Subject: Gene Drive Breakout Group - HexSim Follow-up
From: "Reichman, Jay" <Reichman.Jay@epa.gov>
Date: 5/22/2017 6:22 PM
To: Sarah Carter <carter@sciencepolicyconsulting.com>, "Wegrzyn, Renee" <renee.wegrzyn@darpa.mil>, "esvelt@mit.edu" <esvelt@mit.edu>, "Geoff.Hosack@data61.csiro.au" <Geoff.Hosack@data61.csiro.au>, Royden Saah <royden.saah@islandconservation.org>, "Dass, Brinda" <Brinda.Dass@fda.hhs.gov>, Camilla Beech <cambeaconsults@gmail.com>, "Lunshof, Jeantine E" <jelunshof@genetics.med.harvard.edu>, Jason Delborne <jadelbor@ncsu.edu>, "Tountas, Karen (FNIH) [T]" <ktountas@fnih.org>, "Lance, Richard F ERDC-RDE-EL-MS CIV" <Richard.F.Lance@erdc.dren.mil>
CC: "Schumaker, Nathan" <Schumaker.Nathan@epa.gov>

Gene Drive Breakout Group,
During our discussions, I described the HexSim platform for spatially-explicit, individual-based models, and several people showed some interest in learning more. HexSim has been developed by Nathan Schumaker (CCed above) here at the US EPA, Western Ecology Division. The HexSim website can be accessed at: http://www.hexsim.net/

I think that HexSim could be a very useful tool for evaluating/comparing dynamics of Gene Drive release scenarios. See what you think, and feel free to contact Nathan to ask questions.

Jay R.

****

Jay R. Reichman, Ph.D.
Ecologist
U.S. Environmental Protection Agency
Office of Research & Development
Western Ecology Division
200 SW 35th St
Corvallis, OR 97333
Office 541-754-4643
****