



**LOUISIANA STATE UNIVERSITY**  
**College of Agriculture**  
**School of Plant, Environmental, and Soil Sciences**  
**AGRO 7075 Prediction-based Breeding**



# Kinship matrices

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$G_A$

- $G_A$  – additive genomic relationship matrix
- There are many methods
- The most popular was proposed by VanRaden (2008)

$$G_A = \frac{WW'}{\sum_{i=1}^n (2piqi)}$$

Efeitos aditivos: W

$$W = \begin{cases} Se\ MM; & 2 \rightarrow 2 - 2p = 2q \\ Se\ Mm; & 1 \rightarrow 1 - 2p = q - p \\ Se\ mm; & 0 \rightarrow 0 - 2p = -2p \end{cases}$$

- Another way is to center and scale the matrix first
- `W <- scale(M, scale = TRUE, center = TRUE)`
- `G_A <- tcrossprod(W) / ncol(W)`

	snp2	snp5	snp6	snp7	snp8	snp9	snp10
gid 1	1	1	1	1	0	0	0
gid 2	1	1	0	1	0	0	0
gid 4	2	0	0	2	0	0	0
gid 5	2	2	0	2	2	2	2
gid 6	2	2	2	0	2	2	2
gid 7	0	2	1	2	2	2	2
gid 8	0	1	1	1	2	2	2
gid 9	1	2	2	1	2	2	2
gid 10	2	1	2	2	2	1	1

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.063	1.062	1.016	-0.719	-0.578	-0.625	-0.484	-0.602	-0.133
gid 2	1.062	1.273	1.227	-0.508	-0.789	-0.625	-0.484	-0.812	-0.344
gid 4	1.016	1.227	1.813	-0.344	-1.047	-0.883	-0.742	-1.070	0.031
gid 5	-0.719	-0.508	-0.344	0.875	0.172	0.336	0.055	0.148	-0.016
gid 6	-0.578	-0.789	-1.047	0.172	1.156	0.055	0.195	0.711	0.125
gid 7	-0.625	-0.625	-0.883	0.336	0.055	0.852	0.570	0.453	-0.133
gid 8	-0.484	-0.484	-0.742	0.055	0.195	0.570	0.711	0.383	-0.203
gid 9	-0.602	-0.812	-1.070	0.148	0.711	0.453	0.383	0.688	0.102
gid 10	-0.133	-0.344	0.031	-0.016	0.125	-0.133	-0.203	0.102	0.570

	snp2	snp5	snp6	snp7	snp8	snp9	snp10
gid 1	-0.267	-0.471	0.000	-0.471	-1.333	-1.258	-1.258
gid 2	-0.267	-0.471	-1.155	-0.471	-1.333	-1.258	-1.258
gid 4	0.933	-1.886	-1.155	0.943	-1.333	-1.258	-1.258
gid 5	0.933	0.943	-1.155	0.943	0.667	0.800	0.800
gid 6	0.933	0.943	1.155	-1.886	0.667	0.800	0.800
gid 7	-1.467	0.943	0.000	0.943	0.667	0.800	0.800
gid 8	-1.467	-0.471	0.000	-0.471	0.667	0.800	0.800
gid 9	-0.267	0.943	1.155	-0.471	0.667	0.800	0.800
gid 10	0.933	-0.471	1.155	0.943	0.667	-0.229	-0.229

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	0.780	0.780	0.734	-0.577	-0.387	-0.486	-0.295	-0.436	-0.112
gid 2	0.780	0.970	0.924	-0.386	-0.577	-0.486	-0.295	-0.627	-0.303
gid 4	0.734	0.924	1.656	-0.227	-0.989	-0.737	-0.547	-0.958	0.143
gid 5	-0.577	-0.386	-0.227	0.815	0.053	0.305	-0.076	0.084	0.009
gid 6	-0.387	-0.577	-0.989	0.053	1.197	-0.076	0.114	0.655	0.009
gid 7	-0.486	-0.486	-0.737	0.305	-0.076	0.808	0.427	0.366	-0.121
gid 8	-0.295	-0.295	-0.547	-0.076	0.114	0.427	0.617	0.271	-0.216
gid 9	-0.436	-0.627	-0.958	0.084	0.655	0.366	0.271	0.606	0.039
gid 10	-0.112	-0.303	0.143	0.009	0.009	-0.121	-0.216	0.039	0.552

$$G_A = \frac{WW'}{ncol}$$

$G_D$

- $G_D$  – dominance genomic relationship matrix

- $Aa = 1$

- Otherwise = 0

$$G_D = \frac{SS'}{\sum_{i=1}^n (2piqi)^2}$$

Efeitos de dominância: S

$$S = \begin{cases} Se\ MM; & 0 \rightarrow -2q^2 \\ Se\ Mm; & 1 \rightarrow 2pq \\ Se\ mm; & 0 \rightarrow -2p^2 \end{cases}$$

