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- definitions
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BreedeR: a R-package implementing statistical models specifically suited for forest genetic resources analysts

Multiple trait analysis and breedR

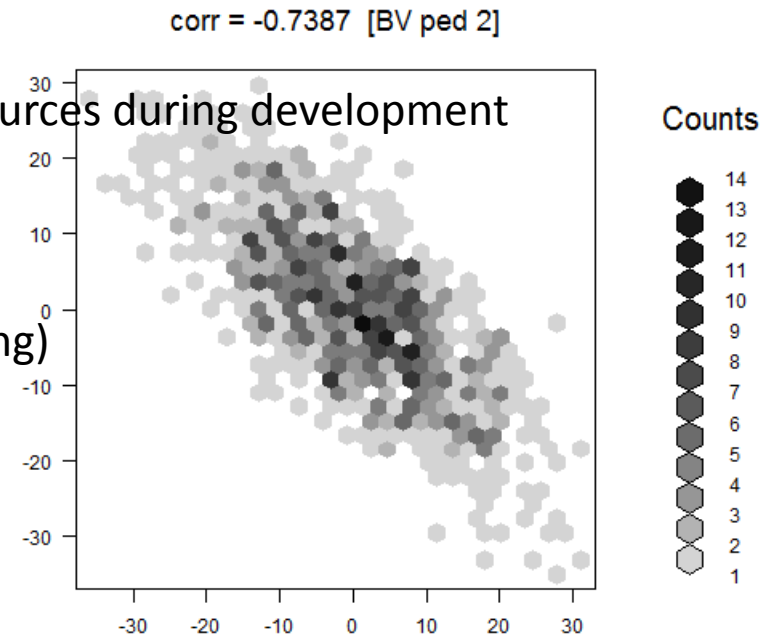
- Multiple trait analyses are not yet available in current breedR release
- From now onwards & up to the end of the project there will be new releases at regular basis
- Next release after the workshop will have the feature of multiple trait analyses
- breedR is based on BLUPF90 family of programs, which already support multiple trait models. BreedR needs a refactoring of the interface to have full benefit of this BLUPF90 feature.

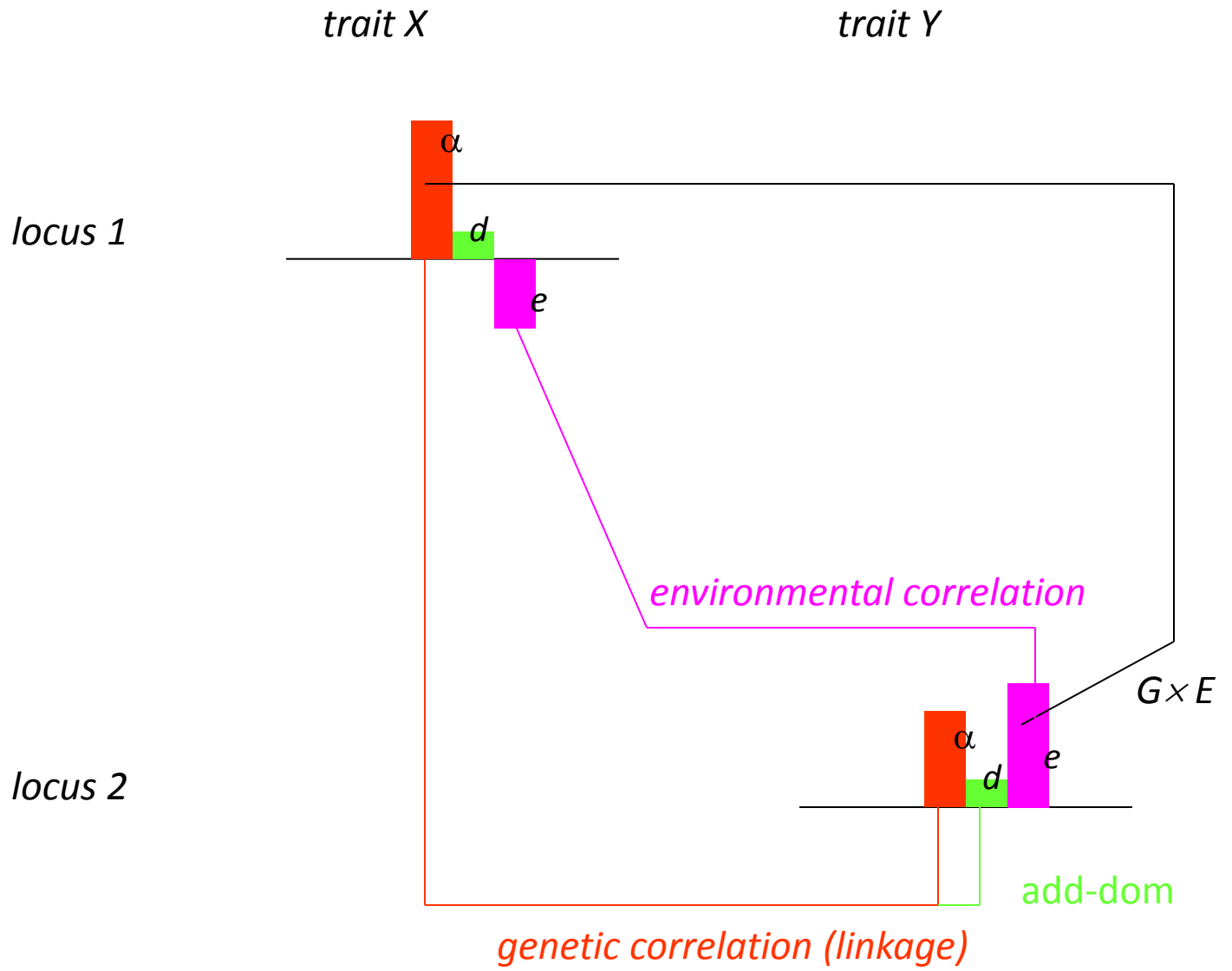
Lynch & Walsh (1998): *“Deciphering the relative contributions of environmental and genetic factors to phenotypic correlations is one of the most powerful and revealing applications of QG”*

