

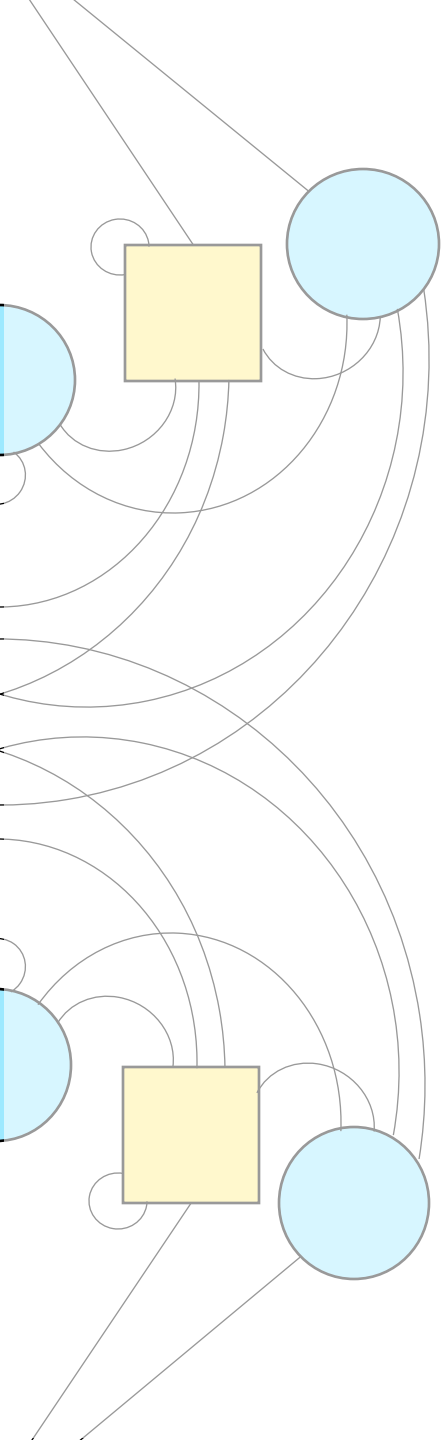
Estimating Parental Effects using Polygenic Scores Part II: Model Extensions

Jared V. Balbona | Yongkang Kim | Matthew C. Keller

Outline of this video:

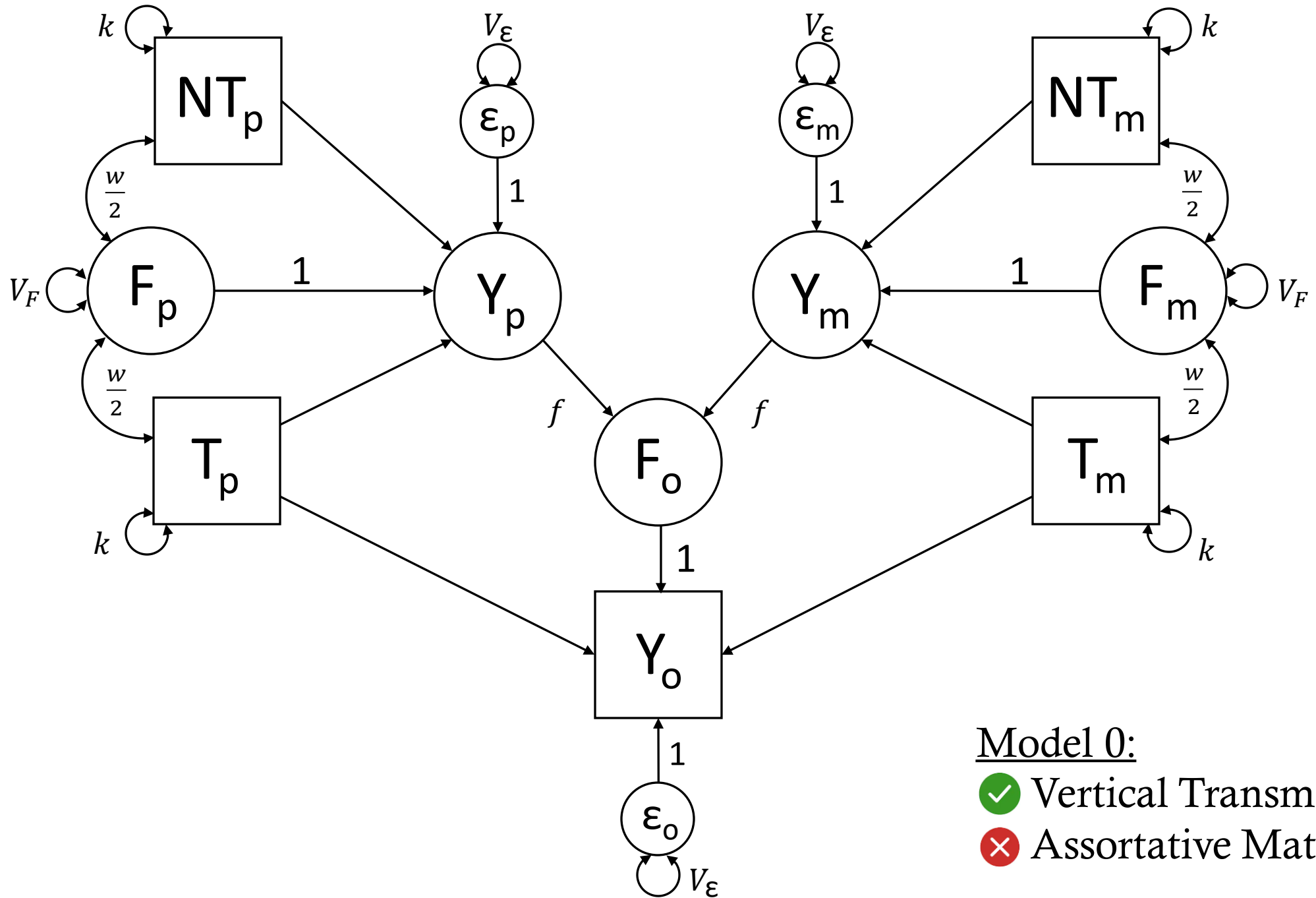
- How SEM-PGS models can detect and estimate different types of assortative mating
 - Disequilibrium vs. Equilibrium
 - Phenotypic, Social, and Genetic Homogamy
- Using latent genetic factors to capture full additive genetic effects
- Other model extensions
 - Different data types that can be leveraged
 - Different questions that can be addressed

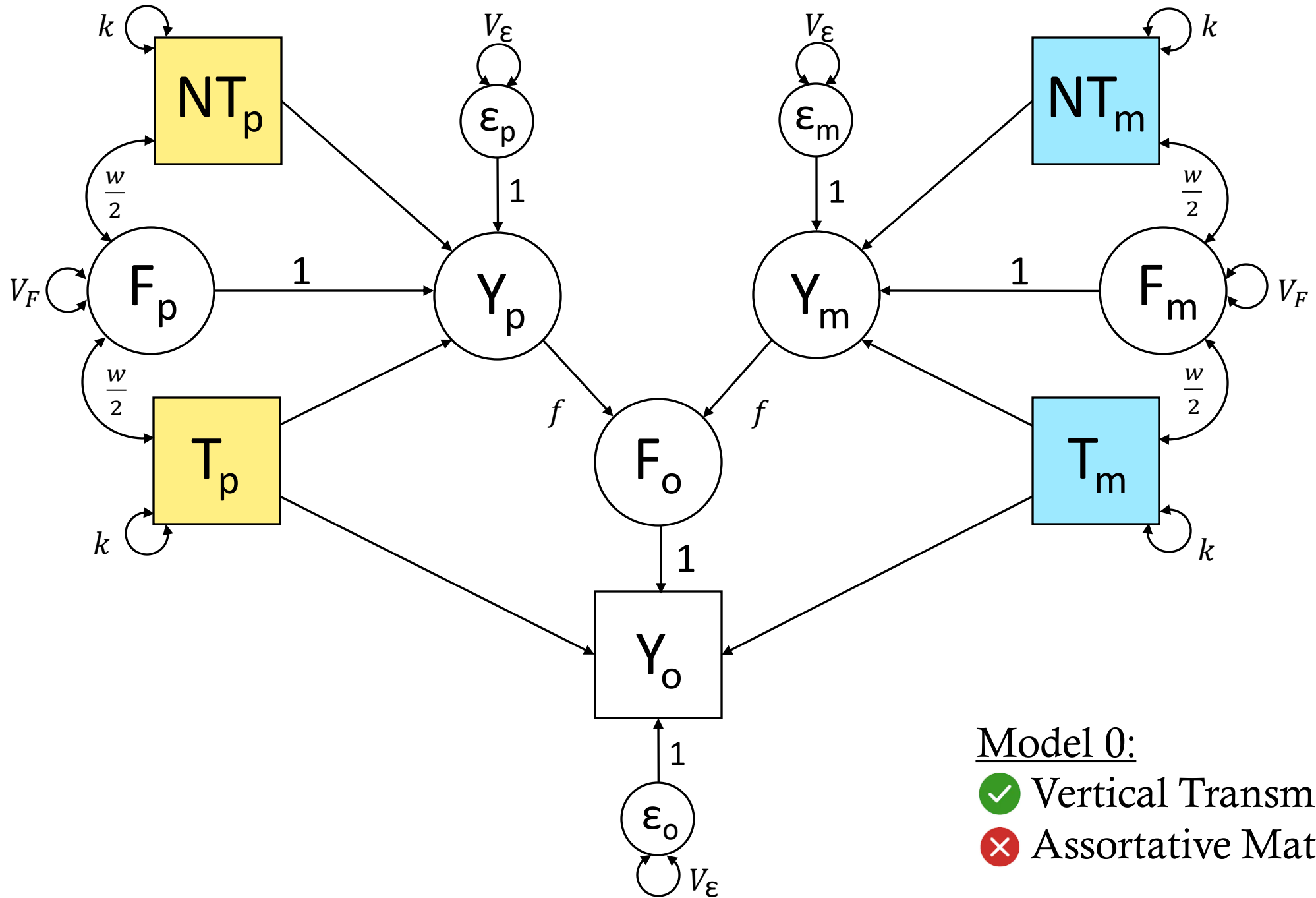
Accounting for Assortative Mating

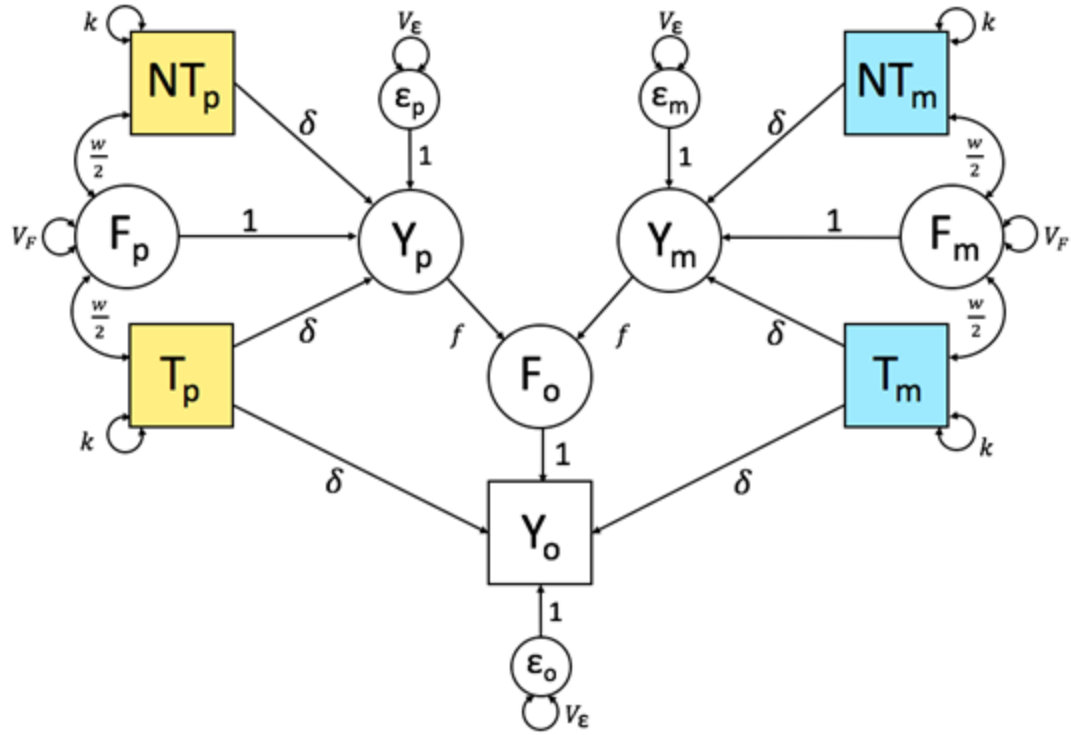


Importance of Assortative Mating

- Assortment is interesting in its own right!
 - Informs about a given population's culture, priorities, and preferences
- Assortment can impact genetic architecture
 - Assortative mating can lead to increases in:
 1. Correlations between trait-increasing alleles
 - *AKA "Gametic Phase Disequilibrium"*
 2. Genetic correlations between traits
 3. Homozygosity
 4. Genetic correlations between relatives
 5. Population phenotypic and genotypic variance







Offspring's Genome

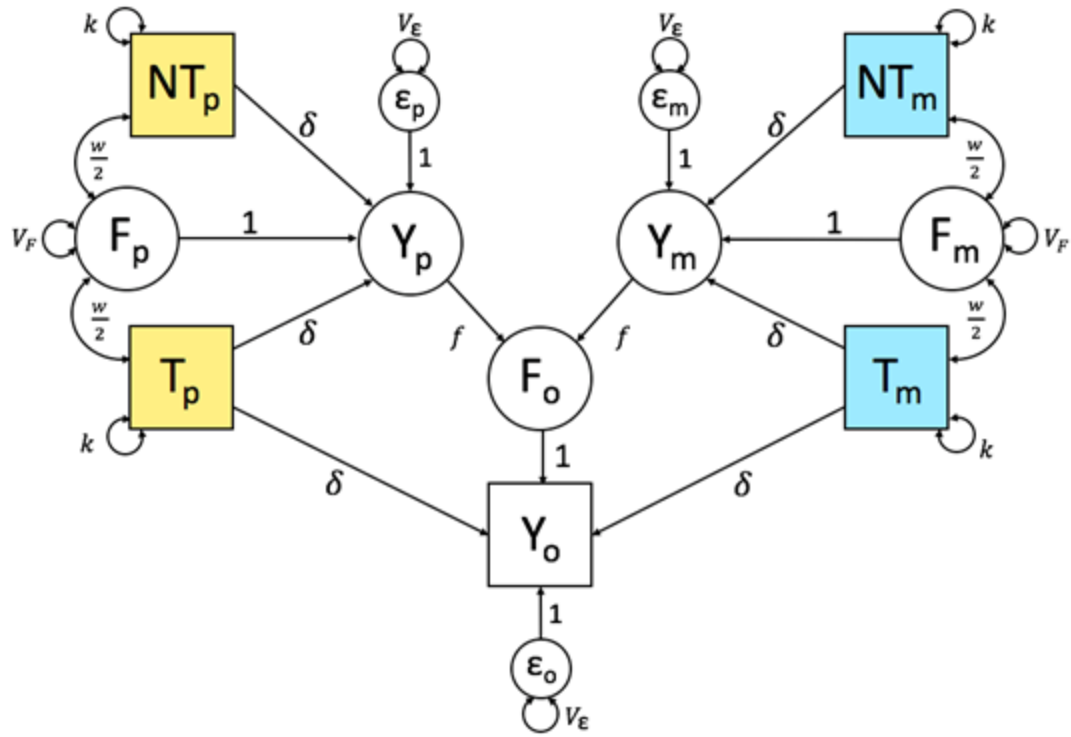
NT_p

NT_M

T_P

T_M

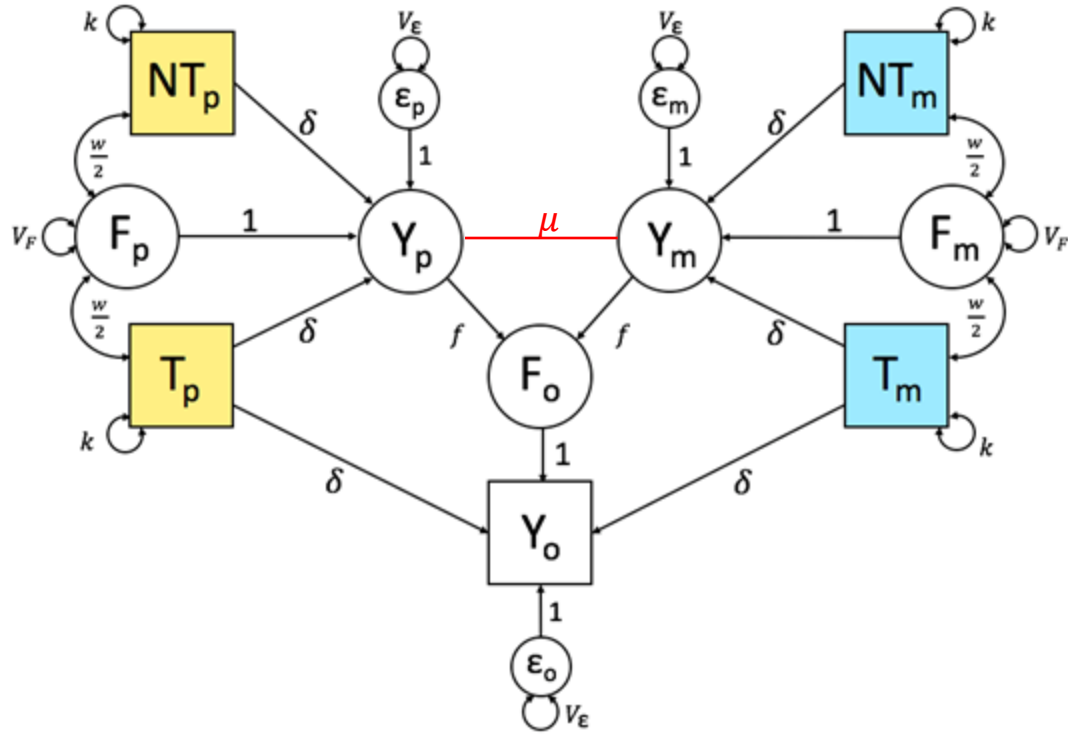
No Assortment



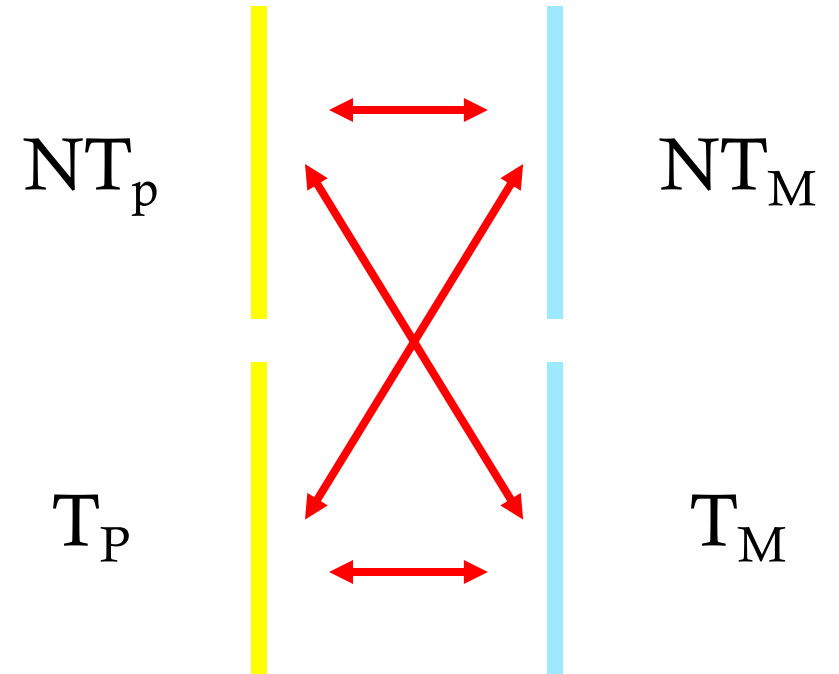
	T_p	NT_p	T_m	NT_m
T_p	k	0	0	0
NT_p		k	0	0
T_m			k	0
NT_m				k

No Assortment

$$\mu = \frac{\text{Spousal Phenotypic Covariance}}{(\text{Spouse Phenotypic Variance})^2}$$

