GROWTH PROFILE AND INVARIANT MEASURES FOR THE WEAKLY SUPERCIRITCAL CONTACT PROCESS ON A HOMGENEOUS TREE

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ABSTRACT. The growth profile V(s) of a weakly supercritical contact process on a homogeneous tree of degree d+1 is defined by $V(s)=\lim_{n\to\infty} n^{-1}\log P\{x_n\in A_{ns}\}$. Here A_t denotes the set of infected sites at time t, x_n is any vertex at distance n from the root e, and $A_0=\{e\}$. Properties of V are related to the values of $\eta=\lim_{t\to\infty} P\{e\in A_t\}^{1/t}$ and $\beta=\lim_{n\to\infty} P\{x_n\in \cup_{t>0}A_t\}^{1/n}$. It was shown in [7] that in the weakly supercritical phase it is always the case that $\beta\leq 1/\sqrt{d}$. Here it is shown that if $\beta<1/\sqrt{d}$ then $\eta<1$, but that if $\beta=1/\sqrt{d}$ then $\eta=1$. The function V is shown to be concave and bounded above by $\log \beta$, and to have asymptotic slope $\lim_{s\to\infty} V(s)/s=\log \eta$. It is also shown that if $N_n(t)$ is the number of vertices $x\in A_t$ at distance n from e that are infected at time t then almost surely on the event of non-extinction,

$$\lim_{n\to\infty}\frac{1}{n}\log N_n(ns)=\max(0,V(s)+\log d).$$

Finally, the function V is related to a function φ introduced in [10], and this relation is used to prove that if $\beta < 1/\sqrt{d}$ then there exists a spherically symmetric invariant measure for the contact process whose density decays exponentially at ∞ .

1. Introduction

This paper is a sequel to [7], in which the weakly supercritical phase of an isotropic contact process on an infinite homogeneous tree was studied. Briefly, an isotropic contact process on the homogeneous tree $\mathcal{T} = \mathcal{T}_d$ of degree d+1 is a continuous time Markov process A_t on the set of finite subsets of \mathcal{T} (henceforth, \mathcal{T} will be identified with the vertex set of the tree) that evolves as follows. Infected sites (members of A_t) recover at rate 1 and upon recovery are removed from A_t ; healthy sites (members of A_t^c) become infected at rate ρ times the number of infected neighbors, and upon infection are added to A_t . Under the default probability measure P, the initial state A_0 is the singleton set $\{e\}$ (where e is a distinguished element of \mathcal{T} called the "root"). See [8] and [3] for general information on the contact process, and [7], especially sections 1 and 2, for background information concerning the contact process on a homogeneous tree. Some of the arguments of this paper (see the proofs of Proposition 9 and Theorem 3 below) are borrowed from [7].

It was discovered by Pemantle [12] for trees of degree greater than 3 and by Liggett [11] (see also Stacey [14] for a relatively simple argument) for the tree of degree 3 that the

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contact process described above has (at least) 3 essentially different "phases": (i) extinction, (ii) weak survival, and (iii) strong survival. In phase (i), $A_t = \emptyset$ eventually, with probability 1; in phase (ii), $|A_t| \to \infty$ with positive probability but for every finite subset Bof T, $A_t \cap B = \emptyset$ eventually, with probability 1; and in phase (iii), with positive probability $e \in A_t$ for arbitrarily large values of t. There exist critical constants $0 < \rho_1 < \rho_2 < \infty$ such that $\rho \leq \rho_1$ implies ultimate extinction; $\rho_1 < \rho \leq \rho_2$ implies weak survival; and $\rho > \rho_2$ implies strong survival. The phase of interest here is weak survival (we also refer to the contact process in this phase as weakly supercritical). This phase is of interest, among other reasons, because it does not occur for the contact process on Euclidean lattices (e.g., on \mathbb{Z}^d). Henceforth we shall discuss only this case. Thus, we make the standing assumption that

$$\rho \in (\rho_1, \rho_2].$$

1.1. Growth Profile and Other Characteristics. The main results of this paper concern a function V(s) which we shall call the *growth profile* of the contact process. Two other parameters also enter into the statements of these results: $\beta = \beta(\rho)$, which determines the size of the "limit set" of the contact process on the event of its survival (see [7]), and $\eta = \eta(\rho)$, the exponential rate of decay of $P\{e \in A_t\}$. The definitions are as follows:

(1)
$$\beta = \lim_{n=d(x,e)\to\infty} (P\{x \in A_t \text{ for some } t\})^n;$$

(2)
$$\eta = \lim_{t \to \infty} (P\{e \in A_t\})^{1/t};$$

(3)
$$V(s) = \log \lim_{n=d(x,e)\to\infty} (P\{x \in A_{ns}\})^{1/n}.$$

The existence of these limits follows from simple subadditivity arguments (see below for η and V(s), and see [7] for β). The main result of [7] is that for all values of $\rho \in (\rho_1, \rho_2]$,

$$\beta \le \frac{1}{\sqrt{d}}.$$

Theorem 1. The growth profile V(s) is a concave, continuous function of s > 0 that is bounded above by $\log \beta$ and satisfies

$$\lim_{s \to 0+} V(s) = -\infty,$$

(6)
$$\lim_{s \to \infty} V(s)/s = \log \eta.$$

Theorem 1 will be proved in section 2 below – see Propositions 1-4.

Theorem 2. If $\beta < 1/\sqrt{d}$ then $\eta < 1$. If $\beta = 1/\sqrt{d}$ then $\eta = 0$.

The first statement of this theorem, that $\beta < 1\sqrt{d}$ implies $\eta < 1$, is the main technical result of the paper. Sections 3 4, and 5 below are devoted to its proof. This statement is also the key to the proof of Theorem 4 below. The second statement, that $\beta = 1/\sqrt{d}$ implies $\eta = 1$, follows by an argument similar to the "backscattering" argument in section 4 of [7]. This argument is sketched in section 6 below. Theorem 2, together with Theorem 1, implies that if $\beta < 1/\sqrt{d}$ then $V(s) \to -\infty$ as $s \to \infty$, but that if $\beta = 1/\sqrt{d}$ then V(s) is nondecreasing in s (since it is concave).

The function V(s) proscribes the shape and size of the set A_t of infected sites at large times t. Define r_t and R_t to be the *smallest* and *largest* distances d(x, e) among the infected sites $x \in A_t$. Also, for any integer n and any s > 0 define $N_n(ns)$ to be the number of vertices $x \in A_{ns}$ at distance n from e that are infected at time ns.

