DISCRETE POISSON HARDCORE 1D MODEL AND REINFECTIONS

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Abstract. We suggest a new hardcore Poisson-type distribution for Young diagrams with the row lengths from some finite list. A discrete variant of the time-ordered Matérn II process in 1D is employed. This approach is related to that based on the interlacing sequences due to Kerov and others, but we restrict the number of rows. The basic lengths are assumed comparable with the total order of the diagram in the quasi-classical limit, which results in new methods and new formulas. An interesting application is to random walks where the steps are at the points satisfying the classical Poisson distribution or our truncated one. In the simplest case, one obtains the distribution \(\{e^{-\alpha}I_r(\alpha), -\infty < r < \infty\}\) for the Bessel \(I\)-functions, which provides some probabilistic interpretation of its many properties. An immediate application of our truncated Poisson distributions is to modeling reinfections in epidemics, which is of obvious importance for the Covid-19 pandemic.

Key words: hardcore Poisson point processes; Matérn processes; epidemics; reinfections; Young diagrams; stochastic processes; Bessel functions.

MSC (2010): 05A15, 05A18, 33C10, 60C05, 60G55, 60E05, 62P10, 91F99

1. Introduction. The main general result of this paper is the definition and calculation of a new Poisson-type distribution for sequences of non-overlapping subsegments of lengths \(\{L_1, \ldots, L_s\}\) in a segment of length \(N\). Equivalently, this distribution is for Young diagrams of order \(\leq N\) with the the row lengths \(\{L_i\}\). This is related to the interlacing sequences due to Kerov and others, a starting point for many far-reaching applications: Jack-Whittaker-Macdonald functions and the corresponding stochastic point processes. From this perspective, we assume that the distances between the points are \(\geq L_i\).

† June 17, 2022. Partially supported by NSF grant DMS–1901796.
The creation of these segments is governed by a discrete variant of the time-ordered Matérn II process in 1D. We assume that that \( \lim_{N \to \infty} L_i / N = \nu_i > 0 \) in the quasi-classical limit, so the edge effects are significant. Taking the limit required a procedure which seems new even for one \( L \), as well as the resulting formulas.

A variant is the probability distribution for random walks with the steps \( \pm 1 \) at the points satisfying the Poisson \( \alpha \)-distribution or our truncated one. In the simplest case, we arrive at \( \{ e^{-\alpha I_r(\alpha)}, -\infty < r < \infty \} \) for the Bessel \( I \)-functions, which provides a probabilistic interpretation of the properties of \( I \)-functions. The restriction of this approach to Catalan (non-negative) paths is considered.

An immediate application of our truncated Poisson distribution is to modeling reinfections in epidemics, aimed at the Covid-19 pandemic. Combinatorially, segments of one or several different lengths are protective immunity intervals; they are placed in a bigger segment, the epidemic cycle. Practically, no greater than 2-3 different strains can be present simultaneously. The case of 1 strain (when \( s = 1 \)) is the key.

Reinfections were relatively rare before Covid-19 (during 1 cycle). The Poisson distribution can be expected if the immunity and the duration of the disease are disregarded. However, immunity is the key here. There were not many papers on modeling reinfections; see e.g. [ADDP], which was SIR-based. We mention that the SIR-models proved to be not applicable to Covid-19; see [Ch1, Ch2].

**Hardcore point processes.** The corresponding mathematical tool is the theory of **Poisson hardcore point processes**, more specifically, the time-ordered **Matérn process II** and in its **lattice** variant. There are quite a few processes where the distances between neighboring objects must be greater than some constant. The usual examples are **forestry**, **ecology**, **vehicular networks**, **cellular networks**, etc. Also, see [Gi] for Tonks gas. In statistical physics, “small systems” are of this type, those far from thermodynamic equilibrium. There is a vast literature on Matérn processes I,II,III, mostly in 2D. See e.g. [KD] on vehicular networks and references there. Modeling **vehicular networks**, clear 1D processes, is somewhat similar to modeling reinfections. The interval between cars is a counterpart of the immunity intervals.

In such and similar examples, the intervals between objects are mostly assumed small vs. the domains where they are considered. Accordingly,
the edge effects are mostly ignored. This is different for epidemics: the immunity intervals are quite comparable with the duration of the epidemic cycle. The continuous distribution we obtain in (6) is a certain truncated version of the classical Poisson distribution; we think it is new. It is not its straightforward truncation via the relative probabilities.

We begin with the following discrete setting: configurations of subsegments of the length \( L + 1 \) with gaps between them in a given segment of the length \( N \). This can be necessary when the process depends on \( N \) and \( L \), not just on \( L/N \) in the limit (see below). In the lattice version, exact formulas can be obtained in terms of binomial coefficients and generalized to subsegments of any lengths, which requires only basic combinatorics. We make them as explicit as possible in Corollary 5.3.

**Edge effects.** This is when the last segment goes beyond \( N \). They naturally result in a sum of \( L + 1 \) binomial coefficients. To perform the continuous limit, we need a formula where the number of terms depends only on the number of subsegments. Generally, the assumption is that the size of the subsegments is comparable with that of the segment where they are considered. For one \( L \), the continuous limit is when \( \lim_{N \to \infty} L/N = \nu > 0 \). The resulting distribution has \( \text{Ceiling}[1/\nu] \) states. The process of finding this limit suggested in the paper is of interest; the procedure we use seems new.

**Several lengths.** A natural extension is from one \( L \) to \( \{L_i, 1 \leq i \leq s\} \) (with different probabilities). We do this in 2 stages: first, for \( s = 2 \) and then the general case. Interestingly, the formulas remain quite compact, and the limiting procedure for one \( L \) can be used almost without modifications. See Theorems 7.1 and 7.2. The probability distribution becomes that for the Young diagrams with \( \leq N \) boxes and the rows of sizes from \( \{L_i\} \). Thus, we restrict the number of rows in contrast to [Ke, BO, Ol] and other papers. Also, the creation of the segments (rows in the Young diagrams) is subject to the Poisson-type distribution. Generally, one can explicitly calculate the correlation functions for these processes; we provide the simplest ones.

**Bessel-type formulas.** A variant of our approach is when we consider \( L_i \) as some jumps of the energy function or similar functions with some probabilities. It is assumed that the energy constantly increases by 1 unless for the jumps. It is natural here to allow the jumps by \( \pm L_i \), not only by \( + L_i \) as for reinfections and similar processes. In the
quasi-classical limit \( \lim_{N \to \infty} L_i/N = \nu_i \), it leads to interesting multi-dimensional Bessel-type functions.

For one \( L \) and when \( \nu \to 0 \), i.e. when the segments become points, we obtain a random walk with probabilities \( p, q \) of the steps \( \pm 1 \) that occur at the points subject to the Poisson \( \alpha \)-distribution. The probability of \( r \) outputs is then \( e^{-\alpha} I_r(\alpha) \) for \( p = \frac{1}{2} = q \). Interestingly, pure Bessel functions \( I_r \) occur here. It is reasonable here to allow only positive \( r \) during the process, i.e. to impose the Catalan condition for the paths; we provide the formulas.

**Reinfections (Covid-19).** The duration of the Covid-19 epidemic (from late 2019) is already beyond 2 years; we are still in its 1st cycle. This epidemic was practically uninterrupted except for minor breaks between the waves (mostly during summer periods). Due to the unusually large number of the strains of Covid-19, all with with very high transmissibility, the natural immunity did not last too long for Covid-19, as well as the immunity due to the vaccinations.

For instance, those infected by the “wild strain” (the G-strain dominated in Europe in early 2020) could be reinfected by Alpha, then by Delta (B.1.617.2 and AY lineages), and then by Omicron (B.1.1.529 and BA lineages). The average immunity durations were not that long, presumably about 5-8 months; the waves of different strains obviously contributed to this. We will disregard below relatively rare cases when someone is infected simultaneously by 2 strains.

The statistics of reinfections and the recurrences for Covid-19 is not very reliable. Some countries reported only the total number of (known) infected individuals, not the total number of detected infections. For instance, this was the case with England until January 31, 2022; the data on Covid-19 in England are generally among the most systematic. According to the UK Health Security Agency (UKHSA), the number of detected reinfections can be about 10% in early 2022. In quite a few countries, it was significantly greater than this and reinfections were present well before 2022.

We note that the available data are for the detected cases. Massive testing began at the end of 2021 in quite a few countries, but very many cases remain unreported. However even the detected cases of double reinfections (3 Covid-19 infections) appeared not too rare. The actual numbers can be significantly higher among all infections, including asymptomatic ones.
We use in this paper a general method, which can be naturally extended to any number of parallel infections with different immunity durations of any any lengths. There is only one constraint: the corresponding subsegments must not overlap.

We note that Covid-19 provides quite a few examples of parallel strains: \{Alpha and Delta\}, \{Delta: AY.1, \ldots, AY.4.2\}, \{Delta, Omicron\}, \{Omicron: BA.1, BA.2, BA.3, \ldots\}. It is really rare when someone could be infected by two parallel strains at the same time.

Main hypotheses. We assume that people are exposed to the infection uniformly during the cycle of the epidemic, which is \(N\) days in the paper, with probability \(\beta\) per day. According to [Ch1, Ch2], the curves of the total number of detected infections in very many countries (all we considered) are essentially of Bessel type for phase 1 and are of linear type for phase 2; a clear phase transition can be seen in many countries. However, it is very reasonable to assume that statistically the process is not far from linear.

