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Invariant Measures for the Multitype Voter Model

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1. Introduction.

The voter model was introduced independently by Clifford and Sudbury [1] and by Holley and Liggett [2]. For this model, a complete description of all invariant measures and ergodic theorems were obtained in [2] and [3]. On the other hand, Spitzer [7] introduced a generalized voter model as a class of infinite systems with locally interacting components, and the same problems were discussed in Liggett and Spitzer [4].

In this paper, we study the multitype voter model which is described as follows. Let S be a countable set and p(x, y) the transition probability for an irreducible Markov chain on S. We regard S as a collection of voters, each having one of countably many possible positions on an issue. Every voter x waits an exponential time with parameter one and then, he chooses a voter y with probability p(x, y) and adopts the position of y. For a set of positions on an issue we take $\mathbb{Z}_{+} = \{0, 1, 2, \cdots\}$, since the structure of the set does not play an important role in our model.

In the case there are only two possible positions, it is a genuine voter model. Our model corresponds to the generalized voter model of Spitzer [7] whose parameter is particularly zero. This case is not treated in [4].

Our model is defined on a state space

$$X = (\mathbf{Z}_+)^S = \{ \eta : S \to \mathbf{Z}_+ \} .$$

Here we equip Z_+ with the discrete topology and X with the product topology. X is then a complete separable metric space. For $\eta \in X$ and $x \in S$, $\eta(x) \in Z_+$ represents the position of the voter x. So $\eta \in X$ is regarded as a configuration of positions of the voters. First we construct a Markov process on X describing the time evolution of our model. We do this by using a stochastic differential equation associated with Poisson random measures. Next we find all extremal invariant measures for this model and determine the domain of attraction of each of them. To do this, we make use of Shiga's method in [6], who discussed the continuous time multi-allelic stepping stone models which

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