[Genetics and Analysis of Quantitative Traits]

multiple natures... ?

- environmental correlations
 - p.e. availability of same basic resources during development
- genetic correlations
 - pleiotropy
 - linkage (by distance, by sampling)





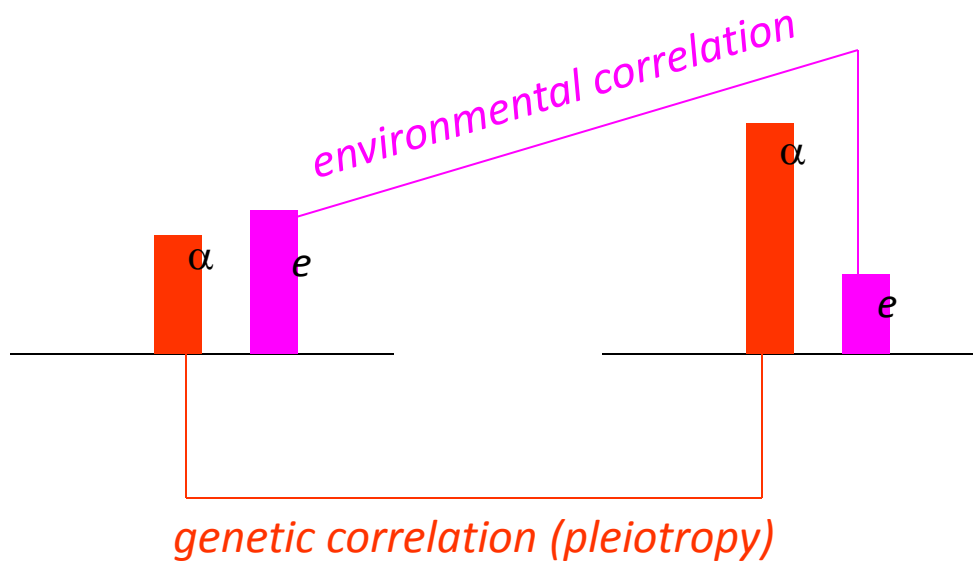
trait X

trait Y

locus 1

locus 3

locus 2



Nature of genetic correlations: linkage vs. pleiotropy

Mather & Jinks (1982): *“...linkage is the more likely explanation”*
[Biometrical Genetics, London]

Jinks et al. (1985): *“...either or both factors may be important, depending on the pair of traits...”*

[Heredity, 55]

Falconer & Mackay (1996): *“...the genetic cause of correlation is chiefly pleiotropy, ... linkage is a cause of transient correlation...”*

Linkage is of minor importance in equilibrium populations ...

