A) Original Design

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

μ_i	Gen.	Native Env.	μ_j
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 ~ Gen. * Experimental Env.}

μ_i	Gen.	Native Env.	μ_j
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 ~ Native Env. * Experimental Env.}

Model for μ_i :
{Phenotype ~ Gen. * Experimental Env.}

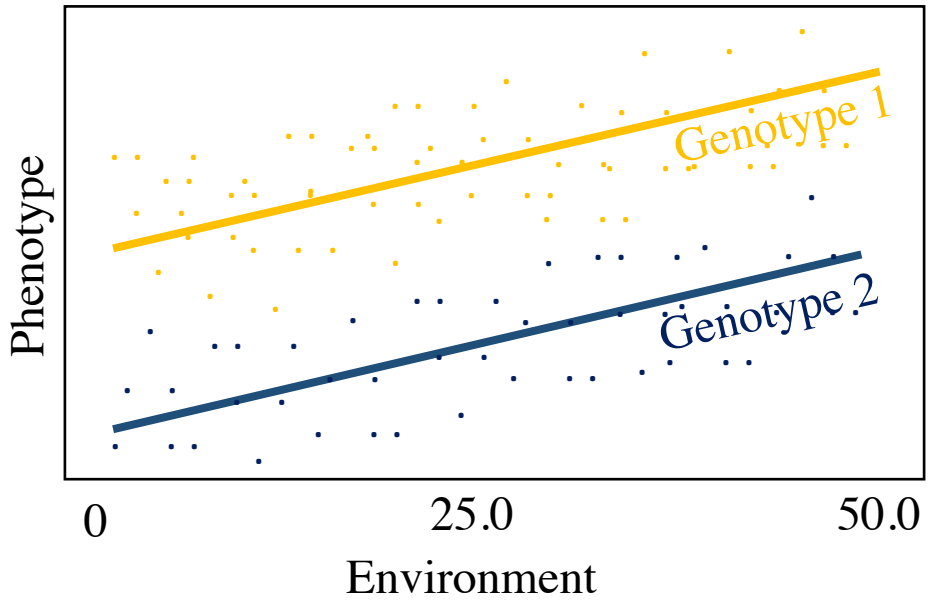
μ_i	Gen.	Native Env.	μ_j	Group
0.68	G_1	E_1	-0.68	A
-0.68	G_5	E_2	0.68	B
-0.68	G_6	E_2	0.68	B
-0.68	G_7	E_2	0.68	B
-0.68	G_8	E_2	0.68	B

