crossrun: Joint Distribution for Number of Crossings and Longest Run in Independent Bernoulli observations

by Tore Wentzel-Larsen and Jacob Anhøj

Abstract An abstract of less than 150 words.

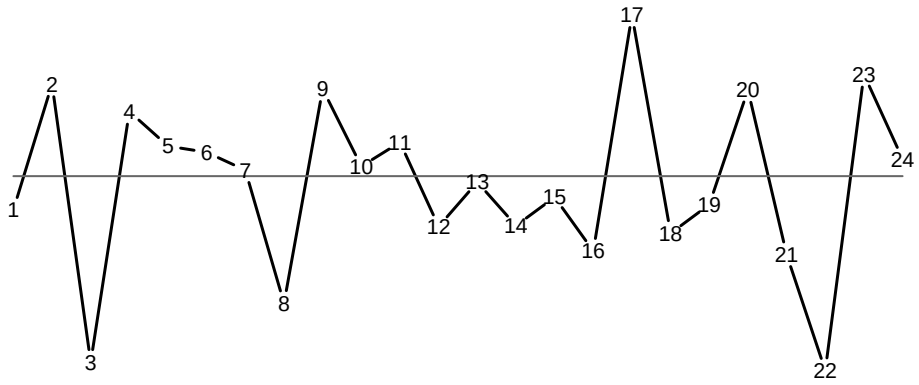
Introduction

The setting is defined by a number of independent observations from a Bernoulli distribution with the same success probability. In statistical process control, our main intended application, this may be the useful observations in a runchart, recording values above and below the median from previous data, disregarding any observations equal to the median (Anhøj, 2015).

The focus of the `crossrun` package is the joint distribution of number of crossings, C, and the length of the longest run, L, in random data sequences. A run is a sequence of successes or failures, delimited by a different observation or the start or end of the entire sequence. A crossing is two adjacent different observations.

Figure 1: illustrates runs and crossings in a run chart with 24 random observations. Observations above and below the median represent successes and failures respectively.

Figure 1: A runchart with n = 24 data points. The longest run consists of observations 12-16 below the median. The length of the longest run is L = 5. The number of crossings of the median is C = 11.



While the number of crossings follows a binomial distribution in the symmetric case (success probability 0.5), no closed form distribution is known for the longest run. The distribution of the longest run has been investigated in a number of articles, including (Schilling, 2012), and (Fazekas et al., 2010) that in fact gives recursion formulas, and approximations have been given. However, what is needed in applications is the joint distribution of these two variables, for which we are not aware of exact results. Our primary aim is to present an iterative procedure for computing this distribution, in principle for an arbitrary number of observations.

The iterative procedure, setting

In n independent Bernoulli observations with success probability p and failure probability $q = 1 - p$, values are denoted by 1 (success with probability p) or 0. A crossing consists of two consecutive different values, and a run of length l consists of l successive observations, delimited by a crossing or the first or last observation. The possible values of the number C of crossings are $c = 0, \ldots, n-1$ and the possible values for the length L of the longest run are $l = 1, \ldots, n$. The joint probabilities of L and C for given n are denoted by $P_n(L = l, C = c)$.

The iterative procedure involves conditioning on the first observation denoted by S, with values 1 for success (probability p) and 0 for failure (probability q). The iterative procedure computes the conditional probabilities

$$P_n(L = l, C = c \mid S = 1), P_n(L = l, C = c \mid S = 0)$$

This conditioning on the first observation is an essential part of the procedure. One way to see that this is reasonable is to consider the case when p is close to 1. Then most observations are successes, most runs are success runs and the conditional joint distribution of runs and crossings is quite different dependent on the first observation. It is sufficient to be able to compute these conditional distributions, because the unconditional joint distribution is

$$P_n(L = l, C = c) = P_n(L = l, C = c \mid S = 1) \cdot p + P_n(L = l, C = c \mid S = 0) \cdot q$$

For the iterative procedure to work it is also necessary to take another variable into account, the first crossing. More precisely, we denote the end position of the first crossing by F, with values $f = 2, \ldots, n$. An additional value $f = 1$ denotes, by convention, the case of no crossing. The joint probabilities for C and L conditional on S are partioned by further conditioning on F as detailed below.

It is important to underline that the conditioning parameters S and F are not parameters of the distribution but useful constructions that help brake down the iterative procedure in manageable parts.

This article first describes the setting for the iterative computation procedure and its initial stage, next introduces conditioning on the starting position and partitioning on the position of the first crossing and the joint distribution of the number of crossings and the longest run conditional on these variables. The computation procedure is different in two cases that are subsequently described.

After the exposition of the iterative procedure follows a brief comment on the simpler symmetric case, and the precision of the procedure is discussed. The resulting joint distribution is described in a simple case also included in the package vignette, and procedures for checking are briefly commented. Finally, the case where the median is determined from the data itself is considered and a similar procedure in that case is outlined. This case is not yet included in the `crossrun` package.

The conditional probabilities with one observation

First we present the starting point of the iterative procedure, the conditional probabilities in the rather redundant case with only one observation. If $n = 1$, 0 is the only possible value of C and 1 the only possible value of L, therefore $P_1(C = 0, L = 1 \mid S = 1) = P_1(C = 0, L = 1 \mid S = 0) = 1$. In this case the joint distribution matrices of C and L conditional on $S = 1$ or $S = 0$ are simple 1 by 1 identity matrices. Moving to more than one observation, the next step is presenting the conditional distribution of the end position F of the first crossing, conditional on the starting position S.

The distribution of the first crossing conditional on the starting position

If the first value is 1 (success), no crossing means that all the remaining $n - 1$ values are also 1, therefore $P_n(F = 1 \mid S = 1) = p^{n-1}$. Similarly, $P_n(F = 1 \mid S = 0) = q^{n-1}$. Next, if the first value is $f = 2, \cdots, n$ and the first value is a success, $F = f$ means that the sequence starts with a success, then $f - 2$ more successes and then one failure. Therefore,

$$P_n(F = f \mid S = 1) = p^{f-2} \cdot q, P_n(F = f \mid S = 0) = q^{f-2} \cdot p, f = 2, \ldots, n$$

where the last formula is based on a similar argument conditional on $S = 0$. In the following, arguments will in many cases be given for $S = 1$ only, and similar results for $S = 0$ will be stated with no explicit arguments. By symmetry, these results will simply involve replacing p by q. In the next step the formulas in this section will be used for partitioning the joint conditional probabilities for C and L given S, by the position F of the first crossing.

