



Optimal generalized truncated sequential Monte Carlo test



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ABSTRACT

When it is not possible to obtain the analytical null distribution of a test statistic U , Monte Carlo hypothesis tests can be used to perform the test. Monte Carlo tests are commonly used in a wide variety of applications, including spatial statistics, and biostatistics. Conventional Monte Carlo tests require the simulation of m independent copies from U under the null hypothesis, what is computationally intensive for large data sets. Truncated sequential Monte Carlo designs can be performed to reduce computational effort in such situations. Different truncated sequential procedures have been proposed. They work under restrictive assumptions on the distribution of U aiming to bound the power loss and to reduce execution time. Since the use of Monte Carlo tests are based on the situations where the null distribution of U is unknown, their results are not valid for the general case of any test statistic. In this paper, we derive an optimal scheme for truncated sequential Monte Carlo hypothesis tests. This scheme minimizes the expected number of simulations under any alternative hypothesis, and bounds the power loss in arbitrarily small values. The first advantage from this scheme is that the results concerning the power and the expected time are valid for any test statistic. Also, we present practical examples of optimal procedures for which the expected number of simulations are reduced by 60% in comparison with some of the best procedures in the literature.

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1. Introduction

The Monte Carlo test (MC) is an important tool to perform hypotheses tests when the distribution of the test statistic under the null hypothesis is unknown. Monte Carlo hypothesis testing is commonly applied in a wide variety of subject areas. The Scan statistic, [9], directed to detect spatial cluster is an example of a Monte Carlo test application in spatial statistics. In [6], Monte Carlo p -value is used to perform a likelihood ratio test for signal detection of adverse events in drug safety data.

Assuming that large values of U lead to the null hypothesis rejection, a Monte Carlo p -value is calculated based on the proportion of m simulated values that are larger than or equal to the observed value of U , with m defined a priori. This procedure can take a long time to run if the test statistic requires a complicated calculation as, for example, those involved in lengthy inferential procedures. These situations are exactly those where the MC tests are likely to be most useful, as analytical exact or asymptotic results concerning the test statistic U are hard to obtain. For example, the multivariate problem of finding spatial clusters of disease outbreak requires the use of computationally intensive testing procedures, like the flexibly shaped scan statistic proposed by [12]. These authors emphasize that the execution time of the flexibly

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shaped scan, which is based on a conventional Monte Carlo test procedure, can take as long as two weeks depending on the application.

The adoption of sequential procedures to carry out *MC* tests is a way to reach a faster decision. In contrast with the fixed *m* conventional *MC* procedure, in the sequential *MC* test the number of simulated statistics is a random variable. The basic idea is to stop simulating as soon as there is enough evidence either to reject or to accept the null hypothesis. For example, it is intuitively clear that, if the observed value u_0 of U is close to the median of the first 100 simulated values, the null hypothesis is not likely to be rejected even if we perform 900 additional simulations. Sequential Monte Carlo tests are procedures that provide decision rules about when to stop the simulations to decide against or for H_0 .

Let X_t be the number of simulated statistics under H_0 exceeding u_0 at t -th simulation. In general, sequential *MC* procedures track the X_t evolution by checking if it crosses an upper or a lower boundary. When it does, the test is halted and a decision is reached. Typically, crossing the lower boundary leads to the rejection of the null hypothesis while the upper boundary crossing leads to the acceptance of the null hypothesis.

There are different proposals for a sequential Monte Carlo test in the statistical literature. Some of these proposals provide a valid p -value, defined as a statistic $0 \leq P \leq 1$ such that, for all $0 \leq \alpha \leq 1$, we have $\mathbb{P}(P \leq \alpha) \leq \alpha$. [2] proposed a very simple scheme that provides a valid p -value for a sequential test with an upper bound n in the number of simulations of U . It depends on a single tuning parameter h , making it extremely simple to use. We stop the simulations when $X_t = h$ for the first time and $t < n + 1$. If $X_n < h$, the simulations are halted. The sequential p -value for this procedure is given by

$$P_{BC} = \begin{cases} X_t/t, & \text{if } X_t = h, \\ (X_t + 1)/(n + 1), & \text{if } X_t < h. \end{cases} \quad (1)$$

The support set of P_{BC} is

$$S = \{1/(n + 1), 2/(n + 1), \dots, h/(n + 1), h/n, \dots, h/(h + 2), h/(h + 1), 1\}.$$

We have $\mathbb{P}(P_{BC} \leq a) = a$ under the null hypothesis for $a \in S$ and therefore, P_{BC} is a valid p -value. Additional randomization can provide a continuous p -value with uniform distribution in the interval $(0, 1)$, rather than distributed on the discrete set S .

Therefore, the boundaries of [2] are given by the horizontal line $X_t = h$ and the vertical line $t = n$. There is no lower boundary but only a predetermined maximum number of simulations. Procedures with a bound on the maximum number n of simulations are called truncated sequential Monte Carlo test. The Besag and Clifford sequential *MC* test brings a reduction in execution time only when the null hypothesis is true. In this case, the number of simulated values greater than the observed u_0 tends to increase quickly. In contrast, when the null hypothesis is false, one will often run the Monte Carlo simulation up to its upper bound n . The observed value u_0 will tend to be large in this situation and the null hypothesis simulated values of U will likely be smaller than u_0 . Hence, X_t is updated very rarely, often not reaching the upper bound h after n simulations. Therefore, additional gains could be obtained by adopting a stopping criterion based on the small values of X_t . For any significance level α , [11] showed that one can design a Besag and Clifford sequential *MC* test with the same power as a conventional Monte Carlo test and with shorter running time. These authors also showed the puzzling result that this sequential Monte Carlo should have a maximum sample size equal to h/α , because the power is constant for $n \geq h/\alpha$.

In addition to [2], alternative sequential Monte Carlo tests have been suggested recently. These other procedures are mainly concerned with the resampling risk (RR), defined by [3] as the probability that the test decision of a realized *MC* test will be different from a theoretical *MC* test with an infinite number of replications. [3] proposed the curtailed sampling design where the procedure is interrupted and H_0 is not rejected if $X_t \geq \lfloor \alpha(n + 1) \rfloor$. If the number $t - X_t$ of simulations not exceeding u_0 is greater or equal to $\lceil (1 - \alpha)(n + 1) \rceil$ or the number of simulations reaches n , the procedure is interrupted and H_0 is rejected, where n is the maximum number of simulations. They also introduced the interactive push out (IPO) procedure that requires an algorithm to define the boundaries of the sequential procedure. This procedure is proven to decrease the sample size with respect to a curtailed sampling design. For all their results, [3] assumed a specific class of distribution for the p -value statistic, that distribution implied by a test statistic U that either follows the standard normal distribution under the null hypothesis and follows a $N(\mu, 1)$ under the alternative hypothesis or U follows a central or non-central $\chi_1^{(2)}$ under the null and alternative hypothesis, respectively. Conditional on this class of distributions, they found numerically the worst distribution to bound the resampling risk. IPO has a smaller expected execution time than the curtailed sampling design but its implementation is not practical for bounding the resampling risk in arbitrarily low values such as 0.01, for example. Also, the class of distributions for the p -value assumed in [3] is too restrictive, and we shall show in the Section 5 that it is not necessary to use restrictions on the p -value distribution to build sequential procedures that are fast and have good power properties.

[4] proposed an algorithm to implement a truncated Sequential Probability Ratio Test (tSPRT) to bound the resampling risk and studied its behavior as a function of the p -value. The algorithm, denoted here as the FKH, allows the calculation of a valid p -value, which depends on the calculation of the number of ways to reach each point on the stopping boundary of the *MC* test.

These previous works are devoted to propose sequential procedures to save execution time in the Monte Carlo test, which is also our main aim. In a different direction, [5] proposed a sequential algorithm whose main objective is to control the resampling risk. His algorithm produces an open-ended sequential procedure that uniformly bounds the resampling risk

in arbitrarily small values for any test statistic. This RR control is possible because the procedure considered is not truncated. In practice, it is necessary to establish a maximum number of simulations. The reason is that when the p -value p is close to α , the expected number of simulations can be unreasonably large. For example, if $p = 0.051$, according to an expression offered in [5], a lower bound for the expected number of simulations is 43,049. Even worse, if $p = \alpha$, [5] shows that the expected number of simulations is infinite. So, the lower bound for the expected number of simulations is inconveniently high when p is close to α , what is not uncommon. Therefore, the procedure proposed in [5] is not indicated to save the execution time. Since all his results are based on asymptotic arguments and valid only when the open-ended strategy is adopted, the effective control of the resampling risk and of the type I error for the procedure proposed by [5] is an open problem in practical terms.

[8] explored the approach from [3] to bound the resampling risk using their same restrictive class of p -value distributions. She used the B -value boundaries proposed by [10] and applied the algorithm of [4] to obtain valid p -values. She was able to obtain arbitrarily low bounds to the resampling risk and showed empirically that the B -value boundaries produce a smaller expected number of simulations than the IPO designs. In that paper, she also defined an approximated B -value procedure, which has analytical formulas that give insights on the choice of parameter values of the exact B -value design and, because it avoids the use of the FKH algorithm, it is simpler to use. These B -value boundaries have the main advantages from the other procedures cited and, in our opinion, it is the best alternative for a sequential MC test at the moment. However, its main results, concerning the resampling risk and the expected number of simulations, depend on the same restrictive class of p -value distributions of [3]. Moreover, important topics were not explored for the B -value boundaries such as, for example, its power with respect to the conventional MC test or the establishment of lower bounds for the expected number of simulations for the general case of any test statistic.

These previous papers do not consider bilateral sequential tests. To decrease the computational burden of bootstrap tests, [7] proposed the *conditional repeated significance test* (CT), a resampling sequential scheme for bilateral tests. The CT procedure defines two outer barriers and two inner barriers. The inner boundaries indicate the moment in which the procedure should be interrupted and the null hypothesis accepted, while the outer boundaries serve to reject the null hypothesis. [7] bounds the power loss with respect to a test with fixed sample size. The main sequential characteristics of this previous work, such as the establishment of bounds for the expected number of simulations under the alternative hypothesis and the obtainment of a valid value- p , were not evaluated as this was not the objective of the paper. The average simulation time of CT method is considerably small but, as we shall show in Section 7, the optimal sequential procedure we propose here is substantially faster.

In this paper, we introduce a generalized truncated sequential Monte Carlo test allowing any monotonic shapes for the boundaries. For example, it is possible to construct boundaries which are close to each other in the beginning of the simulations, departing from each other as the simulations proceed and approaching each other again at the simulations number upper limit. We have been able to provide expressions to calculate the expected number of simulations under the null hypothesis, to bound the expected number of simulations under the alternative hypothesis, and to bound the power loss of the sequential MC test. These expressions are valid for any α level and for the general case of any test statistic. Moreover, we are able to provide the optimal truncated boundaries that lead to a design with minimum expected sampling size and the boundaries are easily calculated. Another advantage of our proposal is the simple calculation of a valid p -value dispensing the use of more elaborate algorithms such as the FKH. We show for many practical values of α and n that our optimal barriers lead to the expected running time considerably smaller than the present alternative sequential procedures, in some cases as small as 60% of the best one presently available. Concerning the resampling risk, we consider a larger class of distributions for the p -value than the class considered in [3]. We show that the class we consider allows to explicit algebraic manipulation leading to the calculation of resampling risk bounds for any sequential MC test design. All our results are extended for two-sided tests.

