ANNIHILATION AND COALESCENCE ON BINARY TREES

ITAI BENJAMINI AND YURI LIMA

Abstract. An infection spreads in a binary tree $T_n$ of height $n$ as follows: initially, each leaf is either infected by one of $k$ states or it is not infected at all. The infection state of each leaf is independently distributed according to a probability vector $\mathbf{p} = (p_1, \ldots, p_{k+1})$. The remaining nodes become infected or not via annihilation and coalescence: nodes whose two children have the same state (infected or not) are infected (or not) by this state; nodes whose two children have different states are not infected; nodes whose only one of the children is infected are infected by this state. In this note we characterize, for every $\mathbf{p}$, the limiting distribution at the root node of $T_n$ as $n$ goes to infinity.

We also consider a variant of the model when $k = 2$ and a mutation can happen, with a fixed probability $q$, at each infection step. We characterize, in terms of $\mathbf{p}$ and $q$, the limiting distribution at the root node of $T_n$ as $n$ goes to infinity.

The distribution at the root node is driven by a dynamical system, and the proofs rely on the analysis of this dynamics.

1. Introduction and statement of results

Let $\Delta_k$ denote the $k$-dimensional simplex

\[
\Delta_k = \left\{ \mathbf{p} = (p_1, \ldots, p_{k+1}) \in \mathbb{R}^{k+1} : \sum_{i=1}^{k+1} p_i = 1 \text{ and } p_i > 0, \forall i \right\},
\]

let $T_n$ denote the binary tree of height $n$, and fix $\mathbf{p} \in \Delta_k$. The nodes of $T_n$ are infected by one of $k$ states $\{1, 2, \ldots, k\}$ or not infected as follows.

**Step 1.** Each leaf is infected i.i.d. according to $\mathbf{p}$:

\[
\mathbb{P}[\text{leaf is infected by } i] = p_i, \quad \mathbb{P}[\text{leaf is not infected}] = p_{k+1}. \quad (1.1)
\]

**Step 2.** A node adjacent to two leaves is infected or not according to the rules:

- (R1) if both leaves are not infected, the node is not infected.
- (R2) if both leaves are infected by the same state, the node is infected by it,
- (R3) if both leaves are infected by different states, the node is not infected,
- (R4) if only one of the leaves is infected, the node is infected by it.

**Step 3.** Repeat Step 2 to each level of $T_n$.

In other words, there is coalescence of infection if the states agree and annihilation if they disagree. Let $\mathbf{p}(n) \in \Delta_k$ denote the distribution of the state in the
root node of $T_n$, i.e.

$$P[\text{root node is infected by } i] = p_i(n) \quad \text{and} \quad P[\text{root node is not infected}] = p_{k+1}(n).$$

In this note, we characterize the limiting behavior of $p(n)$ as $n$ goes to infinity.

**Theorem 1.1.** For any $p \in \Delta_k$, $p(n)$ converges. Assume that $p_1 \geq \cdots \geq p_k$.

(a) If $p_1 = \cdots = p_k$, then $p(n)$ converges to $(\frac{1}{2k-1}, \ldots, \frac{1}{2k-1}, \frac{k-1}{2k-1})$.

(b) If $p_1 = \cdots = p_i > p_{i+1}$ for some $i \in \{1, \ldots, k-1\}$, then $p(n)$ converges to $(\frac{1}{2i-1}, \ldots, \frac{1}{2i-1}, 0, \ldots, 0, \frac{1}{2i-1})$, where the entry $\frac{1}{2i-1}$ repeats $i$ times.

Thus the asymptotic distribution of $p(n)$ is uniquely determined by $p$. This is expected: although Step 1 is random, all the others are deterministic. In particular, if the distribution of $p$ is the Lebesgue measure on $\Delta_k$, then one state will dominate almost surely.

We also analyze a variant of the model when $k = 2$. For a fixed $q \in (0, 1)$, consider the infection process with rules (R1), (R2), (R3) and (R4)’ if only one of the leaves is infected, the node is infected by it with probability $q$ and not infected with probability $1 - q$.

Let $p(n) \in \Delta_2$ denote the distribution of the state in the root node of $T_n$.

