

Subject: Re: Gene Drive Breakout Group - HexSim Follow-up

From: Camilla Beech <cambeaconsults@gmail.com>

Date: 5/23/2017 3:46 AM

To: "Dass, Brinda" <Brinda.Dass@fda.hhs.gov>, "Geoff.Hosack@data61.csiro.au" <Geoff.Hosack@data61.csiro.au>, Jason Delborne <jadelbor@ncsu.edu>, "Lance, Richard F ERDC-RDE-EL-MS CIV" <Richard.F.Lance@erdc.dren.mil>, "Lunshof, Jeantine E" <jelunshof@genetics.med.harvard.edu>, "Reichman, Jay" <Reichman.Jay@epa.gov>, Royden Saah <royden.saah@islandconservation.org>, Sarah Carter <carter@sciencepolicyconsulting.com>, "Tountas, Karen (FNIH) [T]" <ktountas@fnih.org>, "Wegrzyn, Renee" <renee.wegrzyn@darpa.mil>, "esvelt@mit.edu" <esvelt@mit.edu>
CC: "Schumaker, Nathan" <Schumaker.Nathan@epa.gov>

Many thanks

Best wishes

Camilla

On Mon, 22 May 2017 at 23:22, Reichman, Jay <Reichman.Jay@epa.gov> wrote:

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

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Camilla Beech

Director

CAMBEA CONSULTING LTD

t: +44 (0)7811 486410