Appendix. Unifying quantification methods for sexual selection and assortative mating using information theory.

A. Carvajal-Rodríguez*

Centro de Investigación Mariña (CIM), Departamento de Bioquímica, Genética e Inmunología. Universidade de Vigo, 36310 Vigo, Spain.

*: A. Carvajal-Rodríguez. Departamento de Bioquímica, Genética e Inmunología. Universidade de Vigo, 36310 Vigo, Spain. Phone: +34 986813828

email: acraaj@uvigo.es

A. General formula for non-random mating information

Consider two continuous traits, *X* in females and *Y* in males from a population and let the probability distribution $Q'(x,y)$ with probability density $q'(x,y)$ that represents the mating probability for pairs with values in the infinitesimal interval ($[x,x+dx],[y,y+dy]$). Consider alternatively the probability distribution $Q(x,y)$ of random mating with the product of densities $q(x,y) = f(x)g(y)$ from *X* and *Y*, respectively.

Let *x* and *y*, be phenotypes in a mating pair, and let Z_{xy} be any function of the traits (x,y). Now, choose the function $L_{xy} = \log(m_{xy})$ so that $Z_{xy} = L_{xy}$. Then, the average change in *L* caused by non-random mating is given by Jeffreys divergence (Carvajal-Rodríguez, 2018a; Frank, 2012)

$$\Delta L=\int_{-a}^{+a}\int_{-a}^{+a}\Delta q\, L_{xy}\,dxdy \quad \text{so,}$$

$$\Delta L=J=\int_{-a}^{+a}\int_{-a}^{+a}\left(q'(x,y)-q(x,y)\right)\log\frac{q'(x,y)}{q(x,y)}\,dxdy \quad \text{where } q(x,y)=f(x)g(y) \qquad \text{(A1).}$$

However, *Z* can be any function of the pairs (x,y). For example, *Z* may be a linear function of the display (δ) by the courter (sensu Rosenthal, 2017) and the preference (π) of the chooser e.g., $Z_{xy} = a\delta+b\pi$, where *a* and *b* are ad hoc weight functions. If both traits *x* and *y* are size and only one sex chooses (e.g. females), then $\delta = y$, $a = 1$, and $b = 0$, so $Z_{xy} = y$. However, if there is a preference for males of similar size, then it could be, $\delta=0$, $b=1$, $\pi=1-|x-y|/D_{max}$, where D_{max} is the maximum possible difference between *x* and *y*.

The relationship of *J* with the average change in *Z*, caused by mutual mating fitness is

$$\Delta_m Z=\frac{\beta_{Z,m}}{\beta_{L,m}}J$$

where $\beta_{Z,m}$ is the regression of Z on the actual mutual mating propensity m and $\beta_{L,m}$ is the regression of log(m) on m.

With respect to J, the difference $q'(x,y)$ - $q(x,y)$ can be partitioned as follows

$$q'(x,y)-q(x,y)=q'(x,y)-f_1(x)f_2(y)+f_1(x)f_2(y)-q(x,y),$$

where $f_1(x)$ and $f_2(y)$ are the marginal densities for X and Y

$$f_1(x)=\int_{-a}^{+a} q'(x,y)\,dy$$

$$f_2(y)=\int_{-a}^{+a} q'(x,y)\,dx \qquad \text{(A2).}$$

Similarly, the logarithm

$$\log\frac{q'(x,y)}{q(x,y)}=\log\left(\frac{q'(x,y)}{f_1(x)f_2(y)}\frac{f_1(x)f_2(y)}{q(x,y)}\right)=\log\frac{q'(x,y)}{f_1(x)f_2(y)}+\log\frac{f_1(x)f_2(y)}{q(x,y)}.$$

