

# Package: epigrowthfit (via r-universe)

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**URL** <https://github.com/davidearn/epigrowthfit>

**BugReports** <https://github.com/davidearn/epigrowthfit/issues>

**Title** Nonlinear Mixed Effects Models of Epidemic Growth

**Description** Maximum likelihood estimation of nonlinear mixed effects models of epidemic growth using Template Model Builder ("TMB"). Enables joint estimation for collections of disease incidence time series, including time series that describe multiple epidemic waves. Supports a set of widely used phenomenological models: exponential, logistic, Richards (generalized logistic), subexponential, and Gompertz. Provides methods for interrogating model objects and several auxiliary functions, including one for computing basic reproduction numbers from fitted values of the initial exponential growth rate. Preliminary versions of this software were applied in Ma et al. (2014) <[doi:10.1007/s11538-013-9918-2](https://doi.org/10.1007/s11538-013-9918-2)> and in Earn et al. (2020) <[doi:10.1073/pnas.2004904117](https://doi.org/10.1073/pnas.2004904117)>.

**Depends** R (>= 4.3)

**LinkingTo** RcppEigen (>= 0.3.4.0.0), TMB

**Imports** Matrix (>= 1.6-2), TMB, grDevices, graphics, methods, nlme, stats, utils

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**Repository** <https://epiverse-connect.r-universe.dev>

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epigrowthfit-package    R Package **epigrowthfit**

---

## Description

An R package for estimating nonlinear mixed effects models of epidemic growth.

## Details

The “main” model estimating function is [egf](#).

To render a list of available help topics, use `help(package = "epigrowthfit")`. Many of these document methods for the class of objects returned by [egf](#).

To report a bug or request a change, use `bug.report(package = "epigrowthfit")`.

## Author(s)

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---

`coef.egf`                      *Extract Coefficients and Random Effect Covariance Parameters*

---

## Description

Extracts the bottom level parameter vector `c(beta, theta, b)` or a subset. Segments `beta`, `theta`, and `b` contain (respectively) fixed effect coefficients, random effect covariance parameters, and random effect coefficients.

## Usage

```
## S3 method for class 'egf'  
coef(object, random = FALSE, full = FALSE, ...)
```

## Arguments

<code>object</code>	an <a href="#">egf</a> object.
<code>random</code>	a logical. If FALSE, then segment <code>b</code> is excluded.
<code>full</code>	a logical. If FALSE, then mapped elements are excluded, and the result is called “condensed”.
<code>...</code>	unused optional arguments.

**Value**

A numeric vector concatenating beta, theta, and b, without b if `random = FALSE` and without mapped elements if `full = FALSE`.

Attribute `len` is a named integer vector partitioning the result by segment.

Attribute `map` is a named list of integer vectors `i` such that that a full segment `y` and its condensed counterpart `x` are related by  $y = x[i]$ , with the exception that `i[j]` is NA if `y[j]` is mapped to an initial value. NULL is used in place of an integer vector where `x` and `y` are identical.

The result inherits from class `coef.egf`, which has methods for `print`, `as.list`, and `labels`.

**See Also**

The generic function `coef`.

**Examples**

```
example("egf", package = "epigrowthfit")

for (random in c(FALSE, TRUE)) {
  for (full in c(FALSE, TRUE)) {
    cat(sprintf("random = %s, full = %s :\n\n", random, full))
    str(coef(m1, random = random, full = full))
    cat("\n")
  }
}
```

---

confint.egf

*Confidence Intervals*

---

**Description**

Computes confidence intervals on fixed effect coefficients, random effect covariance parameters, and linear combinations thereof, including population fitted values. Intervals on individual fitted values accounting for random effects are supported, but only by `method = "wald"`.

**Usage**

```
## S3 method for class 'egf'
confint(object, parm, level = 0.95,
        A = seq_along(par), method = c("wald", "profile", "uniroot"), scale = 7,
        parallel = egf_parallel(), trace = FALSE,
        top = egf_top(object), subset = NULL, select = NULL,
        class = FALSE, link = TRUE, random = FALSE, ...)

## S3 method for class 'confint.egf'
plot(x, by = 12L,
     subset = NULL, order = NULL, label = NULL, main = NULL, ...)
```

**Arguments**

object	an <a href="#">egf</a> object.
parm	unused argument, for consistency with the generic function.
level	a number in the interval (0, 1) indicating a confidence level.
A	a numeric matrix with 1+p columns, where $p = \text{length}(\text{coef}(\text{object}))$ , in which case each row specifies a linear combination of the elements of $c(1, \text{coef}(\text{fitted}))$ for which intervals are computed; or a valid index vector for $\text{coef}(\text{fitted})$ , in which case intervals are computed for the indexed elements; or NULL, in which case intervals on fitted values are computed.
method	a character string indicating <i>how</i> intervals are computed.
scale	a positive number, for <code>method = "uniroot"</code> . <a href="#">tmbroot</a> will search for roots between $\text{value} - \text{scale} * \text{se}$ and $\text{value} + \text{scale} * \text{se}$ , where <code>value</code> and <code>se</code> are the estimate and standard error.
parallel	an <a href="#">egf_parallel</a> object defining options for R level parallelization.
trace	a logical. If TRUE, then basic tracing messages indicating progress are printed. These may be mixed with optimizer output depending on <code>object[["control"]][["trace"]]</code> .
top	a subset of <a href="#">egf_top</a> (object) naming top level nonlinear model parameters for which intervals on fitted values should be computed.
subset, select	index vectors for the rows and columns of <code>model.frame(object, "combined")</code> or language objects evaluating to such vectors. <code>subset</code> indicates fitting windows for which intervals should be computed; the default indicates all. <code>select</code> indicates variables that should be appended to the result; the default indicates none. Evaluation of language objects follows the implementation of <a href="#">subset.data.frame</a> .
	For the <a href="#">plot</a> method:
	an index vector for <code>seq_len(nrow(x))</code> or a language object evaluating in <code>x</code> to such a vector. <code>subset</code> indicates which intervals are plotted; the default indicates all.
class	a logical. If TRUE and if <code>A = NULL</code> , then the value of the <a href="#">confint</a> call is a <a href="#">confint.egf</a> object, not a matrix.
link	a logical. If FALSE and if <code>A = NULL</code> and <code>class = TRUE</code> , then fitted values and confidence limits are returned on the “natural” (inverse link) scale.
random	a logical, affecting only <code>method = "wald"</code> . If TRUE, then intervals are computed for individual fitted values, which count random effects, rather than population fitted values, which do not.
...	additional arguments passed from or to other methods.
x	a <a href="#">confint.egf</a> object.
by	a positive integer indicating the number of intervals displayed in one plot.
order	a permutation of <code>seq_len(nrow(x))</code> or a language object evaluating in <code>x</code> to such a vector. <code>order</code> indicates the order in which intervals are plotted; the default indicates the original order.
label	a character or expression vector of length <code>nrow(x)</code> or a language object evaluating in <code>x</code> to such a vector. <code>label</code> indicates <i>y</i> -axis labels for intervals; the default is to use <code>as.character(x[["window"]])</code> .

`main` a character or expression vector of length 1 indicating a plot title, to be recycled for all plots.

### Details

Three methods for computing confidence intervals are available:

"wald" confidence limits are calculated as

$$\text{value} + c(-1, 1) * \text{sqrt}(q) * \text{se}$$

where  $q = \text{qchisq}(\text{level}, \text{df} = 1)$ .

"profile", "uniroot" confidence limits are calculated as approximate solutions of the equation

$$2 * (f(x) - f(\text{value})) = q$$

where  $q = \text{qchisq}(\text{level}, \text{df} = 1)$  and  $f$  is the negative log marginal likelihood function expressed as a function of the parameter  $x$  in question. Solutions are approximated by interpolating a likelihood profile ("profile") or by rootfinding ("uniroot").

"wald" assumes asymptotic normality of the maximum likelihood estimator. "profile" and "uniroot" avoid this constraint but are typically expensive, requiring estimation of many restricted models. They are parallelized at the C++ level when there is OpenMP support and `object[["control"]][["omp_num_threads"]]` is set to an integer greater than 1. When there is no OpenMP support, they can still be parallelized at the R level with appropriate setting of argument `parallel`.

### Value

A numeric array in 2 or 3 dimensions containing the lower and upper confidence limits in the last dimension.