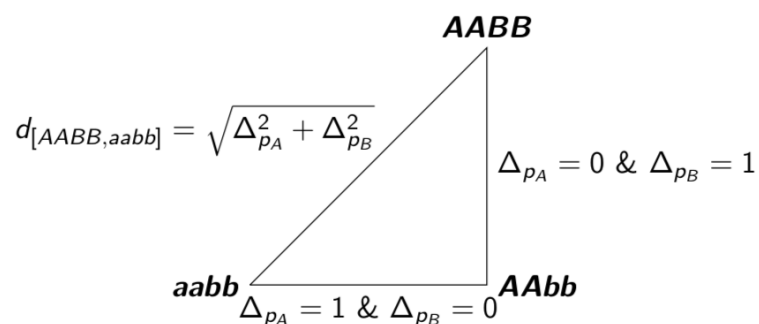
	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.629	1.335	0.597	0.034	-0.140	0.203	0.551	0.425	-0.474
gid 2	1.335	1.629	0.890	0.327	0.154	-0.090	0.258	0.718	-0.180
gid 4	0.597	0.890	1.810	0.726	0.813	0.512	0.077	0.501	-0.303
gid 5	0.034	0.327	0.726	0.394	0.481	0.180	0.006	0.170	0.032
gid 6	-0.140	0.154	0.813	0.481	0.829	0.267	-0.167	-0.004	0.119
gid 7	0.203	-0.090	0.512	0.180	0.267	0.668	0.494	-0.248	-0.183
gid 8	0.551	0.258	0.077	0.006	-0.167	0.494	0.842	-0.161	-0.096
gid 9	0.425	0.718	0.501	0.170	-0.004	-0.248	-0.161	0.560	-0.193
gid 10	-0.474	-0.180	-0.303	0.032	0.119	-0.183	-0.096	-0.193	0.639

	snp2	snp5	snp6	snp7	snp8	snp9	snp10
gid 1	1	1	1	1	0	0	0
gid 2	1	1	0	1	0	0	0
gid 4	2	0	0	2	0	0	0
gid 5	2	2	0	2	2	2	2
gid 6	2	2	2	0	2	2	2
gid 7	0	2	1	2	2	2	2
gid 8	0	1	1	1	2	2	2
gid 9	1	2	2	1	2	2	2
gid 10	2	1	2	2	2	1	1

	snp2	snp5	snp6	snp7	snp8	snp9	snp10
gid 1	1	1	1	1	0	0	0
gid 2	1	1	0	1	0	0	0
gid 4	0	0	0	0	0	0	0
gid 5	0	0	0	0	0	0	0
gid 6	0	0	0	0	0	0	0
gid 7	0	0	1	0	0	0	0
gid 8	0	1	1	1	0	0	0
gid 9	1	0	0	1	0	0	0
gid 10	0	1	0	0	0	1	1

# Gaussian kernel

- **GK – Euclidian genomic distance between individuals**
- Capture additive and non-additive effects



$$GK = \exp\left(-h \frac{dist_{ii'}^2}{median(dist_{ii'}^2)}\right)$$

- $h$  = bandwidth parameters
- Replace the diagonal by 1,00

	snp2	snp5	snp6	snp7	snp8	snp9	snp10
gid 1	1	1	1	1	0	0	0
gid 2	1	1	0	1	0	0	0
gid 4	2	0	0	2	0	0	0
gid 5	2	2	0	2	2	2	2
gid 6	2	2	2	0	2	2	2
gid 7	0	2	1	2	2	2	2
gid 8	0	1	1	1	2	2	2
gid 9	1	2	2	1	2	2	2
gid 10	2	1	2	2	2	1	1