Partitioning by the position of the first crossing

Partitioning on F we have

$$P_n(L = l, C = c \mid S = 1) = \sum_{f=1}^{n} P_n(L = l, C = c \mid S = 1, F = f) \cdot P_n(F = f \mid S = 1)$$

where, as shown in the previous section, $P_n(F = f \mid S = 1) = p^{f-2}q$ if $f \geq 2$ and $P_n(F = 1 \mid S =$

$1) = p^{n-1}$. The formula for $P_n(L = l, C = c \mid S = 0)$ is the same, just interchanging p and q. This implies that the joint probabilities of C and L conditional on S may be computed if it is possible to compute all the joint probabilities of C and L conditional on S and F. This is the next step.

Joint distribution conditional on both S and F

First, if there is no crossing ($F = 1$) the entire sequence constitutes one single run, therefore

$$P_n(C = 0, L = 1 \mid S = 1, F = 1) = P_n(C = 0, L = 1 \mid S = 0, F = 1) = 1$$

and all other conditional probabilities are 0. Thus, the matrices of joint probabilities of C and L conditional on $F = 1$ together with each value of S, are matrices with all components equal to 0, except for a 1 in the upper right corner.

If crossings do occur ($f = 2, \ldots, n$), the conditional probabilities

$$P_n(C = c, L = l \mid S = 1, F = f), P_n(C = c, L = l \mid S = 0, F = f)$$

are more complicated. The key to computing these probabilities is to recognize that, except for the initial run of $f - 1$ observations, the remaining observations constitute $n - (f - 1) = n + 1 - f$ identical and independent Bernoulli observations with success probability p, they represent the same setting as for all n observations, just a shorter sequence. Further, these $n + 1 - f$ observations are also conditional on a fixed value of their first observation, only that this fixed value is the opposite as in the entire sequence. This is because the last $n + 1 - f$ observations start with the observation after the first crossing.

We now have to distinguish between two cases. In case 1, the initial run of $f - 1$ observations before the first crossing are at least as many as the last $n + 1 - f$ ones. In case 2, the initial run is shorter:

Case 1: $f - 1 \geq n + 1 - f$

Case 2: $f - 1 < n + 1 - f$

Case 1, at least as many observations before the first crossing as thereafter

This is the simplest case. Here, the first $f - 1$ observations constitute a run of length $f - 1$, and no run in the last $n + f - 1$ observations may be longer than that. Therefore, the longest run is $f - 1$, and the non-zero probabilities $P_n(C = c, L = l \mid S = 1, F = f)$ are confined to the vertical strip $l = f - 1$. And, in fact, to only a part of this strip. First, there is at least one crossing, from time $f - 1$ to f. Also, any further crossings are within the last $n + 1 - f$ observations, and may be any number between 0 and $(n + 1 - f) - 1$. The total number of crossings may therefore be any number between 1 and $n + 1 - f$, which means that the non-zero probabilities $P_n(C = c, L = l \mid S = 1, F = f)$ are confined to the strip $l = f - 1, 1 \leq c \leq n + 1 - f$. Figure 2: illustrates this in the case $n = 24$ and $f = 16$.

The non-zero probabilities $P_n(C = c, L = l \mid S = 1, F = f), l = f - 1, 1 \leq c \leq n + 1 - f$ are somehow determined by what happens within the last $n + 1 - f$ observations. The precise procedure for computing these probabilities is illustrated by the red arrows in Figure 2 above. The clue is to see that the last $n + 1 - f$ observations constitute a situation identical to the original n observations, only shorter, and with the starting observation fixed on the opposite side of the central line. To put it into a formula,

$$P_n(C = c, L = f - 1 \mid S = 1, F = f) = P_{n+1-f}(C = c - 1 \mid S = 0)$$

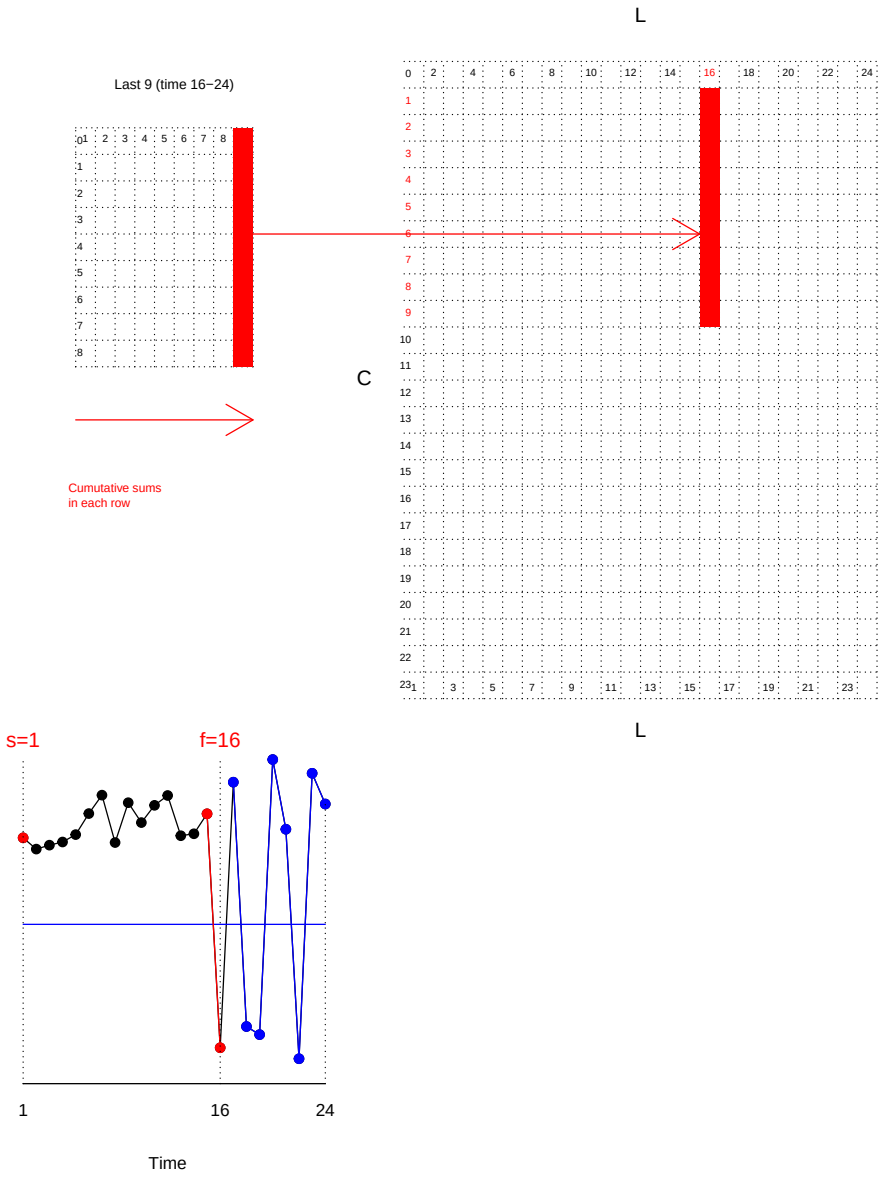
where $C = c - 1$ is because the crossing from $f - 1$ to f is just before the last $n + 1 - f$ observations. Similarly,

