

Estimating Parental Effects using Polygenic Scores Part I: Model Introduction

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



“Okay yeah, that explains a lot.”



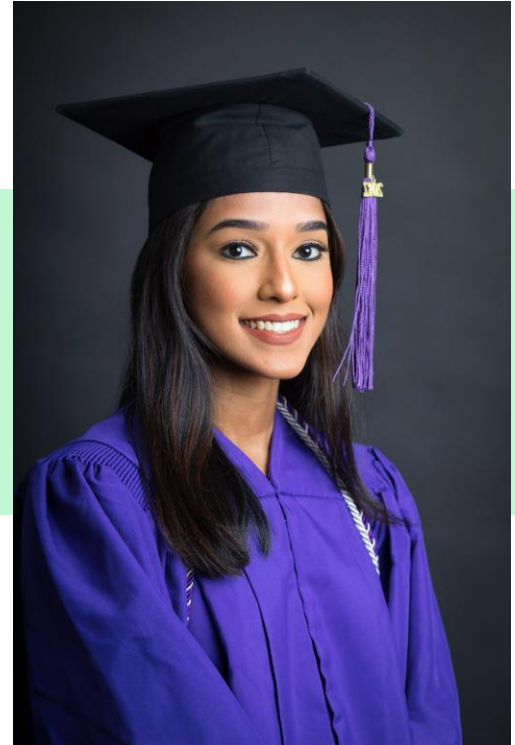
There are so many ways that parents
and offspring resemble one another.

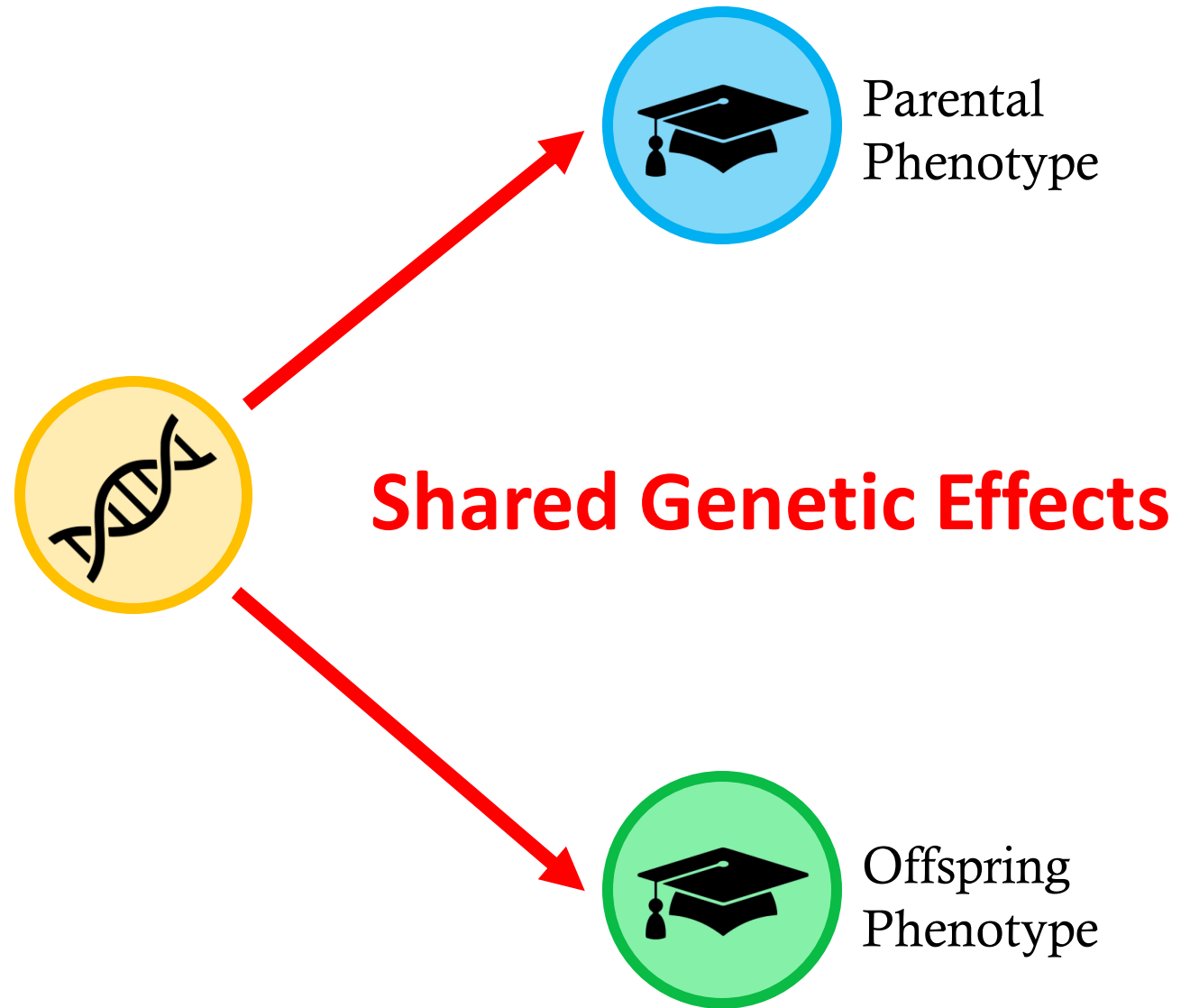


Why?