Theorem 3. Suppose that $\beta < 1/\sqrt{d}$. Then there exist smallest and largest solutions $0 < s_1 \le s_2 < \infty$ of $V(s) = -\log d$. Almost surely on the event of survival,

$$\lim_{t \to \infty} r_t/t = 1/s_2, \qquad and$$

(7)
$$\lim_{t \to \infty} r_t/t = 1/s_2,$$
(8)
$$\lim_{t \to \infty} R_t/t = 1/s_1.$$

Moreover, for any s > 0 such that $V(s) + \log d > 0$,

(9)
$$\lim_{n \to \infty} \frac{1}{n} \log N_n(ns) = V(s) + \log d$$

See section 8 for the proof. This theorem explains the use of the term "growth profile". The function V(s) effectively determines how the contact process "spreads out" in spacetime, and determines roughly how many vertices at each distance from e are infected at any large time t. Together with Theorem 2, it also implies that A_t recedes linearly from the root vertex e if and only if $\beta < 1/\sqrt{d}$.

1.2. Invariant Measures for the Contact Process. The set of invariant measures in the phase of strong survival has a relatively simple structure: every such measure is a mixture of the point mass at \emptyset and the "upper invariant measure" (see Zhang [15]). For weakly supercritical contact processes the set of invariant measures seems in general to be much more complex. Durrett and Schinazi [1] proved that it has infinitely many extreme points. Liggett [10] showed that, at least for $\rho > \rho_1$ sufficiently close to ρ_1 , there are invariant measures ν that are spherically symmetric (about the root vertex e) and have exponentially receding densities, i.e., are such that for all $x \in \mathcal{T}$,

(10)
$$C_1 z^{d(x,e)} \le \nu \{A : x \in A\} \le C_2 z^{d(x,e)},$$

where $0 < C_1 < C_2 < \infty$ are constants independent of x and d(x,e) denotes the distance from x to e in T. Liggett also conjectured that such invariant measures exist for all $\rho \in$ $(\rho_1, \rho_2]$, and gave a sufficient condition for their existence. This condition involves the function

(11)
$$\varphi(z) = \lim_{t \to \infty} \left(E \sum_{x \in A_t} z^{L(x)} \right)^{\frac{1}{t}},$$

where L(x) is the level of the vertex x in the tree (see [10] or section 3 below for the definition). Liggett proved that if there exists a solution $z \in (1/\sqrt{d}, 1)$ of the equation

$$\varphi(z) = 1,$$

then there exists a spherically symmetric invariant measure for the contact process that satisfies the exponential decay law (10).

Our results on the growth profile shed some light on Liggett's conjecture. The function $\varphi(z)$ is intimately related to the growth profile V(s), as the next theorem shows.

Theorem 4. If $\beta < 1/\sqrt{d}$ then for every $z > 1/\sqrt{d}$,

(13)
$$\varphi(z) = \max_{0 < s < \infty} \exp\left(\frac{V(s) + \log(dz)}{s}\right).$$

The proof will be given in section 7, along with the proof of the following corollary.

Corollary 1. If $\beta < 1/\sqrt{d}$, then $\varphi(1/d\beta) = 1$.

Thus, in view of Liggett's results, this implies that spherically symmetric invariant measures satisfying equation (10), with $z = 1/d\beta$, exist whenever $\beta < 1/\sqrt{d}$. It is natural to make the following conjectures:

Conjecture 1. If $\beta(\rho) = 1/\sqrt{d}$ then $\rho = \rho_2$.

Conjecture 2. $\beta = \beta(\rho)$ is strictly increasing for $\rho \in (\rho_1, \rho_2]$.

Both conjectures are highly plausible. The truth of Conjecture 1, together with Corollary 1, would imply Liggett's conjecture, as it would then be the case that $\beta < 1/\sqrt{d}$ for all $\rho < \rho_2$. Conjecture 2 is stronger than Conjecture 1, but is no less believable. It is not unlikely that Conjecture 2 will ultimately be proved by a suitable continuous-time adaptation of the techniques in Chapter 3 of [2].

2. Growth Profile: Basic Properties

By the isotropy of the contact process, the probability that the set A_t of sites infected at time t contains a particular vertex $x \in \mathcal{T}$ depends only on t and |x|. Thus, we may define

$$u_n(t) = P\{x \in A_t\},\,$$

where x is any vertex at distance n from the root e. The Markov and monotonicity properties of the contact process imply that for all nonnegative integers m, n and all times $s, t \ge 0$,

$$(14) u_{m+n}(s+t) \ge u_m(s)u_n(t).$$

Consequently, by the basic subadditivity lemma, for every s > 0 the limit

(15)
$$\lim_{n \to \infty} u_n(ns)^{\frac{1}{n}} \stackrel{\Delta}{=} U(s) \stackrel{\Delta}{=} e^{V(s)}$$

exists, and for every s > 0 and every integer $n \ge 0$,

$$(16) u_n(ns) \le U(s)^n.$$

Proposition 1. $V(s) \leq \log \beta$

Proof. It is clear that $u_n(ns) \leq u_n$ for any $n \in \mathbb{N}$ and any s > 0. Taking nth roots on both sides of this inequality and letting $n \to \infty$, one obtains the desired result.

Proposition 2. V(s) is a concave and, therefore, continuous function of s > 0.

Proof. According to the fundamental inequality (14), for all $0 < s < t < \infty$ and all nonnegative integers m, n,

$$u_m(ms)u_n(nt) \le u_{m+n}(ms+nt).$$

Taking the (m+n)thh root of both sides and letting $m, n \to \infty$ in such a way that the ratio m/(m+n) converges to $\alpha \in (0,1)$, one gets

$$U(s)^{\alpha}U(t)^{1-\alpha} \le U(s+t),$$

which implies that V is concave.

Proposition 3. $\lim_{s\to 0+} V(s) = -\infty$.