Now note that the densities $f(x)$ and $g(y)$ depend on the population distribution, while the marginal densities $f_1(x)$ and $f_2(y)$ depend on the mating distribution so they are not necessarily equal. Then we have

$$J_{PSS}=\int_{-a}^{+a}\int_{-a}^{+a}\left(f_1(x)f_2(y)-q(x,y)\right)\log\frac{f_1(x)f_2(y)}{q(x,y)}\,dxdy$$

and

$$J_{PSI}=\int_{-a}^{+a}\int_{-a}^{+a}\left(q'(x,y)-f_1(x)f_2(y)\right)\log\frac{q'(x,y)}{f_1(x)f_2(y)}\,dxdy$$

therefore, as in the discrete case, the measure of non-random mating can be divided into

$$J=J_{PSS}+J_{PSI}+E \qquad \text{(A3).}$$

The component E is

$$E=\int_{-a}^{+a}\int_{-a}^{+a}(A+B)dxdy=\int_{-a}^{+a}\int_{-a}^{+a}Adxdy+\int_{-a}^{+a}\int_{-a}^{+a}Bdxdy$$

$$A=(f_1(x)f_2(y)-q(x,y))\log\frac{q'(x,y)}{f_1(x)f_2(y)}$$

$$B=(q'(x,y)-f_1(x)f_2(y))\log\frac{f_1(x)f_2(y)}{q(x,y)}.$$

We will show that

$$\int_{-a}^{+a}\int_{-a}^{+a}Bdxdy=\int_{-a}^{+a}\int_{-a}^{+a}[(q'(x,y)-f_1(x)f_2(y))\log\frac{f_1(x)f_2(y)}{q(x,y)}]dxdy=0 \qquad \text{(A4)}$$

so that,

$$E=\int_{-a}^{+a}\int_{-a}^{+a}(f_1(x)f_2(y)-q(x,y))\log\frac{q'(x,y)}{f_1(x)f_2(y)}\neq 0\Leftrightarrow J_{PSS}\neq 0\wedge J_{PSI}\neq 0 \qquad \text{(A5)}.$$

Now, first recall that $q(x,y)=f(x)g(y)$ and then

$$\log\frac{f_1(x)f_2(y)}{q(x,y)}=\log\frac{f_1(x)}{f(x)}+\log\frac{f_2(y)}{g(y)}.$$

Also,

$$\int_{-a}^{+a}f_1(x)dx=\int_{-a}^{+a}\int_{-a}^{+a}q'(x,y)dxdy=\int_{-a}^{+a}f_2(y)dy=1$$

so that,

$$\int_{-a}^{+a}\int_{-a}^{+a}[f_1(x)f_2(y)\log\frac{f_1(x)}{f(x)}]dxdy=\int_{-a}^{+a}f_1(x)\log\frac{f_1(x)}{f(x)}dx\int_{-a}^{+a}f_2(y)dy=\int_{-a}^{+a}f_1(x)\log\frac{f_1(x)}{f(x)}dx$$

(A6),

and similarly

$$\int_{-a}^{+a}\int_{-a}^{+a}[f_1(x)f_2(y)\log\frac{f_2(y)}{g(y)}]dxdy=\int_{-a}^{+a}f_2(y)\log\frac{f_2(y)}{g(y)}dy \qquad \text{(A7).}$$

Also using the marginal density definitions from (A2)

$$\int_{-a}^{+a}\int_{-a}^{+a}[q'(x,y)\log\frac{f_1(x)}{f(x)}]dxdy=\int_{-a}^{+a}\log\frac{f_1(x)}{f(x)}dx\int_{-a}^{+a}q'(x,y)dy=\int_{-a}^{+a}f_1(x)\log\frac{f_1(x)}{f(x)}dx \qquad \text{(A8)}$$

and

$$\int_{-a}^{+a}\int_{-a}^{+a}[q'(x,y)\log\frac{f_2(y)}{g(y)}]dxdy=\int_{-a}^{+a}f_2(y)\log\frac{f_2(y)}{g(y)}dy \qquad \text{(A9).}$$

Finally, noting that (A6) equals (A8) and (A7) equals (A9) and rearranging and substituting in (A4) we obtain

$$\int_{-a}^{+a}\int_{-a}^{+a}Bdxdy=\int_{-a}^{+a}\int_{-a}^{+a}[(q'(x,y)-f_1(x)f_2(y))\log\frac{f_1(x)f_2(y)}{q(x,y)}]dxdy=(A6)+(A7)-(A8)-(A9)=0$$

B. Assortative mating with normally distributed traits

The general formulation is

$$J_{PSI}=\int_{-a}^{+a}\int_{-a}^{+a}(q'(x,y)-r'(x,y))\log\frac{q'(x,y)}{r'(x,y)}dxdy$$

where $r'(x,y) = f_1(x)f_2(y)$.