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.000	0.717	0.513	0.264	0.264	0.275	0.301	0.287	0.368
gid 2	0.717	1.000	0.561	0.275	0.234	0.264	0.287	0.253	0.315
gid 4	0.513	0.561	1.000	0.264	0.195	0.217	0.234	0.209	0.331
gid 5	0.264	0.275	0.264	1.000	0.390	0.475	0.414	0.442	0.414
gid 6	0.264	0.234	0.195	0.390	1.000	0.368	0.414	0.624	0.414
gid 7	0.275	0.264	0.217	0.475	0.368	1.000	0.624	0.561	0.390
gid 8	0.301	0.287	0.234	0.414	0.414	0.624	1.000	0.561	0.390
gid 9	0.287	0.253	0.209	0.442	0.624	0.561	0.561	1.000	0.475
gid 10	0.368	0.315	0.331	0.414	0.414	0.390	0.390	0.475	1.000

# G<sub>AxE</sub>

- Additive by Environment
- Kronecker product
- Environment (diagonal)
- $\otimes$
- $G_A$  matrix

	LN	IN
LN	1	0
IN	0	1

	gid 1	gid 2
gid 1	1.063	1.062
gid 2	1.062	1.273

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.063	1.062	1.016	-0.719	-0.578	-0.625	-0.484	-0.602	-0.133
gid 2	1.062	1.273	1.227	-0.508	-0.789	-0.625	-0.484	-0.812	-0.344
gid 4	1.016	1.227	1.813	-0.344	-1.047	-0.883	-0.742	-1.070	0.031
gid 5	-0.719	-0.508	-0.344	0.875	0.172	0.336	0.055	0.148	-0.016
gid 6	-0.578	-0.789	-1.047	0.172	1.156	0.055	0.195	0.711	0.125
gid 7	-0.625	-0.625	-0.883	0.336	0.055	0.852	0.570	0.453	-0.133
gid 8	-0.484	-0.484	-0.742	0.055	0.195	0.570	0.711	0.383	-0.203
gid 9	-0.602	-0.812	-1.070	0.148	0.711	0.453	0.383	0.688	0.102
gid 10	-0.133	-0.344	0.031	-0.016	0.125	-0.133	-0.203	0.102	0.570

	LNgid 1	LNgid 2	INgid 1	INgid 2
LNgid 1	1.063	1.062	0.000	0.000
LNgid 2	1.062	1.273	0.000	0.000
INgid 1	0.000	0.000	1.063	1.062
INgid 2	0.000	0.000	1.062	1.273

# Epistasis

- **Hadamard product** (Vitezica et al., 2017)

$$Cov_{AA} = \frac{G_A \odot G_A}{tr(G_A \odot G_A)/n} = G_{AA} \sigma_{AA}^2$$

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.063	1.062	1.016	-0.719	-0.578	-0.625	-0.484	-0.602	-0.133
gid 2	1.062	1.273	1.227	-0.508	-0.789	-0.625	-0.484	-0.812	-0.344
gid 4	1.016	1.227	1.813	-0.344	-1.047	-0.883	-0.742	-1.070	0.031
gid 5	-0.719	-0.508	-0.344	0.875	0.172	0.336	0.055	0.148	-0.016
gid 6	-0.578	-0.789	-1.047	0.172	1.156	0.055	0.195	0.711	0.125
gid 7	-0.625	-0.625	-0.883	0.336	0.055	0.852	0.570	0.453	-0.133
gid 8	-0.484	-0.484	-0.742	0.055	0.195	0.570	0.711	0.383	-0.203
gid 9	-0.602	-0.812	-1.070	0.148	0.711	0.453	0.383	0.688	0.102
gid 10	-0.133	-0.344	0.031	-0.016	0.125	-0.133	-0.203	0.102	0.570

