Uncovering the Spread of Chagas Disease in Argentina and Mexico

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Abstract—Chagas disease is a neglected disease, and information about its geographical spread is very scarse. We analyze here mobility and calling patterns in order to identify potential risk zones for the disease, by using public health information and mobile phone records. Geolocalized call records are rich in social and mobility information, which can be used to infer whether an individual has lived in an endemic area. We present two case studies in Latin American countries. Our objective is to generate risk maps which can be used by public health campaign managers to prioritize detection campaigns and target specific areas. Finally, we analyze the value of mobile phone data to infer long-term migrations, which play a crucial role in the geographical spread of Chagas disease.

I. INTRODUCTION

Chagas disease is a neglected tropical disease of global reach, spread mostly across 21 Latin American countries. Caused by the *Trypanosoma cruzi* parasite, its transmission occurs mostly in the American endemic regions via the *Triatoma infestans* insect family. In recent years, due to the globalization of migrations, the disease has become an issue in other continents as well [11], particularly in countries that receive Latin American immigrants such as Spain and the United States.

A crucial characteristic of the infection is that it may last 10 to 30 years in an individual without presenting symptoms [9], which greatly complicates effective detection and treatment. Long-term human mobility (particularly seasonal and permanent rural-urban migration) thus plays a key role in the geographical spread of the disease [1].

In this work, we discuss the use of Call Detail Records (CDRs) for the analysis of mobility patterns and the detection of potential risk zones of Chagas disease in two Latin American countries [5], [10]. We generate predictions of population movements between different regions, providing a proxy for the epidemic spread. We present two case studies, in Argentina and in Mexico, using data provided by mobile phone companies from each country.

II. CHAGAS DISEASE IN ARGENTINA AND MEXICO

A. Endemic Zone in Argentina

The *Gran Chaco*, situated in the northern part of the country, is endemic for the disease [8]. The ecoregion's low socio-

demographic conditions further support the parasite's lifecycle, where domestic interactions between humans, triatomines and animals foster the appearance of new infection cases, particularly among rural and poor areas. This region is considered as the endemic zone E_Z in the analysis described in Section IV.

Recent national estimates indicate that between 1.5 and 2 million individuals carry the parasite, with more than seven million exposed. National health systems face many difficulties to effectively treat the disease. In Argentina, less than 1% of infected people are treated (the same statistic holds at the world level). Even though governmental programs have been ongoing for years now, data on the issue is scarce or hardly accessible.

B. Endemic Zone in Mexico

The Mexican epidemic area [3] covers most of the South region of the country and includes the states of Jalisco, Oaxaca, Veracruz, Guerrero, Morelos, Puebla, Hidalgo and Tabasco. This region is considered as the endemic zone E_Z for the Mexican case.

Despite the lack of official reports, an estimate of the number of *Trypanosoma cruzi* infections by state in the country indicates that the number of potentially affected people in Mexico is about 5.5 million [2]. In recent years there has been a focus on treating the disease with two available medications, benznidazole or nifurtimox, with less than 0.5% of infected individuals receiving treatment in Mexico [7].

People from endemic areas tend to migrate to the industrialized cities of the country, mainly Mexico City, in search for jobs [6]. Therefore, the study of long-term mobility is crucial to understand the geographical spread of the Chagas disease in Mexico.

III. MOBILE PHONE DATA SOURCES

Our data source is anonymized traffic information from two mobile operators. The Argentinian dataset contains CDRs collected over a period of 5 consecutive months. The Mexican dataset contains CDRs for a period of 24 consecutive months.

For our purposes, each record is represented as a tuple $\langle i,j,t,d,l \rangle$, where user i is the encrypted caller, user j is the encrypted callee, t is the date and time of the call, d

is the direction of the call (incoming or outgoing), and l is the location of the tower that routed the communication. The dataset does not include personal information from the users.

We aggregate the call records for a five month period into an edge list $(n_i, n_j, w_{i,j})$ where nodes n_i and n_j represent users i and j respectively, and $w_{i,j}$ is a boolean value indicating whether those two users have communicated during the five month period. This edge list represents our communication graph $\mathcal{G} = \langle \mathcal{N}, \mathcal{E} \rangle$ where \mathcal{N} denotes the set of nodes (users) and \mathcal{E} the set of communication links. We note that only a subset \mathcal{N}_C of nodes in \mathcal{N} are clients of the mobile operator. Since geolocation information is available only for users in \mathcal{N}_C , in the analysis we considered the graph $\mathcal{G}_C = \langle \mathcal{N}_C, \mathcal{E}_C \rangle$ of communications between clients of the operator.

