# Viewing the Phenomenon of Heterosis as a Network of Interacting Parallel Aggregation Processes

UNIVERSITEIT GENT

Computational Biology

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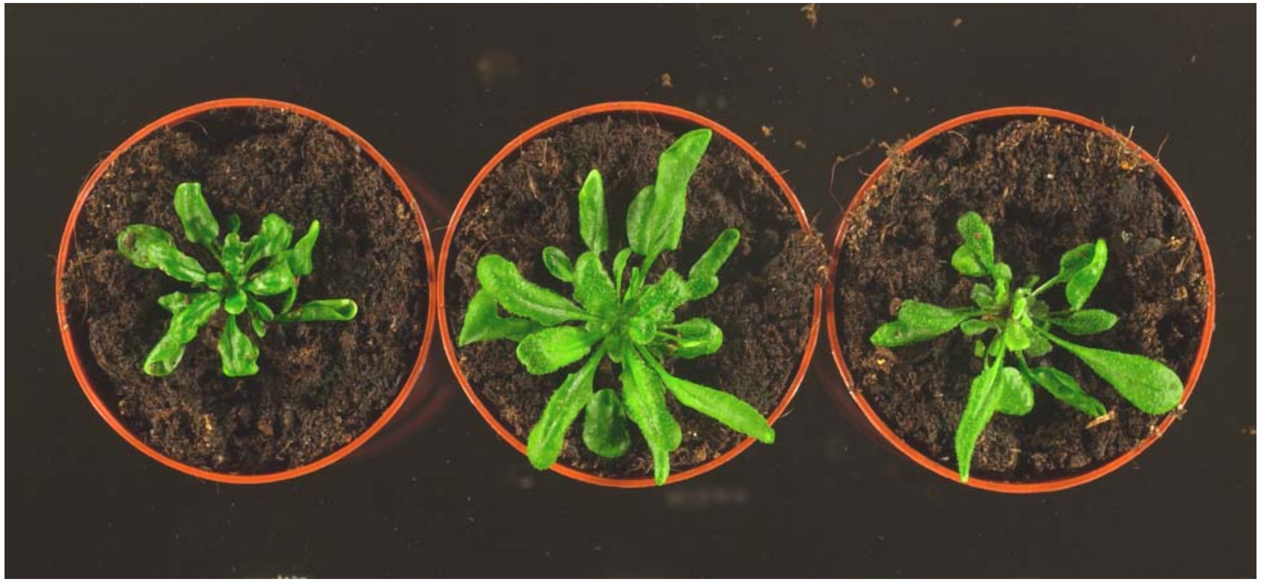
“Heterosis, or hybrid vigor, refers to the phenomenon that a progeny of diverse inbred varieties exhibit greater biomass, speed of development, and fertility than the better of the two parents.”

J.A. Birchler *et al.* (2003) *In Search of the Molecular Basis of Heterosis.* The Plant Cell, Vol. 15, 2236-2239.

# Biomass Heterosis in *Arabidopsis thaliana*



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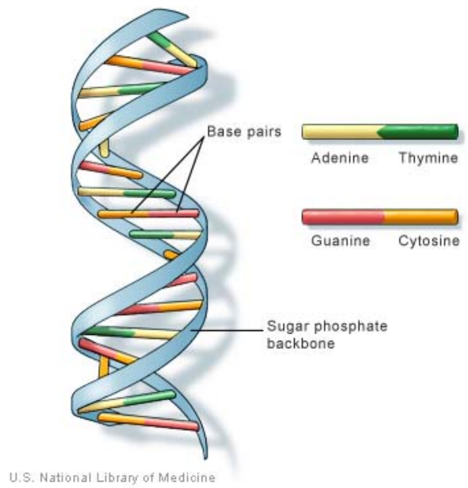
Heterosis is of great commercial importance since it enables the breeder to generate a product with preserved values which in turn, allows the farmer to grow uniform plants expressing these heterosis features.

