REMMA 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**

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 0

Number of false positives: 46

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: 1

Number of false positives: 227

F1 Score: 0.0087

Average true positive position (unpenalized) ranked by p-value: 2

Average true positive position (penalized) ranked by p-value: 2

Impure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 400

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: 0

Number of false positives: 102

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\_InteractionAlpha2

Number of true positives: 1

Number of false positives: 1726

F1 Score: 0.001156737998843262

Average true positive position (unpenalized) ranked by p-value: 38

Average true positive position (penalized) ranked by p-value: 883

Impure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 297

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: 409

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: 48

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: 1

Number of false positives: 535

F1 Score: 0.0037243947858473

Average true positive position (unpenalized) ranked by p-value: 15

Average true positive position (penalized) ranked by p-value: 15

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 1

Number of false positives: 128

F1 Score: 0.015384615384615385

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

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

Pure\_Multiplicative\_OnePair\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 171

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: 10

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: 2

Number of false positives: 1422

F1 Score: 0.002805049088359046

Average true positive position (unpenalized) ranked by p-value: 305

Average true positive position (penalized) ranked by p-value: 305

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 1

Number of false positives: 1239

F1 Score: 0.001610305958132045

Average true positive position (unpenalized) ranked by p-value: 2

Average true positive position (penalized) ranked by p-value: 621.5

Pure\_Multiplicative\_TwoPairs\_BaselineAlpha10\_InteractionAlpha15

Number of true positives: 0

Number of false positives: 15

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: 32

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\_InteractionAlpha3

Number of true positives: 2

Number of false positives: 2145

F1 Score: 0.0018561484918793504

Average true positive position (unpenalized) ranked by p-value: 711.5

Average true positive position (penalized) ranked by p-value: 1788.875

Pure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha2

Number of true positives: 1

Number of false positives: 2673

F1 Score: 0.0007457121551081282

Average true positive position (unpenalized) ranked by p-value: 20

Average true positive position (penalized) ranked by p-value: 2343.125

Impure\_Multiplicative\_EightPairs\_BaselineAlpha10\_InteractionAlpha3

Number of true positives: 0

Number of false positives: 953

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: 2425

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: 1

Number of false positives: 709

F1 Score: 0.0028129395218002813

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

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

Impure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 1023

F1 Score: 0.001951219512195122

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

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

Impure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 2

Number of false positives: 430

F1 Score: 0.009216589861751152

Average true positive position (unpenalized) ranked by p-value: 3

Average true positive position (penalized) ranked by p-value: 3

Impure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 2

Number of false positives: 580

F1 Score: 0.00684931506849315

Average true positive position (unpenalized) ranked by p-value: 2

Average true positive position (penalized) ranked by p-value: 2

Pure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 1

Number of false positives: 914

F1 Score: 0.002183406113537118

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

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

Pure\_Dominant\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 716

F1 Score: 0.002785515320334262

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

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

Pure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 2

Number of false positives: 523

F1 Score: 0.007590132827324478

Average true positive position (unpenalized) ranked by p-value: 2

Average true positive position (penalized) ranked by p-value: 2

Pure\_Dominant\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 2

Number of false positives: 596

F1 Score: 0.006666666666666667

Average true positive position (unpenalized) ranked by p-value: 2

Average true positive position (penalized) ranked by p-value: 2

**RECESSIVE DATASETS**

Impure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 20

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: 29

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: 1

Number of false positives: 1770

F1 Score: 0.0011280315848843769

Average true positive position (unpenalized) ranked by p-value: 77

Average true positive position (penalized) ranked by p-value: 924.5

Impure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 2109

F1 Score: 0.000946969696969697

Average true positive position (unpenalized) ranked by p-value: 38

Average true positive position (penalized) ranked by p-value: 1074.5

Pure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 1

Number of false positives: 2961

F1 Score: 0.0006749915626054674

Average true positive position (unpenalized) ranked by p-value: 359

Average true positive position (penalized) ranked by p-value: 359

Pure\_Recessive\_OnePair\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 1829

F1 Score: 0.0010922992900054614

Average true positive position (unpenalized) ranked by p-value: 256

Average true positive position (penalized) ranked by p-value: 256

Pure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 1

Number of false positives: 1007

F1 Score: 0.0019801980198019802

Average true positive position (unpenalized) ranked by p-value: 186

Average true positive position (penalized) ranked by p-value: 597.5

Pure\_Recessive\_TwoPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 1

Number of false positives: 816

F1 Score: 0.002442002442002442

Average true positive position (unpenalized) ranked by p-value: 11

Average true positive position (penalized) ranked by p-value: 414.5

**XOR DATASETS:**

Pure\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 519

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\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 2140

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\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha16

Number of true positives: 0

Number of false positives: 2416

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\_XOR\_EightPairs\_BaselineAlpha10\_InteractionAlpha8

Number of true positives: 0

Number of false positives: 2154

F1 Score: 0.0

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

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

**DISCUSSION (Page 12-13)**

Unpenalized true positive positions by interaction type.

Multiplicative: 0,2,0,0,38,0,0,0,15,1,0,0,305,2,0,0,711.5,20,0,0

Dominant: 1,1,3,2,1,1,2,2

Recessive: 0,0,77,38,359,256,186,11

XOR: 0,0,0,0

F1 Score by grouped by interaction type.

Multiplicative: 0.0087, 0.0011, 0.0037, 0.015, 0.0028, 0.0016, 0.0018, 0.00074, 0,0,0,0, 0,0,0,0, 0,0,0,0 => 0.0018

Dominant: 0.0028, 0.0019, 0.0092, 0.0068, 0.0022, 0.0028, 0.0076, 0.0067 => 0.005

Recessive: 0, 0, 0.0011, 0.00095, 0.00067, 0.0011, 0.0020, 0.0024 => 0.0010

XOR: 0,0,0,0 => 0.0

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): 0,2,0,0,883,0,0,0,15,1,0,0,305,621.5,0,0,1788.9,2343.1,0,0

Dominant Interaction Average True Positive Positions: 1,1,3,2,1,1,2,2

Recessive Interaction Average True Positive Positions: 0,0,924.5,1074.5,359,256,597.5,414.5

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

REMMA could detect all but XOR interactions.

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, 1/1, 1/1, 2/2, ½, 2/8, 1/8, 1/1, 1/1, 2/2, 2/2, 1/1, 1/1, 2/2, 2/2, ½, ½, 1/1, 1/1, ½, ½