A mathematical approach to differentiate spontaneous and induced evolution to drug resistance during cancer treatment

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Abstract

Resistance to chemotherapy is a major impediment to the successful treatment of cancer. Classically, resistance has been thought to arise primarily through random genetic mutations, after which mutated cells expand via Darwinian selection. However, recent experimental evidence suggests that the progression to drug resistance need not occur randomly, but instead may be induced by the therapeutic agent itself. This process of resistance induction can be a result of genetic changes, or can occur through epigenetic alterations that cause otherwise drug-sensitive cancer cells to undergo phenotype switching. This relatively novel notion of resistance further complicates the already challenging task of designing treatment protocols that minimize the risk of developing drug resistance. In an effort to better understand resistance to treatment, we have developed a mathematical modeling framework that incorporates both random and drug-induced resistance. Our model demonstrates that the ability (or lack thereof) of a drug to induce resistance can result in qualitatively different responses to the same drug dose and delivery schedule. The importance of induced resistance in treatment response led us to ask if, in our model, one can determine the resistance induction rate of a drug for a given treatment protocol. Not only could we prove that the induction parameter in our model is theoretically identifiable, we have also proposed a possible *in vitro* protocol which could potentially be used to determine a treatment's propensity to induce resistance.

Keywords. Drug resistance | Chemotherapy | Phenotype | Identifiability | Control theory

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Tumor resistance to chemotherapy and targeted drugs is a major cause of treatment failure. Both molecular and microenvironmental factors have been implicated in the development of drug resistance [34]. As an example of molecular resistance, the upregulation of drug efflux transporters can prevent sufficiently high intracellular drug accumulation, limiting treatment efficacy [31]. Other molecular causes of drug resistance include modification of drug targets, enhanced DNA damage repair mechanisms, dysregulation of apoptotic pathways, and the presence of cancer stem cells [31, 17, 34, 78, 81]. The irregular tumor vasculature which results in inconsistent drug distribution and hypoxia is an example of a microenvironmental factor that impacts drug resistance [76]. Other characteristics of the tumor microenvironment that influence drug resistance include regions of acidity, immune cell infiltration and activation, and the tumor stroma [27, 76, 56, 15, 34, 55].

Research continues to shed light on the multitude of factors that contribute to cancer drug resistance. Mathematical modeling studies in particular have been used to explore both broad and detailed aspects of cancer drug resistance, as reviewed in [43, 7, 25]. The fundamental question of how the presence of drug resistant cells influences tumor dynamics and treatment outcomes has been thoroughly explored in mathematical models under a wide variety of assumptions [14, 37, 39, 47, 58, 40, 23, 24, 70, 16, 45, 60, 63, 4, 22, 33, 44, 52, 65, 3, 32, 80, 13, 26, 29, 46, 49, 51, 57, 59, 77, 18, 68, 1, 9, 10, 20]. Cancer models have also been utilized to assess how various underlying mechanisms contribute to the resistant phenotype [80, 13, 59, 18, 20], and to calculate the probability that drug resistance emerges within a specified time frame, be it before or during cancer treatment [39, 40, 58, 24, 3, 26, 59]. The question of how frequently, and at what dose, a single cancer drug should be administered given the presence of (or risk of developing) resistant cells has also been explored through mathematical modeling [37, 23, 24, 33, 46, 49, 68, 1, 9]. When multiple drugs are available, mathematical models have been used to determine the drug schedule (number of drugs to use, dose, sequence, timing) that best controls tumor progression in spite of drug resistance [39, 47, 70, 16, 60, 63, 4, 51, 10].

Resistance to cancer drugs can be classified as either pre-existing or acquired [34]. Pre-existing (intrinsic) drug resistance describes the case in which a tumor contains a subpopulation of drug resistant cells at the initiation of treatment, making the therapy (eventually) ineffective due to resistant cell selection [34]. As examples, pre-existing BCR-ABL kinase domain mutations confer resistance to the tyrosine kinase inhibitor imatinib in chronic myeloid leukemia patients [66, 36], and pre-existing MEK1 mutations confer resistance to BRAF inhibitors in melanoma patients [8]. Many mathematical models have considered how the presence of pre-existing resistant cells impact cancer progression and treatment [37, 39, 58, 40, 23, 24, 70, 16, 60, 63, 4, 22, 44, 3, 32, 80, 29, 49, 57, 59, 77, 68, 9, 10].

On the other hand, acquired drug resistance broadly describes the case in which drug resistance develops during the course of therapy from a population of cells that were initially drug sensitive [34]. The term "acquired resistance" is really an umbrella term for two distinct phenomena, which complicates the study of acquired resistance. On the one hand there is resistance that is *randomly acquired* during the course of treatment, be it due to random genetic mutations or stochastic non-genetic phenotype switching [65]. This spontaneous form of acquired resistance has been considered in many mathematical models [14, 39, 47, 58, 40, 23, 24, 45, 4, 22, 33, 44, 52, 32, 80, 26, 46, 51, 57, 10]. On the other hand, drug resistance can be

induced (caused) by the drug itself [62, 61, 69, 65, 64].

The question of whether resistance is an induced phenomenon or the result of random events was first famously studied by Luria and Delbrück in the context of bacterial (*Escherichia coli*) resistance to a virus (T1 phage) [53]. In particular, Luria and Delbrück hypothesized that if selective pressures imposed by the presence of the virus *induce* bacterial evolution, then the number of resistant colonies that formed in their plated experiments should be Poisson distributed, and hence have an approximately equal mean and variance. What Luria and Delbrück found instead was that the number of resistant bacteria on each plate varied drastically, with the variance being significantly larger than the mean. As a result, they concluded that the bacterial mutations are random, and not induced by the presence of the virus [53].

In the case of cancer, there is strong evidence that drugs have the ability to induce resistance. Genomic mutations can be caused by cytotoxic cancer chemotherapeutics [73, 72]. For instance, nitrogen mustards can induce base substitutions and chromosomal rearrangements, topoisomerase II inhibitors can induce chromosomal translocations, and antimetabolites can induce double stranded breaks and chromosomal aberrations [73]. Such drug-induced genomic alterations would generally be non-reversible, and a handful of mathematical models have considered this type of drug-induced resistance [29, 49, 68, 1, 20]. Drug resistance can also be induced at the epigenetic level via DNA methylation and histone modification [62, 65]. As an example, the expression of multidrug resistance 1 (MDR1), an ABC-family membrane pump that mediates the active efflux of drug, can be induced during treatment [34, 65]. Resistance developed in this way can occur quite rapidly, and can often be reversed [69, 65, 35].

Despite these known examples of drug-induced resistance, differentiating between drug-selected and drug-induced resistance is nontrivial. What appears to be drug-induced acquired resistance may simply be the rapid selection of a very small number of pre-existing resistant cells, or the selection of cells that spontaneously acquired resistance [45, 65]. In pioneering work by Pisco and colleagues, the relative contribution of resistant cell selection versus drug-induced resistance was assessed in an experimental system involving HL60 leukemic cells treated with the chemotherapeutic agent vincristine [65]. After 1-2 days of treatment, the expression of MDR1 was shown to be predominantly mediated by cell-individual induction of MDR1 expression, and not by the selection of MDR1-expressing cells [65, 64]. In particular, these cancer cells exploit their heritable, non-genetic phenotypic plasticity (by which one genotype can map onto multiple stable phenotypes) to change their gene expression to a more resistant state in response to treatment-related stress [65, 64].

This experimental work demonstrating drug-induced phenotypic switching was accompanied by two phenomenological mathematical models, one probabilistic and one deterministic, that account for the net growth of a sensitive and a resistant population during treatment, and the transition between those compartments [65]. While the parameters in this model were calibrated to experimental data during treatment, the models themselves do not depend on the drug dose and therefore cannot distinguish between the effects of selection versus induction of resistance. Models of a similar nature are also considered in [30, 11]. To our knowledge, the only other mathematical model to account for drug-induced, reversible phenotypic switching is that in [13]. In that work, an individual-based model and an integro-differential equation model are developed to capture the dynamics of reversible, drug-induced phenotypic switching [13]. Based on experimental data in [69], the models in [13] consider rapidly proliferating drug sensitive cells, slowly proliferating drug resistant cells, and rapidly proliferating drug

resistant cells. An advection term (with the speed depending on the drug levels) is used to model drug-induced adaptation of the cell proliferation level, and a diffusion term for both the level of cell proliferation and survival potential (response to drug) is used to model non-genetic phenotype instability. Results of these models are compared to a separate model of drug-independent genetic mutations, where these spontaneous mutations are represented using a symmetric diffusive term that allows the behavior of cells to drift to both more and less resistant phenotypes [13]. On the other hand, herein we develop what, to our knowledge, is the first mathematical model to incorporate two mechanisms of drug resistance: drug-induced phenotypic switching and drug-independent non-reversible genetic mutations. Further, we use a system of three ordinary differential equations in our model, making it more amenable to analysis than the integro-differential equation and individual based models developed in [13].

This manuscript is organized as follows. We begin by introducing a mathematical model to describe the evolution of drug resistance during treatment with a theoretical resistance-inducing (and non-inducing) drug. We use this mathematical model to explore the role that the drug's resistance induction rate has on treatment dynamics. We demonstrate that the induction rate of a theoretical cancer drug could have a nontrivial impact on the qualitative responses to a given treatment strategy, including the tumor composition and the time horizon of tumor control. In our model, for a *phenotype-preserving* drug (i.e. a drug which does not induce resistance), better tumor control is achieved using a constant therapeutic protocol as compared to a pulsed one. On the other hand, in the case of a resistance-inducing drug, pulsed therapy prolongs tumor control longer than does constant therapy due to sensitive/resistant cell competitive inhibition. Once the importance of induced resistance has been established, we demonstrate that all parameters in our mathematical model are identifiable, meaning that it is theoretically possible to determine the rate at which drug resistance is induced for a given treatment protocol. Since this theoretical result does not directly lend itself to an experimental approach for quantifying a drug's ability to induce resistance, we also describe a potential *in vitro* experiment for approximating this ability for constant therapies. Concluding remarks and potential extensions of our analysis are presented at the end of the text.

