHorder1 - mHfromD^2 rDHorder1 + mHfromD rHDorder1 - \\ & mHfromD^2 rHDorder1 - rHHorder1 + (-1 + mHfromD)^2 \left( rHHorder1 - \frac{\text{const}}{4 cNtot \rho H} \right) - \\ & \frac{\text{const } mHfromD^2}{8 cNtot - 8 cNtot \rho H} - \frac{\text{const } (-2 mDfromH^2 (-1 + \rho H) + mHfromD^2 \rho H)}{8 cNtot (mDfromH + mHfromD)^2 (-1 + \rho H) \rho H} \Big\}, \\ & \frac{1}{8 cNtot} \in \left( - \frac{\text{const } mHfromD^2}{(mDfromH + mHfromD)^2 (-1 + \rho H)} - \frac{1}{(mDfromH + mHfromD)^2 \rho H} \right. \\ & 2 mDfromH (\text{const } (mDfromH^2 + mHfromD^2 + mDfromH (-1 + 2 mHfromD)) + \\ & 4 cNtot (mDfromH + mHfromD)^2 (rHDorder1 - rHHorder1) \rho H) + \frac{1}{(-1 + \rho H) \rho H} \\ & mHfromD (-8 cNtot ((-1 + mDfromH) rDDorder1 + rHDorder1 - mDfromH rDHorder1 + \\ & rHDorder1 - rHHorder1)) (-1 + \rho H) \rho H + \text{const } (mDfromH (-2 + \rho H) + \rho H) \Big\}, \\ & \frac{1}{8 cNtot} \in \left( - \frac{\text{const } mHfromD^2}{(mDfromH + mHfromD)^2 (-1 + \rho H)} - \frac{1}{(mDfromH + mHfromD)^2 \rho H} \right. \\ & 2 mDfromH (\text{const } (mDfromH^2 + mHfromD^2 + mDfromH (-1 + 2 mHfromD)) + 4 cNtot \\ & (mDfromH + mHfromD)^2 (rDHorder1 - rHHorder1) \rho H) + \frac{1}{(-1 + \rho H) \rho H} mHfromD \\ & (-8 cNtot ((-1 + mDfromH) rDDorder1 + rDHorder1 - mDfromH rDHorder1 + mDfromH \\ & (-rHDorder1 + rHHorder1)) (-1 + \rho H) \rho H + \text{const } (mDfromH (-2 + \rho H) + \rho H)) \Big\}, \\ & \in \left( - rDDorder1 + mDfromH rDHorder1 - mDfromH^2 rDHorder1 + mDfromH rHDorder1 - \right. \\ & mDfromH^2 rHDorder1 + mDfromH^2 rHHorder1 + \\ & \frac{(-1 + mDfromH)^2 (\text{const } + 8 cNtot rDDorder1 (-1 + \rho H))}{8 cNtot (-1 + \rho H)} - \\ & \frac{\text{const } mDfromH^2}{4 cNtot \rho H} - \frac{\text{const } (-2 mDfromH^2 (-1 + \rho H) + mHfromD^2 \rho H)}{8 cNtot (mDfromH + mHfromD)^2 (-1 + \rho H) \rho H} \Big\} \Big\}
\end{aligned} \right)

```

```

sol1 = Solve[% == {{0, 0, 0, 0}} && rHHorder1 + rHDorder1 + rDHorder1 + rDDorder1 == 0,
{rHHorder1, rHDorder1, rDHorder1, rDDorder1}]

{{rHHorder1 \rightarrow
( const (-14 mDfromH + 20 mDfromH^2 - 6 mDfromH^3 - 6 mHfromD + 32 mDfromH mHfromD -
18 mDfromH^2 mHfromD + 12 mHfromD^2 - 18 mDfromH mHfromD^2 - 6 mHfromD^3 + 15 mDfromH
ρH - 22 mDfromH^2 ρH + 7 mDfromH^3 ρH + 11 mHfromD ρH - 40 mDfromH mHfromD ρH +
21 mDfromH^2 mHfromD ρH - 18 mHfromD^2 ρH + 21 mDfromH mHfromD^2 ρH + 7 mHfromD^3 ρH) ) /
(32 cNtot (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)^2 (-1 + ρH) ρH) , rHDorder1 \rightarrow
- (( const (-2 + 4 mDfromH - 2 mDfromH^2 + 4 mHfromD - 4 mDfromH mHfromD - 2 mHfromD^2 + ρH -
2 mDfromH ρH + mDfromH^2 ρH - 2 mHfromD ρH + 2 mDfromH mHfromD ρH + mHfromD^2 ρH) ) /
(32 cNtot (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) (-1 + ρH) ρH) , rDHorder1 \rightarrow
- (( const (-2 + 4 mDfromH - 2 mDfromH^2 + 4 mHfromD - 4 mDfromH mHfromD - 2 mHfromD^2 + ρH -
2 mDfromH ρH + mDfromH^2 ρH - 2 mHfromD ρH + 2 mDfromH mHfromD ρH + mHfromD^2 ρH) ) /
(32 cNtot (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) (-1 + ρH) ρH) ) ,
rDDorder1 \rightarrow - (( const (-10 mDfromH + 12 mDfromH^2 - 2 mDfromH^3 - 2 mHfromD +
16 mDfromH mHfromD - 6 mDfromH^2 mHfromD + 4 mHfromD^2 - 6 mDfromH mHfromD^2 -
2 mHfromD^3 + 13 mDfromH ρH - 18 mDfromH^2 ρH + 5 mDfromH^3 ρH +
9 mHfromD ρH - 32 mDfromH mHfromD ρH + 15 mDfromH^2 mHfromD ρH -
14 mHfromD^2 ρH + 15 mDfromH mHfromD^2 ρH + 5 mHfromD^3 ρH) ) /
(32 cNtot (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)^2 (-1 + ρH) ρH) ) } }
}

```

```

rightVapprox =

$$\left( \begin{array}{c} rHHorder0 + rHHorder1 * \epsilon \\ rHDorder0 + rHDorder1 * \epsilon \\ rDHorder0 + rDHorder1 * \epsilon \\ rDDorder0 + rDDorder1 * \epsilon \end{array} \right) /. sol0[[1]] /. sol1[[1]] /. cNtot \rightarrow Ntot * \epsilon // Simplify$$


$$\left\{ \left\{ \frac{1}{32} \text{const} \left( 8 + \left( (-1 + mDfromH + mHfromD) (mDfromH^2 (-6 + 7 \rho H) + mHfromD (6 - 11 \rho H + mHfromD (-6 + 7 \rho H)) + mDfromH (14 - 15 \rho H + 2 mHfromD (-6 + 7 \rho H))) \right) / \right. \right. \right.$$


$$\left. \left. \left. \left( (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)^2 Ntot (-1 + \rho H) \rho H \right) \right\}, \right. \right. \right.$$


$$\left. \left. \left. \left\{ \frac{1}{32} \text{const} \left( 8 - \frac{(-1 + mDfromH + mHfromD)^2 (-2 + \rho H)}{(-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot (-1 + \rho H) \rho H} \right) \right\}, \right. \right. \right.$$


$$\left. \left. \left. \left\{ \frac{1}{32} \text{const} \left( 8 - \frac{(-1 + mDfromH + mHfromD)^2 (-2 + \rho H)}{(-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot (-1 + \rho H) \rho H} \right) \right\}, \right. \right. \right.$$


$$\left. \left. \left. \left\{ \frac{1}{32} \text{const} \left( 8 - \left( (-1 + mDfromH + mHfromD) (mDfromH^2 (-2 + 5 \rho H) + mHfromD (2 - 9 \rho H + mHfromD (-2 + 5 \rho H)) + mDfromH (10 - 13 \rho H + 2 mHfromD (-2 + 5 \rho H))) \right) / \right. \right. \right. \right.$$


$$\left. \left. \left. \left. \left( (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)^2 Ntot (-1 + \rho H) \rho H \right) \right\} \right\} \right\}$$


Total[rightVapprox] // Simplify  

rightVapprox[[2]] = rightVapprox[[3]]  

{const}  

True


```

Using eigenvectors, we define Fst

**CorrHHave =**

$$1 - \frac{rHH}{\frac{Hap^2}{(Hap+2*Dip)^2} * rHH + \frac{2*Hap*(2*Dip)}{(Hap+2*Dip)^2} * rHD + \frac{(2*Dip)^2}{(Hap+2*Dip)^2} * rDD} / . rHH \rightarrow rightVapprox[[1, 1]] / .$$

$$rHD \rightarrow rightVapprox[[2, 1]] / . rDD \rightarrow rightVapprox[[4, 1]] / . Hap \rightarrow Ntot * \rhoH / .$$

$$Dip \rightarrow Ntot * (1 - \rhoH) / . N\tilde{tot} \rightarrow Ntot * \epsilon // FullSimplify$$

$$rHD$$

$$CorrHDave = 1 - \frac{rHH}{\frac{Hap^2}{(Hap+2*Dip)^2} * rHH + \frac{2*Hap*(2*Dip)}{(Hap+2*Dip)^2} * rHD + \frac{(2*Dip)^2}{(Hap+2*Dip)^2} * rDD} / .$$

$$rHH \rightarrow rightVapprox[[1, 1]] / . rHD \rightarrow rightVapprox[[2, 1]] / .$$

$$rDD \rightarrow rightVapprox[[4, 1]] / . Hap \rightarrow Ntot * \rhoH / .$$

$$Dip \rightarrow Ntot * (1 - \rhoH) / . N\tilde{tot} \rightarrow Ntot * \epsilon // FullSimplify$$

$$rDD$$

$$CorrDDave = 1 - \frac{rHH}{\frac{Hap^2}{(Hap+2*Dip)^2} * rHH + \frac{2*Hap*(2*Dip)}{(Hap+2*Dip)^2} * rHD + \frac{(2*Dip)^2}{(Hap+2*Dip)^2} * rDD} / .$$

$$rHH \rightarrow rightVapprox[[1, 1]] / . rHD \rightarrow rightVapprox[[2, 1]] / .$$

$$rDD \rightarrow rightVapprox[[4, 1]] / . Hap \rightarrow Ntot * \rhoH / .$$

$$Dip \rightarrow Ntot * (1 - \rhoH) / . N\tilde{tot} \rightarrow Ntot * \epsilon // FullSimplify$$

For large values of the population size, we do not obtain the same measure of Fst as Rousset's method (by contrast to the Whitlock & Barton method using HD as a comparator, rather than the average, see below):

$$\text{Factor}\left[\text{Normal}\left[\text{Series}\left[\{\text{CorrHHave}, \text{CorrDDave}\} / . \text{Ntot} \rightarrow \frac{Ntot}{\epsilon}, \{\epsilon, 0, 1\}\right]\right] / . \epsilon \rightarrow 1\right]$$

$$\left\{ - \left( \left( 2 (-1 + mDfromH + mHfromD) \right. \right. \right.$$

$$\left. \left. \left. (3 mDfromH - mDfromH^2 + mHfromD - 2 mDfromH mHfromD - mHfromD^2 - 3 mDfromH \rhoH + mDfromH^2 \rhoH - 2 mHfromD \rhoH + 2 mDfromH mHfromD \rhoH + mHfromD^2 \rhoH) \right) / \right. \right. \right.$$

$$\left. \left. \left. \left( (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)^2 Ntot (-2 + \rhoH) \rhoH \right) , \right. \right. \right.$$

$$\left. \left. \left. - \left( \left( (-1 + mDfromH + mHfromD) (4 mDfromH - 5 mDfromH \rhoH + mDfromH^2 \rhoH - 3 mHfromD \rhoH + 2 mDfromH mHfromD \rhoH + mHfromD^2 \rhoH) \right) / \right. \right. \right.$$

$$\left. \left. \left. \left( 2 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)^2 Ntot (-2 + \rhoH) (-1 + \rhoH) \right) \right) \right\}$$

$$\text{Factor}\left[\frac{\%}{FNlarge} / . X \rightarrow mHfromD + mDfromH / . \text{subconstraints} / . \rhoD \rightarrow 1 - \rhoH\right] // FullSimplify$$

$$\left\{ \left( 4 (mHfromD (1 + mHfromD (-1 + \rhoH) - 2 \rhoH) + mDfromH^2 (-1 + \rhoH) + mDfromH (-3 + 2 mHfromD) (-1 + \rhoH)) (-1 + \rhoH) \right) / \right.$$

$$\left. \left( (mHfromD (2 + 2 mHfromD (-1 + \rhoH) - 3 \rhoH) + 2 mDfromH^2 (-1 + \rhoH) + 4 mDfromH (-1 + mHfromD) (-1 + \rhoH)) (-2 + \rhoH) \right) , \right.$$

$$\left. \rhoH (-4 mDfromH - (mDfromH^2 + (-3 + mHfromD) mHfromD + mDfromH (-5 + 2 mHfromD)) \rhoH) \right\}$$

$$\left. / (-2 + \rhoH) (2 mDfromH + ((-3 + mDfromH) mDfromH + 2 (-1 + mDfromH) mHfromD + mHfromD^2) \rhoH) \right)$$

For example, in the symmetric case with large N and small (but not very small) movement rates, this

measure yields Fst values that are half as large:

$$\text{Normal}\left[\text{Series}\left[\% /. \text{mHfromD} \rightarrow m /. \text{mDfromH} \rightarrow m /. \rho H \rightarrow \frac{2}{3}, \{m, 0, 1\}\right]\right] // \text{Factor}$$

$$\left\{\frac{1}{2}, \frac{1}{2}\right\}$$

Alternatively, we can focus on the case where sexuality is nearly complete (asexuality rare, with  $mHfromH$  and  $mDfromD$  of order  $\epsilon$ ):

$$\begin{aligned} \text{Simplify}\left[\text{Normal}\left[\right.\right. \\ \text{Series}\left[\text{CorrHHave} /. \text{mHfromD} \rightarrow 1 - \text{mDfromD} /. \text{mDfromH} \rightarrow 1 - \text{mHfromH} /. \text{mHfromH} \rightarrow \frac{\theta HH}{N_{tot}} /.\right. \\ \left.\left.\text{mDfromD} \rightarrow \frac{\theta DD}{N_{tot}} /.\text{Ntot} \rightarrow c N_{tot} * \frac{1}{\epsilon}, \{\epsilon, 0, 0\}\right]\right], \text{constraints}] \\ - \frac{8 (-1 + \rho H) \rho H}{-4 + 4 (3 + 8 \theta DD + 8 \theta HH) \rho H - 3 (3 + 16 \theta DD + 16 \theta HH) \rho H^2 + 16 (\theta DD + \theta HH) \rho H^3} \end{aligned}$$

which can be written as:

$$\begin{aligned} \text{EqB1WB} = & \frac{4 * \rho H (2 * \rho D)}{-(\rho H - (2 * \rho D))^2 + 8 * \rho H * (2 * \rho D) * (\rho H + (2 * \rho D)) * (\theta HH + \theta DD)} ; \\ & \% - \% /. \rho D \rightarrow 1 - \rho H // \text{Factor} \\ & 0 \end{aligned}$$

This differs substantially from Eq. (B.1) based on Rousset's method (becoming negative as sexuality approaches one rather than approaching one as does Eq. (B.1)), likely because the coalescent events are poorly described by the leading eigenvalue only when the populations are nearly fully sexual:

$$\text{EqB1} = \frac{\rho H + (2 * \rho D)}{\rho H + (2 * \rho D) + 4 * \rho H * (2 * \rho D) * (\theta HH + \theta DD)} ;$$

### Fst measured relative to HD by Whitlock and Barton (1997)

Using the eigenvectors obtained above, we define Fst

```

CorrHHhd = 1 -  $\frac{r_{HH}}{r_{HD}}$  /. rHH → rightVapprox[[1, 1]] /. rHD → rightVapprox[[2, 1]] /.
rDD → rightVapprox[[4, 1]] /. Hap → Ntot * ρH /.
Dip → Ntot * (1 - ρH) /. cNtot → Ntot * ε // FullSimplify
CorrHDhd = 1 -  $\frac{r_{HD}}{r_{HH}}$  /. rHH → rightVapprox[[1, 1]] /. rHD → rightVapprox[[2, 1]] /.
rDD → rightVapprox[[4, 1]] /. Hap → Ntot * ρH /.
Dip → Ntot * (1 - ρH) /. cNtot → Ntot * ε // FullSimplify
CorrDDhd = 1 -  $\frac{r_{DD}}{r_{HH}}$  /. rHH → rightVapprox[[1, 1]] /. rHD → rightVapprox[[2, 1]] /.
rDD → rightVapprox[[4, 1]] /. Hap → Ntot * ρH /.
Dip → Ntot * (1 - ρH) /. cNtot → Ntot * ε // FullSimplify
- ((4 (-1 + mDfromH + mHfromD) (mHfromD (2 + 2 mHfromD (-1 + ρH) - 3 ρH) +
2 mDfromH2 (-1 + ρH) + 4 mDfromH (-1 + mHfromD) (-1 + ρH))) /
((mDfromH + mHfromD) (2 (-1 + mDfromH + mHfromD)2 -
((-1 + mDfromH + mHfromD)2 + 8 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot)
ρH + 8 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot ρH2)))

```

0

$$(4 (-1 + mDfromH + mHfromD) (2 mDfromH + ((-3 + mDfromH) mDfromH + 2 (-1 + mDfromH) mHfromD + mHfromD<sup>2</sup>) ρH)) /
((mDfromH + mHfromD) (2 (-1 + mDfromH + mHfromD)<sup>2</sup> -
((-1 + mDfromH + mHfromD)<sup>2</sup> + 8 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot) ρH +
8 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot ρH<sup>2</sup>))$$

For large values of the population size, we obtain the same measure of Fst as Rousset's method:

```

Factor[Normal[Series[{CorrHHhd, CorrDDhd} /. Ntot →  $\frac{N_{tot}}{\epsilon}$ , {ε, 0, 1}]] /. ε → 1]
{- (((-1 + mDfromH + mHfromD) (4 mDfromH - 2 mDfromH2 + 2 mHfromD - 4 mDfromH mHfromD - 2 mHfromD2 - 4 mDfromH ρH +
2 mDfromH2 ρH - 3 mHfromD ρH + 4 mDfromH mHfromD ρH + 2 mHfromD2 ρH)) /
(2 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)2 Ntot (-1 + ρH) ρH)),
((-1 + mDfromH + mHfromD) (2 mDfromH - 3 mDfromH ρH + mDfromH2 ρH -
2 mHfromD ρH + 2 mDfromH mHfromD ρH + mHfromD2 ρH)) /
(2 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)2 Ntot (-1 + ρH) ρH)}

```

```

Factor[% - FNlarge /. X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH]
{0, 0}

```

Alternatively, we can focus on the case where sexuality is nearly complete (asexuality rare, with mHfromH and mDfromD of order  $\epsilon$ ):

```

Simplify[Normal[
  Series[CorrHHhd /. mHfromD → 1 - mDfromD /. mDfromH → 1 - mHfromH /. mHfromH → θHH/Ntot /.
    mDfromD → θDD/Ntot /. Ntot → cNtot * 1/ε, {ε, 0, 0}], constraints]
  2 (-2 + ρH)
  -2 + (1 - 16 θDD - 16 θHH) ρH + 16 (θDD + θHH) ρH^2

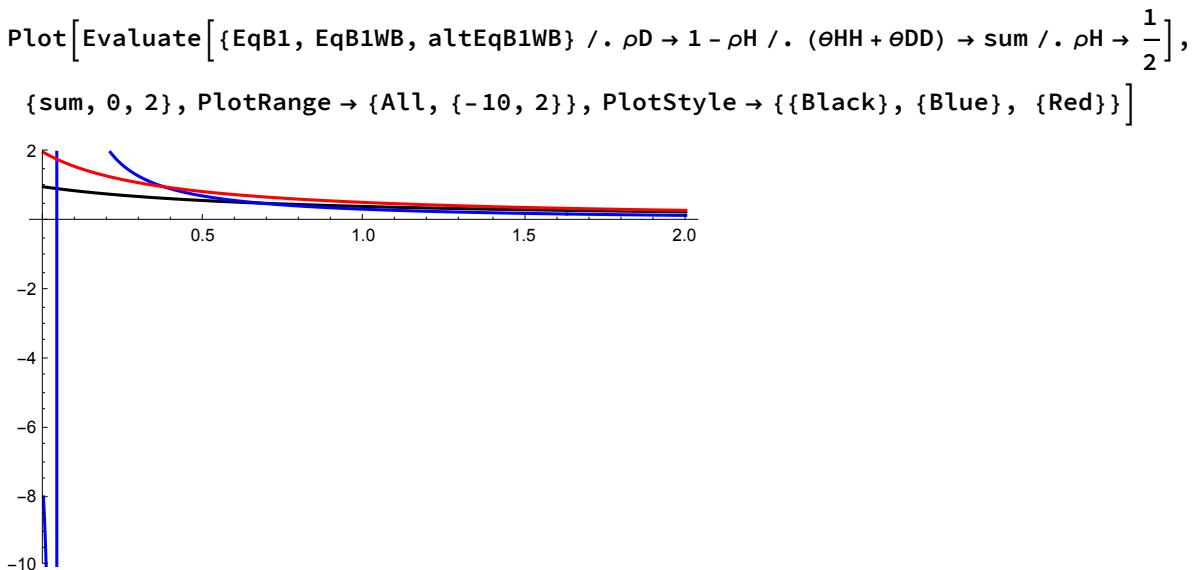
altEqB1WB = 2 * ρH + (2 * ρD) /.
  ρH + (2 * ρD) + 8 * ρH * (2 * ρD) * (θDD + θHH);
%% - % /. ρD → 1 - ρH // Factor
0