$$P_n(C = c, L = f - 1 \mid S = 0, F = f) = P_{n+1-f}(C = c - 1 \mid S = 1)$$

The probabilities on the right hand side of these formulas are for a lower number of observations and are therefore already computed in the iterative procedure.

Note that the $n + 1 - f$ observations after the initial run start on opposite side of the centre line. Therefore it is necessary to compute conditional probabilities conditional on starting values both above and below the centre line in the iterative procedure, they cannot be computed separately. The computations are a bit moe complicated in the second case, when the initial run is the shorter part, but the main idea is the same.

Figure 2: A runs chart with n=24 time points, starting above the midline ($S = 1$), and with the first crossing ending at time 16 ($F = 16$). The last 9 observations, from time 16 on, start below the midline ($S = 0$). The figure also shows (upper right) the joint distribution of crossings and runs for the entire sequence conditional on ($S = 1, F = 16$), and (upper left) the joint distribution among the last 9 observations conditional on ($S = 0$).



Case 2, fewer observations before the first crossing than thereafter

As in case 1, the total number of crossings is between 1 and $n - f + 1$. As to the longest run L, it cannot be shorter than $f - 1$ or longer than $n - f + 1$, and it is necessary to distinguish between values $l = f - 1$ and $l \geq f$. A longest run $f - 1$ in the entire sequence means that all runs in the last $n - f + 1$ observations have length $l \leq f - 1$. Therefore

$$P_n(C = c, L = f - 1 \mid S = 1, F = f) = P_{n+1-f}(C = c - 1, L \leq f - 1 \mid S = 0)$$

(and similarly conditional on $S = 0$). For longer runs, $f \leq l \leq n + 1 - f$ the longest run has to be within the last $n + 1 - f$ observations and we have

$$P_n(C = c, L = l \mid S = 1, F = f) = P_{n+1-f}(C = c - 1, L = l \mid S = 0)$$

(and similarly conditional on $S = 0$). All these conditional probabilies, based on a shorter sequence, have already been computed in an iterative computation procedure. This procedure is illustrated in Figure 3:

Simplifications in the symmetric case

For $p = \frac{1}{2}$ there is a symmetry between crossings up or down, and between success and failure runs. Therefore conditioning on the first observation is not necessary, although it is still necessary to partition on the first crossing F. Also, by an induction argument following the iterative procedure, all these probabilities are integer multiples of $\left(\frac{1}{2}\right)^{n-1}$ and, in fact, represent a partition of the binomial coefficients in the distribution of C, by the values $l = 1, \ldots, n$ of L.