When confidence intervals on fitted values are desired, the user will set `A = NULL` and in that case have the option of passing `class = TRUE` to obtain an augmented result. Thus, alternatively:

A data frame inheriting from class `confint.egf`, with variables:

<code>top</code>	top level nonlinear model parameter, from <code>egf_top(object)</code> .
<code>ts</code>	time series, from <code>levels(model.frame(object)[["ts"]])</code> .
<code>window</code>	fitting window, from <code>levels(model.frame(object)[["window"]])</code> .
<code>value</code>	fitted value.
<code>ci</code>	a numeric matrix with two columns giving the lower and upper confidence limits.
<code>...</code>	further variables from <code>model.frame(object, "combined")</code> specified by argument <code>select</code> .

The confidence level `level` is preserved as an attribute.

### See Also

The generic function `confint`.

**Examples**

```

example("egf", package = "epigrowthfit")

zz1 <- confint(m1, A = NULL, method = "wald", class = TRUE,
              random = TRUE)
str(zz1)

op <- par(mar = c(4.5, 4, 2, 1), oma = c(0, 0, 0, 0))
plot(zz1)
par(op)

zz2 <- confint(m1, A = NULL, method = "profile", class = TRUE,
              top = "log(r)", subset = quote(country == "A" & wave == 1))
zz3 <- confint(m1, A = NULL, method = "uniroot", class = TRUE,
              top = "log(r)", subset = quote(country == "A" & wave == 1))

```

cov2theta

*Compute a Packed Representation of a Covariance Matrix***Description**

Transform covariances matrices to a “packed” representation or compute the inverse transformation.

**Usage**

```

cov2theta(Sigma)
theta2cov(theta)

```

**Arguments**

**Sigma** an  $n$ -by- $n$  real, symmetric positive definite matrix. Only the upper triangle is “seen”.

**theta** a numeric vector of length  $n(n + 1)/2$  whose first  $n$  elements are positive.

**Details**

An  $n$ -by- $n$  real, symmetric, positive definite matrix  $\Sigma$  can be factorized as

$$\Sigma = R'R.$$

The upper triangular Cholesky factor  $R$  can be written as

$$R = R_1 D^{-1/2} D_\sigma^{1/2},$$

where  $R_1$  is a unit upper triangular matrix and  $D = \text{diag}(\text{diag}(R_1'R_1))$  and  $D_\sigma = \text{diag}(\text{diag}(\Sigma))$  are diagonal matrices.

cov2theta takes  $\Sigma$  and returns the vector  $\theta$  of length  $n(n + 1)/2$  containing the log diagonal entries of  $D_\sigma$  followed by (in column-major order) the strictly upper triangular entries of  $R_1$ . theta2cov computes the inverse transformation.

**Value**

A vector like `theta` (`cov2theta`) or a matrix like `Sigma` (`theta2cov`); see ‘Details’.

---

covid19.ontario	<i>COVID-19 in Ontario, Canada</i>
-----------------	------------------------------------

---

**Description**

Time series of COVID-19 cases and tests in Ontario, Canada, daily from February 8, 2020 to May 1, 2022.

**Usage**

```
data(covid19.ontario, package = "epigrowthfit")
```

**Format**

A data frame with 814 rows and 3 variables:

`date` a [Date](#) vector.

`cases` an integer vector. `cases[i]` is the number of cases confirmed by Ontario public health units prior to `date[i]`. This number includes resolved and fatal cases as well as reinfections.

`tests` an integer vector. `tests[i]` is the number of tests completed prior to `date[i]`. This number includes repeated tests by individuals except prior to April 15, 2020, when individuals were counted at most once.

**Source**

This data set is a processed subset of a larger data set downloaded on 2024-01-10 from the It is updated using an installed script:

```
\link{system.file}("scripts", "covid19.ontario.R", package = "epigrowthfit")
```

**Examples**

```
data(covid19.ontario, package = "epigrowthfit")  
plot(1 + diff(c(NA, cases)) ~ date, data = covid19.ontario, log = "y")
```



---

df.residual.egf	<i>Extract the Residual Degrees of Freedom</i>
-----------------	--

---

**Description**

Extracts from a model object the number of observations (see [nobs](#)) minus the number of estimated parameters (fixed effect coefficients and random effect covariance parameters).

**Usage**

```
## S3 method for class 'egf'
df.residual(object, ...)
```

**Arguments**

object	an <a href="#">egf</a> object.
...	unused optional arguments.

**Value**

An integer.

**See Also**

The generic function [df.residual](#).

---

egf	<i>Fit Nonlinear Mixed Effects Models of Epidemic Growth</i>
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---

**Description**

Fits nonlinear mixed effects models of epidemic growth to collections of one or more disease incidence time series.

**Usage**

```
egf(model, ...)

## S3 method for class 'egf_model'
egf(model,
     formula_ts,
     formula_windows,
     formula_parameters = list(),
     formula_priors = list(),
     data_ts,
```

```

data_windows,
subset_ts = NULL,
subset_windows = NULL,
select_windows = NULL,
na_action_ts = c("fail", "pass"),
na_action_windows = c("fail", "omit"),
control = egf_control(),
init = list(),
map = list(),
fit = TRUE,
se = FALSE,
...)
```

### Arguments

**model** an R object specifying a top level nonlinear model, typically of class `egf_model`.

**formula\_ts** a formula of the form `cbind(time, x) ~ ts` specifying one or more disease incidence time series in long format.

`ts` must evaluate to a factor (insofar as `as.factor(ts)` is a factor) grouping the data by time series. `time` must evaluate to a numeric vector that is increasing within levels of `ts`. `Date`, `POSIXct`, and `POSIXlt` vectors are supported and coerced to numeric with `julian(time)`. Finally, `x` must evaluate to a non-negative numeric vector with `x[i]` equal to the number of cases observed over the interval  $(\text{time}[i-1], \text{time}[i])$ . Edge cases like `x[1]` are ignored internally. Elements of `x` that are not integer-valued are rounded with a warning.

`formula_ts = cbind(time, x) ~ 1` can be supplied when there is only one time series; it is equivalent to `formula_ts = cbind(time, x) ~ ts` with `ts` evaluating to `rep(factor(1), length(x))`.

**formula\_windows** a formula of the form `cbind(start, end) ~ ts` specifying disjoint fitting windows  $(\text{start}, \text{end}]$  in long format. If `formula_ts = cbind(time, x) ~ ts1` and `formula_windows = cbind(start, end) ~ ts2`, then observation `x[i]` is associated with window  $(\text{start}[j], \text{end}[j])$  if and only if  $\text{time}[i-1] \geq \text{start}[j]$ ,  $\text{time}[i] \leq \text{end}[j]$ , and  $\text{ts1}[i] == \text{ts2}[j]$ .

**formula\_parameters** a list of formulae of the form `parameter ~ terms` specifying mixed effects models for top level nonlinear model parameters using **lme4**-like syntax (see, e.g., `help("lmer", package = "lme4")`). Alternatively, a formula of the form `~terms` to be recycled for all parameters.

A list of parameters for which formulae may be specified can be retrieved with `egf_top`. Specifically, `deparse(parameter)` must be an element of `egf_top(model)`. The default for parameters not assigned a formula is `~1`.

**formula\_priors** a list of formulae of the form `parameter ~ prior` defining priors on:

- (i) top level nonlinear model parameters,
- (ii) fixed effect coefficients and random effect covariance parameters (elements

of segments beta and theta of the bottom level parameter vector), or (iii) random effect covariance matrices (elements of a list Sigma containing the matrices).

prior must be a call to a [prior function](#) with arguments specifying suitable hyperparameters. In case (i), deparse(parameter) must be an element of [egf\\_top\(model\)](#), and hyperparameters supplied on the right hand side must have length 1. In cases (ii) and (iii), parameter must be beta, theta, or Sigma or a call to [ or [[ referring to a subset or element of beta, theta, or Sigma (e.g., beta[index], where index is a valid index vector for beta), and hyperparameters are recycled to the length of the indicated subset.