**Theorem 1.2.** For any $p \in \Delta_2$, $p(n)$ converges.

(a) If $q > 0.5$, then

$$\lim_{n \to \infty} p(n) = \begin{cases} (1, 0, 0) & \text{if } p_1 > p_2, \\ (0, 1, 0) & \text{if } p_1 < p_2, \\ \left(\frac{2q-1}{2q-1}, \frac{2q-1}{2q-1}, \frac{1}{2q-1}\right) & \text{if } p_1 = p_2. \end{cases}$$

(b) If $q = 0.5$, then

$$\lim_{n \to \infty} p(n) = \begin{cases} (p_1 - p_2, 0, 1 - p_1 + p_2) & \text{if } p_1 > p_2, \\ (0, -p_1 + p_2, 1 + p_1 - p_2) & \text{if } p_1 < p_2, \\ (0, 0, 1) & \text{if } p_1 = p_2. \end{cases}$$

(c) If $q < 0.5$, then $p(n)$ converges to $(0, 0, 1)$.
That is, for large $q$ the behavior is similar to that of Theorem 1.1 (the fixed point inside the simplex varies smoothly with $q$), there is a phase transition at $q = 0.5$, and if $q$ is small then the empty state dominates. We depict the phase spaces in Figure 1.

The model analyzed here is an instance of a wider setup, in which several types of particles move in a space and interact as follows: when particles of the same type meet they coalesce, while when particles of different types meet they annihilate each other. What is the distribution of the survivor particles, if any? We collect this and other variants of the model in Section 4.

Our setup is completely deterministic: the distribution at the root node satisfies a quadratic recursive equation, and the analysis of this dynamics establishes the results. Similar models in trees of larger branching number lead to recursive equations of higher degree. Not much is known about these systems.

Recursions appear naturally in the analysis of probabilistic processes on trees. See e.g. §4.2 of [2] and [4–7]. For a survey on more elaborate recursive equations, see [1].

The paper is organized as follows. In Section 2 we prove Theorem 1, in Section 3 we prove Theorem 2, and in Section 4 we make final comments and collect further questions.

2. Proof of Theorem 1.1

For simplicity of notation, let us assume that the possible states of the nodes on $T_n$ are $\{1, \ldots, k, k+1\}$: $1, \ldots, k$ represent the infections and $k+1$ represents the empty state (no infection). Given $i, j \in \{1, \ldots , k + 1\}$, $i \neq j$, the rules (R1)–(R4) are depicted in Figure 2.

Let $R_{n+1}$ denote the root node of $T_{n+1}$, and $R_{n+1}^1, R_{n+1}^2$ its two children. $R_{n+1}^1$ and $R_{n+1}^2$ are root nodes of two independent binary trees of height $n$, thus their
states are independent and distributed according to $p(n)$. By (R1)–(R4), the following recursions hold:

$$
\begin{align*}
\mathbf{p}_i(n + 1) &= \mathbf{p}_i(n)^2 + 2\mathbf{p}_i(n)\mathbf{p}_{k+1}(n), \quad i = 1, \ldots, k, \text{ and} \\
\mathbf{p}_{k+1}(n + 1) &= \mathbf{p}_{k+1}(n)^2 + 2 \sum_{1 \leq i < j \leq k} \mathbf{p}_i(n)\mathbf{p}_j(n).
\end{align*}
$$

Define the function $F = (F_1, \ldots, F_k, F_{k+1}) : \Delta_k \to \Delta_k$ by

$$
\begin{align*}
F_i(x_1, \ldots, x_{k+1}) &= x_i^2 + 2x_i x_{k+1}, \quad i = 1, \ldots, k, \text{ and} \\
F_{k+1}(x_1, \ldots, x_{k+1}) &= x_{k+1}^2 + 2 \sum_{1 \leq i < j \leq k} x_i x_j.
\end{align*}
$$

Thus $p(n) = F^n(p)$ for every $n \geq 1$.