Education







Parental
Phenotype



Offspring
Phenotype

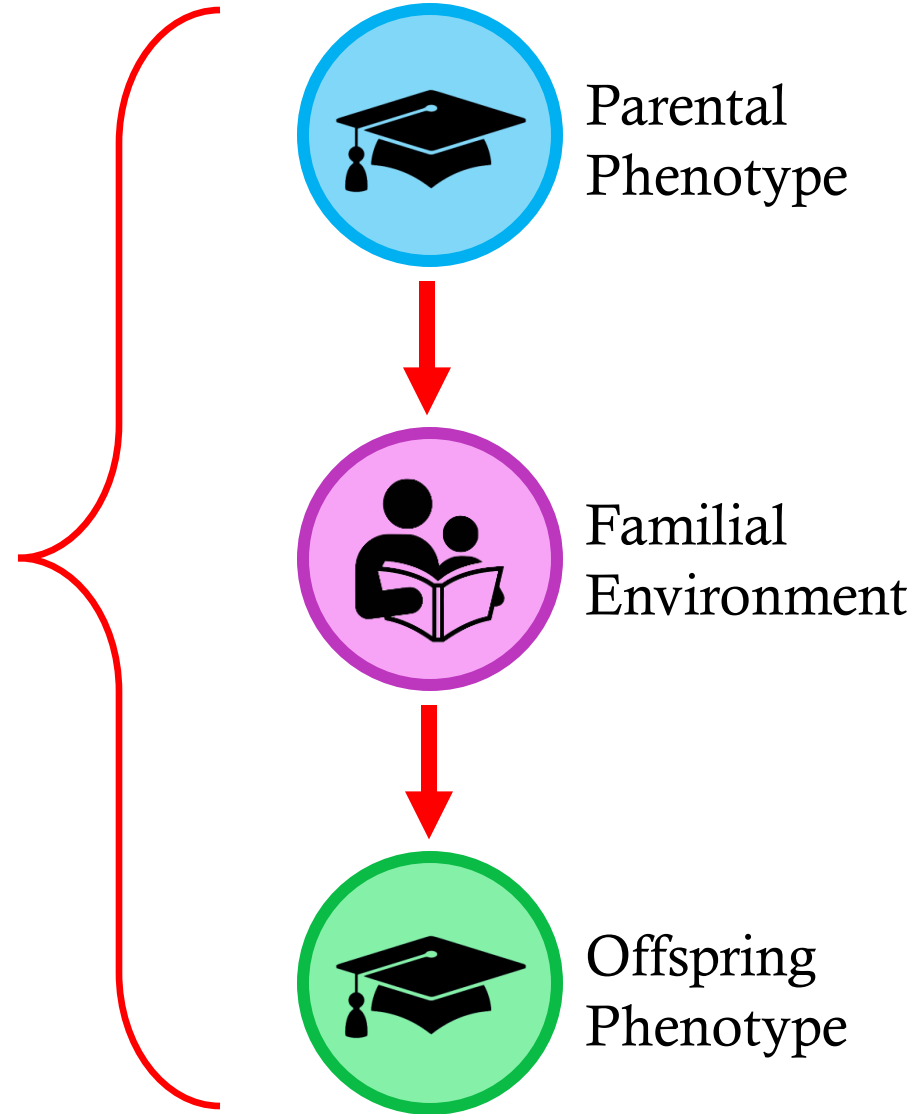


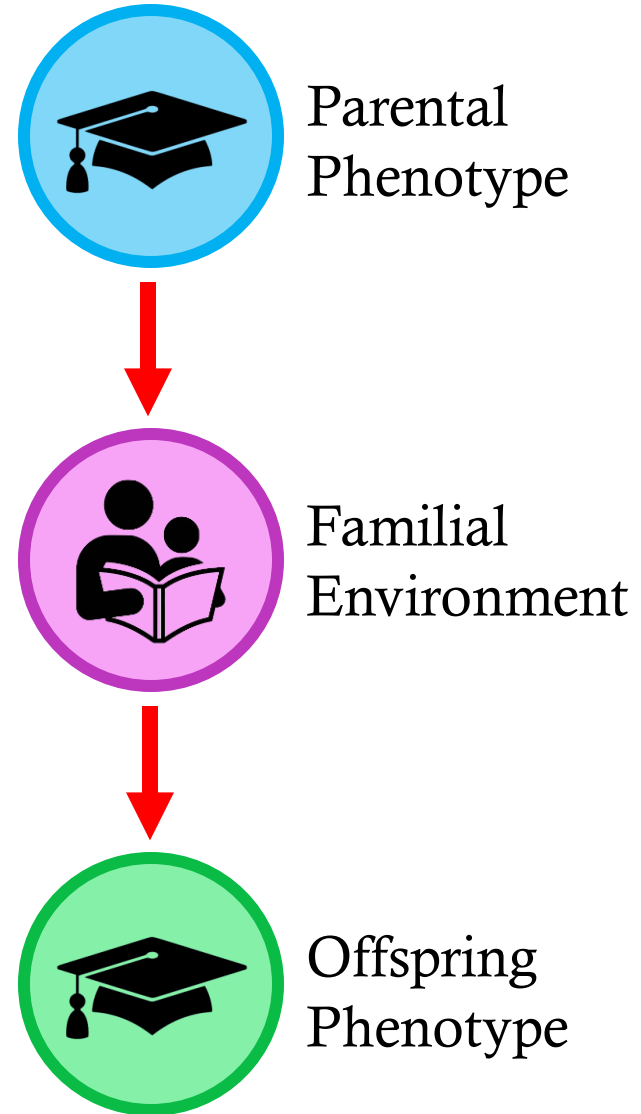
Parental
Phenotype

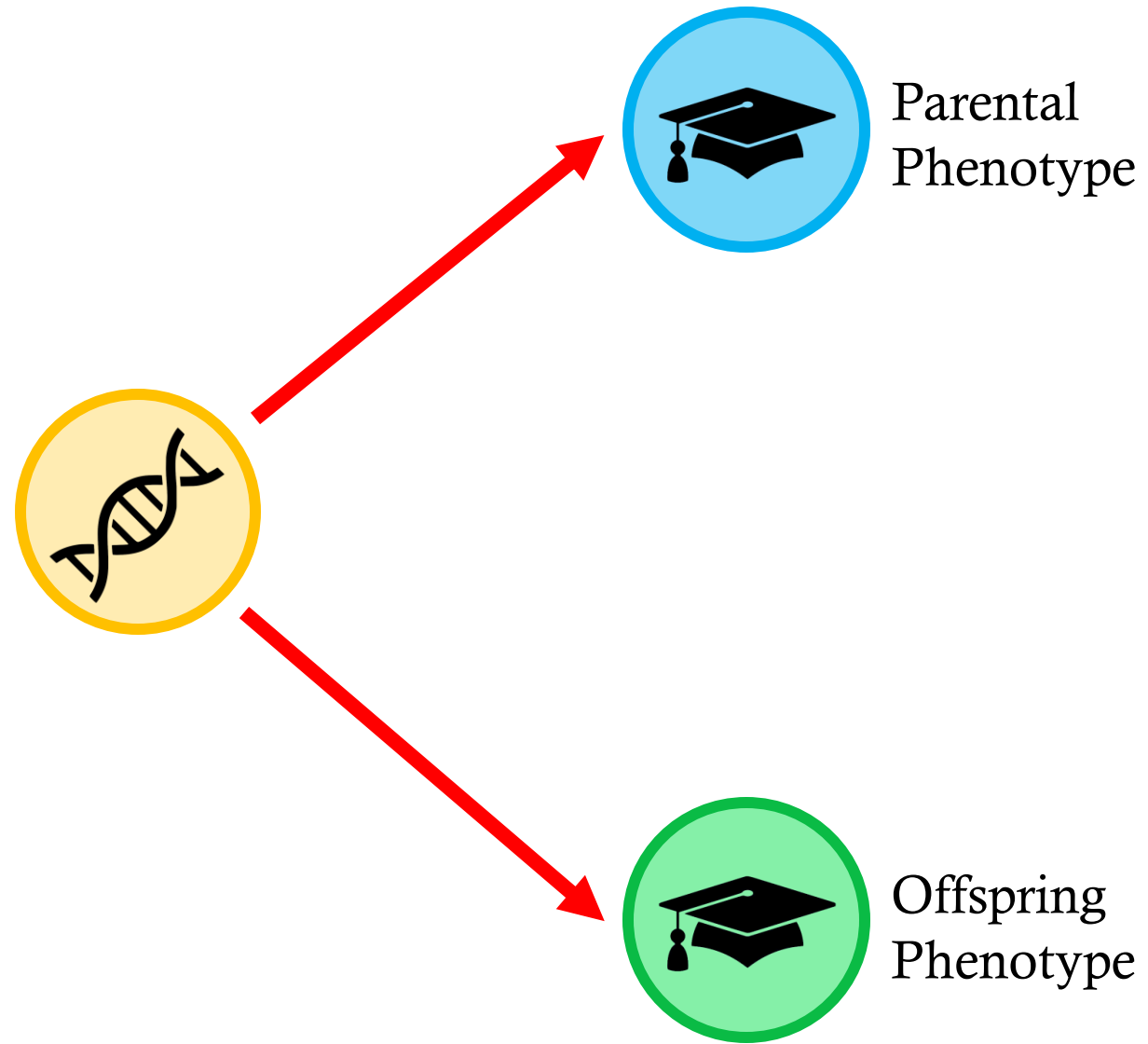


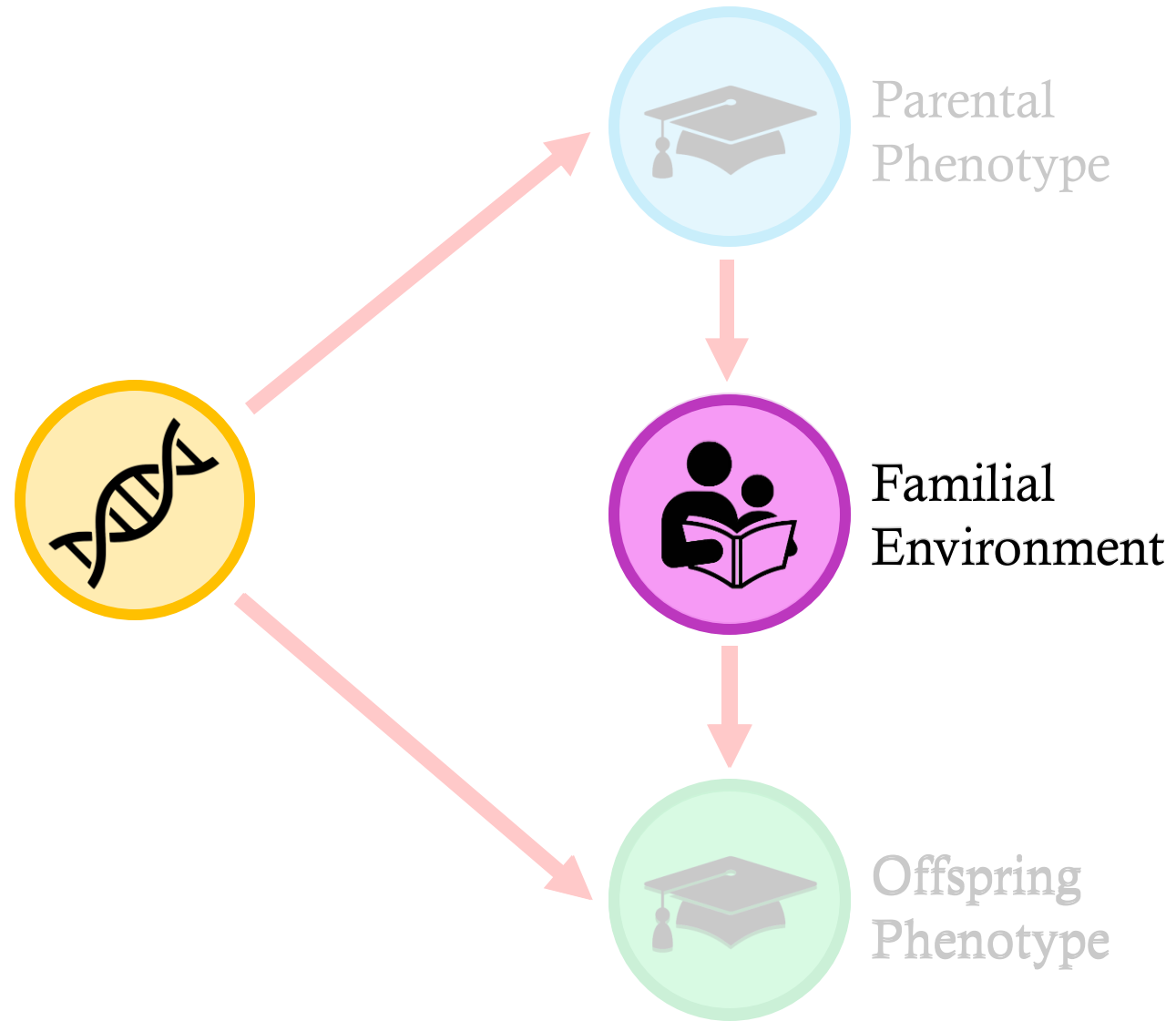
Offspring
Phenotype

**Vertical
Transmission**
(aka "Cultural Transmission")

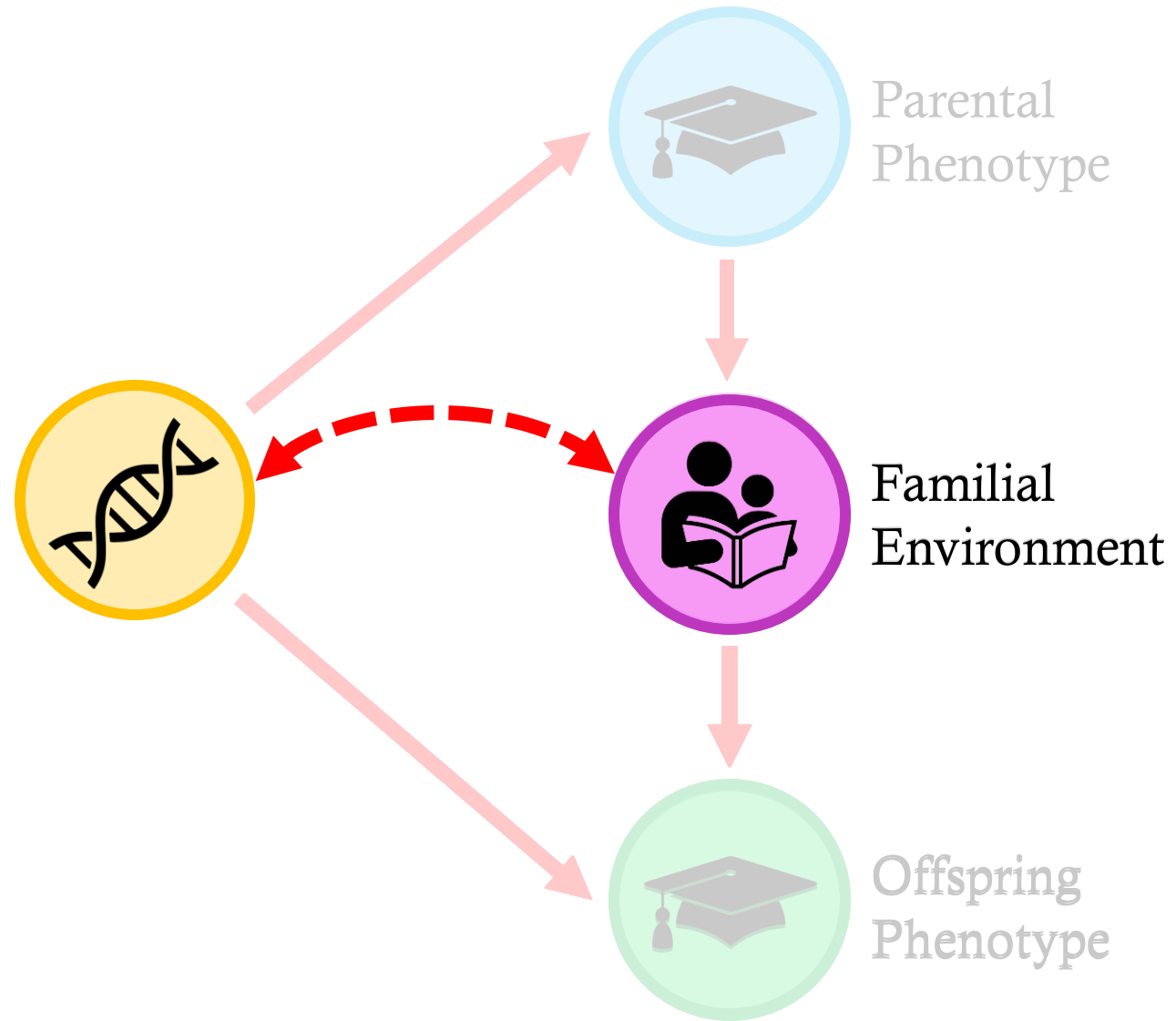


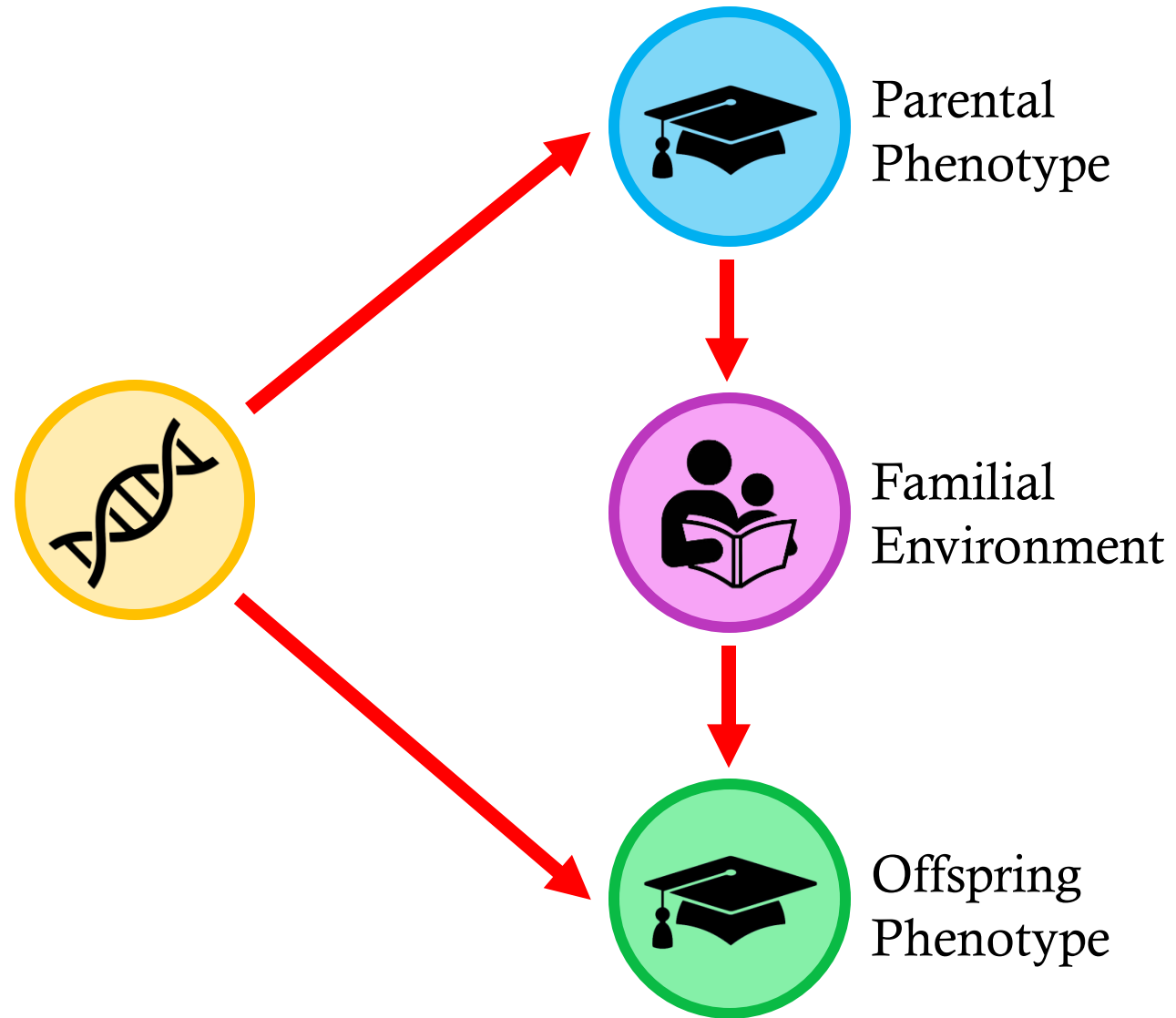


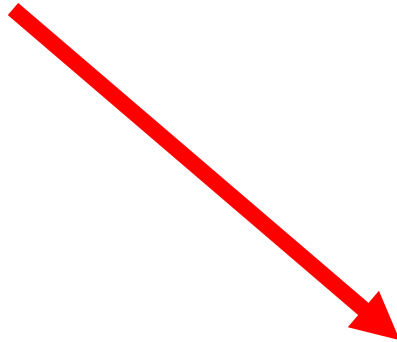




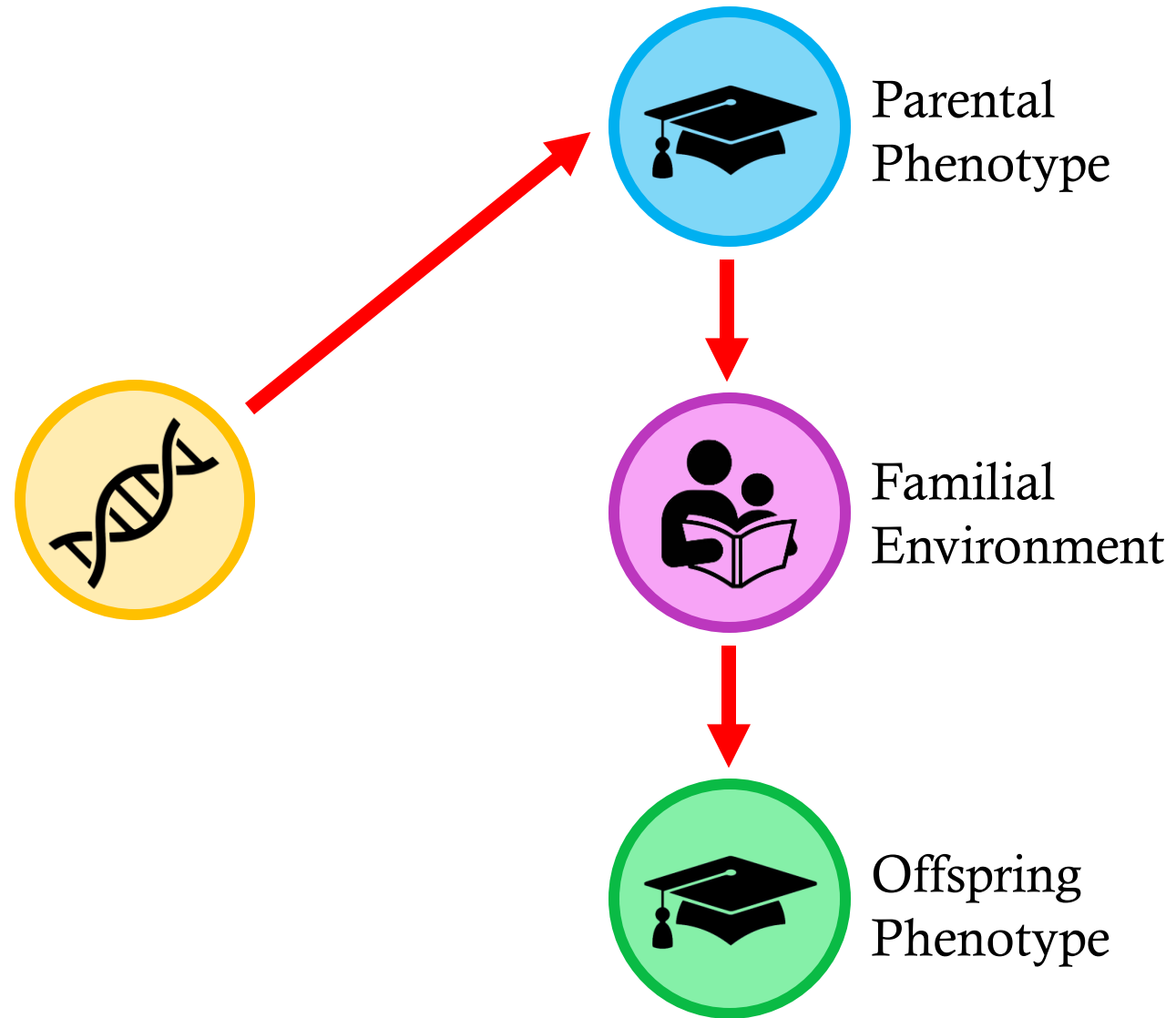
Genetic Nurture
*aka "Passive Gene-
Environment Covariance"*





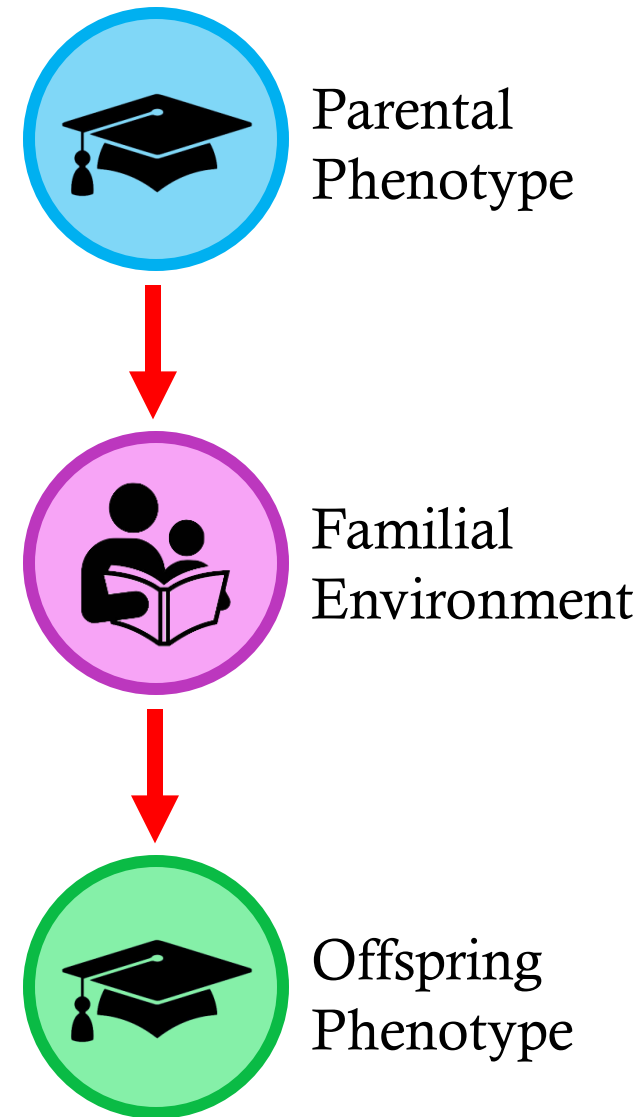


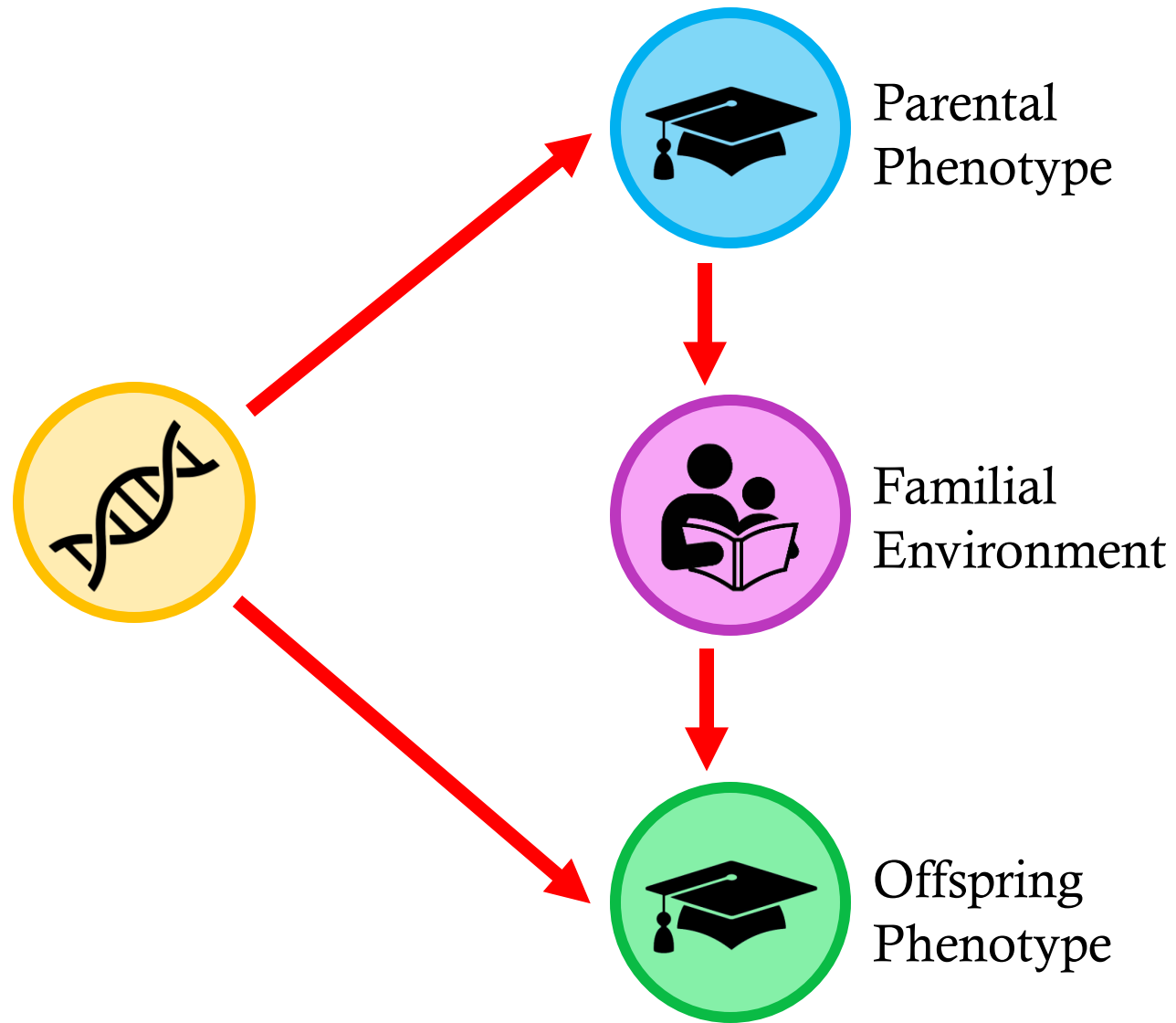
Offspring
Phenotype



If unaccounted for, vertical transmission:

- Will upwardly bias estimates of SNP effects from GWAS
- Will upwardly bias estimates of shared environmental effects (C) in twin ACE models
- Will upwardly bias estimates of additive genetic effects (A) in twin AE and ADE models





Methods

Using structural equation modelling to jointly estimate maternal and fetal effects on birthweight in the UK Biobank

Nicole M Warrington,¹ Rachel M Freathy,^{2,3} Michael C Neale⁴ and David M Evans^{1,3,5*}

Mendelian Randomization

Elucidating the role of maternal environmental exposures on offspring health and disease using two-sample Mendelian randomization

David M Evans ,^{1,2,3*} Gunn-Helen Moen,^{4,5} Liang-Dar Hwang,¹ Debbie A Lawlor^{2,3,6} and Nicole M Warrington¹

RESEARCH ARTICLE

Assessing the Causal Relationship of Maternal Height on Birth Size and Gestational Age at Birth: A Mendelian Randomization Analysis