Expressions prior and index are evaluated in the corresponding formula environment.

data_ts, data_windows	data frames, lists, or environments to be searched for variables named in the corresponding formula_* and subset_* arguments. (formula_parameters uses data_windows.) Formula environments are searched for variables not found here.
subset_ts, subset_windows	expressions to be evaluated in the corresponding data_* data frames. The value should be a valid index vector for the rows of the data frame. Rows that are not indexed are discarded. Rows that are indexed are filtered further (e.g., time series with zero associated fitting windows are discarded regardless of subset_ts). The default is to preserve all rows for further filtering.
select_windows	an expression indicating additional variables in data_windows (if it is a data frame) to be preserved in the returned object for use by methods. The default is to preserve nothing. A dot '.' is to preserve all variables not occurring in formula_windows or formula_parameters. Outside of these two special cases, evaluation of select follows the implementation of <a href="#">subset.data.frame</a> .
na_action_ts	a character string affecting the handling of NA in x if formula_ts = cbind(time, x) ~ ts. "fail" is to throw an error. "pass" is to ignore NA when fitting and replace NA when predicting. NA in time and ts are always an error.
na_action_windows	a character string affecting the handling of NA in formula_windows and formula_parameters variables. "fail" is to throw an error. "omit" is to discard incomplete rows of data.
control	an <a href="#">egf_control</a> object specifying control parameters.
init	a named list of numeric vectors with possible elements beta, theta, and b, specifying values to be used in the first likelihood evaluation for the so-named segments of the bottom level parameter vector. The default value of each segment is a zero vector, with the exception that "(Intercept)" coefficients in beta have default values computed from supplied time series. Use NA to indicate elements that should retain their default value.
map	a named list of factors with possible elements beta, theta, and b, each as long as the so-named segment of the bottom level parameter. Elements of a segment <name> indexed by is.na(map[["<name>"]]) are fixed at their initial values,

rather than estimated, and elements corresponding to a common factor level are constrained to have a common value during estimation. `map[["<name>"]]` can be an index vector for segment <name>, instead of a factor. In this case, the indexed elements of that segment are fixed at their initial values.

<code>fit</code>	a logical. If FALSE, then <code>egf</code> returns early ( <i>before</i> fitting) with a partial model object. The details of the partial result are subject to change and therefore sparsely documented, on purpose ...
<code>se</code>	a logical. If TRUE, then the Hessian matrix of the negative log marginal likelihood function is computed and inverted to approximate the joint covariance matrix of segments <code>beta</code> and <code>theta</code> of the bottom level parameter vector. Standard errors on the fitted values of all top level nonlinear model parameters are computed approximately using the delta method. Computations are preserved in the model object for reuse by methods.
<code>...</code>	additional arguments passed from or to other methods.

### Details

Users attempting to set arguments `formula_priors`, `init`, and `map` should know the structure of the bottom level parameter vector. It is described under topic [egf-class](#).

If

```
formula_ts = cbind(time, x) ~ ts1
formula_windows = cbind(start, end) ~ ts2
```

then it is expected that `time`, `start`, and `end` (after coercion to numeric) measure time on the same scale. To be precise, numeric times should have a common unit of measure and, at least within time series, represent displacements from a common reference time. These conditions will always hold if `time`, `start`, and `end` all evaluate to [Date](#), [POSIXct](#), or [POSIXlt](#) vectors.

When day of week effects are estimated, numeric times are interpreted as numbers of days since midnight on January 1, 1970, so that time points can be mapped unambiguously to days of week. Furthermore, in this case, `time` (after coercion to numeric) is required to be integer-valued with one day spacing in all time series. This means that

```
isTRUE(all.equal(time, round(time))) &&
  all(range(diff(round(time))) == 1)
```

must be TRUE in each level of `ts1`. These conditions ensure that intervals between successive time points represent exactly one day of week.

### Value

A list inheriting from class `egf`. See topic [egf-class](#) for class documentation.

### See Also

The many methods for class `egf`, listed by `methods(class = "egf")`.

**Examples**

```

## Simulate 'N' incidence time series exhibiting exponential growth
set.seed(180149L)
N <- 10L
f <- function(time, r, c0) {
  lambda <- diff(exp(log(c0) + r * time))
  c(NA, rpois(lambda, lambda))
}
time <- seq.int(0, 40, 1)
r <- rlnorm(N, -3.2, 0.2)
c0 <- rlnorm(N, 6, 0.2)
data_ts <-
  data.frame(country = gl(N, length(time), labels = LETTERS[1:N]),
             time = rep.int(time, N),
             x = unlist(Map(f, time = list(time), r = r, c0 = c0)))
rm(f, time)

## Define fitting windows (here, two per time series)
data_windows <-
  data.frame(country = gl(N, 1L, 2L * N, labels = LETTERS[1:N]),
             wave = gl(2L, 10L),
             start = c(sample(seq.int(0, 5, 1), N, TRUE),
                       sample(seq.int(20, 25, 1), N, TRUE)),
             end = c(sample(seq.int(15, 20, 1), N, TRUE),
                     sample(seq.int(35, 40, 1), N, TRUE)))

## Estimate the generative model
m1 <-
  egf(model = egf_model(curve = "exponential", family = "pois"),
      formula_ts = cbind(time, x) ~ country,
      formula_windows = cbind(start, end) ~ country,
      formula_parameters = ~(1 | country:wave),
      data_ts = data_ts,
      data_windows = data_windows,
      se = TRUE)

## Re-estimate the generative model with:
## * Gaussian prior on beta[1L]
## * LKJ prior on all random effect covariance matrices
## (here there happens to be just one)
## * initial value of 'theta' set explicitly
## * theta[3L] fixed at initial value
m2 <-
  update(m1,
        formula_priors = list(beta[1L] ~ Normal(mu = -3, sigma = 1),
                              Sigma ~ LKJ(eta = 2)),
        init = list(theta = c(log(0.5), log(0.5), 0)),
        map = list(theta = 3L))

```

## Description

Class `egf` designates models estimated by function `egf`. Objects of this class hold information about an estimated model. Components can be accessed directly. However, as the components are subject to change without notice, portable code will rely on exported methods for interrogation.

## Details

Currently, a legitimate `egf` object is a list with elements:

`model` a copy of the so-named argument of `egf`.

`frame` a list of the form `list(ts, windows, parameters, extra)`. `ts` and `windows` are data frames preserving time series and fitting window endpoints. `parameters` is a list of mixed effects model frames, with one element for each top level nonlinear model parameter. `extra` is a data frame preserving additional variables specified in `call[["select_windows"]]`. `windows`, the model frames listed in `parameters`, and `extra` all correspond rowwise.

`priors` a list of the form `list(top, bottom = list(beta, theta, Sigma))`, where `top`, `beta`, `theta`, and `Sigma` are all lists of `egf_prior` objects.

`control` a copy of the so-named argument of `egf`.

`tmb_out` the list output of `MakeADFun`.

`optimizer_out` the list output of the optimizer specified by `control[["optimizer"]]`.

`init`, `best` numeric vectors giving the values of the condensed bottom level parameter vector used in the first and maximal likelihood evaluations.

`random` a logical vector indexing the elements of the condensed bottom level parameter vector that are *not* arguments of the negative log marginal likelihood function. It indexes all elements of segment `b` (random effect coefficients) and (but only if `control[["profile"]] = TRUE`) all elements of segment `beta` (fixed effect coefficients).

`value`, `gradient` numeric vectors giving the value and gradient of the negative log marginal likelihood function at `best[!random]`.

`hessian` a logical flag indicating whether the Hessian matrix of the negative log marginal likelihood function is positive definite at `best[!random]`. `NA` means that the matrix has not been computed.

`coefficients` a list of the form `list(fixed, random)`, where `fixed` and `random` are data frames preserving interpretive information about fixed and random effect coefficients.

`contrasts` a list of the form `list(fixed, random)`, where `fixed` and `random` are lists preserving contrasts used to construct the fixed and random effects design matrices.

`call` the call to `egf`, enabling updates to the object by the default method of generic function `update`.

## Bottom Level Parameter Vector

An estimated model is specified by a bottom level parameter vector that is the concatenation of three segments:

`beta` the result of `unlist(lbeta)`, where `lbeta` is a list of numeric vectors of fixed effect coefficients, with one vector for each top level nonlinear model parameter. The order of top level parameters is specified by `egf_top(model)`.

`theta` the result of `unlist(ltheta)`, where `ltheta` is a list of numeric vectors of random effect covariance parameters, with one vector for each distinct random effect term in `formula_parameters`. Each vector parametrizes a random effect covariance matrix via `theta2cov` and its inverse `cov2theta`.

The list `Sigma` mentioned in the description of `egf` argument `formula_priors` is precisely `lapply(ltheta, theta2cov)`.

`b` the result of `unlist(lb)`, where `lb` is a list of numeric matrices of scaled random effect coefficients, corresponding elementwise to `ltheta`. The columns of `lb[[i]]` (one per level of the grouping variable) are interpreted as samples from a zero mean, unit variance multivariate normal distribution with covariance matrix `cov2cor(theta2cov(ltheta[[i]]))`.

When elements of this vector are “mapped” via `egf` argument `map`, likelihood is defined as a function of the condensed vector that excludes mapped elements.

