$z_m = \frac{1}{2}; z_f = 0$

$\rho_{sel} = 1$

$z_m, z_f = \frac{1}{2}$

$\rho_{sel} = \frac{1}{2}$

$z_m, z_f = \frac{1}{2}$

$\rho_{sel} = -\frac{1}{2}$

$z_m, z_f = \frac{1}{2}$

Mean equilibrium

Mean $\alpha$

Small mutations

Large mutations

Phenotypic correlation ($\rho_{mut}$)

- ○ Het. advantage
- ■ Mixed SA
- □ Directional SA

Figure 56  Mean alpha and $\hat{q}$, for $n = 5$, $h = 0.25$, and $\omega_m = \omega_b = \frac{1}{2}$. Each datapoint is based on 100,000 randomly simulated balanced polymorphisms for the given parameter set ($z_m, z_f, \rho_{sel}, \rho_{mut}$). For each parameter combination, mutation magnitudes were generated using a bivariate exponential distribution (gamma with shape parameter $k = 1$), with equal marginal distributions, and correlation of $\rho_{mut} = \text{corr}(r_m, r_f)$. Small mutations use $E[r] = 0.05n^{0.5}$, and large mutations use $E[r] = 0.4n^{0.5}$ (corresponding to male-specific scaled sizes of $E[x_m] = 0.25$, and $E[x_b] = 2$, respectively).