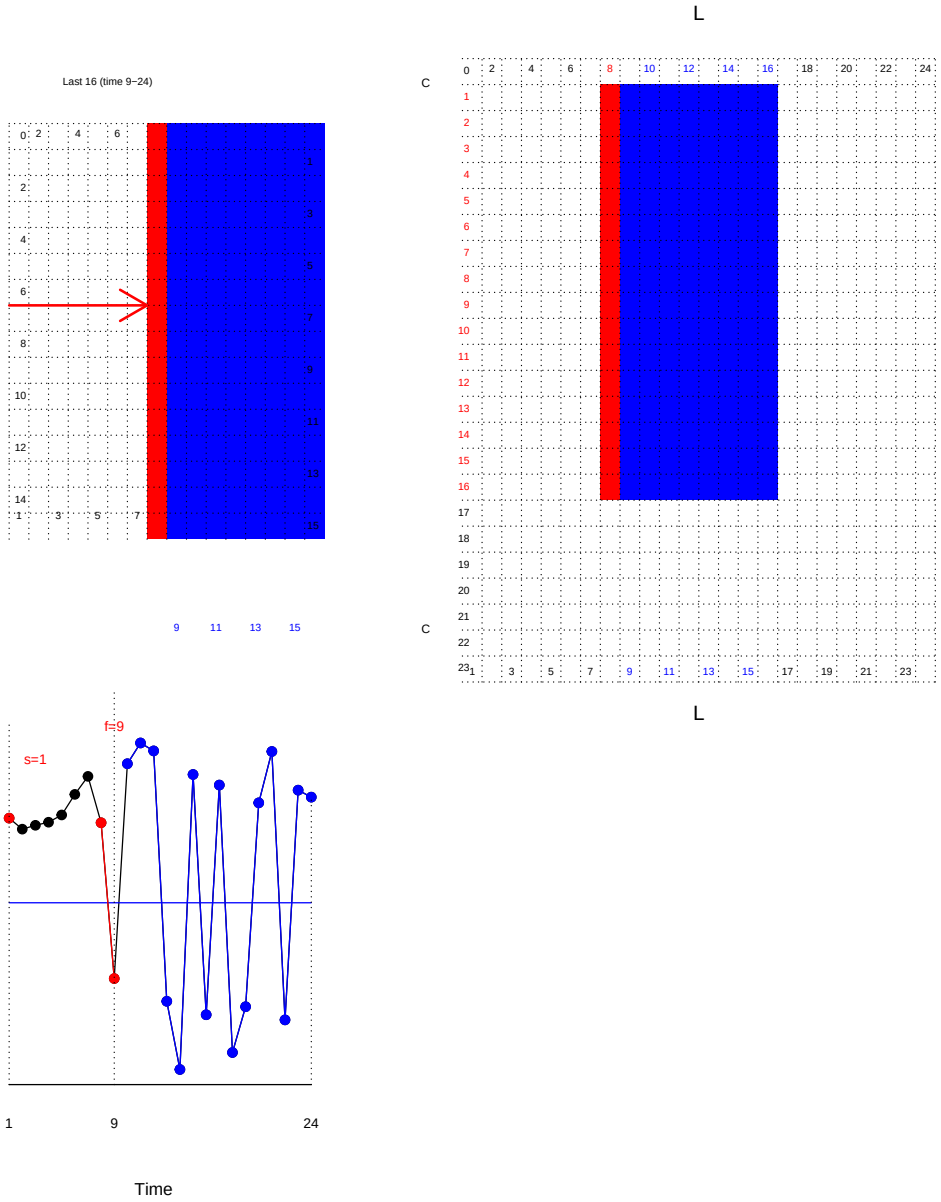
Precision considerations

To enhance precision, computations have been performed in the R package Rmpfr (Maechler, 2018), an R interface to the GNU MPFR library (Fousse et al., 2007). Preliminary investigations pointed to precision problems above values about 50 for sequence length n without this increased precision, but no such problems up to $n = 100$ when using Rmpfr. To further enhance precision, probabilities have been multiplied by m^{n-1} where m is a multiplier with default value 2. Thereby very small numbers are avoided, at least to some extent, and the numbers computed are integers in the symmetric case. The joint probabilities for $n = 15$ are shown below in this representation:

n=15	l=1	l=2	l=3	l=4	l=5	l=6	l=7	l=8	l=9	l=10	l=11	l=12	l=13	l=14	l=15
c= 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
c= 1	0	0	0	0	0	0	0	2	2	2	2	2	2	2	0
c= 2	0	0	0	0	1	9	18	18	15	12	9	6	3	0	0
c= 3	0	0	0	4	48	88	84	60	40	24	12	4	0	0	0
c= 4	0	0	1	100	280	270	175	100	50	20	5	0	0	0	0
c= 5	0	0	50	530	666	420	210	90	30	6	0	0	0	0	0
c= 6	0	0	357	1197	861	392	147	42	7	0	0	0	0	0	0
c= 7	0	8	1008	1456	672	224	56	8	0	0	0	0	0	0	0
c= 8	0	84	1470	1044	324	72	9	0	0	0	0	0	0	0	0
c= 9	0	252	1200	450	90	10	0	0	0	0	0	0	0	0	0
c=10	0	330	550	110	11	0	0	0	0	0	0	0	0	0	0
c=11	0	220	132	12	0	0	0	0	0	0	0	0	0	0	0
c=12	0	78	13	0	0	0	0	0	0	0	0	0	0	0	0
c=13	0	14	0	0	0	0	0	0	0	0	0	0	0	0	0
c=14	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

The corresponding joint probabilities are obtained by dividing these integers by $2^{n-1} = 2^{14} = 16384$, for instance $P(C = 5, L = 6) = 420/16384 = 0.026$. The highest joint probability is $P(C = 8, L = 3) = 1470/16384 = 0.090$. It is also seen that a hight proportion of the joint probabilities consists of zeroes, and except for some very small numbers the joint probabilities are concentrated within a narrow band sloping band. These are fairly general phenomena. For comparison the joint distribution for $n = 15$ is also shown below for $p = 0.6$, a case where observations tend to stay above the midline. These probabilities are still shown in the "times" representation, they are multiplied by $2^{n-1} = 16384$, and are shown with one decimal digit:

Figure 3: A runs chart with n=24 time points, starting above the midline ($S = 1$), and with the first crossing ending at time 9 ($F = 9$). Also (top right) the joint distribution of C and L conditional on ($S = 1, F = 9$), and (top left) the joint distribution among the last 16 observations conditional on ($S = 0$), including a red strip representing the cumulative sum of the first $f - 1 = 8$ columns, and a blue rectangle representing joint probabilities from $L = 9$ on. The corresponding contributions to the joint probabilities for $n = 24$ are shown in the same colors (top right).



p=0.7	l=1	l=2	l=3	l=4	l=5	l=6	l=7	l=8	l=9	l=10	l=11	l=12	l=13	l=14	l=15
c=0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.7
c=1	0	0	0	0	0	0	0	1.5	1.8	2.3	3.2	4.7	6.9	10.3	0
c=2	0	0	0	0	1.1	11.4	29.3	33.7	31.8	29.7	26.8	21.9	13.8	0	0
c=3	0	0	0	3.0	41.7	91.7	105.9	87.8	70.3	51.9	32.6	13.9	0	0	0
c=4	0	0	0.9	99.2	318.3	354.3	260.6	172.1	101.9	49.2	15.1	0	0	0	0
c=5	0	0	39.3	468.8	670.6	483.1	278.4	141.5	57.1	14.1	0	0	0	0	0
c=6	0	0	319.2	1180.3	948.8	485.7	210.1	70.9	14.2	0	0	0	0	0	0
c=7	0	6.0	836.1	1324.0	679.9	257.7	75.4	12.9	0	0	0	0	0	0	0
c=8	0	68.5	1289.2	994.7	341.5	86.5	12.6	0	0	0	0	0	0	0	0
c=9	0	196.4	991.5	402.9	89.8	11.5	0	0	0	0	0	0	0	0	0
c=10	0	267.1	466.8	100.8	11.3	0	0	0	0	0	0	0	0	0	0
c=11	0	170.3	106.7	10.5	0	0	0	0	0	0	0	0	0	0	0
c=12	0	61.2	10.6	0	0	0	0	0	0	0	0	0	0	0	0
c=13	0	10.5	0	0	0	0	0	0	0	0	0	0	0	0	0
c=14	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Limitations

One main limitation is that the iterative procedure cannot in any obvious way be generalized to autocorrelated time series. It may, however be generalized to time series with independent, but not necessarily identical, observations, this is implemented in a function `crossrunchange`. Another limitation is that the code has so far only been checked for $n \leq 100$. In that range it seems to work well. It has been checked with manual computations for $n \leq 6$, and with 100,000 simulations for $n = 100$. Specifically, the mean and standard deviations for both C and L have been computed, as well as the mean of $C \cdot L$ and also the cumulative distribution functions of C and L separately, with no substantial deviations. It has also been checked for $n \leq 100$ that the marginal distribution of C computed from the joint distribion agrees with the correct binomial distribution in the symmetric case. These last investigations were, in fact, what pointed to the necessity to base the code on Rmpfr. The performance of the procedure has not, however, so far been checked for $n > 100$. For applications to statistical process control $n \leq 100$ should be sufficient in most cases, but other applications may require higher n.

