Package 'MGDrivE'

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Type Package

Title Mosquito Gene Drive Explorer

Version 1.0

Description MGDrivE is a model designed to be a reliable testbed where various gene drive interventions for mosquito-borne diseases control.
It is being developed to accommodate the use of various mosquito-specific gene drive systems within a population dynamics framework that allows migration of individuals between patches in landscape.

License GPL-3

Encoding UTF-8

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RdMacros Rdpack

LinkingTo Rcpp, RcppArmadillo

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BugReports https://github.com/MarshallLab/MGDrivE/issues

Author Héctor Manuel Sánchez Castellanos [aut, cre],
Jared Bennett [aut],
Sean Wu [aut],
John M. Marshall [aut]

Maintainer Héctor Manuel Sánchez Castellanos <sanchez.hmsc@berkeley.edu>

R topics documented:

`accumulate_ADMnew_Patch` *Accumulate ADMnew*

Description

Accumulate new ADM males

Usage

```
accumulate_ADMnew_Patch(count)
```

Arguments

`count`	vector of new ADM males

`aggregateFemales` *Aggregate Female Output by Genotype*

Description

Aggregate over male mate genotype to convert female matrix output into vector output.

Usage

```
aggregateFemales(directory, genotypes, remove = FALSE, multiCore = FALSE)
```

Arguments

`directory`	Directory where output was written to; must not end in path seperator
`genotypes`	Character vector of possible genotypes; found in `driveCube$genotypesID`
`remove`	Boolean flag to remove original (unaggregated) file
`multiCore`	Write output using multiple cores? Default is FALSE

`AnalyzeQuantiles` *Summary Statistics for Stochastic MGDrivE*

Description

This function reads in all repetitions for each patch and calculates either the mean, quantiles, or both. User chooses the quantiles, up to 4 decimal places, and enters them as a vector. (order does not matter)

Usage

```
AnalyzeQuantiles(readDirectory, writeDirectory, mean = TRUE,
  quantiles = NULL)
```

Arguments

`readDirectory`	Directory to find repetition folders in
`writeDirectory`	Directory to write output
`mean`	Boolean, calculate mean or not. Default is TRUE
`quantiles`	Vector of quantiles to calculate. Default is NULL

Details

Given the readDirectory, this function assumes the follow file structure:

- readDirectory
  - repetition 1
    - patch 1
    - patch 2
    - patch 3
  - repetition 2
    - patch 1
    - patch 2
    - patch 3
  - repetition 3
  - repetition 4
  - ...

Value

Writes output to files in writeDirectory

`calcAquaticStagesSurvivalProbability` *Calculate Survival Probability of entire Aquatic Stage Life-cycle*

Description

Calculate vector of survival probabilities for each stage of aquatic lifecycle.

Usage

```
calcAquaticStagesSurvivalProbability(eggSurvivalProbability,
  larvaSurvivalProbability, pupaSurvivalProbability)
```

Arguments

`eggSurvivalProbability`
: see `calcAquaticStageSurvivalProbability`

`larvaSurvivalProbability`
: see `calcAquaticStageSurvivalProbability`

`pupaSurvivalProbability`
: see `calcAquaticStageSurvivalProbability`

`calcAquaticStageSurvivalProbability` *Calculate Aquatic Stage Surival Probability*

Description

Calculate θ_{st}, density-independent survival probability, given by:

$$\theta_{st} = (1 - \mu_{st})^{T_{st}}$$

Usage

```
calcAquaticStageSurvivalProbability(mortalityRate, stageDuration)
```

Arguments

`mortalityRate`	daily mortality probability, μ_{st}
`stageDuration`	duration of aquatic stage, T^{st}

`calcAverageGenerationTime`

Calculate Average Generation Time

Description

Calculate g, average generation time, given by:

$$g = T_e + T_l + T_p + \frac{1}{\mu_{ad}}$$

Usage

```
calcAverageGenerationTime(stagesDuration, adultMortality)
```

Arguments

`stagesDuration`	vector of lengths of aquatic stages, T_e, T_l, T_p
`adultMortality`	adult mortality rate, μ_{ad}

`calcDensityDependentDeathRate`

Calculate Density-dependent Larval Mortality

Description

Calculate α, the strength of density-dependent mortality during the larval stage, given by:

$$\alpha = \left(\frac{1/2 * \beta_k * \theta_e * Ad_{eq}}{R_m - 1} \right) * \left(\frac{1 - (\theta_l / R_m)}{1 - (\theta_l / R_m)^{1/T_l}} \right)$$

Usage

```
calcDensityDependentDeathRate(fertility, thetaAq, tAq, adultPopSizeEquilibrium,
  populationGrowthRate)
```

Arguments

`fertility`	number of eggs per oviposition for wild-type females, β_k
`thetaAq`	vector of density-independent survival probabilities of aquatic stages, θ_e, θ_l
`tAq`	vector of lengths of aquatic stages, T_e, T_l, T_p
`adultPopSizeEquilibrium`	adult population size at equilbrium, Ad_{eq}
`populationGrowthRate`	population growth in absence of density-dependent mortality R_m

calcLarvalPopEquilibrium

Calculate Equilibrium Larval Population

Description

Equilibrium larval population to sustain population.

Usage

```
calcLarvalPopEquilibrium(alpha, Rm)
```

Arguments

alpha	see calcDensityDependentDeathRate
Rm	see calcPopulationGrowthRate

calcLarvalStageMortalityRate

Calculate Larval Stage Mortality Rate

Description

Calculate μ_l, the larval mortality, given by

$$\mu_l = 1 - \left(\frac{R_m * \mu_{ad}}{1/2 * \beta_k * (1 - \mu_m)} \right)^{\frac{1}{T_e + T_l + T_p}}$$

Usage

```
calcLarvalStageMortalityRate(generationPopGrowthRate, adultMortality, fertility,
  aquaticStagesDuration)
```

Arguments

generationPopGrowthRate	see calcPopulationGrowthRate
adultMortality	adult mortality rate, μ_{ad}
fertility	number of eggs per oviposition for wild-type females, β_k
aquaticStagesDuration	vector of lengths of aquatic stages, T_e, T_l, T_p

`calcMemoryWindow` *Calculate Memory Window*

Description

Calculates the necessary window of population history required for the model to work

Usage

```
calcMemoryWindow(stagesDuration)
```

Arguments

`egg`	length of egg stage (days)
`larva`	length of larval stage (days)
`pupa`	length of pupal stage (days)

`calcPopulationGrowthRate`
Calculate Population Growth Rate

Description

Calculate R_m, population growth in absence of density-dependent mortality, given by:

$$(r_m)^g$$

Usage

```
calcPopulationGrowthRate(dailyPopGrowthRate, averageGenerationTime)
```

Arguments

`dailyPopGrowthRate`	daily population growth rate, r_m
`averageGenerationTime`	see `calcAverageGenerationTime`

calc_ExpKernel *Calculate Exponential Stochastic Matrix*

Description

Given a distance matrix from calc_haversine, calculate a stochastic matrix where one step movement probabilities follow an exponential density.

Usage

```
calc_ExpKernel(distMat, r)
```

Arguments

distMat	distance matrix from calc_haversine
r	rate parameter of Exponential distribution

calc_GammaKernel *Calculate Gamma Stochastic Matrix*

Description

Given a distance matrix from calc_haversine, calculate a stochastic matrix where one step movement probabilities follow a gamma density.

Usage

```
calc_GammaKernel(distMat, shape, rate)
```

Arguments

distMat	distance matrix from calc_haversine
shape	shape parameter of GammaDist distribution
rate	rate parameter of GammaDist distribution

calc_haversine *Calculate Haversine Distance*

Description

Calculate the great-circle distance (Haversine distance) between sets of longitude - latitude points, see https://en.wikipedia.org/wiki/Haversine_formula

Usage

```
calc_haversine(longlats)
```

Arguments

longlats	numeric matrix where first column is vector of longitudes and second column is vector of latitudes

calc_HurdleExpKernel *Calculate Hurdle Exponential Stochastic Matrix*

Description

Given a distance matrix from calc_haversine, calculate a stochastic matrix where one step movement probabilities follow an zero-truncated exponential density with a point mass at zero.

Usage

```
calc_HurdleExpKernel(distMat, r, pi)
```

Arguments

distMat	distance matrix from calc_haversine
r	rate parameter of Exponential distribution
pi	point mass at zero

calc_LognormalKernel *Calculate Lognormal Stochastic Matrix*

Description

Given a distance matrix from calc_haversine, calculate a stochastic matrix where one step movement probabilities follow a lognormal density.

Usage

```
calc_LognormalKernel(distMat, meanlog, sdlog)
```

Arguments

distMat	distance matrix from calc_haversine
meanlog	log mean of Lognormal distribution
sdlog	log standard deviation of Lognormal distribution

close_allConnections_Network *Close all Output Connections*

Description

Close private$conADM and private$conAF1

Usage

```
close_allConnections_Network()
```

createNamedPopMatrix *Create a Named Matrix*

Description

Create a named matrix of 0s

Usage

```
createNamedPopMatrix(genotypesID)
```

Arguments

genotypesID	character vector of possible genotypes

createNamedPopVector *Create a Named Vector*

Description

Create a named vector of 0s

Usage

```
createNamedPopVector(genotypesID)
```

Arguments

genotypesID	character vector of possible genotypes

cube2csv *Export a Cube to .csv*

Description

Export a cube as multiple .csv files (one for each genotype; slices of z-axis).

Usage

```
cube2csv(cube, directory, digits = 3)
```

Arguments

cube	a cube object (see MGDrivE-Cube for options)
directory	directory to write .csv files to
digits	number of significant digits to retain in .csv output

cubeModifiers *Generate and Modify Default Genotype-specific Parameters*

Description

This is an internal function for cubes.

Usage

```
cubeModifiers(gtype, eta = NULL, phi = NULL, omega = NULL, xiF = NULL,
  xiM = NULL, s = NULL)
```

Arguments

gtype	character vector of genotypes
eta	genotype-specific mating fitness
phi	genotype-specific sex ratio at emergence
omega	genotype-specific multiplicative modifier of adult mortality
xiF	genotype-specific female pupatory success
xiM	genotype-specific male pupatory success
s	genotype-specific fractional reduction(increase) in fertility

Cube_Homing1RA *Inheritance Cube: Homing Drive with 1 Resistance Allele*

Description

This function creates an inheritance cube to model a homing gene drive (such as a CRISPR-Cas9 system) that creates 1 type of resistance allele. It assumes no sex-specific inheritance patterns and the construct is on an autosome.