Moreover, the numbers of consecutive waves in many countries was like 3-6, which provides another reason to assume that the spread of Covid-19 is linear statistically. Generally, the Law of Large Numbers (LLN) is always a rationale for the uniformity assumption. The averages over 3-6 waves are sufficient for this. Similarly, not much will change statistically for reinfections if we try to incorporate the “exact” (Bessel-type) shapes of the curves of the total cases.

The 2nd hypothesis is that the impact of the vaccinations and (significant) number of undetected and asymptomatic cases can be addressed via diminishing the susceptible population of a country. The size of population does not directly appear in the formulas. The vaccinations generally decrease \(\beta\), but the strains of Covid-19 increased their transmissibility during the epidemics.

The 3rd hypothesis is a minor one: we disregard the duration of the disease. It is simply added to the immunity interval.

We think that all 3 assumptions are quite reasonable for the last 2 years of Covid-19. So the challenge is to provide the distribution of the reinfections based on them, and then adjust it to the real data.

The distribution. Under these assumptions, we define and calculate the probabilities \(\pi_r\) for \(r\) infections during the total period. They depend on the duration of an epidemic, \(N\) days, the immunity interval
$L$, and the probability $\beta$ to be exposed to the infection during 1 day. Later, we make $\beta = \frac{\alpha}{N}$ for some parameter $\alpha$. We note that it can be only among reported case; this does not influence our analysis but $\alpha$ and $L/N$ can change.

The parameters $\alpha, \beta$ can be determined if the total number of non-infected people (during the whole cycle) and those with exactly 1 infection are known. In the absence of immunity, $\alpha$ can be estimated as the total number of infected people divided by the size of the population in the area. Generally, $e^{-\alpha}$ is the number of noninfected people (during the whole cycle of epidemic) divided by the population of the country. This is as for the classical Poisson distribution.

Then we (approximately) find $L$ using our formula for $\pi_1$ or its limit $\pi'_1$ (exactly one infection during $N$ days). For the classical Poisson distribution (no immunity), it is $\alpha e^{-\alpha}$. Now it depends on $L$.

So we can assume that $\beta = \alpha/N$ and $L$ are known. Then $\pi_2$ and $\pi_3$ are the probabilities of 2 and 3 infections during $N$ days, which can be compared with reinfection data.

We consider through the paper 3 model situation: $N = 750$ (about 25 months), $L = 150$ (about 5 months), and 3 values of $\alpha = 1, \log(2), 0.5$ in (4). For these values of $\alpha$, about 37%, 50%, 60% of the susceptible population remain noninfected during 25 months. The 3rd case basically matches the number of reinfections for Covid-19 reported in England (until 02/2022).

**Main findings.** The famous Poisson distribution is a straightforward limit of a simple distribution in terms of binomial coefficients, its lattice variant. Our distribution $\{\pi_r\}$ for the probabilities of $r$ infections is a sum of $L+1$ binomial coefficients, where $L$ is the immunity duration. We calculate $\pi_r$ and $\pi'_r = \lim_{N \to \infty} \pi_r$ as $\lim_{N \to \infty} L/N = \nu > 0$; the limiting procedure is interesting. We give other formulas for $\pi_r$ and those for the corresponding generating functions.

In spite of the 1D setup, there are various applications of $\pi_r, \pi'_r$, not only for reinfections. Almost any networks have refractoriness: excited agents cannot be immediately re-excited. Vehicular networks and trading equities in stock markets are typical examples. We focus in this paper on networks with relatively small number of possible states and when $\nu = L/N$ cannot be assumed negligible, which is obviously the case with reinfections.
As far as we know, our distributions \( \{\pi_r\} \) and \( \{\pi'_r\} \) are new, as well as their application to reinfections of epidemics. The number of states is bounded in our approach: \( r \leq \text{Ceiling}[N/L] \). The edge effects are important; we allow one of the subsegments to go beyond \( N \), the right endpoint. This assumption is necessary for reinfections. Stock markets are such too: there can be open positions after the end of the considered period. Mathematically, the corresponding sum of all probabilities will not be 1 without the edge effects.

This approach can be smoothly extended to any number of lengths: \( \{L_i, 1 \leq i \leq s\} \) with the corresponding probabilities. The formulas remain reasonably compact; the limiting procedure is basically the same as for one \( L \). See Theorems 7.1 and 7.2. The probability distribution becomes that for the Young diagrams of size \( \leq N \) with finitely many rows: those of lengths \( L_i \).

An interesting variant here is when the “energy function” can jump by \( \pm L_i \) with probabilities \( p_i, q_i \) and increases by 1 otherwise. This is motivated by physics, networks and share-prices. When \( N \to \infty \) and \( \nu_i \to 0 \), i.e. the segments \( L_i \) become points, we arrive at the random 1D walk with jumps up and down at the points satisfying some Poisson-type distribution or our truncated one. We arrive at generalized Bessel \( I \)-functions. Catalan-type (non-negative) paths are of obvious interest here. We provide only Theorem 4.1 for \( s = 1 \) (for one \( L \)).

2. Hardcore Poisson-type processes. If the immunity factor is omitted, the distribution of reinfections is as follows. Assume that an epidemic lasts \( N \) days and \( \beta = \alpha/N \) is the probability to be infected during one day. Then the probability to be infected \( r \) times during \( N \) days and its continuous limit are given by the classical Poisson distribution and its combinatorial counterpart. Namely:

\[
(1) \quad p_r = \binom{N}{r} \beta^r (1-\beta)^{N-r} \quad \text{for} \quad r = 0, 1, 2, \ldots , \quad p'_r = \lim_{N \to \infty} p_r = \frac{\alpha^r}{r!e^{-\alpha}},
\]

where \( e \) is the Euler number.

Three basic examples. Let \( \alpha = 1, \alpha = \log(2) \approx 0.69, \alpha = 0.5 \). Then,

\[
(2) \quad p'_0 = p'_1 = \frac{1}{e} \approx 0.37, \quad p'_2 = \frac{1}{2e} \approx 0.18, \quad p'_3 = \frac{1}{6e} \approx 0.06 \quad \text{for} \quad \alpha = 1,
\]

\[
p'_0 \approx 0.5, \quad p'_1 \approx \log(2)/2 \approx 0.35, \quad p'_2 \approx 0.12, \quad p'_3 \approx 0.03 \quad \text{for} \quad \alpha = \log(2),
\]

and \( p'_0 \approx 0.61, \quad p'_1 \approx 0.30, \quad p'_2 \approx 0.08, \quad p'_3 \approx 0.01 \quad \text{for} \quad \alpha = 0.5.\)

The corresponding values for the combinatorial \( p_i \) are about the same.
Adding immunity. Assume that an individual infected at day $x$ cannot be infected again for days $x+1, x+2, \ldots, x+L$, i.e. $L < N$ is the duration of the immunity interval.

Let $\pi_r$ be the probability of $r$ infections during $N$ days for $r = 0, 1, \ldots$. If $1 \leq x_1 < x_2 < x_3 < \ldots < x_r \leq N$ are the infection days, then $x_1 < x_2 - L < x_3 - 2L \ldots x_r - (r-1)L$ and there are 2 cases:

(a) $x_r + L \leq N$, and, otherwise, (b) $x_r + L > N$.

Here $x_i$ are for the actual infections, when the disease begins. The potential infections are the days when an individual was exposed to the infection, which is assumed with probability $\beta$. Due to the immunity, not all of the exposures result in the actual infection (disease). Any number of potential infections can occur (anywhere) during the periods $x_i + 1, \ldots, x_i + L$ for $1 \leq i < r$ and during the end period $x_r + 1, \ldots, \min\{x_r + L, N\}$. This means that these periods can be removed from the consideration when counting the probabilities. Switching to $x_i' = x_i(i-1)$ for $1 \leq i \leq r$, the probability of the event “$x_1' < x_2' < \ldots < x_r'$” is $\beta r (1-\beta)^{N-rL-r}$ for (a) and $\beta r (1-\beta)^{(x_r-(r-1)L-r)}$ for (b).

Let $P(r, N, \beta) \overset{\text{def}}{=} (\frac{N-Lr}{r})\beta r (1-\beta)^{N-Lr-r}$, it is 0 if $r < 0$ or when $N < Lr + r$. We obtain the following straightforward formula:

\[(3) \quad \pi_r = P(r, N, \beta) + \beta \sum_{i=1}^{L} P(r - 1, N - i, \beta), \quad r = 0, 1, \ldots . \]

To give an example: for $L = 1$, $\pi_r = \beta r (1-\beta) N^{-2r} \left(\binom{N-r+1}{r} + \beta \binom{N-r}{r}\right)$. Here and for any fixed $L$, $\lim_{N \to \infty} \pi_r = p_r'$, where $p_r'$ are from (1), where we set $\beta = \alpha/N$.

One has: $\sum_{r=0}^{\infty} \pi_r = 1$, where $r \leq \frac{N+L}{L+1}$ are sufficient in this sum. This is some combinatorial identity, which immediately follows from the definition of $\pi_r$. Obviously, $\pi_0 = p_0$ for any $N, L$.