This paper is organized in the following way. In the next section, we describe the B -value boundaries. Section 3 defines our generalized sequential MC test and presents expressions for size, power, and expected number of simulations. In Section 4 we discuss a general class for the p -value distribution and provide some analytical results for the sequential tests. Section 5 presents an optimal design of boundaries, some specific suggestions for practical use, and a comparison with the B -value procedure in terms of execution time. Section 6 has a discussion concerning the flexibility of our sequential procedure for constructing a wide variety of shapes for the stopping boundaries. Section 7 extends all results for two-sided tests, and Section 8 closes the paper with some conclusions.

2. The B -value procedure

Consider a hypothesis test of a null hypothesis H_0 against an alternative hypothesis H_A by means of a test statistic U . When the null distribution of U is known, we can calculate the p -value analytically and we say that we have an exact test. If this null distribution is not available, the MC test can be seen as an estimation procedure for the unknown decision based on the exact test. [8] has adopted this point of view by seeing the MC test as a procedure to decide either the exact p -value associated with the test statistic U belongs either to the rejection region $(0, \alpha]$ or to the acceptance region $(\alpha, 1)$. The parameter α is the significance level of the exact test. This interpretation leads to the following pair of hypotheses:

$$H_0^* : p \leq \alpha$$

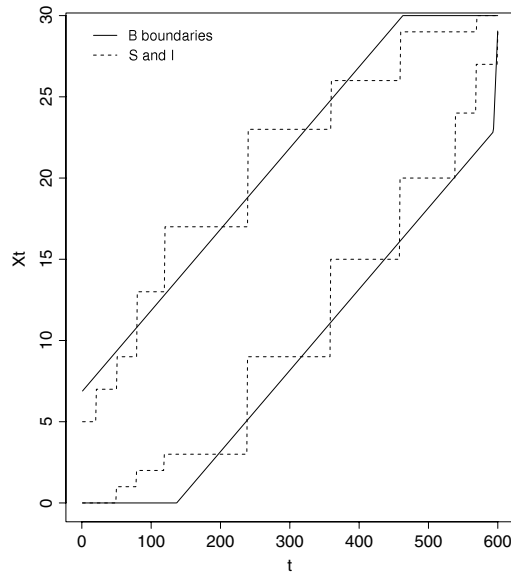


Fig. 1. Example of the MC_G (S and I) and B boundaries with $\alpha = 0.05$ and a maximum number of simulations equal to $n = 600$.

$$H_A^* : p > \alpha \tag{2}$$

where p is the realized and unknown p -value. Viewed as a random variable, we denote the p -value by P . Clearly, the decision in favor of any of the above hypotheses leads to a decision concerning the original hypotheses H_0 and H_A .

Let u_0 be the observed value of the test statistic U based on a fixed sample and let u_1, u_2, \dots be independently simulated values from U under H_0 . Let

$$X_t = \sum_{i=1}^t 1_{\{[u_0, \infty)\}}(u_i),$$

where $1_{\{[u_0, \infty)\}}(u_i)$ is the indicator function that $u_i \geq u_0$.

[8] used the B -value introduced by [10] to propose a sequential procedure to test H_0^* versus H_A^* .

Define $V(t) = \min \{x \geq 0 : x - tx \geq c_1 \{n\alpha(1 - \alpha)\}^{1/2}\}$ and $L(t) = \max \{x \geq 0 : x - t\alpha \leq c_2 \{n\alpha(1 - \alpha)\}^{1/2}\}$.

Let $B_{upper} = \{(t, x) = (t, \min\{V(t), r_1\}) : t = t_0^+, t_0^+ + 1, \dots, n\}$ be the upper boundary, and $B_{lower} = \{(t, x) = (t, \max\{L(t), t - r_0\}) : t = t_0^-, t_0^- + 1, \dots, n\}$ be the lower boundary of a sequential procedure, where t_0^+ is the smaller value of t such that $V(t) \leq t$ and t_0^- is the smaller value of t such that $L(t) \geq 0$. Similarly, let t_1^+ be the smaller value of t such that $V(t) \geq r_1$ and t_1^- the smaller value of t such that $L(t) \leq t - r_0$. The stopping boundaries from [8] are given by $B = B_{lower} \cup B_{upper}$. The B boundaries are formed by the union of linear functions in t . Tuning parameters c_1 and c_2 were specified by [8] using numerical calculations in order to reduce the expected number of simulations. Fig. 1 illustrates with solid lines the B -boundaries B_{upper} and B_{lower} using $c_1 = -c_2 = 1.282$, $n = 600$ and $\alpha = 0.05$. The choice of c_1 and c_2 here is just following the specification used by [8]. This is one among the best choices tabled by [8] in the sense of having small execution times.

The upper boundary B_{upper} is formed by the union of the line $V(t) = c_1 \{n\alpha(1 - \alpha)\}^{1/2} + t\alpha$ until $t = t_1^+$, when the upper boundary becomes the horizontal line with height $r_1 = \lfloor \alpha(n + 1) \rfloor$. The lower boundary B_{lower} is formed by the line $L(t) = c_2 \{n\alpha(1 - \alpha)\}^{1/2} + t\alpha$ up to $t = t_1^-$ when it becomes the vertical line $r_0 = t - \lceil (1 - \alpha)(n + 1) \rceil$.

The simulations are interrupted in the first time that X_t reaches one of the boundaries. [8] uses ϕ_{FKH} , the test criterion based on the valid p -value presented in [4]. The valid p -value is defined as $\hat{p}_v(X_t, t) = F_{\hat{p}_{MLE}}(X_t/t)$, where \hat{p}_{MLE} is the maximum likelihood estimator of p and $F_{\hat{p}}$ is defined in (5.2) from [4]. The estimate $\hat{p}_v(X_t, t)$ of the p -value can be computed using the FKH algorithm. The test adopted by [8] for the B boundaries is given by:

$$\phi_{FKH}(t, x) = \begin{cases} 1, & \text{if } \hat{p}_v(x, t) \leq \alpha \\ 0, & \text{if } \hat{p}_v(x, t) > \alpha. \end{cases}$$

When $\phi_{FKH}(t, x) = 0$, the hypothesis H_0 is not rejected, because $H_0^* : p \leq \alpha$ is rejected. Henceforth, this procedure is called MC_B .

It is important to remark that there is no need to check the value of X_t at every moment t . To see this, note that the boundaries B_{upper} and B_{lower} are composed by non-integer numbers while X_t is a count. As a consequence, there will be times t for which the simulations cannot be interrupted by B_{lower} and therefore there is no need to check against the lower

boundary at these times. To illustrate this, consider the boundaries B_{upper} and B_{lower} between the times 134 and 179 in the Fig. 1 represented by the solid lines. The lower boundary is equal to zero until $t = 136$ and it is formed by numbers smaller than 1 until $t = 156$. Therefore, X_t reaches the lower boundary during this period if $X_{137} = 0$ and there is no need to check against it for $t \leq 156$. Likewise, if X_t is not interrupted by B_{lower} at $t = 157$ (that is, if $X_{157} > 2$), it will not reach it at least until $t = 176$. Therefore, in practice, there is no need to check against the lower boundary for every simulated value. One needs to check only on those times t such that

$$\lceil B_{\text{lower}}(t - 1) \rceil < \lceil B_{\text{lower}}(t) \rceil$$

for $t = t_1, \dots, n$, where t_1 is the greatest value of t such that $B_{\text{lower}}(t) = 0$. This will be explored by our generalized sequential Monte Carlo method described in Section 3.

Since B_{upper} will typically be non-integer, it is always possible to define step functions equivalent to the upper boundary. To see this, consider again Fig. 1. From $t = 134$ to $t = 143$, the slowly increasing values of $B_{\text{upper}}(t)$ could be all substituted by 14 and the procedure would remain the same.

2.1. Bounding the resampling risk of MC_B

[3] considered the IPO procedure, which adjusts an initial set of boundaries as the simulations proceeds. This method allows the bounding of the resampling risk. The IPO procedure is not described in details here, but it should be noted that it is a computationally intensive procedure, and its implementation is intractable for small values of resampling risk. [3] considered a rather restrictive class of p -value distributions, with cumulative distribution function given by:

$$H_{\alpha, 1-\beta}(p) = 1 - \Phi \left\{ \Phi^{-1}(1-p) - \Phi^{-1}(1-\alpha) + \Phi^{-1}(\beta) \right\} \quad (3)$$

where $\Phi(\cdot)$ is the cumulative distribution function of a standard Normal distribution, α is the desired significance level and β is the type II error probability. When $\alpha = 1 - \beta$, the cumulative distribution $H_{\alpha, 1-\beta}(p)$ has a uniform distribution on $(0, 1)$, as is expected when H_0 is true.

The p -value distribution defined in (3) assumes a variety of shapes, but the analytical manipulation of the resampling risk or of the expected number of simulations is intractable. To circumvent this problem, [3] used a Beta(a, b) distribution to approximate $H_{\alpha, 1-\beta}(p)$, and this approximation is denoted by $\tilde{H}_{\alpha, 1-\beta}(p)$. This approximation is chosen such that the expected value of P coincides with that from $H_{\alpha, 1-\beta}(p)$ and such that $\tilde{H}_{\alpha, 1-\beta}(\alpha) = H_{\alpha, 1-\beta}(\alpha) = 1 - \beta$. Numerical studies were performed by [3] to obtain the worst case \tilde{F} within the class (3) in the sense of having the largest resampling risk. Let \tilde{F}^* be the correspondent Beta distribution approximation to \tilde{F} .

Although MC_B is simpler and it presents a smaller expected time execution than the IPO procedure, it depends on the FKH algorithm which requires rather complex modifications for each type of sequential design. [8] proposes an approximation for the MC_B procedure. With this approximation, if B_{upper} is reached before B_{lower} , H_0^* is rejected, while H_A^* is accepted if B_{lower} is reached first. The approximation may be used to gain analytic insights on the properties of the MC_B procedure or to help on choosing the parameters c_1 , c_2 , and n , as well as providing an approximation for the expected number of simulations. An undesirable characteristic of the approximated MC_B is that it is not truncated and the expected number of simulations must be calculated letting the maximum number of simulations go to infinity. Moreover, the approximation to MC_B does not offer a guarantee that the type I error probability is under control for any choice of c_1 and c_2 . For this reason, the approximated MC_B will not be explored here.

3. Our proposed generalized truncated sequential Monte Carlo test

The analytical treatment of the MC test power function is a cumbersome task when it is based on two interruption boundaries. The reason is that it involves the calculation of the large number of possible trajectories of the random variable X_t responsible for the rejection of H_0 . [4] present an algorithm to calculate this number, and they used this algorithm to obtain both, the expected number of simulations and the resampling risk, for each fixed p -value. [4] emphasize that such algorithm is valid only for the specific sequential procedure treated in that article, and adjustments are needed to use it with other sequential designs. [8] also used that algorithm for her calculations, and the approximated MC_B is an attempt to escape from the dependence on special algorithms.

Aiming to overcome this limitation, we propose a truncated sequential procedure with two boundaries that have the shape of step functions. The values of X_t are checked against the upper boundary for every t while they are checked against the lower boundary in an arbitrary set of predetermined discrete moments, possibly a smaller set than all integers between 1 and n . The motivation for this design, where the lower boundary monitoring is not carried out for every time t , is to allow for the analytical treatment of the power function, to allow for the building of optimal boundaries in the sense of minimizing the expected simulation time, and to allow for the calculation of the expected number of simulations of the sequential MC test for any test statistic. We also bound the resampling risk of our sequential MC test.