EqB1WB
  8 ρD ρH
  - (-2 ρD + ρH)^2 + 16 (θDD + θHH) ρD ρH (2 ρD + ρH)

```

This differs substantially from Eq. (B.1) based on Rousset's method (being nearly twice as large when asexuality is very rare and  $\theta_{DD}+\theta_{HH}$  near zero), likely because the coalescent events are poorly described by the leading eigenvalue only when the populations are nearly fully sexual, as assumed by the Whitlock and Barton method.

The following graph illustrates the discrepancies that arise with the Whitlock & Barton method when asexuality is very rare, where the asymptotic properties focusing on the leading eigenvalue fail to capture the dynamics when there is a nearly strict alternation of generations.



## Complete symmetry case

```

MatrixG /. subconstraints /. mHfromD → m /. mDfromH → m /. Hap → ρH * Ntot /.
Dip → (1 - ρH) * Ntot /. ρH →  $\frac{2}{3}$  // Simplify;
% // MatrixForm
FullSimplify[Eigenvalues[%], 0 < Ntot]
RightV = FullSimplify[Eigenvectors[%], 0 < Ntot]


$$\begin{pmatrix} \frac{(-1+m)^2 (-3+2 Ntot)}{2 Ntot} & -(-1+m) m & -(-1+m) m & m^2 \left(1 - \frac{3}{2 Ntot}\right) \\ (1-m) m \left(1 - \frac{3}{2 Ntot}\right) & (-1+m)^2 & m^2 & (1-m) m \left(1 - \frac{3}{2 Ntot}\right) \\ (1-m) m \left(1 - \frac{3}{2 Ntot}\right) & m^2 & (-1+m)^2 & (1-m) m \left(1 - \frac{3}{2 Ntot}\right) \\ m^2 \left(1 - \frac{3}{2 Ntot}\right) & -(-1+m) m & -(-1+m) m & \frac{(-1+m)^2 (-3+2 Ntot)}{2 Ntot} \end{pmatrix}$$



$$\left\{ 1 - 2 m + \frac{3 (-1 + 2 m)}{2 Ntot}, 1 - 2 m,$$


$$-\frac{3 + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{4 Ntot} - 4 Ntot - 2 (-1 + m) m (-3 + 4 Ntot),$$


$$-\frac{-3 + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{4 Ntot} + 4 Ntot + 2 (-1 + m) m (-3 + 4 Ntot) \right\}$$



$$\left\{ \{-1, 0, 0, 1\}, \{0, -1, 1, 0\},$$


$$\left\{ 1, \frac{-3 - 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{8 (-1 + m) m Ntot},$$


$$\frac{-3 - 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{8 (-1 + m) m Ntot}, 1 \right\},$$


$$\left\{ 1, -\frac{3 + 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{8 (-1 + m) m Ntot},$$


$$-\frac{3 + 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{8 (-1 + m) m Ntot}, 1 \right\}$$


RightVG = RightV[[4]]
RightVG[[2]] == RightVG[[3]]


$$\left\{ 1, -\frac{3 + 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{8 (-1 + m) m Ntot},$$


$$-\frac{3 + 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}}{8 (-1 + m) m Ntot}, 1 \right\}$$


```

True

```

CorrHHsym =

$$1 - \frac{r_{\text{HH}}}{\frac{Hap^2}{(Hap+2*Dip)^2} * r_{\text{HH}} + \frac{2*Hap*(2*Dip)}{(Hap+2*Dip)^2} * r_{\text{HD}} + \frac{(2*Dip)^2}{(Hap+2*Dip)^2} * r_{\text{DD}}} / . r_{\text{HH}} \rightarrow \text{RightVG}[[1]] / .$$


$$r_{\text{HD}} \rightarrow \text{RightVG}[[2]] / . r_{\text{DD}} \rightarrow \text{RightVG}[[4]] / . Hap \rightarrow Ntot * \rho H / .$$


$$Dip \rightarrow Ntot * (1 - \rho H) / . \rho H \rightarrow \frac{2}{3} // \text{FullSimplify}$$


$$\frac{r_{\text{HD}}}{\frac{Hap^2}{(Hap+2*Dip)^2} * r_{\text{HH}} + \frac{2*Hap*(2*Dip)}{(Hap+2*Dip)^2} * r_{\text{HD}} + \frac{(2*Dip)^2}{(Hap+2*Dip)^2} * r_{\text{DD}}} / .$$


$$r_{\text{HH}} \rightarrow \text{RightVG}[[1]] / . r_{\text{HD}} \rightarrow \text{RightVG}[[2]] / . r_{\text{DD}} \rightarrow \text{RightVG}[[4]] / .$$


$$Hap \rightarrow Ntot * \rho H / . Dip \rightarrow Ntot * (1 - \rho H) / . \rho H \rightarrow \frac{2}{3} // \text{FullSimplify}$$


$$\frac{r_{\text{DD}}}{\frac{Hap^2}{(Hap+2*Dip)^2} * r_{\text{HH}} + \frac{2*Hap*(2*Dip)}{(Hap+2*Dip)^2} * r_{\text{HD}} + \frac{(2*Dip)^2}{(Hap+2*Dip)^2} * r_{\text{DD}}} / .$$


$$r_{\text{HH}} \rightarrow \text{RightVG}[[1]] / . r_{\text{HD}} \rightarrow \text{RightVG}[[2]] / . r_{\text{DD}} \rightarrow \text{RightVG}[[4]] / .$$


$$Hap \rightarrow Ntot * \rho H / . Dip \rightarrow Ntot * (1 - \rho H) / . \rho H \rightarrow \frac{2}{3} // \text{FullSimplify}$$


$$\frac{1}{3} \left( \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} + 2 (-1 + m) m (-3 + 4 Ntot) \right)$$


$$\frac{1}{3} \left( -\sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} - 2 (-1 + m) m (-3 + 4 Ntot) \right)$$


$$\frac{1}{3} \left( \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} + 2 (-1 + m) m (-3 + 4 Ntot) \right)$$


EqC4a =

$$\frac{1}{3} * \left( \sqrt{9 - 4 * m * (1 - m) * (9 - m * (1 - m) * (4 * Ntot - 3)^2)} - 2 * m * (1 - m) * (4 Ntot - 3) \right);$$

EqC4a - CorrHHsym // Simplify

$$0$$

CorrHHsym == CorrDDsym

$$\text{True}$$

Limit[CorrHHsym, m \rightarrow 0]

$$\text{Limit[CorrHHsym, m \rightarrow 1]}$$


$$1$$


$$1$$


```

```

Limit[CorrHHsym, m → 1/2]
Simplify[% , 1 < Ntot]

$$\frac{1}{6} \left( 3 - 4 Ntot + \sqrt{(-3 + 4 Ntot)^2} \right)$$

0

Series[CorrHHsym /. m → cm * ε /. Ntot → cNtot * 1/ε, {ε, 0, 0}] // Simplify
Normal[%] /. cm → m / . cNtot → Ntot * ε / . Ntot → 3 * Ndeem // Simplify

$$\frac{1}{3} \left( -8 cm cNtot + \sqrt{9 + 64 cm^2 cNtot^2} \right) + O[\epsilon]^1$$


$$-8 m Ndeem + \sqrt{1 + 64 m^2 Ndeem^2}$$


```

```

Series[CorrHHsym /. m → cm * ε /. Ntot → cNtot * 1/ε, {ε, 0, 0}] // Simplify
Normal[%] /. cm → m / . cNtot → Ntot * ε / . Ntot → 3/2 * Nlocal // Simplify

$$\frac{1}{3} \left( -8 cm cNtot + \sqrt{9 + 64 cm^2 cNtot^2} \right) + O[\epsilon]^1$$


$$-4 m Nlocal + \sqrt{1 + 16 m^2 Nlocal^2}$$


```

This approximation is only half that obtained by Rousset's method ( $\frac{1}{1+4\theta_{local}}$ , where  $\theta_{local}=m Nlocal$ ) when  $\theta_{local}$  is large:

```

Limit[(-4 θlocal + √(1 + 16 θlocal^2)) / (1 / (1 + 4 θlocal)), θlocal → Infinity]

$$\frac{1}{2}$$


Series[CorrHHsym /. m → cm * ε^2 /. Ntot → cNtot * 1/ε, {ε, 0, 1}] // Simplify
Normal[%] /. cm → m / . cNtot → Ntot * ε / . Ntot → 3/2 * Nlocal // Simplify

$$1 - \frac{8}{3} (cm cNtot) \epsilon + O[\epsilon]^2$$


$$1 - 4 m Nlocal$$


```

```

Simplify[Series[CorrHHsym /. m → cm*ε /. Ntot → cNtot * 1/ε^2, {ε, 0, 1}],
          0 < cm && 0 < cNtot]
Simplify[Normal[%] /. cm → m/ε /. cNtot → Ntot*ε^2 /. Ntot → 3/2*Nlocal, {ε > 0}]

$$\frac{3\epsilon}{16cmcNtot} + O[\epsilon]^2$$


$$\frac{1}{8mNlocal}$$


```

Alternatively, we can focus on the case where sexuality is nearly complete (asexuality rare, with mHH and mDD of order  $\epsilon$ ):

```

FullSimplify[Normal[Series[CorrHHsym /. m → 1 - θii/Ntot /. Ntot → cNtot * 1/ε, {ε, 0, 0}],
          cNtot → Ntot*ε, {0 < θii, Ntot > 0}]]

$$\frac{1}{3} \left( -8\theta ii + \sqrt{9 + 64\theta ii^2} \right)$$


```

This approaches 1, as it should, when there is very little asexual reproduction ( $\theta ii$  approaches 0):

```
Limit[%, θii → 0]
```

```
1
```

But note that this is not generally true when there is very rare sexuality and the case is not fully symmetric.

### Fst measured relative to HD for the complete symmetry case

If we instead compare sampling within a ploidy population to between ploidy populations (instead of the average) we get:

```

CorrHHsym2 = 1 - rHH/rHD /. rHH → RightVG[[1]] /. rHD → RightVG[[2]] /. rDD → RightVG[[4]] /.
Hap → Ntot * ρH /. Dip → Ntot * (1 - ρH) // FullSimplify
CorrDDsym2 = 1 - rDD/rHD /. rHH → RightVG[[1]] /. rHD → RightVG[[2]] /. rDD → RightVG[[4]] /.
Hap → Ntot * ρH /. Dip → Ntot * (1 - ρH) // FullSimplify

$$1 + \frac{8(-1+m)mNtot}{3 + 6(-1+m)m + \sqrt{9 + 4(-1+m)m(9 + (-1+m)m(3 - 4Ntot)^2)}}$$


$$1 + \frac{8(-1+m)mNtot}{3 + 6(-1+m)m + \sqrt{9 + 4(-1+m)m(9 + (-1+m)m(3 - 4Ntot)^2)}}$$


```

```
CorrHHsym2 == CorrDDsym2
```

True

This is no longer EqC4a:

**EqC4a =**

$$\frac{1}{3} * \left( \sqrt{9 - 4 * m * (1 - m) * (9 - m * (1 - m) * (4 * Ntot - 3)^2)} - 2 * m * (1 - m) * (4 * Ntot - 3) \right);$$

**FullSimplify[EqC4a - CorrHHsym2, {m > 0, Ntot > 0}]**

$$\frac{8 (-1 + m) m Ntot \left( \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} + 2 (-1 + m) m (-3 + 4 Ntot) \right)}{3 \left( 3 + 6 (-1 + m) m + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} \right)}$$

By multiplying top and bottom of the fraction in CorrHH2 by

$3 + 6 (-1 + m) m - \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)}$ , we can simplify it to:

$$1 + \frac{8 (-1 + m) m Ntot \left( 3 + 6 (-1 + m) m - \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} \right)}{(3 + 6 (-1 + m) m)^2 - (9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2))};$$

**FullSimplify[Factor[%], {m > 0, Ntot > 0}]**

$$\frac{-3 + \sqrt{9 + 4 (-1 + m) m (9 + (-1 + m) m (3 - 4 Ntot)^2)} + 2 (-1 + m) m (-9 + 4 Ntot)}{4 (-1 + m) m (-3 + 2 Ntot)}$$

**EqC4b =**

$$\frac{3 + 2 * m * (1 - m) * (4 * Ntot - 9) - \sqrt{9 - 4 * m * (1 - m) * (9 - m * (1 - m) * (4 * Ntot - 3)^2)}}{4 * m * (1 - m) * (2 * Ntot - 3)};$$

**FullSimplify[EqC4b - CorrHHsym2, {m > 0, Ntot > 0}]**

0

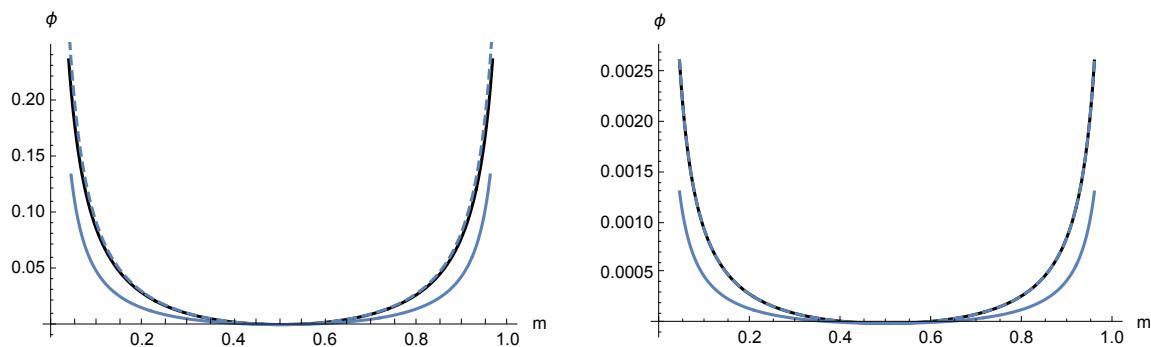
The alternative definition (dashed) is nearly twice the Fst value obtained by comparing to the average (solid), especially when the population size is large, but this alternative measure better matches Rousset's Fst (black):

$$\text{Eq3} = \frac{(1 - 2 * m)^2}{\frac{2}{3} * Ntot - (1 - 2 * m)^2 * \left( \frac{2}{3} * Ntot - 1 \right)};$$

```

GraphicsGrid[
{{Show[
  Plot[Eq3 /. Ntot -> 30, {m, 0, 1}, PlotStyle -> Black, AxesLabel -> {"m", "\u03c6"}],
  Plot[EqC4a /. Ntot -> 30, {m, 0, 1}],
  Plot[EqC4b /. Ntot -> 30, {m, 0, 1}, PlotStyle -> Dashed]
], 
Show[
  Plot[Eq3 /. Ntot -> 3000, {m, 0, 1}, PlotStyle -> Black, AxesLabel -> {"m", "\u03c6"}],
  Plot[EqC4a /. Ntot -> 3000, {m, 0, 1}],
  Plot[EqC4b /. Ntot -> 3000, {m, 0, 1}, PlotStyle -> Dashed]
]}]}
]

```



which reduces to the classic Fst prediction when expressing the total population size in terms of the effective number of diploids:

```

Limit[CorrHHsym2, m -> 0]
Limit[CorrHHsym2, m -> 1]

1
1

Limit[CorrHHsym2, m ->  $\frac{1}{2}$ ]
Simplify[%, 1 < Ntot]

$$1 - \frac{4 \text{Ntot}}{3 + \sqrt{(-3 + 4 \text{Ntot})^2}}$$

0

```

```

Series[CorrHHsym2 /. m → cm*ε /. Ntot → cNtot * 1/ε, {ε, 0, 0}] // Simplify
Normal[%] /. cm → m/ε /. cNtot → Ntot*ε /. Ntot → 3*Ndeem // Simplify

$$\left(1 - \frac{8 cm cNtot}{3 + \sqrt{9 + 64 cm^2 cNtot^2}}\right) + O[\epsilon]^1$$


$$1 - \frac{8 m Ndeem}{1 + \sqrt{1 + 64 m^2 Ndeem^2}}$$


Series[CorrHHsym2 /. m → cm*ε /. Ntot → cNtot * 1/ε, {ε, 0, 0}] // Simplify
Normal[%] /. cm → m/ε /. cNtot → Ntot*ε /. Ntot → 3/2 * Nlocal // Simplify

$$\left(1 - \frac{8 cm cNtot}{3 + \sqrt{9 + 64 cm^2 cNtot^2}}\right) + O[\epsilon]^1$$


$$1 - \frac{4 m Nlocal}{1 + \sqrt{1 + 16 m^2 Nlocal^2}}$$


```

Multiplying the top and bottom of the first by  $3 - \sqrt{9 + 64 cm^2 cNtot^2}$  and simplifying:

$$1 - \frac{8 cm cNtot (3 - \sqrt{9 + 64 cm^2 cNtot^2})}{9 - (9 + 64 cm^2 cNtot^2)} // Simplify$$

$$1 - \frac{-3 + \sqrt{9 + 64 cm^2 cNtot^2}}{8 cm cNtot}$$

Multiplying the top and bottom of the second by  $1 - \sqrt{1 + 16 m^2 Nlocal^2}$  and simplifying:

$$1 - \frac{4 m Nlocal (1 - \sqrt{1 + 16 m^2 Nlocal^2})}{1 - (1 + 16 m^2 Nlocal^2)} // Simplify$$

$$1 - \frac{-1 + \sqrt{1 + 16 m^2 Nlocal^2}}{4 m Nlocal}$$

For large  $\theta_{local}=m Nlocal$ , this matches the Rousset result ( $\frac{1}{1+4 \theta_{local}}$ ):

$$\text{Limit}\left[\frac{\frac{1 - \frac{-1 + \sqrt{1 + 16 \theta_{local}^2}}{4 \theta_{local}}}{\frac{1}{1+4 \theta_{local}}}, \theta_{local} \rightarrow \text{Infinity}}{\frac{1}{1+4 \theta_{local}}}\right]$$

## Very rare sexuality and large population for the complete symmetry case

```

Eq6 = 
$$\frac{(1 - 2 * m)^2}{\frac{2}{3} * N_{tot} - (1 - 2 * m)^2 * \left(\frac{2}{3} * N_{tot} - 1\right)};$$


Series[% /. m → cm * ε² /. Ntot → cNtot *  $\frac{1}{\epsilon}$ , {ε, 0, 1}] // Simplify
Normal[%] /. cm →  $\frac{m}{\epsilon^2}$  /. cNtot → Ntot * ε /. Ntot → 3 * Ndeem // Simplify
 $1 - \frac{8}{3} (cm cNtot) \epsilon + O[\epsilon]^2$ 
1 - 8 m Ndeem

Series[CorrHHsym /. m → cm * ε² /. Ntot → cNtot *  $\frac{1}{\epsilon}$ , {ε, 0, 1}] // Simplify
Normal[%] /. cm →  $\frac{m}{\epsilon^2}$  /. cNtot → Ntot * ε /. Ntot → 3 * Ndeem // Simplify
 $1 - \frac{8}{3} (cm cNtot) \epsilon + O[\epsilon]^2$ 
1 - 8 m Ndeem

Series[CorrHHsym2 /. m → cm * ε² /. Ntot → cNtot *  $\frac{1}{\epsilon}$ , {ε, 0, 1}] // Simplify
Normal[%] /. cm →  $\frac{m}{\epsilon^2}$  /. cNtot → Ntot * ε /. Ntot → 3 * Ndeem // Simplify
 $1 - \frac{4}{3} (cm cNtot) \epsilon + O[\epsilon]^2$ 
1 - 4 m Ndeem