A Mathematical Model for the Evolution of Drug Resistance

In this section, we introduce a general modeling framework to describe the evolution of drug resistance during treatment. We assume resistance is generated via two distinct cellular processes: stable genetic mutations and phenotypic alterations that are at least in part influenced by treatment. The former correspond to purely random mutations conferring drug resistance (e.g. point mutations or gene amplification), which may occur either prior to or during treatment. Drug-induced resistance is resistance specifically activated by the drug, and as such, depends on the effective dosage encountered by a cell. Such a formulation allows us to distinguish the contributions of both drug-dependent and drug-independent mechanisms, as well as any dependence on pre-existing (i.e. prior to treatment) resistant populations.

General Model

We consider the tumor to be composed of two types of cells: sensitive (S) and resistant (R). Sensitive (or wild-type) cells are fully susceptible to treatment, while treatment affects resistant cells to a lesser degree. As per the above discussion, the drug resistant population can be further categorized by the cell's mechanism of origin as either genetic and hence purely spontaneous (population R_g) or phenotypic, arising spontaneously or possibly induced by the presence of the drug (population R_p). Thus, to analyze the role of both phenomena, we utilize a system of three ordinary differential equations (ODEs) to describe the dynamics between the S, R_g, and R_p subpopulations:

$$\frac{dS}{dt} = r\left(1 - \frac{V}{K}\right)S - (\epsilon_1 + \epsilon_2)S - \alpha u(t)S - du(t)S + \gamma R_p, \tag{1}$$

$$\frac{dR_g}{dt} = r_g\left(1 - \frac{V}{K}\right)R_g + \epsilon_1 S - d_g u(t)R_g, \tag{2}$$

$$\frac{dR_p}{dt} = r_p\left(1 - \frac{V}{K}\right)R_p + \epsilon_2 S + \alpha u(t)S - \gamma R_p - d_p u(t)R_p. \tag{3}$$

Here V denotes the entire tumor population, i.e.

$$V := S + R_g + R_p. \tag{4}$$

All parameters are non-negative. In the absence of treatment, we assume that the tumor grows logistically, with each population contributing equally to competitive inhibition. Phenotypes S, R_g, and R_p may each possess individual intrinsic growth rates, but we make the assumption in the remainder of the work that $0 < r_g, r_p < r$; otherwise treatment acts to select a both faster dividing and more resistant cellular population, and it is clearly optimal to never apply treatment when analyzing a clinically realistic metric. Furthermore, there is experimental evidence to support this assumption [48, 67, 6].

Transitions are allowed to occur between the three populations. As compartment R_g represents drug-resistant cells arising via spontaneous genetic mutations, the transition rate $\epsilon_1 S$ is independent of treatment, where ϵ_1 is generally considered small [50]. Note however that recent experimental evidence into error prone DNA polymerases suggests that cancer cells may have increased mutation rates due to the over-expression of such polymerases [41, 54, 42]. For example, in [41], mutation rates due to such polymerases are characterized by probabilities as high as 7.5×10^{-1} per base substitution, and it is known that many point mutations in cancer arise from these DNA polymerases [42]. This is indeed an interesting phenomenon which could be studied using our model, but for this work we adopt the classical notion that random point mutations leading to drug resistance are rare. Furthermore, since the rate of spontaneous back mutations would be substantially smaller (on the order of ϵ_1^2, correlating mutation rates with probabilities, and assuming independence), we do not consider mutations from the spontaneous resistance compartment back to wild-type ($R_g \not\to S$).

Cancer cells exhibiting phenotypic (i.e. non-genetic) resistance are represented by the R_p compartment. As detailed above, there are non-genetic mechanisms which cause resistance to be induced more rapidly on the phenotypic scale. For example, there is experimental evidence that the over-expression of the P-glycoprotein gene, a well-known mediator of multi-drug resistance,

may be induced by the application of chemotherapy [34, 74]. Such acquired resistance has been observed to occur on time scales inconsistent with known genetic mutation rates, and thus must be due to a phenotype-switching phenomena [65]. The transition to phenotypic resistance can be described with a net term of the form $\epsilon_2 S + \alpha u(t) S$. Mathematically, the drug-induced term $\alpha u(t) S$, where $u(t)$ is the effective applied drug dosage at time t, describes the effect of treatment on promoting the resistant phenotype. Note that we assume the simplest form of induced resistance, with a dose-dependent per-capita induced transition rate. Phenotype instability is considered in the $\epsilon_2 S$ term, which permits a phenotype-switching phenomena even in the absence of treatment. This is consistent (and indeed necessary) to understand the experimental results in [65], where a stable distribution of MDR1 expressions is observed even in the absence of treatment. We also allow back transitions from the R_p compartment, with rate γR_p, since phenotype-switching is often reversible, with the reverse transition (sensitive to resistant) occurring at a non-negligible rate [65].

To model the effect of treatment, we assume the log-kill hypothesis [75], where a given dose of chemotherapy eliminates the same fraction of tumor cells, regardless of tumor size. We allow for each cellular compartment to have a different drug-induced death rate (d, d_g, d_p); however, to accurately describe resistance we assume that $0 \leq d_g, d_p < d$.

Finally, we note that the effective drug concentration $u(t)$ can be thought of as a control input. For simplicity, in this work we assume that it is directly proportional to the applied drug concentration. However, pharmacodynamic/pharmacokinetic considerations could be incorporated to more accurately describe the uptake/evolution of the drug *in vivo* or *in vitro*; for example, as in [2, 79, 21].

Two Population Reduction

In this work, we are primarily interested in the role of induced phenotypic alterations in treatment dynamics and outcome, compared with canonical random genetic changes. Thus, we consider a simplification of the system (1)-(3) highlighting the comparison between these mechanisms. Specifically, we assume that back mutations do not occur ($\gamma = 0$) and that both resistant subpopulations divide at the same rate ($r_r := r_g = r_p$). Drug-independent transition rates are taken as identical ($\epsilon := \epsilon_1 = \epsilon_2$). Furthermore, the drug is assumed to be completely ineffective against both R_g and R_p, so that $d_g = d_p = 0$. Under these assumptions, and defining the total resistant population as

$$R = R_g + R_p, \tag{5}$$

allows system (1)-(3) to be reduced to a two population model:

$$\frac{dS}{dt} = r\left(1 - \frac{S+R}{K}\right) S - (\epsilon + \alpha u(t))S - du(t)S, \tag{6}$$

$$\frac{dR}{dt} = r_r\left(1 - \frac{S+R}{K}\right) R + (\epsilon + \alpha u(t))S. \tag{7}$$

For the remainder of the manuscript, we focus on system (6)-(7).

To understand the above system of drug resistance evolution, we reduce the number of parameters via non-dimensionalization. Rescaling S and R by their (joint) carrying capacity

K, and time t by the sensitive cell growth rate r,

$$\begin{aligned} \tilde{S}(\tau) &= \frac{1}{K} S\left(\frac{1}{r}\tau\right), \\ \tilde{R}(\tau) &= \frac{1}{K} R\left(\frac{1}{r}\tau\right), \end{aligned} \tag{8}$$

system (6)-(7) can be written in the form

$$\frac{dS}{dt} = (1 - (S + R))\, S - (\epsilon + \alpha u(t))S - du(t)S, \tag{9}$$

$$\frac{dR}{dt} = p_r\,(1 - (S + R))\, R + (\epsilon + \alpha u(t))S. \tag{10}$$

For convenience, we have relabeled S, R, and t to coincide with the non-dimensionalization, so that the parameters ϵ, α, and d must be scaled accordingly (by $1/r$). As r_r was assumed to satisfy $0 \leq r_r < r$, the relative resistant population growth rate p_r satisfies $0 \leq p_r < 1$.

One can show (see Supporting Information (SI) Section A) that asymptotically, under any treatment regime $u(t) \geq 0$, the entire population will become resistant:

$$\begin{pmatrix} S(t) \\ R(t) \end{pmatrix} \xrightarrow{t\to\infty} \begin{pmatrix} 0 \\ 1 \end{pmatrix}. \tag{11}$$

However, tumor control is still possible, where one can combine therapeutic efficacy and clonal competition to influence transient dynamics and possibly prolong patient life. Indeed, the modality of adaptive therapy has shown promise in utilizing real-time patient data to inform therapeutic modulation aimed at increasing quality of life and survival times [28]. This work will focus on such dynamics and controls.

Effect of Induction on Treatment Efficacy

We investigate the role of a drug's induction capability (parameter α in (9)-(10)) on treatment dynamics. Specifically, the value of α may have a substantial impact on the relative success of two standard therapy protocols: constant dosage and periodic pulsing.

Treatment Protocol

To quantify the effects of induced resistance, a treatment protocol must be specified. We adopt a clinical perspective over the course of the disease, which is summarized in Figure 1. We assume that the disease is initiated by a small number of wild-type cells:

$$S(0) = S_0, \quad R(0) = 0, \tag{12}$$

where $0 < S_0 < 1$. The tumor then progresses untreated until a specific volume V_d is detected (or, for hematologic tumors, via appropriate blood markers), which utilizing existing nuclear imaging techniques corresponds to a tumor with diameter on the order of 10 mm [19]. The time

to reach V_d is denoted by t_d, which in general depends on all parameters appearing in (9)-(10). Note that, assuming $\epsilon > 0$, a non-zero resistant population will exist at the onset of treatment. Therapy, represented through $u(t)$, is then applied, until the tumor reaches a critical size V_c, which we equate with treatment failure. Since the $(S, R) = (0, 1)$ state is globally asymptotically stable in the first quadrant, $V_c < 1$ is guaranteed to be obtained in finite time. Time until failure, t_c, is then a measure of efficacy of the applied $u(t)$.