If q' is bivariate normal and f_1 and f_2 are normally distributed we have

$$q'(x,y)=\frac{1}{|2\Pi\Sigma_1|^{0.5}}\exp[-\frac{1}{2}(z-\mu_1)'\Sigma_1^{-1}(z-\mu_1)]$$

where Σ_1 is the variance-covariance matrix (see below), $|\Sigma_1|$ is the determinant, z is the column vector of the two variables x,y and z' is the row vector of x,y and μ_1 is the column vector (μ_{1x},μ_{1y}).

Similarly, the product of the two marginals is

$$r'(x,y)=\frac{1}{|2\Pi\Sigma_2|^{0.5}}\exp\left[-\frac{1}{2}(z-\mu_2)'\Sigma_2^{-1}(z-\mu_2)\right]$$

where μ_2 is the column vector (μ_{2x}, μ_{2y}).

Note that in our case, using males and females from matings (joint distribution versus random mating distribution obtained from mating data) implies that mean and variances are equal between distributions ($\mu_1 = \mu_2$, $\sigma_1 = \sigma_2$), i.e. $\mu_{1x} = \mu_{2x}$, $\mu_{1y} = \mu_{2y}$ and $\sigma_{1x} = \sigma_{2x}$, $\sigma_{1y} = \sigma_{2y}$.

Let

$$\Sigma_1=\begin{pmatrix}\sigma_{xx} & \sigma_{xy}\\ \sigma_{xy} & \sigma_{yy}\end{pmatrix},\ \ \Sigma_1^{-1}=\frac{1}{S}\begin{pmatrix}\sigma_{yy} & -\sigma_{xy}\\ -\sigma_{xy} & \sigma_{xx}\end{pmatrix}\ \text{with}\ S=\sigma_{xx}\sigma_{yy}-\sigma_{xy}^2$$

and

$$\Sigma_2=\begin{pmatrix}\sigma_{xx} & 0\\ 0 & \sigma_{yy}\end{pmatrix},\ \ \Sigma_2^{-1}=\frac{1}{\sigma_{xx}\sigma_{yy}}\begin{pmatrix}\sigma_{yy} & 0\\ 0 & \sigma_{xx}\end{pmatrix}$$

In this case the Kullback-Leibler divergences are (c.f. Kullback, 1997 (1.6) p. 190)

$$KL(q'\|r')=\frac{1}{2}\log\frac{|\Sigma_2|}{|\Sigma_1|}-1+\frac{1}{2}tr(\Sigma_1\Sigma_2^{-1})=\frac{1}{2}\log\frac{\sigma_{xx}\sigma_{yy}}{S}$$

and

$$KL(r'\|q')=\frac{1}{2}\log\frac{|\Sigma_1|}{|\Sigma_2|}-1+\frac{1}{2}tr(\Sigma_2\Sigma_1^{-1})=\frac{1}{2}\log\frac{S}{\sigma_{xx}\sigma_{yy}}-1+\frac{\sigma_{xx}\sigma_{yy}}{S}$$

where *tr* is the trace (sum of diagonal elements) of a square matrix.

Therefore,

$$J_{PSI} = KL(q' \| r') + KL(r' \| q') = \frac{\sigma_{xx}\sigma_{yy}}{S} - 1 = \frac{\sigma_{xy}{}^2}{\sigma_{xx}\sigma_{yy} - \sigma_{xy}{}^2} = \frac{\rho^2}{1-\rho^2}.$$

C. Total *J* with normally distributed traits

$$J = \int_{-a}^{+a}\int_{-a}^{+a} (q'(x,y) - q(x,y)) \log \frac{q'(x,y)}{q(x,y)} dxdy, \quad \text{where } q(x,y) = f(x)g(y)$$

If q' is $N(\mu_1, \Sigma_1)$ and q $N(\mu_2, \Sigma_2)$ where Σ_i is the variance-covariance matrix, we have that the *KL* divergence has the following closed form (Pardo, 2018)

$$KL(q' \| q) = \frac{1}{2}\left(\log \frac{|\Sigma_2|}{|\Sigma_1|} - 2 + tr(\Sigma_2^{-1}\Sigma_1) + (\mu_2 - \mu_1)'\Sigma_2^{-1}(\mu_2 - \mu_1)\right) \qquad \text{(C1)}$$

where *tr* is the trace (sum of diagonal elements) of a square matrix, $|\Sigma|$ is the determinant, μ_i is the column vector (μ_{ix}, μ_{iy}), μ' is the row vector.

