

Chapman & Hall/CRC
Handbooks of Modern
Statistical Methods

**Handbook of
Methods for
Designing, Monitoring,
and Analyzing
Dose-Finding Trials**

Edited by

John O'Quigley

Alexia Iasonos

Björn Bornkamp



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A CHAPMAN & HALL BOOK

**Handbook of
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Handbooks of Modern Statistical Methods

Series Editor

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Preface

This volume covers recent developments in the design and analysis of dose-finding clinical trials. While the theory is closely examined, the unifying driving force is the clinical applications themselves. Given the high failure rate of Phase III confirmatory clinical trials, together with an increasing need to look at new agents in a timely manner, it has become apparent that poor accuracy in the early-phase trials can have significant consequences further down the line in the overall drug development. The aim of recent developments in early-phase trials is to greatly improve this accuracy and to achieve this while strictly respecting ethical requirements governing clinical trials in human subjects. In the long term, the end result will be a speedier and more reliable drug development process so that patients can more quickly see the real benefit from scientific advances in the laboratory.

In Phase I first-in-human trials, little is known on how the probability of encountering adverse events relates to dose when the drug is given to humans based on preclinical data. One objective of a trial is to learn more about this relationship, although we are severely hampered by the need to avoid overdosing. Further, underdosing is also a concern for oncology patients who participate in these trials, if there is no hope of benefit one should not offer to include patients in the trial. We need a trade-off between information gained via experimentation at various dose levels and the requirements of the treated patients themselves on a particular study. The statistical setting is thus unusual. This presents a considerable statistical challenge and has formed the basis of several of the model-based approaches that are discussed here. Challenges in Phase II dose-finding studies include the fact that efficacy information evaluated on the different dose levels is limited not only by a typically rather low sample size but also by the fact that biomarker, or short-term, endpoints are used compared to more definitive endpoints used in more extensive and longer-term Phase III clinical trials.

Explicitly characterizing the relation between the amount of a given drug and its effect, i.e., how the body reacts to given doses of the drug, has not traditionally been an objective of Phase I trials. Even some Phase II dose-finding trials do not aim to do this. As a result of this lack of precision, the goals of the older, or classical, standard dose-finding designs, such as the well-known 3 + 3, are not clear. In the absence of clear goals, it is not possible to say whether or not any proposed statistical methodology works well or is even fit for its purpose. In Phase II dose-finding clinical trials, a major focus has traditionally been statistical testing based on pairwise comparisons of the efficacy endpoint, which is not aligned with the goal of determining the efficacy dose-response curve. An aim in this current volume is to make very clear and explicit early on the goals of an early-phase study under different settings, and then to critically investigate how any statistical approach can meet these goals. In practice, the level of clinical complexity can increase rapidly, for example, studies in targeted therapies, combination therapies, bridging between different patient populations or several heterogeneous groups, and errors in recording adverse events. The several authors in this volume, through the many different approaches presented, never lose sight of the initial motivation and the study's objective. No statistical complexity, for

its own sake, is presented, and the methods described are being currently used to provide answers in applied clinical research. The material presented here, along with references to further work, provides an overview of various existing methods that can help a practicing statistician select an appropriate clinical trial design to match the objective of the study.

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Part I

Phase I Designs



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1

Overview of Phase I Designs

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Though many differing approaches for conducting phase I trials have been proposed over the past three decades, they all aim to target a specific dose level while minimizing the risk of patients in the trial experiencing intolerable toxicities. Here, we cover the two main types of phase I designs—rule-based and model-based—and provide an overview of the many designs available. We also discuss other design aspects, such as start-up rules and stopping rules, and summarize how clinical practice has changed over the years when it comes to designing a phase I trial.

1.1 Introduction

The primary objective of a phase I clinical trial is to investigate the safety profile of a novel drug or drug combination and identify a tolerable dose schedule that is likely to benefit patients (Chang and Chow, 2006). For cytotoxic therapies in oncology, such trials

are conducted using a small number of cancer patients for whom standard therapies have not worked (Horstmann et al., 2005). Due to the possibility of experimental treatments causing severe side effects, trials are conducted as *dose-escalation studies*. In general, patients are recruited into the trial and treated in small cohorts of one, two, or three, with the first cohort treated at an exceedingly low dose level considered safe in humans (Von Hoff et al., 1984; Eisenhauer et al., 2000). The number and severity of toxic reactions, as defined by the National Cancer Institute’s Common Terminology Criteria for Adverse Events [NCI CTCAE (National Cancer Institute, 2009)], observed in patients undergoing treatment are recorded, and based on the results for the current cohort (and possibly previous cohorts), the next cohort of patients will be treated at either a higher dose level, a lower dose level, or the same dose level. The trial continues in this manner until all available patients have been treated, or some other stopping criterion is satisfied, such as a target number of patients have been consecutively dosed at one dose level, or the proportion of patients experiencing severe toxicity at a dose level exceeds a prespecified threshold (see Section 1.4.2).

Commonly, toxicity frequency and severity data are reduced to a single binary outcome known as *dose-limiting toxicity* (DLT) (Le Tourneau et al., 2009), and this response is used to determine whether dose escalation occurs or not. What constitutes a DLT will vary from trial to trial (Le Tourneau et al., 2011), but it is often the case that a DLT is said to have occurred in a patient if at least one severe toxicity [grade 3 or higher under the NCI CTCAE (NCI, 2009)] in a particular body system or organ of interest is observed in the first cycle of treatment (Babb and Rogatko, 2004).

The main objective of phase I trials is to identify the *maximum tolerated dose* (MTD) of the new drug. Although definitions of the MTD vary (Le Tourneau et al., 2009), it is often defined as the dose that, at the end of the trial, has an estimated probability of causing a DLT as close to some predetermined *target toxicity level* (TTL) as possible (Babb and Rogatko, 2004). In oncology, the TTL is fixed often at some probability between 0.20 and 0.35 (Neuenschwander et al., 2008; Le Tourneau et al., 2009). An alternative definition of the MTD is the dose with no more than a certain proportion (e.g., 33%) of patients at that dose experiencing DLT. If an MTD is successfully identified in a phase I trial, the drug is then taken forward into a phase II trial, with the MTD or a slightly lower dose designated as the recommended phase II dose (RP2D) (Le Tourneau et al., 2012).