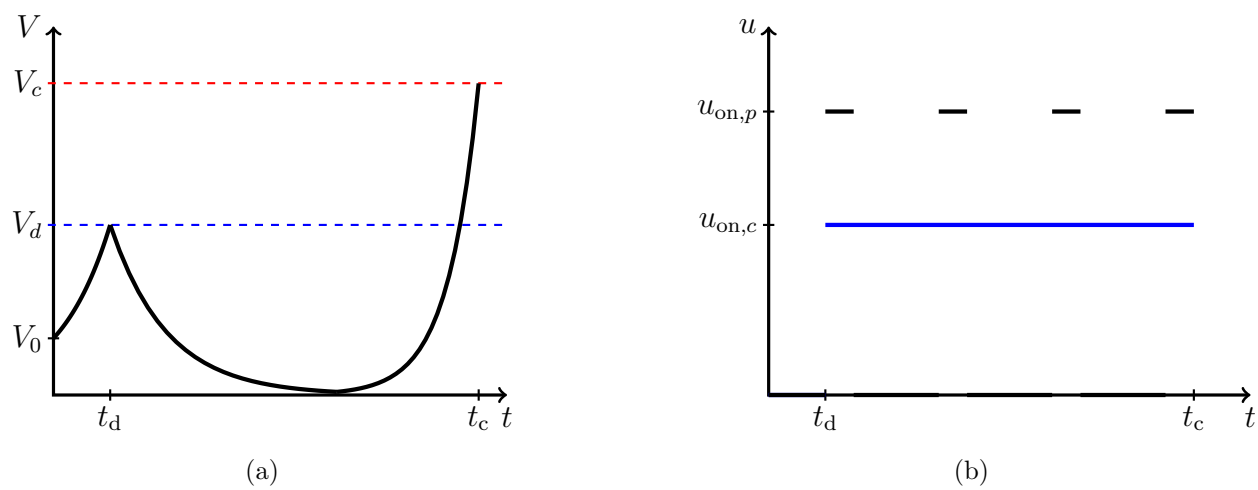


Figure 1: Schematic of tumor dynamics under two treatment regimes. (a) Tumor volume V in response to treatment initiated at time t_d. Cancer population arises from a small sensitive population at time $t = 0$, upon which the tumor grows to detection at volume V_d. Treatment is begun at t_d, and continues until the tumor reaches a critical size V_c (at a corresponding time t_c), where treatment is considered to have failed. (b) Illustrative constant and pulsed treatments, both initiated at $t = t_d$.

Although a diverse set of inputs $u(t)$ may be theoretically applied, presently we consider only strategies as illustrated in Figure 1(b). The blue curve in Figure 1(b) corresponds to a constant effective dosage $u_c(t)$ initiated at t_d (administered approximately utilizing continuous infusion pumps and/or slow-release capsules), while the black curve represents a corresponding pulsed strategy $u_p(t)$, with fixed treatment windows and holidays. In general, we may allow for different magnitudes, $u_{\text{on},c}$ and $u_{\text{on},p}$, for constant and pulsed therapies respectively; for example to relate the total dosage applied per treatment cycle (AUC in clinical literature). However for simplicity we assume the same magnitude in the subsequent section (although see SI Section B for a normalized comparison). While these represent idealized therapies, such $u(t)$ may form an accurate approximation to *in vitro* and/or *in vivo* kinetics. Note that the response $V(t)$ illustrated in Figure 1(a) will not be identical (or even qualitatively similar) for both presented strategies, as will be demonstrated numerically.

Constant vs. Pulsed Therapy Comparison

To qualitatively demonstrate the role induced resistance plays in designing schedules for therapy, we consider two drugs with the same cytotoxic potential (i.e. same drug-induced death rate

Parameter	Biological Interpretation	Value (dimensionless)
S_0	Initial sensitive population	0.01
R_0	Initial resistant population	0
V_d	Detectable tumor volume	0.1
V_c	Tumor volume defining treatment failure	0.9
ϵ	Background mutation rate	10^{-6}
d	Cytotoxicity of sensitive cells	1
p_r	Resistant growth fraction	0.2
u_{on}	Treatment magnitude, constant dose	1.5
Δt_{on}	Pulsed treatment window	1
Δt_{off}	Pulsed holiday length	3

Table 1: Parameters utilized in Figure 2

d), each possessing a distinct level of resistance induction (parameter α). A fundamental question is then whether there exist qualitative distinctions between treatment responses for each chemotherapy. More specifically, how does the survival time compare when scheduling is altered between constant therapy and pulsing? Does the optimal strategy (in this case, optimal across only two schedulings) change depending on the extent to which the drug induces resistance?

We fix two values of the induction parameter α:

$$\alpha_s = 0, \qquad \alpha_i = 10^{-2}.$$

Recall that we are studying the non-dimensional model (9)-(10), so no units are specified. Parameter $\alpha = 0$ corresponds to no therapy-induced resistance (henceforth denoted as *phenotype-preserving*), and therefore considering this case permits a comparison between the classical notion of random evolution towards resistance ($\alpha = 0$) and drug-induced resistance ($\alpha > 0$). For the remainder of the section, parameters are fixed as in Table 1. Importantly, all parameters *excluding* α are identical for each drug, enabling an unbiased comparison. Treatment magnitudes $u_{\text{on},c}$ and $u_{\text{on},p}$ are selected to be equal: $u_{\text{on},c} = u_{\text{on},p} = u_{\text{on}}$.

Note that selecting parameter $V_d = 0.1$ implies that the carrying capacity has a diameter of 100 mm, as V_d corresponds to a detectable diameter of 10 mm. Assuming each cancer cell has volume 10^{-6} mm^3, tumors in our model can grow to a carrying capacity of approximately 12.4 cm in diameter, which is in qualitative agreement with the parameters estimated in [12] ($\approx$ 12.42 cm, assuming a tumor spheroid).

By examining Figures 2(a)-2(b), we clearly observe an improved response to constant therapy when using a phenotype-preserving drug, with a treatment success time t_c nearly seven times as long compared to the resistance-inducing therapy. It can be seen that the tumor composition at treatment conclusion is quite different for each therapy (not shown for this simulation, but see a comparable result in Figures S1(b) and S1(d)), and it appears that the pulsed therapy was not sufficiently strong to hamper the rapid growth of the sensitive population. Indeed, treatment failed quickly due to insufficient treatment intensity in this case, as the population remains almost entirely sensitive. Thus, for this patient under these specific treatments, assuming drug resistance only arises via random stochastic mutations, constant therapy

