The supplementary material is intended to provide mathematical details the text leaves out for clarity. We begin with a section describing how we approximate genotype frequencies from allele frequencies. We then calculate fitness for the autosomal case. We repeat the calculations for an X-linked allele. We add additional details of equilibria calculations and we attach the Maple code for the equilibria calculations. Finally, we include supplementary figures.

I. Understanding the relationship between genotype frequency and *Medea* allele frequency.

In a *Medea*-bearing population the fate of an individual depends on the genotype of its mother as well as its own genotype. Thus, knowledge of one genotype frequency after a single round of random mating is not sufficient to characterize the population.

We approach this problem first by presenting an example, a Medea with a 20% multiplicative embryonic fitness cost. We plot, on a DeFinetti diagram, the trajectories of genotype frequencies over 1000 generations when present in a population initially composed of different proportions of *Medea* homozygotes and non-*Medea* individuals (points along the horizontal axis), non-*Medea* individuals and *Medea* heterozygotes (points along the left axis), or *Medea* homozygotes and heterozygotes (points along the right axis) (Fig. S1A). For this set of parameters, all populations converge to one of two stable equilibrium points, composed of either non-*Medea* individuals, or of two thirds *Medea* homozygotes and one third *Medea* heterozygotes, the stable internal equilibrium allele frequency (SIEAF) (Fig. S1A). The regions of initial conditions that converge to each stable equilibrium are separated by a set of gamete frequencies, known as a separatrix, that define a threshold between *Medea* allele loss and fixation. The separatrix is the stable manifold of the unstable equilibrium (a saddle). This family of points includes one, the unstable internal equilibrium allele frequency (the UIEAF), discussed further below. Importantly, all populations initiating on either side of the separatrix approach and ultimately follow a common trajectory in moving towards one or the other stable equilibrium (the common trajectory is the unstable manifold of the unstable equilibrium). This observation implies that one can calculate genotype frequencies, and thus allele fitness, as a function of *Medea* allele frequency, by calculating the approximate positions of points on this common trajectory. To do this we take a number of starting parental genotypes distributed throughout the parameter space of all possible parental genotypes, indicated by the black dots in the DeFinetti diagrams in Fig. S1B. Each genotype in the distribution is advanced one generation and all possible genotype distributions for that generation are plotted, indicated by the green region. The procedure is repeated for a second generation, resulting in the region of possible genotypes indicated in red; for a third generation, resulting in the region of possible genotypes indicated in yellow; and for a fourth generation, resulting in the region of possible genotypes indicated in blue. After four generations the genotype space distribution is very tight (the blue region that resembles a line in Fig. S1B). Throughout the remainder of the text we use the constrained values of genotype space during the fourth generation to calculate genotype frequencies and fitness values with respect to *Medea* allele frequency. Plots of genotype or fitness as a function of *Medea* allele frequency (as in Fig. 1A,C; Fig. 4B; Fig. 5A) which appear line-like, are not one-dimensional lines, but narrow two-dimensional bands around a line. Places where the bands cross are not points but small areas.

II. Fitness Calculations

By fitness of a particular genotype we mean the average number of progeny a zygote of that genotype will have, given a particular zygote genotype distribution. A zygote with a fitness of 1 exactly replaces itself (has one progeny). Fitness of a particular allele refers to the average number of progeny an individual with that allele will have, given a particular genotype distribution. Fitness has three components. 1) The ability of an organism to survive to reproductive maturity, $l_{genotype}$. This is the embryonic fitness. 2) The ability of an organism to make gametes (a parental fertility or fecundity loss), $m_{genotype}$. 3) A component specific to *Medea*, the ability of the gametes to survive fusion to form a viable zygote, $n_{gametetype}$. In order to calculate fitness we must track the fate of the 8 types of gametes. Gametes have 3 essential attributes, 1) whether they are sperm or egg, 2) whether they carry the *Medea* or non-*Medea* allele and 3) the genotype of the gamete's parent.

To find fitnesses, we begin by finding the distribution of gametes given a distribution of zygotes. We start by introducing the following terminology. A zygote has already undergone death by the *Medea* mechanism but has not experienced any fitness costs. Zygotes can be $zygote_{++}$, $zygote_{M+}$, or $zygote_{MM}$ for the fraction of zygotes that are homozygous non-*Medea*, heterozygous for *Medea*, or homozygous *Medea*, respectively. Egg/sperm sub gamete genotype, gamete's parent's genotype. Gamete genotype can be *p* or *q* for *Medea* and non *Medea* respectively. Gamete's parent's genotype can be *MM*, *M+*, or *++* for homozygous *Medea*, heterozygous *Medea* and homozygous non-*Medea*, respectively. For example, we define spm_{q++} as the the fraction of male gametes that are non-*Medea* from a non-*Medea* parent. V_P is the parental fitness cost. In the case of an egg, it is V_D and in the case of a sperm it is V_S. We do not consider the case where V_D is not equal to V_S. Mathematically,

$$egg_{q++} = spm_{q++} = \frac{zygote_{++}}{zygote_{++} + zygote_{M+}V_EV_P + zygote_{MM}V_E^2V_P^2}$$

$$egg_{qM+} = egg_{pM+} = spm_{qM+} = spm_{pM+} = \frac{\frac{1}{2}\,zygote_{M+}V_EV_P}{zygote_{++} + zygote_{M+}V_EV_P + zygote_{MM}V_E^2V_P^2}$$

$$egg_{pMM} = spm_{pMM} = \frac{zygote_{MM}V_E^2V_P^2}{zygote_{++} + zygote_{M+}V_EV_P + zygote_{MM}V_E^2V_P^2}$$

Now we examine the fitness of each type of gamete (part 3). To find fitness, we examine the fate of the gamete when it joins with all other possible gametes. For example, a non-*Medea* sperm from a non-*Medea* parent will always survive when it joins a non-*Medea* egg from a non-*Medea* parent, will die a fraction (1-t_0) of the time when it joins a non-*Medea* egg from a heterozygous parent, will always survive when it joins a *Medea* egg from a heterozygous parent, and will die a fraction (1-t_1) of the time when it joins a *Medea* egg from a homozygous *Medea* female. To find the fitness of the genotype, we find the mean of the fitness of sperm and egg of the same genotype.

$$n_{spermq++} = egg_{q++} + egg_{qM+}(1-t_0) + egg_{pM+} + egg_{pMM}(1-t_1)$$

$$n_{eggq++} = spm_{q++} + spm_{qM+} + spm_{pM+} + spm_{pMM}$$

$$n_{q++} = \tfrac{1}{2}\left(n_{spermq++} + n_{eggq++}\right)$$

$$n_{spermqM+} = egg_{q++} + egg_{qM+}(1-t_0) + egg_{pM+} + egg_{pMM}(1-t_1)$$

$$n_{eggqM+} = spm_{q++}(1-t_0) + spm_{qM+}(1-t_0) + spm_{pM+} + spm_{pMM}$$

$$n_{qM+} = \tfrac{1}{2}\left(n_{spermqM+} + n_{eggqM+}\right)$$

$$n_{spermpM+} = egg_{q++} + egg_{qM+} + egg_{pM+} + egg_{pMM}$$

$$n_{eggpM+} = spm_{q++} + spm_{qM+} + spm_{pM+} + spm_{pMM}$$

$$n_{qM+} = \tfrac{1}{2}\left(n_{spermqM+} + n_{eggqM+}\right)$$

$$n_{spermpMM} = egg_{q++} + egg_{qM+} + egg_{pM+} + egg_{pMM}$$

$$n_{eggpMM} = spm_{q++}(1-t_1) + spm_{qM+}(1-t_1) + spm_{pM+} + spm_{pMM}$$

$$n_{qMM} = \tfrac{1}{2}\left(n_{spermqMM} + n_{eggqMM}\right)$$

III. Genotype fitness

The genotype fitness is calculated by multiplying each component of fitness.

$$fitness_{\hom ozygousMedea} = l_{MM}m_{MM}n_{pMM}$$
$$fitness_{heterozygousMedea} = \tfrac{1}{2}l_{M+}m_{M+}\left(n_{pM+} + n_{qM+}\right)$$
$$fitness_{\hom ozygousnonMedea} = l_{++}m_{++}n_{p++}$$

IV. Allele fitness

The *Medea* allele fitness is calculated by finding the fitness of the heterozygote multiplied by the fraction of *Medea* alleles in heterozygotes and adding the fitness of homozygous *Medea* multiplied by the fraction of *Medea* alleles in homozygotes. Fitness of the non-*Medea* allele is calculated similarly.

$$fitness_{MedeaAllele} = l_{M+} m_{M+} n_{pM+} \frac{zygote_{M+}}{zygote_{M+} + 2zygote_{MM}} + l_{MM} m_{MM} n_{pMM} \frac{2zygote_{MM}}{zygote_{M+} + 2zygote_{MM}}$$

$$fitness_{nonMedeaAllele} = l_{M+} m_{M+} n_{pM+} \frac{2zygote_{M+}}{zygote_{M+} + 2zygote_{++}} + l_{++} m_{++} n_{p++} \frac{2zygote_{++}}{zygote_{M+} + 2zygote_{++}}$$

V. Population fitness

The population fitness is the sum of the products of each genotype and the fraction of zygotes with that genotype.

$$fitness_{population} = zygote_{MM}\ fitness_{\mathrm{hom}\,ozygousMedea} + zygote_{M+}\ fitness_{heterozygousMedea} + zygote_{++}\ fitness_{\mathrm{hom}\,ozgousnonMedea}$$

VI. X chromosome

An X-linked *Medea* is different from autosomal *Medea* in that the ratio of males to females is not 1 to 1. There are only 2 male genotypes *Medea* Y and non-*Medea* Y.

	Parental Genotype Frequency			Male Offspring Frequency		Female Offspring Frequency		
Family	Male	Female	Mating	*Medea*	non-*Medea*	Homo	Het	WT
1	S_{MY}	D_{MM}	S_{MY}*D_{MM}	V_E		V_E^2		
2	S_{+Y}	D_{MM}	S_{+Y} *D_{MM}	V_E			V_E	
3	S_{MY}	D_{M+}	S_{MY}*D_{M+}	½ V_E	½	½ V_E^2	½ V_E	
4	S_{+Y}	D_{M+}	S_{+Y}*D_{M+}	½ V_E	½		½ V_E	½
5	S_{MY}	D_{++}	S_{MY}*D_{++}		1		V_E	
6	S_{+Y}	D_{++}	S_{+Y}*D_{++}		1			1

Equations are shown in the text.

VII. X Chromosome Fitness:

We use the same definitions of fitness and symbols as defined in the autosomal fitness cost case.

$$egg_{q++} = \frac{femalezygote_{++}}{femalezygote_{++} + femalezygote_{M+}V_E + femalezygote_{MM}V_E^2}$$

$$egg_{qM+} = egg_{pM+} = \frac{\frac{1}{2}\, femalezygote_{M+}V_E}{femalezygote_{++} + femalezygote_{M+}V_E + femalezygote_{MM}V_E^2}$$

$$egg_{pMM} = spm_{pMM} = \frac{femalezygote_{MM}V_E^2V_P^2}{femalezygote_{++} + femalezygote_{M+}V_E + femalezygote_{MM}V_E^2}$$

$$spm_{q+Y} = \frac{\frac{1}{2}\, malezygote_{+Y}}{malezygote_{+Y} + malezygote_{MY} V_E}$$

$$spm_{Y+Y} = \frac{\frac{1}{2}\, malezygote_{+Y}}{malezygote_{+Y} + malezygote_{MY} V_E}$$

$$spm_{pMY} = \frac{\frac{1}{2}\, malezygote_{MY} V_E}{malezygote_{+Y} + malezygote_{MY} V_E}$$

$$spm_{YMY} = \frac{\frac{1}{2}\, malezygote_{MY} V_E}{malezygote_{+Y} + malezygote_{MY} V_E}$$

Now we examine the fitness of each type of gamete (part 3). To find fitness, we examine the fate of the gamete when it joins with all other possible gametes.

$$n_{spermq+Y} = egg_{q++} + egg_{pM+} + egg_{pMM}$$

$$n_{eggq+Y} = spm_{q+Y} + spm_{Y+Y} + spm_{pMY} + spm_{YMY}$$

$$n_{spermYM+} = egg_{q++} + egg_{pM+} + egg_{pMM}$$

$$n_{eggqM+} = spm_{pMY}$$

$$n_{spermpM+} = egg_{q++} + egg_{qM+} + egg_{pM+} + egg_{pMM}$$

$$n_{eggpM+} = spm_{q+Y} + spm_{YMY} + spm_{pMY} + spm_{Y+Y}$$

$$n_{spermpMY} = egg_{q++} + egg_{qM+} + egg_{pM+} + egg_{pMM}$$

$$n_{eggpMM} = spm_{q+Y} + spm_{qMY} + spm_{pMY} + spm_{pMY}$$

VIII. X Chromosome Allele fitness

The *Medea* allele fitness is calculated by finding the fitness of the heterozygous females multiplied by the fraction of *Medea* alleles in heterozygous, adding the fitness of homozygous *Medea* females multiplied by the fraction of *Medea* alleles in a homozygous female *Medea* background and adding the fitness of male *Medea* individuals and multiplying by the fraction of *Medea* alleles in a male *Medea* background. Fitness of the non-*Medea* allele and Y are calculated similarly.

IX. X Chromosome Population fitness

The population fitness is the sum of the fitness of each genotype multiplied by the fraction of zygotes with that genotype.

X. Equilibria Calculations

The attached code calculates equilibrium values and stability for both autosomal and X-linked *Medea*. The code contains much of the output. Some of the equilibria take many pages to output; therefore that output has been suppressed. Some calculations take minutes to days to run on a PC with 2 gigabytes of RAM with and an Intel® Core2™ CPU . We provide appropriate warnings.

Here we provide a summary of the calculations with more details than are present in the text. Some cumbersome equations are not reproduced. Equilibria are calculated by simultaneously solving $G_{++}^{'} = G_{++}$ and $G_{MM}^{'} = G_{MM}$. To find stability, the modulus of the eigenvalues of the Jacobian must be less than 1.

Recall the Jacobian matrix is defined as

$$\begin{pmatrix} \dfrac{\partial G_{MM}^{'}}{\partial G_{MM}} & \dfrac{\partial G_{MM}^{'}}{\partial G_{++}} \\ \dfrac{\partial G_{++}^{'}}{\partial G_{MM}} & \dfrac{\partial G_{++}^{'}}{\partial G_{++}} \end{pmatrix}.$$

XI. Embrynoic Fitness Costs

$V_{D,Het}=V_{D,Homo}=V_{S,Het}=V_{S,Homo}=1$, $t_1=0$, $t_0=1$

There are 4 equilibria.

1. $G_{++} = 1$, $G_{M+} = G_{MM} = 0$

The eigenvalues are

$$\begin{pmatrix} 0 \\ V_{E,Het} \end{pmatrix}$$

2. $G_{++} = -\dfrac{V_{E,Het}^2 - V_{E,Het} + V_{E,Homo}}{-V_{E,Homo} + V_{E,Het} - 1}$

$$G_{MM} = -\frac{1 + V_{E,Het}^2 - 2V_{E,Het}}{-V_{E,Homo} + V_{E,Het} - 1}$$

Feasibility:

Using $G_{++} = 0$

$$V_{E,Homo} \geq V_{E,Het} - V_{E,Het}^2$$

Using other genotype boundaries, no additional feasibility conditions are found.

Stability: the eigenvalues are cumbersome expressions (see expression 22 in the maple code). In the biologically feasible realm, the modulus of each eigenvalue is equal to 1 when $V_{E,Het} = 1$ and $V_{E,Homo} = V_{E,Het} - V_{E,Het}^2$. These boundaries are coincident with feasibility. Except at boundaries, all feasible solutions are unstable.

3. $G_{++} = 0$

$$G_{MM} = \frac{V_{E,Homo}}{2V_{E,Het} - V_{E,Homo}}$$

Biological feasibility:

$$V_{E,Het} \geq V_{E,Homo}$$

The eigenvalues are

$$\begin{pmatrix} \dfrac{-V_{E,Homo}+V_{E,Het}}{V_{E,Het}^2} \\ \dfrac{V_{E,Homo}}{V_{E,Het}} \end{pmatrix}$$

The second eigenvalue shows a change in stability that is coincident with feasibility. Therefore, no examination $V_{E,Het} \geq V_{E,Homo}$ is necessary.

The modulus of the first eigenvalue equals 1 when

$V_{E,Homo} = V_{E,Het} + V_{E,Het}^2$ and $V_{E,Homo} = V_{E,Het} - V_{E,Het}^2$

The first solution is never biologically feasible. The second solution is stable when $V_{E,Homo} > V_{E,Het} - V_{E,Het}^2$.