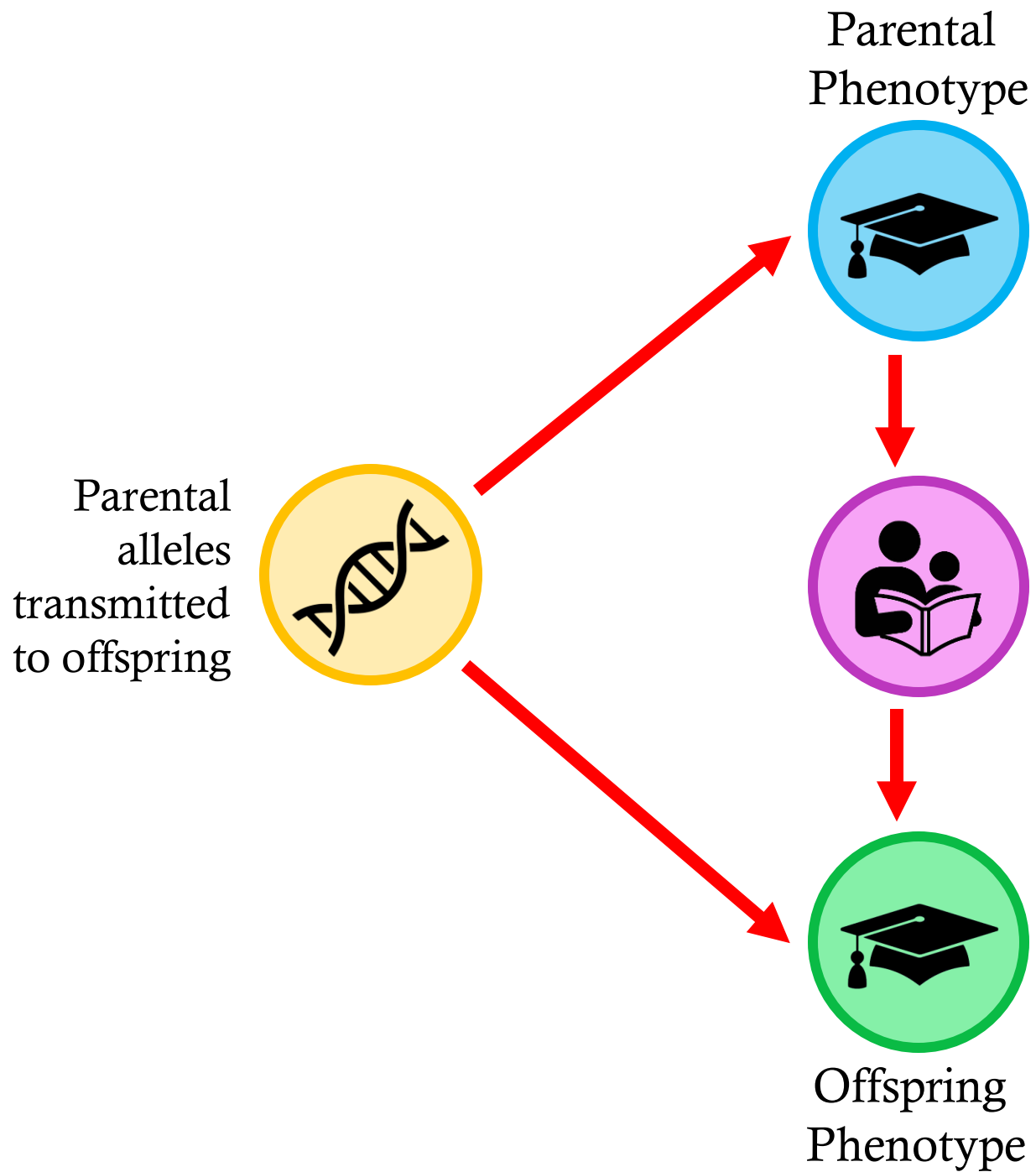
Ge Zhang^{1,2*}, Jonas Bacelis³, Candice Lengyel², Kari Teramo⁴, Mikko Hallman⁵, Øyvind Helgeland⁶, Stefan Johansson^{6,7}, Ronny Myhre⁸, Verena Sengpiel³, Pål Rasmus Njølstad^{6,9}, Bo Jacobsson^{8,10}, Louis Muglia^{2*}

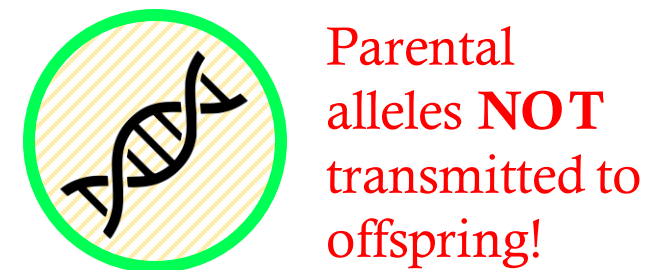
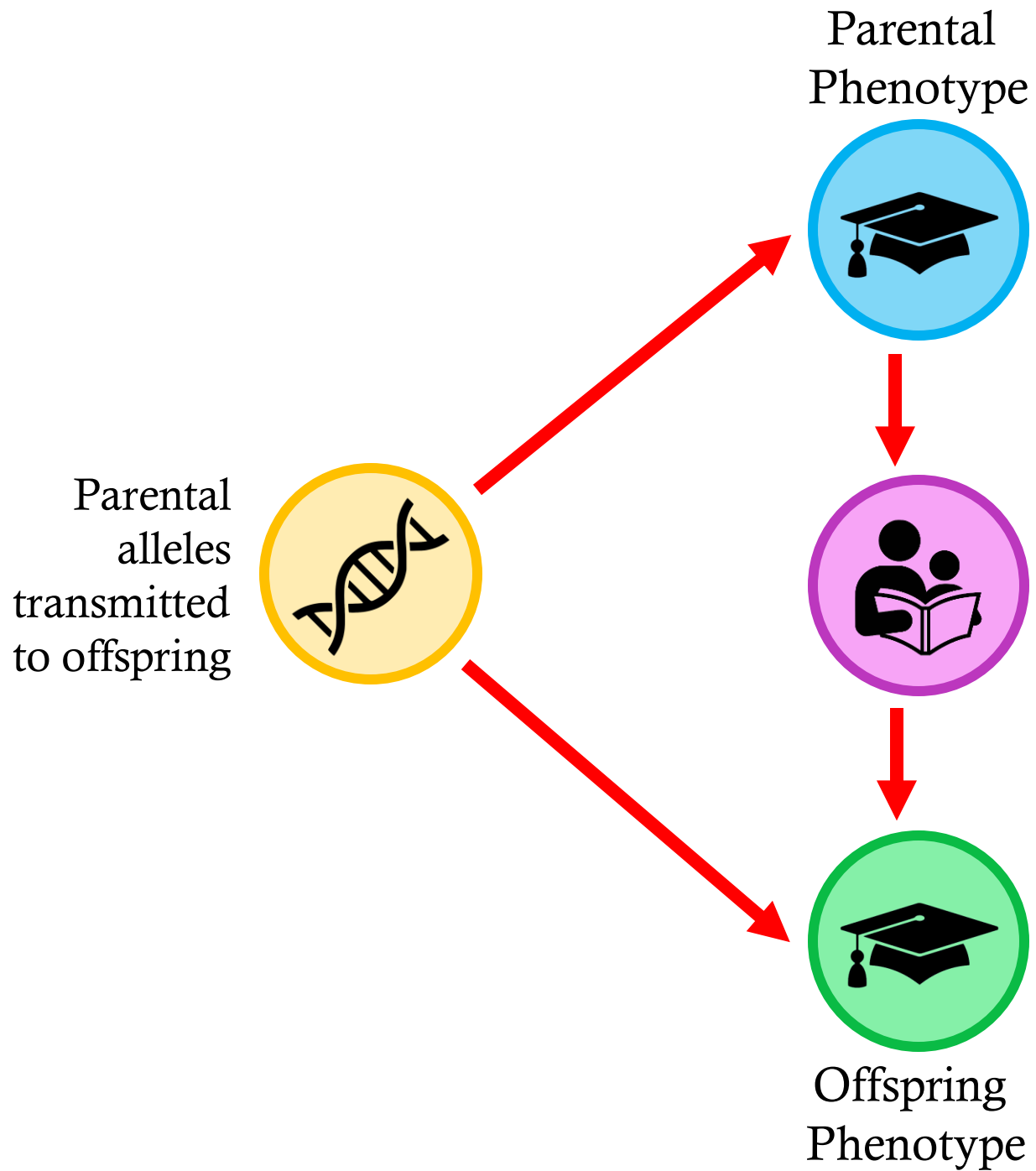
RESEARCH

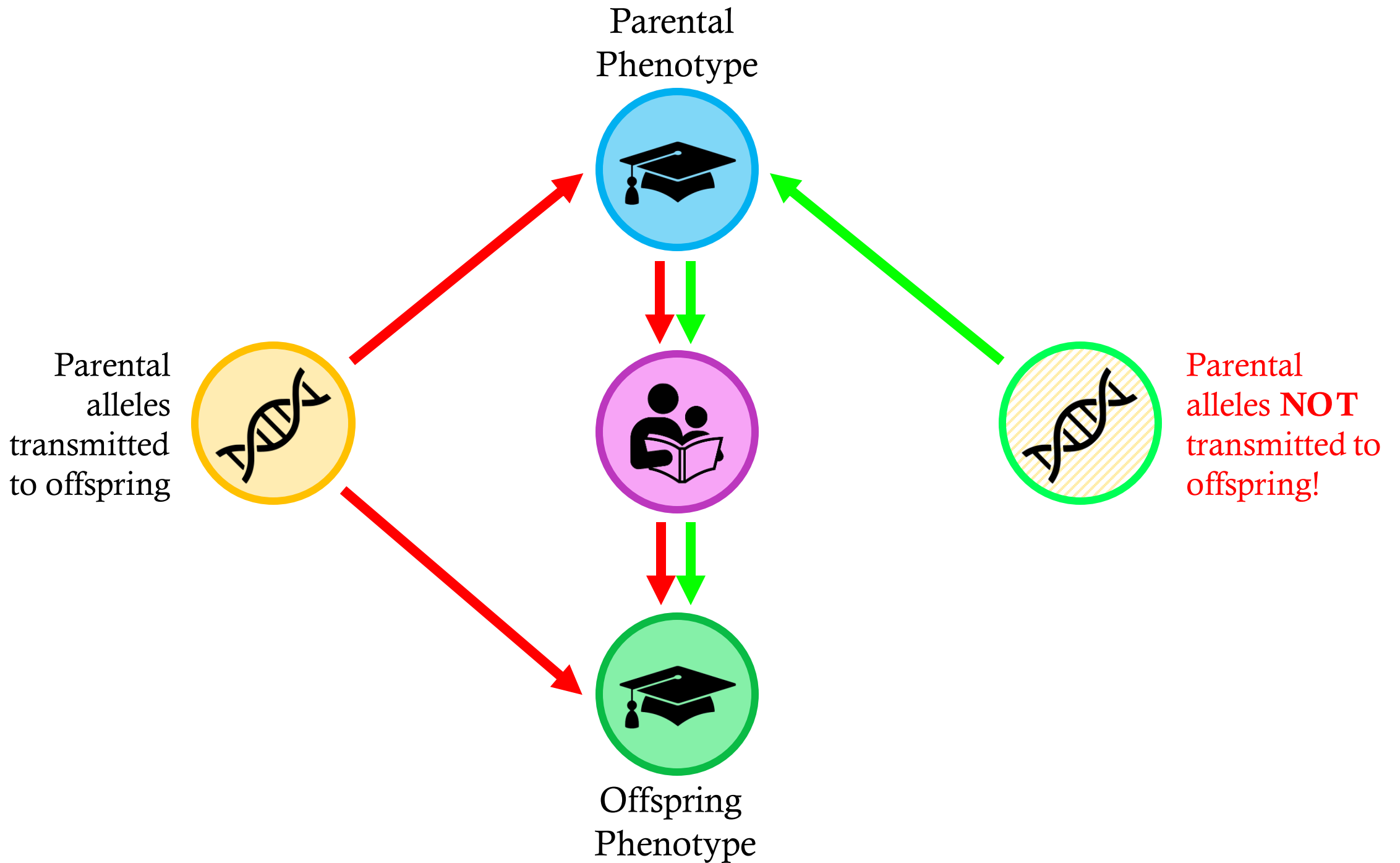
HUMAN GENOMICS

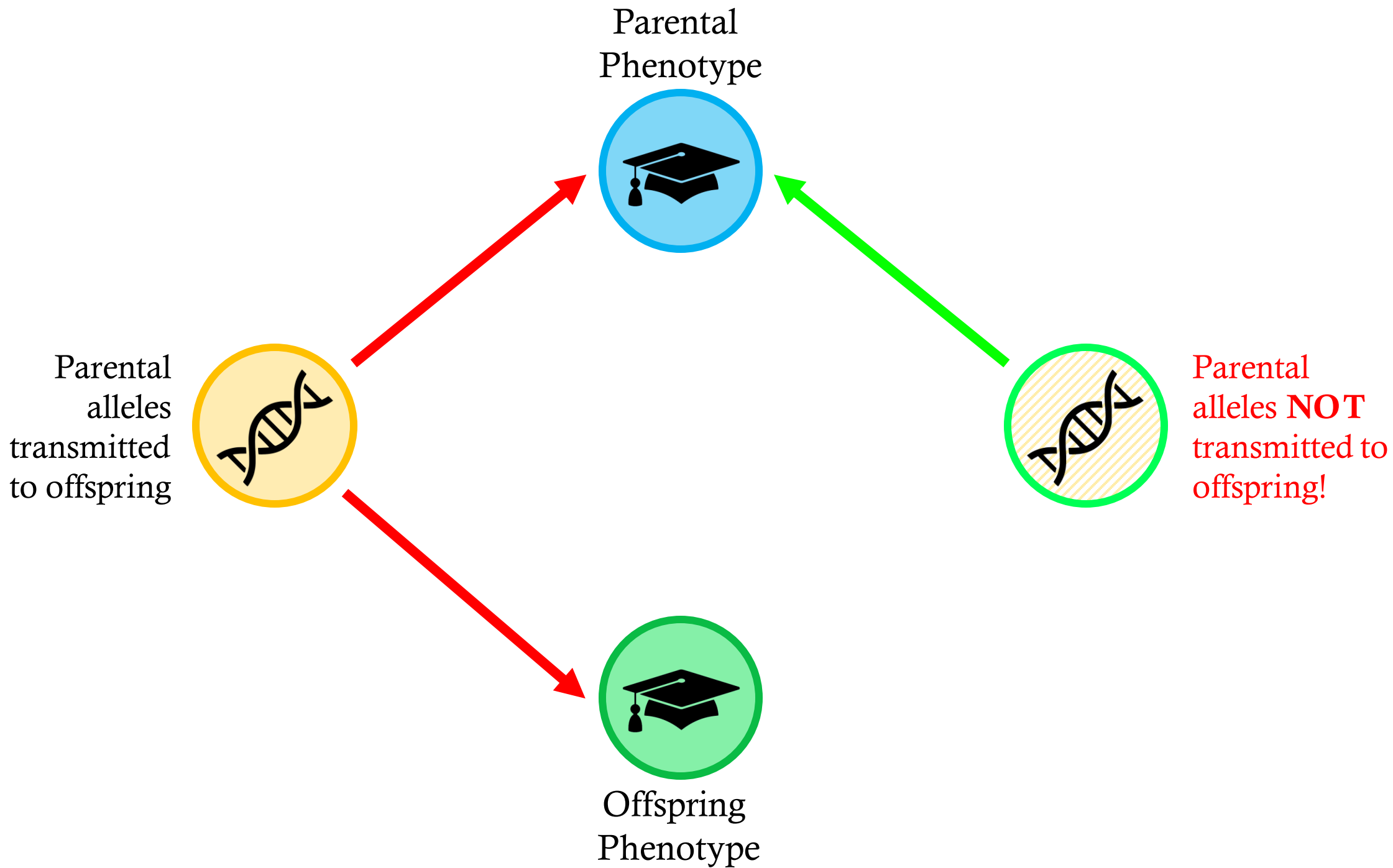
The nature of nurture: Effects of parental genotypes

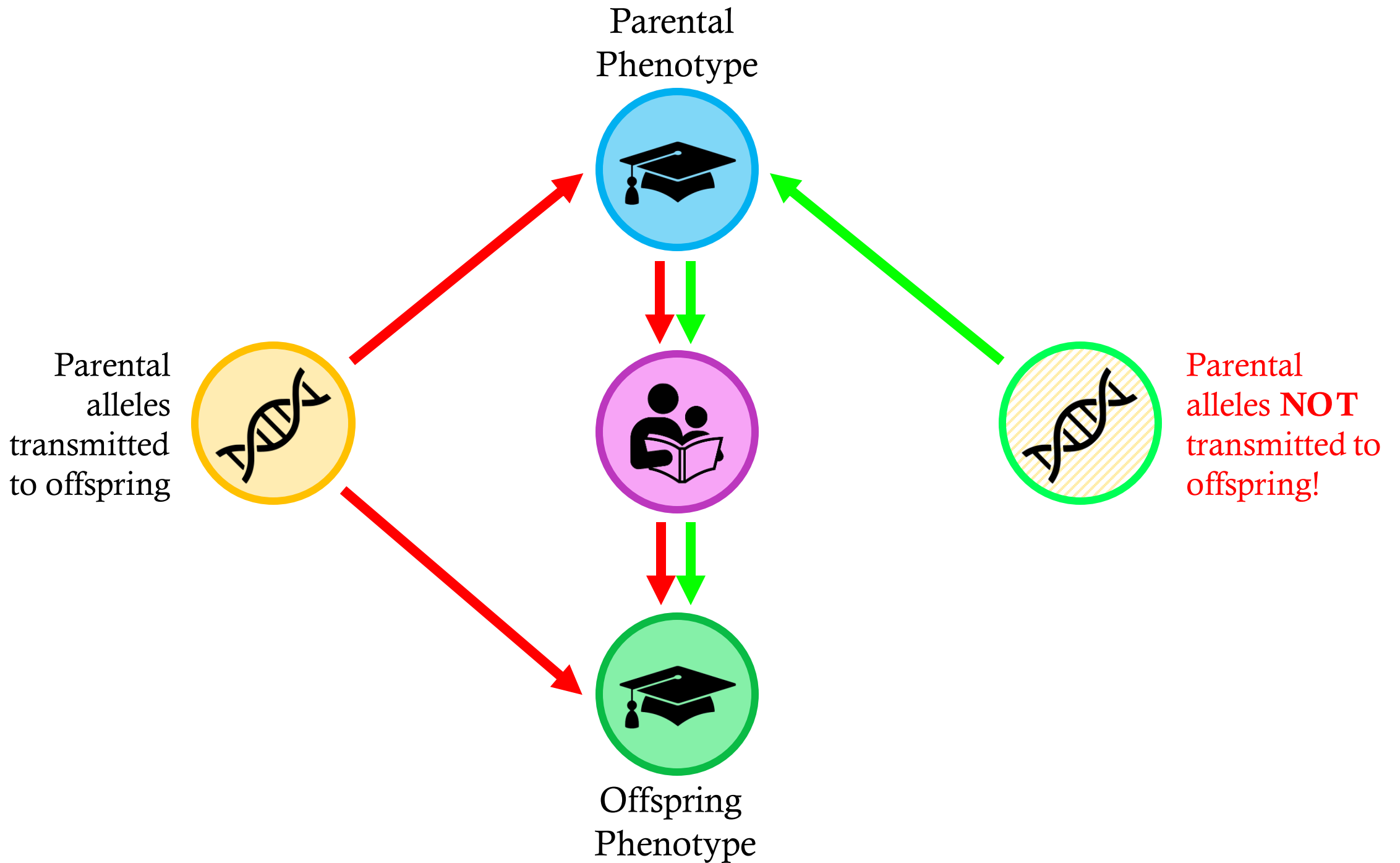
Augustine Kong,^{1,2,3*} Gudmar Thorleifsson,¹ Michael L. Frigge,¹ Bjarni J. Vilhjalmsdottir,^{4,5} Alexander I. Young,^{1,2,6} Thorgeir E. Thorgeirsson,¹ Stefania Benonisdottir,¹ Asmundur Oddsson,¹ Bjarni V. Halldorsson,¹ Gisli Masson,¹ Daniel F. Gudbjartsson,^{1,3} Agnar Helgason,^{1,7} Gyda Bjornsdottir,¹ Unnur Thorsteinsdottir,^{1,8} Kari Stefansson^{1,8*}