Methods are defined for generic functions `coef`, `fixef`, and `ranef` to allow users to interrogate the structure of the vector.

## Examples

```
methods(class = "egf")
help.search("\\.egf$", fields = "alias", package = "epigrowthfit")
## less verbosely: alias??`\\.egf`
```

---

egf\_control

*Define Control Parameters*

---

## Description

Set parameters controlling the behaviour of `egf`.

## Usage

```
egf_control(outer_optimizer = egf_optimizer(nlminb),
            inner_optimizer = egf_optimizer(newton),
            trace = FALSE, profile = FALSE, sparse_X = FALSE,
            omp_num_threads = getOption("egf.cores", 1L))
```

## Arguments

<code>outer_optimizer</code> , <code>inner_optimizer</code>	<code>egf_optimizer</code> objects specifying “outer” and “inner” optimization methods.
<code>trace</code>	an integer determining the amount of tracing performed; see ‘Details’.
<code>profile</code>	a logical. If TRUE, then fixed effect coefficients are profiled out of the likelihood, which may stabilize optimization for models with many fixed effects. This “feature” should be considered experimental, and in fact it may <i>destabilize</i> optimization, as it relies on assumptions about the optimization problem that are not necessarily satisfied by the nonlinear mixed effects models fit by <code>egf</code> .

`sparse_X` a logical. If TRUE, then the fixed effects design matrix is represented as a (sparse) `dgCMatrix`, rather than as a traditional (dense) matrix.

`omp_num_threads` an integer indicating a number of OpenMP threads to be used when evaluating the objective function, provided that **epigrowthfit** was compiled with OpenMP support.

### Details

`trace` affects the amount of information printed during likelihood evaluations:

- 0 likelihood evaluations are always silent.
- 1 a message is printed whenever a negative log marginal likelihood term is NaN or exceeds  $1e+09$ .
- 2 all negative log marginal likelihood terms are printed.

`egf` passes `silent = trace == 0L` to `MakeADFun`. A corollary is that nonzero values of `trace` have a number of additional side effects:

- error messages are printed during function and gradient evaluations;
- the maximum absolute gradient element is printed with each gradient evaluation; and
- trace flags set by `config` are turned on.

### Value

A list inheriting from class `egf_control` containing the validated arguments.

### Warning

Setting `trace > 0L` and `omp_num_threads > 0L` simultaneously should be avoided, because tracing messages are printed using R API functions that are not thread-safe.

### Examples

```
control <- egf_control()
str(control)
```

---

`egf_control_plot`      *Define Control Parameters for Plotting*

---

### Description

Sets parameters controlling the graphical output of `plot` for objects of class `egf`. Supplied values override package defaults (retrievable as `defaults <- egf_control_plot()`), which in turn override global defaults set via `par`.

Below, `x`, `type`, `time_as`, and `delta` refer to the so-named arguments of `plot.egf`.



**Usage**

```
egf_control_plot(window, data, predict, asymptote, box, axis, title, doubling)
```

**Arguments**

window	a named list of arguments to <code>rect</code> affecting the appearance of fitting windows.
data	a named list of the form <code>list(main, short, long)</code> . <code>main</code> is a named list of arguments to <code>points</code> affecting the appearance of observed data. <code>short</code> and <code>long</code> are alternatives to <code>main</code> used for counts over intervals shorter or longer than <code>delta</code> when <code>type = "interval"</code> . <code>short</code> and <code>long</code> default to <code>main</code> (element-wise).
predict	a named list of the form <code>list(value, ci)</code> . <code>value</code> and <code>ci</code> are named lists of arguments to <code>lines</code> and <code>polygon</code> affecting the appearance of predicted curves and corresponding confidence bands. <code>ci[["col"]]</code> defaults to <code>value[["col"]]</code> with added transparency.
asymptote	a named list of arguments to <code>segments</code> affecting the appearance of line segments drawn at <code>y = &lt;initial exponential growth rate&gt;</code> when <code>type = "rt"</code> and <code>x[["model"]][["curve"]] = "logistic" or "richards"</code> .
box	a named list of arguments to <code>box</code> affecting the appearance of the box drawn around the plot region on the device.
axis	a named list of the form <code>list(x, y)</code> . <code>x</code> and <code>y</code> are named lists of arguments to <code>axis</code> affecting the appearance of the bottom and left axes. When <code>time_as = "Date"</code> , there are minor and major bottom axes. In this case, the major axis uses a modified version of <code>x</code> that tries to ensure that it is displayed below the minor axis in a slightly larger font.
title	a named list of the form <code>list(main, sub, xlab, ylab)</code> . The elements are named lists of arguments to <code>title</code> affecting the appearance of plot (sub)titles and axis labels. <code>sub[["adj"]]</code> defaults to <code>main[["adj"]]</code> .
doubling	a named list of the form <code>list(legend, estimate, ci)</code> . The elements are named lists of arguments to <code>mtext</code> affecting the appearance of initial doubling times printed in the top margin.

**Details**

Setting an argument (or an element thereof in the case of nested lists) to `NULL` has the effect of suppressing the corresponding plot element.

**Value**

A named list containing the package defaults modified according to the arguments in the call.

---

egf\_has\_converged      *Test for Convergence*

---

### Description

Performs simple diagnostic tests to assess whether the optimizer that produced an estimated model actually converged to a local minimum point of the negative log marginal likelihood function.

### Usage

```
egf_has_converged(object, check = TRUE, tol = 1)
```

### Arguments

object	an <a href="#">egf</a> object.
check	a logical. If TRUE, then an error is thrown if object does not actually inherit from class <a href="#">egf</a> .
tol	a positive number. Convergence requires all gradient elements to be less than or equal to tol in absolute value.

### Value

TRUE if all tests pass. FALSE if any test fails. NA if no test fails, but the test for a positive definite Hessian matrix is indeterminate because the matrix has not been computed.

---

egf\_has\_random      *Test for Random Effects*

---

### Description

Tests whether an object specifies a model with random effects.

### Usage

```
egf_has_random(object, check = TRUE)
```

### Arguments

object	an <a href="#">egf</a> object.
check	a logical. If TRUE, then an error is thrown if object does not actually inherit from class <a href="#">egf</a> .

### Value

TRUE or FALSE.

---

egf_model	<i>Define a Top Level Nonlinear Model</i>
-----------	---

---

## Description

Sets flags defining a top level nonlinear model of epidemic growth to be estimated by [egf](#).

## Usage

```
egf_model(curve = c("logistic", "richards", "exponential",
                   "subexponential", "gompertz"),
          excess = FALSE,
          family = c("nbinom", "pois"),
          day_of_week = FALSE)
```

## Arguments

curve	a character string specifying a model for expected cumulative incidence as a function of time.
excess	a logical flag. If TRUE, then a constant baseline mortality rate is estimated.
family	a character string specifying a family of discrete probability distributions assigned to observations, which are the first order differences of observed cumulative incidence.
day_of_week	an integer flag. If positive, then day of week effects are estimated as offsets relative to the indicated day of week (1=Sunday, 2=Monday, and so on).

## Value

A list inheriting from class `egf_model` containing the validated arguments.

## See Also

[simulate.egf\\_model](#).

## Examples

```
model <- egf_model()
str(model)
```

---

egf\_optimizer      *Define an Optimization Method*

---

## Description

Utilities for linking an optimizer with optional arguments and control parameters to define an optimization method for use by [egf](#).

## Usage

```
egf_optimizer(f = nlminb, args = list(), control = list())
```

## Arguments

f	a function performing optimization. Supported are <a href="#">newton</a> , <a href="#">optim</a> , <a href="#">nlminb</a> , <a href="#">nlm</a> , and any <code>optim</code> -like function.
args	a list of optional arguments to f not including control. If f = <a href="#">optim</a> and args does not have method as an element, then method = "BFGS" is appended.
control	a list of control parameters to be passed to f.

## Details

An [optim](#)-like function is a function f such that:

- the first three arguments of f specify an initial parameter vector, an objective function, and a gradient function, respectively;
- f accepts control as a fourth (or later) argument; and
- f returns a named list with elements par, value, convergence, and message.

## Value

A list inheriting from class `egf_optimizer` containing the validated arguments, wherein f may be a new function wrapping the supplied one to make it [optim](#)-like.

## Examples

```
optimizer <- egf_optimizer(nlminb)
str(optimizer)
```

---

`egf_parallel`*Define a Parallelization Method*

---

## Description

Defines instructions for parallelization by linking a method with options.

