

# Modeling the effect of aneuploidy on cancer evolution

Remus Stana<sup>1</sup>, Uri Ben-David<sup>2</sup>, Daniel B. Weissman<sup>3</sup>, and Yoav Ram<sup>1,\*</sup>

<sup>1</sup>School of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel

<sup>2</sup>Department of Human Molecular Genetics and Biochemistry, Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel

<sup>3</sup>Department of Physics, Emory University, Atlanta, GA

\*Corresponding author: yoav@yoavram.com

June 4, 2023

## Abstract

Evolutionary rescue is the process by which a population is able to survive a sudden environmental change which initially causes the population to decline towards extinction. A prime example of evolutionary rescue is the ability of cancer to survive being exposed to various treatments. We are interested in the mechanisms through which a population of cancer cells are able to adapt to chemotherapy, and in particular, the role played by chromosomal instability (aneuploidy). Cancer cells which have aneuploidy are hypothesized to have a higher fitness in an environment altered by anti-cancer drugs as they have incomplete pathways which drugs activate in order to kill the cells. Aneuploidy is highly prevalent in tumors and certain drugs which attempt to combat cancers through increasing chromosomal instability. As a result, the question we wish to answer is how aneuploidy impacts the fate of the population of cancer cells. We propose to model evolutionary rescue with the help of multi-type branching processes to obtain the probability that cancer will survive. Additionally, we will utilize large genomic datasets to assess the effects of aneuploidy on the probability of evolutionary rescue.

## 24 Introduction

**Aneuploidy in cancer.** Chromosomal instability (CIN) is the mitotic process in which cells suffer from chromosome mis-segregation that leads to aneuploidy, where cells are characterized by structural changes of the chromosomes and copy number alterations (Schukken and Fojer, 2018). Interestingly, aberrations in chromosome copy number have been shown to allow cancer cells to survive under stressful conditions such as drug therapy. Indeed, cancer cells are often likely to be aneuploid, and aneuploidy is associated with poor patient outcomes (Ben-David and Amon, 2020).

The role of chromosomal instability (CIN) in the emergence of cancer has been studied extensively in the past decades (Michor et al., 2005; Christine et al., 2018; Nowak et al., 2002; Pavelka et al., 2010; Komarova et al., 2003; Zhu et al., 2018). One hypothesis is that CIN facilitates tumor genesis by accelerating the removal of tumor suppression genes (TSG) and subsequent appearance of cancer. The deletion of tumor suppression genes can happen in two ways: two point mutations deleting both alleles of the TSG (assuming a diploid genotype), or one point mutation and one chromosomal loss event. Initial theoretical studies have shown that aneuploidy can have a significant role in the deletion of the the tumor suppressing genes when compared to two consecutive point mutations (Nowak et al., 2002; Komarova et al., 2003; Michor et al., 2005; Komarova et al., 2008). However, when taking into account that the appearance of aneuploidy requires a mutation to trigger CIN, the probability that CIN precedes tumor genesis is highly unlikely.

**Evolutionary rescue.** Populations adapted to a certain environment are vulnerable to environmental changes, which might cause extinction of the population. Examples of such environmental changes include climate change, invasive species or the onset of drug therapies. Adaptation is a race against time as the population size decreases in the new environment (Tanaka and Wahl, 2022). *Evolutionary rescue* is the process where the population acquires a trait that increases fitness in the new environment such that extinction is averted. It is mathematically equivalent to the problem of crossing of fitness valley (Weissman et al., 2009, 2010). There are three potential ways for a population to survive environmental change: migration to a new habitat similar to the one before the onset of environmental change (Cobbold and Stana, 2020); adaptation by phenotypic plasticity without genetic modification (Carja and Plotkin, 2019, 2017; Levien et al., 2021); and adaptation through genetic modifications, e.g., mutation (Uecker et al., 2014; Uecker and Hermisson, 2016, 2011).

Models of evolutionary rescue usually assume that the fitness of the wildtype and mutant are homogeneous in time. An exception was given by Marrec and Bitbol (2020), who modeled the fitness of the wildtype and mutant as time dependent. Additionally, Uecker and Hermisson (2011) investigated the probability of fixation of a beneficial mutation in a variable environment with arbitrary time-dependent selection coefficient and population size. Most models focus on the probability that at least one mutation rescues the population. How multiple mutations contribute to the survival of the population is less explored, but Wilson et al. (2017) have shown that evolutionary rescue is significantly enhanced by soft selective sweeps when multiple mutations contribute. Evolutionary rescue that requires two successive mutations has been investigated using diffusion approximation by Martin et al. (2013).

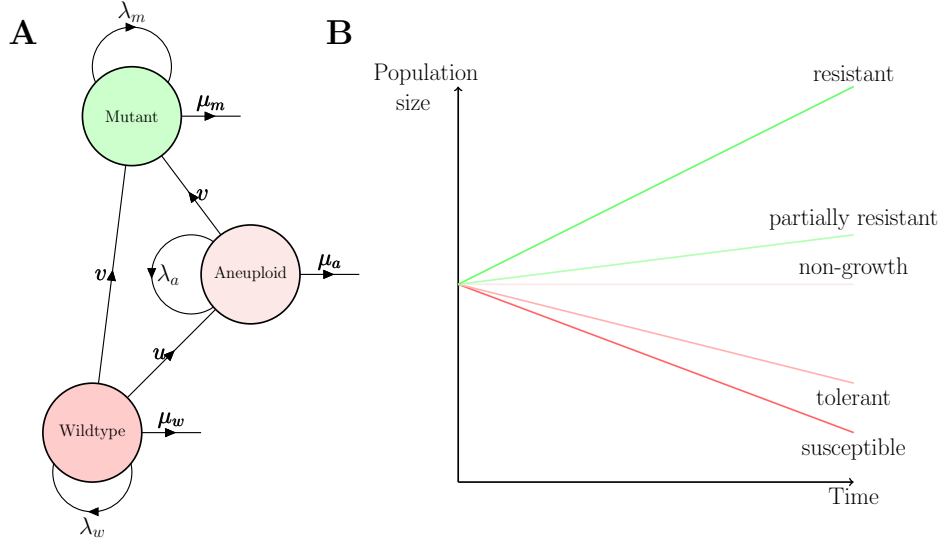


Figure 1: **Model illustration.** (A) A population of cancer cells is composed of wildtype, aneuploid, and mutant cells, which divide with rates  $\lambda_w$ ,  $\lambda_a$ , and  $\lambda_m$  and die at rates  $\mu_w$ ,  $\mu_a$ , and  $\mu_m$ , respectively. Wildtype cells can become aneuploid at rate  $u$ . Both aneuploid and wildtype cells can acquire a beneficial mutation with rate  $v$ . Color denotes the relative growth rates of the three genotypes such that  $\lambda_w - \mu_w < \lambda_a - \mu_a < \lambda_m - \mu_m$ . (B) The wildtype and the mutant are susceptible and resistant, respectively, to the drug. The aneuploid may be tolerant, non-growing, or partially resistant.

## 66 Methods

### Evolutionary model

68 We follow the number of cancer cells that have one of three different genotypes at time  $t$ :  
 wildtype,  $w_t$ ; aneuploid,  $a_t$ ; and mutant,  $m_t$ . These cells divide and die with rates  $\lambda_k$  and  $\mu_k$   
 70 (for  $k = w, a, m$ ). The difference between the division and death rate is  $\Delta_k = \lambda_k - \mu_k$ . We  
 assume the population of cells is under a strong stress, such as drug therapy, to which the  
 72 wildtype genotype is susceptible and therefore  $\Delta_w < 0$ , whereas the mutant is resistant to the  
 stress,  $\Delta_m > 0$ . We analyze three scenarios: in the first, aneuploid cells are partially resistant,  
 74  $\Delta_m > \Delta_a > 0$ ; in the second, aneuploid cells are tolerant,  $0 > \Delta_a > \Delta_w$  (see Brauner et al.,  
 2016, for the distinction between susceptible, resistant, and tolerant); in the third, aneuploid  
 76 cells are non-growing or "barely growing", that is, either slightly tolerant or slightly resistant,  
 such that  $\Delta_a \approx 0$ . Wildtype cells may missegregate to become aneuploids at rate  $u$ . Both  
 78 aneuploid and wildtype cells may mutate to become mutants at rate  $v$  (Figure 1).

### Stochastic simulations

80 Simulations are performed using a *Gillespie algorithm* (Gillespie, 1976, 1977) implemented in  
 Python (Van Rossum and Others, 2007). The simulation monitors the number of cells of each  
 82 type: wildtype, aneuploid, and mutant. The wildtype population initially consists of  $w_0$  cells,  
 whereas the other cell types are initially absent.

The state of the stochastic system at time  $t$  is represented by the triplet  $(w_t, a_t, m_t)$ . The  
 following describes the events that may occur (right column), the rates at which they occur

	Name	Value	Units	References
$N$	Initial tumor size	$10^7 - 10^9$	cells	Del Monte (2009)
$\lambda_w$	Wildtype division rate	0.14	1/days	(Bozic et al., 2013)
$\mu_w$	Wildtype death rate	0.17	1/days	Bozic et al. (2013)
$\lambda_a$	Aneuploid division rate*	0.14	1/days	-
$\mu_a$	Aneuploid death rate*	0.13 - 0.17	1/days	-
$\lambda_m$	Mutant division rate	0.14	1/days	Bozic et al. (2013)
$\mu_m$	Mutant death rate	0.13	1/days	Bozic et al. (2013)
$u$	Missegregation rate	$10^{-3} - 10^{-2}$	1/cell division	Nowak et al. (2004); Bakker et al. (2023)
$v$	Mutation rate	$10^{-7} - 10^{-9}$	1/gene/cell division	Nowak et al. (2004)

Table 1: **Model parameters.** Aneuploid birth rate  $\lambda_a$  is set to the same value as the wildtype and mutant birth rates,  $\lambda_w$  and  $\lambda_m$ . Aneuploid death rate  $\mu_a$  is set to an intermediate value between the wildtype and mutant death rates,  $\mu_w$  and  $\mu_m$ .