Therefore,

$$\Sigma_1 = \begin{pmatrix} \sigma_{1xx} & \sigma_{1xy} \\ \sigma_{1xy} & \sigma_{1yy} \end{pmatrix}, \; |\Sigma_1| = \sigma_{1xx}\sigma_{1yy} - \sigma_{1xy}^2$$

and

$$\Sigma_2 = \begin{pmatrix} \sigma_{2xx} & \sigma_{2xy} \\ \sigma_{2xy} & \sigma_{2yy} \end{pmatrix}, \quad \Sigma_2^{-1} = \frac{1}{S_2}\begin{pmatrix} \sigma_{2yy} & -\sigma_{2xy} \\ -\sigma_{2xy} & \sigma_{2xx} \end{pmatrix}$$

where

$$|\Sigma_2| = S_2 = \sigma_{2xx}\sigma_{2yy} - \sigma_{2xy}^2 = \sigma_{2xx}\sigma_{2yy} \quad \text{because} \quad \sigma_{2xy} = 0$$

Now, let

$$T = \sigma_{1xx}\sigma_{2yy} + \sigma_{1yy}\sigma_{2xx}$$

then

$$tr\left(\Sigma_2^{-1}\Sigma_1\right)=T/S_2=\frac{\sigma_{1xx}}{\sigma_{2xx}}+\frac{\sigma_{1yy}}{\sigma_{2yy}}$$

and,

$$(\mu_2-\mu_1)'\Sigma_2^{-1}(\mu_2-\mu_1)=\frac{(\mu_{2x}-\mu_{1x})^2}{\sigma_{2xx}}+\frac{(\mu_{2y}-\mu_{1y})^2}{\sigma_{2yy}}$$

The other divergence is

$$KL(q\|q')=\frac{1}{2}\left(\log\frac{|\Sigma_1|}{|\Sigma_2|}-2+tr\left(\Sigma_1^{-1}\Sigma_2\right)+(\mu_1-\mu_2)'\Sigma_1^{-1}(\mu_1-\mu_2)\right) \qquad \text{(C2)}$$

$$\Sigma_1^{-1}=\frac{1}{S_1}\begin{pmatrix}\sigma_{1yy} & -\sigma_{1xy}\\ -\sigma_{1xy} & \sigma_{1xx}\end{pmatrix} \text{ with } S_1=|\Sigma_1|$$

$$tr\left(\Sigma_1^{-1}\Sigma_2\right)=T/S_1=\frac{\sigma_{1xx}\sigma_{2yy}+\sigma_{1yy}\sigma_{2xx}}{\sigma_{1xx}\sigma_{1yy}-\sigma_{1xy}^2}$$

$$(\mu_1-\mu_2)'\Sigma_1^{-1}(\mu_1-\mu_2)=\frac{\sigma_{1yy}(\mu_{1x}-\mu_{2x})^2+\sigma_{1xx}(\mu_{1y}-\mu_{2y})^2-2\sigma_{1xy}(\mu_{1x}-\mu_{2x})(\mu_{1y}-\mu_{2y})}{S_1}$$

Finally,

$$J=KL(q'\|q)+KL(q\|q')$$

with nJ asymptotically χ^2 distributed with 5 degrees of freedom where n is the sample size of matings.