Usage

```
Cube_Homing1RA(e = 1, p = 0, eta = NULL, phi = NULL, omega = NULL,
  xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

e	Homing rate
p	Resistance allele generation rate
eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list(inheritance cube, viability mask, genotypes ID, genotypes number, wild-type allele, mating fitness, sex ratio, adult mortality modifier, female pupatory success, male pupatory success, fertility modifier, release genotype)

`Cube_HomingDrive` *Inheritance Cube: CRISPR (Clustered Regularly Interspaced SWort Palindromic Repeats) witW 2 Resistance Allele*

Description

This is a sex-specific version of the original cube. It assumes that the construct is on an autosome and there can be different male/female homing rates

Usage

```
Cube_HomingDrive(eM = 1, eF = 1, rM = 0, bM = 0, rF = 0, bF = 0,
  eta = NULL, phi = NULL, omega = NULL, xiF = NULL, xiM = NULL,
  s = NULL)
```

Arguments

`eM`	Male homing rate
`eF`	Female homing rate
`rM`	Male no-cost resistance generation rate
`bM`	Male detrimental resistance generation rate
`rF`	Female no-cost resistance generation rate
`bF`	Female detrimental resistance generation rate
`eta`	Genotype-specific mating fitness
`phi`	Genotype-specific sex ratio at emergence
`omega`	Genotype-specific multiplicative modifier of adult mortality
`xiF`	Genotype-specific female pupatory success
`xiM`	Genotype-specific male pupatory success
`s`	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

`Cube_KillerRescue` *Inheritance Cube: Killer-Rescue System*

Description

This function creates an inheritance cube to model a Killer-Rescue system. Killer-Resuce is a 2-locus system: one locus has a toxin and the other locus contains the antidote. The loci are assumed independent and are non-homing.
This drive has 3 alleles at locus 1 and 2 alleles and locus 2:

- Locus 1
  - T: Wild-type allele
  - K: "Killer" toxin allele
  - R: Rroken toxin allele
- Locus 2
  - W: Wild-type allele
  - A: Antidote allele

Usage

```
Cube_KillerRescue(eR = 0, Keff = 1, Aeff = 1, eta = NULL, phi = NULL,
  omega = NULL, xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

`eR`	Conversion of K allele to R allele, a basal mutation rate
`Keff`	Toxin efficacy
`Aeff`	Antidote efficacy
`eta`	Genotype-specific mating fitness
`phi`	Genotype-specific sex ratio at emergence
`omega`	Genotype-specific multiplicative modifier of adult mortality
`xiF`	Genotype-specific female pupatory success
`xiM`	Genotype-specific male pupatory success
`s`	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_MEDEA *Inheritance Cube: MEDEA (Maternal Effect Dominant Embryonic Arrest)*

Description

This function creates an inheritance cube to model a MEDEA drive system. This system was first discovered in flour beetles. It biases inheritance by expressing a maternal toxin such that offspring die unless they express a zygotic antidote.
This drive has 3 alleles at 1 locus:

- W: Wild-type allele
- M: MEDEA allele
- R: Resistance allele

Usage

```
Cube_MEDEA(rM = 0, rW = 0, Teff = 1, eta = NULL, phi = NULL,
  omega = NULL, xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

rM	Breakdown of MEDEA allele, no homing/toxin/antidote, M -> R conversion
rW	De novo resistance generation, W -> R conversion
Teff	Efficacy of the toxin
eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_Mendelian *Inheritance Cube: Mendelian*

Description

This function creates a Mendelian Inheritance Cube. It only handles simple, alphabetic genotypes. The default is 3 alleles at 1 locus, but this can be extended to however many alleles one is interested in, but only at 1 locus.

Usage

```
Cube_Mendelian(gtype = c("AA", "Aa", "aa"), eta = NULL, phi = NULL,
  omega = NULL, xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

gtype	Vector of genotypes, with the wild-type in the first position
eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_oneLocusTA *Inheritance Cube: 1 Locus Maternal-Toxin/Zygotic-Antidote System*

Description

This function creates a 1 locus maternal-toxin/zygotic-antidote system. This is similar to the construct called UDmel. There is no resistance generation in this model.
This drive has 3 alleles at 1 locus:

- A: Maternal-toxin 1, zygotic-antidote 2
- B: Maternal-toxin 2, zygotic-antidote 1
- W: Wild-type allele

Usage

```
Cube_oneLocusTA(TAEfficacy = 1, TBEfficacy = 1, eta = NULL, phi = NULL,
  omega = NULL, xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

TAEfficacy	Maternal toxin A efficacy
TBEfficacy	Maternal toxin B efficacy
eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_ReciprocalTranslocations

Inheritance Cube: Reciprocal Translocation

Description

This function creates an inheritance cube to model a reciprocal translocation. This technology was the original form of underdominant system. It involves 2 chromosomes, each with two alleles. This drive has 4 alleles at 2 loci:

- a: Wild-type at locus A
- A: Translocation at locus A
- b: Wile-type at locus B
- B: Translocation at locus B

Usage

```
Cube_ReciprocalTranslocations(eta = NULL, phi = NULL, omega = NULL,
  xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_RIDL *Inheritance Cube: RIDL (Release of Insects with Dominant Lethality)*

Description

This function creates a RIDL system RIDL (Release of Insects with Dominant Lethality), is a form of SIT. Created by Oxitec, this is based on a positive feedback loop using the toxic tTAV gene, contolled under lab conditions by the TetO promoter. This has 2 alleles at 1 locus

- W: Wild-type allele
- R: OX513 RIDL allele

Usage

```
Cube_RIDL(eta = NULL, phi = NULL, omega = NULL, xiF = NULL,
  xiM = NULL, s = NULL)
```

Arguments

eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_twoLocusTA *Inheritance Cube: 2 Locus Maternal-Toxin/Zygotic-Antidote System*

Description

This function creates a 2 locus maternal-toxin/zygotic-antidote system. This is similar to the construct called UDmel. There is no resistance generation in this model.
This drive has 2 unlinked alleles, 1 allele each at 2 loci:

- A: Maternal-toxin 1, zygotic-antidote 2
- a: Wild-type at locus A
- B: Maternal-toxin 2, zygotic-antidote 1
- b: Wild-type at locus B

Usage

```
Cube_twoLocusTA(TAEfficacy = 1, TBEfficacy = 1, eta = NULL, phi = NULL,
  omega = NULL, xiF = NULL, xiM = NULL, s = NULL)
```

Arguments

TAEfficacy	Maternal toxin A efficacy
TBEfficacy	Maternal toxin B efficacy
eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

Cube_Wolbachia *Inheritance Cube: Wolbachia*

Description

This function creates an inheritance cube to model a Wolbachia infection. Wobachia is a parasite that can infect mosquitoes. It biases its inheritance through cytoplasmic incompatibility.
This drive has 2 alleles at 1 locus:

- W: has Wolbachia
- w: does not have Wolbachia

Usage

```
Cube_Wolbachia(eta = NULL, phi = NULL, omega = NULL, xiF = NULL,
  xiM = NULL, s = NULL)
```

Arguments

eta	Genotype-specific mating fitness
phi	Genotype-specific sex ratio at emergence
omega	Genotype-specific multiplicative modifier of adult mortality
xiF	Genotype-specific female pupatory success
xiM	Genotype-specific male pupatory success
s	Genotype-specific fractional reduction(increase) in fertility

Details

Cytoplasmic Incompatibility:

- male W cross female w -> all offspring die (complete penetrance)
- male w cross female W -> all offspring inherit Wolbachia

Value

Named list containing the inheritance cube, transition matrix, genotypes, wild-type allele, and all genotype-specific parameters.

`eraseDirectory` *Erase all files in a directory*

Description

Given a directory path, check it exists and if so delete all its contents.

Usage

```
eraseDirectory(directory)
```

Arguments

`directory`	directory whose contents will be deleted

`generateReleaseVector` *Make List of Modified Mosquito Releases*

Description

Sets up a release schedule for a single patch, calls `Release_basicRepeatedReleases` internally.

Usage

```
generateReleaseVector(driveCube = driveCube,
  releasesParameters = releasesParameters, sex = "M")
```

Arguments

`driveCube`	gene-drive cube
`releasesParameters`	A list containing the releasesStart, releasesNumber releasesInterval, and releaseProportion named values.
`sex`	character in 'M','F'

`get_ADMdly_Patch` *Get ADMdly*

Description

Return adult male stage delay window population

Usage

```
get_ADMdly_Patch()
```

get_ADMnew_Patch *Get ADMnew*

Description

Return the new ADM females

Usage

```
get_ADMnew_Patch()
```

get_ADM_Patch *Get ADM*

Description

Return adult male stage population

Usage

```
get_ADM_Patch()
```

get_AdPopEQ_Network *Get AdPopEQ*

Description

Return equilibrium adult population

Usage

```
get_AdPopEQ_Network(ix)
```

Arguments

ix	index of patch

get_AF1dly_Patch *Get AF1dly*

Description

Return adult female stage delay window population

Usage

```
get_AF1dly_Patch()
```

get_AF1new_Patch *Get AF1new*

Description

Return the new AF1 females

Usage

```
get_AF1new_Patch()
```

get_AF1_Patch *Get AF1*

Description

Return adult female stage population

Usage

```
get_AF1_Patch()
```

get_alpha_Network *Get alpha*

Description

Return density dependent mortality, see calcDensityDependentDeathRate

Usage

```
get_alpha_Network(ix)
```

Arguments

ix	index of patch

get_beta_Network *Get beta*

Description

Return size of wild-type egg batch

Usage

```
get_beta_Network()
```

get_conADM_Network *Get conADM*

Description

Return connection where adult male dynamics are written to

Usage

```
get_conADM_Network()
```

get_conAF1_Network *Get conAF1*

Description

Return connection where adult female dynamics are written to

Usage

```
get_conAF1_Network()
```

get_directory_Network *Get directory*

Description

Return character string of directory being written to

Usage

```
get_directory_Network()
```

get_driveCube_genotype_Network *Get Element(s) of Drive Cube by Genotype*

Description

Return elements or slices of drive cube. If all NULL return entire cube.

Usage

```
get_driveCube_genotype_Network(fG = NULL, mG = NULL, oG = NULL)
```

Arguments

fG	female genotype
mG	male genotype
oG	offspring genotype

get_driveCube_index_Network *Get Element(s) of Drive Cube by Index*

Description

Return elements or slices of drive cube. If all NULL return entire cube.