The rationale for targeting a dose level that is potentially harmful with small probability is due to the belief that the higher the dose of a cytotoxic drug, the better the speed or extent of tumor response (Marshall, 2012). Therefore, the MTD of a cytotoxic drug is seen as a proxy for an efficacious dose level with limited toxicity potential. When considering molecularly targeted agents, which affect particular molecules required for cancer cells to mutate (carcinogenesis) rather than all cells, this may not necessarily be the case (Le Tourneau et al., 2009); in some cases, it has been observed that the dose–response relationship may be nonmonotonically increasing (Conolly and Lutz, 2004; Bretz et al., 2008). Most methods for phase I trials are based on the *assumption of monotonicity* (Box 1.1); that is, if a patient has a DLT at a given dose level, then the same patient would have had a DLT had they been given a higher dose level than the one they received. Conversely, had the patient not had a DLT at a given dose level, then the same patient would not have had a DLT had they been given a lower dose level than the one they received (O’Quigley and Zohar, 2006). This assumption can be summarized on a population level by saying that the probability of a DLT occurring in a patient is monotonically increasing with dose.

Box 1.1 The Assumption of Monotonicity

The probability of observing a dose-limiting toxicity (DLT) is monotonically increasing with dose.

Methods for conducting dose-escalation studies are usually dichotomized into two families: *rule-based designs*, where fixed rules applied to empirical counts of DLT/non-DLT responses govern the escalation and de-escalation of doses, and *model-based designs*, where statistical models are employed to describe the relationship between the dose given to a patient and the probability of DLT occurring (Rosenberger and Haines, 2002). O’Quigley and Zohar (2006) stated that any method considered for use in a phase I trial should aim to (1) minimize the number of patients treated at dose levels below the true MTD, (2) minimize the number of patients treated at dose levels above the true MTD, (3) minimize the number of patients used in the study in its entirety, and (4) be able to respond quickly to errors in initial guesses or incorrect dose allocations. In this chapter, we describe the main rule-based and model-based approaches for conducting phase I dose-escalation studies with a single binary DLT endpoint. We follow these up with discussions on modifications to these designs that have been used in clinical practice, the popularity of particular designs in clinical practice, and available software for various methods.

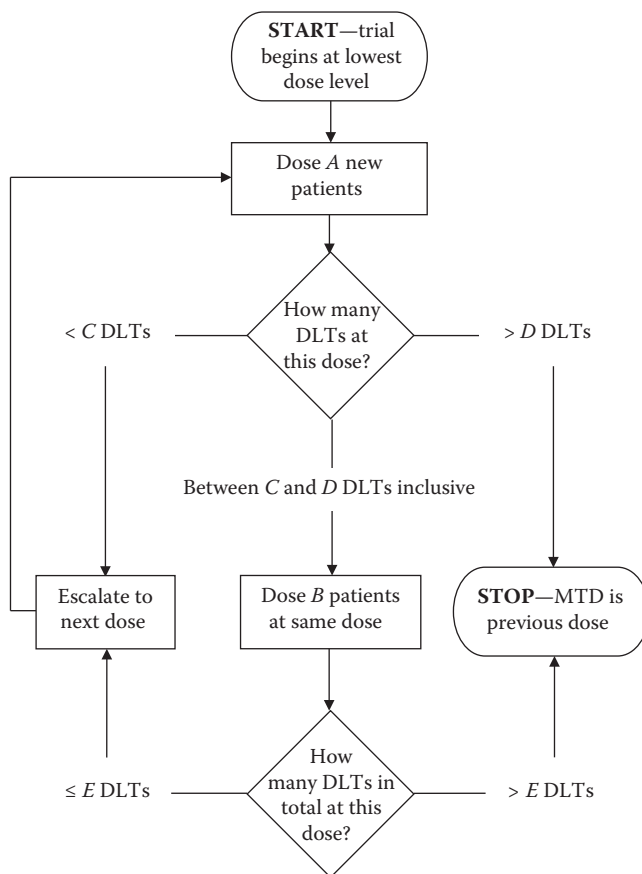
1.2 Rule-Based Designs

Rule-based designs have long been popular with clinicians in cytotoxic drug experimentation (Storer, 1989; Rogatko et al., 2007). The fundamental aspect of rule-based designs is that they do not require the dose–toxicity relationship to be modeled according to some function of dose level. Many of the methods proposed stem from the work on the *up-and-down design* by Dixon and Mood (1948), who sought to identify the mean or median height from which a weight may be dropped upon an explosive compound without detonation occurring. Over time, variations of the up-and-down design made their way into medical research.

1.2.1 The 3 + 3 design

The 3 + 3 design (Carter, 1973; Storer, 1989) is one of the first methods used to conduct dose-escalation studies in humans. The 3 + 3 design is the most commonly used design in phase I clinical trials (Rogatko et al., 2007; Penel et al., 2009; Le Tourneau et al., 2009, 2012) and has long been considered the routine method by clinicians for estimating the MTD of novel drugs in oncology (Penel et al., 2009).

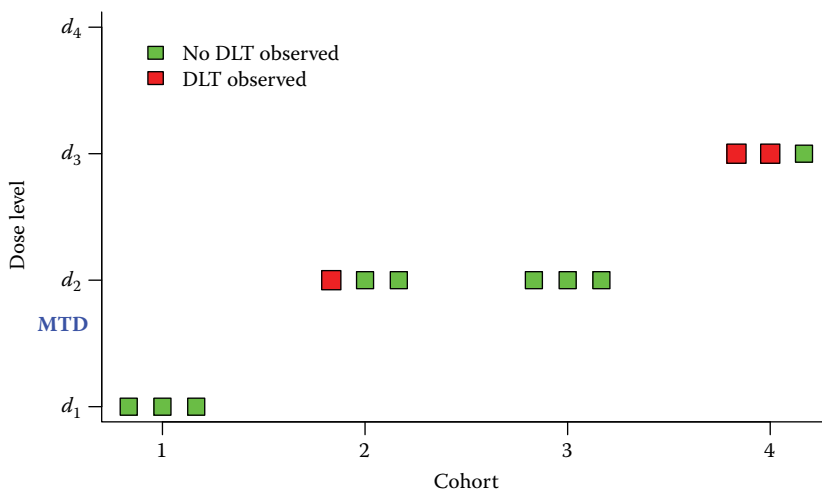
For a trial of k dose levels of a new drug, denoted as $D = \{d_1, \dots, d_k\}$, patients are treated in cohorts of three for the 3 + 3 design. The first cohort of patients are treated at d_1 , the lowest dose level. If no patients in a cohort experience a DLT, then the next cohort is treated at the next highest dose level. If one out of the three patients experiences a DLT, then the next cohort is treated at the same dose level. If at dose level d_i at least two out of the three or six patients experience a DLT, the trial is terminated and d_{i-1} is deemed to be the MTD; if $d_{i-1} = d_0$, then no MTD is identified for safety reasons. The 3 + 3 design may be adapted so that excessive toxicity leads to dose de-escalation rather than trial termination (Storer, 1989; Dignam et al., 2006; Skolnik et al., 2008; Chow, 2011). That is, if d_i is deemed excessively toxic, and only three patients have received dose d_{i-1} , then another three patients are dosed at d_{i-1} . If at most one out of the six patients experiences a DLT, then the trial is terminated and d_{i-1} is the MTD; otherwise, the dose is de-escalated again under the same rules. If six patients had been treated at d_{i-1} , and d_i was deemed excessively toxic, then the trial would terminate and d_{i-1} would be recommended as the MTD. Figure 1.1 illustrates the trial schematic for the 3 + 3 design with dose de-escalation not permitted, and Figure 1.2 illustrates an example trial using data from a real

