# Close-kin mark-recapture methods to estimate demographic parameters of mosquitoes



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### Talk outline

- 1. Overview of research program
- 2. Review of malaria & mosquito modeling work
- 3. Application of close-kin markrecapture methods to mosquito populations
- 4. Opportunities for collaboration



#### Mathematical modeling of infectious diseases





#### Mathematical modelling of malaria



#### What do you think the $R_0$ for malaria is?



#### Basic reproductive number, R<sub>0</sub>, for malaria



 $R_0 =$  $R_{0,H \rightarrow V}$ x $R_0$ Average number of mosquitoesAverage numinfected by a typical infectious personinfected by a typical

 $R_{0,V \rightarrow H}$ Average number of people infected by a typical infectious mosquito

#### Basic reproductive number, R<sub>0</sub>, for malaria



• Smith DL, McKenzie FE, Snow RW, Hay SI (2007) PLoS Biology 5: e42

#### Why we need new malaria control tools

#### Fig. 8.1.

Comparison of global progress in malaria a) case incidence and b) mortality rate, considering two scenarios: current trajectory maintained (blue) and GTS targets achieved (green) *Source: WHO estimates*.



#### • World Health Organization (2023) 2023 World Malaria Report

#### Current interventions are not sufficient



• Walker PGT, Griffin JT, Ferguson NM, Ghani AC (2016) Lancet Global Health

#### Integrated vector management



Kiware SS, Chitnis N, Tatarsky A, Wu SL et al. (2017) PLoS ONE

#### Gene drive strategies for mosquito control





• Raban R, Marshall JM et al. (2023) Annual Review of Genetics

#### Predator Free 2050



Stas Kulesh / Getty Images

#### SCIENCE

#### NEW ZEALAND'S WAR ON RATS COULD CHANGE THE WORLD

The nation wants to eradicate all invasive mammal predators by 2050. Gene-editing technology could help—or it could trigger an ecological disaster of global proportions.

By Ed Yong



Esvelt KM, Gemmell NJ (2017) PLoS Biology

# Modeling needs for gene drive mosquito projects



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Raban R, Marshall JM et al. (2023) Annual Review of Genetics

# Mosquito gene drive explorer model



• Wu SL, Bennett JB, Sánchez HM et al. (2021) PLoS Computational Biology

#### Inheritance models



A. Inheritance



• Carballar-Lejarazú R, Dong Y, Pham TB, Tushar T et al. (2023) PNAS

#### Mosquito life history models



• White MT, Griffin JT, Churcher TS et al. (2011) Parasites & Vectors

#### Landscape models



• Wu SL, Bennett JB, Sánchez HM et al. (2021) PLoS Computational Biology

# Epidemiology models



• Griffin JT, Hollingsworth DT, Okell LC, Churcher TS, White M et al. (2010) PLoS Medicine 7: e1000324

#### Gene drive spatial simulation in São Tomé

#### Close-kin mark-recapture to estimate dispersal





• Williamson DH, Harrison HB, Almany GR, Berumen ML et al. (2016) Mol. Ecol. 25L 6039-6054

#### Close-kin mark-recapture framework



 $\mathbb{P}[i \text{ is } j \text{ s mother} | z_i, z_j] = \mathbb{E}\left[\frac{i \text{ s reproductive output in } j \text{ s year-of-birth}}{\text{Total female reproductive output in } j \text{ s year-of-birth} | z_i, z_j]}\right]$ 

Bravington MV, Grewe PM, Campbell RD (2016) Nature Communications

#### Close-kin mark-recapture to estimate abundance



• Hillary RM, Bravington MV, Patterson TA, Grewe P, Bradford R et al. (2018) Scientific Reports

#### Mosquito life history model



# Mother-larval offspring pairs

 $P_{MOL}(t_2|t_1) = \frac{\mathbb{E}\left[\text{Larval offspring at time } t_2 \text{ from an adult female sampled at time } t_1\right]}{\mathbb{E}\left[\text{Larval offspring at time } t_2 \text{ from all adult females}\right]} = \frac{E_{MOL}(t_2|t_1)}{E_L}$ 



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$$E_{MOL}(t_2|t_1) = \sum_{y_2=t_2-T_E-(T_L-1)}^{t_2-T_E} (1-\mu_A)^{(t_1-y_2)} \times \left(\mathbb{I}[(t_1-T_A) < y_2 \le t_1] \times \beta \times (1-\mu_E)^{T_E} \times (1-\mu_L)^{(t_2-y_2-T_E)}\right)$$

$$E_L = \sum_{y_2=0-T_E-(T_L-1)}^{0-T_E} N_F \times \beta \times (1-\mu_E)^{T_E} \times (1-\mu_L)^{(0-y_2-T_E)}$$

 $L(k_{MOL}(t_1, t_2)) =$  Binomial  $(k_{MOL}(t_1, t_2) : n_L(t_2), p_{MOL}(t_1, t_2))$ 

$$\Lambda_{MOL} = \sum_{t_1} \sum_{t_2=t_1+T_E - (T_A - 1)}^{t_1 + T_E + (T_L - 1)} \log L(k_{MOL}(t_1, t_2))$$

# Larva-larva full-sibling pairs

 $P_{FSLL}(t_2|t_1) = \frac{\mathbb{E}\left[\text{Larvae at time } t_2 \text{ that are full-siblings of a larva sampled at time } t_1\right]}{\mathbb{E}\left[\text{Larval offspring at time } t_2 \text{ from all adult females}\right]} = \frac{E_{FSLL}(t_2|t_1)}{E_L}$ 