(a) Assume that $\mathbf{p}_1 = \cdots = \mathbf{p}_k$. Clearly, $\mathbf{p}_1(n) = \cdots = \mathbf{p}_k(n)$ for every $n \geq 1$. So $\{\mathbf{p}_1(n)\}_{n \geq 1}$ satisfies the recursion

$$
\mathbf{p}_1(n + 1) = \mathbf{p}_1(n)^2 + 2\mathbf{p}_1(n)\{1 - k\mathbf{p}_1(n)\} = \{1 - 2k\}\mathbf{p}_1(n)^2 + 2\mathbf{p}_1(n).
$$

Define $f : (0, k^{-1}] \to \mathbb{R}$ by $f(x) = (1 - 2k)x^2 + 2x$. Thus $\mathbf{p}_1(n) = f^n(\mathbf{p}_1)$ for every $n \geq 1$.

**Lemma 2.1.** $\bar{x} = \frac{1}{2k-1}$ is a global attractor of $f$.

**Proof.** Note that (see Figure 3)

(i) $\bar{x}$ is the unique fixed point of $f$,

(ii) $f(0, k^{-1}] \subset (0, \bar{x}]$, and

(iii) $f|_{(0, \bar{x})} : (0, \bar{x}) \to (0, \bar{x})$ is strictly increasing.

![Figure 3. Graph of $f$.](image)

For every $x \in (0, k^{-1}]$, the sequence $\{f^n(x)\}_{n \geq 1}$ is increasing and converges to the unique fixed point $\bar{x}$ of $f$. □

By Lemma 2.1 $p(n)$ converges to $(\frac{1}{2k-1}, \ldots, \frac{1}{2k-1}, \frac{k-1}{2k-1})$. 


(b) Assume that 
\[ p_1 = \cdots = p_i > p_{i+1} \geq \cdots \geq p_k \]
for some \( i \in \{1, 2, \ldots, k-1\} \). We will prove that
\[
\lim_{n \to \infty} F^n(p) = \left( \frac{1}{2i-1}, \ldots, \frac{1}{2i-1} \right) \quad \text{for} \quad i = 2, \ldots, k-1.
\]

The proof is divided into a few lemmas.

**Lemma 2.2.** If \( x \in \Delta_k \) with \( x_1 \geq x_2, \ldots, x_k \), then \( F_{k+1}(x) \geq F_2(x) + \cdots + F_k(x) \).

**Proof.**

\[
F_{k+1}(x) - F_2(x) - \cdots - F_k(x) = x_{k+1}^2 + 2 \sum_{1 \leq i < j \leq k} x_i x_j - \sum_{i=2}^{k} (x_i^2 + 2x_i x_{k+1})
\]

\[
= x_{k+1}^2 - 2x_{k+1} \sum_{i=2}^{k} x_i + 2 \sum_{1 \leq i < j \leq k} x_i x_j - \sum_{i=2}^{k} x_i^2
\]

\[
= \left( x_{k+1} - \sum_{i=2}^{k} x_i \right)^2 - \left( \sum_{i=2}^{k} x_i \right)^2 + 2 \sum_{1 \leq i < j \leq k} x_i x_j - \sum_{i=2}^{k} x_i^2
\]

\[
= \left( x_{k+1} - \sum_{i=2}^{k} x_i \right)^2 - \sum_{i=2}^{k} x_i^2 - 2 \sum_{2 \leq i < j \leq k} x_i x_j
\]

\[
= \left( x_{k+1} - \sum_{i=2}^{k} x_i \right)^2 - \sum_{i=2}^{k} x_i^2 + \sum_{1 \leq i < j \leq k} x_i x_j
\]

and every term in the expression above is nonnegative. \( \square \)

**Lemma 2.3.** \( \{p_1(n) - p_{i+1}(n)\}_{n \geq 1} \) converges.

**Proof.** We have

\[
p_1(n+1) - p_{i+1}(n+1) = \{p_1(n)^2 + 2p_1(n)p_{k+1}(n)\} - \{p_{i+1}(n)^2 + 2p_{i+1}(n)p_{k+1}(n)\}
\]

\[
= \{p_1(n) - p_{i+1}(n)\} \{p_1(n) + p_{i+1}(n) + 2p_{k+1}(n)\},
\]

that is:

\[
p_1(n+1) - p_{i+1}(n+1) = \{p_1(n) - p_{i+1}(n)\} \{p_1(n) + p_{i+1}(n) + 2p_{k+1}(n)\}.
\]