The case when the median is determined by the data itself

Another important limitation of the package crossrun is that the case when the median is determined from the data itself is not covered. This is common in statistical process control. Some progress has been made on this case since the package was submitted to CRAN, and we plan to include a procedure for this case in a subsequent update. This section describes the procedure in general terms.

The setting is n independent and identically observations of a continuous variable. The empirical median in the sequence is computed, and C and L is the number of crossings of the median line and the longest run above or below the median. Observations at the median neither contribute to the run nor do they break it (Anhøj, 2015). Therefore, limiting to the observations used we may without loss of generality assume that the number n of observations is even, with half the observations above and half the observations below the median. Thus, this case is by definition symmetric.

First, we note that by symmetry, all placements of the $m = n/2$ observations above the median are equally probable. Therefore, if all sequences of n Bernoulli observations are enumerated, we may simply count the sequences with each combinations of C and L and divide by the total number of sequences, this will give the joint probability. This procedure has been implemented and it is checked that the resulting joint distribution is in close agreement with simulations. The main drawback with this procedure is that the algorithmic complexity in terms of storage requirements and time consumption is prohibitive except for small n. It is practical only up to about $n = 28$. This procedure is therefore not discussed further.

To sum up, we want to find the number of sequences of $m = n/2$ zeroes (below the median) and m ones for each combination of C and L. This problem, it turns out, is not in itself tractable. However, if the requirement that exactly half the observations are 1 and the others are 0 is relaxed, the problem is relaxed it turns out that the problem may be solved by an iterative procedure that in fact resembles the procedure used in `crossrun`. This reflects a general phenomenon, in an iterative procedure "more may be less", because then more information is available from earlier stages. This we set out to compute the number of

sequences of m ones and n - m zeroes for each value c of C and l of L, $1 \leq c \leq n-1, 1 \leq l \leq n$.

This problem has higher algorithmic complexity than the corresponding problem already teeated in crossrunbin since the numer for sequences has to be computed for all m, $0 \leq m \leq n$. And also for al n, not only for even numbers. This increases complexity by a factor roughly equal to 2n, and only a tiny fraction of the information produced is actually used, for even n and $m = n/2$. Still the algorithmic complexity is appreciably lower than the procedure using full enumaration of all sequences, and we have been able to reach $n = 64$ within resonable time. In the following we introduce some notation before describing the iterative procedure in more detail.

We set $\text{NFI}_{n,m}(C = c, L = l)$ equal to the number of sequences of m ones and n-m zeroes with c crossings and longest run l, starting with a 1. Similarly $\text{NFN}_{n,m}(C = c, L = l)$ is the number of sequences of m ones and n - m zeroes with c crossings and longest run l, starting with a 0 (number of subsets, first element included and not included, respectively). We want to compute these two numbers for all m, $0 \leq m \leq n$ and all c and l, $0 \leq c \leq n-1, 1 \leq l \leq n$. The cases $m = 0$, n are simple. If $m = 0$, NFI is all zeroes and in $\text{NFN}_{n,0}(C = 0, L = n) = 1$ and the rest of the NFN matrix is 0. Similarly, for $m = n$, NFN is all zeroes and $\text{NFI}_{n,n}(C = 0, L = n) = 1$ and the rest of the NFI matrix is 0. In the following we assume that $1 \leq m \leq n-1$. We partition on the length G of the initial run, with values $1 \leq g \leq m$ in computation of NFI and $1 \leq g \leq n - m$ in computation of NFN. Then

$$\text{NFI}_{n,m}(C = c, L = l) = \sum_{g=1}^{m} \text{NFI}_{n,m}(C = c, L = l, G = g)$$

$$\text{NFN}_{n,m}(C = c, L = l) = \sum_{g=1}^{n-m} \text{NFN}_{n,m}(C = c, L = l, G = g)$$

Much as in crossrunbin there are two cases,

Case 1: $g \geq n - g$

Case 2: $g < n - g$

Case 1 is the simplest one. Then no runs within the last $n - g$ is longer than the initial run and the total number of crossings is one more than the number of crossings within these last part of the sequence. Therefore non-zero numbers are confined to $1 \leq c \leq n - g, l = g$ and

$$\text{NFI}_{n,m}(C = c, L = l, G = g) = \text{NFN}_{n-g,m-g}(C = c - 1)$$
$$\text{NFN}_{n,m}(C = c, L = l, G = g) = \text{NFi}_{n-g,m}(C = c - 1)$$

Note that the $G = g$ contribution to NFI, resp. NFN, is computed from NFN, resp. NFI within the last $n - g$ observations, it is not possible to compute NFI or NFN without the other. This is because the first observation after the initial run is opposite to the first observation in the entire sequence. This also applies in case 2.

In case 2 the longest run in the last $n - g$ observations may be longer than the initial run. For the entire sequence, $l = g$ may occur, this is when the longest run in the last $n - q$ observations is $\leq g$,

$$\text{NFI}_{n,m}(C = c, L = g, G = g) = \text{NFN}_{n-g,m-g}(C = c - 1, L \leq g)$$
$$\text{NFN}_{n,m}(C = c, L = g, G = g) = \text{NFI}_{n-g,m}(C = c - 1, L \leq g)$$

$L > g$ may also occur if the longest run is within the last $n - g$ observations. Then

$$\text{NFI}_{n,m}(C = c, L = l, G = g) = \text{NFN}_{n-g,m-g}(C = c - 1, L = l)$$
$$\text{NFN}_{n,m}(C = c, L = l, G = g) = \text{NFN}_{n-g,m}(C = c - 1, L = l)$$

Now all cases are covered, and together these formulas make it possible to compute all

$\text{NFI}_{n,m}(C = c, L = l)$ and $\text{NFN}_{n,m}(C = c, L = l)$ based on the smaller sequence after the initial run.