Tureli (1985), Hastings (1989), Bürger (1989)

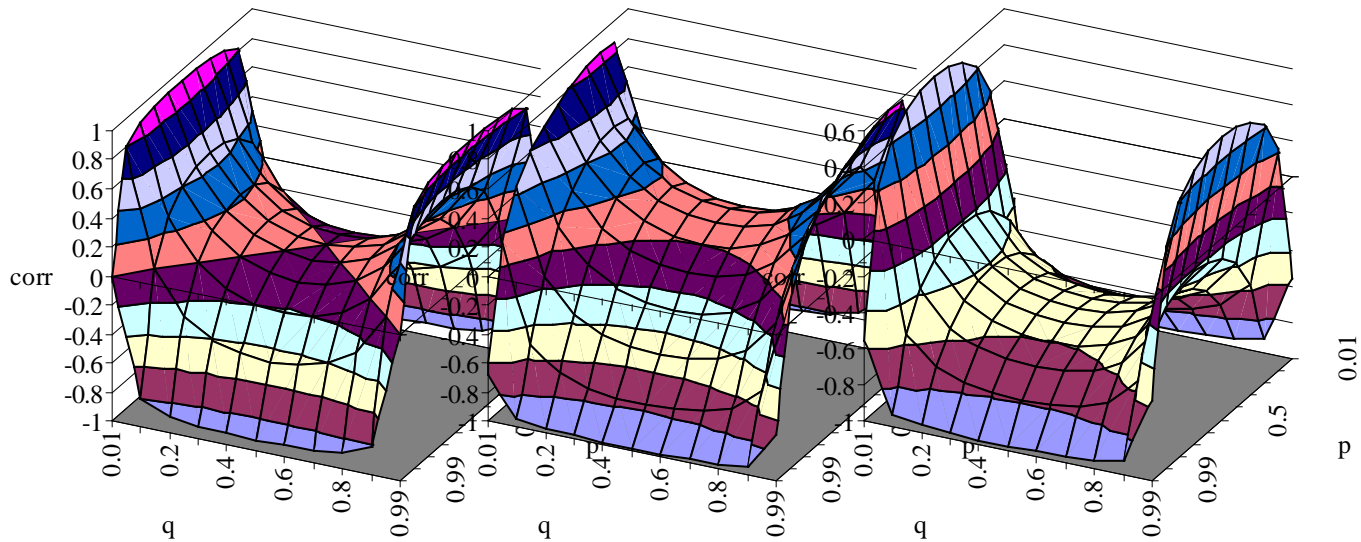
[Genetics, 111; 121; 121]

Correlations and gene frequencies

Génotype	A1A1	A1A2	A2A2	B1B1	B1B2	B2B2
caractère X		-1	0	1	1	0
caractère Y		-1	0	1	-1	0

Génotype	A1A1	A1A2	A2A2	B1B1	B1B2	B2B2
caractère X		1	1	-1	1	0
caractère Y		1	0	-1	-1	0

Génotype	A1A1	A1A2	A2A2	B1B1	B1B2	B2B2
caractère X		1	0	-1	1	0
caractère Y		1	0	-1	-5	0



Pleiotropy: several sources

Hodgkin (1998): “... pleiotropy is for the geneticist what ambiguity is for the critic, multiple functions embedded in the same object...”

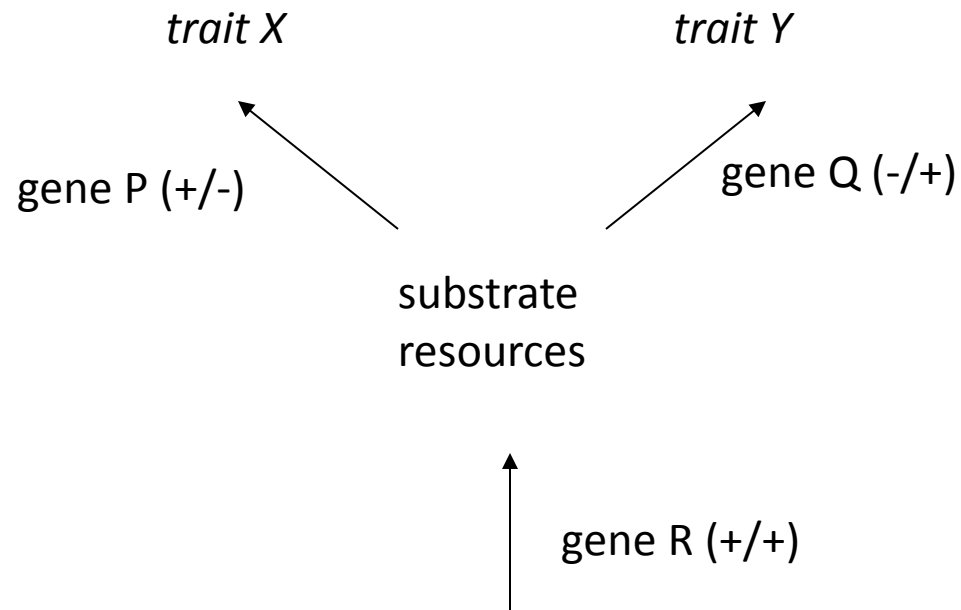
[Journal of Developmental Biology, 42]

