R documentation

of all in 'EpiPv'

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R topics documented:

| APdata_simulator | *Simulate Access Period Data for Virus Transmission Assays* |

Description

The APdata_simulator function receives event rate parameters for virus transmission (μ, α, β, γ) as well as assay feeding durations and returns simulated access period data. The simulation considers how events occur during assays, accounting for periods of acquisition, latency progression, inoculation and loss of infectiousness.

Usage

```
APdata_simulator(lmark_in, smarkpams_in, WF_in, nReps_in)
```

Arguments

lmark_in	A numeric vector representing assay feeding durations.
smarkpams_in	A numeric vector containing event rate parameters for virus transmission, including alpha, beta, gamma and mu.
WF_in	An integer indicating the number of whitefly in a cohort per replication
nReps_in	An integer representing the number of replications for the simulation.

Details

This function simulates the random times of event occurrence in AP (Access Period: Acquisition Access Period, Latent Access Period, and Inoculation Access Period) experiments. The simulation reflects the contingent nature of inoculation duration, which varies depending on when latency progression and loss of infectiousness occurs.

Value

A binary vector of dimension nReps_in representing the simulated access period data (test plant infection or no test plant infection) based on the input parameters.

Examples

```
# Example of how to use the APdata_simulator function
lmark <- c(10, 15, 20)  # Assay feeding durations
smarkpams <- c(0.5, 2, 1, 0.3)  # Event rate parameters: alpha, beta, mu
WF <- 5  # Number of workflow iterations
nReps <- 100  # Number of repetitions

# Simulate access period data
simulated_data <- APdata_simulator(lmark, smarkpams, WF, nReps)
print(simulated_data)
```

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calculate_epidemic_probability

Calculate Epidemic Probability given Plant Virus Transmission rates and local parameters

---

Description

This function calculates the epidemic probability for different types of inoculum state based on event rate parameters for virus transmission, local parameters, and user inputs.

Usage

```
calculate_epidemic_probability(numberInsects, interv, localParameters, virusParameters)
```

Arguments

numberInsects   An integer representing the local level for insect vector burden i.e. the number of vectors per plant.

interv   A numeric value indicating the initial time interval resolution (minutes) for the probability calculations (recommend using 10 and the routine will increase this by 1 if step size is too big until step size is appropriate (i.e., probability no event occurs >0)).

localParameters

A numeric vector containing local event rate parameters (θ, r, h, b_f, nu_pl) (vector dispersal, roguing, harvesting, vector field mortality, plant latency progression rates, all day^-1).

virusParameters

A numeric vector containing virus transmission parameters (α, β, μ) (acquisition, inoculation and virus clearance rates, all day^-1).

Value

A numeric array or matrix representing the epidemic probabilities for various inoculum states.

Examples

```
# Example of how to use the calculate_epidemic_probability function
numberInsects <- 10
interv <- 10
localParameters <- c(1, 0.1, 0.01, 0.1, 0.05)
virusParameters <- c(0.3, 0.4, 0.5)

epidemic_probabilities <- calculate_epidemic_probability(numVars,starting_guess, numberInsects, interv, loc
print(epidemic_probabilities)
```

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estimate_virus_parameters_PT

Estimate Virus Parameters for Persistently Transmitted Plant Viruses

---

Description

This function estimates virus transmission parameters from access period data for a given vector-PT virus-plant combination.

Usage

```
estimate_virus_parameters_PT(assay1, assay2, assay3, offdiag_array, IVD, lsEst, virus)
```

Arguments

assay1	A matrix or data frame containing access period data for the first assay (acquisition access period), structured with the first row as feeding durations, the second row as the number of insect vectors used, and the third row as the number of infections.
assay2	A matrix or data frame containing access period data for the second assay (latent access period), structured similarly to assay1.
assay3	A matrix or data frame containing access period data for the third assay (inoculation access period), structured similarly to assay1.
offdiag_array	A numerical array containing the fixed access period durations for those durations that are not varied in the assay.
IVD	An integer value representing the number of insects in a cohort for each replication.
lsEst	An integer value representing the estimated survival of insects in the laboratory (in minutes).
virus	A character string representing the name of the virus for output file naming.

Details

The function runs a Stan model for parameter estimation based on access period assays for persistent transmission viruses. It exports summary parameter estimates and the full Markov chains to the main home directory.

Value

Returns a matrix containing the posterior parameter distributions for transmission rates mu, alpha, beta, and gamma.

Examples

```
# Example of how to call the function
result <- estimate_virus_parameters_PT(assay1, assay2, assay3, offdiag_array, IVD, lsEst, virus_name)
```

---

estimate_virus_parameters_SPT

Estimate Virus Transmission Parameters for SPT

Description

This function estimates virus transmission parameters from access period data for a given vector-SPT virus-plant combination.

Usage

```
estimate_virus_parameters_SPT(assay1, assay2, offdiag_array, IVD, lsEst, virus)
```

Arguments

assay1	A matrix or data frame containing access period data for the first assay (acquisition access period), structured with the first row as feeding durations, the second row as the number of insect vectors used, and the third row as the number of infections.
assay2	A matrix or data frame containing access period data for the second assay (inoculation access period), structured similarly to assay1.
offdiag_array	A numerical array containing the fixed access period durations for the duration that is not varied in the assay (e.g. where acquisition access period is varied this is typically followed by a fixed inoculationa access period and vice versa).
IVD	An integer value representing the number of insects in a cohort for each replication.
lsEst	An integer value representing the estimated survival of insects in the laboratory (in minutes).
virus	A character string representing the name of the virus for output file naming.

Details

The function runs a Stan model for parameter estimation based on access period assays for persistent transmission viruses. It exports summary parameter estimates and the full Markov chains to the main home directory.

Value

Returns a matrix containing the posterior parameter distributions for transmission rates mu, alpha and beta.

Examples

```
# Example usage
result <- estimate_virus_parameters_SPT(assay1_data, assay2_data, offdiag_data, IVD_value, lsEst_value, "vi
```

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