## Appendix: analytical derivations

In this appendix, we detail the analytical derivations leading to the equations given in the main text, in four sections. First, in section I. "Settings and general results", we briefly recall the derivations from Martin et al. (2013) leading to the evolutionary rescue (ER) probability. Then, in section II. "Application to Fisher's Geometric Model (FGM)", we apply this framework to the FGM, yielding the ER probability in the SSWM regime. In section III. "Small mutational effects approximation (SME)", we derive explicit approximations under the assumption of weak mutation effects (limit as $\lambda / r_{\max } \rightarrow 0$ ), illustrated by numerical examples (Supplementary Figs.3-4). Then, in section "IV. Key properties of the model" we use these approximations to provide simple insights into key properties of the model: proportion of ER caused by standing variance, characteristic stress and stress window over which ER changes from highly likely to highly unlikely.

All along $\mathbb{E}_{X}($.$) denotes an expectation taken over the distribution of X$ (which can be multivariate), and $X \mid Y$ denotes a random variable $X$ conditional on $Y$. Most computations are checked in a Mathematica ${ }^{\circledR}$ notebook (Supplementary file S1), provided as a .cdf file that can be ran using a freely available "CDF player" from the Wolfram website.

## I. Settings and general results

We recall the general model and approximations described in Martin et al. (2013), which apply to Fisher's Geometrical Model (FGM), in the limit of Strong Selection Weak Mutation (SSWM). We call 'new environment' the environment imposed at the onset of stress $(t=0)$ : it induces a decay of the population under study, at $t=0$. The environment in which the population was before the onset of stress is called 'previous environment'.

1. General stochastic demography: Each genotype $i$ present at $t=0$ or later produced by mutation (via a Poisson process) is characterized by the parameters ( $r_{i}, \sigma_{i}$ ) of a Feller diffusion approximating its stochastic demography. Let $N_{i}(t)$ be the size of the genotypic class $i$ at time $t$. The growth rate $r_{i}$ and reproductive variance $\sigma_{i}$ give the expectation and variance of the change, over $d t$, in $\log N_{i}(t)$ (which is $\left.\Delta N_{i} / N_{i}\right)$, given $N_{i}(t)$. We have $r_{i}=\mathbb{E}\left(\Delta N_{i} \mid N_{i}\right) /$
( $d t N_{i}$ ) over some time interval (infinitesimal in the diffusion limit), and $\sigma_{i}=V\left(\Delta N_{i} \mid N_{i}\right) /$ $\left(d t N_{i}\right)$. In the diffusion limit, the population size of the genotypic class is characterized by the stochastic differential equation $d N_{i}(t)=r_{i} N_{i}(t) d t+\sqrt{\sigma_{i} N_{i}(t)} d B_{t}$ where $B_{t}$ is a standard Brownian motion.
2. Application to a discrete time model with Poisson offspring distribution: In our case, we consider, as an example, discrete non-overlapping generations where the subclass consisting of individuals of genotype $i$ produces $N_{i}(t+1) \sim \operatorname{Poisson}\left(W_{i} N_{i}(t)\right)$ offspring over one generation, where $W_{i}$ is the absolute Darwinian (i.e., multiplicative) fitness of this genotype. In this case $r_{i}=\mathbb{E}\left(N_{i}(t+1)-N_{i}(t)\right) / N_{i}(t)=W_{i}-1$, while $\quad \sigma_{i}=V\left(N_{i}(t+1)-N_{i}(t)\right) /$ $N_{i}(t)=W_{i}$ are two constant coefficients for any genotype. The diffusion limit applies when the demographic changes per generation are small, which requires $W_{i} \rightarrow 1$. In this case we retrieve a Feller diffusion where $r_{i}=W_{i}-1 \rightarrow \log \left(W_{i}\right)$ is the absolute Malthusian fitness of genotype $i$, while $\sigma_{i}=W_{i} \rightarrow 1$ is constant across genotypes (Martin et al. 2013).

Extinction of the population occurs if none of the genotypes present or produced over the course to extinction avoids extinction: following classic notation, non-extinction (over infinite time) is denoted "establishment". The probability of establishment, for a lineage started in single copy, with growth rate $r$ and stochastic variance $\sigma$ in the new environment, is $\pi(r)=$ $\left(1-e^{-2 r / \sigma}\right) \Theta(r)$ where $\Theta($.$) is the Heaviside theta function (\Theta(x)=0$ if $x \leq 0$ and $\Theta(x)=$ 1 if $x>0$ ) and the reproductive variance $\sigma \approx 1$ (as in our simulation example mentioned above considering a Poisson reproduction).
3. Strong selection weak mutation (SSWM): In this work we use a SSWM approximation (Gillespie 1983; McCandlish and Stoltzfus 2014). We consider that the mutation rate is low relative to the strength of selection, so that rescue mutations are typically single step mutants (sampled from the pool of possible mutants), be it present before the onset of stress (from standing variance, hereafter 'SV') or arising after it (de novo hereafter 'DN'). We thus only consider rescue from a single allele, which is randomly drawn among all possible alleles, weighted by their probability to produce a rescue (illustrated in Supplementary Fig.1). Under the SSWM approximation, all possible rescue events (SV or DN, from any given allele) arise as
alternative Poisson events (Martin et al. 2013). The overall probability of extinction is thus simply the zero class of a Poisson distribution and the probability of evolutionary rescue (ER) is that of the complementary event ('no extinction'). The key to describing the process is therefore to derive the rate of these Poisson events, over all possible mutations in the model considered.

(A) Proportion of individuals carrying different numbers of de novo mutations in rescued populations.

(B) Proportion of individuals carrying different numbers of de novo resistant mutations in rescued populations.