Usage

```
get_driveCube_index_Network(fG = NULL, mG = NULL, oG = NULL)
```

Arguments

fG	female genotype index
mG	male genotype index
oG	offspring genotype index

get_EGGdly_Patch *Get EGGdly*

Description

Return egg stage delay window population

Usage

```
get_EGGdly_Patch()
```

get_EGG_Patch *Get EGG*

Description

Return egg stage population

Usage

```
get_EGG_Patch()
```

get_eta_Network *Get eta*

Description

Return genotype-specific mating fitness

Usage

```
get_eta_Network()
```

get_femaleMigration_Patch *Get maleMigration*

Description

Return outbound males (nGenotypes X nGenotypes X nPatch array)

Usage

```
get_femaleMigration_Patch()
```

get_genotypesID_Network *Get genotypesID*

Description

Return character vector of possible genotypes

Usage

```
get_genotypesID_Network()
```

get_genotypesN_Network *Get genotypesN*

Description

Return number of possible genotypes

Usage

```
get_genotypesN_Network()
```

get_g_Network *Get g*

Description

Return average generation time, see calcAverageGenerationTime

Usage

```
get_g_Network()
```

get_LARdly_Patch *Get LARdly*

Description

Return larval stage delay window population

Usage

```
get_LARdly_Patch()
```

get_LAR_Patch *Get LAR*

Description

Return larval stage population

Usage

```
get_LAR_Patch()
```

get_Leq_Network *Get Leq*

Description

Return equilibrium larval population, see calcLarvalPopEquilibrium

Usage

```
get_Leq_Network(ix)
```

Arguments

ix	index of patch

get_maleMigration_Patch *Get maleMigration*

Description

Return outbound males (nGenotypes X nPatch integer matrix)

Usage

```
get_maleMigration_Patch()
```

get_migrationFemaleRow_Network *Get Row of Female Migration Matrix*

Description

Return a matrix object (does not drop dimensions)

Usage

```
get_migrationFemaleRow_Network(ix)
```

Arguments

ix	index of row

get_migrationFemale_Network *Get Female Migration Matrix*

Description

Return a matrix object

Usage

```
get_migrationFemale_Network()
```

get_migrationMaleRow_Network *Get Row of Male Migration Matrix*

Description

Return a matrix object (does not drop dimensions)

Usage

```
get_migrationMaleRow_Network(ix)
```

Arguments

ix	index of row

get_migrationMale_Network *Get Male Migration Matrix*

Description

Return a matrix object

Usage

```
get_migrationMale_Network()
```

get_moveVar_Network *Get moveVar*

Description

Return numeric variance in Dirchlet-Multinomial movement

Usage

```
get_moveVar_Network()
```

get_muAd_Network *Get muAd*

Description

Return adult mortality

Usage

```
get_muAd_Network()
```

get_muAq_Network *Get muAq*

Description

Return larval mortality, see calcLarvalStageMortalityRate

Usage

```
get_muAq_Network()
```

get_NetworkPointer_Patch *Get Network Pointer*

Description

Return a reference to the enclosing Network object

Usage

```
get_NetworkPointer_Patch()
```

get_nPatch_Network *Get nPatch*

Description

Return number of patches

Usage

```
get_nPatch_Network()
```

get_omega_Network *Get omega*

Description

Return genotype-specific multiplicative modifier of adult mortality

Usage

```
get_omega_Network()
```

get_patches_Network *Get all Patches*

Description

Return a list of Patch objects

Usage

```
get_patches_Network()
```

get_patchID_Patch *Get patchID*

Description

Return the ID of this patch

Usage

```
get_patchID_Patch()
```

get_patchReleases_Network *Get Patch Release Schedule*

Description

Return the release schedule for a patch for male or female

Usage

```
get_patchReleases_Network(ix, sex = "M")
```

Arguments

ix	index of patch
sex	character in 'M', 'F'

get_patch_Network *Get Patch*

Description

Return a Patch object

Usage

```
get_patch_Network(ix)
```

Arguments

ix	integer id of patch to return

get_phi_Network *Get phi*

Description

Return genotype-specific sex ratio at emergence

Usage

```
get_phi_Network()
```

get_PUPdly_Patch *Get PUP*

Description

Return pupae stage delay window population

Usage

```
get_PUPdly_Patch()
```

get_PUP_Patch *Get PUP*

Description

Return pupae stage population

Usage

```
get_PUP_Patch()
```

get_releaseType_Network *Get releaseType*

Description

Return genotype of release

Usage

```
get_releaseType_Network()
```

get_Rm_Network *Get Rm*

Description

Return population growth rate, see calcPopulationGrowthRate

Usage

```
get_Rm_Network()
```

get_simTime_Network *Get simTime*

Description

Return maximum time to run simulation

Usage

```
get_simTime_Network()
```

get_s_Network *Get s*

Description

Return genotype-specific fractional reduction(increase) in fertility

Usage

```
get_s_Network()
```

get_tau_Network *Get Viability Mash (tau)*

Description

Return matrix

Usage

```
get_tau_Network()
```

get_thetaAq_Network *Get thetaAq*

Description

Return aquatic stage survival probability, see calcAquaticStagesSurvivalProbability and calcAquaticStageSurvi

Usage

```
get_thetaAq_Network(stage)
```

Arguments

stage	character in 'E', 'L', 'P'

get_timeAq_Network *Get timeAq*

Description

Return duration of aquatic stages, see initStagesDurations

Usage

```
get_timeAq_Network(stage = NULL)
```

Arguments

stage	character in 'E', 'L', 'P'; if NULL return total duration

get_tNow_Network *Get tNow*

Description

Return current simulation time

Usage

```
get_tNow_Network()
```

get_wildType_Network *Get wildType*

Description

Return wild-type genotype

Usage

```
get_wildType_Network()
```

get_windowSize_Network *Get windowSize*

Description

Return memory window size, see calcMemoryWindow

Usage

```
get_windowSize_Network()
```

get_xiF_Network *Get xiF*

Description

Return genotype-specific female pupatory success

Usage

```
get_xiF_Network()
```

get_xiM_Network *Get xiM*

Description

Return genotype-specific male pupatory success

Usage

```
get_xiM_Network()
```

ggCol_utility *Utility to Imitate ggplot2 Colors*

Description

Sample at equally spaced intervals along the color wheel

Usage

```
ggCol_utility(n, alpha = 1)
```

Arguments

n	number of colors
alpha	transparency

initPopMatrixArray *Create a population array of matrices*

Description

Creates an array for the population history to be stored. The length of the array is equal to the window required for the model to run (in our specific case it is equal to the sum of aquatic stages lengths).

Usage

```
initPopMatrixArray(genotypesID, memoryWindow)
```

Arguments

genotypesID	character vector of possible genotypes
memoryWindow	integer size of list structure

initPopVectorArray *Create a population array of vectors*

Description

Creates an array for the population history to be stored. The length of the array is equal to the window required for the model to run (in our specific case it is equal to the sum of aquatic stages lengths).

Usage

```
initPopVectorArray(genotypesID, memoryWindow)
```

Arguments

genotypesID	character vector of possible genotypes
memoryWindow	integer size of list structure

initStagesDurations *Initialize Aquatic Stages Durations*

Description

Initialises the vector that holds the duration of each aquatic stage

Usage

```
initStagesDurations(egg = 1, larva = 14, pupa = 1)
```

Arguments

egg	length of egg stage (days)
larva	length of larval stage (days)
pupa	length of pupal stage (days)

kernels *Kernels Parameters*

Description

A named list containing maximum likelihood fitted parameter values from mosquito dispersal estimates.

Usage

```
data(kernels)
```

Format

named list with 5 elements:

lnorm_mean log mean of log-normal density

lnorm_sd log standard deviation of log-normal density

gamma_shape shape parameter of gamma density

gamma_sd rate parameter of gamma density

exp_rate rate parameter of exponential density

MGDrivE *MGDrivE: Mosquito Gene Drive Explorer*

Description

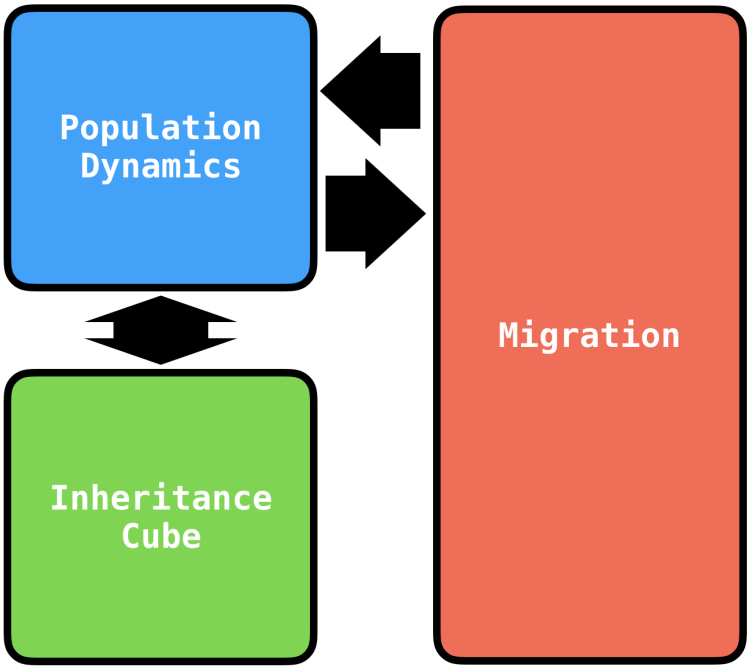
MGDrivE: Mosquito Gene Drive Explorer

Introduction

Recent developments of CRISPR-Cas9 based homing endonuclease gene drive systems for the suppression or replacement of mosquito populations have generated much interest in their use for control of mosquito-borne diseases (such as dengue, malaria, chikungunya and Zika). This is because genetic control of pathogen transmission may complement or even substitute traditional vector-control interventions, which have had limited success in bringing the spread of these diseases to a halt. Despite excitement for the use of gene drives for mosquito control, current modeling efforts have analyzed only a handful of these new approaches (usually studying just one per framework). Moreover, these models usually consider well-mixed populations with no explicit spatial dynamics. To this end, we are developing MGDrivE (Mosquito Gene DRIVe Explorer), in cooperation with the 'UCI Malaria Elimination Initiative', as a flexible modeling framework to evaluate a variety of drive systems in spatial networks of mosquito populations. This framework provides a reliable testbed to evaluate and optimize the efficacy of gene drive mosquito releases. What separates MGDrivE from other models is the incorporation of mathematical and computational mechanisms to simulate a wide array of inheritance-based technologies within the same, coherent set of equations. We do this by treating the population dynamics, genetic inheritance operations, and migration between habitats as separate processes coupled together through the use of mathematical tensor operations. This way we can conveniently swap inheritance patterns whilst still making use of the same set of population dynamics equations. This is a crucial advantage of our system, as it allows other research groups to test their ideas without developing new models and without the need to spend time adapting other frameworks to suit their needs.