IV. RISK MAPS FOR CHAGAS DISEASE

A. Methodology for Risk Map Generation

The first step is to determine the area where each user lives. For each user $u \in \mathcal{N}_C$, we compute its *home antenna* H_u as the antenna in which user u spends most of the time during weekday nights [4]. The users such that H_u is located in the endemic zone E_Z are considered the *residents of* E_Z .

The second step is to find users highly connected with the residents of E_Z . To do this, we compute the list of calls for each user and then determine his set of neighbors in the social graph \mathcal{G}_C . For each resident of the endemic zone, we tag all his neighbors as *vulnerable*.

The third step is to aggregate this data by antenna. For every antenna a, we compute: the total number of residents N_a , the total number of residents which are vulnerable V_a , the total volume of outgoing calls C_a , and the number of outgoing calls whose receiver lives in the endemic area VC_a .

We generated heatmaps to visualize these antenna indicators, overlapping these heatmaps with political maps. Each antenna is represented by a circle whose area depends on the population living in the antenna N_a and whose color depends of the fraction V_a/N_a of vulnerable users living there. We used two filtering parameters: each antenna is plotted if its fraction of vulnerable users is higher than β , and if its population is bigger than m_v .

B. Results and Observations

Fig. 1 shows the risk maps for Argentina, generated with two values for the β parameter and fixing $m_v=50$ inhabitants per antenna. After filtering with $\beta=0.15$, we see that large portions of the country harbor potentially vulnerable individuals. Namely, Fig. 1(b) shows antennas where more that 15% of the population has social ties with the endemic region E_Z .

Advised by Mundo Sano Foundation's experts, we then focused on areas whose results were unexpected to the epidemiological experts. Focused areas included the provinces of Tierra del Fuego, Chubut, Santa Cruz and Buenos Aires, with special focus on the metropolitan area of Greater Buenos Aires whose heatmap is shown in Fig. 2.

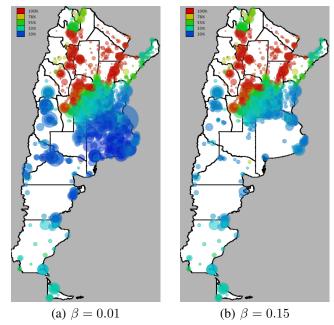


Figure 1. Risk map for Argentina, filtered according to β .

High risk antennas were separately listed and manually located in political maps. This information was made available to the Mundo Sano Foundation collaborators who used it as an aid for their campaign planning and for the education of community health workers.

V. PREDICTION OF LONG-TERM MIGRATIONS

In this section, we describe our work on the prediction of long-term mobility. The CDR logs available in the Mexican dataset span 24 months, from January 2014 to December 2015, making them suitable for this study.

We divide the available data into two distinct periods: T_0 , from January 2014 to July 2015, considered as the "past" in

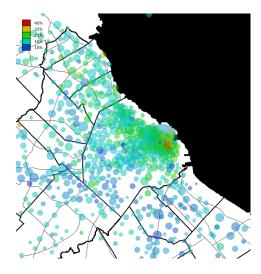


Figure 2. Risk map for the metropolitan area of Buenos Aires, filtered with $\beta=0.02$.

our experiment; and T_1 , from August 2015 to December 2015, considered as the "present". Knowing which users live in the endemic region E_Z and how they communicate during period T_1 , we want to infer whether they lived in E_Z in the past (period T_0).

A. Model Features

The features constructed reflect calling and mobility patterns. Each week is divided into 3 time periods: (i) weekday from Monday to Friday, on working hours (8hs to 20hs); (ii) weeknight from Monday to Friday, between 20hs and 8hs of the following day; and (iii) weekend is Saturday and Sunday. The model consists of the following features, which can be classified in 4 categories:

- 1) Used and home antennas: For each user $u \in \mathcal{N}_C$, we register the top ten most used antennas, considering all calls or only calls made during the *weeknight* period. Users were tagged as 'endemic' if their home antenna is in the endemic zone E_Z and 'exposed' if any of the top ten antennas is in the risk area.
- 2) Mobility diameter: The user's logged antennas define a convex hull in space and the radius of the hull is taken as the mobility diameter. We generate two values, considering (i) all antennas and (ii) only the antennas used during the weeknight.
- 3) Communications graph: We enrich the social graph \mathcal{G}_C built from the CDRs. For each edge $\langle n_i, n_j \rangle \in \mathcal{E}_C$, we gather the number of calls exchanged, the sum of call durations (in seconds), the direction (incoming or outgoing), segmented according to the periods weekday, weeknight, and weekend.

Since the samples in our dataset are users, we aggregate these variables by grouping interactions at the user level. The combination of different variables amounts to a total of 130 features per user.