Supplementary Figure 1: Proportion of individuals carrying different numbers of de novo mutations (all mutations in (A) or only resistant mutations in (B)) in rescued populations, from exact simulations. These proportions were evaluated in those populations having been rescued, at the time where they reached our stop criterion, that is
when their current mean growth rate and population size imply a very low probability of future extinction, even in the absence of future adaptation (see simulation methods in the main text). The distributions are given for different mutation rates (x-axis), given relative to the critical mutation rate ( $U_{c}=n^{2} \lambda / 4=0.1$ here) below which the SSWM assumption should hold. Populations were initially composed of a single clone, with $N_{0}=10^{5}, n=4$, $\bar{s}=0.01, r_{\max }=1.5, r_{D}=(0.042,0.129,0.23,0.32)$ from right to left in each panel. Whenever $U \ll U_{c}$, rescued populations mostly consist of the wild type ( 0 mutation, not shown here) and single mutants (purple bars). As $U$ approaches $U_{C}$, a substantial proportion of multiple mutants is found in late rescued populations (fewer when focusing on the resistant mutants that are the potential rescuers of the populations). Note however that this illustration does not ascertain whether these multiple mutants are the cause of rescue or not.
4. Rescue from de novo mutation: We first consider rescue starting from a clonal population (of inoculum size $N_{0}$ ), so that any rescue event is caused by de novo mutations ('DN'). We define the rate of 'DN' rescue events $\omega_{D N}$ per individual present at the onset of stress, such that $N_{0} \omega_{D N}$ is the parameter of the Poisson number of ' $D N$ ' rescue events. Ignoring stochasticity in the decay dynamics of the wild-type (large $N_{0} r_{D}$ ), the total number, over time, of rescue mutations for those mutants with growth rate $r$ (more precisely, within the infinitesimal class $[r, r+d r])$ is $N_{0} U \pi(r) f(r) d r / r_{D}$. Here $U \pi(r) f(r) d r$ is the rate, per capita per unit time, of mutations towards this class, weighted by their probability $\pi(r)$ to generate a rescue. After integrating over the whole distribution of possible resistant mutants we get (following Martin et al. 2013):

$$
\begin{equation*}
\omega_{D N}=U \frac{\mathbb{E}_{r}(\pi(r))}{r_{D}}=\frac{U}{r_{D}} \int_{0}^{r_{\max }}\left(1-e^{-2 r / \sigma}\right) f(r) d r \tag{A1}
\end{equation*}
$$

where the random variable $r$ denotes mutant growth rates in the new environment and $f(r)$ their probability density function. The corresponding probability of extinction is then $P_{\text {ext }}=$ $e^{-N_{0} \omega_{D N}}$ (Martin et al. 2013).
5. Rescue from standing variance: In an alternative scenario, the initial population (of size $N_{0}$ ) is previously at equilibrium in the non-stressful 'previous environment'. In the SSWM regime, the rescue process results from the contributions from two independent processes: rescue caused by a mutant appearing after the onset of stress and rescue caused by a mutant already present at the onset of stress. The numbers of each event overall are approximately Poisson distributed,
with rates $N_{0} \omega_{D N}$ (given in Eq.(A1)) and $N_{0} \omega_{S V}$, respectively. The latter depends on the joint distribution of the cost $c$ of resistance mutations in the previous environment, and of their growth rate $r$ in the new environment. The cost $c$ (in the previous environment) is equal to minus the selection coefficient, relative to the dominant background, of random mutations arising in this very background (Martin et al. 2013); we then have:

$$
\begin{equation*}
\omega_{S V}=U \mathbb{E}_{c, r}\left(\frac{\pi(r)}{c}\right)=U \mathbb{E}_{r}\left(\pi(r) \mathbb{E}_{c}\left(\left.\frac{1}{c} \right\rvert\, r\right)\right) . \tag{A2}
\end{equation*}
$$

This Poisson approximation applies under the SSWM regime (Martin et al. 2013), regardless of whether the population is initially at stochastic mutation-selection-drift balance at constant size $N_{0}$, or at quasi-deterministic mutation-selection balance (at some size $N \gg N_{0}$ ) followed by a bottleneck at the onset of stress (to reach size $N_{0}$ ). The extinction probability in the presence of both initial standing variance and de novo mutations is $P_{\text {ext }}=e^{-N_{0}\left(\omega_{D N}+\omega_{S V}\right)}$, and because rescue events are Poisson distributed, the proportion $\phi_{S V}$ of rescue from standing variants (over all rescue events) is

$$
\begin{equation*}
\phi_{S V}=\frac{\omega_{S V}}{\omega_{D N}+\omega_{S V}} . \tag{A3}
\end{equation*}
$$

## II. Application to Fisher's Geometric Model (FGM)

In our case, the joint distribution of $c$ and $r$ emerges from the FGM: growth rates (both in the previous and new environment) are quadratic functions of phenotype, around an environmentdependent optimum. We recall that we directly give the results in the case of a Poisson offspring number as mentioned in section I subsection 2 (where $\sigma \approx 1$ for all genotypes). In the following, we derive the above quantities in this context.

1. Definitions: Define $n$ the number of dimensions of the fitness landscape (number of traits under stabilizing selection) and $\lambda$, the variance of mutational effects. In our model, $\lambda$ varies with both the strength of selection and the effect of mutations. To see this, consider an isotropic model on some arbitrary phenotypic space: we can define the Malthusian fitness of a phenotype $\mathbf{z}$ as $r(\mathbf{z})=r_{\max }-\lambda_{S}\|\mathbf{z}\|^{2} / 2$ with $\lambda_{S}$ the strength of stabilizing selection on each
trait. Each mutation creates a random perturbation $\mathbf{d z} \sim N\left(\mathbf{0}, \lambda_{M} \mathbf{I}_{n}\right)$ with $\mathbf{I}_{n}$ the identity matrix in $\mathbb{R}^{n}$ and $\lambda_{M}$ the variance of mutational effects on each trait. As we focus only on fitness here, we can consider the model in a scaled phenotypic space, with phenotypes $\mathbf{x}=\sqrt{\lambda_{S}} \mathbf{z}$ so that $r(\mathbf{x})=r_{\max }-\|\mathbf{x}\|^{2} / 2$ and $\mathbf{d x} \sim N\left(\mathbf{0}, \lambda \mathbf{I}_{\mathrm{n}}\right)$ where $\lambda=\lambda_{S} \lambda_{M}$. Thus, we need not separate selective and mutational scalings, and simply 'measure' phenotypic traits in convenient units of 'selection strength'. The mean fitness effect of random mutations is $|\mathbb{E}(s)|=\lambda n / 2$, in absolute value (Martin and Lenormand 2015). Therefore, $\lambda$ directly gives a measure of mutant selective effects per trait.