# Genomes and Genes

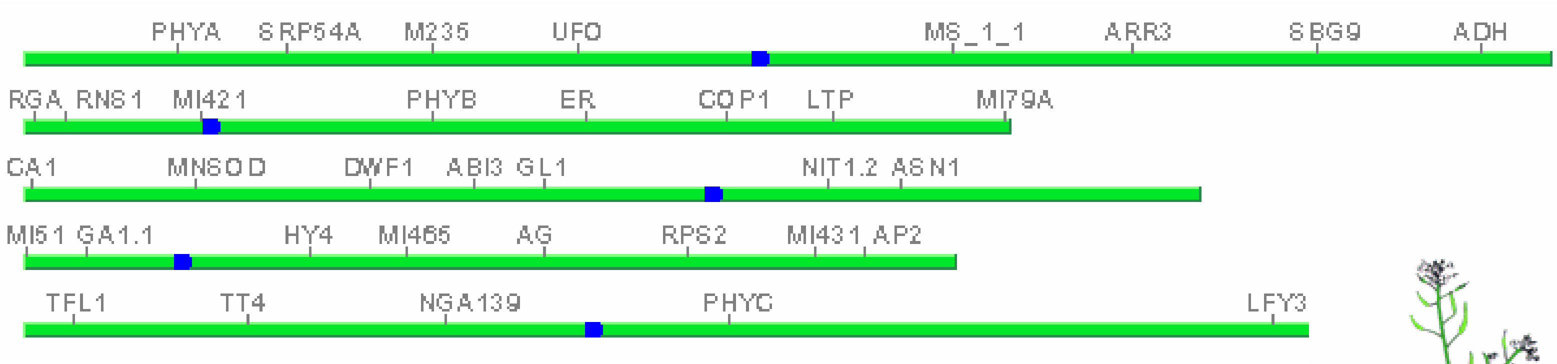



**Genes** are certain regions in the DNA molecule of the organism.

The **genome** is the totality of the genetic information of an organism.

DNA: the physical carrier of the genetic information.

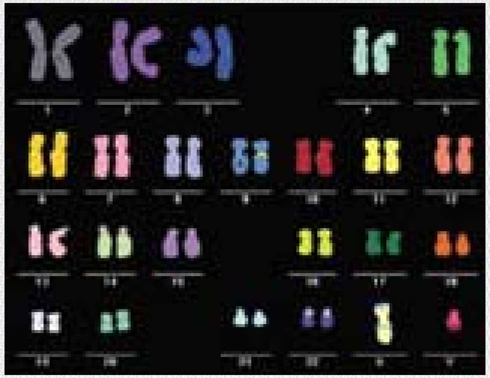
# The Genome of *Arabidopsis thaliana*




*Small genome (114.5 Mb/125 Mb total, 5 chromosomes) has been sequenced in the year 2000.*

# Genotype and Phenotype

Human male karyotype



A **chromosome** is a very long, continuous piece of DNA, contained in the cell's nucleus.

The **karyotype** is the collection of chromosomes.

The **genotype** is the totality of the genetic information of an organism.

The **phenotype** is the expression of organism’s genotype.

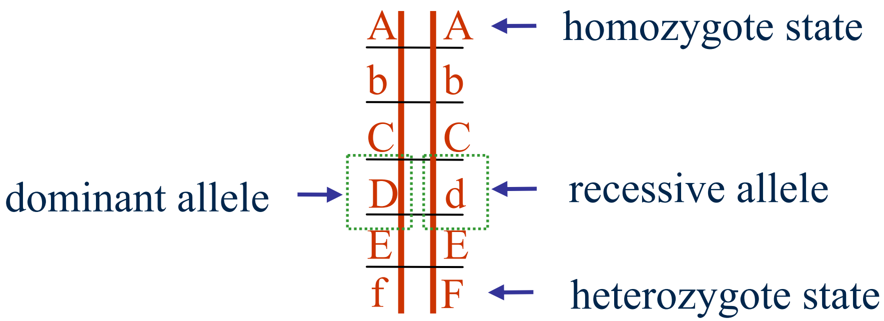
# Diploid Organisms

An **allele** is a variant of gene.