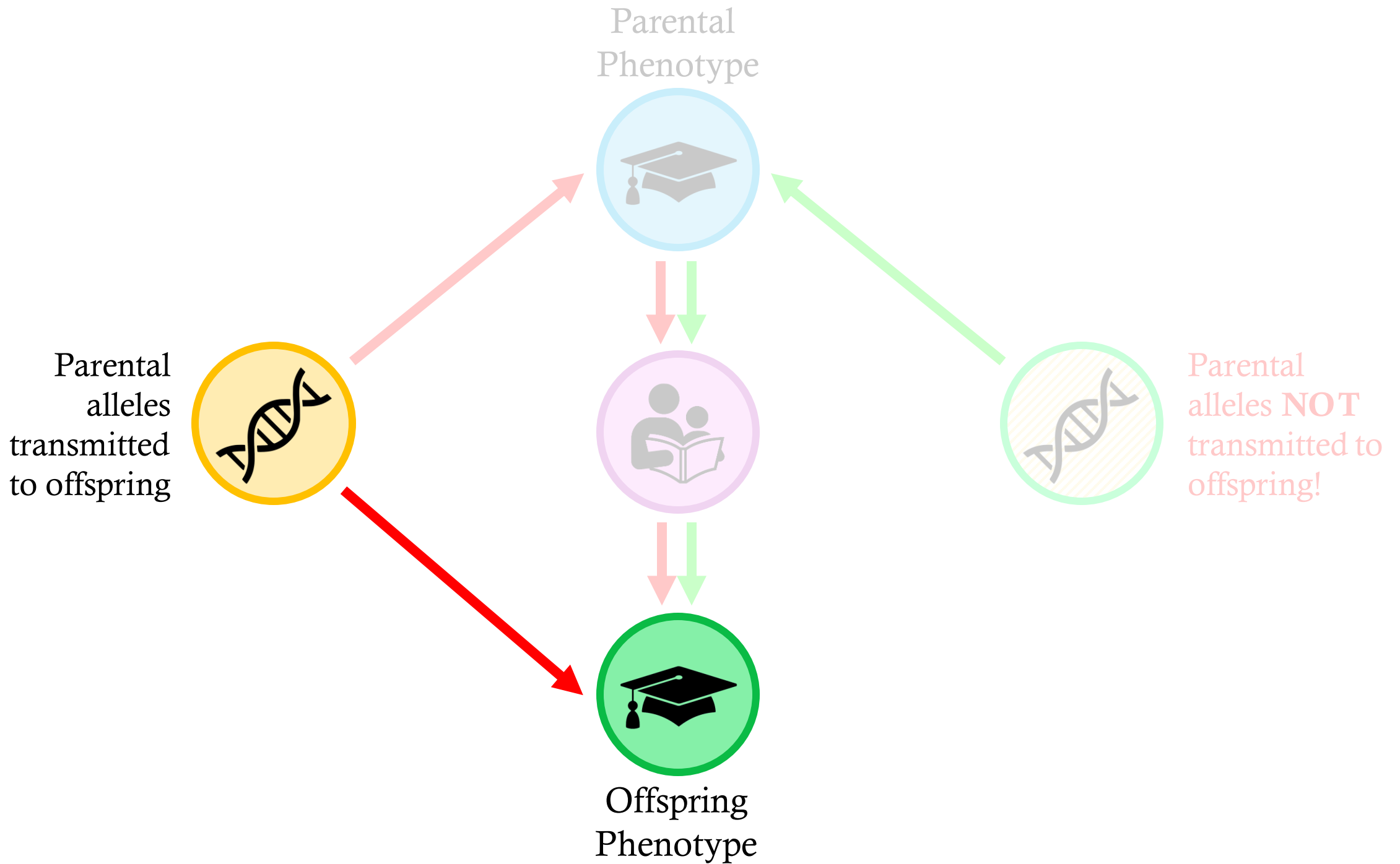












Parental
Phenotype



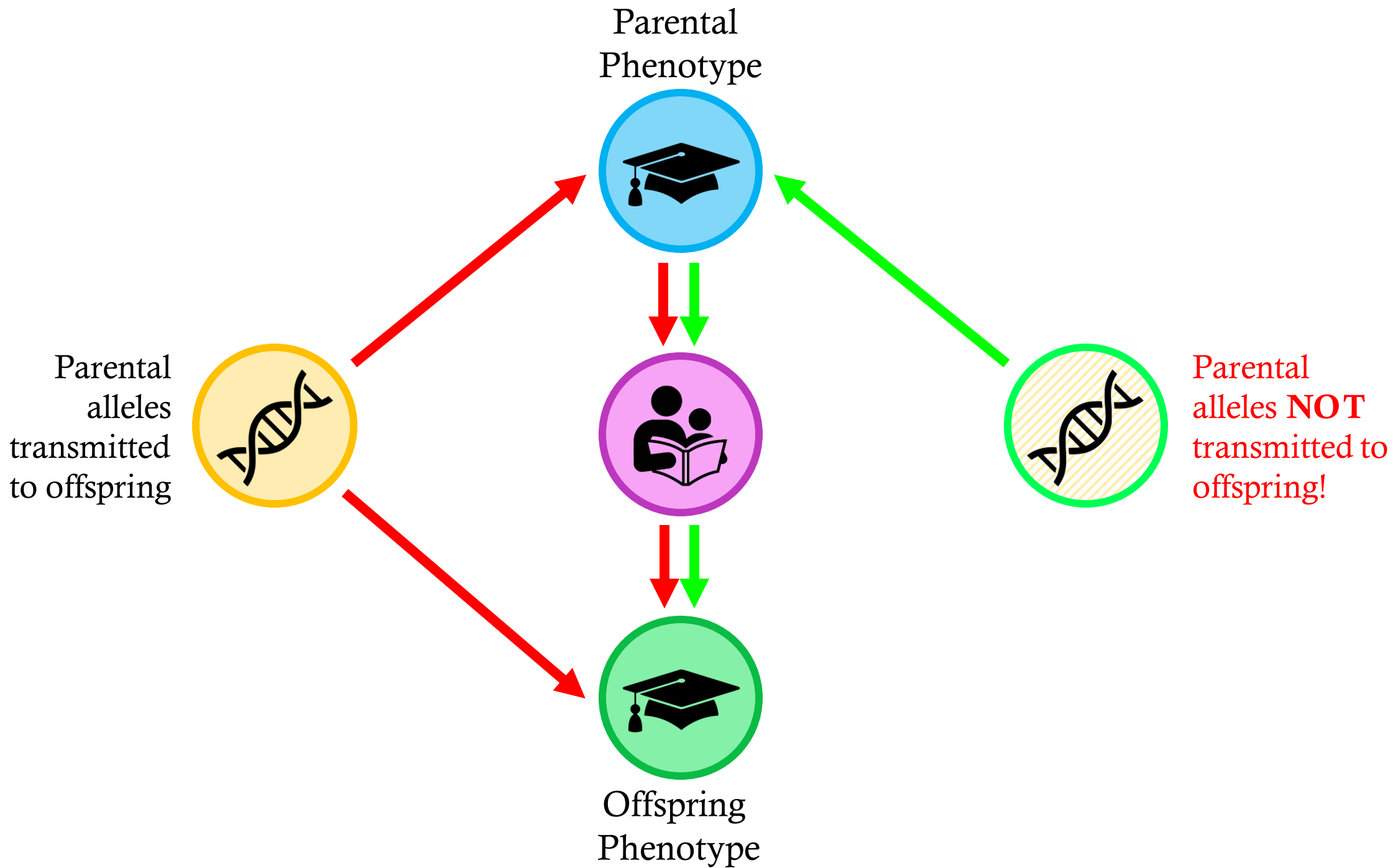
Offspring
Phenotype

Parental
alleles
transmitted
to offspring



Parental
alleles **NOT**
transmitted to
offspring!







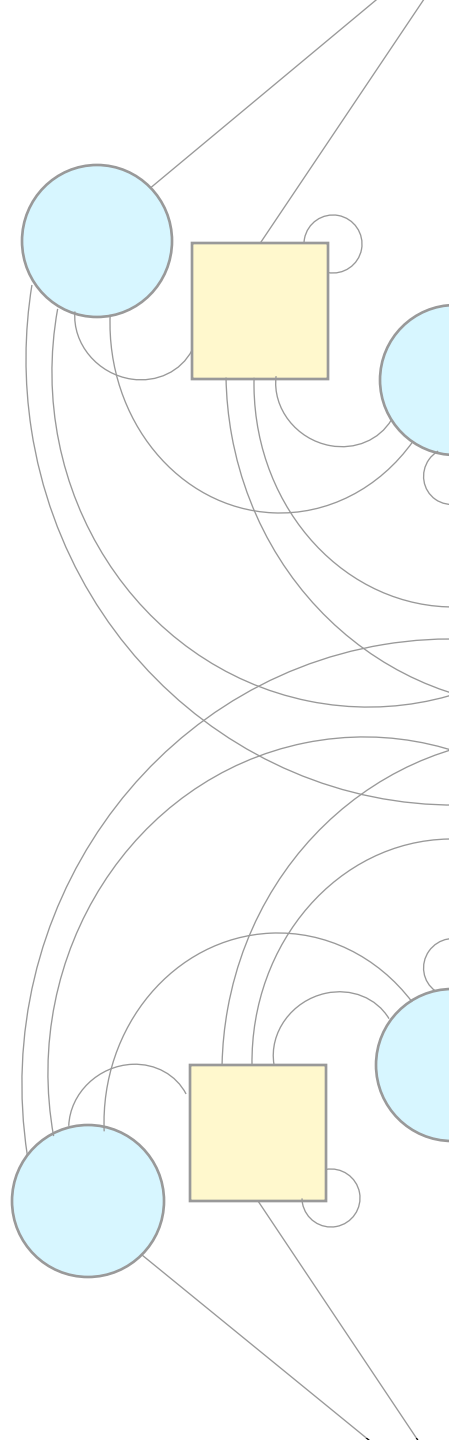
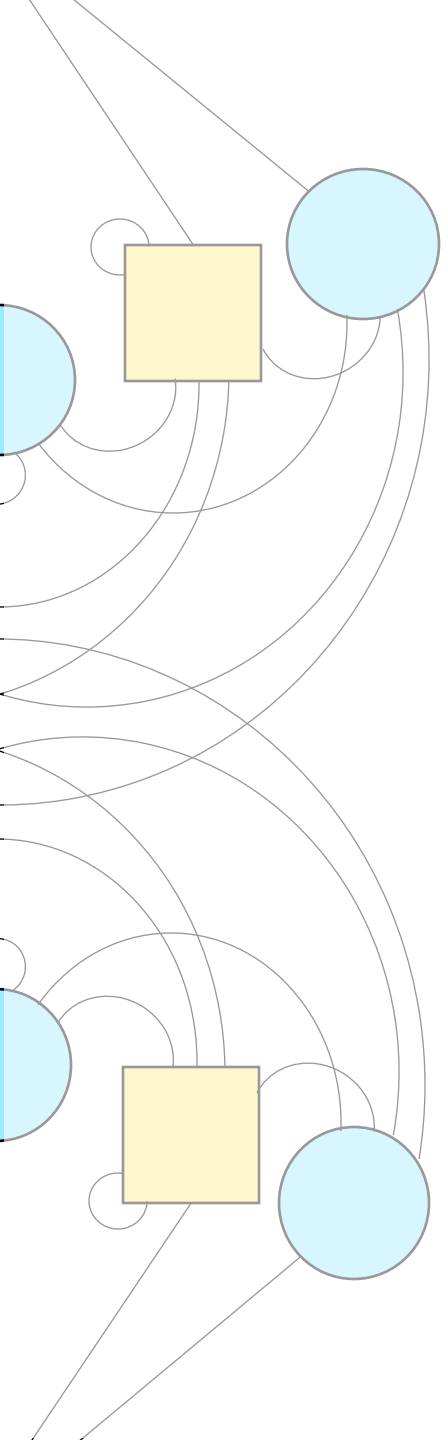
Estimation of Parental Effects Using Polygenic Scores

Jared V. Balbona^{1,2}  · Yongkang Kim¹ · Matthew C. Keller^{1,2}

Received: 7 August 2020 / Accepted: 20 November 2020 / Published online: 2 January 2021

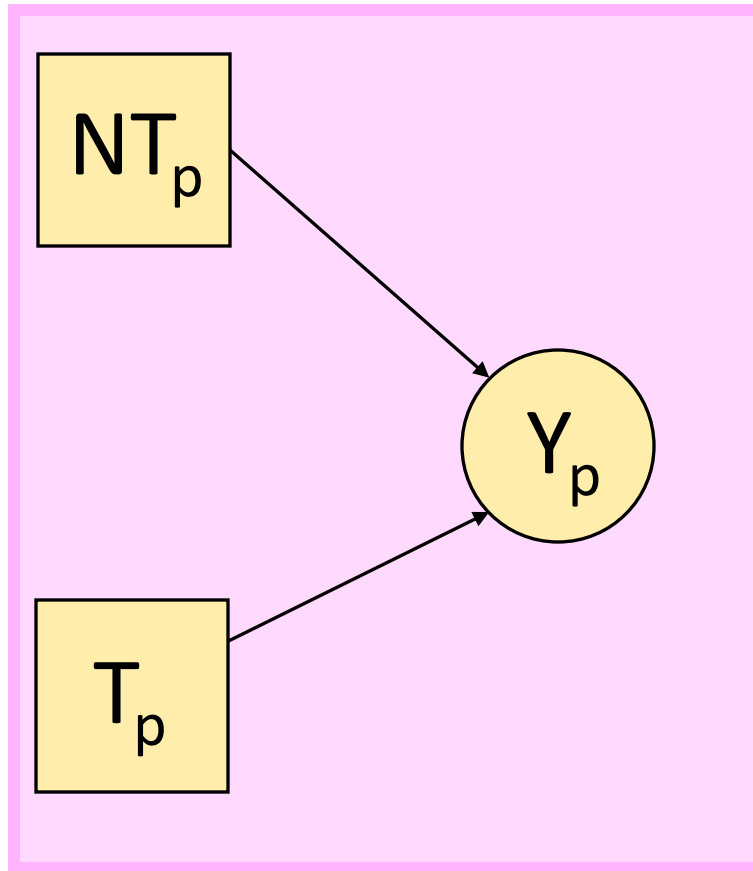
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SEM-PGS

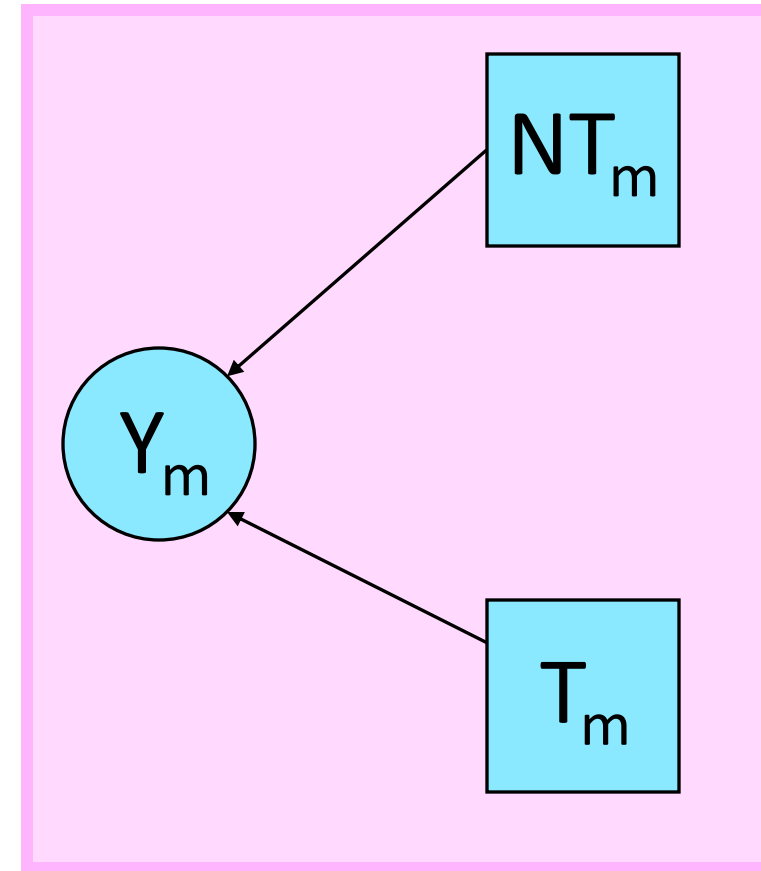


SEM-PGS

1. Unbiased estimates of h^2 , vertical transmission, and genetic nurture— Even when the PGS being used is not very predictive
2. Properly accounts for various types of assortative mating at both equilibrium and disequilibrium
3. In principle, is not biased by missing data-- Thus, it does not require complete trios
4. Is very easy to use, relying on relatively simple math
5. Allows for a vast number of extensions to best fit the trait and data being worked with