It proves handy to define the scaled variable $y=r / r_{\max } \in[0,1]$ and the corresponding scaled decay rate $y_{D}=r_{D} / r_{\text {max }}$ (which are also used in the main text). For the sake of compactness, in the derivations of this appendix only, we also define a scaled height of the fitness peak $\rho_{\max }=r_{\max } / \lambda$ (scaled by the variance of mutational effects $\lambda$ ) and a measure of dimensionality $\theta=n / 2$.
2. Distribution of mutant growth rates: The initial clone lies at fitness distance $s_{0}=r_{\max }+r_{D}$ from the optimum in the new environment, which, together with $n$ and $\lambda$, fully determines the distribution of mutant selection coefficients (and hence growth rates $r$ ). The distribution of selection coefficients $s=r+r_{D}$ of random mutants relative to the ancestor has known exact form for the isotropic FGM (eq.(3) in Martin and Lenormand 2015). From it, the distribution of growth rates $r$ among random mutants, within the new environment, is readily obtained. It has stochastic representation

$$
r=r_{\max }-\frac{\lambda}{2} \chi_{n}^{2}\left(2 \rho_{\max }\left(1+y_{D}\right)\right)
$$

where $\chi_{n}^{2}(v)$ is a non-central chisquare with $n$ degree of freedom and non-centrality parameter $v$. The scaled growth rate $y=r / r_{\max } \in[0,1]$ has stochastic representation $y=$ $1-\chi_{n}^{2}\left(2 \rho_{\max }\left(1+y_{D}\right)\right) /\left(2 \rho_{\max }\right)$ with corresponding probability density function (see also Supplementary file S1)

$$
\begin{equation*}
f_{y}(y)=e^{-\rho_{\max }\left(2+y_{D}-y\right)} \rho_{\max }^{\theta}(1-y)^{\theta-1} \frac{{ }_{0} F_{1}\left(\theta, \rho_{\max }^{2}\left(1+y_{D}\right)(1-y)\right)}{\Gamma(\theta)} \tag{A4}
\end{equation*}
$$

where ${ }_{0} F_{1}(. .$.$) is the confluent hypergeometric function.$
3. Rescue from de novo mutation: The rate of ER from de novo mutations in Eq.(A1) can be equivalently computed by integrating over the distribution of the scaled growth rate $y=$ $r / r_{\max }$. The non-extinction probability, given $y$, is $\pi(y)=\left(1-e^{-2 r_{\max } y}\right) \Theta(y)$ where $\Theta($.$) is$ the Heaviside theta function $\left(\Theta(x)=1\right.$ for $x \in \mathbb{R}^{+}$and $\Theta(x)=0$ for $\left.x \in \mathbb{R}^{-}\right)$:

$$
\begin{equation*}
\omega_{D N}=U \frac{\mathbb{E}_{y}(\pi(y))}{r_{D}}=\frac{U}{r_{D}} \int_{0}^{1}\left(1-e^{-2 r_{\max } y}\right) f_{y}(y) d y \tag{A5}
\end{equation*}
$$

where $f_{y}(y)$ is given by Eq.(A4). This integral can readily be computed numerically.
4. Rescue from standing variance ( $\boldsymbol{n} \geq \mathbf{2}$ ): For rescue from standing variants ('SV'), the distribution of the cost, in the previous environment, of mutations with growth rate $r$ (or scaled growth rate $y$ ), in the new environment, must also be known (see Eq.(A2)). In the SSWM approximation, we neglect the effect of standing background variation on the distribution of fitness effects of mutations generated before the onset of stress. We thus consider that the joint distribution of $(c, r)$ is the one generated if all mutants arose from the dominant genotype in the previous environment, which is optimal in this environment (same as the initial clone in the DN rescue problem. For the FGM, the distribution of $c$ has a known form, conditional on the effect of the mutant $\left(s=r+r_{D}\right)$ in the new environment. Consider a background optimal in the previous environment, not too close to the optimum of the new environment and with $n \geq 2$. The conditional cost then has a simple stochastic representation (from eq. (9) in Martin and Lenormand 2015): $c \mid s \sim c_{\min }+\gamma$, where $\gamma \sim \Gamma(\theta-1 / 2, \lambda)$ is a gamma deviate and $c_{\text {min }}=2 s_{0}-s-2 s_{0} \sqrt{1-s / s_{0}}$ is a constant, with $s_{0}=r_{\max }+r_{D}$. Expressed in terms of scaled growth rates $y\left(s=y r_{\max }+r_{D}\right)$, we have $c_{\min }=c_{\min }(y)=\left(2+y_{D}-\right.$ $\left.2 \sqrt{\left(1+y_{D}\right)(1-y)}-y\right) r_{\text {max }}$ and we have $c \mid y \sim c_{\min }(y)+\gamma$. The cost $c_{\text {min }}(y)$ can be simply interpreted as an "incompressible cost": the minimum cost that mutants within the class $[y, y+d y]$ must pay, because they cannot get close to the new optimum without moving away from the former one. The stochastic component $\gamma$ describes the variation in distance to the former optimum, of those mutants within the class $[y, y+d y]$, i.e. lying on the subspace of phenotypes equally distant to the new optimum. This component happens to be independent of $y$, which simplifies our derivations.

From Martin et al. (2013), the key to predict ER from standing variance is the harmonic mean of $c \mid y$ (among random mutants with effect $y$ ), which we denote $c_{H}(y)$. From the stochastic representation of $c \mid y$ described above, it is given by (see also Supplementary file S1):

$$
\begin{equation*}
c_{H}(y)=\frac{1}{\mathbb{E}_{c}\left(\left.\frac{1}{c} \right\rvert\, y\right)}=\frac{1}{\mathbb{E}_{\gamma}\left(\frac{1}{\gamma+c_{\min }(y)}\right)}=\frac{\lambda e^{-v(y)}}{E_{\theta-1 / 2}(v(y))} \tag{A6}
\end{equation*}
$$

with $v(y)=\mathrm{c}_{\min }(y) / \lambda=\rho_{\max }\left(2+y_{D}-2 \sqrt{\left(1+y_{D}\right)(1-y)}-y\right)$
where $\mathbb{E}_{\gamma}($.$) is taken over the distribution of \gamma \sim \Gamma(\theta-1 / 2, \lambda)$ and $E_{k}(z)=\int_{1}^{\infty} e^{-z t} / t^{k} d t$ is the exponential integral function. Using Eq.(A6), Eq.(A2) yields the rate of ER from standing variance:

$$
\begin{equation*}
\omega_{S V} \approx U \mathbb{E}_{y}\left(\frac{\pi(y)}{c_{H}(y)}\right)=\frac{U}{\lambda} \int_{0}^{1}\left(1-e^{-2 r_{\max } y}\right) e^{v(y)} E_{\theta-1 / 2}(v(y)) f_{y}(y) d y \tag{A7}
\end{equation*}
$$