## Usage

```
egf_parallel(method = c("serial", "multicore", "snow"),
            outfile = "", cores = getOption("egf.cores", 1L),
            args = list(), cl = NULL)
```

## Arguments

<code>method</code>	a character string indicating a method of parallelization. "serial" indicates no parallelization. "multicore" indicates R level forking. It is intended for use from a terminal rather than from a GUI. "snow" indicates socket clusters. On Windows, "multicore" is equivalent to "serial". "snow" is supported on both Unix-alikes and Windows.
<code>outfile</code>	a character string indicating a file path where console output should be diverted. An empty string indicates no diversion. If <code>method = "snow"</code> , then diversion may be necessary to view output.
<code>cores</code>	a positive integer indicating a number of threads/processes to fork/spawn when <code>parallel != "serial"</code> . <code>detectCores</code> can be called to detect the theoretical maximum.
<code>args</code>	a list of optional arguments to <code>mclapply</code> ( <code>method = "multicore"</code> ) or <code>makePSOCKcluster</code> ( <code>method = "snow"</code> ).
<code>cl</code>	an existing <a href="#">socket cluster</a> ( <code>method = "snow"</code> ). The default is to create a new cluster stop it upon job completion.

## Value

A list inheriting from class "egf\_parallel" containing the arguments (after possible matching and coercion).

## See Also

[vignette\("parallel", "parallel"\)](#).

## Examples

```
parallel <- egf_parallel()
str(parallel)
```

egf\_prior

*Prior Distributions***Description**

Functions used by `egf` to specify prior distributions of bottom level mixed effects model parameters.

**Usage**

```
Normal(mu = 0, sigma = 1)
LKJ(eta = 1)
Wishart(df, scale, tol = 1e-06)
InverseWishart(df, scale, tol = 1e-06)
```

**Arguments**

<code>mu</code>	a numeric vector listing means.
<code>sigma</code>	a positive numeric vector listing standard deviations.
<code>eta</code>	a positive numeric vector listing values for the shape parameter, with 1 corresponding to a uniform distribution over the space of real, symmetric, positive definite matrices with unit diagonal elements. Lesser (greater) values concentrate the probability density around such matrices whose determinant is nearer to 0 (1).
<code>df</code>	a numeric vector listing degrees of freedom. <code>df</code> must be greater than <code>nrow(scale) - 1</code> . If either <code>df</code> or <code>scale</code> has length greater than 1, then this condition is checked elementwise after recycling.
<code>scale</code>	a list of real, symmetric, positive definite matrices or a matrix to be placed in a list of length 1.
<code>tol</code>	a non-negative number specifying a tolerance for indefiniteness of <code>scale</code> . All eigenvalues of <code>scale</code> must exceed <code>-tol * rho</code> , where <code>rho</code> is the spectral radius of <code>scale</code> . However, regardless of <code>tol</code> , <code>diag(scale)</code> must be positive, as standard deviations are stored on a logarithmic scale.

**Value**

A list inheriting from class `egf_prior`, with elements:

<code>family</code>	a character string specifying a family of distributions.
<code>parameters</code>	a named list of numeric vectors specifying parameter values.

**Examples**

```
Normal(mu = 0, sigma = 1)
Normal(mu = -5:5, sigma = c(0.1, 1))

LKJ(eta = 2)
```

```
u <- matrix(rnorm(9L), 3L, 3L)
utu <- crossprod(u)
uut <- tcrossprod(u)
Wishart(df = 6, scale = utu)
InverseWishart(df = 6, scale = list(utu, uut))
```

---

egf\_shiny

*Installed Shiny Applications*

---

### Description

Launches one of the **Shiny** applications installed with package **epigrowthfit**. To halt execution, interrupt R by typing Ctrl+C or Esc. An error is thrown if package **shiny** is not installed.

### Usage

```
egf_shiny(app = c("toplevel", "windowselect"), ...)
```

### Arguments

app	a character string naming an application.
...	optional arguments to <a href="#">runApp</a> .

### Details

Currently, two applications are available:

"toplevel" a tool for the exploring top level nonlinear models implemented in **epigrowthfit** and their dependence on parameter values. Expected incidence is plotted as a function of time together with simulated incidence time series.

"windowselect" a tool for viewing collections of incidence time series and interactively selecting suitable fitting windows. Users upload time series data in **.rds** format and download the results of their session in the same format. The result is a list containing arguments to be passed directly to **egf**. The element of the list specifying fitting windows can itself be uploaded to a session, allowing users to modify or delete existing windows and define new ones.

### Value

The value of the [runApp](#) call, though typically execution is terminated before the function can return.

### Examples

```
## Not run:
egf_shiny("toplevel")
egf_shiny("windowselect")

## End(Not run)
```

---

 egf\_top

*Top Level Nonlinear Model Parameter Names*


---

**Description**

Retrieves the names used internally for top level nonlinear model parameters.

**Usage**

```
egf_top(object, ...)

## S3 method for class 'egf_model'
egf_top(object, link = TRUE, ...)
## S3 method for class 'egf'
egf_top(object, link = TRUE, ...)
```

**Arguments**

object	an R object specifying a top level nonlinear model, typically of class <a href="#">egf_model</a> or <a href="#">egf</a> .
link	a logical flag. If TRUE, then " <code>&lt;link&gt;(&lt;name&gt;)</code> " is returned instead of " <code>&lt;name&gt;</code> ".
...	unused optional arguments.

**Value**

A character vector listing names relevant to object.

---

 epigrowthfit-defunct *Defunct Functions in Package* **epigrowthfit**


---

**Description**

The functions and other objects listed here are no longer part of **epigrowthfit** as they are no longer needed.

**Usage**

```
## Nothing yet!
```

**Details**

These either are stubs reporting that they are defunct or have been removed completely (apart from being documented here).

**See Also**

[Deprecated](#), [base-deprecated](#), [epigrowthfit-deprecated](#), [epigrowthfit-notyet](#).



---

epigrowthfit-deprecated

*Deprecated Functions in Package **epigrowthfit***

---

### **Description**

The functions and other objects listed here are provided only for compatibility with older versions of **epigrowthfit** and may become defunct as soon as the next release.

### **Usage**

```
## Nothing yet!
```

### **See Also**

[Defunct](#), [base-defunct](#), [epigrowthfit-defunct](#), [epigrowthfit-notyet](#).

---

epigrowthfit-notyet

*Not Yet Implemented Functions in Package **epigrowthfit***

---

### **Description**

The functions listed here are defined but not yet implemented. Use [bug.report](#)(package = "epigrowthfit") to request an implementation.

### **Usage**

```
## Nothing yet!
```

### **See Also**

[NotYetImplemented](#), [epigrowthfit-deprecated](#), [epigrowthfit-defunct](#).

---

extractAIC.egf	<i>Extract the (Generalized) AIC</i>
----------------	--------------------------------------

---

**Description**

Extracts from a model object the generalized Akaike Information Criterion (AIC).

**Usage**

```
## S3 method for class 'egf'
extractAIC(fit, scale, k = 2, ...)
```

**Arguments**

fit	an <a href="#">egf</a> object.
scale	unused argument, for generic consistency.
k	a number giving a weight for the equivalent degrees of freedom. $k=2$ and $k=\log(\text{nobs}(\text{fit}))$ give the standard Akaike Information Criterion and Bayesian Information Criterion.
...	unused optional arguments.

**Value**

An numeric vector of length 2 giving the equivalent degrees of freedom and criterion value.

**See Also**

The generic function [extractAIC](#).

---

finalsize	<i>Compute the Expected Epidemic Final Size</i>
-----------	---

---

**Description**

Computes the proportion of a population expected to be infected over the course of an epidemic, as a function of the basic reproduction number.

**Usage**

```
finalsize(R0, S0, I0)
```

**Arguments**

R0	a numeric vector listing non-negative values for the basic reproduction number.
S0, I0	numeric vectors listing values in the interval $[0, 1]$ for the proportions of the population that are susceptible and infected, respectively, at the start of the epidemic. Hence $S0 + I0$ must be less than or equal to 1.

### Details

At least one of  $S_0$  and  $I_0$  must be supplied. If  $S_0$  ( $I_0$ ) is supplied but not  $I_0$  ( $S_0$ ), then the latter is assigned the value of one minus the former.

$R_0$ ,  $S_0$ , and  $I_0$  are recycled to a common length (the maximum of their lengths).

### Value

A numeric vector listing values in the interval  $[0, 1]$  for the expected epidemic final size.