Brief Description

MGDrivE is based on the idea that we can decouple the genotype inheritance process from the population dynamics equations. This allows the system to be treated and developed in three semi-indpendent modules that come together to form the system. The way this is done will be described later in this document but a reference diagram is shown here.



Previous Work

The original version of this model was based on work by (Deredec et al. 2011; Hancock and Godfray 2007) and adapted to accommodate CRISPR homing dynamics in a previous publication by our team (Marshall et al. 2017). As it was described, we extended this framework to be able to handle a variable number of genotypes, and migration across spatial scenarios. We did this by adapting the equations to work in a tensor-oriented manner, where each genotype can have different processes affecting their particular strain (death rates, mating fitness, sex-ratio bias, et cetera).

Notation and Conventions

Before beginning the full description of the model we will define some of the conventions we followed for the notation of the written description of the system.

- Overlines are used to denote the dimension of a tensor
- Subscript brackets are used to indicate an element in time. For example: $L_{[t-1]}$ is the larval population at time: $t-1$.
- Parentheses are used to indicate the parameter(s) of a function. For example: $\overline{O(T_e + T_l)}$ represents the function O evaluated with the parameter: $T_e + T_l$
- Matrices follow a 'row-first' indexing order (i: row, j: column)

In the case of one dimensional tensors, each slot represents a genotype of the population. For example, the male population is stored in the following way:

$$\overline{Am} = \begin{pmatrix} g_1 \\ g_2 \\ g_3 \\ \vdots \\ g_n \end{pmatrix}_i$$

All the processes that affect mosquitoes in a genotype-specific way are defined and stored in this way within the framework.

There are two tensors of squared dimensionality in the model: the adult females matrix, and the genotype-specific viability mask. In the case of the former the rows represent the females' genotype, whilst the columns represent the genotype of the male they mated with:

$$\overline{\overline{Af}} = \begin{pmatrix} g_{11} & g_{12} & g_{13} & \cdots & g_{1n} \\ g_{21} & g_{22} & g_{23} & \cdots & g_{2n} \\ g_{31} & g_{32} & g_{33} & \cdots & g_{3n} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ g_{n1} & g_{n2} & g_{n3} & \cdots & g_{nn} \end{pmatrix}_{ij}$$

The genotype-specific viability mask, on the other hand, stores the mothers' genotype in the rows, and the potential eggs' genotype in the columns of the matrix.

References

Deredec A, Godfray HCJ, Burt A (2011). "Requirements for effective malaria control with homing endonuclease genes." *Proceedings of the National Academy of Sciences of the United States of America*, **108**(43), E874–80. ISSN 1091-6490, doi: 10.1073/pnas.1110717108, http://www.ncbi.nlm.nih.gov/pubmed/21976487{%}5Cnhttp://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC3203790.

Hancock PA, Godfray HCJ (2007). "Application of the lumped age-class technique to studying the dynamics of malaria-mosquito-human interactions." *Malaria journal*, **6**, 98. ISSN 1475-2875, doi: 10.1186/14752875698, http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1971713{&}tool=pmcentrez{&}rendertype=abstract.

Marshall J, Buchman A, C. HMS, Akbari OS (2017). "Overcoming evolved resistance to population-suppressing homing-based gene drives." *Nature Scientific Reports*, 1–46. ISSN 2045-2322, doi: https://doi.org/10.1101/088427.

`MGDrivE-Cube` *MGDrivE: Inheritance Cube*

Description

To model an arbitrary number of genotypes efficiently in the same mathematical framework we use a 3-dimensional array structure (cube) where each axis represents the following information:

- x: female adult mate genotype
- y: male adult mate genotype
- z: proportion of the offspring that inherits a given genotype (layer)

Details

The cube structure gives us the flexibility to apply tensor operations to the elements within our equations, so that we can calculate the stratified population dynamics rapidly; and within a readable, flexible computational framework. This becomes apparent when we define the equation we use for the computation of eggs laid at any given point in time:

$$\overline{O(T_x)} = \sum_{j=1}^{n} \left(\left((\beta * \overline{s} * \overline{\overline{Af_{[t-T_x]}}}) * \overline{\overline{\overline{Ih}}} \right) * \Lambda \right)^{\top}_{ij}$$

In this equation, the matrix containing the number of mated adult females ($\overline{\overline{Af}}$) is multiplied element-wise with each one of the layers containing the eggs genotypes proportions expected from this cross ($\overline{\overline{\overline{Ih}}}$). The resulting matrix is then multiplied by a binary 'viability mask' (Λ) that filters out female-parent to offspring genetic combinations that are not viable due to biological impediments (such as cytoplasmic incompatibility). The summation of the transposed resulting matrix returns us the total fraction of eggs resulting from all the male to female genotype crosses ($\overline{O(T_x)}$).

Note: For inheritance operations to be consistent within the framework the summation of each element in the z-axis (this is, the proportions of each one of the offspring's genotypes) must be equal to one.

Drive-specific Cubes

An inheritance cube in an array object that specifies inheritance probabilities (offspring genotype probability) stratified by male and female parent genotypes. MGDrivE provides the following cubes to model different gene drive systems:

- `Cube_oneLocusTA`: 1 Locus Maternal-Toxin/Zygotic-Antidote System
- `Cube_twoLocusTA`: 2 Locus Maternal-Toxin/Zygotic-Antidote System
- `Cube_Homing1RA`: Homing Drive with 1 Resistance Allele
- `Cube_HomingDrive`: CRISPR (Clustered Regularly Interspaced SWort Palindromic Repeats) witW 2 Resistance Allele
- `Cube_KillerRescue`: Killer-Rescue System
- `Cube_MEDEA`: MEDEA (Maternal Effect Dominant Embryonic Arrest)
- `Cube_ReciprocalTranslocations`: Reciprocal Translocation
- `Cube_RIDL`: RIDL (Release of Insects with Dominant Lethality)
- `Cube_Mendelian`: Mendelian
- `Cube_Wolbachia`: Wolbachia

Functions for Cubes

There are several functions to operate on cube objects.

- `cube2csv`: Export slices of a cube to .csv format

`MGDrivE-Model` *MGDrivE: Model's Mathematical Description*

Description

The original version of this model was based on work by (Deredec, Godfray, and Burt 2011; Hancock and Godfray 2007) and adapted to accommodate CRISPR homing dynamics in a previous publication by our team (Marshall, Buchman, C., and Akbari 2017). As it was described, we extended this framework to be able to handle a variable number of genotypes, and migration across spatial scenarios. We did this by adapting the equations to work in a tensor-oriented manner, where each genotype can have different processes affecting their particular strain (death rates, mating fitness, sex-ratio bias, etcetera).

Inheritance Cube and Oviposition

To allow the extension of the framework to an arbitrary number of genotypes we decided to transform traditional inheritance matrices into inheritance cubes where each of the axis represents the following information:

- x: female adult mate genotype
- y: male adult mate genotype
- z: proportion of the offspring that inherits a given genotype (slice)

The 'cube' structure gives us the flexibility to apply tensor operations to the elements within our equations, so that we can calculate the stratified population dynamics rapidly; and within a readable, flexible computational framework. This becomes apparent when we define the equation we use for the computation of eggs laid at any given point in time:

$$\overline{O(T_x)} = \sum_{j=1}^{n} \left(\left((\beta * \overline{s} * \overline{\overline{Af_{[t-T_x]}}}) * \overline{\overline{\overline{Ih}}} \right) * \Lambda \right)^{\top}_{ij}$$

In this equation, the matrix containing the number of mated adult females ($\overline{\overline{Af}}$) is multiplied element-wise with each one of the slices containing the eggs genotypes proportions expected from this cross ($\overline{\overline{\overline{Ih}}}$). The resulting matrix is then multiplied by a binary 'viability mask' (Λ) that filters out female-parent to offspring genetic combinations that are not viable due to biological impediments (such as cytoplasmic incompatibility). The summation of the transposed resulting matrix returns us the total fraction of eggs resulting from all the male to female genotype crosses ($\overline{O(T_x)}$).

Note: For inheritance operations to be consistent within the framework the summation of each element in the 'z' axis (this is, the proportions of each one of the offspring's genotypes) must be equal to one.

Population Dynamics

During the three aquatic stages, a density-independent mortality process takes place:

$$\theta_{st} = (1 - \mu_{st})^{T_{st}}$$

Along with a density dependent process dependent on the number of larvae in the environment:

$$F(L[t]) = \left(\frac{\alpha}{\alpha + \sum \overline{L[t]}} \right)^{1/T_l}$$

where α represents the strength of the density-dependent process. This parameter is calculated with:

$$\alpha = \left(\frac{1/2 * \beta_k * \theta_e * Ad_{eq}}{R_m - 1} \right) * \left(\frac{1 - (\theta_l / R_m)}{1 - (\theta_l / R_m)^{1/T_l}} \right)$$

in which β_k is the species' fertility in the absence of gene-drives, Ad_{eq} is the adult mosquito population equilibrium size, and R_m is the population growth in the absence of density-dependent mortality. This population growth is calculated with the average generation time (g), the adult mortality rate (μ_{ad}), and the daily population growth rate (r_m):

$$g = T_e + T_l + T_p + \frac{1}{\mu_{ad}} R_m = (r_m)^g$$

Larval Stages: The computation of the larval stage in the population is crucial to the model because the density dependent processes necessary for equilibrium trajectories to be calculated occur here. This calculation is performed with the following equation:

$$D(\theta_l, T_x) = \begin{cases} \theta'_{l[0]} = \theta_l & i = 0 \\ \theta'_{l[i+1]} = \theta'_{l[i]} * F(\overline{L_{[t-i-T_x]}}) & i \leq T_l \end{cases}$$

In addition to this, we need the larval mortality (μ_l):

$$\mu_l = 1 - \left(\frac{R_m * \mu_{ad}}{1/2 * \beta_k * (1 - \mu_m)} \right)^{\frac{1}{T_e + T_l + T_p}}$$

With these mortality processes, we are now able to calculate the larval population:

$$\overline{L_{[t]}} = \overline{L_{[t-1]}} * (1 - \mu_l) * F(\overline{L_{[t-1]}}) + \overline{O(T_e)} * \theta_e - \overline{O(T_e + T_l)} * \theta_e * D(\theta_l, 0)$$

where the first term accounts for larvae surviving one day to the other; the second therm accounts for the eggs that have hatched within the same period of time; and the last term computes the number of larvae that have transformed into pupae.

