Phenotype Binarization Thresholds:

The threshold is selected such that if there is an effective interaction between at least one disease SNP pair the phenotype is case.

Multiplicative Interaction Alpha 1.25: 15

Multiplicative Interaction Alpha 1.5: 22

Multiplicative Interaction Alpha 2: 40

Multiplicative Interaction Alpha 3: 90

Recessive Interaction Alpha 8: 30

Recessive Interaction Alpha 16: 60

Dominant Interaction Alpha 8: 30

Dominant Interaction Alpha 16: 60

XOR Interaction Alpha 8: 30

XOR Interaction Alpha 16: 60

Control: 20

Multiplicative dataset specifications:

* Epistasis Type: Pure, Impure
* Interaction Order: 2nd
  + Number of Interacting (non-overlapping) Pairs: 1, 2, and 8
  + There are 8 datasets with 1 interacting pair, 8 datasets with 2 interacting pairs, and 4 datasets with 8 interacting pairs
* Interaction Models: multiplicative (all pairs are same interaction model with same interaction alpha)
* Number of SNPs: 1000
* Number of Individuals: 1000
* Minor Allele Frequency Range: 0.05 - 0.2
* Chromosome: 1
* Population: CEU
* Phenotype: quantitative
* Baseline Alpha: 10
* Marginal Model: additive + recessive + dominant (mixed for impure, all recessive for pure)
* Number of Disease SNPs:
  + 5 such that there are 1 or 2 interacting pairs
  + 20 such that there are 8 interacting pairs
* For datasets with 5 disease SNPs (16 datasets):
  + Interaction Alpha: 1.25, 1.5, 2, 3
    - Four datasets with interaction alpha 1.25
    - Four datasets with interaction alpha 1.5
    - Four datasets with interaction alpha 2
    - Four datasets with interaction alpha 3
  + Marginal Alpha:
    - Pure: recessive model with alpha 1.0 (no impact)
      * Ten datasets are pure with no individual main effects
    - Impure:
      * Two SNPs are recessive marginal model with alpha 0.5
      * Two SNPs are additive marginal model with alpha 2
      * One SNPs is dominant marginal model with alpha 3
      * Ten datasets are impure with above-stated individual main effects
* For datasets with 20 disease SNPs (4 datasets):
  + Interaction Alpha:
    - Two datasets with interaction alpha 2
    - Two datasets with interaction alpha 3
  + Marginal Alpha:
    - Pure: recessive model with alpha 1.0 (no impact)
      * Two datasets are pure with no individual main effects
    - Impure:
      * Ten SNPs are recessive marginal model with alphas: 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9
      * Five SNPs are additive marginal model with alphas: 0.8, 0.85, 0.9, 0.95, 1.0
      * Five SNPs are dominant marginal model with alpha: 1.25
      * Two datasets are impure with above-stated individual main effects

Resulting multiplicative datasets:

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha125\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha15\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha2\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha3\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha125\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha15\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha2\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha3\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha2\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha3\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha125\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha15\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha2\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha3\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha125\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha15\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha2\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha3\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha2\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha3\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Recessive and dominant datasets:

* Epistasis Type: Pure, Impure
* Interaction Order: 2nd
  + Number of Interacting (non-overlapping) Pairs: 1, 2 pairs
  + There are 8 datasets with 1 interacting pair and 8 datasets with 2 interacting pairs
    - Four 1 pair datasets and four 2 pair datasets are dominant interaction
    - Four 1 pair datasets and four 2 pair datasets are recessive interaction
* Interaction Models: recessive, dominant (all pairs are same interaction model with same interaction alpha)
* Number of SNPs: 1000
* Number of Individuals: 1000
* Minor Allele Frequency Range: 0.25-0.4 for recessive datasets, 0.05-0.2 for dominant datasets
* Chromosome: 1
* Population: CEU
* Phenotype: quantitative
* Baseline Alpha: 10
* Marginal Model: additive + recessive + dominant (mixed for impure, all recessive for pure)
* Number of Disease SNPs: 5
* Interaction Alpha 2, 3
  + Eight datasets with interaction alpha 2
  + Eight datasets with interaction alpha 3
* Marginal Alpha:
  + Pure: recessive model with alpha 1.0 (no impact)
    - Eight datasets are pure with no individual main effects
  + Impure:
    - Two SNPs are recessive marginal model with alpha 0.5
    - Two SNPs are additive marginal model with alpha 2
    - One SNPs is dominant marginal model with alpha 3
    - Ten datasets are impure with above-stated individual main effects

Resulting recessive and dominant datasets:

Pure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Pure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Pure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Pure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Impure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Impure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Impure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Impure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF025\_04

Pure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

XOR Datasets:

* Epistasis Type: Pure, Impure
* Interaction Order: 2nd
  + Number of Interacting (non-overlapping) Pairs: 8 pairs
  + There are 4 datasets with 8 interacting pairs
* Interaction Models: XOR (all pairs are same interaction model with same interaction alpha)
* Number of SNPs: 1000
* Number of Individuals: 1000
* Minor Allele Frequency Range: 0.05-0.2 for dominant datasets
* Chromosome: 1
* Population: CEU
* Phenotype: quantitative
* Baseline Alpha: 10
* Marginal Model: additive + recessive + dominant (mixed for impure, all recessive for pure)
* Number of Disease SNPs: 20
* Interaction Alpha: 8, 16
  + Two datasets with interaction alpha 8
  + Two datasets with interaction alpha 16
* Marginal Alpha:
  + Marginal Alpha:
    - Pure: recessive model with alpha 1.0 (no impact)
      * Two datasets are pure with no individual main effects
    - Impure:
      * Ten SNPs are recessive marginal model with alphas: 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9
      * Five SNPs are additive marginal model with alphas: 0.8, 0.85, 0.9, 0.95, 1.0
      * Five SNPs are dominant marginal model with alpha: 1.25
      * Two datasets are impure with above-stated individual main effects

Resulting XOR datasets:

Impure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Impure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha8\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02

Pure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha16\_Chr1\_CEU\_SNP1000\_IND1000\_MAF005\_02