5. Case $\boldsymbol{n}=1$ : Eq. (9) in Martin and Lenormand (2015) applies for all $n \geq 2$, but not if $n=1$. In this case, the geometry of the landscape is more constrained, and the cost distribution is simplified. We can use elementary computations (see Supplementary file S1) from the results of (Martin and Lenormand 2015) to see that the conditional cost $c \mid y$ is a constant $c \mid y=$ $c_{\text {min }}(y)=\lambda v(y)$, so that its harmonic mean is also $c_{H}(y)=\lambda v(y)$. Intuitively this result arises because, in one dimension, there is no freedom in the position of a mutant relative to its ancestor and to the optimum in the new environment (all three phenotypes must be aligned). The ER rate from standing variance, in this case, is simply

$$
\begin{equation*}
\omega_{S V} \approx U \mathbb{E}_{y}\left(\frac{\pi(y)}{c_{H}(y)}\right)=\frac{U}{\lambda} \int_{0}^{1}\left(1-e^{-2 r_{\max } y}\right) \frac{f_{y}(y)}{v(y)} d y \tag{A8}
\end{equation*}
$$

## III. Small mutational effects approximation (SME)

Eqs. (A5) and (A7) provide a mathematical framework to predict rescue from both de novo mutants and standing variants, in the SSWM regime. However, they do not provide simple closed form expressions (the integrals must be computed numerically). To gain more analytical
insight, we rely on a further approximation: we look for limit expressions for these rates, as the variance of mutational effects $\lambda$ becomes small relative to the maximal growth rate $r_{\max }$. As we have seen above (Section II subsection 1), $\lambda$ measures the average mutant selective effect per trait. Therefore, we denote these limits "small mutation effect (SME) approximations", in the sense that we let $\lambda / r_{\max }=\rho_{\max }^{-1} \rightarrow 0$ or $\rho_{\max } \rightarrow \infty$, holding all other parameters fixed. This approximation implies that most resistant mutants grow much less than the optimal phenotype: they remain far from the optimum of the new environment so that $y=r / r_{\max } \ll$ 1.

1. Approximate probability density function of $\boldsymbol{y}$ : As the SME implies both that $1-y=O(1)$ while $\rho_{\max } \gg 1$, the second argument in the hypergeometric function in Eq.(A4) is large: $h=$ $\rho_{\max }^{2}\left(1+y_{D}\right)(1-y)=O\left(\rho_{\max }^{2}\right) \gg 1$ for any $y_{D}$. Therefore, we can use an asymptotic expansion, when $|h| \rightarrow \infty$, for this function: $\quad{ }_{0} F_{1}(\theta, h) / \Gamma(\theta) \approx h^{1 / 4-\theta / 2} e^{2 \sqrt{h}} /(2 \sqrt{\pi})$ (Wolfram Research 2001). Plugging this into Eq.(A4) yields a simplified expression for the pdf of the scaled mutant growth rate distribution (see Supplementary file S1):

$$
\begin{equation*}
f_{y}(y) \approx \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}}\left(1+y_{D}\right)^{1 / 4-\theta / 2} e^{-v(y)}(1-y)^{\theta / 2-3 / 4}, \quad y \in[0,1] \tag{A9}
\end{equation*}
$$

where $v(y)=\rho_{\max }\left(2+y_{D}-2 \sqrt{\left(1+y_{D}\right)(1-y)}-y\right)$ was defined in Eq.(A6). Convergence to this limit is faster with (i) stronger stress ( $z$ increases with $y_{D}$ ) and (ii) lower dimensionality. It is roughly exact, for any $\rho_{\max }$, when $\theta=1 / 2$ (see Supplementary file S 1 ).
2. Change of variables $\boldsymbol{y} \rightarrow \boldsymbol{\psi}$ : The distribution in Eq.(A9) takes a more compact form by using a bijective change of variable, which corresponds to an alternative measure of the mutant growth rate $y$. More precisely, we consider $\psi=\psi(y)=2(1-\sqrt{1-y})$ as a measure of growth rate, so that, conversely, $y=y(\psi)=\psi(1-\psi / 4)$. The scaled growth rate of the initial clone is $-y_{D}$ which yields a corresponding decay rate $\psi_{D}=\left|\psi\left(-y_{D}\right)\right|=2\left(\sqrt{1+y_{D}}-\right.$ 1). The transformation is bijective and strictly increasing $\left(\psi^{\prime}(y)=1 / \sqrt{1-y}>0\right)$, from $y \in$ $[0,1]$ to $\psi \in[0,2]$. A linear approximation $\psi_{D} \approx y_{D}+o\left(y_{D}\right)$ yields a relative error $\leq 20 \%$ for all $y_{D} \in[0,1]$, as illustrated in Supplementary Figure 2 below.


Supplementary Figure 2: Relative error implied by the approximation $\psi_{D}=y_{D}$.

The probability density function $f_{\psi}($.$) of the transformed variable \psi$, based on the approximate probability density function of $y$ in Eq.(A9), is $y^{\prime}(\psi) f_{y}(y(\psi))$ yielding:

$$
\begin{align*}
& f_{\psi}(\psi)=y^{\prime}(\psi) f_{y}(y(\psi)) \approx \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}} e^{-\rho_{\max } q(\psi)}\left(\frac{1-\psi / 2}{1+\psi_{D} / 2}\right)^{\theta-1 / 2}  \tag{A10}\\
& q(\psi)=\frac{1}{4}\left(\psi+\psi_{D}\right)^{2}, \quad \psi \in[0,2]
\end{align*} .
$$

This form makes it more visible how the SME corresponds to small $y$ (here to small $\psi=y+$ $o(y))$. Indeed, as $\rho_{\max }$ gets larger, the probability density function in Eq.(A10) is dominated by $e^{-\rho_{\max } q(\psi)}$, which falls off sharply with $\psi$, so that most $\psi$ values are small.
3. Approximate ER rate $\omega_{D N}$ from de novo mutations: Using the $\psi$-scale, the ER rate in Eqs.(A5) is amenable to the so-called Laplace method of approximation for integrals (Breitung 1994). Broadly speaking, this method studies integrals over some domain for $\psi$, involving integrands of the form $h(\psi) e^{-\rho q(\psi)}$ (with some functions $q($.$) and h($.$) , independent of \rho$ ). As $\rho \rightarrow \infty$, such integrals are dominated by terms in the vicinity of the minimum of $q($.$) , over the$ integration domain. They can thus be computed approximately, by (i) using the leading order of $h($.$) (and possibly q($.$) , although we do not require this) around this minimum, and by (ii)$ integrating over any domain that proves handy, away from the minimum.