- “*Artefactual*” (... , mutagenesis affecting adjacent but unrelated genes)
- “*Adoptive & opportunistic*” (... , 1 gene different purposes)
- “*Parsimonious*” (1 gene same purposes different pathways)
- “*Combinatorial*” (genes as bricks of larger functional products)
- “*Unifying*” (several genes coding a common biol. function)
- ...

Pleiotropy: resources model

Sheridan and Barker (1974)

[Aust. J. biol. Sci., 27]



Genetic correlations and evolution

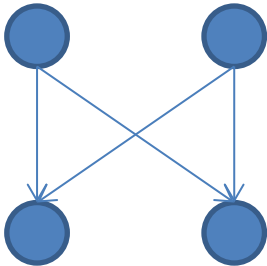
Armbruster & Schwaegerle (1996): “... covariation of traits that are functionally related, adaptative character complexes, that have evolved by natural selection favouring certain combinations of genetically independent traits.”

[J.Evol.Biol., 9]

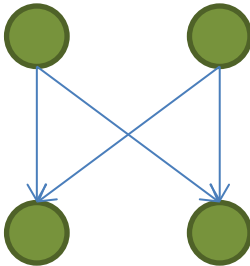
Pleiotropy is a constraint in evolution (**Arnold, 1992**)

[American Naturalist, 140]

