BOOST Report (with EpiGEN)

Ways of evaluating epistasis detection algorithm performance:

1. Number of interacting pairs (true positives) identified.
2. Number of false positives.
3. Position of true positive(s) (averaged if multiple) when ranked by p-value. If any true positives are missing their position is considered to be the “last” in the list.
   1. The above definition will be referred to as penalized true positive position.
   2. Alternatively, average true positive position can be computed only using the detected true positives. This will be referred to as unpenalized true positive position.
4. Runtime (~1second for 1000 SNPs, NA for 100000 SNPs)

Compare these performance parameters across:

1. Multiplicative vs Dominant vs Recessive vs XOR Interaction.
2. Interaction Alpha: 1.25, 1.5, 2, 3, 8, 16.
3. Pure vs Impure.

Each EpiGEN dataset is named as follows: PURE/IMPURE (indicates presence of marginal effects) \_ MULTIPLICATIVE/DOMINANT/RECESSIVE/XOR (indicates type of interaction) \_ ONEPAIR / TWOPAIRS / EIGHTPAIRS (indicates number of interacting disease snp pairs) \_ BASELINEALPHA10 (indicates quantitative phenotype value in absence of marginal and interaction effects) \_ InteractionAlpha 1.25/1.5/2/3/8/16 (indicates strength of interaction effect)

**RESULTS (pages 1-11)**

**MULTIPLICATIVE DATASETS**

Pure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha125

Number of true positives: 1

Number of false positives: 0

F1 Score: 1.0

Average true positive position (unpenalized) ranked by p-value: 1

Average true positive position (penalized) ranked by p-value: 1

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha125

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha125

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha125

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

**DOMINANT DATASETS**

Impure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 1

Number of false positives: 0

F1 Score: 0.66

Average true positive position (unpenalized) ranked by p-value: 1

Average true positive position (penalized) ranked by p-value: 1.5

Impure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 0

F1 Score: 0.66

Average true positive position (unpenalized) ranked by p-value: 1

Average true positive position (penalized) ranked by p-value: 1.5

Pure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 1

Number of false positives: 0

F1 Score: 0.66

Average true positive position (unpenalized) ranked by p-value: 1

Average true positive position (penalized) ranked by p-value: 1.5

Pure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

**RECESSIVE DATASETS**

Impure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Impure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

Pure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 0

F1 Score: 0.0

Average true positive position (unpenalized) ranked by p-value: 0

Average true positive position (penalized) ranked by p-value: 0

**XOR DATASETS:**

Impure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 2

Number of false positives: 1

F1 Score: 0.36

Average true positive position (unpenalized) ranked by p-value: 1.5

Average true positive position (penalized) ranked by p-value: 3.375

Impure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 2

Number of false positives: 0

F1 Score: 0.40

Average true positive position (unpenalized) ranked by p-value: 1.5

Average true positive position (penalized) ranked by p-value: 2.625

Pure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 0

F1 Score: 0.22

Average true positive position (unpenalized) ranked by p-value: 1

Average true positive position (penalized) ranked by p-value: 1.875

Pure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 1

Number of false positives: 0

F1 Score: 0.22

Average true positive position (unpenalized) ranked by p-value: 1

Average true positive position (penalized) ranked by p-value: 1.875

**DISCUSSION (Page 12-13)**

Unpenalized true positive positions by interaction type.

Multiplicative: 0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0

Dominant: 0,0,1,1,0,0,1,0

Recessive: 0,0,0,0,0,0,0,0

XOR: 1.5,1.5,1,1

F1 Score by grouped by interaction type.

Multiplicative: 0,0,0,0,0, 0,0,0,0,0, 0,0,0,0,0, 0,0,0,0,1 => 0.05

Dominant: 0,0,0.66,0.66, 0,0,0.66,0 => 0.25

Recessive: 0,0,0,0, 0,0,0,0 => 0

XOR: 0.36, 0.4, 0.22, 0.22 => 0.3

From this point onward assume all true positive positions are penalized.

Multiplicative Interaction Average True Positive Positions (note that 0 means no true positives were detected): 0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0

Dominant Interaction Average True Positive Positions: 0,0,1.5,1.5,0,0,1.5,0

Recessive Interaction Average True Positive Positions: 0,0,0,0,0,0,0,0

XOR Interaction Average True Positive Positions: 3.375, 2.625, 1.875, 1.875

Boost could not detect recessive interactions. Multiplicative interactions were almost never detected.

Pairs Detected (# of SNP pairs correctly detected / total # of interacting disease SNP pairs) – only count if at least one pair was detected: 1/1, ½, ½, ½, 2/8, 2/8, 1/8, 1/8

Rarely detected more than one pair.