For our three basic examples above, we will take $N = 750, L = 150$. Then, $\nu = 0.2$ and

\[(4) \quad \pi_0 \approx 0.37, \quad \pi_1 \approx 0.44, \quad \pi_2 \approx 0.17, \quad \pi_3 \approx 0.02 \quad \text{for } \alpha = 1, \]
\[\pi_0 \approx 0.50, \quad \pi_1 \approx 0.39, \quad \pi_2 \approx 0.10, \quad \pi_3 \approx 0.01 \quad \text{for } \alpha = \log(2), \]
\[\pi_0 \approx 0.61, \quad \pi_1 \approx 0.33, \quad \pi_2 \approx 0.06, \quad \pi_3 \approx 0.004 \quad \text{for } \alpha = 0.5. \]

The change is not dramatic vs. (2) since $\alpha$ and $\nu$ are relatively small. For instance, $\pi_1 \approx 0.51$ if $\nu = 0.4$ for $\alpha = 1$ (with the same $\pi_0 \approx 0.37$).
Let us rewrite the formula for $\pi_r$ without the $L$-summation.

**Theorem 2.1.** Let $F_r(X) = d^{r-1} \left( X^{N-Lr} \frac{1-X^L}{1-X} \right) / dX^{r-1}$ (the $(r-1)$th derivative), where $r > 0$, $L > 0$ and $N - Lr > 0$. Then

\begin{equation}
\pi_r = \left( \frac{N - Lr}{r} \right) \beta^r (1 - \beta)^{N-Lr-r} + \frac{\beta^r}{(r-1)!} F_r(X \mapsto 1 - \beta). \quad \square
\end{equation}

The number of terms in this formula depends only on $r$ (not on $L$), which is the key when considering its limit as $L, N \to \infty$.

**3. Continuous limit.** Let us provide the first 4 cases of (5), where we use directly the theorem:

\begin{align*}
\pi_0 &= (1 - \beta)^N, \\
\pi_1 &= \beta(N - L)(1 - \beta)^{N-L-1} + (1 - (1 - \beta)^L)(1 - \beta)^{N-L}, \\
\pi_2 &= \beta^2 \left( \frac{N-2L}{2} \right) (1 - \beta)^{N-2L-2} + \beta(N - 2L)(1 - (1 - \beta)^L)(1 - \beta)^{N-2L-1} \\
&\quad + \left( 1 - (1 - \beta)^L - \beta L(1 - \beta)^{L-1} \right) (1 - \beta)^{N-2L}, \\
\pi_3 &= \frac{\beta^3}{6} \left( (N-3L)(N-3L-1)(N-3L-2)x^{N-3L-3} + \\
&\quad 3 \left( -2Lx^{L-1} \frac{x^{N-3L}}{\beta^2} + \frac{(N-3L)x^{N-3L-1}}{\beta} - \frac{L(L-1)x^{N-2L-2}}{\beta} \right) \\
&\quad (1-x^L) \left( \frac{2x^{N-3L-3}}{\beta^2} + \frac{2(N-3L)x^{N-3L-1}}{\beta} + \frac{(N-3L)(N-3L-1)x^{N-3L-2}}{\beta} \right) \right).
\end{align*}

Here we set $x \overset{\text{def}}{=} 1 - \beta$. Also, $N \geq L$, $N \geq 2L$ and $N \geq 3L$ correspondingly; generally, $r \leq \frac{N}{L}$. Recall that $\pi_r > 0$ for $N \geq L(r-1)+r$, i.e. for $r \leq \frac{N+L}{L+1}$. For instance, $\pi_1 = 1 - (1 - \beta)^N$ for any $L$ such that $L > N$.

Notice that $\pi_0$ does not depend on $L$; this is obvious because the duration of the immunity interval does not affect those non-infected.

Setting $\beta \overset{\text{def}}{=} \alpha/N$ and $\lim_{N \to \infty} N/L = \nu \geq 0$, the limits $\pi'_r = \lim_{N \to \infty} \pi_r$ for $r = 0, 1, 2$ are as follows:

\begin{align*}
\pi'_0 &= e^{-\alpha}, \\
\pi'_1 &= e^{(\nu-1)\alpha} \left( 1 + \alpha(1 - \nu) \right) - e^{-\alpha}, \\
\pi'_2 &= e^{(2\nu-1)\alpha} \left( 1 + \alpha(1 - 2\nu) + \frac{\alpha(1 - 2\nu)^2}{2} \right) - e^{(\nu-1)\alpha} \left( 1 + \alpha(1 - \nu) \right).
\end{align*}
We assume here that \( r \nu \leq 1 \). Generally, under this assumption:

\[
\pi'_r = e^{(r \nu - 1)\alpha} \left( 1 + \alpha(1 - r \nu) + \frac{\alpha^2(1 - r \nu)^2}{2} + \ldots + \frac{\alpha^{r-1}(1 - r \nu)^{r-1}}{(r-1)!} \right) 
- e^{((r-1)\nu - 1)\alpha} \left( 1 + \alpha(1 - (r-1)\nu) + \ldots + \frac{\alpha^{r-1}(1 - (r-1)\nu)^{r-1}}{(r-1)!} \right).
\]

The last value of \( r \) here is \( r_\nu = \text{Floor}[\frac{1}{\nu}] \), where \( \text{Floor}[x] \) is the integer part of \( x \). The initial inequality \( r \leq \frac{N+L}{L+1} \) gives that the last nonzero \( \pi'_r \) is for \( r_\nu = \text{Ceiling}[N/L] \), which is \( r_\nu + 1 \) if \( \frac{1}{\nu} \) is not an integer, and \( \pi_\beta \) if \( 1/\nu \in \mathbb{Z}_+ \). Indeed, \( \frac{N}{L} + 1 > \frac{N+L}{L+1} > \frac{N}{L} \). When \( r_\nu = r_\beta + 1 \), one has:

\[
\pi'_{r_\nu+1} = 1 - e^{(r_\nu \nu - 1)\alpha} \left( 1 + \alpha(1 - r_\nu \nu) + \frac{\alpha^2(1 - r_\nu \nu)^2}{2} + \ldots + \frac{\alpha^{r_\nu}(1 - r_\nu \nu)^{r_\nu}}{(r_\nu)!} \right).
\]

The positivity of \( \pi'_r \) for \( 0 \leq r \leq r_\nu + 1 \) can be readily seen from these formulas, though it of course follows from the origin of \( \pi'_r \). Here we calculated \( \pi'_{r_\nu+1} \) directly from the definition. Alternatively, it can be obtained from the identity \( \sum_{r=0}^{r_\nu} \pi'_r = 1 \). This sum is obviously 1 (the telescoping summation), which holds \textit{a priori} because \( \sum_{r=0}^{r_\nu} \pi_r = 1 \), which is due to the definition of \( \pi_r \). We arrive at the following theorem.

**Theorem 3.1.** Assume that \( N \to \infty, \beta = \alpha/N, \lim_{N \to \infty} L/N = \nu \) for some \( \alpha > 0 \) and \( 0 \leq \nu \leq 1 \). Then formula (6) holds for any \( 0 \leq r \leq r_\nu \), as well as the additional formula above for \( r_\nu = r_\beta + 1 \) when \( \frac{1}{\nu} \) is not an integer.

**Proof.** We can simplify \( F_r \) from (5) considered in the limit as follows. Let \( \Phi_r \overset{\text{def}}{=} \mathcal{B}^{-1} \left( \frac{X^{N-Lr} - X^{N-Lr(-1)}}{1-X} \right) \) for the following formal differentiation \( \mathcal{B} \) of the ring generated by \( X^{N-sL} \) and \( 1/(1-X) \) treated as independent symbols:

\[
\mathcal{B}^p(X^{N-sL}) = (1-s\nu)^p X^{N-sL}, \quad \mathcal{B}^p \left( \frac{1}{1-X} \right) = \frac{\beta^p p!}{(1-X)^{p+1}}, \quad p = 0, 1, 2, \ldots.
\]

This differentiation is \( \beta d/dX \) with the following simplifications due to taking the limit. First, we replace \( \binom{N-sL}{r} \) by \( \frac{N^r}{r!} \) for \( s \leq r \) due to \( r \ll N - sL \). Second, \( X^{N-sL} \pm p \) is replaced by \( X^{N-sL} \) for \( 0 \leq p \leq r \) because these powers will be finally evaluated at \( X = 1 - \beta = 1 - \frac{\alpha}{N} \to 1 \).

We obtain that \( \pi'_r = \frac{\alpha^{(1-r\nu)\nu}}{r!} e^{(r\nu - 1)\alpha} + \frac{1}{(r-1)!} \Phi'_r \), where \( \Phi'_r \) is the limit of \( \beta \Phi_r \) after the evaluation \( 1 - X \to \beta, X^{N-sL} \to e^{\alpha(\nu - 1)} \).
One has: \( \Phi_r = \sum_{s=0}^{r-1} \binom{r-1}{s} B_s \left( X^{N-Lr} - X^{N-L(r-1)} \right) B^{r-s} \left( \frac{1}{1-X} \right) = \sum_{s=0}^{r-1} \beta^{r-s-1} \frac{(r-1)!}{s!} \left( \frac{\alpha^s(1-r\nu)^s X^{N-Lr} - \alpha^s(1-(r-1)\nu)^s X^{N-L(r-1)}}{(1-X)^{r-s}} \right) \).