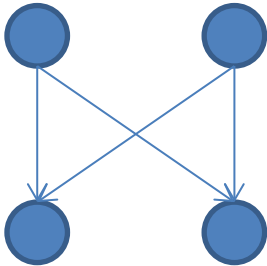
computing genetic correlations



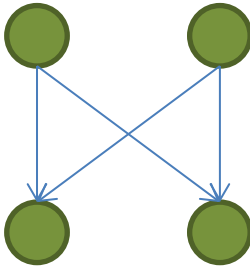
$$y_i - X_b \quad y_j - X_b$$



$$y_k - X_b \quad y_l - X_b$$

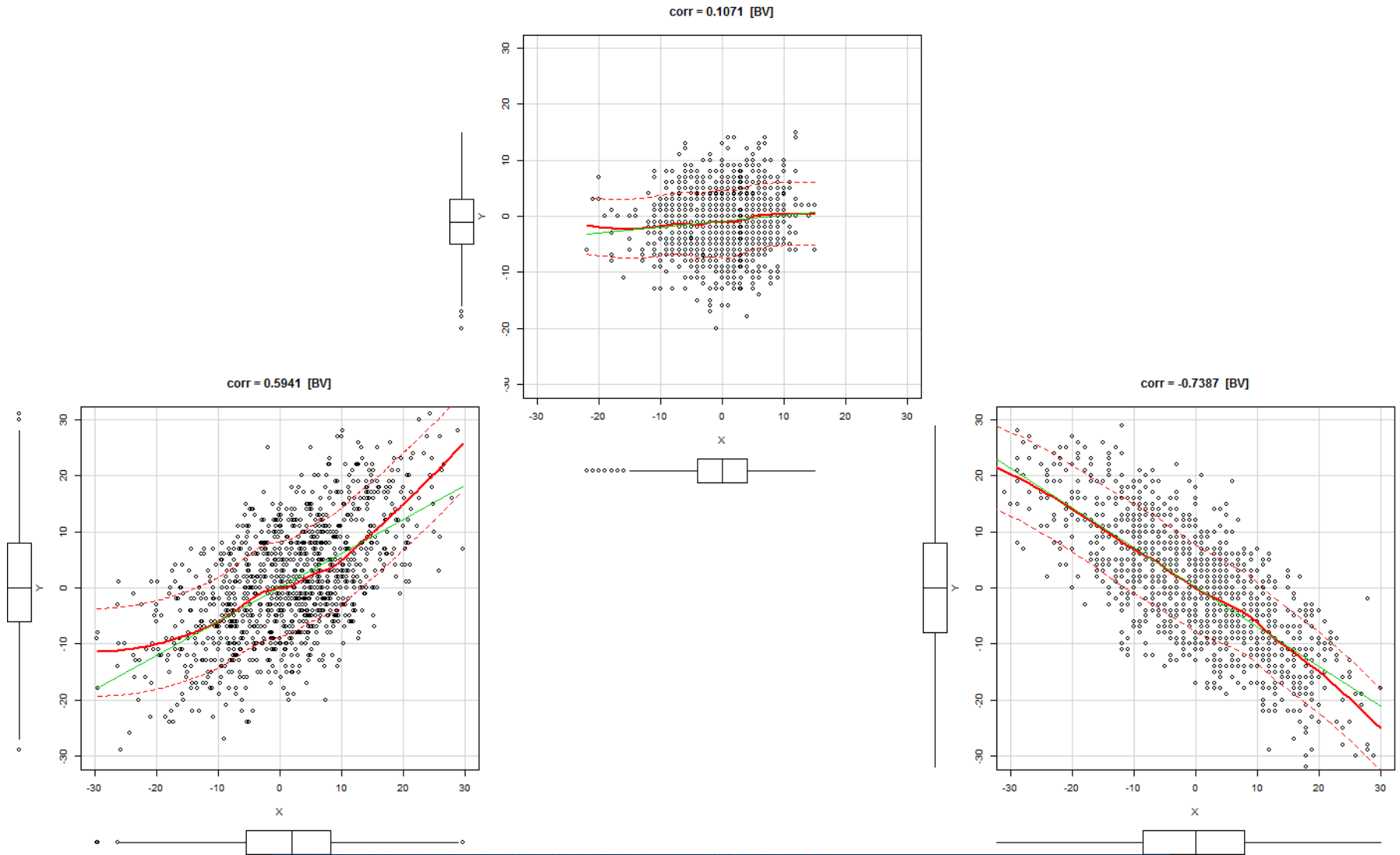


$$y_i - X_b \quad x_j - X_b$$



$$y_k - X_b \quad x_l - X_b$$

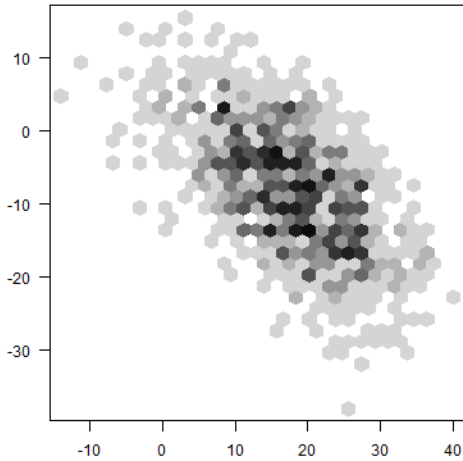
scenarios of genetic & phenotypic correlations



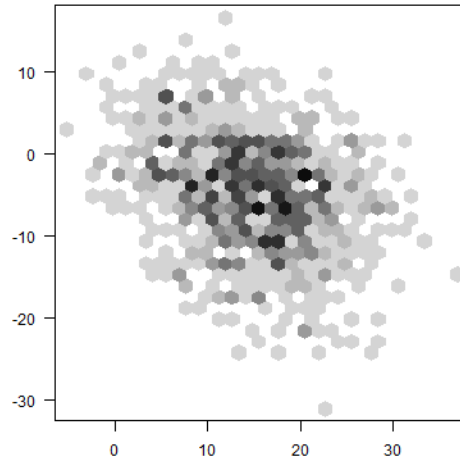
```
correl <- round(corr_2_gen_1_bv, digits = 4)
heading <- paste("corr =", correl, " [BV]")
scatterplot(ped_2_gen_1$BV_Y, ped_2_gen_1$BV_X, xlab = "X", ylab = "Y",
            main = heading, xlim = c(-30, 30), ylim = c(-30, 30))
```

