

Extended Abstract

Modelling Two Dimensional Affected Regions by “Seca” Disease with Proximity Diagrams †

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Abstract: In this work we propose a mathematical model to determine the potentially propagation areas of the Mediterranean Quercus disease commonly referred to as “seca” in specific areas of Extremadura. To do it we will use optimal computational geometry algorithms based on proximity diagrams that permit to design a pathogen transmission map and to determine causing agents.

Keywords: phytophthora cinnamomi; proximity diagrams; computational

1. Introduction

The Mediterranean Quercus disease is characterized by progressive decay and death of individuals specially belonging to holm oak and cork oak species. Initially observed in the 80s, this disease was at first attributed to *Phytophthora cinnamomi* that was responsible for the death of chestnut trees throughout Spain. Nowadays, the sickness particularly affects the southwest of the Iberian Peninsula, and specifically the regions of Alentejo and Algarve in Portugal and Extremadura and Andalucía in Spain. The most damaged areas in the region of Extremadura are Sierra de San Pedro, the swampy zone of la Siberia and the Alagón and Tiétar valleys in Cáceres [1,2,3]. Recently, it has been tested that this affection is motivated by different agents without a clear pattern. Some of them are long-term predisposing factors that severely weaken the trees [4] as devastating pruning, pollution, insects, or changes in soil conditions, its composition and compaction [5] due to agricultural activity, livestock farming, or actual climatic setting that influences to the erosion, the temperature and variations in annual rainfall. Also, some geographical conditions as altitude, orography and orientation have been observed as conditioning agents [3]. Others, that finally cause the death of the trees, correspond to the presence of pathogens as *Phytophthora cinnamomi*. Although the diseased trees do not follow an obvious spatial disposal, it seems that generally are allocated in groups and close to ponds, streams, reservoirs or standing water [1,3]. Some mitigation strategies depending on the predominant responsible agent of the decay have been proposed [3,4] to control the pathogen invasion. Following these premises, our aim here is to develop a pathogen invasion model to delimit the sensible predispose invasion zones of trees with possible decline symptoms in order to implement those specific measures depending on the causing agent. To do it, we construct Voronoi diagrams of the region using the sets of the seca focus and water channels locations as generators of the diagrams. Using proper numerical software we display some subregions of the tessellation, called as Voronoi cells, that contains exactly one generator and that represent all points that are closer to this local focus than any other. All points that are closer to the Voronoi diagrams display the regions of ‘attraction’ for each agent and allow us identified its

susceptible influence region and also safe areas. We also analyze the interaction of both factors in the context disease.

Additionally, we stress the interest of this numerical simulation within actual pathogen transmission map since it can be applied to different agents of transmissions by considering their locations as generators of the respective diagrams.

2. Materials and Methods

Voronoi diagrams have been revealed as an extremely graphical tool for the solution of proximity problems and constitute the inspiration of an amount of applications (see [6], [7]). Now, we how to construct this diagram and its principal properties that help us to analyze the disease propagation.

Definition 1. Given two point $p, q \in R^2$, $p = (p_x, p_y)$, $q = (q_x, q_y)$, the Euclidean distance is defined as

$$dis(p, q) = \sqrt{\{(p_x - q_x)^2 + (p_y - q_y)^2\}}$$

Definition 2. Let $P = \{p_1, p_2, \dots, p_n\}$ a set of n different points in the plane, in the following denoted by “sites”. We define the Voronoi diagram of p , and we will denote by $Vor(P)$ as the subdivision of the plane into n cells, one for each site in p , with the property that a point q lies in the cell corresponding to a site p_i , if and only if

$$dist(q, p_i) < dist(q, p_j), \forall p_j \in P \text{ with } j \neq i.$$

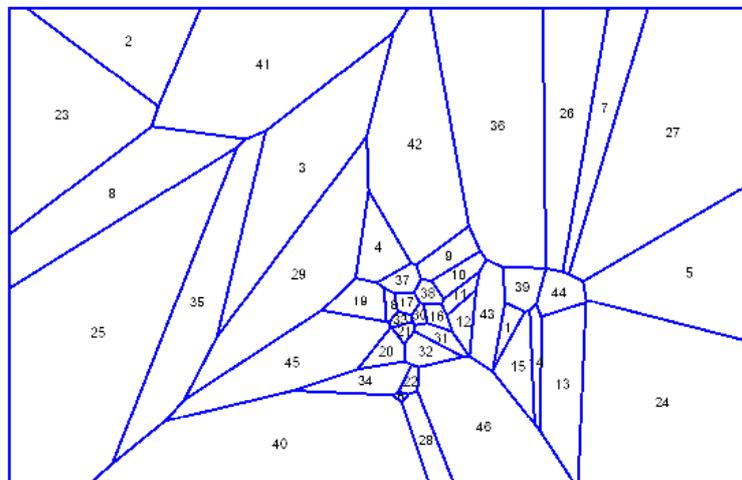
The corresponding cell to a site p_i will be denoted by $v(p_i)$ and it constitutes the set of points on the plane that are closer to p_i than other site.