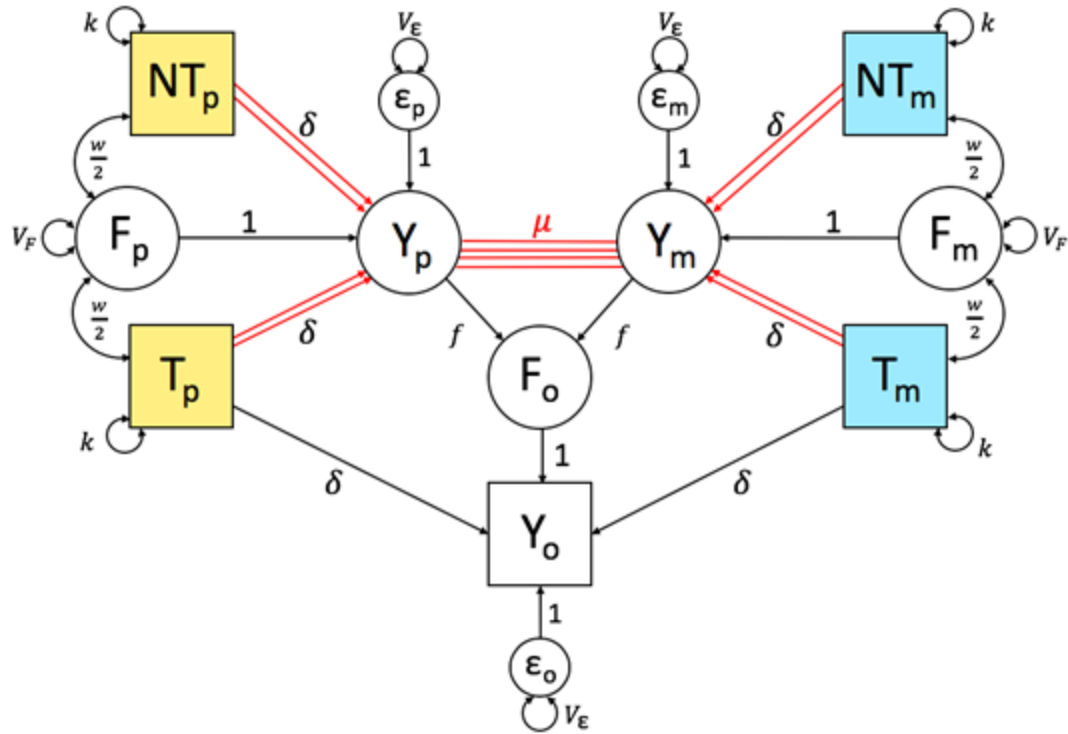


Offspring's Genome

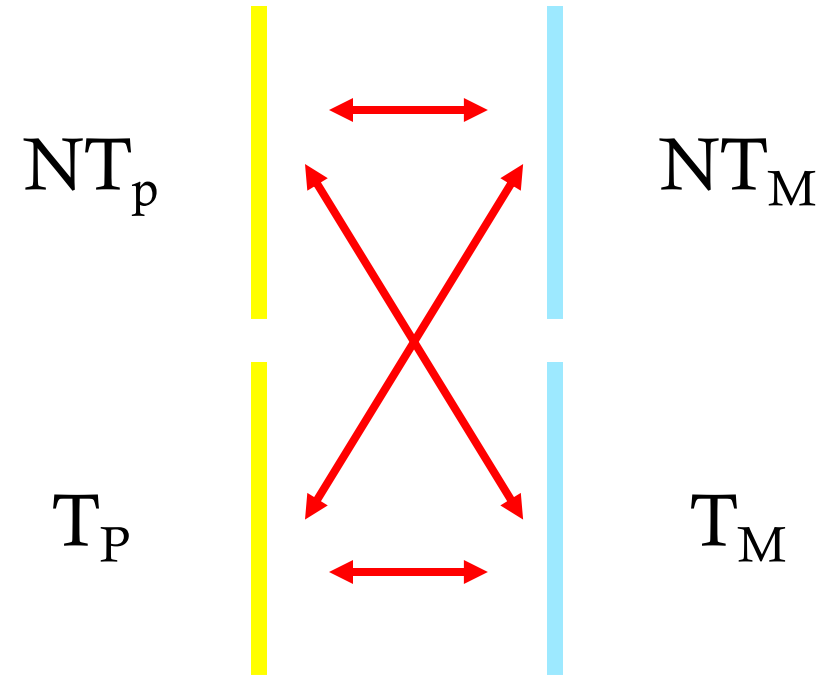


1 Generation of Assortment

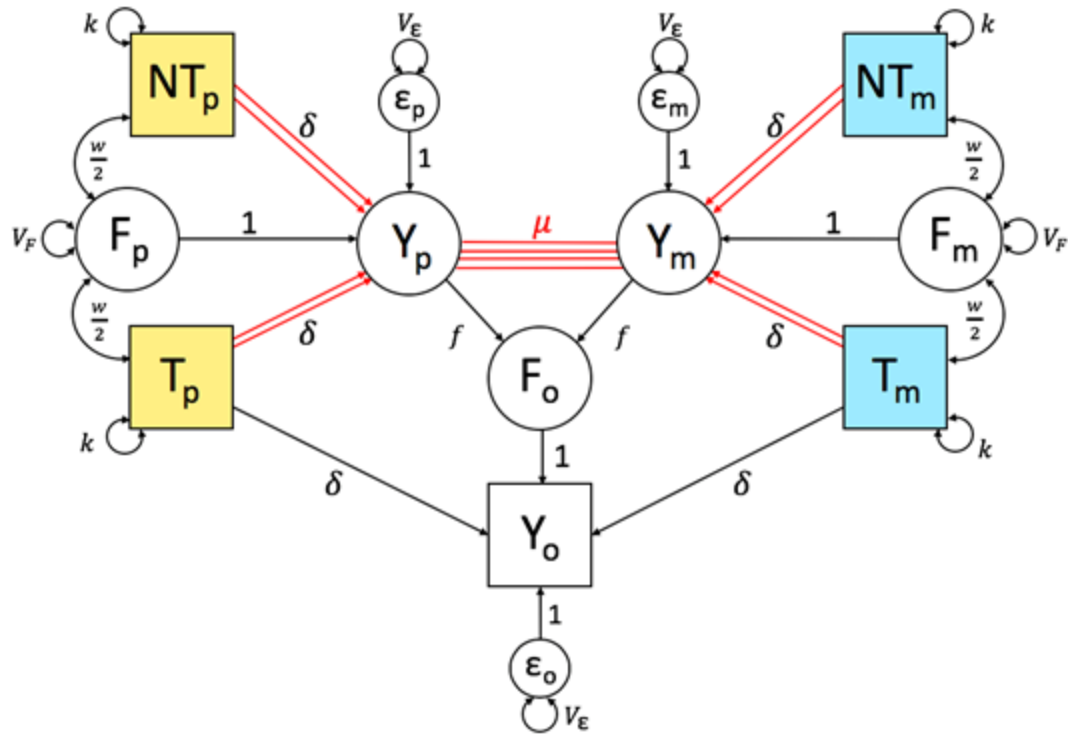
$$\mu = \frac{\text{Spousal Phenotypic Covariance}}{(\text{Spouse Phenotypic Variance})^2}$$



Offspring's Genome

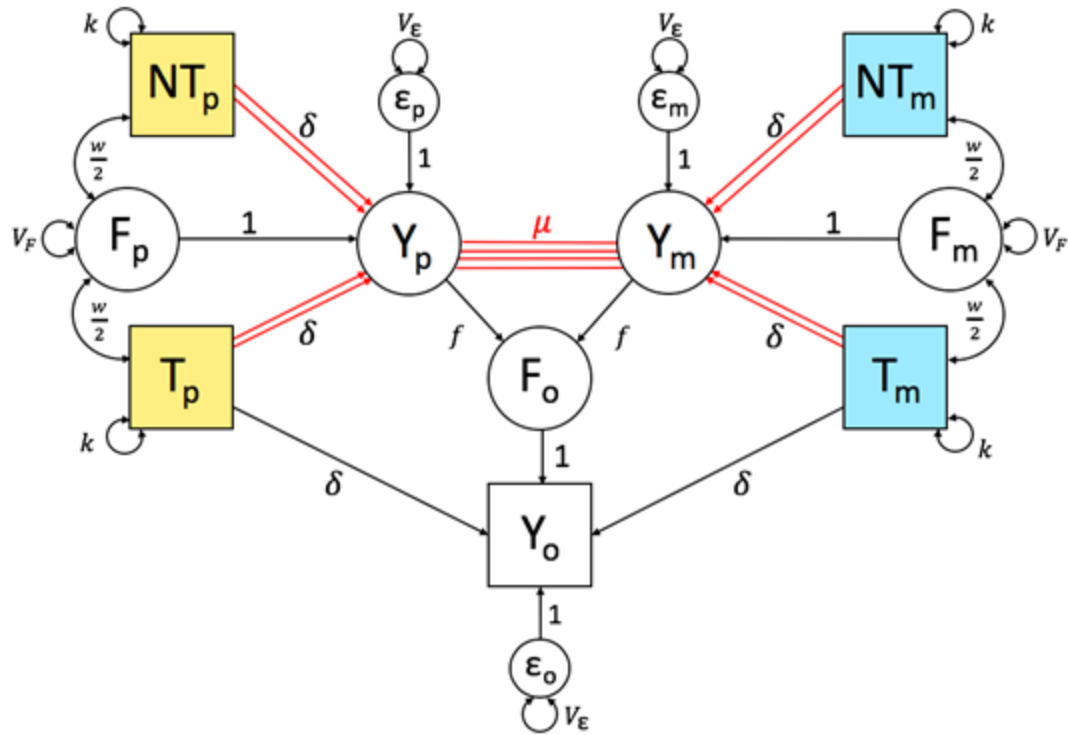


1 Generation of Assortment



	T_p	NT_p	T_m	NT_m
T_p	k	0	0	0
NT_p		k	0	0
T_m			k	0
NT_m				k

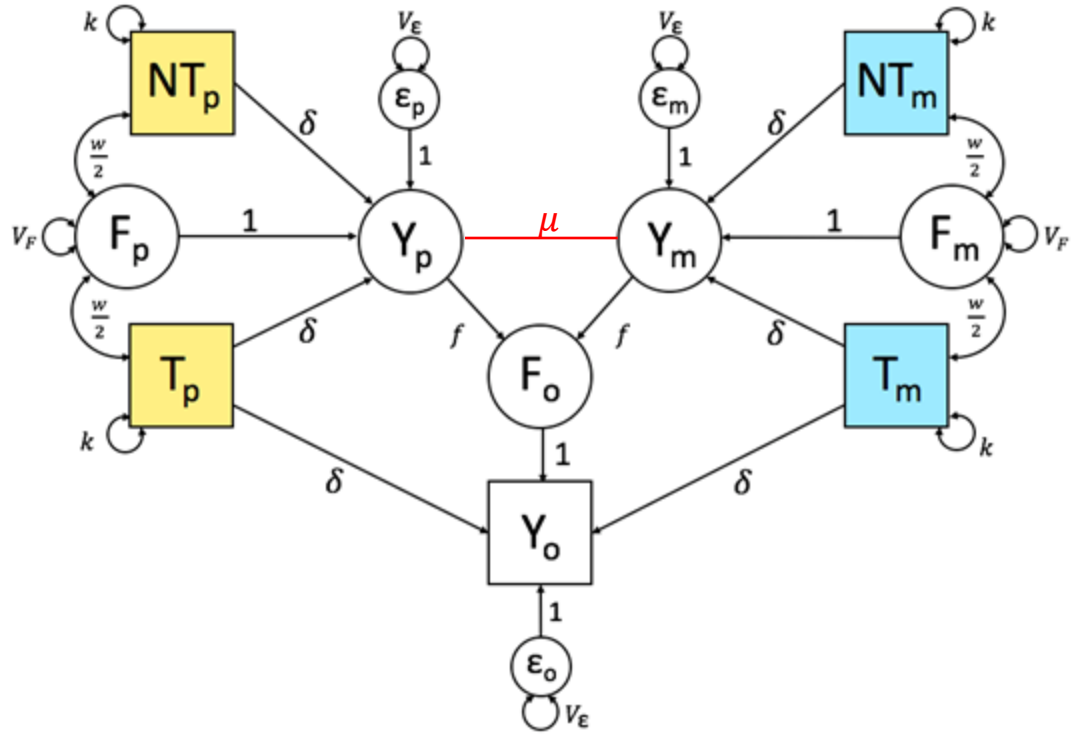
1 Generation of Assortment



g : Increase in PGS covariances due to AM

	T_p	NT_p	T_m	NT_m
T_p	k	0	g	g
NT_p		k	g	g
T_m			k	0
NT_m				k

1 Generation of Assortment

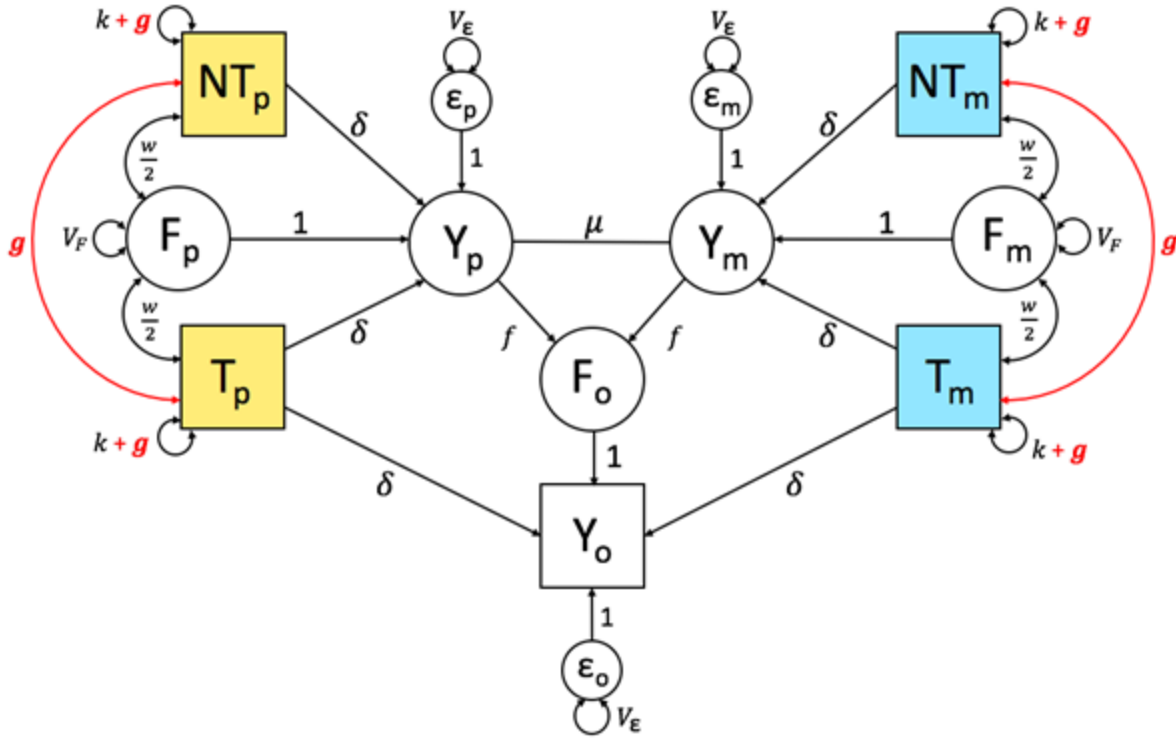


g : Increase in PGS covariances due to AM

	T_p	NT_p	T_m	NT_m
T_p	k	0	g	g
NT_p		k	g	g
T_m			k	0
NT_m				k

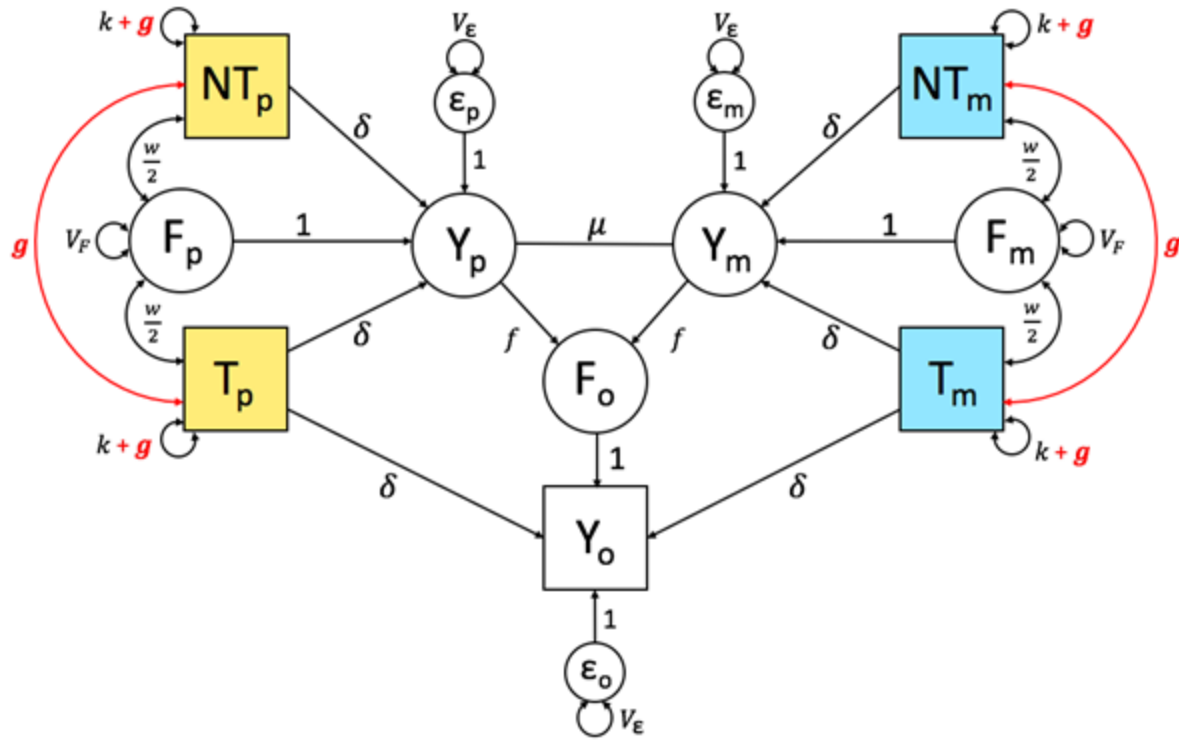
>1 Generation of Assortment

g : Increase in PGS (co)variances due to AM

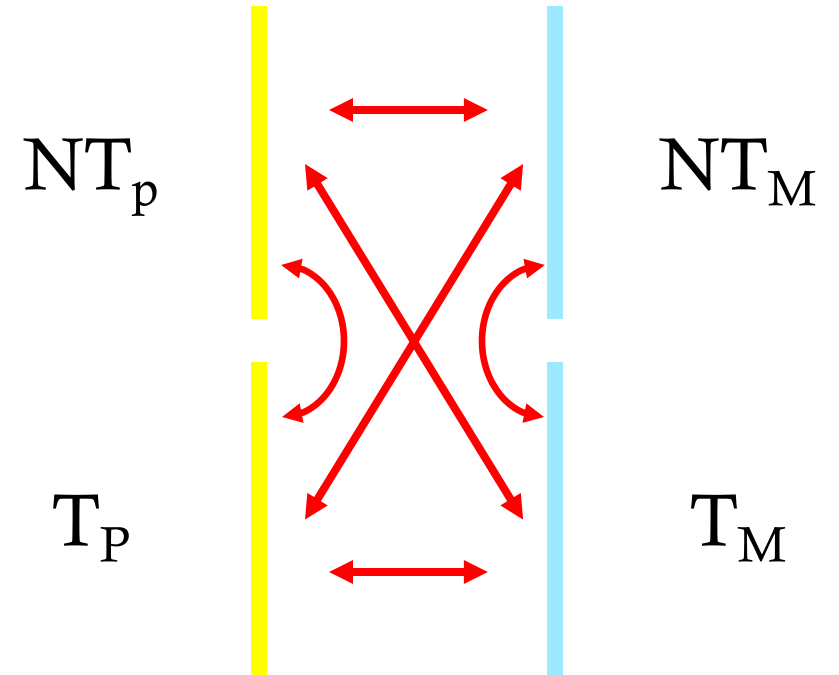


	T_p	NT_p	T_m	NT_m
T_p	$k + g$	g	g	g
NT_p		$k + g$	g	g
T_m			$k + g$	g
NT_m				$k + g$

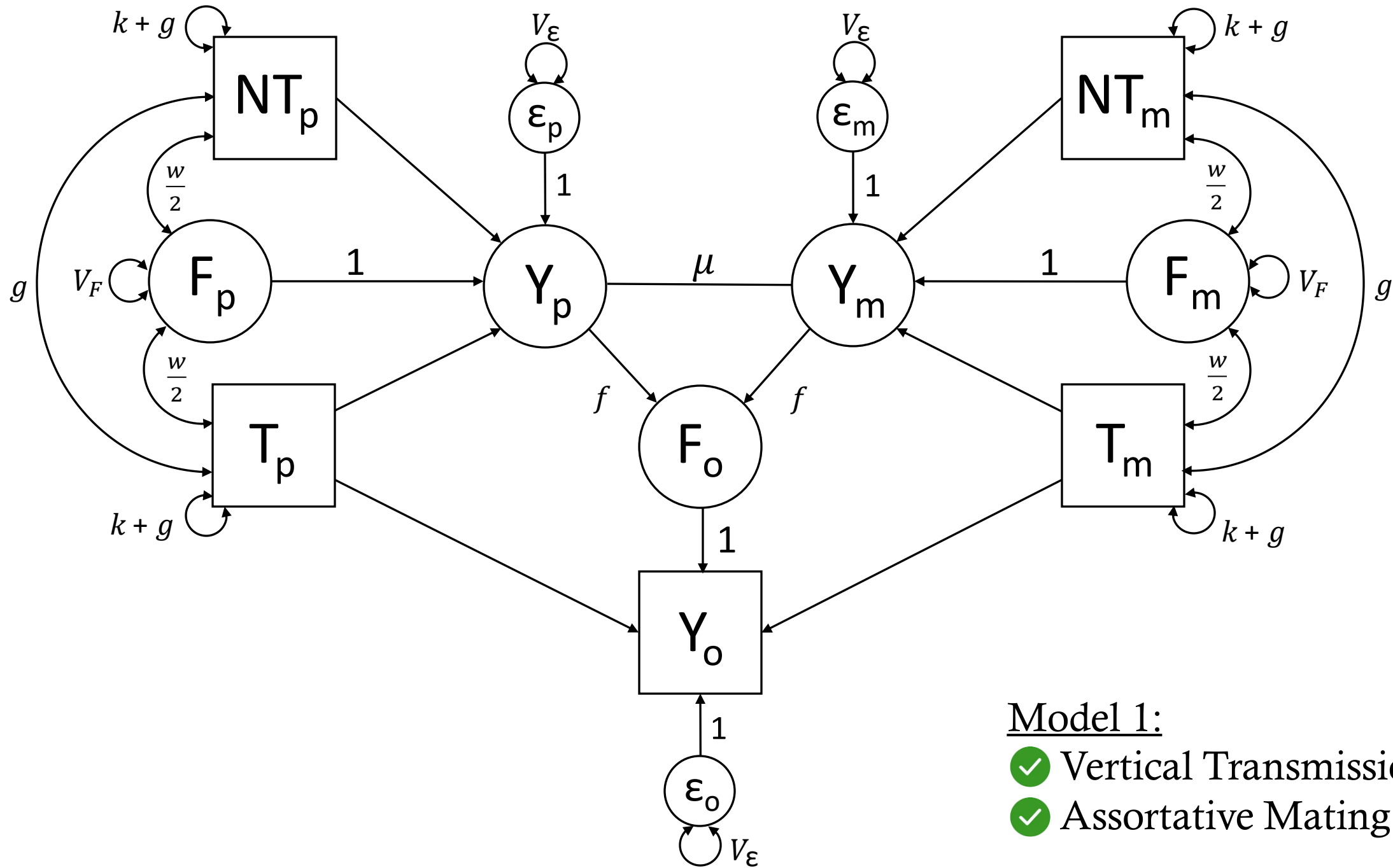
>1 Generation of Assortment



Offspring's Genome

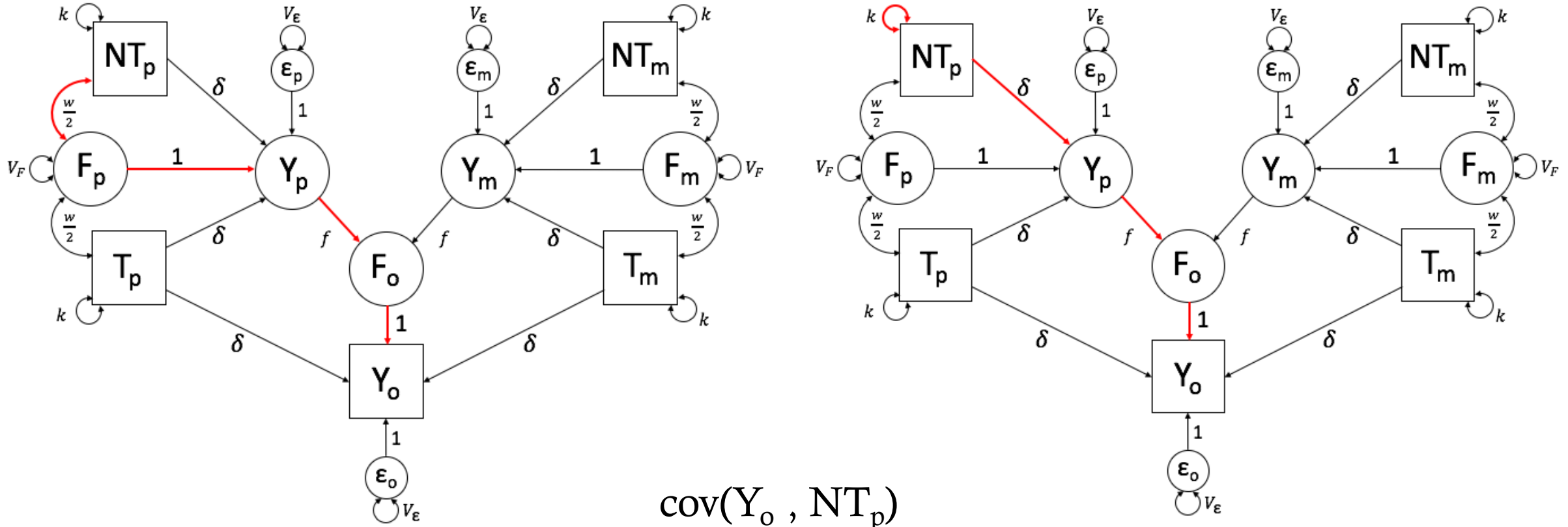


>1 Generation of Assortment



Model 0:

- ✓ Vertical Transmission,
- ✗ Assortative Mating



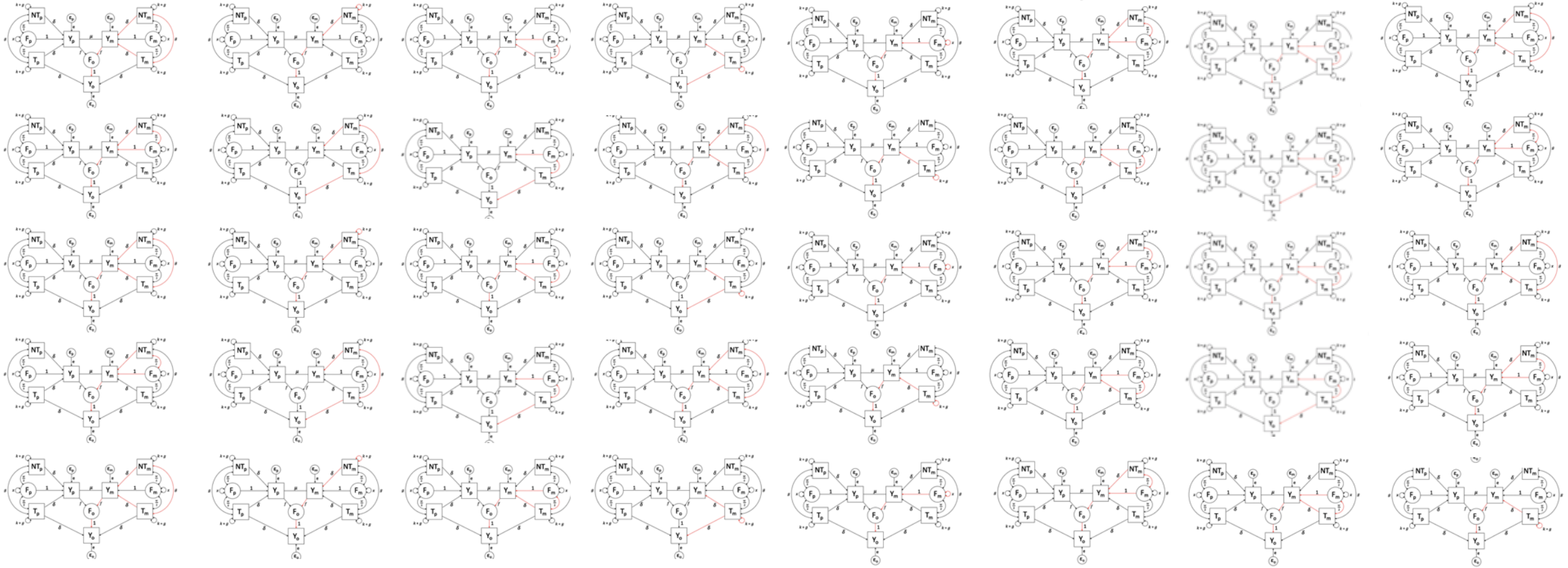
$$\text{cov}(Y_o, NT_p)$$

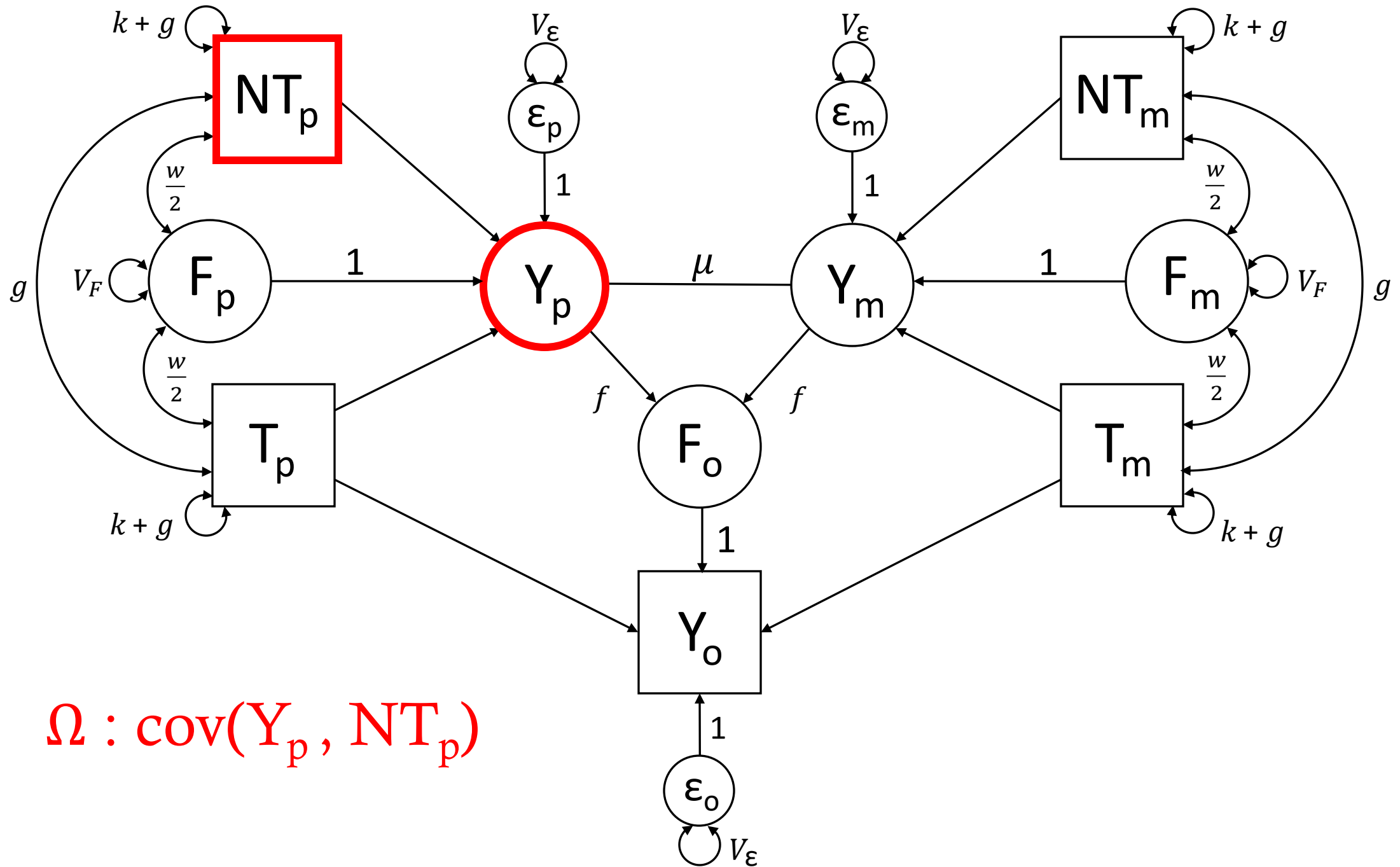
$$= \left(1 * f * 1 * \frac{w}{2} \right) + \left(1 * f * \delta * k \right)$$

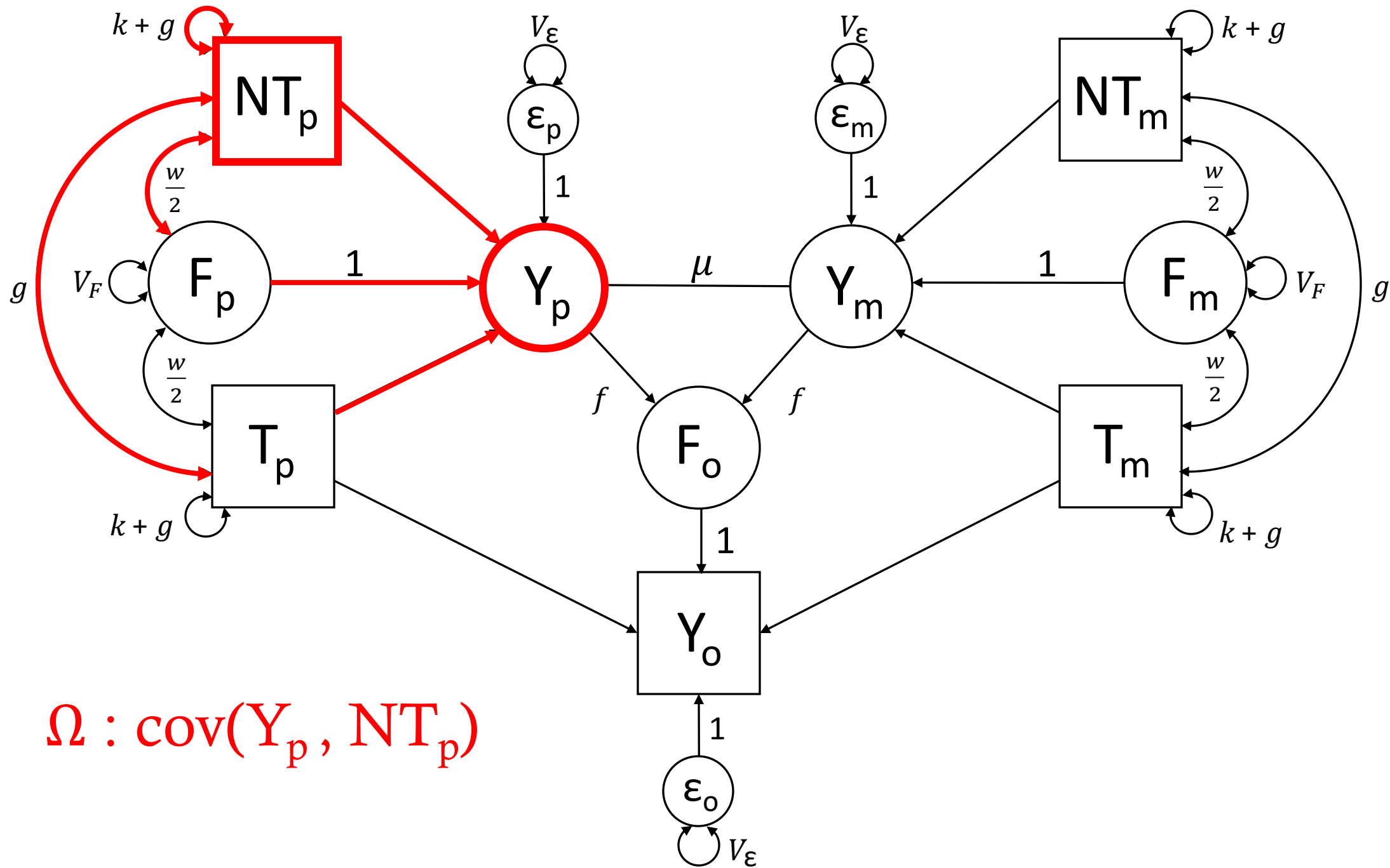
$$= \frac{1}{2}fw + f\delta k$$

Model 1:

- ✓ Vertical Transmission,
- ✓ Assortative Mating

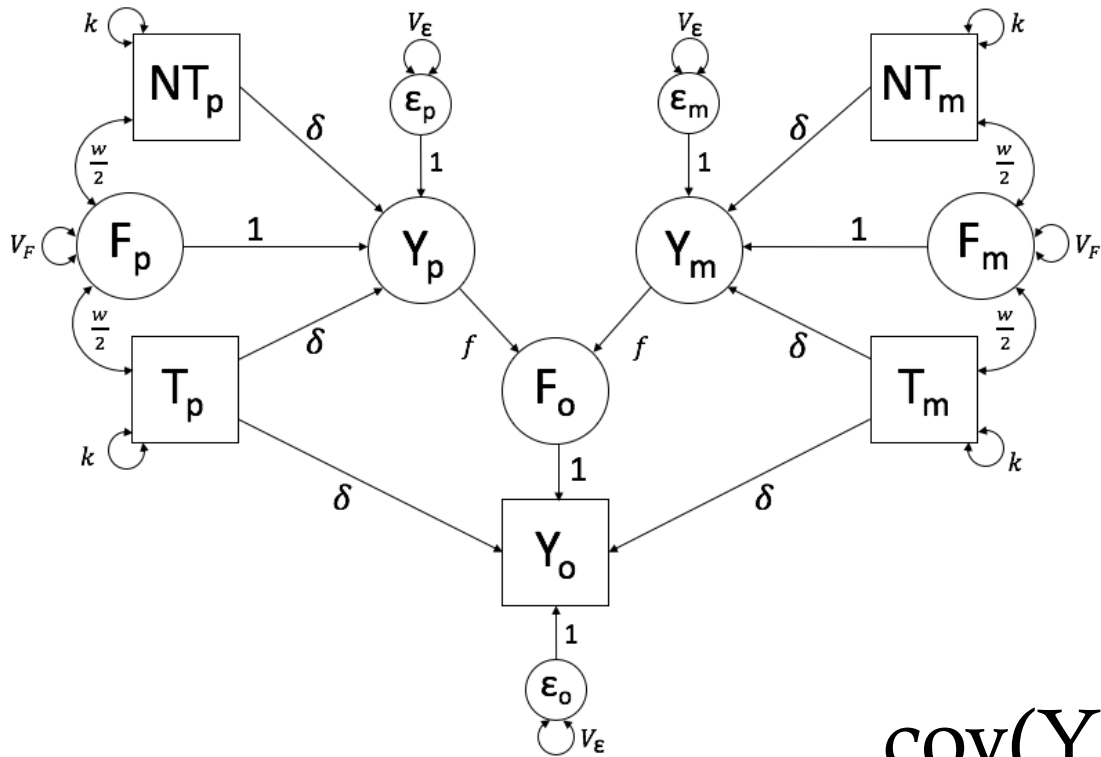






Model 0:

- ✓ Vertical Transmission,
- ✗ Assortative Mating



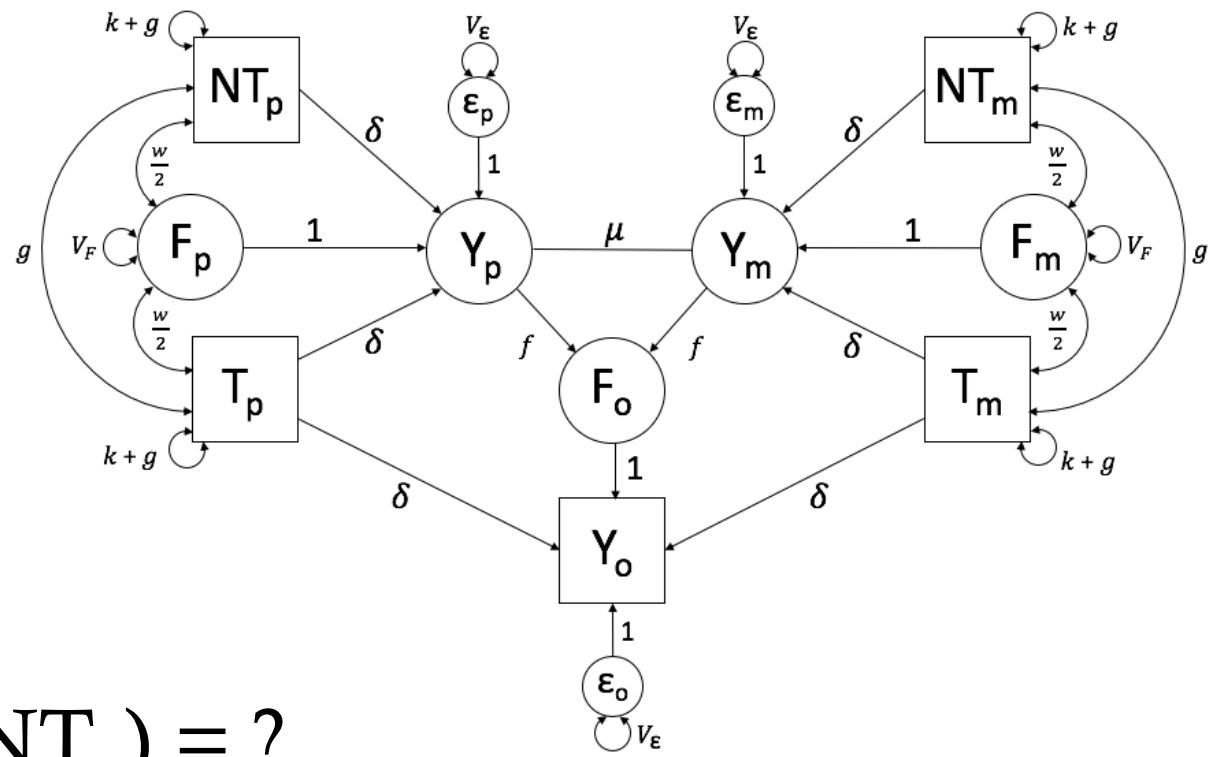
$$= f\left(\frac{w}{2} + \delta k\right)$$

$$= f\Omega$$

$$\text{cov}(Y_o, NT_p) = ?$$

Model 1:

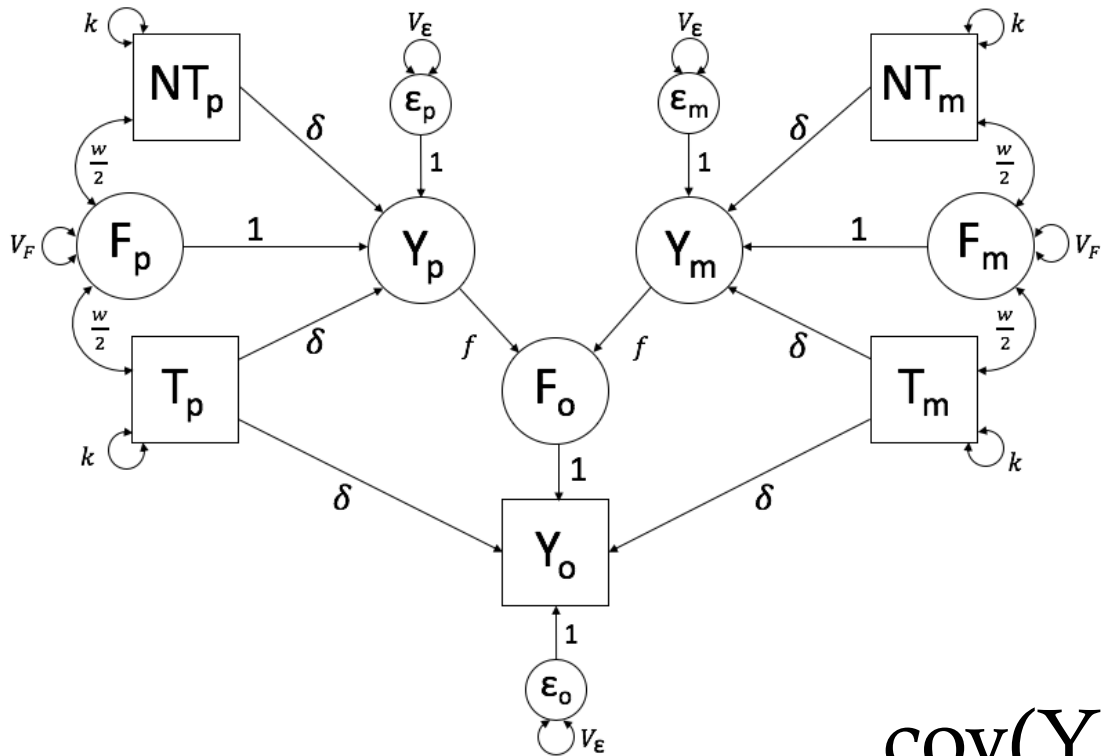
- ✓ Vertical Transmission,
- ✓ Assortative Mating



$$= f\Omega(1 + V_y\mu) + 2\delta g$$

Model 0:

- ✓ Vertical Transmission,
- ✗ Assortative Mating



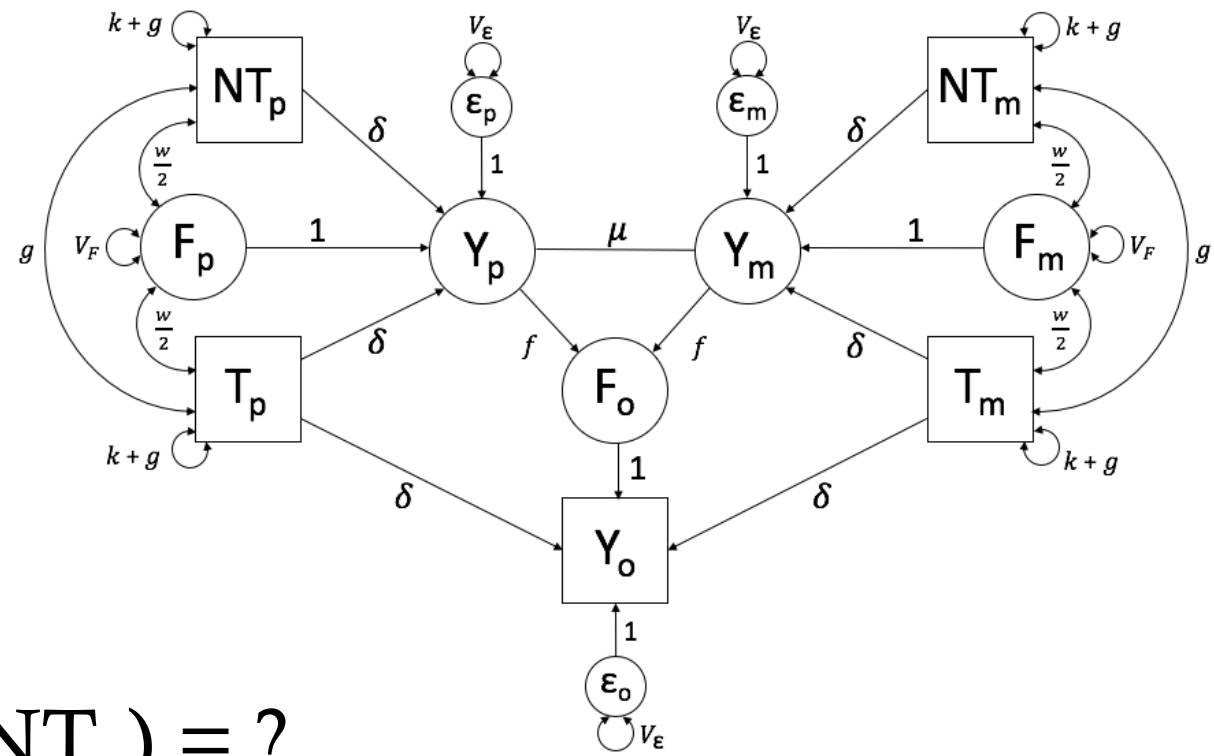
$$= f\left(\frac{w}{2} + \delta k\right)$$

$$= f\Omega$$

$$\text{cov}(Y_o, NT_p) = ?$$

Model 1:

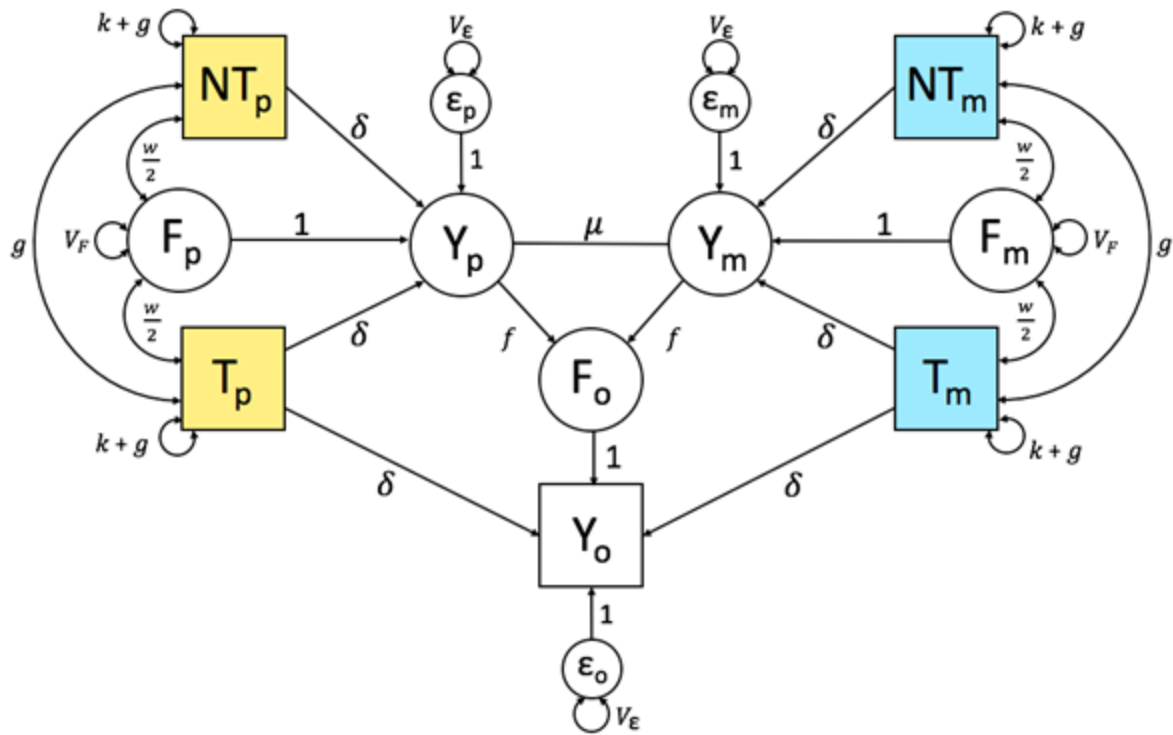
- ✓ Vertical Transmission,
- ✓ Assortative Mating



$$= f\Omega(1 + V_y\mu) + 2\delta g$$



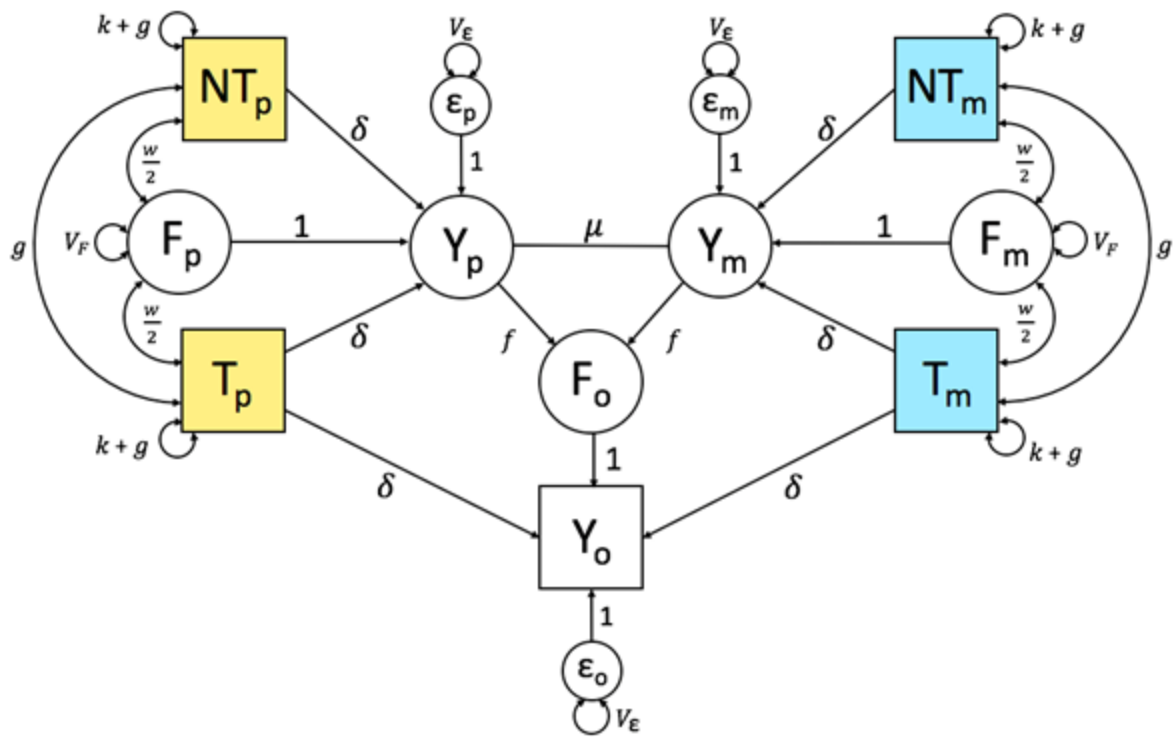
Determining if AM is changing over time



	T _p NT _p		T _m NT _m	
T _p	$k + g$	g	g	g
NT _p		$k + g$	g	g
T _m			$k + g$	g
NT _m				$k + g$

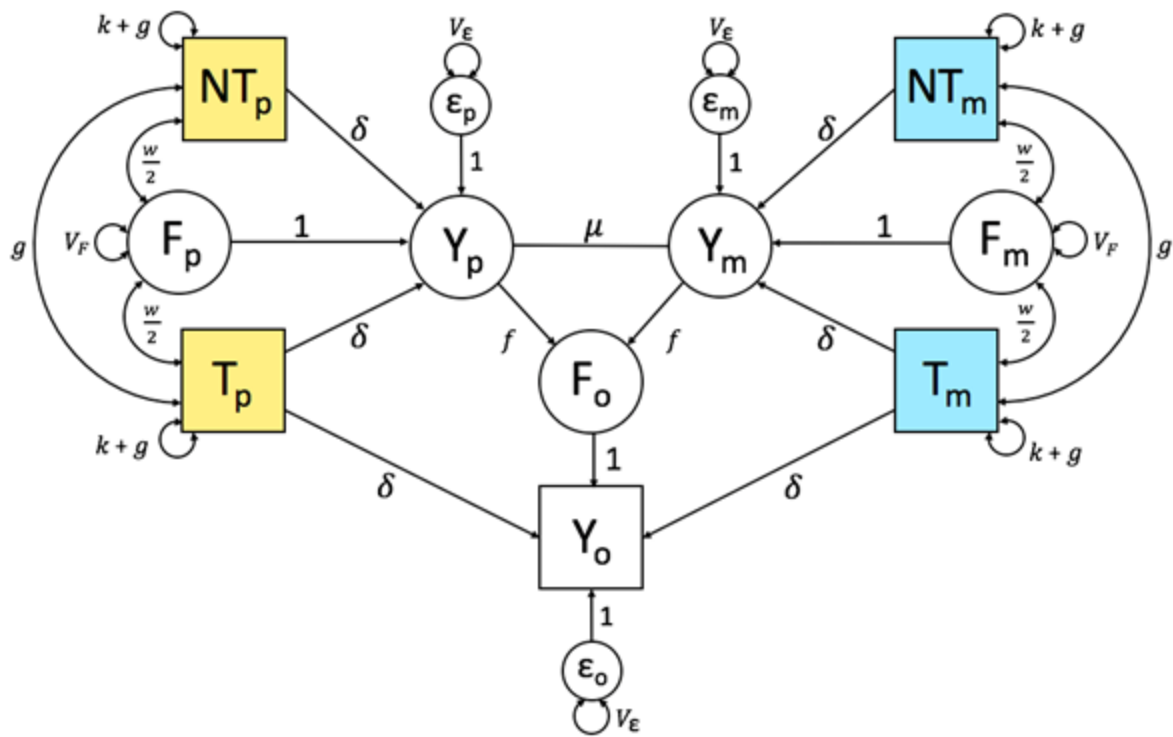
Model 1:

- ✓ Vertical Transmission
- ✓ Assortative Mating



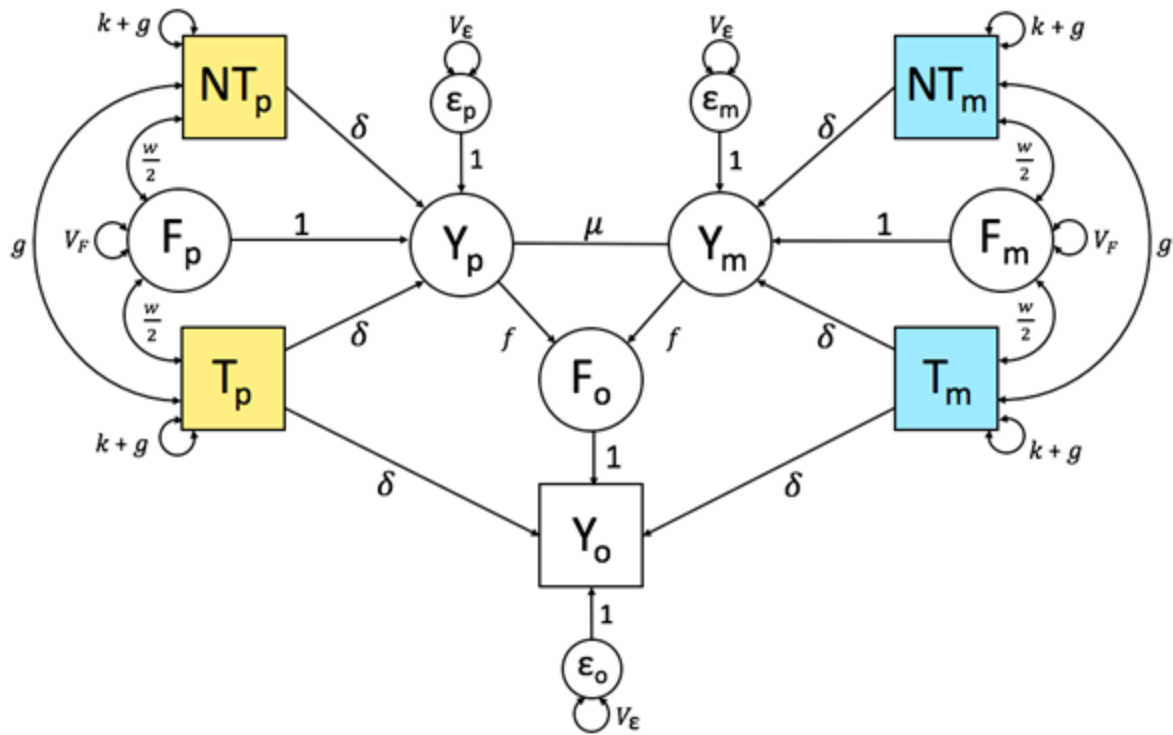
	T_p	NT_p	T_m	NT_m
T_p	$k + g$	g	g	g
NT_p		$k + g$	g	g
T_m			$k + g$	g
NT_m				$k + g$

Equilibrium



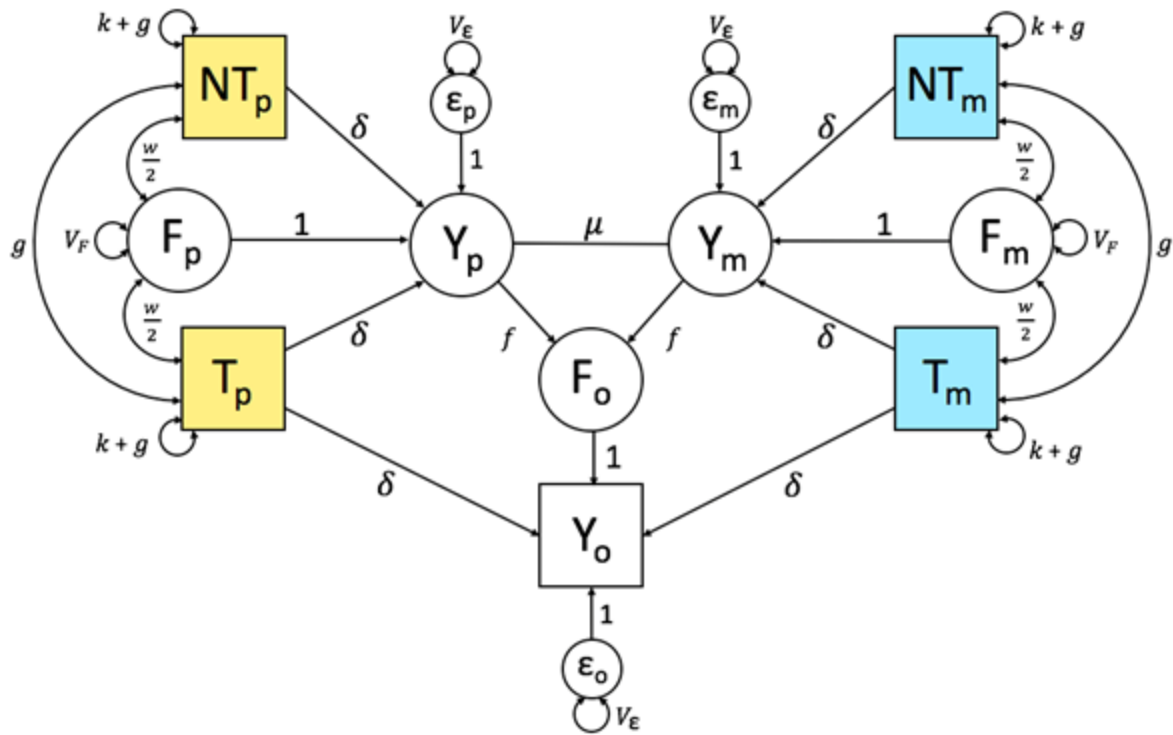
	T _p NT _p		T _m NT _m	
T _p	$k + g$	g	g	g
NT _p		$k + g$	g	g
T _m			$k + g$	g
NT _m				$k + g$

Disequilibrium



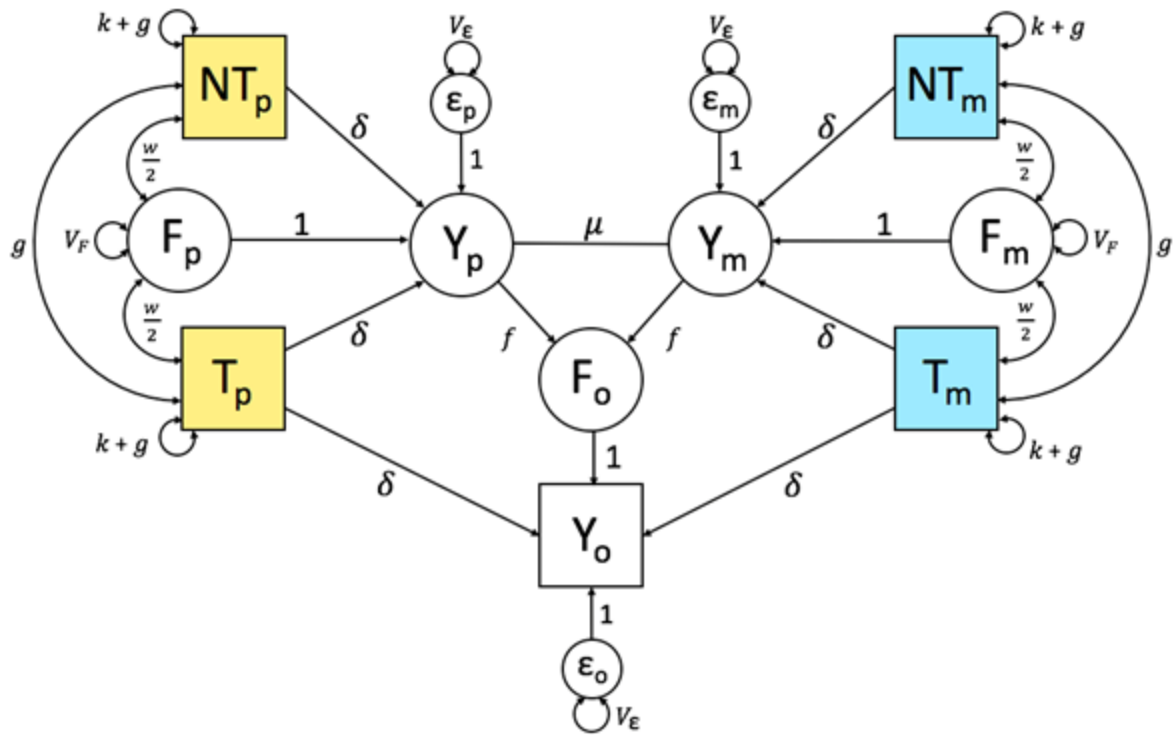
	T _p NT _p		T _m NT _m	
T _p	$k + g_{cis}$	g_{cis}	g_{trans}	g_{trans}
NT _p		$k + g_{cis}$	g_{trans}	g_{trans}
T _m			$k + g_{cis}$	g_{cis}
NT _m				$k + g_{cis}$

Disequilibrium



	T_p	NT_p	T_m	NT_m
T_p	$k + g_c$	g_c	g_t	g_t
NT_p		$k + g_c$	g_t	g_t
T_m			$k + g_c$	g_c
NT_m				$k + g_c$

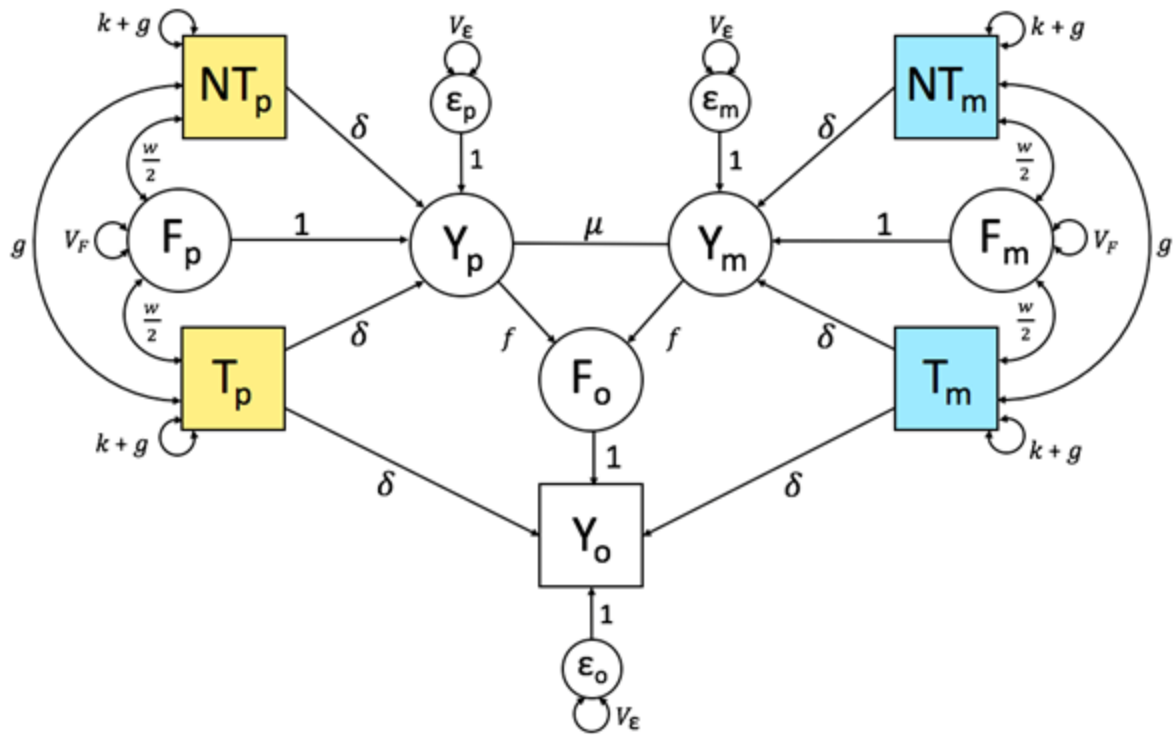
Disequilibrium



g_t is a between-spouse estimate, and tells us about AM in the parental generation