**FIGURE 1.1**

Design schematic of the $A + B$ design without dose de-escalation.

3 + 3 trial conducted by Park et al. (2005). The trial investigated the dose escalation of 5-fluorouracil (5-FU) in combination with a fixed dose of docetaxel in patients with advanced gastric cancer. Four dose levels were planned for experimentation: 250, 500, 750 and 1000 mg/m²/day. In the first cohort, no patients experienced a DLT at the first dose level. The second cohort was given the dose level of 500 mg/m²/day, at which one out of the three patients experienced a DLT. Therefore, the third cohort was also given the second dose level. No patients in the third cohort experienced a DLT, and so the fourth cohort was given the dose level of 750 mg/m²/day. As two out of the three patients in the fourth cohort experienced a DLT, the trial was terminated after 12 patients and the MTD was identified as 500 mg/m²/day.

There exist several variants of the traditional 3 + 3 design, including generic $A + B$ trials where A and B are positive integers that denote cohort sizes to be used in the trial (Lin and Shih, 2001). For example, a 2 + 4 trial would dose a cohort of two patients at a dose level and then add another four patients to that dose level if one of the initial two patients treated experienced a DLT. There are also $A + B + C$ designs where an extra cohort of C patients may be added onto a dose level if a predetermined number of DLTs are observed in $A + B$ patients. Examples include the 3 + 1 + 1 design, which offers more aggressive dose escalation than the 3 + 3 design (Storer, 2001), and the 3 + 3 + 3 design (Hamberg

**FIGURE 1.2**

Example of dose-escalation pathway in a real 3 + 3 trial (Park et al., 2005). After observing one DLT in cohort 2 at dose level d_2 , cohort 3 were dosed at dose level d_2 also. After escalating to dose level d_3 , excessive toxicity leads to termination of the trial and dose level d_2 is the final MTD.

and Verweij, 2009), which after observing two DLTs in six patients, doses another cohort of three patients at the same dose level.

The main advantages of the 3 + 3 design are that neither a statistician nor highly technical computer software are required to help design or run the trial (Le Tourneau et al., 2009), and exact operating characteristics can be calculated (Lin and Shih, 2001; Wheeler et al., 2016). Additionally, the 3 + 3 design may be ideal for screening drugs very quickly to identify a dose level that exhibits very little toxicity in a small number of patients (Rosenberger and Haines, 2002). However, the pitfalls associated with the 3 + 3 design perhaps outweigh these benefits (Harrington et al., 2013). The 3 + 3 design is a *memoryless* design (Ratain et al., 1993; O’Quigley and Zohar, 2006), i.e., dose-escalation decisions are based on the observed results at the current dose, and the distribution of toxicities in previous cohorts is ignored (Zohar and O’Quigley, 2009). Furthermore, many of the trial participants are treated at subtherapeutic doses due to the slow dose-escalation process that the algorithm enforces (O’Quigley et al., 1990; Ratain et al., 1993), and a new cohort cannot be enrolled until toxicity outcomes have been observed for all patients in the current cohort. A common misconception is that the MTD determined in a 3 + 3 trial always has an expected toxicity rate of 33% since the dose selected as the MTD has an empirical toxicity rate of at most 33%. Large-scale simulation studies have shown that the expected toxicity rate at the estimated MTD depends on the number of doses under experimentation and is often much lower than 33% (Kang and Ahn, 2001, 2002; He et al., 2006; Chen et al., 2009). In fact, the 3 + 3 design does not have a TTL to target per se, meaning that the design is searching for an unknown dose with an unspecified toxicity probability.

1.2.2 Rolling-6 design

In order to shorten trial duration for the 3 + 3 design, Skolnik et al. (2008) proposed the *rolling-6 design*, in which dose-escalation/de-escalation decisions can be made for the next cohort of three patients, even when not all three patients in the previous cohort have a

definitive DLT/no-DLT response. These decisions depend on the number of patients currently enrolled in the cohort, the number of patients with DLTs, and the number of patients enrolled but not yet evaluable for DLT. The trial is run as a 3 + 3 design, but with several modifications: if DLT data are unavailable for one or more of the three patients at dose d_i , or if one DLT is observed at d_i , then the fourth patient (the first patient in the next cohort) is also dosed at d_i ; if two or more DLTs have been observed, even if the third patient is not yet evaluable for DLT, then the fourth patient is given dose d_{i-1} . These rules also apply to the fifth and sixth patients (patients 2 and 3 of the next cohort). Several comparative simulation studies have shown that trials using the rolling-6 design are shorter in duration than those using the 3 + 3 design, but on average require more patients to identify an MTD and are more likely to result in excessive numbers of DLTs (at least three per dose) occurring (Onar-Thomas and Xiong, 2010; Sposto and Groshen, 2011; Doussau et al., 2012). The design has been implemented in practice, particularly in pediatric oncology trials (Mossé et al., 2013; Hoffman et al., 2015). However, it still possesses many of the pitfalls of the 3 + 3 design, and model-based alternatives have been shown to offer much better performance (Onar-Thomas and Xiong, 2010; Zhao et al., 2011).

1.2.3 Accelerated titration designs

An alternative class of rule-based methods to the traditional 3 + 3 design are accelerated titration designs (Simon et al., 1997), which permit inpatient dose escalation in order to reduce the total sample size and the number of patients treated at subtherapeutic doses. Under accelerated titration designs, dose-escalation/de-escalation decisions are made within patients as well as between patients/cohorts and are based on the toxicity observed in the current treatment cycles and/or the largest toxicity in the first treatment cycle. A drawback of such designs is that inpatient dose escalation may lead to difficulty in the analysis of trial data since cumulative or delayed toxicities may be masked (Hansen et al., 2014). Simon et al. found that the number of high-grade toxicities increased under accelerated titration compared to a design without inpatient dose escalation. Although not exhaustive, the 3 + 3 design and accelerated titration designs are the primary rule-based designs used in phase I oncology trials (Rogatko et al., 2007).