Conclusions

The crossrun package includes functions for computing the probabilities of the joint distribution of longest run and number of crossings in random data series. To our knowledge, this distribution has not been studied before.

The ability to calculate exact probabilities for the joint distribution allows for the development of better prediction limits for longest run and crossings in random data series. In turn, this allows for better separation of signal and noise, i.e. random and non-random variation, in, for example, statistical process control, gaming fraud detection, or search for extraterrestrial life, to name a few.

Appendix 1: R code for the iteration procedure

The iterative procedure is coded in the function crossrunbin.

```
crossrunbin <- function(nmax   = 100,
                        prob   = 0.5,
                        mult   = 2,
                        prec   = 120,
                        printn = FALSE) {
  nill   <- mpfr(0, prec)
  one    <- mpfr(1, prec)
  multm  <- mpfr(mult, prec)
  pm     <- mpfr(prob, prec)
  qm     <- one - pm
  pmultm <- pm * multm
  qmultm <- qm * multm

  # conditioning of S = first value, pat: above 0, pbt: below 0
  # suffix t: probabilities times multm^(n - 1).
  # n = 1:

  pat <- list(pt1=mpfr2array(one, dim = c(1, 1)))
  pbt <- list(pt1=mpfr2array(one, dim = c(1, 1)))
  pt  <- list(pt1=mpfr2array(one, dim = c(1, 1)))
  qat <- list(pt1=mpfr2array(one, dim = c(1, 1)))
  qbt <- list(pt1=mpfr2array(one, dim = c(1, 1)))
  qt  <- list(pt1=mpfr2array(one, dim = c(1, 1)))

  for (nn in 2:nmax) {
    pat[[nn]]           <- mpfr2array(rep(nill,nn*nn), dim=c(nn,nn))
    pbt[[nn]]           <- mpfr2array(rep(nill,nn*nn), dim=c(nn,nn))
    rownames(pat[[nn]]) <- c(0:(nn-1))
    rownames(pbt[[nn]]) <- c(0:(nn-1))
    colnames(pat[[nn]]) <- c(1:nn)
    colnames(pbt[[nn]]) <- c(1:nn)
    pat[[nn]][1, nn]     <- (pmultm^(nn-1)) # from cond on no crossing
    pbt[[nn]][1, nn]     <- (qmultm^(nn-1)) # from cond on no crossing

    for (ff in 2:nn) { # from cond on first crossing at ff
      if (nn - ff + 1 <= ff - 1) { # if last part shortest:
        f1 <- ff # unnecessary, but makes code checking easier
        pat[[nn]][2:(nn - f1 + 2), f1 - 1] <-
          pat[[nn]][2:(nn - f1 + 2), f1 - 1] +
```

```
          (pmultm^(f1-2)) * qmultm *
            qbt[[nn - f1 + 1]][1:(nn - f1 + 1), nn - f1 + 1]
        pbt[[nn]][2:(nn - f1 + 2), f1 - 1] <-
          pbt[[nn]][2:(nn - f1 + 2), f1 - 1] +
            (qmultm^(f1 - 2)) * pmultm *
              qat[[nn - f1 + 1]][1:(nn - f1 + 1), nn - f1 + 1]
      } # end if last part shortest

      if (nn - ff + 1 > ff - 1) { # if last part longest
        f2 <- ff # unnecessary, but makes code checking easier
        pat[[nn]][2:(nn - f2 + 2), f2 - 1] <-
          pat[[nn]][2:(nn - f2 + 2), f2 - 1] +
            (pmultm^(f2 - 2)) *
              qmultm *
                qbt[[nn - f2 + 1]][1:(nn - f2 + 1), f2 - 1]
        pat[[nn]][2:(nn - f2 + 2), f2:(nn - f2 + 1)] <-
          pat[[nn]][2:(nn - f2 + 2), f2:(nn - f2 + 1)] +
            (pmultm^(f2 - 2)) *
              qmultm *
                pbt[[nn - f2 + 1]][1:(nn - f2 + 1), f2:(nn - f2 + 1)]
        pbt[[nn]][2:(nn - f2 + 2), f2 - 1] <-
          pbt[[nn]][2:(nn - f2 + 2), f2 - 1] +
            (qmultm^(f2 - 2)) *
              pmultm * qat[[nn - f2 + 1]][1:(nn - f2 + 1), f2 - 1]
        pbt[[nn]][2:(nn - f2 + 2), f2:(nn - f2 + 1)] <-
          pbt[[nn]][2:(nn - f2 + 2), f2:(nn - f2 + 1)] +
            (qmultm^(f2 - 2)) *
              pmultm *
                pat[[nn - f2 + 1]][1:(nn - f2 + 1),f2:(nn - f2 + 1)]
      } # end if last part longest
    } # end for ff

    pt[[nn]]            <- pm * pat[[nn]] + qm * pbt[[nn]]
    qat[[nn]]           <- cumsumm(pat[[nn]])
    qbt[[nn]]           <- cumsumm(pbt[[nn]])
    qt[[nn]]            <- pm*qat[[nn]] + qm*qbt[[nn]]
    rownames(pt[[nn]])  <- c(0:(nn - 1))
    colnames(pt[[nn]])  <- c(1:nn)
    rownames(qat[[nn]]) <- c(0:(nn - 1))
    colnames(qat[[nn]]) <- c(1:nn)
    rownames(qbt[[nn]]) <- c(0:(nn - 1))
    rownames(qat[[nn]]) <- c(0:(nn - 1))
    colnames(qt[[nn]])  <- c(1:nn)
    colnames(qt[[nn]])  <- c(1:nn)

    if (printn) {
      print(nn)
      print(Sys.time())
    } # end optional timing information
  } # end for nn

  names(pat) <-paste("pat", 1:nmax, sep="")
  names(pbt) <-paste("pbt", 1:nmax, sep="")
  names(pt)  <-paste("pt",  1:nmax, sep="")
  names(qat) <-paste("qat", 1:nmax, sep="")
  names(qbt) <-paste("qbt", 1:nmax, sep="")
  names(qt)  <-paste("qt",  1:nmax, sep="")

  return(list(pat = pat, pbt = pbt, pt = pt, qat = qat, qbt = qbt, qt = qt))
```

```
} # end function crossrunbin
```