Finally, \( \Phi_r' = \sum_{s=0}^{r-1} \binom{r-1}{s} \frac{(r-1)!}{s!} \left( \alpha^s(1-r\nu)^s e^{(r-1)\nu} e^{\alpha((r-1)\nu-1)} - \alpha^s(1-(r-1)\nu)^s e^{\alpha((r-1)\nu-1)} \right) \).

This gives formula (6). The calculation is similar for \( \pi_r' \).

The \( \nu \)-dependence of \( \pi_r' \) is interesting. For instance, since \( \pi_0' \) does not depend on \( \nu \), \( \pi_1' \) increases if \( \nu \) increases. Indeed, the chances of reinfections (counted by \( \pi_r' \) for \( r \geq 2 \)) diminish. Similarly, \( \pi_r' \) decreases if present (if \( 1/\nu \) is not an integer). Generally, we have the following straightforward corollary.

**Corollary 3.2.** Let \( \delta_r = \frac{r \alpha e^{(r-1)\alpha} \alpha^{(1-r\nu)r}}{r!} \) for \( 0 \leq r \leq r_z \), and \( \delta_{-1} = \delta_{r_z} = 0 \). Then \( d \pi_r'/d\nu = \delta_{r} - \delta_{r-1} \) for \( 0 \leq r \leq r_z \). In particular, \( d \pi_r'/d\nu \geq 0 \) for \( 1 \leq r \leq \frac{1}{\nu} \) if and only if \( \nu \alpha e^{\nu} \geq (r-1)(1+z)^{r-1}z \) for \( z = \frac{\nu}{1-r\nu} \). Otherwise, this derivative is negative.

Practically, triple reinfections (\( r = 4 \)) are hardly possible for one cycle of any epidemic. Though there can be other random processes of this kind where big \( r \) make sense. The distribution in (6) is some quantization of the Poisson distribution, where \( \nu \to 0 \) is the quasi-classical limit. Accordingly, (3) is its “quantization” with 2 parameters, \( L \) and \( N \). One more parameter can be added to (3) by switching to the \( q \)-binomial coefficients there, which we will not discuss.

**Reinfections in England.** As a demonstration, let us try to employ these formula to the Covid-19 data from England. “As of 31 January (2022), updated figures for England show 14845382 episodes of infection since the start of the pandemic with 588114 (4.0%) reinfections covering the whole pandemic.” So, approximately \( 14845382 - 588114 = 14257268 \) people were detected to be infected at least once. Let us assume conditionally that about 35M were involved in collecting the data; the population of England is about 57M. Our approach can be applied if only detected cases and reinfections are taken into account; however, \( \alpha \) depends on the number of all infections, including the asymptomatic...
and undetected ones. Technically, we diminish 57M to 35M, but this can be done directly via $\alpha$ (to adjust $\pi_0, \pi_1$).

As in the 3 basic cases, we take $N = 750$ and $L = 150$. Then $\alpha \approx 0.5$; indeed, $\pi_0' = e^{-0.5} \approx 0.6 \approx 1 - 14/35$. This is basically the 3rd case in (4): $\pi_1 \approx 0.33$, $\pi_2 \approx 0.06$. Qualitatively, 0.06 matches the data from UKHSA: about 0.04 for $\pi_2$ (until January 31, 2022).

4. Poisson-Catalan distribution. Let us assume that a system is subject to $N$ random events of 3 sorts: (i) adding $1/N$ to its energy $E$ with probability $(1 - \alpha N)$, (ii) adding $L/N$ to $E$ with probability $\alpha p N$ and (iii) subtracting $L/N$ with probability $\alpha q N$, where $p, q \geq 0$ and $p + q = 1$. This can be a “slow” linear growth of energy with more significant accidental transitions to excited states and back. Another interpretation is when $E$ is a share-price subject to some constant trend with relatively rare $\pm L/N$ fluctuations.

We begin with $E = 0$ and fix the final energy in the range $1 \leq E < 1 + L/N$. It is allowed for $E$ to take any non-negative values before the final point but the intermediate balances of additions and subtractions of $L/N$ must be always non-negative (the gains due to other points are disregarded). I.e. it must be a Catalan path.

We assume that $\lim_{N \to \infty} L/N = \nu \leq 1$ and consider below only this limit. Accordingly, $P'_{r,m}$ be the probability that $E$ changes from 0 to the final value in the range $0 \leq E < 1 + \nu$ for Catalan paths with $r + m$ events of adding $\nu$ and $m$ events of subtracting $\nu$.

In the following proposition, $\pi'_{r,m}$ denotes $\pi'_{r+2m}$ calculated for the parameters $\alpha_m = (1+2m\nu)\alpha$ and $\nu_m = \frac{\nu}{1+2m\nu}$. In fact, only $\alpha_m$ must be changed from $\alpha$ in $\pi'_{r+2m}$ because the dependence on $\nu_m$ is via the product $\nu_m\alpha_m = \nu\alpha$.

**Theorem 4.1.** (i) For $m \geq 0$ and $0 \leq r \leq \text{Ceiling}[1/\nu]$ , one has:

$$P'_{r,m} = \pi'_{r,m} p^{r+m} q^m \left( \frac{r + 2m}{m} \right)^{r + 1} \frac{1}{r + m + 1}.$$  

(ii) Let $P^0_{r,m} \overset{\text{def}}{=} \lim_{\nu \to 0} P'_{r,m}$. Then $P^0_{r,m} = \frac{\alpha^{r+2m} \nu^{r+m} p^m e^{-\alpha}}{m!(r+m)!} \frac{r+1}{r+m+1}$. I.e. we count Catalan paths with the number of steps satisfying the $\alpha$-Poisson distribution. Furthermore, let $p = \frac{1}{2} = q$ and $\sigma^0_r \overset{\text{def}}{=} \sum_{m=0}^{\infty} P^0_{r,m}$. Then $\sigma^0_r = \frac{r+1}{\alpha/2} e^{-\alpha} I_{r+1}(\alpha)$ for the hyperbolic Bessel function $I_u(z) = \sum_{m=0}^{\infty} \frac{(z/2)^{2m+u}}{m!(m+u+1)}$. Note that $I_0(z) = \sum_{m=0}^{\infty} \frac{(z/2)^{2m}}{(m!)^2}$, $I_1(z) = dI_0(z)/dz$. 

(iii) Under \( p = 1/2 = q \) and for \( \nu = 0 \) as in (ii), the probability \( \sigma^0_r = \sum_{r=0}^{\infty} a^0_r \) to obtain a Catalan path with arbitrary \( r \geq 0 \) and \( m \geq 0 \) equals \( e^{-\alpha} (I_0(\alpha) + I_1(\alpha)) \). Also, the average value \( T = \sum_{r=0}^{\infty} (r+1) \sigma^0_r \) of the parameter \( (r+1) \) over such Catalan paths is \( T = 1 \).

(iv) Setting \( \nu = 0 \), let us consider all paths, i.e. we disregard the Catalan condition and \( r \) can be negative, and let \( p_r(m) \) be the corresponding probability with \( m \) steps and the output \( r \). Then

\[
p_r(m) = p^{r+m} q^m \left( \frac{r+2m}{m} \right) \frac{e^{-\alpha}}{(r+2m)!} \quad \text{for } r \geq -m , \quad \text{and}
\]

\[
P_r = \sum_{m=0}^{\infty} p_r(m) = e^{-\alpha} \left( \frac{p}{q} \right)^{r/2} I_r(2\alpha(pq)^{1/2}).
\]

In particular, \( \sum_{r=-\infty}^{\infty} P_r = 1 \).

**Proof.** (i,ii) The number of sequences \( \{a_i = \pm 1, 1 \leq i \leq n\} \) such that \( \sum_{i=1}^{k} a_i \geq 0 \) for any \( 1 \leq k \leq n \) and \( \sum_{i=1}^{n} a_i = r \geq 0 \) is as follows: \( C_{n-r}^{0} = \binom{n}{(n-r)/2} \frac{r+1}{(n+r)/2+1} \), where \( n-r \) must be even. This is a standard formula in the theory of Catalan numbers. For \( n = r+2m \), we obtain \( C_{r+2m}^{0} = \left( \frac{r+2m}{m} \right) \frac{r+1}{r+m+1} \). Then we multiply the latter expression by \( p^{r+m} q^m \) and by \( \pi_{r,m} \). This proves (i); the justification of (ii) is straightforward.