1.2.4 Pharmacologically guided dose escalation

Another variation is pharmacologically guided dose escalation (PGDE) (Collins et al., 1990), which relies on *in vivo* data to predict DLT outcomes in humans. Dose escalation of one-patient cohorts is based on whether the area under the curve (AUC) of drug concentration over time is less than some target level. When such a level is exceeded, or when DLTs begin to occur, the design switches to the traditional 3 + 3 design. The PGDE method has had mixed results in clinical practice, in that reliable phase II doses have been recommended for some cytotoxic compounds that have high interpatient variability/heterogeneity (Graham and Workman, 1992; Hansen et al., 2014).

1.2.5 Improvements to conventional rule-based designs

Ivanova et al. (2003) proposed various up-and-down rules that incorporate more trial information than approaches based on the 3 + 3 design (i.e., the most recent cohort) in order to guide dose escalation. Among these is the Narayana rule, derived from the unpublished work of Narayana (1953), which recommends dose escalation or de-escalation from the current dose level based on the empirical proportions of DLTs observed and the k most recent dose-toxicity outcomes at the current level. The authors also considered different procedures

for estimating the MTD of a drug, including isotonic regression (Robertson et al., 1988), which adjusts the empirical DLT rates at different doses via the pooled adjacent violators algorithm (PAVA) to maintain monotonicity of toxicity in doses (Barlow et al., 1972).

The approaches discussed here aim to develop the early up-and-down design work of Dixon and Mood (1948) while keeping dose-escalation decisions dependent on the empirical DLT rates at each dose level. However, more statistical approaches for conducting dose-escalation studies have been proposed, which use mathematical models to quantify the relationship between the dose of a drug and the probability of a DLT occurring.

1.3 Model-Based Designs

Over the past two decades, there has been widespread interest in adaptive model-based designs for phase I clinical trials (Whitehead, 1997), particularly Bayesian designs, in order to overcome the shortcomings identified with the 3 + 3 design and other rule-based methods. Model-based designs use statistical models to estimate the underlying dose–toxicity relationship and can easily incorporate all trial data as well as *a priori* beliefs into the dose–toxicity relationship to help determine dose allocation and MTD recommendation.

1.3.1 The continual reassessment method

One of the first model-based designs for phase I clinical trials was the *continual reassessment method* (CRM) (O’Quigley et al., 1990). Under the CRM, the dose–toxicity curve is assumed to have some monotonically increasing functional form (Table 1.1), which is characterized by a single parameter a and dose level d or a transformed set of dose levels based on the initial dose–toxicity probability guesses, known as the *dose–toxicity skeleton*. The models presented in Table 1.1 are the two simplest and most commonly used; other model structures have been proposed, but under certain conditions, these are equivalent to either the power or logistic model (Cheung, 2011). The models are parameterized with respect to $\exp(a)$ to ensure that the dose–toxicity function is increasing in dose. Transformed dose levels are used to ensure that the chosen model is a sensible fit for the dose–toxicity skeleton (the prior guesses for the dose–toxicity probabilities at each dose level) and can easily be computed by backward substitution (Cheung, 2011).

In a Bayesian setting, a prior belief about the shape of the dose–toxicity curve, along with any surrounding uncertainty, is expressed as a prior distribution on parameter a ; this information may be elicited from clinical opinion and data from previous studies if available and calibrated so that it does not dominate over the data that are accrued during the trial (Legedza and Ibrahim, 2001; Rosenberger et al., 2005; Cheung, 2011). As the trial progresses, patient data are used to update the prior distribution on a to obtain a posterior belief about the shape of the dose–toxicity curve. Let $D = \{d_1, \dots, d_k\}$ be the set of k dose

TABLE 1.1
Common models for one-parameter CRM.

Model	$\psi(d, a)$	Restrictions
Power	$d^{\exp(a)}$	$0 < d < 1$
Logistic	$\frac{\exp(a_1 + \exp(a)d)}{1 + \exp(a_1 + \exp(a)d)}$	a_1 fixed $-\infty < d < \infty$

labels, obtained from the dose–toxicity skeleton of a new drug under experimentation. Let $x_j \in D$ be the dose level that patient j receives and Y_j be the binary DLT outcome for patient j , i.e.,

$$Y_j = \begin{cases} 1 & \text{if patient } j \text{ experiences a DLT} \\ 0 & \text{otherwise} \end{cases} \quad (1.1)$$

Let $\Omega_j = \{x_1, y_1, \dots, x_j, y_j\}$ denote the set of trial data (doses given and DLT outcomes) for the first j patients and $g(a)$ denote the prior distribution of a , which is defined on the set $\mathcal{A} = (-\infty, \infty)$. Then using Bayes' theorem (Bayes, 1763), we may obtain the posterior distribution of a , denoted as $f(a | \Omega_j)$:

$$f(a | \Omega_j) = \frac{g(a)L(a | \Omega_j)}{\int_{a \in \mathcal{A}} g(a)L(a | \Omega_j) da}, \quad (1.2)$$

where the likelihood $L(a | \Omega_j)$ is of the form

$$L(a | \Omega_j) = \prod_{l=1}^j \psi(x_l, a)^{y_l} [1 - \psi(x_l, a)]^{1-y_l}. \quad (1.3)$$

The posterior belief about the shape of the dose–toxicity curve, derived from the posterior distribution of a , allows us to select a dose level that has an estimated probability of DLT as close to the desired TTL as possible; we denote the TTL as θ here. O'Quigley et al. (1990) propose two different, but closely related, estimators. One obtains the posterior mean of a , denoted as \hat{a} , and uses this plug-in estimate to find x_{j+1} , the dose for the next patient, i.e.,

$$\hat{a} = \int_{a \in \mathcal{A}} a f(a | \Omega_j) da, \quad (1.4)$$

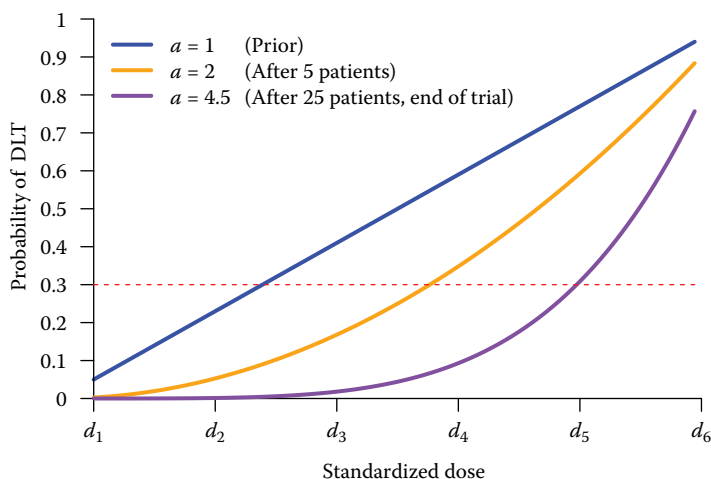
$$x_{j+1} = \arg \min_{d_i \in D} (\psi(d_i, \hat{a}) - \theta)^2. \quad (1.5)$$