C.1 Mating covariance greater than 0 with equal means and variances

Note that from (C1) and (C2), if we assume that the means and variances between the two distributions are the same, i.e. $\mu_1 = \mu_2$, $\sigma_{1xx} = \sigma_{2xx}$, $\sigma_{1yy} = \sigma_{2yy}$ but $\sigma_{1xy} > 0$ and $\sigma_{2xy} = 0$ then

$$J = KL(q'\|q) + KL(q\|q') = 0 + \frac{\sigma^2_{1xy}}{\sigma_{xx}\sigma_{yy} - \sigma^2_{1xy}} = \frac{\rho^2}{1-\rho^2} = J_{PSI}$$

which is the assortative mating component without sexual selection (J_{PSI}) obtained in the Appendix B.

C.2 No covariance within matings

On the other side, if we assume $\sigma_{1xy} = \sigma_{2xy} = 0$ then from C1 and C2 we get

$$J = -2 + \frac{1}{2}\left(\frac{\sigma_{1xx}}{\sigma_{2xx}} + \frac{\sigma_{2xx}}{\sigma_{1xx}} + \frac{\sigma_{1yy}}{\sigma_{2yy}} + \frac{\sigma_{2yy}}{\sigma_{1yy}}\right) + \frac{1}{2}(\mu_{1x} - \mu_{2x})^2\left(\frac{1}{\sigma_{1xx}} + \frac{1}{\sigma_{2xx}}\right) + \frac{1}{2}(\mu_{1y} - \mu_{2y})^2\left(\frac{1}{\sigma_{1yy}} + \frac{1}{\sigma_{2yy}}\right)$$

which can be expressed as

$$J = -1 + \frac{1}{2}\left(\frac{\sigma_{1xx}}{\sigma_{2xx}} + \frac{\sigma_{2xx}}{\sigma_{1xx}}\right) + \frac{1}{2}(\mu_{1x} - \mu_{2x})^2\left(\frac{1}{\sigma_{1xx}} + \frac{1}{\sigma_{2xx}}\right) - 1 + \frac{1}{2}\left(\frac{\sigma_{1yy}}{\sigma_{2yy}} + \frac{\sigma_{2yy}}{\sigma_{1yy}}\right) + \frac{1}{2}(\mu_{1y} - \mu_{2y})^2\left(\frac{1}{\sigma_{1yy}} + \frac{1}{\sigma_{2yy}}\right)$$

and by taking $\Phi_1 = \sigma_{1xx}/\sigma_{2xx}$ and $\Phi_2 = \sigma_{1yy}/\sigma_{2yy}$ and noting that

$$\left(\frac{1}{\sigma_{1xx}} + \frac{1}{\sigma_{2xx}}\right) = \frac{\Phi_1 + 1}{\sigma_{2xx}\Phi_1} \text{ and } \left(\frac{1}{\sigma_{1yy}} + \frac{1}{\sigma_{2yy}}\right) = \frac{\Phi_2 + 1}{\sigma_{2yy}\Phi_2}$$

then

$J = J_{S1} + J_{S2}$ as defined in (6), which is sexual selection without assortative mating.

C.3 No covariance and equal means

Even if we assume only differences in variances, we obtain the information gain due to the pattern of sexual selection as

$$J = -1 + \frac{1}{2}\left(\frac{\sigma_{1xx}}{\sigma_{2xx}} + \frac{\sigma_{2xx}}{\sigma_{1xx}}\right) - 1 + \frac{1}{2}\left(\frac{\sigma_{1yy}}{\sigma_{2yy}} + \frac{\sigma_{2yy}}{\sigma_{1yy}}\right)$$

that corresponds to (6) when the means are assumed to be equal.

D. Simulation results tables

Table S1. One sex is choosy. Choice implies preference for similarity with a bias of 1.5. Mating is with replacement. *N* is the population size and *n* the sample size of matings. The quantitative trait distribution is *Z*(0,1). Number of runs: 10,000. % sig: The % of tests with *p*-value ≤ 0.05. The values in parentheses correspond to the average value of the statistic for the total number of significant runs.