Simplify[Series[CorrHHsym2 /. m → cm * ε /. Ntot → cNtot *  $\frac{1}{\epsilon^2}$ , {ε, 0, 1}],
0 < cm && 0 < cNtot]
Simplify[Normal[%] /. cm →  $\frac{m}{\epsilon}$  /. cNtot → Ntot * ε² /. Ntot →  $\frac{3}{2} * N_{local}$ , {ε > 0}]
 $\frac{3 \epsilon}{8 cm cNtot} + O[\epsilon]^2$ 
 $\frac{1}{4 m N_{local}}$ 

```

```

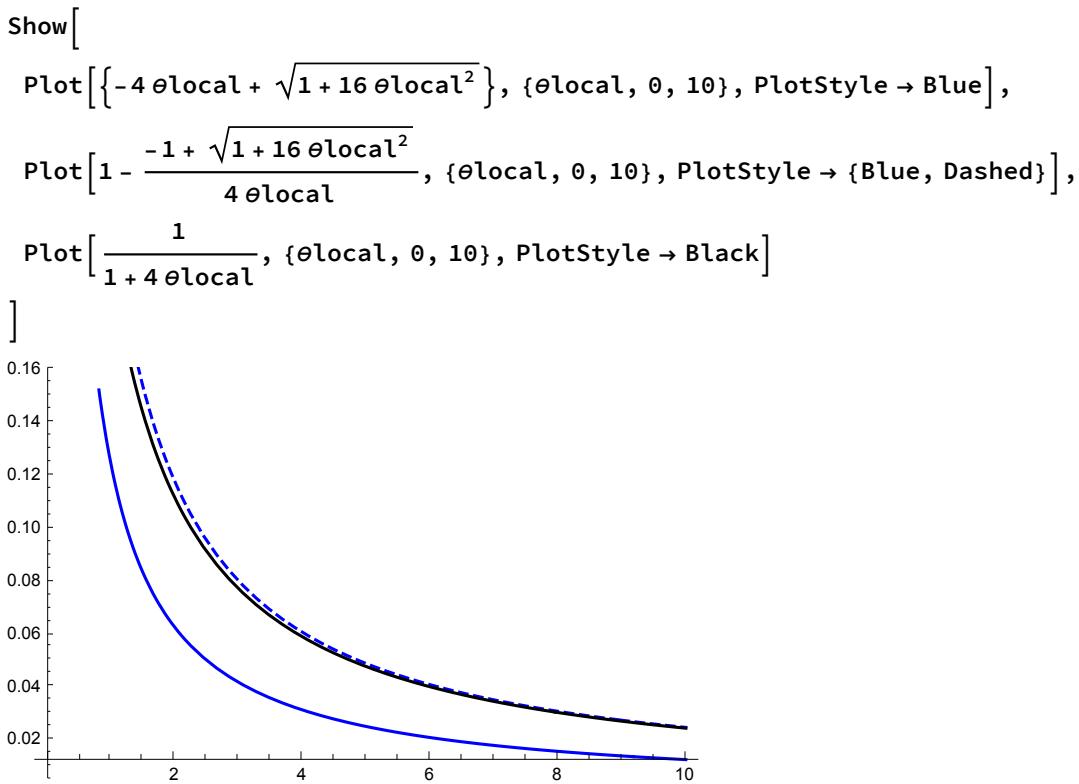
FullSimplify[Normal[Series[
  
$$\frac{1}{3} * \left( \sqrt{9 - 4 * m * (1 - m) * (9 - m * (1 - m) * (4 * Ntot - 3)^2)} - 2 * m * (1 - m) * (4 * Ntot - 3) \right) / .$$

  
$$m \rightarrow \frac{\theta}{Ntot} /. Ntot \rightarrow Ntot/\epsilon, \{\epsilon, 0, 0\}\right], \{\theta > 0, Ntot > 0\}]]

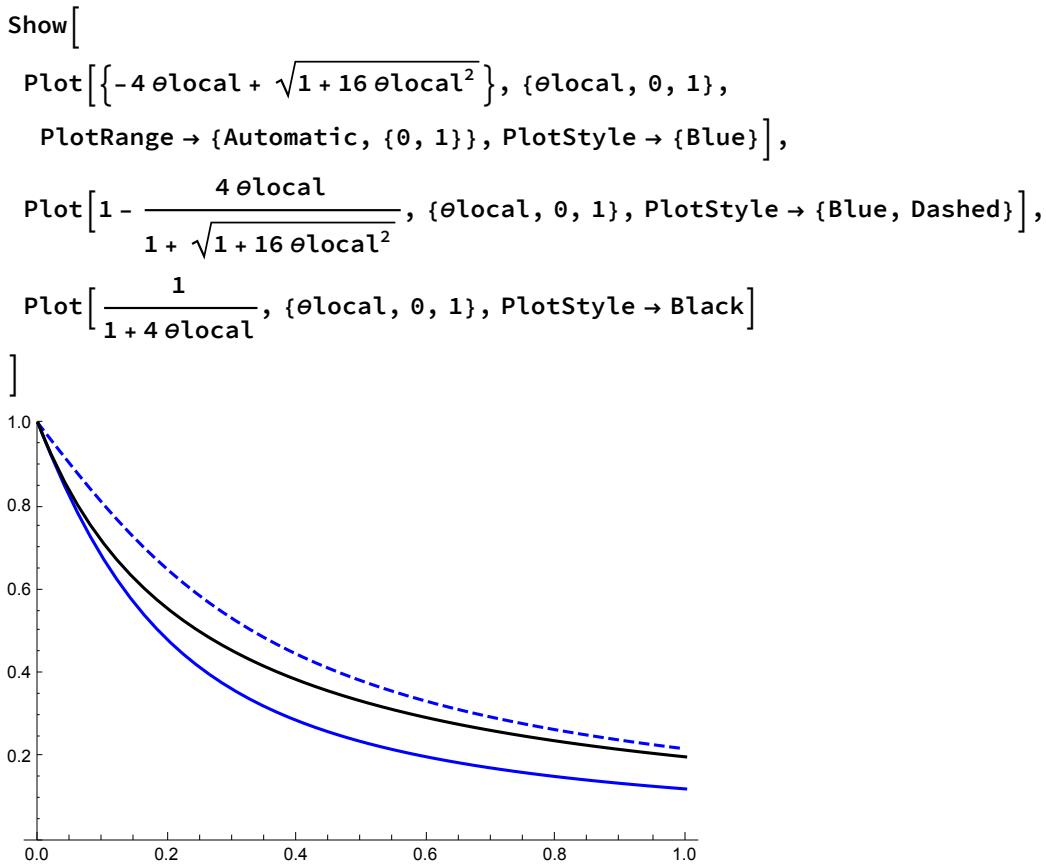

$$\frac{1}{3} \left( -8 \theta + \sqrt{9 + 64 \theta^2} \right)$$$$

```

Defining  $\theta_{local} = m N_{local} = \frac{2}{3} m N_{tot}$ , we can compare the three approximations, finding that the alternative definition using HD sampling (dashed) better matches Rousset (black) than does using the average (blue):



unless migration is very rare ( $\theta_{local} \ll 1$ ), in which case it is the average and Rousset's method that match (at  $\sim 1-4\theta_{local}$ ):



Alternatively, we can focus on the case where sexuality is nearly complete (asexuality rare, with mHH and mDD of order  $\epsilon$ ):

```
FullSimplify[
  Normal[Series[CorrHH2 /. m -> 1 - θii / Ntot /. Ntot -> Ntilde /. Ntilde -> ε Ntot,
    {0 < θii, Ntot > 0}]] /. Ntilde -> ε Ntot,
  1 - 8 θii / (3 + Sqrt[9 + 64 θii^2])
```

This approaches 1, as it should, when there is very little asexual reproduction ( $\theta_{ii}$  approaches 0):

```
Limit[% , θii -> 0]
1
```

But note that this is not generally true when there is very rare sexuality and the case is not fully symmetric.

## Appendix D

### Variance effective size in Bessho and Otto (2022)

$$\text{varianceNe} = \frac{\rho H * \rho D}{cD^2 * \rho H + 2 * cH^2 * \rho D} * N_{\text{tot}};$$

For the global regulation model, we have

$$\begin{aligned} \text{solH} &= \left( aH * wH + aD * wD - 2 * wD + \sqrt{4 * (1 - aH) * (1 - aD) * \frac{f * wH}{2} * wD + (aH * wH - aD * wD)^2} \right) / \\ &\quad \left( 2 * \left( aH * wH + \frac{f * wH}{2} * (1 - aH) - wD \right) \right); \\ \text{NeG} &= \text{varianceNe} / . \text{cH} \rightarrow \frac{(1 - aH) * \frac{f}{2} * wH * \rho H^2}{(1 - aH) * \frac{f}{2} * wH * \rho H^2 + (1 - aD) * wD * \rho D^2} / . \\ cD &\rightarrow \frac{(1 - aD) * wD * \rho D^2}{(1 - aH) * \frac{f}{2} * wH * \rho H^2 + (1 - aD) * wD * \rho D^2} / . \rho D \rightarrow 1 - \rho H / . \rho H \rightarrow \text{solH} // \text{Simplify} \\ &\left( 4 N_{\text{tot}} \left( wD - aH wH + \frac{1}{2} (-1 + aH) f wH \right)^4 \right. \\ &\quad \left( (-1 + aH) f wH \left( -2 wD + aD wD + aH wH + \sqrt{2 (-1 + aD) (-1 + aH) f wD wH + (aD wD - aH wH)^2} \right)^2 + \right. \\ &\quad \left. 2 (-1 + aD) wD \left( aD wD - aH wH - f wH + aH f wH + \sqrt{2 (-1 + aD) (-1 + aH) f wD wH + (aD wD - aH wH)^2} \right)^2 \right)^2 \Big/ \\ &\left( (2 wD + (aH (-2 + f) - f) wH)^4 \left( -wD + aH wH - \frac{1}{2} (-1 + aH) f wH \right) \left( (-1 + aH)^2 f^2 wH^2 \right. \right. \\ &\quad \left. \left( -2 wD + aD wD + aH wH + \sqrt{2 (-1 + aD) (-1 + aH) f wD wH + (aD wD - aH wH)^2} \right)^3 - 2 (-1 + aD)^2 \right. \\ &\quad \left. wD^2 \left( aD wD - aH wH - f wH + aH f wH + \sqrt{2 (-1 + aD) (-1 + aH) f wD wH + (aD wD - aH wH)^2} \right)^3 \right) \Big/ \end{aligned}$$

For the local regulation model, we have

$$\begin{aligned} \text{NeL} &= \text{varianceNe} / . \text{cH} \rightarrow \frac{1 + \frac{aH * wH * \rho H}{(1 - aD) * wD * \rho D}}{2 + \frac{aH * wH * \rho H}{(1 - aD) * wD * \rho D} + \frac{2}{f} * \frac{aD * wD * \rho D}{(1 - aH) * wH * \rho H}} / . \\ cD &\rightarrow \frac{1 + \frac{2}{f} * \frac{aD * wD * \rho D}{(1 - aH) * wH * \rho H}}{2 + \frac{aH * wH * \rho H}{(1 - aD) * wD * \rho D} + \frac{2}{f} * \frac{aD * wD * \rho D}{(1 - aH) * wH * \rho H}} / . \rho D \rightarrow 1 - \rho H; \end{aligned}$$

### Equations (from above)

Migration rates are backwards rates so that  $mH_{\text{fromH}} + mH_{\text{fromD}}$  sum to one:

```

constraints = {mHfromH + mHfromD == 1, mDfromH + mDfromD == 1, ρD + ρH == 1};

subconstraints = {mHfromH → 1 - mHfromD, mDfromD → 1 - mDfromH};

FNlarge = { (1 - X) * ((2 - X) * X * (2 * ρD) - mHfromD * (ρH + 2 * ρD)) / (2 - X) * X^2 * ρH * (2 * ρD) * Ntot,
            (1 - X) * ((2 - X) * X * ρH - mDfromH * (ρH + 2 * ρD)) / (2 - X) * X^2 * ρH * (2 * ρD) * Ntot };

NextQHH = (1 - μ)^2 * (mHfromH^2 * (1/Hap + (1 - 1/Hap) * QHH) + mHfromH * mHfromD * QHD +
            mHfromD * mHfromH * QDH + mHfromD^2 * (1/(2 * Dip) + (1 - 1/(2 * Dip)) * QDD));
NextQHD = (1 - μ)^2 * (mHfromH * mDfromH * (1/Hap + (1 - 1/Hap) * QHH) + mHfromH * mDfromD * QHD +
            mHfromD * mDfromH * QDH + mHfromD * mDfromD * (1/(2 * Dip) + (1 - 1/(2 * Dip)) * QDD));
NextQDH = (1 - μ)^2 * (mDfromH * mHfromH * (1/Hap + (1 - 1/Hap) * QHH) + mDfromH * mHfromD * QHD +
            mDfromD * mHfromH * QDH + mDfromD * mHfromD * (1/(2 * Dip) + (1 - 1/(2 * Dip)) * QDD));
NextQDD = (1 - μ)^2 * (mDfromD^2 * (1/(2 * Dip) + (1 - 1/(2 * Dip)) * QDD) + mDfromH * mDfromD * QHD +
            mDfromD * mDfromH * QDH + mDfromH^2 * (1/Hap + (1 - 1/Hap) * QHH));

```

The recursion equations for Q can be described as,  $(1 - \mu)^2 A(Q + c)$ ;

(this equation corresponds to Eq. (9.30) in Rousset (2004))

$$\text{MatrixA} = \begin{pmatrix} mHfromH * mHfromH & mHfromH * mHfromD & mHfromD * mHfromH & mHfromD * mHfromD \\ mHfromH * mDfromH & mHfromH * mDfromD & mHfromD * mDfromH & mHfromD * mDfromD \\ mDfromH * mHfromH & mDfromH * mHfromD & mDfromD * mHfromH & mDfromD * mHfromD \\ mDfromH * mDfromH & mDfromH * mDfromD & mDfromD * mDfromH & mDfromD * mDfromD \end{pmatrix};$$

$$\text{VectC} = \begin{pmatrix} \frac{1}{Hap} * (1 - QHH) \\ 0 \\ 0 \\ \frac{1}{2*Dip} * (1 - QDD) \end{pmatrix};$$

$$\begin{pmatrix} \text{NextQHH} \\ \text{NextQHD} \\ \text{NextQDH} \\ \text{NextQDD} \end{pmatrix} - (1 - \mu)^2 * \text{MatrixA} \cdot \begin{pmatrix} QHH \\ QHD \\ QDH \\ QDD \end{pmatrix} + \text{VectC} // \text{Simplify}$$

{ {0}, {0}, {0}, {0} }

Note that, we can write,  $A = \text{TensorProduct}[F, F]$

```

MatrixF = {{mHfromH, mHfromD}, {mDfromH, mDfromD}};
TensorProduct[MatrixF, MatrixF] // MatrixForm
MatrixA // MatrixForm

$$\left( \begin{array}{cc} \left( \begin{array}{cc} mHfromH^2 & mHfromD mHfromH \\ mDfromH mHfromH & mDfromD mHfromH \end{array} \right) & \left( \begin{array}{ccc} mHfromD mHfromH & mHfromD^2 \\ mDfromH mHfromD & mDfromD mHfromD \\ mDfromD mHfromH & mDfromD mHfromD \end{array} \right) \\ \left( \begin{array}{cc} mDfromH mHfromH & mDfromH mHfromD \\ mDfromH^2 & mDfromD mDfromH \end{array} \right) & \left( \begin{array}{ccc} mDfromD mHfromH & mDfromD mHfromD \\ mDfromD mDfromH & mDfromD^2 \\ mDfromD mDfromH & mDfromD mHfromD \end{array} \right) \end{array} \right)$$


$$\left( \begin{array}{cccc} mHfromH^2 & mHfromD mHfromH & mHfromD mHfromH & mHfromD^2 \\ mDfromH mHfromH & mDfromD mHfromH & mDfromH mHfromD & mDfromD mHfromD \\ mDfromH mHfromH & mDfromH mHfromD & mDfromD mHfromH & mDfromD mHfromD \\ mDfromH^2 & mDfromD mDfromH & mDfromD mDfromH & mDfromD^2 \end{array} \right)$$


```

Note that, the matrix A is a probability matrix;

```

MatrixA. {{1}, {1}, {1}, {1}} // Simplify
{{1}, {1}, {1}, {1}}

```

Furthermore, this can be represented as,  $(1 - \mu)^2 (GQ + A\delta)$  and  $(1 - \mu)^2 (GQ + (I - G) 1)$ ;  
(this equation corresponds to Eq. (4.4) in Rousset (2004))

```
MatrixG =
```

$$\begin{pmatrix} mHfromH^2 * \left(1 - \frac{1}{Hap}\right) & mHfromH * mHfromD & mHfromD * mHfromH & mHfromD^2 * \left(1 - \frac{1}{2*D}\right) \\ mHfromH * mDfromH * \left(1 - \frac{1}{Hap}\right) & mHfromH * mDfromD & mHfromD * mDfromH & mHfromD * mDfromD * \left(1 - \frac{1}{2*D}\right) \\ mDfromH * mHfromH * \left(1 - \frac{1}{Hap}\right) & mDfromH * mHfromD & mDfromD * mHfromH & mDfromD * mHfromD * \left(1 - \frac{1}{2*D}\right) \\ mDfromH^2 * \left(1 - \frac{1}{Hap}\right) & mDfromH * mDfromD & mDfromD * mDfromH & mDfromD^2 * \left(1 - \frac{1}{2*D}\right) \end{pmatrix}$$

$$\Bigg);$$

$$Vect\delta = \begin{pmatrix} \frac{1}{Hap} \\ 0 \\ 0 \\ \frac{1}{2*Dip} \end{pmatrix};$$

$$\begin{pmatrix} NextQHH \\ NextQHD \\ NextQDH \\ NextQDD \end{pmatrix} - (1 - \mu)^2 * \left( MatrixG. \begin{pmatrix} QHH \\ QHD \\ QDH \\ QDD \end{pmatrix} + MatrixA.Vect\delta \right) // Simplify$$

$$\begin{pmatrix} NextQHH \\ NextQHD \\ NextQDH \\ NextQDD \end{pmatrix} - (1 - \mu)^2 * \left( MatrixG. \begin{pmatrix} QHH \\ QHD \\ QDH \\ QDD \end{pmatrix} + \left( \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} - MatrixG \right). \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \end{pmatrix} \right) /.$$

