

Package ‘CWDsims’

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Type Package

Title CWDsims: An R package for simulating chronic wasting disease scenarios

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Description Collections of functions to run an interactive Shiny application of CWD disease models. Currently there are deterministic and stochastic models that are intended to project out scenarios for a 5 to 10 year window. The models are sex and age structured with direct and indirect transmission.

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Depends R (>= 3.4)

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dplyr (>= 0.8.3),
forcats (>= 0.4.0),
ggplot2 (>= 3.0.0),
ggridges (>= 0.5.0),
knitr (>= 1.25),
magrittr (>= 1.2),
markdown (>= 1.0),
plyr (>= 1.8.0),
popbio (>= 2.0),
reshape2 (>= 1.4.0),
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R topics documented:

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allocate_deaths	<i>Randomly allocates deaths in the stochastic CWD model</i>
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Description

Randomly allocates deaths in the stochastic CWD model

Usage

```
allocate_deaths(deaths, pop)
```

Arguments

deaths	A vector of how many die in each age category
pop	A matrix of age.categories = rows and number of I categories = columns

Value

A new matrix of the # of individuals in each I and age category

CWDsims

CWDsims: An R package for chronic wasting disease simulations

Description

Collections of functions to run an interactive Shiny application of CWD disease models. Currently there are deterministic and stochastic models that are intended to project out scenarios for a 5 to 10 year window. The models are sex and age structured with direct and indirect transmission.

Model functions

`cwd_det_model` runs the deterministic CWD model

`cwd_stoch_model` runs the stochastic CWD model

`cwd_det_model_wiw` similar to `cwd_det_model`, but allows for different male-male male-female, and female-male transmission rates.

`cwd_stoch_model_wiw` similar to `cwd_stoch_model`, but allows for different male-male male-female, and female-male transmission rates.

`cwd_stoch_wrapper` runs the stochastic CWD model multiple times for the same parameter set

`launchCWDapp` launches the Shiny applications.

Helper functions

`est_beta_params` converts from a mean and variance to the shape and scale parameters of the Beta distribution

`allocate_deaths` randomly allocates deaths among the 10 infectious subcategories

Plotting functions

`plot_age_dist` plots the age distribution at the last timepoint

`plot_buck_doe` plots the adult male to female ratio over time

`plot_fawn_doe` plots the fawn to adult female ratio over time

`plot_deaths` plots how types of deaths change over time.

`plot_prev_age_end` plots the prevalence versus age curve at the last timepoint.

`plot_prev_time` plots the prevalence over time.

`plot_tots` plots the total population size over time

`plot_ttd` plots the distribution of years until disease-induced death given a rate of movement among the infectious subcategories

`plot_vitals` plots the distribution of survival and reproductive rates

Stochastic plotting functions

plot_stoch_age_dist plots the stochastic age distribution plot for the last time point
 plot_stoch_buck_doe plots the stochastic adult male to adult female ratio
 plot_stoch_deaths plots how types of deaths change in the stochastic model over time.
 plot_stoch_disease plots the number of positive and negative individuals over time
 plot_stoch_fawn_doe fawns to adult females ratio over time
 plot_stoch_perc_deaths plots how the stochastic model over time.
 plot_stoch_prev plot the prevalence over time for the stochastic model
 plot_stoch_prev_age plot stochastic prevalence by age over time
 plot_stoch_prev_age_end Prevalence versus age plot at the last time point
 plot_stoch_tots plot the total number of individuals over time

Comparison plotting functions

plot_compare_all_det barplot to compare the output of two different deterministic scenarios
 plot_compare_all_stoch density plot to compare the output of two different scenarios for the stochastic model
 plot_compare_hunted density plot to look at how the number of hunted individuals compares for the stochastic model.
 plot_compare_prev density plot comparing prevalence for the stochastic model.
 plot_compare_tots density plot comparing the total population size for the stochastic model.

cwg_det_model

CWD deterministic model function

Description

Deterministic monthly age and sex structured model with constant environmental transmission and dynamic direct transmission