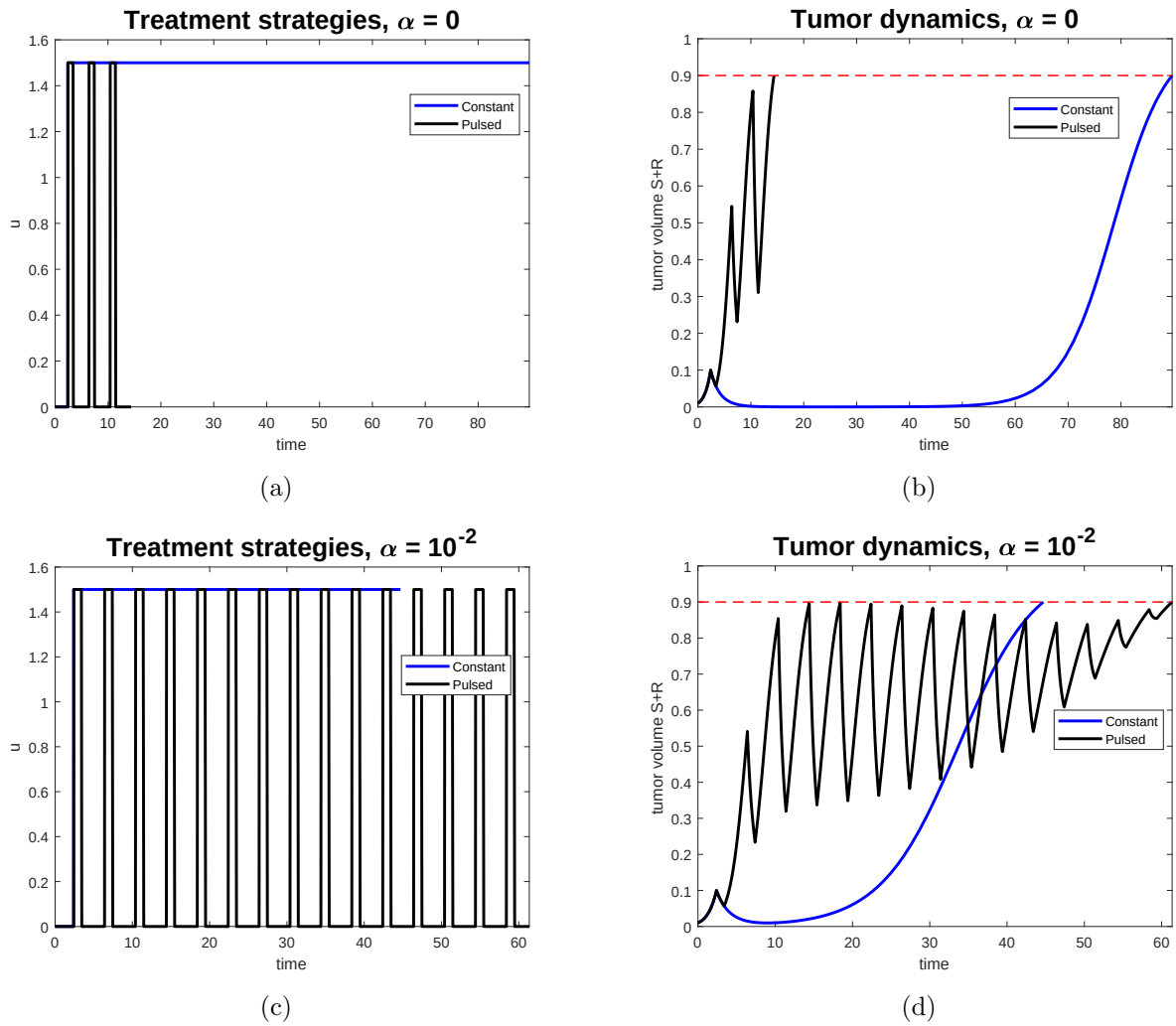


Figure 2: Comparison of treatment efficacy for *phenotype-preserving* ($\alpha = 0$) and resistance-inducing ($\alpha = 10^{-2}$) drugs. Left column indicates treatment strategy, while right indicates corresponding tumor volume response. Note that the dashed red line in the right column indicates the tumor volume representing treatment failure, V_c. (a) Constant and pulsed therapies after tumor detection for $\alpha = 0$. (b) Responses corresponding to treatment regimens in (a). (c) Constant and pulsed therapies after tumor detection for $\alpha = 10^{-2}$. (d) Responses corresponding to treatment regimens in (c).

would be preferred. One might argue that a pulsed, equal-magnitude treatment is worse when $\alpha = 0$ simply because less total drug (i.e. AUC) is applied. However, we see that even in this case, intermediate dosages may be optimal (see Figure 4(a) below). Thus, it is not the larger total drug *per se* that is responsible for the superiority of the constant protocol in this case, a point that is reinforced by the fact that the results remain qualitatively unchanged even if the total drug is controlled for (see SI Section B).

Compare this to Figures 2(c)-2(d), which considers the same patient and cytotoxicity, but for a highly inductive drug. The results are strikingly different, and suggest that pulsed therapy

is now not worse, and in fact substantially improves patient response ($t_d \approx 61$ for pulsed, compared to $t_d \approx 45$ for constant). In this case, both tumors are now primarily resistant (see Figures S2(b) and S2(d)), but the pulsed therapy allows prolonged tumor control via sensitive/resistant competitive inhibition. Furthermore, treatment holidays reduce the overall flux into resistance, since the application of the drug itself promotes this evolution. The total amount of drug (AUC) is also smaller for the pulsed therapy (22.5 compared to ≈ 64), so that the pulsed therapy is both more efficient in terms of treatment efficacy, and less toxic to the patient, as side effects are typically correlated with the total administered dose, which is proportional to the AUC.

For these specific parameter values, differences between the constant and pulsed therapy for the inductive drug are not as extensive as in the phenotype-preserving case. However, recall that time has been non-dimensionalized, and hence scale may indeed be clinically relevant. Such differences can be further amplified, and in fact since exact parameters are difficult or even (currently) impossible to measure, qualitative distinctions are paramount. Thus, at this stage, the ranking of therapies, rather than their precise quantitative efficacy, should act as the more important clinical criterion.

From these results, we observe a qualitative difference in the treatment strategy to apply, based entirely on the value of α, the degree to which the drug itself induces resistance. Thus, in administering chemotherapy, the resistance-promotion rate α of the treatment is a clinically significant parameter. In the next section, we use our model and its output to propose *in vitro* methods for experimentally measuring a drug's α parameter.

Identifying the Rate of Induced Drug Resistance

The effect of treatment on the evolution of phenotypic resistance may have a significant impact on the efficacy of conventional therapies. Thus, it is essential to understand the value of the induction parameter α prior to administering therapy. In this section, we discuss both the theoretical possibility and practical feasibility of determining α from different input strategies $u(t)$.

Theoretical Identifiability

We first show that all parameters in system (9)-(10) are identifiable utilizing a relatively small set of controls $u(t)$ via classical methods from control theory. We provide a self-contained discussion; for a thorough review of theory and methods, see the recent article [71] and the references therein.

Assuming that time and tumor volume are the only clinically observable outputs (i.e. that one cannot readily determine sensitive and resistant proportions in a given population), we measure $V(t)$ and its derivatives at time $t = t_d$ for different controls $u(t)$. For simplicity, we assume that $t_d = 0$, so that treatment is initiated with a purely wild-type (sensitive) population. Although the results remain valid if $t_d > 0$, this assumption will simplify the subsequent computations. For a discussion of the practical feasibility of such methods, see the following section.

Specifically, consider the system (9)-(10) with initial conditions (12). Measuring $V(t) = S(t) + R(t)$ at time $t = 0$ implies that we can identify S_0:

$$V(0) = S(0) + R(0) = S_0 =: Y_0,$$

where we adopt the notation $Y_i, i \geq 0$ for measurable quantities. Similarly, define the following for the given input controls:

$$\begin{aligned}
Y_1 &:= V'(0), \quad u(t) \equiv 0, \\
Y_2 &:= V'(0), \quad u(t) \equiv 1, \\
Y_3 &:= V''(0), \quad u(t) \equiv 0, \\
Y_4 &:= V''(0), \quad u(t) \equiv 1, \\
Y_5 &:= V''(0), \quad u(t) \equiv 2, \\
Y_6 &:= V'''(0), \quad u(t) \equiv 0, \\
Y_7 &:= V'''(0), \quad u(t) = t.
\end{aligned} \tag{13}$$

All quantities $Y_i, i = 0, 1, \ldots, 7$ are measurable, as each requires only knowledge of $V(t)$ in a small positive neighborhood of $t = 0$. Note that the set of controls $u(t)$ is relatively simple, with Y_7 exclusively determined via a non-constant input.

Each measurable Y_i may also be written in terms of a subset of the parameters d, ϵ, p_r, and α, as all derivatives can be calculated in terms of the right-hand sides of equations (9)-(10). For more details, see SI Section C. Equating the expressions yields a system of equations for the model parameter, which we are able to solve. Carrying out these computations yields the following solution:

$$d = -\frac{Y_2 - Y_1}{Y_0}, \tag{14}$$

$$\epsilon = \frac{Y_7 - Y_6 + \frac{1}{2}Y_5 - 2Y_4 - \frac{3}{2}Y_3 + dY_0(1 - Y_0)}{dY_0}, \tag{15}$$

$$p_r = \frac{Y_3 - (1 - \epsilon)Y_0 + (3 - \epsilon)Y_0^2 - 2Y_0^3}{\epsilon Y_0(1 - Y_0)}, \tag{16}$$

$$\alpha = \frac{\frac{1}{2}Y_5 - Y_4 + \frac{1}{2}Y_3 - d^2 Y_0}{dY_0}. \tag{17}$$

Note that in system (14)-(17), each quantity is determined by the Y_i and the parameter values previously listed; we do not write the solution in explicit form for the sake of clarity, as the resulting equations are unwieldy. Furthermore, the solution of this system relies on the assumption of strictly positive initial conditions ($S_0 = Y_0 > 0$), wild-type drug induction death rate (d), and background mutation rate (ϵ), all of which are made in this work.

Equation (17) is the desired result of our analysis. It demonstrates that the drug-induced phenotype switching rate α may be determined by a relatively small set of input controls $u(t)$. As discussed in the previous section, the value of α may have a large impact on treatment efficacy, and thus determining its value is clinically significant. Our results now prove that it is possible to compute the induction rate, and hence utilize this information in designing treatment protocols. In the next section, we investigate other qualitative properties that could also be applied to understand the rate of drug-induced resistance.

An *in vitro* Experimental Protocol to Distinguish Random and Drug-Induced Resistance

We have demonstrated that all parameters in (9)-(10) are identifiable, so that it is theoretically possible to determine the phenotype switching rate α from a class of input controls $u(t)$. However, we see that the calculation involved measuring derivatives at the initial detection time $t = t_d$. Furthermore, the utilized applied controls (see equation (13)) are non-constant and thus require fractional dosages to be administered. Clinically, such strategies and measurements may be difficult and/or impractical. In this section, we describe an *in vitro* method for estimating α utilizing *constant therapies only*. Specifically, our primary goal is to distinguish drugs with $\alpha = 0$ (phenotype-preserving) and $\alpha > 0$ (resistance inducing). Such experiments, which are described below, may be implemented for a specific drug, even if its precise mechanism of promoting resistance' remains uncertain.

Before describing the *in vitro* experiment, we note that we are interested in qualitative properties for determining α. Indeed, in most modeling scenarios, we have little or no knowledge of precise parameter values, and instead must rely on characteristics that distinguish the switching rate α independently of quantitative measurements. Furthermore, as a general framework for drug resistance, the only guaranteed clinically observable output variables are the critical tumor volume V_c and the corresponding time t_c (for a description of the treatment protocol, see above); we cannot expect temporal clonal subpopulation measurements. Assuming V_c is fixed for a given cancer, t_c is thus the only observable that we consider.