4. $G_{++} = 0$, $G_{M+} = 0$, $G_{MM} = 1$

The eigenvalues are

$$\begin{pmatrix} 0 \\ \dfrac{V_{E,Het}}{V_{E,Homo}} \end{pmatrix}$$

The stability boundary is

$V_{E,Het} = V_{E,Homo}$

Stability occurs when

$V_{E,Het} < V_{E,Homo}$

XII. Parental Fitness Costs

$V_{D,Het}=V_{S,Het}$, $V_{D,Homo}=V_{S,Homo}$, $V_{E,Homo}=V_{E,Het}=1$, $t_1=0$, $t_0=1$

Stability and feasibility analysis yields the same boundaries as with embryonic costs. Detailed analysis is shown in Maple Code. As noted in the text, the equilibrium values are different from those associated with embryonic costs.

XIII. Maternal Fitness Costs

$V_{E,Het}=V_{S,Het}=V_{E,Homo}=V_{S,Homo}=1$, $t_1=0$, $t_0=1$

1. $G_{++} = 1$, $G_{M+} = G_{MM} = 0$

The eigenvalues are

2. $G_{++} = 0$

$$G_{MM} = \frac{V_{D,\,Homo} - V_{D,\,Het} \pm \sqrt{V_{D,\,Homo}^{2} - 2V_{D,\,Het}V_{D,\,Homo} + 2V_{D,\,Het}^{2}}}{V_{D,\,Het}}$$

Only the (+) solution is relevant, when $V_{D,Het} \geq V_{D,Homo}$

Stability:

The only boundary condition other than feasibility is

$$V_{D,Homo} = \frac{V_{D,Het}^{2} - V_{D,Het} + 1 - \sqrt{4V_{D,Het}^{3} - 7V_{D,Het}^{2} + 2V_{D,Het} + 1}}{V_{D,Het} - 2}$$

. This equilibrium is stable when homozygous fitness is greater than the expression.

3. The all genotypes equilibrium is a very cumbersome expression. However, by solving for no non-*Medea* individuals in the population, we find that the biological feasibility boundary is the same as the stability boundary for equilibrium 2. There are no other stability boundaries. The equilibrium is always unstable when feasible.

4. $G_{++} = 0$, $G_{MM} = 1$

The eigenvalues are

$$\begin{pmatrix} 0 \\ \dfrac{V_{D,Homo} + V_{D,Het}}{2V_{D,Homo}} \end{pmatrix}$$

This equilibrium is stable when $V_{D,Het} > V_{D,Homo}$

Figure S2 partitions (V_{Het}, V_{Homo}) fitness parameter space into regions in which linear stability analysis indicate qualitatively similar behaviors are observed. The case for embryonic fitness costs is illustrated in Fig. S2A (see also Fig. 2); the case of maternal fitness costs is illustrated in Figure S2B.

XIV. Embryonic Fitness Costs and t_1

$V_{D,Het}=V_{D,Homo}=V_{S,Het}=V_{S,Homo}=1$, $t_1=0$, $t_0=1$

There are 4 equilibria.

1. $G_{++} = 1$, $G_{M+} = G_{MM} = 0$

The eigenvalues are

$$\begin{pmatrix} 0 \\ V_{E,Het} \end{pmatrix}$$

2. $$G_{++} = -\frac{V_{E,Het}^3 t_1^2 - 4V_{E,Het}^2 t_1 - 2V_{E,Het} t_1 + 8V_{E,Het} - 4 + 2t_1}{t_1^2 V_{E,Het}^4 - 4V_{E,Het}^3 t_1 + 4V_{E,Het}^2 + 2V_{E,Het}^2 t_1 - 4V_{E,Het} - 2V_{E,Het} t_1 + 4}$$

$$G_{MM} = -\frac{4(-2V_{E,Het}) + 1 + V_{E,Het}^2}{t_1^2 V_{E,Het}^4 - 4V_{E,Het}^3 t_1 + 4V_{E,Het}^2 + 2V_{E,Het}^2 t_1 - 4V_{E,Het} - 2V_{E,Het} t_1 + 4}$$

Feasibility:

Using $G_{++} = 0$

$$t_1 = \frac{2V_{E,Het}^2 + V_{E,Het} + 1 \pm \sqrt{-4V_{E,Het}^4 + 8V_{E,Het}^3 - 3V_{E,Het}^2 - 2V_{E,Het} + 1}}{V_{E,Het}^3}$$

Only the (-) solution is relevant.

Stability: No eigenvalues are less than or equal to 1 within the biologically feasible region. Therefore the equilibrium is unstable.

3. $G_{++} = 0$

$$G_{MM} = -\frac{V_{E,Het} - 1 \pm \sqrt{1 - 2V_{E,Het} t_1}}{V_{E,Het} + 2t_1 - 2}$$

Only the (+) solution is biologically relevant.

Biological feasibility:

$V_{E,Het} \leq 1 - \frac{1}{2} t_1$

The eigenvalues are cumbersome functions that are not reproduced here – see Maple code.

The modulus of the first eigenvalue equals 1 when

(a) $V_{E,Het} = 1 - \frac{1}{2} t_1$,

(b) $V_{E,Het} = \frac{1}{2t_1}$,

(c) $V_{E,Het} = -\frac{-\frac{1}{2} - \frac{1}{2}\sqrt{1+4t_1} + t_1}{t_1}$,

(d) $t_1 = \frac{2V_{E,Het}^2 + V_{E,Het} - 1 + \sqrt{-4V_{E,Het}^4 + 8V_{E,Het}^3 - 3V_{E,Het}^2 - 2V_{E,Het} + 1}}{V_{E,Het}^3}$

In case (a), this is the feasibility boundary.

In case (b), this solution is entirely outside the range of biological feasibility.

In case (c), no change of stability is found after passing this curve.

In case (d), solutions are stable above the curve and unstable below it.

No additional boundaries are found with solutions of the second eigenvalue.

4. $G_{++} = 0$, $G_{M+} = 0$, $G_{MM} = 1$

The eigenvalues are

$$\begin{pmatrix} 0 \\ -\frac{t_1 - 2}{2V_{E,Het}} \end{pmatrix}$$

The stability boundary is

$$V_{E,Het} = 1 - \tfrac{1}{2}t_1$$

Stability occurs when

$$V_{E,Het} < 1 - \tfrac{1}{2}t_1$$

Figure S3 partitions (t_1, V_{Het}) parameter space for embryonic and parental fitness costs (Fig. S3A), or maternal fitness costs (Fig. S3B) into regions in which linear stability analysis indicates qualitatively similar behaviors are observed. Qualitative behavior changes as we cross each of these curves, with the occurrence of a bifurcation, as described in the legend to Fig. 2 and Fig. S2.

XV. X-linked Element

1. D_{MM}=0; D_{M+}=0; D_{++}=1/2; S_{MY}=0; S_{+Y}=1/2

The eigenvalues are 0, -.5V and V. This equilibrium is always stable except when the fitness equals 1.

2. All genotypes. See Maple Code for expressions for the genotype fractions at equilibrium. This equilibrium is unstable. The Maple code shows this by plotting the modulus of the eigenvalues for all possible fitnesses.

3. No non-*Medea* individuals

$$D_{MM} = -\frac{V_{E,Het}}{V_{E,Het} - 2}$$

$$D_{M+} = \frac{2V_{E,Het} - 1}{V_{E,Het} - 2}$$

$$D_{++} = 0$$

$$S_{++} = 0$$

This equilibrium only exists for fitness values greater than or equal to 0.5. The eigenvalues are 0 and $2V_{E,Het}$. This equilibrium is stable when it exists, except at the boundaries where the analysis is inconclusive.

4. No non-*Medea* alleles.

$$D_{MM} = \frac{V_{E,Het}}{V_{E,Het} + 1}$$
$$D_{M+} = 0$$
$$D_{++} = 0$$
$$S_{++} = 0$$

The eigenvalues are 0 and $\frac{1}{2V_{E,Het}}$. Therefore this equilibrium is stable for fitnesses greater than 0.5, and unstable for lower fitnesses; stability at the equality is inconclusive.

```
> #Ward, Catherine
> #Supplemental Materials: Calculations for feasibility and
  stability of autosomal Medeas
> #This is a long file organized into 5 sections:
> #1) Loading the Model
> #2) Embryonic only fitness costs starts after execution group
  (2).
> #3) Maternal only fitness costs starts after execution group
  (35).
> #4) Parental fitness costs starts after execution group (72)
> #5) t1 fitness cost starts after execution group (95).
>
> #Each section begins with simplifying assumptions.  We calculate
  equilibria.  Then we look at the feasibility of the equilibrium
  through parameter space.  Then we calculate the stability by
  finding conditions such that the eigenvalues of the Jacobian
  matrix have modulus one (potential boundaries for stability
  changes).  There are usually several pages of analysis to
  determine which potential boundaries are biologically relevant
  (ie, fitness between 0 and 1).  Having determined all boundary
  conditions, we check the stability of the equilibrium in each
  region of space.
>

>
>
> restart : clear : with(LinearAlgebra) : with(SolveTools) :
>

> #We begin by defining the general equations.
> #Terms are as defined in the text except the next generation is
  nextGmm rather than Gmm', non-Medea individuals are Gpp,
  heterozygotes are Gmp rather than Gm+ and, of course, suscripts
  are not used.
```

$$
> W := VEHomo\cdot\Big(Gmm\cdot Gmm\cdot VSHomo\cdot VDHomo + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gmm\cdot VSHet\cdot VDHomo + \left(\frac{1}{2}\right)\cdot Gmm\cdot Gmp\cdot VSHomo\cdot VDHet + \left(\frac{1}{4}\right)\cdot Gmp\cdot Gmp\cdot VSHet\cdot VDHet\Big) + VEHet\cdot\Big(\Big(\left(\frac{1}{2}\right)\cdot Gmp\cdot Gmm\cdot VSHet\cdot VDHomo\cdot mu1 + Gpp\cdot Gmm\cdot VDHomo\cdot mu1 + \left(\frac{1}{2}\right)\cdot Gmm\cdot Gmp\cdot VSHomo\cdot VDHet + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gmp\cdot VSHet\cdot VDHet + \left(\frac{1}{2}\right)\cdot Gpp\cdot Gmp\cdot VDHet
$$

$$+ Gmm\cdot Gpp\cdot VSHomo + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gpp\cdot VSHet\Big) + \left(\frac{1}{4}\right)\cdot Gmp\cdot Gmp\cdot VSHet\cdot VDHet \cdot mu0 + \left(\frac{1}{2}\right)\cdot Gpp\cdot Gmp\cdot VDHet\cdot mu0 + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gpp\cdot VSHet + Gpp\cdot Gpp :$$

```
>
```

$$> nextGmm := subs\Big(Gmp = 1 - Gmm - Gpp, \frac{VEHomo}{W}\cdot\Big(Gmm\cdot Gmm\cdot VSHomo\cdot VDHomo + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gmm\cdot VSHet\cdot VDHomo + \left(\frac{1}{2}\right)\cdot Gmm\cdot Gmp\cdot VSHomo\cdot VDHet + \left(\frac{1}{4}\right)\cdot Gmp\cdot Gmp\cdot VSHet\cdot VDHet\Big)\Big) :$$

$$> nextGmp := subs\Big(Gmp = 1 - Gmm - Gpp, \frac{VEHet}{W}\cdot\left(\frac{1}{2}\right)\cdot Gmp\cdot Gmm\cdot VSHet\cdot VDHomo\cdot mu1 + Gpp\cdot Gmm\cdot VDHomo\cdot mu1 + \left(\frac{1}{2}\right)\cdot Gmm\cdot Gmp\cdot VSHomo\cdot VDHet + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gmp\cdot VSHet\cdot VDHet + \left(\frac{1}{2}\right)\cdot Gpp\cdot Gmp\cdot VDHet + Gmm\cdot Gpp\cdot VSHomo + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gpp\cdot VSHet\Big) :$$

$$> nextGpp := subs\Big(Gmp = 1 - Gmm - Gpp, \frac{1}{W}\Big(\left(\frac{1}{4}\right)\cdot Gmp\cdot Gmp\cdot VSHet\cdot VDHet\cdot mu0 + \left(\frac{1}{2}\right)\cdot Gpp\cdot Gmp\cdot VDHet\cdot mu0 + \left(\frac{1}{2}\right)\cdot Gmp\cdot Gpp\cdot VSHet + Gpp\cdot Gpp\Big)\Big) :$$

```
>
> #We now give the code that will generate the general solutions.
The general solution is too complex to be useful.  A PC with 2
gigs of RAM takes days to solve this and then crashes if any
further manipulations are attempted.  Macs with 5 gigs of RAM
simply do not run this calculation.
> #genEq:=solve( {nextGpp = Gpp, nextGmm = Gmm}, [Gpp, Gmm]) :
>
> #In order to do linear stability analysis we find the Jacobian
Matrix
```

$$> MyJacobian := simplify(Matrix([[diff(nextGmm, Gmm), diff(nextGmm, Gpp)], [diff(nextGpp, Gmm), diff(nextGpp, Gpp)]])) :$$

```
>
> #For the two trivial solutions to the general equation (no non-
Medea alleles and no Medea alleles), we present the stability
analysis.
> #First no Medea alleles
```

$$> simplify(Eigenvalues(subs(Gpp = 1, Gmp = 0, Gmm = 0, MyJacobian)));$$

$$\begin{bmatrix} 0 \\ \frac{1}{2}\, VEHet\, VDHet + \frac{1}{2}\, VEHet\, VSHet \end{bmatrix} \tag{1}$$

```
> #No non-Medea alleles
> simplify(Eigenvalues(subs(Gpp = 0, Gmp = 0, Gmm = 1, MyJacobian)));
```

$$\begin{bmatrix} 0 \\ \frac{1}{2}\,\frac{VEHet\,(VSHet\,VDHomo\,\mu 1 + VSHomo\,VDHet)}{VSHomo\,VDHomo\,VEHomo} \end{bmatrix} \tag{2}$$

```
>
> #Now we present the stability analysis for a selection of
  simplifications
>
```

```
> #Case 1) Embryonic Fitness Cost, No parental
  effects; mu0=0 and mu1=1
```

```
> #We begin by introducing the simplified senarios
> nextGppEmbryonic := subs(VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, μ0 = 0, μ1 = 1,
      nextGpp) :
> nextGmmEmbryonic := subs(VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, μ0 = 0, μ1
      = 1, nextGmm) :
> nextGmpEmbryonic := subs(VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, μ0 = 0, μ1
      = 1, nextGmp) :
> #Solve for the 4 biologically relevant equilibria
> embryonicEq := solve({nextGppEmbryonic = Gpp, nextGmmEmbryonic = Gmm}, [Gpp,
      Gmm]) :
```

```
> #Medea Homozygous Equilibrium
> embryonicEq[1];
```

$$[Gpp = 0,\ Gmm = 1] \tag{3}$$

```
> simplify(Eigenvalues(subs(embryonicEq[1], VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet
      = 1, μ0 = 0, μ1 = 1, MyJacobian)));
```

$$\begin{bmatrix} 0 \\ \frac{VEHet}{VEHomo} \end{bmatrix} \tag{4}$$

```
> #Note the conditions for stability are the modulus of each of
  the eigenvalues must be less than 1.  This equilibrium is stable
  when VEHomo>VEHet, unstable VEHet>VEHomo, and the linear
  analysis is inconclusive at the equality.  Recall, VEHet and
  VEHomo must both be non-negative.
```

```
> #No non-Medea Genotype Equilibrium
> embryonicEq[2];
```

$$\left[Gpp = 0,\ Gmm = \frac{VEHomo}{-VEHomo + 2\,VEHet}\right] \tag{5}$$

`> #First we find the boundaries such that 0≤Gmm≤1.`

$$> \mathit{solve}\left(\frac{\mathit{VEHomo}}{-\mathit{VEHomo}+2\,\mathit{VEHet}}=0\right);$$

$$\{\mathit{VEHet}=\mathit{VEHet},\ \mathit{VEHomo}=0\} \tag{6}$$

$$> \mathit{solve}\left(\frac{\mathit{VEHomo}}{-\mathit{VEHomo}+2\,\mathit{VEHet}}=1\right);$$

$$\{\mathit{VEHet}=\mathit{VEHomo},\ \mathit{VEHomo}=\mathit{VEHomo}\} \tag{7}$$

`> #We test VEHet<VEHomo and VEHomo<VEHet to find feasiblity.`

$$> \mathit{subs}(\mathit{VEHomo}=.9,\ \mathit{VEHet}=.8,\ \mathit{embryonicEq}[2]);$$

$$[\mathit{Gpp}=0,\ \mathit{Gmm}=1.285714286] \tag{8}$$

$$> \mathit{evalf}(\mathit{simplify}(\mathit{subs}(\mathit{VEHomo}=.7,\ \mathit{VEHet}=.9,\ \mathit{embryonicEq}[2])));$$

$$[\mathit{Gpp}=0.,\ \mathit{Gmm}=0.6363636364] \tag{9}$$

`> #This equilibrium is feasible when VEHomo≤VEHet.`

`>`

`> #Now, we examine stability.`

$$> \mathit{EV} := \mathit{simplify}(\mathit{Eigenvalues}(\mathit{subs}(\mathit{embryonicEq}[2],\ \mathit{VSHomo}=1,\ \mathit{VDHomo}=1,\ \mathit{VSHet}=1,\ \mathit{VDHet}=1,\ \mu 0=0,\ \mu l=1,\ \mathit{MyJacobian})));$$

$$\mathit{EV} := \begin{bmatrix} \dfrac{\mathit{VEHomo}}{\mathit{VEHet}} \\[2ex] \dfrac{-\mathit{VEHomo}+\mathit{VEHet}}{\mathit{VEHet}^2} \end{bmatrix} \tag{10}$$

$$> \mathit{solve}(\mathit{EV}[1]=1);$$

$$\{\mathit{VEHet}=\mathit{VEHomo},\ \mathit{VEHomo}=\mathit{VEHomo}\} \tag{11}$$

$$> \mathit{solve}(\mathit{EV}[1]=-1);$$

$$\{\mathit{VEHet}=-\mathit{VEHomo},\ \mathit{VEHomo}=\mathit{VEHomo}\} \tag{12}$$