Proof. This is equivalent to showing that $\lim_{s\to 0+} U(s) = 0$. Recall that

$$U(s) = \lim_{n \to \infty} u_n(ns)^{1/n},$$

and that $u_n(ns)$ is the probability that a particular vertex x at distance n from e will be infected at time ns. Let $x_0, x_1, x_2, \ldots, x_n$ be the successive vertices on the geodesic segment from $e = x_0$ to $x = x_n$, and for each $1 \le m \le n$ define τ_m to be the elapsed time between the first infection of x_{m-1} and the first infection of m. In order that x_n be infected at time ns, it must be the case that at least half of the times τ_m are no greater than 2s. But the distribution of τ_m , conditional on the history of the contact process up to the time of first infection of x_{m-1} , is stochastically larger than an exponential random variable with mean $1/\rho$, so the conditional probability that $\tau_m \le 2s$ is no larger than $1 - e^{-2\rho s}$. Thus, the probability that at least half of the random variables τ_m , $1 \le m \le n$, are $\le 2s$ is no larger than

$$\sum_{k=[n/2]}^{n} \binom{n}{k} (1 - e^{-2\rho s})^k (e^{-2\rho s})^{n-k} \le (n+1)2^n (1 - e^{-2\rho s})^{[n/2]}$$

Taking nth roots, one finds that

$$U(s) = \limsup_{n \to \infty} (u_n(ns))^{1/n} \le 2\sqrt{1 - e^{-2\rho s}},$$

which converges to 0 as $s \to \infty$.

By definition, $u_0(t) = P\{e \in A_t\}$ is the probability that the root vertex e is infected at time t. If e is infected at time t and if there is an infection trail from (e,t) to (e,t+s), then clearly e is infected at time t+s. Hence, by the Markov and monotonicity properties of the contact process, $u_0(t+s) \ge u_0(t)u_0(s)$ for all s,t>0. It follows that

$$\eta = \lim_{t \to \infty} u_0(t)^{\frac{1}{t}} \le 1$$

exists, and that $u_0(t) \leq \eta^t$ for all t > 0.

Proposition 4. $\lim_{s\to\infty} V(s)/s = \log \eta$.

Proof. The concavity of V implies that the limit exists and is nonpositive, so it suffices to consider only integer values of s. Fix $\varepsilon = 1/m > 0$ smaller than 1, and let n > 0 be an integer such that $n\varepsilon \in \mathbb{N}$. Let x be a vertex at distance $n\varepsilon$ from the root e. If there are infection trails that extend from (e,0) to $(e,n-n\varepsilon)$ and from $(e,n-n\varepsilon)$ to (x,n), then their concatenation is an infection trail from (e,0) to (x,n). Hence, by the Markov and monotonicity properties,

$$u_{n\varepsilon}(n) \ge u_0(n-n\varepsilon)u_{n\varepsilon}(n\varepsilon)$$

Taking nth roots of both sides and letting $n \to \infty$ through integer multiples of $1/\varepsilon$ gives

$$U(1/\varepsilon)^{\varepsilon} \ge \eta^{1-\varepsilon} U(1)^{\varepsilon}.$$

Taking logarithms and letting $\varepsilon \to 0$ yields

$$\lim_{s \to \infty} \frac{V(s)}{s} \ge \log \eta.$$

The reverse inequality is obtained in much the same way. Let x be a vertex at distance $n\varepsilon$ from the root e. If there are infection trails that extend from (e,0) to (x,n) and from

(x, n) to $(e, n + n\varepsilon)$ then their concatenation is an infection trail from (e, 0) to $(e, n + n\varepsilon)$; consequently,

$$u_{n\varepsilon}(n)u_{n\varepsilon}(n\varepsilon) \le u_0(n+n\varepsilon).$$

Taking nth roots and letting $n \to \infty$ gives

$$U(1/\varepsilon)^{\varepsilon}U(1)^{\varepsilon} \leq \eta^{1+\varepsilon}$$

and letting $\varepsilon \to 0$ yields

$$\lim_{s \to \infty} \frac{V(s)}{s} \le \log \eta.$$

Proposition 5. If $\lim_{s\to\infty} V(s) = -\infty$ then

$$\max_{0 \le s \le \infty} V(s) = \log \beta.$$

Proof. By Proposition 3, $V(s) \to -\infty$ as $s \to 0+$, and by Proposition 2, V(s) is continuous in s. Consequently, if $V(s) \to -\infty$ as $s \to \infty$ then V(s) attains its maximum value v_{max} . Moreover, since V is concave, the hypothesis that $V \to -\infty$ as $s \to \infty$ implies that there exist constants a < 0 and $0 < s_* < \infty$ such that

$$(17) V(s) \le as - as_* + v_{\max} - 1 if s_* \le s < \infty$$

Let x be any vertex of \mathcal{T} . If x is infected for a first time at time τ , then conditional on the history of the contact process up to time τ the probability that x will remain infected until time $\tau + 1$ is at least 1/e, because the death rate is 1. On this event, x will remain infected at the first *integer* time after τ . Hence,

(18)
$$u_n \le e \sum_{m=1}^{\infty} u_n(m)$$
$$= e \sum_{m=1}^{\infty} \exp\{nV(m/n)\}$$
$$= e(\sum_{A} + \sum_{B}),$$

where

$$m \in A$$
 if $m/n \le s_*$
 $m \in B$ if $m/n > s_*$.

By (17), sum B is dominated by a convergent geometric series whose first term is no larger than $\exp\{n(v_{\max}-1)\}$. On the other hand, sum A contains at most ns_*+1 terms, none larger than $\exp\{nv_{\max}\}$. Thus,

$$\sum_{A} \le \exp\{nv_{\max}\}(ns_* + 1),$$

$$\sum_{B} \le \exp\{nv_{\max} - n\}/(1 - e^{-a})$$

and so the dominant term is sum A. Taking nth roots in (18) and letting $n \to \infty$ gives $\log \beta \le v_{\text{max}}$. Proposition 1 implies the reverse inequality.

3. Counting Paths in \mathcal{T}

The proof of Theorem 2 will require estimates of the number of "k-paths" in the tree of a given length connecting eto e. For any $k \geq 1$, define a k-path γ of length n to be a sequence $\gamma = x_0x_1x_2...x_n$ of n+1 vertices of \mathcal{T} such that for each $0 \leq m \leq n-2$,

$$d(x_m, x_{m+1}) = k \qquad \forall \ 0 \le m \le n-2 \text{ and}$$

$$d(x_{n-1}, x_n) \le k$$

For any two vertices $x, y \in \mathcal{T}$, define $\Gamma_n^k(x, y)$ to be the set of all k-paths of length n with initial vertex x and terminal vertex y, and let $N_n^k(x, y)$ be the cardinality of $\Gamma_n^k(x, y)$. As usual, let e be the root node of \mathcal{T} .

Proposition 6. For any vertex $x \in \mathcal{T}$,

$$N_n^k(e,x) \le 2(d+1)d^k\left((k+1)d^{\frac{k}{2}}\right)^n.$$

Proof. The vertices of \mathcal{T} may be arranged in "levels" $\mathcal{L}_n, n \in \mathbb{Z}$, in such a way that

- (1) every vertex $y \in \mathcal{L}_n$ has exactly d neighbors in \mathcal{L}_{n+1} and exactly one neighbor in \mathcal{L}_{n-1} ;
- (2) the root vertex e is in level \mathcal{L}_0 ; and
- (3) the terminal vertex x is in \mathcal{L}_r for some $r \leq 0$.