A **locus** is a certain position in the genome.

A **homozygote state** is a locus having two identical alleles.

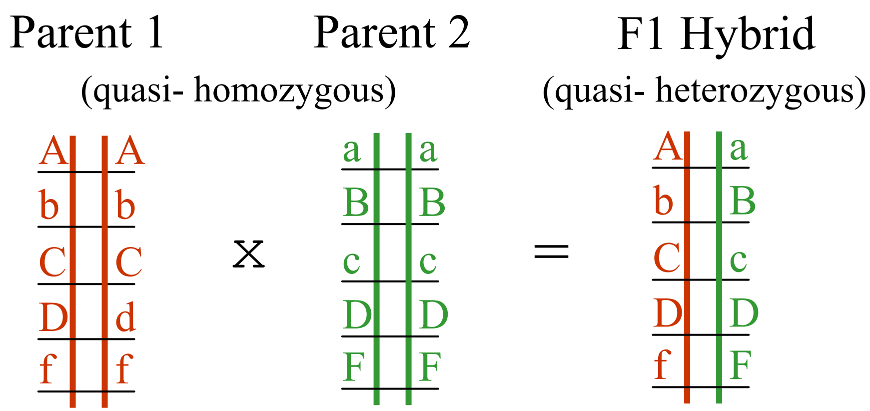
Diploid organism
(2n choromosomes)




Genomes can be present in one or more copies per cell.

Two copies of the genome are found in the **diploid organisms**.

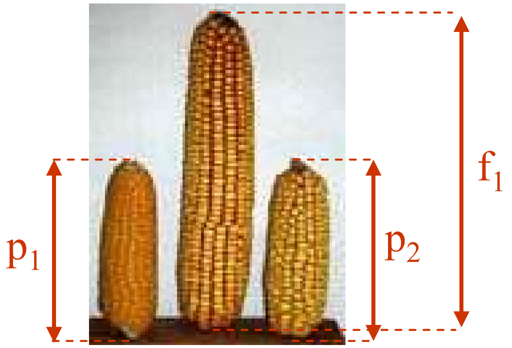
# Molecular Models of Heterosis




1. **Additive-Dominance Model**: heterosis in F1 is due to increased number of loci of the genome where the heterozygote state is superior than any of the parental homozygote states.

2. **Epistatic Model**: heterosis in F1 is due to complex interaction between different genes on different loci of the genome.

# Additive versus Dominance Effects




$p_1$, $p_2$ : phenotypic values of the parents
$f_1$: phenotypic values of the hybrid