(middle column), and the effect these events have on the state (Figure 1):

$$\begin{aligned}
(+1, 0, 0) : & \quad \lambda_w w_t \quad (\text{birth of wildtype cell}), \\
(-1, 0, 0) : & \quad \mu_w w_t \quad (\text{death of wildtype cell}), \\
(-1, +1, 0) : & \quad u w_t \quad (\text{wildtype cell becomes aneuploid}), \\
(-1, 0, +1) : & \quad v w_t \quad (\text{wildtype cell becomes mutant}), \\
(0, +1, 0) : & \quad \lambda_a a_t \quad (\text{birth of aneuploid cell}), \\
(0, -1, 0) : & \quad \mu_a a_t \quad (\text{death of aneuploid cell}), \\
(0, -1, +1) : & \quad v a_t \quad (\text{aneuploid cell becomes mutant}), \\
(0, 0, +1) : & \quad \lambda_m m_t \quad (\text{birth of mutant cell}), \\
(0, 0, -1) : & \quad \mu_m m_t \quad (\text{death of mutant cell}).
\end{aligned}$$

Each iteration of the simulation loop starts with computing the rates  $\nu_j$  of each event  $j$ . We then draw the time until the next event,  $\Delta t$ , from an exponential distribution whose rate parameter is the sum of the rates of all events, such that  $\Delta t \sim \text{Exp}(\sum_j \nu_j)$ . Then, we randomly determine which event occurred, where the probability for event  $j$  is  $p_j = \nu_j / \sum_i \nu_i$ . Finally, we update the number of cells of each type according to the event that occurred and update the time from  $t$  to  $t + \Delta t$ . We repeat these iterations until either the population becomes extinct (the number of cells of all types is zero) or the number of mutant cells is high enough so that its extinction probability is  $< 0.1\%$ , that is until

$$m_t > \left\lceil -\frac{3 \log 10}{\log\left(\frac{\mu_m}{\lambda_m}\right)} \right\rceil + 1,$$

84  **$\tau$ -leaping.** When simulations are slow (e.g. due to large population size), we utilize  $\tau$ -leaping (Gillespie, 2001), where change in number of cells of genotype  $i$  in a fixed time interval  $\Delta t$  is

86 Poisson distributed with mean  $\nu_i \Delta t$ . If the change in number of cells is negative and larger than the subpopulation size then the subpopulation size is updated to be zero.

**Density-dependent growth.** In our analysis we assume that lineages produced by cells from the initial population divide and die independently of each other, which may be unrealistic, as cells usually compete for resources. A more realistic model includes competition for limited resources and spatial structure, which may play an important role in the development of cancer (e.g., Martens et al., 2011). To simulate birth and death rates that depend on the number of cells in the population, we transform the rates of division and death to the following:

$$\begin{aligned}\lambda'_w &= \lambda_w, \\ \mu'_w &= \mu_w, \\ \lambda'_a &= C_1 + (\lambda_a - \mu_a) \left(1 - \frac{w + a + m}{K}\right), \\ \mu'_a &= C_1, \\ \lambda'_m &= C_2 + (\lambda_m - \mu_m) \left(1 - \frac{w + a + m}{K}\right), \\ \mu'_m &= C_2,\end{aligned}$$

88 where  $C_1, C_2 > 0$  are constants.

## Code and data availability.

90 All source code is available online at <https://github.com/yoavram-lab/EvolutionaryRescue>.

## Results

### 92 Survival probability

To analyze evolutionary rescue in this model, we use the framework of *multitype branching processes* (Rybnikov et al., 2021; Harris et al., 1963). This allows us to find explicit expressions for the *survival probability*: the probability that a lineage descended from a single cell does not become extinct.

Let  $p_w$ ,  $p_a$ , and  $p_m$  be the survival probabilities of a population consisting initially of single wildtype cell, aneuploid cell, or mutant cell, respectively. The complements  $1 - p_w$ ,  $1 - p_a$ , and  $1 - p_m$  are the extinction probabilities, which satisfy each its respective equation,

$$\begin{aligned}1 - p_w &= \frac{\mu_w}{\lambda_w + \mu_w + u + v} + \frac{u}{\lambda_w + \mu_w + u + v} (1 - p_a) + \\ &\quad \frac{\lambda_w}{\lambda_w + \mu_w + u + v} (1 - p_w)^2 + \frac{v}{\lambda_w + \mu_w + u + v} (1 - p_m), \\ 1 - p_a &= \frac{\mu_a}{\lambda_a + \mu_a + v} + \frac{v}{\lambda_a + \mu_a + v} (1 - p_m) + \frac{\lambda_a}{\lambda_a + \mu_a + v} (1 - p_a)^2, \\ 1 - p_m &= \frac{\mu_m}{\lambda_m + \mu_m} + \frac{\lambda_m}{\lambda_m + \mu_m} (1 - p_m)^2.\end{aligned}\tag{2}$$

The survival probabilities are given by the smallest solution for each quadratic equation (Uecker et al., 2015). Therefore we have

$$\begin{aligned} p_w &= \frac{\lambda_w - \mu_w - u - v + \sqrt{(\lambda_w - \mu_w - u - v)^2 + 4\lambda_w(up_a + vp_m)}}{2\lambda_w}, \\ p_a &= \frac{\lambda_a - \mu_a - v + \sqrt{(\lambda_a - \mu_a - v)^2 + 4\lambda_a vp_m}}{2\lambda_a}, \\ p_m &= \frac{\lambda_m - \mu_m}{\lambda_m}. \end{aligned} \quad (3)$$

Note that the equation for  $p_w$  depends on both  $p_a$  and  $p_m$ , and the equation for  $p_a$  depends on  $p_m$ . To proceed, we can plug the solution for  $p_m$  and  $p_a$  into the solution for  $p_w$ . We perform this for three different scenarios.

### Scenario 1: Aneuploid cells are partially resistant

We first assume that aneuploidy provides partial resistance to drug therapy,  $\lambda_a > \mu_a$ , and that this resistance is significant,  $(\lambda_a - \mu_a - v)^2 > 4\lambda_a vp_m$ . We thus rewrite eq. (3) as

$$\begin{aligned} p_w &= \frac{\lambda_w - \mu_w - u - v}{2\lambda_w} \left( 1 - \sqrt{1 + \frac{4\lambda_w(vp_m + up_a)}{(\lambda_w - \mu_w - u - v)^2}} \right), \text{ and} \\ p_a &= \frac{\lambda_a - \mu_a - v}{2\lambda_a} \left( 1 + \sqrt{1 + \frac{4\lambda_a vp_m}{(\lambda_a - \mu_a - v)^2}} \right). \end{aligned}$$

Using the quadratic Taylor expansion  $\sqrt{1+x} = 1 + x/2 + O(x^2)$  and assuming  $u, v \ll 1$ , we obtain the following approximation for the survival probability of a population initially consisting of a single wildtype cell,

$$\begin{aligned} p_w &\approx -\frac{vp_m + up_a}{\lambda_w - \mu_w - u - v} \\ &\approx -\frac{1}{\lambda_w - \mu_w} \left[ \frac{u(\lambda_a - \mu_a)}{\lambda_a} + \frac{uv(\lambda_m - \mu_m)}{\lambda_m(\lambda_a - \mu_a)} + \frac{v(\lambda_m - \mu_m)}{\lambda_m} \right] \end{aligned} \quad (4)$$

**Second-order approximation.** To improve our approximation, we can consider the second term of the Taylor series expansion,

$$\left( 1 + \frac{4\lambda_a vp_m}{(\lambda_a - \mu_a - v)^2} \right)^{\frac{1}{2}} = 1 + \frac{2\lambda_a vp_m}{(\lambda_a - \mu_a - v)^2} - \frac{(\lambda_a vp_m)^2}{4(\lambda_a - \mu_a - v)^4} + \dots,$$

which gives us the following approximation,

$$p_a \approx \frac{\lambda_a - \mu_a - v}{\lambda_a} + \frac{vp_m}{\lambda_a - \mu_a - v} - \frac{\lambda_a (vp_m)^2}{8(\lambda_a - \mu_a - v)^3}. \quad (6)$$

We therefore have

$$p_w \approx -\frac{1}{\lambda_w - \mu_w - u - v} \left[ \frac{u(\lambda_a - \mu_a - v)}{\lambda_a} + \frac{uv(\lambda_m - \mu_m)}{\lambda_m(\lambda_a - \mu_a - v)} + \frac{v(\lambda_m - \mu_m)}{\lambda_m} - \frac{uv^2\lambda_a(\lambda_m - \mu_m)^2}{8\lambda_m^2(\lambda_a - \mu_a - v)^3} \right]$$

$$\approx -\frac{1}{\lambda_w - \mu_w} \left[ \frac{u(\lambda_a - \mu_a)}{\lambda_a} + \frac{uv(\lambda_m - \mu_m)}{\lambda_m(\lambda_a - \mu_a)} + \frac{v(\lambda_m - \mu_m)}{\lambda_m} - \frac{uv^2\lambda_a(\lambda_m - \mu_m)^2}{8\lambda_m^2(\lambda_a - \mu_a)^3} \right], \quad (7)$$

108 and using  $\Delta_k = \lambda_k - \mu_k$ , we can write the above equation as

$$p_w \approx -\frac{1}{\Delta_w} \left( \frac{u\Delta_a}{\lambda_a} + \frac{uv\Delta_m}{\lambda_m\Delta_a} + \frac{v\Delta_m}{\lambda_m} - \frac{uv^2\lambda_a\Delta_m^2}{8\lambda_m^2\Delta_a^3} \right). \quad (8)$$

## 110 Scenario 2: Aneuploid cells are tolerant.

We now assume that aneuploidy provides tolerance to drug therapy, that is, the number of  
 112 aneuploid cells significantly declines over time, but at a lower rate than the number of wildtype  
 cells,  $\lambda_w - \mu_w < \lambda_a - \mu_a < 0$ . We also assume that the decline are significant,  $(\lambda_a - \mu_a - v)^2 >$   
 114  $4\lambda_a vp_m$ . We rewrite eq. (3) as

$$p_w = \frac{\lambda_w - \mu_w - u - v}{2\lambda_w} \left( 1 - \sqrt{1 + \frac{4\lambda_w(vp_m + up_a)}{(\lambda_w - \mu_w - u - v)^2}} \right), \text{ and} \quad (9)$$

$$p_a = \frac{\lambda_a - \mu_a - v}{2\lambda_a} \left( 1 - \sqrt{1 + \frac{4\lambda_a vp_m}{(\lambda_a - \mu_a - v)^2}} \right).$$

