INSTAR: simulating the biological cycle of a forest pest in Mediterranean pine stands

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The pine processionary moth (Thaumetopoea pityocampa) is a typically Mediterranean forest pest feeding on pine needles during its larval stages. The outbreaks of this pest cause important landscape impacts and public health problems (i.e. larvae are very urticant). Larvae feed during winter months and cold temperature is the main limiting factor in their development. Therefore, rising temperatures are thought to benefit this species. Indeed, observations suggest that outbreaks are becoming more frequent and populations are shifting uphill.

The objective of this work is to simulate the biological cycle of T. pityocampa to make predictions about where and when outbreaks will occur. Thus, we have created a model called INSTAR that will help to identify hotspots and foresee massive defoliation episodes. This will enhance the information available for the control of this pest.

INSTAR is an Agent-Based Model, which allows the inclusion of important characteristics of the system: emergence, feedback (i.e. interaction between agents and their environment), adaptation (i.e. decision based on the mentioned interactions) and path dependence (i.e. possibilities at one time point are determined by past conditions). These characteristics arise from a set of functions simulating pine growth, processionary development, mortality and movement. These functions are easily extrapolable to other similar biological processes and therefore INSTAR aims at serving of example for other forest pest models.

INSTAR is the first comprehensive approach to simulate the biological cycle of T pityocampa. It simulates the pest development in a given area, from which elevation and pine trees are considered. Moreover, it is also a good example of integrating environmental information into a population dynamic model: meteorological variables and soil moisture are obtained from a hydrological model (WiMMed, Herrero et al. 2009) executed for the area of interest. These variables are the inputs of the model, which feed the functions that simulate the processionary life cycle.

Model's executions in two different areas and for relatively long time frames (1993-2014 and 2000-2014) yield relevant information about the biological cycle of the forest pest: the simulated peaks of larvae are followed by minimal values of pine biomass and pine infections are more abundant at the edge of the stands. Moreover, emerging patterns such as denso-dependency can be observed.

To sum up, INSTAR is a promising tool for modeling T. pityocampa population dynamics. The obtained model will help to improve the decision making process regarding the control of the forest pest. Moreover, its simple structure of functions will facilitate the design of new models simulating other forest pests.