Eq.(A5), once expressed in terms of $\psi$, with probability density function given in Eq.(A10), is of this form. We have $\pi(y(\psi))=1-e^{-2 r_{\max } \psi(1-\psi / 4)}$ so that Eq. (A5) can be written:

$$
\begin{align*}
& \omega_{D N}=\frac{U}{r_{D}} \mathbb{E}_{\psi}(\pi(y(\psi))) \approx \frac{U}{r_{D}} \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}} \int_{0}^{2} h(\psi) e^{-\rho_{\max } q(\psi)} d \psi  \tag{A11}\\
& h(\psi)=\left(\frac{1-\psi / 2}{1+\psi_{D} / 2}\right)^{\theta-1 / 2}\left(1-e^{-2 r_{\max } \psi(1-\psi / 4)}\right)
\end{align*}
$$

where the function $q($.$) (Eq.(A10)) has a unique minimum, over \psi \geq 0$, at $\psi=0$. Therefore, an approximation to the integral in Eq.(A11), as $\rho_{\max } \rightarrow \infty$, is obtained by approximating $h($.) by its leading order around $\psi=0: h(\psi)=h_{*}(\psi)+o(\psi)$, with $h_{*}(\psi)=2 r_{\max } \psi(1+$ $\left.\psi_{D} / 2\right)^{1 / 2-\theta}$. Plugging this into the integral, expressing $r_{D}$ as $r_{D}=\psi_{D}\left(1+\psi_{D} / 4\right) r_{\max }$, and computing the integral over $\psi \in[0, \infty]$ yields (see Supplementary file S1):

$$
\begin{align*}
& \omega_{D N} \underset{\rho_{\max } \rightarrow \infty}{\rightarrow} \omega_{D N}^{*}=\frac{U}{r_{D}} \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}} \int_{0}^{\infty} h_{*}(\psi) e^{-\rho_{\max } q(\psi)} d \psi \\
& \omega_{D N}^{*}=U \frac{\left(1+\psi_{D} / 2\right)^{1 / 2-\theta}}{1+\psi_{D} / 4} g(\alpha) \tag{A12}
\end{align*}
$$

$$
\text { with } \alpha=\psi_{D}^{2} \frac{\rho_{\max }}{4} \text { and } g(\alpha)=\frac{e^{-\alpha}}{\sqrt{\pi \alpha}}-\operatorname{erfc}(\sqrt{\alpha})
$$

where $\operatorname{erfc}($.$) is the complementary error function. It can be checked numerically that the$ 'exact' rate $\omega_{D N}$ (Eq.(A5)) indeed converges to this limit as $\lambda / r_{\max } \rightarrow 0$ (i.e. as $\rho_{\max } \rightarrow \infty$ ). This is illustrated in Supplementary Fig.3: the convergence to $\omega_{D N}^{*}$, as $\lambda / r_{\max } \rightarrow 0$, is faster for higher stress levels (higher $y_{D}$ ).


Supplementary Figure 3: relative error between $\omega_{D N}^{*}$ and $\omega_{D N}$ (here $\theta=2$ and $r_{\max }=0.5$ ), for different stress levels (scaled decay rates $y_{D}$ indicated in legend).
4. Effect of FGM parameters on the rate of rescue from de novo mutations: Here we detail how each of the FGM parameters ( $r_{D}, \lambda, n, r_{\max }$ ) qualitatively affects the rate of rescue from de novo mutations. First, we note that both $\psi_{D}$ and $\alpha$ (Eq.(6) of the main text) are increasing functions of $r_{D}$, while $g($.$) (Eq.(7) of the main text) is a decreasing function of \alpha$ and the factor $\left(1+\psi_{D} / 2\right)^{1 / 2-\theta} /\left(1+\psi_{D} / 4\right)$ (Eq.(7) of the main text) is a decreasing function of $\psi_{D}$. Overall, when $r_{D}$ increases, the rate of ER (Eq.(A12)) decreases, and so does the ER probability. Second, the only effect of decreasing the variance of mutational effects $(\lambda)$ is to increase $\alpha$ and thus to decrease the ER probability. Third, the effect of dimensionality $(\theta=n / 2)$ is straightforward: increasing $n$ decreases the factor $\left(1+\psi_{D} / 2\right)^{1 / 2-\theta}$, thus decreasing the ER probability. Finally, the effect of the fitness peak height $\left(r_{\max }\right)$ is less obvious from the formula, as increased $r_{\max }$ decreases $\psi_{D}$ but increases $\rho_{\text {max }}$ (and hence potentially $\alpha$ ).

In fact, from the definitions in Eq.(A12) and replacing by $\psi_{D}=2\left(\sqrt{1+y_{D}}-1\right), \partial_{r_{\max }} \alpha=$ $-\left(\sqrt{1+y_{D}}-1\right)^{2} /\left(\sqrt{1+y_{D}} \lambda\right)<0$. Thus, increased $r_{\max }$ decreases both $\alpha$ and $\psi_{D}$ and thus increases the ER probability.
5. Approximate ER rate $\omega_{S V}$ from standing variance: We can follow the same approach used to approximate $\omega_{D N}$ to compute an approximation for $\omega_{S V}$ in Eq.(A7). Expressed in terms of $\psi$,
we find that $v(y(\psi))=q(\psi) \rho_{\max }$ (with $v($.$) from Eq.(A6) and q($.$) from Eq.(A10)). The$ integral in Eq.(A7) thus becomes:

$$
\begin{equation*}
\omega_{S V}=U \mathbb{E}_{\psi}\left(\frac{\pi(y(\psi))}{c_{H}(v(y(\psi)))}\right) \approx \frac{U}{\lambda} \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}} \int_{0}^{2} h(\psi) E_{\theta-1 / 2}\left(\rho_{\max } q(\psi)\right) d \psi \tag{A13}
\end{equation*}
$$