Usage

cwg_det_model(params)

Arguments

params	A list with the following parameters included: fawn.an.sur, juv.an.sur, ad.an.f.sur, ad.an.m.sur, fawn.repro, juv.repro, ad.repro, hunt.mort.fawn, hunt.mort.juv.f, hunt.mort.juv.m, hunt.mort.ad.f, hunt.mort.ad.m, ini.fawn.prev, ini.juv.prev, ini.ad.f.prev, ini.ad.m.prev, n.age.cats, p, env.foi, beta.f, beta.m, theta, n0, n.years = 10, rel.risk
--------	---

Value

A list with 2 dataframes: 1. counts of the # of individuals in the susceptible and infectious categories by over time. 2. deaths—how individuals died over time (hunting, natural or disease).

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.08, beta.m = 0.08,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwg_det_model(params)

plot_tots(out$counts)
```

cwg_det_model_wiw

CWD who-infects-who deterministic model

Description

Deterministic monthly age and sex structured model with constant environmental transmission and dynamic direct transmission. 2x2 matrix of transmission rates between males and females.

Usage

```
cwg_det_model_wiw(params)
```

Arguments

params	A list with the following parameters included: fawn.an.sur, juv.an.sur, ad.an.f.sur, ad.an.m.sur, fawn.repro, juv.repro, ad.repro, hunt.mort.fawn, hunt.mort.juv.f, hunt.mort.juv.m, hunt.mort.ad.f, hunt.mort.ad.m, ini.fawn.prev, ini.juv.prev, ini.ad.f.prev, ini.ad.m.prev, n.age.cats, p, env.foi, beta.ff, gamma.mm, gamma.mf, gamma.fm, theta, n0, n.years = 10, rel.risk
--------	--

Value

A list with 2 dataframes: 1. counts of the # of individuals in the susceptible and infectious categories by over time. 2. deaths—how individuals died over time (hunting, natural or disease).

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.ff = 0.06,
  gamma.mm = 2, gamma.mf = 2, gamma.fm = 1,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwg_det_model_wiw(params)

plot_tots(out$counts)
```

cwd_stoch_model	<i>CWD stochastic model function</i>
-----------------	--------------------------------------

Description

Stochastic monthly age and sex structured model with constant environmental transmission and dynamic direct transmission. The function conducts one run of the model.

Usage

```
cwd_stoch_model(params)
```

Arguments

params	A list with the following parameters included: fawn.an.sur, juv.an.sur, ad.an.f.sur, ad.an.m.sur, fawn.repro, juv.repro, ad.repro, hunt.mort.fawn, hunt.mort.juv.f, hunt.mort.juv.m, hunt.mort.ad.f, hunt.mort.ad.m, ini.fawn.prev, ini.juv.prev, ini.ad.f.prev, ini.ad.m.prev, n.age.cats, p, env.foi, beta.f, beta.m, theta, n0, n.years, rel.risk, repro.var, fawn.sur.var, sur.var, and hunt.var
--------	--

Value

A list with 2 dataframes: 1. counts of the # of individuals in the susceptible and infectious categories by over time. 2. deaths—how individuals died over time (hunting, natural or disease).

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.08, beta.m = 0.08,
theta = 1, n0 = 1000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_model(params)

plot_tots(out$counts)
```

cwd_stoch_model_wiw	<i>CWD who-infects-who stochastic model</i>
---------------------	---

Description

Stochastic monthly age and sex structured model with constant environmental transmission and dynamic direct transmission. The function conducts one run of the model. 2x2 matrix of transmission rates between males and females.

Usage