For an arbitrary vertex $y \in \mathcal{T}$, define the depth L(y) of y to be the index of its level (i.e., the unique integer n such that $y \in \mathcal{L}_n$). Thus, L(x) = r.

Let $y \in \mathcal{T}$ be an arbitrary vertex, at an arbitrary depth m; and let $\partial B_k(y)$ be the set of all vertices in \mathcal{T} at distance k from y. By the homogeneity of \mathcal{T} , the cardinality M_{ν}^k of $\partial B_k(y) \cap \mathcal{L}_{m+\nu}$ depends only on ν and k, and is given by

(19)
$$\begin{aligned} M_{\nu}^{k} &= 1 & \text{if } \nu = -k; \\ M_{\nu}^{k} &= d^{k} & \text{if } \nu = k; \\ M_{\nu}^{k} &= (d-1)d^{j-1} \leq d^{j} & \text{if } \nu = -k + 2j \text{ and } -k < \nu < k; \\ M_{\nu}^{k} &= 0 & \text{otherwise.} \end{aligned}$$

Now consider the set $\Gamma_n^k(e, \mathcal{L}_r)$ of k-paths $\gamma = x_0 x_1 x_2 \dots x_n$ of length n, starting at $x_0 = e$ and terminating at an arbitrary vertex x_n in level \mathcal{L}_r . Each path $\gamma \in \Gamma_n^k(e, \mathcal{L}_r)$ determines a unique sequence of depths $l_j = L(x_j)$. Observe that there are no more than $2(k+1)^n$ allowable depth sequences l_j , because for each 0 < j < n there are only (k+1) possibilities for the increment $l_j - l_{j-1}$, and there at most 2(k+1) possibilities for $l_n - l_{n-1}$. To complete the proof, we will show that for any allowable depth sequence $l = l_0 l_1 l_2 \dots l_n$ the number of possible k-paths $\gamma \in \Gamma_n^k(e, \mathcal{L}_r)$ with depth sequence l is no larger than

$$d^{nk/2}(d+1)d^{2k}.$$

Fix an allowable depth sequence $l = l_0 l_1 l_2 \dots l_n$. Suppose that the first i points $x_0 x_1 \dots x_i$ of the path γ have been determined. Then by equations (19), the number of possible choices for x_{i+1} is, for any $0 \le i \le n-2$, no larger than

$$d^{(k+l_{i+1}-l_i)/2},$$

and for i = n - 1 is no larger than $(d+1)d^k$ (since the distance between x_{n+1} and x_n is no larger than k). Consequently, the total number of paths $\gamma \in \Gamma_n^k(e, \mathcal{L}_r)$ with depth sequence

l is no larger than

$$(d+1)d^k \prod_{i=0}^{n-2} d^{(k+l_{i+1}-l_i)/2} = (d+1)d^k d^{kn/2} d^{l_i-1}$$

$$\leq (d+1)d^{2k} d^{kn/2}.$$

Note: In effect, the upper bound in Proposition 6 provides a lower bound for the spectral radius of the random walk in \mathcal{T} whose one-step distribution is the uniform distribution on the sphere of radius k. The exact value of the spectral radius, as well as much more precise estimates on $N_n^k(e,x)$ for fixed x, may be deduced from the results of either [5] or [13]. When k=1, Proposition 6 implies that the number of 1-paths grows no faster than $O((2\sqrt{d})^n)$, which agrees with Kesten's formula [4] for the spectral radius of simple random walk on \mathcal{T} .

4. Expected Number of Infections

If a vertex $x \in \mathcal{T}$ is ever infected, then eventually it will recover (recall that the recovery rate is 1). It may then be re-infected at a future time, but will again eventually recover. The cycle of infection/ recovery may continue, but eventually it will cease, because in the weakly supercritical phase the infection must ultimately vacate every finite subset of \mathcal{T} , with probability 1. Consequently, for every vertex x the total number J_x of recoveries is almost surely finite. (Because the recovery process at x is a Poisson process with rate 1, the number of recoveries in any finite time interval is finite, w.p.1).

Proposition 7. If $\beta < 1/\sqrt{d}$ then there exists a constant C, depending only on β and d, such that for every vertex $x \in \mathcal{T} - \{e\}$,

$$EJ_x \le C(d(x,e)+1)\beta^{d(x,e)}$$
.

Proof. Fix vertex x at distance $k \geq 1$ from e. Let $0 \leq \nu_1 < \tau_1 < \nu_2 < \ldots$ denote the times of first infection, first recovery, second infection, second recovery, etc. at x. Observe that these are Markov times for the contact process. The event that $\nu_1 < \infty$ is just the event that x is ever infected, hence has probability $u_k \leq \beta^k$.

Consider the event that $\nu_{j+1} < \infty$ for some $j \ge 1$: if this event occurs, there must be a vertex Y_j (not necessarily unique) in the set A_{τ_j} of sites infected at time τ_j from which the infection spreads to x at time ν_{j+1} . The entries of the finite sequence $Y_1, Y_2, \ldots, Y_{J_x-1}$ are all members of $A_* = \bigcup_{t \ge 0} A_t$; multiple occurrences of an element $y \in A_*$ in the sequence $Y_1, Y_2, \ldots, Y_{J_x-1}$ are possible. Let $y \in T$ be any vertex of the tree, and denote by m its distance from x. The probability that y occurs at least $n \ge 1$ times in the sequence $Y_1, Y_2, \ldots, Y_{J_x-1}$ is no greater than $u_m^n \le \beta^{mn}$, because each such occurrence entails that infection travels from y to x in a new time interval $(\tau_i, \nu_{i+1}]$ (keep in mind also that the times τ_i are Markov times). It follows that the expected length of the sequence $Y_1, Y_2, \ldots, Y_{J_x-1}$ is bounded above by

$$\sum_{y\neq x} \beta^{d(e,y)} \sum_{n=1}^{\infty} \beta^{nd(y,x)} \le \sum_{y\neq x} \beta^{d(e,y)} \beta^{d(x,y)} / (1-\beta).$$

To evaluate the latter sum we must estimate the number of vertices $y \in \mathcal{T}$ such that d(e,y) + d(y,x) = n, for $n \geq 0$. By the triangle inequality, there are no such vertices if

n < d(e,x) = k. If n = k then there are exactly k such vertices - the vertices y on the geodesic segment from e to x. Finally, if y is a vertex such that d(e,y) + d(y,x) > k then d(e,y) + d(y,x) = k + 2m for a positive integer m, and the number of such vertices is no larger than $(k+1)d^{2m}$. (To see this, partition them according to the closest vertex z on the geodesic segment from e to x. There are (k+1) possibilities for z, including x. The vertex y must be at some distance m from z. The number of possibilities is bounded by d^m , because for each of the m steps leading from z to y there are at most d possibilities.) Thus,

$$\sum_{y \neq x} \beta^{d(e,y)} \beta^{d(x,y)} \leq \beta^k \sum_{m=0}^{\infty} (k+1) d^m \beta^{2m} = (k+1) \beta^k / (1 - d\beta^2).$$

Together with the result of the preceding paragraph, this proves the proposition for all vertices $x \neq e$.