Adult Stages: We are ultimately interested in calculating how many adults of each genotype exist at any given point in time. For this, we first calculate the number of eggs that are laid and survive to the adult stages with the equation:

$$\overline{E'} = \overline{O(T_e + T_l + T_p)} \left(\overline{\xi_m} * (\theta_e * \theta_p) * (1 - \mu_{ad}) * D(\theta_l, T_p) \right)$$

With this information we can calculate the current number of male adults in the population by computing the following equation:

$$\overline{Am_{[t]}} = \overline{Am_{[t-1]}} * (1 - \mu_{ad}) * \overline{\omega_m} + (1 - \overline{\phi}) * \overline{E'} + \overline{\nu m_{[t-1]}}$$

in which the first term represents the number of males surviving from one day to the next; the second one, the fraction of males that survive to adulthood ($\overline{E'}$) and emerge as males ($1 - \phi$); the last one is used to add males into the population as part of gene-drive release campaigns.
Female adult populations are calculated in a similar way:

$$\overline{\overline{Af_{[t]}}} = \overline{\overline{Af_{[t-1]}}} * (1 - \mu_{ad}) * \overline{\omega_f} + \left(\overline{\phi} * \overline{E'} + \overline{\nu f_{[t-1]}} \right)^\top * \left(\frac{\overline{\eta} * \overline{Am_{[t-1]}}}{\sum \overline{Am_{[t-1]}}} \right)$$

where we first compute the surviving female adults from one day to the next; and then we calculate the mating composition of the female fraction emerging from pupa stage. To do this, we obtain the surviving fraction of eggs that survive to adulthood ($\overline{E'}$) and emerge as females (ϕ), we then add the new females added as a result of gene-drive releases ($\overline{\nu f_{[t-1]}}$). After doing this, we calculate the proportion of males that are allocated to each female genotype, taking into account their respective mating fitnesses ($\overline{\eta}$) so that we can introduce the new adult females into the population pool.

Gene Drive Releases and Effects

As it was briefly mentioned before, we are including the option to release both male and/or female individuals into the populations. Another important thing to emphasize is that we allow flexible releases sizes and schedules. Our model handles releases internally as lists of populations compositions so, it is possible to have releases performed at irregular intervals and with different numbers of mosquito genetic compositions as long as no new genotypes are introduced (which have not been previously defined in the inheritance cube).

$$\overline{\nu} = \left\{ \begin{pmatrix} g_1 \\ g_2 \\ g_3 \\ \vdots \\ g_n \end{pmatrix}_{t=1}, \begin{pmatrix} g_1 \\ g_2 \\ g_3 \\ \vdots \\ g_n \end{pmatrix}_{t=2}, \cdots, \begin{pmatrix} g_1 \\ g_2 \\ g_3 \\ \vdots \\ g_n \end{pmatrix}_{t=x} \right\}$$

So far, however, we have not described the way in which the effects of these gene-drives are included into the mosquito populations dynamics. This is done through the use of various modifiers included in the equations:

- $\overline{\omega}$: Relative increase in mortality (zero being full mortality effects and one no mortality effect)
- $\overline{\phi}$: Relative shift in the sex of the pupating mosquitoes (zero biases the sex ratio towards males, whilst 1 biases the ratio towards females).
- $\overline{\eta}$: Standardized mating fitness (zero being complete fitness ineptitude, and one being regular mating skills).
- $\overline{\beta}$: Fecundity (average number of eggs laid).
- $\overline{\xi}$: Pupation success (zero being full mortality and one full pupation success).

Migration

To simulate migration within our framework we are considering patches (or nodes) of fully-mixed populations in a network structure. This allows us to handle mosquito movement across spatially-distributed populations with a transitions matrix, which is calculated with the tensor outer product of the genotypes populations tensors and the transitions matrix of the network as follows:

$$\overline{Am^i_{(t)}} = \sum \overline{A^j_m} \otimes \overline{\overline{\tau m_{[t-1]}}} \overline{\overline{Af^i_{(t)}}} = \sum \overline{\overline{A^j_f}} \otimes \overline{\overline{\tau f_{[t-1]}}}$$

In these equations the new population of the patch i is calculated by summing the migrating mosquitoes of all the j patches across the network defined by the transitions matrix τ, which stores the mosquito migration probabilities from patch to patch. It is worth noting that the migration probabilities matrices can be different for males and females; and that there's no inherent need for them to be static (the migration probabilities may vary over time to accommodate wind changes due to seasonality).

Parameters

This table compiles all the parameters required to run MGDrivE clustered in six categories:

- Life Stages: These deal with the structure of mosquito population.
- Bionomics: This set of parameters is related to the behavior of the specific mosquito species being modeled.
- Gene Drive: Genotype-specific vectors of parameters that affect how each gene-drive modifies the responses of populations to them.

- Releases: List of vectors that control the release of genetically-modified mosquitoes.
- Population: General mosquito-population parameters that control environmentally-determined variables.
- Network: Related to migration between nodes of population units

Stochasticity

MGDrivE allows stochasticity to be included in the dynamics of various processes; in an effort to simulate processes that affect various stages of mosquitoes lives. In the next section, we will describe all the stochastic processes that can be activated in the program. It should be noted that all of these can be turned on and off independently from one another as required by the researcher.

Mosquito Biology: Oviposition

Stochastic egg laying by female/male pairs is separated into two steps: calculating the number of eggs laid by the females and then distributing laid eggs according to their genotypes. The number of eggs laid follows a Poisson distribution conditioned on the number of female/male pairs and the fertility of each female.

$$Poisson(\lambda = numFemales * Fertility)$$

Multinomial sampling, conditioned on the number of offspring and the relative viability of each genotype, determines the genotypes of the offspring.

$$Multinomial\left(numOffspring, p_1, p_2 \dots p_b\right) = \frac{numOffspring!}{p_1!\, p_2\, \dots p_n} p_1^{n_1} p_2^{n_2} \dots p_n^{n_n}$$

Sex Determination

Sex of the offspring is determined by multinomial sampling. This is conditioned on the number of eggs that live to hatching and a probability of being female, allowing the user to design systems that skew the sex ratio of the offspring through reproductive mechanisms.

$$Multinomial(numHatchingEggs, p_{female}, p_{female})$$

Mating Stochastic mating is determined by multinomial sampling conditioned on the number of males and their fitness. It is assumed that females mate only once in their life, therefore each female will sample from the available males and be done, while the males are free to potentially mate with multiple females. The males' ability to mate is modulated with a fitness term, thereby allowing some genotypes to be less fit than others (as seen often with lab releases).

$$Multinomial(numFemales, p_1 f_1, p_2 f_2, \dots p_n f_n)$$

Hatching

Other Stochastic Processes All remaining stochastic processes (larval survival, hatching , pupating, surviving to adult hood) are determined by multinomial sampling conditioned on factors affecting the current life stage. These factors are determined empirically from mosquito population data.

Migration: Variance of stochastic movement (not used in diffusion model of migration). It affects the concentration of probability in the Dirchlet simplex, small values lead to high variance and large values lead to low variance.

References

Deredec A, Godfray HCJ, Burt A (2011). "Requirements for effective malaria control with homing endonuclease genes." *Proceedings of the National Academy of Sciences of the United States of America*, **108**(43), E874–80. ISSN 1091-6490, doi: 10.1073/pnas.1110717108, http://www.ncbi.nlm.nih.gov/pubmed/21976487{%}5Cnhttp://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC3203790.

Hancock PA, Godfray HCJ (2007). "Application of the lumped age-class technique to studying the dynamics of malaria-mosquito-human interactions." *Malaria journal*, **6**, 98. ISSN 1475-2875, doi: 10.1186/14752875698, http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1971713{&}tool=pmcentrez{&}rendertype=abstract.

Marshall J, Buchman A, C. HMS, Akbari OS (2017). "Overcoming evolved resistance to population-suppressing homing-based gene drives." *Nature Scientific Reports*, 1–46. ISSN 2045-2322, doi: https://doi.org/10.1101/088427.

`MGDrivE.Setup` *Setup MGDrivE*

Description

Initialize methods in `Patch` to run deterministic or stochastic simulations. This function must be called prior to any objects being created.

Usage

```
MGDrivE.Setup(stochasticityON = FALSE)
```

Arguments

`stochasticityON`
: enable/disable stochastic simulation.

`moveMatAll2` *Movement Matrix: All 2*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatAll2)
```

Format

A matrix with 3 rows and 3 columns:

Patches 1 and 3 are sources for patch 2 which is a sink.

moveMatCascade3 *Movement Matrix: Cascade 3*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatCascade3)
```

Format

A matrix with 3 rows and 3 columns:

Mosquitoes in patch 1 have equal probability to stay or move to 2; mosquitoes in patch 2 have equal probability to stay or move to 3; mosquitoes in patch 3 stay there.

moveMatDiag *Movement Matrix: Diagonal*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatDiag)
```

Format

A matrix with 3 rows and 3 columns:

3 independent patches.

moveMatDiagOneCity *Movement Matrix: Diagonal One City*

Description

A movement matrix for simulation with 1 patch.

Usage

```
data(moveMatDiagOneCity)
```

Format

A matrix with 1 rows and 1 columns:

A 1 by 1 matrix with entry 1.

moveMatDie *Movement Matrix: Die*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatDie)
```

Format

A matrix with 3 rows and 3 columns:

All entries of matrix are 0 for testing that all mosquitoes will be killed.

moveMatIndependent3 *Movement Matrix: Independent 3*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatIndependent3)
```

Format

A matrix with 3 rows and 3 columns:

Mosquitoes in patch 1 stay with probability 0.975, move to patch 2 with probability 0.025, mosquitoes in patch 2 and 3 stay in their patches.

moveMatMixedSpil *Movement Matrix: Mixed Spill*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatMixedSpil)
```

Format

A matrix with 3 rows and 3 columns:

Mosquitoes in patch 1 stay with probability 0.999, move to patch 2 with probability 0.001, mosquitoes in patch 2 and 3 stay in their patches.

moveMatTaleOfTwoCities *Movement Matrix: Tale of Two Cities*

Description

A movement matrix for simulation with 2 patches.

Usage

```
data(moveMatTaleOfTwoCities)
```

Format

A matrix with 2 rows and 2 columns:

Mosquitoes do not move between the two patches.

moveMatTriDiagonal *Movement Matrix: Tri-diagonal*

Description

A movement matrix for simulation with 12 patches.

Usage

```
data(moveMatTriDiagonal)
```

Format

A matrix with 12 rows and 12 columns:

Tri-diagonal matrix with approximately 0.985 probability on diagonal and rest of probability mass on k-1 and k+1 off-diagonal elements.

moveMatTriple *Movement Matrix: Triple*

Description

A movement matrix for simulation with 3 patches.