$\mu = 0.00$

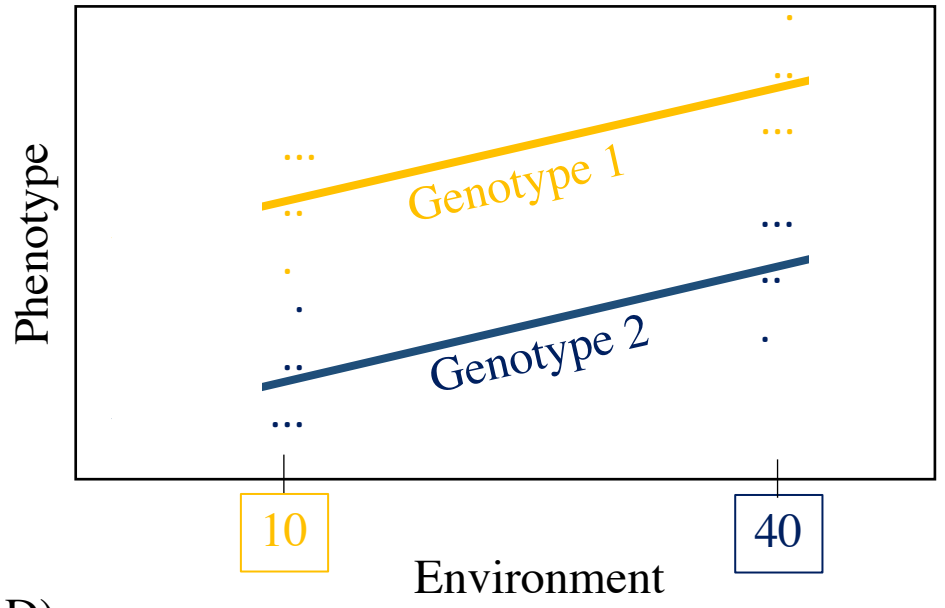
Incompatible Designs

Compatible Designs

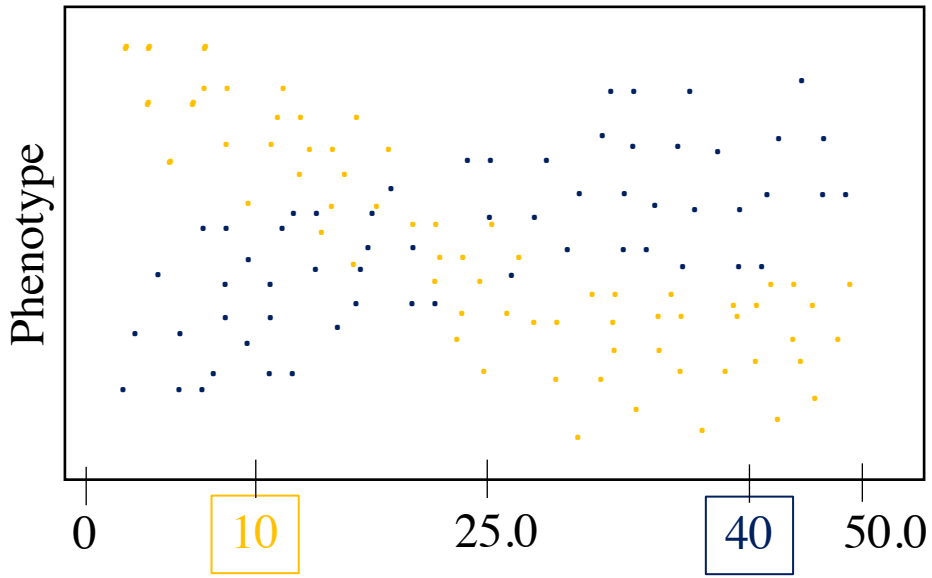
A)



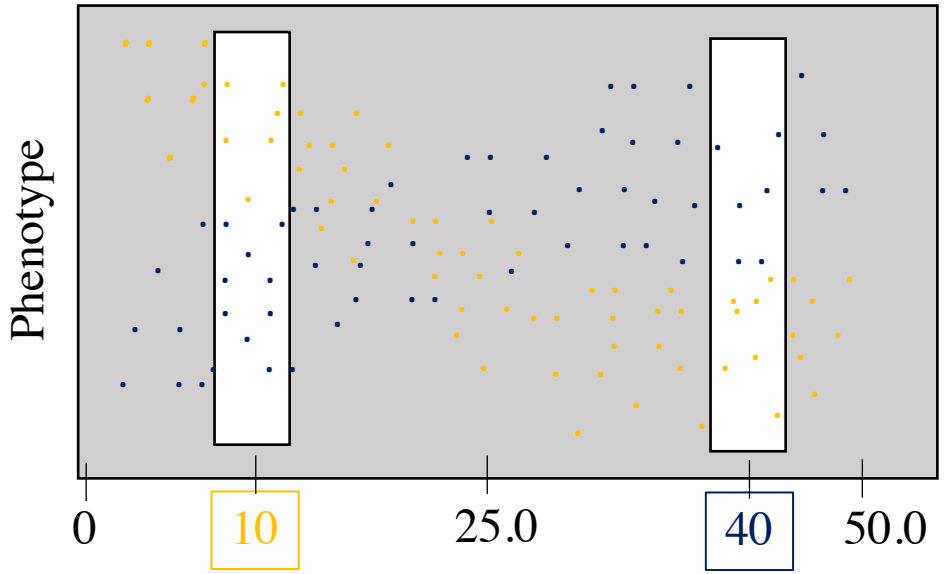
B)



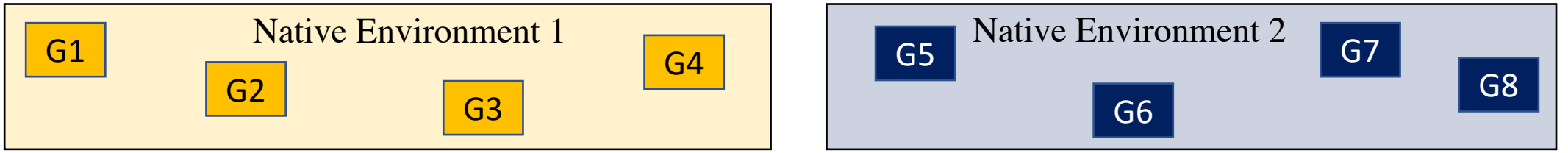
C)



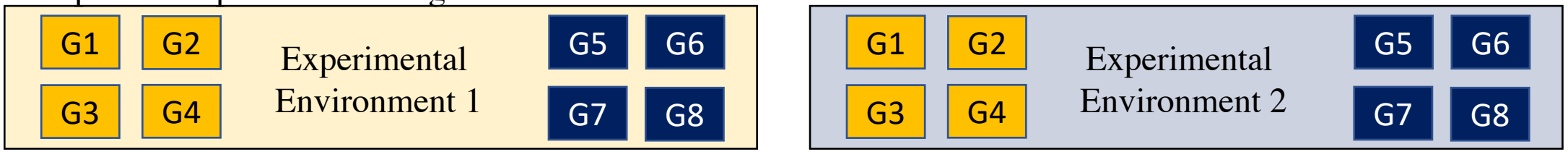
D)