5. Behavior of the Growth Profile for Large s

Recall that an infection trail is a (continuous) path in the percolation structure that does not pass through any "death marks" *. Define the 1-skeleton of an infection trail to be the sequence of vertices in \mathcal{T} through which the infection trail passes; note that this is a 1-path, in the terminology of section 3. For any 1-path $\gamma = x_0x_1x_2...x_n$, define the associated k-path to be the subsequence $\gamma' = x_{m_0}x_{m_1}...x_{m_r}$ such that $m_0 = 0$, $m_r = n$, $d(x_{m_{r-1}}, x_n) \leq k$, and for every $0 \leq j \leq r-2$, m_j is the first index $i > m_{j-1}$ such that $d(x_{m_{j-1}}, x_i) = k$. Define the k-skeleton of an infection trail to be the associated k-path of its 1 - skeleton.

Lemma 1. Let $\xi = x_0 x_1 x_2 \dots x_n$ be any k-path of length n. Then the probability that ξ is the k-skeleton of an infection trail starting at x_0 is no greater than

$$C^n(k+1)^n\beta^{nk}$$
,

where C is as in the statement of Proposition 7.

Proof. This is by induction on the length n of the k-path ξ . Let F be the event that ξ is the k-skeleton of an infection trail. In order that the event F occur, it is necessary that (i) the contact process initiated at x_0 eventually infects x_1 , at some time σ_1 , and (ii) there is an infection trail starting at (x_1, σ_1) and ending at x_n whose k-skeleton is $x_1x_2 \dots x_n$. Note that σ_1 need not be the first time that the contact process initiated at $x_0 = e$ infects x_1 , nor that σ_1 be a Markov time for the contact process. However, σ_1 must be one of the times ν_i , $1 \le i \le J_x$, at which an infection cycle at $x = x_1$ begins. Let F_i be the event that there is an infection trail starting at (x_1, ν_i) and ending at x_n whose k-skeleton is $x_1x_2 \dots x_n$. Then

(20)
$$F \subset \bigcup_{i=1}^{\infty} (\{\nu_i < \infty\} \cap F_i).$$

If n=1 then the event F_i is certain, given that $\nu_i < \infty$. If n>1 then since ν_i is a Markov time, $P(F_i | \nu_i < \infty) = P(F')$, where F' is the event that $x_1 x_2 \dots x_n$ is the k-skeleton of an infection trail starting at $(x_1, 0)$. By the induction hypothesis, $P(F') \leq (C(k+1))^{n-1} \beta^{nk-k}$. Hence, by the Bonferroni inequality and (20),

$$P(F) \le \sum_{i=1}^{\infty} P(\{\nu_i < \infty\} \cap F_i) \le EJ_{x_1}(C(k+1))^{n-1}\beta^{nk-k},$$

and the result now follows from Proposition 7.

For $k \in \mathbb{N}$, t > 0, $\varepsilon > 0$, and $x \in \mathcal{T}$, define $F_x(t, k, \varepsilon)$ to be the event that there is an infection trail from (e, 0) to (x, t) whose k-skeleton has length less than εt .

Lemma 2. For each $k \in \mathbb{N}$ there exist constants $\varepsilon > 0$ and $r \in (0,1)$ such that

$$\sup_{x \in \mathcal{T}} \sup_{t > 1} \frac{P(F_x(t, k, \varepsilon))}{r^t} < \infty$$

Proof. It suffices to prove this with the supremum over all $t \geq 1$ replaced by the supremum over all integers $t \geq 1$, because conditional on the event $F_x(t,k,\varepsilon)$ the probability that the infection trail to (x,t) extends to (x,[t]+1) without leaving the vertex x is at least e^{-1} (recall that the instantaneous death rate in the contact process is 1). Similarly, it suffices to prove the result with the supremum over all t>0 replaced by the supremum over all t>0 in some fixed arithmetic progression.

Let $B_k = B_k(e)$ denote the set of all vertices in \mathcal{T} at distance $\leq k$ from e, and consider the part of the percolation structure over B_k for times between 0 and 1. There is a positive probability δ that in this part of the percolation structure there are no infection arrows originating at vertices of B_k and that there is a death over every vertex $x \in B_k$. Note that on this event there cannot be an infection trail from $B_k \times \{0\}$ to $B_k \times \{1\}$ that does not exit B_k . It follows from the independence between nonoverlapping parts of the percolation structure that for any integer $n \geq 1$ the probability that there is an infection trail from $B_k \times \{0\}$ to $B_k \times \{n\}$ that does not exit B_k is no larger than $(1-\delta)^n$. Consequently, by the isotropy of the contact process, for any ball $B_k(y)$ in \mathcal{T} of radius k and any time $k \geq 0$, the probability that there is an infection trail from $B_k(y) \times \{t\}$ to $B_k(y) \times \{t+n\}$ that does not exit $B_k(y)$ is no larger than $(1-\delta)^n$.

Let $\xi = x_0 x_1 x_2 \dots x_m$ be a fixed, but arbitrary, k-path. Suppose that there is an infection trail of duration $n \geq m$ whose k-skeleton is ξ ; then for at least half of the indices $j \in \{0, 1, \dots, m-1\}$ the infection trail must stay in the ball $B_k(x_j)$ for a time exceeding n/2m. Hence, the probability that such an infection trail exists is no greater than

$$\sum_{j=[m/2]}^{m} {m \choose j} (1-\delta)^{j[n/2m]} (1-(1-\delta)^{[n/2m]})^{m-j} \le (m+1)2^m (1-\delta)^{n/4-1}.$$

By Proposition 6, the number of distinct k-paths of length m with initial vertex e and terminal vertex x is bounded above by cC_k^m for constants c, C_k not depending on x or m. Thus, by the result of the preceding paragraph, the probability that there is an infection trail from (e,0) to (x,n) with k-skeleton of length $\leq \varepsilon n$ is bounded above by

$$c(n/\varepsilon+1)(2C_k)^{n/\varepsilon}(1-\delta)^{n/4-1}$$
.