scenarios of genetic & phenotypic correlations

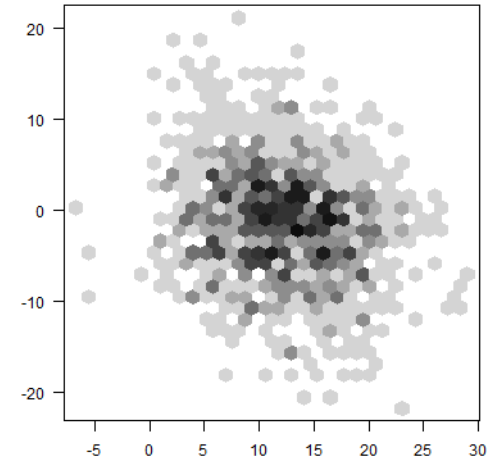
corr = -0.586 [BV 23]



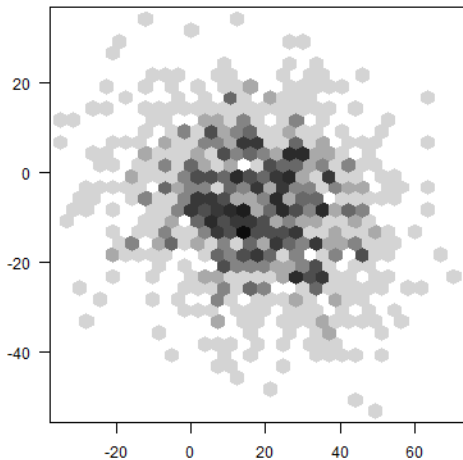
corr = -0.312 [BV 13]



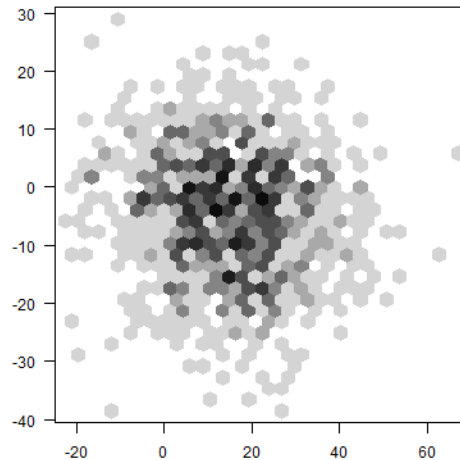
corr = -0.188 [BV 33]



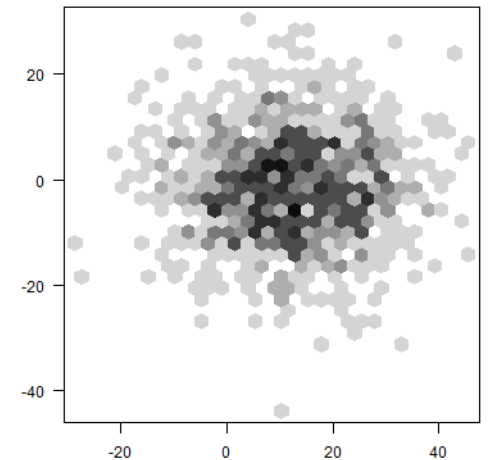
corr = -0.1764 [phe 23]



corr = -0.0979 [phe 13]