### Computation

The basic reproduction number  $R_0$  defines the expected epidemic final size  $Z$  through an implicit equation,

$$Z = S_0 * (1 - \exp(-R_0 * (Z + I_0))) ,$$

which admits an explicit solution

$$Z = S_0 + (1/R_0) * W(-R_0 * S_0 * \exp(-R_0 * (S_0 + I_0))) .$$

Here,  $W$  denotes the **Lambert  $W$  function**. `finalsize` computes this solution, relying on function `lambertW` from package **emdbook**.

### References

Ma, J. & Earn, D. J. D. (2006). Generality of the final size formula for an epidemic of a newly invading infectious disease. *Bulletin of Mathematical Biology*, 68(3), 679-702. doi:10.1007/s11538-00590477

### See Also

[timescale](#), [R0](#).

### Examples

```
R0 <- 10^seq(-3, 1, length.out = 151L)
plot(R0, finalsize(R0, S0 = 1, I0 = 0), type = "l", las = 1,
     xlab = "basic reproduction number",
     ylab = "final size")
```

fitted.egf

*Fitted Values***Description**

Retrieves fitted values of top level nonlinear model parameters. The fitted value of a given parameter for a given fitting window is obtained by adding (i) the population fitted value computed as a linear combination of fixed effect coefficients and (ii) all applicable random effects, with random effects set equal to their conditional modes.

**Usage**

```
## S3 method for class 'egf'
fitted(object,
        top = egf_top(object), subset = NULL, select = NULL,
        class = FALSE, se = FALSE, ...)

## S3 method for class 'fitted.egf'
confint(object, parm = seq_len(nrow(object)), level = 0.95,
        class = FALSE, ...)
```

**Arguments**

object	an <a href="#">egf</a> or <code>fitted.egf</code> object.
top	a subset of <code>egf_top(object)</code> naming top level nonlinear model parameters whose fitted values should be retrieved.
subset, select	index vectors for the rows and columns of <code>model.frame(object, "combined")</code> or language objects evaluating to such vectors. <code>subset</code> indicates fitting windows for which fitted values should be retrieved; the default indicates all. <code>select</code> indicates variables that should be appended to the result; the default indicates none. Evaluation of language objects follows the implementation of <a href="#">subset.data.frame</a> .
class	a logical. If TRUE, then the value of the method call is a <code>fitted.egf</code> or <a href="#">confint.egf</a> object, not a matrix.
se	a logical. If TRUE and if <code>class = TRUE</code> , then the result is augmented with approximate delta method standard errors.
...	additional arguments passed from or to other methods.
parm	a valid index vector for the rows of <code>object</code> indicating a subset of the fitted values.
level	a number in the interval (0, 1) indicating a confidence level.

**Value**

A numeric matrix containing fitted values.

Users can pass `class = TRUE` to obtain an augmented result. Thus, alternatively:

A data frame inheriting from class `fitted.egf`, with variables:

top	top level nonlinear model parameter, from <code>egf_top(object)</code> .
ts	time series, from <code>levels(model.frame(object)[["ts"]])</code> .
window	fitting window, from <code>levels(model.frame(object)[["window"]])</code> .
value	fitted value.
se	approximate delta method standard error (only if requested).
...	further variables from <code>model.frame(object, "combined")</code> specified by argument <code>select</code> .

**See Also**

The generic function `fitted`.

**Examples**

```
example("egf", package = "epigrowthfit")

zz <- fitted(m1, class = TRUE, se = TRUE)
str(zz)

confint(zz, class = TRUE)
```

---

fixef.egf

*Details about Fixed Effect Coefficients*


---

**Description**

Extracts from a model object details about the fixed effect coefficients, namely segment beta of the bottom level parameter vector.

**Usage**

```
## S3 method for class 'egf'
fixef(object, ...)
```

**Arguments**

object	an <code>egf</code> object.
...	unused optional arguments.

**Value**

A data frame with one row per coefficient and variables:

bottom	label for a bottom level mixed effects model parameter, in this case for a fixed effect coefficient. This is a string with format "beta[%d]".
top	name of the top level nonlinear model parameter whose fitted value is a function of bottom, from <code>egf_top(object)</code> .
term	term from the fixed effects component of the mixed effects model formula for parameter top.
colname	column name in the fixed effects design matrix <code>model.matrix(object, "fixed")</code> .
value	coefficient estimate, from segment beta of <code>coef(object, full = TRUE)</code> .

**See Also**

The generic function `fixef`.

---

formula.egf

*Extract Model Formulae*

---

**Description**

Extracts from a model object the mixed effects model formula corresponding to a top level nonlinear model parameter.

**Usage**

```
## S3 method for class 'egf'
formula(x, top = egf_top(x), split = FALSE, ...)
```

**Arguments**

x	an <code>egf</code> object.
top	a character string specifying a top level nonlinear model parameter.
split	a logical flag. If TRUE, then random effect terms are deleted from the formula and preserved as an attribute.
...	unused optional arguments.

**Value**

By default, the mixed effects model formula corresponding to top. If `split = TRUE`, then the same formula without random effect terms. The deleted terms are stored in an expression vector and preserved as attribute `random` of the result.

**See Also**

The generic function `formula`.

---

`getCall.egf`*Extract Model Calls*

---

**Description**

Extracts from a model object the call to `egf` that produced it. This method exists mainly to enable compatibility with the default method of generic function `update`.

**Usage**

```
## S3 method for class 'egf'  
getCall(x, ...)
```

**Arguments**

`x` an `egf` object.  
`...` unused optional arguments.

**Value**

A call to `egf`.

**See Also**

The generic function `getCall`.

---

`gi`*Generation Interval Distribution*

---

**Description**

Generation interval density function (`dgi`), distribution function (`pgi`), quantile function (`qgi`), and sampling (`rgi`). Results are conditional on supplied latent and infectious period distributions. It is assumed

- that the latent period and infectious waiting time are independent,
- that infectiousness is constant over the infectious period, and
- that the latent and infectious periods are positive and integer-valued (in arbitrary but common units of time).

**Usage**

```
dgi(x, latent, infectious)  
pgi(q, latent, infectious)  
qgi(p, latent, infectious)  
rgi(n, latent, infectious)
```

**Arguments**

`x, q` a numeric vector listing generation intervals.

`p` a numeric vector listing probabilities.

`n` a non-negative integer indicating a sample size. If `length(n) > 1`, then `length(n)` is taken to be the sample size.

`latent, infectious` numeric vectors such that `latent[i]` and `infectious[i]` are the probabilities that the latent and infectious periods, respectively, are `i` units of time. It is sufficient to supply probability weights, as internally both vectors are divided by their sums.

**Value**

A numeric vector with length equal to the that of the first argument or length `n` in the case of `rgi`.

**References**

Svensson, Å. (2007). A note on generation times in epidemic models. *Mathematical Biosciences*, 208(1), 300-311. doi:10.1016/j.mbs.2006.10.010

**Examples**

```
latent <- c(0.026, 0.104, 0.182, 0.246, 0.318, 0.104,
           0.013, 0.004, 0.003)
m <- length(latent)

infectious <- c(0.138, 0.462, 0.256, 0.078, 0.041, 0.007,
               0.004, 0.004, 0.006, 0.004)
n <- length(infectious)

## Histogram of samples
y <- rgi(1e06, latent, infectious)
hist(y, breaks = seq(0, m + n + 1), freq = FALSE, las = 1,
     ylab = "relative frequency",
     main = "")

## Density and distribution functions
x <- seq(0, m + n + 1, by = 0.02)
fx <- dgi(x, latent, infectious)
Fx <- pgi(x, latent, infectious)
plot(x, fx, type = "l", las = 1, # consistent with histogram
     xlab = "generation interval",
     ylab = "density function")
plot(x, Fx, type = "l", las = 1,
     xlab = "generation interval",
     ylab = "distribution function")

## Quantile function
p <- seq(0, 1, by = 0.001)
qp <- qgi(p, latent, infectious)
```



```
plot(p, qp, type = "l", las = 1,
     xlab = "probability",
     ylab = "quantile function")
```

---

logLik.egf

*Extract the Log (Marginal) Likelihood*


---

### Description

Extracts from a model object the value of the log marginal likelihood. Whether the result represents a local maximum depends on, among other things, convergence of the optimizer.

### Usage

```
## S3 method for class 'egf'
logLik(object, ...)
```

### Arguments

object            an [egf](#) object.  
...                unused optional arguments.

### Value

A numeric vector of length 1 inheriting from class `logLik`. Attribute `df` is the number of estimated parameters (fixed effect coefficients and random effect covariance parameters). Attribute `nobs` is the number of observations of disease incidence used in estimation.