```
cwg_stoch_model_wiw(params)
```

Arguments

params A list with the following parameters included: fawn.an.sur, juv.an.sur, ad.an.f.sur, ad.an.m.sur, fawn.repro, juv.repro, ad.repro, hunt.mort.fawn, hunt.mort.juv.f, hunt.mort.juv.m, hunt.mort.ad.f, hunt.mort.ad.m, ini.fawn.prev, ini.juv.prev, ini.ad.f.prev, ini.ad.m.prev, n.age.cats, p, env.foi, beta.ff, gamma.mm, gamma.mf, gamma.fm, theta, n0, n.years, rel.risk, repro.var, fawn.sur.var, sur.var, and hunt.var

Value

A list with 2 dataframes: 1. counts of the # of individuals in the susceptible and infectious categories by over time. 2. deaths—how individuals died over time (hunting, natural or disease).

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.ff = 0.06,
gamma.mm = 2, gamma.mf = 2, gamma.fm = 1,
theta = 1, n0 = 1000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwg_stoch_model_wiw(params)

plot_tots(out$counts)
```

cwg_stoch_wrapper	<i>CWD stochastic model wrapper</i>
-------------------	-------------------------------------

Description

Wrapper function to run the stochastic CWD model many times.

Usage

```
cwg_stoch_wrapper(params, nsims)
```

Arguments

params A list with the parameters needed for the stochastic model: fawn.an.sur, juv.an.sur, ad.an.f.sur, ad.an.m.sur, fawn.repro, juv.repro, ad.repro, hunt.mort.fawn, hunt.mort.juv.f, hunt.mort.juv.m, hunt.mort.ad.f, hunt.mort.ad.m, ini.fawn.prev, ini.juv.prev, ini.ad.f.prev, ini.ad.m.prev, n.age.cats, p, env.foi, beta.f, beta.m, theta, n0, n.years, rel.risk, repro.var, fawn.sur.var, sur.var, and hunt.var

nsims The number of simulations to run.

Value

A list with 2 dataframes: 1. counts of the # of individuals in the susceptible and infectious categories by over time. 2. deaths—how individuals died over time (hunting, natural or disease).

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 10)

plot_stoch_tots(out$counts, all.lines = TRUE, error.bars = c(0.05, 0.95),
by.sexage = TRUE)
```

est_beta_params

Beta distribution conversion function

Description

Converts mean and variance parameters to the shape and scale parameters of a Beta distribution

Usage

```
est_beta_params(mu, var)
```

Arguments

mu	mean
var	variance

Value

A list of alpha and beta values

Examples

```
est_beta_params(mu = 0.9, var = 0.005)
```

launchApp	<i>launches the shinyCWDAp</i>
-----------	--------------------------------

Description

launches the shinyCWDAp

Usage

```
launchApp(example)
```

Arguments

example	name of the application to run
---------	--------------------------------

plot_age_dist	<i>Plot the age distribution at the end</i>
---------------	---

Description

Plot the age distribution at the end

Usage

```
plot_age_dist(dat)
```

Arguments

dat	counts provided as output from the CWD model functions
-----	--

Value

a plot the age distribution at the end point

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_age_dist(out$counts)
```

plot_buck_doe	<i>Plot the buck:doe ratio</i>
---------------	--------------------------------

Description

Plot the buck:doe ratio

Usage

```
plot_buck_doe(dat)
```

Arguments

dat	counts provided as output from the CWD model functions
-----	--

Value

a plot the buck:doe ratio

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_buck_doe(out$counts)
```

plot_compare_all_det	<i>Deterministic Comparison plot</i>
----------------------	--------------------------------------

Description

Deterministic Comparison plot

Usage

```
plot_compare_all_det(outa, outb)
```

Arguments

outa	counts as provided as output from the CWD model functions for the first simulation
outb	counts as provided as output from the CWD model functions for the second simulation

Value

a bar plot comparison

Examples

```
params.a <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)
```

```
params.b <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.5, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)
```

```
out.a <- cwd_det_model(params.a)
out.b <- cwd_det_model(params.b)
```

```
plot_compare_all_det(out.a, out.b)
```

plot_compare_all_stoch

Stochastic Comparison plot

Description

Stochastic Comparison plot

Usage