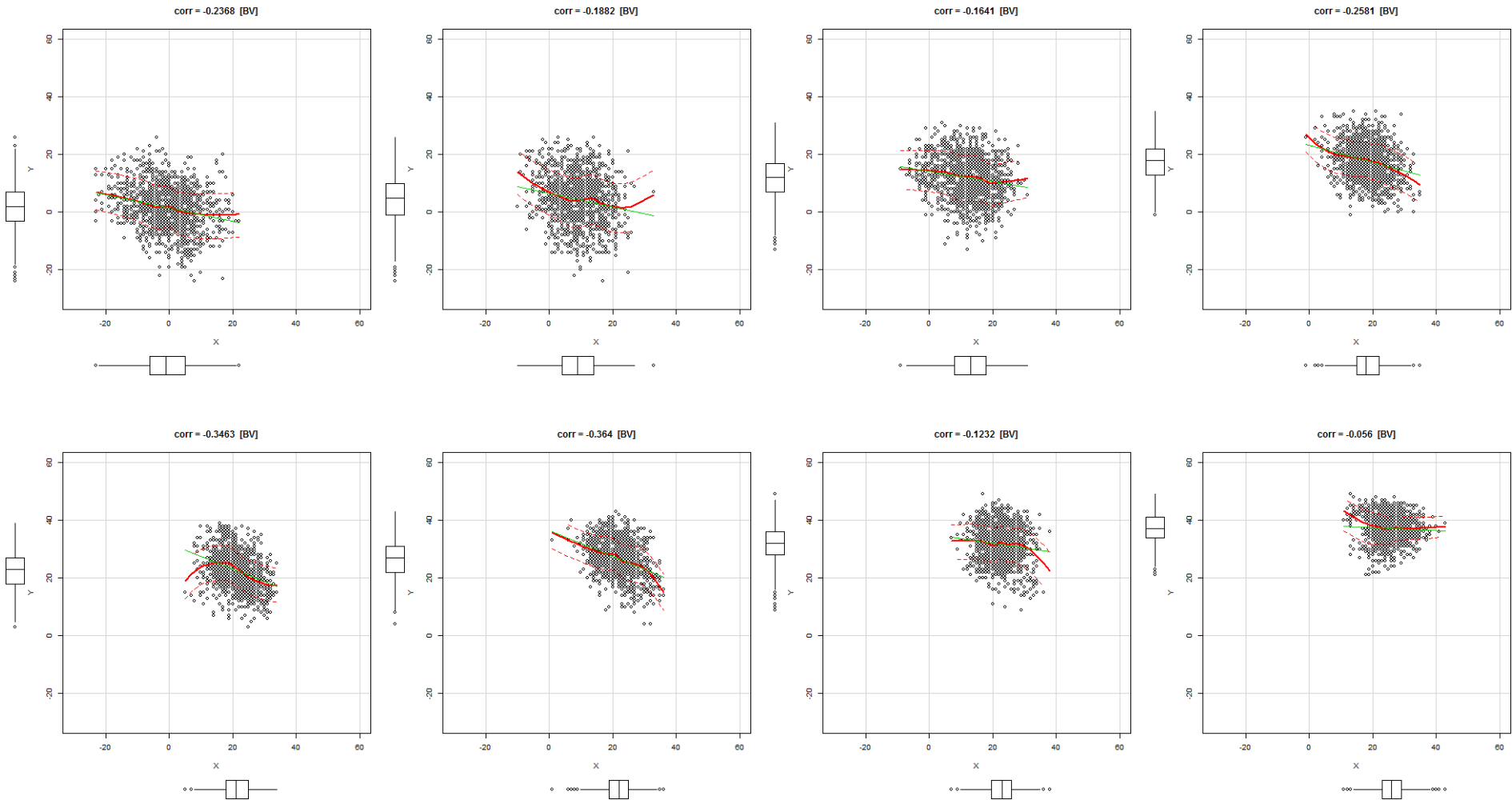


corr = -0.0224 [phe 33]



```
bin<-hexbin(data_phe_X_33, data_phe_Y_33, xbins=30)
correl <- round(correl_phe_33, digits = 4)
heading <- paste("corr =", correl, " [phe 33]")
plot(bin, main=heading, xlab=" ", ylab=" ")
```