### See Also

The generic function [logLik](#).

---

model.frame.egf

*Extract Model Frames*


---

### Description

Extracts from a model object any of several data frames used to specify the model, including the mixed effects model frames.

### Usage

```
## S3 method for class 'egf'
model.frame(formula,
            which = c("ts", "windows", "parameters", "extra", "combined"),
            top = egf_top(formula), full = FALSE, ...)
```

**Arguments**

formula	an <a href="#">egf</a> object.
which	a character string controlling what is returned: "ts" disease incidence time series. "windows" fitting window endpoints. "parameters" the mixed effects model frame corresponding to top. "extra" variables preserved in formula due to setting of <a href="#">egf</a> argument select_windows. "combined" the result of concatenating (in the sense of <code>cbind</code> ) all mixed effects model frames and the data frame corresponding to "extra", then deleting any duplicated variables.
top	a character string specifying a top level nonlinear model parameter, for which = "parameters".
full	a logical, for which = "ts". If TRUE, then complete time series are returned. Otherwise, only observations belonging to fitting windows are returned.
...	unused optional arguments.

**Value**

A data frame.

**See Also**

The generic function [model.frame](#).

---

model.matrix.egf	<i>Extract Design Matrices</i>
------------------	--------------------------------

---

**Description**

Extracts from a model object fixed and random effects design matrices.

**Usage**

```
## S3 method for class 'egf'
model.matrix(object, which = c("fixed", "random"),
             top = NULL, random = NULL, ...)
```

**Arguments**

object	an <a href="#">egf</a> object.
which	a character string controlling what is returned: "fixed" the fixed effects design matrix X corresponding to top. "random" the random effects design matrix Z corresponding to top and random.

top	a character string specifying a top level nonlinear model parameter. NULL indicates “all of them”; see ‘Details’.
random	a random effect term, which is a call to binary operator  . NULL indicates “all of them”; see ‘Details’.
...	unused optional arguments.

### Details

`model.matrix(which = "fixed", top = NULL)` returns the result of combining (in the sense of `cbind`) all fixed effects design matrices.

`model.matrix(which = "random", top = "<name>", random = NULL)` returns the result of combining all random effects design matrices associated with parameter `top`.

`model.matrix(which = "random", top = NULL, random = NULL)` returns the result of combining all random effects design matrices *and* permuting the columns to obtain a convenient ordering of random effect coefficients. (Coefficients are sorted by relation to a common random vector. Random vectors are sorted by relation to a common covariance matrix.)

None of these “combined” design matrices possesses attributes `assign` and `contrasts`.

### Value

A (sparse) [dgCMatrix](#) or a traditional (dense) matrix, with attributes `assign` and `contrasts` except in special cases; see ‘Details’.

### See Also

The generic function [model.matrix](#).

---

nobs.egf

*Extract the Number of Observations*

---

### Description

Returns the number of observations of disease incidence that were used in estimation of a model. This number excludes missing values and observations not belonging to a fitting window, which, despite being preserved in model objects, do not affect estimation.

### Usage

```
## S3 method for class 'egf'
nobs(object, ...)
```

### Arguments

object	an <a href="#">egf</a> object.
...	unused optional arguments.

**Value**

An integer.

**See Also**

The generic function [nobs](#).

---

plot.egf

*Plot Nonlinear Mixed Effects Models of Epidemic Growth*

---

**Description**

A method for printing objects of class [egf](#).

**Usage**

```
## S3 method for class 'egf'
plot(x, type = c("interval", "cumulative", "rt"),
     time_as = c("Date", "numeric"), delta = 1, log = TRUE, zero = NA,
     show_predict = TRUE, show_doubling = FALSE, level = 0.95,
     control = egf_control_plot(), cache = NULL, plot = TRUE,
     subset = NULL, order = NULL, xlim = NULL, ylim = NULL,
     main = NULL, sub = NULL, xlab = NULL, ylab = NULL, ...)
```

**Arguments**

x	an <a href="#">egf</a> object.
type	a character string indicating a type of plot. The options are: interval incidence ("interval"), cumulative incidence ("cumulative"), and per capita growth rate ("rt").
time_as	a character string indicating how numeric times are displayed on the bottom axis. The options are: as is ("numeric") and with a calendar ("Date"). In the latter case, horizontal user coordinates on measure time in days since midnight on January 1, 1970.
delta	a positive number indicating a step size on the time axis. Predicted curves are evaluated on a grid with this spacing. When type = "interval", counts observed over shorter or longer intervals $\Delta_0$ are scaled by a factor of $\Delta/\Delta_0$ so that their scale matches that of predicted incidence. Scaled counts can be highlighted via control. If x specifies a model with day of week effects, then $\Delta = 1$ is used unconditionally.
log	a logical. If TRUE, then the dependent variable is plotted on a logarithmic scale.
zero	a positive number indicating a line on which to plot zeros when log = TRUE and type = "interval" or "cumulative". NA is to place zeros on the bottom axis. NULL is to suppress zeros.

show_predict	an integer flag: 2 is to draw predicted curves with confidence bands, 1 is draw predicted curves only, 0 is to draw neither.
show_doubling	an integer flag: 2 is to print initial doubling time estimates in the top margin with confidence intervals, 1 is to print estimates only, 0 is to print neither. Nothing is printed for models without a well-defined initial exponential growth rate.
level	a number in the interval (0, 1) indicating confidence level, used when show_predict = 2 or show_doubling = 2.
control	an <a href="#">egf_control_plot</a> object controlling the appearance of most plot elements.
cache	a <code>plot.egf</code> object returned by a previous evaluation of <code>plot(x, ...)</code> . Fitted and predicted values and standard errors stored in cache are reused to avoid recomputation.
plot	a logical. If FALSE, then plotting does not occur. Useful when only the returned <code>plot.egf</code> object is desired.
subset	an index vector for the rows of <code>mf = model.frame(object, "combined")</code> or a language object evaluating to such a vector. Only time series corresponding to indexed rows are plotted and only fitting windows corresponding to indexed rows are highlighted; the default is to plot all series and to highlight all windows. Evaluation of language objects follows the implementation of <a href="#">subset.data.frame</a> .
order	a permutation of <code>seq_len(nrow(mf))</code> or a language object evaluating in <code>mf</code> to such a vector. <code>order</code> indicates the order in which time series are plotted; the default indicates the original order.
xlim, ylim	numeric vectors of length 2 specifying axis limits, which are recycled for all plots. If <code>time_as = "Date"</code> , then <code>xlim</code> can instead be a <a href="#">Date</a> , <a href="#">POSIXct</a> , or <a href="#">POSIXlt</a> vector.
main, sub, xlab, ylab	character or expression vectors or (main, sub) language objects evaluating in <code>mf</code> to such vectors. These are used to generate plot (main, sub) and axis (xlab, ylab) labels.
...	unused optional arguments.

## Details

Computation of fitted and predicted values and standard errors is performed before any plots are created. To avoid waste of computation time, cached computations are returned *even if* an error is thrown during plotting. To ensure that the cache is preserved, assign the result of the function call to a name:

```
cache <- plot(x, \dots)
```

. Caching functionality must be used with care, as mismatch between `x` and `cache` will not be detected. Constructions such as `plot(y, cache = plot(x, ...), ...)`, where `x` and `y` are different `egf` objects, should not be expected to produce correct results.

**Value**

A data frame inheriting from class `plot.egf`.

If argument `cache` was supplied in the function call, then this data frame is the result of augmenting `cache` with any new computations.

**See Also**

The generic function `plot`.

**Examples**

```
example("egf", package = "epigrowthfit")

l <- list(legend = list(cex = 0.8),
         value = list(cex = 0.8, font = 2),
         ci = list(cex = 0.8))
control <- egf_control_plot(doubling = 1)

op <- par(mar = c(3.5, 5, 5, 1))
plot(m1,
     type = "interval",
     show_predict = 2L,
     show_doubling = 2L,
     control = control)
plot(m1,
     type = "cumulative",
     main = "Fitted exponential model",
     sub = quote(paste("Country", country)))
par(op)

op <- par(mar = c(3.5, 9.5, 5, 1))
plot(m1, type = "rt", subset = quote(country %in% LETTERS[4:6]))
par(op)
```

---

predict.egf

*Predicted Values*

---

**Description**

Computes predicted values of top level nonlinear model parameters. These are conditional on an estimated nonlinear mixed effects model and, optionally, new data.