The other approach integrates over the distribution of a to obtain a posterior mean estimate of $\psi(d_i, a)$ for $i = 1, \dots, k$ and finds the dose with mean probability of DLT closest to θ :

$$x_{j+1} = \arg \min_{d_i \in D} \left(\int_{a \in \mathcal{A}} \psi(d_i, a) f(a | \Omega_j) da - \theta \right)^2. \quad (1.6)$$

Once the dose has been chosen for patient $j + 1$, the trial repeats the above computation based on the trial data set Ω_{j+1} , which is formed by the union of Ω_j and $\{x_{j+1}, y_{j+1}\}$, the dose and DLT outcome of patient $j + 1$. The trial is either stopped after an MTD estimate has been reached with a sufficient level of certainty or when a maximum number of patients have been treated (see Section 1.4.2). The CRM may also be used using maximum likelihood estimation to update the parameter a and determine dose escalation for future patients (O'Quigley and Shen, 1996). Rather than using a prior distribution $g(a)$ for a , the 3 + 3 design is used as a start-up rule until the first DLT response is observed (estimation of \hat{a} requires at least one DLT response and one non-DLT response). After this, maximum likelihood estimation is used to estimate a , with dose escalation and MTD selection conducted as shown in Equation 1.5. An example of how the shape of the dose–toxicity curve changes with more data is shown in Figure 1.3.

There are several advantages to using the CRM instead of the 3 + 3 design. First, the CRM incorporates all trial information into the dose-escalation decision-making process, rather than just the current cohort as in the 3 + 3 design. Furthermore, an explicit TTL θ can be stated, which means that the MTD identified at the end of the trial has a meaning

**FIGURE 1.3**

Example of how dose–toxicity curve changes with patient data, assuming a power model for the CRM design. Here, at the end of the trial seeking a dose with probability of DLT as close to $\theta = 0.30$ as possible, dose level d_5 is selected as the MTD.

to both statisticians and clinicians. The CRM provides faster dose escalation and more accurate convergence to the true MTD than the 3 + 3 design (O’Quigley et al., 1990; Le Tourneau et al., 2009), as shown in numerous simulation studies (O’Quigley, 1999; Thall and Lee, 2003; Iasonos et al., 2008; Onar et al., 2009; Onar-Thomas and Xiong, 2010). In its original form, the faster dose-escalation had the potential to lead to patients being assigned to high dose levels. The model and dose-escalation schematic of the CRM are easily adaptable to circumvent this problem, and several papers have proposed various changes to aspects of the original CRM design. In particular, it is now common practice to start the trial at the lowest dose under experimentation and to not escalate more than one dose level per patient (O’Quigley and Chevret, 1991; Faries, 1994; Goodman et al., 1995; Møller, 1995). There have also been investigations into how the prior distribution and dose–toxicity skeleton should be chosen (Cheung, 2011; Lee and Cheung, 2011; Iasonos and O’Quigley, 2012), as well as appropriate stopping rules for trials using the CRM (O’Quigley and Reiner, 1998; Zohar and Chevret, 2001) (Section 1.4.2) and how the CRM performs under model misspecification. While one can never truly know if they have chosen the correct model for the dose–toxicity curve, several studies have shown that while operating characteristics may be different under different model choices, a simple one-parameter CRM is likely to be more robust in targeting the correct MTD (Paoletti and Kramar, 2009; Iasonos et al., 2016).

1.3.2 Escalation with overdose control (EWOC)

In order to overcome concerns about quickly escalating doses and overdosing patients under the CRM, Babb et al. (1998) proposed the *escalation with overdose control* (EWOC) design. Under the EWOC design, the posterior distribution of the MTD is updated after each patient, and a chosen percentile of the MTD distribution is used to select doses for future patients. This percentile, denoted as α , is known as the *feasibility bound* and reflects how conservative investigators are in escalating dose levels between patients. The feasibility bound can be interpreted via a decision-theoretic loss function, which describes the relative

preference of underdosing a patient compared to overdosing a patient. For some dose level d and MTD μ , the loss function for feasibility bound α is

$$\text{Loss}(d, \mu) = \begin{cases} \alpha(\mu - d) & \text{if } d \text{ is an underdose, i.e., } d \leq \mu \\ (1 - \alpha)(d - \mu) & \text{if } d \text{ is an overdose, i.e., } d \geq \mu. \end{cases} \quad (1.7)$$

In words, for any $\delta > 0$, the loss incurred by overdosing a patient (with respect to the MTD μ) by δ units is $\frac{1-\alpha}{\alpha}$ times greater than underdosing a patient by δ units (Babb et al., 1998; Babb and Rogatko, 2001). For $\alpha < 0.50$, the loss function in Equation 1.7 places a higher penalty on overdosing, whereas if $\alpha = 0.50$, one is indifferent between overdosing and underdosing patients. In order to conduct dose escalation, Babb et al. (1998) proposed a two-parameter logistic function to model the probability of DLT, given dose level d_i :

$$\psi(d_i, a_1, a_2) = \frac{\exp(a_1 + \exp(a_2)d_i)}{1 + \exp(a_1 + \exp(a_2)d_i)}, \quad (1.8)$$

where a_1 and a_2 are model parameters. If for MTD μ , we denote $\psi(\mu, a_1, a_2) = \theta$ and for the lowest dose level d_1 , we denote $\psi(d_1, a_1, a_2) = \rho_0$ for some probability $\rho_0 \in (0, 1)$, one can transform these expressions and rewrite a_1 and a_2 as

$$a_1 = \frac{\mu \text{logit}(\rho_0) - d_1 \text{logit}(\theta)}{\mu - d_1} \quad \text{and} \quad a_2 = \log \left(\frac{\text{logit}(\theta) - \text{logit}(\rho_0)}{\mu - d_1} \right). \quad (1.9)$$