	T_p	NT_p	T_m	NT_m
T_p	$k + g_c$	g_c	g_t	g_t
NT_p		$k + g_c$	g_t	g_t
T_m			$k + g_c$	g_c
NT_m				$k + g_c$

g_c is a within-person estimate, and tells us about AM in the grandparental generation and earlier

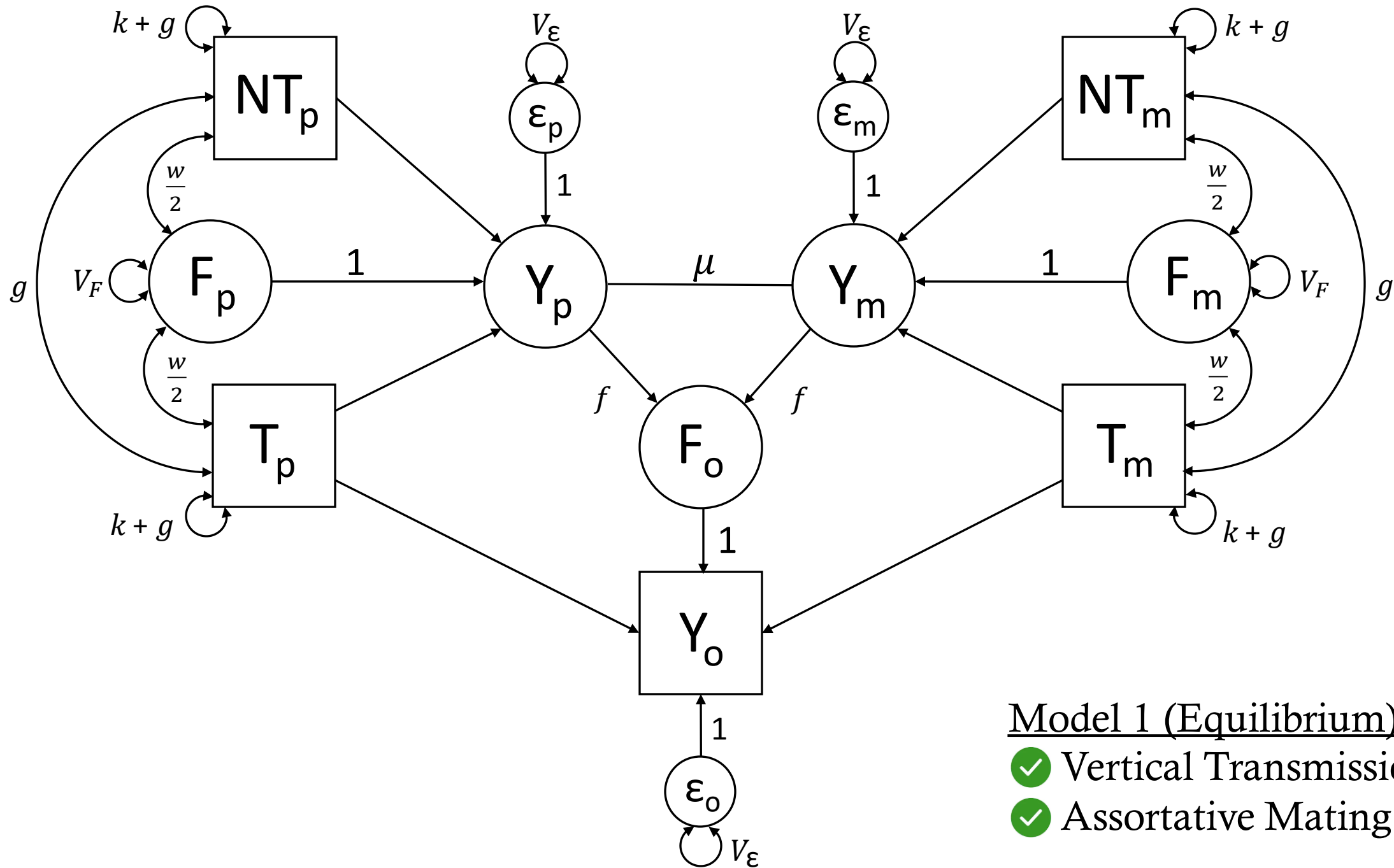


g_t is a between-spouse estimate, and tells us about AM in the *parental generation*

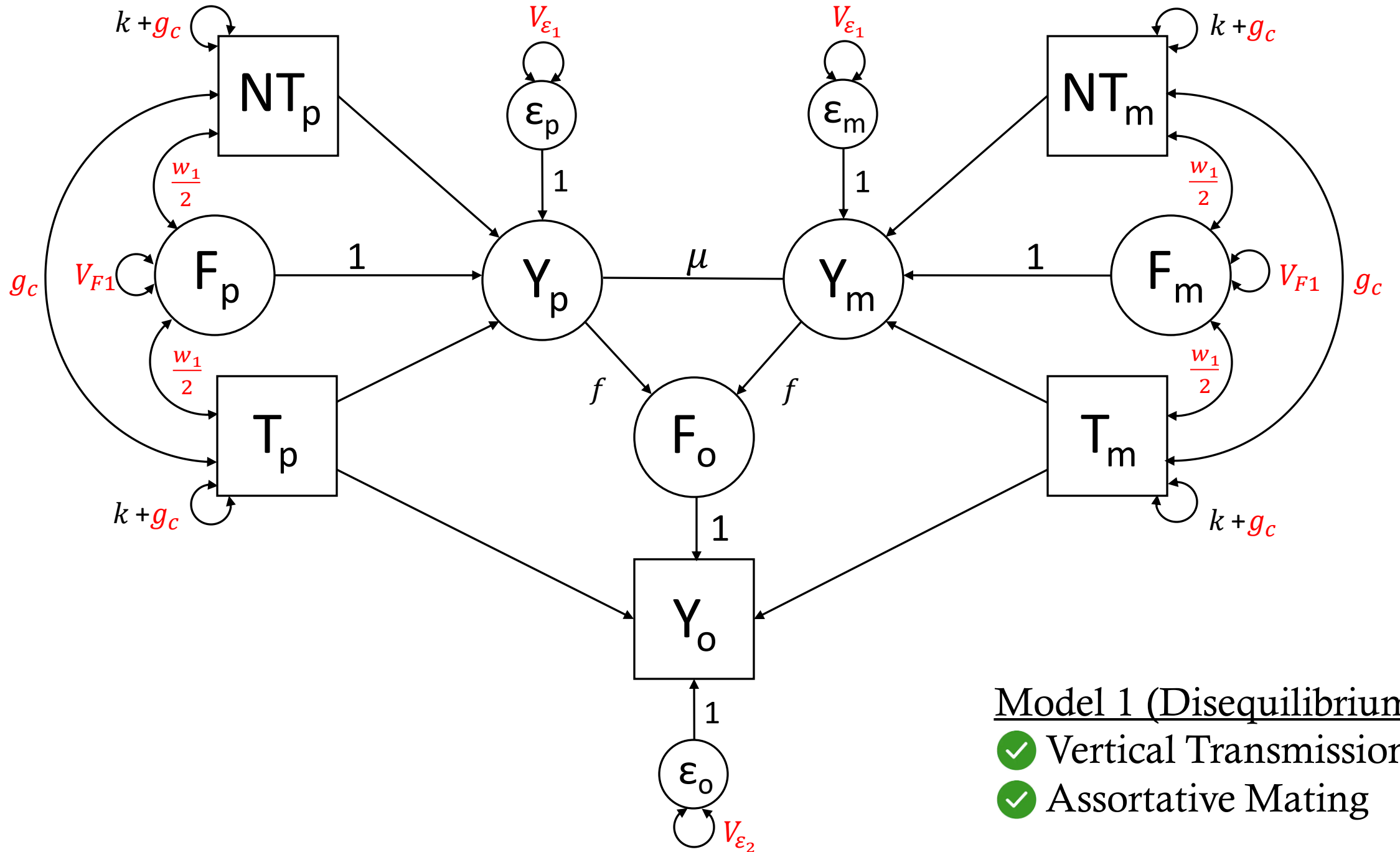
	T_p	NT_p	T_m	NT_m
T_p	$k + g_c$	g_c	g_t	g_t
NT_p		$k + g_c$	g_t	g_t
T_m			$k + g_c$	g_c
NT_m				$k + g_c$



g_c is a within-person estimate, and tells us about AM in the *grandparental generation and earlier*



Model 1 (Equilibrium):
 ✓ Vertical Transmission
 ✓ Assortative Mating



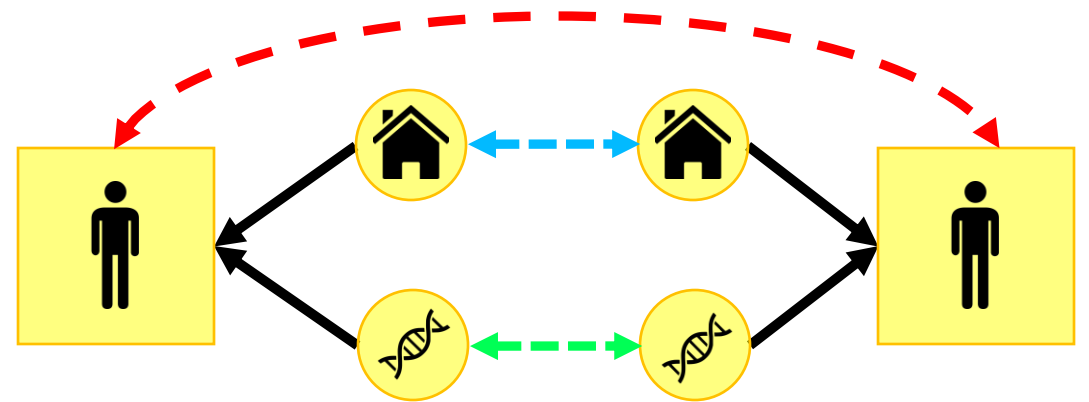


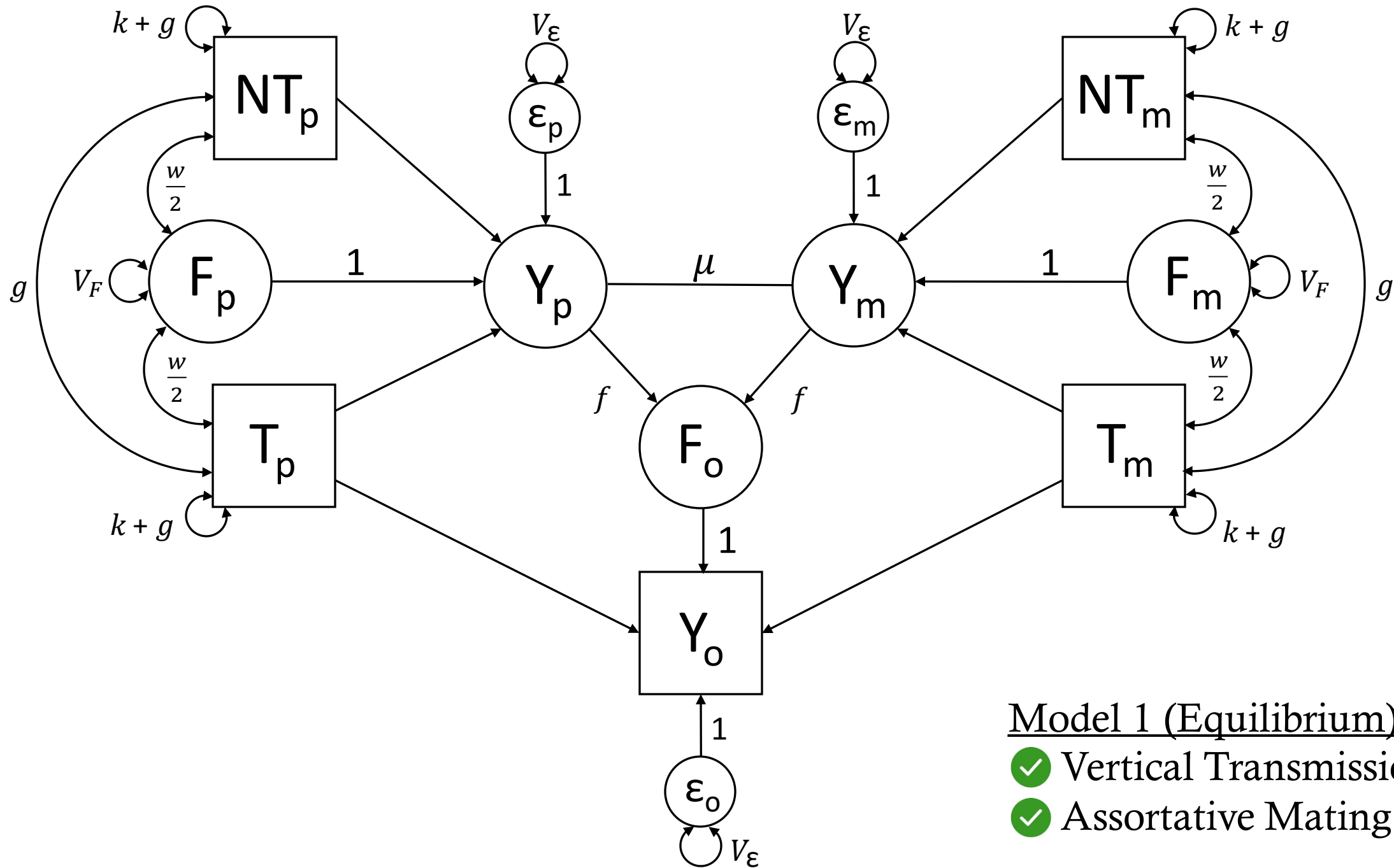
Determining what is causing AM



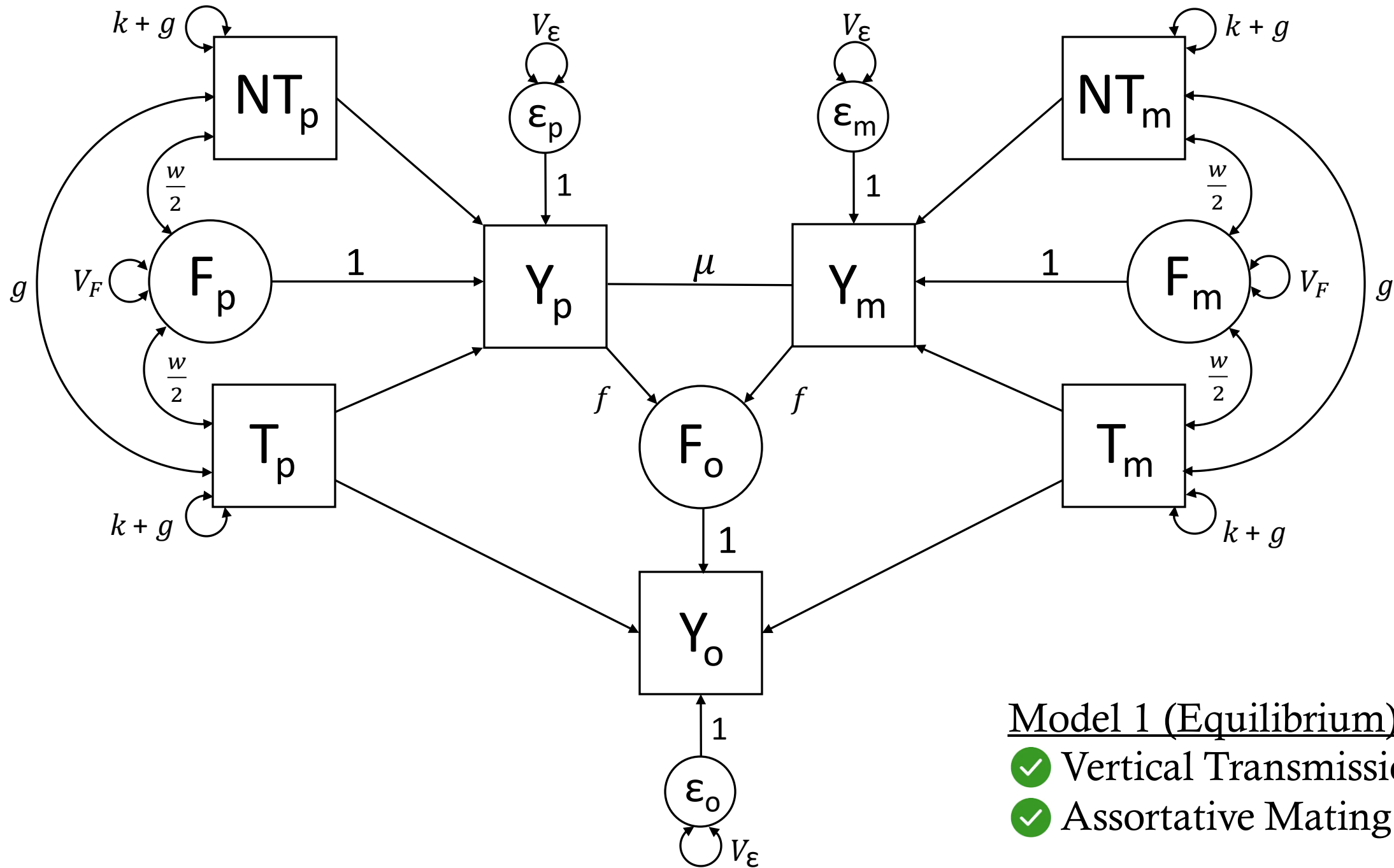
Types of Assortative Mating

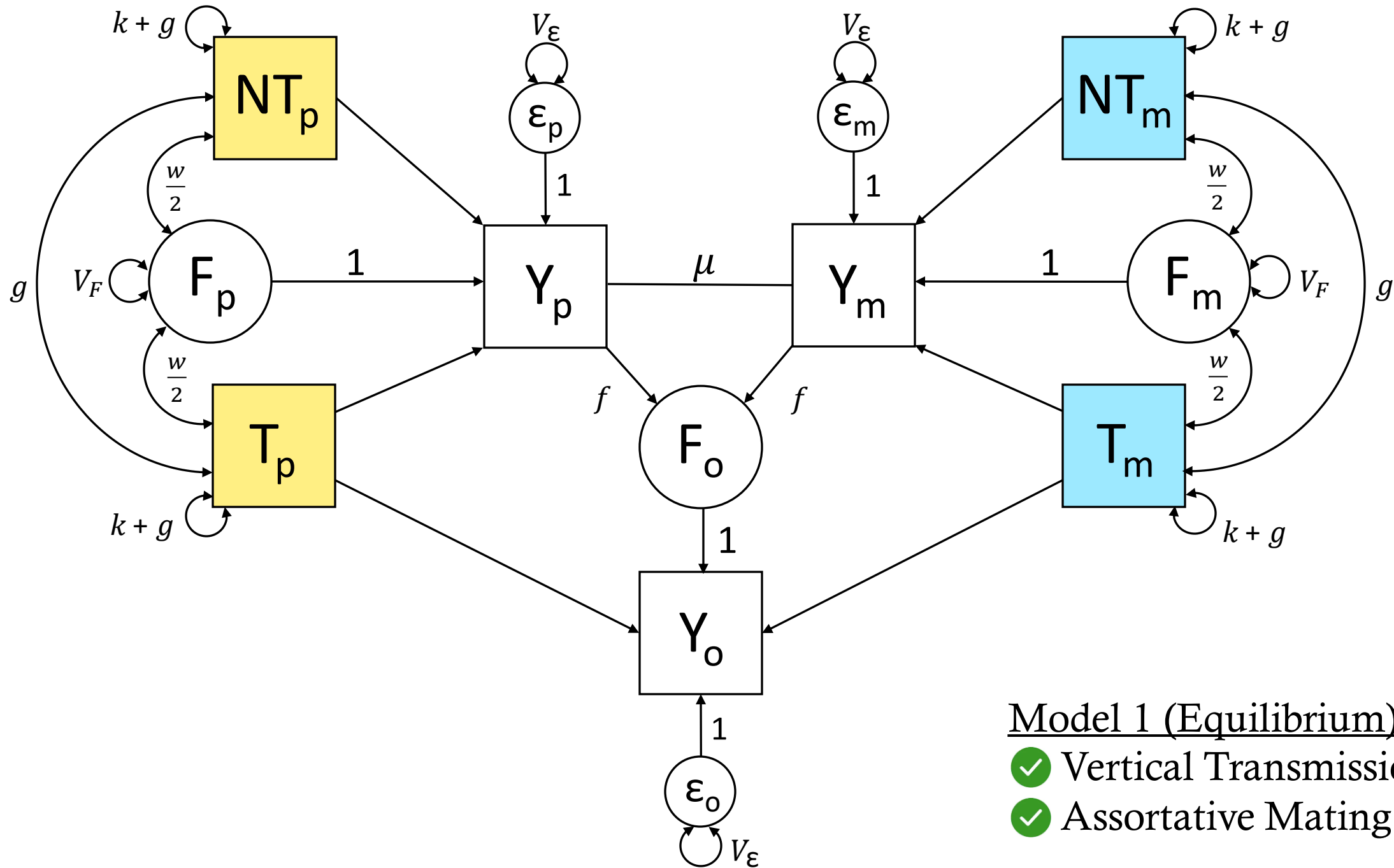
- Phenotypic Homogamy
 - *AKA Primary Phenotypic Assortment*
 - E.g., Mating based on height
- Social Homogamy
 - E.g., Mating based on geographic location
 - Doesn't impact genetic architecture
- Genetic Homogamy
 - Phenotypic homogamy on a different, genetically correlated trait