It is clear that if $\varepsilon > 0$ is sufficiently small then this is exponentially decreasing in n. \square

Proposition 8. If $\beta < 1/\sqrt{d}$ then $\eta < 1$.

Proof. Fix $k \in \mathbb{N}$, and let $\varepsilon > 0$ and $r \in (0,1)$ be as in the statement of Lemma 2. Then the probability that there is an infection trail from (e,0) to (e,t) whose k-skeleton has length less than εt is $O(r^t)$. Hence, to prove the proposition it suffices to prove that if $K_{\varepsilon t}$ is the number of k-paths from e to e of length $n \ge \varepsilon t$ that are k-skeletons of infection trails beginning and ending at e, then

$$EK_{\varepsilon t} = O(q^{\varepsilon t})$$

for some q < 1. It will then follow that $\eta \leq \max(r, q^{\varepsilon})$.

By Proposition 6, the number of k-paths from e to e of length $n \ge \varepsilon t$ is no larger than $2(d+1)d^k((k+1)d^{k/2})^n$. Let $\xi = x_0x_1\cdots x_n$ be any such k-path. By Lemma 1, the probability that ξ is the k-skeleton of an infection trail is no larger than $C^n(k+1)^n\beta^{nk}$. Thus, the expected number of k-paths of length n that are k-skeletons of infection trails beginning and ending at e is no greater than

$$2(d+1)d^k\left(C(k+1)^2(\beta\sqrt{d})^k\right)^n.$$

For all k sufficiently large it will be the case that $q = C(k+1)^2(\beta\sqrt{d})^k < 1$, so

$$EK_{\varepsilon t} \le 2(d+1)d^k \sum_{n>\varepsilon t} (C(k+1)^2 (\beta \sqrt{d})^k)^n = O(q^{\varepsilon t}).$$

6. THE CRITICAL CASE

This section is devoted to the proof of the following proposition, which will complete the roof of Theorem 2. The argument is largely borrowed from [7], section 4.

Proposition 9. If $\beta = 1/\sqrt{d}$ then $\eta = 1$.

For any integer $n \geq 1$, define F_n to be the event that there is an infection trail that begins at the root e at time t=0, reaches a vertex x at distance n from e, and then returns from x to e. Since the contact process is, by hypothesis, weakly supercritical, $P(F_n) \to 0$ as $n \to \infty$ (see [7] section 4). Define

$$\zeta = \limsup_{n \to \infty} P(F_n)^{\frac{1}{n}}.$$

Lemma 3. If $\zeta = 1$ then $\eta = 1$.

Proof. Let H_n be the event that $e \in A_t$ for some $t \ge n$, and let H'_n be the event that $e \in A_t$ for some integer $t \ge n$. Since the recovery rate in the contact process is 1, for any n the conditional probability is at least $\exp\{-1\}$ that e remains infected for $n \le t \le n+1$, given that e is infected at time n. Hence, $P(H_n) \le \exp\{1\}P(H'_n)$, and it follows that

$$P(H_n) \le \exp\{1\} \sum_{m=0}^{\infty} P(e \in A_{n+m}) \le \exp\{1\} \eta^n / (1-\eta).$$

Thus, to prove that $\eta = 1$ it suffices to prove that

$$\limsup_{n\to\infty} P(H_n)^{1/n} = 1.$$

Fix $\varepsilon > 0$, and let G_n be the event that there is an infection trail starting at (e,0) that reaches a vertex at distance n from e and then returns to e by time εn . On the event G_n , some vertex at distance n from e is infected at some time $t < \varepsilon n$; hence, summing over all such vertices and all integer times $< \varepsilon n$, using again the fact that the recovery rate is 1, we obtain that

$$P(G_n) < (d+1)d^{n-1} \left(\exp\{1\} \sum_{m=1}^{\varepsilon n} \exp nV(m/n) + \rho^n \exp\{-\rho\}/n! \right)$$

 $(\rho^n e^{-\rho}/n!)$ is an upper bound for the probability that a particular vertex x at distance n from e is infected before time 1). Consequently, by Proposition 3, if $\varepsilon > 0$ is sufficiently small then

$$\limsup_{n\to\infty} P(G_n)^{\frac{1}{n}} < 1.$$

Now by hypothesis, $\limsup_{n\to\infty} P(F_n)^{1/n} = 1$. Consequently, if $\varepsilon > 0$ is sufficiently small then, by the result of the preceding paragraph, $\limsup_{n\to\infty} P(F_n \cap G_n^c)^{1/n} = 1$. But the event $F_n \cap G_n^c$ is contained in $H_{[\varepsilon n]}$, so it follows that

$$\limsup_{n\to\infty} P(H_{[\varepsilon n]})^{\frac{1}{n}} = 1.$$

Proof of Proposition 9. By Lemma 3, it suffices to show that $\zeta = 1$. For this we adapt from [7] (section 3) the notion of a downward infection trail. Let $x, y \in \mathcal{T}$ be vertices such that L(x) = m < L(y) = m + k; here L(z) denotes the depth of the vertex z (the index of its level $\mathcal{L}_{L(z)}$ – see the proof of Proposition 6). A downward infection trail from x to y is an infection trail that begins at x, never enters level \mathcal{L}_{m-1} , and first reaches \mathcal{L}_{m+k} at y, where it terminates. Observe that a downward infection trail is the same as an outward infection trail (see section 3 of [7]) provided that the initial vertex x is at depth L(x) > 0. By the isotropy of the contact process, the probability that there is a downward infection trail from x to y depends only on k = d(x, y), so we may define

$$w_k = P\{\exists \text{ downward infection trail } x \to y\}.$$

By Proposition 1 of [7], $w_k^{1/k} \to \beta$ as $k \to \infty$. Thus, the probability that there is a downward infection trail from e to x is, in exponential size, just as large as the probability that there is any infection trail from e to x.

