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# Some approaches of modeling geographical Chagas disease expansion's by applying orthogonal polynomials, integrodifference equations and agent-based simulations.

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## Abstract:

Chagas disease is a potentially fatal disease that affects 10 to 12 million people worldwide and is responsible for about 50 000 deaths per year. It is caused by a flagellated parasite called *Tripanosoma Cruzi* (*T.Cruzi*).

The main transmission mode of the disease is based on the biological system: parasite (*T.Cruzi*)-vector (triatominae)-host (mammals). This complex system is considered as: (1) an epidemiological one if the interest is on the absence or presence of *T.Cruzi*; (2) a population's ecology system if the study is on population dynamics of vectors; (3) or both types at the same time. In addition, if the spatial dispersal of the parasite encompasses an area of human habitation, the transmission is said to be domestic. Otherwise, it is sylvatic (transmission in a domain like the forest).

These different approaches allow the application of various mathematical tools. In the case of sylvatic transmission, we present, a first model, via the ecology of populations, by application of orthogonal polynomials [1], then an epidemiological one by application of integrodifference equations [2] and a third one by application of agent-based simulations [3].

**Keywords:** Chagas disease, population dynamics, orthogonal polynomials, integrodifference equations, agent-based model.

## References

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