Paternal Genes and
Phenotype

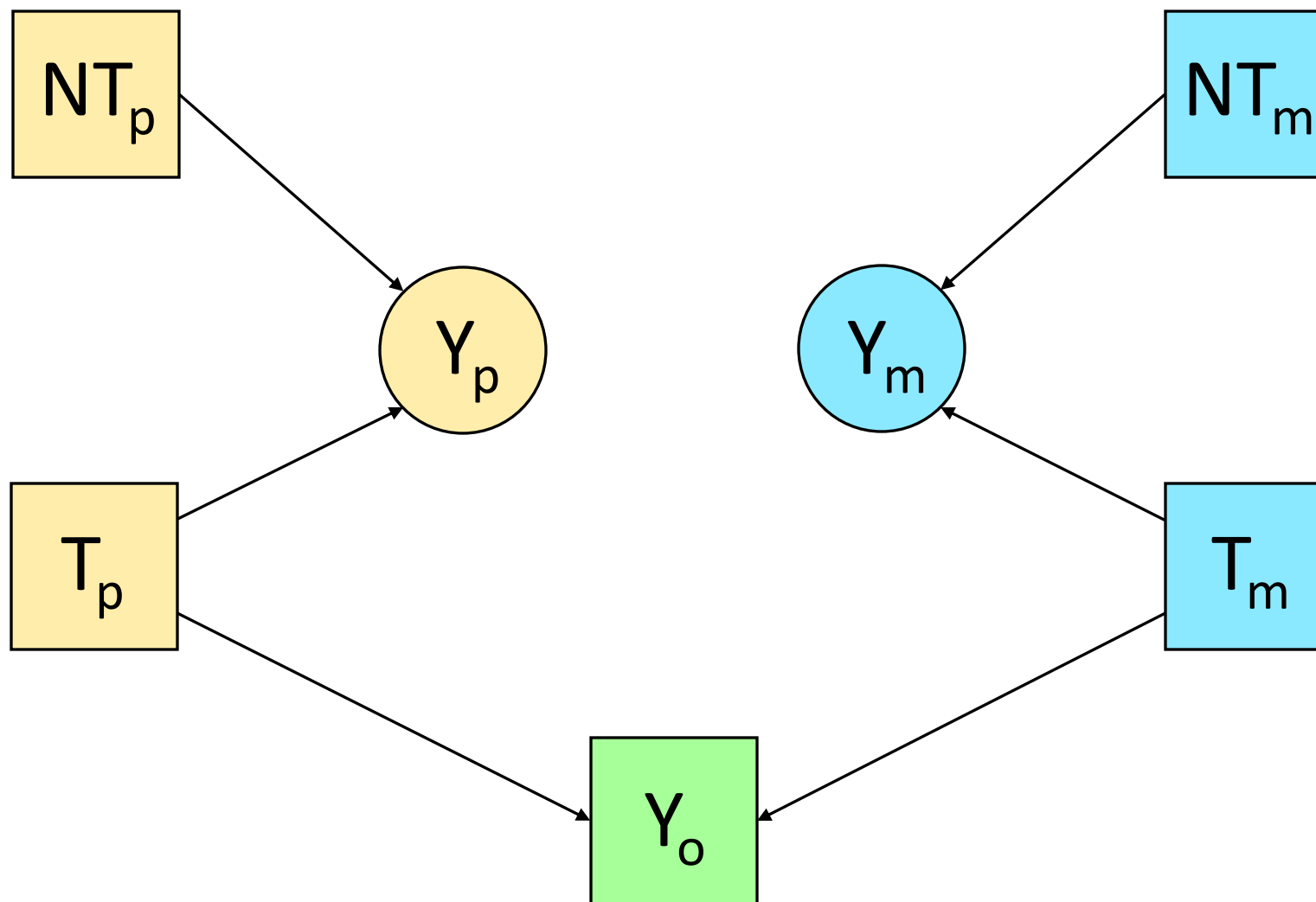


Maternal Genes and
Phenotype

Y: Phenotypic Value

T: PGS made from the parent's *transmitted* alleles

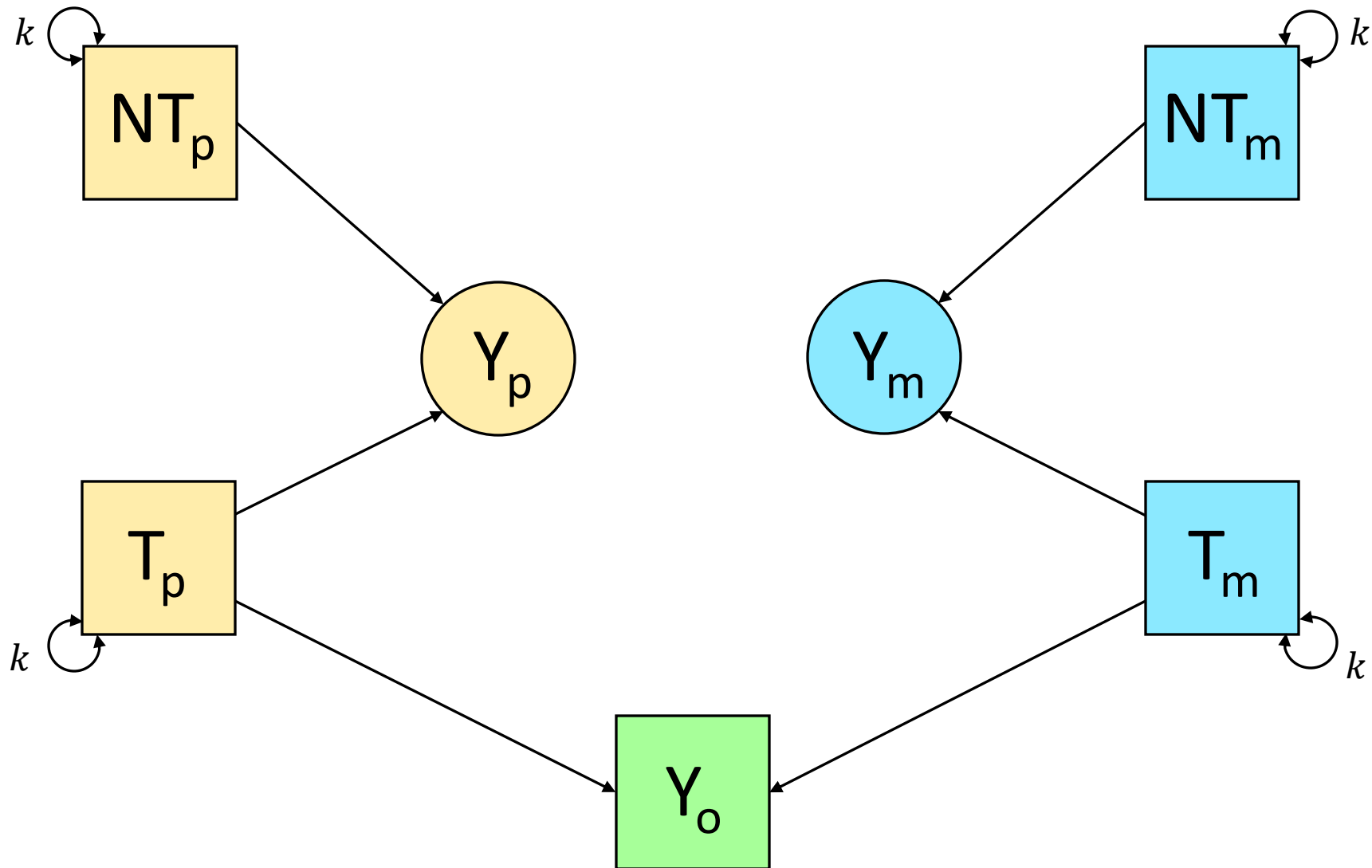
NT: PGS made from the parent's *non-transmitted* alleles



Y: Phenotypic Value

T: PGS made from the parent's *transmitted* alleles

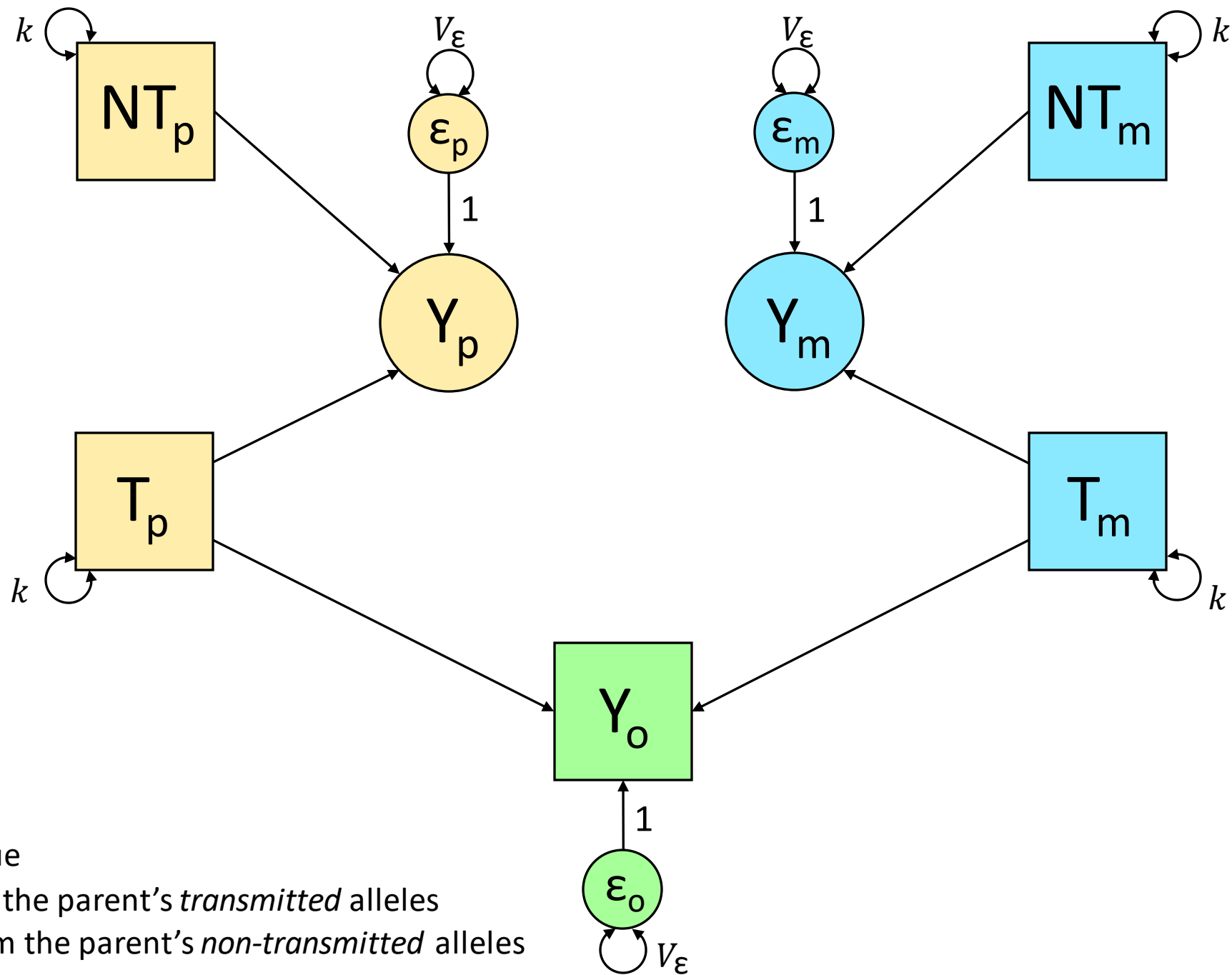
NT: PGS made from the parent's *non-transmitted* alleles



Y: Phenotypic Value

T: PGS made from the parent's *transmitted* alleles

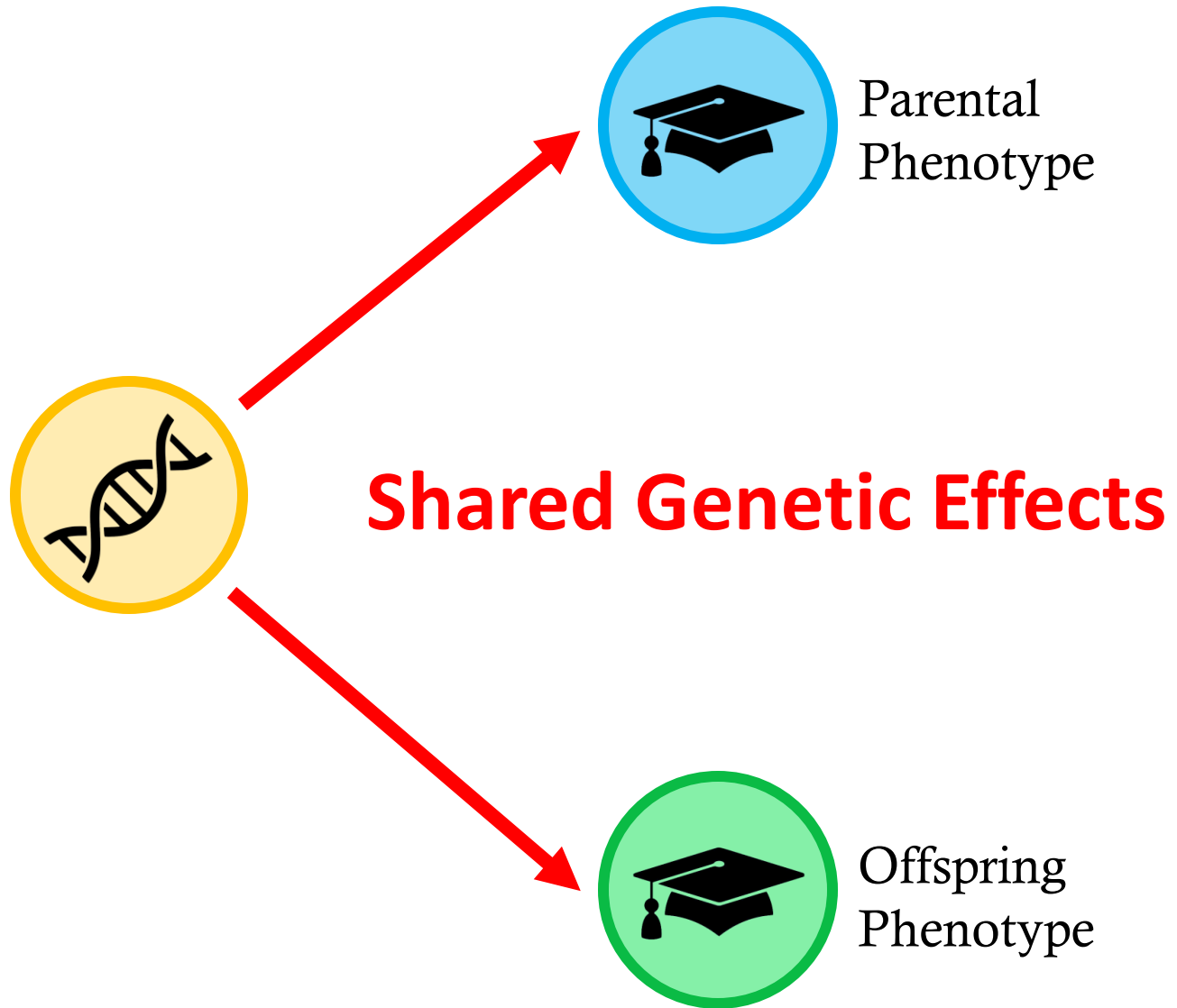
NT: PGS made from the parent's *non-transmitted* alleles