By examining (9)-(10), we see that the key parameters dictating the progression to the steady state $(S, R) = (0, 1)$ are d and α, as these determine the effectiveness and resistance-induction of the treatment, respectively. Recall that ϵ is the fixed background mutation rate, and p_r the relative fitness of the resistant cells. Thus, we perform a standard dose-response experiment for each value of drug sensitivity d, and measure the time t_c to reach critical size V_c as a function of d. The response t_c will then depend on the applied dosage u (recall that we are only administering constant therapies) and the sensitivity of the wild-type cells d, as well as the induction rate α:

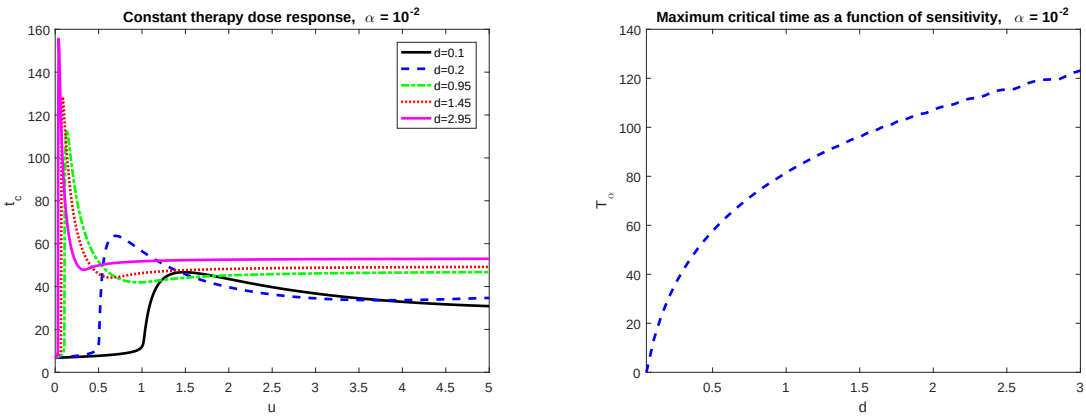
$$t_c = t_c(u, d, \alpha). \tag{18}$$

We further imagine that it is possible to adjust the wild-type drug sensitivity d. For example, in the case of multi-drug resistance in which the over-abundance of P-glycoprotein affects drug pharmacokinetics, altering the expression of MDR1 via ABCBC1 or even CDX2 [38] may yield a quantifiable relationship between wild-type cell and d, thus producing a range of drug-sensitive cell types. Figure 3(a) exhibits a set of dose response curves for representative drug sensitivities d, for the case of a resistance-inducing drug ($\alpha = 10^{-2}$).

For each of these cell-types, we then define the supremum response time over administered doses:

$$T_\alpha(d) := \sup_u \{t_c(u, d, \alpha)\}. \tag{19}$$

Note that in a laboratory setting, only a finite number of doses will be administered, so that the above supremum is actually a maximum, but for mathematical precision we retain supremum.



(a) (b)

Figure 3: Variation in response time t_c for a treatment inducing resistance. Constant therapy $u(t) \equiv u$ is applied for $t_d \leq t \leq t_c$. Induction rate $\alpha = 10^{-2}$, with all other parameters as in Table 1. (a) Time until tumor reaches critical size V_c for various drug sensitivities d. (b) Maximum response time $T_\alpha(d)$ for a treatment inducing resistance. Note that time $T_\alpha(d)$ increases with drug sensitivity; compare to Figure 4(b) for purely random resistance evolution.

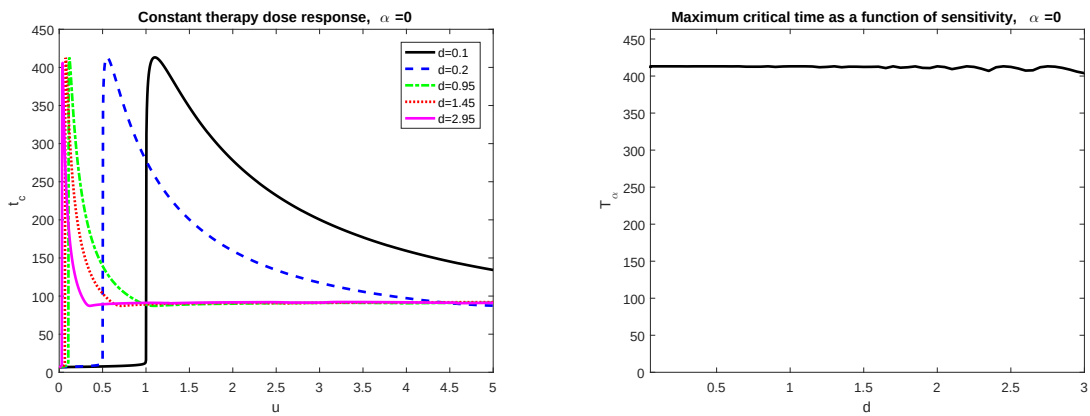
Thus, we obtain a curve $T_\alpha = T_\alpha(d)$ for each value of the induced resistance rate α. We then explore the properties of these curves for different α values.

Consider first the case of a phenotype-preserving drug, so that $\alpha = 0$. As $u(t) \equiv u$, we see that the system (9)-(10) depends only on the product of u and d. Hence, the dependence in (18) becomes of the form $t_c(u \cdot d, 0)$, and thus the supremum in (19) is instead across the joint parameter $D := u \cdot d$:

$$T_0 := \sup_D \{t_c(D, 0)\}. \tag{20}$$

Clearly, this is independent of d, so that T_0 is simply a horizontal line for $\alpha = 0$. Qualitatively, the resulting curve will have no variation among the engineered sensitive phenotypes, save for experimental and measurement noise. See Figure 4 for both representative curves (Figure 4(a), comparable to Figure 3(a))) and a plot of $T_0(d)$ (Figure 4(b)) verifying its independence of d. We make two minor technical notes. First, it is important that we assume $d > 0$ here, as otherwise $D \equiv 0$, independent of dose u and the supremum is over a one element set. See below for more details and the implications for α identifiability. Second, the slight variation for large values of d is due to numerical error, as the maximum of t_c occurs at decreasing dosages (see SI Section D and Figure S3 for more details).

Comparing Figures 3(a) and 4(a), we observe similar properties: small t_c for small doses, a sharp increase about a critical u_c, followed by smooth decrease and eventual horizontal asymptote (for mathematical justification, see SI Section D). However, note that for a resistance-inducing drug, (Figure 3(a)), the maximum critical time $T_\alpha(d)$ increases as a function of d. This is in stark contrast with the constant behavior obtained for $\alpha = 0$, argued above and demonstrated in Figure 4(b). To understand this phenomena further, we plot $T_\alpha(d)$ for a fixed induction rate $\alpha = 10^{-2}$ in Figure 3(b). The behavior of this curve is a result of the fact that the critical dosage u_c at which $T_\alpha(d)$ is obtained is a decreasing function of d (see equation (S8)



(a) (b)

Figure 4: Change in critical time t_c for differing drug sensitivities in the case of a phenotype-preserving treatment. (a) Time until tumor reaches critical size V_c for various drug sensitivities d. Comparable to Figure 3(a), with $\alpha = 0$. (b) Maximum critical time $T_0(d)$. Note that the curve is essentially constant.

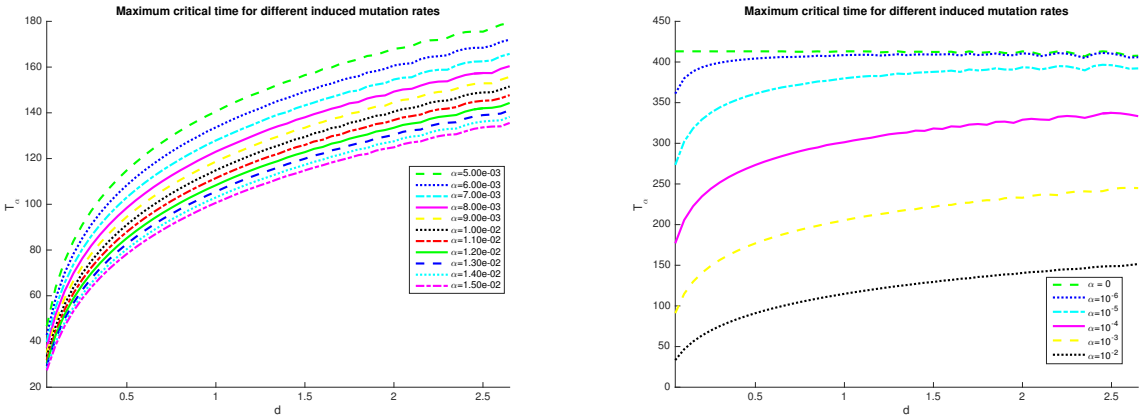
and Figure S3 in SI Section D). But since u_c also controls the amount of resistant cells generated (via the $\alpha u(t)S$ term), resistance growth is impeded by a decreasing u_c. Thus, as a non-negligible amount of resistant cells are necessary to yield $T_\alpha(d)$, more time is required for resistant cells to accumulate as d increases. Hence, $T_\alpha(d)$ increases a function of d.

The behavior observed in Figures 3(b) and 4(b) is precisely the qualitative distinction that could assist in determining the induced resistance rate α. In the case of a phenotype-preserving drug, the proposed *in vitro* experiment would produce a flat curve, while a resistance-inducing drug ($\alpha > 0$) would yield an increasing function $T_\alpha(d)$. Furthermore, we could utilize this phenomena to, in principle, measure the induction rate from the experimental $T_\alpha(d)$ curve. For example, Figure 5(a) displays a range of $T_\alpha(d)$ for α near 10^{-2}.