(2.2)
By Lemma 2.2,
\[ p_1(n) + p_{i+1}(n) + 2p_{k+1}(n) > p_1(n) + 2p_{k+1}(n) \]
\[ \geq p_1(n) + \cdots + p_{k+1}(n) = 1, \]
so \( \{p_1(n) - p_{i+1}(n)\}_{n \geq 1} \) is a bounded and strictly increasing sequence. □

**Lemma 2.4.** \( \{p_{i+1}(n)\}_{n \geq 1}, \ldots, \{p_k(n)\}_{n \geq 1} \) all converge to zero.

**Proof.** Because \( p_{i+1}(n) \geq \cdots \geq p_k(n) \) for every \( n \geq 1 \), it is enough to prove that \( \{p_{i+1}(n)\}_{n \geq 1} \) converges to zero.

By equality (2.2), \( \{p_1(n) + p_{i+1}(n) + 2p_{k+1}(n)\}_{n \geq 1} \) converges to 1: otherwise, \( \{p_1(n) - p_{i+1}(n)\}_{n \geq 1} \) would be unbounded. Writing
\[ p_1(n) + p_{i+1}(n) + 2p_{k+1}(n) = 1 + \left( p_{k+1}(n) - \sum_{j=2, j \neq i+1}^{k} p_j(n) \right) =: 1 + y(n), \]
this means that \( \{y(n)\}_{n \geq 1} \) converges to zero. Now write
\[ z(n) = p_{k+1}(n) - \sum_{j=2}^{k} p_j(n). \] (2.3)

By Lemma 2.2, \( y(n) \geq z(n) \geq 0 \), so \( \{z(n)\}_{n \geq 1} \) also converges to zero. Consequently, the difference \( \{p_{i+1}(n) = y(n) - z(n)\}_{n \geq 1} \) converges to zero. □

Lemmas 2.3 and 2.4 imply that
\[ \lim_{n \to \infty} F^n(p) = (x, \ldots, x, 0, \ldots, 0, 1 - ix). \]
By continuity, \( x \in (0, i^{-1}] \) is a fixed point of \( f = f_i \) as defined in Lemma 2.1, i.e. \( x = \frac{1}{i^{1-i}} \). This concludes the proof of Theorem 1.1.

3. A VARIANT OF THE MODEL WHEN \( k = 2 \): PROOF OF THEOREM 1.2

Here, we fix a parameter \( q \in (0, 1) \) and consider the infection process with rules (R1)–(R3) and (R4)’. Like in the previous section, we denote the empty state by 3. The rules are depicted in Figure 4.
Although in each step the output is random, the distribution of the state in the root node is again driven by a dynamical system.

Let \( p \in \Delta_2 \), and let \( p(n) \in \Delta_2 \) denote the distribution of the state in the root node of \( T_n \). Let \( G = (G_1, G_2, G_3) : \Delta_2 \to \Delta_2 \) be

\[
\begin{align*}
G_1(x_1, x_2, x_3) &= x_1^2 + 2qx_1x_3 \\
G_2(x_1, x_2, x_3) &= x_2^2 + 2qx_2x_3 \\
G_3(x_1, x_2, x_3) &= x_3^2 + 2x_1x_2 + 2(1-q)x_1x_3 + 2(1-q)x_2x_3.
\end{align*}
\]

Thus \( p(n) = G^n(p) \) for every \( n \geq 1 \).

(a) \( q > 0.5 \): assume first that \( p_1 > p_2 \).

