Hwang, Krapivsky, and Redner Reply: The Comment by Sayama and Bar-Yam (SB) [1] raises concerns about our Letter [2]. We argue below that their objections do not invalidate our general conclusions.

(1) There are several ways to describe the age structure of the population. SB use the inverse average death rate L to represent the lifespan (defined as the average time between the birth and death of each individual), whereas we use the average age of the population A as the longevity measure. Both quantities are easily derived from the fundamental age distribution derived in our Letter. In the supercritical and critical cases, L and A are asymptotically identical. In the subcritical case, we verified that L exhibits the same qualitative dependence on mutational bias as A.

(2) SB introduce a variant of our model, with geometric death rate h^n ($0 < h < 1$, $-\infty < n < \infty$) for individuals of fitness n, as opposed to our death rate $1/n$. However, a geometric death rate appears biologically irrelevant, since individuals can become arbitrarily unfit and still reproduce.

(3) SB also consider the somewhat tangential issue of an immature nonreproductive period of length λn. It is not obvious whether a fixed or a proportional immature period is more realistic. Our results apply to the former case while SB's apply to the latter.

(4) Finally, SB compare lifetimes of different individuals in a given society. Clearly, in a given society, individuals with higher fitness live longer. What we meant by the title of our Letter is the comparison of the average ages in separate societies with different mutational biases. Hence the "interpretational" problem they cite is semantical.

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[1] H. Sayama and Y. Bar-Yam, preceding Comment, Phys. Rev. Lett. **86**, 4718 (2001).
[2] W. Hwang, P. Krapivsky, and S. Redner, Phys. Rev. Lett. **83**, 1251 (1999); a comprehensive account of this work appears in W. Hwang, P. Krapivsky, and S. Redner, adap-org/9912004.

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