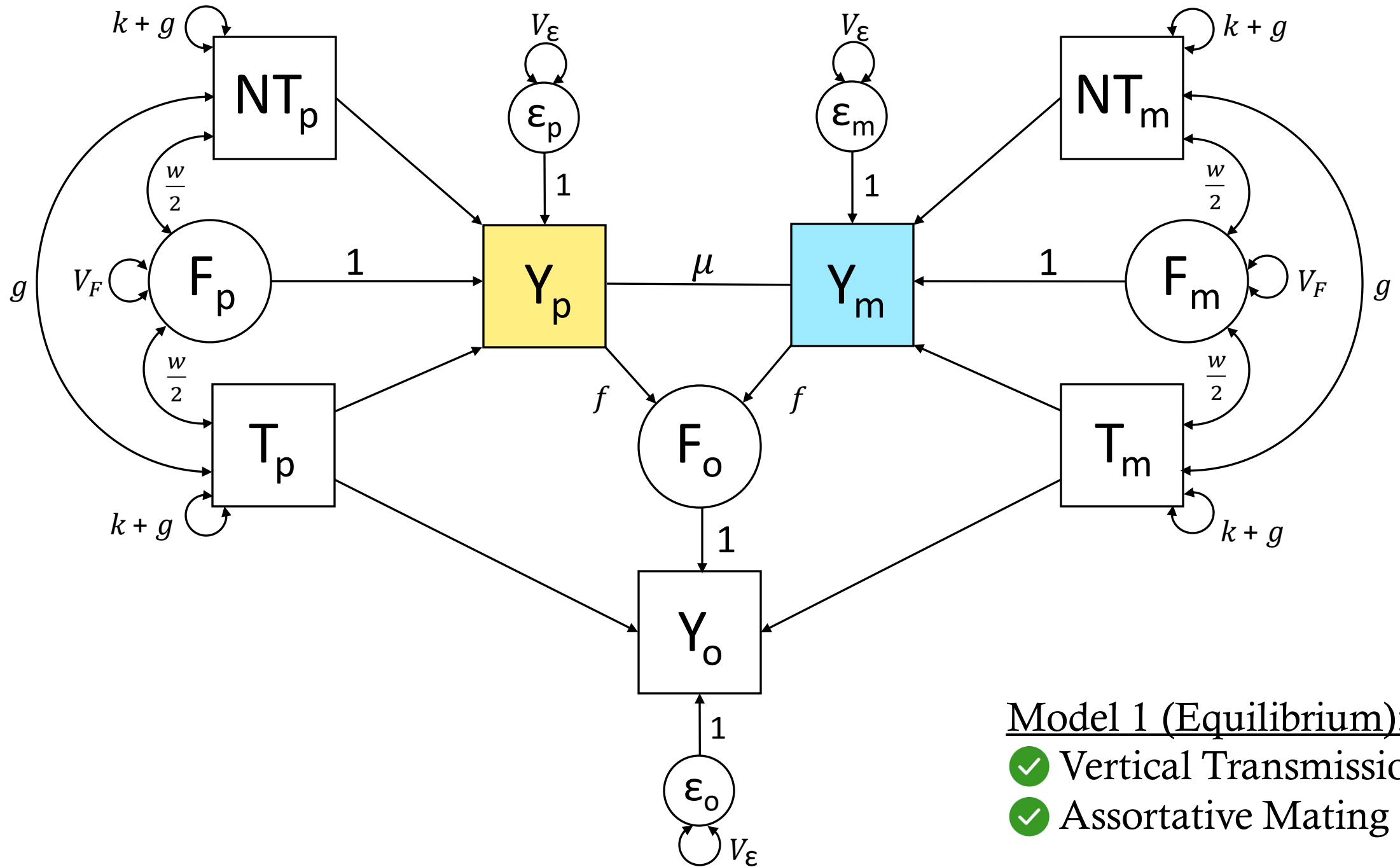




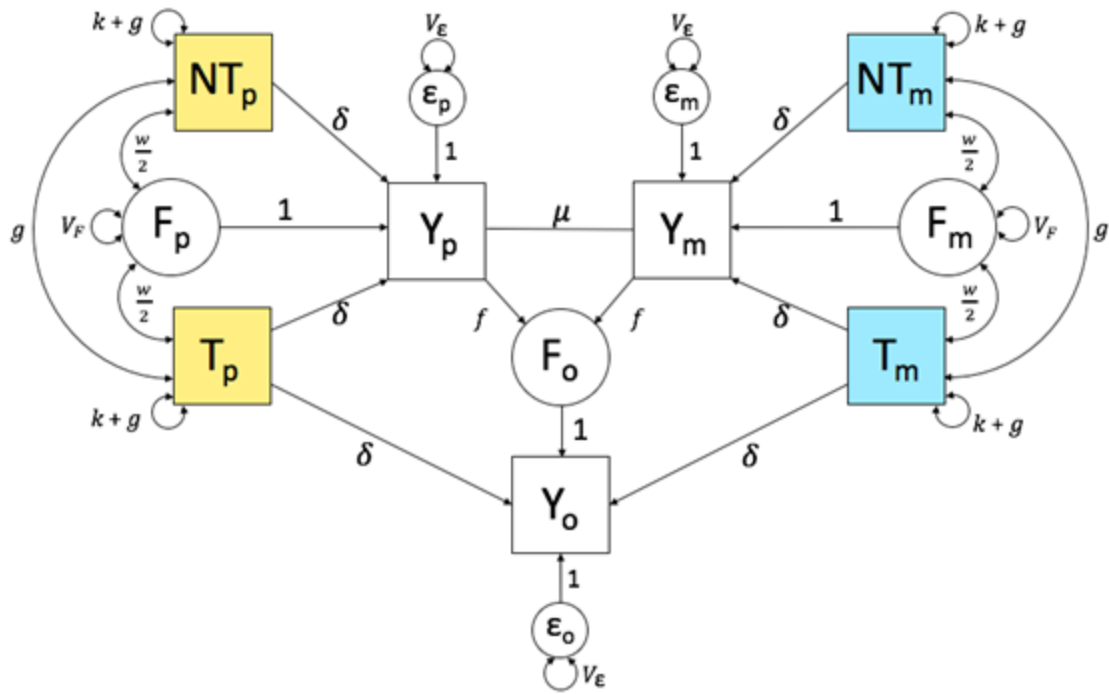
Model 1 (Equilibrium):
 ✓ Vertical Transmission
 ✓ Assortative Mating





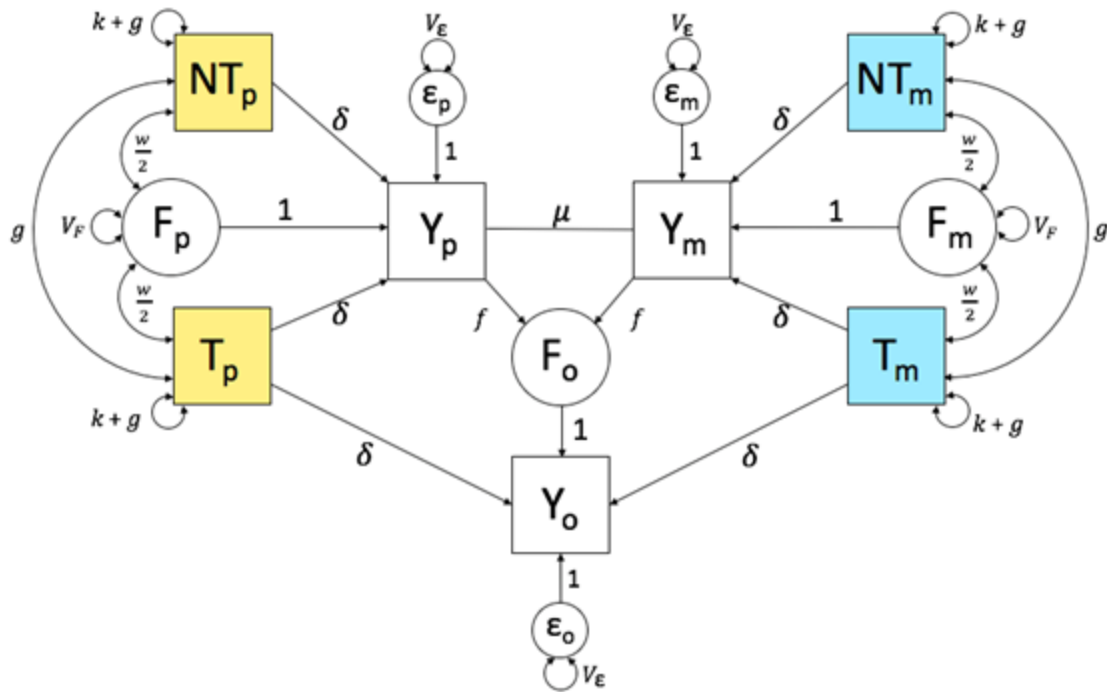


Observed g



	T_p	NT_p	T_m	NT_m
T_p	$k+g$	g	g	g
NT_p		$k+g$	g	g
T_m			$k+g$	g
NT_m				$k+g$

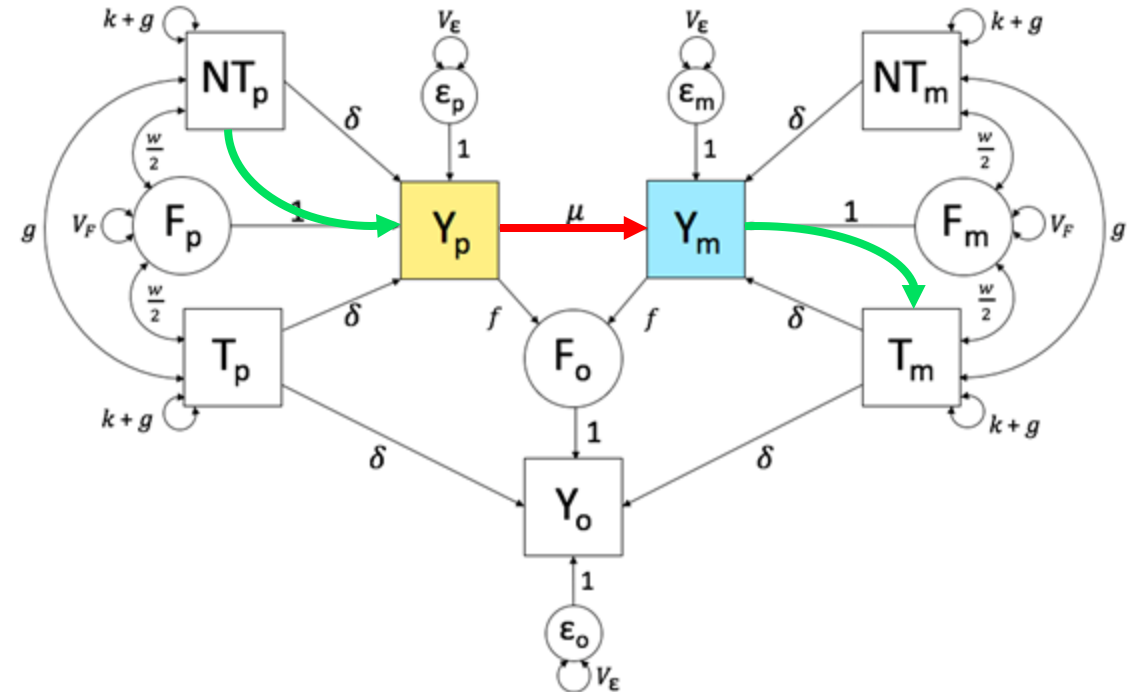
Observed g



	T_p	NT_p	T_m	NT_m
T_p	$k+g$	g	g	g
NT_p		$k+g$	g	g
T_m			$k+g$	g
NT_m				$k+g$

Expected g

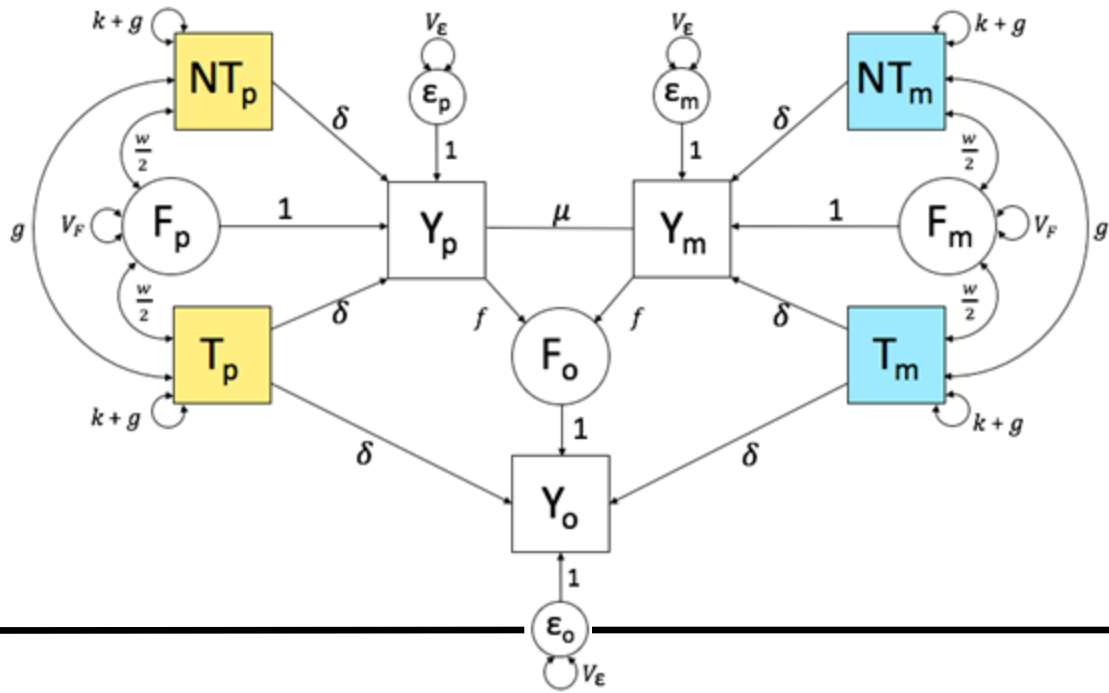
based on spousal phenotypic covariance



$$E(g) = \text{cov}([N]T_p, [N]T_m) = \Omega \mu \Omega = \Omega^2 \mu$$

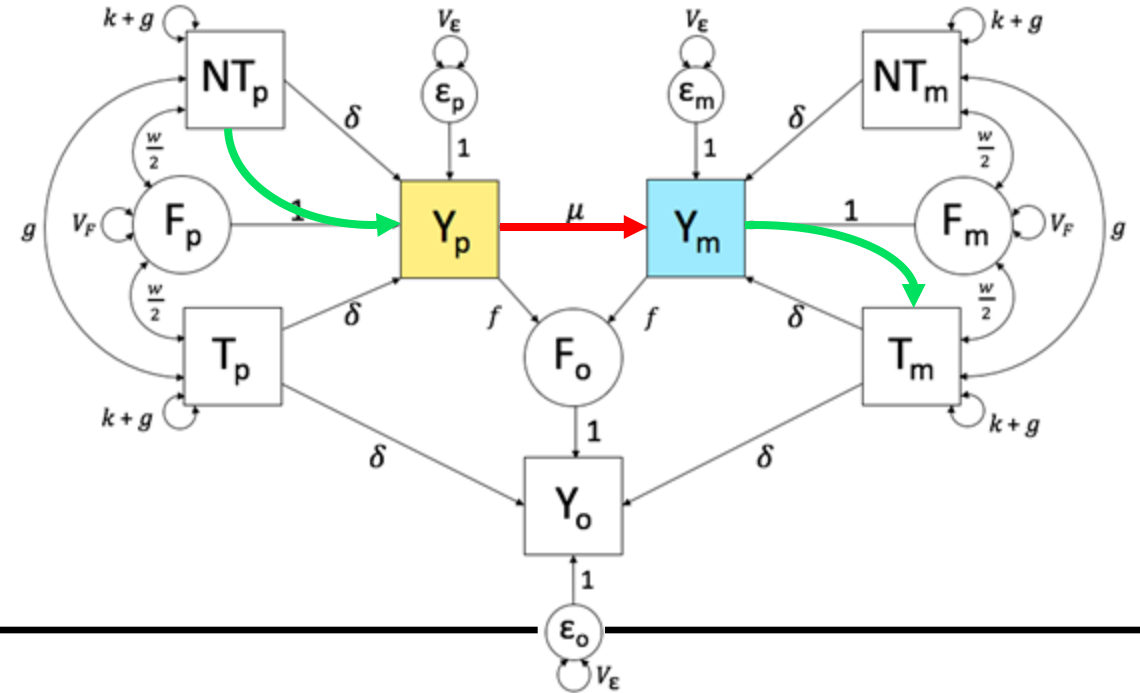
$$\mu = \frac{\text{Spousal Phenotypic Covariance}}{(\text{Spouse Phenotypic Variance})^2}$$

Observed g



Expected g

based on spousal phenotypic covariance

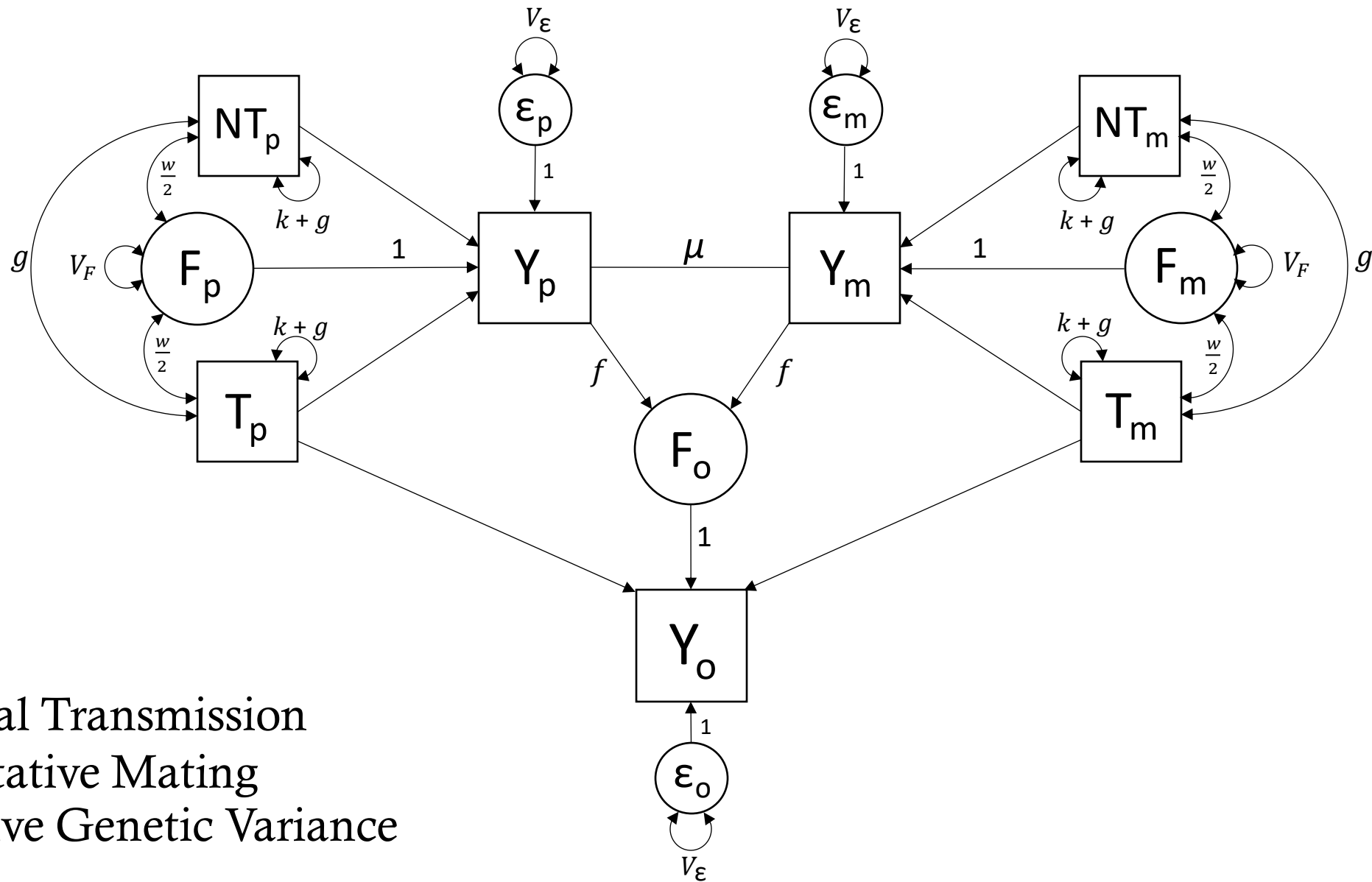


- If Observed $g =$ Expected $g \rightarrow$ Phenotypic Homogamy
- If Observed $g <$ Expected $g \rightarrow$ Social Homogamy
- If Observed $g >$ Expected $g \rightarrow$ Genetic Homogamy



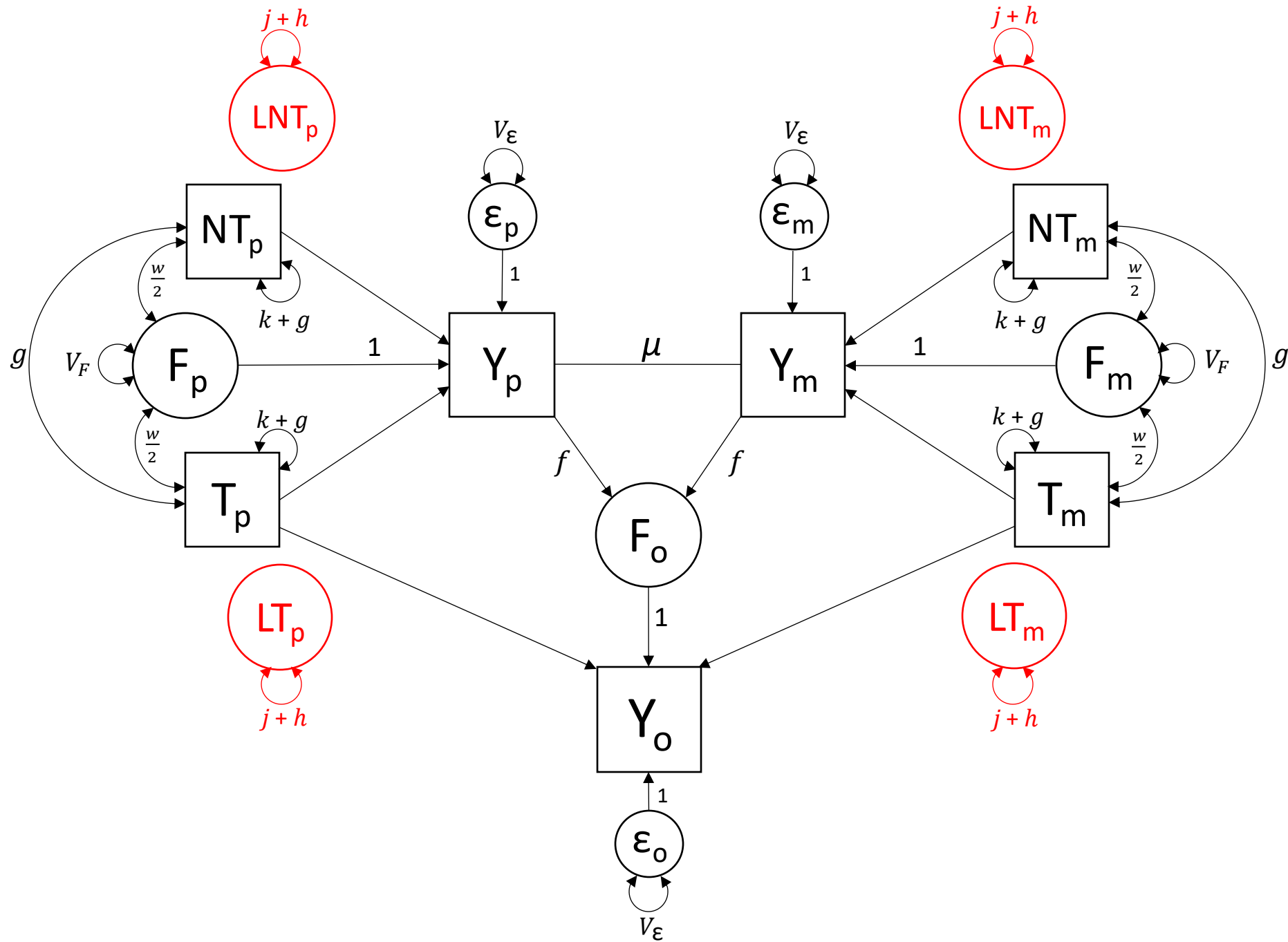
What if the PGS explains a small fraction of total h^2 ?

