# A novel detection method for high-order SNP epistatic interactions based on explicit-encoding-based multitasking harmony search

### 1. disease models

#### 1.1 8 EINME models

**Table S1. Eight EINME models.** The 3<sup>rd</sup> column denotes whether the model satisfies the Hardy-Weinberg equilibrium (**HWE**). In column 4–column 8, the values represent the prediction accuracy from k-order (k=1, 2,...,5) epistatic interaction.

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Model	k- order	HWE	1-order(sd)	2-order(sd)	3-order(sd)	4-order(sd)	5-order(sd)	tar.gz link
EINME-1	3	No	.502(.001)	.511(.007)	.886(.023)			threewayBests
EINME-2	3	Yes	.504(.002)	.509(.003)	.680(.024)			<u>HWthreewayBests</u>
EINME-3	4	No	.502(.001)	.510(.003)	-	.897(.018)		<u>fourwayBests</u>
EINME-4	4	Yes	.507(.003)	.513(.003)	-	.673(.009)		<u>HWfourwayBests</u>
EINME-5	4	No	.501(.000)	.504(.001)	.518(.003)	.567(.010)		<u>fourwayNoLowBests</u>
EINME-6	5	No	.502(.001)	.510(.002)	-	-	.895(.009)	fivewayBests
EINME-7	5	Yes	.511(.003)	.518(.003)	-	-	.693(.008)	<u>HWfivewayBests</u>
EINME-8	5	No	.503(.001)	.508(.001)	.518(.002)	.543(.004)	.690(.008)	fivewayNoLowBests

The eight datasets are generated by Himmelstein et al, 2011[1], which disables the discovery of disease-causing models for certain existing heuristic methods due to the lack of clues of causative SNP markers.

#### 1.2 12 EIME models

Table S2. The parameters and the values of penetrance of 12 EIME models.

Model type	EIME	order	Heritability(H <sup>2</sup> )	MAF	Heterogeneity proportion
	EIME -1	5	0.1	0.1	1.0
Additive model	EIME -2	5	0.1	0.25	1.0
Additive illoder	EIME -3	5	0.1	0.5	1.0
	EIME -4	5	0.1	0.2	1.0
	EIME -5	5	0.1	0.1	1.0
Threshold model	EIME -6	5	0.25	0.1	1.0
Threshold model	EIME -7	5	0.5	0.1	1.0
	EIME -8	5	0.1	0.2	1.0
	EIME -9	4	0.005	0.1	1.0
Multiplicative	EIME -10	4	0.005	0.2	1.0
model	EIME -11	4	0.005	0.4	1.0
	EIME -12	4	0.004	0.05	1.0

 $H^2$  denotes the genetic heritability. MAF represents the minor allele frequencies.

The datasets are generated using GAMETES software.

## 2. References

[1] Himmelstein et al. Evolving hard problems: Generating human genetics datasets with a complex etiology. BioData Mining 4, 21(2011). doi:10.1186/1756-0381-4-21. http://discovery.dartmouth.edu/model\_free\_data/.