Appendix 2: Detailed computation, illustrated for n = 7

This section should be removed before publication, but is included to aid our own comprehension of the procedure. First some generalities on the times representation

$$\mathrm{Pt}_n(C = c, L = l \mid S = 1) = m^{n-1} P_n(C = c, L = l \mid S = 1)$$

where m is a multiplier normally set as m=2 (the case of conditioning on S=0, starting below the midline, is similar). Denoting the success probability as p and the failure probability as q=1-p the main decomposition for probabilities is

$$P_n(C = c, L = l \mid S = 1) = p^{n-1} \cdot P_n(C = c, L = l \mid S = 1, F = 1) +$$

$$\sum_{f=2}^{n} p^{f-2} \cdot q \cdot P_n(C = c, L = l \mid S = 1, F = f)$$

where the first term conditions on F=1, by convention corresponding to no crossing, and each of the remaining terms condition on $F = f, f = 2, \ldots, n$ corresponds to the first crossing from f-1 to f. The corresponding decomposition in the times representation is

$$\mathrm{Pt}_n(C = c, L = l \mid S = 1) = (pm)^{n-1} \cdot P_n(C = c, L = l \mid S = 1, F = 1) +$$

$$\sum_{f=2}^{n} (pm)^{f-2} \cdot qm \cdot m^{n-f} P_n(C = c, L = l \mid S = 1, F = f)$$

In the first term for no crossing the probability is simply 1 if $C = 0, L = n$ and 0 otherwise. This term is the same in the times representation except for the initial factor in which p^{n-1} is replaced by $(pm)^{n-1}$. In the symmetric case both pm and qm are equal to 1, thus the initial factor is 1 and the term as a whole is actually simpler in the times representation in the symmetric case.

In the remaining terms, for the first crossing from f-1 to f, there there is first a factor $(pm)^{f-2} \cdot qm$ that is similar to the corresponding factor in the original representation, except that p is replaced by pm and q by qm. Again this first factor is actually 1 in the symmetric case. The rest of the term is $m^{n-f} P_n(C = c, L = l \mid S = 1, F = f)$. In the following we will show that the probabilities $P_n(C = c, L = l \mid S = 1, F = f)$ are determined by the joint distribution $P_{n+1-f}(C = c', L = l' \mid S = 0)$ for the observations starting at the end of the first crossing. Here we condition on the opposite starting value S=0 since this last part of the sequence starts just where the first crossing has occurred. As to the main part of the term $P_n(C = c, L = l \mid S = 1, F = f)$ we more specifically have seen, ands will illustrate in an example, that it is determinded by the joint distribution $P_{n+1-f}(C = c', L = l' \mid S = 0)$ by simple operations in terms of additions and reshuffling only. The corresponding joint distribution on the times representation is

$$\mathrm{Pt}_{n+1-f}(C = c', L = l' \mid S = 0) = m^{(n+1-f)-1} \cdot P_{n+1-f}(C = c', L = l' \mid S = 0)$$

where the leading factor $m^{(n+1-f)-1} = m^{n-f}$ is exactly the same as the leadning factor in $m^{n-f} P_n(C = c, L = l \mid S = 1, F = f)$. Therefore the term

$$m^{n-f} P_n(C = c, L = l \mid S = 1, F = f)$$

is determined by the joint distribution

$$\mathrm{Pt}_{n+1-f}(C = c', L = l' \mid S = 0)$$

on the times scale by exactly the same additions and reshufflings as apply on the original probability scale.

We take as an example n=7 in the symmetric case. The joint distributions for $n = 1, \ldots, 6$ are taken for granted throughout, this is an illustration of step 7 in the sequential computation procedure. Then

$$P_7(C = c, L = l \mid S = 1) = (0.5)^6 \cdot P_7(C = c, L = l \mid S = 1, F = 1) +$$

$$(0.5) \cdot P_7(C = c, L = l \mid S = 1, F = 2) + (0.5)^2 \cdot P_7(C = c, L = l \mid S = 1, F = 3) + \ldots +$$

$$(0.5)^6 \cdot P_7(C = c, L = l \mid S = 1, F = 7)$$

In the times representation these probabilities are multiplied by 2^6.

In the contribution from F=1, $P_7(C = c, L = l \mid S = 1, F = 1)$ is 1 if C=0 and L=7 and 0 elsewhere, since F=1 is defined as no crossing. This, the contribution from this first term, in the times representation, is a 7x7 matrix with a 1 in the upper right corner and zeroes elsewhere.

In the remaining terms for $f = 2, \ldots, 7$ there is a distinction between case 1 when the initial run of f-1 observations is at least as long as the rest, and case 2 when this is not the case. For n=7, case 1 corresponds to f=5,6,7, and case 2 corresponds to f=2,3,4.

In case 1 we start with f=7. Then the first 6 observations are above the midline and the last observation is below. This means that C=1 and L=6. The contribution from this term in the times representation is a matrix with a 1 in the position (c=1,l=6) and zeroes elsewhere.

The term for f=6 is

$$(0.5)^5 \cdot P_7(C = c, L = l \mid S = 1, F = 6)$$

The longest run is the initial one, with l=5. There is one crossing from observation 5 to 6. In addition, the last two observations start below the midline and constitute a sequence on its own, with equal probabilities 0.5 for zero and for one crossing. Thus

$$P_7(C = 1, L = 5 \mid S = 1, F = 6) = P_7(C = 2, L = 5 \mid S = 1, F = 6) = 0.5$$

The 0.5 here gives $(0.5)^6$ when multiplied by the initial factor $(0.5)^5$ in the term. Thus in the times representation this contribution is a matrix with ones at positions (c=1,l=5) and (c=2,l=5) and zeroes elsewhere.

The term for f=5 is

$$(0.5)^4 \cdot P_7(C = c, L = l \mid S = 1, F = 5)$$

The longest run is the initial one, with l=4. There is one crossing from observation 4 to 5. In addition, the last 3 observations start below the midline and constitute a sequence on its own. The joint distribution of C and L in this sequence is

n=3	l=1	l=2	l=3
c= 0	0	0	1
c= 1	0	2	0
c= 2	1	0	0

From this we get the marginal distribution for the number of crossings in this last 3 observations in the times representation:

n=3	c=0	c=1	c=2
	1	2	1

The number of crossings in the entire sequence is one more, thus these three numbers are placed at positions (c=1,l=4), (c=2,l=4) and (c=3,l=4), respectively. In the original representation these numbers are multiplied with $(0.5)^2$ which together with the initial factor $(0.5)^4$ gives $(0.5)^6$, therefore this matrix is the contribution from this term in the times representation of the entire sequence.