If there is a downward infection trail from an infected site x at level $L(x) \geq 0$ (beginning at x during the first infection epoch of x) to a site $x^* \in T(x)$, say that x^* is a descendant of x. Fix an integer $L \geq 1$ and define Y_L to be the number of descendants of e at depth L. Then by Proposition 2 of [7], there is a Galton-Watson process Z_n^L with mean offspring number $d^L w_L$ such that $Y_{nL} \geq Z_n^L$ for all n. Since $w_L^{1/L} \to \beta = 1/\sqrt{d}$ as $L \to \infty$, if L is sufficiently large then the Galton-Watson Z_n^L is supercritical. Hence, for any $\beta_- < \beta$, if k is sufficiently large then

(21)
$$p_k \stackrel{\triangle}{=} P\{Y_k > (d\beta_-)^k\} > \varepsilon > 0,$$

where $\varepsilon > 0$ is the probability that the Galton-Watson process Z_n^L does not reach extinction. Consider now the event F_n^k that there is an infection trail that begins at the root e at time t = 0, reaches a vertex $x \in Y_{nk}$, and then returns from x to e. Clearly, $P(F_n^k) \leq P(F_{nk})$, where F_{nk} is as in Lemma 3 above. The event F_n^k will occur if there is just one descendant x of e at depth e such that (i) there is a descendant e of e at depth e and an infection trail from e to e, beginning at the instant of initial infection of e, and (ii) there is a subsequent infection trail from e to e. Now conditional on the set e of descendants of e at depth e, the events (i) for the different e e e non-overlapping parts of the percolation structure), and each has probability e (by the isotropy of the contact process). Moreover, given that event (i) occurs for some e e e is e.

the conditional probability of event (ii) is at least u_k . Consequently, if $r_n = P(F_n^k)$, then

$$r_n \ge P\{Y_k \ge (d\beta_-)^k\} P(\bigcup_{x \in \mathcal{Y}_k} (i) \& (ii) \mid Y_k \ge (d\beta_-)^k)$$

$$\ge p_k (1 - (1 - r_{n-1})^{(d\beta_-)^k}) u_k$$

$$\ge p_k u_k (1 - \exp\{-(d\beta_-)^k r_{n-1}\})$$

For each fixed k, $r_n = P(F_n^k) \to 0$ as $n \to \infty$, as the contact process is weakly supercritical. This implies that the last exponential displayed above is well-approximated by the first term of its Taylor series around 0. Furthermore, if k is sufficiently large then $u_k > \beta_-^k$, and $p_k > \varepsilon$ by the last paragraph. Thus, for all large n,

$$r_n \geq \varepsilon (d\beta_-^2)^k r_{n-1}/2$$
.

It follows that $\liminf_{n\to\infty} P(F_n^k)^{1/n} \ge \varepsilon (d\beta_-^2)^k/2$. Since $P(F_n^k) \le P(F_{nk})$, this implies that $\limsup_{n\to\infty} P(F_n)^{1/n} \ge d\beta_-^2$; but $\beta_- < \beta = 1/\sqrt{d}$ was arbitrary, so this proves that

$$\lim_{n\to\infty} P(F_n)^{1/n} = \eta = 1.$$

7. The Growth Profile and Liggett's φ -Function

In this section we make the connection between the growth profile V and Liggett's φ -function. The main result is Theorem 4. The proof will use the following intermediate characterization of φ .

Lemma 4. For every $z > 1/\sqrt{d}$,

$$\varphi(z) = \lim_{t \to \infty} \left(\sum_{n=0}^{\infty} u_n(t) (dz)^n \right)^{\frac{1}{t}}.$$

Proof. Recall that $\varphi(z) = \lim_{t\to\infty} (Ew_z(A_t))^{1/t}$, where A_t denotes the set of infected vertices at time t and $w_z(A) = \sum_{x\in A} z^{L(x)}$. Here L(x) denotes the depth of x, as in the proof of Proposition 6. Let M_{ν}^k denote the number of vertices of \mathcal{T} at distance k from the root e and at depth ν ; recall that $M_{\nu}^k = 0$ unless $\nu = -k + 2j$ for some integer $j \leq k$, by equations (19). Thus,

$$Ew_z(A_t) = \sum_{k=0}^{\infty} \sum_{j=0}^{k} z^{-k+2j} M_{-k+2j}^k u_k(t).$$

Since $M_k^k = d^k$, it follows directly that

$$Ew_z(A_t) \ge \sum_{k=0}^{\infty} z^k d^k u_k(t).$$

On the other hand, the inequalities (19) and the hypothesis that $z^2d > 1$ imply that

$$Ew_{z}(A_{t}) \leq \sum_{k=0}^{\infty} \sum_{j=0}^{k} z^{k} d^{k} u_{k}(t) z^{-2j} d^{-j}$$
$$\leq \sum_{k=0}^{\infty} z^{k} d^{k} u_{k}(t) (1 - (z^{2} d)^{-1})^{-1}$$

Since the limit $\lim_{t\to\infty} (Ew_z(A_t))^{1/t}$ exists and equals $\varphi(z)$ (see [10]), the desired result follows from the last two displayed inequalities.

Proof of Theorem 4. Fix $z > 1/\sqrt{d}$, set $V_z(s) = V(s) + \log(dz)$, and define

$$\sigma = \sup_{s>0} V_z(s)/s = \sup_{s>0} (V(s) + \log(dz))/s.$$

By Propositions 3,8 and 4, $V_z(s)/s$ converges to $-\infty$ as $s \to 0+$ and $V_z(s)/s$ converges to $\log \eta < 0$ as $s \to \infty$. Consequently, $\sigma < \infty$.

By definition of σ and the intermediate value theorem, for all $\sigma_* < \sigma$ sufficiently close to σ , the line of slope σ_* through the origin must intersect the graph of V. Thus, there exists $s_* \in (0, \infty)$ such that $V_z(s_*) = \sigma_*$. Now

$$\left(\sum_{n=0}^{\infty} u_n(t)d^n z^n\right)^{\frac{1}{t}} \ge \left(u_{[t/s_*]}(t)(dz)^{[t/s_*]}\right)^{\frac{1}{t}}$$

$$\to \left(U(s_*)dz\right)^{\frac{1}{s_*}}$$

$$= \exp\{\sigma_*\}$$

as $t \to \infty$. This implies, by Lemma 4, that $\varphi(z) \geq e^{\sigma_*}$. Since $\sigma_* < \sigma$ was arbitrary, it follows that

$$\varphi(z) \geq e^{\sigma}$$
.