So, a_1 and a_2 can be expressed in terms of μ , the MTD, and ρ_0 , the probability of toxicity at dose d_1 . These parameters are more meaningful to clinicians and can be used in the Bayesian updating procedure by placing prior distributions upon μ and ρ_0 (Kadane et al., 1980; Babb et al., 1998). For prior distributions on μ and ρ_0 , Babb et al. (1998) suggest a uniform distribution over the interval $[d_1, d_k]$ for μ and a uniform distribution over the interval $[0, \theta]$ for ρ_0 , though others have been proposed (Tighiouart et al., 2005). Similar to Equation 1.2, the joint posterior distribution for μ and ρ_0 given trial data Ω_j and prior distribution $g(\mu, \rho_0)$, denoted as $f(\mu, \rho_0 | \Omega_j)$, can be obtained. With this, the marginal cumulative distribution function of μ , $H_j(\mu')$ is

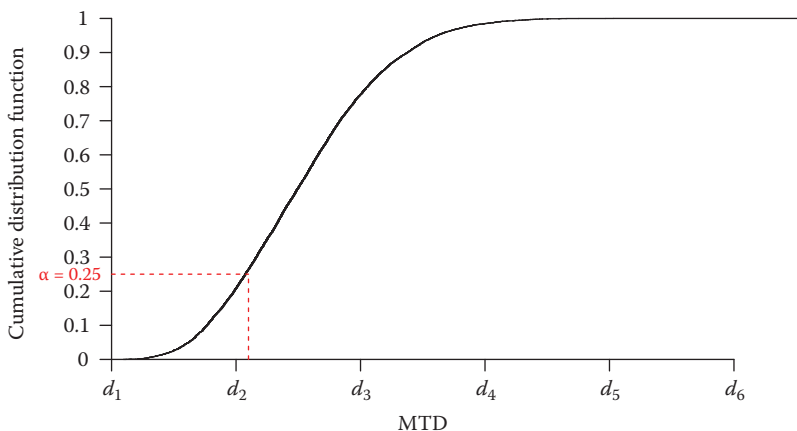
$$H_j(\mu') = \mathbb{P}(\mu \leq \mu' | \Omega_j) = \int_{x_1}^{\mu'} \int_0^{\theta} f(\mu, \rho_0 | \Omega_j) d\rho_0 d\mu, \quad (1.10)$$

and the dose for patient $j + 1$, x_{j+1} is chosen as

$$x_{j+1} = \arg \min_{d_i \in D} \left\{ (H_j(d_i) - \alpha)^2 \right\}. \quad (1.11)$$

Figure 1.4 illustrates how dose is chosen based on the cumulative distribution function of the MTD; in this instance with $\alpha = 0.25$ (i.e., overdosing is three times worse than underdosing), d_2 is the closest dose level and so would be chosen as the dose for the next patient.

The EWOC model is more conservative in dose escalation relative to the CRM. However, in some cases, the MTD estimated at the end of the trial may be a dose level not used for any patient throughout the trial (Berry et al., 2010). To overcome this, several trials have let the feasibility bound α increase as more patients are accrued (Babb and Rogatko, 2001, 2004; Cheng et al., 2004; Chu et al., 2009; Tighiouart and Rogatko, 2010). As information accrues during the trial, one can afford to be less conservative and escalate more quickly in order to identify the MTD. This can be achieved by letting α increase toward some upper limit, say 0.50, at which point the EWOC approach with $\alpha = 0.50$ is equivalent to a CRM model that uses the posterior median of the MTD distribution to select the next dose level [see Appendix B.3.1 of Carlin and Louis (2009)]. However, the mechanism by which α changes during the trial requires careful consideration (Wheeler, 2016).

**FIGURE 1.4**

Example of dose selection for the EWOC approach with feasibility bound $\alpha = 0.25$.

1.3.3 Toxicity probability interval designs

The toxicity probability interval (TPI) (Ji et al., 2007) and modified TPI (mTPI) (Ji et al., 2010) designs are model-based alternatives to the 3 + 3 design where posterior probabilities for the risk of DLT belonging to each of three intervals determine whether the dose for the next cohort is escalated, held at the current dose, or de-escalated. Each dose level's probability of causing a DLT is assigned a vague prior distribution (Ji et al., 2007, 2010, use beta distributions), and the number of patients and the number of DLTs at each dose are used to update these prior distributions, using what is known as a beta-binomial model. Three intervals, $U = [0, \theta - \epsilon_1]$, known as the underdosing interval, $P = [\theta - \epsilon_1, \theta + \epsilon_2]$, the proper dosing interval, and $O = (\theta + \epsilon_2, 1]$, the overdosing interval, are specified; the cutoffs ϵ_1 and ϵ_2 can be elicited from clinicians. Under the mTPI design at current dose level d_i , with the probability of DLT parameter p_i , the ratio between the area of the distribution p_i within each interval and its width is calculated. If the ratio is maximized for interval U , then the dose is escalated; if the ratio is maximized for interval P , then the dose stays at the same level; if the ratio is maximized for interval O , then the dose is de-escalated. The use of a beta-binomial model means that calculations to obtain the posterior probability distribution of DLT at each dose are computationally fast and simple. Furthermore, the simple escalate/stay/de-escalate rules are analogous to the 3 + 3 design, which many clinicians are familiar with, except that under the mTPI design, a TTL can be explicitly targeted and estimates of p_i at the end of the trial (using isotonic regression, for example) can be used to choose the MTD. Ji and Wang (2013) conducted a simulation study that showed the mTPI design recommended the correct MTD more often and overdoses less often than the 3 + 3 design, and the mTPI design can even be run using Microsoft Excel, making it accessible to those without advanced statistical programs.