```
plot_compare_all_stoch(outa, outb)
```

Arguments

outa	counts as provided as output from the CWD model functions for the first simulation
outb	counts as provided as output from the CWD model functions for the second simulation

Value

a density plot comparison

Examples

```

params.a <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

params.b <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.05, hunt.mort.ad.m = 0.6, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)
out.a <- cwd_stoch_wrapper(params.a, nsims = 20)
out.b <- cwd_stoch_wrapper(params.b, nsims = 20)

plot_compare_all_stoch(out.a, out.b)

```

plot_compare_hunted *Stochastic Comparison plot of all hunted*

Description

Stochastic Comparison plot of all hunted

Usage

```
plot_compare_hunted(outa, outb, end, males.only, old.only)
```

Arguments

outa	deaths data as provided as output from the CWD model functions for the first simulation
outb	deaths data as provided as output from the CWD model functions for the second simulation
end	TRUE/FALSE for whether to show just the last timepoint (end = TRUE), or the cumulative number over the whole simulation. Default = FALSE.
males.only	TRUE/FALSE for whether to show only males Default = FALSE.
old.only	TRUE/FALSE for whether to show just those hunted over 3yrs. Default = FALSE.

Value

a density plot comparison

Examples

```

params.a <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

params.b <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.05, hunt.mort.ad.m = 0.6, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)
out.a <- cwd_stoch_wrapper(params.a, nsims = 20)
out.b <- cwd_stoch_wrapper(params.b, nsims = 20)

plot_compare_hunted(out.a$deaths, out.b$deaths)

```

plot_compare_prev

*Stochastic Comparison plot of prevalence over time***Description**

Stochastic Comparison plot of prevalence over time

Usage

```
plot_compare_prev(outa, outb)
```

Arguments

outa	counts as provided as output from the CWD model functions for the first simulation
outb	counts as provided as output from the CWD model functions for the second simulation

Value

a comparison plot of prevalence

Examples

```

params.a <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,

```

```

n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

params.b <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.05, hunt.mort.ad.m = 0.6, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)
out.a <- cwd_stoch_wrapper(params.a, nsims = 20)
out.b <- cwd_stoch_wrapper(params.b, nsims = 20)

plot_compare_prev(out.a$counts, out.b$counts)

```

plot_compare_tots	<i>Stochastic Comparison plot of totals over time</i>
-------------------	---

Description

Stochastic Comparison plot of totals over time

Usage

```
plot_compare_tots(outa, outb)
```

Arguments

outa	counts as provided as output from the CWD model functions for the first simulation
outb	counts as provided as output from the CWD model functions for the second simulation

Value

a density plot comparison

Examples

```

params.a <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

params.b <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,

```

```

hunt.mort.ad.f = 0.05, hunt.mort.ad.m = 0.6, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)
out.a <- cwd_stoch_wrapper(params.a, nsims = 20)
out.b <- cwd_stoch_wrapper(params.b, nsims = 20)

plot_compare_tots(out.a$counts, out.b$counts)

```

plot_deaths	<i>Plot the deaths by category.</i>
-------------	-------------------------------------

Description

Plot the deaths by category.

Usage

```
plot_deaths(dat, percents)
```

Arguments

dat	deaths as provided as output from the CWD model functions
percents	TRUE/FALSE on whether to plot the totals or the percentage absolute totals are the default

Value

a plot deaths by category

Examples

```

params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_deaths(out$deaths, percents = TRUE)
plot_deaths(out$deaths, percents = FALSE)

```

plot_fawn_doe	<i>Plot the fawn to doe ratio over time</i>
---------------	---

Description

Plot the fawn to doe ratio over time

Usage

```
plot_fawn_doe(dat)
```

Arguments

dat counts provided as output from the CWD model functions

Value

a plot the fawn:doe ratio

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_fawn_doe(out$counts)
```

plot_prev_age_end	<i>Plot the prevalence by age at the end of the simulation</i>
-------------------	--

Description

Plot the prevalence by age at the end of the simulation

Usage

```
plot_prev_age_end(dat)
```

Arguments

dat counts provided as output from the CWD model functions

Value

a plot of the prevalence by age

Examples

```

params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_prev_age_end(out$counts)