`>`

`> #When VEHomo<VEHet(1-VEHet), this equilibrium is unstable.`

`> #When VEHet(1-VEHet)<VEHomo<VEHet, this equilibrium is stable.`

`>`

`>`

> #The all non-Medea equilibrium

$$> \mathit{embryonicEq}[3];$$

$$[\mathit{Gpp}=1,\ \mathit{Gmm}=0] \tag{13}$$

$$> \mathit{simplify}(\mathit{Eigenvalues}(\mathit{subs}(\mathit{embryonicEq}[3],\ \mathit{VDHomo}=1,\ \mathit{VSHomo}=1,\ \mathit{VDHet}=1,\ \mathit{VSHet}=1,\ \mu 0=0,\ \mu l=1,\ \mathit{MyJacobian})));$$

$$\begin{bmatrix} 0 \\ \mathit{VEHet} \end{bmatrix} \tag{14}$$

`> #If VEHet<1, this equilibrium is stable.`

`> #If VEHet=1, linear analysis is inconclusive.`

`>`

`> #All 3 genotypes in the equilibrium population`

$> \mathit{embryonicEq}[4];$

$$\left[Gpp = -\frac{VEHet^2 - VEHet + VEHomo}{-VEHomo + VEHet - 1},\ Gmm = -\frac{-2\,VEHet + VEHet^2 + 1}{-VEHomo + VEHet - 1}\right] \tag{15}$$

`> #First we find the boundaries such that 0≤Gpp≤1 and 0≤Gmm≤1 .`

$> myGpp := -\dfrac{VEHet^2 - VEHet + VEHomo}{-VEHomo + VEHet - 1}:$

$> myGmm := -\dfrac{1 - 2\,VEHet + VEHet^2}{-VEHomo + VEHet - 1}:$

$> \mathit{solve}(myGpp = 0);$

$$\{VEHet = VEHet,\ VEHomo = -VEHet^2 + VEHet\} \tag{16}$$

$> \mathit{subs}(VEHomo = (-VEHet^2 + VEHet)\cdot 1.1,\ VEHet = .8,\ myGpp);$

$$0.04255319149 \tag{17}$$

$> \mathit{subs}(VEHomo = (-VEHet^2 + VEHet)\cdot .9,\ VEHet = .8,\ myGpp);$

$$-0.04651162791 \tag{18}$$

$> \mathit{subs}(VEHomo = (-VEHet^2 + VEHet)\cdot 1.1,\ VEHet = .8,\ myGmm);$

$$0.1063829787 \tag{19}$$

$> \mathit{solve}(myGmm = 0);$

$$\{VEHet = 1,\ VEHomo = VEHomo\},\ \{VEHet = 1,\ VEHomo = VEHomo\} \tag{20}$$

`>`

`> #This equilibrium is feasible when VEHomo>VEHet-VEHet^2.`

`>`

$> Eq4EV := \mathit{simplify}(\mathit{Eigenvalues}(\mathit{subs}(\mathit{embryonicEq}[4],\ VDHomo = 1,\ VSHomo = 1,\ VDHet = 1,\ VSHet = 1,\ \mu0 = 0,\ \mu1 = 1,\ MyJacobian)));$

$$Eq4EV := \left[\left[\frac{1}{2}\,\frac{1}{VEHomo}\left(2\,VEHomo - VEHomo\,VEHet + \left(-VEHomo\left(-4\,VEHomo + 4\,VEHomo\,VEHet - VEHet^2\,VEHomo - 8\,VEHet^2 + 4\,VEHet^3 + 4\,VEHet\right)\right)^{1/2}\right)\right],\ \left[-\frac{1}{2}\,\frac{1}{VEHomo}\left(-2\,VEHomo + VEHomo\,VEHet + \left(-VEHomo\left(-4\,VEHomo + 4\,VEHomo\,VEHet - VEHet^2\,VEHomo - 8\,VEHet^2 + 4\,VEHet^3 + 4\,VEHet\right)\right)^{1/2}\right)\right]\right] \tag{21}$$

`>`

`> #To be unstable, the modulus of an eigenvalue has to be >1.`
`Let's find when they are equal to 1.`

$> solns := \mathit{solve}(\mathrm{abs}(Eq4EV[1]) = 1):$

$> solns[1];$

$$\{VEHet = 1,\ VEHomo < 0\} \tag{22}$$

`> #Does not apply; VEHomo>0`

> *solns*[2];

$$\{VEHet = 1, VEHomo = 0, VEHomo < 0\} \tag{23}$$

> **#a boundary; coincident with feasibility**

> *solns*[3];

$$\{VEHomo = -VEHet^2 + VEHet, -VEHet^2 + VEHet = -VEHet^2 + VEHet, VEHet < 0\} \tag{24}$$

> **#Does not apply; VEHomo>0**

> *solns*[4];

$$\{VEHomo = -VEHet^2 + VEHet, -VEHet^2 + VEHet = -VEHet^2 + VEHet, 1 < VEHet\} \tag{25}$$

> **#coincident with feasiblity**

> *solns*[5];

$$\{VEHet = 1, 0 < VEHomo\} \tag{26}$$

> *solns*[6];

$$\{VEHet = 1, VEHomo = 0, 0 < VEHomo\} \tag{27}$$

> *solns*[7];

$$\{VEHomo = -VEHet^2 + VEHet, -VEHet^2 + VEHet = -VEHet^2 + VEHet, 0 < VEHet, VEHet < 1\} \tag{28}$$

> **#soln[7] is feasible**

> *solns*[8];

$$\left\{VEHomo = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet} = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, 0 < VEHet, VEHet < 1\right\} \tag{29}$$

> $plot\left(\frac{VEHet\,(-2\,VEHet + 1 + VEHet^2)}{-3 + VEHet}, VEHet = 0\,..1\right):$

> **#We plot this function for 0<VEHet<1. VEHomo<0, therefore boundary condition does not apply.**

> *solns*[9];

$$\left\{VEHomo = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet} = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, 1 < VEHet, VEHet < 3\right\} \tag{30}$$

> *solns*[10];

$$\left\{VEHomo = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet} = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, VEHet < 0\right\} \tag{31}$$

> *solns*[11];

$$\left\{VEHomo = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet} = \frac{VEHet\,(-2\,VEHet + VEHet^2 + 1)}{-3 + VEHet}, 3 < VEHet\right\} \tag{32}$$

```
> solns[12];
Error, invalid subscript selector
> #No more solutions
> #Find when the modulus of the second eigenvalue is 1.
> solns := solve(abs(Eq4EV[2]) = 1) :
> #No additional solutions found.
> #This means the stability at VEHet=1 and VEHomo=VEHet-VEHet^2 is
  inconclusive.  This equilibrium does not exist when
  VEHomo<VEHet-VEHET^2.  We need to test VEHomo>VEHet-VEHet^2
  while VEHet is not 1.
>
> #Take a point, VEHet=.8, VEHomo=.9
> subs(VEHet = .8, VEHomo = 9, Eq4EV[1]);
                              1.197029685                                (33)
> #This equilibrium is unstable for VEHomo>VEHet-VEHet^2.
> #Let's work on the VEHet=1 condition.
> subs(VEHet = 1, myGpp);
                                   1                                     (34)
> subs(VEHet = 1, myGmm);
                                   0                                     (35)
> #The VEHet=1 condition collapses to all non-Medea individuals in
  the population.
>
> #Case 2) Maternal Fitness only, No
  parental fitness effects; mu0=0 and mu1=1
> #We begin by introducing the simplifications.
>
> nextGppMaternal := subs(VSHomo = 1, VEHomo = 1, VSHet = 1, VEHet = 1, μ0 = 0, μ1 = 1,
      nextGpp) :
> nextGmmMaternal := subs(VSHomo = 1, VEHomo = 1, VSHet = 1, VEHet = 1, μ0 = 0, μ1 = 1,
      nextGmm) :
> nextGmpMaternal := subs(VSHomo = 1, VEHomo = 1, VSHet = 1, VEHet = 1, μ0 = 0, μ1 = 1,
      nextGmp) :
>
> #Solve for the 4 biologically relevant equilibria
> maternalEq := solve({nextGppMaternal = Gpp, nextGmmMaternal = Gmm}, [Gpp, Gmm]) :
>
> #All Medea alleles
> maternalEq[1];
                           [Gpp = 0, Gmm = 1]                            (36)
```

```
> EV1 := simplify(Eigenvalues(subs(maternalEq[1], VEHomo=1, VSHomo=1, VSHet=1,
      VEHet=1, μ0=0, μ1=1, MyJacobian)));
```

$$EV1 := \begin{bmatrix} 0 \\ \frac{1}{2}\,\frac{VDHomo + VDHet}{VDHomo} \end{bmatrix} \tag{37}$$

```
> solve(EV1[2]=1);
```

$$\{VDHet = VDHomo,\ VDHomo = VDHomo\} \tag{38}$$

```
> #When VDHet>VDHomo, this equilibrium is unstable.  It is stable
  at VDHomo>VDHet and inconclusive at the equality.
```

```
> #No non-Medea Individuals
```

```
> allvalues(maternalEq[2]);
```

$$\left[Gpp = 0,\ Gmm = \frac{VDHomo - VDHet + \sqrt{VDHomo^2 - 2\ VDHet\ VDHomo + 2\ VDHet^2}}{VDHet}\right], \tag{39}$$

$$\left[Gpp = 0,\ Gmm = -\frac{-VDHomo + VDHet + \sqrt{VDHomo^2 - 2\ VDHet\ VDHomo + 2\ VDHet^2}}{VDHet}\right]$$

```
> #First determine which radical is relevant
```

```
> solve({(VDHomo-VDHet + sqrt(VDHomo^2-2*VDHet*VDHomo + 2*VDHet^2))
      /VDHet=1}, VDHomo);
```

$$\{VDHomo = VDHet\} \tag{40}$$

```
> allvalues(subs(VDHomo=.8, VDHet=.7, maternalEq[2]));
```

$$[Gpp = 0,\ Gmm = 1.153009688],\ [Gpp = 0,\ Gmm = -0.8672954017] \tag{41}$$

```
>
```

```
> allvalues(subs(VDHomo=.7, VDHet=.8, maternalEq[2]));
```

$$[Gpp = 0,\ Gmm = 0.8827822185],\ [Gpp = 0,\ Gmm = -1.132782219] \tag{42}$$

```
> #The second radical is relevant.
```

```
> #Find when the relevant radical equals 0.
```

```
> myGmm := (VDHomo - VDHet + sqrt(VDHomo^2 - 2 VDHet VDHomo + 2 VDHet^2))/VDHet;
```

$$myGmm := \frac{VDHomo - VDHet + \sqrt{VDHomo^2 - 2\ VDHet\ VDHomo + 2\ VDHet^2}}{VDHet} \tag{43}$$

```
>
```

```
> solve(myGmm=1);
```

$$\{VDHet = VDHomo,\ VDHomo = VDHomo\} \tag{44}$$

```
> solve(myGmm=0);
```

$$\{VEHet = 1,\ VEHomo = VEHomo\},\ \{VEHet = 1,\ VEHomo = VEHomo\} \tag{45}$$

```
> #Only the solution with the positive radical is feasible.
```

```
> #When VDHomo≤VDHet, this solution is biologically feasible.
> #When VDHet≤VDHomo, this solution is biologically not feasible.
>
```

> $EV2 := simplify(Eigenvalues(subs(Gpp = 0, Gmm = myGmm, Gmp = 1 - myGmm, VEHomo = 1, VSHomo = 1, VSHet = 1, VEHet = 1, \mu 0 = 0, \mu 1 = 1, MyJacobian))) :$

```
> #These eigenvalues are complicated.  The stategy is to solve for
  when modulus of the eigenvalues equal 1 to divide parameter
  space into regions and then test stability in each region.
  These are potential boundaries.  We only consider 0<VDHet<1 and
  0<VDHomo<1.
```

> $checkEV21 := solve(\operatorname{abs}(EV2[1]) = 1) :$

> $checkEV21[1];$

$$\left\{VDHet = \left(\frac{1}{2} - \frac{1}{2}\,\mathrm{I}\right) VDHomo,\ VDHomo = VDHomo\right\} \tag{46}$$

```
> #Not a boundary; complex.
```

> $checkEV21[2];$

$$\left\{VDHet = \left(\frac{1}{2} + \frac{1}{2}\,\mathrm{I}\right) VDHomo,\ VDHomo = VDHomo\right\} \tag{47}$$

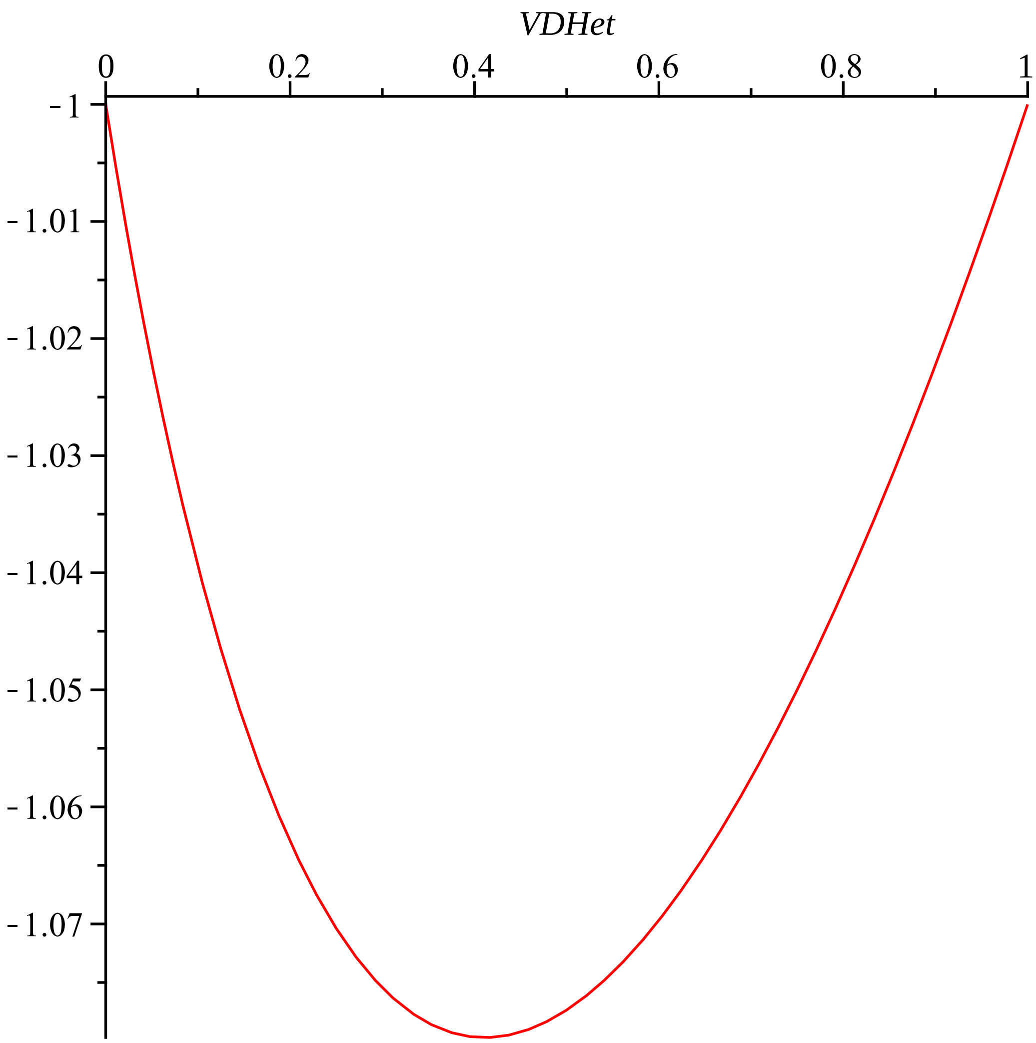
```
> #Not a boundary; complex.
```

> $checkEV21[3];$

$$\left\{VDHet = VDHet,\ VDHomo = \frac{-VDHet + VDHet^2 + 1 + \sqrt{-7\,VDHet^2 + 4\,VDHet^3 + 2\,VDHet + 1}}{VDHet - 2}\right\} \tag{48}$$

```
> #To see if solution [3] has solutions in biologically relevant
  space, we plot this solution.
```