```
subconstraints // Simplify
```

```
{ {0}, {0}, {0}, {0} }
```

```
{ {0}, {0}, {0}, {0} }
```

### Asymptotic inbreeding effective size by Rousset (2004)

At equilibrium, we have

$$Q = (1 - \mu)^2 (I - (1 - \mu)^2 G)^{-1} (I - G) 1.$$

We describe  $(I-G)1$  by the linear combination by eigen vector of matrix  $G$  ( $v1, v2, v3, v4$ ),  
 $(I-G)1 = a1 v1 + a2 v2 + a3 v3 + a4 v4$ .

Using this, we have

$$Q = (1 - \mu)^2 \left( \frac{1}{1-\lambda_1} a_1 v_1 + \frac{1}{1-\lambda_2} a_2 v_2 + \frac{1}{1-\lambda_3} a_3 v_3 + \frac{1}{1-\lambda_4} a_4 v_4 \right),$$

where  $\lambda_1, \lambda_2, \lambda_3, \lambda_4$  are eigen value of matrix G.

Furthermore, because of  $(1 - \mu)^2 \lambda^0 + (1 - \mu)^4 \lambda^1 + (1 - \mu)^6 \lambda^2 + \dots = \frac{(1-\mu)^2}{1-(1-\mu)^2 \lambda}$ , we have

$$Q = ((1 - \mu)^2 \lambda_1^0 a_1 v_1 + (1 - \mu)^4 \lambda_1^1 a_1 v_1 + \dots) + ((1 - \mu)^2 \lambda_2^0 a_2 v_2 + (1 - \mu)^4 \lambda_2^1 a_2 v_2 + \dots) + \\ ((1 - \mu)^2 \lambda_3^0 a_3 v_3 + (1 - \mu)^4 \lambda_3^1 a_3 v_3 + \dots) + ((1 - \mu)^2 \lambda_4^0 a_4 v_4 + (1 - \mu)^4 \lambda_4^1 a_4 v_4 + \dots)$$

It becomes

$$Q = (1 - \mu)^2 (\lambda_1^0 a_1 v_1 + \lambda_2^0 a_2 v_2 + \lambda_3^0 a_3 v_3 + \lambda_4^0 a_4 v_4) + (1 - \mu)^4 (\lambda_1^1 a_1 v_1 + \lambda_2^1 a_2 v_2 + \lambda_3^1 a_3 v_3 + \lambda_4^1 a_4 v_4) + \dots$$

Here the probability of IBD, Q, can be described as

$$Q = (1 - \mu)^2 C(1) + (1 - \mu)^4 C(2) + \dots,$$

where C indicates that the probability of coalecence.

Comparing these equations, we have the probabiltiy of coalecence using the eigenvalue of matrix G.

Using the leading eigenvalue of the matrix G, we have the inbreeding effective population size,

$$C(t) = (\lambda_1^{t-1} a_1 v_1 + \lambda_2^{t-1} a_2 v_2 + \lambda_3^{t-1} a_3 v_3 + \lambda_4^{t-1} a_4 v_4)$$

The inbreeding effective size comparing haploid WF population is defined as,

$$\frac{1}{N_e} = \text{Limit} \left[ \frac{C(t+1)}{1 - (C(1) + C(2) + \dots + C(t))}, t \rightarrow \infty \right]$$

Using the probability of coalecence, we have

$$\text{Limit} \left[ \frac{C(t+1)}{1 - (C(1) + C(2) + \dots + C(t))}, t \rightarrow \infty \right] = 1 - \lambda_1,$$

where  $\lambda_1$  is the leading eigenvalue of matrix G.

Hence, we have the inbreeding effective population size,

$$N_e = \frac{1}{1 - \lambda_1}$$

If we define the effective population size comparing with diploid WF model, it becomes

$$N_e = \frac{1}{2} \frac{1}{1 - \lambda_1}$$

We consider the perturbation, G - A;

**MatrixG - MatrixA // MatrixForm // Simplify**

$$\begin{pmatrix} -\frac{mHfromH^2}{Hap} & 0 & 0 & -\frac{mHfromD^2}{2 Dip} \\ -\frac{mDfromH mHfromH}{Hap} & 0 & 0 & -\frac{mDfromD mHfromD}{2 Dip} \\ -\frac{mDfromH mHfromH}{Hap} & 0 & 0 & -\frac{mDfromD mHfromD}{2 Dip} \\ -\frac{mDfromH^2}{Hap} & 0 & 0 & -\frac{mDfromD^2}{2 Dip} \end{pmatrix}$$

Because this perturbation is very small when we assume a large population size, we can derive the change in leading eigenvalue, using  $\Delta\lambda = \frac{\text{LeftEigenVector}(G-A)\times\text{RightEigenvector}}{\text{LeftEigenVector}\times v}$ .

Because the matrix A is probability matrix, the leading eigenvalue and right eigenvector is one and unit vector.

$$\text{LeftEigenVectorA} = \begin{pmatrix} \text{VHH} \\ \text{VHD} \\ \text{VDH} \\ \text{VDD} \end{pmatrix};$$

$$\text{RightEigenVectorA} = \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \end{pmatrix};$$

```
DeltaApproximationλG =
    
$$\frac{\text{Transpose}[\text{LeftEigenVectorA}] . (\text{MatrixG} - \text{MatrixA}) . \text{RightEigenVectorA}}{\text{Transpose}[\text{LeftEigenVectorA}] . \text{RightEigenVectorA}} // \text{Simplify}$$

    \{ \{ - ( ( \text{Hap} ( \text{mDfromD}^2 \text{VDD} + \text{mDfromD} \text{mHfromD} ( \text{VDH} + \text{VHD} ) + \text{mHfromD}^2 \text{VHH} ) + 2 \text{Dip} ( \text{mDfromH}^2 \text{VDD} + \text{mDfromH} \text{mHfromH} ( \text{VDH} + \text{VHD} ) + \text{mHfromH}^2 \text{VHH} ) ) / ( 2 \text{Dip} \text{Hap} ( \text{VDD} + \text{VDH} + \text{VHD} + \text{VHH} ) ) ) \} \}
```

The left eigenvector of matrix A (VHH, VHD, VDH, VDD) can be described as (VH\*VH, VH\*VD, VH\*VD, VD\*VD), where the VH and VD are the left eigenvector of the simpler 2x2 matrix F, normalized by their sum ( $VH = \frac{\text{mDfromH}}{\text{mHfromD}+\text{mDfromH}}$ ,  $VD = \frac{\text{mHfromD}}{\text{mHfromD}+\text{mDfromH}}$ ).

```
Eigenvalues[Simplify[Transpose[MatrixA] /. subconstraints]]
Eigenvectors[Simplify[Transpose[MatrixA] /. subconstraints]]
Eigenvalues[Simplify[Transpose[MatrixF] /. subconstraints]]
Eigenvectors[Simplify[Transpose[MatrixF] /. subconstraints]]
\{1, 1 - mDfromH - mHfromD, 1 - mDfromH - mHfromD, (-1 + mDfromH + mHfromD)^2\}
\{ \{ \frac{mDfromH^2}{mHfromD^2}, \frac{mDfromH}{mHfromD}, \frac{mDfromH}{mHfromD}, 1 \},
  \{ -\frac{mDfromH}{mHfromD}, -\frac{-mDfromH + mHfromD}{mHfromD}, 0, 1 \}, \{0, -1, 1, 0\}, \{1, -1, -1, 1\} \}
\{1, 1 - mDfromH - mHfromD\}
\{ \{ \frac{mDfromH}{mHfromD}, 1 \}, \{-1, 1\} \}
\{ \frac{\%[[1, 1]]}{\%[[1, 1]] + \%[[1, 2]]}, \frac{\%[[1, 2]]}{\%[[1, 1]] + \%[[1, 2]]} \} // \text{Simplify}
\{ \frac{mDfromH}{mDfromH + mHfromD}, \frac{mHfromD}{mDfromH + mHfromD} \}
```

$$\text{subV} = \left\{ VH \rightarrow \frac{mDfromH}{mHfromD + mDfromH}, VD \rightarrow \frac{mHfromD}{mHfromD + mDfromH} \right\};$$

The leading eigenvalue of the matrix G is approximated as  $1 / Ne = \lambda G = 1 - \frac{VH^2}{Hap} - \frac{VD^2}{2*Dip}$ .

This means that two gene lineages are in the same ploidy with probability V and they can coalesce with probability 1/number of chromosomes (Eq.9.32, in Rousset 2004).

```
Part[DeltaApproximationλG[[1]], 1] /. VHH → VH * VH /. VHD → VH * VD /. VDH → VD * VH /.
```

```
VDD → VD * VD /. subconstraints /. subV // Simplify
```

$$\% - \left( -\frac{VH^2}{Hap} - \frac{VD^2}{2 * Dip} \right) /. subV // Simplify$$

$$-\frac{2 * Dip * mDfromH^2 + Hap * mHfromD^2}{2 * Dip * Hap * (mDfromH + mHfromD)^2}$$

0

Then, the leading eigenvalue of the matrix G is approximated as  $1 - \frac{VH^2}{Hap} - \frac{VD^2}{2*Dip}$  and we have approximated inbreeding effective size comparing with classical diploid WF model,  $Ne = \frac{1}{2} \frac{1}{1-\lambda_1}$ ;

$$\text{ApproximationλG} = 1 - \frac{VH^2}{Hap} - \frac{VD^2}{2 * Dip};$$

InbreedingNe =

$$\frac{1}{2} * \frac{1}{1 - \text{ApproximationλG}} /. subV /. mHD \rightarrow \frac{(1 - aH) * \frac{f}{2} * wH * \rhoH}{(1 - aH) * \frac{f}{2} * wH * \rhoH + aD * wD * \rhoD} /.$$

$$mDH \rightarrow \frac{(1 - aD) * wD * \rhoD}{aH * wH * \rhoH + (1 - aD) * wD * \rhoD} /. Hap \rightarrow Ntot * \rhoH /.$$

$$Dip \rightarrow Ntot * \rhoD /. \rhoD \rightarrow 1 - \rhoH // Simplify;$$

$$NeG - (InbreedingNe /. \rhoH \rightarrow solH) // Simplify$$

0

$$NeL - InbreedingNe // Simplify$$

0

## Effective size by Whitlock and Barton (1997)

Using the formulae Eq.(8) and (9) in Whitlock and Barton (1997), we have

```

Hap2 =  $\frac{\text{Hap}}{2}$ ;
Nave =  $\frac{\text{Hap2} + \text{Dip}}{2}$ ;
 $\varphi H = \frac{\text{Hap2} * mHfromH + \text{Dip} * mDfromH}{\text{Hap2}}$ ;
(*Numerator represents number of individuals in the next
generation that descend from haploids, with mHD being the fraction
of the next generation of diploids that descend from haploids.*)
 $\varphi D = \frac{\text{Hap2} * mHfromD + \text{Dip} * mDfromD}{\text{Dip}}$ ;
Eq8inWB =  $\frac{1}{4 * \text{Nave}^2} * \left( \left( \frac{\text{Hap2} * \varphi H^2}{2} * (1 - \text{CorrHHave}) + \frac{\text{Dip} * \varphi D^2}{2} * (1 - \text{CorrDDave}) \right) + (\text{Hap2}^2 * \varphi H^2 * \text{CorrHHave} + \right.$ 
 $\left. 2 * \text{Hap2} * \text{Dip} * \varphi H * \varphi D * \text{CorrHDave} + \text{Dip}^2 * \varphi D^2 * \text{CorrDDave}) \right) // \text{Simplify};$ 

```

```

NewB =  $\frac{1}{2 * \text{Eq8inWB}}$  /. subconstraints /. Hap  $\rightarrow$  Ntot *  $\rho H$  /. Dip  $\rightarrow$  Ntot *  $(1 - \rho H)$  // Simplify

$$(N_{\text{tot}} (-2 + \rho H) (-1 + \rho H) \rho H (\text{mDfromH}^3 (-4 + 4 (3 + 4 N_{\text{tot}}) \rho H - 3 (3 + 8 N_{\text{tot}}) \rho H^2 + 8 N_{\text{tot}} \rho H^3) +$$


$$\text{mDfromH}^2 (24 - 32 (2 + N_{\text{tot}}) \rho H + 6 (7 + 8 N_{\text{tot}}) \rho H^2 - 16 N_{\text{tot}} \rho H^3 +$$


$$3 \text{mHfromD} (-4 + 4 (3 + 4 N_{\text{tot}}) \rho H - 3 (3 + 8 N_{\text{tot}}) \rho H^2 + 8 N_{\text{tot}} \rho H^3)) + \text{mHfromD}$$


$$(-4 + 20 \rho H - 21 \rho H^2 + \text{mHfromD} (8 - 32 (1 + N_{\text{tot}}) \rho H + 6 (5 + 8 N_{\text{tot}}) \rho H^2 - 16 N_{\text{tot}} \rho H^3) +$$


$$\text{mHfromD}^2 (-4 + 4 (3 + 4 N_{\text{tot}}) \rho H - 3 (3 + 8 N_{\text{tot}}) \rho H^2 + 8 N_{\text{tot}} \rho H^3)) + \text{mDfromH} (-20 +$$


$$52 \rho H - 33 \rho H^2 - 8 \text{mHfromD} (-4 + 4 (3 + 2 N_{\text{tot}}) \rho H - 3 (3 + 4 N_{\text{tot}}) \rho H^2 + 4 N_{\text{tot}} \rho H^3) +$$


$$3 \text{mHfromD}^2 (-4 + 4 (3 + 4 N_{\text{tot}}) \rho H - 3 (3 + 8 N_{\text{tot}}) \rho H^2 + 8 N_{\text{tot}} \rho H^3))) /$$


$$(4 \text{mDfromH}^5 (-1 + \rho H)^2 (12 - 28 \rho H + 19 \rho H^2) + 4 \text{mDfromH}^4 (-1 + \rho H)$$


$$(40 - 152 \rho H + 198 \rho H^2 - 86 \rho H^3 + \text{mHfromD} (-36 + 132 \rho H - 169 \rho H^2 + 76 \rho H^3)) +$$


$$\text{mHfromD} \rho H (-8 + 64 \rho H - 114 \rho H^2 + 58 \rho H^3 + \text{mHfromD}^4 \rho H (12 - 28 \rho H + 19 \rho H^2) -$$


$$2 \text{mHfromD}^3 \rho H (28 - 72 \rho H + 49 \rho H^2) +$$


$$4 \text{mHfromD} (-1 + \rho H) (-4 + 16 (2 + N_{\text{tot}}) \rho H - (43 + 16 N_{\text{tot}}) \rho H^2 + 4 N_{\text{tot}} \rho H^3) + \text{mHfromD}^2$$


$$(-8 + 4 (31 + 8 N_{\text{tot}}) \rho H - 2 (151 + 32 N_{\text{tot}}) \rho H^2 + (193 + 40 N_{\text{tot}}) \rho H^3 - 8 N_{\text{tot}} \rho H^4)) +$$


$$\text{mDfromH} \rho H (-40 + 160 \rho H - 202 \rho H^2 + 82 \rho H^3 - 32 \text{mHfromD} (-4 + 22 \rho H - 33 \rho H^2 + 15 \rho H^3) -$$


$$8 \text{mHfromD}^3 (-20 + 92 \rho H - 139 \rho H^2 + 69 \rho H^3) +$$


$$\text{mHfromD}^4 (-48 + 196 \rho H - 272 \rho H^2 + 133 \rho H^3) + \text{mHfromD}^2$$


$$(-200 + 4 (267 + 8 N_{\text{tot}}) \rho H - 2 (839 + 32 N_{\text{tot}}) \rho H^2 + (813 + 40 N_{\text{tot}}) \rho H^3 - 8 N_{\text{tot}} \rho H^4)) +$$


$$\text{mDfromH}^3 (-8 \text{mHfromD} (32 - 188 \rho H + 404 \rho H^2 - 377 \rho H^3 + 129 \rho H^4) +$$


$$\text{mHfromD}^2 (144 - 768 \rho H + 1536 \rho H^2 - 1384 \rho H^3 + 475 \rho H^4) + 2 (-1 + \rho H)$$


$$(-56 - 4 (-81 + 8 N_{\text{tot}}) \rho H + (-530 + 64 N_{\text{tot}}) \rho H^2 + (263 - 40 N_{\text{tot}}) \rho H^3 + 8 N_{\text{tot}} \rho H^4)) +$$


$$\text{mDfromH}^2 (-4 (-1 + \rho H) \rho H (60 + 8 N_{\text{tot}} (-2 + \rho H)^2 (-1 + \rho H) - 144 \rho H + 85 \rho H^2) +$$


$$\text{mHfromD}^3 (48 - 352 \rho H + 864 \rho H^2 - 912 \rho H^3 + 361 \rho H^4) -$$


$$2 \text{mHfromD}^2 (48 - 448 \rho H + 1256 \rho H^2 - 1424 \rho H^3 + 571 \rho H^4) + 2 \text{mHfromD} (-1 + \rho H)$$


$$(-24 - 4 (-89 + 8 N_{\text{tot}}) \rho H + (-874 + 64 N_{\text{tot}}) \rho H^2 + (567 - 40 N_{\text{tot}}) \rho H^3 + 8 N_{\text{tot}} \rho H^4)))$$


Series[ $\frac{\text{NewB}}{N_{\text{tot}}}$  /. Ntot  $\rightarrow$  cNtot *  $\frac{1}{\epsilon}$ , { $\epsilon$ , 0, 0}] // Simplify
NewBlargeN = Normal[% * Ntot /. mDfromH  $\rightarrow$   $\frac{(1 - aH) * \frac{f}{2} * wH * \rho H}{(1 - aH) * \frac{f}{2} * wH * \rho H + aD * wD * \rho D}$  /.
mHfromD  $\rightarrow$   $\frac{(1 - aD) * wD * \rho D}{aH * wH * \rho H + (1 - aD) * wD * \rho D}$  /.  $\rho D \rightarrow 1 - \rho H$ ] // Simplify

$$\frac{(mDfromH + mHfromD)^2 (-1 + \rho H) \rho H}{2 mDfromH^2 (-1 + \rho H) - mHfromD^2 \rho H} + O[\epsilon]^1$$


$$\frac{2 N_{\text{tot}} (-1 + \rho H) \left( \frac{(-1+aD) wD (-1+\rho H)}{(-1+aD) wD (-1+\rho H)+aH wH \rho H} + \frac{(-1+aH) f wH \rho H}{2 aD wD (-1+\rho H)+(-1+aH) f wH \rho H} \right)^2}{-\frac{2 (-1+aD)^2 wD^2 (-1+\rho H)^2}{((-1+aD) wD (-1+\rho H)+aH wH \rho H)^2} + \frac{4 (-1+aH)^2 f^2 wH^2 (-1+\rho H) \rho H}{(2 aD wD (-1+\rho H)+(-1+aH) f wH \rho H)^2}}$$


```

```
NeG = (NeWBlargeN /. pH → solH) // Simplify
```

```
0
```

```
NeL = NeWBlargeN // Simplify
```

```
0
```

Note that even if we measure Fst relative to a sample from haploids and diploids (HD) rather than the average sample across the full population, we must still rephrase the HD-based Fst values in terms of the average-based Fst values in order to use equations (8) and (9) of Barton and Whitlock:

$$\begin{aligned} \frac{\text{Corrij} - \text{fave}}{1 - \text{fave}} / . \text{Corrij} &\rightarrow \frac{\text{Fij} - \text{FHD}}{1 - \text{FHD}} / . \\ \text{fave} &\rightarrow \frac{\text{Hap}^2}{(\text{Hap} + 2 * \text{Dip})^2} * \frac{\text{FHH} - \text{FHD}}{1 - \text{FHD}} + \frac{\text{Hap} * (2 * \text{Dip})}{(\text{Hap} + 2 * \text{Dip})^2} * \frac{\text{FHD} - \text{FHD}}{1 - \text{FHD}} + \\ &\quad \frac{\text{Hap} * (2 * \text{Dip})}{(\text{Hap} + 2 * \text{Dip})^2} * \frac{\text{FDH} - \text{FHD}}{1 - \text{FHD}} + \frac{(2 * \text{Dip})^2}{(\text{Hap} + 2 * \text{Dip})^2} * \frac{\text{FDD} - \text{FHD}}{1 - \text{FHD}} // \text{Simplify}; \\ \frac{\text{Fij} - \text{Fave}}{1 - \text{Fave}} / . \text{Fave} &\rightarrow \frac{\text{Hap}^2}{(\text{Hap} + 2 * \text{Dip})^2} * \text{FHH} + \frac{\text{Hap} * (2 * \text{Dip})}{(\text{Hap} + 2 * \text{Dip})^2} * \text{FHD} + \\ &\quad \frac{\text{Hap} * (2 * \text{Dip})}{(\text{Hap} + 2 * \text{Dip})^2} * \text{FDH} + \frac{(2 * \text{Dip})^2}{(\text{Hap} + 2 * \text{Dip})^2} * \text{FDD} // \text{Simplify}; \\ \% - \\ \% // \\ \text{Simplify} \\ 0 \\ \text{altEq8inWB} = \\ \frac{1}{4 * \text{Nave}^2} * \left( \left( \frac{\text{Hap}^2 * \varphi H^2}{2} * \left( 1 - \left( \frac{\text{CorrHHhd} - \text{fave}}{1 - \text{fave}} \right) \right) + \frac{\text{Dip} * \varphi D^2}{2} * \left( 1 - \left( \frac{\text{CorrDDhd} - \text{fave}}{1 - \text{fave}} \right) \right) \right) + \right. \\ \left( \text{Hap}^2 * \varphi H^2 * \left( \frac{\text{CorrHHhd} - \text{fave}}{1 - \text{fave}} \right) + 2 * \text{Hap}^2 * \text{Dip} * \varphi H * \varphi D * \left( \frac{\text{CorrHDhd} - \text{fave}}{1 - \text{fave}} \right) + \right. \\ \left. \text{Dip}^2 * \varphi D^2 * \left( \frac{\text{CorrDDhd} - \text{fave}}{1 - \text{fave}} \right) \right) / . \text{fave} \rightarrow \frac{\text{Hap}^2}{(\text{Hap} + 2 * \text{Dip})^2} * \text{CorrHHhd} + \\ \frac{2 * \text{Hap} * (2 * \text{Dip})}{(\text{Hap} + 2 * \text{Dip})^2} * \text{CorrHDhd} + \frac{(2 * \text{Dip})^2}{(\text{Hap} + 2 * \text{Dip})^2} * \text{CorrDDhd} // \text{Simplify}; \\ \text{Eq8inWB} = \frac{1}{4 * \text{Nave}^2} * \\ \left( \left( \frac{\text{Hap}^2 * \varphi H^2}{2} * (1 - \text{CorrHHave}) + \frac{\text{Dip} * \varphi D^2}{2} * (1 - \text{CorrDDave}) \right) + (\text{Hap}^2 * \varphi H^2 * \text{CorrHHave} + \right. \\ \left. 2 * \text{Hap}^2 * \text{Dip} * \varphi H * \varphi D * \text{CorrHDave} + \text{Dip}^2 * \varphi D^2 * \text{CorrDDave}) \right) // \text{Simplify}; \end{aligned}$$

(recall that CorrHD2=0).

The above is the same equation as derived above, once put back in the terms used by Whitlock and Barton, and so gives the same Ne:

```
altEq8inWB - Eq8inWB /. subconstraints /. Hap → Ntot * ρH /. Dip → Ntot * (1 - ρH) // Factor
0
```

---

## Figures

Figure 1-4: Fst with different m

### Equations

```
subconstraints = {mHfromH → 1 - mHfromD, mDfromD → 1 - mDfromH};

FaiHHstrict = ((1 - X)3 + Ntot * (1 - X) * ((2 - X) * X * (2 * ρD) - mHfromD * (ρH + 2 * ρD))) /
((1 - X)3 - Ntot * (1 - X) * ((1 - X)2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) +
Ntot2 * X2 * (2 - X) * (2 * ρD) * ρH) /.

