

A) Original Design

Model for μ_j and μ_i and μ :
 {Phenotype \sim Gen. * Experimental Env.}

μ_i	Gen.	Native Env.	μ_j
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0.68	G_1	E_1	-0.68
0.68	G_2	E_1	-0.68
0.68	G_3	E_1	-0.68
0.68	G_4	E_1	-0.68
-0.68	G_5	E_2	0.68
-0.68	G_6	E_2	0.68
-0.68	G_7	E_2	0.68
-0.68	G_8	E_2	0.68

$\mu = 0.00$

B) Imbalanced Design

Model for μ_j and μ_i and μ :
 {Phenotype \sim Gen. * Experimental Env.}

μ_i	Gen.	Native Env.	μ_j
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0.68	G_1	E_1	-0.98
-0.68	G_5	E_2	0.27
-0.68	G_6	E_2	0.27
-0.68	G_7	E_2	0.27
-0.68	G_8	E_2	0.27

$\mu = -0.21$

C) Imbalanced Design using correction

Model for μ_j and μ :
 {Phenotype \sim Native Env. * Experimental Env.}
 Model for μ_i :
 {Phenotype \sim Gen. * Experimental Env.}

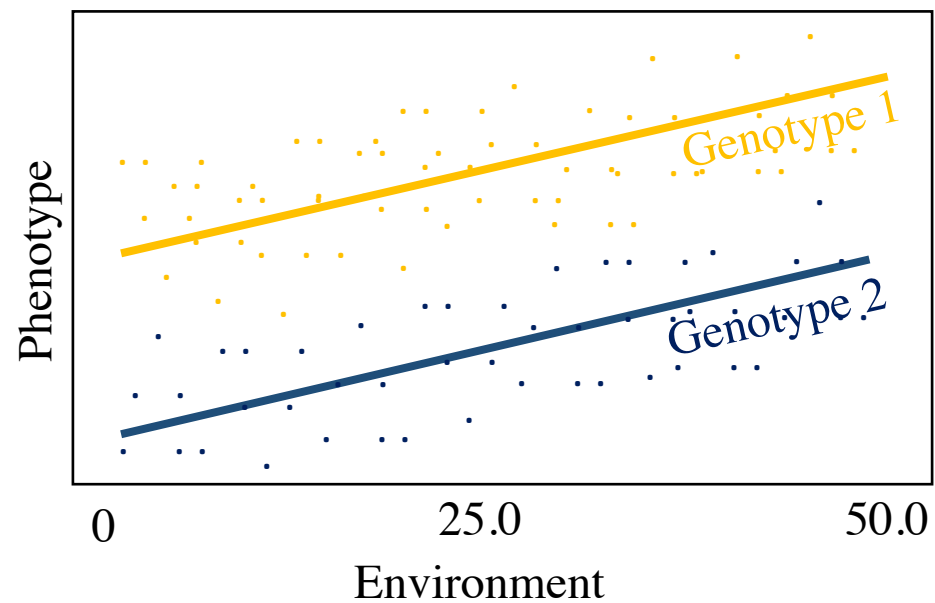
μ_i	Gen.	Native Env.	μ_j
---------	------	-------------	---------

0.68	G_1	E_1	-0.68
-0.68	G_5	E_2	0.68
-0.68	G_6	E_2	0.68
-0.68	G_7	E_2	0.68
-0.68	G_8	E_2	0.68

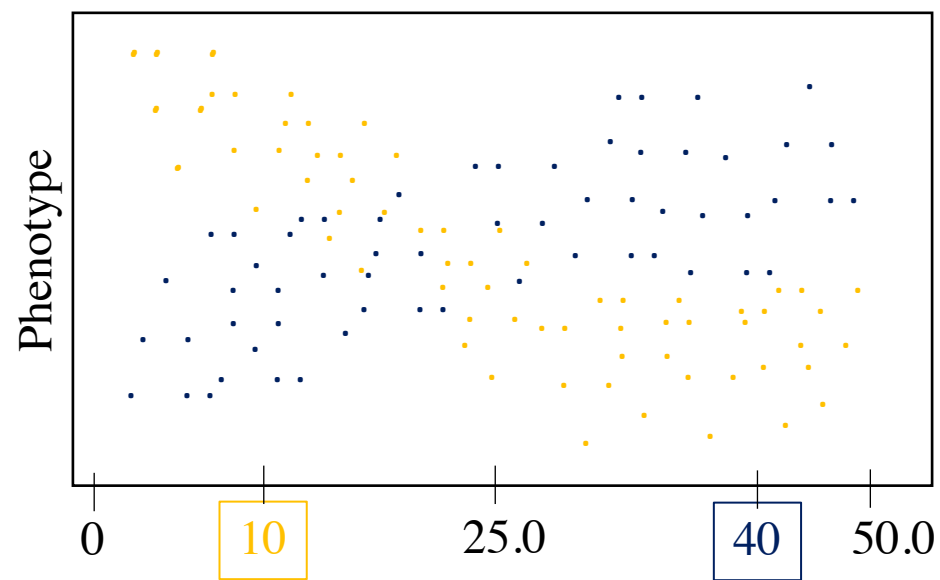
$\mu = 0.00$

Incompatible Designs

A)