Figure 5(a) shows a clear dependence of $T_\alpha(d)$ on the value of α. Quantitatively characterizing such curves would allow us to reverse engineer the induction rate α. However, we note that in general the precise characteristics will depend on the other fixed parameter values, such as p_r, V_c, and ϵ. Indeed, only order of magnitude estimates may be feasible; illustrative sample curves are provided in Figure 5(b). Two such characteristics are apparent from this figure, both related to the slope of $T_\alpha(d)$. First, as $d \to 0^+$, we observe an increase in the slope of $T_\alpha(d)$ as α decreases (note that in Figure 5(b), only $d \geq 0.05$ are plotted). This follows from continuity of solutions on parameters and the fact that $T_0(d)$ possesses a jump discontinuity at $d = 0$, i.e. its distributional derivative is given by

$$\frac{\partial}{\partial d}\Big|_{d=0} T_0(d) = k\delta(d), \tag{21}$$

where δ is the Dirac function, and k is a positive constant. As discussed previously (see (20) and the subsequent paragraph), $T_0(d)$ is flat, except at $d = 0$ where the vector field contains no u dependence. Therefore the set over which the maximum is taken is irrelevant, and $T_0(d)$ is thus proportional to the Heaviside function, which possesses the distributional derivative (21).



(a) (b)

Figure 5: Variation in maximum response time for different induction rates α. For details on computation of $T_\alpha(d)$, see Figure S3. All other parameters given as in Table 1. (a) Plot of $T_\alpha(d)$ for α near 10^{-2}. (b) Analogous to (a), where α is now varied over several orders of magnitude. Non-mutagenic case ($\alpha = 0$) is included for reference.

The constant k is determined by the size of the discontinuity of $T_0(d)$. Continuous dependence on parameters then implies that as α increases, the resulting derivative decreases away from positive infinity, since the corresponding derivative for $T_\alpha(d)$ with $\alpha > 0$ is defined in the classical sense for $\alpha > 0$:

$$\frac{\partial}{\partial \alpha}\frac{\partial}{\partial d}\bigg|_{d=0} T_\alpha(d) \leq 0.$$

The above argument implies that measuring the slope of $T_\alpha(d)$ at $d = 0$ will give a characterization of the phenotypic alteration rate α of the treatment. However, such experiments may be impractical, as fine-tuning a cell's sensitivity near complete resistance may be difficult. Alternatively, one could analyze the degree of flatness for a relatively large d (so to be sufficiently far from $d = 0$) and correlate this measure with α. For example, examining $d = 2$ in Figure 5(b), we see that the relative slope of $T_\alpha(d)$ with respect to d should correlate with decreasing α. A similar argument to the above makes this rigorous, for d sufficiently large. Practical issues still arise, but this second method does provide a more global method for possibly computing α. Indeed, slopes at a given d can be approximated by a wider range of secant approximations, as the result holds for a range of d, as compared to the previously-discussed case when d is near zero. Furthermore, our focus is largely on the qualitative aspects of α determination (such as the differences in Figures 3(a) and 4(a)) and determining whether the treatment itself induces resistance to emerge.

Conclusions and Future Work

In this work, we have analyzed mechanisms of drug resistance. Specifically, a mathematical model is proposed which describes both the traditional genetic origin of resistance, as well as

drug-induced resistance which can occur at both the genetic and epigenetic level, with the latter being reversible (phenotype-switching). Utilizing this model, we contrasted the effect of standard therapy protocols, and demonstrated that the rate of resistance induction may have a significant effect on treatment outcome. Thus, understanding the dynamics of resistance evolution in regards to the applied therapy is crucial.

To demonstrate that one can theoretically determine the induction rate, we performed an identifiability analysis on the parameter α, and showed that it can be obtained via a set of appropriate perturbation experiments $u(t)$. Furthermore, we presented an alternative method, utilizing only constant therapies, for understanding qualitative differences between the purely spontaneous and induced cases. Such properties could possibly be used to design *in vitro* experiments on different pharmaceuticals, allowing one to determine the induction rate of drug resistance without an *a priori* understanding of the precise mechanism. We do note, however, that such experiments may still be difficult to perform in a laboratory environment, as engineering cells with various drug sensitivities d may be challenging. Indeed, this work can be considered as a thought experiment to identify qualitative properties that the induction rate α yields in our modeling framework. Future work will focus on expanding the set of feasible controls away from purely constant therapies, and thus determine α for cancer cells with a fixed drug sensitivity d.

We have also limited our analysis to a simplified version of the proposed framework by considering both resistant phenotypes to exhibit the same cellular dynamics, as well as assuming that all resistance is non-reversible. The analysis can be extended to the full three-compartment model to better differentiate the roles of both genetic and phenotypic alterations in cases where these cell types exhibit distinct characteristics. Adaptive/metronomic therapies, as well as optimal control techniques, are also being investigated and analyzed, to assist in our understanding of how resistance mechanisms impact therapeutic response.

Overcoming drug resistance is crucial for the success of chemotherapy. Furthermore, the added complexity of induced drug resistance complicates therapy design, as the simultaneous effects of tumor reduction and resistance propagation confound one another. Mathematically, we have presented a clear framework for differentiating the two resistance mechanisms, which will allow for clinically actionable analysis on a biologically subtle, yet important, issue.

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Author Contributions

All authors contributed equally to this work.

Conflict of Interest

None declared.

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Supporting Information (SI)

The supplement contains results on the mathematical characteristics of solutions of system (9)-(10), as well as an expanded discussion on the maximum critical time $T_\alpha(d)$ (see (19)).

A Fundamental Solution Properties of Resistance Model

For convenience, system (9)-(10) is reproduced below:

$$\frac{dS}{dt} = (1-(S+R))\,S - (\epsilon + \alpha u(t))S - du(t)S, \tag{S1}$$

$$\frac{dR}{dt} = p_r\,(1-(S+R))\,R + (\epsilon + \alpha u(t))S. \tag{S2}$$

We begin with a standard existence/uniqueness result, as well as the dynamical invariance of the triangle

$$T := \{(S,R)|S \geq 0, R \geq 0, S+R \leq 1\}\,. \tag{S3}$$

Note that T represents the region of non-negative tumor sizes below 1. Biologically, this implies that all solutions remain physical (non-negative) and bounded above by the carry capacity (non-dimensionalized to 1 here, generally K in (6)-(7)).

Theorem 1. *For any bounded measurable control $u : [0,\infty) \to [0, u_{\max}]$, with $u_{\max} < \infty$, and $(S_0, R_0) \in T$, the initial value problem* (S1)-(S2)*,*

$$S(0) = S_0, \qquad R(0) = R_0,$$

has a unique solution $(S(t), R(t))$ defined for all times $t \in \mathbb{R}$. Furthermore, under the prescribed dynamics, region T is invariant.

Proof. Existence and uniqueness of local solutions follow from standard results in the theory of differential equations; see for example Theorem 2.1.1 and 2.1.3 in [5]. Since the vector field

$$F(S,R,t) := \begin{pmatrix} (1-(S+R))S - (\epsilon + \alpha u(t))\,S - du(t)S \\ p_r\,(1-(S+R))\,R + (\epsilon + \alpha u(t))S \end{pmatrix}.$$

is analytic for $(S,R) \in \mathbb{R}^2$, the existence of maximal solutions defined for all $t \in \mathbb{R}$ will follow from boundedness (see Theorem 2.1.4 in [5]), which we demonstrate below.

Uniqueness implies that solutions remain in the first quadrant for all $t \geq 0$. Indeed, we first note that $(0,0)$ and $(0,1)$ are steady states for any control $u(t)$. As $S = 0$ implies that $\dot{S} = 0$, we see that the R-axis in invariant, with $R(t) \xrightarrow{t\to\infty} 1$. Similarly, $R = 0$ implies $\dot{R} \geq 0$, and hence all trajectories with $(S_0, R_0) \in T$ remain non-negative for all t. As $V = S + R$ satisfies the differential equation

$$\dot{V} = \alpha(t)(1-V) - \beta(t),$$

where $\alpha(t) := S(t) + p_r R(t)$, $\beta(t) := du(t)S(t)$ are both non-negative, $V_0 < 1 \Rightarrow V(t) < 1$. Thus, if the initial conditions (S_0, R_0) reside in T, we are guaranteed that $(S(t), R(t)) \in T$ for all time t, as desired. □

We now prove that asymptotically the cells will evolve to become entirely resistant. For simplicity, we assume that the tumor is initially below carrying capacity, although a similar result holds for $V_0 > 1$.

Theorem 2. *For any bounded measurable control $u : [0, \infty) \to [0, u_{\max}]$, with $u_{\max} < \infty$, and initial conditions $(S_0, R_0) \in T$, solutions of system* (S1)-(S2) *will approach the steady state $(S, R) = (0, 1)$:*

$$(S(t), R(t)) \xrightarrow{t\to\infty} (0, 1).$$

Proof. From Theorem 1, we have that $0 \leq S(t) + R(t) \leq 1$, so that (S2) implies

$$\frac{dR}{dt} \geq 0.$$

As $0 \leq R(t) \leq S(t) + R(t) \leq 1$, $R(t)$ must converge, so that there exists $0 \leq R_* \leq 1$ such that

$$R(t) \xrightarrow{t\to\infty} R_*.$$

By uniqueness, for all admissible controls $u(t)$, the line $R = R_*$ is attracting and invariant, and thus the corresponding sensitive component $S(t)$ along this line must satisfy

$$p_r\,(1 - R_* - S(t))\,R_* + (\epsilon + \alpha u(t))S(t) \equiv 0. \tag{S4}$$

Since $\epsilon > 0$ and $u(t) \geq 0$, and both terms on the left-hand side of (S4) are non-negative, this is only possible if $S(t) \equiv 0, R_* = 1$. Hence the line $R = R_*$ is in actuality the point $(S, R) = (0, 1)$, so that $(S(t), R(t)) \xrightarrow{t\to\infty} (0, 1)$ for all $(S_0, R_0) \in T$, as desired. □

B Treatment comparison for equal AUC

Here we provide an analogous comparison of treatment outcomes between constant and pulsed therapy as in the main text. However, treatment magnitudes $u_{\text{on},c}$ and $u_{\text{on},p}$ are chosen such that

$$\int_{t_d}^{t_d+\Delta t_{\text{on}}+\Delta t_{\text{off}}} u_c(t)\,\mathrm{d}t = \int_{t_d}^{t_d+\Delta t_{\text{on}}+\Delta t_{\text{off}}} u_p(t)\,\mathrm{d}t, \tag{S5}$$

which is equivalent to the conservation of total administered dose between both strategies over a single pulsing cycle. In (S5), $u_c(t)$ and $u_p(t)$ denote the constant and pulsed therapy schedules, respectively. The constant therapy magnitude $u_{\text{on},c}$ is fixed (arbitrarily) at 0.5, which by (S5) implies that $u_{\text{on},p} = 5$. We also adjust $\Delta t_{\text{on}} = 0.5, \Delta t_{\text{off}} = 4.5$, and all other parameter values remain as in Table 1.