(iv) To allow any sequences of \( \pm 1 \), we must omit the terms \( \frac{r+1}{m+r+1} \). Then \( \sum_{r=-\infty}^{\infty} P_r = 1 \), which is the classical identity

\[
e^{\frac{\pi i}{2} (t+\frac{1}{2})} = \sum_{r=-\infty}^{\infty} I_r(\alpha)t^r, \quad \text{where } I_r(\alpha) = I_{-r}(\alpha).
\]

Indeed, \( p_r(m) + p_{-r}(m) \) for \( r > 0 \) equals

\[
(p^{r+m} q^m + p^{r+m} q^m) \left( \frac{r+2m}{m} \right) \frac{e^{-\alpha}}{(r+2m)!} = (pq)^{r+2m} \left( \frac{p}{q} \right)^{r/2} + (\frac{q}{p})^{r/2} \frac{e^{-\alpha}}{m!(r+m)!}.
\]

The sum of these terms and the one for \( r = 0 \) is

\[
P_r = e^{-\alpha} I_0(2\alpha(pq)^{1/2}) + e^{-\alpha} \sum_{r=1}^{\infty} \left( \frac{p}{q} \right)^{r/2} + (\frac{q}{p})^{r/2} \right) I_r(2\alpha(pq)^{1/2})
\]

\[
= \exp \left( -\alpha + \alpha(pq)^{1/2} \left( \frac{p}{q} \right)^{1/2} + (\frac{q}{p})^{1/2} \right) = 1 \text{ due to } p + q = 1.
\]

Since we know that the sum must be 1, this proves formula (9). Indeed, we can make \( t = (p/q)^{1/2} \) arbitrary here.
Accordingly, for roulette is a 0-sum game, and 2
ence of 1-minos. Here we count the tilings with the weights as above.
statistical physics. Though there are no exact 2D formulas in the pres-
with dominos and monominos (dimers and monomers) is important in
T
= 1. Indeed, \( \frac{t^{r+1}-t^{-r-1}}{t^{r}} \). To obtain \( \sigma^{0}_{\ast} \), observe
that the latter sum contains 1 for even \( r \) and \( t \) for odd \( r \); then use (9)
for \( r = 0, 1 \).

Actually, we do not need (9) for (iii). The total number of all Catalan paths with \( n \) steps is \( \binom{n}{n/2} \) for even \( n \) and \( \binom{n}{(n-1)/2} \) for odd \( n \). It is
\( C^{0\rightarrow\ast}_{n} = \sum_{r=0}^{\infty} C^{0\rightarrow r}_{n} \), where \( n-r \) is even, in the notation above. Thus, the total probability to obtain a Catalan path is
\[
\sum_{r=0}^{\infty} \sigma^{0}_{r} = \sum_{n=0}^{\infty} e^{-\alpha} \frac{\alpha^{n}}{n!} \left( \binom{n}{\text{Floor}[n/2]} \right) = e^{-\alpha} (I_{0}(\alpha) + I_{1}(\alpha)).
\]

Then, \( 2^{n} - \binom{n}{\text{Floor}[n/2]} \sum_{r=0}^{\infty} r C^{0\rightarrow r}_{n} \) for even \( n-r \), since the ideal roulette is a 0-sum game, and \( 2^{n} = \sum_{r=0}^{\infty} (r+1) C^{0\rightarrow r}_{n} \) using the formula above for \( C^{0\rightarrow\ast}_{n} \). This results in \( T = 1 \).

Proposition 4.2. Let \( p = 1/2 = q \) and \( \nu = 0 \) as in Part (iii) of Problem 4.1. Now the starting level will be \( k \geq 0 \) and the corresponding probability of Catalan paths will be \( \sigma^{0}_{\ast}(k) = e^{-\alpha} \sum_{n=0}^{\infty} \frac{\alpha^{n}}{n!} C^{k\rightarrow\ast}_{n} \). Then
\[
C^{k\rightarrow\ast}_{n} = \sum_{n=0}^{\infty} \left( \binom{n}{\text{Floor}[n-k]} \right) + \left( \binom{n}{\text{Floor}[n-k]+1} \right) + \cdots + \left( \binom{n}{\text{Floor}[n+k]} \right).
\]

Accordingly, \( \sigma^{0}_{\ast}(k) = e^{-\alpha} (I_{-k}(\alpha) + I_{-k+1} + \cdots + I_{k+1}(\alpha)) \).

5. Generating functions. We will provide the generating function for \( \pi_{r}(N,L) \). We will show now the dependence of \( \pi_{r} \) on \( N,L \). Let
\( G(t,u) \) be \( \sum_{N=0}^{\infty} t^{N} \pi_{r}(N,L) u^{r} \). We fix \( L \) here and below.

Theorem 5.1. \( G(t,u) = \frac{1}{1-t} + \frac{\beta (u-1) t}{(1-t)(1-(1-\beta) t - \beta u t^{r+1})} \).

Proof. First of all, let us calculate \( G^{\alpha}_{N} = \sum_{r=0}^{\infty} P(r,N,\beta) u^{r} = \sum_{r=0}^{\infty} u^{r} \beta^{r} (1 - \beta)^{N-L r} r^{N-L r} \). This is the classical problem about tiling the segment with \( N \) boxes by \( (L+1) \)-minos, sequences of \( L+1 \) consecutive boxes, and with 1-minos. Its variant in a 2D square lattice with dominos and monominos (dimers and monomers) is important in statistical physics. Though there are no exact 2D formulas in the presence of 1-minos. Here we count the tilings with the weights as above.
For \(u = 1, \beta = 1/2, L = 1\): \(G_N^\circ = f_{N+1}/2^N\) for the Fibonacci numbers \(f_N\). Generally:

\[
G_N^\circ = (1 - \beta)G_{N-1}^\circ + \beta u G_{N-L-1}^\circ, \quad G_0^\circ = 1, \quad G_i^\circ = (1 - \beta)^i \quad \text{for} \quad 1 \leq i \leq L.
\]

For instance, \(G_{L+1}^\circ = (1 - \beta)^{L+1} + \beta u\). Using the standard facts in the theory of generating functions or a straightforward consideration:

\[
G^\circ(t, u) = \sum_{N=0}^{\infty} G_N^\circ t^N = \frac{1}{1 - (1 - \beta)t - \beta ut^{L+1}}.
\]

Due to formula (3), \(G_N = \sum_{r=0}^{\infty} \pi_r(N, L)u^r\) satisfies the same recurrence as for \(G_N^\circ\), but with different initial conditions. Namely, \(G(t, u) = (1 + \beta ut + \beta ut^2 + \ldots + \beta ut^L)G^\circ(t, u)\). Finally,

\[
G(t, u) = \frac{1 - t + \beta ut(1 - t^L)}{(1 - t)(1 - (1 - \beta)t - \beta ut^{L+1})} = \frac{1}{1 - t} \left( 1 + \frac{\beta (u - 1)t}{1 - (1 - \beta)t - \beta ut^{L+1}} \right).
\]

For \(u = 0\): \(\sum_{N=0}^{\infty} \pi_0(N, L) = \frac{1}{1 - (1 - \beta)t}\), which we know without any calculations. For \(u = 1\): \(\sum_{r=0}^{\infty} \pi_r(N, L)t^N = \frac{1}{1 - t}\), which gives a combinatorial proof of the identities \(\sum_{r=0}^{\infty} \pi_r(N, L) = 1\) for any \(N, L\).

**Explicit formulas.** The theorem readily gives that

\[
(10) \quad \pi_r(N, L) = \frac{d^r}{du^r} \left( \frac{1}{1 - t} \left( 1 + \frac{\beta (u - 1)t}{1 - (1 - \beta)t - \beta ut^{L+1}} \right) \right) (u \rightarrow 0).
\]

Performing the differentiation, we obtain the following “telescopic-type” presentation of \(\pi_r\).

**Corollary 5.2.** Let \(\Pi_r(L) = \frac{\beta^r u^{(L+1)r-L}}{(1-t)(1-(1-\beta)t)}\) for \(r \geq 1\) and \(\Pi_0(L) = \frac{1}{1 - t}\). Then \(\sum_{N=0}^{\infty} \pi_r(N, L)t^N = \Pi_r(L) - \Pi_{r+1}(L)\) for \(r \geq 1\). This immediately gives that \(\sum_{r=0}^{\infty} \pi_r(N, L) = 1\) for any \(N, L\). \(\square\)

One can use this corollary to make the formulas for \(\pi_r\) quite explicit: directly expressed in terms of the binomial coefficients. The sums there can be calculated using the standard combinatorial identities.

**Corollary 5.3.** Provided that \(N - L(r - 1) - r \geq 0\),

\[
\pi_r(N, L) = \beta^r \sum_{s=0}^{m} \binom{s+r-1}{r-1} (1 - \beta)^{\max\{m-L,s\}}, \quad m = N - L(r - 1) - r,
\]
where there are $L + 1$ powers of $(1 - \beta)$ with integral positive coefficients for $m \geq L$. These powers are $(1 - \beta)^{m-L+k}$ for $k = 0, 1, \ldots, L$ and the coefficients depend only on $k, r$ unless $k = 0$. For $m < L$, these powers are $(1 - \beta)^k$, where $0 \leq k \leq m$ and all coefficients depend only on $k, r$.

\[ \square \]

6. Two processes. It is quite possible that several strains (point processes) can be present simultaneously. They can be generally with different immunity intervals $L$ and $\beta$.

Let $\beta_1$ and $\beta_2$ be the probabilities of being infected by strain 1 and strain 2 during 1 day, assuming that that the simultaneous infections by 1 and 2 are negligible. We set $\beta_0 = \beta_1 + \beta_2$. The corresponding immunity intervals after the infections will be $L_1, L_2$. Let $\pi_{r_1, r_2}(N, L_1, L_2)$ be the probability to have $r_1$ cases for strain 1 and $r_2$ for 2. Accordingly, we need to calculate the generating function $G = \sum_{N=0}^{\infty} G_N t^N$, where $G_N = \sum_{r_1, r_2=0}^{\infty} u_1^{r_1} u_2^{r_2} \pi_{r_1, r_2}(N, L_1, L_2)$.