scenarios of genetic & phenotypic correlations

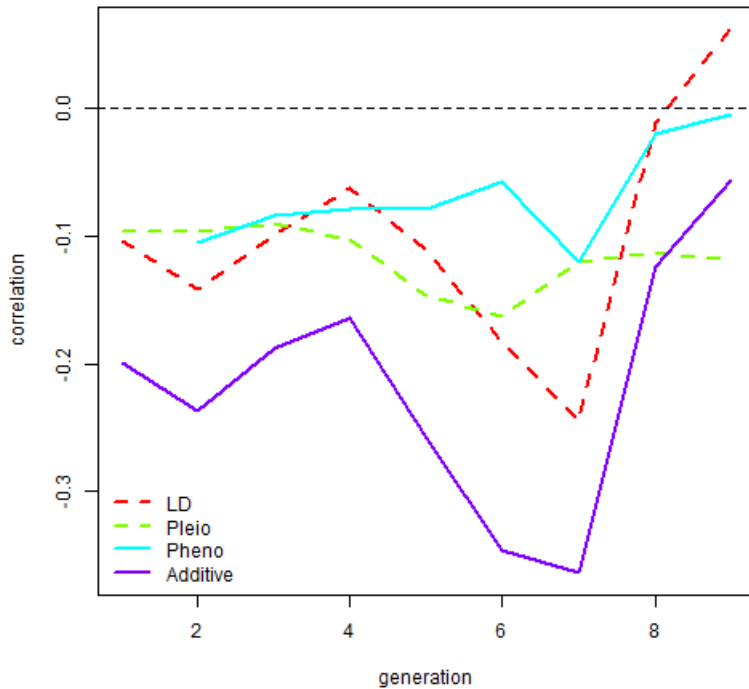


time lapse of genetic correlations over $t=8$

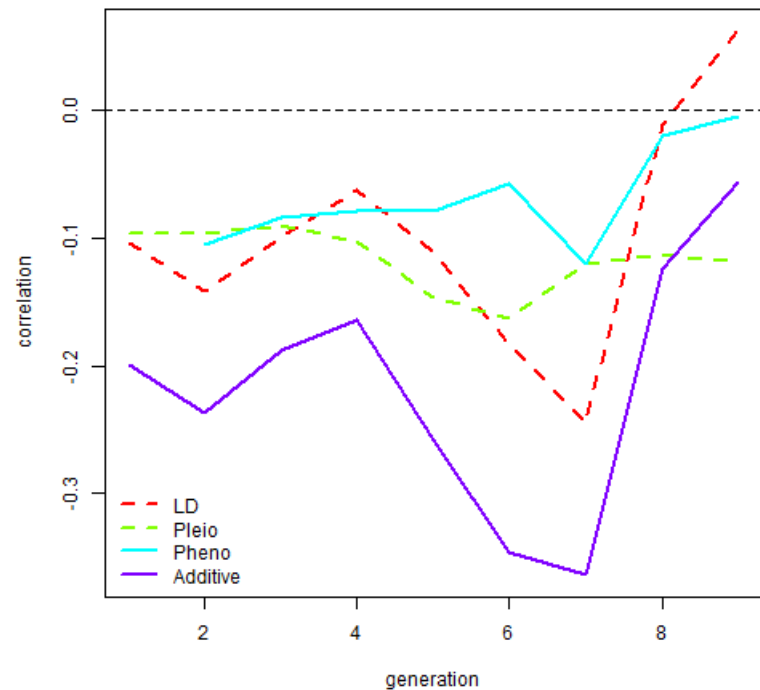
scenarios of genetic & phenotypic correlations

$$r[X, Y]_0 = \frac{\sigma_{AA[X,Y]LD} + \sigma_{DD[X,Y]LD} + \sigma_{AA[X,Y]P} + \sigma_{DD[X,Y]P}}{\sqrt{\left(\sigma_a^2[X] + \sigma_{AA[X]LD} + \sigma_{DD[X]LD}\right)\left(\sigma_a^2[Y] + \sigma_{AA[Y]LD} + \sigma_{DD[Y]LD}\right)}}$$

contributions to numerator

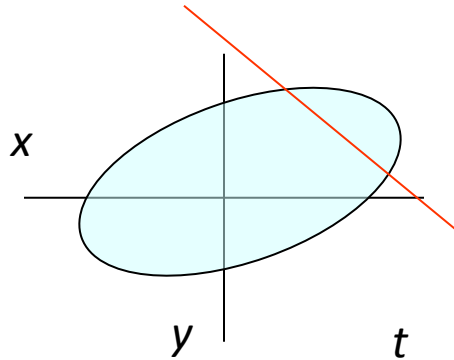


contributions to numerator



Sanchez, L., Yanchuk, A., King, J., 2007. Gametic models for multitrait selection schemes to study variance of response and drift under adverse genetic correlations. *Tree Genetics & Genomes*.

Index selection



$$l = b^T z = (P^{-1} G a)^T z$$

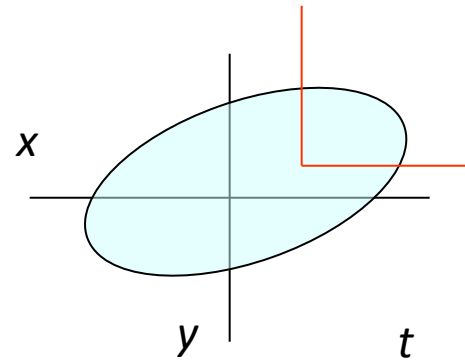
Optimal if...

- known **G** and **P**

Inefficient if...

- poor estimations of **G** et **P**
- *drift* of genetic parameters over generations

Independent culling



selected x \cap *selected y*

- simple
- economic advantages (multistage)
- cumbrous computing of optimal thresholds with many traits