N	***n***	***Choice***	***s***	**% sig. (ρ)**	**%sig. ($\rho^2/(1-\rho^2)$)**
10^4	500	0	--	4.8 (0.004)	4.9 (0.01)
10^4	500	0.2	0.08	99.9 (0.22)	99.9 (0.05)
10^4	500	0.4	0.08	100 (0.54)	100 (0.41)
10^4	500	0.8	0.08	100 (0.87)	100 (3.19)
10^4	500	1	0.08	100 (0.89)	100 (3.99)
500	50	0	--	5 (-0.025)	5.9 (0.12)
500	50	0.2	0.08	44.7 (0.37)	48.2 (0.17)
500	50	0.4	0.08	100 (0.67)	100 (0.90)
500	50	0.8	0.08	100 (0.84)	100 (2.54)
500	50	1	0.08	100 (0.90)	100 (4.43)
500	50	0.2	0.01	100 (0.97)	100 (64.72)
500	50	0.4	0.01	100 (0.99)	100 (41.97)
500	50	0.8	0.01	100 (1)	100 (115.87)
500	50	1	0.01	100 (1)	100 (3935.1)

Table S2. Mating under a logistic model with α = 2. There is no preference for similarity. *N* is the population size and *n* the sample size of matings. The quantitative trait distribution is *Z*(0,1). Number of runs: 10,000. % sig: The % of tests with *p*-value ≤ 0.05. The values in parentheses correspond to the average value of the statistic for the total number of significant runs.

N	***n***	**Mating**	**% sig. (ρ)**	**%sig. ($\rho^2/(1-\rho^2)$)**
10^4	500	replacement	5.3 (0.003)	5.4 (0.01)

10^4	500	individual	4.9 (0.003)	5.0 (0.01)
10^4	500	mass-encounter	4.7 (0.004)	4.8 (0.01)
500	50	replacement	5.0 (-0.01)	6.0 (0.12)
500	50	individual	5.2 (0.02)	6.3 (0.12)
500	50	mass-encounter	5.4 (0.03)	6.4 (0.12)

Table S3. Bimodal populations with mixture proportion $\pi = 0.5$, μ_2-μ_1- = 3 and $\sigma_1 + \sigma_2 = 2$. One sex is choosy. Choice implies preference for similarity. Mating is with replacement. *N* is the population size and *n* the sample size of matings. The quantitative trait distribution is *Z*(0,1). Number of runs: 10,000. % sig: The % of tests with *p*-value ≤ 0.05. The values in parentheses correspond to the average value of the statistic for the total number of significant runs.

N	***n***	***Choice***	***s***	**% sig. (ρ)**	**%sig. ($\rho^2/(1-\rho^2)$)**
10^4	500	0	--	5.1 (0.004)	5.2 (0.01)
10^4	500	0.2	0.08	90 (0.15)	90.1 (0.03)
10^4	500	0.4	0.08	100 (0.43)	100 (0.22)
10^4	500	0.8	0.08	100 (0.82)	100 (1.98)
10^4	500	1	0.08	100 (0.89)	100 (3.79)
10^4	500	0.2	0.01	100 (0.95)	100 (9.99)
10^4	500	0.4	0.01	100 (0.99)	100 (48.67)
10^4	500	0.8	0.01	100 (1.0)	100 (242.35)
10^4	500	1	0.01	100 (1.0)	100 (397.16)
500	50	0	--	5.1 (-0.01)	6.1 (0.12)
500	50	0.2	0.08	43.2 (0.38)	46.2 (0.18)
500	50	0.4	0.08	99.7 (0.59)	99.7 (0.58)
500	50	0.8	0.08	100 (0.93)	100 (6.58)
500	50	1	0.08	100 (0.94)	100 (7.74)

500	50	0.2	0.01	100 (0.97)	100 (18.57)
500	50	0.4	0.01	100 (0.99)	100 (47.17)
500	50	0.8	0.01	100 (1.0)	100 (177.0)
500	50	1	0.01	100 (1.0)	100 (324.56)

Table S4. Both sexes are choosy. Mating with replacement. *N* is the population size and *n* the sample size of matings. Choice implies preference for similarity. The quantitative trait distribution is *Z*(0,1). Number of runs: 1,000. % sig: The % of tests with *p*-value ≤ 0.05. The values in parentheses correspond to the average value of the statistic for the total number of significant runs.