116 Since  $u, v \ll 1$ , the term in the root can be approximated using a 1st-order Taylor expansion.  
 So, substituting the expressions for  $p_a$  and  $p_m$ , we have

$$\begin{aligned} p_w &\approx -\frac{vp_m + up_a}{\lambda_w - \mu_w - u - v} \\ 118 \quad &\approx \frac{1}{\lambda_w - \mu_w - u - v} \left[ \frac{uv(\lambda_m - \mu_m)}{\lambda_m(\lambda_a - \mu_a - v)} - \frac{v(\lambda_m - \mu_m)}{\lambda_m} \right] \\ &\approx \frac{v(\lambda_m - \mu_m)}{\lambda_m(\lambda_w - \mu_w)} \left[ \frac{u}{(\lambda_a - \mu_a)} - 1 \right] \end{aligned} \quad (10)$$

## Scenario 3: Aneuploid cells are non-growing

120 We now assume that the growth rate of aneuploid cells is close to zero (either positive or  
 negative), such that  $(\lambda_a - \mu_a - v)^2 < 4\lambda_a vp_m$ . We rewrite eq. (3) as

$$122 \quad p_a = \frac{\lambda_a - \mu_a - v + 2\sqrt{\lambda_a vp_m} \left( 1 + \frac{(\lambda_a - \mu_a - v)^2}{4\lambda_a vp_m} \right)^{\frac{1}{2}}}{2\lambda_a}. \quad (11)$$

Using a following Taylor series expansion

$$\left( 1 + \frac{(\lambda_a - \mu_a - v)^2}{4\lambda_a vp_m} \right)^{\frac{1}{2}} = 1 + \frac{(\lambda_a - \mu_a - v)^2}{8\lambda_a vp_m} + \dots,$$

we obtain the approximation

$$\begin{aligned}
p_a &\approx \frac{\lambda_a - \mu_a - v + 2\sqrt{\lambda_a v p_m} \left[ 1 + \frac{(\lambda_a - \mu_a - v)^2}{8\lambda_a v p_m} \right]}{2\lambda_a} \\
&= \frac{\lambda_a - \mu_a - v + 2\sqrt{\lambda_a v p_m} + \frac{(\lambda_a - \mu_a - v)^2}{4\sqrt{\lambda_a v p_m}}}{2\lambda_a} \\
&= \frac{(\lambda_a - \mu_a - v + 2\sqrt{\lambda_a v p_m})^2 + 4\lambda_a v p_m}{8\lambda_a \sqrt{\lambda_a v p_m}} \\
&= \frac{4\lambda_a v p_m + 4\lambda_a v p_m \left( 1 + \frac{\lambda_a - \mu_a - v}{2\sqrt{\lambda_a v p_m}} \right)^2}{8\lambda_a \sqrt{\lambda_a v p_m}} \\
&= \frac{1}{2\lambda_a} \left( \lambda_a - \mu_a - v + 2\sqrt{\lambda_a v p_m} \right).
\end{aligned} \tag{12}$$

Plugging this in eq. (10), the survival probability of a population starting from one wildtype individual is

$$\begin{aligned}
p_w &\approx -\frac{1}{\lambda_w - \mu_w - u - v} \left[ v \frac{\lambda_m - \mu_m}{\lambda_m} + \frac{u}{2\lambda_a} \left( \lambda_a - \mu_a - v + 2\sqrt{\lambda_a v p_m} \right) \right] \\
&= -\frac{1}{\lambda_w - \mu_w - u - v} \left[ v \frac{\lambda_m - \mu_m}{\lambda_m} + \frac{u}{2\lambda_a} (\lambda_a - \mu_a - v) + u \sqrt{\frac{v(\lambda_m - \mu_m)}{\lambda_a \lambda_m}} \right].
\end{aligned} \tag{13}$$

## Evolutionary rescue probability

In our model, *evolutionary rescue* occurs when resistant cells appear and fixate ( $m_t \gg 1$ ) in the population before the population becomes extinct ( $w_t = a_t = m_t = 0$ ). Aneuploidy may contribute to evolutionary rescue by either preventing (when  $\Delta_a > 0$ ) or delaying (when  $0 > \Delta_a > \Delta_w$ ) the extinction of the population before mutant cells appear and fixate.

To estimate the rescue probability  $p_{\text{rescue}}$ , we assume independence between clonal lineages starting from an initial population of  $N$  wildtype cells (we check the effect of density-dependent growth on our results below). Thus, the rescue probability is given by

$$p_{\text{rescue}} = 1 - (1 - p_w)^N \tag{14a}$$

$$\approx 1 - e^{-Np_w}, \tag{14b}$$

where the approximation  $(1 - p_w) \approx e^{-p_w}$  assumes that  $p_w$  (but not  $Np_w$ ) is small.

Applying the approximations for the survival probability  $p_w$  from eqs. (4), (10) and (13) in eq. (14b) and substituting  $\Delta_k = \lambda_k - \mu_k$ , we find that the rescue probability can be approximated by

$$\begin{aligned}
p_{\text{rescue}} &\approx \begin{cases} 1 - \exp \left[ \frac{N}{\Delta_w - u - v} \left( v \frac{\Delta_m}{\lambda_m} + \frac{u(\Delta_a - v)}{2\lambda_a} + u \sqrt{\frac{v\Delta_m}{\lambda_a \lambda_m}} \right) \right], & 4\lambda_a v p_m > (\Delta_a - v)^2, \\ 1 - \exp \left[ \frac{v\Delta_m N}{\lambda_m \Delta_w} \left( 1 - \frac{u}{\Delta_a} \right) \right], & \Delta_a < 0 \quad \text{and} \quad 4\lambda_a v p_m < (\Delta_a - v)^2, \\ 1 - \exp \left[ \frac{N}{\Delta_w} \left( \frac{u\Delta_a}{\lambda_a} + \frac{uv\Delta_m}{\lambda_m \Delta_a} + \frac{v\Delta_m}{\lambda_m} \right) \right], & \Delta_a > 0 \quad \text{and} \quad 4\lambda_a v p_m < (\Delta_a - v)^2. \end{cases}
\end{aligned} \tag{15}$$

We validate these approximations by comparing them to results of stochastic evolutionary simulations. We find that the approximations work very well (Figures 2 to 5).



**Density-dependent growth.** In our analysis we used branching processes, which assume that growth (division and death) are density-independent. However, growth may be limited by resources (oxygen, nutrients, etc.) and therefore depend on cell density. We therefore performed stochastic simulations of a logistic growth model with carrying capacity  $K$  (Methods). We find that our approximations agree with results of simulations with density-dependent growth for biologically relevant parameter values (Figure 5).

**Standing vs. de-novo genetic variation** In the above we assumed that upon beginning of drug therapy, the initial tumor consisted entirely of wildtype cells. However, aneuploid cells are likely generated even before onset of treatment at some rate  $\tilde{u} \leq u$  (because the treatment itself may promote generation of aneuploid cells REF), which are likely to have a deleterious effect (REF). But if the number of cells in the tumor  $N$  is large, as expected if drug treatment is applied, there may already be a fraction  $f = \tilde{u}/s$  of aneuploid cells in the population, where  $s$  is the cost of aneuploidy (REF).

In this scenario, the probability of evolutionary rescue by cells with aneuploidy from the initial population is

$$p_{sgv} = 1 - (1 - p_a)^{fN} \approx 1 - e^{-fNp_a}.$$

The total probability of evolutionary rescue is given by

$$\begin{aligned} p_{rescue} &= p_{sgv} + (1 - p_{sgv}) p_{de-novo} \\ &= 1 - \exp(-[(1 - f)p_w + fp_a]N). \end{aligned} \quad (16)$$

The fraction of cases in which the population is rescued by pre-existing aneuploid cells (i.e., standing genetic variation) is given by  $F(f) = \frac{p_{sgv}}{p_{total}}$  (Figure 6).

## Effect of aneuploidy on evolutionary rescue

To determine the extent to which aneuploidy may affect evolutionary rescue, we define  $H$  to be the ratio of the rescue probability with aneuploidy ( $u > 0$ ) and the rescue probability without aneuploidy ( $u = 0$ ),

$$H = \frac{p_{rescue}(u > 0)}{p_{rescue}(u = 0)}. \quad (17)$$

Plugging in our approximations from eq. (14a), we have

$$H = \begin{cases} \frac{1 - \exp\left[\frac{N}{\Delta_w - u - v} \left(v \frac{\Delta_m}{\lambda_m} + \frac{u(\Delta_a - v)}{2\lambda_a} + u \sqrt{\frac{v\Delta_m}{\lambda_a \lambda_m}}\right)\right]}{1 - \exp\left[\frac{vN\Delta_m}{(\Delta_w - v)\lambda_m}\right]}, & 4\lambda_a v p_m > (\Delta_a - v)^2, \\ \frac{1 - \exp\left[\frac{v\Delta_m N}{\lambda_m \Delta_w} \left(1 - \frac{u}{\Delta_a}\right)\right]}{1 - \exp\left(\frac{v\Delta_m N}{\lambda_m \Delta_w}\right)}, & \Delta_a < 0 \quad \text{and} \quad 4\lambda_a v p_m < (\Delta_a - v)^2, \\ \frac{1 - \exp\left[\frac{N}{\Delta_w} \left(\frac{u\Delta_a}{\lambda_a} + \frac{uv\Delta_m}{\lambda_m \Delta_a} + \frac{v\Delta_m}{\lambda_m}\right)\right]}{1 - \exp\left[\frac{v\Delta_m N}{\lambda_m \Delta_w}\right]}, & \Delta_a > 0 \quad \text{and} \quad 4\lambda_a v p_m < (\Delta_a - v)^2. \end{cases} \quad (18)$$

We find that the rescue ratio increase with the aneuploidy growth rate  $\Delta_a$ , because the better aneuploid cells are in growth, the better they are at rescuing the population (when they provide partial resistance) or delaying the extinction of the population (when they provide tolerance). However, the rescue decreases with the wildtype growth rate  $\Delta_w$ , because the better the wildtype is at growth, the less is depends on aneuploidy for rescue or delay, and the more likely it is to directly produce mutant cells, rather than relying on aneuploid cells for producing mutant cells (Figure 7). The effect of the initial tumor size  $N$  is the similar to that of the wildtype growth rate. Importantly, in large tumors, the ratio converges to unity, that is, aneuploidy does not affect the probability for evolutionary rescue.