with $h($.$) given in Eq.(A11).$
The approximation is in two steps. In a first step, we find an asymptotic expression for the exponential integral function as $\rho_{\max } \rightarrow \infty$, via the Laplace method. By the definition of this function, we have $E_{\theta-1 / 2}\left(\rho_{\max } q(\psi)\right)=\int_{1}^{\infty} e^{-\rho_{\max } q(\psi) u} u^{1 / 2-\theta} d u$. With $0 \leq \psi \leq 2$, we have $\alpha \leq \rho_{\max } q(\psi) \leq \alpha\left(2+\psi_{D} / 2\right)^{2}$ where $\alpha=\psi_{D}^{2} \rho_{\max } / 4$ as given in Eq. (A12). Assume that $\rho_{\max } \rightarrow \infty$, but further conditioning on $\psi_{D}$ non-vanishing, e.g. letting $\lambda \rightarrow 0$ with $r_{D}$ and $r_{\max }$ held constant. These criterions guarantee that $\alpha$ is large, so that $\rho_{\max } q(\psi) \geq \alpha$ is large too. We can then use the Laplace method as $\rho_{\max } q(\psi) \rightarrow \infty$, to approximate the integral $E_{\theta-1 / 2}\left(\rho_{\max } q(\psi)\right)$. We apply the approximation around the minimum of the exponential term in the integrand $\left(e^{-\rho_{\max } q(\psi) u}\right)$, over the integration domain $u \in[1, \infty]$, namely around $u=1$. Using the approximation $u^{1 / 2-\theta} \approx e^{(\theta-1 / 2)(u-1)}$ in the vicinity of $u=$ 1, we get the following approximation for the exponential integral term:

$$
\begin{equation*}
E_{\theta-1 / 2}\left(\rho_{\max } q(\psi)\right) \underset{\rho_{\max } \overrightarrow{\psi_{D}^{2} / 4 \rightarrow \infty}}{\overrightarrow{\theta-1 / 2+\rho_{\max } q(\psi)}} \tag{A14}
\end{equation*}
$$

In a second step, we now plug this asymptote into Eq.(A13). We retrieve the required form for our integral to apply the Laplace method as in section III subsection 3 for the whole expression of $\omega_{S V}$ :

$$
\begin{align*}
& \omega_{S V} \underset{\rho_{\max } \overrightarrow{\psi_{D}^{2} / 4 \rightarrow \infty}}{ } \frac{U}{\lambda} \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}} \int_{0}^{2} \eta(\psi) e^{-\rho_{\max } q(\psi)} d \psi  \tag{A15}\\
& \eta(\psi)=\frac{h(\psi)}{\theta-1 / 2+\rho_{\max } q(\psi)}
\end{align*}
$$

We thus apply the exact same method as in Eq. (A12) with the leading order for $\eta(\psi)$, when $\rho_{\max } \rightarrow \infty$, in the vicinity of $\psi=0$, given by $\eta_{*}(\psi)=2 r_{\max } \psi\left(1+\psi_{D} / 2\right)^{1 / 2-\theta} /(\alpha+$ $\theta-1 / 2$ ). The resulting asymptotic approximation for $\omega_{S V}$, as $\rho_{\max } \rightarrow \infty$ (with non-
vanishing $\psi_{D}$ ), then satisfies the following relationship with the asymptotic ER rate from de novo mutations ( $\omega_{D N}^{*}$ in Eq. (A12)):

$$
\begin{align*}
& \omega_{S V} \underset{\rho_{\max } \overrightarrow{\psi_{D}^{2}} / 4 \rightarrow \infty}{ } \omega_{S V}^{*}=\frac{U}{\lambda} \frac{\sqrt{\rho_{\max }}}{2 \sqrt{\pi}} \int_{0}^{\infty} \eta_{*}(\psi) e^{-\rho_{\max } q(\psi)} d \psi  \tag{A16}\\
& \omega_{S V}^{*}=\omega_{D N}^{*} \frac{1+\psi_{D} / 4}{\epsilon / \psi_{D}+\psi_{D} / 4} \text { with } \epsilon=\frac{\theta-1 / 2}{\rho_{\max }}
\end{align*}
$$

The convergence of the ER rate $\omega_{S V}$ to its SME approximation ( $\omega_{S V}^{*}$, Eq.(A16)) is illustrated in Supplementary Fig.4. The convergence pattern is slightly more complex than for $\omega_{D N}$, especially at low stress levels (e.g. with $y_{D}=0.05$ in the figure): indeed, this SME limit now requires both $\rho_{\max } \rightarrow \infty$ and $\psi_{D}$ non-vanishing (i.e. $\alpha \rightarrow \infty$ ). Logically, convergence is again faster with higher stress levels (higher $y_{D}$ ).


Supplementary Figure 4: same as Supplementary Fig. 3 but for the relative error between $\omega_{S V}$ and $\omega_{S V}^{*}$.

## IV. Some key properties of the model

1. Characteristic stress level: The relationship between the parameters characterizing the stress $\left(r_{\max }, r_{D}, \lambda\right)$ and the rate of rescue shows a sharp drop from no extinction to nearly certain extinction. We here derive a heuristic characterization of this behavior, for de novo rescue (rescue from standing variance is discussed in a later section). We start by the heuristic behavior
suggested by Eq.(A12), in the limit of mild decay (Eq. 7b, main text): whenever $\psi_{D} \ll 2, \omega_{D N}^{*} \approx$ $U g(\alpha)$. Second, we further simplify the model by taking a series expansion of $g(\alpha) \approx$ $e^{-\alpha} \alpha^{-3 / 2} / 2 \sqrt{\pi}$, when $\alpha$ is large. This approximation yields a relative error of less than $20 \%$ as long as $\alpha \geq 7$. Note that this approximation can apply (i.e., alpha can be that large) even for mild stress $\psi_{D} \ll 2$, as long as $\rho_{\max }$ is large enough.

We define $\alpha_{p}$ of level $p$ by the set of parameter values such that $\alpha=\alpha_{p}$ and $P_{R}=p$ a given ER probability. Under the approximate heuristic derived above, $\alpha_{p}$ is characterized by $p=P_{R} \approx 1-\exp \left(-N_{0} U g\left(\alpha_{p}\right)\right)$, with $g(\alpha) \approx e^{-\alpha} \alpha^{-3 / 2} / 2 \sqrt{\pi}$. This implies $g\left(\alpha_{p}\right)=$ $-\log (1-p) / N_{0} U$, and inversion of $g($.$) then yields$

$$
\begin{equation*}
\alpha_{p} \approx \frac{3}{2} \mathcal{W}\left(\left(\frac{2}{\pi}\right)^{1 / 3} \frac{1}{3}\left(\frac{N_{0} U}{\log (1 /(1-p))}\right)^{2 / 3}\right) \tag{A17}
\end{equation*}
$$

where $\mathcal{W}($.$) is Lambert's ('productlog') function. A linear regression of \mathcal{W}(x) v s . \log (x)-1$ (checked by visual inspection, see Supplementary file S1) suggests that, over a biologically relevant range $\in\left[10,10^{12}\right]: \mathcal{W}(x) \approx 0.9(\log (x)-1)$. This yields the approximation (see numerical check in Supplementary file S1)

$$
\begin{equation*}
\alpha_{p} \approx 0.9\left(\log \left(N_{0} U\right)-\log \left(\log \left(\frac{1}{1-p}\right)\right)\right)-3 \tag{A18}
\end{equation*}
$$