Usage

```
data(moveMatTriple)
```

Format

A matrix with 3 rows and 3 columns:

All entries of matrix are 1 for testing that mosquitoes will be produced.

`Network` *Network Class Definition*

Description

A `Network` class object stores all the information for a simulation on a defined landscape.

Usage

```
Network
```

Format

An `R6Class` generator object

Constructor

- networkParameters: see `Network.Parameters`
- driveCube: an inheritance cube, see `MGDrivE-Cube` for available cubes
- patchReleases: see `Release_basicRepeatedReleases` for examples on how to set up release schedules
- migrationMale: a stochastic matrix whose dimensions conform to the number of patches
- migrationFemale: a stochastic matrix whose dimensions conform to the number of patches
- directory: character string of output directory

Methods

- get_moveVar: see `get_moveVar_Network`
- get_timeAq: see `get_timeAq_Network`
- get_thetaAq: see `get_thetaAq_Network`
- get_windowSize: see `get_windowSize_Network`
- get_beta: see `get_beta_Network`
- get_muAd: see `get_muAd_Network`
- get_rm: see `get_rm_Network`
- get_AdPopEQ: see `get_AdPopEQ_Network`
- get_g: see `get_g_Network`
- get_Rm: see `get_Rm_Network`
- get_muAq: see `get_muAq_Network`
- get_alpha: see `get_alpha_Network`
- get_Leq_Network: see `get_Leq_Network`
- get_driveCube_genotype: see `get_driveCube_genotype_Network`
- get_driveCube_index: see `get_driveCube_index_Network`
- get_tau: see `get_tau_Network`
- get_genotypesID: see `get_genotypesID_Network`
- get_genotypesN: see `get_genotypesN_Network`

- get_wildType: see get_wildType_Network
- get_eta: see get_eta_Network
- get_phi: see get_phi_Network
- get_omega: see get_omega_Network
- get_xiF: see get_xiF_Network
- get_xiM: see get_xiM_Network
- get_s: see get_s_Network
- get_releaseType: see get_releaseType_Network
- get_patch: see get_patch_Network
- get_patches: see get_patches_Network
- get_nPatch: see get_nPatch_Network
- get_directory: see get_directory_Network
- get_simTime: see get_simTime_Network
- get_conADM: see get_conADM_Network
- get_conAF1: see get_conAF1_Network
- close_allConnections: see close_allConnections_Network
- get_tNow: see get_tNow_Network
- get_migrationMale: see get_migrationMale_Network
- get_migrationMaleRow: see get_migrationMaleRow_Network
- set_migrationMale: see set_migrationMale_Network
- get_migrationFemale: see get_migrationFemale_Network
- get_migrationFemaleRow: see get_migrationFemaleRow_Network
- set_migrationFemale: see set_migrationFemale_Network
- get_patchReleases: see get_patchReleases_Network
- oneDay_Migration: see oneDay_Migration_Network
- reset: see reset_Network
- oneRun: see oneRun_Network
- oneDay: see oneDay_Network

Fields

- parameters: see Network.Parameters
- patches: a list of Patch objects
- nPatch: number of patches
- simTime: maximum time of simulation
- driveCube: an inheritance cube
- tNow: current time of simulation (time starts at 2 because time 1 is the initial equilibrium state)
- runID: an identifier for the current simulation run, useful for Monte Carlo simulation
- directory: a character string of where to store output
- conADM: a connection to write male population dynamics out to
- conAF1: a connection to write female population dynamics out to
- migrationMale: a stochastic matrix whose dimensions conform to the number of patches
- migrationFemale: a stochastic matrix whose dimensions conform to the number of patches
- patchReleases: a list of release schedules for each patch

`Network.Parameters` *Network Parameters*

Description

Generate parameters for simulation on a `Network`. Parameters average generation time g, population growth rate R_m, aquatic mortality μ_{Aq}, and aquatic survival θ_{Aq} are shared between patches and calculated by `calcAverageGenerationTime`, `calcPopulationGrowthRate`, `calcLarvalStageMortalityRate`, and `calcAquaticStagesSurvivalProbability`.
Patch-specific parameters α and L_{eq} are calculated for each patch by `calcDensityDependentDeathRate` and `calcLarvalPopEquilibrium`.

Usage

```
Network.Parameters(nPatch, simTime, parallel = FALSE, moveVar = 1000,
  tEgg = 1L, tLarva = 14L, tPupa = 1L, beta = 32, muAd = 0.123,
  popGrowth = 1.096, AdPopEQ, runID = 1L)
```

Arguments

`nPatch`	number of `Patch`
`simTime`	maximum time to run simulation
`parallel`	append process id (see `link[base]{Sys.getpid}`) to output files for running in parallel
`moveVar`	variance of stochastic movement (not used in diffusion model of migration). It affects the concentration of probability in the Dirchlet simplex, small values lead to high variance and large values lead to low variance.
`tEgg`	length of egg stage
`tLarva`	length of larval instar stage
`tPupa`	length of pupal stage
`beta`	female egg batch size of wild-type
`muAd`	wild-type daily adult mortality (1/muAd is average wild-type lifespan)
`popGrowth`	daily population growth rate (used to calculate equilibrium)
`AdPopEQ`	vector of adult population size at equilibrium
`runID`	begin counting runs with this set of parameters from this value

`normalise` *Normalise a Numeric Vector*

Description

Normalise a numeric vector to sum to one

Usage

```
normalise(vector)
```

Arguments

`vector`	numeric vector

`oneDay_admPupating_deterministic_Patch`

Determinstc Adult Male Pupation

Description

Adult male emergence is calculated based on the number of male pupae multiplied by

$$\left(\overline{\xi_m} * (\theta_e * \theta_p) * (1 - \mu_{ad}) * D(\theta_l, T_p)\right)$$

, where $\overline{\xi_m}$ is the genotype-specific pupation success probability.

Usage

```
oneDay_admPupating_deterministic_Patch()
```

`oneDay_admPupating_stochastic_Patch`

Stochastic Adult Male Pupation

Description

Pupation from male pupae to adults is sampled from a binomial distribution for each genotype where the probability of pupation is given by

$$\left(\overline{\xi_m} * (\theta_e * \theta_p) * (1 - \mu_{ad}) * D(\theta_l, T_p)\right)$$

, where $\overline{\xi_m}$ is the genotype-specific pupation success probability.

Usage

```
oneDay_admPupating_stochastic_Patch()
```

`oneDay_admSurvival_deterministic_Patch`

Determinstc Adult Male Survival

Description

Daily adult male survival is calculated according to

$$\overline{\overline{Am_{[t-1]}}} * (1 - \mu_{ad}) * \overline{\omega_m}$$

, where μ_{ad} is adult mortality rate and $\overline{\omega_m}$ correponds to genotype-specific mortality effects.

Usage

```
oneDay_admSurvival_deterministic_Patch()
```

oneDay_admSurvival_stochastic_Patch
Stochastic Adult Male Survival

Description

Daily adult male survival is sampled from a binomial distribution where survival probability is given by

$$(1 - \mu_{ad}) * \overline{\omega_m}$$

, where μ_{ad} is adult mortality rate and $\overline{\omega_m}$ correponds to genotype-specific mortality effects.

Usage

```
oneDay_admSurvival_stochastic_Patch()
```

oneDay_af1Mating_deterministic_Patch
Determinstc Mating

Description

Mating is calculated as the outer product of newly emerging adult females and adult males, modulated by $\overline{\eta}$, genotype-specific male mating fitness.

Usage

```
oneDay_af1Mating_deterministic_Patch()
```

oneDay_af1Mating_stochastic_Patch
Stochastic Mating

Description

Mating for each newly emerging adult female genotype is sampled from a multinomial distribution with probabilities equal to the adult male population vector multiplied by $\overline{\eta}$, genotype-specific male mating fitness.

Usage

```
oneDay_af1Mating_stochastic_Patch()
```

`oneDay_af1Pupation_deterministic_Patch`
Determinstc Adult Female Pupation

Description

Adult female emergence is calculated based on the number of female pupae multiplied by

$$\left(\overline{\xi_f} * (\theta_e * \theta_p) * (1 - \mu_{ad}) * D(\theta_l, T_p)\right)$$

, where $\overline{\xi_f}$ is the genotype-specific pupation success probability.

Usage

```
oneDay_af1Pupation_deterministic_Patch()
```

`oneDay_af1Pupation_stochastic_Patch`
Stochastic Adult Female Pupation

Description

Pupation from female pupae to adults is sampled from a binomial distribution for each genotype where the probability of pupation is given by

$$\left(\overline{\xi_f} * (\theta_e * \theta_p) * (1 - \mu_{ad}) * D(\theta_l, T_p)\right)$$

, where $\overline{\xi_f}$ is the genotype-specific pupation success probability.

Usage

```
oneDay_af1Pupation_stochastic_Patch()
```

`oneDay_af1Survival_deterministic_Patch`
Determinstc Adult Female Survival

Description

Daily adult female survival is calculated according to

$$\overline{\overline{Af_{[t-1]}}} * (1 - \mu_{ad}) * \overline{\omega_f}$$

, where μ_{ad} is adult mortality rate and $\overline{\omega_f}$ correponds to genotype-specific mortality effects.

Usage

```
oneDay_af1Survival_deterministic_Patch()
```

oneDay_af1Survival_stochastic_Patch
Stochastic Adult Female Survival

Description

Daily adult female survival is sampled from a binomial distribution where survival probability is given by

$$(1 - \mu_{ad}) * \overline{\omega_f}$$

, where μ_{ad} is adult mortality rate and $\overline{\omega_f}$ correponds to genotype-specific mortality effects.

Usage

```
oneDay_af1Survival_stochastic_Patch()
```

oneDay_calcCumulativeLarvalDensityDependentFactor_Patch
Calculate Cumulative Larval density-dependent Mortality

Description

Calculate

$$F(L[t]) = \left(\frac{\alpha}{\alpha + \sum \overline{L[t]}} \right)^{1/T_l}$$

, the cumulative effect of density-dependence on larval mortality over the entire duration of larval stage.

Usage

```
oneDay_calcCumulativeLarvalDensityDependentFactor_Patch()
```

oneDay_calcCumulativePupaDensityDependentFactor_Patch
Calculate Cumulative Pupae density-dependent Mortality

Description

Calculate

$$D(\theta_l, T_P) = \begin{cases} \theta'_{l[0]} = \theta_l & i = 0 \\ \theta'_{l[i+1]} = \theta'_{l[i]} * F(\overline{L_{[t-i-T_P]}}) & i \leq T_P \end{cases}$$

, the cumulative effect of density-dependence on larval mortality over the entire duration of larval and pupal stages.