**Single Gene Model**

Additive effect: $\boldsymbol{a = |p_1 - p_2| / 2}$

Dominance effect: $\boldsymbol{d = f_1 - (p_1 + p_2) / 2}$

Potence ratio: $\boldsymbol{hp = d / a}$

Heterosis: $\boldsymbol{hp > 1}$

Additivity: $\boldsymbol{hp = 0}$

Partial dominance: $\boldsymbol{-1 < hp < 0}$ **or** $\boldsymbol{0 < hp < 1}$

Complete dominance: $\boldsymbol{hp = -1}$ **or** $\boldsymbol{hp = 1}$

Over-dominance: $\boldsymbol{hp < -1}$ **or** $\boldsymbol{hp > 1}$

# Additive versus Dominance Effects

**Multiple Gene Model**

Net additive effect: $\boldsymbol{a = \mathrm{r_a} \cdot \Sigma_{i=1,m}\, a_i}$

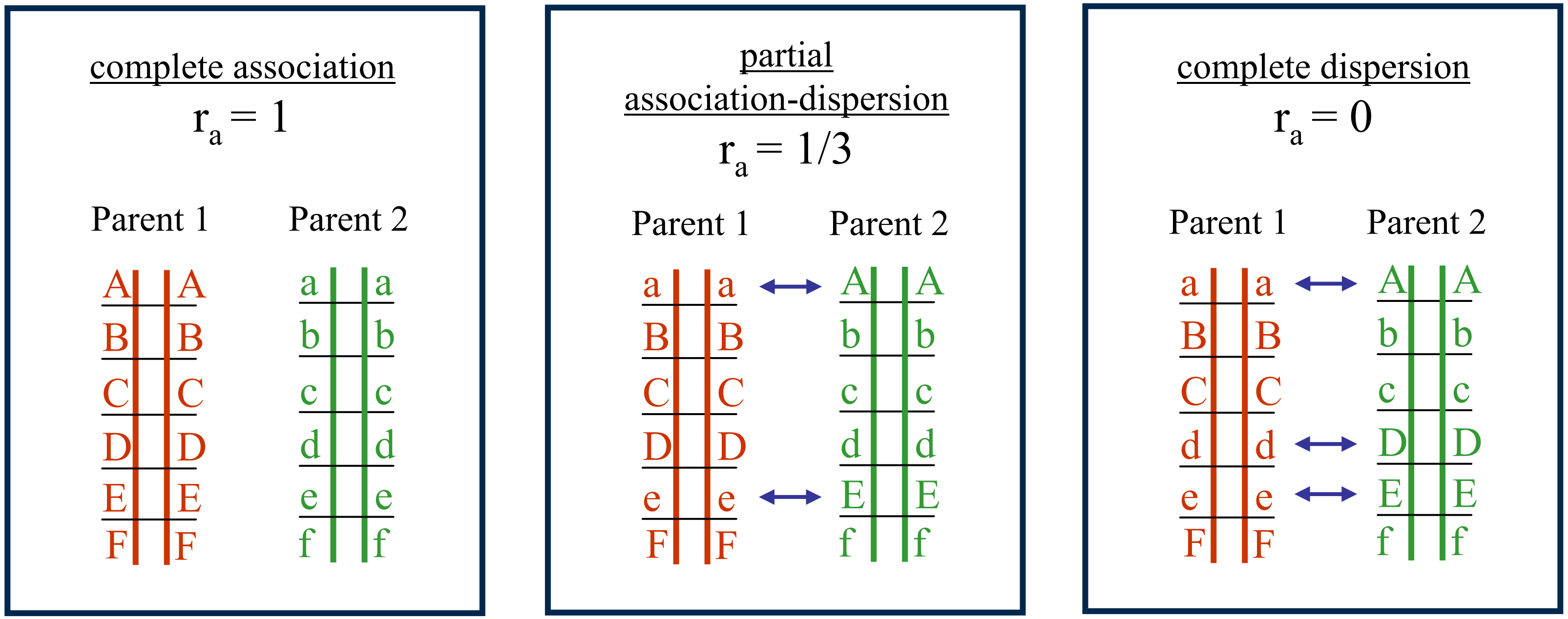
Net dominance effect: $\boldsymbol{d = \Sigma_{i=1,m}\, d_i}$

$\boldsymbol{a_i}$ : additive effect of gene *i*

$\boldsymbol{d_i}$ : dominance effect of gene *i*

$\mathbf{r_a}$ : coefficient of gene association-dispersion

# Coefficient of Gene Association-Dispersion




$$\mathbf{r_a = 1 - 2\Sigma_{\mathit{j}\in \mathit{J}}\, \mathit{a_j} \,/\, \Sigma_{\mathit{j}}\, \mathit{a_j}}$$

$J$ : the set of genes with dispersed alleles between the parents

# Heterosis Potential

## Net Potence Ratio

$$hp = \underbrace{\Sigma_{i=1,m}\, d_i}_{\text{net dominance effect}} \;/\; \underbrace{(r_a\, .\, \Sigma_{i=1,m}\, a_i)}_{\text{net additive effect}}$$

$$hp = 1 \;/\; r_a\, .\, \Sigma_{i=1,m}\, \underbrace{(a_i \;/\; \Sigma_{i=1,m}\, a_i)}_{\lambda_i} \;.\; \underbrace{d_i \,/\, a_i}_{hp_i}$$