A characteristic stress level $\alpha_{c}$ can be defined as the value of $\alpha$ where the ER probability is $50 \%: \alpha_{c}=\alpha_{1 / 2}$. It characterizes the level of stress about which rescue drops from highly likely to highly unlikely. Setting $p=1 / 2$ in Eq.(A18), the characteristic stress is approximately

$$
\begin{equation*}
\alpha_{c} \approx 0.9 \log \left(N_{0} U\right)-2.7 \tag{A19}
\end{equation*}
$$

2. Self-consistency at large $\boldsymbol{N}_{\mathbf{0}} \boldsymbol{U}$ : We have used both (i) a large $\alpha$ approximation and (ii) a small $\psi_{D} \ll 2$ approximation (Eq. 7b) to derive the characteristic stress in Eq.(A19). We argue that they are self-consistent as long as $N_{0} U$ is large.

We have (Eq.(A19)) $\alpha_{c} \approx 0.9 \log \left(N_{0} U\right)-2.7$, which is indeed large provided $N_{0} U$ is large. We have seen that approximating $g(\alpha) \approx e^{-\alpha} \alpha^{-3 / 2} / 2 \sqrt{\pi}$ should be reasonably accurate ( $<20 \%$ relative error) as long as $\alpha_{c} \geq 7$, which corresponds to $N_{0} U \geq 5.10^{4}$, a condition quite easily
met in microbial experiments, for example. Furthermore, as $\alpha_{c}=\rho_{\max }\left(\psi_{D}^{c}\right)^{2} / 4$ (Eq.(A12)), the corresponding characteristic $\psi_{D}$ is equal to $\psi_{D}^{c}=2 \sqrt{\left(0.9 \log \left(N_{0} U\right)-2.7\right) / \rho_{\max }}$ (Eq.(A19) and is indeed negligible relative to 1 as long as $N_{0} U \ll 20 e^{\rho_{\max }}$. This second criterion is in fact so easily met that it does not constrain the results; for example, with $\rho_{\max }=50$, the requirement is simply that $N_{0} U \ll 10^{25}$ ! Overall, it appears that Eq.(A19) is self-consistent whenever $N_{0} U$ is large.
3. Characteristic stress window: Around the characteristic stress, the ER probability falls off more or less sharply. We define a characteristic stress window of level $q$ over which $P_{R}$ drops from $1 / 2+q$ to $1 / 2-q$. As an illustration, we use $q=0.25$, so that the window characterizes the drop from $75 \%$ to $25 \%$ ER. This window can be directly computed from Eq.(A17) as $\Delta \alpha=$ $\alpha_{1 / 4}-\alpha_{3 / 4}$. It is also approximately given by the inverse of the slope of the ER probability with $\alpha, \quad$ at $\alpha=\alpha_{c}=\alpha_{1 / 2}, \quad$ namely: $\Delta \alpha \approx 2 q /\left|P_{R}^{\prime}\left(\alpha_{c}\right)\right|=1 /\left(2\left|P_{R}^{\prime}\left(\alpha_{c}\right)\right|\right), \quad$ with $q=1 / 4$. Letting $P_{R}(\alpha)=1-e^{-N_{0} U g(\alpha)}$ (Eq. 7b, main text), and using the large $\alpha$ approximation to $g($.) $\left(g(\alpha) \approx e^{-\alpha} \alpha^{-3 / 2} / 2 \sqrt{\pi}\right)$, we have $g^{\prime}(\alpha) \approx-g(\alpha)(1+3 /(2 \alpha))$, so that $P_{R}{ }^{\prime}\left(\alpha_{p}\right)=(1-$ $p) \log (1-p)\left(1+3 / 2 \alpha_{p}\right)$ for any level $p$. Setting $p=1 / 2$ so that $\alpha=\alpha_{c}$ we have

$$
\begin{equation*}
\Delta \alpha \approx \frac{1 / 2}{\left|P_{R}^{\prime}\left(\alpha_{c}\right)\right|} \approx \frac{2 \alpha_{c}}{\log 8+\log 4 \alpha_{c}} \approx \frac{\alpha_{c}}{1+0.7 \alpha_{c}} . \tag{A20}
\end{equation*}
$$

The width of the window can be scaled by the value of the characteristic stress $\alpha_{c}$ around which the drop occurs, in order to characterize how sharp the drop is, as is done in Eq. (9) of the main text. Obviously, this simple heuristic, based on a linear approximation for $P_{R}$, gets more accurate over narrower windows, e.g. it is very accurate for describing the decay from $70 \%$ to $30 \%$, and less accurate for describing the decay from $95 \%$ to $5 \%$.
4. Proportion of rescue from standing variance: The result in Eq. (A16) shows the relationship between $\omega_{S V}^{*}$ and $\omega_{D N}^{*}$ in the SME approximation. Then, from Eq.(A3), the proportion $\phi_{S V}$ converges to a simple limit $\phi_{S V}^{*}$ :

$$
\begin{equation*}
\phi_{S V}^{*}=\frac{\omega_{S V}^{*}}{\omega_{D N}^{*}+\omega_{S V}^{*}}=\frac{1+\psi_{D} / 4}{\epsilon / \psi_{D}+1+\psi_{D} / 2} \tag{A21}
\end{equation*}
$$

Obviously, in the limit where $\epsilon \ll \psi_{D}$ (with $\epsilon$ in Eq.(A16)), the proportion $\phi_{S V}^{*}$ simplifies to $1 / 2+1 /\left(2+\psi_{D}\right)$, being always above $50 \%$, and decreasing with higher stress-scaled decay rates.