Usage

```
oneDay_calcCumulativePupaDensityDependentFactor_Patch()
```

`oneDay_calcLarvalDensityDependentFactor_Patch`
Calculate Larval density-dependent Mortality

Description

Calculate

$$D(\theta_l, T_x) = \begin{cases} \theta'_{l[0]} = \theta_l & i = 0 \\ \theta'_{l[i+1]} = \theta'_{l[i]} * F(\overline{L_{[t-i-T_x]}}) & i \leq T_l \end{cases}$$

, the effect of density-dependence on larval mortality for one day.

Usage

```
oneDay_calcLarvalDensityDependentFactor_Patch()
```

`oneDay_eggsFract2_deterministic_Patch`
Determinstc Larval Pupation

Description

Calculate the number of larvae that will pupate prior to calculating density-dependent effects in `oneDay_calcCumulativeLarvalDensityDependentFactor_Patch`.

Usage

```
oneDay_eggsFract2_deterministic_Patch()
```

`oneDay_eggsFract2_stochastic_Patch`
Stochastic Larval Pupation

Description

Calculate the number of larvae that will pupate prior to calculating density-dependent effects in `oneDay_calcCumulativeLarvalDensityDependentFactor_Patch`.

Usage

```
oneDay_eggsFract2_stochastic_Patch()
```

`oneDay_femaleReleases_Patch`
Release Female Mosquitoes in a Patch

Description

Based on this patch's release schedule, handle daily releases.

Usage

```
oneDay_femaleReleases_Patch()
```

`oneDay_hatchingFract_deterministic_Patch`
Determinstc Fraction of Eggs Maturing to Hatch

Description

Calculate the fraction of hatching eggs accounting for delay given by: $\overline{O(T_e)}$

Usage

```
oneDay_hatchingFract_deterministic_Patch()
```

`oneDay_hatchingFract_stochastic_Patch`
Stochastic Fraction of Eggs Maturing to Hatch

Description

Calculate the fraction of hatching eggs accounting for delay given by: $\overline{O(T_e)}$ Stochasticity is introduced by assuming $\overline{O(T_e)}$ defines the mean of a Poisson distributed number of eggs that can hatch.

Usage

```
oneDay_hatchingFract_stochastic_Patch()
```

`oneDay_initOutput_Patch`
Initialize Output from Focal Patch

Description

Writes output to the text connections specified in the enclosing `Network`

Usage

```
oneDay_initOutput_Patch()
```

`oneDay_larHatching_deterministic_Patch`
Stochastic Egg Hatching to Larval Stage

Description

Calculate the eggs that have survived and hatched during a day given by: $\overline{O(T_e)} * \theta_e$

Usage

```
oneDay_larHatching_deterministic_Patch()
```

`oneDay_larHatching_stochastic_Patch`
Stochastic Egg Hatching to Larval Stage

Description

Calculate the eggs that have survived and hatched during a day given by: $\overline{O(T_e)} * \theta_e$ The number of eggs that survive to hatch follows a binomial distribution.

Usage

```
oneDay_larHatching_stochastic_Patch()
```

`oneDay_larPupating_deterministic_Patch`
Deterministc Larval Pupation

Description

Calculate the number of larvae that have transformed into pupae given by $\overline{O(T_e + T_l)} * \theta_e * D(\theta_l, 0)$

Usage

```
oneDay_larPupating_deterministic_Patch()
```

`oneDay_larPupating_stochastic_Patch`
Stochastic Larval Pupation

Description

Calculate the number of larvae that have transformed into pupae given by $\overline{O(T_e + T_l)} * \theta_e * D(\theta_l, 0)$ This number follows a binomial distribution.

Usage

```
oneDay_larPupating_stochastic_Patch()
```

oneDay_larSurvival_deterministic_Patch
Determinstc Larval Survival

Description

Calculate the number of larvae surviving from day to day, given by:

$$\overline{L_{[t-1]}} * (1 - \mu_l) * F(\overline{L_{[t-1]}})$$

Usage

```
oneDay_larSurvival_deterministic_Patch()
```

oneDay_larSurvival_stochastic_Patch
Stochastic Larval Survival

Description

Calculate the number of larvae surviving from day to day, given by:

$$\overline{L_{[t-1]}} * (1 - \mu_l) * F(\overline{L_{[t-1]}})$$

Stochasticity is introduced by assuming $(1-\mu_l) * F(\overline{L_{[t-1]}})$ defines binomial likelihood of survival for each genotype of larvae.

Usage

```
oneDay_larSurvival_stochastic_Patch()
```

oneDay_maleReleases_Patch
Release Male Mosquitoes in a Patch

Description

Based on this patch's release schedule, handle daily releases.

Usage

```
oneDay_maleReleases_Patch()
```

`oneDay_migrationIn_Patch`
Inbound Migration

Description

Accumulate all inbound migration to this patch.

Usage

```
oneDay_migrationIn_Patch(maleIn, femaleIn)
```

Arguments

`maleIn`	vector of inbound migration
`femaleIn`	matrix of inbound migration

`oneDay_migrationOut_deterministic_Patch`
Deterministic Oubound Migration from a Patch

Description

Determinstc model of outbound migration of `AF1new` females from this patch, fills up the `femaleMigration` array.

Usage

```
oneDay_migrationOut_deterministic_Patch()
```

`oneDay_migrationOut_stochastic_Patch`
Stochastic Oubound Migration

Description

Stochastic model of migration of `AF1new` females from this patch, fills up the `femaleMigration` array. Migration is modeled as a Dirichlet-Multinomial process parameterized by `moveVar` multiplied by the row corresponding to this patch from the stochastic matrix. A Dirichlet distributed random variate is sampled from `rdirichlet` according to that parameter vector and then movement is sampled from `rmultinom`.

Usage

```
oneDay_migrationOut_stochastic_Patch()
```

oneDay_Migration_Network *Inter-Patch Migration*

Description

Simulate migration between patches. See MGDrivE-Model, 'Migration' section for more details on how inter-patch migration is handled.

Usage

```
oneDay_Migration_Network()
```

oneDay_Network *Run a Single Day on a Network*

Description

Runs a single day of simulation on a Network object, handling population dynamics, migration, population update, and output.

Usage

```
oneDay_Network()
```

oneDay_numMaleFemale_deterministic_Patch *Determinstc Sex Ratio*

Description

Calculate the number of males, $(1-\overline{\phi}) * \overline{E'}$ and females, $\overline{\phi} * \overline{E'}$

Usage

```
oneDay_numMaleFemale_deterministic_Patch()
```

oneDay_numMaleFemale_stochastic_Patch *Stochastic Sex Ratio*

Description

Calculate the number of males, $(1-\overline{\phi}) * \overline{E'}$ and females, $\overline{\phi} * \overline{E'}$ These counts are follow a binomial distribution.

Usage

```
oneDay_numMaleFemale_stochastic_Patch()
```

`oneDay_ovipositG1_deterministic_Patch`
Determinstc Oviposition

Description

Calculate the number of eggs oviposited by female mosquitoes following:

$$\overline{O(T_x)} = \sum_{j=1}^{n} \left(\left((\beta * \overline{s} * \overline{\overline{Af_{[t-T_x]}}}) * \overline{\overline{Ih}} \right) * \Lambda \right)_{ij}^{\top}$$

Usage

```
oneDay_ovipositG1_deterministic_Patch()
```

`oneDay_ovipositG1_stochastic_Patch`
Stochastic Oviposition

Description

Calculate the number of eggs oviposited by female mosquitoes following:

$$\overline{O(T_x)} = \sum_{j=1}^{n} \left(\left((\beta * \overline{s} * \overline{\overline{Af_{[t-T_x]}}}) * \overline{\overline{Ih}} \right) * \Lambda \right)_{ij}^{\top}$$

The deterministic result for number of eggs is used as the mean of a Poisson-distributed number of actual eggs oviposited.

Usage

```
oneDay_ovipositG1_stochastic_Patch()
```

`oneDay_PopDynamics_Patch`
Daily Population Dynamics for a Patch

Description

Run population dynamics (not including migration) for this patch.

Usage

```
oneDay_PopDynamics_Patch()
```

oneDay_updatePopulation_Patch *Shift Population*

Description

Update larval and adult populations daily at end of time step, calls shiftAndUpdatePopVector

Usage

```
oneDay_updatePopulation_Patch()
```

oneDay_writeOutput_Patch *Write Output from Focal Patch*

Description

Writes output to the text connections specified in the enclosing Network

Usage

```
oneDay_writeOutput_Patch()
```

oneRun_Network *Run Simulation*

Description

Run a single simulation on this network.

Usage

```
oneRun_Network(conADM = NULL, conAF1 = NULL)
```

Arguments

conADM	an optional connection to write male population dynamics to, if NULL use the directory specified in the constructor of Network with the current runID appended to the file.
conAF1	an optional connection to write female population dynamics to, if NULL use the directory specified in the constructor of Network with the current runID appended to the file.

`Patch` *Patch Class Definition*

Description

A Patch is a single well-mixed population that is the smallest unit of simulation for MGDrivE.