Let $\eta^l = \{n_1^l, \dots, n_{k_1}^l\}$, with $n_j^l < n_{j+1}^l$, be a set containing the moments when X_t must be checked against the lower boundary given by the values $I = \{I_1, \dots, I_{k_1}\}$. If $X_{n_j^l} < I_j$, the simulations are interrupted and H_0 is rejected.

The monitoring of X_t with respect to the upper boundary crossing is carried out at all moments $t = 1, \dots, n$ and this upper boundary is also a step function. Let $\eta^S = \{n_1^S, \dots, n_{k_2}^S\}$, with $n_j^S < n_{j+1}^S$ be the jump moments for the upper boundary. For $n_{j-1}^S < t \leq n_j^S$, the upper boundary is given by S_j where $n_0^S = 0$ and $S_1 < S_2 \dots < S_{k_2}$. Let $S = \{S_1, \dots, S_{k_2}\}$. Therefore, the simulations are interrupted if $D_t = 1$, where:

$$D_t = \begin{cases} 1, & \text{if } (t \in \eta^l \text{ and } X_t < I_j) \text{ or } (X_t = S_j, \text{ for } n_{j-1}^S < t \leq n_j^S) \\ 0, & \text{otherwise} \end{cases} \tag{4}$$

or if the number of simulations reaches a predetermined maximum equal to n .

Let x_t be the observed value of the random variable X_t . The p -value can be estimated by:

$$p_G = \begin{cases} x_t/t, & \text{if } x_t = S_j \text{ and } n_{j-1}^S < t \leq n_j^S \\ (x_t + 1)/(t + 1), & \text{if } x_t < I_j \text{ and } t = n_j^l. \end{cases} \tag{5}$$

We define the test decision function for this sequential test by:

$$\phi_G(t, x) = \begin{cases} 1, & \text{if the lower boundary } I \text{ is reached before } S \text{ or } t = n \\ 0, & \text{if the upper boundary } S \text{ is reached before } I. \end{cases}$$

The hypothesis H_0 is rejected if $\phi_G = 1$ and it is not rejected if $\phi_G = 0$. This sequential MC test will be denoted by MC_G . As an example, take $k_1 = k_2 = 10, n = 600$, and consider $\eta^l = \eta^S = \{20, 50, 79, 119, 239, 359, 459, 539, 569, 600\}$. For the lower and upper boundary values, consider the sets $I = \{0, 1, 2, 3, 9, 15, 20, 24, 27, 29\}$ and $S = \{5, 7, 9, 13, 17, 23, 26, 29, 29, 30\}$, respectively. Fig. 1 shows these boundaries as dashed lines.

The choice of the boundaries is closely linked to the desired α_{mc} , which is equal to 0.05 in this example. In Section 5, we show how to find in a simple way the optimal boundaries to minimize the expected number of simulations for any α_{mc} and n .

3.1. Power and size of the MC_G

In the MC_G procedure, the rejection of H_0 occurs in the first moment $t = n_j^l$ such that $x_t < I_j$. The power calculation is simpler if we merge the two sets η^l and η^S . Define $\eta = \eta^l \cup \eta^S = \{n_1, \dots, n_k\}$ with $k = \#\eta$. Let $S' = \{S'_1, \dots, S'_k\}$ be the upper boundary adjusted for each $n_i \in \eta$ in the following way. If $n_i = n_j^S \in \eta^S$ for some j , then $S'_i = S_j$. If $n_i \in \eta^l \cap (\eta^S)^c$, then $S'_i = S_j$ where j is such that $n_j^S = \max_r \{n_r^S : n_r^S < n_i\}$. Thus, if n_i matches with some jump time in the set η^S , then S'_i is equal to the value in S for the time n_i . If n_i is not an element in η^S , then S'_i is the jump value of the η^S time immediately preceding n_i .

Similarly, let $I' = \{I'_1, \dots, I'_k\}$ be the adjusted lower boundary. That is, when $n_i = n_j^l \in \eta^l$ for some j , then $I'_i = I_j$. If $n_i \in \eta^S$ but $n_i \notin \eta^l$, then $I'_i = I_j$ where j is such that $n_j^l = \max_r \{n_r^l : n_r^l < n_i\}$.

Thus, for a given value of $p \in (0, 1)$, the power function of the MC_G procedure, is given by:

$$\begin{aligned} \pi_G(p) = & \sum_{x_1=0}^{I'_1-1} C_{x_1}^{n_1} p^{x_1} (1-p)^{n_1-x_1} + \sum_{x_1=I'_1}^{\min\{S'_1-1, I'_2-1\}} \sum_{y=0}^{\min\{I'_2-x_1-1, n_2-n_1\}} C_y^{n_2-n_1} C_{x_1}^{n_1} p^{y+x_1} (1-p)^{n_2-y-x_1} \\ & + \sum_{j=2}^{k-1} \sum_{x_j=I'_j}^{\min\{S'_j-1, I'_{j+1}-1\}} \sum_{y=0}^{\min\{I'_{j+1}-x_j-1, n_{j+1}-n_j\}} \sum_{x_{j-1}=I'_{j-1}}^{\min\{S'_{j-1}-1, x_j\}} \\ & \dots \sum_{x_1=I'_1}^{\min\{S'_1-1, x_2\}} C_y^{n_{j+1}-n_j} C_{x_1}^{n_1} p^{y+x_j} (1-p)^{n_{j+1}-y-x_j} \prod_{i=2}^j C_{x_i-x_{i-1}}^{n_i-n_{i-1}} \end{aligned} \tag{6}$$

where $C_a^b = b!/a!(b-a)!$. This expression is composed by k summands. If k is not too large, the direct application of this expression is simple and quick. However, for large values of k this calculation is computationally harder, as is the case in the MC_B procedure, where $k = 2 \lfloor \alpha_{mc} n \rfloor$, especially for large values of n , as 9999, for example.

Under the null hypothesis, P follows the $U(0, 1)$ distribution. Hence, by integrating out (6) with respect to P with a $U(0, 1)$ density, we obtain the type I error probability for MC_G :

$$\begin{aligned} \mathbb{P}(\text{type I error}) = & \int_0^1 \pi_G(p) dp = \frac{I'_1}{n_1 + 1} + \sum_{x_1=I'_1}^{\min\{S'_1-1, I'_2-1\}} \sum_{y=0}^{\min\{I'_2-x_1-1, n_2-n_1\}} \frac{C_y^{n_2-n_1} C_{x_1}^{n_1}}{(n_2 + 1) C_{y+x_1}^{n_2}} \\ & + \sum_{j=2}^{k-1} \sum_{x_j=I'_j}^{\min\{S'_j-1, I'_{j+1}-1\}} \sum_{y=0}^{\min\{I'_{j+1}-x_j-1, n_{j+1}-n_j\}} \sum_{x_{j-1}=I'_{j-1}}^{\min\{S'_{j-1}-1, x_j\}} \dots \sum_{x_1=I'_1}^{\min\{S'_1-1, x_2\}} \frac{C_y^{n_{j+1}-n_j} C_{x_1}^{n_1} \prod_{i=2}^j C_{x_i-x_{i-1}}^{n_i-n_{i-1}}}{(n_{j+1} + 1) C_{y+x_j}^{n_{j+1}}}. \end{aligned} \tag{7}$$

An upper bound b_G for the power difference between MC_G and the exact test can be obtained:

$$b_G = \max_{p \in (0,1)} \{1_{(0,\alpha]} - \pi_G(p)\}, \tag{8}$$

where α is the significance level of the exact test. Observe that α is also implicitly the nominal significance level for MC_G . Section 5.1 gives the details about how to build boundaries in order to guarantee a Type I error smaller than or equal to α .

The power function $\pi_G(p)$ evaluated for a fixed p is equal to the probability of X_t reaching l before reaching S , and this probability is decreasing with p . In this way, as compared to the exact test, the largest power loss of MC_G is given by:

$$b_G = \max_{p \in (0,\alpha]} \{1 - \pi_G(\alpha)\} = 1 - \pi_G(\alpha). \tag{9}$$

Let MC_m be the conventional MC test performed with a fixed number m of simulations. An upper bound for the power difference between MC_m and MC_G is given by:

$$b_{m,G} = \max_{p \in (0,1)} \{\pi_m(p) - \pi_G(p)\}, \tag{10}$$

where $\pi_m(p) = \mathbb{P}(G \leq \lfloor m\alpha_{mc} \rfloor - 1)$ is the power function of MC_m for a given p , and G is distributed according to a binomial distribution with parameters m and p .

3.2. Expected number of simulations for MC_G

Let L be the random variable that represents the number of simulations carried out until the halting moment. To perform the computation of the expectation of L , obtained by $\mathbb{E}(L|P = p) = \sum_{l=1}^{n_k} l \mathbb{P}(L = l|P = p)$, for each fixed p . The probability $\mathbb{P}(L = l|P = p)$ for $l \leq n_2$ is given by:

$$\mathbb{P}(L = l|P = p) = \begin{cases} C_{l-S'_1}^{l-1} p^{l-S'_1} (1-p)^{S'_1} & \text{if } l < n_1 \\ C_{l-S'_1}^{l-1} p^{l-S'_1} (1-p)^{S'_1} + \sum_{x=0}^{l'_1-1} C_x^{n_1} p^x (1-p)^{n_1-x} & \text{if } l = n_1 \\ \sum_{x=0}^{l'_1-1} C_x^{n_1} C_{l-n_1-(S'_2-x)}^{l-n_1-1} p^{S'_2} (1-p)^{l-S'_2} & \text{if } n_1 < l < n_2 \\ \sum_{x=0}^{l'_1-1} C_x^{n_1} C_{l-n_1-(S'_2-x)}^{l-n_1-1} p^{S'_2} (1-p)^{l-S'_2} \\ + \sum_{x=l'_1}^{\min\{S'_1-1, l'_2-1\}} \sum_{y=0}^{\min\{l'_2-x-1, n_2-n_1\}} \\ \times C_y^{n_2-n_1} p^y (1-p)^{n_2-n_1-y} C_x^{n_1} p^x (1-p)^{n_1-x} & \text{if } l = n_2. \end{cases}$$

For $l = n_j$, with $j = 3, \dots, k-1$, we have:

$$\begin{aligned} \mathbb{P}(L = l|P = p) = & \sum_{x_{j-1}=l'_{j-1}}^{\min\{S'_{j-1}-1, l'_j-1\}} \sum_{y=0}^{\min\{l'_j-x_{j-1}-1, n_j-n_{j-1}\}} \sum_{x_{j-2}=l'_{j-2}}^{\min\{S'_{j-2}-1, x_{j-1}\}} \\ & \dots \sum_{x_1=l'_1}^{\min\{S'_1-1, x_2\}} C_y^{n_j-n_{j-1}} C_{x_1}^{n_1} p^{y+x_{j-1}} (1-p)^{n_j-y-x_{j-1}} \prod_{i=2}^{j-1} C_{x_i-x_{i-1}}^{n_i-n_{i-1}} \\ & + \sum_{x_{j-1}=l'_{j-1}}^{\min\{S'_{j-1}-1, l'_j-1\}} \sum_{x_{j-2}=l'_{j-2}}^{\min\{S'_{j-2}-1, x_{j-1}\}} \\ & \dots \sum_{x_1=l'_1}^{\min\{S'_1-1, x_2\}} C_{n_j-n_{j-1}-(S'_j-x_{j-1})}^{n_j-n_{j-1}-1} C_{x_1}^{n_1} p^{l-S'_j} (1-p)^{S'_j} \prod_{i=2}^{j-1} C_{x_i-x_{i-1}}^{n_i-n_{i-1}}. \end{aligned}$$