1.3.4 Curve-free methods

Several approaches exist for dose-finding studies where an explicit model relating dose level to the probability of DLT is not required. Gasparini and Eisele (2000, 2001) proposed the use of a *product of beta prior* (PBP) approach, which induces a monotonic relationship between dose and probability of toxicity without specifying a particular model form. Given dose and toxicity outcome data for current patients in the trial, the dose for the next cohort

of patients is that with a posterior probability of DLT closest to the TTL θ . A potential problem with the curve-free approach of Gasparini and Eisele (2000) is that it becomes stuck at a dose level and is unable to escalate even after observing many non-DLT responses (Cheung, 2002, 2011). Whitehead et al. (2010) also proposed a curve-free approach, where decisions to escalate are based on maximizing the probability of the risk of toxicity being equal to θ . In essence, discrete risks of toxicity are specified at the start of trial (say, 0.05, 0.10, 0.20, 0.30, and 0.60), and after observing dose and toxicity data, the posterior probability that the risk of toxicity is equal to each of the discrete risks is calculated. This form of design has been adapted for a trial of two agents in combination (Whitehead et al., 2012), including an extension with both toxicity and efficacy outcomes (Whitehead et al., 2011) (see Section 1.4.3). While curve-free methods do not assume a specific form for the relationship between dose and toxicity, separate assumptions are required to be made on the prior probabilities of DLT at each dose to be considered in the trial. O’Quigley (2002) provides a discussion on the equivalence of the CRM and the curve-free approach of Gasparini and Eisele (2000), in the sense that identical operating characteristics can be obtained from each method by specifying appropriate design quantities for each design.

1.3.5 Optimal design theory approaches

Haines et al. (2003) proposed the use of optimal design theory for dose-escalation decision making. In particular, Bayesian D -optimality was proposed, which chooses the dose level that minimizes the global variance of the model parameters, or equivalently, maximizes the information that can be obtained about the shape of the dose-toxicity relationship, subject to additional toxicity constraints. Other optimal design theoretic approaches for phase I trials have been proposed, particularly for trials with multiple outcomes and for combination therapies, though they require additional constraints or penalization in order to prevent unethical dose recommendations (Mats et al., 1998; Dragalin and Fedorov, 2006; Dragalin et al., 2008; Roy et al., 2009; Pronzato, 2010; Fedorov and Leonov, 2013; Azriel, 2014; Haines and Clark, 2014).

1.4 Modifications to Proposed Designs

The designs in Sections 1.2 and 1.3 are not necessarily fixed in how they are conducted. Methodologists and clinicians have proposed several modifications to these approaches in order to overcome potential design pitfalls, or because of specific requirements/constraints in their trials.

1.4.1 Start-up rules

A clinician may deem it problematic to immediately use a statistical model to determine dose escalation for the first few patients, especially if very little is known about how a novel drug behaves in human patients. For example, when using a Bayesian model, if the prior distributions for the model parameters are highly variable, one may not be comfortable in using these distributions to determine dose-escalation decisions until some data are obtained. Similarly, if one wishes to use maximum likelihood estimation methods to estimate parameters, we will not be able to obtain maximum likelihood estimates of the parameters until we observe heterogeneous DLT responses, i.e., at least one non-DLT response and at least one DLT response. Therefore, an initial dose-escalation rule may be used in order to

obtain preliminary toxicity data before the statistical model is implemented. For example, the likelihood approach of the CRM (O’Quigley and Shen, 1996) uses the 3 + 3 design as a start-up rule until the first DLT outcome is observed, before then reverting to the CRM modeling approach described in Section 1.3.1. Iasonos and O’Quigley (2012) recommend using data from the first stage of the design to inform the structure of the skeleton to be used for the CRM in the second stage. Ivanova et al. (2003) proposed an alternative start-up rule that depends on the TTL, primarily aiming to conserve patient resources and enable the first dose given under the main design to be closer to the MTD. For optimal design approaches, Haines et al. (2003) constructed a constrained optimal design in the first stage, i.e., allocated a small number of patients across the dose levels so that information about the dose–toxicity curve was maximized, yet patients were not placed at toxic doses. After data on these patients were obtained, they proceeded with their sequential dose-escalation approach.

1.4.2 Stopping rules

As well as considerations for how to start a trial, the criteria for stopping a dose-escalation trial need to be stated. Stopping a trial before a maximum number of patients have been treated is considered for two reasons; either the MTD is judged to be outside of the planned set of doses to be experimented on (i.e., all doses are too toxic, or all doses have a probability of DLT well below the TTL), or the addition of more patients into the trial is unlikely to yield any more information that would change the current MTD estimate. There exist several different approaches for determining when it is suitable to stop a phase I trial. For example, Thall and Russell (1998) recommend terminating a trial if the posterior probability of all dose levels having a DLT rate above (or below) the TTL is at least 0.90, and this has been implemented as a safety constraint in many other dose-escalation designs (Yin et al., 2006). With respect to stopping a trial early when a suitably accurate MTD estimate has been obtained, several rules have been proposed, particularly for the CRM. These include stopping a trial when a fixed number of patients have been consecutively dosed at one dose level (Korn et al., 1994), when the width of the confidence interval for the MTD reaches a particular level (O’Quigley et al., 1990), or stopping when the probability that the next m patients to be dosed in the trial are given the same dose level exceeds some level (e.g., 0.90) (O’Quigley and Reiner, 1998; Zohar and Chevret, 2001; O’Quigley, 2002). The choice of one or more stopping rules for a trial is ultimately dependent on the number of patients available, as well as the statistical expertise at hand, the prior knowledge of the dose–toxicity relationship, and the number of dose levels under consideration.

1.4.3 Choice of endpoints

The methods discussed so far all use a single binary outcome for the occurrence of DLT. While conveniently simple, there are pitfalls to using such an endpoint. First, one has to wait for DLT outcomes to be recorded before making dose recommendations for the next cohort, thus potentially leading to long trial durations. Using a time-to-event (TITE) endpoint (see Chapter 3) can help to reduce trial duration, while still providing informed dose-escalation decision making. Also, toxicity outcomes are graded from 0 (no toxicity) to 5 (death), as per the NCI CTCAE (NCI, 2009), with intermediate gradings relating to the severity of a side effect. Rather than using a binary endpoint for DLT, a categorical endpoint for toxicity could be used so that recording of low-grade toxicities can provide information as to how toxic other doses might be; this can be done throughout the trial, or in the first stage of a two-stage design (Iasonos et al., 2011). Approaches incorporating toxicity gradings are discussed in Chapter 3. Furthermore, toxicities occurring in different

body systems may be more or less important to clinicians, and one may wish to reduce the number of different DLTs or high-grade toxicities a patient might receive on treatment; approaches using multiple toxicity constraints have been developed to this end (Bekele and Thall, 2004; Lee et al., 2011).

In addition to using toxicity information, efficacy outcomes may also be used to inform dose-escalation and end-of-trial dose recommendation; it may be the case that a biologically optimal dose (BOD) is sought, rather than an MTD. Several joint-outcome models have been proposed, using binary, categorical, and continuous efficacy outcomes, and these are explored in Chapter 5.