For non-vanishing $\epsilon / \psi_{D}$, as $\psi_{D}$ varies, the proportion $\phi_{S V}^{*}$ reaches a maximum at the unique positive $\psi_{D}$ where $\partial \phi_{S V}^{*} / \partial \psi_{D}=0$, which is at $\psi_{D}=\psi_{D}^{0}=\epsilon+\sqrt{\epsilon(4+\epsilon)}$. At that point, its value is

$$
\begin{equation*}
\max \phi_{S V}^{*}=\phi_{S V}^{*}\left(\psi_{D}^{0}\right)=\frac{1-\epsilon / 2-\sqrt{\epsilon(1+\epsilon / 4)}}{1-2 \epsilon}=1-\sqrt{\epsilon}+o(\sqrt{\epsilon}) . \tag{A22}
\end{equation*}
$$

5. Stability of $\boldsymbol{\phi}_{S V}^{*}$ across a range of stress: In fact, as $P_{R}$ drops sharply with $\psi_{D}$ (or $y_{D}$ ), the proportion $\phi_{S V}^{*}$ happens to be fairly stable across stress levels, if stress only affects decay rates. To see this, we can derive the curvature, as $\psi_{D}$ varies, of $\phi_{S V}^{*}$ with respect to the log of the extinction probability $\left|\log P_{E}\right|$, in the presence of de novo mutation and standing variance. We study this curvature around the value of $\psi_{D}$ where the proportion is maximal, namely around $\psi_{D}=\psi_{D}^{0}$. It is equivalent and proves convenient to study this curvature by defining the two quantities as functions of $\alpha$, and studying the curvature when $\alpha$ varies. Because $\psi_{D}^{0}=O(\epsilon)$, we can use the small $\psi_{D}$ approximation (Eq. 7b) $\omega_{D N}^{*} \approx U g(\alpha)$. From Eq. (A16) and using $\psi_{D}=$ $\sqrt{\alpha / \rho_{\max }}$, we can write the ratio of ER rates as

$$
\begin{equation*}
\frac{\omega_{S V}^{*}}{\omega_{D N}^{*}}=2 \frac{\sqrt{\alpha \rho_{\max }}}{\alpha+\theta-1 / 2}\left(1-\frac{\psi_{D}}{4}\right), \tag{A23}
\end{equation*}
$$

Again, as we study this ratio in the vicinity of $\psi_{D}^{0}=O(\epsilon)$, we can ignore the factor $1-\psi_{D} / 4$ in Eq.(A23) and compute the proportion of ER from standing variance as:

$$
\begin{equation*}
Y(\alpha)=\phi_{S V}^{*} \approx \frac{2 \sqrt{\alpha \rho_{\max }}}{\alpha+\theta-1 / 2+2 \sqrt{\alpha \rho_{\max }}} \tag{A24}
\end{equation*}
$$

This is maximal at $\alpha=\theta-1 / 2$, which is consistent with the expression for $\alpha=\rho_{\max } \psi_{D}^{2} / 4$ when using the leading order for $\psi_{D}^{0}=2 \sqrt{\epsilon}+o(\sqrt{\epsilon})$. The total ER rate from de novo mutations plus standing variance ( $\left.\omega^{*}=\omega_{D N}^{*}+\omega_{S V}^{*}\right)$ is also simplified, once we ignore the factor $1-$
$\psi_{D} / 4$ in Eq.(A23). This yields a relatively simple form for the log of the extinction probability (recalling that $P_{E}=e^{-N_{0} \omega^{*}}$ ):

$$
\begin{equation*}
X(\alpha)=\left|\log P_{E}\right| \approx N_{0} U\left(\omega_{D N}^{*}+\omega_{S V}^{*}\right) \approx N_{0} U g(\alpha)\left(1+\frac{2 \sqrt{\alpha \rho_{\max }}}{\alpha+\theta-1 / 2}\right) \tag{A25}
\end{equation*}
$$

The two quantities $(X(\alpha), Y(\alpha))$ define a parametric curve as $\alpha$ varies, with a maximum in $Y($. at $\alpha=\theta-1 / 2$. The curvature of $Y=\phi_{S V}^{*}$ with $X=\log P_{R}$, at this point $\alpha_{0}$, is given by (see e.g. Goldman 2005)

$$
\begin{equation*}
\kappa=\frac{X^{\prime}(\theta-1 / 2) Y^{\prime \prime}(\theta-1 / 2)-Y^{\prime}(\theta-1 / 2) X^{\prime \prime}(\theta-1 / 2)}{\left(X^{\prime}(\theta-1 / 2)^{2}+Y^{\prime}(\theta-1 / 2)^{2}\right)^{3 / 2}} \tag{A26}
\end{equation*}
$$

using the expressions for $X($.$) and Y($.$) in \operatorname{Eqs}(\mathrm{A} 24)$ and (A25), we get

$$
\begin{equation*}
\kappa=\frac{e^{2(\theta-1 / 2)} \pi(\theta-1 / 2)^{5 / 2} \sqrt{\rho_{\max }}}{N_{0}^{2} U^{2}\left(\sqrt{\theta-1 / 2}+\sqrt{\rho_{\max }}\right)^{4}} . \tag{A27}
\end{equation*}
$$

This curvature is obviously very small, of order $1 /\left(N_{0}^{2} U^{2} \rho_{\text {max }}^{3 / 2}\right)$. This flatness of the proportion $\phi_{S V}^{*}$ with $\left|\log P_{E}\right|$ (extinction probability on a log-scale), shows formally that it is almost unaffected by changes in decay rates, over a wide range of stress levels, spanning several orders of magnitude of change in $P_{E}$ (or equivalently $P_{R}$ ).

## Bibliography

Breitung K. W., 1994 Asymptotic approximations for probability integrals. Springer-Verlag, Berlin ; New York.

Gillespie J. H., 1983 Some Properties of Finite Populations Experiencing Strong Selection and Weak Mutation. Am. Nat. 121: 691-708.

Goldman R., 2005 Curvature formulas for implicit curves and surfaces. Comput. Aided Geom. Des. 22: 632-658.

Martin G., Aguilée R., Ramsayer J., Kaltz O., Ronce O., 2013 The probability of evolutionary rescue: towards a quantitative comparison between theory and evolution experiments. Phil Trans R Soc B 368: 20120088.

Martin G., Lenormand T., 2015 The fitness effect of mutations across environments: Fisher's geometrical model with multiple optima. Evolution 69: 1433-1447.

McCandlish D. M., Stoltzfus A., 2014 Modeling Evolution Using the Probability of Fixation: History and Implications. Q. Rev. Biol. 89: 225-252.

Wolfram Research, 2001 Confluent hypergeometric function OF1: Series representations.