```

plot_prev_time	<i>Plot the prevalence over time</i>
----------------	--------------------------------------

Description

Plot the prevalence over time

Usage

```
plot_prev_time(dat)
```

Arguments

dat counts provided as output from the CWD model functions

Value

a plot of the prevalence over time

Examples

```

params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_prev_time(out$counts)

```

plot_stoch_age_dist *Age distribution plot*

Description

Age distribution plot

Usage

```
plot_stoch_age_dist(dat)
```

Arguments

dat counts as provided as output from the CWD model

Value

a plot of the percent of the population in each age class

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
  repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 10)
plot_stoch_age_dist(out$counts)
```

plot_stoch_buck_doe *Buck:doe stochastic plot*

Description

Buck:doe stochastic plot

Usage

```
plot_stoch_buck_doe(dat, all.lines, error.bars)
```

Arguments

dat counts as provided as output from the CWD model

all.lines TRUE/FALSE for whether to plot a line for every simulation

error.bars error bars = vector of high and low percentiles (2 values only). If missing, no error bars are shown.

Value

a plot of the ratio of adult males to adult females over time

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_buck_doe(out$counts, all.lines = TRUE,
error.bars = c(0.05, 0.95))
```

plot_stoch_deaths	<i>Death types stochastic plot</i>
-------------------	------------------------------------

Description

Death types stochastic plot

Usage

```
plot_stoch_deaths(dat, error.bars)
```

Arguments

dat	counts as provided as output from the CWD model
error.bars	error bars = vector of high and low percentiles (2 values only). If missing, no error bars are shown.

Value

a plot of death types over time.

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_deaths(out$deaths, error.bars = c(0.05, 0.95))
```

plot_stoch_disease	<i>Plot stochastic totals of positives and negatives over time</i>
--------------------	--

Description

Plot stochastic totals of positives and negatives over time

Usage

```
plot_stoch_disease(dat, error.bars)
```

Arguments

dat	counts as provided as output from the CWD model
error.bars	error bars = vector of high and low percentiles (2 values only). If missing, no error bars are shown.

Value

a multiple line plot of the simulation over time

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_disease(out$counts, error.bars = c(0.05, 0.95))
```

plot_stoch_fawn_doe	<i>Fawn:doe stochastic plot</i>
---------------------	---------------------------------

Description

Fawn:doe stochastic plot

Usage

```
plot_stoch_fawn_doe(dat, all.lines, error.bars)
```

Arguments

<code>dat</code>	counts as provided as output from the CWD model
<code>all.lines</code>	TRUE/FALSE for whether to plot a line for every simulation
<code>error.bars</code>	2 value vector for the hi and lo percentiles on the error bars. If missing, no error bars will be shown.

Value

a plot of the percent of the population in each age class

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
  repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_fawn_doe(out$counts, error.bars = c(0.05, 0.95))
```

plot_stoch_perc_deaths

Percentage death types stochastic plot

Description

Percentage death types stochastic plot

Usage

```
plot_stoch_perc_deaths(dat, error.bars)
```

Arguments

<code>dat</code>	counts as provided as output from the CWD model
<code>error.bars</code>	2 value vector for the hi and lo percentiles on the error bars. If missing, no error bars are shown.

Value

a plot of

Examples

```

params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_perc_deaths(out$deaths, error.bars = c(0.05, 0.95))

```

plot_stoch_prev

*Plot stochastic prevalence over time***Description**

Plot stochastic prevalence over time

Usage

```
plot_stoch_prev(dat, all.lines, error.bars)
```

Arguments

dat	counts as provided as output from the CWD model
all.lines	TRUE/FALSE for whether to plot a line for every simulation. Default = TRUE.
error.bars	2 value vector for the hi and lo percentiles on the error bars. If missing, no error bars are shown

Value

a multiple line plot of the simulation over time

Examples