1.4.4 Combination therapies and schedules

Combination therapies are used frequently in the treatment of cancer, and many designs for escalating two or more drugs together have been proposed, though not necessarily implemented (Harrington et al., 2013). Combination dose-escalation studies can present difficulties not observed in single-agent trials, such as modeling interactive treatment/toxicity effects between drugs, deciding on the escalation strategy, attributing toxicity to one specific drug or a combination of several, and in order to explore several combinations, more patients are likely to be required. Furthermore, it is possible to recommend multiple MTDs to take forward to phase II trials. Nevertheless, the aforementioned designs and modifications discussed in this chapter have all motivated the design of dose-escalation studies with multiple drugs, some of which include graded outcomes, efficacy endpoints, and attributing toxicity to specific agents; these are explored in Chapter 6. Furthermore, approaches for conducting dual-agent dose-escalation studies can be used for single-agent trials to optimize both dose and schedule of treatment administration; these designs are discussed in Chapter 7.

1.5 Usage of Different Designs in Clinical Practice

Several reviews have shown that model-based designs have been used rarely for conducting phase I dose-escalation studies. One review of 1,235 phase I dose-escalation studies testing new anticancer agents between 1991 and 2006 found that 1,215 (98.4%) of such trials used the traditional 3 + 3 design or some variant, with only 17 trials (1.4%) using the CRM method and 3 trials using the EWOC design (Rogatko et al., 2007). Further, Le Tourneau et al. (2009) found that of 181 phase I clinical trials conducted between January 2007 and December 2008, 168 trials used the traditional 3 + 3 design (1 of which featured inpatient dose escalation) and 7 used the accelerated titration design. Of the remaining six trials, five used the modified CRM and one used the CRM design with a TITE endpoint (TITE-CRM) (see Chapter 3). In a review of single-agent phase I trials of molecularly targeted agents published between 2000 and 2010, Le Tourneau et al. (2012) found 6 (7.1%) out of 84 trials used a model-based design (specifically the modified CRM approach), and Rivoirard et al. (2016) assessed 228 radiochemotherapy phase I trials published between 1990 and 2015, finding 3 (1.3%) that used a model-based design (all TITE-CRM). With respect to planned phase I trials, a survey of 35 clinical trial units (CTUs) registered with the UK Clinical Research Collaboration showed that in the 7 CTUs involved in phase I trials, all ongoing studies were implementing the 3 + 3 design, with only 1 study being planned with the CRM (Jaki, 2013). While these reviews generally indicate few phase I trials have used model-based designs, there is a growing movement for changes in clinical practice. In particular, Iasonos and O'Quigley (2014) found 53 trials published between 2003 and 2013 that implemented

either the CRM, EWOC, or TITE-CRM designs, and recent papers have called for more early-phase cancer trials to use novel adaptive designs in practice (Petroni et al., 2017; Wong et al., 2016).

1.5.1 Barriers to adopting novel designs

The reluctance to use adaptive model-based designs for phase I dose-escalation studies has been attributed to numerous reasons, including lack of understanding of statistical methods, fears of lending control to statistical models, concerns about obtaining regulatory approval, lack of user-friendly software, or even just reluctance to break from traditional methods (Bailey et al., 2009; Gönen, 2009; Mandrekar et al., 2010; Harrington et al., 2013; Jaki, 2013). However, Bailey et al. (2009) described how in a phase I trial of nilotinib and imatinib in patients with imatinib-resistant gastrointestinal stromal tumors (GISTs), a close working relationship between the trial statisticians and clinicians with nontechnical training in related statistical concepts allowed all parties to be clear on interpreting trial findings and making dose-escalation decisions based on the model's recommendations. With respect to obtaining regulatory approval, the American Society of Clinical Oncology (ASCO), the US Food and Drug Administration (FDA), and the European Medicines Agency (EMA) have introduced guidance to encourage the use of Bayesian adaptive designs in oncology trials (Gaydos et al., 2006, 2012).

One of the more technical barriers to implementing adaptive model-based designs that Gönen (2009) highlighted was the specification of prior distributions for model parameters. However, for phase I trials, prior distributions can be obtained by working closely with clinical experts to elicit opinions about dose-toxicity relationships, by using information from past dose-escalation studies and other trials, and conducting sensitivity analyses and fine-tuning prior distributions so that unrealistic and unwanted model behavior is avoided (Legedza and Ibrahim, 2001; Geller, 2004; Rosenberger et al., 2005; Adamina et al., 2009; Cheung, 2011).

Perhaps the main reason for the infrequent use of novel adaptive designs in phase I trials is that an investigator insists on using a particular method (Jaki, 2013), either because the investigator has used it in past work or because previous studies in that disease area have used the same method. For phase I oncology trials, this means that the ubiquity of published trials using the 3 + 3 design will likely influence other investigators to use the 3 + 3 design also. Gönen (2009) also mentioned the challenge of motivating investigators to consider novel methods. While extensive simulation studies have shown several model-based designs to have much better operating characteristics than the standard 3 + 3 design (see Section 1.3.1), motivating investigators to consider new methods for future trials is dependent on overcoming all of the above barriers. Therefore, establishing good collaborative relationships between clinical and statistical experts [as discussed in the example trial of Bailey et al. (2009)] is likely to be fundamental to overcoming practical, technical, and motivational barriers (Harrington et al., 2013).

1.5.2 Available tools and software

Increases in computational power mean that advanced simulation studies to investigate model characteristics such as dose-escalation behavior and MTD recommendation can be conducted quickly with free, user-friendly software (Berry et al., 2010; Sweeting et al., 2013). Examples include the open software library of the MD Anderson Cancer Center*

* Division of Quantitative Sciences—Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Software Download Site: <https://biostatistics.mdanderson.org/SoftwareDownload>

and the Comprehensive R Archive Network (CRAN) library[†], which provide open-source programs for, among many other things, conducting and simulating dose-escalation studies. More information on available software for designing and assisting with phase I dose-finding studies is presented in Chapter 10.

1.6 Summary

Over the past three decades, many approaches have been proposed for conducting phase I dose-escalation studies. These include both rule-based and model-based approaches that, as this chapter and the rest of this handbook will show, can be tailored to suit a wide range of trials defined by the disease and treatments under study, the endpoints of interest, the patient population, as well as the clinical, statistical, and computational expertise available. The uptake of novel designs that exhibit vast improvements upon the traditional up-and-down methods, such as the 3 + 3 design, has long been hindered by several barriers, but there is a growing movement to design new trials using these methods and for more widespread changes to be made to clinical practice. A collaborative effort between clinicians and statisticians can help to overcome the barriers documented, leading to well-designed trials that will benefit trial participants and future patients.

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