The proof of the reverse inequality is similar to the proof of Proposition 5. First note that by Proposition 3, $V(s) \to -\infty$ as $s \to 0+$, so for any z > 0 there exists $\delta \in (0,1)$ sufficiently small that for all $s \in (0,\delta)$,

$$V(s) + \log(dz) < \min(-1, \sigma - 1)$$

Now

$$\begin{split} \sum_{n=0}^{\infty} u_n(t) d^n z^n &\leq \sum_{n=0}^{\infty} U(t/n)^n d^n z^n \\ &= \sum_{n=0}^{\infty} \exp\{n(V(t/n) + \log(dz))\} \\ &= \sum_A + \sum_B, \end{split}$$

where \sum_A extends over all $n \leq \delta t$, and \sum_B over all $n > \delta t$. There are at most δt terms in \sum_A , none larger than $e^{\sigma t}$, since $\sigma t \geq V(t) + \log(dz)$ by definition of σ . By our choice of δ , the terms of \sum_B are dominated by the terms of a geometric series with ratio $\leq e^{-1}$ and with initial term no larger than $e^{t(\sigma-1)/\delta} < e^{t(\sigma-1)}$. Hence, by Lemma 4,

$$\varphi(z) = \limsup_{t \to \infty} \left(\sum_{n=0}^{\infty} u_n(t) d^n z^n \right)^{\frac{1}{t}} \le e^{\sigma}.$$

Proof of Corollary 1. By Proposition 8, if $\beta < 1/\sqrt{d}$ then $\lim_{s\to\infty} V(s) = -\infty$. Thus, Theorem 4 implies that for every $z > 1/\sqrt{d}$ the value of $\varphi(z)$ is given by equation (13). By

Proposition 5, the function V(s) attains its maximum value of $\log \beta$ at some $s = s_* \in (0, \infty)$. When $z = 1/(d\beta)$,

$$\max_{s>0}(V(s) + \log(dz)) = (V(s_*) + \log(dz)) = 0,$$

so by (13), $\varphi(z) = 1$.

8. THE GROWTH PROFILE AND THE SPREAD OF THE INFECTION

Proof of Theorem 3. When $\beta < 1/\sqrt{d}$, by Propositions 8 and 5, $\max_s V(s) = \log \beta$. Also, $\beta \ge -\log d$ because otherwise the expected number of sites ever infected would be finite, which would preclude the possibility of weak survival. Consequently, there is at least one solution s of $V(s) = -\log d$. Let s_1 be the smallest solution and s_2 the largest solution. Recall that r_t and R_t are the smallest and largest distances d(x, e) among the infected sites $x \in A_t$, and for any interval (a, b), $N_t(a, b)$ is the number of vertices $x \in A_t$ such that at < d(x, e) < bt.

Proof of Relations (7)-(8)(Sketch). We will show that a.s. on the event of survival, for any $\varepsilon > 0$, $N_t(t/s_1 + \varepsilon t, \infty) = 0$ eventually and $N_t(0, t/s_1 - \varepsilon t) = 0$ eventually. This will imply that a.s. on survival, $\limsup R_t/t \le 1/s_1$ and $\liminf r_t/t \ge 1/s_2$. The reverse inequalities $\liminf R_t/t \ge 1/s_1$ and $\limsup r_t/t \le 1/s_2$ will follow from relation (9) proved below.

A routine argument using estimates like those developed in the proof of Proposition 3 shows that it is enough to consider *integer* times t (the probability that an infection trail moves a distance $\geq \varepsilon t$ in time 1 decreases more rapidly than any exponential e^{-ct}). For a fixed large integer t, the probability that $N_t(t/s_1 + \varepsilon t, \infty) > 0$ is smaller than

$$\sum_{n\geq t/s_1+\varepsilon t} u_n(t) d^n(d+1).$$

But $u_n(t) \leq \exp\{nV(t/n)\}$, so by an argument like that used in the proof of Theorem 4 the terms in the above sum are bounded by the terms of a geometric series with sum smaller than $O(e^{-t\delta}$ for some $\delta > 0$ depending only on ε . Since $\sum_t \in \mathbb{N}e^{-t\delta} < \infty$, the Borel-Cantelli Lemma implies that a.s. $N_t(t/s_1 + \varepsilon t, \infty) = 0$ eventually. A similar argument proves that a.s. $N_t(t/s_1 + \varepsilon t, \infty) = 0$ eventually.

Proof of Relation (9)(Sketch): Fix s > 0 such that $V(s) + \log d > 0$. The probability $u_n(ns)$ that a particular vertex at distance n from the root will be infected at time ns is no larger than $\exp\{nV(s)\}$. The number of vertices in \mathcal{T} at distance n from e is $(d+1)d^{n-1}$. It follows that the expected number of such vertices that are infected at time ns is no larger than

$$(d+1)d^n e^{nV(s)}.$$

Consequently, by a routine application of the Borel-Cantelli lemma and the Markov inequality,

$$\limsup_{n\to\infty}\frac{1}{n}\log N_n(ns)\leq V(s)+\log d.$$

The proof of the reverse direction uses again the notion of a downward infection trail, which was introduced in the proof of Proposition 9. Let x be a vertex at depth n > 0, and let $u_n^*(t)$ be the probability that there is a downward infection trail from (e,0) to (x,t). Then for any s > 0,

(22)
$$\lim_{n \to \infty} u_n^* (ns)^{1/n} = e^{V(s)}.$$

This may be proved in much the same manner as Proposition 1 of [7].

The virtue of considering only vertices infected via downward infection trails is that the existence (or nonexistence) of these infection trails depends only on the part of the percolation structure above the vertices of the tree in the sector between the initial and terminal vertices. Thus, for any distinct vertices x, x', \ldots at depth m and any times t, s, the numbers $\xi_x(s,t), \xi_{x'}(s,t), \ldots$ of vertices y, y', \ldots that are infected at time t by downward infection trails starting at $(x,s), (x',s), \ldots$, respectively, are mutually independent. Consequently, if $N_{nm}(nms)$ denotes the number of vertices at distance nm that are infected at time nms (by infection trails starting at (e,0)), then $N_{nm}(nms)$ dominates a Galton-Watson chain Z_n whose mean offspring number is

$$d^m u_m^*(ms)$$
.

(See [7], Proposition 2 for a similar result about time-independent infection trails.) It follows that on the event of non-extinction of this Galton-Watson process,

$$\liminf_{n\to\infty}\frac{1}{n}\log N_{nm}(nms)\geq \log d^m u_m^*(ms).$$

By choosing m large, we can (i) make the event of non-extinction of the G-W process arbitrarily close to the event of non-extinction of the contact process, and (ii) push $u_m^*(ms)^{1/m}$ close to $e^{V(s)}$, by (22). Therefore, almost surely on the event of non-extinction,

$$\liminf_{t\to\infty}\frac{1}{t}\log N_n(ns)\geq V(s)+\log d.$$

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