A) Data collection:

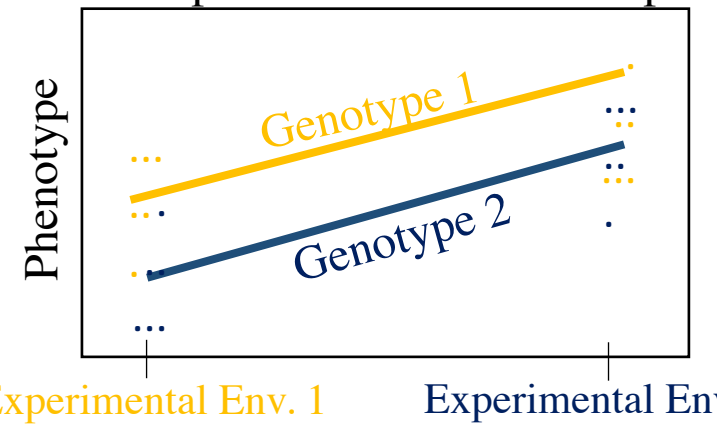


B) Compatible Experimental design:

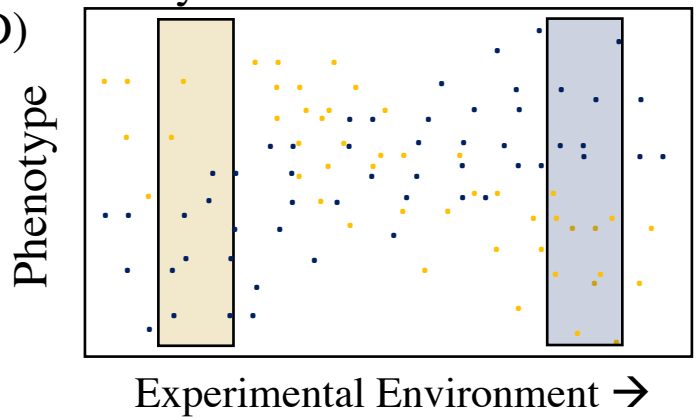


Example reaction norms compatible with analysis:

C)

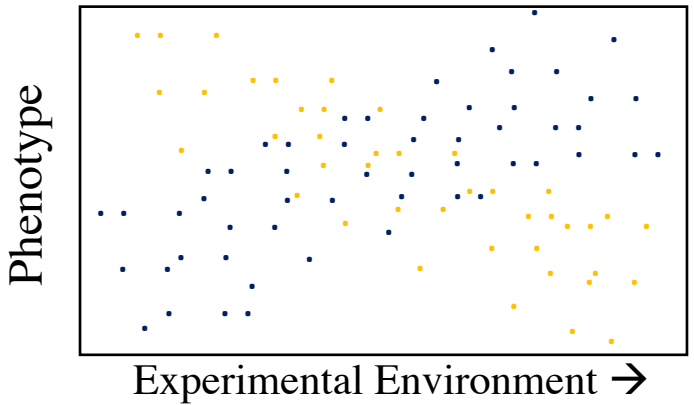


D)

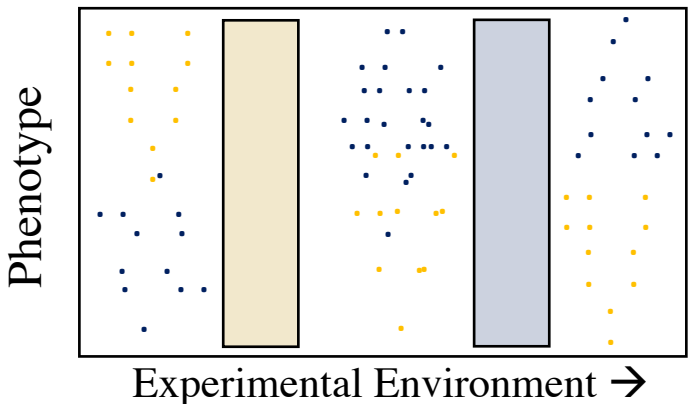


Example reaction norms incompatible with analysis:

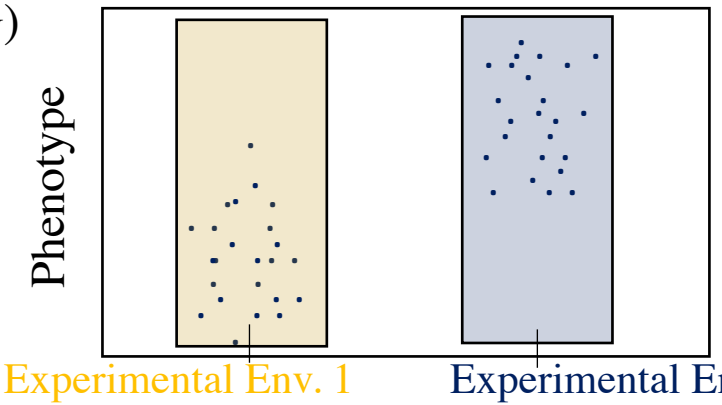
E)

