Parameterization and sensitivity analysis of a honey bee colony dynamics model for neonicotinoid exposure events using Markov Chain Monte Carlo methods

Jeffrey M. Minucci  
ORISE at U.S. EPA, jminucci2@gmail.com

Robert Curry  
Crystal River Consulting

Gloria DeGrandi-Hoffman  
USDA Agricultural Research Service

Kris Garber  
U.S. EPA, Office of Pesticide Programs

Reed M. Johnson  
The Ohio State University

See next page for additional authors

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Presenter/Author Information
Jeffrey M. Minucci, Robert Curry, Gloria DeGrandi-Hoffman, Kris Garber, Reed M. Johnson, Andrew Kanarek, Chia-Hua Lin, and Thomas S. Purucker
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Jeffrey M. Minucci, Robert Curry, Gloria DeGrandi-Hoffman, Kris Garber, Reed Johnson, Andrew Kanarek, Chia Lin, S. Thomas Purucker

a Oak Ridge Institute for Science and Education at U.S. EPA (Minucci.Jeffrey@epa.gov)
b Crystal River Consulting (stratpilot@gmail.com)
c USDA Agricultural Research Service (Gloria.Hoffman@ars.usda.gov)
d U.S. Environmental Protection Agency (Garber.Kristina@epa.gov, Kanarek.Andrew@epa.gov, Purucker.Tom@epa.gov)
e The Ohio State University (johnson.5005@osu.edu, lin.724@osu.edu)

Abstract: Honey bee (Apis mellifera) colony losses have increased in recent decades in both Europe and North America. While multiple stressors to honey bee colonies appear to be driving this decline (including disease, nutrition, genetics), direct exposure to pesticides has been identified as a factor leading to increased bee declines. The simulation model VarroaPop is currently being modified by the USDA and USEPA to predict honey bee hive dynamics in response to pesticide exposure. However, applying this model to pesticides is complicated due to a lack of parameterization information from the supporting literature for many variables, especially those related to in-hive pesticide dynamics. Here, we utilize data from a field study which measured residues of several neonicotinoid insecticides in pollen and tracked population dynamics of exposed hives to improve our estimation of colony simulation model parameters relevant to VarroaPop and the new model components related to pesticides. We use Markov Chain Monte Carlo methods to sample the probability distribution of model parameters and examine the likelihood of each parameter combination, given the field-derived population data. Through this procedure, we obtain posterior distributions which represent the most likely parameter values given a realistic neonicotinoid exposure scenario. We use these pesticide-optimized parameter distributions to run a global sensitivity analysis for the updated posteriors in order to contrast with a sensitivity analysis based on the priors. This helps determine what factors are most important in driving hive success or failure following exposure events.

Keywords: Apis mellifera; pesticides; neonicotinoids; sensitivity analysis; Markov Chain Monte Carlo