For $n_{j-1} < l < n_j$, with $j = 3, \dots, k$:

$$\mathbb{P}(L = l|P = p) = \sum_{x_{j-1}=l'_{j-1}}^{\min\{S'_{j-1}-1, l'_j-1\}} \sum_{x_{j-2}=l'_{j-2}}^{\min\{S'_{j-2}-1, x_{j-1}\}} \dots \sum_{x_1=l'_1}^{\min\{S'_1-1, x_2\}} C_{n_j-n_{j-1}-(S'_j-x_{j-1})}^{n_j-n_{j-1}-1} C_{x_1}^{n_1} p^{l-S'_j} (1-p)^{S'_j} \prod_{i=2}^{j-1} C_{x_i-x_{i-1}}^{n_i-n_{i-1}}.$$

Finally, for $l = n_k$, we have:

$$\begin{aligned} \mathbb{P}(L = l | P = p) &= \sum_{x_{j-1}=l'_{j-1}}^{\min\{S'_{j-1}-1, l'_{j-1}\}} \sum_{y=0}^{\min\{l'_{j-1}-x_{j-1}-1, n_j-n_{j-1}\}} \sum_{x_{j-2}=l'_{j-2}}^{\min\{S'_{j-2}-1, x_{j-1}\}} \\ &\dots \sum_{x_1=l'_1}^{\min\{S'_1-1, x_2\}} C_y^{n_j-n_{j-1}} C_{x_1}^{n_1} p^{y+x_{j-1}} (1-p)^{n_j-y-x_{j-1}} \prod_{i=2}^{j-1} C_{x_i-x_{i-1}}^{n_i-n_{i-1}}. \end{aligned} \tag{11}$$

Using that P has a $U(0, 1)$ distribution under the null hypothesis, we have

$$\mathbb{E}(L | H_0 \text{ is true}) = \int_0^1 \mathbb{E}(L | P = p) dp. \tag{12}$$

To calculate $\mathbb{E}(L)$ under H_A it is necessary to know the p -value distribution. However, a bound is easier to calculate as

$$b_{E(L)} = \max_{p \in (0, 1)} \{\mathbb{E}(L | P = p)\}. \tag{13}$$

The value $b_{E(L)}$ is a very conservative upper bound for $E(L)$. However, as we will illustrate in Section 5, in practical situations it is useful to bound the expectation of L as $\mathbb{E}(L) \leq 0.523(n + 1)$.

4. A class of distributions for the p -value

Let the set \mathfrak{S} be the class of probability distributions for the p -value P . [8] showed that, for $p = \alpha$, the resampling risk is at least 0.5. Hence, it is not possible to bound the resampling risk in relevant values for all P in \mathfrak{S} if this class includes possible distributions. This is the reason we restrict \mathfrak{S} to be the set of all continuous probability distributions $f_p(p)$ in $(0, 1)$ with differentiable densities that are non-increasing in p . From the p -value definition, its probability distribution function can be written in the following way:

$$\mathbb{P}(P \leq p) = \begin{cases} 1 - F_A(F_0^{-1}(1-p)), & \text{if } U \text{ is large under } H_A, \\ F_A(F_0^{-1}(p)), & \text{if } U \text{ is small under } H_A \end{cases} \tag{14}$$

where F_A denotes the probability distribution function of the test statistic U under H_A and F_0 is the distribution of U under H_0 .

Assuming the existence of density functions $f_A(u)$ and $f_0(u)$ of U under H_A and H_0 , respectively, the p -value density can be written as:

$$f_p(p) = \begin{cases} \frac{f_A(F_0^{-1}(1-p))}{f_0(F_0^{-1}(1-p))}, & \text{if } U \text{ tends to be large under } H_A, \\ \frac{f_A(F_0^{-1}(p))}{f_0(F_0^{-1}(p))}, & \text{if } U \text{ tends to be small under } H_A. \end{cases} \tag{15}$$

Hence, we can study the behavior of the p -value distribution by studying the behavior of the ratio between $f_A(u)$ and $f_0(u)$.

In the majority of the real applications, the ratio (15) is non-increasing with p , and this is the motivation to restrict the analysis of the resampling risk to the set \mathfrak{S} . For example, suppose that $f_A(u)$ and $f_0(u)$ belong to the same single-parameter exponential family with parameters θ_0 and θ_A under H_0 and H_A , respectively. From the expression (15), for $\theta_0 \leq \theta_A$, the p -value density is proportional to $F_0^{-1}(1-p)(\theta_0 - \theta_A)$, which is non-increasing with p . For $\theta_0 \geq \theta_A$, the p -value density is proportional to $F_0^{-1}(p)(\theta_0 - \theta_A)$, which is also a non-increasing function of p . Therefore, \mathfrak{S} matches with a considerable variety of real applications.

Let \mathfrak{S}_B be the class of p -value distributions defined in [3] with cumulative distribution $H_{\alpha, 1-\beta}(p)$, as described in Section 2. Let π be the power of the exact test. We will show now that, for unbiased tests (that is, with $\pi \geq \alpha$), \mathfrak{S} is more general than \mathfrak{S}_B .

From the expression (3), the densities $h(p) \in \mathfrak{S}_B$ can be indexed by α and β and they are given by:

$$h_{\alpha, 1-\beta}(p) = \exp \left\{ -\frac{1}{2} [\Phi^{-1}(\beta) - \Phi^{-1}(1-\alpha)] [\Phi^{-1}(\beta) - \Phi^{-1}(1-\alpha) + 2\Phi^{-1}(1-p)] \right\} \tag{16}$$

where Φ^{-1} is the inverse function of the standard normal cumulative distribution function $\Phi(\cdot)$. The first derivative of $h_{\alpha, 1-\beta}(p)$ with respect to p is equal to:

$$h'_{\alpha, 1-\beta}(p) = \frac{[\Phi^{-1}(\beta) - \Phi^{-1}(1-\alpha)]}{\phi(\Phi^{-1}(1-p))} h_{\alpha, 1-\beta}(p) \tag{17}$$

where $\phi(\cdot)$ is the density function of the standard normal distribution. For $1 - \beta \geq \alpha$, we have $h'_{\alpha,1-\beta}(p) \leq 0$ for all $p \in (0, 1)$.

Consider the subset of densities $\mathfrak{S}_B^* = \{f_p(p) \in \mathfrak{S}_B : 1 - \beta \geq \alpha\}$. That is, \mathfrak{S}_B^* is a subset from \mathfrak{S}_B formed only by densities that implies unbiased tests. Therefore, $\mathfrak{S}_B^* \subset \mathfrak{S}$. Thus, the class \mathfrak{S}_B is a particular case from \mathfrak{S} in the class of unbiased tests. Since biased tests are typically useless, we proved that our class is larger than \mathfrak{S}_B in all relevant cases.

Furthermore, the class \mathfrak{S}_B does not cover all cases of interest. For example, the spatial scan statistic developed by [9] to detect spatial clusters follows very closely a Gumbel distribution under the null hypothesis and a chi-square distribution under H_A [1]. Therefore, even in interesting applied situations, there is not guarantee that $f_p(p) \in \mathfrak{S}_B$ and a larger class, such as ours, may be useful.

There is another example where we can show analytically that \mathfrak{S}_B is too restrict for practical purposes. For $1 - \beta \geq \alpha$ and $p \leq 0.5$, the density $h_{\alpha,1-\beta}(p) \in \mathfrak{S}_B$ is a convex function. To see this, it is enough to show that its second derivative with respect to p is positive. Since

$$h''_{\alpha,1-\beta}(p) = \frac{[\Phi^{-1}(\beta) - \Phi^{-1}(1 - \alpha) - \phi'(\Phi^{-1}(1 - p))]}{\phi(\Phi^{-1}(1 - p))} h'_{\alpha,1-\beta}(p) \tag{18}$$

and we have that

$$\phi'(\Phi^{-1}(1 - p)) = \frac{\Phi^{-1}(1 - p)}{\sqrt{2\pi}\phi(\Phi^{-1}(1 - p))} \exp\left\{-1/2 [\Phi^{-1}(1 - p)]^2\right\} \geq 0$$

if $p \leq 0.5$, we conclude that $h''_{\alpha,1-\beta}(p) \geq 0$. However, in many practical cases, the density $h_{\alpha,1-\beta}(p) \in \mathfrak{S}_B$ is not a convex function. For example, suppose $U_0 \sim \chi_1^2(0)$ and $U_A \sim \chi_{1.01}^2(0)$. The corresponding p -value density from this conjecture is not convex for $p > 0.32$.

Our more general \mathfrak{S} family is not restricted to families such as the normal, chi-square or F distributions. It also contains p -value densities with mixed shapes, with concave and convex parts. However, it is important to point out that the class \mathfrak{S} is not required to use our MC_G procedure. In particular, we do not need this class to calculate a bound for the power loss with respect to the MC_m or to the exact test. We do not need this class either to establish the bound for the expected number of simulations under H_A . The results in Sections 3.1 and 3.2 are valid for any test statistic.

When the additional assumption that the p -value density $f_p(p)$ belongs to \mathfrak{S} holds, stronger results can be obtained. In the next subsections, we show that assuming \mathfrak{S} allows the bounding of the resampling risk in a very simple way, as well as to obtain better results for the power and the expected number of simulations of our generalized Monte Carlo test procedure than those in Section 3.

4.1. Upper bound for the power difference between the exact test and MC_G

The power of the generalized Monte Carlo test is given by integrating out the probability $\pi_G(p)$ of rejecting the null hypothesis conditioned on the p -value p with respect to the p -value density:

$$\pi_G = \int_0^1 \pi_G(p) f_p(p) dp. \tag{19}$$

The power difference between the exact test and MC_G is given by:

$$\delta_G = \int_0^1 (1_{(0,\alpha_{mc})}(p) - \pi_G(p)) f_p(p) dp. \tag{20}$$

An upper bound b_G^* for the power loss δ_G can be obtained if we take the worst possible case for $f_p(p)$. That is, assume that the p -value density is given by $f_{p,w}(p) = 1/\alpha_{mc}$, if $p \in (0, \alpha_{mc}]$, and by $f_{p,w}(p) = 0$, otherwise. Therefore, the bound is given by

$$\begin{aligned} b_G^* &= \int_0^1 (1_{(0,\alpha_{mc})}(p) - \pi_G(p)) f_{p,w}(p) dp = \int_0^{\alpha_{mc}} \frac{1}{\alpha_{mc}} dp - \int_0^{\alpha_{mc}} \pi_G(p) \frac{1}{\alpha_{mc}} dp \\ &= 1 - \frac{1}{\alpha_{mc}} \int_0^{\alpha_{mc}} \pi_G(p) dp. \end{aligned} \tag{21}$$

Because the function (6) is a sum of Beta(a, b) density kernels, the integral (21) can be rewritten as a function of incomplete Beta(a, b) functions, all of them evaluated at $p = \alpha_{mc}$, with a and b depending only of the parameters I, S and η . In the same way, an upper bound for the power difference between MC_m and MC_G is given by:

$$b_{m,G}^* = \int_0^{\alpha_{mc}} (\pi_m(p) - \pi_G(p)) \frac{1}{\alpha_{mc}} dp. \tag{22}$$

As before, (22) can also be expressed using incomplete beta functions.