Similar to the above consideration, the basic combinatorial problem is now to count the number of coverings of an $N$-segment by non-overlapping ($L_1 + 1$)-subsegments, ($L_2 + 1$)-subsegments, and 1-subsegments (monomers). One of the subsegments can go through $N$, the endpoint of the $N$-segment. Then $G_N$ satisfies the recurrence relation $G_N = (1 - \beta_0)G_{N-1} + \beta_1 u_1 G_{N-1-L_1} + \beta_2 u_2 G_{N-1-L_2}$, and:

\[
G = \frac{1 + u_1 \beta_1 t (1 + t + \ldots + t^{L_1-1}) + u_2 \beta_2 t (1 + t + \ldots + t^{L_2-1})}{1 - (1 - \beta_0) t - u_1 \beta_1 t^{L_1+1} - u_2 \beta_2 t^{L_2+1}}
\]

\[= \frac{1 - t + u_1 \beta_1 t (1 - t^{L_1}) + u_2 \beta_2 t (1 - t^{L_2})}{(1 - t)(1 - (1 - \beta_0) t - u_1 \beta_1 t^{L_1+1} - u_2 \beta_2 t^{L_2+1})}\]

\[= \frac{1}{1 - \frac{\beta_1 (u_1 - 1) t + \beta_2 (u_2 - 1) t}{1 - (1 - \beta_0) t - u_1 \beta_1 t^{L_1+1} - u_2 \beta_2 t^{L_2+1}}}.
\]

Several processes. The latter formula can be readily extended to any number of simultaneous processes (strains). For $\beta_0 = \sum_i \beta_i$ in the natural notation:

\[
G = \frac{1}{1 - t} \left(1 + \frac{\sum_i \beta_i (u_i - 1) t}{1 - (1 - \beta_0) t - \sum_i u_i \beta_i t^{L_i+1}}\right).
\]

Using that the dependence of $u_1, u_2$ is linear in the numerator and denominator, it is not difficult to perform the necessary $u$-differentiations and calculate the generating functions with fixed $r_1, r_2$. For instance,
let $u_1 = u = u_2$, $\pi_r(N, L_1, L_2)$ be the probability that $r_1 + r_2 = r$, and $P_r(t) = \sum_{N=0}^{\infty} \pi_r(N, L_1, L_2)t^N$. Then

$$P_1(t) = \frac{t(\beta_1 + \beta_2)(1 - t(1 - \beta_1 - \beta_2) - \beta_1 tL_1 + \beta_2 tL_2)}{(1 - t)(1 - t(1 - \beta_1 - \beta_2))^2}.$$ 

This is for 1 infection by any strain (from two). When $L_1 = L = L_2$ and $\beta = \beta_0 = \beta_1 + \beta_2$, we arrive at the case of one type of infection. For $r > 1$, this is generally not true: even if $L_1 = L_2$, the order of the strains in their sequences matters. An explicit combinatorial formula for $N > L_2 \geq L_1$ is as follows:

$$\beta_0^{-1} \pi_1(N, L_1 \leq L_2) = x^{N-L_2-1}\left(x^0(N - L_2)(1 - \beta_1) + x^1(1 - (N - L_2 + 1)\beta_1) + x^2(1 - (N - L_2)\beta_1) + \ldots + x^{L_2 - L_1 - 1}(1 - (N - L_1 - 1)\beta_1)
+ x^{L_2 - L_1} + x^{L_2 - L_1 + 1} + \ldots + x^{L_2}\right), \quad \text{where } x \overset{\text{def}}{=} 1 - \beta_1 - \beta_2.$$

It becomes somewhat simpler combinatorially in terms of $x, \beta_2$:

$$\beta_0^{-1} \pi_1(N, L_1 \leq L_2) = x^{N-L_2-1}\left(x^0(N - L_2)\beta_2 + x^1(N - L_2 + 1)\beta_2 + x^2(N - L_2 + 2)\beta_2 + \ldots + x^{L_2 - L_1 - 1}(N - L_1 - 1)\beta_2 + x^{L_2 - L_1}(N - L_1)
+ x^{L_2 - L_1 + 1} + \ldots + x^{L_2}\right), \quad \text{where } x \overset{\text{def}}{=} 1 - \beta_1 - \beta_2, \quad N > L_2 \geq L_1.$$

There are $L_2 + 1$ powers of $x$ here; the terms $x^1(1 - (N - L_2 + 1)\beta_1)$, $x^1(N - L_2 + 1)\beta_2$ are present only if $L_2 > L_1 + 1$. For $N \leq L_2$, the number of terms is $N$: they are exactly the top $N$ terms in the formulas above. The sums of the binomial coefficients in this formula can be readily calculated, which is useful for obtaining the limits as $N \rightarrow \infty$, when $N\beta_i \rightarrow \alpha_i, L_i/N \rightarrow \nu_i$ for $i = 1, 2$. We note that by setting $\beta_1 = 0, \beta = \beta_2, L = L_2$ in the 1st formula, we obtain the 2nd where $\beta_2 = 0, \beta = \beta_1, L = L_1$. This is our formula for $\pi_1(N, L)$.

Similarly, one calculates $\pi_{(1)} = \pi_{1,0}$ and $\pi_{(2)} = \pi_{0,1}$, which are the coefficients of $u_1$ and $u_2$ of $G$; $\pi_{(i)}$ depends only on $L_i$. For $N > L_i$:

$$\pi_{(i)}(N, L_i) = x^{N-L_i-1}\beta_i\left(x^0(N - L_i) + x^1 + \ldots + x^{L_i}\right), \quad i = 1, 2.$$

where $x \overset{\text{def}}{=} 1 - \beta_1 - \beta_2$. Accordingly, the top $N$ terms must be taken if $N \leq L_i$. Obviously, $\pi_1(N, L_1 \leq L_2) = \pi_{(1)}(N, L_1) + \pi_{(2)}(N, L_2)$. In the
limit $\beta_i N \to \alpha_i$ and $L_i/N \to \nu_i$, we obtain for $\alpha_0 = \alpha_1 + \alpha_2$:

$$\pi'_i = \lim_{N \to \infty} \pi_{(i)} = e^{\alpha_0(\nu_i - 1)} \alpha_i \left(1 - \nu_i + \frac{1 - e^{-\alpha_0 \nu_i}}{\alpha_0}\right), \quad i = 1, 2.$$

Similar to Corollary 3.2 for $r = 1$:

$$\frac{d\pi'_i}{d\nu_i} = \alpha_i \alpha_0 e^{\alpha_0(\nu_i - 1)} (1 - \nu_i),$$

We see that $\pi'_i$ increases in terms of the corresponding $\nu_i$ for $0 \leq \nu_i < 1$ and fixed $\alpha_i > 0$. This could be expected: the greater $\nu_i$ the smaller the total number of the corresponding reinfections. This is because $\pi'_0$ does not depend on the immunity intervals.

### 7. Generalizations

Let us now provide the generalizations of Theorems 2.1, 3.1 to the case of any $L_i$ for $i = 1, 2, \ldots, s$ and the corresponding $\beta_i$. We set $\beta_0 = \beta_1 + \ldots + \beta_s$, $\beta_i = \alpha_i/N$ and $\alpha_0 = \alpha_1 + \ldots + \alpha_s$. Let $\pi_{r_1, \ldots, r_s}$ be the probability as above, where $r_i$ is the number of segments of the length $L_i + 1$ in $[1, N]$ corresponding to $\beta_i$. One has: $\pi_0, \ldots, 0 = (1 - \beta_0)^N$. We will assume below that $r \overset{\text{def}}{=} r_1 + \ldots + r_s$ is positive. Note that in the formulas below, we set $\beta_i^{r_i} = 1 = \alpha_i^{r_i}$ for $r_i = 0$ even when $\beta_i = 0 = \alpha_i$.