# Net Potence Ratio

$$\boldsymbol{hp} \,.\, \mathbf{r_a} = \Sigma_{i=1,m}\, \lambda_i \,.\, \boldsymbol{hp_i}$$

$\boldsymbol{hp_i = d_i / a_i}$ : heterosis potential of gene *i*

$\lambda_i = \boldsymbol{a_i} / \Sigma_{i=1,m}\, \boldsymbol{a_i}$ : relative additive effect of gene *i*

$\Sigma_{i=1,m}\, \lambda_i = 1$

# Net Potence Ratio and Heterosis

$$\min_{i=1,m} hp_i \leq hp \,.\, r_a \leq \max_{i=1,m} hp_i$$

If $\Sigma_{i=1,m} \lambda_i \,.\, hp_i > r_a$ then <u>heterosis</u>.

If <u>heterosis</u> then $\max_{i=1,m} hp_i > r_a$ .

# Heterosis and Coefficient of Association-Dispersion

If heterosis then:

- in case of *complete association* there must exist at least one positively *over-dominant gene*;
- otherwise, in *all other cases*, at least one gene exhibiting positive *partial-dominance* must be present.

# Heterosis as a Network of Interacting Parallel Aggregation Processes

genes = interacting agents

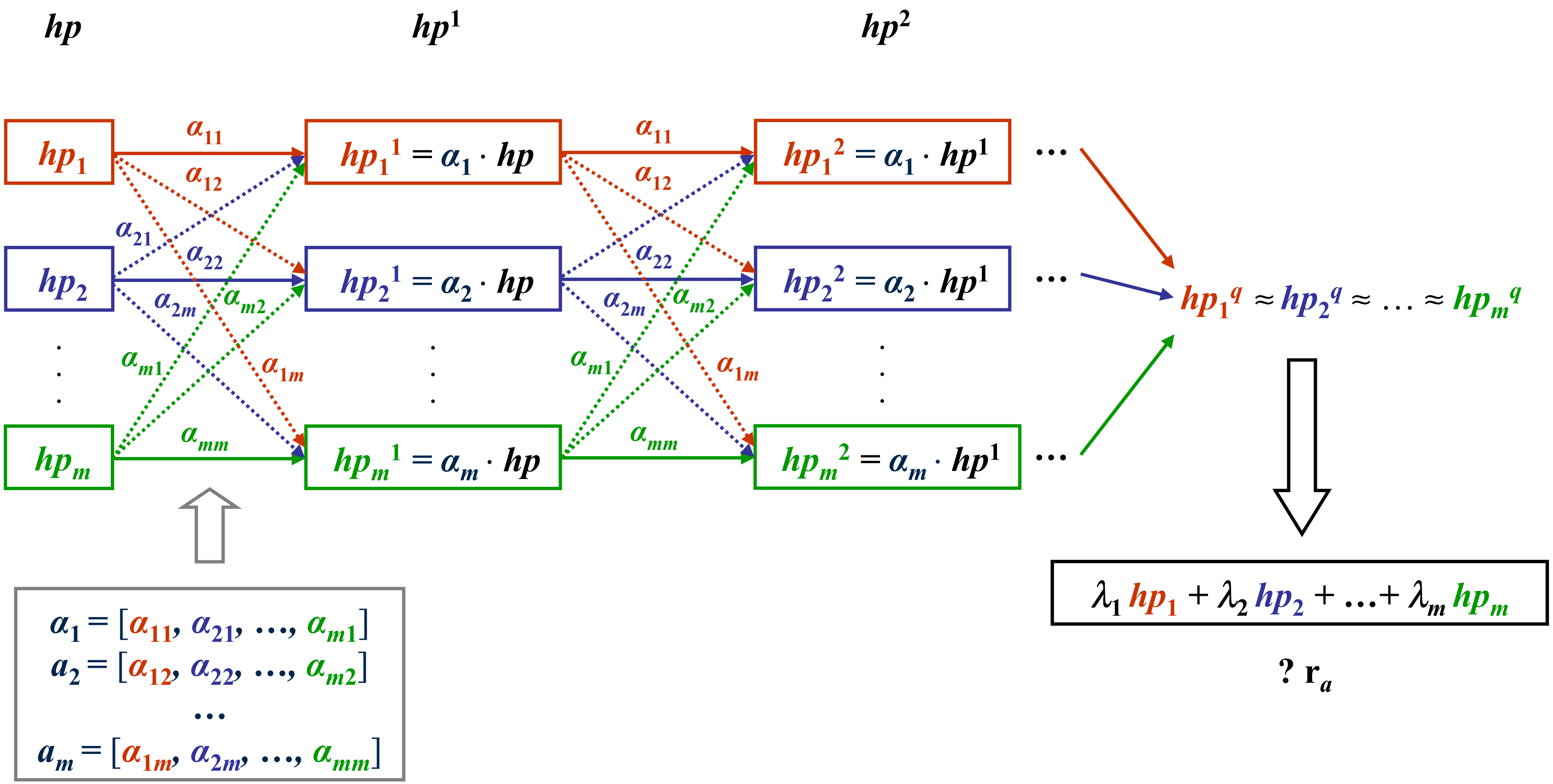
$\boldsymbol{\alpha_i = [\alpha_{i1}, \alpha_{i2}, \ldots, \alpha_{im}]}$: interaction coefficients for agent i