## Evolutionary rescue time

Even evolutionary rescue occurs, it may take a long time; therefore, it is crucial to estimate the mean waiting time for rescue and the effect aneuploidy may have on it. We therefore calculate the mean time for the appearance of the first mutant that rescues the cell population. This can occur either through the evolutionary trajectory *wildtype*  $\rightarrow$  *mutant* or through the trajectory *wildtype*  $\rightarrow$  *aneuploid*  $\rightarrow$  *mutant*. We start with the former.

Assuming no aneuploidy ( $u = 0$ ), we define  $T_1$  to be the time at which the first mutant cell appears that will avoid extinction and will therefore rescue the population. Note that if extinction occurs, that is  $m_\infty = 0$ , then it is implied that  $T_1 = \infty$ , and vice versa if  $T_1 < \infty$  then  $m_\infty > 0$ .

The number of successful mutants generated until time  $t$  can be approximated by an inhomogeneous Poisson process with rate  $R(t) = up_a w_t$ , where  $w_t = Ne^{\Delta_w t}$  is the number of wildtype cells at time  $t$ . Note that

$$\int_0^t R(z) dz = up_a N \frac{\exp[\Delta_w t] - 1}{\Delta_w} \approx up_a N t, \quad (19)$$

by integrating the exponential and because  $\frac{\exp[\Delta_w t] - 1}{\Delta_w} = \frac{1 + \Delta_w t + O(t^2) - 1}{\Delta_w} = t + O(t^2)$ . The probability density function of  $T_1$  is thus  $R(t) \exp\left(-\int_0^t R(z) dz\right)$ . Therefore, the probability density function of  $(T_1 | T_1 < \infty)$  is  $f_1(t) = \frac{R(t) \exp(-\int_0^t R(z) dz)}{p_{\text{rescue}}}$ .

We are interested in the mean conditional time,  $\tau_1 = \mathbb{E}[T_1 | T_1 < \infty]$ , which is given by

$$\tau_1 = \int_0^\infty t f_1(t) dt = \frac{\int_0^\infty t R(t) \exp\left(-\int_0^t R(z) dz\right) dt}{p_{\text{rescue}}} = \frac{\int_0^\infty \exp\left(-\int_0^t R(z) dz\right) dt}{p_{\text{rescue}}} \quad (20)$$

after applying integration by parts. Therefore, plugging eqs. (14b) and (19) in eq. (20),

$$\tau_1 = \frac{\int_0^\infty \exp(-up_a N t) dt}{1 - e^{-N p_w}} \approx (1 + e^{-N p_w}) \int_0^\infty e^{-up_a N t} dt = \frac{1 + e^{-N p_w}}{up_a N}, \quad (21)$$

where we use the approximation  $(1 - e^{-N p_w})^{-1} \approx 1 + e^{-N p_w}$  and performed the integration of the exponent. We plot the expansion (21) in Figure 8 and observe that it is a very good fit for intermediate and large values of the initial wildtype population size.

When  $Nu \gg 1$  the aneuploid population can be assumed to be deterministic and approximated by the solution to the system of ODEs:

$$a_t = \frac{Nu e^{\Delta_w t}}{\Delta_w - \Delta_a} [1 - e^{(\Delta_w - \Delta_a)t}]. \quad (22)$$

As a result, when  $N \gg 1$  the number of successful mutants created by direct mutation or though aneuploidy are an inhomogeneous Poisson processes with the rates:

$$\begin{aligned} r_1(t) &= v p_m \int_0^t a_\tau d\tau = \frac{uv N p_m}{\Delta_w - \Delta_a} \left( \frac{e^{\Delta_w t} - 1}{\Delta_w} - \frac{e^{\Delta_a t} - 1}{\Delta_a} \right), \\ r_2(t) &= v p_m \int_0^t w_\tau d\tau = v N p_m \frac{e^{\Delta_w t} - 1}{\Delta_w}. \end{aligned}$$

For large initial population sizes we can assume that both rescue mutations produced through direct mutation and aneuploidy are independent and, as a result, they can be merged into a single Poisson process with rate  $(r_1 + r_2)(t)$ . Consequently, the mean time to the appearance of the first rescue mutant is:

$$\tau_2 = \frac{\int_0^\infty e^{-(r_1+r_2)} d\tau}{1 - (1 - p_w)^N} = \frac{\int_0^\infty \exp \left[ -\frac{uvNp_m}{\Delta_w - \Delta_a} \left( \frac{e^{\Delta_w \tau} - 1}{\Delta_w} - \frac{e^{\Delta_a \tau} - 1}{\Delta_a} \right) - vNp_m \frac{e^{\Delta_w \tau} - 1}{\Delta_w} \right] d\tau}{1 - (1 - p_w)^N}, \quad (23)$$

which we plot in Figure 9 as a function of the initial population size.

We wish to obtain a simpler formula for  $\tau_2$  in an analogous way to (21). For this, we make use of the following expansions:

$$\begin{aligned} \frac{e^{\Delta_w \tau} - 1}{\Delta_w} &= \frac{1 + \Delta_w \tau + \frac{\Delta_w^2 \tau^2}{2} + O(\tau^3) - 1}{\Delta_w} = \tau + \frac{\Delta_w}{2} \tau^2 + O(\tau^3). \\ \frac{e^{\Delta_a \tau} - 1}{\Delta_a} &= \frac{1 + \Delta_a \tau + \frac{\Delta_a^2 \tau^2}{2} + O(\tau^3) - 1}{\Delta_a} = \tau + \frac{\Delta_a}{2} \tau^2 + O(\tau^3), \end{aligned}$$

which allow us to write:

$$\frac{e^{\Delta_w \tau} - 1}{\Delta_w} - \frac{e^{\Delta_a \tau} - 1}{\Delta_a} \approx \frac{(\Delta_w - \Delta_a)}{2} \tau^2.$$

As a result, the integrand in (23) can be written as:

$$\begin{aligned} \exp \left[ -\frac{uvNp_m}{\Delta_w - \Delta_a} \left( \frac{e^{\Delta_w \tau} - 1}{\Delta_w} - \frac{e^{\Delta_a \tau} - 1}{\Delta_a} \right) - vNp_m \frac{e^{\Delta_w \tau} - 1}{\Delta_w} \right] &\approx \exp(-uvNp_m \tau^2 - vNp_m \tau) \\ &= \exp\left(\frac{vNp_m}{2}\right) \exp\left[-\frac{uvNp_m}{2} \left(\tau + \frac{1}{u}\right)\right]. \end{aligned}$$

Consequently, the mean time  $\tau_2$  is obtained to be:

$$\tau_2 \approx [1 + \exp(-Np_w)] \exp\left(\frac{vNp_m}{2u}\right) \frac{\text{erfc}\left(\sqrt{\frac{vNp_m}{2u}}\right)}{\sqrt{\frac{2uvNp_m}{\pi}}}, \quad (24)$$

200 where  $\text{erfc}$  is the complementary error function. We plot the expansion (24) in Figure 9 and observe that it is a very good fit for large values of the initial wildtype population size.

If we select only linear terms in the following expansions:

$$\begin{aligned} \frac{e^{\Delta_w \tau} - 1}{\Delta_w} &= \frac{1 + \Delta_w \tau + O(\tau^2) - 1}{\Delta_w} = \tau + O(\tau^2). \\ \frac{e^{\Delta_a \tau} - 1}{\Delta_a} &= \frac{1 + \Delta_a \tau + O(\tau^2) - 1}{\Delta_a} = \tau + O(\tau^2), \end{aligned}$$

we obtain the first order approximation for  $\tau_2$ :

$$\tau_2 \approx (1 + e^{-Np_w}) \int_0^\infty e^{-uNp_m \tau} d\tau = \frac{(1 + e^{-Np_w})}{uNp_m}, \quad (25)$$

202 which we plot in Figure 9 and observe that it offer as a good a fit to (23) as (24). Additionally,  
 204 we observe that for large initial wildtype populations sizes direct mutation drives evolutionary  
 rescue while aneuploidy plays a role for intermediate sized tumors. This is consistent with the  
 information obtained from Figure ?? where aneuploidy improves the probability of evolutionary  
 206 rescue only for small and intermediate values of  $N$ .

## Contribution of aneuploidy to mean evolutionary rescue time

$$\begin{aligned}
 I = \frac{\tau_2}{\tau_1} &= \frac{\int_0^\infty \exp \left[ -\frac{uvNp_m}{\Delta_w - \Delta_a} \left( \frac{e^{\Delta_w t} - 1}{\Delta_w} - \frac{e^{\Delta_a t} - 1}{\Delta_a} \right) - vNp_m \frac{e^{\Delta_w \tau} - 1}{\Delta_w} \right] d\tau}{\int_0^\infty e^{-uNp_m \frac{e^{\Delta_w \tau} - 1}{\Delta_w}} d\tau} \times \frac{1 - (1 - p_w|_{u=0})^N}{1 - (1 - p_w|_{u>0})^N} \\
 &= \frac{\int_0^\infty \exp \left[ -\frac{uvNp_m}{\Delta_w - \Delta_a} \left( \frac{e^{\Delta_w t} - 1}{\Delta_w} - \frac{e^{\Delta_a t} - 1}{\Delta_a} \right) - vNp_m \frac{e^{\Delta_w \tau} - 1}{\Delta_w} \right] d\tau}{\int_0^\infty e^{-vNp_m \frac{e^{\Delta_w \tau} - 1}{\Delta_w}} d\tau} \frac{1}{H}, \tag{26}
 \end{aligned}$$

where  $H$ , is the ratio of the probability of evolutionary rescue with and without aneuploidy, defined in (17). We plot (26) in Figure 10 as a function of the initial wildtype population for varying values of the Malthusian fitness of aneuploid cells  $\Delta_a$ .

## Discussion

Evolutionary rescue is the process where the population acquires a trait that increases fitness in the new environment such that extinction is averted. Here, we have modeled a tumor—a population of cancer cells—exposed to drug therapy that causes the cell population to decline towards extinction. The cancer cell population can escape extinction either by a mutation that confers resistance, or by first generating aneuploid cells in which the effect of the drug is diminished, and then producing a mutation that confers full resistance (Figure 1).