```

params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_prev(out$counts, error.bars = c(0.05, 0.95))

```

plot_stoch_prev_age *Plot stochastic prevalence by age over time*

Description

Plot stochastic prevalence by age over time

Usage

```
plot_stoch_prev_age(dat, by.sex)
```

Arguments

dat counts as provided as output from the CWD model
by.sex TRUE/FALSE on whether to facet by sex. Default = FALSE

Value

a multiple line plot of the simulation over time

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_prev_age(out$counts, by.sex = TRUE)
```

plot_stoch_prev_age_end
 Prevalence versus age plot

Description

Prevalence versus age plot

Usage

```
plot_stoch_prev_age_end(dat, error.bars)
```

Arguments

dat counts as provided as output from the CWD model
error.bars vector with 2 values for the low and high percentiles. If missing, then no error bars will be shown.

Value

a plot of prevalence versus age at the last timepoint of the simulation

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_prev_age_end(out$counts, error.bars = c(0.05, 0.95))
```

plot_stoch_tots

Plot stochastic totals over time

Description

Plot stochastic totals over time

Usage

```
plot_stoch_tots(dat, all.lines, error.bars, by.sexage)
```

Arguments

dat	counts as provided as output from the CWD model
all.lines	TRUE/FALSE for whether to plot a line for every simulation
error.bars	error bars = vector of high and low percentiles (2 values only). If missing, no error bars will be shown.
by.sexage	TRUE/FALSE for whether to facet by sex and age.

Value

a multiple line plot of the simulation over time

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.1, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)
```



```
out <- cwd_stoch_wrapper(params, nsims = 20)
plot_stoch_tots(out$counts, all.lines = TRUE, by.sexage = TRUE,
error.bars = c(0.05, 0.95))
```

plot_tots

*Plot the total of S and I over time***Description**

Plot the total of S and I over time

Usage

```
plot_tots(dat)
```

Arguments

dat counts provided as output from the CWD model functions

Value

a plot of the population totals split by age.

Examples

```
params <- list(fawn.an.sur = 0.6, juv.an.sur = 0.8, ad.an.f.sur = 0.95,
ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.2, ini.fawn.prev = 0.02,
ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0)

out <- cwd_det_model(params)
plot_tots(out$counts)
```

plot_ttd

*Plot Time to disease-induced death***Description**

Creates a plot of the time (in years) to disease-induced death based on the proportion or probability of movement through the 10 infectious sub-categories. Uses 1000 draws from a Gamma distribution.

Usage

```
plot_ttd(p)
```

Arguments

`p` proportion or probability of progressing through the infections categories. Must be between 0 and 1.

Value

a density plot of time to death.

Examples

```
plot_ttd(p = 0.043)
```

plot_vitals	<i>Vital rate plot</i>
-------------	------------------------

Description

Creates a plot of the survival and reproduction distributions that are defined by the CWD model parameters

Usage

```
plot_vitals(params)
```

Arguments

`params` list of the parameters provided to the CWD model

Value

a plot of the vital rate distributions

Examples

```
params <- list(fawn.an.sur = 0.4, juv.an.sur = 0.6, ad.an.f.sur = 0.95,
  ad.an.m.sur = 0.9, fawn.repro = 0, juv.repro = 0.6, ad.repro = 1,
  hunt.mort.fawn = 0.01, hunt.mort.juv.f = 0.1, hunt.mort.juv.m = 0.1,
  hunt.mort.ad.f = 0.2, hunt.mort.ad.m = 0.4, ini.fawn.prev = 0.02,
  ini.juv.prev = 0.03, ini.ad.f.prev = 0.04, ini.ad.m.prev = 0.04,
  n.age.cats = 12, p = 0.43, env.foi = 0, beta.f = 0.15, beta.m = 0.15,
  theta = 1, n0 = 2000, n.years = 10, rel.risk = 1.0,
  repro.var = 0.005, fawn.sur.var = 0.005, sur.var = 0.005, hunt.var = 0.005)

plot_vitals(params = params)
```

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