**Lemma 3.1.** If \( x \in \Delta_2 \) with \( x_1 > x_2 \), then \( G_3(x) > G_2(x) \).

*Proof.* \( G_3(x) - G_2(x) = (x_3^2 + 2x_1x_2) - (x_2^2 + 2x_2x_3) = (x_2-x_3)^2 + 2(x_1-x_2)x_2 \). \( \square \)

**Lemma 3.2.** \( \{p_3(n)\}_{n \geq 1} \) converges to zero.

*Proof.* We have

\[
p_1(n + 1) - p_2(n + 1) = \{p_1(n) - p_2(n)\} \{p_1(n) + p_2(n) + 2q p_3(n)\} = \{p_1(n) - p_2(n)\} \{1 + (2q-1)p_3(n)\}.
\]

Because \( \{p_1(n) - p_2(n)\}_{n \geq 1} \) is bounded and nonzero, the claim follows. \( \square \)

By Lemma 3.1 \( \{p_2(n)\}_{n \geq 1} \) also converges to zero, and so \( \{p(n)\}_{n \geq 1} \) converges to \((1, 0, 0)\). Analogously, if \( p_1 < p_2 \) then \( \{p(n)\}_{n \geq 1} \) converges to \((0, 1, 0)\).

Now assume that \( p_1 = p_2 \). In this case, \( \{p_1(n)\}_{n \geq 1} \) satisfies the recursion

\[
p_1(n + 1) = p_1(n)^2 + 2qp_1(n)\{1 - 2p_1(n)\} = (1 - 4q)p_1(n)^2 + 2qp_1(n).
\]

Define \( g : (0, 0.5) \to \mathbb{R} \) by \( g(x) = (1 - 4q)x^2 + 2qx \). Thus \( p_1(n) = g^n(p_1) \) for every \( n \geq 1 \).

![Figure 5. The graph of g.](image)

Arguing similarly to the proof of Lemma 2.1 \( g \) has a global attracting fixed point \( \frac{2q-1}{4q-1} \) (see Figure 5), so \( \{p(n)\}_{n \geq 1} \) converges to \( \left( \frac{2q-1}{4q-1}, \frac{2q-1}{4q-1}, 1 \right) \).
If \( q < 0.5 \): we have
\[
P_1(n + 1) = P_1(n)\{P_1(n) + 2qP_3(n)\} < P_1(n)\{P_1(n) + P_3(n)\} < P_1(n)
\]
so \( \{P_1(n)\}_{n \geq 1} \) is strictly decreasing. Analogously, \( \{P_2(n)\}_{n \geq 1} \) is strictly decreasing. In particular, these two sequences converge, and so does \( \{P(n)\}_{n \geq 1} \). By continuity, its limit \( \bar{p} = (\bar{p}_1, \bar{p}_2, \bar{p}_3) \in \Delta_2 \) satisfies
\[
\begin{aligned}
\bar{p}_1 &= \bar{p}_1(\bar{p}_1 + 2q\bar{p}_3) \\
\bar{p}_2 &= \bar{p}_2(\bar{p}_2 + 2q\bar{p}_3).
\end{aligned}
\]
If \( \bar{p}_1 \neq 0 \), then \( \bar{p}_1 + 2q\bar{p}_3 = 1 \), so
\[
1 = \bar{p}_1 + 2q\bar{p}_3 \leq \bar{p}_1 + \bar{p}_3 \leq \bar{p}_1 + \bar{p}_2 + \bar{p}_3 = 1,
\]
with equality only if \( \bar{p}_1 = 1 \). This cannot happen, because \( \bar{p}_1 \) is the limit of a strictly decreasing sequence. Thus \( \bar{p}_1 = 0 \), and analogously \( \bar{p}_2 = 0 \), so \( \{P(n)\}_{n \geq 1} \) converges to \((0, 0, 1)\).

(b) \( q = 0.5 \): as in (c), \( \{P_1(n)\}_{n \geq 1} \) and \( \{P_2(n)\}_{n \geq 1} \) are strictly decreasing, so \( \{P(n)\}_{n \geq 1} \) converges to some \( \bar{p} = (\bar{p}_1, \bar{p}_2, \bar{p}_3) \in \Delta_2 \) satisfying
\[
\begin{aligned}
\bar{p}_1 &= P_1(\bar{p}_1 + \bar{p}_3) \\
\bar{p}_2 &= P_2(\bar{p}_2 + \bar{p}_3).
\end{aligned}
\]
By the first equality,
\[
\bar{p}_1\bar{p}_2 = P_1(1 - \bar{p}_1 - \bar{p}_3) = 0. \tag{3.1}
\]