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.000	0.998	0.914	0.458	0.296	0.346	0.207	0.321	0.016
gid 2	0.998	1.434	1.332	0.228	0.551	0.346	0.207	0.584	0.105
gid 4	0.914	1.332	2.909	0.105	0.970	0.690	0.487	1.013	0.001
gid 5	0.458	0.228	0.105	0.678	0.026	0.100	0.003	0.019	0.000
gid 6	0.296	0.551	0.970	0.026	1.183	0.003	0.034	0.447	0.014
gid 7	0.346	0.346	0.690	0.100	0.003	0.642	0.288	0.182	0.016
gid 8	0.207	0.207	0.487	0.003	0.034	0.288	0.447	0.130	0.036
gid 9	0.321	0.584	1.013	0.019	0.447	0.182	0.130	0.419	0.009
gid 10	0.016	0.105	0.001	0.000	0.014	0.016	0.036	0.009	0.288

$$Cov_{DD} = \frac{G_D \odot G_D}{tr(G_D \odot G_D)/n} = G_{DD} \sigma_{DD}^2$$

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.629	1.335	0.597	0.034	-0.140	0.203	0.551	0.425	-0.474
gid 2	1.335	1.629	0.890	0.327	0.154	-0.090	0.258	0.718	-0.180
gid 4	0.597	0.890	1.810	0.726	0.813	0.512	0.077	0.501	-0.303
gid 5	0.034	0.327	0.726	0.394	0.481	0.180	0.006	0.170	0.032
gid 6	-0.140	0.154	0.813	0.481	0.829	0.267	-0.167	-0.004	0.119
gid 7	0.203	-0.090	0.512	0.180	0.267	0.668	0.494	-0.248	-0.183
gid 8	0.551	0.258	0.077	0.006	-0.167	0.494	0.842	-0.161	-0.096
gid 9	0.425	0.718	0.501	0.170	-0.004	-0.248	-0.161	0.560	-0.193
gid 10	-0.474	-0.180	-0.303	0.032	0.119	-0.183	-0.096	-0.193	0.639

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	2.113	1.419	0.284	0.001	0.016	0.033	0.242	0.144	0.179
gid 2	1.419	2.113	0.631	0.085	0.019	0.006	0.053	0.410	0.026
gid 4	0.284	0.631	2.609	0.420	0.526	0.209	0.005	0.200	0.073
gid 5	0.001	0.085	0.420	0.124	0.184	0.026	0.000	0.023	0.001
gid 6	0.016	0.019	0.526	0.184	0.547	0.057	0.022	0.000	0.011
gid 7	0.033	0.006	0.209	0.026	0.057	0.355	0.194	0.049	0.027
gid 8	0.242	0.053	0.005	0.000	0.022	0.194	0.565	0.021	0.007
gid 9	0.144	0.410	0.200	0.023	0.000	0.049	0.021	0.250	0.030
gid 10	0.179	0.026	0.073	0.001	0.011	0.027	0.007	0.030	0.325

$$Cov_{AD} = \frac{G_A \odot G_D}{tr(G_A \odot G_D)/n} = G_{AD} \sigma_{AD}^2$$

	gid 1	gid 2	gid 4	gid 5	gid 6	gid 7	gid 8	gid 9	gid 10
gid 1	1.512	1.238	0.530	-0.021	0.071	-0.111	-0.233	-0.223	0.055
gid 2	1.238	1.811	0.954	-0.145	-0.106	0.049	-0.109	-0.509	0.054
gid 4	0.530	0.954	2.865	-0.218	-0.743	-0.395	-0.050	-0.468	-0.008
gid 5	-0.021	-0.145	-0.218	0.301	0.072	0.053	0.000	0.022	0.000
gid 6	0.071	-0.106	-0.743	0.072	0.837	0.013	-0.028	-0.002	0.013
gid 7	-0.111	0.049	-0.395	0.053	0.013	0.497	0.246	-0.098	0.021
gid 8	-0.233	-0.109	-0.050	0.000	-0.028	0.246	0.523	-0.054	0.017
gid 9	-0.223	-0.509	-0.468	0.022	-0.002	-0.098	-0.054	0.336	-0.017
gid 10	0.055	0.054	-0.008	0.000	0.013	0.021	0.017	-0.017	0.318

# SCA

- **Kronecker product** (Lópes-Cruz et al., 2015)
- $G_1 \otimes G_2$
- Females  $\otimes$  Males
- `SCA <- kronecker(Ga.male, Ga.female)`
- Generates all possible hybrids

	gid 1	gid 2
gid 1	1.063	1.062
gid 2	1.062	1.273

	gid 9	gid 10
gid 9	0.688	0.102
gid 10	0.102	0.570

		1 9	2 9	1 10	2 10
1 9		0.73	0.11	0.73	0.11
2 9		0.11	0.61	0.11	0.61
1 10		0.73	0.11	0.88	0.13
2 10		0.11	0.61	0.13	0.73