Using multitype branching processes, we derived the probability of evolutionary rescue of the population of cancer cells under various scenarios for the effect of aneuploidy, including both tolerance and partial resistance to the drug. We obtained both exact and approximate expressions for the probability of evolutionary rescue. As expected, our analytic results in eq. (14a) show that the probability of evolutionary rescue increases with the initial tumor size  $N$ , the wildtype growth rate  $\Delta_w = \lambda_w - \mu_w$ , and the mutation  $v$  and aneuploidy  $u$  rates.

When aneuploid cells are partially resistant to the drug ( $\Delta_w \ll 0 \ll \Delta_a \ll \Delta_m$ ), evolutionary rescue can be approximated by a one-step evolutionary rescue process where aneuploidy itself rescues the population (Figure 2). When aneuploidy only provides tolerance to the drug ( $\Delta_w \ll \Delta_a \ll 0 \ll \Delta_m$ ), it cannot rescue the population. Instead, aneuploidy acts as a *stepping stone* through which the resistant mutant can appear in a more expedient fashion, given that the aneuploid cell population declines slower than the wildtype cell population. In this case, aneuploidy provides two benefits. First, it delays the extinction of the population—providing more time for appearance of the resistance mutations. Second, it increases the population size relative to a wildtype population—providing more cells for generating mutations, i.e., it increases the mutation supply.

We find that aneuploidy can have a significant effect on evolutionary rescue (Figure 7). For example, when aneuploidy cells are “barely-resistant” (they grow at a very low rate,  $\Delta_a = 10^{-3}$ ) the probability of evolutionary rescue is 1000-fold higher with aneuploidy than without it (for parameters previously described in cancer Table 1). Interestingly, aneuploidy is unlikely to contribute to evolutionary rescue in primary tumors, as the number of cells in such tumors ( $N > 10^7$ ) is large enough for the appearance of resistant mutation directly before the extinction of wildtype cells (Figure 7). However, aneuploidy may play a crucial role in evolutionary rescue of secondary tumors, whose size may be below the detection threshold of  $\sim 10^7$  (Bozic et al., 2013). Given the fact that the mean time for such secondary tumors to overcome chemotherapy

can be of the order of 100 days (Figure 9), this can explain the reappearance of cancer even  
244 after initial remission.

We hypothesized that presence of "standing variation"—a subpopulation of aneuploid cancer  
246 cells—at the onset of chemotherapy may facilitate evolutionary rescue by reducing the waiting  
time for the appearance of aneuploid cells. Indeed, we observe that even when a small fraction  
248 of the initial tumor is aneuploid, evolutionary rescue is more likely to occur through this existing  
standing variation, rather than through "de novo" aneuploid cells (Figure 6).

250 We have assumed that cancer cell lineages are independent of each other. However, this may  
not be the case, as cancer cells compete for resources (e.g., blood supply). Nevertheless, we  
252 find that when the carrying capacity is large our approximation for the probability of evolutionary  
rescue agrees with results of stochastic simulations with density-dependent growth  
254 (Figure 5). Future work may focus on scenarios with small carrying capacity by analysing  
density-dependent branching processes.

256 Our model predictions may be tested by experiments (Martin et al., 2013). For example, to  
study the effects of initial tumor size on the probability of evolutionary rescue, a large culture  
258 mass can be propagated from a single cancer cell in permissive conditions and then diluted to  
a range of starting tumor sizes. Afterwards, these tumors may be exposed to anti-cancer drugs  
260 that induces aneuploidy or to saline solution for control. Cell density can then be measured  
and compared to the predictions of our model.

## 262 Acknowledgements

We thank XXX for discussions and comments. This work was supported in part by the Israel Science  
Foundation (ISF 552/19, YR), the US-Israel Binational Science Foundation (BSF 2021276, YR), Min-  
erva Stiftung Center for Lab Evolution (YR), and the Ela Kodesz Institute for Research on Cancer  
Development and Prevention (RS).

## References

- Bakker, B., Schubert, M., Bolhaqueiro, A. C., Kops, G. J., Spierings, D. C. and Foijer, F.  
(2023), 'Predicting cin rates from single-cell whole genome sequencing data using an in silico  
model', *bioRxiv* pp. 2023–02.
- Ben-David, U. and Amon, A. (2020), 'Context is everything: aneuploidy in cancer', *Nature  
Reviews Genetics* **21**(1), 44–62.
- Bozic, I., Reiter, J. G., Allen, B., Antal, T., Chatterjee, K., Shah, P., Moon, Y. S., Yaquibie, A.,  
Kelly, N., Le, D. T. et al. (2013), 'Evolutionary dynamics of cancer in response to targeted  
combination therapy', *elife* **2**, e00747.
- Brauner, A., Fridman, O., Gefen, O. and Balaban, N. Q. (2016), 'Distinguishing between  
resistance, tolerance and persistence to antibiotic treatment', *Nature Reviews Microbiology*  
**14**(5), 320–330.
- Carja, O. and Plotkin, J. B. (2017), 'The evolutionary advantage of heritable phenotypic het-  
erogeneity', *Scientific reports* **7**(1), 1–12.
- Carja, O. and Plotkin, J. B. (2019), 'Evolutionary rescue through partly heritable phenotypic  
variability', *Genetics* **211**(3), 977–988.

- Christine, J. Y., Regan, S., Liu, G., Alemara, S. and Heng, H. H. (2018), ‘Understanding aneuploidy in cancer through the lens of system inheritance, fuzzy inheritance and emergence of new genome systems’, *Molecular cytogenetics* **11**(1), 1–13.
- Cobbold, C. A. and Stana, R. (2020), ‘Should I stay or should I go: partially sedentary populations can outperform fully dispersing populations in response to climate-induced range shifts’, *Bulletin of Mathematical Biology* **82**(2), 1–21.
- Del Monte, U. (2009), ‘Does the cell number 109 still really fit one gram of tumor tissue?’, *Cell cycle* **8**(3), 505–506.
- Gillespie, D. T. (1976), ‘A general method for numerically simulating the stochastic time evolution of coupled chemical reactions’, *Journal of computational physics* **22**(4), 403–434.
- Gillespie, D. T. (1977), ‘Exact stochastic simulation of coupled chemical reactions’, *The journal of physical chemistry* **81**(25), 2340–2361.
- Gillespie, D. T. (2001), ‘Approximate accelerated stochastic simulation of chemically reacting systems’, *The Journal of chemical physics* **115**(4), 1716–1733.
- Harris, T. E. et al. (1963), *The theory of branching processes*, Vol. 6, Springer Berlin.
- Komarova, N. L., Sadovsky, A. V. and Wan, F. Y. (2008), ‘Selective pressures for and against genetic instability in cancer: a time-dependent problem’, *Journal of The Royal Society Interface* **5**(18), 105–121.
- Komarova, N. L., Sengupta, A. and Nowak, M. A. (2003), ‘Mutation–selection networks of cancer initiation: tumor suppressor genes and chromosomal instability’, *Journal of theoretical biology* **223**(4), 433–450.
- Levien, E., Min, J., Kondev, J. and Amir, A. (2021), ‘Non-genetic variability in microbial populations: survival strategy or nuisance?’, *Reports on Progress in Physics* **84**(11), 116601.
- Marrec, L. and Bitbol, A.-F. (2020), ‘Adapt or perish: Evolutionary rescue in a gradually deteriorating environment’, *Genetics* **216**(2), 573–583.
- Martens, E. A., Kostadinov, R., Maley, C. C. and Hallatschek, O. (2011), ‘Spatial structure increases the waiting time for cancer’, *New journal of physics* **13**(11), 115014.
- Martin, G., Aguilée, R., Ramsayer, J., Kaltz, O. and Ronce, O. (2013), ‘The probability of evolutionary rescue: towards a quantitative comparison between theory and evolution experiments’, *Philosophical Transactions of the Royal Society B: Biological Sciences* **368**(1610), 20120088.
- Michor, F., Iwasa, Y., Vogelstein, B., Lengauer, C. and Nowak, M. A. (2005), Can chromosomal instability initiate tumorigenesis?, in ‘Seminars in cancer biology’, Vol. 15, Elsevier, pp. 43–49.
- Nowak, M. A., Komarova, N. L., Sengupta, A., Jallepalli, P. V., Shih, I.-M., Vogelstein, B. and Lengauer, C. (2002), ‘The role of chromosomal instability in tumor initiation’, *Proceedings of the National Academy of Sciences* **99**(25), 16226–16231.
- Nowak, M. A., Michor, F., Komarova, N. L. and Iwasa, Y. (2004), ‘Evolutionary dynamics of tumor suppressor gene inactivation’, *Proceedings of the National Academy of Sciences* **101**(29), 10635–10638.
- Pavelka, N., Rancati, G. and Li, R. (2010), ‘Dr Jekyll and Mr Hyde: role of aneuploidy in cellular adaptation and cancer’, *Current opinion in cell biology* **22**(6), 809–815.

- Rybniakov, S., Weissman, D. B., Hübner, S. and Korol, A. B. (2021), ‘Fitness dependence preserves selection for recombination across diverse mixed mating strategies’, *Journal of Theoretical Biology* **528**, 110849.
- Schukken, K. M. and Fojier, F. (2018), ‘Cin and aneuploidy: different concepts, different consequences’, *Bioessays* **40**(1), 1700147.
- Tanaka, M. M. and Wahl, L. M. (2022), ‘Surviving environmental change: when increasing population size can increase extinction risk’, *Proceedings of the Royal Society B* **289**(1976), 20220439.
- Uecker, H. and Hermisson, J. (2011), ‘On the fixation process of a beneficial mutation in a variable environment’, *Genetics* **188**(4), 915–930.
- Uecker, H. and Hermisson, J. (2016), ‘The role of recombination in evolutionary rescue’, *Genetics* **202**(2), 721–732.
- Uecker, H., Otto, S. P. and Hermisson, J. (2014), ‘Evolutionary rescue in structured populations’, *The American Naturalist* **183**(1), E17–E35.
- Uecker, H., Setter, D. and Hermisson, J. (2015), ‘Adaptive gene introgression after secondary contact’, *Journal of mathematical biology* **70**, 1523–1580.
- Van Rossum, G. and Others (2007), Python Programming Language., in ‘USENIX Annu. Tech. Conf.’.
- Weissman, D. B., Desai, M. M., Fisher, D. S. and Feldman, M. W. (2009), ‘The rate at which asexual populations cross fitness valleys’, *Theoretical population biology* **75**(4), 286–300.
- Weissman, D. B., Feldman, M. W. and Fisher, D. S. (2010), ‘The rate of fitness-valley crossing in sexual populations’, *Genetics* **186**(4), 1389–1410.
- Wilson, B. A., Pennings, P. S. and Petrov, D. A. (2017), ‘Soft selective sweeps in evolutionary rescue’, *Genetics* **205**(4), 1573–1586.
- Zhu, J., Tsai, H.-J., Gordon, M. R. and Li, R. (2018), ‘Cellular stress associated with aneuploidy’, *Developmental cell* **44**(4), 420–431.