X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH // Simplify;

FaiDDstrict = ((1 - X)3 + Ntot * (1 - X) * ((2 - X) * X * ρH - mDfromH * (ρH + 2 * ρD))) /
((1 - X)3 - Ntot * (1 - X) * ((1 - X)2 * (ρH + 2 * ρD) - mDfromD * ρH - mHfromH * (2 * ρD)) +
Ntot2 * X2 * (2 - X) * (2 * ρD) * ρH) /.

X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH // Simplify;

FaiAverage =  $\frac{\rho H}{\rho H + 2 * \rho D} * FaiHHstrict + \frac{2 * \rho D}{\rho H + 2 * \rho D} * FaiDDstrict$  /. ρD → 1 - ρH // Simplify
- (( (- (-1 + mDfromH + mHfromD)3 + (1 - mDfromH - mHfromD) Ntot
(mHfromD (-2 + ρH) + 2 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) (-1 + ρH)))
ρH + 2 (1 - ρH) (- (-1 + mDfromH + mHfromD)3 + (-1 + mDfromH + mHfromD) Ntot
(mDfromH2 ρH + (-2 + mHfromD) mHfromD ρH + mDfromH (2 + (-3 + 2 mHfromD) ρH))) ) )
((2 - ρH) ((-1 + mDfromH + mHfromD)3 + (-1 + mDfromH + mHfromD) Ntot
(mHfromD (2 + mHfromD (-2 + ρH)) +
mDfromH (4 + 2 mHfromD (-2 + ρH) - 3 ρH) + mDfromH2 (-2 + ρH)) -
2 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD)2 Ntot2 (-1 + ρH) ρH))) )
```

```

FaiHHstrict /. mHfromD → 1 /. mDfromH → 1 // Simplify
FaiHHstrict /. mHfromD → 1 /. mDfromH → 0 // Simplify
FaiHHstrict /. mHfromD → 0 /. mDfromH → 1 // Simplify
FaiHHstrict /. mHfromD → 0 /. mDfromH → 0 // Simplify

1
0
0
1

FaiDDstrict /. mHfromD → 1 /. mDfromH → 1 // Simplify
FaiDDstrict /. mHfromD → 1 /. mDfromH → 0 // Simplify
FaiDDstrict /. mHfromD → 0 /. mDfromH → 1 // Simplify
FaiDDstrict /. mHfromD → 0 /. mDfromH → 0 // Simplify

1
0
0
1

```

**Figure 1: Equal movement, Equal chromosome**

```

FaiHHstrict /. mHfromD → m /. mDfromH → m // Simplify
FaiDDstrict /. mHfromD → m /. mDfromH → m // Simplify
- (((-1 + 2 m) (1 + m (-4 + Ntot (6 - 7 ρH)) + m2 (4 + 8 Ntot (-1 + ρH))) ) /
(1 - 3 m (2 + Ntot (-2 + ρH)) + 8 m3 (-1 - Ntot (-2 + ρH) + 2 Ntot2 (-1 + ρH) ρH) -
2 m2 (-6 - 5 Ntot (-2 + ρH) + 8 Ntot2 (-1 + ρH) ρH)) )
((-1 + 2 m) (-1 + m (4 + Ntot (2 - 5 ρH)) + 4 m2 (-1 + Ntot ρH))) /
(1 - 3 m (2 + Ntot (-2 + ρH)) + 8 m3 (-1 - Ntot (-2 + ρH) + 2 Ntot2 (-1 + ρH) ρH) -
2 m2 (-6 - 5 Ntot (-2 + ρH) + 8 Ntot2 (-1 + ρH) ρH))

```

```

FaiHHstrict /. mHfromD → m /. mDfromH → m /. ρH →  $\frac{2}{3}$  // Simplify
FaiDDstrict /. mHfromD → m /. mDfromH → m /. ρH →  $\frac{2}{3}$  // Simplify
%- %% // Simplify

$$-\frac{3 (1 - 2 m)^2}{-3 + m (12 - 8 Ntot) + 4 m^2 (-3 + 2 Ntot)}$$


$$-\frac{3 (1 - 2 m)^2}{-3 + m (12 - 8 Ntot) + 4 m^2 (-3 + 2 Ntot)}$$

0
Eq3 = 
$$\frac{(1 - 2 * m)^2}{\frac{2}{3} * Ntot - (1 - 2 * m)^2 * \left(\frac{2}{3} * Ntot - 1\right)};$$

Eq3 - FaiHHstrict /. mHfromD → m /. mDfromH → m /. ρH →  $\frac{2}{3}$  // Simplify
0
Limit[Eq3, m → 0]
Limit[Eq3, m →  $\frac{1}{2}$ ]
Limit[Eq3, m → 1]
1
0
1

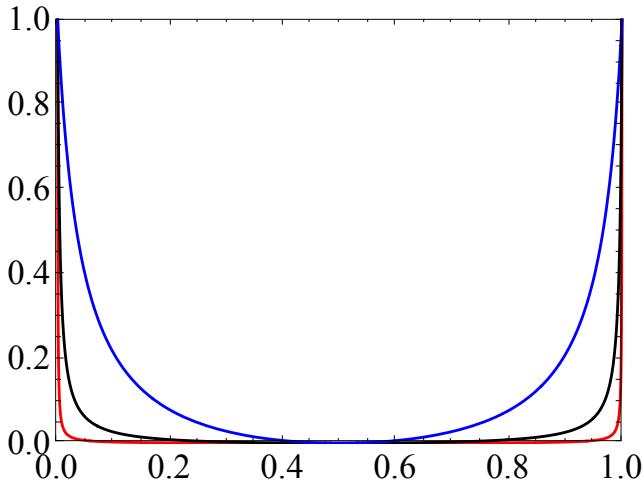
```

```

Plot[Eq3 /. Ntot -> 10, {m, 0, 1}, PlotRange -> {{0, 1}, {0, 1}},
  PlotStyle -> {Thickness[0.005], Blue}, AspectRatio -> 0.75];
Plot[Eq3 /. Ntot -> 100, {m, 0, 1}, PlotRange -> {{0, 1}, {0, 1}},
  PlotStyle -> {Thickness[0.005], Black}, AspectRatio -> 0.75];
Plot[Eq3 /. Ntot -> 1000, {m, 0, 1}, PlotRange -> {{0, 1}, {0, 1}},
  PlotStyle -> {Thickness[0.005], Red}, AspectRatio -> 0.75];
Show[%, %%, %%%];

Show[% , AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
  Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
  Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
  FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
  Style["", 20, FontFamily -> "Times New Roman"]}]

```



**Figure 2: Equal movement**

```

FaiHHstrict /. mHfromD -> m /. mDfromH -> m // Simplify
FaiDDstrict /. mHfromD -> m /. mDfromH -> m // Simplify
- (( (-1 + 2 m) (1 + m (-4 + Ntot (6 - 7 ρH)) ) + m^2 (4 + 8 Ntot (-1 + ρH)) ) ) /
(1 - 3 m (2 + Ntot (-2 + ρH)) ) + 8 m^3 (-1 - Ntot (-2 + ρH) + 2 Ntot^2 (-1 + ρH) ρH) -
2 m^2 (-6 - 5 Ntot (-2 + ρH) + 8 Ntot^2 (-1 + ρH) ρH) )
(( -1 + 2 m) (-1 + m (4 + Ntot (2 - 5 ρH)) ) + 4 m^2 (-1 + Ntot ρH)) ) /
(1 - 3 m (2 + Ntot (-2 + ρH)) ) + 8 m^3 (-1 - Ntot (-2 + ρH) + 2 Ntot^2 (-1 + ρH) ρH) -
2 m^2 (-6 - 5 Ntot (-2 + ρH) + 8 Ntot^2 (-1 + ρH) ρH)

```

```
FaiHHstrict /. mHfromD → m /. mDfromH → m /. m → 0 // Simplify
FaiHHstrict /. mHfromD → m /. mDfromH → m /. m → 1 // Simplify
FaiDDstrict /. mHfromD → m /. mDfromH → m /. m → 0 // Simplify
FaiDDstrict /. mHfromD → m /. mDfromH → m /. m → 1 // Simplify

1
1
1
1

FaiHHstrict /. mHfromD → m /. mDfromH → m /. m →  $\frac{1}{2}$  // Simplify
FaiDDstrict /. mHfromD → m /. mDfromH → m /. m →  $\frac{1}{2}$  // Simplify

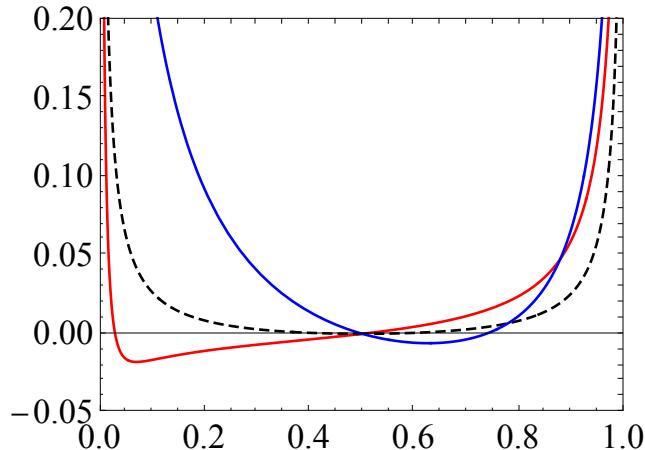
0
0
```

```

g1 = Plot[FaiHHstrict /. mHfromD → m /. mDfromH → m /. ρH → 0.9 /. Ntot → 100,
{m, 0, 1}, PlotRange → {{0, 1}, {-0.1, 0.3}},
PlotStyle → {Thickness[0.005], Red}, AspectRatio → 0.75];
g2 = Plot[FaiHHstrict /. mHfromD → m /. mDfromH → m /. ρH → 2/3 /. Ntot → 100,
{m, 0, 1}, PlotRange → {{0, 1}, {-0.1, 0.3}},
PlotStyle → {Thickness[0.005], Black, Dashed}, AspectRatio → 0.75];
g3 = Plot[FaiHHstrict /. mHfromD → m /. mDfromH → m /. ρH → 0.1 /. Ntot → 100,
{m, 0, 1}, PlotRange → {{0, 1}, {-0.1, 0.3}},
PlotStyle → {Thickness[0.005], Blue}, AspectRatio → 0.75];
Show[g1, g2, g3, PlotRange → {{0, 1}, {-0.05, 0.2}}];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],
Style["\"", 20, FontFamily → "Times New Roman"]}]

```



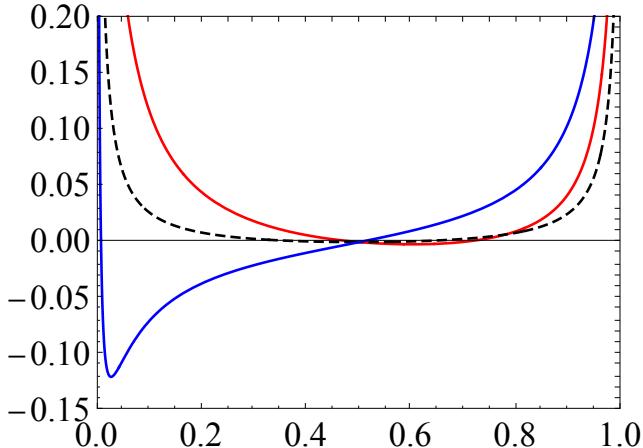
```

g1 = Plot[FaiDDstrict /. mHfromD → m /. mDfromH → m /. ρH → 0.9 /. Ntot → 100,
{m, 0, 1}, PlotRange → {{0, 1}, {-0.15, 0.5}},
PlotStyle → {Thickness[0.005], Red}, AspectRatio → 0.75];
g2 = Plot[FaiDDstrict /. mHfromD → m /. mDfromH → m /. ρH → 2/3 /. Ntot → 100,
{m, 0, 1}, PlotRange → {{0, 1}, {-0.15, 0.5}},
PlotStyle → {Thickness[0.005], Black, Dashed}, AspectRatio → 0.75];
g3 = Plot[FaiDDstrict /. mHfromD → m /. mDfromH → m /. ρH → 0.1 /. Ntot → 100,
{m, 0, 1}, PlotRange → {{0, 1}, {-0.15, 0.5}},
PlotStyle → {Thickness[0.005], Blue}, AspectRatio → 0.75];
Show[g1, g2, g3, PlotRange → {{0, 1}, {-0.15, 0.2}}];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],

Style["\"", 20, FontFamily → "Times New Roman"]}]

```



**Figure 3: Asymmetry movement, Equal chromosome number**

```

MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

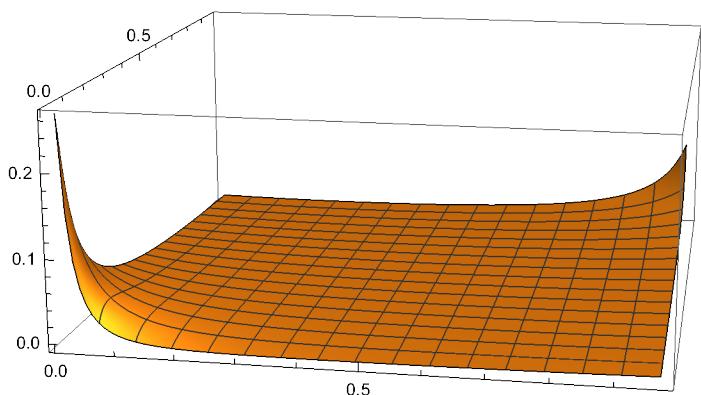
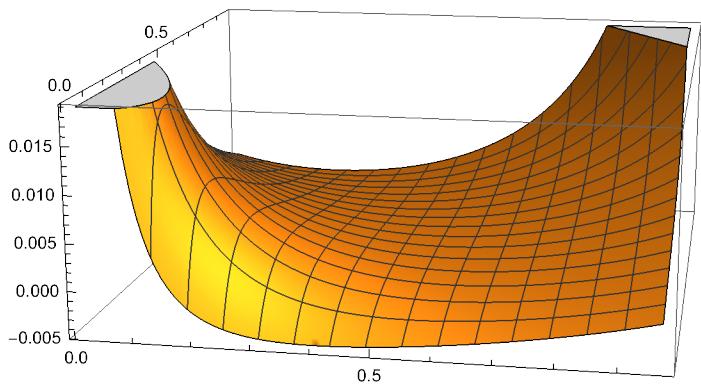
FQHH = FaiHHstrict /. pH →  $\frac{2}{3}$  /. Ntot → 100;
FQDD = FaiDDstrict /. pH →  $\frac{2}{3}$  /. Ntot → 100;

OmegaQHH = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
OmegaQDD = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
repeat = 0;
For[repeat1 = 1, repeat1 ≤ RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 ≤ RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(MaxV - MinV)}{RepeatMax} * (repeat1 - 1)$ ;
    x2 = MinV +  $\frac{(MaxV - MinV)}{RepeatMax} * (repeat2 - 1)$ ;
    OmegaQHH[[repeat, 1]] = x1;
    OmegaQHH[[repeat, 2]] = x2;
    OmegaQHH[[repeat, 3]] = FQHH /. mHfromD → x1 /. mDfromH → x2;

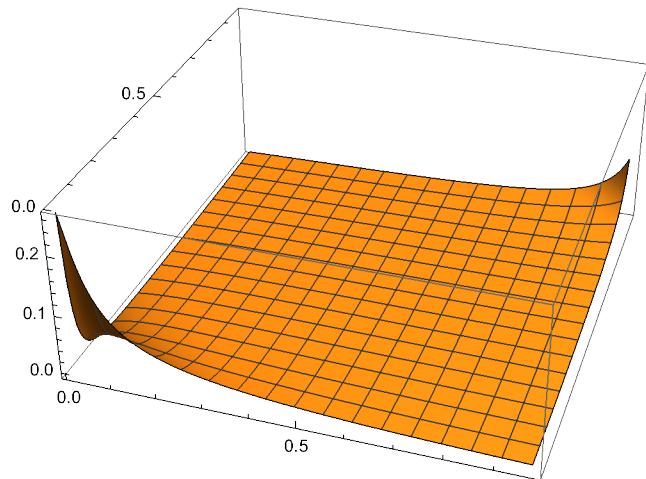
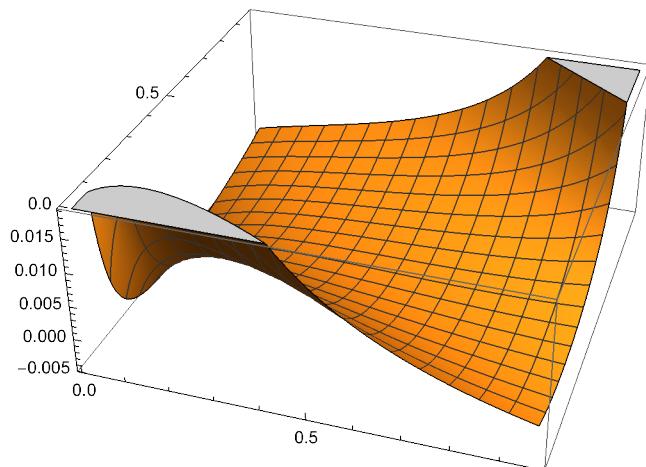
    OmegaQDD[[repeat, 1]] = x1;
    OmegaQDD[[repeat, 2]] = x2;
    OmegaQDD[[repeat, 3]] = FQDD /. mHfromD → x1 /. mDfromH → x2;
  ];
];
];

```

```
ListPlot3D[OmegaQHH]
ListPlot3D[OmegaQHH, PlotRange → All]
```

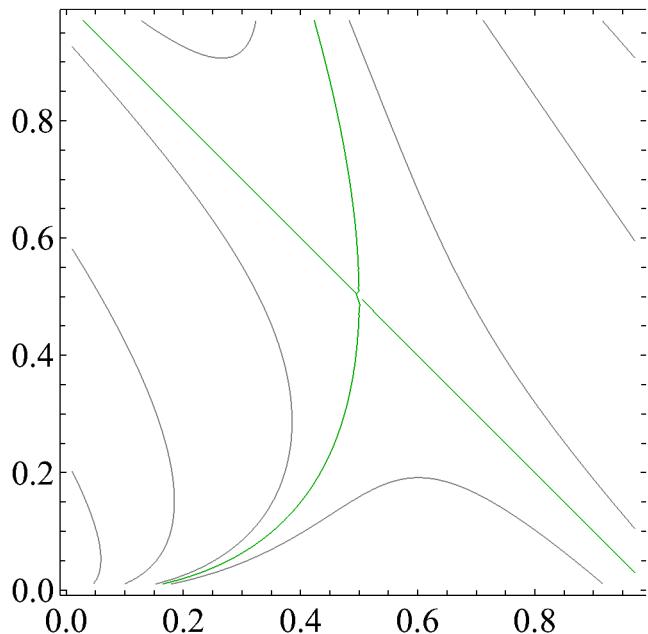