$\boldsymbol{\Sigma_k \alpha_{ik} = 1}$

$\boldsymbol{\alpha_{ik}}$ : the relative degree of influence agent *k* accepts from agent *i*

$\boldsymbol{\alpha_{ii}}$ : the relative degree of self-influence of agent *i* in the interaction

# Interacting Parallel Aggregation Processes



# Parallel Aggregation Processes in Terms of Matrix Operations

**Initialization**

$\boldsymbol{hp}^0 = [\boldsymbol{hp}_1, \boldsymbol{hp}_2, \ldots, \boldsymbol{hp}_m]^T$ : vector of initial heterosis potentials

$$\boldsymbol{A} = [\boldsymbol{\alpha}_1^T, \boldsymbol{\alpha}_2^T, \ldots, \boldsymbol{\alpha}_m^T] = \begin{pmatrix} \alpha_{11} & \alpha_{12} & \ldots & \alpha_{1m} \\ \alpha_{21} & \alpha_{22} & \ldots & \alpha_{2m} \\ \ldots & \ldots & \ldots & \ldots \\ \alpha_{m1} & \alpha_{m2} & \ldots & \alpha_{mm} \end{pmatrix}$$ : interaction matrix

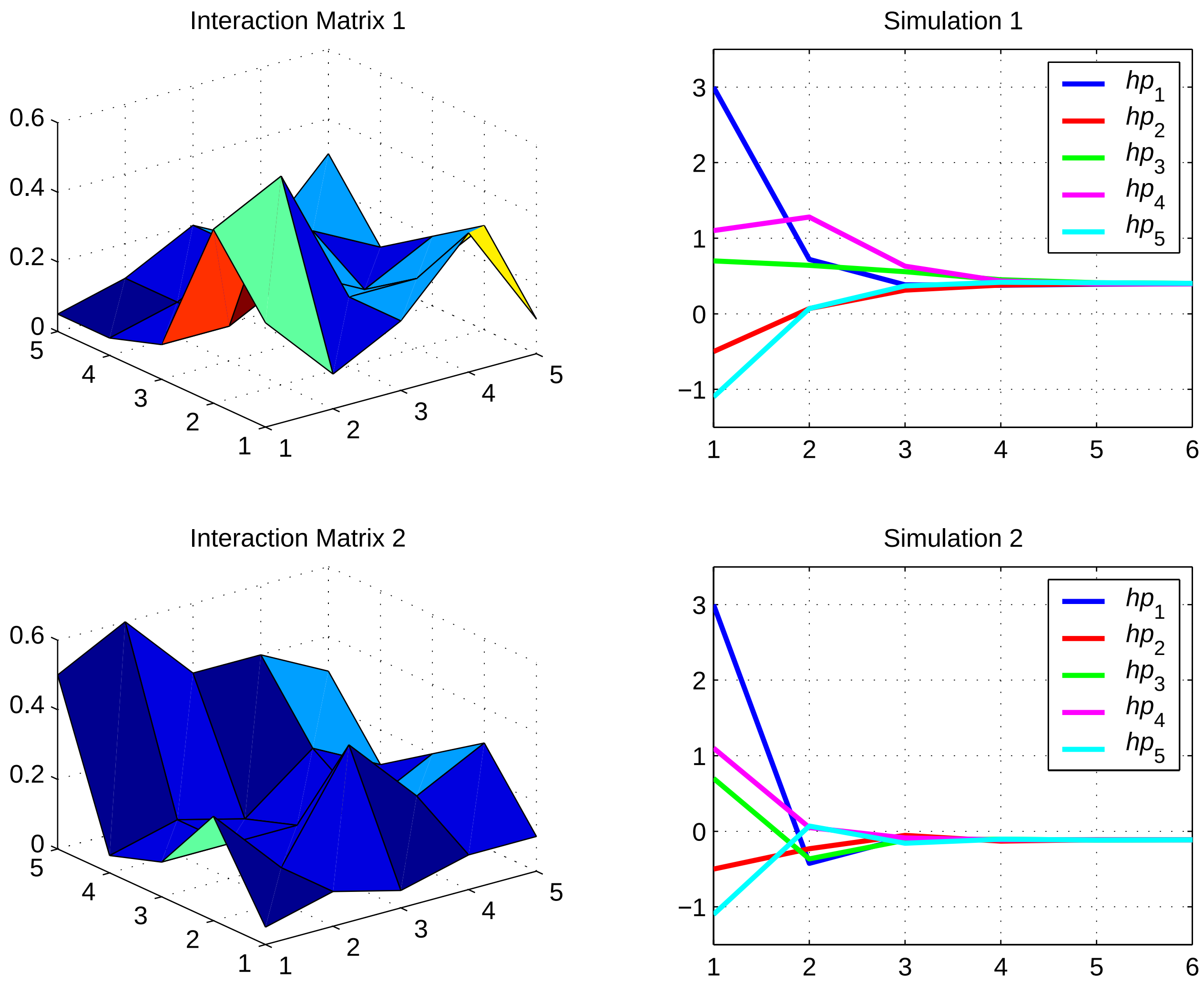
**Recursion**

For $k = 1, 2, \ldots$ $\boldsymbol{hp}^k = \boldsymbol{A}^T \boldsymbol{hp}^{k-1}$: vector of heterosis potentials at step $k$.

**Convergence**

Guaranteed for all $\alpha_{ij} > \mathbf{0}$.

After $q$ steps $\boldsymbol{hp}^q = \boldsymbol{A}^T \boldsymbol{hp}_m^{q-1} = \boldsymbol{A}^T \ldots \boldsymbol{A}^T \boldsymbol{hp}^0 = (\boldsymbol{A}^q)^T \boldsymbol{hp}^0$ and $\boldsymbol{hp}_1^q \approx \ldots \approx \boldsymbol{hp}_m^q$



Interaction Matrix 1
0.6
0.4
0.2
0
5
4
3
2
1
1
2
3
4
5
Simulation 1
3
2
1
0
−1
1
2
3
4
5
6
$hp_1$
$hp_2$
$hp_3$
$hp_4$
$hp_5$
Interaction Matrix 2
0.6
0.4
0.2
0
5
4
3
2
1
1
2
3
4
5
Simulation 2
3
2
1
0
−1
1
2
3
4
5
6
$hp_1$
$hp_2$
$hp_3$
$hp_4$
$hp_5$