We also compute the user's degree and the total count of endemic neighbors, labeling each user i as *vulnerable* whenever he has an edge with a user j who lives in the endemic region E_Z .

4) Validation data: We perform an analysis similar to the home antenna detection previously described, but considering the time period T_0 (from January 2014 to July 2015), in order to determine the home antenna of users during T_0 .

B. Supervised Classification

We used most common techniques for this task: Support Vector Machines, Random Forest, Logistic Regression, and Multinomial Naive Bayes. The data was split into 70% for training and 30% for testing.

The Multinomial Bayes classifier has a linear time complexity, and thus serves as a fast benchmark. Support Vector Machines (SVM) and Logistic Regression performed better than Multinomial Bayes. We tuned the standard hyperparameters: L2-penalty regularization for Logistic Regression and kernel bandwidth for the Gaussian Kernel SVM. Both learning routines were executed in parallel and in each iteration 5% of the training set was sampled for cross validation. The best model was a Logistic Regression Classifier with an L2-penalty

value of 0.01. The scores obtained by the selected model on the out-of-sample set are F1-score: 0.964537; accuracy: 0.980670; AUC: 0.991593; precision: 0.970838; recall: 0.958316.

High values across all scoring measures are achieved. These results can be explained by the fact that communication and mobility patterns are in essence highly correlated across time periods. In this case, a user being endemic in T_1 is correlated to being endemic in T_0 , and the same holds with a user's interaction with vulnerable neighbors during T_1 .

VI. CONCLUSION

The heatmaps shown in Section IV expose an expected "temperature" descent from the endemic regions outwards. We also found out communities atypical compared to their neighboring region, which stand out for their strong communication ties with the endemic region E_Z . The detection of these communities is of great value to health campaign managers, providing them tools to target specific areas and prioritize resources and calls to action more effectively.

In Section V, we tackled the problem of predicting long-term migrations. In particular, we showed that it is possible to use the mobile phone records of users during a bounded period of time in order to predict whether they have lived in the endemic zone E_Z in a previous time frame.

To conclude, we showed here the value of generating risk maps in order to prioritize effectively detection and treatment campaigns for the Chagas disease. The results stand as a proof of concept which can be extended to other countries with similar characteristics.

REFERENCES

- R. Briceño-León. Chagas disease in the Americas: an ecohealth perspective. Cadernos de Saúde Pública, 25:S71–S82, 2009.
- [2] A. Carabarin-Lima, M. C. González-Vázquez, O. Rodríguez-Morales, L. Baylón-Pacheco, J. L. Rosales-Encina, P. A. Reyes-López, and M. Arce-Fonseca. Chagas disease (american trypanosomiasis) in Mexico: an update. *Acta tropica*, 127(2):126–135, 2013.
- [3] A. Cruz-Reyes and J. M. Pickering-López. Chagas disease in Mexico: an analysis of geographical distribution during the past 76 years-A review. *Memorias do Instituto Oswaldo Cruz*, 101(4):345–354, 2006.
- [4] B. C. Csáji, A. Browet, V. Traag, J.-C. Delvenne, E. Huens, P. Van Dooren, Z. Smoreda, and V. D. Blondel. Exploring the mobility of mobile phone users. *Physica A: Statistical Mechanics and its* Applications, 2012.
- [5] J. de Monasterio, A. Salles, C. Lang, D. Weinberg, M. Minnoni, M. Travizano, and C. Sarraute. Analyzing the spread of Chagas disease with mobile phone data. In 2016 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM). IEEE, aug 2016.
- [6] C. Guzmán-Bracho. Epidemiology of Chagas disease in Mexico: an update. TRENDS in Parasitology, 17(8):372–376, 2001.
- [7] J. M. Manne, C. S. Snively, J. M. Ramsey, M. O. Salgado, T. Bärnighausen, and M. R. Reich. Barriers to treatment access for Chagas disease in Mexico. *PLoS Negl Trop Dis*, 7(10):e2488, 2013.
- [8] OPS. Mapa de Transmisión vectorial del Mal de Chagas. Organizacion Panamericana de la Salud, 2014.
- [9] A. Rassi and J. M. de Rezende. American trypanosomiasis (Chagas disease). *Infectious disease clinics of North America*, 26(2):275–291, 2012.
- [10] C. Sarraute, C. Lang, J. de Monasterio, and D. Weinberg. Descubriendo Chagas con big data. In XVII Simposio Internacional sobre Enfermedades Desatendidas, Aug 2015.
- [11] G. A. Schmunis and Z. E. Yadon. Chagas disease: a Latin American health problem becoming a world health problem. *Acta tropica*, 115(1):14–21, 2010.