```
ListPlot3D[OmegaQDD]
ListPlot3D[OmegaQDD, PlotRange → All]
```



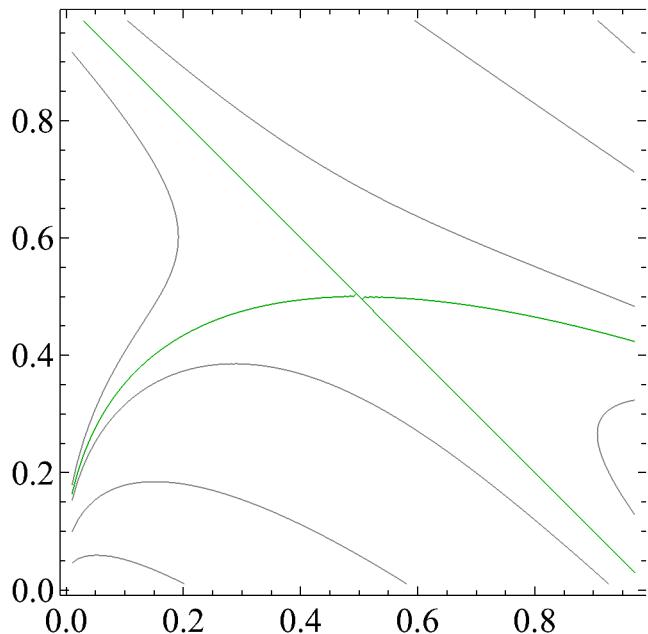
```
ListContourPlot[OmegaQHH,
Contours → {{-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],
Style["\"", 20, FontFamily → "Times New Roman"]}]
```

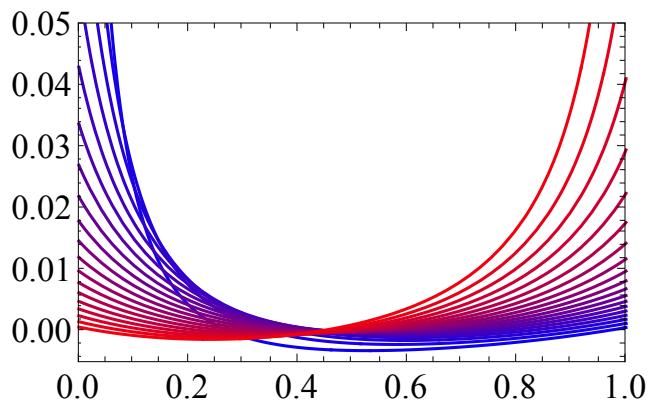


```
ListContourPlot[OmegaQDD,
Contours → {{-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["", 20, FontFamily → "Times New Roman"],
Style["", 20, FontFamily → "Times New Roman"]}]
```



```
Plot[Evaluate[  
  FaiHHstrict /. pH ->  $\frac{2}{3}$  /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}],  
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],  
  PlotRange -> {{0, 1}, {-0.005, 0.05}}]  
];  
  
Show[% , AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],  
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->  
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],  
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],  
Style["", 20, FontFamily -> "Times New Roman"]}]
```

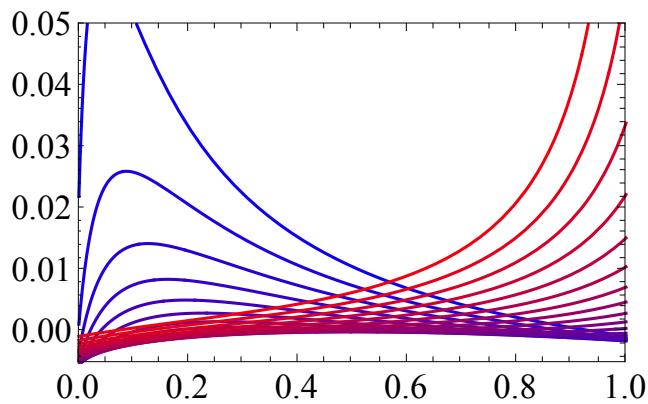


```

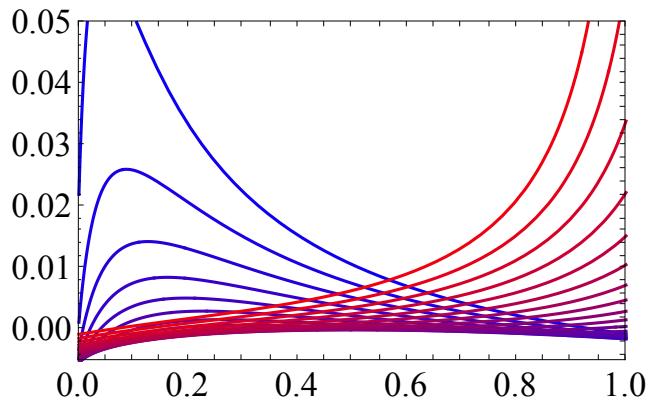
Plot[Evaluate[
  FaiHHstrict /. pH ->  $\frac{2}{3} / . N_{tot} \rightarrow 100 / . mHfromD \rightarrow Table[i, \{i, 0.05, 0.95, 0.05\}]$ ],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.005, 0.05}}];
];

```

Show[% , AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]



```
Plot[Evaluate[  
  FaiDDstrict /. pH ->  $\frac{2}{3}$  /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}],  
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],  
  PlotRange -> {{0, 1}, {-0.005, 0.05}}]  
];  
  
Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],  
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->  
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],  
FrameLabel -> {Style["\"", 20, FontFamily -> "Times New Roman"],  
Style["\"", 20, FontFamily -> "Times New Roman"]}]
```

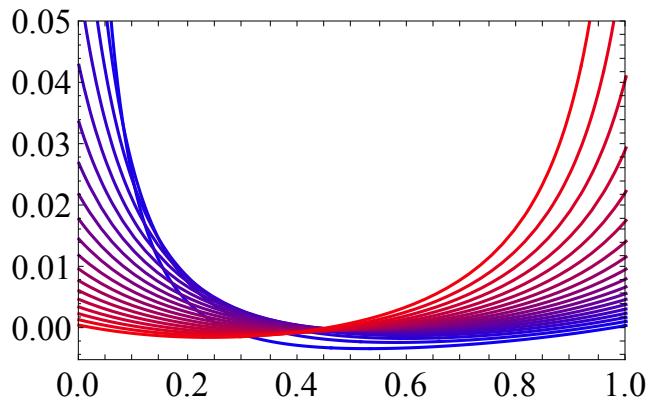


```

Plot[Evaluate[
  FaiDDstrict /. pH ->  $\frac{2}{3}$  /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.005, 0.05}}
];

```

Show[% , AxesOrigin -> {0, 0} , AxesStyle -> Directive[Black, AbsoluteThickness[0.5]] ,
Frame -> True, FrameStyle -> AbsoluteThickness[0.5] , FrameTicksStyle ->
Directive[AbsoluteThickness[0.5] , FontFamily -> "Times New Roman" , FontSize -> 18] ,
FrameLabel -> {Style["" , 20, FontFamily -> "Times New Roman"] ,
Style["" , 20, FontFamily -> "Times New Roman"]}]



## Figure 4: Asymmetry movement

```

MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

FQHH = FaiHHstrict /. ρH → 0.1 /. Ntot → 100;
FQDD = FaiDDstrict /. ρH → 0.1 /. Ntot → 100;

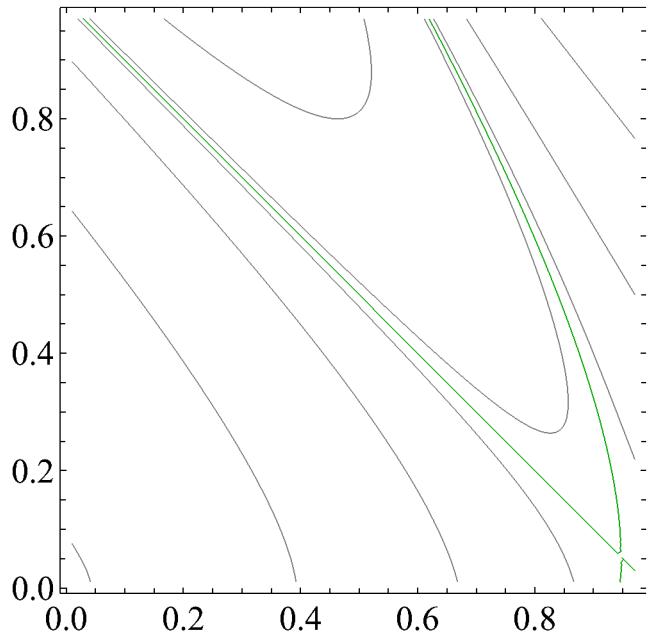
OmegaQHH = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
OmegaQDD = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
repeat = 0;
For[repeat1 = 1, repeat1 ≤ RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 ≤ RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQHH[[repeat, 1]] = x1;
    OmegaQHH[[repeat, 2]] = x2;
    OmegaQHH[[repeat, 3]] = FQHH /. mHfromD → x1 /. mDfromH → x2;

    OmegaQDD[[repeat, 1]] = x1;
    OmegaQDD[[repeat, 2]] = x2;
    OmegaQDD[[repeat, 3]] = FQDD /. mHfromD → x1 /. mDfromH → x2;
  ];
];
];

```

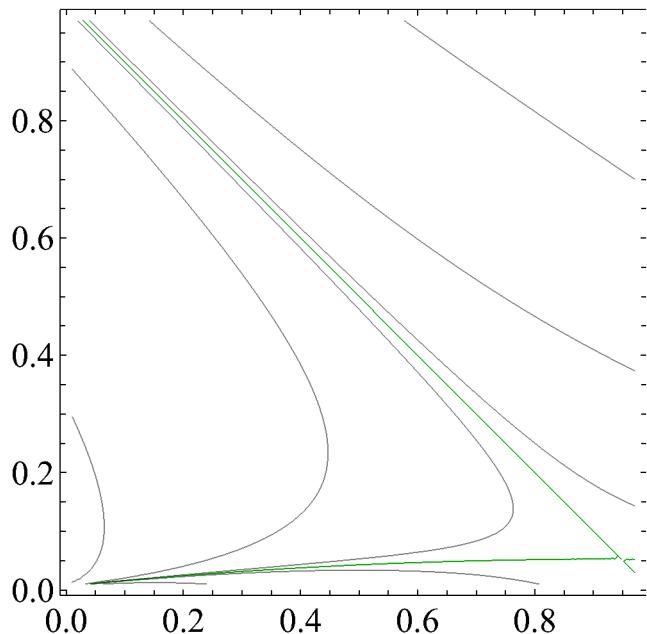
```
ListContourPlot[OmegaQHH,
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}, {0.5}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["", 20, FontFamily → "Times New Roman"],
Style["", 20, FontFamily → "Times New Roman"]}]
```



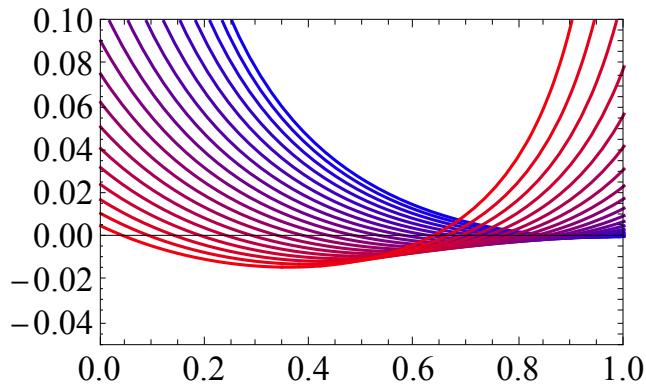
```
ListContourPlot[OmegaQDD, Contours ->
  {{-0.1}, {-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}, {0.5}},
  PlotRange -> All, ContourShading -> None];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
 Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
 Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
 FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
 Style["", 20, FontFamily -> "Times New Roman"]}]
```



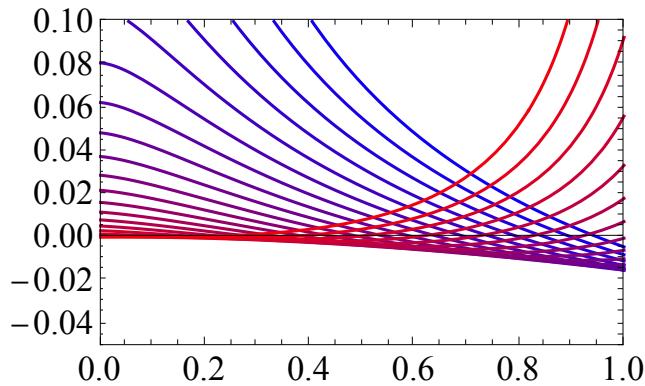
```
Plot[Evaluate[
  FaiHHstrict /. pH -> 0.1 /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```



```
Plot[Evaluate[
  FaiHHstrict /. pH -> 0.1 /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```



```

MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

FQHH = FaiHHstrict /. ρH → 0.5 /. Ntot → 100;
FQDD = FaiDDstrict /. ρH → 0.5 /. Ntot → 100;

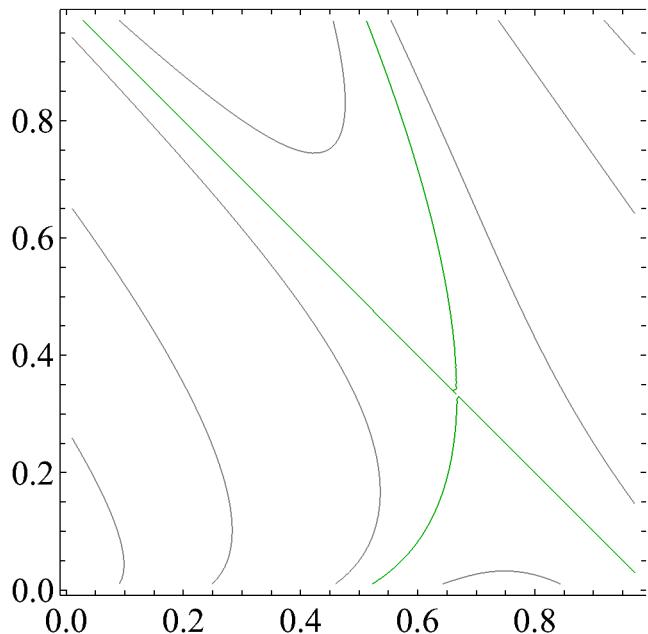
OmegaQHH = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
OmegaQDD = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
repeat = 0;
For[repeat1 = 1, repeat1 ≤ RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 ≤ RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQHH[[repeat, 1]] = x1;
    OmegaQHH[[repeat, 2]] = x2;
    OmegaQHH[[repeat, 3]] = FQHH /. mHfromD → x1 /. mDfromH → x2;

    OmegaQDD[[repeat, 1]] = x1;
    OmegaQDD[[repeat, 2]] = x2;
    OmegaQDD[[repeat, 3]] = FQDD /. mHfromD → x1 /. mDfromH → x2;
  ];
];
];

```

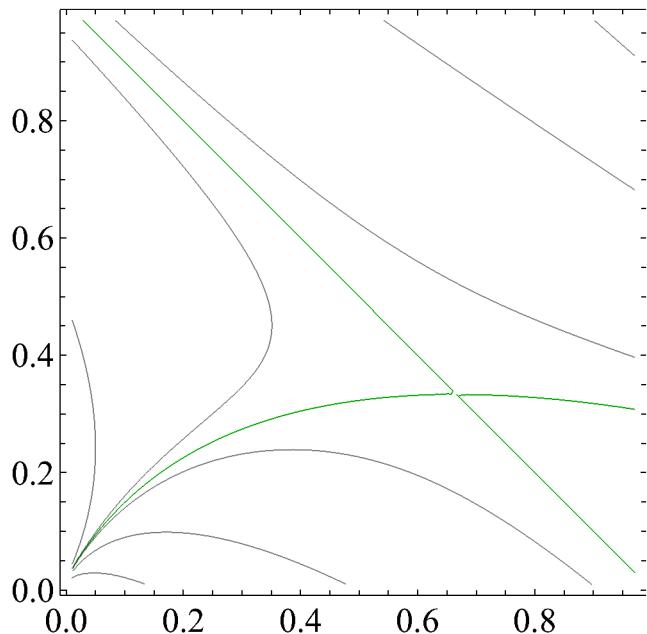
```
ListContourPlot[OmegaQHH,
Contours → {{-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["", 20, FontFamily → "Times New Roman"],
Style["", 20, FontFamily → "Times New Roman"]}]
```



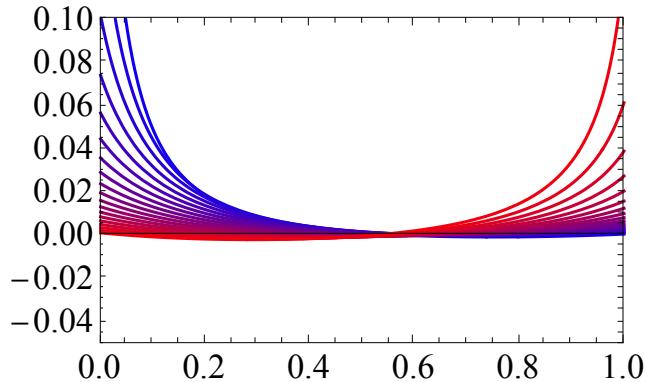
```
ListContourPlot[OmegaQDD,
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["", 20, FontFamily → "Times New Roman"],
Style["", 20, FontFamily → "Times New Roman"]}]
```



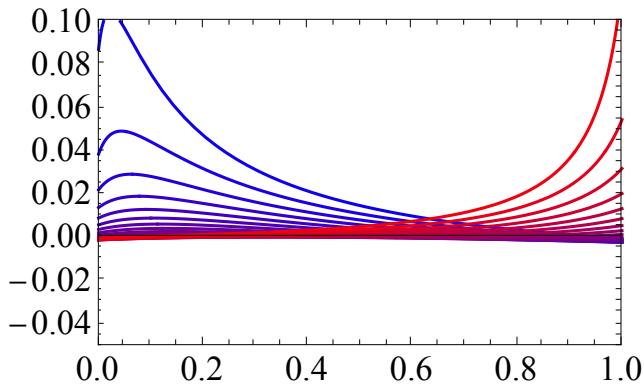
```
Plot[Evaluate[
  FaiHHstrict /. pH -> 0.5 /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```



```
Plot[Evaluate[
  FaiHHstrict /. pH -> 0.5 /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```



```

MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

FQHH = FaiHHstrict /. ρH → 0.9 /. Ntot → 100;
FQDD = FaiDDstrict /. ρH → 0.9 /. Ntot → 100;

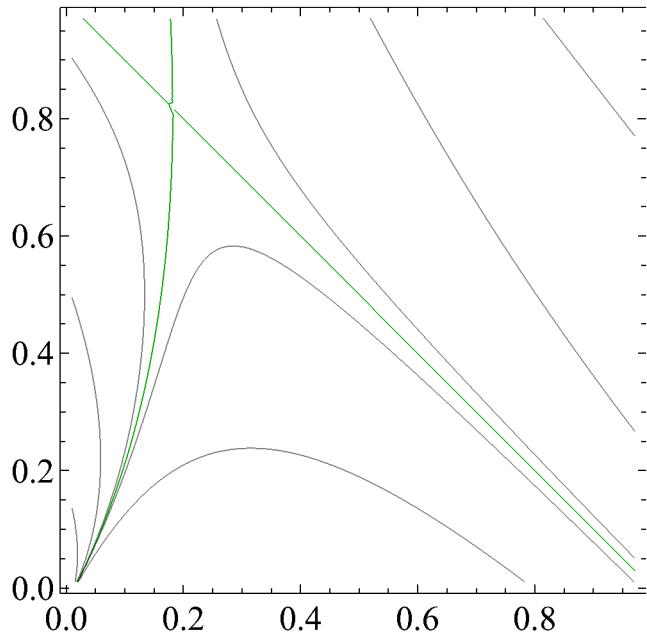
OmegaQHH = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
OmegaQDD = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];
repeat = 0;
For[repeat1 = 1, repeat1 ≤ RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 ≤ RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQHH[[repeat, 1]] = x1;
    OmegaQHH[[repeat, 2]] = x2;
    OmegaQHH[[repeat, 3]] = FQHH /. mHfromD → x1 /. mDfromH → x2;