Results of the simulations are presented in Figures S1 and S1. Note that here Figure S1 displays the results for the phenotype-preserving drug ($\alpha = 0$), while Figure S2 represents the resistance-inducing drug ($\alpha = 10^{-2}$). Each drug is simulated for the two distinct strategies; each strategy is represented in the left column of the respective figures. The right column illustrates the population response, for both the individual populations (sensitive S and resistant R cells), as well as for the total tumor volume $V = S+R$. As previously discussed, treatment is continued

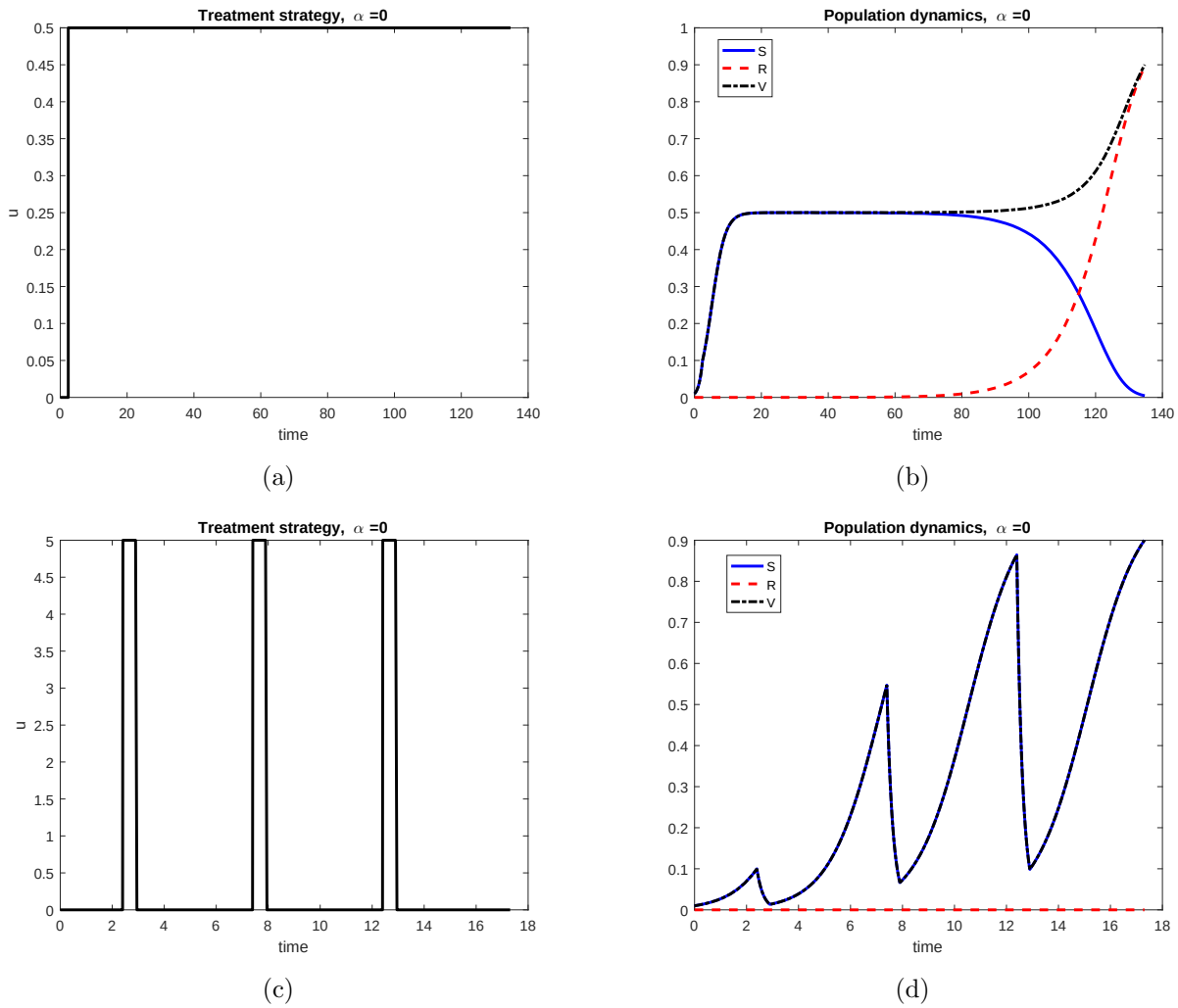

Figure S1: Treatment dynamics for phenotype-preserving drug ($\alpha = 0$). Left column indicates treatment strategy, while right indicates corresponding population response. (a) Constant treatment after tumor detection. (b) Response to constant treatment. Note that at the time of treatment failure, the tumor is essentially entirely resistant. (c) Pulsed therapy after tumor detection. (d) Response to pulsed therapy. Note that the treatment fails much earlier than for the constant dosage, and that the tumor is primarily drug sensitive.

until a critical tumor size V_c is obtained, and the corresponding time t_c is utilized as measure of treatment efficacy, with a larger t_c indicating a better response.

Our results are qualitatively in agreement with those presented in the main text (Figure 2), where no preservation of total administered drug (AUC) was considered. Specifically, we observe a superior response with constant therapy for the phenotype-preserving drug ($\alpha = 0$), while the situation is reversed for the resistance inducing drug ($\alpha = 10^{-2}$).

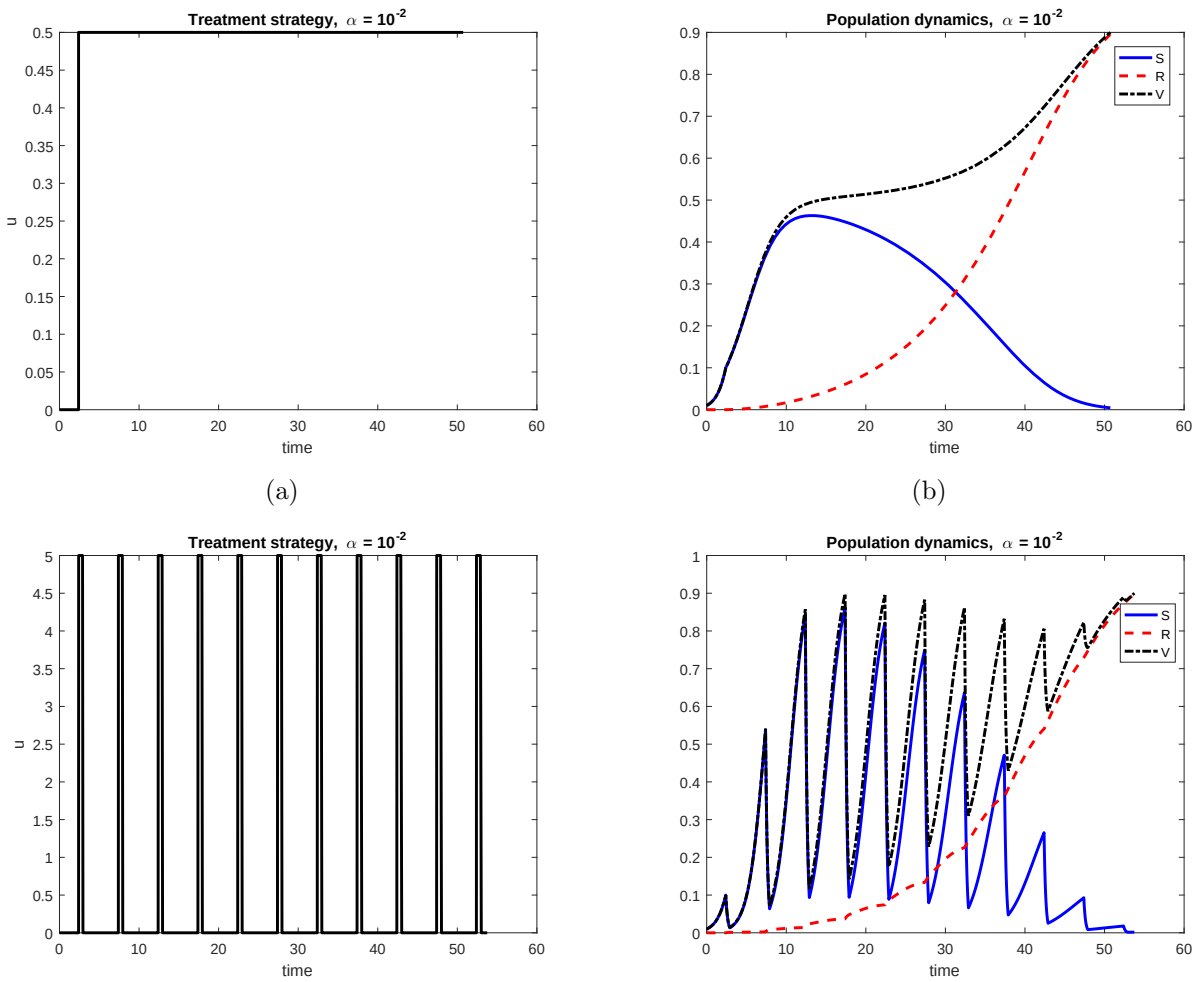

Figure S2: Treatment dynamics for resistance-inducing drug ($\alpha = 10^{-2}$). Left column indicates treatment strategy, while right indicates corresponding population response. (a) Constant treatment after tumor detection. (b) Response to constant treatment. Note that at the time of treatment failure, the tumor is essentially entirely resistant. Similar dynamics to Figure 1(b), although with a shorter survival time. (c) Pulsed therapy after tumor detection. (d) Response to pulsed therapy. Note that here, in contrast to case of a phenotype-preserving drug as shown in Figure S1, pulsed therapy exhibits a longer survival time.