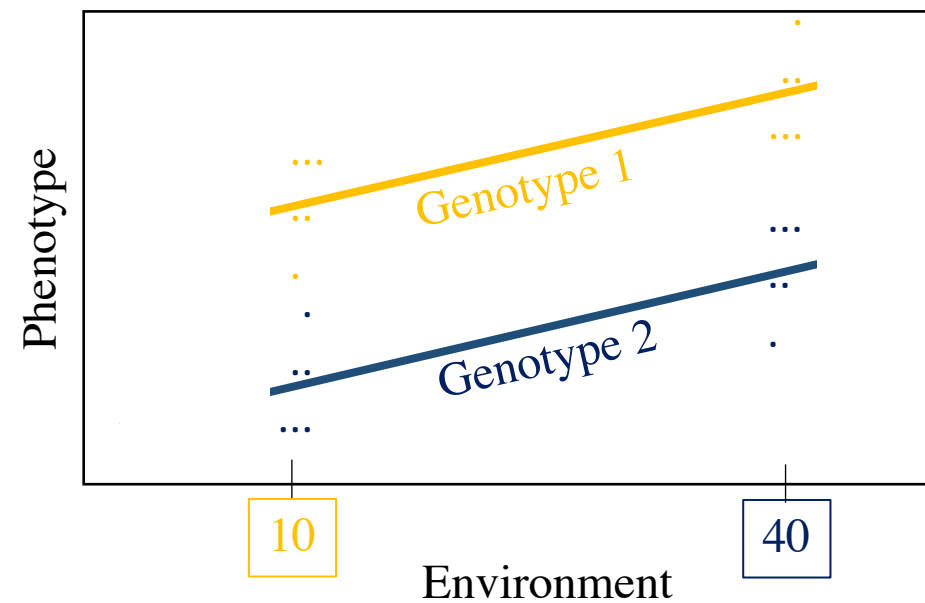


C)

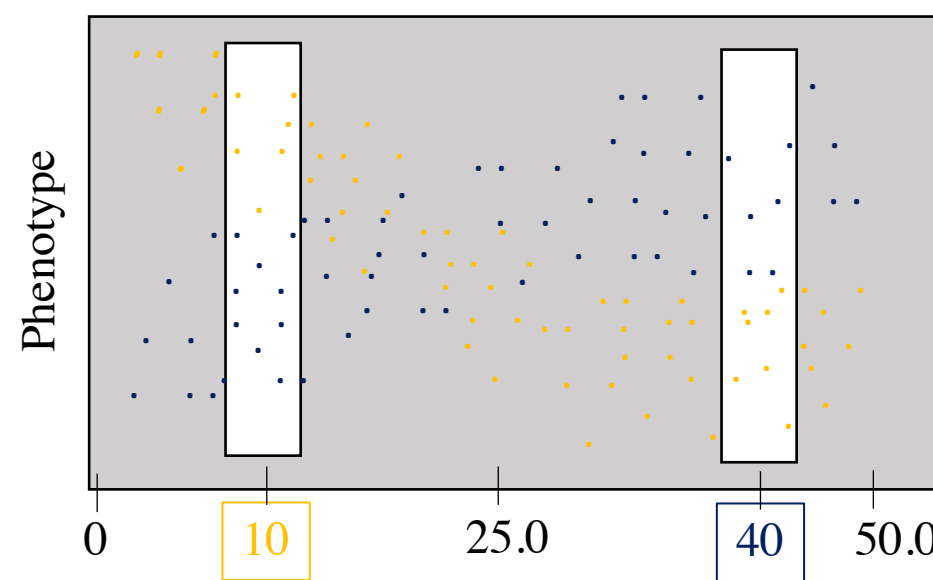


Compatible Designs

B)