    OmegaQDD[[repeat, 1]] = x1;
    OmegaQDD[[repeat, 2]] = x2;
    OmegaQDD[[repeat, 3]] = FQDD /. mHfromD → x1 /. mDfromH → x2;
  ];
];
];

```

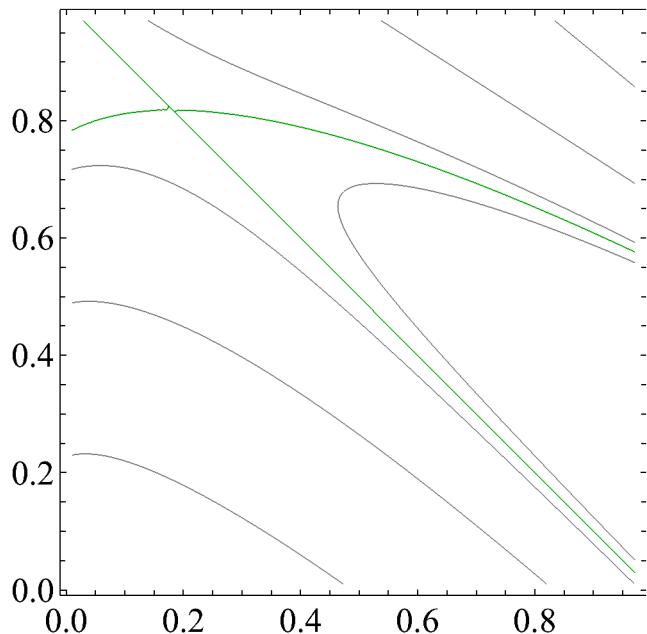
```
ListContourPlot[OmegaQHH,
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["", 20, FontFamily → "Times New Roman"],
Style["", 20, FontFamily → "Times New Roman"]}]
```



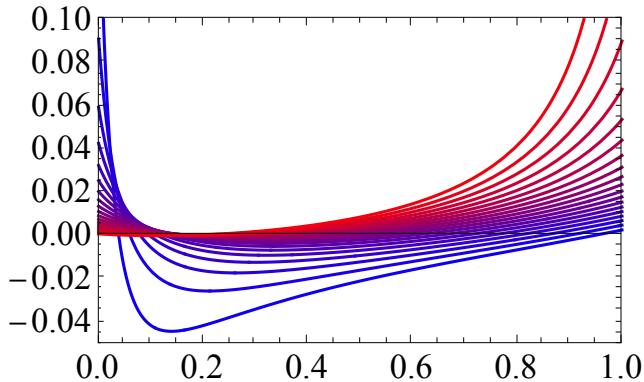
```
ListContourPlot[OmegaQDD,
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}},
PlotRange → All, ContourShading → None];

Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],
FrameLabel → {Style["", 20, FontFamily → "Times New Roman"],
Style["", 20, FontFamily → "Times New Roman"]}]
```



```
Plot[Evaluate[
  FaiHHstrict /. pH -> 0.9 /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```



```

Plot[Evaluate[
  FaiHHstrict /. pH -> 0.1 /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}]],
{mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]

```

### Supplementary: Average Fst, Equal chromosome number

```

FaiAverage /. pH ->  $\frac{2}{3}$  // FullSimplify
Eq8 = 
$$\frac{(1-X)^2}{\frac{2}{3} * Ntot - (1-X)^2 * \left(\frac{2}{3} * Ntot - 1\right)}$$
 /. X -> mHfromD + mDfromH;
% - %% // Simplify

$$-\frac{3 (-1 + mDfromH + mHfromD)^2}{-3 (-1 + mDfromH + mHfromD)^2 + 2 (-2 + mDfromH + mHfromD) (mDfromH + mHfromD) Ntot}$$

0

```

```

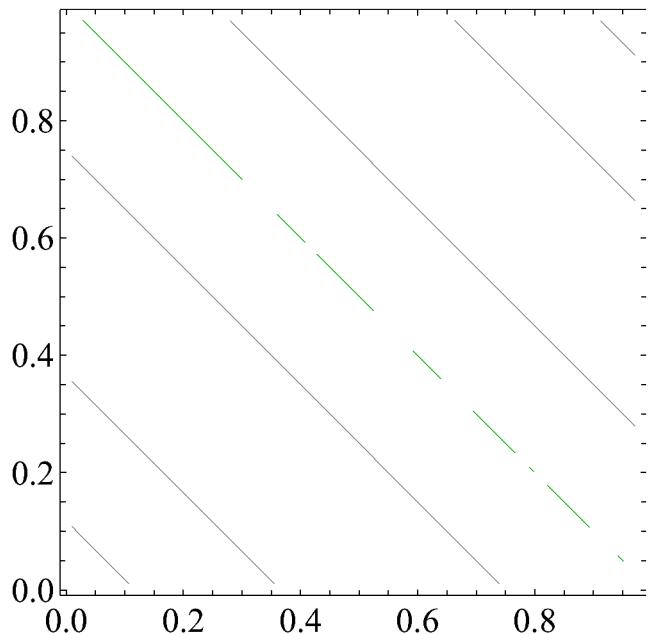
MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

OmegaQave = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];

repeat = 0;
For[repeat1 = 1, repeat1 < RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 < RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQave[[repeat, 1]] = x1;
    OmegaQave[[repeat, 2]] = x2;
    OmegaQave[[repeat, 3]] =
       $\frac{2}{3} \text{FaiAverage} / . \rho\text{H} \rightarrow 100 / . \text{mHfromD} \rightarrow x1 / . \text{mDfromH} \rightarrow x2$ ;
  ];
];
];

```

```
ListContourPlot[OmegaQave,  
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}, {0.5}},  
PlotRange → All, ContourShading → None];  
  
Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],  
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →  
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],  
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],  
Style["\"", 20, FontFamily → "Times New Roman"]}]
```

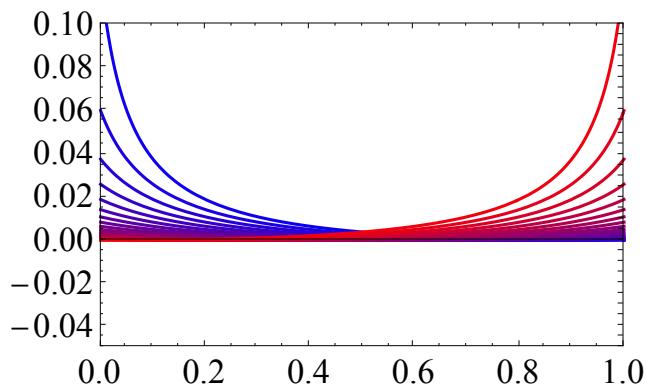


```

Plot[Evaluate[
  FaiAverage /. pH ->  $\frac{2}{3} / . N_{tot} \rightarrow 100 / . mD_{fromH} \rightarrow Table[i, \{i, 0.05, 0.95, 0.05\}]$ ],
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

```

Show[% , AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]

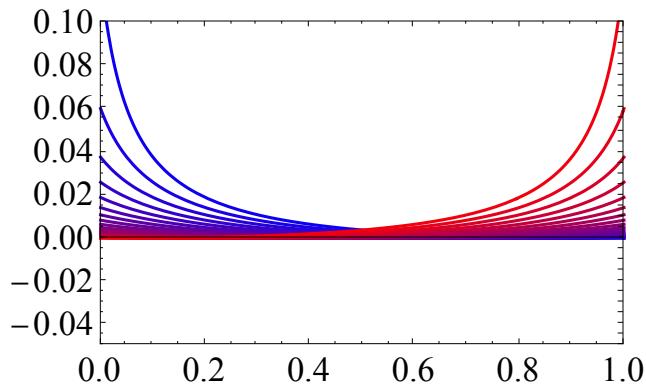


```

Plot[Evaluate[
  FaiAverage /. pH ->  $\frac{2}{3} / . N_{tot} \rightarrow 100 / . mHfromD \rightarrow Table[i, \{i, 0.05, 0.95, 0.05\}]$ ],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

```

Show[% , AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style[""], 20, FontFamily -> "Times New Roman"},  
Style["", 20, FontFamily -> "Times New Roman"]}]



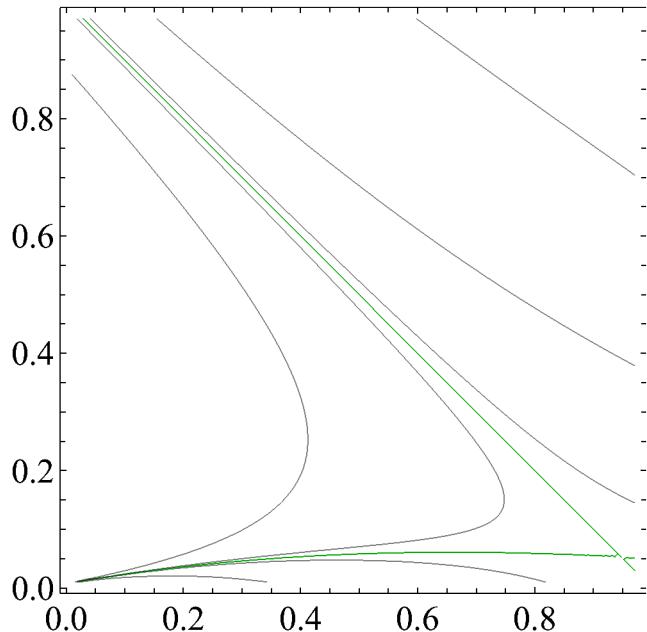
## Figure 5: Average Fst

```
MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

OmegaQave = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];

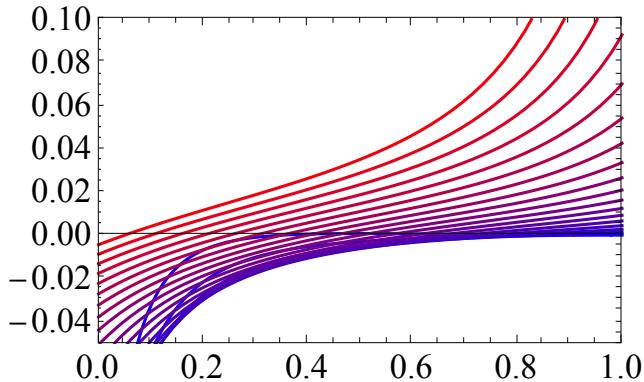
repeat = 0;
For[repeat1 = 1, repeat1 < RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 < RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQave[[repeat, 1]] = x1;
    OmegaQave[[repeat, 2]] = x2;
    OmegaQave[[repeat, 3]] =
      FaiAverage /. pH → 0.1 /. Ntot → 100 /. mHfromD → x1 /. mDfromH → x2;
  ];
];
];
```

```
ListContourPlot[OmegaQave,  
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}, {0.5}},  
PlotRange → All, ContourShading → None];  
  
Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],  
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →  
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],  
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],  
Style["\"", 20, FontFamily → "Times New Roman"]}]
```

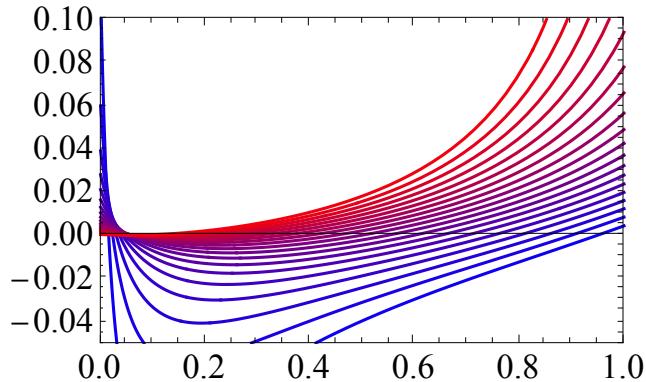


```
Plot[Evaluate[
  FaiAverage /. pH -> 0.1 /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}]], 
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}], 
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
  Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
  Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
  FrameLabel -> {Style["\"", 20, FontFamily -> "Times New Roman"],
  Style["\"", 20, FontFamily -> "Times New Roman"]}]
```



```
Plot[Evaluate[  
  FaiAverage /. pH -> 0.1 /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}]],  
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],  
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]  
];  
  
Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],  
  Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->  
  Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],  
  FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],  
  Style["", 20, FontFamily -> "Times New Roman"]}]
```

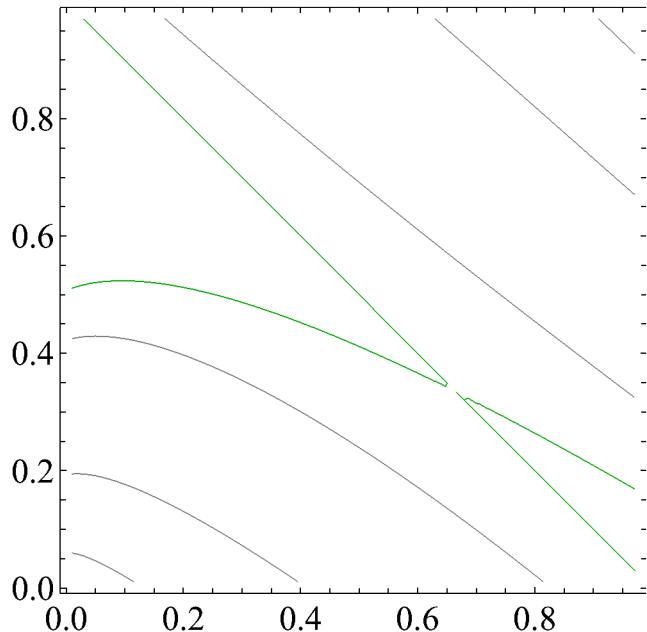


```
MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

OmegaQave = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];

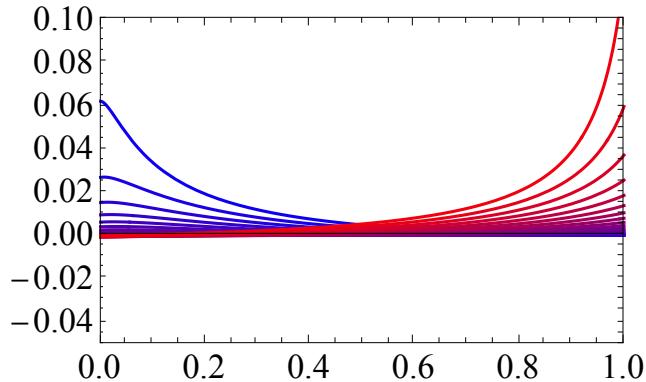
repeat = 0;
For[repeat1 = 1, repeat1 < RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 < RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQave[[repeat, 1]] = x1;
    OmegaQave[[repeat, 2]] = x2;
    OmegaQave[[repeat, 3]] =
      FaiAverage /. pH -> 0.5 /. Ntot -> 100 /. mHfromD -> x1 /. mDfromH -> x2;
  ];
];
];
```

```
ListContourPlot[OmegaQave,  
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}, {0.5}},  
PlotRange → All, ContourShading → None];  
  
Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],  
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →  
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],  
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],  
Style["\"", 20, FontFamily → "Times New Roman"]}]
```



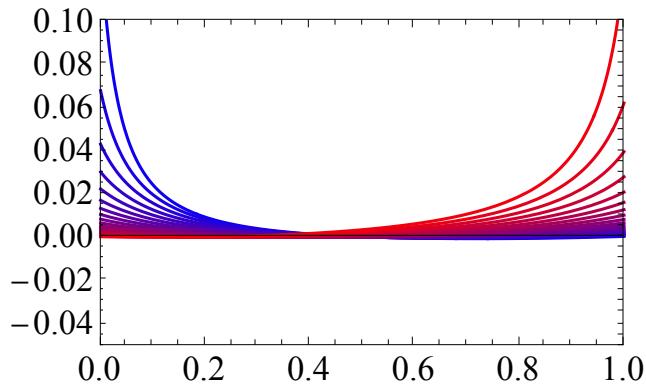
```
Plot[Evaluate[
  FaiAverage /. pH -> 0.5 /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}]], 
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}], 
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
  Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
  Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
  FrameLabel -> {Style["\"", 20, FontFamily -> "Times New Roman"],
  Style["\"", 20, FontFamily -> "Times New Roman"]}]
```



```
Plot[Evaluate[
  FaiAverage /. pH -> 0.5 /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```

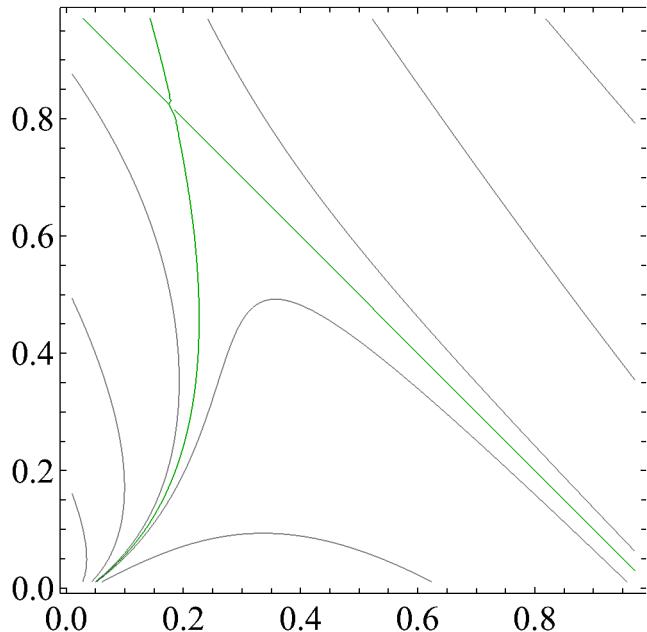


```
MaxV = 0.99;
MinV = 0.01;
RepeatMax = 101;

OmegaQave = Table[10, {i, (RepeatMax - 1) * (RepeatMax - 1)}, {j, 3}];

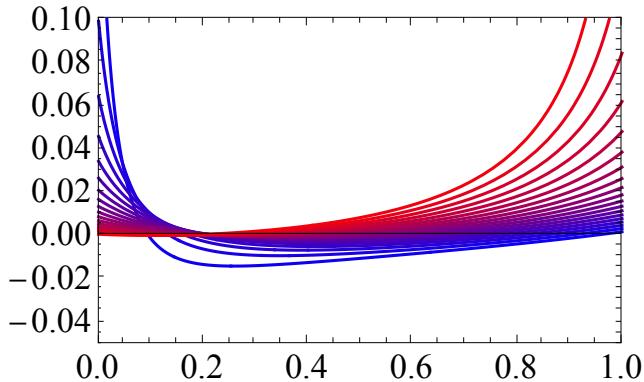
repeat = 0;
For[repeat1 = 1, repeat1 ≤ RepeatMax - 1, repeat1 = repeat1 + 1,
  For[repeat2 = 1, repeat2 ≤ RepeatMax - 1, repeat2 = repeat2 + 1,
    repeat = repeat + 1;
    x1 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat1} - 1)$ ;
    x2 = MinV +  $\frac{(\text{MaxV} - \text{MinV})}{\text{RepeatMax}} * (\text{repeat2} - 1)$ ;
    OmegaQave[[repeat, 1]] = x1;
    OmegaQave[[repeat, 2]] = x2;
    OmegaQave[[repeat, 3]] =
      FaiAverage /. pH → 0.9 /. Ntot → 100 /. mHfromD → x1 /. mDfromH → x2;
  ];
];
];
```

```
ListContourPlot[OmegaQave,  
Contours → {{-0.01}, {-0.001}, {0, Darker[Green]}, {0.001}, {0.01}, {0.05}, {0.5}},  
PlotRange → All, ContourShading → None];  
  
Show[%, AxesOrigin → {0, 0}, AxesStyle → Directive[Black, AbsoluteThickness[0.5]],  
Frame → True, FrameStyle → AbsoluteThickness[0.5], FrameTicksStyle →  
Directive[AbsoluteThickness[0.5], FontFamily → "Times New Roman", FontSize → 18],  
FrameLabel → {Style["\"", 20, FontFamily → "Times New Roman"],  
Style["\"", 20, FontFamily → "Times New Roman"]}]
```



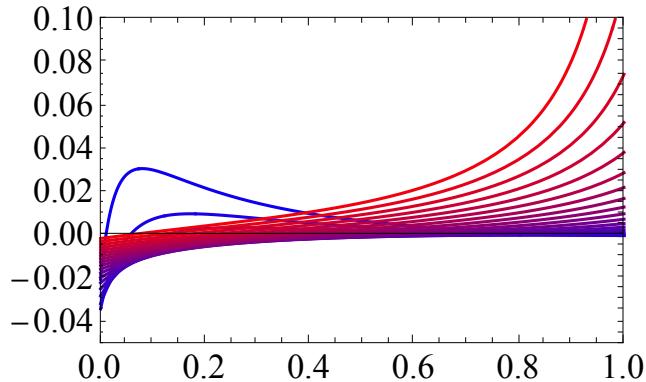
```
Plot[Evaluate[
  FaiAverage /. pH -> 0.9 /. Ntot -> 100 /. mDfromH -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mHfromD, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["", 20, FontFamily -> "Times New Roman"],
Style["", 20, FontFamily -> "Times New Roman"]}]
```



```
Plot[Evaluate[
  FaiAverage /. pH -> 0.9 /. Ntot -> 100 /. mHfromD -> Table[i, {i, 0.05, 0.95, 0.05}]],
  {mDfromH, 0, 1}, PlotStyle -> Table[RGBColor[i, 0, 1-i], {i, 0.05, 0.95, 0.05}],
  PlotRange -> {{0, 1}, {-0.05, 0.1}}]
];