Now, note that
\[
P_1(n + 1) - P_2(n + 1) = \{P_1(n) - P_2(n)\}\{P_1(n) + P_2(n) + P_3(n)\}
= P_1(n) - P_2(n),
\]
so \( P_1(n) - P_2(n) = P_1 - P_2 \) for every \( n \geq 1 \). Passing to the limit, \( \bar{p}_1 - \bar{p}_2 = P_1 - P_2 \). This, together with equality \((3.1)\), implies
\[
\bar{p} = \begin{cases} 
(P_1 - P_2, 0, 1 - P_1 + P_2) & \text{if } P_1 > P_2, \\
(0, -P_1 + P_2, 1 + P_1 - P_2) & \text{if } P_1 < P_2.
\end{cases}
\]
If \( P_1 = P_2 \), then
\[
\bar{p}_1 = \bar{p}_1(\bar{p}_1 + \bar{p}_3) = P_1(1 - \bar{p}_1),
\]
i.e. \( \bar{p}_1 \) is a fixed point of the map \( x \mapsto x(1 - x) \). This implies that \( \bar{p} = (0, 0, 1) \), and the proof of Theorem \( 1.2 \) is complete.

4. Final comments

1. As remarked in the introduction, we can consider a wider class of models. Assume that particles, placed in the vertices of a graph, perform simple random walks independently, and they annihilate/coalesce when they meet, depending whether their states are different or not. What is the distribution of the survivor particles, if any?
For example, on the circle $\mathbb{R}/\mathbb{Z}$ place $2n + 1$ particles uniformly and independently. Each particle moves on $\mathbb{R}/\mathbb{Z}$ with a random independent speed, distributed according to the Gaussian $\mathcal{N}(0, 1)$. All particles move simultaneously and when two of them collide they annihilate each other. What is the speed of the remaining particle? Does it converge to zero as $n$ grows, or is there a nontrivial limiting distribution? Another variant is to allow the particles to perform an independent Brownian motion, each of them with an independent Gaussian diffusion constant.

Variants of our model can also be considered. Here we mention three of them. The first is to change the rules of annihilation/coalescence. Assume there are $k$ possible states $1, 2, \ldots, k$ and we are given a matrix $A = (a_{ij})_{1 \leq i, j \leq k}$ with $a_{ij} \in \{1, 2, \ldots, k\}$. At each step, the particles perform simple random walks independently and interact according to $A$: when a particle with state $i$ meets a particle with state $j$, they become a single particle with state $a_{ij}$.

The second variant is to consider annihilation/coalescence in a regular tree of degree $d$, $d \geq 3$, with rules similar to ours: nodes whose all $d$ children have the same state (infected or not) are infected (or not) by it; nodes with two children with different states are not infected; nodes whose some children are infected by a single state and the others are not infected are infected by it.

The third variant is to start with other measures on the initial configuration of the leaves rather than the product measure.

2. Sensitivity of iterated majority with random inputs was studied in [6]. It is of interest to consider noise sensitivity and the influence of leaves subsets in this context, including all the variants, as well.

3. There is no uniform rate of convergence in Theorems 1.1 and 1.2. As an illustration, we prove this for Theorem 1.1. Let $z(n)$ as in 2.3. By Lemma 2.2, $z(n)$ converges to zero. This convergence can be arbitrarily slow: by Lemma 2.2,

$$z(n) = z(n) + 2 \sum_{i=2}^{k} (p_i(n) - p_i(n))p_i(n) \geq z(n),$$

thus $z(n) \geq z(0)^2$. In particular, if $z(0) = 2^{-2^{n}}$, then $z(n) = 0.5$.

4. We would like to point out that the quadratic family appears in the proof of Theorem 1.2 but in a simple way: for each parameter there is a global attracting fixed point. It would be interesting to describe a set of rules for the model to force the quadratic family to appear with nontrivial parameters, e.g., parameters with more periodic points, or even parameters with a horseshoe. See [3] for a discussion on the quadratic family.

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Weizmann Institute of Science, Faculty of Mathematics and Computer Science, POB 26, 76100, Rehovot, Israel.

E-mail address: itai.benjamini, yuri.lima@weizmann.ac.il