4.2. An upper bound for the expected number of simulations

For values of p near 0, the simulation time is around n_1 , the first checking point of the lower boundary in the sequential procedure. For values of p near 1, the simulation time is around S'_1 , the smallest height of the upper boundary. Numerically, we find that $\mathbb{E}(L|P = p)$ is maximized for p around α_{mc} . Let

$$p_{\max} = \arg \max_p \mathbb{E}(L|P = p)$$

and define $\bar{f}_{p,\max}(p) = 1/p_{\max}$, for $p \in (0, p_{\max}]$, and $\bar{f}_{p,\max}(p) = 0$, otherwise. Thus, it follows that

$$\begin{aligned} \mathbb{E}(L) &= \int_0^1 \mathbb{E}(L|P = p)\bar{f}_p(p)dp \leq \int_0^1 \mathbb{E}(L|P = p)\bar{f}_{p,\max}(p)dp \\ &= \int_0^{1/p_{\max}} \mathbb{E}(L|P = p) \frac{1}{p_{\max}} dp. \end{aligned} \tag{23}$$

The right hand side of the inequality (23) defines an upper bound $b_{E(L)}^*$ for $\mathbb{E}(L)$.

4.3. An upper bound for the resampling risk

Let RR be the resampling risk in a MC test defined as:

$$RR = \mathbb{P}_{mc}(H_0 \text{ is not rej. } |P \leq \alpha) \mathbb{P}(P \leq \alpha) + \mathbb{P}_{mc}(H_0 \text{ is rej. } |P \geq \alpha) \mathbb{P}(P \geq \alpha) \tag{24}$$

where \mathbb{P}_{mc} is the probability measure associated with the events generated by MC simulations. For the MC_G test, denote its resampling risk by RR_G , which is computed as:

$$RR_G = \int_0^\alpha [1 - \pi_G(p)]f_p(p)dp + \int_\alpha^1 \pi_G(p)f_p(p)dp. \tag{25}$$

As $\pi_G(p)$ is a decreasing function of p , the function $1_{p \in (0, \alpha]}(p) - \pi_G(p)$ is maximum at $p = \alpha$. Thus, RR_G is maximum when $f_p(p)$ puts the largest possible mass at α , which is the worst case $f_{p,w}(p)$. Substituting $f_p(p)$ in (25) by $f_{p,w}(p)$ and setting $\alpha = \alpha_{mc}$, we have:

$$RR_G \leq 1 - \frac{1}{\alpha_{mc}} \int_0^{\alpha_{mc}} \pi_G(p)dp. \tag{26}$$

Therefore, an upper bound for RR_G is equal to the upper bound (21) for the power loss with respect to the exact test. That is, $b_{RR_G}^* = b_G^*$.

Recall that π is the power of the exact test and π_G is the power of the generalized sequential test calculated as shown in (19). The expression (25) can be rewritten in a way that emphasizes another property. When $\pi < \pi_G$ we should obviously prefer the sequential test and there would be issue concerning the resampling risk. Therefore, the control of RR_G is important only when $\pi \geq \pi_G$. This inequality implies that $RR_G \geq \delta_G$, where δ_G is the power difference between the exact test and MC_G . Therefore, equal power of the exact test and the MC_G test does not imply a null resampling risk. To see this, note that:

$$\begin{aligned} RR_G &= \int_0^{\alpha_{mc}} f_p(p)dp - \int_0^{\alpha_{mc}} \pi_G(p)f_p(p)dp + \int_{\alpha_{mc}}^1 \pi_G(p)f_p(p)dp \\ &= \pi - \pi_G + 2 \int_{\alpha_{mc}}^1 \pi_G(p)f_p(p)dp = \delta_G + 2 \int_{\alpha_{mc}}^1 \pi_G(p)f_p(p)dp. \end{aligned} \tag{27}$$

5. Optimal boundaries

This section presents a constructive way to find the MC_G optimal in the sense of minimizing the expected number of simulations among all the procedures controlling the sequential risk. Let $R_S(t|H_0)$ be the sequential risk associated with the upper boundary S defined as the H_0 probability that the sequential test do not reject the null hypothesis at t and the fixed m conventional MC test does reject H_0 . That is,

$$\begin{aligned} R_S(t|H_0) &= \mathbb{P}(X_t \geq S_j, X_m < \lfloor \alpha_{mc}(m + 1) \rfloor | H_0) \\ &= \sum_{x=S_j}^{x_0} \sum_{y=0}^{y_0} C_y^{m-t} C_x^t B(x + y + 1, m - x - y + 1) \end{aligned} \tag{28}$$

with $B(a, b) = \Gamma(a)\Gamma(b)/\Gamma(a + b)$, $j = \max\{r : n_r^S \leq t\}$, $x_0 = \min\{\lfloor \alpha_{mc}(m + 1) \rfloor - 1, t\}$ and $y_0 = \min\{m - t, \lfloor \alpha_{mc}(m + 1) \rfloor - 1 - x\}$. Similarly, $R_l(t|H_0)$ is the sequential risk associated with the lower boundary l , and it is given by

$$\begin{aligned} R_l(t|H_0) &= \mathbb{P}(X_t < l_j, X_m \geq \lfloor \alpha_{mc}(m + 1) \rfloor | H_0) \\ &= I_j/(t + 1) - \sum_{x=0}^{j-1} \sum_{y=0}^{y_0} C_y^{m-t} C_x^t B(x + y + 1, m - x - y + 1) \end{aligned} \tag{29}$$

with $j = \max\{r : n_r^l \leq t\}$.

In our definition, the optimal procedure has the minimum expected value for the number of simulations among all procedures that bound the sequential risk for all t in arbitrarily small values. More specifically, let $M(\Delta)$ be the set of all MC_G procedures such that $R_S(t|H_0) \leq \delta_u(t)$ and $R_l(t|H_0) \leq \delta_l(t)$, where $\delta_u(t) \geq 0$ and $\delta_l(t) \geq 0$, $t = 1, \dots, m$ are arbitrary sequences. We let $\Delta = \{\Delta_u, \Delta_l\}$ with $\Delta_u = \{\delta_u(1), \dots, \delta_u(m)\}$ and $\Delta_l = \{\delta_l(1), \dots, \delta_l(m)\}$. Then, the optimal procedure has the minimum $\mathbb{E}(L)$ among all sequential procedures MC_G in $M(\Delta)$.

The rationale that explains the use of the sequential risk to specify an optimal procedure can be seen through a simple example. Consider the situation with $n = 19$, $\alpha_{mc} = 0.05$ and an upper boundary constant and equal to 1. This is the optimal MC_G with level 0.05 and with $\mathbb{E}(L) = 3.55$. However, this procedure has much lower power than a conventional test with $m = 999$, for example. Therefore, it is important to take into account the power loss with respect to MC_m in the definition of an optimal procedure because we want to reduce simulation time without efficiency loss. We do not use the resampling risk to define the optimal procedure because it is not possible to bound this risk in the case of an arbitrary f_p for truncated procedures, while the power loss with respect to MC_m can always be bounded.

Let MC_G be an arbitrary element of the set $M(\Delta)$. Therefore,

$$\begin{aligned} \mathbb{P}(MC_G \text{ rejects } H_0 \text{ in opposition to } MC_m | H_0) &\leq \sum_{t \in \eta^l} R_l(t|H_0) \\ &\leq \sum_{t \in \eta^l} \delta_l(t) = \delta_l \end{aligned} \tag{30}$$

and

$$\begin{aligned} \mathbb{P}(MC_G \text{ do not reject } H_0 \text{ in opposition to } MC_m | H_0) &\leq \sum_t R_S(t|H_0) \\ &\leq \sum_{t=1}^{m-1} \delta_u(t) = \delta_u. \end{aligned} \tag{31}$$

Therefore, for $MC_G \in M(\Delta)$, the type I error probability is always under control:

$$\alpha_{mc} - \delta_u \leq \mathbb{P}(\text{type I error with } MC_G) \leq \alpha_{mc} + \delta_l. \tag{32}$$

The tuning parameters δ_u and δ_l are used to bound the power loss of the optimal procedure and to set the Type I error of the optimal boundaries accordingly to the nominal significance level. Section 5.1 gives a general rule concerning the choice of the tuning parameter δ_l , for fixed δ_u , in order to have a valid p -value. An example of use for this rule is given on page 14. On page 15 we show that δ_u can be directly interpreted as the arbitrary upper bound for the power loss for the optimal procedure.

We point out the relevance of (32) by defining the p -value δ -valid. We say that a p -value \widehat{P} is δ -valid if $\mathbb{P}(\widehat{P} \leq \alpha_{mc}) \leq \alpha_{mc} + \delta$, with $\delta > 0$. By (32), every procedure from $M(\Delta)$ is δ_l -valid.

For $t = 1, 2, \dots, m$, the optimal boundaries $L(t)$ and $U(t)$ are given by:

$$\begin{aligned} L(t) &= \max\{r : \mathbb{P}(X_t < r, X_m \geq h | H_0) \leq \delta_l(t)\}; \\ U(t) &= \min\{r : \mathbb{P}(X_t \geq r, X_m < h | H_0) \leq \delta_u(t)\} \end{aligned} \tag{33}$$

where $h = \lfloor \alpha_{mc}(m + 1) \rfloor$. As a consequence of this construction, the maximum number of simulations n of the optimal procedure is equal to m .

Denote the optimal sequential procedure by MC_0 . The vertical steps of the upper and lower boundaries of MC_0 will be denoted by $I_0 = \{I_1^O, \dots, I_{k_1}^O\}$ and $S_0 = \{S_1^O, \dots, S_{k_2}^O\}$, respectively, and their corresponding jumping points by $\eta_0^l = \{t_1^l, \dots, t_{k_1}^l\}$ and $\eta_0^s = \{t_1^s, \dots, t_{k_2}^s\}$. Note that the sets η_0^l and η_0^s are the jumping points of $L(t)$ and $U(t)$, while I_0 and S_0 are the values of $L(t)$ and $U(t)$ evaluated at these jumping points. We will call either I_0 and S_0 or, equivalently, $L(t)$ and $U(t)$, as optimal boundaries.

5.1. Power and size of MC_O

Consider a particular MC_G scheme, in which the upper boundary is constant with height $h = \lfloor \alpha_{mc}(m + 1) \rfloor$. Then, the rejection of H_0 by the conventional MC_m implies the rejection H_0 by MC_G . That is, MC_G rejects H_0 with probability at least equal to α_{mc} . Hence, the power loss of MC_G , in the general case, is due to the events where S is reached before I and, at the same time, MC_m rejects H_0 . As a consequence, $\pi_m(p) - \pi_O(p) \leq \sum_{t=1}^m \mathbb{P}(X_t \geq S_j^O, X_m < \lfloor \alpha_{mc}(m + 1) \rfloor | P = p)$, with $j = \max \{r, r : t_r^S \leq t\}$, where $\pi_m(p)$ and $\pi_O(p)$ are the power functions of the MC_m and MC_O procedures for a given realized p , respectively. If $f_p(p) \in \mathfrak{S}$, then:

$$\begin{aligned} \pi_m - \pi_O &\leq \int_0^{\bar{p}} \bar{p}^{-1} \sum_{t=1}^m \mathbb{P}(X_t \geq S_j^O, X_m < \lfloor \alpha_{mc}(m + 1) \rfloor | P = p) dp \\ &\leq \sum_{t=t_1^S}^{m-1} \sum_{x=S_j^O}^{x_0} \sum_{y=0}^{y_0} C_y^{m-t} C_x^t B(x + y + 1, m - x - y + 1) / \bar{p} \\ &= \bar{p}^{-1} \sum_{t=1}^{m-1} R_S(t) \leq \bar{p}^{-1} \delta_u \end{aligned} \tag{34}$$

where \bar{p} is the argument maximizing $\mathbb{P}(X_t \geq S_j^O, X_m < \lfloor \alpha_{mc}(m + 1) \rfloor | P = p)$ in p .