**Theorem 7.1.** Setting $\sigma = N - \sum_{i=1}^{s} r_i L_i$, for $\sigma \geq r$:

$$\pi_{r_1, \ldots, r_s} = \frac{(\beta_1^{r_1} \cdots \beta_s^{r_s})(1 - \beta_0)^{\sigma - r}\sigma!}{(r_1! \cdots r_s!)(\sigma - r)!} + \frac{\beta_1^{r_1} \cdots \beta_s^{r_s}}{r_1! \cdots r_s!} \frac{d^{r-1}}{dX^{r-1}} \left(\sum_{k=1}^{s} r_k X^{\sigma - 1} - X^{L_k} \right) \left(X \mapsto 1 - \beta_0\right).$$

Provided that $\beta_i > 0$ for any $i$, the nonzero $\pi_{r_1, \ldots, r_s}$ are exactly when $\sigma - r \geq L_k$ for at least one $k$. Accordingly, for $\sigma < r$:

$$\pi_{r_1, \ldots, r_s} = \frac{\beta_1^{r_1} \cdots \beta_s^{r_s}}{r_1! \cdots r_s!} \frac{d^{r-1}}{dX^{r-1}} \left(\sum_{k=1}^{s} r_k X^{\sigma - 1} - X^{\sigma + L_k - r + 1} \right) \left(X \mapsto 1 - \beta_0\right),$$

where the summation is only over $k$ such that $L_k \geq r - \sigma$. \hfill $\square$

**Theorem 7.2.** We assume that $L_k/N \to \nu_k$ for $1 \leq k \leq s$ as $N \to \infty$. Let $\pi'_{r_1, \ldots, r_s} = \lim_{N \to \infty} \pi_{r_1, \ldots, r_s}$, $\mu = 1 - (\nu_1 r_1 + \ldots + \nu_s r_s)$ and $\mu_k = \mu + \nu_k$. 
Then $\pi_{0,\ldots,0}' = e^{-\alpha_0}$. For $r > 0$ and $\mu \geq 0$:

\begin{equation}
\pi_{r_1,\ldots,r_s}' = \frac{\mu^r \alpha_1^{r_1} \cdots \alpha_s^{r_s}}{r_1! \cdots r_s!} e^{-\alpha_0 \mu}
+ \frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s} (r-1)!}{\alpha_0^{r_1} r_1! \cdots r_s!} \sum_{k=1}^{s} \sum_{i=0}^{r-1} \frac{r_k}{i!} \left( e^{-\alpha_0 \mu (\alpha_0 \mu)^i} - e^{-\alpha_0 \mu (\alpha_0 \mu_k)^i} \right)
\end{equation}

\begin{equation}
= \frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s} (r-1)!}{\alpha_0^{r_1} r_1! \cdots r_s!} \sum_{k=1}^{s} \left( \sum_{i=0}^{r-1} \frac{r_k}{i!} e^{-\alpha_0 \mu (\alpha_0 \mu)^i} - \sum_{i=0}^{r-1} \frac{r_k}{i!} e^{-\alpha_0 \mu_k (\alpha_0 \mu_k)^i} \right).
\end{equation}

Additionally, the nonzero values occur if $-\nu_k < \mu \leq 0$ for at least one $k$:

\begin{equation}
\pi_{r_1,\ldots,r_s}' = \frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s} (r-1)!}{\alpha_0^{r_1} r_1! \cdots r_s!} \sum_{k=1}^{s} \left( \sum_{i=0}^{r-1} \frac{r_k}{i!} e^{-\alpha_0 \mu (\alpha_0 \mu_k)^i} \right),
\end{equation}

where the summation is over $k$ such that $\mu_k = \mu + \nu_k > 0$. If $\mu = 0$ here, then (13) coincides with the formula above; recall that $0^0 = 1$.

**Proof.** For the first term in (11):

\[
\frac{(\beta_1^{r_1} \cdots \beta_s^{r_s}) (1 - \beta_0)^{\sigma-r} \sigma!}{(r_1! \cdots r_s!) (\sigma-r)!} \rightarrow \frac{\mu^r \alpha_1^{r_1} \cdots \alpha_s^{r_s}}{r_1! \cdots r_s!} e^{-\alpha_0 \mu}.
\]

Following the proof of Theorem 3.1, the remaining summation in (11) becomes the limit of

\[
\sum_{k=1}^{s} \sum_{i=0}^{r-1} \frac{r_k \beta_1^{r_1} \cdots \beta_k^{r_k}}{r_1! \cdots r_s!} \binom{r-1}{i} \left( \sigma - (\sigma + L_k)^i \right) \frac{(r-1-i)!}{\beta_0^{r-1}}.
\]

Then we perform the substitutions $\beta_i = \alpha_i/N$ and $L_i = \nu_i N$, $\beta_0^\sigma i = (\alpha_0 \mu)^i$, $\beta_0^\sigma (\sigma + L_k)^i = (\alpha_0 \mu_k)^i$ and tend $N$ to $\infty$.

When $\mu < 0$, the above sum becomes:

\[
\sum_{k=1}^{s} \sum_{i=0}^{r-1} \frac{r_k \beta_1^{r_1} \cdots \beta_k^{r_k}}{r_1! \cdots r_s!} \binom{r-1}{i} \left( (r-1) \cdots (r-i) - (\sigma + L_k)^i \right) \frac{(r-1-i)!}{\beta_0^{r-1}},
\]

where $(r-1) \cdots (r-i) \beta_0^i$ vanishes in the limit unless $i = 0$. The summation is over $k$ such that $\sigma + L_k \geq r$, which gives $\mu_k > 0$. \hfill $\square$

Assuming that $0 < \nu_1 \leq \nu_2 \leq \ldots \leq \nu_s$, we can define $\kappa(\mu) = \min \{ k \mid \mu + \nu_k > 0 \}$ for $-\nu_s < \mu \leq 0$; the corresponding $\{ r_k \}$ are called extreme. The condition $\mu_k = \mu + \nu_k > 0$ in (13) becomes $k \geq \kappa(\mu)$ and
this formula reads for \(-\nu_s < \mu \leq 0\):

\[
\pi_{r_1,\ldots,r_s}' = \frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s}}{\alpha_0^s r_1! \cdots r_s!} \sum_{k=\kappa(\mu)}^{s} \left( r_k - \sum_{i=0}^{r_k-1} \frac{r_k}{i!} e^{-\alpha_0 \mu k \left(\alpha_0 \mu k\right)^i} \right).
\]

The extreme configurations have little to do with epidemics, but can have potential applications in physics and networks. For instance, let us estimate \(\pi_{r_1,\ldots,r_s}'\) at the resonances: when \(\mu = 0\). Then \(\kappa = 1\) and the Taylor formulas gives that for some \(0 < \epsilon < \epsilon\):

\[
\frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s}}{r_1! \cdots r_s!} e^{-\alpha_0 \nu_s} < \pi_{r_1,\ldots,r_s}' = \frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s}}{r_1! \cdots r_s!} \sum_{k=1}^{s} \frac{r_k}{r} e^{-\alpha_0 \nu k} < \frac{\alpha_1^{r_1} \cdots \alpha_s^{r_s}}{r_1! \cdots r_s!}.
\]

The dependence on \(\mu\) is of interest. It takes values in the set \(\{\mu\} = \{1 - \sum_{k=1}^{s} r_k \nu_k > -\nu_s \mid r_k \geq 0\}\): we can define \(\pi'(\mu)\) as the sum of \(\pi_{r_1,\ldots,r_s}'\) over the configurations with \(1 - \sum_{k=1}^{s} r_k \nu k = \mu\). The sequence \(\{r_k\}\) is uniquely determined by \(\mu\) if \(\nu_k\) are in a general position. For rational \(\nu_k = \ell_k/N\; \{\mu\} = \{N - \sum_{k=1}^{s} r_k \ell_k > -\ell_s \mid r_k \geq 0\}/N\). The extreme \(\mu\) are then for \(\{r_k\}\) such that \(N + \ell_s > \sum_{k=1}^{s} r_k \ell_k \geq N\), which is linked to the Frobenius coin problem.

**Extreme configurations.** There is a natural way to obtain a distribution of probabilities only on the extreme configurations. We set \(\rho_i = \alpha_i/\alpha_0\) and consider \(\tilde{\pi}_{r_1,\ldots,r_s}' \overset{\text{def}}{=} \lim_{\alpha_0 \to \infty} \pi_{r_1,\ldots,r_s}'\). For \(r > 0\):

\[
\tilde{\pi}_{r_1,\ldots,r_s}' = \frac{\rho_1^{r_1} \cdots \rho_s^{r_s} r!}{r_1! \cdots r_s!} \sum_{k=\kappa(\mu)}^{s} \frac{r_k}{r}, \quad \mu = 1 - \sum_{k=1}^{s} r_k \nu k,
\]

for extreme \(\{r_k\}\), and 0 otherwise. For finite \(\alpha_0\), all \(\mu > 0\) occur; generally, the “defects” (gaps) play a very significant role.

The combinatorial counterpart of (15) is straightforward. We assume that \(\beta_0\) is significantly larger than \(1/N\) and that the powers \((1 - \beta_0)^{r_kN}\) can be disregarded. This means that we cover \([1, N]\) by \(L_k\)-segments without gaps between them (the last segment can go beyond \(N\)). The lengths of the segments are here \(\ell_k \geq 1\), not \((L_k+1)\) as in Theorem 7.1. Then \(\beta_0 = 1\) and we set \(\rho_k = \beta_k\). Let \(0 < \ell_1 \leq \ell_2 \leq \ldots \leq \ell_s\); as above, \(\sigma = N - \sum_{k=1}^{s} r_k \ell k\), \(\sigma_k = \sigma + \ell_k\). Then, provided that \(-\ell_s < \sigma \leq 0\),

\[
\tilde{\pi}_{r_1,\ldots,r_s}' = \frac{\rho_1^{r_1} \cdots \rho_s^{r_s} r!}{r_1! \cdots r_s!} \sum_{k=\kappa(\sigma)}^{s} \frac{r_k}{r}, \quad \sigma = \min\{k \mid \sigma_k > 0\},
\]
which coincides with (15) in the limit \( \ell_i/N \to \nu_i \). We obtain that
\[
\sum_{\{r_k\}} \tilde{r}_{r_1 \ldots r_s} = 1 \quad \text{and deduce from it that} \quad \sum_{\{r_k\}} \tilde{r}^\prime_{r_1 \ldots r_s} = 1.
\]