> $plot\left(\frac{VDHet^2 + 1 - VDHet + \sqrt{-7\,VDHet^2 + 4\,VDHet^3 + 1 + 2\,VDHet}}{VDHet - 2}, VDHet = 0..1, VDHomo\right);$



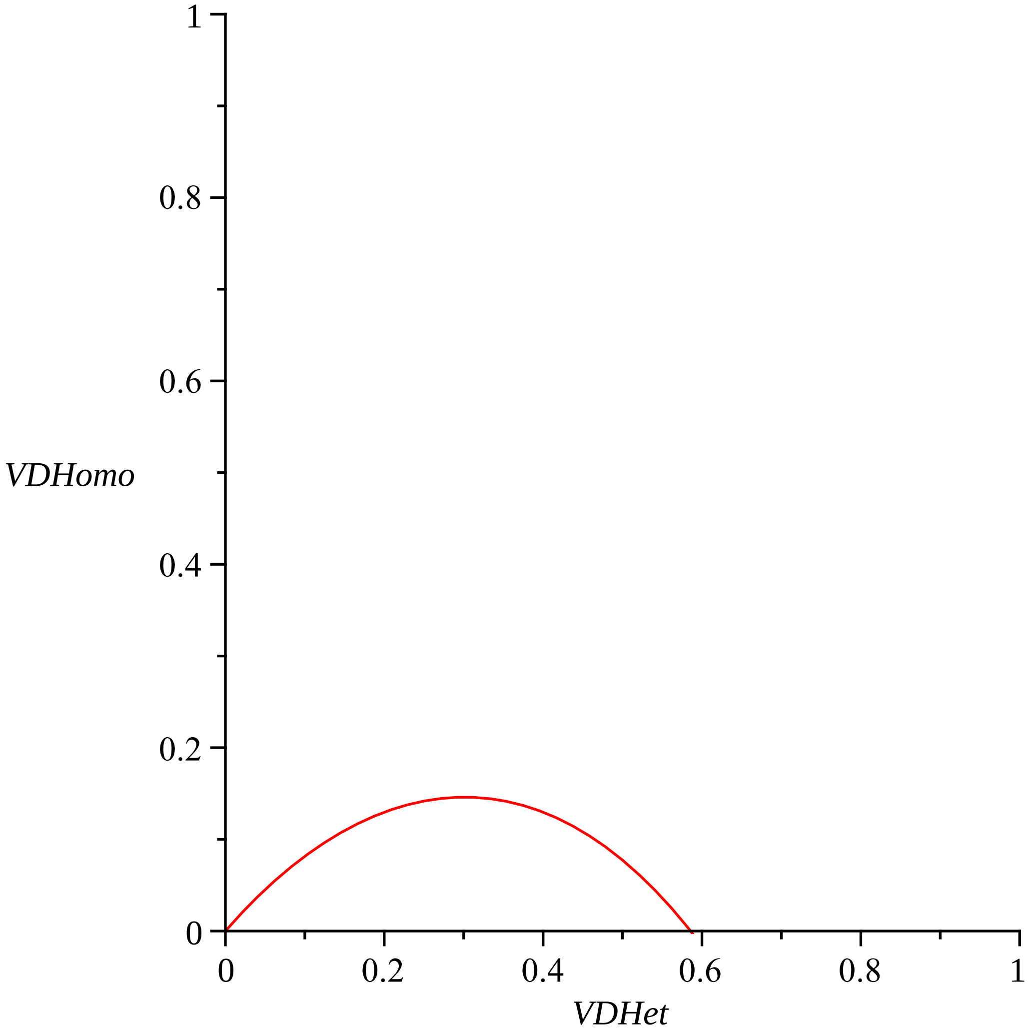
> **#VDHomo<0, therefore this solution is therefore biologically not relevant.**

> $checkEV21[4];$

$$\left\{VDHet = VDHet, VDHomo = -\frac{VDHet - VDHet^2 - 1 + \sqrt{-7\ VDHet^2 + 4\ VDHet^3 + 2\ VDHet + 1}}{VDHet - 2}\right\} \tag{49}$$

> **#To see if solution [4] has solutions in biologically relevant space, we plot this solution.**

> $$plot\left(\left\{-\frac{-VDHet^2 - 1 + VDHet + \sqrt{-7\ VDHet^2 + 4\ VDHet^3 + 2\ VDHet + 1}}{VDHet - 2}\right\}, VDHet = 0\,..1, VDHomo = 0\,..1\right);$$



```
> #This solution is biologically relevant.
> checkEV21[5];
```

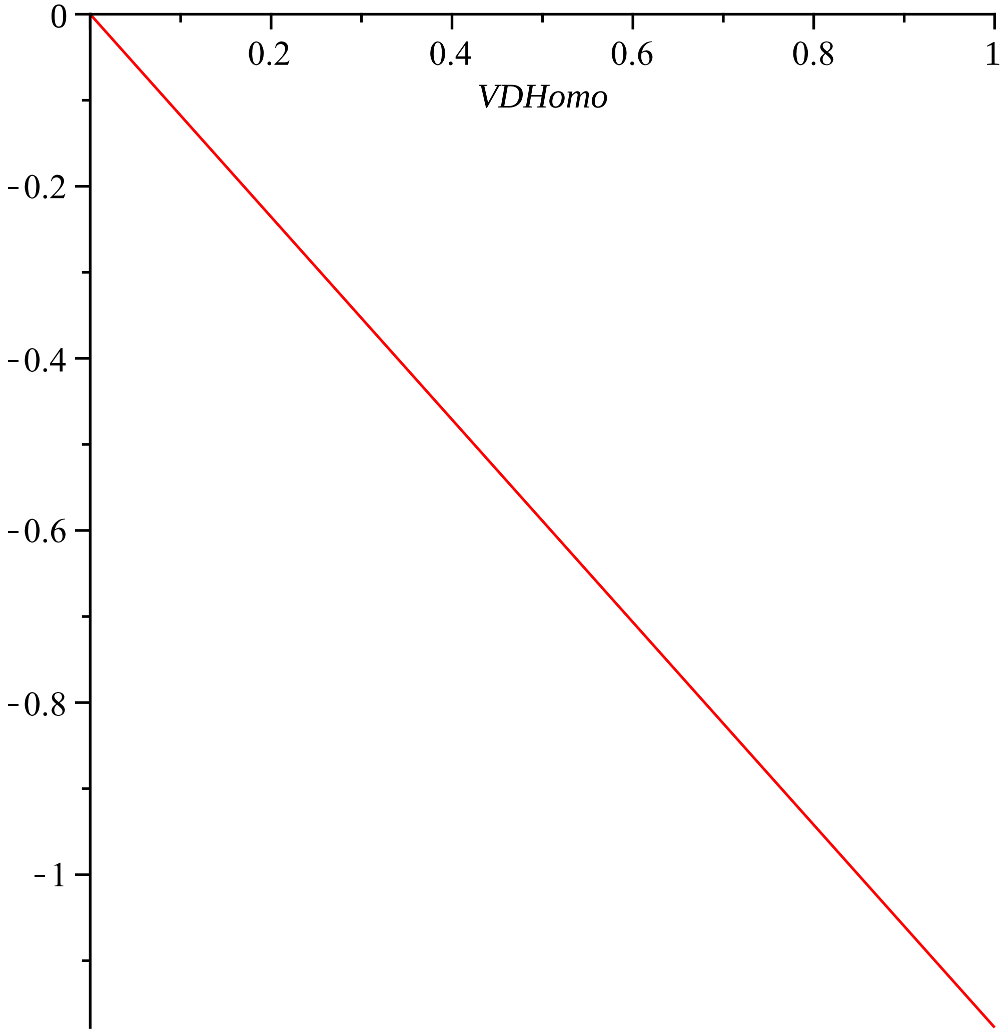
$$\left\{ VDHet = \left(\frac{1}{4}\left(3+2\sqrt{2}\right)^{1/3} + \frac{1}{4\left(3+2\sqrt{2}\right)^{1/3}} - \frac{1}{2}\,\mathrm{I}\sqrt{3}\left(-\frac{1}{2}\left(3+2\sqrt{2}\right)^{1/3} + \frac{1}{2\left(3+2\sqrt{2}\right)^{1/3}} \right) \right) VDHomo,\ VDHomo = VDHomo \right\} \tag{50}$$

```
> #This solution contains imaginary terms.
> checkEV21[6]
```

$$\left\{ VDHet = \left(-\frac{1}{2}\left(3+2\sqrt{2}\right)^{1/3} - \frac{1}{2\left(3+2\sqrt{2}\right)^{1/3}} \right) VDHomo,\ VDHomo = VDHomo \right\} \tag{51}$$

```
> #To see if solution [6] has solutions in biologically relevant
  space, we plot this solution.
```

$$> plot\left(\left(-\frac{1}{2}\left(3+2\sqrt{2}\right)^{1/3} - \frac{1}{2\left(3+2\sqrt{2}\right)^{1/3}} \right) VDHomo,\ VDHomo = 0..1 \right);$$



```
> #VDHet<0; therefore solution not biologically feasible.
>
> checkEV21[7];
```

$$\left\{ VDHet = \left(\frac{1}{4}\left(3+2\sqrt{2}\right)^{1/3} + \frac{1}{4\left(3+2\sqrt{2}\right)^{1/3}} + \frac{1}{2}\, \mathrm{I}\sqrt{3}\left(-\frac{1}{2}\left(3+2\sqrt{2}\right)^{1/3} + \frac{1}{2\left(3+2\sqrt{2}\right)^{1/3}} \right) \right) VDHomo,\ VDHomo = VDHomo \right\} \tag{52}$$

```
> #complex; no transition
> checkEV21[8];
```

$$\left\{ VDHet = VDHet,\ VDHomo = \frac{VDHet^2 + 1 + VDHet + \sqrt{-7\, VDHet^2 - 4\, VDHet^3 + 1 - 2\, VDHet}}{VDHet + 2} \right\} \tag{53}$$

```
> #complex, no transition
> checkEV21[9];
```

$$\left\{VDHet = VDHet,\ VDHomo = -\frac{-VDHet^2 - 1 - VDHet + \sqrt{-7\,VDHet^2 - 4\,VDHet^3 + 1 - 2\,VDHet}}{VDHet + 2}\right\} \tag{54}$$

$$> plot\left(\frac{VDHet^2 - VDHet + 1 + \sqrt{4\,VDHet^3 - 7\,VDHet^2 + 2\,VDHet + 1}}{VDHet - 2},\ VDHet = 0\,..1\right):$$

```
> #VDHomo is negative over the range of VDHet.
```

$$> checkEV21[10];$$

$$\left\{VDHet = \frac{235}{128} + \frac{25}{128}\left(827 + 384\sqrt{2}\right)^{1/3} + \frac{1825}{128\left(827 + 384\sqrt{2}\right)^{1/3}} - \frac{9}{8}\left(\frac{1}{12}\left(827 + 384\sqrt{2}\right)^{1/3} + \frac{73}{12\left(827 + 384\sqrt{2}\right)^{1/3}} + \frac{11}{12}\right)^2,\ VDHomo = -\frac{3}{4}\left(\frac{1}{12}\left(827 + 384\sqrt{2}\right)^{1/3} + \frac{73}{12\left(827 + 384\sqrt{2}\right)^{1/3}} + \frac{11}{12}\right)^2 + \frac{283}{192} + \frac{41}{192}\left(827 + 384\sqrt{2}\right)^{1/3} + \frac{2993}{192\left(827 + 384\sqrt{2}\right)^{1/3}}\right\} \tag{55}$$

$$> evalf(checkEV21[10])$$

$$\{VDHet = -1.136861168,\ VDHomo = 0.965363643\} \tag{56}$$

```
> #solution has negative values of VDHet.  Therefore, not
  relevant.
```

$$> checkEV21[11];$$

```
Error, invalid subscript selector
```

```
> #No more solutions
```

```
> #We now focus on boundary conditions based on the second
  eigenvalue.
```

$$> checkEV22 := solve(\mathrm{abs}(EV2[1]) = 1):$$

```
> #These solutions are the same as those for the first eigenvalue.
   No additional boundary conditions.
```

```
> #We now test points on each side of the boundary condition.
```

$$> subs(VDHet = .4,\ VDHomo = .2,\ EV2);$$

$$\begin{bmatrix} 0.7294901198 \\ 0.6737621252 \end{bmatrix} \tag{57}$$

$$> subs(VDHet = .4,\ VDHomo = .05,\ EV2);$$

$$\begin{bmatrix} 1.292279986 \\ 0.3131437669 \end{bmatrix} \tag{58}$$

```
> #The first eigenvalue is greater than one when VDHomo<-(-VDHet^2
  -VDHet+1+sqrt(4VDHet^3-7VDHet&2+2VDHet+1))/(VDHet-2).  Thefore,
```

the equilibrium is unstable. It is stable when the inequality reverses and the analysis is inconclusive at the equality.

```
>
> #All non-Medea individuals
> maternalEq[3];
```

$$[Gpp = 1, Gmm = 0] \tag{59}$$

```
> simplify(Eigenvalues(subs(maternalEq[3], VSHomo = 1, VEHomo = 1, VSHet = 1, VEHet = 1,
     μ0 = 0, μ1 = 1, MyJacobian)));
```

$$\begin{bmatrix} 0 \\ \frac{1}{2}\,VDHet + \frac{1}{2} \end{bmatrix} \tag{60}$$

```
> #If VDHet<1, this equilibrium is stable.
> #If VDHet=1, linear analysis is inconclusive.
>
> #All genotypes

> allvalues(maternalEq[4]) :
> #Those expressions are very complicated.
> myGpp := subs(maternalEq[4], Gpp) :
> myGmm := subs(maternalEq[4], Gmm) :
> #We begin by solving this at the boundary conditions (any
  Genotype = 0 or 1).
> soln := solve(myGpp = 0, VDHomo);
```

$$soln := 0, \frac{-VDHet + VDHet^2 + 1 + \sqrt{-7\,VDHet^2 + 4\,VDHet^3 + 2\,VDHet + 1}}{VDHet - 2}, \\ -\frac{VDHet - VDHet^2 - 1 + \sqrt{-7\,VDHet^2 + 4\,VDHet^3 + 2\,VDHet + 1}}{VDHet - 2} \tag{61}$$

```
> #These expressions are identical to the the expressions for
  stability of the heterozygous and homozygous Medea equilibrium.
  Only the third expression has VDHomo and VDHet both between 0
  and 1.  Now we check for solutions that contain Gpp, Gmm and Gmp
  all between 0 and 1.
>
> allvalues(subs(VDHet = .2, VDHomo = .4, myGmm))
```

$$0.4116671269, -0.8955380947 \tag{62}$$

```
> allvalues(subs(VDHet = .2, VDHomo = .4, myGpp));
```

$$0.09560911490, -8.579480088 \tag{63}$$

```
> allvalues(subs(VDHet = .2, VDHomo = .4, 1 - myGmm - myGpp));
```

$$0.4927237582, 10.47501818 \tag{64}$$

```
> allvalues(subs(VDHet = .2, VDHomo = .05, myGmm))
```

$$0.8670141061, -1.345483006 \tag{65}$$

```
> allvalues(subs(VDHet = .2, VDHomo = .05, myGpp))
```

$$-0.008581188400, -8.469887707 \tag{66}$$

```
> #Only the first value of the maternalEq solutions are valid.
> #This equilibrium does not have a solution below the boundary.
> #We now examine the other boundary conditions (each genotype
  equals 0 and 1)
> solns := solve(myGpp = 1, VDHomo);
```