For procedures in $M(\Delta)$, the boundaries S and I are determined by the (X_t, X_m) null distribution. Hence, if $\max\{\delta_u(t), \delta_l(t)\} \leq \alpha_{mc}$ for $t \in [1, m]$, then $S_j/t > \alpha_{mc}$, for $j = \max \{r, r : n_r^S \leq t\}$, and $(I_i + 1)/(t + 1) \leq \alpha_{mc}$, for $i = \max \{r, r : n_r^I \leq t\}$. If α_{mc} is a rational number, we have $(I_{k_1} + 1)/(n + 1) = \alpha_{mc}$ and $S_{k_2}/n = \lfloor \alpha_{mc}(m + 1) \rfloor / m > \alpha_{mc}$. Therefore, an $M(\Delta)$ procedure rejects H_0 if, and only if, $P_G \leq \alpha_{mc}$. We use this fact to obtain a valid p -value for the optimal procedure. Denote by P_O the p -value for MC_O calculated according to (5). As $P_O \in M(\Delta)$, then P_O is δ_l -valid. A stronger result is that we can select Δ_u and Δ_l to guarantee that P_O is a valid p -value. A simple way is to select $\delta_u(t_1^S)$ such that $R_S(t_1^S | H_0) \geq \delta_l$. As a consequence, the fraction of the X_t trajectories intercepted by S^O (and implying on the rejection of H_0 by MC_m) is larger than the fraction of trajectories intercepted by I^O (and implying in the acceptance of H_0 by MC_m). Therefore,

$$\mathbb{P}(P_O \leq \alpha_{mc}) = \mathbb{P}(MC_O \text{ error type I}) \leq \alpha_{mc} - R_S(t_1^S | H_0) + \delta_l \leq \alpha_{mc}. \tag{35}$$

For example, take $\delta_u = 0.01$ and $t_1^S = 1$ ($S_1^O = 1$). With $m = 999$ and $\alpha_{mc} = 0.05$, this gives us $R_S(t_1^S | H_0) = 0.00123$. We can take then $\delta_u(t_1^S) = 0.00123$. The other elements of the set Δ_u can be conveniently fixed as $\delta_u(t) = 0.00877/(m - t_1^S)$, for $t = t_1^S + 1, \dots, m$. If we take $\delta_l = 0.00123$, by (35), the resulting p -value is valid. Using (28) with $\alpha_{mc} = 0.05$, for $m = 99, 119, \dots, 99999$, and fixing $t_1^S = 1$ for all cases, we find $0.001 \leq R_S(1 | H_0) \leq 0.00125$ and as an increasing function of m . Thus, in these cases, the p -value is valid if $\delta_l \leq 0.001$. We can invert the direction by initially fixing δ_l . A valid p -value is produced if we take S_1^O and t_1^S such that $R_S(t_1^S | H_0) \leq \delta_l$. If we take $m = 999$, $\alpha_{mc} = 0.05$, $\delta_l = 0.001$, and $S_1^O = 3$, we obtain $t_1^S = 21$ as the smallest value of t for which $R_S(t | H_0) \leq 0.001$, implying in $R_u(21 | H_0) = 0.00113$, which satisfies (35) for a valid p -value. In any case, the exact size of the test can be calculated with (7).

Expression (35) is useful for the error type I control in those cases in which we want to reduce the execution time in exchange for a moderate bound for the power loss. This is so because the average execution time is a decreasing function of δ_l and δ_u . Obviously, for practical reasons, when δ_l and δ_u are both reasonably small, such as 10^{-5} , independently of the structure of Δ , the interval provided by (32) guaranteed an error type I probability reasonably close to α_{mc} .

5.2. MaxMin upper boundary

We can use (34) to bound the MC_O power loss but it depends on the assumption that $f_p(p) \in \mathfrak{S}$. To guarantee that MC_O has the same power as MC_m for any test statistic, we will define the MaxMin upper boundary. A MaxMin boundary maximizes the expectation of the number of simulations with respect to p after having minimize the value of the upper boundary for fixed t keeping under control the sequential risk for all $p \in (0, 1)$. Define the sequential risk of the upper boundary in t , for a given p , by:

$$\begin{aligned} R_S(t, p) &= \mathbb{P}(X_t \geq S_j, X_m < \lfloor \alpha_{mc}(m + 1) \rfloor | P = p) \\ &= \sum_{x=S_j}^{x_0} \sum_{y=0}^{y_0} C_y^{m-t} C_x^t p^{x+y} (1 - p)^{m-x-y}. \end{aligned} \tag{36}$$

Define the MaxMin upper boundary as

$$U_x(t) = \max_{p \in (0,1)} \{U(t, p)\} \tag{37}$$

with $U(t, p) = \min \{r : R_S(t, p) \leq \delta_u(t)\}$.

Table 1

Expected number of simulations for MC_O and MC_{Ox} with m equal to 999 and 9999, α_{mc} equal to 0.01 and 0.05, and $\delta_u = 0.01$, $\delta_l = 0.001$, and valid p -value.

m	α_{mc}	Scheme	Under H_0	$\hat{H}_{\alpha_{mc};0.5}(p)$	$\tilde{f}_{p,\max}(p)$	$b_{E(L)}$
999	0.05	MC_O	45.253	159.848	350.011	713.129
		MC_{Ox}	63.955	196.001	370.413	816.388
	0.01	MC_O	14.520	212.873	406.009	522.683
		MC_{Ox}	16.354	225.485	410.812	544.334
9999	0.05	MC_O	170.554	595.507	1520.297	7424.930
		MC_{Ox}	205.231	692.770	1533.952	7842.827
	0.01	MC_O	78.892	939.793	2285.425	6822.213
		MC_{Ox}	93.421	1095.163	2294.486	7152.269

Table 2

Expected number of simulations for comparison among MC_O (using $\delta_u = 0.01$ and $\delta_l = 0.001$), MC_B (using $c_1 = -c_2 = 1.282$), and MC_h (using $h = \lfloor \alpha_{mc} m \rfloor$) with $\alpha_{mc} = 0.05$.

n	Scenario for $f_p(p)$	MC_O	MC_B	MC_h
599	$U(0, 1)$, $RR = 0.007$	33.851	51.169	61.293
	$\hat{H}_{\alpha_{mc};0.47}(p)$, $RR = 0.025$	119.788	163.118	391.131
	Point mass at α_{mc} , $RR = 0.523$	427.049	494.378	539.786
3619	$U(0, 1)$, $RR = 0.003$	94.295	155.840	363.300
	$\hat{H}_{\alpha_{mc};0.47}(p)$, $RR = 0.01$	331.401	510.256	2370.435
	Point mass at α_{mc} , $RR = 0.511$	2623.359	3076.974	3399.298

Denote by MC_{Ox} the optimal procedure based on the upper boundary $U_x(t)$. The power loss of MC_{Ox} is at most δ_u , and the global sequential risk, the probability that the sequential scheme leads to an opposite decision with respect to the conventional Monte Carlo test, is at most $\delta_l + \delta_u$.

Table 1 shows the average simulation time for optimal schemes with α_{mc} equal to 0.01 and 0.05, m equal to 999 and 9999, and $\delta_l = 0.001$, and $\delta_u = 0.01$. For the set Δ_l , we used $\delta_l(t_1^s) = \delta_l/2$ and $\delta_l(t_i^s) = \delta_l/2(h - 2)$ for $i = 2, \dots, k_1$, where $h = \lfloor \alpha_{mc} m \rfloor$. For the set Δ_u , to guarantee a valid p -value, fixing $S_1^0 = 2$ when $m = 999$ and fixing $S_1^0 = 3$ when $m = 9999$, we chose t_1^s to produce the smallest $R_S(t_1^s)$ that is greater than δ_l . With this, we took $\delta_u(t_1^s) = R_S(t_1^s)$ and $\delta_u(t) = (\delta_u - \delta_u(t_1^s))/(m - t_1^s - 1)$ for $t = t_1^s + 1, \dots, m - 1$. The bounds calculated for the power loss of these schemes are smaller than 10^{-3} . Fig. 2(A) and (B) illustrate the MC_O and MC_{Ox} boundaries, with $m = 999$, for α_{mc} equal to 0.05 and 0.01, respectively.

In Table 1, we consider three scenarios to calculate the average simulation time under the alternative hypothesis. In the first scenario, we used the worst case distribution in \mathfrak{S}_B . Concerning the use of \mathfrak{S}_B , the numerical explorations of [3] were not used here to define the worst case of a p -value distribution with shape $H_{\alpha;1-\beta}(p)$. As discussed in Sections 4 and 4.3, $h_{\alpha;1-\beta}(p)$ (for $1 - \beta \geq \alpha$) and π_G decrease with p . Therefore, the worst case within the class \mathfrak{S}_B , in the sense of bounding the power loss, occurs at the point of maximum with respect to β of the function $H_{\alpha;1-\beta}(\alpha)$. For $1 - \beta \geq \alpha$, this point of maximum is 0.5. Then, the analytical worst case is given by $H_{\alpha;0.5}(p)$. We used this fact to compute the expectations in column 5, using a Beta(a, b) approximation, denoted by $\hat{H}_{\alpha;0.5}(p)$, with $a = 0.3$ and $b = 7.6$ for $\alpha_{mc} = 0.01$. For $\alpha_{mc} = 0.05$, we took $a = 0.359$ and $b = 2.523$. The second scenario is shown in column 6 and it is more general than the first one because it considers the worst case in class \mathfrak{S} . According to (23), this is given by $\tilde{f}_{p,\max}(p)$. The third scenario is the last column and it is given by the bound in (13), which is valid for any test statistic. We see that, even in the conservative scenario in column 7, the optimal procedure presents substantial reductions in the simulation time when compared to the conventional procedure. This reduction is approximately 30% of m , reaching up to 50% of m in some cases.

5.3. Execution time reduction from MC_O

In this section, we offer a comparison between the MC_B and our MC_G sequential test procedure. We use the same example of the MC_B test given by [8]. We built the MC_O boundaries and, by securing an upper bound for the resampling risk to MC_O equal to that presented by the MC_B scheme developed in [8], we compared the average simulation time of the two procedures.

An obvious fact is that the B boundaries are particular cases of I and S , because MC_G was designed to be a generalized sequential procedure with two stopping boundaries. We can rewrite the B boundaries using the MC_G notation, based on the sets I, S, η^I and η^S . In this way, for an MC_B test, the user can apply the general expressions for the power and the expected number of simulations developed in Section 3.

It should be noted that some important shapes for I and S , as the funnel behavior of MC_O , cannot be represented by the MC_B boundaries. The funnel shape is an important characteristic to reduce execution time.