The remaining terms are in case 2 when the initial run is no longer as long as the rest. Continuing downwards the contribution from f=4 is

$$(0.5)^3 \cdot P_7(C = c, L = l \mid S = 1, F = 4)$$

Now, the initial run of f-1=3 observations may or may not be a longest run. To further investigate this we have to look at the joint distribution of the remaining 4 observations whose times representation is

n=4	l=1	l=2	l=3	l=4
c= 0	0	0	0	1
c= 1	0	1	2	0
c= 2	0	3	0	0
c= 3	1	0	0	0

The initial run is a longest run if and only of $l \leq 3$ in the last 4 observations:

n=4	$l \leq 3$	l=4
c= 0	0	1
c= 1	3	0
c= 2	3	0
c= 3	1	0

In the joint distribution for the entire sequence, l is therefore 3 or 4, and the contribution to the joint distribution of C and L for the entire sequence is given by the table above, only with one more crossing:

n=7	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	1	0	0	0
c= 2	0	0	3	0	0	0	0
c= 3	0	0	3	0	0	0	0
c= 4	0	0	1	0	0	0	0
c= 5	0	0	0	0	0	0	0
c= 6	0	0	0	0	0	0	0
c= 7	0	0	0	0	0	0	0

Continuing with f=3, the term is

$$(0.5)^2 \cdot P_7(C = c, L = l \mid S = 1, F = 4)$$

The initial run of f-1=2 observations may or may not be a longest run. The joint distribution for the last 5 observations in the times representation is

n=5	l=1	l=2	l=3	l=4	l=5
c= 0	0	0	0	0	1
c= 1	0	0	2	2	0
c= 2	0	3	3	0	0
c= 3	0	4	0	0	0
c= 4	1	0	0	0	0

The initial run of 2 observations is a longest run if and only if $l \leq 2$ in the last 5 observations, given by the following table:

n=7	$l \leq 2$	l=3	l=4	l=5
c= 0	0	0	0	1
c= 1	0	2	2	0
c= 2	3	3	0	0
c= 3	4	0	0	0
c= 4	1	0	0	0

The corresponding contribution to the joint distribution for the entire sequence includes these numbers, just that the number of crossings in the entire sequence is one more:

n=7	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	0	1	0	0
c= 2	0	0	2	2	0	0	0
c= 3	0	3	3	0	0	0	0
c= 4	0	4	0	0	0	0	0
c= 5	0	1	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

Finally, f=2. Then there is a crossing from observation 1 to observation 2. The joint distribution of C and L in the last 6 observations is:

n=6	l=1	l=2	l=3	l=4	l=5	l=6
c= 0	0	0	0	0	0	1
c= 1	0	0	1	2	2	0
c= 2	0	1	6	3	0	0
c= 3	0	6	4	0	0	0
c= 4	0	5	0	0	0	0
c= 5	1	0	0	0	0	0

The first "run" of just 1 observation is longest if there are all crossings in the last 6 observations, so this is also the contribution to the joint distribution for the entire sequence, jutst with one crossing more:

n=7	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	0	0	1	0
c= 2	0	0	1	2	2	0	0
c= 3	0	1	6	3	0	0	0
c= 4	0	6	4	0	0	0	0
c= 5	0	5	0	0	0	0	0
c= 6	1	0	0	0	0	0	0

Adding all contributions we get

n=7,f=1	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	1
c= 1	0	0	0	0	0	0	0
c= 2	0	0	0	0	0	0	0
c= 3	0	0	0	0	0	0	0
c= 4	0	0	0	0	0	0	0
c= 5	0	0	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

+

n=7,f=2	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	0	0	1	0
c= 2	0	0	1	2	2	0	0
c= 3	0	1	6	3	0	0	0
c= 4	0	6	4	0	0	0	0
c= 5	0	5	0	0	0	0	0
c= 6	1	0	0	0	0	0	0

+

n=7,f=3	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	0	1	0	0
c= 2	0	0	2	2	0	0	0
c= 3	0	3	3	0	0	0	0
c= 4	0	4	0	0	0	0	0
c= 5	0	1	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

+

n=7,f=4	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	1	0	0	0
c= 2	0	0	3	0	0	0	0
c= 3	0	0	3	0	0	0	0
c= 4	0	0	1	0	0	0	0
c= 5	0	0	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

+

n=7,f=5	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	1	0	0	0
c= 2	0	0	0	2	0	0	0
c= 3	0	0	0	1	0	0	0
c= 4	0	0	0	0	0	0	0
c= 5	0	0	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

+

n=7,f=6	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	0	1	0	0
c= 2	0	0	0	0	1	0	0
c= 3	0	0	0	0	0	0	0
c= 4	0	0	0	0	0	0	0
c= 5	0	0	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

n=7,f=7	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	0
c= 1	0	0	0	0	0	1	0
c= 2	0	0	0	0	0	0	0
c= 3	0	0	0	0	0	0	0
c= 4	0	0	0	0	0	0	0
c= 5	0	0	0	0	0	0	0
c= 6	0	0	0	0	0	0	0

+

n=7	l=1	l=2	l=3	l=4	l=5	l=6	l=7
c= 0	0	0	0	0	0	0	1
c= 1	0	0	0	2	2	2	0
c= 2	0	0	6	6	3	0	0
c= 3	0	4	12	4	0	0	0
c= 4	0	10	5	0	0	0	0
c= 5	0	6	0	0	0	0	0
c= 6	1	0	0	0	0	0	0

=

In these calculations we have tacitly used that the joint distributions are the same whether the sequence starts above or below the midline. This is correct in the symmetric case. In non-symmetric cases it is necessary to distinguish between sequences starting above or below the midline, this is precisely why the computations are somewhat simpler in the symmetric case.

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Tore Wentzel-Larsen
Centre for Child and Adolescent Mental Health, Eastern and Southern Norway
Norwegian Centre of Violence and Traumatic Stress Studies
Norway
tore.wentzellarsen@gmail.com

Jacob Anhøj
Rigshospitalet, University of Copenhagen
Denmark
(ORCiD https://orcid.org/0000-0002-7701-1774)
jacob@anhoej.net