$$solns := \frac{1}{2}\ VDHet - \frac{3}{4} + \frac{1}{4}\sqrt{8\ VDHet + 1}, \frac{1}{2}\ VDHet - \frac{3}{4} - \frac{1}{4}\sqrt{8\ VDHet + 1} \tag{67}$$

```
> #We now test this solution with the other two genotypes.  Gmm
  and Gmp must equal 0 for this solution to be relevant.  Gmm and
  Gmp are not 0 for any values of 0<VDHet<1.
```

$$> testGmm := subs\left(VDHomo = \frac{1}{2}\ VDHet - \frac{3}{4} - \frac{1}{4}\sqrt{8\ VDHet + 1}, myGmm\right):$$

$$> testGmp := subs\left(VDHomo = \frac{1}{2}\ VDHet - \frac{3}{4} - \frac{1}{4}\sqrt{8\ VDHet + 1}, 1 - myGpp - myGmm\right):$$

```
> plot({testGmp, testGmm}, VDHet =-5 ..5, Genotypes = 0 ..1) :

> solve(myGmm = 0);
```

$$\{VDHet = 1, VDHomo = VDHomo\}, \{VDHet = 1, VDHomo = VDHomo\} \tag{68}$$

```
> solve(myGmm = 1);
```

$$\{VDHet = VDHet, VDHomo = 0\}, \{VDHet = 2 + VDHomo, VDHomo = VDHomo\}, \{VDHet = 2 + VDHomo, VDHomo = VDHomo\} \tag{69}$$

```
> solns := solve(myGmm + myGpp = 0, VDHomo) :
> plot({solns}, VDHet = 0 ..1, VDHomo = 0 ..1) :
> #Plot shows no biologially interesting values
>
> solns := solve(myGmm + myGpp = 1, VDHomo);
```

$$solns := 0 \tag{70}$$

```
> #There are no other boundaries for feasiblity.
> #The only values possible are when VDHomo>-(-VDHet^2-1+VDHet+
  sqrt(4*VDHet^3-7*VDHet^2+2*VDHet+1))/(VDHet-2)
>
> #We now look at stability.  We begin by finding eigenvalues.
>
> Eq4EV := simplify(Eigenvalues(subs(maternalEq[4], VEHomo = 1, VSHomo = 1, VEHet = 1,
      VSHet = 1, μ0 = 0, μ1 = 1, MyJacobian))) :
> #To be unstable, the eigenvalues have to be >1.  Let's find when
  they are equal to 1.
```

```
> Eq4EV1 := solve(abs(Eq4EV[1]) = 1);
Warning, solutions may have been lost
```

$$Eq4EV1 := \tag{71}$$

```
>
> solve(abs(Eq4EV[2]) = 1);
Warning, solutions may have been lost
> #Maple was unable to find any solutions to these equations.  One
  possibility is that are no solutions in the biologically
  relevant range.  The second possibility is that Maple could not
  find them.  Therefore we turn to simulation.
>
> #By simulation we find that the eigenvalues are always greater
  than 1 for all values of VDHomo and VDHet in the feasible
  region.
```

```
> #Case 3) Parental Fitness only, No
  embryonic fitness effects; mu0=0 and mu1=1
> #We begin by introducing the simplifications
> nextGppParental := subs( VSHomo = VDHomo, VSHet = VDHet, VEHet = 1, VEHomo = 1, μ0
      = 0, μ1 = 1, nextGpp) :
> nextGmmParental := subs( VSHomo = VDHomo, VSHet = VDHet, VEHet = 1, VEHomo = 1, μ0
      = 0, μ1 = 1, nextGmm) :
> nextGmpParental := subs( VSHomo = VDHomo, VSHet = VDHet, VEHet = 1, VEHomo = 1, μ0
      = 0, μ1 = 1, nextGmp) :
> parentalEq := solve( {nextGppParental = Gpp, nextGmmParental = Gmm}, [Gpp, Gmm]) :
```

```
>
> #Solve for the 4 biologically relevant equilibria
> #Only Medea Homozygotes
> parentalEq[1];
```

$$[Gpp = 0, Gmm = 1] \tag{72}$$

```
> Eq1EV := subs( VDHet = VPHet, VDHomo = VPHomo,
      simplify( Eigenvalues( subs( parentalEq[1], VSHomo = VDHomo, VSHet = VDHet, VEHet
      = 1, VEHomo = 1, μ0 = 0, μ1 = 1, MyJacobian ) ) ) );
```

$$Eq1EV := \begin{bmatrix} 0 \\ \frac{VPHet}{VPHomo} \end{bmatrix} \tag{73}$$

```
> #If VPHomo>VPHet the equilibrium is unstable.  If VPHomo<VPHet
```

```
  is stable.  The equality is inconclusvie.
>
> #Only Medea Individuals
> parentalEq[2];
```

$$\left[Gpp=0,\ Gmm=\frac{VDHet}{-2\ VDHomo+3\ VDHet}\right] \tag{74}$$

```
> solve(VDHet/(-2 VDHomo + 3 VDHet) = 0);
```

$$\{VDHet=0,\ VDHomo=VDHomo\} \tag{75}$$

```
> solve(VDHet/(-2 VDHomo + 3 VDHet) = 1)
```

$$\{VDHet=VDHomo,\ VDHomo=VDHomo\} \tag{76}$$

```
> #Solutions only exist when VDHet>VDHomo.
> Eq2EV := simplify(Eigenvalues(subs(parentalEq[2], VSHomo = VDHomo, VSHet = VDHet,
      VEHet = 1, VEHomo = 1, μ0 = 0, μ1 = 1, MyJacobian)));
```

$$Eq2EV := \begin{bmatrix} \dfrac{VDHomo}{VDHet} \\ \dfrac{-VDHomo+VDHet}{VDHet^2} \end{bmatrix} \tag{77}$$

```
>
> #This equilibrium is stable when VDHomo>VDHet-VDHet*VDHet

> #Only non-Medea alleles in the population
> parentalEq[3];
```

$$[Gpp=1,\ Gmm=0] \tag{78}$$

```
> subs(simplify(Eigenvalues(subs(parentalEq[3], VSHomo = VDHomo, VSHet = VDHet, VEHet
      = 1, VEHomo = 1, μ0 = 0, μ1 = 1, MyJacobian))));
```

$$\begin{bmatrix} 0 \\ VDHet \end{bmatrix} \tag{79}$$

```
> #If VDHet<1, this equilibrium is stable.
> #If VDHet=1, linear analysis is inconclusive.
>
> #All 3 genotypes in the equilibrium population
> simplify(parentalEq[4]);
```

$$\Big[Gpp \tag{80}$$

$$= \left(\left(VDHet^2 - VDHet + VDHomo\right)\ VDHomo\right) \Big/ \left(1 + VDHomo^2 - 2\ VDHet\right.$$

$$+\mathit{VDHet}^2+2\,\mathit{VDHomo}-3\,\mathit{VDHet}\,\mathit{VDHomo}+\mathit{VDHet}^2\,\mathit{VDHomo}\big),\ \mathit{Gmm}=\big(\mathit{VDHet}^2+1-2\,\mathit{VDHet}\big)\big/\big(1+\mathit{VDHomo}^2-2\,\mathit{VDHet}+\mathit{VDHet}^2+2\,\mathit{VDHomo}-3\,\mathit{VDHet}\,\mathit{VDHomo}+\mathit{VDHet}^2\,\mathit{VDHomo}\big)\,\big]$$

> $\mathit{myGpp} := \big(\big(\mathit{VDHet}^2-\mathit{VDHet}+\mathit{VDHomo}\big)\,\mathit{VDHomo}\big)\big/\big(-2\,\mathit{VDHet}+1+\mathit{VDHet}^2+2\,\mathit{VDHomo}+\mathit{VDHomo}^2-3\,\mathit{VDHet}\,\mathit{VDHomo}+\mathit{VDHet}^2\,\mathit{VDHomo}\big);$

$$\mathit{myGpp} := \big(\big(\mathit{VDHet}^2-\mathit{VDHet}+\mathit{VDHomo}\big)\,\mathit{VDHomo}\big)\big/\big(1+\mathit{VDHomo}^2-2\,\mathit{VDHet}+\mathit{VDHet}^2+2\,\mathit{VDHomo}-3\,\mathit{VDHet}\,\mathit{VDHomo}+\mathit{VDHet}^2\,\mathit{VDHomo}\big) \tag{81}$$

> $\mathit{myGmm} := \big(1-2\,\mathit{VDHet}+\mathit{VDHet}^2\big)\big/\big(-2\,\mathit{VDHet}+1+\mathit{VDHet}^2+2\,\mathit{VDHomo}+\mathit{VDHomo}^2-3\,\mathit{VDHet}\,\mathit{VDHomo}+\mathit{VDHet}^2\,\mathit{VDHomo}\big);$

$$\mathit{myGmm} := \big(\mathit{VDHet}^2+1-2\,\mathit{VDHet}\big)\big/\big(1+\mathit{VDHomo}^2-2\,\mathit{VDHet}+\mathit{VDHet}^2+2\,\mathit{VDHomo}-3\,\mathit{VDHet}\,\mathit{VDHomo}+\mathit{VDHet}^2\,\mathit{VDHomo}\big) \tag{82}$$

> $\mathit{solve}(\mathit{myGpp}=0);$

$$\{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=-\mathit{VDHet}^2+\mathit{VDHet}\},\ \{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=0\} \tag{83}$$

> $.8-.64$

$$0.16 \tag{84}$$

> $\mathit{subs}(\mathit{VDHet}=.8,\ \mathit{VDHomo}=.2,\ \mathit{myGpp});$

$$0.06250000000 \tag{85}$$

> $\mathit{subs}(\mathit{VDHet}=.8,\ \mathit{VDHomo}=.1,\ \mathit{myGpp});$

$$-0.08108108108 \tag{86}$$

> $\mathit{solve}(\mathit{myGpp}=1);$

$$\{\mathit{VDHet}=1,\ \mathit{VDHomo}=\mathit{VDHomo}\},\ \{\mathit{VDHet}=1+2\,\mathit{VDHomo},\ \mathit{VDHomo}=\mathit{VDHomo}\} \tag{87}$$

```
> #Solution is not when feasible VDHomo<VDHet(1-VDHet).
```

> $\mathit{solve}(\mathit{myGmm}=0);$

$$\{\mathit{VDHet}=1,\ \mathit{VDHomo}=\mathit{VDHomo}\},\ \{\mathit{VDHet}=1,\ \mathit{VDHomo}=\mathit{VDHomo}\} \tag{88}$$

> $\mathit{solve}(\mathit{myGmm}=1);$

$$\{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=0\},\ \big\{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=3\,\mathit{VDHet}-\mathit{VDHet}^2-2\big\} \tag{89}$$

```
> #Transitions not in biologically relevant space.
```

> $\mathit{solve}(\mathit{myGmm}+\mathit{myGpp}=0);$

$$\left\{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=\left(-\frac{1}{2}\,\mathit{VDHet}+\frac{1}{2}\,\sqrt{\mathit{VDHet}^2-4}\right)(\mathit{VDHet}-1)\right\},\ \left\{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=\left(-\frac{1}{2}\,\mathit{VDHet}-\frac{1}{2}\,\sqrt{\mathit{VDHet}^2-4}\right)(\mathit{VDHet}-1)\right\} \tag{90}$$

> $\mathit{solve}(\mathit{myGmm}+\mathit{myGpp}=1);$

$$\{\mathit{VDHet}=\mathit{VDHet},\ \mathit{VDHomo}=0\},\ \{\mathit{VDHet}=1,\ \mathit{VDHomo}=\mathit{VDHomo}\} \tag{91}$$

```
> #Now look at stability
```

> $\mathit{Eq4EV} := \mathit{subs}\big(\mathit{simplify}\big(\mathit{Eigenvalues}\big(\mathit{subs}\big(\mathit{parentalEq}[4],\ \mathit{VSHomo}=\mathit{VDHomo},\ \mathit{VSHet}=\mathit{VDHet},\ \mathit{VEHet}=1,\ \mathit{VEHomo}=1,\ \mu 0=0,\ \mu 1=1,\ \mathit{MyJacobian}\big)\big)\big)\big);$

$$Eq4EV := \left[\left[\frac{1}{2}\,\frac{1}{VDHomo}\left(2\,VDHomo - VDHet\,VDHomo + \left(-VDHomo\left(-4\,VDHomo + 4\,VDHet\,VDHomo - VDHet^{2}\,VDHomo + 4\,VDHet^{3} + 4\,VDHet - 8\,VDHet^{2}\right)\right)^{1/2}\right)\right], \left[-\frac{1}{2}\,\frac{1}{VDHomo}\left(-2\,VDHomo + VDHet\,VDHomo + \left(-VDHomo\left(-4\,VDHomo + 4\,VDHet\,VDHomo - VDHet^{2}\,VDHomo + 4\,VDHet^{3} + 4\,VDHet - 8\,VDHet^{2}\right)\right)^{1/2}\right)\right]\right] \tag{92}$$

```
> #To be unstable, the modulus of the eigenvalues have to be >1.
  We find when they are equal to 1.
```

```
> solve(abs(Eq4EV[1]) = 1);
```

$$\begin{aligned}&\{VDHet = 1, VDHomo < 0\}, \{VDHet = 1, VDHomo = 0, VDHomo < 0\}, \{VDHomo = -VDHet^{2} + VDHet, -VDHet^{2} + VDHet = -VDHet^{2} + VDHet, VDHet < 0\},\\ &\{VDHomo = -VDHet^{2} + VDHet, -VDHet^{2} + VDHet = -VDHet^{2} + VDHet, 1 < VDHet\}, \{VDHet = 1, 0 < VDHomo\}, \{VDHet = 1, VDHomo = 0, 0 < VDHomo\},\\ &\{VDHomo = -VDHet^{2} + VDHet, -VDHet^{2} + VDHet = -VDHet^{2} + VDHet, 0 < VDHet, VDHet < 1\},\\ &\left\{VDHomo = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet} = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, 0 < VDHet, VDHet < 1\right\},\\ &\left\{VDHomo = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet} = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, 1 < VDHet, VDHet < 3\right\},\\ &\left\{VDHomo = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet} = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, VDHet < 0\right\},\\ &\left\{VDHomo = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet} = \frac{(VDHet^{2} + 1 - 2\,VDHet)\,VDHet}{-3 + VDHet}, 3 < VDHet\right\}\end{aligned} \tag{93}$$

```
>
```

```
> #The only solution that has solutions in the biologically
  feasible range is VDHomo=VDHet-VDHet^2.
```

```
> subs(VDHet = .9, VDHomo = .8, Eq4EV[1]);
```

$$1.089675829 \tag{94}$$

```
> #VDHomo<VDHet-VDHet*VDHet is not feasible.
> #VDHomo>VDHet-VDHet*VDHet is not stable.
> solve(abs(Eq4EV[2]) = 1);
```

$$
\begin{gathered}
\left\{VDHomo = \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet} \right.\\
\left. = \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, 0 < VDHet, VDHet < 1\right\}, \left\{VDHomo \right.\\
= \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}\\
\left. = \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, 1 < VDHet, VDHet < 3\right\}, \left\{VDHomo \right.\\
= \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}\\
\left. = \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, VDHet < 0\right\}, \left\{VDHomo \right.\\
= \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}\\
\left. = \frac{\left(VDHet^2+1-2\,VDHet\right)\,VDHet}{-3+VDHet}, 3 < VDHet\right\}, \{VDHet = 1, VDHomo < 0\}, \{VDHet\\
= 1, VDHomo = 0, VDHomo < 0\}, \{VDHomo = -VDHet^2 + VDHet, -VDHet^2 + VDHet =\\
-VDHet^2 + VDHet, VDHet < 0\}, \{VDHomo = -VDHet^2 + VDHet, -VDHet^2 + VDHet =\\
-VDHet^2 + VDHet, 1 < VDHet\}, \{VDHet = 1, 0 < VDHomo\}, \{VDHet = 1, VDHomo = 0,\\
0 < VDHomo\}, \{VDHomo = -VDHet^2 + VDHet, -VDHet^2 + VDHet = -VDHet^2\\
+ VDHet, 0 < VDHet, VDHet < 1\}
\end{gathered}
\tag{95}
$$

```
> #No new criteria

> #Case t1 varies, VEHomo=VEHet^2, Parental
  fitnesses=1
> #We begin by introducing the simplifications
> nextGppEmbryonicMt := subs(VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, VEHomo
      = VEHet·VEHet, μ0 = 0, μ1 = 1 − t1, nextGpp) :
> nextGmmEmbryonicMt := subs(VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, VEHomo
      = VEHet·VEHet, μ0 = 0, μ1 = 1 − t1, nextGmm) :
> nextGmpEmbryonicMt := subs(VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, VEHomo
      = VEHet·VEHet, μ0 = 0, μ1 = 1 − t1, nextGmp) :
>
> #Solve for the 4 biologically relevant equilibria
> embryonicEqMt := solve({nextGppEmbryonicMt = Gpp, nextGmmEmbryonicMt = Gmm},
      [Gpp, Gmm]) :
```