Our interest in this paper yields in the geometric application to the model above. The assumptions in the pattern follows from consider all the focus of “seca” in Extremadura as the set of sites $P = \{p_1, p_2, \dots, p_n\}$ in our diagram and therefore, to induce a subdivision of the total area into regions that will represent all the nearest points of Extremadura to each focus (the sites in our model).

As a first step, following [8] and using the spatial reference system UTM29N, ETRS89—EPSG:25829, we extracted the coordinates of 46 locations of Holm oaks that are diagnosed with the *Phytophthora cinnamomi* disease. Therefore, following Definition 1, we have a set of 46 sites

$$P = \{p_1, p_2, \dots, p_n\} \text{ with } n = 46.$$

Next, using numerical software [9] we construct the corresponding Voronoi diagram $Vor(P)$ that we show in Figure 2 for all the “Sierra de San Pedro”. The sites (focus) in red and the vertices (in green) of the diagram are also shown in Figure 1.



(a)

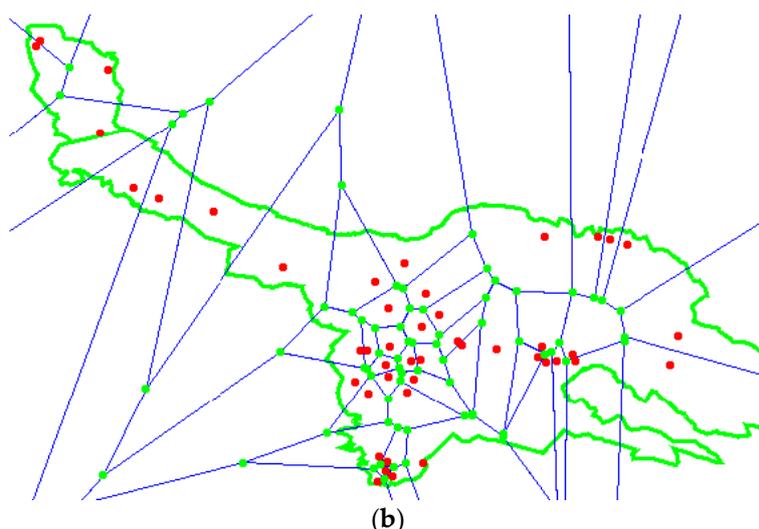


Figure 1. (a) Vor(P) and Voronoi regions (cell) in “Sierra de San Pedro” obtained using the “seca” focus as generators (sites) of the diagram. They are labeled with numbers from 1 to 46. The townships where they were prescribed are included in Table 1. (b) Voronoi regions, sites (Phytophthora cinnamomi focus in Holm oak) and Voronoi vertices of Vor(P) overprinted on the affected areas.

Table 1. Number of focus of the disease and places where they are located. The corresponding label employed in the diagram (see Figure 1) are also shown. Information on the focus and their location has been extracted from [8].

Thownship	Number of Focus	Labels
Santiago de Alcántara	2	2, 23
Membrío	1	41
Valencia de Alcántara	3	8, 25, 35
San Vicente de Alcántara	2	3, 29
Alburquerque	21	4, 42, 37, 9, 10, 11, 12, 13, 38, 19, 8, 17, 33, 30, 16, 45, 21, 31, 20, 32, 34, 22, 6, 40, 28
Villar del Rey	4	10, 6, 28, 46
Aliseda	1	36
Cáceres	12	26, 7, 27, 43, 39, 1, 15, 14, 44, 13, 5, 24

3. Results and Discussion

In this work we employ the versatile geometric structure of Voronoi diagrams to derive information about the safe and sick areas (see Figure 2), where they are located and how many hectares do they measure (see Figure 3). We also can guess possible agents that favor the transmission and therefore to design a map to determine the potentially propagation areas of the Mediterranean Quercus disease commonly referred to as “seca” in the Sierra the San Pedro in Extremadura. Namely, using different tools that can be derived from these kind of diagrams, we conclude that the south of the zone next of Alburquerque is a risk area and that the presence of water constitute a possible agent that contributes to the presence and the propagation of the disease.