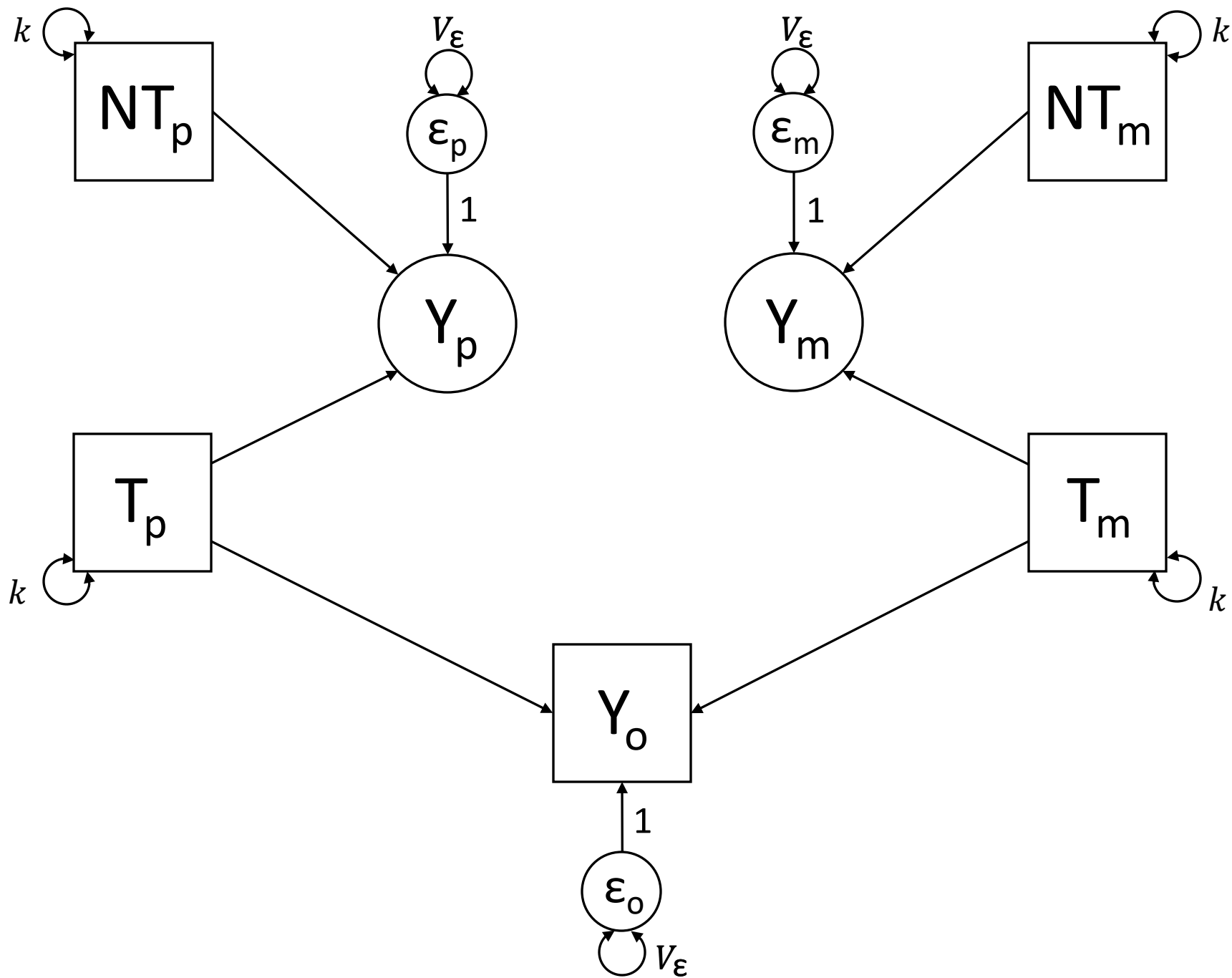


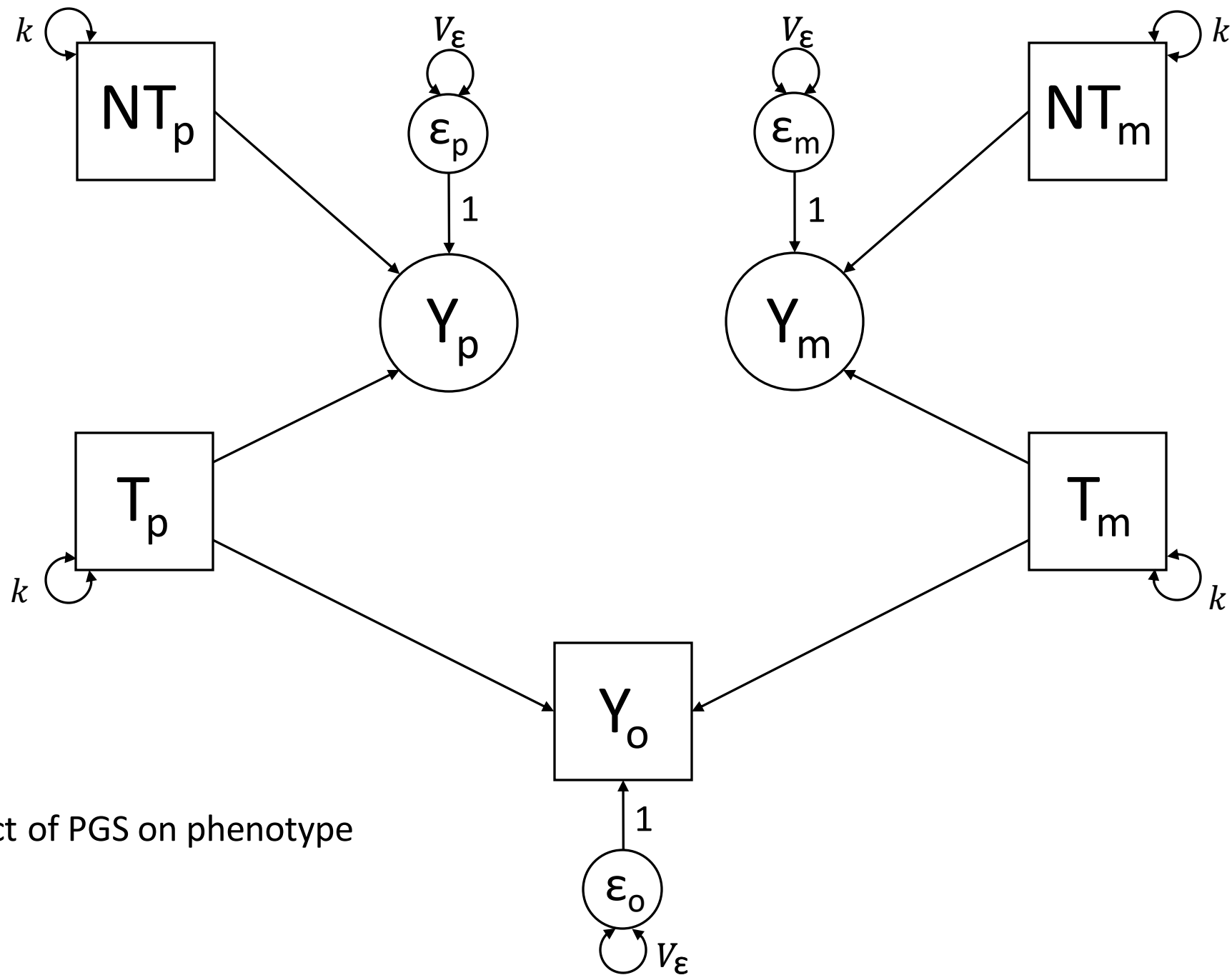
Y: Phenotypic Value

T: PGS made from the parent's *transmitted* alleles

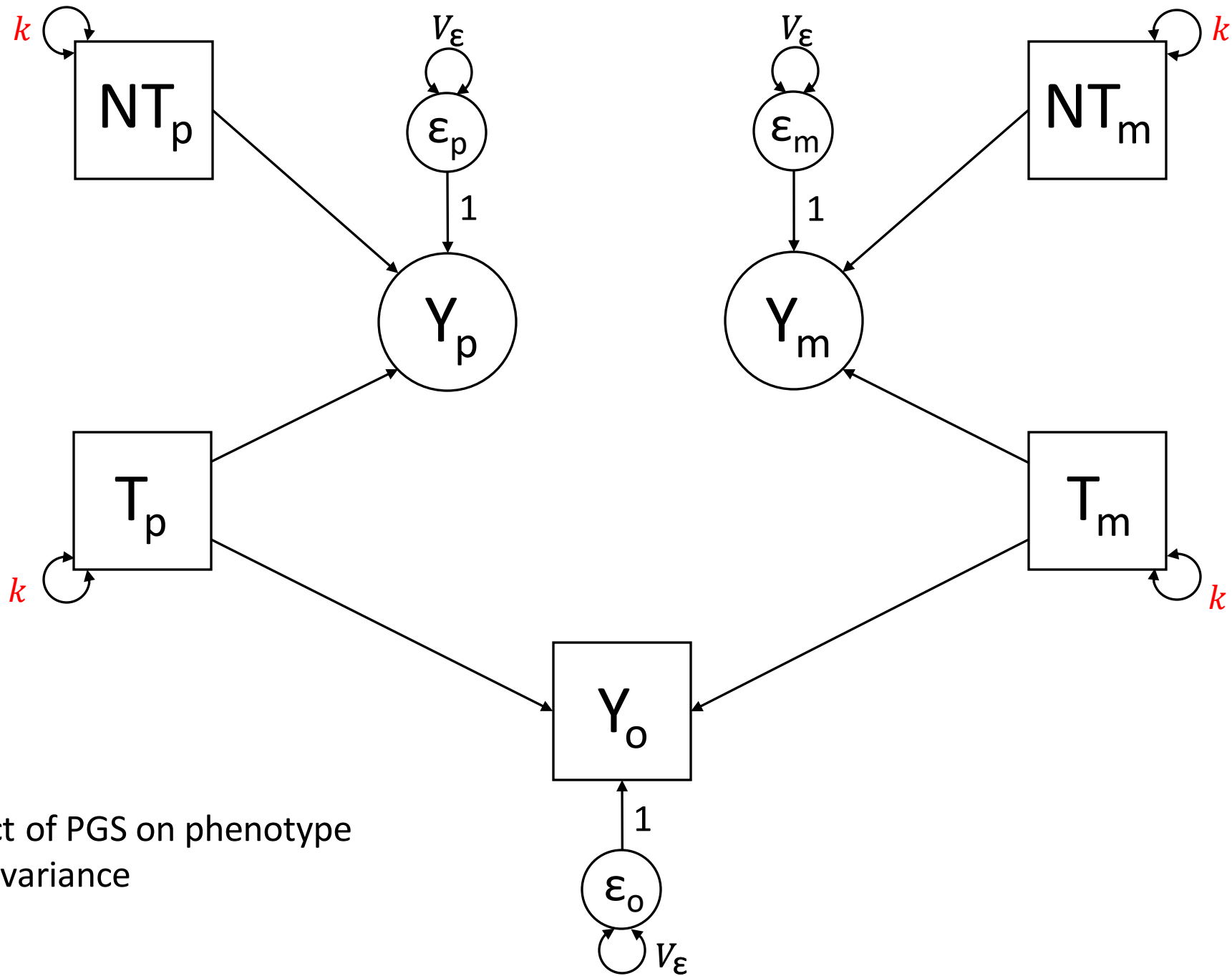
NT: PGS made from the parent's *non-transmitted* alleles