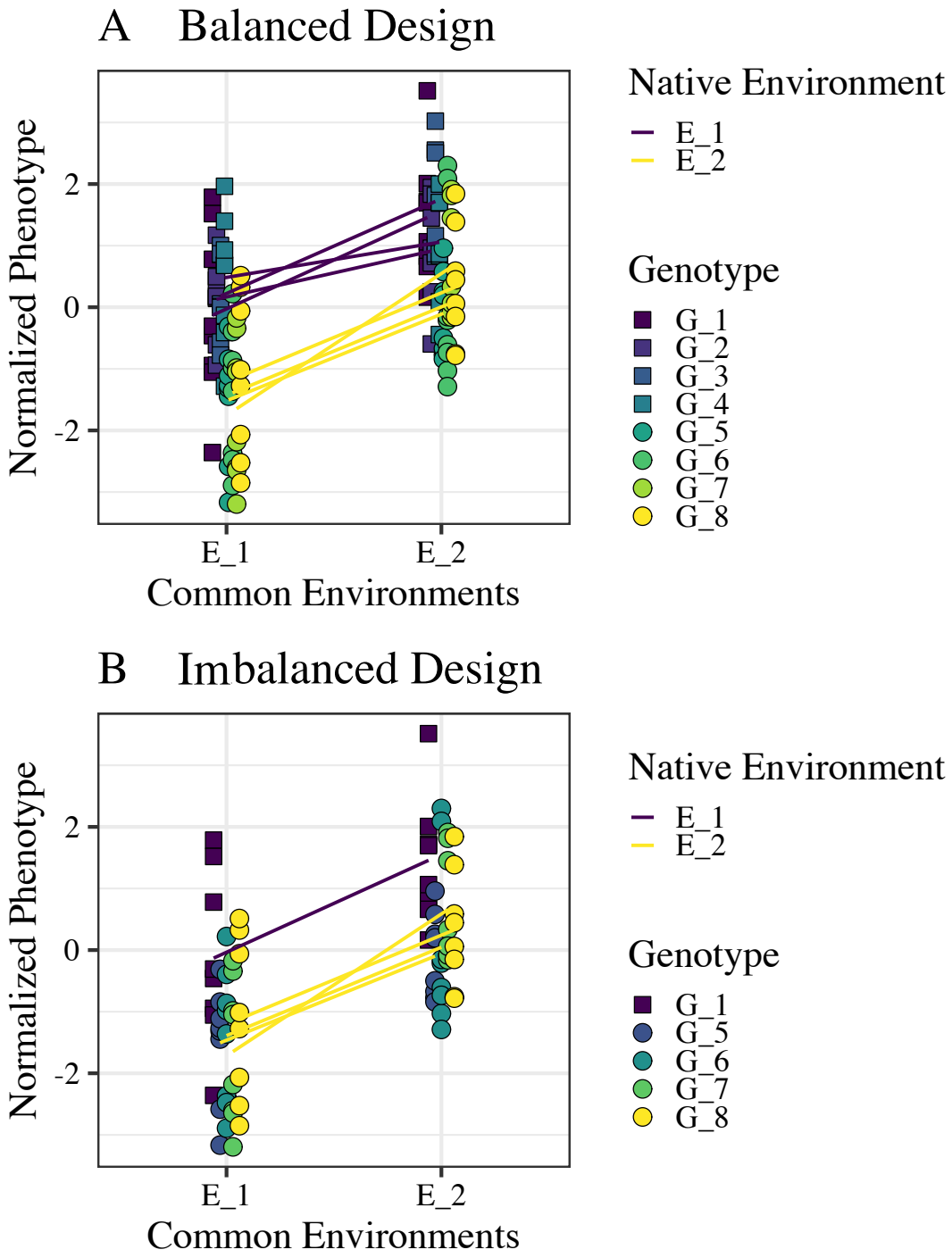


F)



G)




A Balanced Design
Normalized Phenotype
2
0
-2
E_1
E_2
Common Environments
Native Environment
E_1
E_2
Genotype
G_1
G_2
G_3
G_4
G_5
G_6
G_7
G_8
B Imbalanced Design
Normalized Phenotype
2
0
-2
E_1
E_2
Common Environments
Native Environment
E_1
E_2
Genotype
G_1
G_5
G_6
G_7
G_8