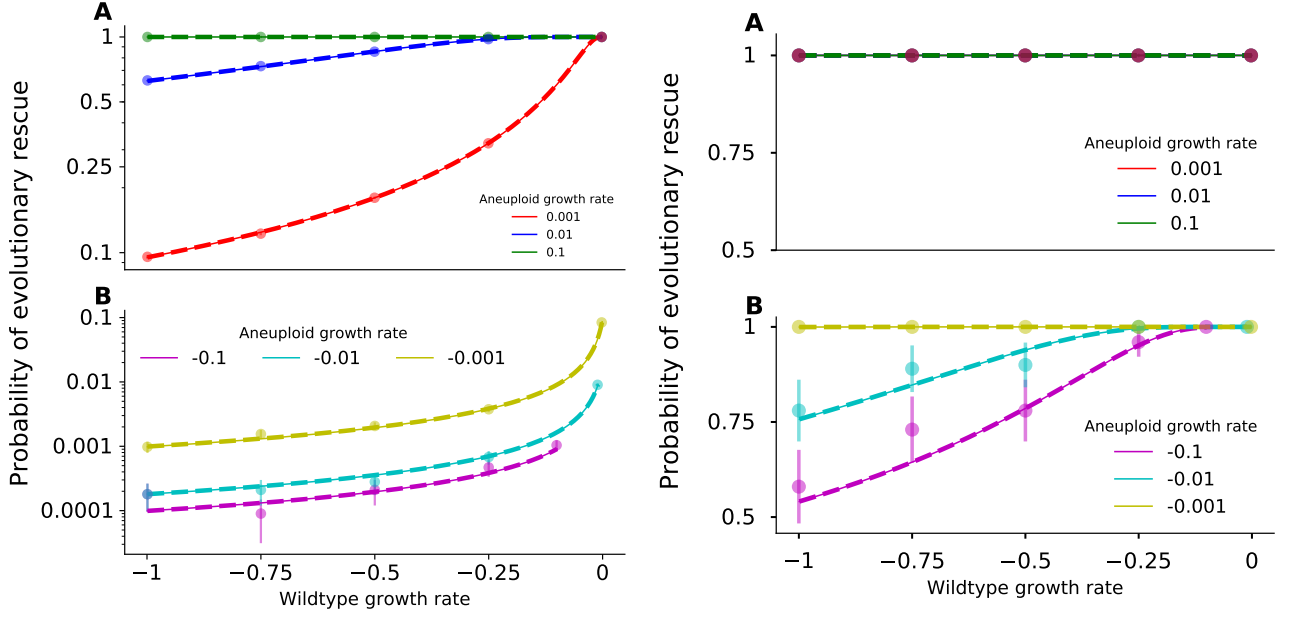


Figure 2: **Evolutionary rescue probability with partially resistant or tolerant aneuploid cells.** Rescue probability is very high when aneuploidy provides partial resistance, in an initially small tumor (**Aleft**,  $N = 10^4$ ) and even more so in an initially large tumor (**Aright**,  $N = 10^8$ ). When aneuploidy provides tolerance (**Bleft**,  $N = 10^4$ ; (**Bright**,  $N = 10^8$ ), the rescue probability is much lower. In both scenarios, rescue probability increase with both the wildtype growth rate (x-axis) and the aneuploidy growth rate (colors). Markers represent simulation results with 95% CI; solid and dashed lines for the exact formula (eq. (3) in eq. (14a)); dashed lines for the approximate formula (eq. (15)), demonstrating that they all agree.

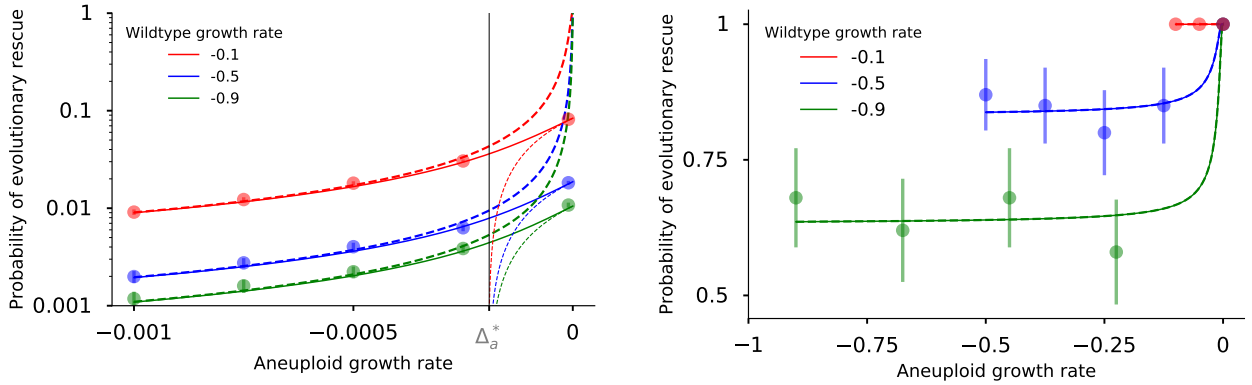


Figure 3: **Evolutionary rescue probability with tolerant or non-growing aneuploid cells.** Rescue probability grows with the aneuploid growth rate  $\Delta_a$  (x-axis), and is much higher in an initially large tumor than in a small one ((A)  $N = 10^4$ ; (B)  $N = 10^8$ ). Markers represent simulation results with 95% CI; solid and dashed lines for the exact formula (eq. (3) in eq. (14a)); dashed lines for the approximate formula (eq. (15)). The approximation agrees with the simulation and exact solution when the initial tumor size is large (panel B). When the tumor size is small (panel A), we switch between the approximation for tolerant and for non-growing aneuploid cells; the switch occurs at  $\Delta_a^* = 2vp_m + v + 2\sqrt{vp_m(vp_m + \mu_a + v)}$ .



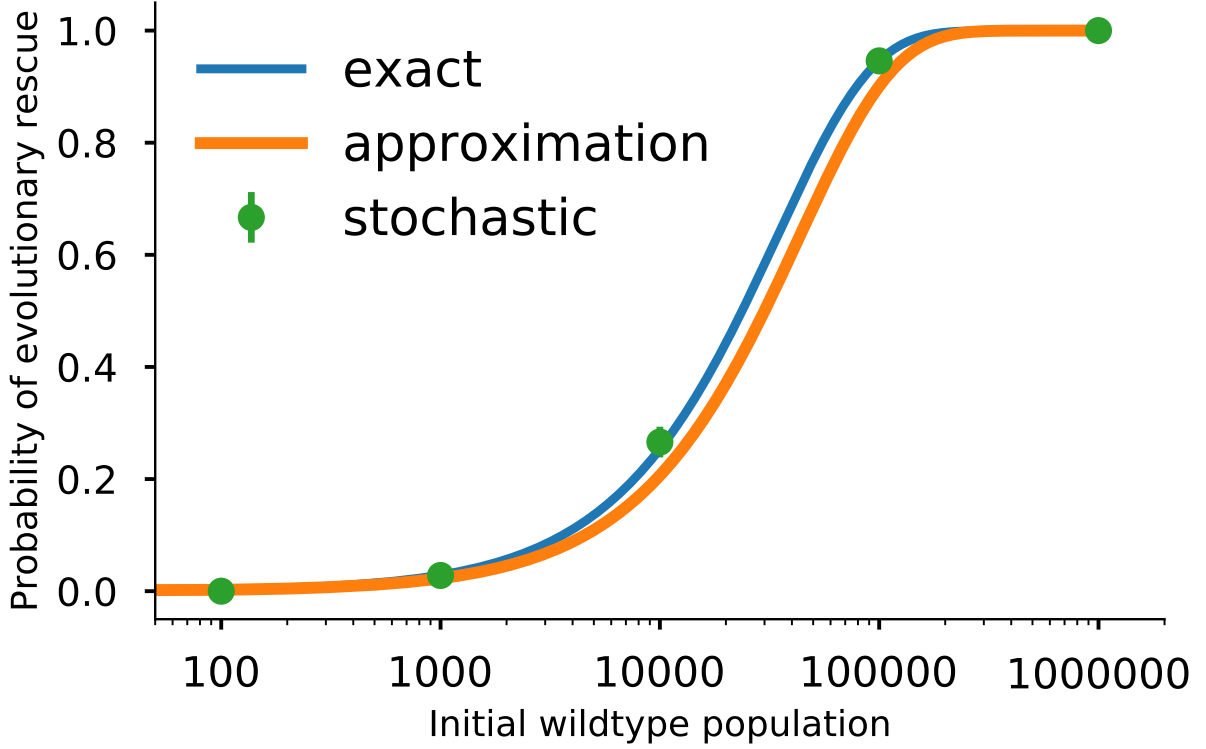


Figure 4: Plot of the probability of evolutionary rescue of a population, consisting of  $N$  wildtype cells, as a function of the initial population size of wildtype cells. The blue line represent the exact result (??) while the orange lines represent the approximation (??). The green dots represent numerical simulations where the error bars represent 95% confidence interval of the form  $p \pm 1.96\sqrt{p(1-p)/n}$  where  $p$  is the mean probability of evolutionary rescue and  $n$  is the number of simulations. The error bars are present but are not visible given the fact that we have used  $n = 10^5$  simulations for each combination of parameters. Here the population initially consists of  $N$  wildtype cells and for the simulations we have chosen the following parameters:  $\lambda_m = 1 + 10^{-1}$ ,  $\mu_w = 1$ ,  $\mu_a = 1$ ,  $\mu_m = 1$ .