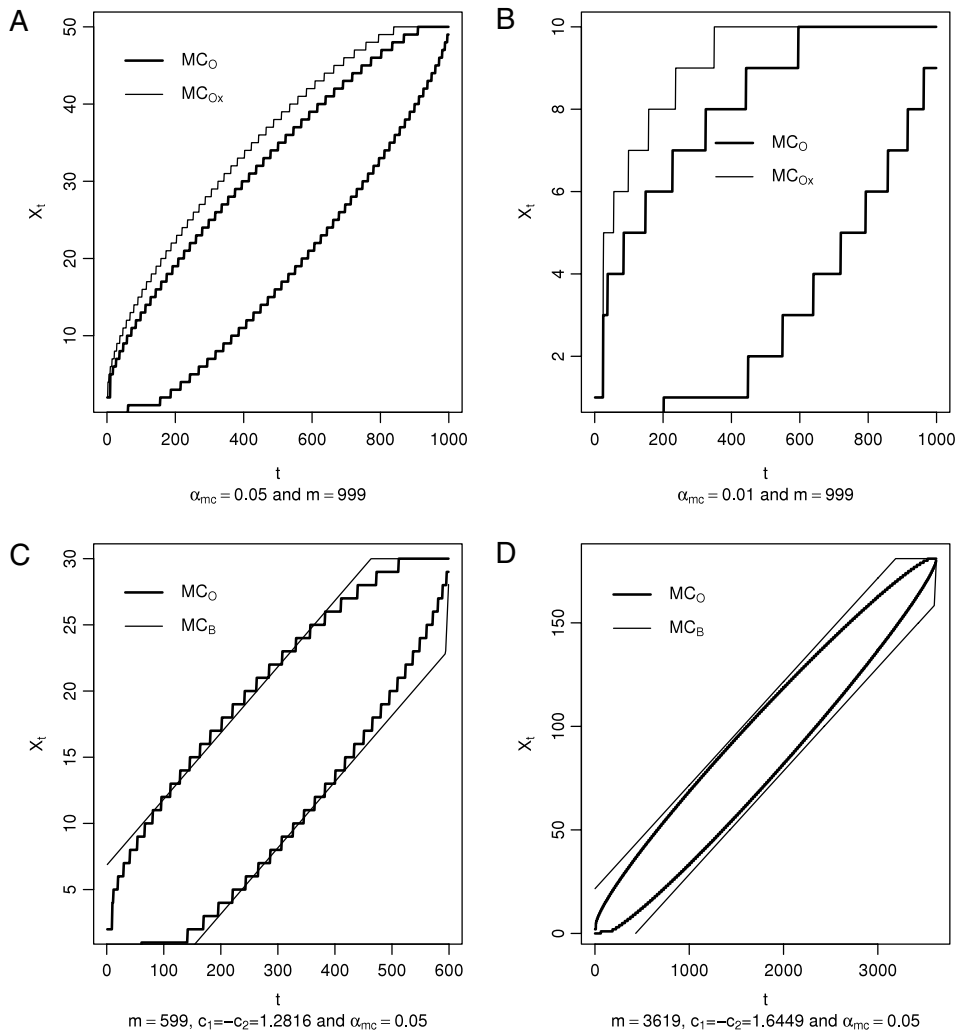


Fig. 2. Examples for MC_O and MC_{Ox} using $\delta_l = 0.001$ and $\delta_u = 0.01$.

Table 2 shows the expected number of simulations presented in [8] for n equal to 599 (using $c_1 = -c_2 = 1.2816$) and n equal to 3619 (using $c_1 = -c_2 = 1.6449$). It also shows the bounds associated to MC_O using $\delta_u = 0.01$ and $\delta_l = 0.001$. All scenarios consider $\alpha_{mc} = 0.05$. Concerning the worst case distribution within the class \mathfrak{S}_B , [8] adopted the numerical studies from [3] and she found $H_{0.05;0.47}(p)$ for $\alpha = 0.05$, with approximation $\tilde{H}_{0.05;0.47}(p) \approx \text{Beta}(0.389; 2.523)$. These bounds are also computed here for the sequential procedure proposed by [2], which will be denoted by MC_h . [11] showed that MC_h has the same power than MC_m if $h = \alpha_{mc}(m + 1)$ and its power is constant for $n \geq h/\alpha_{mc}$, noting that the combination of this two last rules implies that MC_m must be replaced by MC_h , because they have the same power for a maximum number of simulations practically equal (that is, for $n = m + 1$). This table covers three scenarios. In the first, the expected number of simulations is calculated under H_0 , which implies a uniform distribution in $(0,1)$ for the p -value. The second scenario considers the worst case $H_{0.05;0.47}(p)$ used by [8]. The third scenario evaluates the case where the p -value distribution is degenerate at α_{mc} . For these examples, MC_O is substantially faster than the MC_B procedure and their expected time ratio are between 61% and 86%. This illustrates the gain provided by our MC_O procedure. The boundaries for $m = 599$ and $\alpha_{mc} = 0.05$ for the MC_O procedure are available in Fig. 2(C). It is clear that the greater flexibility is given by the MC_O boundaries. While the B boundaries are parallel almost up to the end of the experiment, the I_0 and S_0 boundaries are tapered when t gets close to the maximum number of simulations. This can be intuitively thought as if the boundaries are using the information that X_t not touching the boundaries after a long time should induce a narrower surveillance.

6. Flexibility of MC_G

As MC_G is defined for any boundaries shapes, it is possible to consider a mix of optimal and non-optimal boundaries. One example when this would be relevant is when one wishes to calculate the p -value with a certain precision when the null

Table 3
Resampling risk for fixed m MC test using classes \mathfrak{S} and \mathfrak{S}_B and $\alpha_{mc} = 0.05$.

m	999	2999	4999	9999	19999
$f_{p,w}(p)$	0.0549	0.0317	0.0246	0.0174	0.0123
$\hat{H}_{\alpha_{mc},0.5}(p)$	0.0187	0.0108	0.0083	0.0059	0.0042

hypothesis is rejected but there is no concern to its precision when the null hypothesis is accepted. An early stop due to the null rejection will imply in a p -value with few decimal places and hence not very precise. This situation leads to consider the sequential interruption due only to reaching the upper boundary, when the null hypothesis is accepted. For the rejection of the null hypothesis, one would require the simulations to run up to the last maximum m . Using the MC_G notation, such scheme would be based in an upper boundary given by S^0 and a lower boundary parametrized as $l = \lfloor \alpha_{mc}(m + 1) \rfloor$ with $\eta^l = \{m\}$. Obviously, this procedure will not be as efficient as that based on the optimal two-boundaries procedure in terms of execution time. However, one can control the power loss, the error type I probability, the upper bound for the expected number of simulations, and the upper bound for the resampling risk. Consider the design with $S_i = S_{i-1} + 1$ for $i = 2, \dots, k_2$. For arbitrary S_1 and n_1^S , the most powerful test jumps at $n_i^S = n_1^S + 2(i - 1)$, for $i = 2, \dots, k_2$ and $k_2 = \lfloor \alpha_{mc}(m + 1) \rfloor - S_1 + 1$. This scheme simplifies substantially the power loss calculation for a realized p -value p , which is given by:

$$\begin{aligned}
 b_{m,G}(p) = & \sum_{x=S_1}^{\min\{h-1, n_1^S\}} \sum_{y=0}^{h-1-x} C_x^{n_1^S} C_y^{m-n_1^S} p^{x+y} (1-p)^{m-x-y} + \sum_{y=0}^{h-1-S_1+1} C_{S_1-1}^{n_1^S} C_y^{m-n_1^S-2} p^{S_1+y+1} (1-p)^{m-y-S_1-1} \\
 & + 2 \sum_{y=0}^{h-1-S_1} C_{S_1-1}^{n_1^S} C_y^{m-n_1^S-4} p^{S_1+y+2} (1-p)^{m-y-S_1-2} \\
 & + \dots + 2^{k_2-3} \sum_{y=0}^{h-S_1-(k_2-3)} C_{S_1-1}^{n_1^S} C_y^{m-n_1^S-2(k_2-2)} p^{S_1+y+k_2-2} (1-p)^{m-y-S_1-(k_2-2)}. \tag{38}
 \end{aligned}$$

To illustrate, take $S_1 = 3$, $n_1^S = 3$, $\alpha_{mc} = 0.05$ and $m = 9999$. Maximizing (38) with respect to p gives $p_{\max} = 0.0468$, which implies in a power loss smaller than 1.094×10^{-4} .

The technique used in Section 5.1 to obtain a valid p -value is not restricted to the construction of the optimal procedure, but it can also be applied in the construction of more general sequential procedures. For that, it suffices to calculate the lower boundary sequential risk sum and, conveniently, to select S_1 such that $R_S(n_1^S)$ be greater or equal than this sum.

If the control of the resampling risk RR is important, we can select the smallest m for which the resampling risk of MC_m is smaller than an arbitrary bound. Fixing δ_l and δ_u in sufficiently small values, we can obtain the test MC_{Ox} with the same power and size than MC_m . Table 3 illustrates the RR_m for the worst cases in the classes \mathfrak{S} and \mathfrak{S}_B , given by $f_{p,w}(p)$, described in Section 5.3, and $H_{\alpha_{mc},0.5}(p)$, approximated by $\hat{H}_{\alpha_{mc},0.5}(p)$, respectively. As one can anticipate, RR_m decreases with m . As \mathfrak{S} is larger than \mathfrak{S}_B , the risks calculated for the first class are higher than those for the worst case in \mathfrak{S}_B .

7. Two-sided optimal boundaries

All the results derived until now considered only one-sided tests. For two-sided tests, we need to redefine the simulation interruption criteria. [7] proposed a truncated sequential scheme based on two internal and two external boundaries. If X_t reaches the region between the inner boundaries before crossing the external boundaries, the simulations are halted and the null hypothesis is accepted. If X_t crosses one of the external boundaries before reaching the inner region, the null hypothesis is rejected. [7] was also interested in bounding the power loss with respect to the conventional MC_m . He proposed the *conditional repeated significance test* (CT). This test bounds the rejection probability at time t conditionally on the information produced by X_m . The random variable $X_t|X_m$ is distributed as a hypergeometric with parameters m , X_m and t . This was used to build boundaries formed by the worst cases for the percentiles of this conditional distribution. This approach allows to arbitrarily bound the probability of disagreement between the sequential and the conventional procedures. However, with respect to the execution time, it produces conservative boundaries relative to those obtained directly from the distribution of X_t , as we did in our optimal boundaries proposed here.

Let $\underline{ln} = \{\underline{ln}_1, \dots, \underline{ln}_{k_{ln,1}}\}$, and $\overline{ln} = \{\overline{ln}_1, \dots, \overline{ln}_{k_{ln,2}}\}$ be the lower and upper inner boundaries, respectively. Define also $\underline{O} = \{\underline{O}_1, \dots, \underline{O}_{k_{O,1}}\}$, and $\overline{O} = \{\overline{O}_1, \dots, \overline{O}_{k_{O,2}}\}$ as the lower and upper outer boundaries, respectively. Let $\eta^{\underline{ln}} = \{n_1^{\underline{ln}}, \dots, n_{k_{ln,1}}^{\underline{ln}}\}$ and $\eta^{\overline{ln}} = \{n_1^{\overline{ln}}, \dots, n_{k_{ln,2}}^{\overline{ln}}\}$ be the jump moments for the lower and upper inner boundaries. Similarly, denote by $\eta^{\underline{O}}$ and $\eta^{\overline{O}}$ the sets with the jump moments for the lower and upper outer boundaries. Therefore, the simulations

are interrupted if the number of simulations reaches n or if $D_t = 1$, where:

$$D_t = \begin{cases} 1, & \text{if } (\underline{In}_{j_1} \leq X_t \leq \overline{In}_{j_2}) \text{ or } (X_t < \underline{O}_{g_1}) \text{ or } (X_t = \overline{O}_{g_2}) \\ 0, & \text{otherwise} \end{cases} \tag{39}$$

with $j_1 = \max \left\{ r, r : n_r^{\underline{In}} \leq t \right\}$, $j_2 = \max \left\{ r, r : n_r^{\overline{In}} \leq t \right\}$, $n_{g_1-1}^{\underline{O}} < t \leq n_{g_1}^{\underline{O}}$ and $n_{g_2-1}^{\overline{O}} < t \leq n_{g_2}^{\overline{O}}$.