N	***n***	***Choice***	***s***	**% sig. (ρ)**	**%sig. ($\rho^2/(1-\rho^2)$)**
10^4	500	0	--	4.4 (0.03)	5.4 (0.06)
10^4	500	0.2	0.08	24.6 (0.25)	26.1 (0.07)
10^4	500	0.4	0.08	100 (0.47)	100 (0.3)
10^4	500	0.8	0.08	100 (0.75)	100 (1.39)
10^4	500	0.2	0.01	100 (0.93)	100 (7)
10^4	500	0.4	0.01	100 (0.98)	100 (26)
10^4	500	0.8	0.01	100 (1)	100 (106)
500	50	0	--	4.5 (0.017)	5.7 (0.12)
500	50	0.2	0.08	36.3 (0.36)	38.5 (0.16)
500	50	0.4	0.08	99.8 (0.58)	99.9 (0.57)
500	50	0.8	0.08	100 (0.81)	100 (2.1)
500	50	0.2	0.01	100 (0.96)	100 (12.7)
500	50	0.4	0.01	100 (0.99)	100 (56.7)
500	50	0.8	0.01	100 (1.0)	100 (206)

Table S5. Comparison of ρ and J_{PSI} for lower choice values. One sex is choosy. Choice implies preference for similarity. Mating is with replacement. *N* is the population size and *n* the sample size of matings. The quantitative trait distribution is *Z*(0,1). Number of runs: 10,000. % sig: The % of tests with *p*-value ≤ 0.05. The values in parentheses correspond to the average value of the statistic for the total number of significant runs.

N	***n***	***Choice***	***s***	**% sig. (ρ)**	**%sig. ($\rho^2/(1-\rho^2)$)**
500	50	0.05	0.08	5.1 (0.05)	6.2 (0.12)
500	50	0.1	0.08	11 (0.32)	13 (0.13)
500	50	0.2	0.08	38.6 (0.37)	41.7 (0.16)
500	50	0.3	0.08	86 (0.44)	88 (0.27)
500	50	0.4	0.08	99.95 (0.61)	99.97 (0.64)
500	50	0.5	0.08	100 (0.71)	100 (1.1)
500	50	0.05	0.01	99.9 (0.64)	100 (0.78)
500	50	0.1	0.01	100 (0.90)	100 (4.6)
500	50	0.2	0.01	100 (0.96)	100 (13.54)
500	50	0.3	0.01	100 (0.99)	100 (47.6)
500	50	0.4	0.01	100 (0.99)	100 (56.68)
500	50	0.5	0.01	100 (1.0)	100 (188.6)

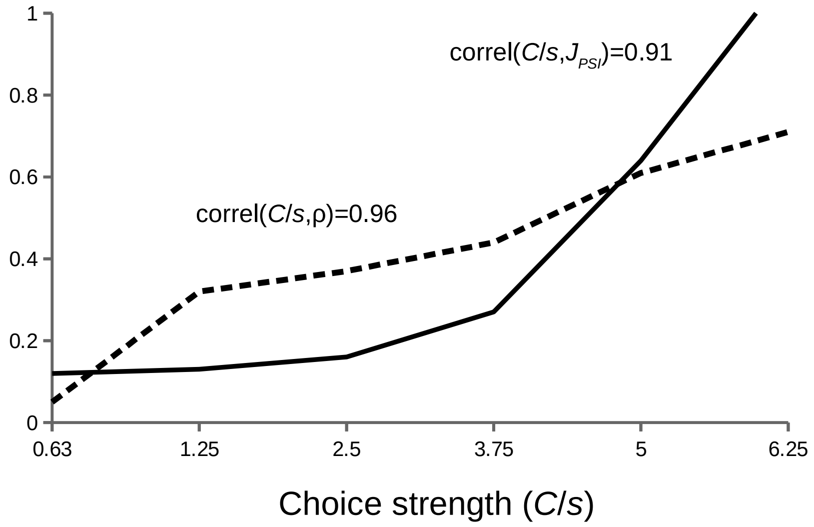

Figure S1. Graphic representation of values of the rho (dashed line) and J_{PSI} (continuous line) statistics with respect to the strength of the choice. The value of the correlation between each statistic and the strength of the choice is given. Population size $N = 500$, sample size $n = 50$. The values of ρ and J_{PSI} are those in Table S5 ordered by increasing C/s.

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