C Identifiability analysis

In this section, we provide additional details on the theoretical identifiability of model parameters. As mentioned in the main text, all higher-order derivatives at initial time $t = 0$ may be calculated in terms of the initial conditions $(S(0), R(0))$ and the control function $u(t)$. For example, for an arbitrary system

$$\dot{x}(t) = f(x(t), u(t)),$$

with external control $u(t)$, the second derivative $\ddot{x}$ may calculated using the chain rule:

$$\ddot{x} = J_f(x,u)f + \nabla_u f(x,u)\dot{u},$$

where $J_f(x)$ is the Jacobian matrix of f, evaluated at state x and control u. If $x(0) = x_0$ is known, the above expression is a relation among parameters, together with u and $\dot{u}$ evaluated at time $t = 0$. An analogous statement holds for a measurable output $y = h(x)$, but will involve the Jacobian of h as well. Concretely, for the model of induced drug resistance (9)-(10), first derivatives of the tumor volume may be calculated as

$$\begin{aligned} V'(0) &= S'(0) + R'(0), \\ &= \left((1-(S+R))\,S - (\epsilon + \alpha u(t))S - du(t)S\right) \\ &\quad + \left(p_r\left(1-(S+R)\right)R + (\epsilon+\alpha u(t))S\right)\Big|_{t=0}, \\ &= (1-S_0)\,S_0 - du(0)S_0, \end{aligned}$$

for any control $u(t)$ (recall that $R(0) = 0$). Similarly, for the second derivative, we compute:

$$\begin{aligned} V''(0) = S_0\big(1-S_0 - (\epsilon+d)u(0)\big)\big(1-2S_0 - du(0)\big) \\ + S_0\big(\alpha u(0)+\epsilon\big)\big(p_r - S_0(1+p_r)\big) - dS_0\dot{u}(0). \end{aligned}$$

Using such expressions (or, more precisely, the Lie derivatives of the vector field, see [71]) for the controls in (13), one is able to obtain a set of equations between the set of $Y_i, i = 0, 1, \ldots, 7$ and the parameters d, ϵ, p_r, and α. Solving these equations allows us to determine the parameters with respect to the measurable quantities. The algebraic solution is system (14)-(17).

D Analysis of critical time $\mathbf{T}_\alpha(\mathbf{d})$

We provide a qualitative understanding of the properties of $T_\alpha(d)$, the maximum time, across all constant dosages, for the tumor to reach size V_c. This appendix is designed to explain the basic properties discussed in the *In Vitro* Identifiability section of the main text.

We first note that $T_\alpha(d)$ is achieved at a medium dosage u_c. More precisely, we describe the qualitative properties of Figures 3(a) and 4(a). Fix a drug sensitivity d. For small u, the sensitive subpopulation is not sufficiently inhibited, and hence expands rapidly to cross the threshold V_c, with an essentially homogenous population of sensitive cells. Indeed, as $u \to 0$, the dynamics of (S1)-(S2) approach those of

$$\frac{d\tilde{S}}{dt} = \left(1-(\tilde{S}+\tilde{R})\right)\tilde{S}, \tag{S6}$$

$$\frac{d\tilde{R}}{dt} = p_r\left(1-(\tilde{S}+\tilde{R})\right)\tilde{R}, \tag{S7}$$

for small finite times, as $\epsilon \ll 1$. Trajectories of (S6)-(S7) remain on the curve

$$R(S) = \frac{R_0}{S_0^{p_r}} S^{p_r}$$

as the solution approaches the line $S + R = 1$. The critical time t_c is then determined by the intersection of this curve with $S + R = V_c$, and hence has sensitive population S_c at t_c given by the unique solution in the first quadrant of

$$S_c + \frac{R_0}{S_0^{p_r}} S_c^{p_r} = V_c.$$

As $R_0 \ll 1$ (since $\epsilon \ll 1$), $S_c \approx V_c$, as claimed. Time t_c is thus small for small u.

Increasing values of u imply t_c to also increase, since the overall growth rate of the sensitive cells is decreased. However, there exists a critical dose u_c such that sensitive cells alone are not able to multiply sufficiently to attain V_c, so that the critical volume must have non-negligible contributions from the resistant fraction. This then leads to the bifurcation apparent in Figures 3(a) and 4(a). We can even approximate the critical dosage maximizing t_c, as V_c must be an approximation for the carrying capacity of the sensitive cells:

$$S_K \approx V_c.$$

By examining the right-hand side of (S1), and assuming that the dynamics of the resistant population are negligible (which is accurate in the early stages of treatment; see Figures 1(b) and 2(b)) we see that the dose yielding the maximum temporal response should be

$$u_c \approx \frac{1 - \epsilon - V_c}{\alpha + d}. \tag{S8}$$

That is, the dosage where $T_\alpha(d)$ is obtained is given approximately by the expression in (S8). For a sample numerical comparison of the predicted formula (S8) and a numerical optimization over a range of drug sensitivities d, see Figure S3. Note that in actuality, $S_K < V_c$, as the resistant dynamics cannot be ignored entirely. Thus, the precise value of u_c will be smaller than that provided in the previous formula, as we numerically observe. Lastly, u_c decreases with increasing values of parameter d, and thus requires an increasingly fine discretization to numerically locate the maximum value. Hence, some numerical error is observed in Figure 4(b).

Lastly, as u is increased further, the dosage becomes sufficiently large so that the inhibition of S via therapy implies that S cannot approach the critical volume V_c, and hence V_c is again reached by an essentially homogeneous population, but of resistant cells. Since resistant cells divide at a slower rate ($p_r < 1$), the corresponding time t_c is smaller. For a schematic of the three regimes described above, see Figure S4.

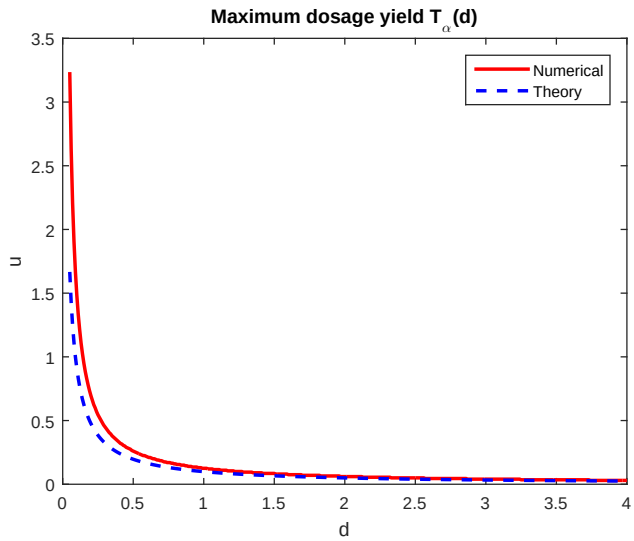

Figure S3: Dose yielding maximal response time $T_\alpha(d)$ computed numerically, as well as the approximation given by (S8). All parameters appear as in Table 1, and $\alpha = 10^{-2}$. The numerical maximum is computed over a discretization of constant dosage procedures $u(t) \equiv u$, for $u \in [0, 5]$, with a mesh size $\Delta u = 0.005$.

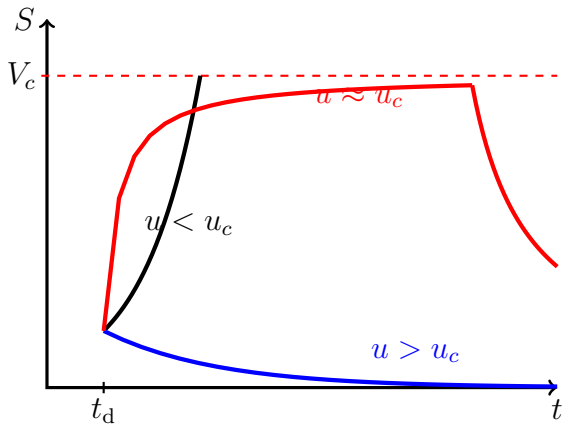

Figure S4: Schematic demonstrating dynamics of variation in t_c on dosage u. Sensitive cell population plotted as a function of time, for three representative doses. For $u < u_c$, sensitive cells grow and reach V_c in a short amount of time. As $u \to u_c^-$, the sensitive population approaches its approximate carrying capacity of V_c, but subsequently decreases due to the dynamics of resistance. Here t_c is maximized, as the sensitive population spends a large amount of time near V_c. For $u > u_c$, the sensitive population is eliminated quickly, and V_c is obtained by a primarily resistant population.