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$$E_{FSLL}(t_2|t_1) = \sum_{y_1=t_1-T_E-(T_L-1)}^{t_1-T_E} p_L(t_1-y_1-T_E) \times \sum_{t_i=y_1-(T_A-1)}^{y_1} p_A(y_1-t_i) \times E_{FSLL}(t_2|t_1,y_1,t_i)$$

$$E_{FSLL}(t_2|t_1, y_1, t_i) = \sum_{y_2=t_i}^{t_i + (T_A - 1)} (1 - \mu_A)^{(y_2 - t_i)} \times \left( \begin{array}{c} \mathbb{I}[(t_2 - T_E - T_L) < y_2 \le (t_2 - T_E)] \\ \times \beta \times (1 - \mu_E)^{T_E} \times (1 - \mu_L)^{(t_2 - y_2 - T_E)} \end{array} \right)$$

$$L(k_{FSLL}(t_2|i), k_{HSLL}(t_2|i)) =$$
Multinomial  $\begin{pmatrix} \{k_{FSLL}(t_2|i), k_{HSLL}(t_2|i)\} : \\ n_L(t_2), \{P_{FSLL}(t_2|t_1(i)), P_{HSLL}(t_2|t_1(i))\} \end{pmatrix}$ 

$$\Lambda_{SLL} = \sum_{i=1}^{n_L - 1} \sum_{t_2 = t_1(i) - 2(T_A - 1) - (T_L - 1)}^{t_1(i) + 2(T_A - 1) + (T_L - 1)} \log L(k_{FSLL}(t_2|i), k_{FHLL}(t_2|i))$$

#### Inference of demographic parameters





#### Inference of dispersal parameters

001 002 003 004 005 006 007 008 009 010 011 012 013 014 015 016 017 018 019 020 021 022 023 024 025 026 027 028 029 030 031 032 033 034 035 036 037 038 039 040 041 042 043 044 045 046 047 048 049 050 051 052 053 054 055 056 057 058 059 060 061 062 063 064 065 066 067 068 069 070 071 072 073 074 075 076 077 078 079 080 **081** 082 **083** 084 **085** 086 **087** 088 **089** 090 **091** 092 093 094 095 096 097 098 099 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 **119** 120 **121** 122 **123** 124 **125** 126 **127** 128 **129** 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 **157** 158 **159** 160 **161** 162 **163** 164 **165** 166 **167** 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 **195** 196 **197** 198 **199** 200 **201** 202 **203** 204 **205** 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 **233** 234 **235** 236 **237** 238 **239** 240 **241** 242 **243** 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361



#### Ongoing field work in Singapore



#### Areas for collaboration

- 1. Variance estimation for close-kin mark-recapture studies
- 2. Application of close-kin mark-recapture methods to populations with seasonal trends
- 3. Sampling strategies to estimate propagule size for an invasive species (or allele)
- 4. Availability for co-advising University of Auckland PhD students
- 5. Current postdoc & researcher positions available at UC Berkeley

### Detection of allele before it becomes too prevalent

- Explore optimal density & placement of traps & frequency of sampling to detect drive alleles, drive-resistant alleles or non-functional effector genes early enough to be managed.
- Expected to be a major cost driver.



• Rašić G, Lobo NF, Jeffrey Gutiérrez EH, Sánchez C. HM, Marshall JM (2022) Frontiers in Genetics

### Trap placement to minimize time to detection

MGSurvE 0.7	.2.0	✓ Latest version		
pip install MGSurvI		Released: Aug 11, 2022		
MGSurvE				
Navigation	Project description			
➡ Project description	MGSurvE: Mosquito Gene Surveilla	ncE		
<ul> <li>Release history</li> <li>Download files</li> </ul>	MGSurvE is a project that optimizes mosquito traps' placement in complex heterogeneous landscapes in an effort to minimize the time to detection of genetic variants of interest.			
Project links	Please have a look at the <u>documentation</u> for more info and our <u>pypi</u> package for detailed <u>installation instructions</u> , and <u>tutorials</u> .			
A Homepage	python 3.9   3.10 pypi package 0.7.2.0 docker img v0.7.2.0 Plake8 passing O CondaEnv passing License GPLv3 O Open	PyTests     passing       Source ?     Yes!		
Statistics	To install the package's latest stable version run (usage of <u>an</u> management is strongly recommended):	aconda for environment		
GitHub statistics:	pip install MGSurvE			
<ul> <li>Forks: 1</li> <li>Open issues/PRs:</li> <li>0</li> <li>View statistics for this project via Libraries.io L, or by using our public dataset on Google BigOuery C</li> </ul>	MGSurvE requires the installation of the <u>DEAP</u> optimization p be installed automatically with our previous <u>pip</u> command. be installed with <u>conda install deap</u> , if needed; or by hav <u>documentation</u> for additional methods. Please have a look at <u>instructions</u> for common issues with some of the dependence build images from <u>our Dockerhub</u> can be pulled and used to issues.	backage, which should This package can also ring a look at <u>DEAP's</u> t our <u>installation</u> ies. Alternatively, pre- avoid dependencies		

 MGSurvE can inform trap numbers & distribution to detect unwanted spread of H or R alleles within a desired timeframe.



Sánchez C. HM, Smith DL, Marshall JM (2022) <u>https://pypi.org/project/MGSurvE/</u>

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