>

> **#The equilibrium with only Medea homozygous individuals**

> $embryonicEqMt[1];$

$$[Gpp = 0, Gmm = 1] \tag{96}$$

> **#Check the stability of only Medea homozygous equilibrium**

> $Eqt1 := simplify(Eigenvalues(subs(embryonicEqMt[1], VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet = 1, VEHomo = VEHet \cdot VEHet, \mu0 = 0, \mu1 = 1 - t1, MyJacobian)));$

$$Eqt1 := \begin{bmatrix} 0 \\ -\frac{1}{2}\,\frac{-2+t1}{VEHet} \end{bmatrix} \tag{97}$$

> $solve(Eqt1[2] = 1, VEHet)$

$$1 - \frac{1}{2}\,t1 \tag{98}$$

>

> $subs(t1 = .1, VEHet = .8, Eqt1[2])$

$$1.187500000 \tag{99}$$

> $subs(t1 = .7, VEHet = .9, Eqt1[2]);$

$$0.7222222222 \tag{100}$$

>

> **#When VEHet less than 1-.5*t1, the equlibrium is not stable. The equilibrium is stable VEHet>1-.5*t1 and analysis is inconclusive at the equality.**

>

> **#The equilibrium with homozygous and heterozygous Medea individuals**

>

> $aEqMt2 := allvalues(embryonicEqMt[2]);$

$$aEqMt2 := \left[Gpp = 0, Gmm = \frac{-VEHet + 1 + \sqrt{1 - 2\,VEHet\,t1}}{VEHet + 2\,t1 - 2}\right], \left[Gpp = 0, Gmm = -\frac{VEHet - 1 + \sqrt{1 - 2\,VEHet\,t1}}{VEHet + 2\,t1 - 2}\right] \tag{101}$$

> *#The first solution is biologically irrelevant because without the radical, the numerator is positive and the denominator is negative..*

> $myGmm := -\frac{VEHet - 1 + \sqrt{1 - 2\,VEHet\,t1}}{VEHet + 2\,t1 - 2};$

$$myGmm := -\frac{VEHet - 1 + \sqrt{1 - 2\,VEHet\,t1}}{VEHet + 2\,t1 - 2} \tag{102}$$

> $solve(\ myGmm = 0);$

$$\{VEHet = 0, t1 = t1\} \tag{103}$$

> $solve(\mathrm{myGmm}=1, \mathrm{VEHet});$

$$1-\frac{1}{2}\,t1 \tag{104}$$

> $subs(t1=.01, VEHet=.51, myGmm);$

$$0.3434604954 \tag{105}$$

> $subs(t1=.4, VEHet=.9, myGmm);$

$$1.430500874 \tag{106}$$

> `#This equilibrium is only biologically feasible when VEHet<=1-(1/2)t1.`

> $Eqt2 := simplify(Eigenvalues(subs(\mathrm{Gpp}=0, \mathrm{Gmm}=\mathrm{myGmm}, \mathrm{Gmp}=1-\ \mathrm{myGmm}, VSHomo=1, VDHomo=1, VSHet=1, VDHet=1, VEHomo=VEHet\cdot VEHet, \mu 0=0, \mu 1=1-t1, MyJacobian))):$

> $solns := solve(\mathrm{abs}(Eqt2[1])=1):$

> $solns[1];$

$$\left\{VEHet=1-\frac{1}{2}\,t1,\ t1=t1\right\} \tag{107}$$

> $$plot\left(\left\{-\frac{1}{2}\,\frac{1}{t1}\left(\left(\frac{1}{3}\left(-64+54\,t1+6\sqrt{-192\,t1+81\,t1^2}\right)^{1/3}+\frac{16}{3\left(-64+54\,t1+6\sqrt{-192\,t1+81\,t1^2}\right)^{1/3}}-\frac{1}{3}\right)^2-1\right)\right\}, t1=0..1\right):$$

> `#Plot indicates solutions when VEHet<0 for 0<t1<1`

> $solns[2];$

$$\left\{VEHet=VEHet,\ t1=\frac{2\,VEHet+\sqrt{-4\,VEHet^2+1}-\frac{-VEHet+1+\sqrt{-4\,VEHet^2+1}}{VEHet}}{VEHet^2}\right\} \tag{108}$$

> $$plot\left(-\frac{1}{2}\,\frac{-\frac{1}{2}+\frac{1}{2}\sqrt{1+4\,t1}+t1}{t1}, t1=0..1\right):$$

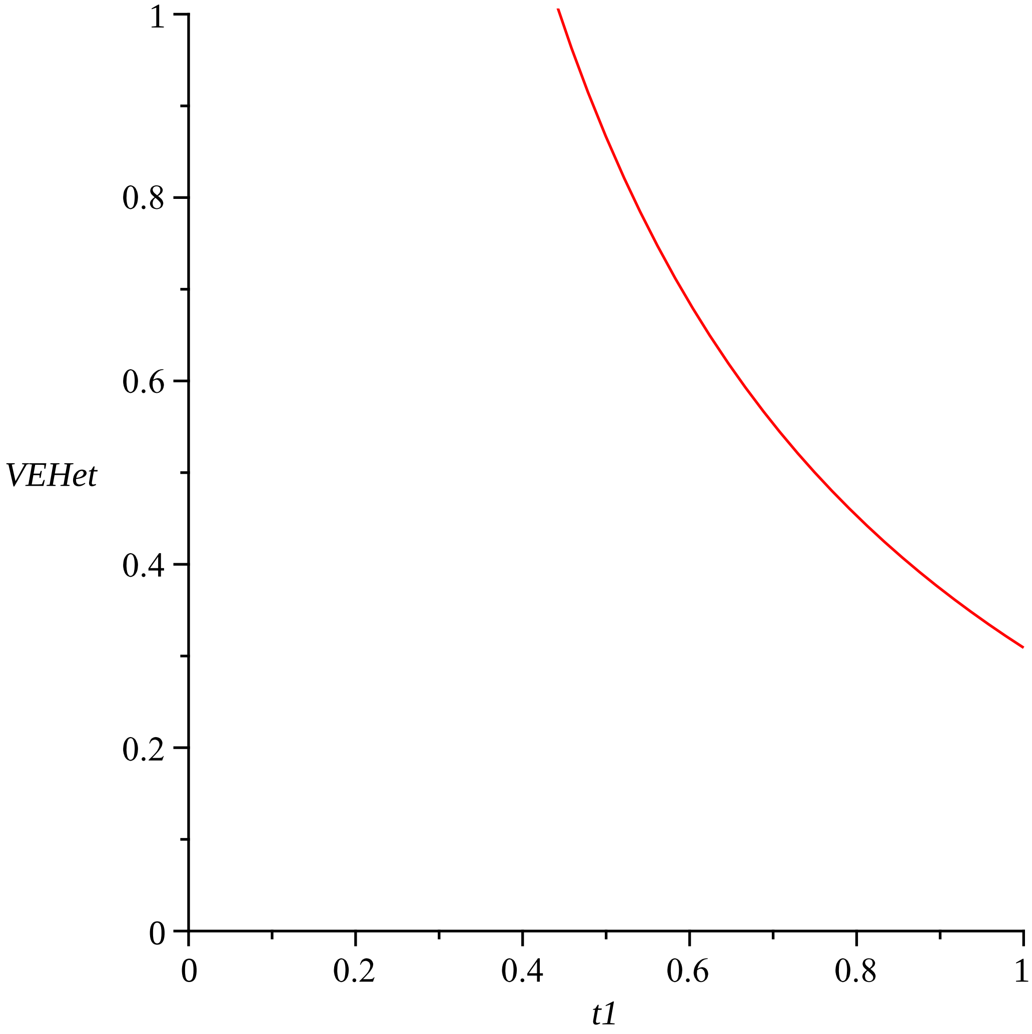
> `#Plot indicates solutions when VEHet<0 for 0<t1<1`

> $solns[3];$

$$\left\{VEHet=VEHet,\ t1=\frac{2\,VEHet-\sqrt{-4\,VEHet^2+1}+\frac{VEHet-1+\sqrt{-4\,VEHet^2+1}}{VEHet}}{VEHet^2}\right\} \tag{109}$$

>

> $$plot\left(-\frac{1}{2}\,\frac{-\frac{1}{2}-\frac{1}{2}\sqrt{1+4\,t1}+t1}{t1}, t1=0..1, VEHet=0..1\right);$$



> **#This solution is biologically relevant.**

> $solns[4];$

$$\left\{ VEHet = VEHet,\ t1 = \frac{1}{2\ VEHet} \right\} \tag{110}$$

> **#This solution is biologically relevant.**

>

> $solns[5];$

$$\left\{ VEHet = -\frac{1}{2}\ \frac{1}{t1} \left(\left(\frac{1}{3} \left(-64 + 54\ t1 + 6\sqrt{-192\ t1 + 81\ t1^2}\right)^{1/3} + \frac{16}{3\left(-64 + 54\ t1 + 6\sqrt{-192\ t1 + 81\ t1^2}\right)^{1/3}} - \frac{1}{3} \right)^2 - 1 \right), t1 = t1 \right\} \tag{111}$$

> $plot\left(\frac{2\ VEHet + \sqrt{-4\ VEHet^2 + 1} - \frac{-VEHet + 1 + \sqrt{-4\ VEHet^2 + 1}}{VEHet}}{VEHet^2}, VEHet = 0\,..1, t1\right.$

$$= 0\,..1\Big) :$$

```
> ##This solution is not biologically relevant.
```

```
> solns[6];
```

$$\left\{ VEHet = -\frac{1}{2}\,\frac{-\frac{1}{2}+\frac{1}{2}\sqrt{1+4\,t1}+t1}{t1},\ t1 = t1 \right\} \tag{112}$$

$$> \mathit{plot}\left(\frac{2\,VEHet-\sqrt{-4\,VEHet^{2}+1}+\frac{VEHet-1+\sqrt{-4\,VEHet^{2}+1}}{VEHet}}{VEHet^{2}},\ VEHet = 0\,..1,\ t1 = 0\,..1\right) :$$

```
> #This solution is biologically relevant.
```

```
> solns[7];
```

$$\left\{ VEHet = -\frac{1}{2}\,\frac{-\frac{1}{2}-\frac{1}{2}\sqrt{1+4\,t1}+t1}{t1},\ t1 = t1 \right\} \tag{113}$$

$$> \mathit{solve}\left(t1 = \frac{1}{2\,VEHet},\ VEHet\right);$$

$$\frac{1}{2\,t1} \tag{114}$$

```
>
```

```
> solns[8];
Error, invalid subscript selector
```

```
> #No more solutions.
```

$$> solns := \mathit{solve}(\mathrm{abs}(Eqt2[2]) = 1) :$$

```
> #No additional boundaries from the second eigenvalue
```

```
> #Now I plot all biologically relevant solutions below
```

```
> #We now rewrite all biologically relevant boundary conditions as
  functions of t1.
```

$$> \mathit{solve}\left(\frac{1}{2\,VEHet} = t1,\ VEHet\right);$$

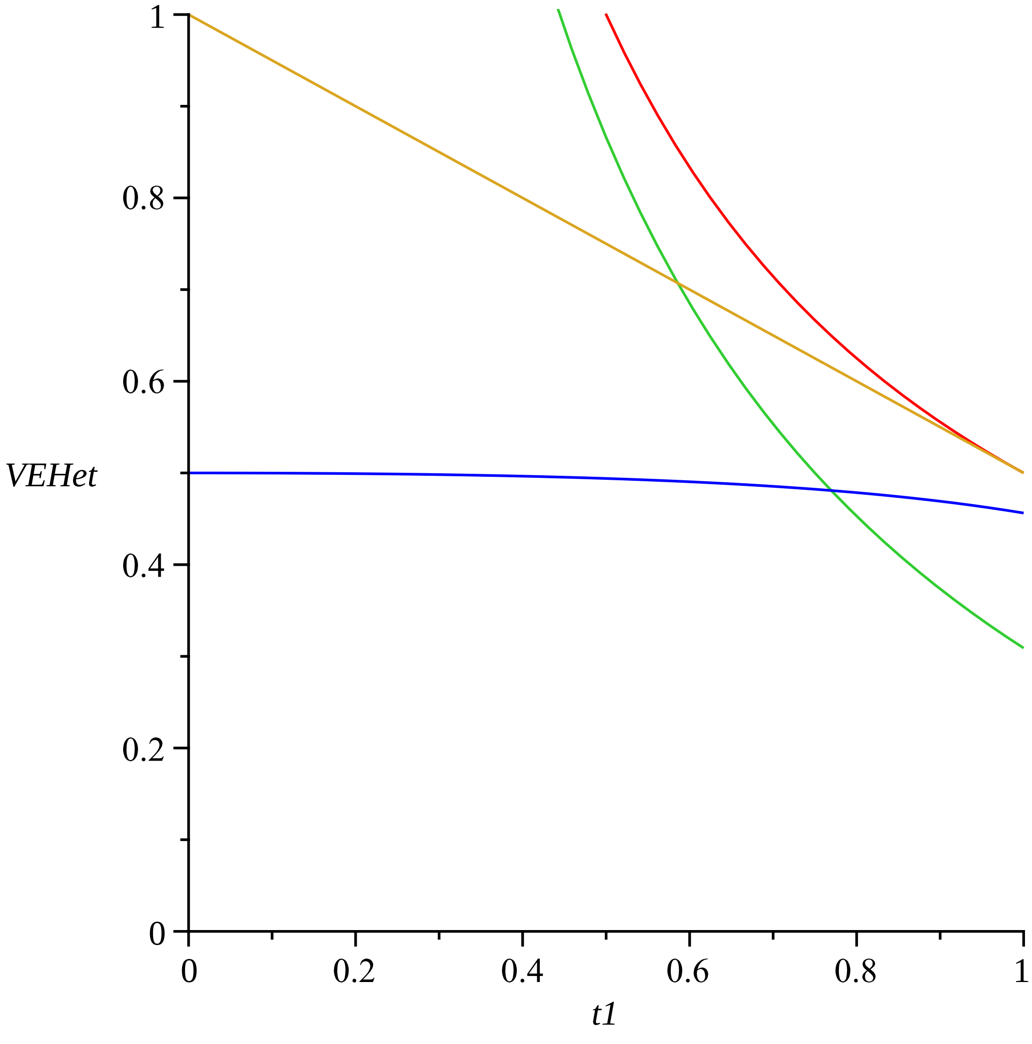
$$\frac{1}{2\,t1} \tag{115}$$

$$> possibleSolution := \mathit{solve}\left(\frac{2\,VEHet-\sqrt{-4\,VEHet^{2}+1}+\frac{VEHet-1+\sqrt{-4\,VEHet^{2}+1}}{VEHet}}{VEHet^{2}}\right.$$

$$= t1,\ VEHet\Big) :$$

$$> plot\left(\left\{\frac{1}{4}\ \frac{1-2\,t1+\sqrt{1+4\,t1}}{t1},\ 1-\frac{1}{2}\ \mathrm{t1},\ \frac{1}{2\,t1},\ possibleSolution\right\},\ t1=0..1,\ VEHet=0..1\right)$$

```
Warning, unable to evaluate 2 of the 6 functions to numeric 
values in the region; see the plotting command's help page to 
ensure the calling sequence is correct
```



```
> #The red curve is 1/(2t1).
> #The gold curve is 1-(1/2)t1.
> #The blue curve is 1/4 (1-2t1 + sqrt(1+4t1))/t1.
> #The green curve corresponds to the first solution of the 
  possibleSolutions variable.
```

```
> #The warning occurs because the other solutions of the
  possibleSolutions curves lie outside the biologially relevant
  (plotted range).
> #We now test points within each region.
> subs(t1 = .1, VEHet = .1, myGmm);
                              0.05291146688                          (116)
> evalf(subs(t1 = .1, VEHet = .1, abs(Eqt2)));
                              [ 9.039257285 ]
                              [             ]                        (117)
                              [0.1061727130 ]
> subs(t1 = .1, VEHet = .6, myGmm);
                              0.4484026267                           (118)
> evalf(subs(t1 = .1, VEHet = .1, abs(Eqt2)));
                              [ 9.039257285 ]
                              [             ]                        (119)
                              [0.1061727130 ]
> subs(t1 = .59, VEHet = .56, myGmm);
                              0.5477261196                           (120)
> evalf(subs(t1 = .95, VEHet = .4, abs(Eqt2)));
                              [ 1.553967066 ]
                              [             ]                        (121)
                              [0.6954858985 ]
> evalf(subs(t1 = .95, VEHet = .2, abs(Eqt2)));
                              [ 4.342682219 ]
                              [             ]                        (122)
                              [0.3161136814 ]
> #The gold line defines the region of infeasibility.  Points
  above the line are not feasible.  Points below are feasible.
> #The red curve is irrelevant because it is in the region of
  biological infeasibility.
> #Points above the blue line are stable (modulus of all
  eigenvalues is less than 1) and points below the blue line are
  not stable (modulus of at least one eigenvalue greater than 1).
> The green line corresponds to points with a modulus of 1 but
  does not correspond to changes in stability.
>
>
> #The equilibrium with only non-Medea individuals
> embryonicEqMt[3];
                           [Gpp = 1, Gmm = 0]                        (123)
> simplify(Eigenvalues(subs(embryonicEqMt[3], VSHomo = 1, VDHomo = 1, VSHet = 1, VDHet
      = 1, VEHomo = VEHet·VEHet, μ0 = 0, μ1 = 1 − t1, MyJacobian)));
```