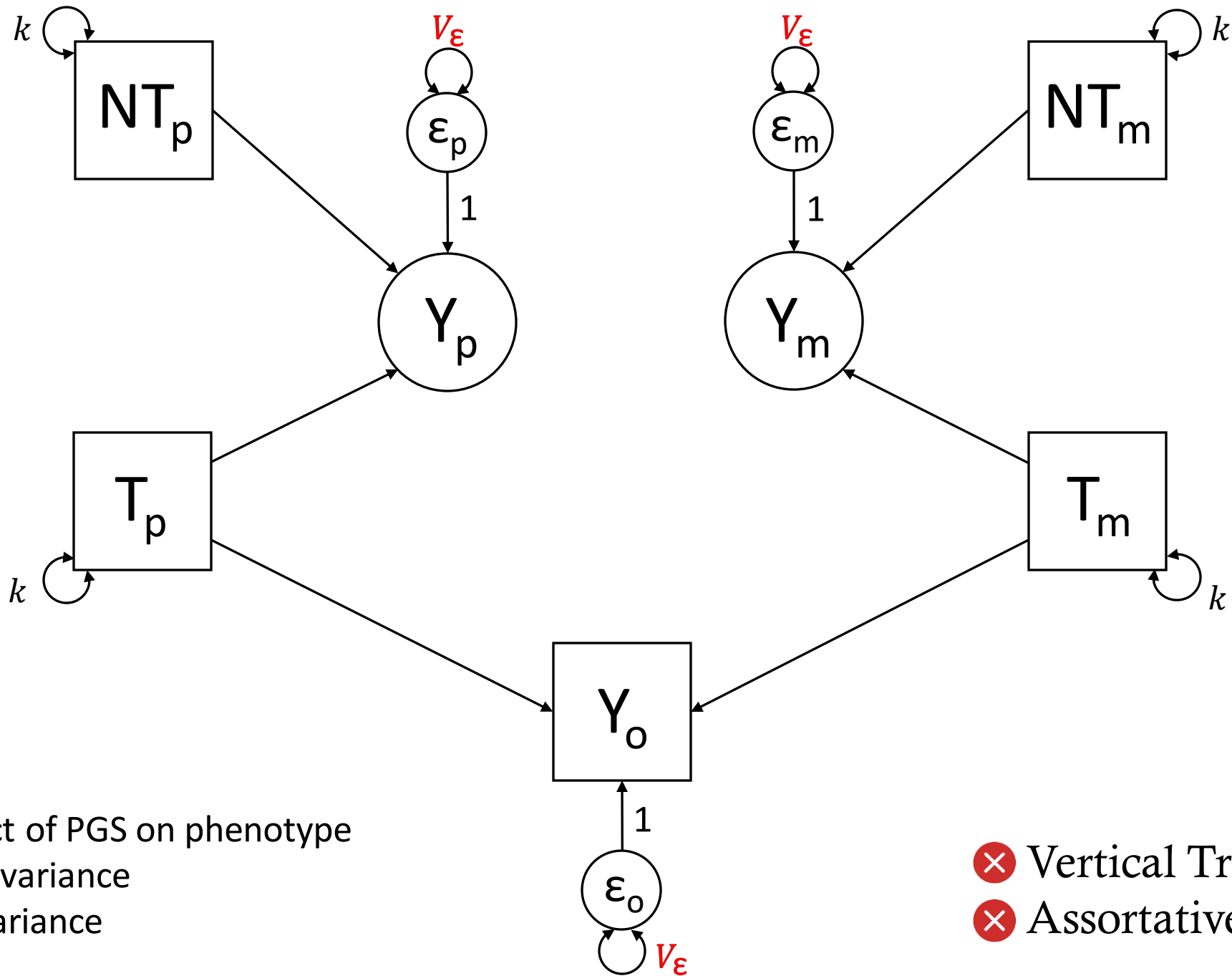


δ : Direct effect of PGS on phenotype



δ : Direct effect of PGS on phenotype

k : Haplotypic variance



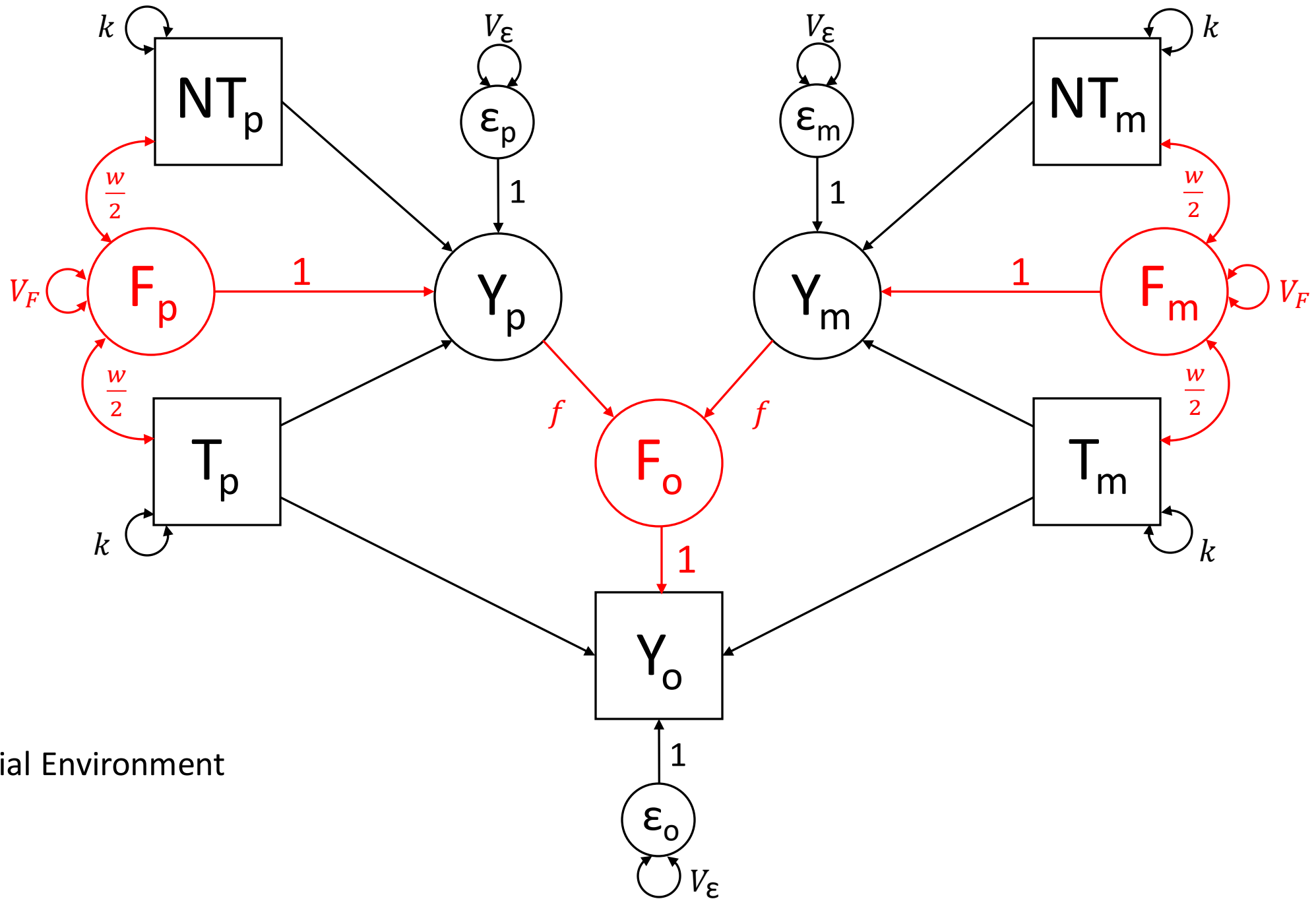
δ : Direct effect of PGS on phenotype

k : Haplotypic variance

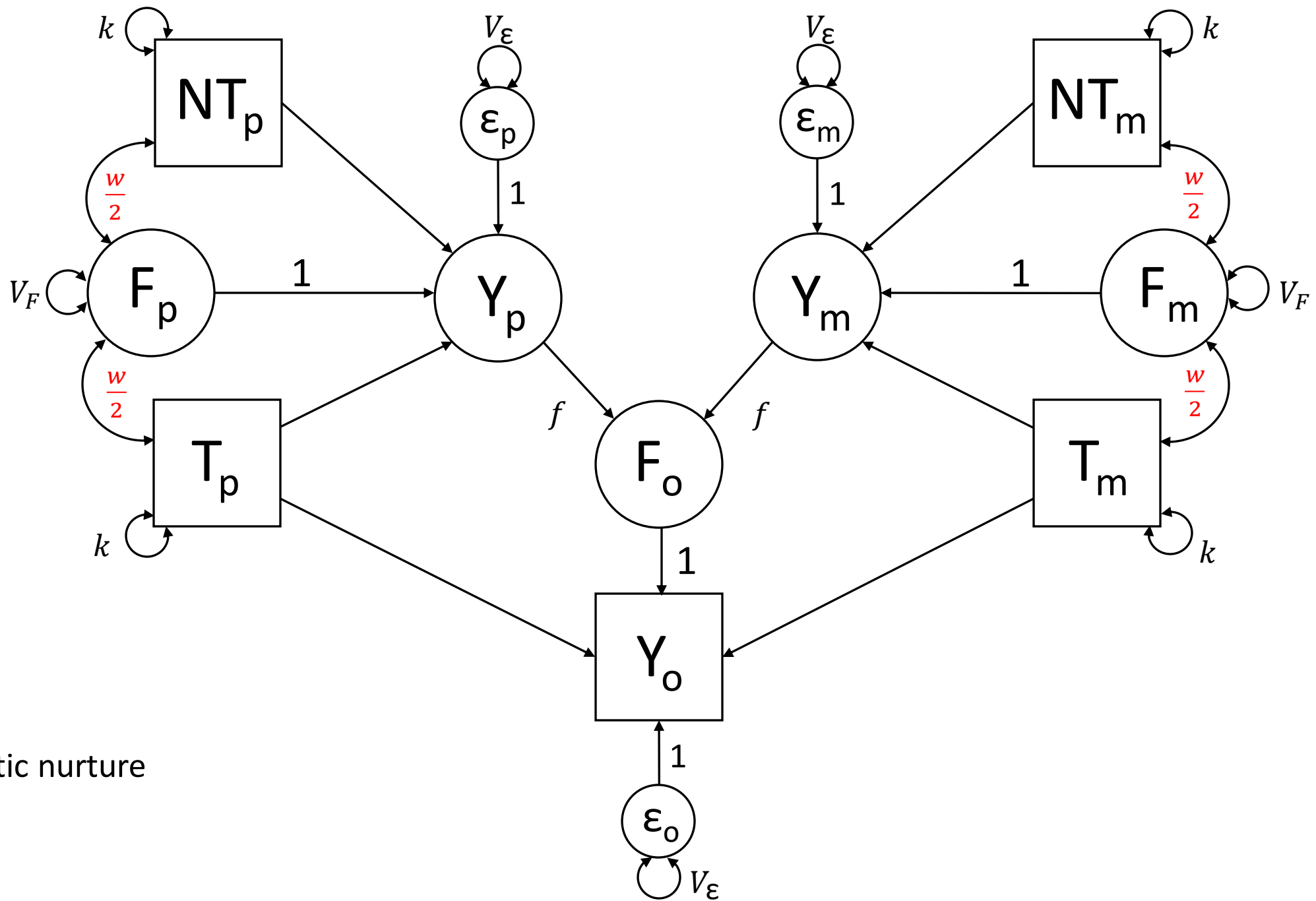
V_ϵ : Residual variance

⊗ Vertical Transmission

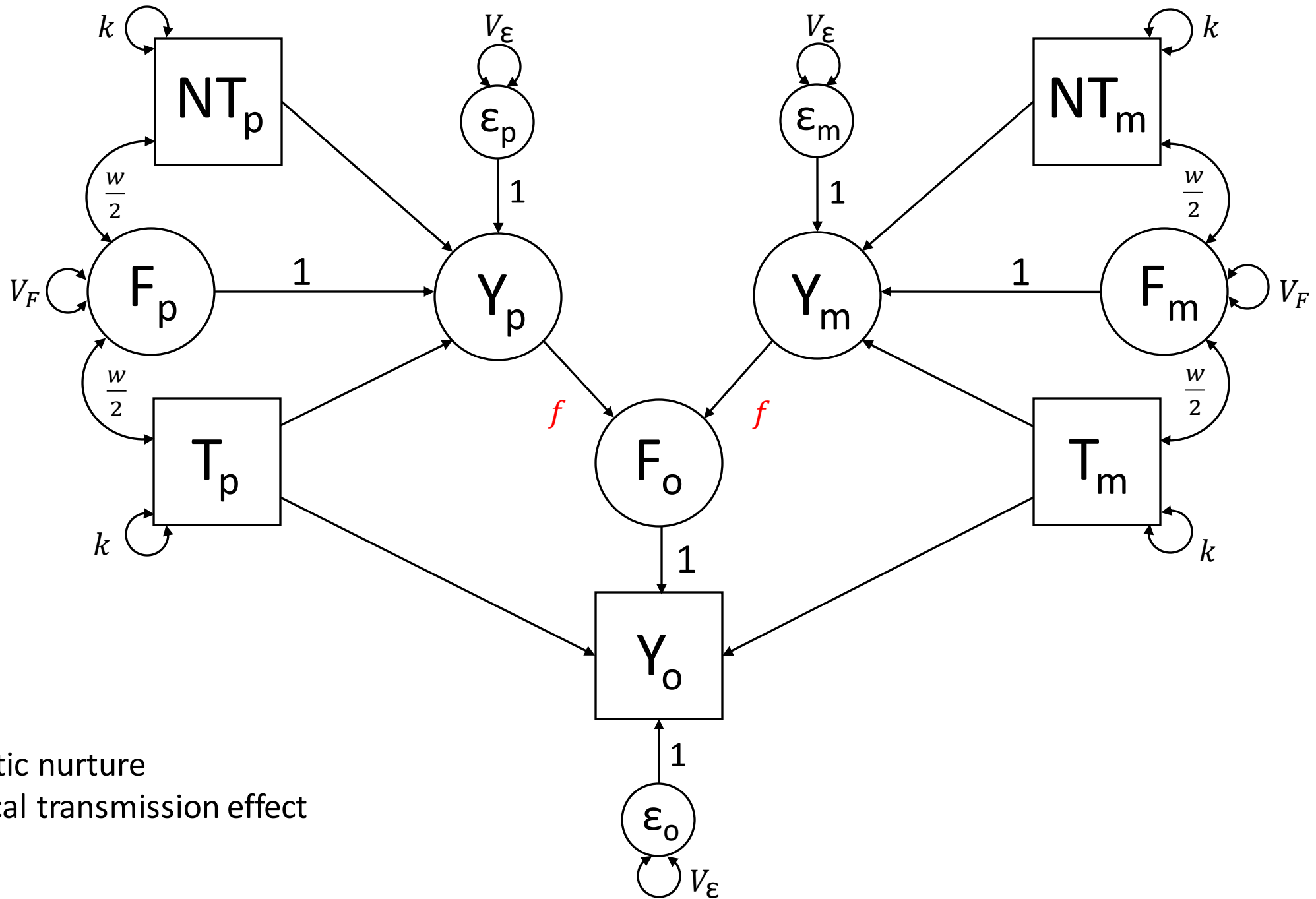
⊗ Assortative Mating



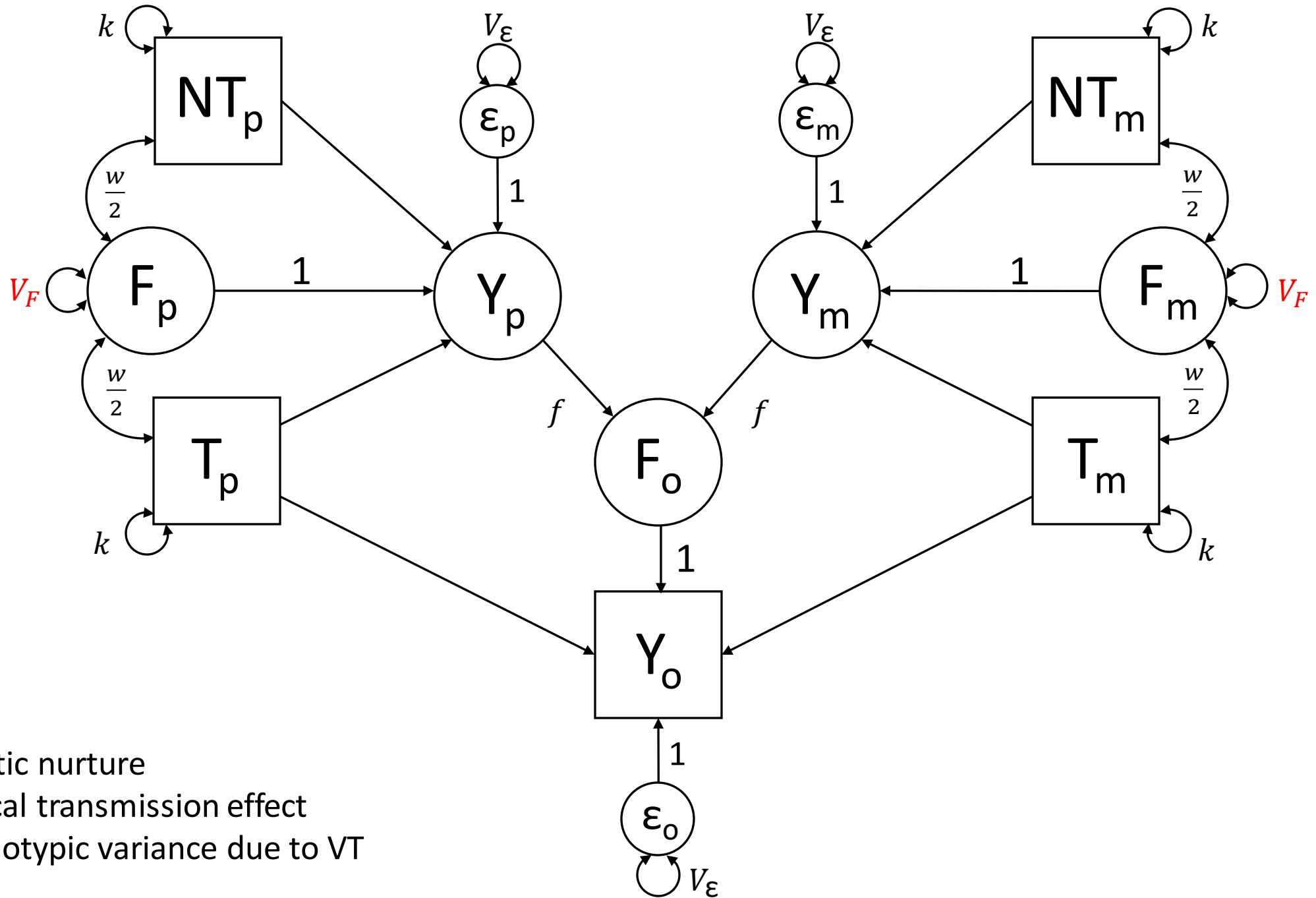
F : Familial Environment

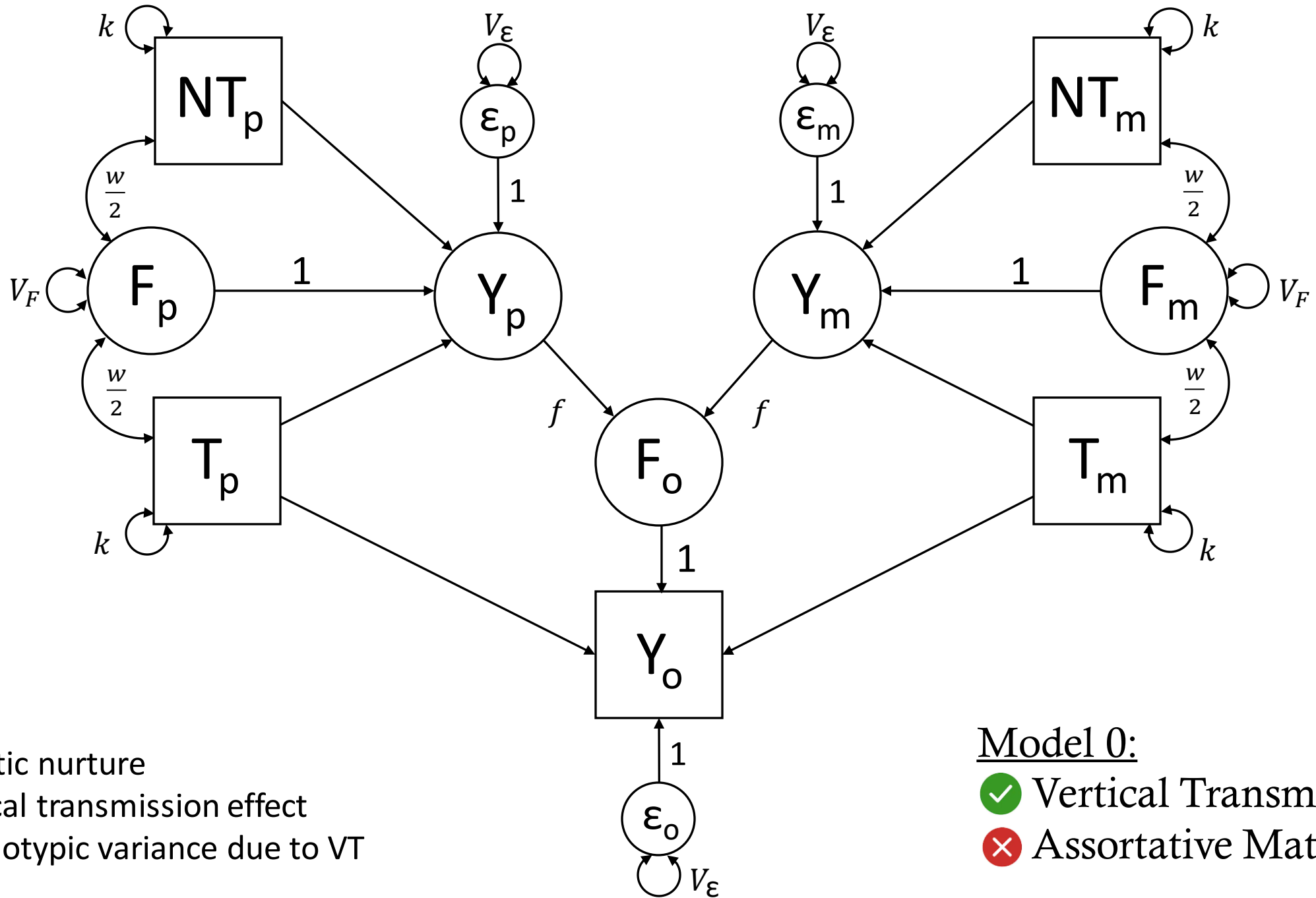


w : Genetic nurture



w : Genetic nurture
 f : Vertical transmission effect

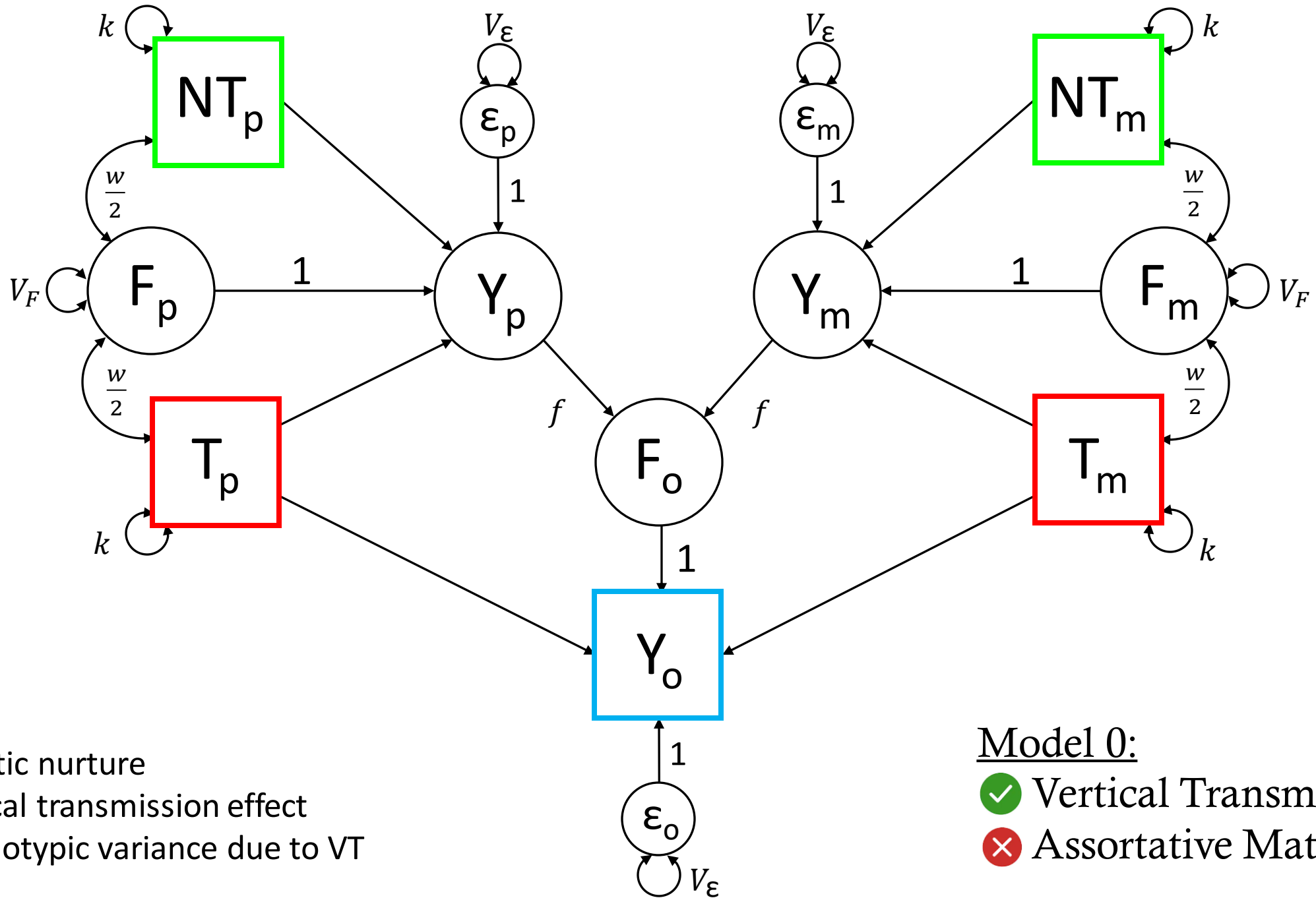


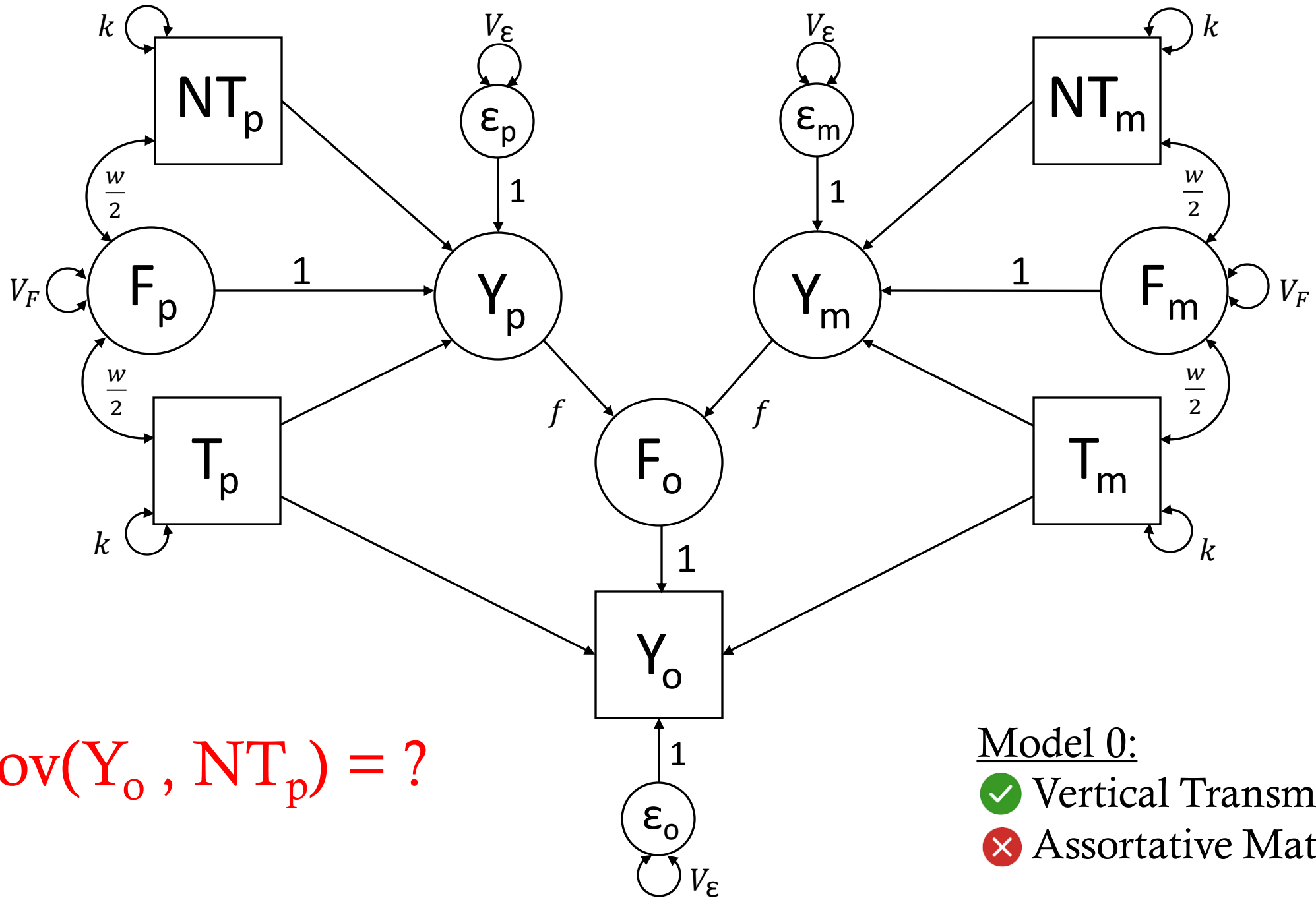


w : Genetic nurture
 f : Vertical transmission effect
 V_F : Phenotypic variance due to VT

Model 0:

- ✓ Vertical Transmission
- ✗ Assortative Mating

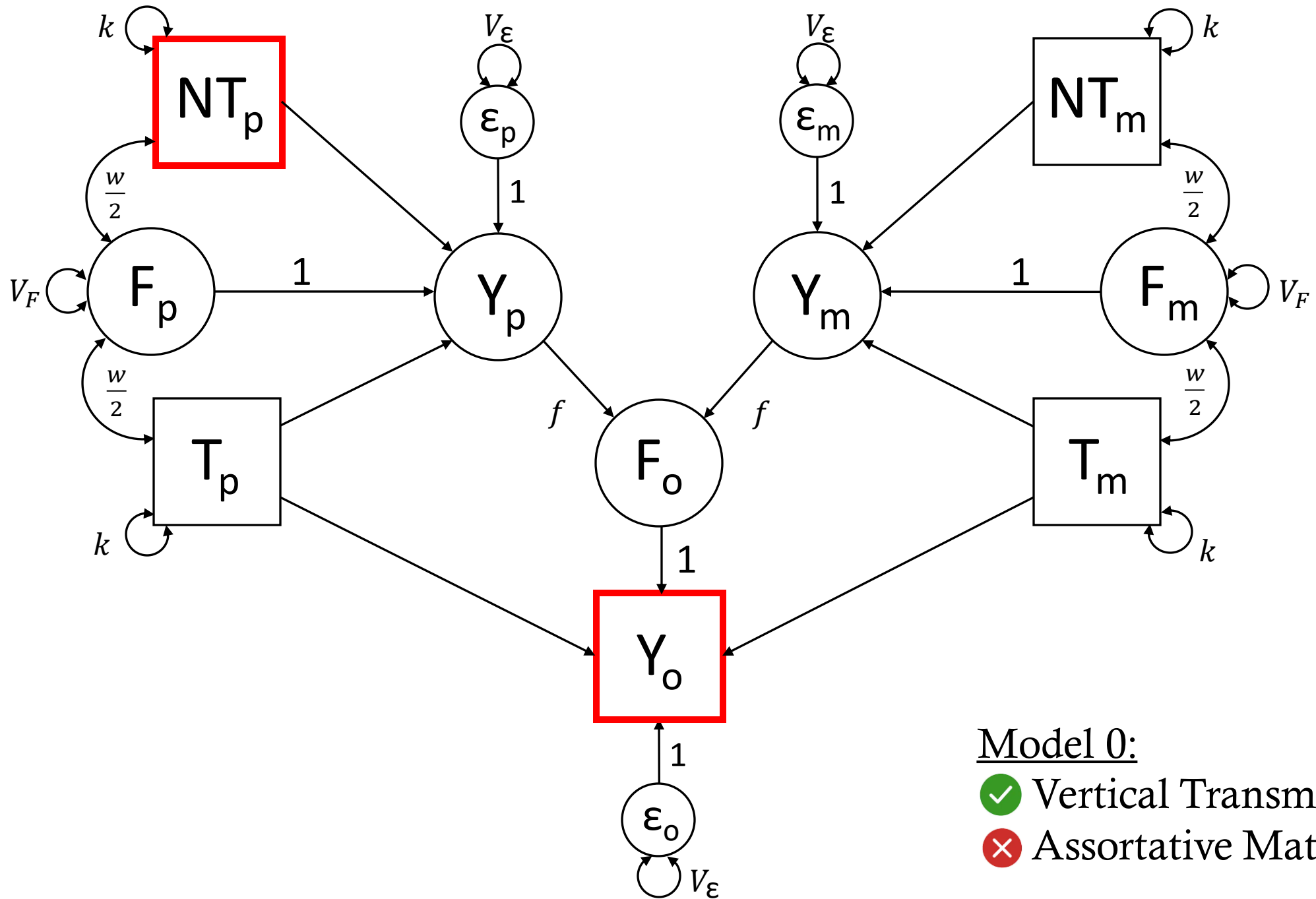




$$\text{cov}(Y_o, NT_p) = ?$$

Model 0:

- ✓ Vertical Transmission
- ✗ Assortative Mating

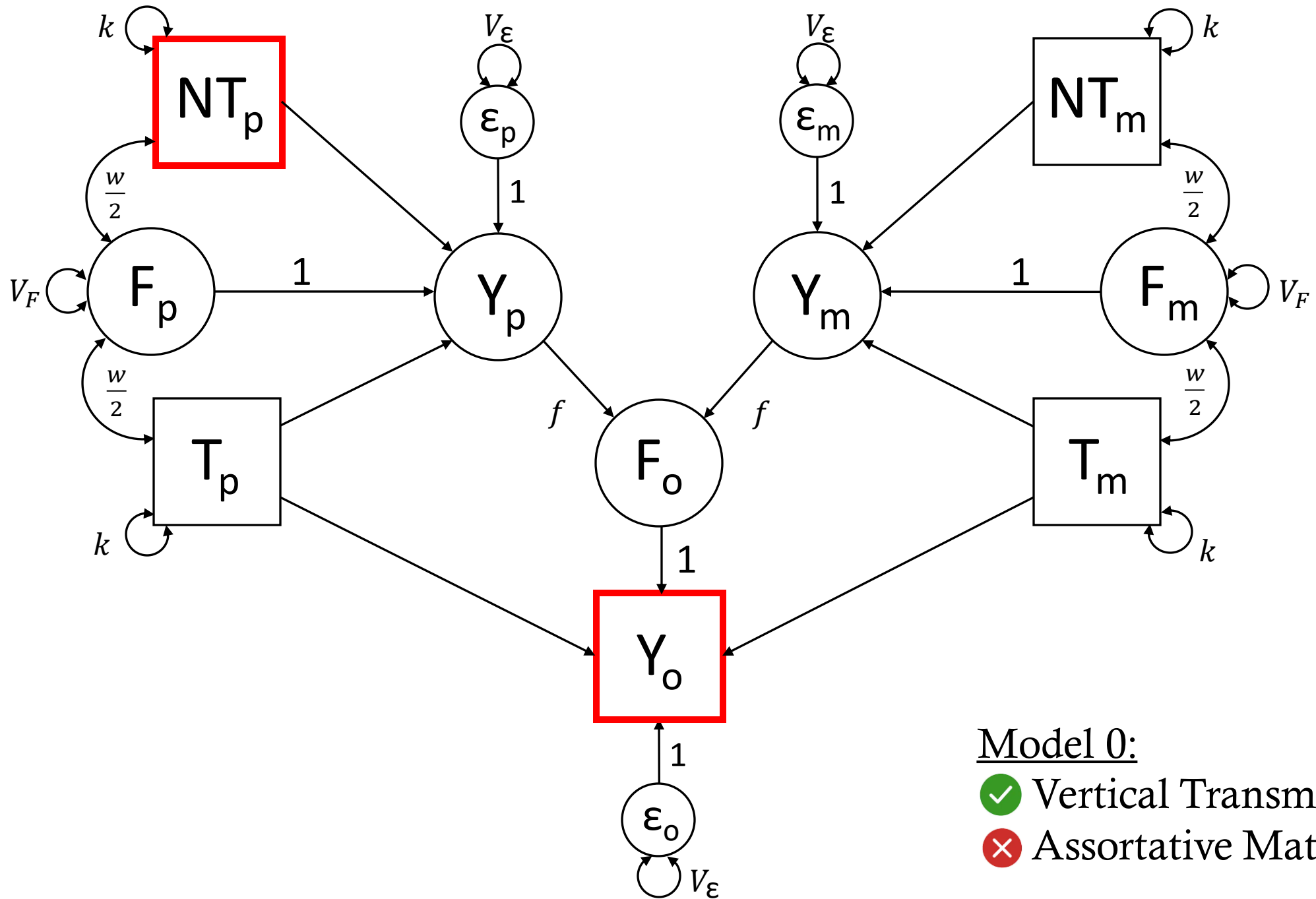


Model 0:

- ✓ Vertical Transmission
- ✗ Assortative Mating

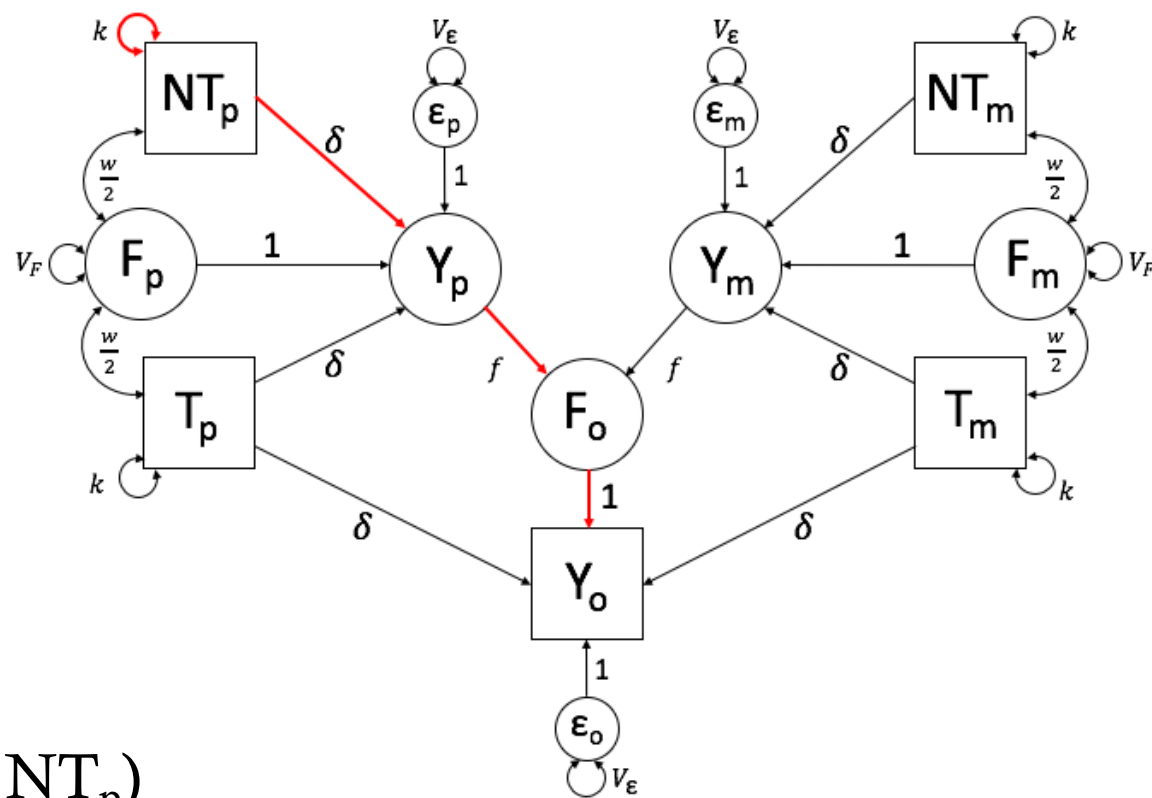
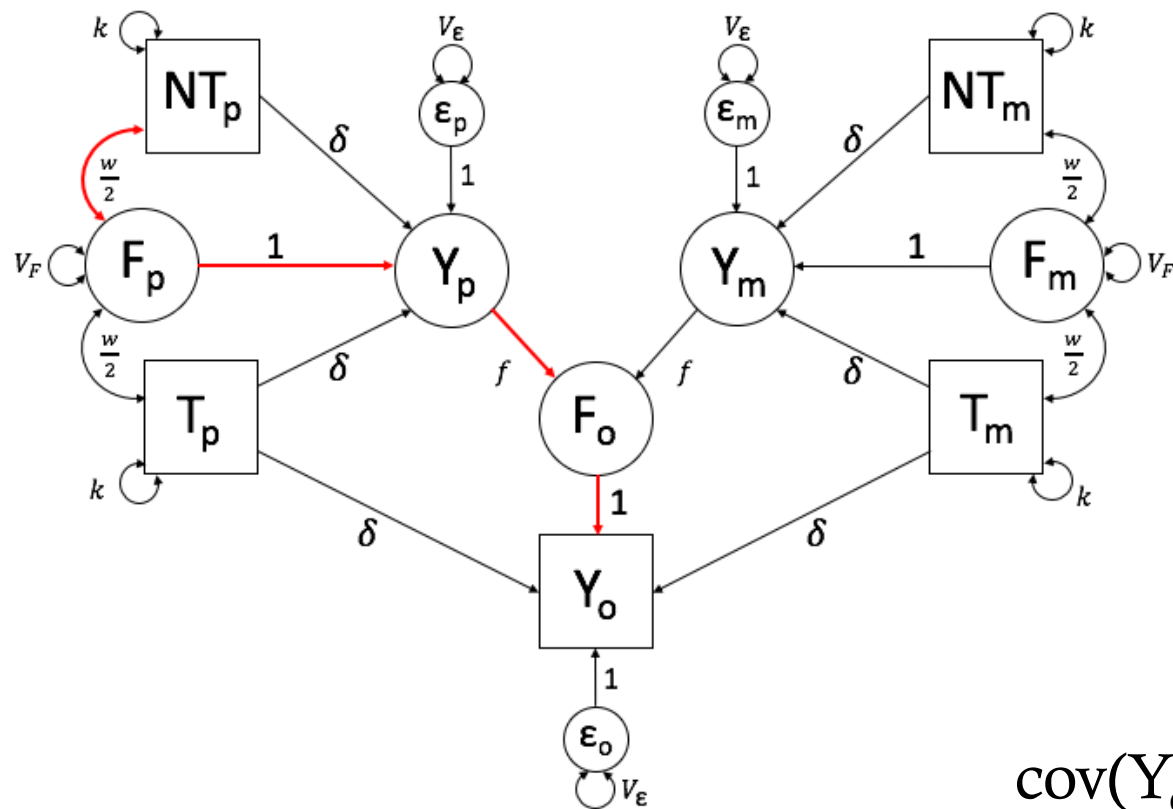
Path Tracing Rules (described in Balbona et al., 2021)

1. A chain begins by travelling backwards against the direction of a single or double-headed arrow (from the arrow's head to its tail). However, once a double-headed arrow has been traversed, the direction reverses such that the chain now travels forwards, in the direction of the arrows.
2. A chain must include exactly one double-headed arrow (a variance or a covariance term), which is equivalent to stating that a chain must change directions exactly once. This is necessary because double-headed arrows provide the proper scaling for the coefficients in each chain.
3. All chains must be counted exactly once and each must be unique. However, the order of the links in the chains matters. For example, despite being algebraically equivalent, the chain $Y_p \rightarrow NT_p \rightarrow T_p \rightarrow Y_p$ is distinct from the chain $Y_p \rightarrow T_p \rightarrow NT_p \rightarrow Y_p$ in Figure 1. Both are unique and both must be counted in determining the variance of Y_p .
4. Co-paths may only be traversed once in a given chain, and a chain must be legitimate before traversing the co-path. However, once the co-path is crossed, the first two rules above reset. A chain must therefore contain exactly one double-headed arrow before traversing the co-path, and one double-headed arrow after traversing the co-path. Thus, co-paths connect two legitimate chains to create a single, longer chain.



Model 0:

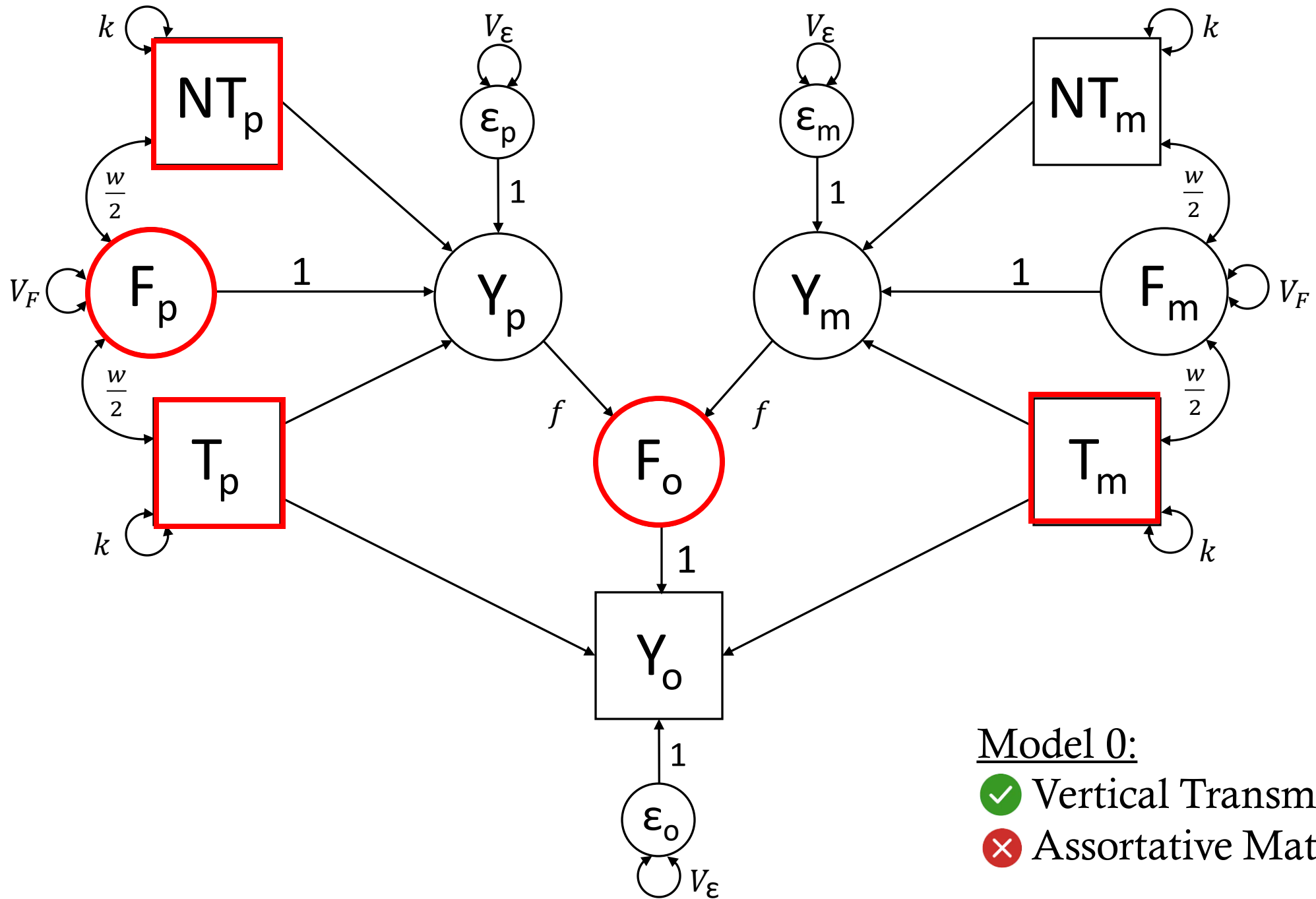
- ✓ Vertical Transmission,
- ✗ Assortative Mating



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

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

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



Model 0:

- ✓ Vertical Transmission
- ✗ Assortative Mating

Thank you!