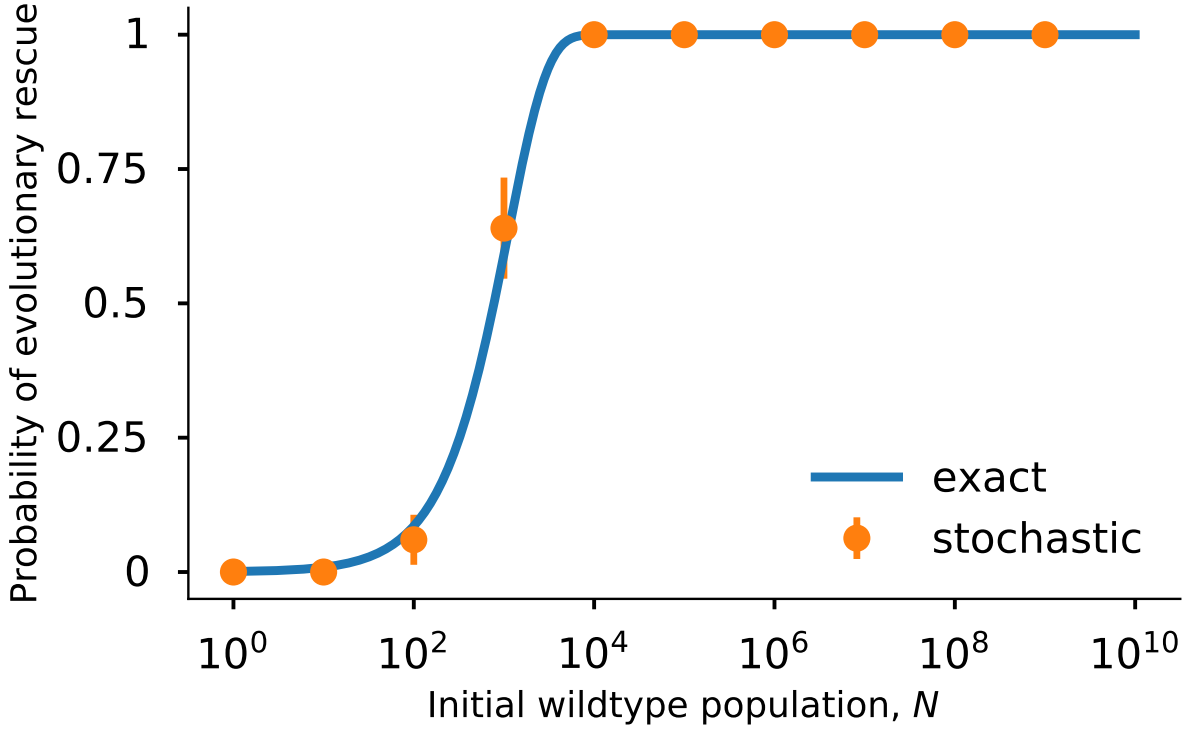


Figure 5: Plot of the probability of evolutionary rescue of a population, consisting of  $N$  wildtype cells, as a function of the initial population size of wildtype cells where maximum population size is constrained by the carrying capacity  $K$ . The blue line represent the exact result (??) while the orange dots represent numerical simulations where the error bars represent 95% confidence interval of the form  $p \pm 1.96\sqrt{p(1-p)/n}$  where  $p$  is the mean probability of evolutionary rescue and  $n$  is the number of simulations. Here the population initially consists of  $N$  wildtype cells and for the simulations we have chosen the following parameters:  $\lambda_w = 1 - 10^{-1}$ ,  $\lambda_a = 1 + 10^{-4}$ ,  $\lambda_m = 1 + 10^{-1}$ ,  $\mu_w = 1$ ,  $\mu_m = 1$ ,  $u = 10^{-2}$ ,  $v = 10^{-7}$ ,  $C_1 = C_2 = 1$ ,  $K = 10^9$ .

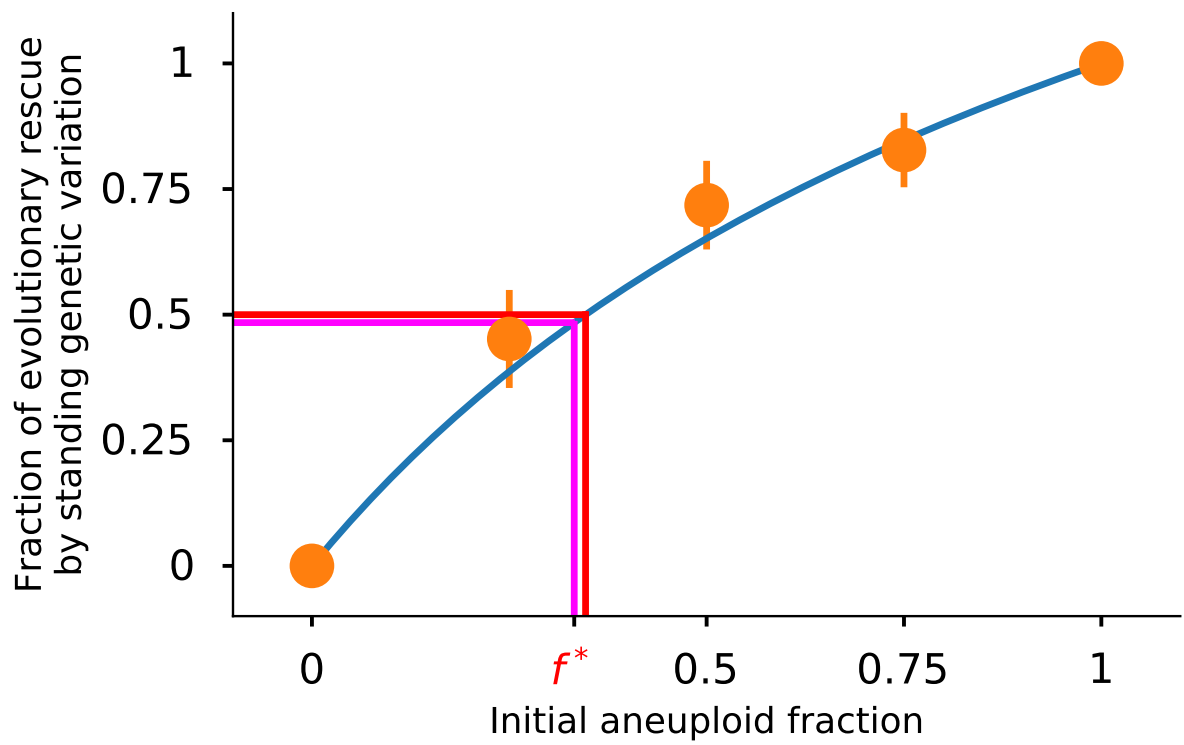


Figure 6: **Effect of standing variation on evolutionary rescue.** In aneuploid cells already exist in the population at the onset of drug therapy as standing genetic variation, then evolutionary rescue is more likely...

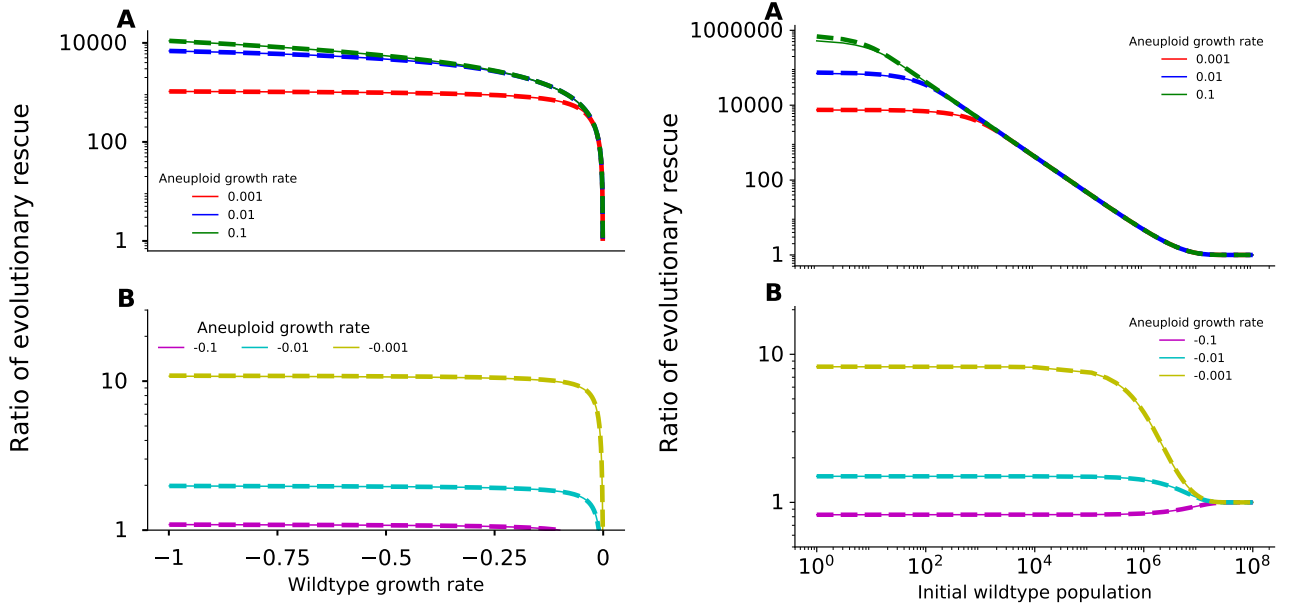


Figure 7: **Effect of aneuploidy on evolutionary rescue.** The ratio of rescue probability with and without aneuploid ( $H$ , eq. (18)) increases with the aneuploid growth rate (colors) and decreases with the wildtype growth rates and initial tumor size (x-axis), except for large tumors where aneuploid cells are tolerant (see right side of panel B-right). **(A-left, A-right)** Aneuploidy provides partial resistance. **(B-left, B-right)** Aneuploidy provides tolerance. Solid and dashed lines apply  $p_{\text{rescue}}$  from the exact formula of (eq. (3) in eq. (14a)); dashed lines apply  $p_{\text{rescue}}$  from the approximate formula (eq. (15)), with good agreement.