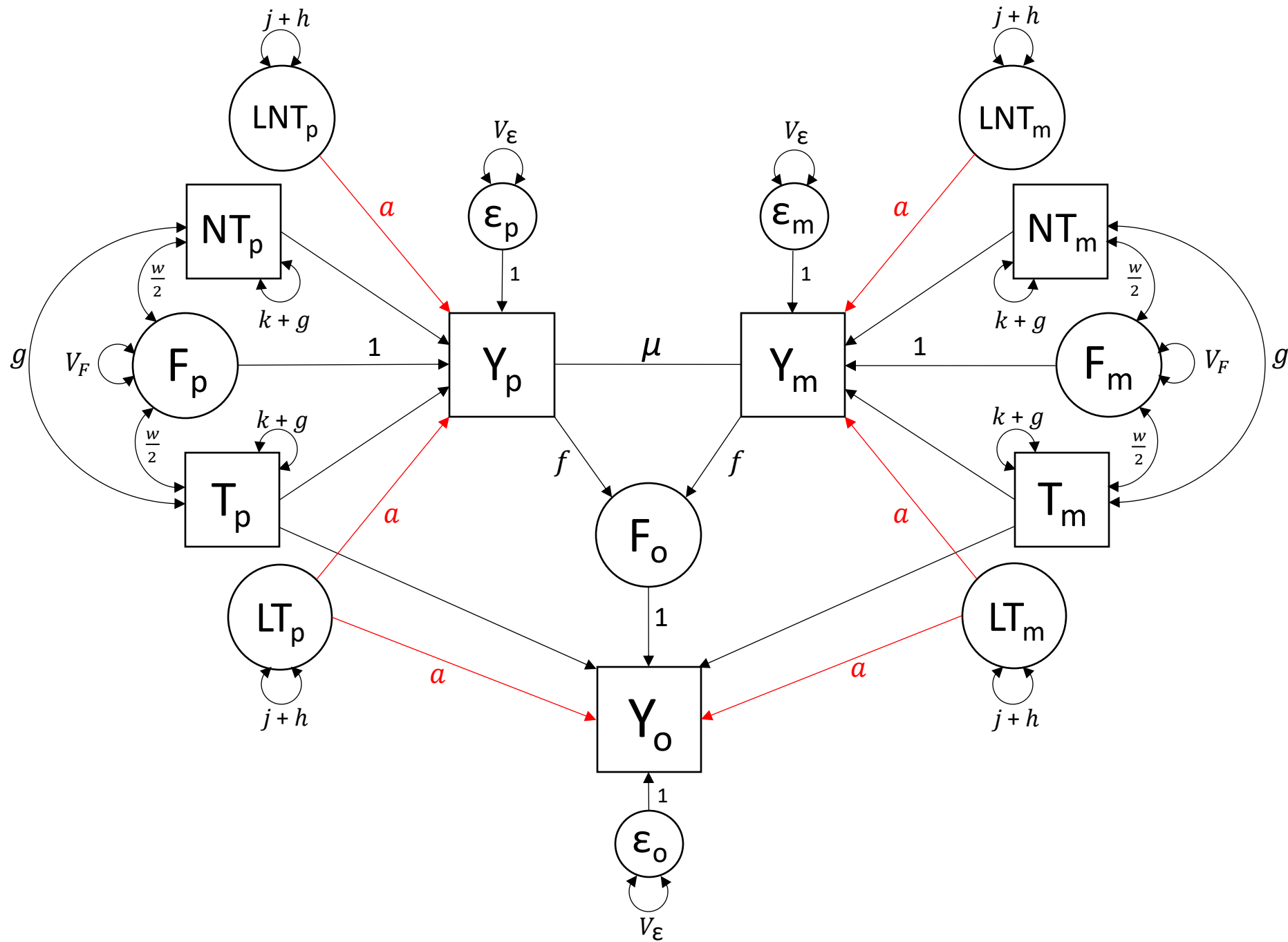


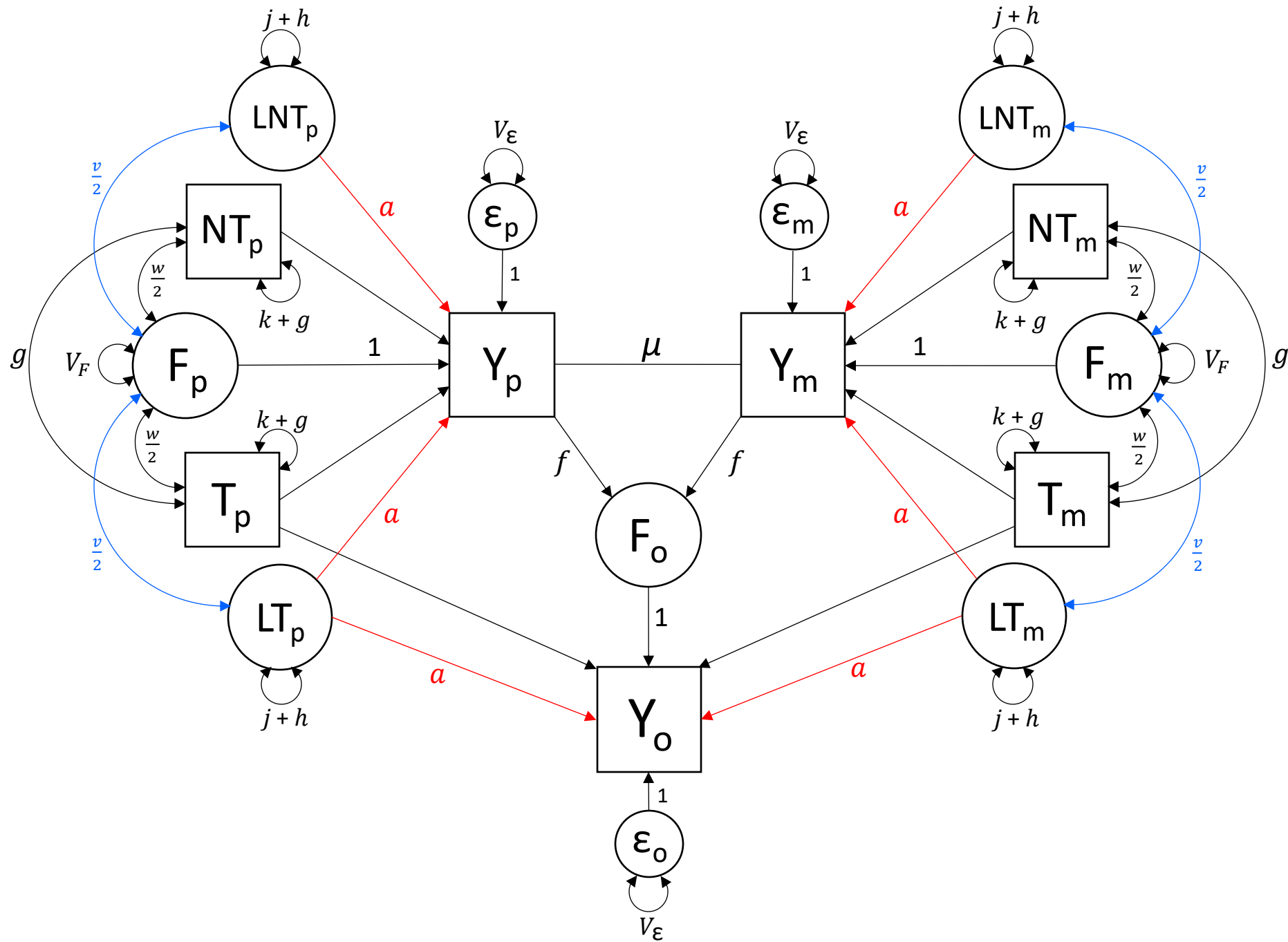


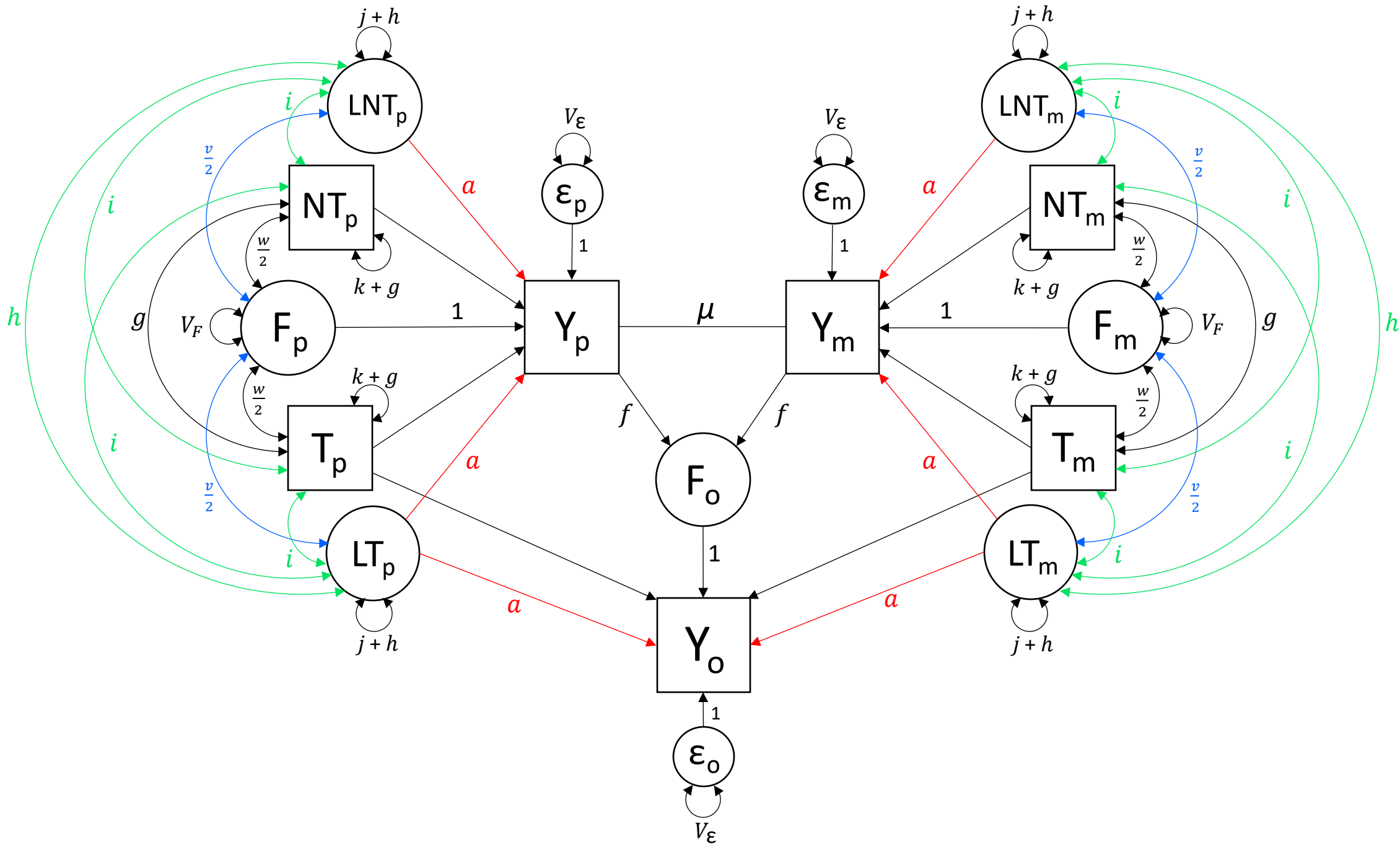
Model 1:

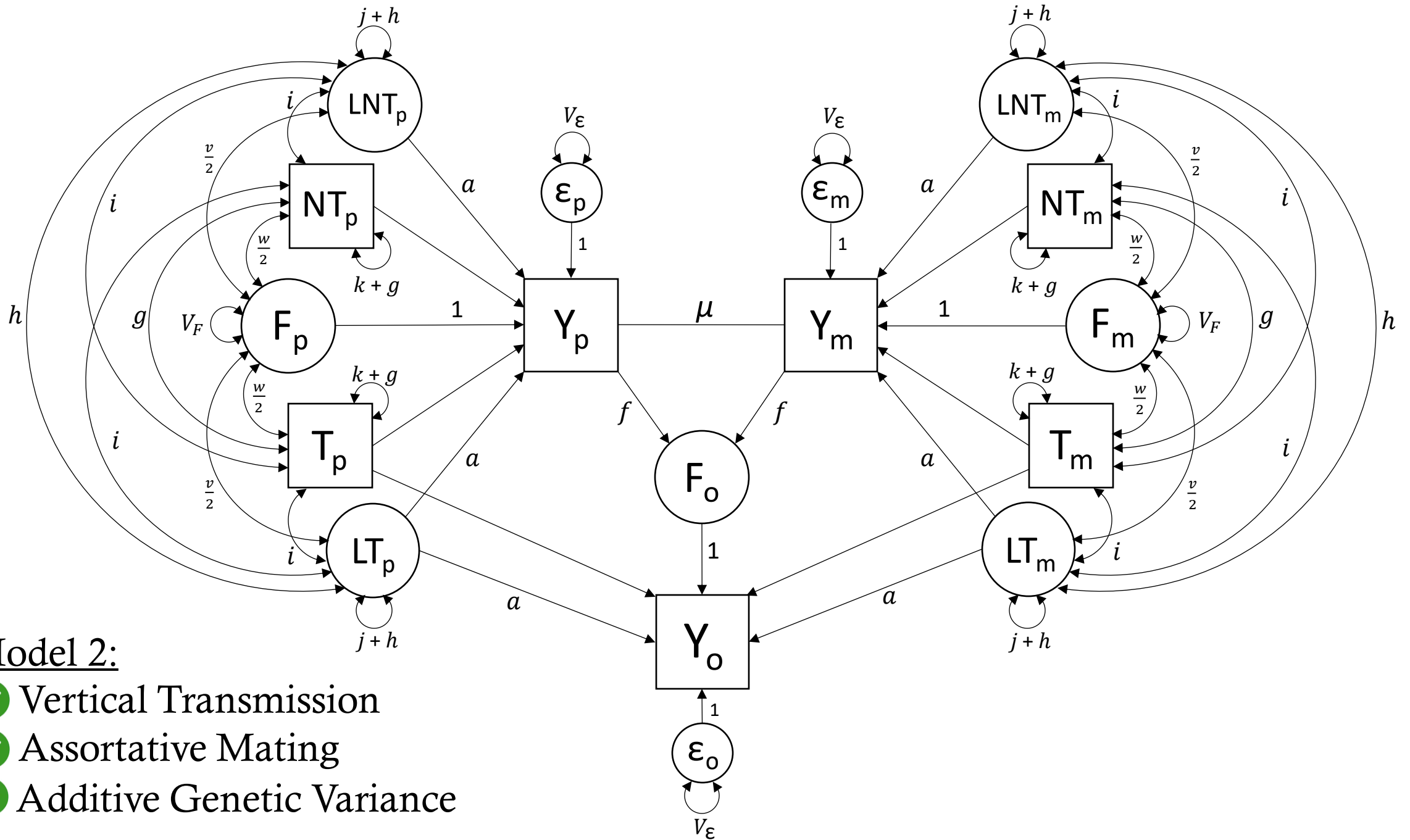
- ✓ Vertical Transmission
- ✓ Assortative Mating
- ✗ Additive Genetic Variance





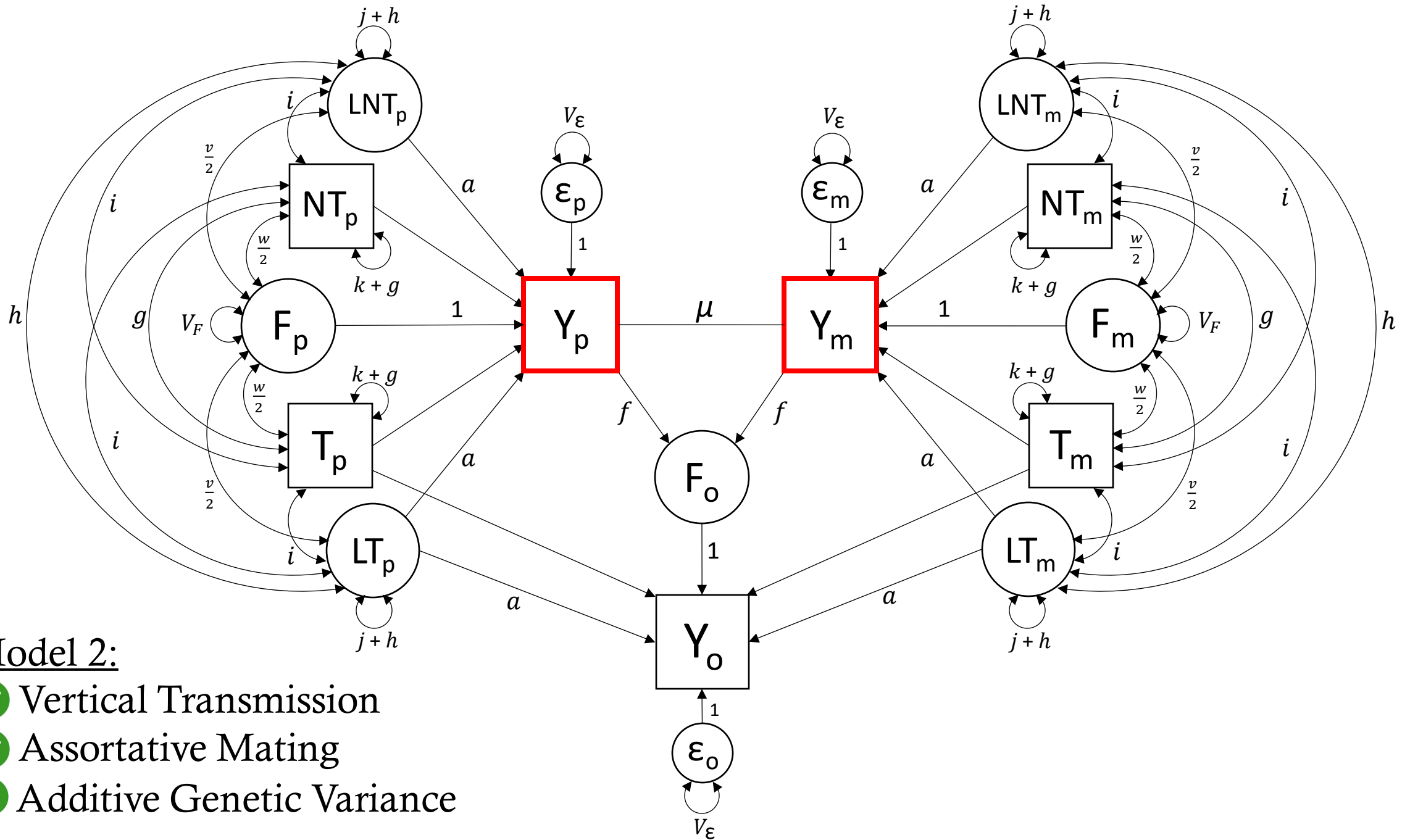






Model 2:

- ✓ Vertical Transmission
- ✓ Assortative Mating
- ✓ Additive Genetic Variance

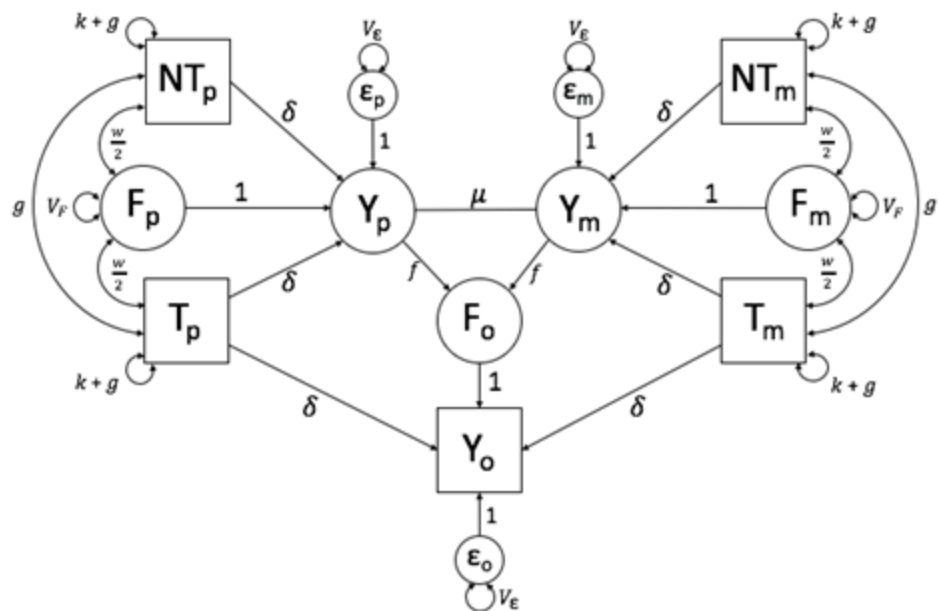


Model 2:

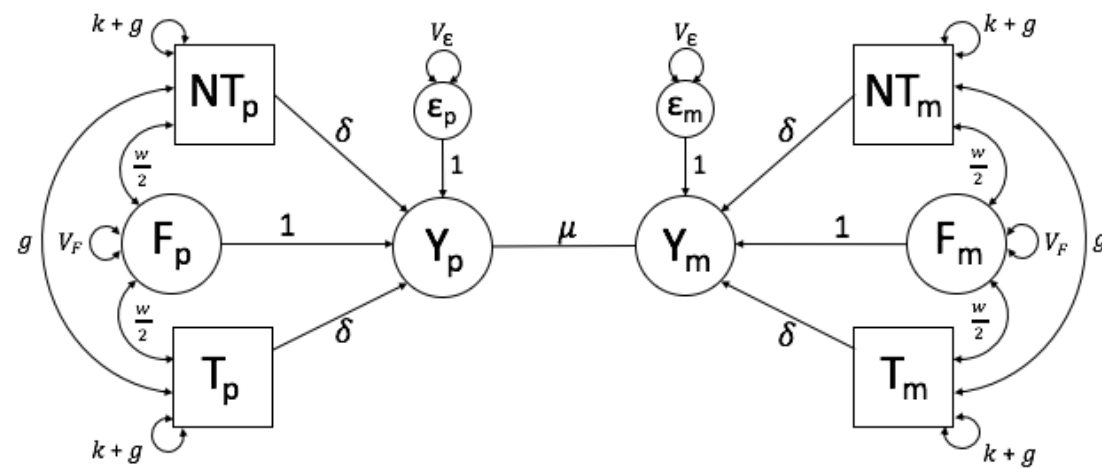
- ✓ Vertical Transmission
- ✓ Assortative Mating
- ✓ Additive Genetic Variance



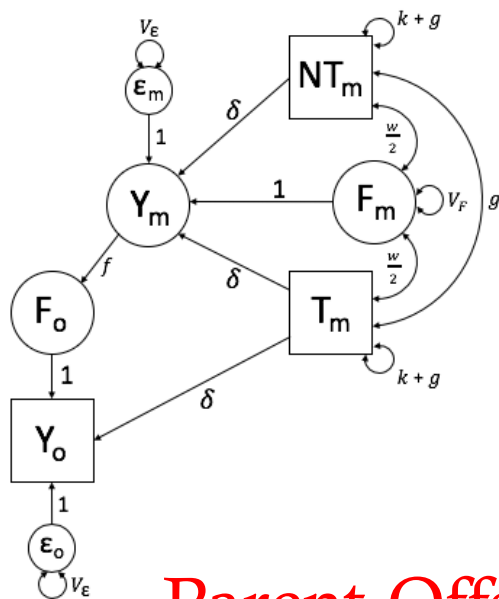
Some other extensions we're working on



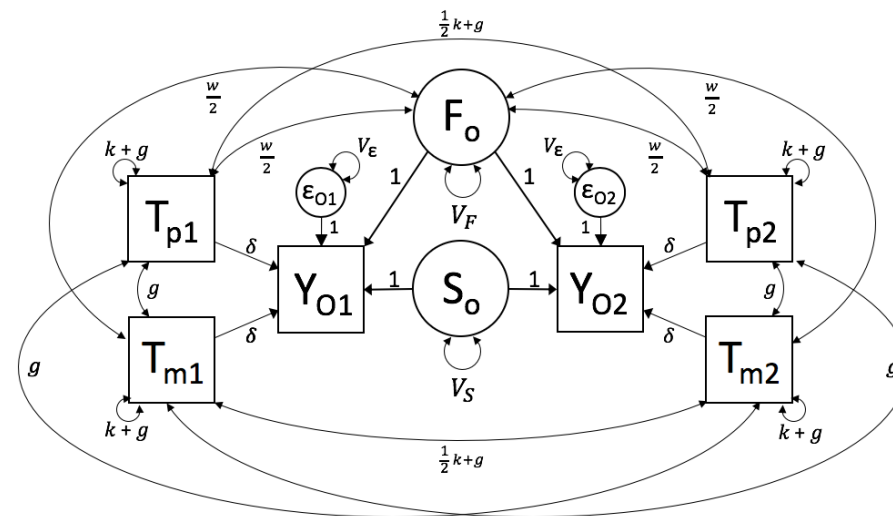
Trio



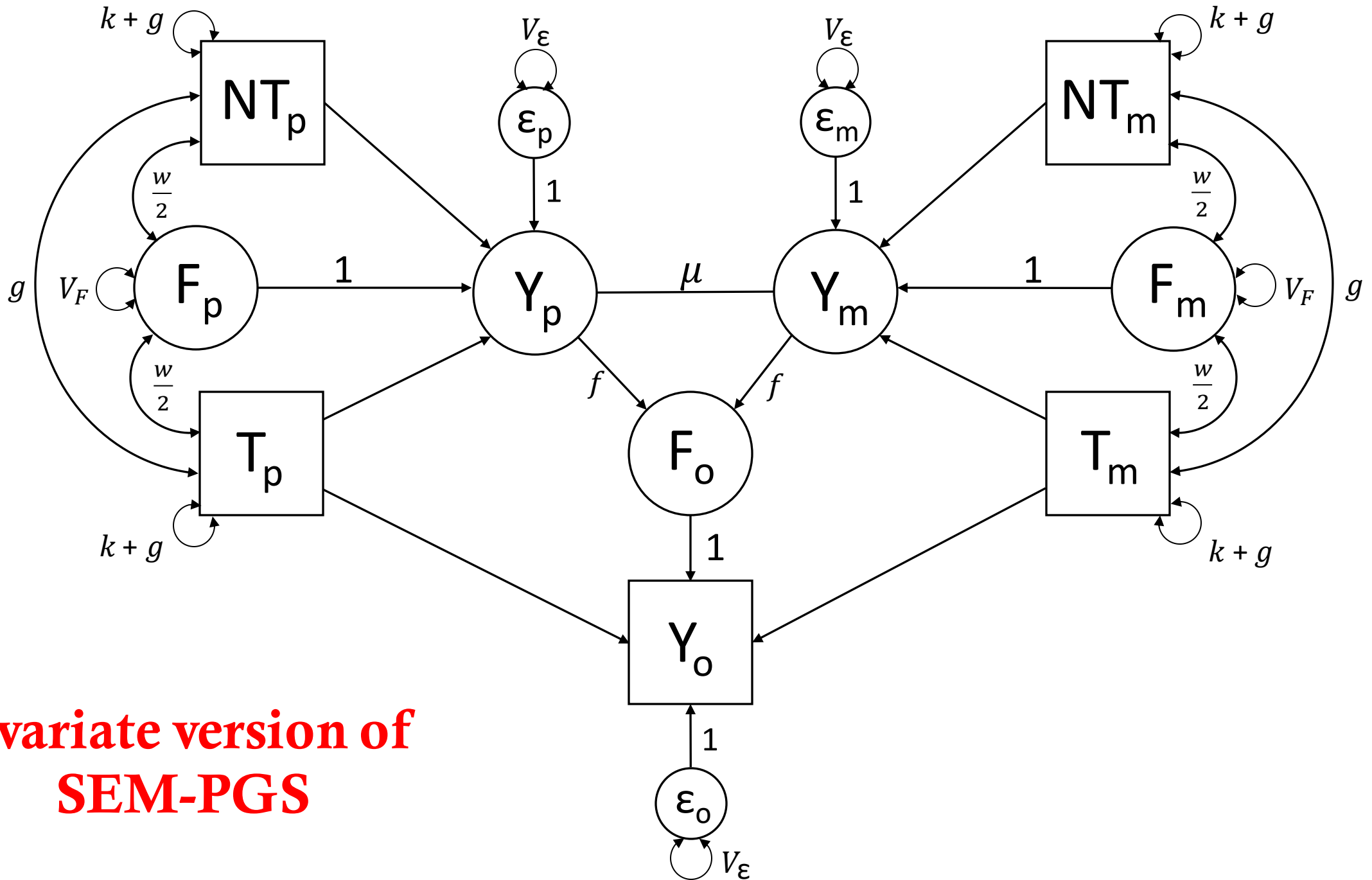
Spouse



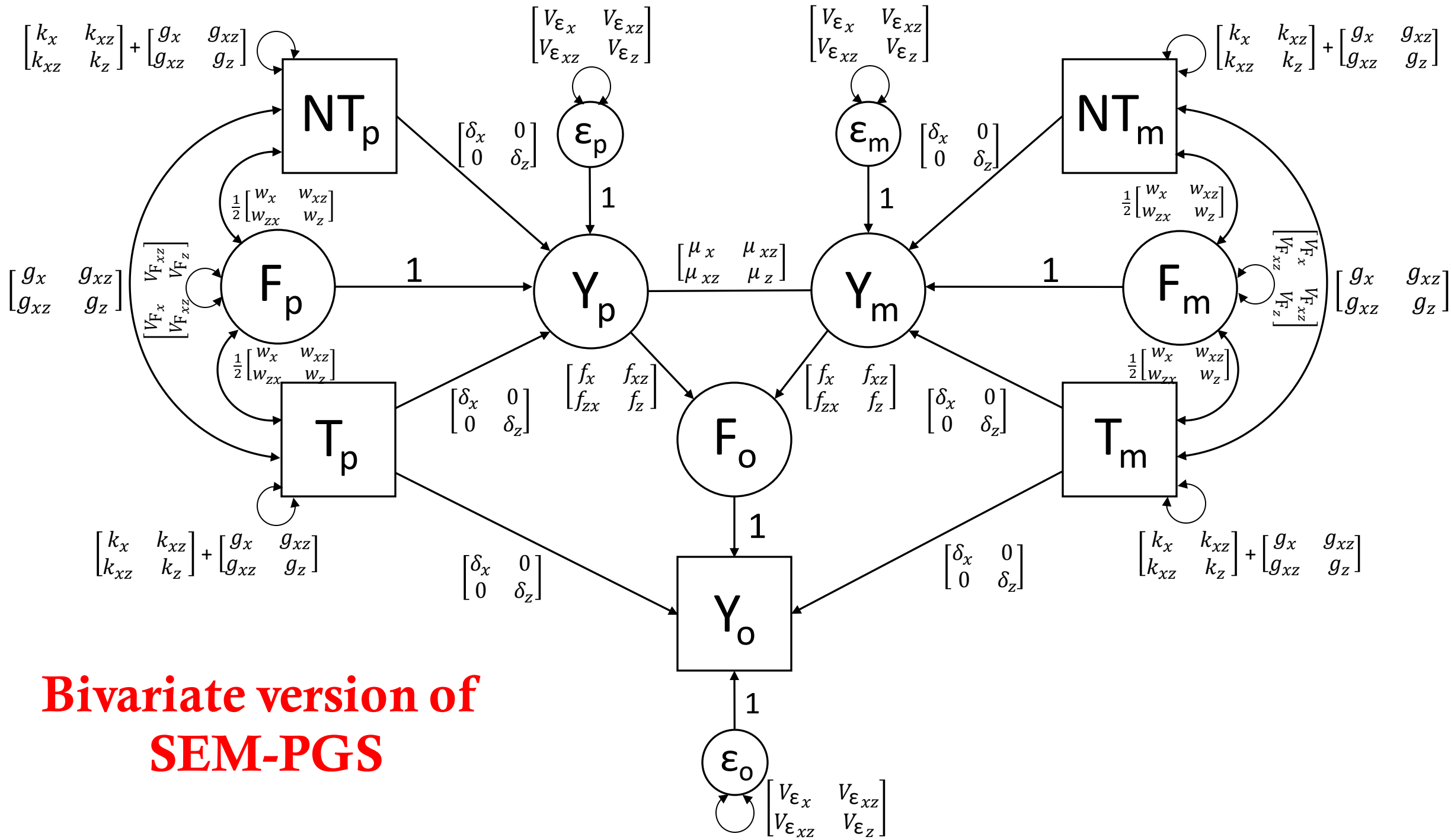
Parent-Offspring



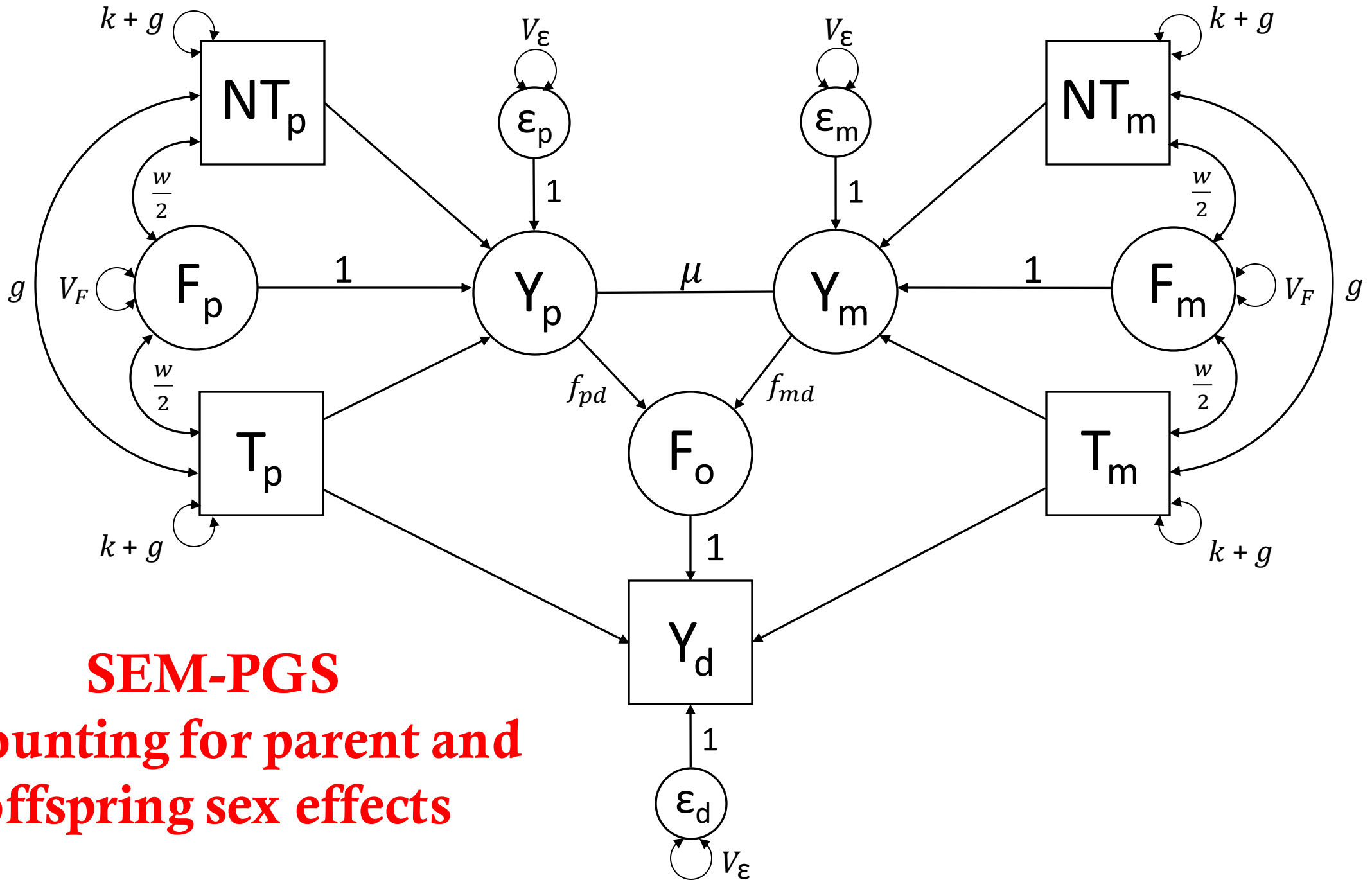
Sibling



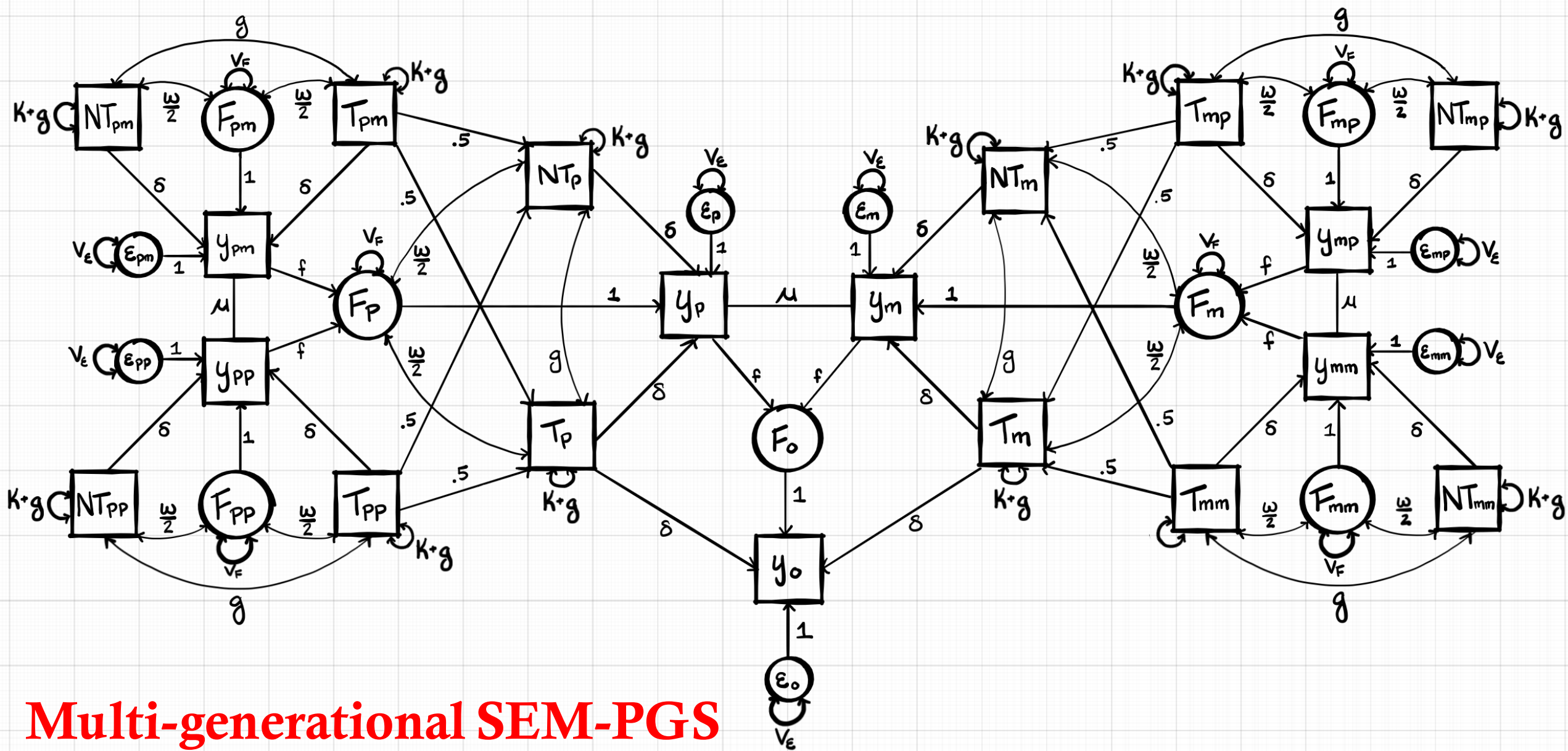
**Bivariate version of
SEM-PGS**



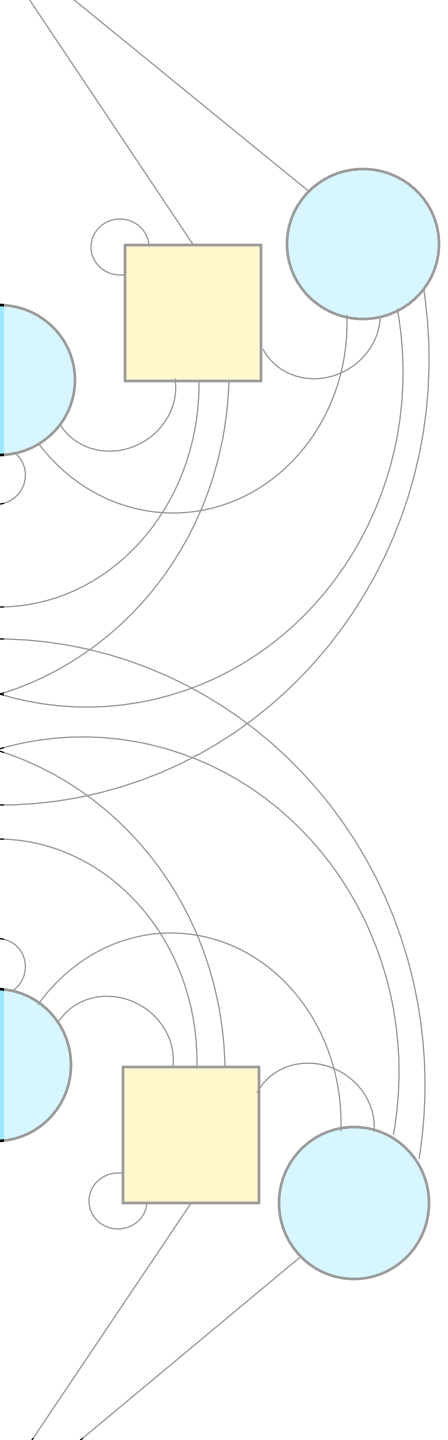
Bivariate version of SEM-PGS



SEM-PGS
accounting for parent and
offspring sex effects



Multi-generational SEM-PGS



Thank you!