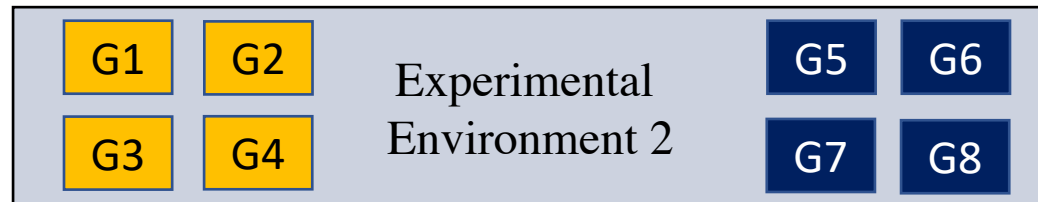
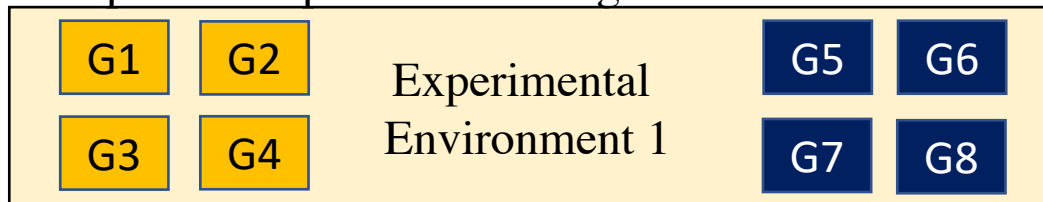
D)



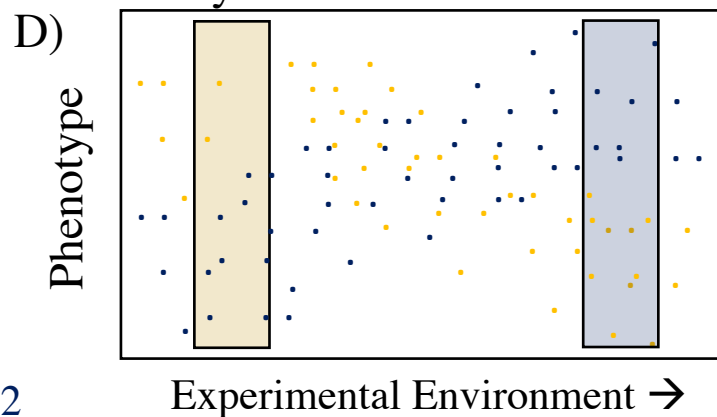
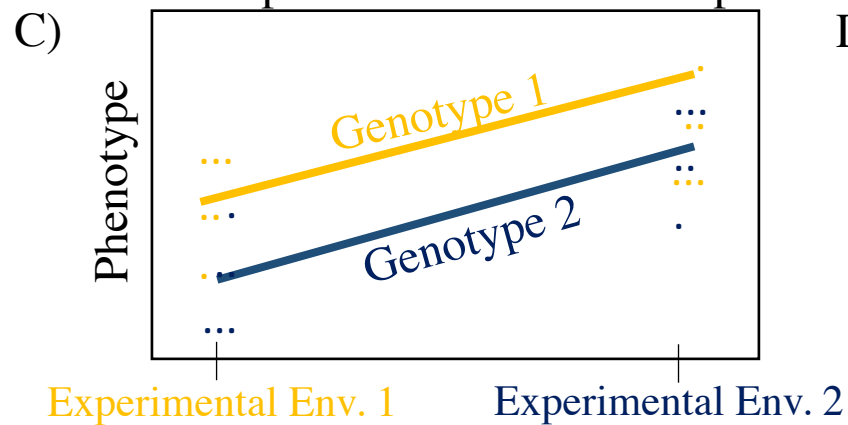
A) Data collection:



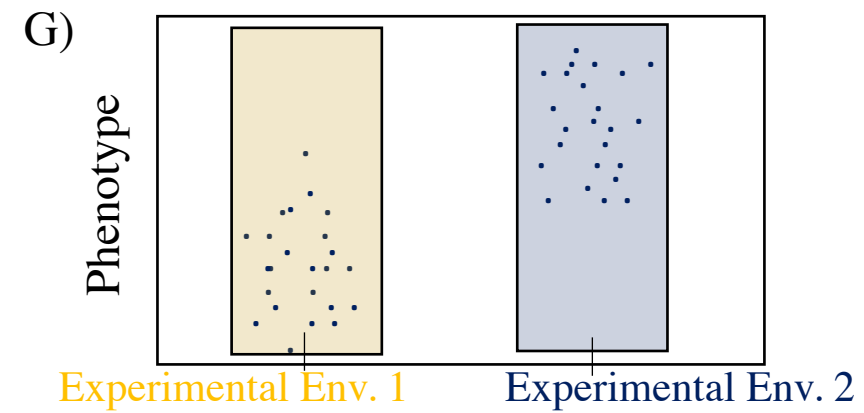
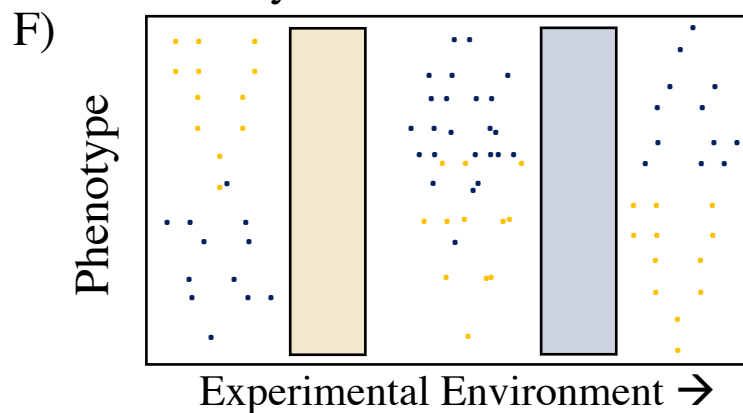
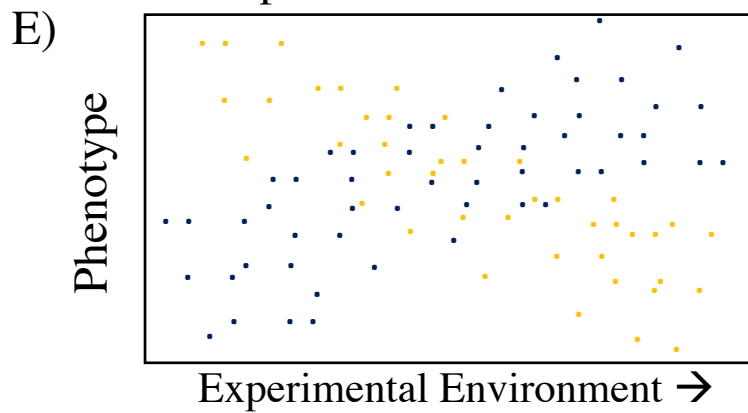
B) Compatible Experimental design:



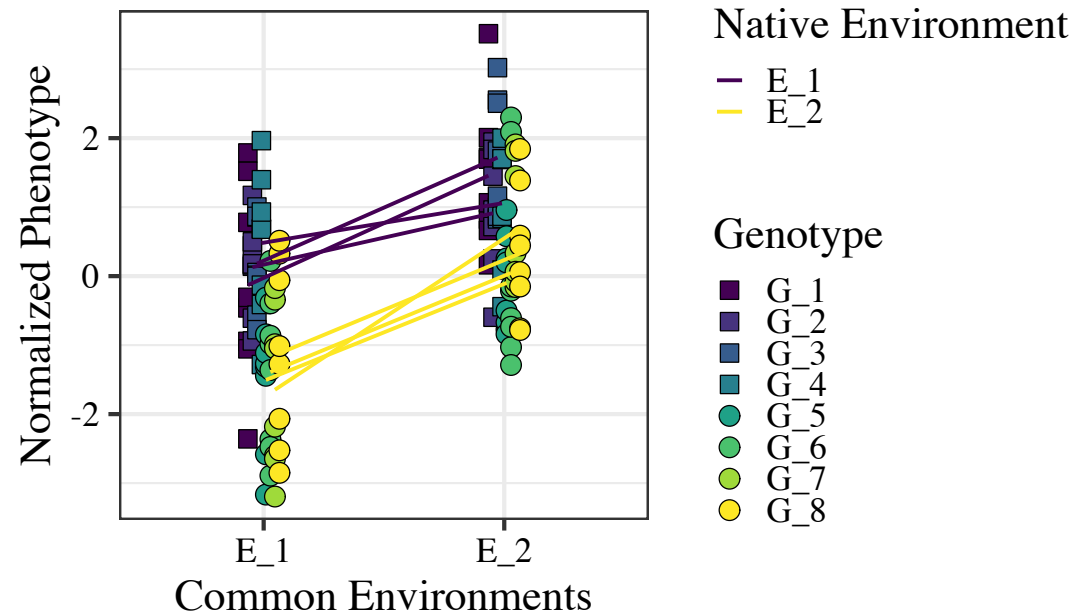
Example reaction norms compatible with analysis:



Example reaction norms incompatible with analysis:



A Balanced Design



B Imbalanced Design