We define the p -value for this two-sided procedure as $P_{TS} = (X_t + 1)/(t + 1)$, if $X_t < \underline{O}_{g_1}$ or $X_t = \overline{O}_{g_2}$, and $P_{TS} = X_t/t$, otherwise. We define the test decision function for this two-sided MC_C test by $\phi_{TS}(t, x) = 1$, if the outer boundaries are reached before the inner ones ($X_t < \underline{O}_{g_1}$ or $X_t = \overline{O}_{g_2}$) or the simulations reach n , and $\phi_{TS}(t, x) = 0$, if the inner boundaries are reached before the outer boundaries ($\underline{In}_{j_1} \leq X_t \leq \overline{In}_{j_2}$). The hypothesis H_0 is rejected if $\phi_{TS} = 1$ and it is not rejected if $\phi_{TS} = 0$.

The conventional two-sided MC test of level α_{mc} rejects H_0 if $X_m < C$ or if $X_m > m - C$, with $C = \lfloor \alpha_{mc}(m + 1) \rfloor / 2$. Define the sequential risks at t , $R_{\underline{O}}(t|H_0)$ and $R_{\overline{O}}(t|H_0)$, associated to the outer boundaries by:

$$\begin{aligned} R_{\underline{O}}(t|H_0) &= \mathbb{P}(X_t < \underline{O}_{g_1}, C \leq X_m \leq m - C | H_0) \\ R_{\overline{O}}(t|H_0) &= \mathbb{P}(X_t \geq \overline{O}_{g_2}, C \leq X_m \leq m - C | H_0). \end{aligned} \tag{40}$$

Similarly, $R_{In}(t|H_0)$ is the sequential risk associated with the inner boundaries and it is given by:

$$R_{In}(t|H_0) = \mathbb{P}(\underline{In}_{j_1} \leq X_t \leq \overline{In}_{j_2}, \{X_m \in C \cup X_m\} m - C | H_0). \tag{41}$$

The simplest two-sided boundaries are those of the curtailed design and their sequential risks are equal to zero for all t with the inner lower and upper boundaries given, respectively, by the straight lines C and $C - t$, and the outer lower and upper boundaries given, respectively, by $\max \{0, C - m + t\}$ and $m - C$.

Let $M(\Delta_{TS})$ be the set of all symmetric two-sided MC_C procedures such that $R_{\underline{O}}(t|H_0) \leq \delta_{\underline{O}}(t)$, $R_{\overline{O}}(t|H_0) \leq \delta_{\overline{O}}(t)$ and $R_{In}(t|H_0) \leq \delta_{In}(t)$, where $\delta_{\underline{O}}(t)$, $\delta_{\overline{O}}(t)$, and $\delta_{In}(t)$ are positive arbitrary sequences, for $t = 1, \dots, m$. Define also $\Delta_{TS} = \{\Delta_{\underline{O}}, \Delta_{\overline{O}}, \Delta_{In}\}$, for $\Delta_{\underline{O}} = \{\delta_{\underline{O}}(1), \dots, \delta_{\underline{O}}(m)\}$, $\Delta_{\overline{O}} = \{\delta_{\overline{O}}(1), \dots, \delta_{\overline{O}}(m)\}$, and $\Delta_{In} = \{\delta_{In}(1), \dots, \delta_{In}(m)\}$. We call symmetric the procedures for which $\underline{In}_{j_1} \leq C$, $\overline{In}_{j_2} \geq t - C$ and $C - \underline{In}_{j_1} = \overline{In}_{j_2} - (t - C)$ for $t \in [1, m]$.

The two-sided optimal procedure has the minimum $\mathbb{E}(L)$ among all MC_C procedures in $M(\Delta_{TS})$.

Denote by $L_{In}(t)$ and $U_{In}(t)$ the lower and upper inner optimal boundaries, respectively. For the optimal outer ones, define $L_{\underline{O}}(t)$ and $U_{\overline{O}}(t)$. These optimal boundaries are given by:

$$\begin{aligned} L_{In}(t) &= t - U_{In}(t) \\ &= \max \{ r : \mathbb{P}(r \leq X_t \leq t - r, \{X_m \in C \cup X_m\} m - C | H_0) \leq \delta_{In}(t) \} \end{aligned} \tag{42}$$

and

$$\begin{aligned} L_{\underline{O}}(t) &= \max \{ r : \mathbb{P}(X_t < r, C \leq X_t \leq m - C | H_0) \leq \delta_{\underline{O}}(t) \}; \\ U_{\overline{O}}(t) &= \max \{ r : \mathbb{P}(X_t > r, C \leq X_t \leq m - C | H_0) \leq \delta_{\overline{O}}(t) \}. \end{aligned} \tag{43}$$

As in the one-sided case, we can also define the minimax inner boundaries:

$$Lx_{In}(t) = t - Ux_{In}(t) = \max_{p \in (0,1)} \{ Ux_{In}(t, p) \} \tag{44}$$

with $Ux_{In}(t, p) = \min \{ r : R_{In}(t, p) \leq \delta_{In}(t) \}$, where $R_{In}(t, p)$ is the sequential risk of the inner boundaries for a given p .

For the optimal scheme, $P_{TS} \leq \alpha_{mc}/2$, or $P_{TS} \geq 1 - \alpha_{mc}/2$, iff $\phi_{TS} = 1$. The expressions we found earlier to bound the power loss, the resampling risk, and the expectation of L can be adapted for the two-sided procedure.[7] exemplified the CT test for $\alpha_{mc} = 0.1$, with boundaries built with the $(1 - 10^{-6})$ 100% and 10^{-6} 100% percentiles of $X_t|X_m$ for the upper and lower boundaries, respectively. Fig. 3 illustrates the CT test with the dashed lines for $m = 999$. The dotted lines represent the curtailed scheme. To compare the results of [7], with $m = 999$ and $\alpha_{mc} = 0.1$, we took $\delta_{In}(t) = \delta_{\underline{O}}(t) = \delta_{\overline{O}}(t) = 10^{-6}$ to produce the optimal scheme, illustrated by the continuous lines in Fig. 3. We evaluated these tests under H_0 and under the worst case in \mathfrak{S} , given by $\hat{f}_{p_{\max}}(p)$. The null $\mathbb{E}(L)$ value for the optimal test is equal to 139, around 74% of the value obtained using CT. Using $\hat{f}_{p_{\max}}(p)$, we have $\mathbb{E}(L) = 493$ for the optimal test, and equal to 663 for CT, keeping the ratio 0.74 seen before. This substantial reduction in the average simulation time is due to the CT boundaries being calculated out of the tails of the conditional distribution of $X_t|X_m$. The optimal boundaries are obtained directly from the (X_t, X_m) joint distribution. Fig. 3 shows that the inner boundaries of the optimal test are external to those from CT, while the optimal outer boundaries are within those of CT.

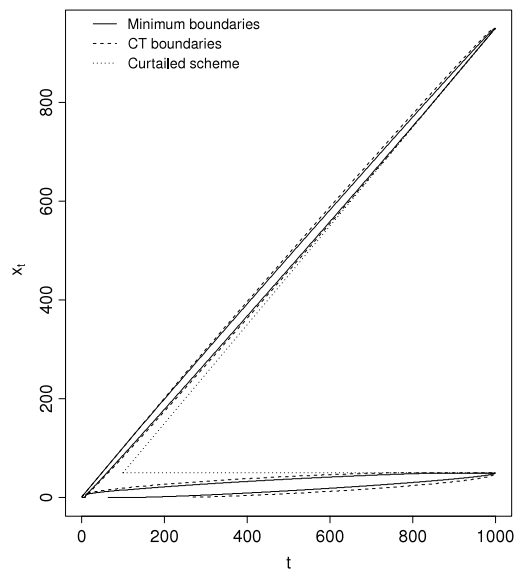


Fig. 3. Curtailed test, CT and minimum boundaries with $\delta_m(t) = \delta_{\underline{0}}(t) = \delta_{\bar{0}}(t) = 10^{-6}$, $m = 999$, and $\alpha_{mc} = 0.1$ ($C = 50$).

8. Concluding remarks

Exact calculations for some specific and practical designs indicate that the optimal sequential procedure proposed in this paper has a considerably smaller execution time than the other sequential methods proposed in the literature. The construction of the optimal boundaries is simple, what favors an easy computational implementation. By using expressions developed in Section 3, these optimal boundaries, or any other generalized designs, can be evaluated by calculating the size, the expected number of simulations under H_0 , and the upper bounds for the power loss and for the expected number of simulations under H_A . These results are valid for any test statistic. Thus, given such control of power loss, significance level, and expected execution time, in the cases where saving execution time is imperative, our optimal truncated generalized sequential Monte Carlo test can be recommended to replace the conventional Monte Carlo test.

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References

- [1] A. Abrams, K. Kleinman, M. Kulldorff, Gumbel based p -value approximations for spatial scan statistics, *International Journal of Health Geographics* 9 (2010) 1–12.
- [2] J. Besag, P. Clifford, Sequential Monte Carlo p -value, *Biometrika* 78 (1991) 301–304.
- [3] M. Fay, D. Follmann, Designing Monte Carlo implementations of permutation or bootstrap hypothesis tests, *The American Statistician* 56 (2002) 63–70.
- [4] M. Fay, H.J. Kim, M. Hachey, On using truncated sequential probability ratio test boundaries for Monte Carlo implementation of hypothesis tests, *Journal of Computational and Graphical Statistics* 16 (2007) 946–967.
- [5] A. Gandy, Sequential implementation of Monte Carlo tests with uniformly bounded resampling risk, *Journal of the American Statistical Association* 104 (2009) 1504–1511.
- [6] L. Huang, J. Zalkikar, R. Tiwari, A likelihood ratio test based method for signal detection with application to FDA's drug safety data, *Journal of the American Statistical Association* 106 (2011) 1230–1241.
- [7] C. Jennison, Bootstrap tests and confidence intervals for a hazard ratio when the number of observed failures is small, with applications to group sequential survival studies, *Computing Science and Statistics* 22 (1992) 89–97.
- [8] H.J. Kim, Bounding the resampling risk for sequential Monte Carlo implementation of hypothesis tests, *Journal of Statistical Planning and Inference* 140 (2010) 1834–1843.
- [9] M. Kulldorff, Prospective time periodic geographical disease surveillance using a scan statistic, *Journal of the Royal Statistical Society* 164A (2001) 61–72.
- [10] K. Lan, J. Wittes, The b -value: a tool for monitoring data, *Biometrics* 44 (1988) 579–585.
- [11] I. Silva, R. Assunção, M. Costa, Power of the sequential Monte Carlo test, *Sequential Analysis* 28 (2009) 163–174.
- [12] T. Tango, K. Takahashi, A flexibly shaped spatial scan statistic for detecting clusters, *International Journal of Health Geographics* 4 (2005).