Show[%, AxesOrigin -> {0, 0}, AxesStyle -> Directive[Black, AbsoluteThickness[0.5]],
Frame -> True, FrameStyle -> AbsoluteThickness[0.5], FrameTicksStyle ->
Directive[AbsoluteThickness[0.5], FontFamily -> "Times New Roman", FontSize -> 18],
FrameLabel -> {Style["\"", 20, FontFamily -> "Times New Roman"],
Style["\"", 20, FontFamily -> "Times New Roman"]}]
```



## Supplementary: Coalescence process considering FIS

### Equations

$$\begin{aligned}
 \text{NextQHH} = & (1 - \mu)^2 * \left( mHfromH^2 * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) + mHfromH * mHfromD * QHD + \right. \\
 & \left. mHfromD * mHfromH * QDH + mHfromD^2 * \left( \frac{1}{2 * Dip} + \frac{1}{2 * Dip} * QDDw + \left( 1 - \frac{2}{2 * Dip} \right) * QDDb \right) \right); \\
 \text{NextQHD} = & (1 - \mu)^2 * \left( mHfromH * mDfromH * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) + \right. \\
 & mHfromD * mDfromH * QDH + mHfromH * mDfromD * QHD + \\
 & \left. mHfromD * mDfromD * \left( \frac{1}{2 * Dip} + \frac{1}{2 * Dip} * QDDw + \left( 1 - \frac{2}{2 * Dip} \right) * QDDb \right) \right); \\
 \text{NextQDH} = & (1 - \mu)^2 * \left( mDfromH * mHfromH * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) + \right. \\
 & mDfromD * mHfromH * QDH + mDfromH * mHfromD * QHD + \\
 & \left. mDfromD * mHfromD * \left( \frac{1}{2 * Dip} + \frac{1}{2 * Dip} * QDDw + \left( 1 - \frac{2}{2 * Dip} \right) * QDDb \right) \right); \\
 \text{NextQDDb} = & (1 - \mu)^2 * \left( mDfromD^2 * \left( \frac{1}{2 * Dip} + \frac{1}{2 * Dip} * QDDw + \left( 1 - \frac{2}{2 * Dip} \right) * QDDb \right) + \right. \\
 & \left. mDfromH * mDfromD * QHD + mDfromD * mDfromH * QDH + mDfromH^2 * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) \right); \\
 \text{NextQDDw} = & (1 - \mu)^2 * \left( mDfromD * QDDw + mDfromH * \left( \frac{1}{Hap} + \left( 1 - \frac{1}{Hap} \right) * QHH \right) \right);
 \end{aligned}$$

Recall that these are backwards rates so that mDD+mHD sum to one:

```

constraints = {mHfromH + mHfromD == 1, mDfromH + mDfromD == 1, rhoD + rhoH == 1};
subconstraints = {mHfromH -> 1 - mHfromD, mDfromD -> 1 - mDfromH};

```

### Exact FST and FIS

At equilibrium, we have

```

sol =
Simplify[Solve[(NextQHH == QHH && NextQDDb == QDDb && NextQDDw == QDDw && NextQHD == QHD &&
NextQDH == QDH), {QHH, QHD, QDH, QDDb, QDDw}], constraints];

```

When there is not mutation, because of a finite population size, Q must be 1.

```

sol /. subconstraints /. mu -> 0 // Simplify
{{QHH -> 1, QHD -> 1, QDH -> 1, QDDb -> 1, QDDw -> 1}}

```

```

EqQHH = Simplify[QHH /. sol[[1]], constraints];
EqQHD = Simplify[QHD /. sol[[1]], constraints];
EqQDH = Simplify[QDH /. sol[[1]], constraints];
EqQDDb = Simplify[QDDb /. sol[[1]], constraints];
EqQDDw = Simplify[QDDw /. sol[[1]], constraints];

```

Note that, we can show QHD = QDH,

```
EqQHD == EqQDH
```

```
True
```

Using Q, we define the F-like measures for the haploid-diploid population.

$$\begin{aligned}
& \text{FaiHstrict} = \text{Simplify}\left[\frac{\text{EqQHH} - \text{EqQHD}}{1 - \text{EqQHD}}, \text{constraints}\right] \\
& ((\text{mDfromH} - \text{mHfromH}) \\
& ((2 - 2 \text{Dip}) \text{mDfromH}^3 + 4 (-1 + \text{Dip}) \text{mDfromH}^2 \text{mHfromH} - (-1 + \text{mHfromH}) \text{mHfromH} + \\
& \text{mDfromH} (-1 + \text{Hap} (-1 + \text{mHfromH}) + \text{mHfromH} + 2 \text{Dip} \text{mHfromH} + (2 - 2 \text{Dip}) \text{mHfromH}^2))) / \\
& (-(\text{mDfromH} - \text{mHfromH}) (\text{mDfromH} + 2 (-1 + \text{Dip}) \text{mDfromH}^3 + (-1 - 2 \text{Dip}) \text{mDfromH} \text{mHfromH} + \\
& (4 - 4 \text{Dip}) \text{mDfromH}^2 \text{mHfromH} + (-1 + \text{mHfromH}) \text{mHfromH} + \\
& 2 (-1 + \text{Dip}) \text{mDfromH} \text{mHfromH}^2) + \text{Hap} (2 (-1 + \text{Dip}) \text{mDfromH}^4 - \\
& (-1 + \text{mHfromH})^2 (1 + \text{mHfromH}) - 2 (-1 + \text{Dip}) \text{mDfromH}^3 (-1 + 3 \text{mHfromH}) - \\
& \text{mDfromH} (-1 + \text{mHfromH}) (1 - 2 \text{Dip} - 4 \text{mHfromH} + 2 (-1 + \text{Dip}) \text{mHfromH}^2) + \\
& \text{mDfromH}^2 (3 - 2 \text{Dip} + \text{mHfromH} - 4 \text{Dip} \text{mHfromH} + 6 (-1 + \text{Dip}) \text{mHfromH}^2)))
\end{aligned}$$

$$\begin{aligned}
& \text{FaiDbstrict} = \text{Simplify}\left[\frac{\text{EqQDDb} - \text{EqQHD}}{1 - \text{EqQHD}}, \text{constraints}\right] \\
& - ((\text{mDfromH} (\text{mDfromH} - \text{mHfromH}) (2 \text{Dip} \text{mDfromH} - (\text{mDfromH} - \text{mHfromH})^2 + \\
& \text{Hap} (-1 + \text{mDfromH} + \text{mDfromH}^2 - 2 \text{mDfromH} \text{mHfromH} + \text{mHfromH}^2))) / \\
& (-(\text{mDfromH} - \text{mHfromH}) (\text{mDfromH} + 2 (-1 + \text{Dip}) \text{mDfromH}^3 + (-1 - 2 \text{Dip}) \text{mDfromH} \text{mHfromH} + \\
& (4 - 4 \text{Dip}) \text{mDfromH}^2 \text{mHfromH} + (-1 + \text{mHfromH}) \text{mHfromH} + \\
& 2 (-1 + \text{Dip}) \text{mDfromH} \text{mHfromH}^2) + \text{Hap} (2 (-1 + \text{Dip}) \text{mDfromH}^4 - \\
& (-1 + \text{mHfromH})^2 (1 + \text{mHfromH}) - 2 (-1 + \text{Dip}) \text{mDfromH}^3 (-1 + 3 \text{mHfromH}) - \\
& \text{mDfromH} (-1 + \text{mHfromH}) (1 - 2 \text{Dip} - 4 \text{mHfromH} + 2 (-1 + \text{Dip}) \text{mHfromH}^2) + \\
& \text{mDfromH}^2 (3 - 2 \text{Dip} + \text{mHfromH} - 4 \text{Dip} \text{mHfromH} + 6 (-1 + \text{Dip}) \text{mHfromH}^2)))
\end{aligned}$$

```

FaiDwstrict = Simplify[Limit[(EqQDDw - EqQHD)/(1 - EqQHD), μ → 0], constraints]
((-1 + mHfromH) (2 Dip mDfromH - (mDfromH - mHfromH)^2 +
Hap (-1 + mDfromH + mDfromH^2 - 2 mDfromH mHfromH + mHfromH^2))) /
(- (mDfromH - mHfromH) (mDfromH + 2 (-1 + Dip) mDfromH^3 + (-1 - 2 Dip) mDfromH mHfromH +
(4 - 4 Dip) mDfromH^2 mHfromH + (-1 + mHfromH) mHfromH +
2 (-1 + Dip) mDfromH mHfromH^2) + Hap (2 (-1 + Dip) mDfromH^4 -
(-1 + mHfromH)^2 (1 + mHfromH) - 2 (-1 + Dip) mDfromH^3 (-1 + 3 mHfromH) -
mDfromH (-1 + mHfromH) (1 - 2 Dip - 4 mHfromH + 2 (-1 + Dip) mHfromH^2) +
mDfromH^2 (3 - 2 Dip + mHfromH - 4 Dip mHfromH + 6 (-1 + Dip) mHfromH^2))) )

FISstrict = Simplify[Limit[(EqQDDw - EqQDDb)/(1 - EqQDDb) /. subconstraints, μ → 0], constraints]
((-1 + mDfromH) (1 + mDfromH - mHfromH) (2 Dip mDfromH - (mDfromH - mHfromH)^2 +
Hap (-1 + mDfromH + mDfromH^2 - 2 mDfromH mHfromH + mHfromH^2))) /
(- (mDfromH - mHfromH) (mDfromH + (-1 + 2 Dip) mDfromH^3 + (-1 - 2 Dip) mDfromH mHfromH +
(-1 + mHfromH) mHfromH + (-1 + 2 Dip) mDfromH mHfromH^2 -
2 mDfromH^2 (Dip - mHfromH + 2 Dip mHfromH)) +
Hap (1 + mDfromH - mHfromH) (-1 + (-1 + 2 Dip) mDfromH^3 + (2 - 4 Dip) mDfromH^2 mHfromH +
mHfromH^2 + mDfromH (2 - 2 Dip - 2 mHfromH + (-1 + 2 Dip) mHfromH^2))) )

```

we can rewrite FaiHstrict as:

```

numerator =
(1 - X)^3 + Hap * mHfromD * mDfromH * (1 - X) + 2 * Dip * mDfromH * ((1 - X)^2 - mHfromH) * (1 - X) -
(1 - X)^2 * (1 + mDfromH * (1 - 2 * X)) // Simplify;
denominator = (1 - X)^3 + Hap * ((1 - X)^2 - mDfromD) * (X + mDfromH * (1 - 2 * X)) +
2 * Dip * mDfromH * ((1 - X)^2 - mHfromH) * (1 - X) - 2 * Hap * Dip * mDfromH * (2 - X) * X^2 -
(1 - X)^2 * (1 + mDfromH * (1 - 2 * X)) // Simplify;
numerator
-----
denominator // FullSimplify;
% - FaiHstrict /. X → mHfromD + mDfromH /. subconstraints /. ρD → 1 - ρH // Factor
0

```

While this doesn't equal FaiHHstrict obtained without considering between and within diploid sampling, it does when the population size is large (here assuming intermediate migration rates):

```

FaiHstrict /. Hap → Ntot * ρH /. Dip → Ntot * ρD // Simplify
( (mDfromH - mHfromH)
  (- (-1 + mHfromH) mHfromH + mDfromH^3 (2 - 2 Ntot ρD) + 4 mDfromH^2 mHfromH (-1 + Ntot ρD) +
   mDfromH (-1 + mHfromH + 2 mHfromH Ntot ρD + mHfromH^2 (2 - 2 Ntot ρD) +
   (-1 + mHfromH) Ntot ρH)) ) /
(- (mDfromH - mHfromH) (mDfromH + (-1 + mHfromH) mHfromH +
   mDfromH^2 mHfromH (4 - 4 Ntot ρD) + 2 mDfromH^3 (-1 + Ntot ρD) +
   2 mDfromH mHfromH^2 (-1 + Ntot ρD) - mDfromH mHfromH (1 + 2 Ntot ρD) ) +
 Ntot (- (-1 + mHfromH)^2 (1 + mHfromH) + 2 mDfromH^4 (-1 + Ntot ρD) -
   2 mDfromH^3 (-1 + 3 mHfromH) (-1 + Ntot ρD) -
   mDfromH (-1 + mHfromH) (1 - 4 mHfromH - 2 Ntot ρD + 2 mHfromH^2 (-1 + Ntot ρD) ) +
   mDfromH^2 (3 + mHfromH - 2 Ntot ρD - 4 mHfromH Ntot ρD + 6 mHfromH^2 (-1 + Ntot ρD) ) ) ρH)

```

If  $N$  is large (total population size) relative to the migration rates (i.e., none of the migration rates is very rare) these reduce to the same  $\text{FNlarge}$  obtained above without considering sampling within and between diploids:

```

Factor[Normal[Series[{FaiHstrict, FaiDbstrict} /. Hap → Ntot * ρH /. Dip → Ntot * ρD /.
  Ntot → Ntot/ε, {ε, 0, 1}]]] /. ε → 1
{ - (( (mDfromH - mHfromH) (2 mDfromH^2 ρD -
  2 mHfromH ρD - 4 mDfromH mHfromH ρD + 2 mHfromH^2 ρD + ρH - mHfromH ρH) ) /
  (2 (-1 + mDfromH - mHfromH) (1 + mDfromH - mHfromH)^2 Ntot ρD ρH) ) ,
 - (( (mDfromH - mHfromH) (2 mDfromH ρD - ρH + mDfromH ρH +
   mDfromH^2 ρH - 2 mDfromH mHfromH ρH + mHfromH^2 ρH) ) /
  (2 (-1 + mDfromH - mHfromH) (1 + mDfromH - mHfromH)^2 Ntot ρD ρH) ) }

```

From above (ignoring between/within), we derived the following in this case:

$$\text{FNlarge} = \left\{ \frac{\frac{(1-X) * ((2-X) * X * (2 * \rhoD) - mHfromD (\rhoH + 2 * \rhoD))}{(2-X) * X^2 * \rhoH * (2 * \rhoD) * Ntot},}{\frac{(1-X) * ((2-X) * X * \rhoH - mDfromH * (\rhoH + 2 * \rhoD))}{(2-X) * X^2 * \rhoH * (2 * \rhoD) * Ntot}} \right\};$$

As expected this equals the same large  $N$  approximation as found without considering within and between sampling:

```

Factor[% - FNlarge /. X → mDfromH + mHfromD /. ρD → 1 - ρH /. subconstraints]
{0, 0}

```

```

Factor[Normal[Series[
  FaiDwstrict /. Hap → Ntot * ρH /. Dip → Ntot * ρD /. Ntot → Ntot / ε, {ε, 0, 1}]]] /. ε → 1
Factor[% - mHfromD * (- (2 - X) * X * ρH + mDfromH * (ρH + 2 * ρD)) /.
  mDfromH * (2 - X) * X^2 * ρH * (2 * ρD) * Ntot
  ρD → 1 - ρH /. subconstraints]
((-1 + mHfromH)
(2 mDfromH ρD - ρH + mDfromH ρH + mDfromH^2 ρH - 2 mDfromH mHfromH ρH + mHfromH^2 ρH) ) /
(2 mDfromH (-1 + mDfromH - mHfromH) (1 + mDfromH - mHfromH)^2 Ntot ρD ρH)

0

Factor[Normal[Series[
  FISstrict /. Hap → Ntot * ρH /. Dip → Ntot * ρD /. Ntot → Ntot / ε, {ε, 0, 1}]]] /. ε → 1
Factor[% - mDfromD * (- (2 - X) * X * ρH + mDfromH * (ρH + 2 * ρD)) /.
  mDfromH * (2 - X) * X * ρH * (2 * ρD) * Ntot
  ρD → 1 - ρH /. subconstraints]
((-1 + mDfromH)
(2 mDfromH ρD - ρH + mDfromH ρH + mDfromH^2 ρH - 2 mDfromH mHfromH ρH + mHfromH^2 ρH) ) /
(2 mDfromH (-1 + mDfromH - mHfromH) (1 + mDfromH - mHfromH) Ntot ρD ρH)

0

```

## Rare sexuality in a large population

We consider the case when there is frequent asexual reproduction ( $\alpha \approx 1$ , and then  $mHfromD$  and  $mDfromH$  is small), and large population size. We assume;

- $mHfromD = O(\epsilon)$
- $mDfromH = O(\epsilon)$
- $Ntot = O(1/\epsilon)$

These assumptions indicates,  $\thetaHD = mHfromD Ntot = O(1)$  and  $\thetaDH = mDfromH Ntot = O(1)$ .

```

FaiH♦RS = Simplify[
  Normal[Series[FaiHstrict /. subconstraints /. Hap → Ntot * ρH /. Dip → Ntot * ρD /.
    mHfromD → θHD / Ntot /. mDfromH → θDH / Ntot /. Ntot → cNtot * 1 / ε, {ε, 0, 0}]]]
(θHD + 4 θDH^2 ρD + θDH (2 + 2 θHD ρD - θHD ρH) ) / (4 θDH^3 ρD ρH + θHD (1 + 2 θHD ρH) +
  θDH (2 + 2 θHD ρD + 5 θHD ρH + 4 θHD^2 ρD ρH) + 2 θDH^2 (ρH + ρD (2 + 4 θHD ρH) ) )

```

```

FaiDb◆RS = Simplify[
  Normal[Series[FaiDbstrict /. subconstraints /. Hap → Ntot * ρH /. Dip → Ntot * ρD /.
    mHfromD → θHD / Ntot /. mDfromH → θDH / Ntot /. Ntot → cNtot * 1/ε, {ε, 0, 0}]]]
  (θDH (1 + 2 θHD ρH + θDH (-2 ρD + ρH))) / (4 θDH³ ρD ρH + θHD (1 + 2 θHD ρH) +
   θDH (2 + 2 θHD ρD + 5 θHD ρH + 4 θHD² ρD ρH) + 2 θDH² (ρH + ρD (2 + 4 θHD ρH)))

FaiDw◆RS = Simplify[
  Normal[Series[FaiDwstrict /. subconstraints /. Hap → Ntot * ρH /. Dip → Ntot * ρD /.
    mHfromD → θHD / Ntot /. mDfromH → θDH / Ntot /. Ntot → cNtot * 1/ε, {ε, 0, 0}]]]
  - ((θHD (1 + 2 θHD ρH + θDH (-2 ρD + ρH))) / (4 θDH³ ρD ρH + θHD (1 + 2 θHD ρH) +
   θDH (2 + 2 θHD ρD + 5 θHD ρH + 4 θHD² ρD ρH) + 2 θDH² (ρH + ρD (2 + 4 θHD ρH))))]

FIS◆RS = Simplify[
  Normal[Series[FISstrict /. subconstraints /. Hap → Ntot * ρH /. Dip → Ntot * ρD /.
    mHfromD → θHD / Ntot /. mDfromH → θDH / Ntot /. Ntot → cNtot * 1/ε, {ε, 0, 0}]]]
  ((θDH + θHD) (-1 + 2 θDH ρD - θDH ρH - 2 θHD ρH)) / (4 θDH³ ρD ρH + θHD (1 + 2 θHD ρH) +
   θDH (1 + 2 θHD ρD + 3 θHD ρH + 4 θHD² ρD ρH) + θDH² (ρH + ρD (6 + 8 θHD ρH)))

FaiH◆RS
  (θHD + 4 θDH² ρD + θDH (2 + 2 θHD ρD - θHD ρH)) / (4 θDH³ ρD ρH + θHD (1 + 2 θHD ρH) +
   θDH (2 + 2 θHD ρD + 5 θHD ρH + 4 θHD² ρD ρH) + 2 θDH² (ρH + ρD (2 + 4 θHD ρH)))

FaiDave◆RS = Simplify[
  Normal[Series[1/(2 * Dip - 1) * FaiDwstrict + (2 * Dip - 2)/(2 * Dip - 1) * FaiDbstrict /. subconstraints /.
    Hap → Ntot * ρH /. Dip → Ntot * ρD /. mHfromD → θHD / Ntot /.
    mDfromH → θDH / Ntot /. Ntot → cNtot * 1/ε, {ε, 0, 0}]]]
  (θDH (1 + 2 θHD ρH + θDH (-2 ρD + ρH))) / (4 θDH³ ρD ρH + θHD (1 + 2 θHD ρH) +
   θDH (2 + 2 θHD ρD + 5 θHD ρH + 4 θHD² ρD ρH) + 2 θDH² (ρH + ρD (2 + 4 θHD ρH)))

```