$$\begin{bmatrix} 0 \\ \mathit{VEHet} \end{bmatrix} \quad \textbf{(124)}$$

```
> #If VEHet<1, this equilibrium is stable.
> #If VEHet=1, linear analysis is inconclusive.
>
> #All 3 genotypes in the equilibrium population
> #We find where this equilibrium is biologically feasible
> embryonicEqMt[4];
```

$$\left[Gpp = \frac{\left(VEHet^3\, t1^2 - 4\, VEHet^2\, t1 - 2\, VEHet\, t1 + 8\, VEHet - 4 + 2\, t1\right) VEHet}{t1^2\, VEHet^4 - 4\, VEHet^3\, t1 + 4\, VEHet^2 + 2\, VEHet^2\, t1 - 4\, VEHet - 2\, VEHet\, t1 + 4}, \right. \quad \textbf{(125)}$$

$$\left. Gmm = \frac{4\left(-2\, VEHet + VEHet^2 + 1\right)}{t1^2\, VEHet^4 - 4\, VEHet^3\, t1 + 4\, VEHet^2 + 2\, VEHet^2\, t1 - 4\, VEHet - 2\, VEHet\, t1 + 4} \right]$$

```
>
> myGpp := subs(embryonicEqMt[4], Gpp) :
> myGmm := subs(embryonicEqMt[4], Gmm) :
> boundary := solve(myGpp = 0, t1);
```

$$boundary := \frac{2\, VEHet^2 + VEHet - 1 + \sqrt{-4\, VEHet^4 + 8\, VEHet^3 - 3\, VEHet^2 - 2\, VEHet + 1}}{VEHet^3}, \quad \textbf{(126)}$$

$$-\frac{-2\, VEHet^2 - VEHet + 1 + \sqrt{-4\, VEHet^4 + 8\, VEHet^3 - 3\, VEHet^2 - 2\, VEHet + 1}}{VEHet^3}$$

```
>
> #Only the first radical is postive, 0<VEHet≤1
> boundary1
```

$$:= \frac{2\, VEHet^2 + VEHet - 1 + \sqrt{-4\, VEHet^4 + 8\, VEHet^3 - 3\, VEHet^2 - 2\, VEHet + 1}}{VEHet} :$$

```
>
> subs(VEHet = .49, boundary1);
```

$$0.1463035073 \quad \textbf{(127)}$$

```
> subs(VEHet = .49, t1 = .6, myGpp);
```

$$-0.0003789866153 \quad \textbf{(128)}$$

```
> subs(VEHet = .49, t1 = 0.62, myGpp);
```

$$0.0004404844116 \quad \textbf{(129)}$$

```
> subs(VEHet = .49, t1 = 0.62, myGmm);
```

$$0.4297549764 \quad \textbf{(130)}$$

```
> #This equilibrium only exists when VEHet>=boundary1.
> solve(myGpp = 1);
```

$$\{VEHet = 1, t1 = t1\}, \left\{VEHet = VEHet, t1 = \frac{VEHet + 1}{VEHet}\right\} \quad \textbf{(131)}$$

```
> #The VEHet+1/VEHet boundary causes t1>1, therefore it is not
```

biologically relevant.

```
> solve(myGmm = 1);
```

$$\{\mathit{VEHet}=0,\ t1=t1\},\ \left\{\mathit{VEHet}=\mathit{VEHet},\ t1=\frac{2\,\mathit{VEHet}^2-\mathit{VEHet}+1+\sqrt{4\,\mathit{VEHet}^4-8\,\mathit{VEHet}^3+5\,\mathit{VEHet}^2-2\,\mathit{VEHet}+1}}{\mathit{VEHet}^3}\right\},\ \left\{\mathit{VEHet}=\mathit{VEHet},\ t1=-\frac{-2\,\mathit{VEHet}^2+\mathit{VEHet}-1+\sqrt{4\,\mathit{VEHet}^4-8\,\mathit{VEHet}^3+5\,\mathit{VEHet}^2-2\,\mathit{VEHet}+1}}{\mathit{VEHet}^3}\right\} \tag{132}$$

```
> #This is the same boundary as discovered with Gpp=0;
>
> solve(myGmm = 0);
```

$$\{\mathit{VEHet}=1,\ t1=t1\},\ \{\mathit{VEHet}=1,\ t1=t1\} \tag{133}$$

```
> solve(myGmm + myGpp = 0);
```

$$\left\{\mathit{VEHet}=\mathit{VEHet},\ t1=\frac{2\,\mathit{VEHet}^2+\mathit{VEHet}-1+\sqrt{-8\,\mathit{VEHet}^4+16\,\mathit{VEHet}^3-7\,\mathit{VEHet}^2-2\,\mathit{VEHet}+1}}{\mathit{VEHet}^3}\right\},\ \left\{\mathit{VEHet}=\mathit{VEHet},\ t1=-\frac{-2\,\mathit{VEHet}^2-\mathit{VEHet}+1+\sqrt{-8\,\mathit{VEHet}^4+16\,\mathit{VEHet}^3-7\,\mathit{VEHet}^2-2\,\mathit{VEHet}+1}}{\mathit{VEHet}^3}\right\} \tag{134}$$

```
> #same boundaries as above

> solve(myGmm + myGpp = 1);
```

$$\{\mathit{VEHet}=0,\ t1=t1\},\ \{\mathit{VEHet}=\mathit{VEHet},\ t1=2\},\ \{\mathit{VEHet}=1,\ t1=t1\} \tag{135}$$

```
> #boundary is not biologically relevant
> #Moving on to stability
> Eq4EV := allvalues(simplify(Eigenvalues(subs(embryonicEqMt[4], VSHomo = 1, VDHomo
      = 1, VSHet = 1, VDHet = 1, VEHomo = VEHet·VEHet, μ0 = 0, μ1 = 1 − t1, MyJacobian)))
      ) :
> EqEV4 := solve(abs(Eq4EV[1]) = 1)
```

$$\mathit{EqEV4} := \{\mathit{VEHet}=1,\ t1=t1\},\ \{\mathit{VEHet}=\mathit{VEHet},\ t1 \tag{136}$$

$$= \frac{2\,\mathit{VEHet}^2 + \mathit{VEHet} - 1 + \sqrt{-4\,\mathit{VEHet}^4 + 8\,\mathit{VEHet}^3 - 3\,\mathit{VEHet}^2 - 2\,\mathit{VEHet} + 1}}{\mathit{VEHet}^3}\Bigg\},$$

$$\Bigg\{\mathit{VEHet} = \mathit{VEHet},\ t1 =$$

$$- \frac{-2\,\mathit{VEHet}^2 - \mathit{VEHet} + 1 + \sqrt{-4\,\mathit{VEHet}^4 + 8\,\mathit{VEHet}^3 - 3\,\mathit{VEHet}^2 - 2\,\mathit{VEHet} + 1}}{\mathit{VEHet}^3}\Bigg\},$$

$$\Bigg\{\mathit{VEHet} = \mathit{VEHet},\ t1 = \frac{1}{\mathit{VEHet}^3\ (3\,\mathit{VEHet} - 1)} \Big(2\,\mathit{VEHet}^3 + 3\,\mathit{VEHet}^2 - 2\,\mathit{VEHet} + 1$$

$$+ \sqrt{4\,\mathit{VEHet}^6 - 7\,\mathit{VEHet}^4 - 4\,\mathit{VEHet}^3 + 10\,\mathit{VEHet}^2 - 4\,\mathit{VEHet} + 1}\Big)\Bigg\},\ \Bigg\{\mathit{VEHet} = \mathit{VEHet},$$

$$t1 = -\frac{1}{\mathit{VEHet}^3\ (3\,\mathit{VEHet} - 1)} \Big(-2\,\mathit{VEHet}^3 - 3\,\mathit{VEHet}^2 + 2\,\mathit{VEHet} - 1$$

$$+ \sqrt{4\,\mathit{VEHet}^6 - 7\,\mathit{VEHet}^4 - 4\,\mathit{VEHet}^3 + 10\,\mathit{VEHet}^2 - 4\,\mathit{VEHet} + 1}\Big)\Bigg\}$$

$$> \ plot\Bigg(-\frac{1}{\mathit{VEHet}^3\ (3\,\mathit{VEHet} - 1)} \Big(-2\,\mathit{VEHet}^3 - 3\,\mathit{VEHet}^2 + 2\,\mathit{VEHet} - 1 + \sqrt{4\,\mathit{VEHet}^6 - 7\,\mathit{VEHet}^4 - 4\,\mathit{VEHet}^3 + 10\,\mathit{VEHet}^2 - 4\,\mathit{VEHet} + 1}\Big),\ \mathit{VEHet} = 0\,..1\Bigg) :$$

```
> #This boundary condition is identical to the boundary that
  seperates biologically relevant and irrelevant boundaries.
```

```
> subs(VEHet = .49, t1 = .6, Eq4EV);
```

$$\begin{bmatrix} 0.6879413467 \\ 0.9978382558 \end{bmatrix} \qquad (137)$$

```
> subs(VEHet = .49, t1 = 0.62, Eq4EV);
```

$$\begin{bmatrix} 0.6901475134 \\ 1.002540850 \end{bmatrix} \qquad (138)$$

```
>
> #The second eignvalue shows the equilibrium is unstable in the
  feasible region.
>
> #We now look for stability boundaries with the second
  eigenvalue.
> solve(abs(Eq4EV[2]) = 1);
```

$$\Bigg\{\mathit{VEHet} = \mathit{VEHet},\ t1 = \frac{1}{\mathit{VEHet}^3\ (3\,\mathit{VEHet} - 1)} \Big(2\,\mathit{VEHet}^3 + 3\,\mathit{VEHet}^2 - 2\,\mathit{VEHet} + 1 \qquad (139)$$

$$+ \sqrt{4\,\mathit{VEHet}^6 - 7\,\mathit{VEHet}^4 - 4\,\mathit{VEHet}^3 + 10\,\mathit{VEHet}^2 - 4\,\mathit{VEHet} + 1}\Big)\Bigg\},\ \Bigg\{\mathit{VEHet} = \mathit{VEHet},$$

$$t1 = -\frac{1}{VEHet^{3}\,(3\,VEHet - 1)}\Big(-2\,VEHet^{3} - 3\,VEHet^{2} + 2\,VEHet - 1 + \sqrt{4\,VEHet^{6} - 7\,VEHet^{4} - 4\,VEHet^{3} + 10\,VEHet^{2} - 4\,VEHet + 1}\Big)\Big\}, \{VEHet = 1, t1 = t1\}, \Big\{VEHet = VEHet, t1 = \frac{2\,VEHet^{2} + VEHet - 1 + \sqrt{-4\,VEHet^{4} + 8\,VEHet^{3} - 3\,VEHet^{2} - 2\,VEHet + 1}}{VEHet^{3}}\Big\},$$

$$\Big\{VEHet = VEHet, t1 = -\frac{-2\,VEHet^{2} - VEHet + 1 + \sqrt{-4\,VEHet^{4} + 8\,VEHet^{3} - 3\,VEHet^{2} - 2\,VEHet + 1}}{VEHet^{3}}\Big\}$$

```
> #No additional boundary conditions.
>
> #Eigenvalue[2] is greater than 1 for biologically feasible
  parameter space.
> subs(VEHet=1, t1=t1, Eq4EV[2]);
```

$$-\frac{1}{2}\,\frac{-t1 + 2 + \sqrt{t1^{2} - 4\,t1 + 4}}{-2 + t1} \qquad \textbf{(140)}$$

```
> #Eigenvalue[2] is equal to 1 when VEHet=1, therefore linear
  analysis is inconclusive
> #When VEHet≠1, and the equilibrium exists, it is unstable.
>
```

```
> #Ward, Catherine
> #Supplemental Materials: Calculations for feasibility and
  stability of X-linked Medeas
>

> We load the model and calculate equilibria and the eigenvalues
  of the Jacobian.
>
>
>
> #clear memory and initialize packages
> restart : clear : with(LinearAlgebra) : with(SolveTools) :

> #The following equations are for each genotype in the next
  generation
> #We begin by defining intermediate quantities.
> #The naming convention is slightly different in this file.  W is
  still the divisor, but genotypes are now instead of using SM+,
  S++, DMM, DM+, and D++, we use HetM, WTM, HomoF, HetF, and WTF.
  Note that F at the end means female while M indicates male.  All
  fitnesses are embryonic and we simply use V and V^2.
> W := ((1/4) * HetF * (HetM + WTM) + (1/2) * HomoF * (WTM + HetM)) * V + ((1/2)
      * WTF * WTM + (1/2) * WTF * HetM) + (HetF * HetM * (1/4) + HomoF * HetM * (1
      /2)) * V * V + (WTF * HetM * (1/2) + HetF * WTM * (1/4) + HetF * HetM * (1/4)
      + HomoF * WTM * (1/2)) * V + (1/2) * WTF * WTM :
> #Now make non-Medea (wildtype) females
> nextWTF := subs(HetM = 1 - WTF - HetF - HomoF - WTM, (1/2) * WTF * WTM / W) :
> #Now all genotypes
> nextHetF := subs(HetM = 1 - WTF - HetF - HomoF - WTM, (WTF * HetM * (1/2) + HetF
      * WTM * (1/4) + HetF * HetM * (1/4) + HomoF * WTM * (1/2)) * V / W) :
> nextHomoF := subs(HetM = 1 - WTF - HetF - HomoF - WTM, (HetF * HetM * (1/4) + HomoF
      * HetM * (1/2)) * V * V / W) :
> nextWTM := subs(HetM = 1 - WTF - HetF - HomoF - WTM, ((1/2) * WTF * WTM + (1/2)
      * WTF * HetM) / W) :
> nextHetM := subs(HetM = 1 - WTF - HetF - HomoF - WTM, ((1/4) * HetF + (1/2) * HomoF)
      * (WTM + HetM) * V / W) :

> #Solve for all the equilibria (takes about 30 secs on a PC with
  2 gigs of RAM)
> equilibria := solve({nextHomoF = HomoF, nextHetF = HetF, nextWTF = WTF, nextWTM
      = WTM}, [HomoF, HetF, WTF, WTM]) :
> equilibria[1];
                                                                          (1)
```

$$\left[HomoF=\frac{V}{1+V},\ HetF=0,\ WTF=0,\ WTM=0\right] \qquad (1)$$

```
>
```

```
> equilibria[2];
```

$$\left[HomoF=-\frac{V}{V-2},\ HetF=\frac{2\,V-1}{V-2},\ WTF=0,\ WTM=0\right] \qquad (2)$$

```
> #Note that when V>.5, HetF is negative (biologially infeasible).
```

```
> equilibria[3];
```

$$\left[HomoF=0,\ HetF=0,\ WTF=\frac{1}{2},\ WTM=\frac{1}{2}\right] \qquad (3)$$

```
> #Warning: this equilibrium takes a few seconds to load (PC with
  2 gigs of RAM).  Output is supressed because expressions for the
  equilibrium fill about 200 pages of output.
> allvalues(equilibria[4]) :
>
> #Now we move on to stability.  Recall that if the modulus of any
  the eigenvalues of the Jacobian evaluated at a particular
  equilibrium is greater than 1, the equilibrium is unstable.
> #Calculate the Jacobian Matrix
> MyMatrix := Matrix([[diff(nextWTF, WTF), diff(nextWTF, HetF), diff(nextWTF, HomoF),
     diff(nextWTF, WTM)], [diff(nextHetF, WTF), diff(nextHetF, HetF), diff(nextHetF,
    HomoF), diff(nextHetF, WTM)], [diff(nextHomoF, WTF), diff(nextHomoF, HetF),
     diff(nextHomoF, HomoF), diff(nextHomoF, WTM)], [diff(nextWTM, WTF),
     diff(nextWTM, HetF), diff(nextWTM, HomoF), diff(nextWTM, WTM)]]) :
```

```
> #Check stability of Medea Homozygote only equilibria
> MyMatrix1 := Eigenvalues(subs(equilibria[1], MyMatrix));
```

$$MyMatrix1 := \begin{bmatrix} 0 \\ 0 \\ 0 \\ \frac{1}{2\,V} \end{bmatrix} \qquad (4)$$

```
> #When V<.5, this eqilibrium is unstable.  When V>.5, it is
  stable.
```

```
> #Check stability of no non-Medea (has hets and homozygotes)
> MyMatrix2 := Eigenvalues(subs(equilibria[2], MyMatrix));
```