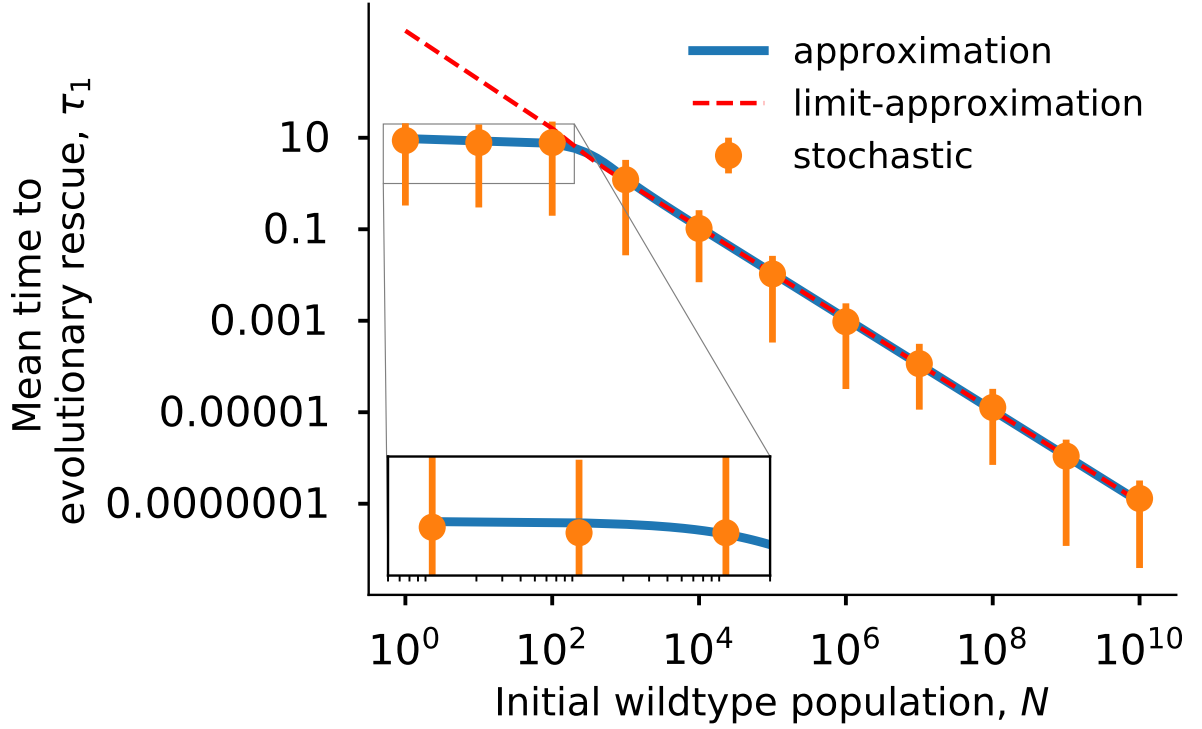


Figure 8: Plot of the mean time until the appearance of a resistance mutation which rescues the population in the case when evolutionary rescue is possible only through mutation but not aneuploidy and mutation. The blue line represents the approximation (20) and the dashed red line represents the first order approximation (21). The orange dots represent the numerical simulations while the error bars represent the interval centered at the mean which containing 95% of the simulated values. Here the population initially consists of  $N$  wildtype cells and for the simulations we have chosen the following parameters:  $\lambda_w = 1 - 10^{-1}$ ,  $\lambda_m = 1 + 10^{-1}$ ,  $\mu_w = 1$ ,  $\mu_m = 1$ ,  $u = 10^{-2}$ ,  $v = 10^{-7}$ .

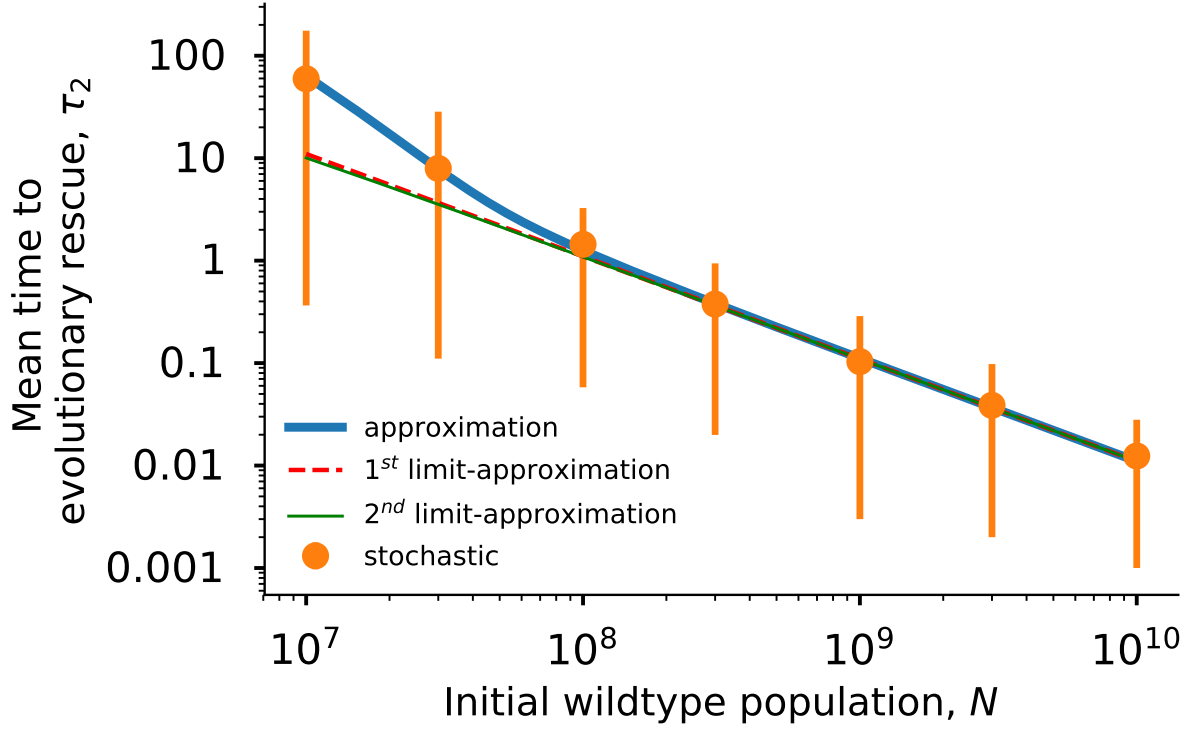


Figure 9: Plot of the mean time until the appearance of a resistance mutation which rescues the population in the case when evolutionary rescue is possible through mutation and aneuploidy. Here the population initially consists of  $N$  wildtype cells and for the simulations we have chosen the following parameters:  $\lambda_w = 1 - 10^{-1}$ ,  $\lambda_a = 1 - 10^{-2}$ ,  $\lambda_m = 1 + 10^{-1}$ ,  $\mu_w = 1$ ,  $\mu_a = 1$ ,  $\mu_m = 1$ ,  $u = 10^{-2}$ ,  $v = 10^{-7}$ . The blue line represents the approximation (23), the dashed red line represents the second order approximation (24) and the green line is first order approximation (25). The orange dots represent the numerical simulations while the error bars represent the interval centered at the mean which containing 95% of the simulated values.

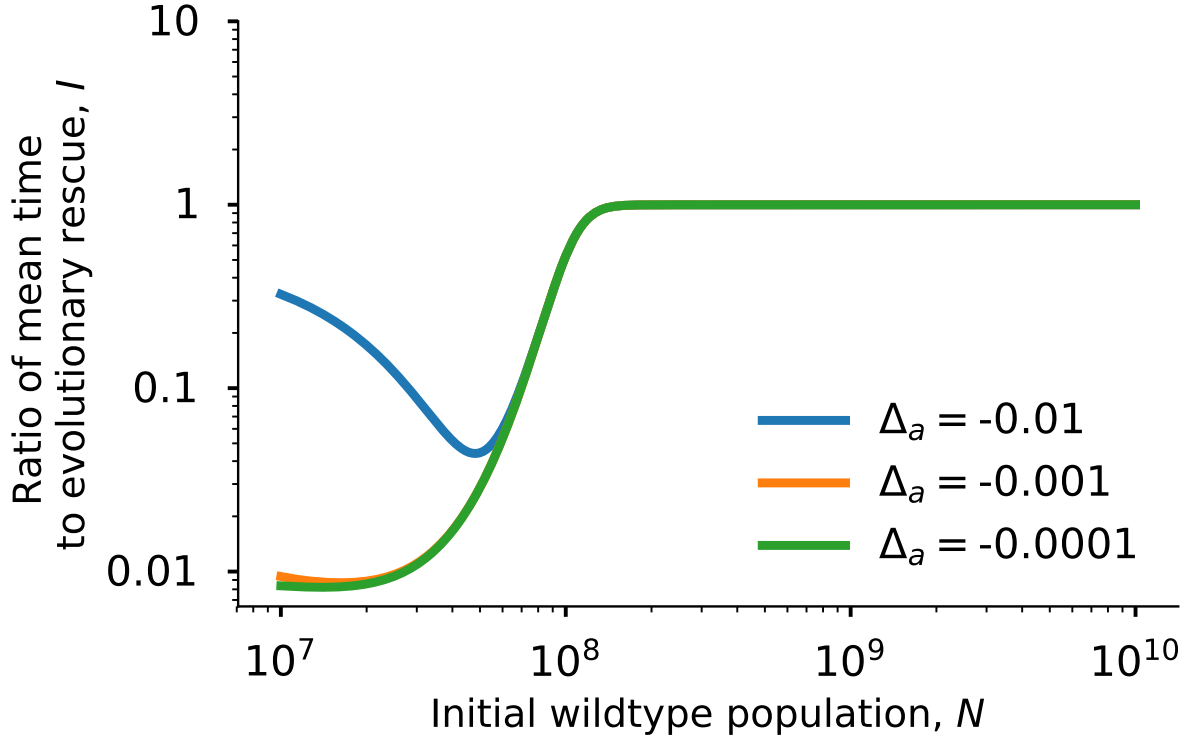


Figure 10: Plot of the ratio of the mean time to evolutionary rescue when aneuploidy can play a role in rescue ( $u > 0$ ) to the mean time where acquisition of aneuploidy is not possible ( $u = 0$ ) as a function of the initial population size of wildtype cells. The continuous lines represent the approximation (26). Here the population initially consists of  $N$  wildtype cells and for the simulations we have chosen the following parameters:  $\lambda_w = 1 - 10^{-1}$ ,  $\lambda_m = 1 + 10^{-1}$ ,  $\mu_w = 1$ ,  $\mu_a = 1$ ,  $\mu_m = 1$ .