Usage

```
Patch
```

Format

An `R6Class` generator object

Constructor

- patchID: integer ID of this patch
- genotypesID: character vector of genotypes
- simTime: maximum time of simulation
- windowSize: necessary memory window size for model
- EGGt0: initial egg population, L_{eq}
- LARt0: initial larval population
- PUPt0: initial pupae population
- ADMt0: initial adult male population, Ad_{eq}
- AF1t0: initial adult female population, Ad_{eq}
- maleReleases: integer ID of this patch
- femaleReleases: female release schedule for this patch, see `Release_basicRepeatedReleases`

Methods

- get_patchID: see `get_patchID_Patch`
- get_AF1new: see `get_AF1new_Patch`
- set_AF1new: see `set_AF1new_Patch`
- get_ADMnew: see `get_ADMnew_Patch`
- set_ADMnew: see `set_ADMnew_Patch`
- accumulate_ADMnew: see `accumulate_ADMnew_Patch`
- get_EGG: see `get_EGG_Patch`
- get_LAR: see `get_LAR_Patch`
- get_PUP: see `get_PUP_Patch`
- get_ADM: see `get_ADM_Patch`
- get_AF1: see `get_AF1_Patch`
- get_EGGdly: see `get_EGGdly_Patch`
- get_LARdly: see `get_LARdly_Patch`

- get_PUPdly: see get_PUPdly_Patch
- get_ADMdly: see get_ADMdly_Patch
- get_AF1dly: see get_AF1dly_Patch
- get_maleMigration: see get_maleMigration_Patch
- get_femaleMigration: see get_femaleMigration_Patch
- set_NetworkPointer: see set_NetworkPointer_Patch
- get_NetworkPointer: see get_NetworkPointer_Patch
- reset: see reset_Patch
- oneDay_initOutput: see oneDay_initOutput_Patch
- oneDay_writeOutput: see oneDay_writeOutput_Patch
- oneDay_migrationIn: see oneDay_migrationIn_Patch
- oneDay_maleReleases: see oneDay_maleReleases_Patch
- oneDay_femaleReleases: see oneDay_femaleReleases_Patch
- oneDay_PopDynamics: see oneDay_PopDynamics_Patch
- oneDay_updatePopulation: see oneDay_updatePopulation_Patch
- oneDay_calcLarvalDensityDependentFactor: see oneDay_calcLarvalDensityDependentFactor_Patch
- oneDay_calcCumulativeLarvalDensityDependentFactor: see oneDay_calcCumulativeLarvalDensityDependent
- oneDay_calcCumulativePupaDensityDependentFactor: see oneDay_calcCumulativePupaDensityDependentFac
- oneDay_migrationOut: see oneDay_migrationOut_stochastic_Patch or oneDay_migrationOut_determinist
- oneDay_ovipositG1: see oneDay_ovipositG1_stochastic_Patch or oneDay_ovipositG1_deterministic_Pat
- oneDay_larSurvival: see oneDay_larSurvival_stochastic_Patch or oneDay_larSurvival_deterministic_P
- oneDay_hatchingFract: see oneDay_hatchingFract_stochastic_Patch or oneDay_hatchingFract_determini
- oneDay_larHatching: see oneDay_larHatching_stochastic_Patch or oneDay_larHatching_deterministic_
- oneDay_eggsFract2: see oneDay_eggsFract2_stochastic_Patch or oneDay_eggsFract2_deterministic_Pat
- oneDay_larPupating: see oneDay_larPupating_stochastic_Patch or oneDay_larPupating_deterministic_P
- oneDay_numMaleFemale: see oneDay_numMaleFemale_stochastic_Patch or oneDay_numMaleFemale_determ
- oneDay_admSurvival: see oneDay_admSurvival_stochastic_Patch or oneDay_admSurvival_deterministic_
- oneDay_admPupating: see oneDay_admPupating_stochastic_Patch or oneDay_admPupating_deterministic
- oneDay_af1Survival: see oneDay_af1Survival_stochastic_Patch or oneDay_af1Survival_deterministic_P
- oneDay_af1Pupation: see oneDay_af1Pupation_stochastic_Patch or oneDay_af1Pupation_deterministic_
- oneDay_af1Mating: see oneDay_af1Mating_stochastic_Patch or oneDay_af1Mating_deterministic_Patch

Fields

- patchID: integer ID of this patch
- EGGt0: vector of initial egg stage population
- LARt0: vector of initial larval stage population
- PUPt0: vector of initial pupae stage population
- ADMt0: vector of initial adult male stage population
- AF1t0: matrix of initial adult female stage population
- EGG: egg stage population

- LAR: larvae stage population
- PUP: pupae stage population
- ADM: adult male stage population
- AF1: adult female stage population
- EGGdly: delay egg stage population
- LARdly: delay larvae stage population
- PUPdly: delay pupae stage population
- ADMdly: delay adult male stage population
- AF1dly: delay adult female stage population
- LARnew: new larval population after difference equations; needed to store population prior to migration exchange
- ADMnew: new adult male population after difference equations; needed to store population prior to migration exchange
- AF1new: new adult female population after difference equations; needed to store population prior to migration exchange
- maleMigration: matrix of outbound migrating males of dimension nGenotypes X nPatch
- femaleMigration: array of outbound migrating females of dimension nGenotypes X nGenotypes X nPatch
- NetworkPointer: a reference to enclosing `Network`
- ovipositG1: new eggs after oviposition by mated female mosquitoes
- larSurvival: surviving larvae
- hatchingFract: fraction of larvae that hatch
- larPupating: fraction of larvae that undergo pupation
- numMaleFemale: number of male vs. female emerging imago stage adults
- admSurvival: number of surviving adult males
- admPupating: number of pupating imago stage adults that become males
- af1Survival: number of surviving adult females
- af1Pupation: number of pupating imago stage adults that become females
- maleMatrix: row of male migration matrix corresponding to migration from this patch
- femaleMatrix: row of female migration matrix corresponding to migration from this patch
- larDDMortal: larval mortality
- f: density dependent factor in larval mortality

primePopMatrixArray *Create a primed population array of matrices*

Description

Primes an array for the population history to be stored. The length of the array is equal to the window required for the model to run (in our specific case it is equal to the sum of aquatic stages lengths).

Usage

```
primePopMatrixArray(primingMatrix, memoryWindow)
```

Arguments

primingMatrix	a named matrix population
memoryWindow	integer size of list structure

primePopVectorArray *Create a primed population array of vectors*

Description

Primes an array for the population history to be stored. The length of the array is equal to the window required for the model to run (in our specific case it is equal to the sum of aquatic stages lengths).

Usage

```
primePopVectorArray(primingVector, memoryWindow)
```

Arguments

primingVector	a named vector population
memoryWindow	integer size of list structure

quantileC *Quantiles Function*

Description

Calculate the given quantiles of a matrix.

Usage

```
quantileC(Trials, Probs)
```

Arguments

Trials	Integer matrix to calculate quantiles over
Probs	Vector of quantiles

Details

This function calculates the given quantiles over the rows of an integer matrix. It uses method 8 of the stat::quantiles() function. It gives the same result, to numerical accuracy, and is designed to handle matrix input. It is only designed to work on integer matrices!

Value

Numeric Matrix

Examples

```
Trials <- matrix(data = sample(x=1:100, size = 150, replace = TRUE), nrow=15, ncol=10)
DrawSize <- c(.25, .5, .75)

quantileC(Trials, Probs)
```

rDirichlet *Dirichlet Distribution*

Description

Make a single draw from a dirichlet distribution with the shape parameter one. This replaces the MCMCpack rDirichlet function, which was wholly written in R.

Usage

```
rDirichlet(migrationPoint)
```

Arguments

migrationPoint	Vector of weights for draws. Must be positive.

Release_basicRepeatedReleases *Make List of Modified Mosquito Releases*

Description

Sets up a release schedule for a single patch, returns a list to be used in oneDay_maleReleases_Patch or oneDay_femaleReleases_Patch.

Usage

```
Release_basicRepeatedReleases(genotypes, releaseStart, releaseEnd,
  releaseInterval, releaseVector, sex = "M")
```

Arguments

genotypes	possible genotypes
releaseStart	day releases start
releaseEnd	day releases end
releaseInterval	interval between releases
releaseVector	named character vector of release composition
sex	character in 'M','F'

Examples

```
# to setup for 3 patches but only release in the first with a defined release schedule:

patchReleases = replicate(n = 3,expr = {
  list(maleReleases = NULL,femaleReleases = NULL)
},simplify = FALSE)

patchReleases[[1]]$femaleReleases = Release_basicRepeatedReleases(genotypes = Cube_Homing1RA$genotypesID,rel
patchReleases[[1]]$maleReleases = Release_basicRepeatedReleases(genotypes = Cube_Homing1RA$genotypesID,relea
```

reset_Network *Reset Network*

Description

Reset a Network between runs, useful for Monte Carlo simulation. This calls reset_Patch on each patch and resets tNow = 2 and increments the runID.

Usage

```
reset_Network()
```

reset_Patch *Reset Patch to Initial Conditions*

Description

Resets a patch to its initial configuration so that a new one does not have to be created and allocated in the network (for Monte Carlo simulation).

Usage

```
reset_Patch()
```

retrieveOutput *Retrieve Output*

Description

Read in output from directory. The resulting object will be a nested list; outermost nesting dimension indexes runID, within runID elements are split by sex and innermost nesting is over patches.

Usage

```
retrieveOutput(directory, genotypes)
```

Arguments

directory	directory where output was written to; must not end in path seperator
genotypes	character vector of possible genotypes; found in driveCube$genotypesID

set_ADMnew_Patch *Set ADMnew*

Description

Set an element in new ADM males

Usage

```
set_ADMnew_Patch(count, genotype_M)
```

Arguments

count	number of mosquitoes
genotype_M	genotype of male

set_AF1new_Patch *Set AF1new*

Description

Set an element in new AF1 females

Usage

```
set_AF1new_Patch(count, genotype_F, genotype_M)
```

Arguments

count	number of mosquitoes
genotype_F	genotype of female (row of matrix)
genotype_M	genotype of male (column of matrix)

set_migrationFemale_Network *Set Female Migration Matrix*

Description

Sets link{private$migrationFemale} field

Usage

```
set_migrationFemale_Network(migrationFemale)
```

Arguments

migrationFemale	matrix object (rows must sum to one)

set_migrationMale_Network *Set Male Migration Matrix*

Description

Sets link{private$migrationMale} field

Usage

```
set_migrationMale_Network(migrationMale)
```

Arguments

migrationMale	matrix object (rows must sum to one)

set_NetworkPointer_Patch *Set Network Pointer*

Description

Set a reference to the enclosing Network object

Usage

```
set_NetworkPointer_Patch(NetworkPointer)
```

Arguments

NetworkPointer	a Network object

shiftAndUpdatePopVector *Shift a Vector*

Description

Shift a population vector by one day and insert the new population. This was written to remove the dependency "binhf".

Usage

```
shiftAndUpdatePopVector(popVector, newPop)
```

Arguments

popVector	List of population vectors of length(Tegg+Tlarva+Tpupa)
newPop	Vector of length equal to the number of genotypes

splitOutput *Split Output by Patch*

Description

Split output into multiple files by patches.

Usage

```
splitOutput(directory, multiCore = FALSE)
```

Arguments

directory	Directory where output was written to; must not end in path seperator
multiCore	Write output using multiple cores? Default is FALSE

SymCubeC *Make a Symmetric Cube*

Description

This function makes a lower-triangular cube symmetric over the z-axis. It was written to remove the dependency "Matrix". It is only used in building cubes.

Usage

```
SymCubeC(lowerMat)
```

Arguments

lowerMat	A lower-triangular matrix of depth 1 or more

turnStochasticityOnOrOff *Enable or Disable Stochastic Model*

Description

Set switches for deterministic or stochastic model

Usage

```
turnStochasticityOnOrOff(on = TRUE)
```

Arguments

on	enable/disable stochastic behaviour

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