(5)

$$MyMatrix2 := \begin{bmatrix} 0 \\ 0 \\ 0 \\ 2\,V \end{bmatrix} \tag{5}$$

```
> #When V is less than 0.5, this equilibrium is stable.  It is not
  biologically feasible V>.5.
```

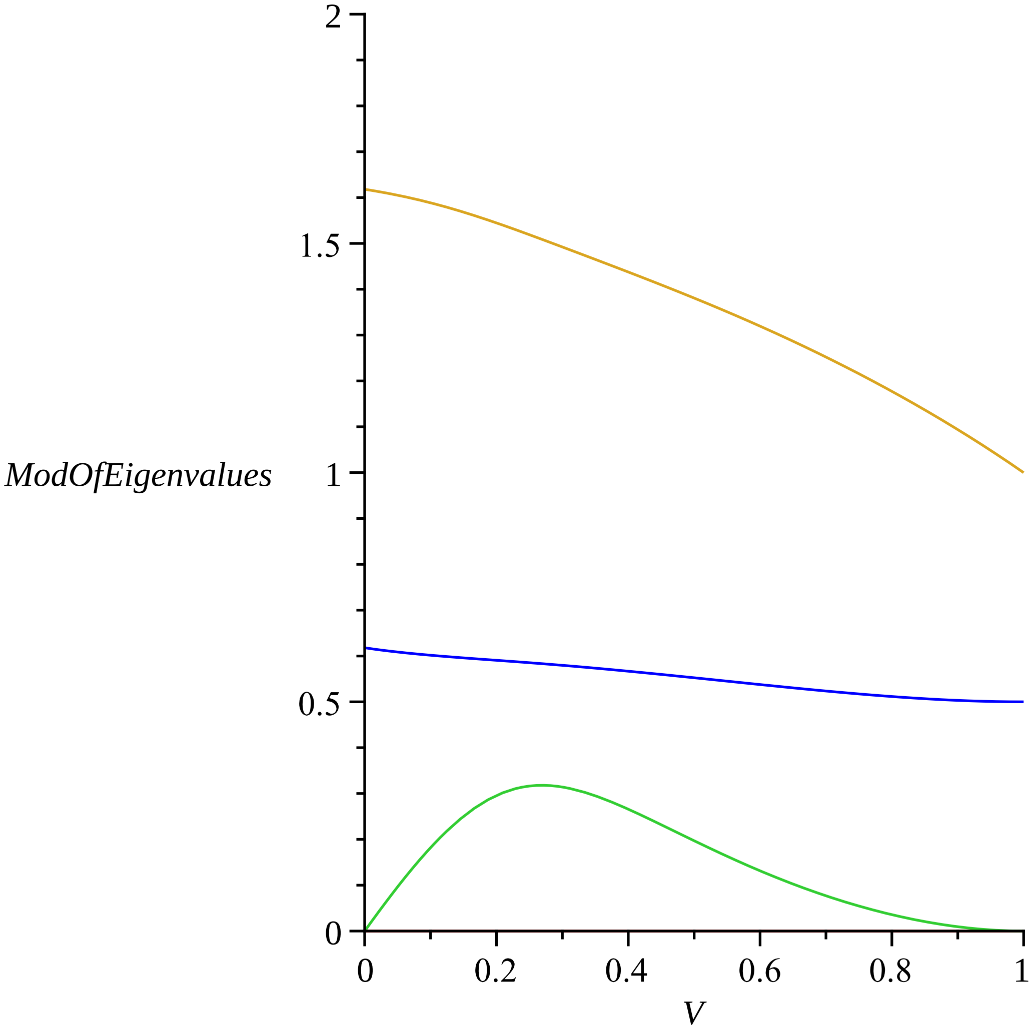
```
> #Check the stability of the all non-Medea equilibria
> MyMatrix3 := Eigenvalues(subs(equilibria[3], MyMatrix));
```

$$MyMatrix3 := \begin{bmatrix} 0 \\ 0 \\ -\frac{1}{2}\,V \\ V \end{bmatrix} \tag{6}$$

```
> #The equilibria is stable except at V=1 where the analysis is
  inconclusive.
```

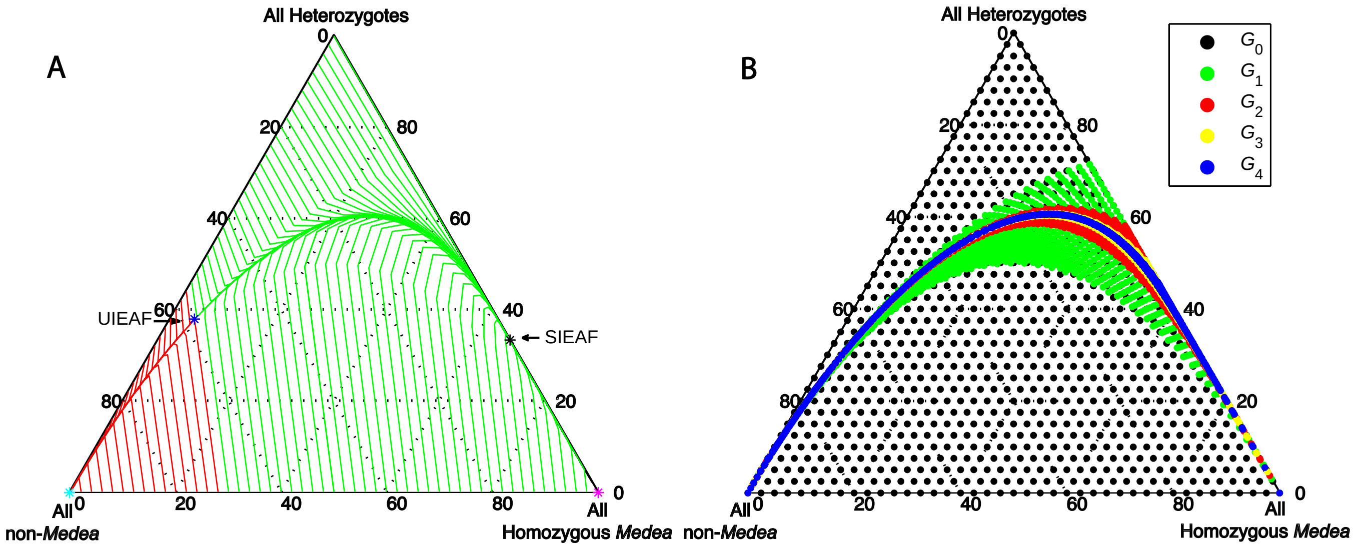
```
> #Checks the stability of the all non-Medea equilibria
> #Warning: this calculation takes a 5-10 mins on a PC with 2 gigs
  of RAM.  Output is suppressed because the expressions have
  several pages worth of terms.
>
> MyMatrix4 := Eigenvalues(subs(equilibria[4], MyMatrix)) :
```

```
> #  Instead of solving for the modulus=1, we plot each modulus of
  the 4 eigenvalues for the all non-Medea equilibrium.  Only three
  appear on the graph because the modulus of one of the
  eigenvalues is 0 for all values of V.  Recall that if any
  eigenvalue is greater than 1, the equilibrium is unstable.
> plot({abs(MyMatrix4[1]), abs(MyMatrix4[2]), abs(MyMatrix4[3]), abs(MyMatrix4[4])}, V
      = 0 ..1, ModOfEigenvalues = 0 ..2);
```



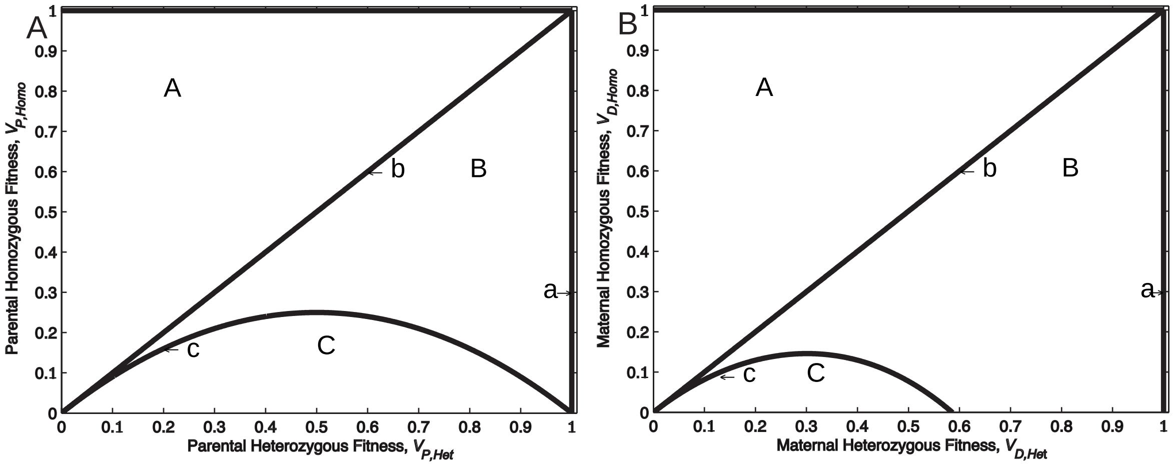
```
> #Because the modulus of one of the eigenvalues is greater than 1
  for all values of V, except V=1, the equilibrium is unstable.
>
```

Figure S1



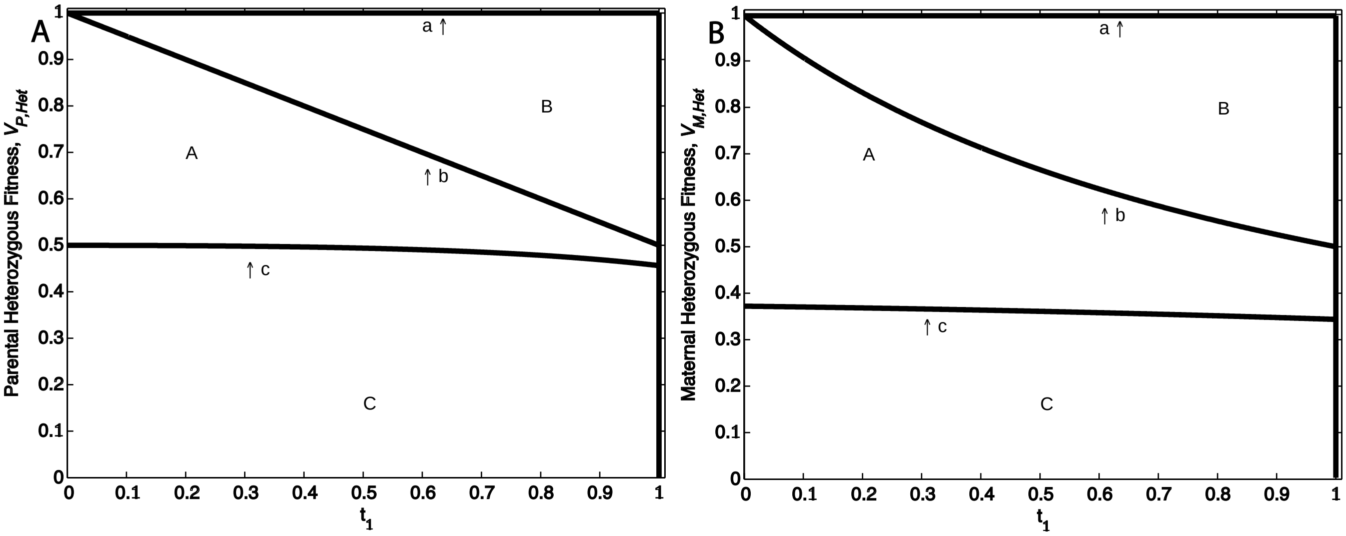
DeFinetti diagrams showing genotype trajectories for a *Medea* with a fitness cost. (A) The DeFinetti diagram plots the change in genotype frequencies over generations for a *Medea* with a 20% embryonic, multiplicative fitness cost, and values of t_1=0 and t_1=1. Population trajectories start with different ratios of two of the three genotypes (genotypes corresponding to points along each of the sides of the triangle). Green lines show trajectories that end at 2/3 *Medea* homozygotes, 1/3 *Medea* heterozygotes and no non-*Medea* individuals, the SIEAF (the stable internal equilibrium allele frequency). Red lines indicate population trajectories that end with loss of *Medea* individuals from the population. The unstable internal equilibrium frequency (UIEAF) is a point on the common trajectory taken by *Medea*-bearing populations that separates populations in which *Medea* spreads from those in which *Medea* is lost. (B) Plot of genotype frequencies over four generations for the *Medea* allele in (A), introduced into a population at a number of different starting genotype frequencies (black circles). When adults from within the G_0 genotype distributions (each of the black circles) mate randomly with each other, a range of possible G_1 genotype distributions, indicated by the green region, is obtained. When adults from G_1 genotype distributions mate randomly, a set of possible G_2 offspring genotype distributions defined by the red region is obtained; matings within each G_2 genotype distribution result in the set of possible G_3 offspring distributions defined by the yellow region; and G_3 matings result in the G_4 (blue) distribution. The G_4 distribution, which is highly constrained, can be used to approximate genotype frequencies and allele fitness for specific *Medea* allele frequencies.

Figure S2



Diagrams partitioning (V_{Het} , V_{Homo}) fitness parameter space into regions in which linear stability analysis indicates qualitatively similar behaviors are observed. (A) Parameter space diagram of ($V_{P,Het}$, $V_{P,Homo}$) space (this diagram is identical for a *Medea* with embryonic fitness cost) . Qualitative behavior changes as each curve is crossed, with the occurrence of a bifurcation. Equilibrium 1, which consists of only the non-*Medea* genotype, is stable in all regions except at line a where the analysis is inconclusive. Equilibrium 2, which consists of all genotypes, is unstable in regions A and B and infeasible in C. Equilibrium 3, which consists of heterozygous and homozygous *Medea*, is infeasible in A, stable in B and unstable in C. Equilibrium 4, which consists of only the homozygous Medea genotype, is stable in A and unstable in B and C. Line a corresponds to a region in which Equilibrium 1 and 2 are coincident. Line b separates regions A and B. On this line, Equilibrium 3 and 4 are coincident. Transcritical bifurcation occurs as Equilibrium 3 moves through Equilibrium 4 (i.e. the two collide), with the two equilibria exchanging stability. Curve c separates regions B and C. On this curve, Equilibrium 2 and 3 are coincident. Transcritical bifurcation occurs as the two equilibria collide, with the two equilibria exchanging stability. (B) Parameter space diagram of ($V_{D,Het}$, $V_{D,Homo}$) space. Explanations are as in (A).

Figure S3



(A) Diagram partitioning (t_1, $V_{P,Het}$) parameter space into regions in which linear stability analysis indicates qualitatively similar behaviors are observed. Qualitative behavior changes as we cross each of these curves, with the occurrence of a bifurcation. Black lines partition parameter space for *Medea* elements with a parental fitness costs. Equilibrium 1, which consists of only the non-*Medea* genotype, is stable in all regions. Equilibrium 2, which consists of all genotypes, is unstable in regions A and B and infeasible in C. Equilibrium 3, which consists of heterozygous and homozygous *Medea* genotypes, is infeasible in C, stable in A and unstable in B. Equilibrium 4, which consists of only the homozygous Medea genotype, is stable in B and unstable in A and C. Line a corresponds to a Medea with no fitness cost. At line a, the stability of equilibrium 1, the all non-Medea equilibrium, is inconclusive. Line b separates regions A and B. On this line, Equilibrium 3 and 4 are coincident. Transcritical bifurcation occurs as Equilibrium 3 moves through Equilibrium 4 (i.e. the two collide), with the two equilibria exchanging stability. Curve c separates regions A and C. On this curve, the Equilibrium 2 and 3 are coincident. (B) As in (A) except fitness costs are maternal.