**Correlation functions.** As above, we will cover \([1, N]\) by \( r = r_1 + \ldots + r_s \) segments of lengths \( \ell_1, \ldots, \ell_s \) (with probabilities \( \rho_1, \ldots, \rho_s \)). The corresponding \( m \)-point function is defined for \( m \geq 1 \), \( 1 \leq k_i \leq s \), and \( 1 \leq N_1 \leq N_2 \leq \ldots \leq N_m \). It is the probability \( \mathcal{P}^{k_1, \ldots, k_m}_{N_1, \ldots, N_m}(r_1, \ldots, r_s) \) of such coverings subject to the following:

\[
N_1 \in X[k_1] \quad \text{and} \quad N_i + \ell_{k_1} + \ldots + \ell_{k_{i-1}} \in X[k_i] \quad \text{for any} \quad 1 < i \leq m,
\]

where \( X[k] \) is the corresponding consecutive segment of the configuration; \( k \) denotes its length: \( |X[k]| = \ell_k \). For instance, the 1-point function is when \( X[k_1] \) covers \( N_1 \) such that \( 1 \leq N_1 \leq \). Let \( r_k^{(i)} \geq 0 \) for \( i = 1, 2, \ldots, m+1 \) be the number of segments of types \( k = 1, 2, \ldots, s \) strictly between \( X[k_i-1] \) and \( X[k_i] \) before \( X[k_1] \) for \( i = 1 \), and (strictly) after \( X_{km} \). Thus, \( r_k - \sum_{i=1}^{m+1} r_k^{(i)} \) is the number of \( k_i = k \) in the sequence \( \{k_i, 1 \leq i \leq m\} \); this relation will be imposed below. We set \( \varsigma^{(i)} \defeq \sum_{j=1}^i (r_1^{(j)} \ell_1 + \ldots + r_s^{(j)} \ell_s) \) for \( 1 \leq i \leq m+1 \). For instance, \( \varsigma^{(m+1)} = \sum_{i=1}^m r_i \ell_i - (\ell_{k_1} + \ldots + \ell_{km}) \). We obtain the following formula in terms of the multinomial coefficients \( (a+b+c+...) \):

\[
\mathcal{P}^{k_1, \ldots, k_m}_{N_1, \ldots, N_m}(r_1, \ldots, r_s) = \sum r_1^{(1)} \cdots r_s^{(1)} \cdot \rho_1 \cdots \rho_s \\
\quad \cdot \rho_1^{(1)} \cdots \rho_s^{(1)} \\
\quad \cdot r_1^{(m)} \cdots r_s^{(m)} \\
\quad \cdot r_1^{(m+1)} + \cdots + r_s^{(m+1)} - 1, \\
\quad \cdot r_1^{(m+1)} + \cdots + r_s^{(m+1)} - 1, \\
\quad \cdot r_1^{(m+1)} + \cdots + r_s^{(m+1)} - 1, \\
\quad \cdot r_1^{(m+1)} + \cdots + r_s^{(m+1)} - 1, \\
\quad \cdot \ldots, \\
\quad \cdot \ldots, \\
\quad \cdot \ldots, \\
\quad \end{array}
\]

where the summation is over \( 1 \leq k \leq s \) and \( \{r_k^{(i)} \geq 0\} \) such that

\[
N_1 + \ell_{k_1} > \varsigma^{(1)} \geq N_1, N_2 + \ell_{k_2} > \varsigma^{(2)} \geq N_2, \ldots, N_m + \ell_{k_m} > \varsigma^{(m)} \geq N_m,
\]

and \( N + \ell_k > \varsigma^{(m+1)} + \ell_{k_1} + \ldots + \ell_{k_m} \geq N \), equivalently, \( N \in X[k] \).

The last term in the product occurs only if \( r_1^{(m+1)} + \ldots + r_s^{(m+1)} \geq 1 \), i.e. when the last segment is not fixed in the \( m \)-point function.

The \( m \)-point function serving Theorem 7.1 is when \( \rho_k = \beta_k \), \( \ell_k = L_k + 1 \), and we add \( \ell_0 = 1 \), \( \rho_0 = 1 - \beta_0 \). It is \( \mathcal{P}^{k_1, \ldots, k_m}_{N_1, \ldots, N_m}(r_0, r_1, \ldots, r_s) \), where now \( k_i \geq 0 \). We can omit \( r_0 \) here, the number of positions not covered by the segments, and fix only the corresponding numbers of segments: \( r_1, \ldots, r_s \). We will not discuss the limit as \( N \to \infty \), providing only the following simple example.
Let \( s = 1 \), so we have only 1 length \( L \). Accordingly \( \beta = \alpha/N \), and we use below the formulas for \( \pi'_r \) from Theorem 3.1 in terms of \( \beta, N, L: \alpha \mapsto \beta N, \nu \mapsto L/N \). We will write \( \pi'_r(N; L, \beta) \).

Then for \( m = 1 \), the limit \( N \to \infty \) of \( \mathcal{P}^0 N_1(r) \), which is when the position \( N_1 \leq N \) is not covered by a segment, is

\[
\mathcal{P}^0_{N_1}(r) = \sum_{i_1, i_2} e^{(i_1 L - N_1) \beta} \pi'_{i_2}(N - N_1; L, \beta) \quad \text{for}
\]

\[
0 \leq i_1 < \frac{N_1 + 1}{L + 1}, \quad 0 \leq i_2 \leq \frac{N_1 + 1}{L + 1}, \quad i_1 + i_2 = r.
\]

Here we do not need the limiting procedure; this is a direct calculation with probabilities. Also, \( \mathcal{P}^0_{N_1}(r) \), the 1-point function when \( N_1 \) is covered by an \((L + 1)\)-segment, is \( \pi'_r(N; L, \beta) - \mathcal{P}^0_{N_1}(r) \).

8. Some perspectives. The consideration of ensembles of segments of various lengths \((L_k + 1)\) links our paper to stochastic processes, namely to Whittaker-type processes, those based on the distances between neighboring particles. See [BC]. In our approach, \( L_k \) with the corresponding multiplicities \( r_k \) are some substitutes for these distances with one reservation: recall that we allow “defects”, the gaps between our segments. Thus, \( \{r_k, L_k\} \) basically give these distances.

Here the Matérn II statistics is employed. Namely, for consecutive time moments \( i = 1, 2, \ldots, N \), the segment \([i, i + L_k]\) can be created at any such \( i \) with the probability \( \beta_k \). This is unless \( i \) belongs to the previously created segment, when the point is deleted (this operation of thinning). We allow only finitely many possible \( L_k: 1 \leq k \leq s \).

Generally, one can always expected some formulas in terms of binomial coefficients for other kinds of statistics.

There is an almost immediate link to the so-called interlacing sequences \( x_1 < y_1 < x_2 < y_2 < \ldots < x_{n-1} < y_n < x_{n+1} \). They are sequences of \( n \) non-overlapping segments \([x_i, y_i]\) of lengths \( y_i - x_i \) in \([x_1, x_{n+1}]\). The corresponding transitional probabilities are associated with the \( t \)-residues of the function \( F(t) = \frac{(t-y_1)(t-y_2)\ldots(t-y_n)}{(t-x_1)(t-x_2)\ldots(t-x_{n+1})} \) at its poles: \( x_1, \ldots, x_{n+1} \). See [Ke, BO, Ol]. In our approach, these segments are \([x_i, y + i = x_i + L_k]\) where \( L_k \) is the length of the segment from \( x_k \).

Then we calculate the generating function \( G(t) \) and expand it; its coefficient of \( t^N u_1^{r_1} u_2^{r_2} \ldots \) is the probabilistic measure of the corresponding
Young diagram of order $\leq N$; $r_k$ is the number of rows of the length $L_k + 1$.

For instance, one can take here $L_i = i$ for $i = 1, 2, \ldots, n$. Then our approach becomes close to the theory of the transitional probabilities. The denominator of $G(t)$ is basically that in $F(t)$ with undetermined coefficients, which are our $u_i \beta_i$. The numerator of $G(t)$, a polynomial of degree $n$, incorporates the edge effects. It is not “generic” in this approach; this is different. The points $x_i, y_i$ do not appear; the aim is to obtain the corresponding distribution of $\{r_k\}$ in terms of the probabilities $\beta_k$. The latter can depend on the corresponding $L_k$, and even on the whole configuration of segments.

The classical theory results in the distribution of probabilities for Young diagrams related to the celebrated hook-formula and Jack polynomials. Our probabilities of Young diagrams from (11) and (12) are of different nature; we think that this approach is new.

A variant of our approach is for “Poisson-Catalan processes,” where $\pm L_i$ are considered as the jumps up and down of the “energy function”. Theorem 4.1 is stated only for one $L$ (for $s = 1$). The probabilities $P'_{r,m}$ there can be extended to multi-dimensional (type $A_s$) Catalan paths, where the steps are at the points subject to the Poisson-type distribution from Theorem 7.2. Generally, one needs here formulas for the number of standard Young tableau for a given skew Young diagram, for instance the Naruse hook-length formula. See e.g. [MPP]. Certain multi-dimension Bessel-type functions occur here, which can be interesting to study.

Acknowledgements. The author thanks very much Alexei Borodin for important discussions, and Evgeny Feigin for his help.

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