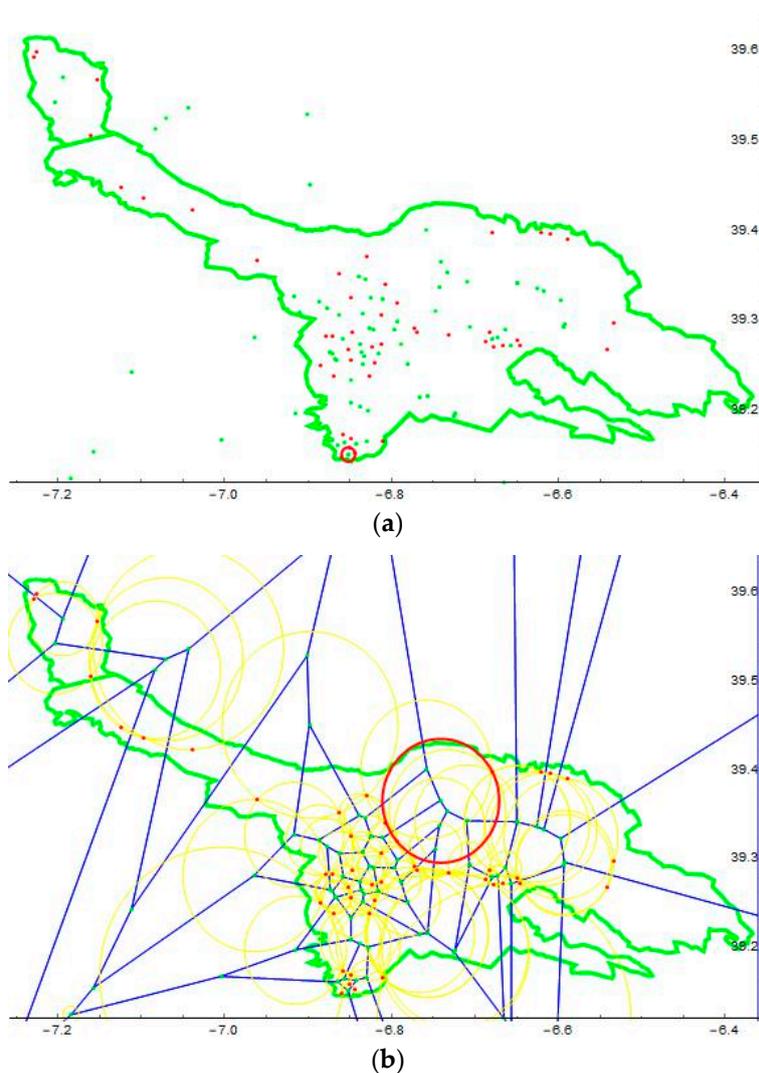


Figure 2. Location of the region with the greatest risk of infection ((a) focus 6) and the least one ((b) focus 43).

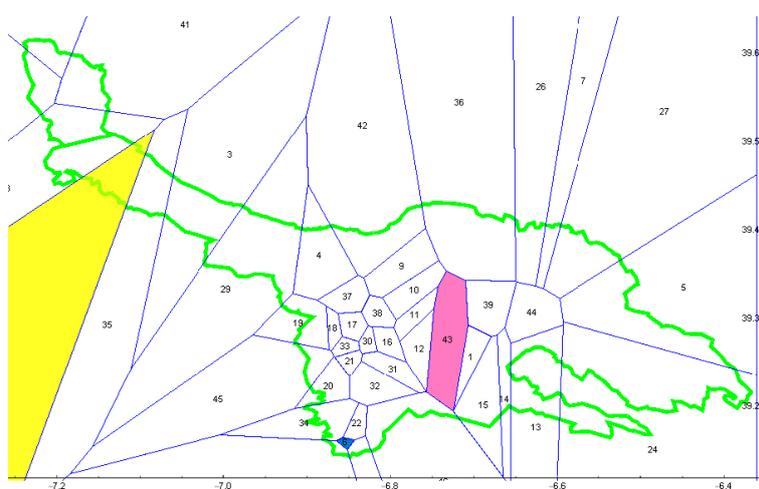


Figure 3. In yellow, Voronoi cell with the largest area (outside our area of interest). In blue the smallest one (26.2116 Ha) and in pink the largest one inside our study area (891.306 Ha).

Author Contributions: Both authors have been conceived the need to address the problem using other techniques to those already existing and analyzed its benchmark. Calvo performed the experiments and wrote the paper. Both authors discussed the results obtained by contrasting them with reality.

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Conflicts of Interest: The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

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