**Usage**

```
## S3 method for class 'egf'
predict(object, newdata = NULL, class = FALSE, se = FALSE, ...)
```

**Arguments**

object	an <a href="#">egf</a> object.
newdata	a data frame containing variables to replace those in the model frame. The default is to use the model frame as is, and currently that is the only implemented behaviour.
class	a logical. If TRUE, then the value of the method call call is a <a href="#">predict.egf</a> object, not a matrix.
se	a logical. If TRUE and if class = TRUE, then the result is augmented with approximate delta method standard errors.
...	additional arguments passed from or to other methods.

**Value**

A numeric matrix containing predicted values.

Users can pass class = TRUE to obtain an augmented result. Thus, alternatively:

A data frame inheriting from class `predict.egf`, with variables:

top	top level nonlinear model parameter, from <a href="#">egf_top</a> (object).
ts	time series, from <code>levels(model.frame(object)[["ts"]])</code> .
window	fitting window, from <code>levels(model.frame(object)[["window"]])</code> .
value	predicted value.
se	approximate delta method standard error (only if requested).

**See Also**

The generic function [predict](#).

---

print.egf

*Printing Model Objects*

---

**Description**

A method for printing objects of class [egf](#).

**Usage**

```
## S3 method for class 'egf'
print(x, width = 0.9 * getOption("width"), indent = 2L, ...)
```

**Arguments**

x	an <a href="#">egf</a> object.
width	an integer width for header text.
indent	an integer indent for body text.
...	unused optional arguments.

**Value**

The argument `x`, unchanged but [invisible](#).

**See Also**

The generic function [print](#).

---

 profile.egf

*Univariate Likelihood Profiles*


---

**Description**

Computes univariate likelihood profiles of fixed effect coefficients, random effect covariance parameters, and linear combinations thereof, including population fitted values.

**Usage**

```
## S3 method for class 'egf'
profile(fitted, level = 0.95,
        A = seq_along(par), grid = 12L,
        parallel = egf_parallel(), trace = FALSE,
        top = egf_top(fitted), subset = NULL, select = NULL, ...)

## S3 method for class 'profile.egf'
confint(object, parm = seq_along(object), level = attr(object, "level"),
        class = FALSE, ...)

## S3 method for class 'profile.egf'
plot(x, parm = seq_along(x), level = attr(x, "level"),
     type = c("z", "abs(z)", "z^2"), ...)
```

**Arguments**

<code>fitted</code>	an <a href="#">egf</a> object.
<code>level</code>	a number in the interval $(0, 1)$ indicating a confidence level. Profiles are computed up to a change in deviance equal to <code>qchisq(level, df = 1)</code> .
<code>A</code>	a numeric matrix with $1+p$ columns, where $p = \text{length}(\text{coef}(\text{fitted}))$ , in which case each row specifies a linear combination of the elements of <code>c(1, coef(fitted))</code> to be profiled; or a valid index vector for <code>coef(fitted)</code> , in which case the indexed elements are profiled; or <code>NULL</code> , in which case population fitted values are profiled.
<code>grid</code>	a positive integer. Step sizes chosen adaptively by <a href="#">tmbprofile</a> will generate approximately this many points on each side of a profile's minimum point.
<code>parallel</code>	an <a href="#">egf_parallel</a> object defining options for R level parallelization.
<code>trace</code>	a logical. If <code>TRUE</code> , then basic tracing messages indicating progress are printed. These may be mixed with optimizer output depending on <code>fitted[["control"]][["trace"]]</code> .



top	a subset of <code>egf_top(fitted)</code> naming top level nonlinear model parameters for which profiles on population fitted values should be profiled.
subset, select	index vectors for the rows and columns of <code>model.frame(fitted, "combined")</code> or language objects evaluating to such vectors. <code>subset</code> indicates fitting windows for which profiles should be computed; the default indicates all. <code>select</code> indicates variables that should be appended to the result; the default indicates none. Evaluation of language objects follows the implementation of <code>subset.data.frame</code> .
...	additional arguments passed from or to other methods.
object, x	a <code>profile.egf</code> object.
parm	a valid index vector for <code>object</code> or <code>x</code> indicating a subset of the profiles.
class	a logical. If TRUE and if <code>object</code> was created by <code>profile(A = NULL)</code> , then the value of the method call is a <code>confint.egf</code> object, not a matrix.
type	a character string indicating which of $z$ , $ z $ , and $z^2$ is plotted.

### Details

Computation of likelihood profiles is typically expensive, requiring estimation of many restricted models. It is parallelized at the C++ level when there is OpenMP support and `fitted[["control"]][["omp_num_threads"]]` is set to an integer greater than 1. When there is no OpenMP support, it can still be parallelized at the R level with appropriate setting of argument `parallel`.

### Value

A list of length `nrow(A)` inheriting from classes `profile.egf` and `profile`. Each element is a data frame specifying a profile, with two variables:

<code>z</code>	a numeric vector containing profile $z$ -statistics. The profile $z$ -statistic is the appropriately signed square root of the change in deviance under the restricted model.
<code>par.vals</code>	a numeric matrix with one column containing values of the linear combination specified by <code>A[i, ]</code> .

The confidence level `level` is preserved as an attribute.

### See Also

The generic function `profile`. The more basic “next” method for generic function `plot`, namely `plot.profile`.

### Examples

```
example("egf", package = "epigrowthfit")

zz <- profile(m1, A = NULL,
             top = "log(r)", subset = quote(country == "A" & wave == 1))
str(zz)

confint(zz, class = TRUE)
```

```
pty <- c("z", "abs(z)", "z^2")
bty <- c("l", "u", "u")
for (i in 1:3)
  plot(zz, type = pty[i], bty = bty[i], las = 1)
```

---

R0

---

*Compute the Basic Reproduction Number*


---

### Description

Computes the basic reproduction number as a function of the initial exponential growth rate, conditional on a binned generation interval distribution.

### Usage

```
R0(r, breaks, probs)
```

### Arguments

r	a non-negative numeric vector listing initial exponential growth rates.
breaks	an increasing numeric vector of length 2 or greater listing break points in the support of the generation interval distribution, in reciprocal units of r.
probs	a numeric vector of length length(breaks)-1. probs[i] is the probability that the generation interval is between breaks[i] and breaks[i+1]. It is sufficient to supply probability weights, as internally the vector is divided by its sum.

### Value

A numeric vector listing basic reproduction numbers.

### Computation

For an initial exponential growth rate r, the basic reproduction number is computed as

$$r / \sum(\text{probs} * (\exp(-r * \text{breaks}[-n]) - \exp(-r * \text{breaks}[-1L])) / (\text{breaks}[-1L] - \text{breaks}[-n])) ,$$

where n = length(breaks).

### References

Wallinga, J. & Lipsitch M. (2007). How generation intervals shape the relationship between growth rates and reproductive numbers. *Proceedings of the Royal Society B: Biological Sciences*, 274(1609), 599-604. doi:10.1098/rspb.2006.3754

### See Also

[timescale](#), [finalsize](#).

**Examples**

```

r <- seq(0, 1, 0.02)
breaks <- seq(0, 20, 1)
probs <- diff(pgamma(breaks, shape = 1, scale = 2.5))

plot(r, R0(r, breaks, probs), las = 1,
      xlab = "initial exponential growth rate",
      ylab = "basic reproduction number")

```

---

ranef.egf

*Details about Random Effect Coefficients*


---

**Description**

Extracts from a model object details about the random effect coefficients, namely segment b of the bottom level parameter vector.

**Usage**

```

## S3 method for class 'egf'
ranef(object, makeSigma = FALSE, ...)

```

**Arguments**

object	an <code>egf</code> object.
makeSigma	a logical flag. If TRUE, then random effect covariance matrices are constructed from segment theta of <code>coef(object, full = TRUE)</code> and preserved as an attribute of the result.
...	unused optional arguments.

**Value**

A data frame with one row per coefficient and variables:

cov	label for a covariance matrix. This is the interaction of term and group, but using levels with format "Sigma[%d]".
vec	label for a random vector. This is the interaction of term, group, and level, but using levels with format "u[%d]".
bottom	label for a bottom level mixed effects model parameter, in this case for a random effect coefficient; this is a string with format "b[%d]".
top	name of the top level nonlinear model parameter whose fitted value is a function of bottom, from <code>egf_top(object)</code> .
term, group	term from the random effects component of the mixed effects model formula for parameter top. term and group give the left and right hand sides of the term, which is a call to binary operator  .

level	level of the factor or interaction indicated by group.
colname	column name in the random effects design matrix <code>model.matrix(object, "random")</code> .
value	random effect conditional mode (unit variance scale), from segment b of <code>coef(object, full = TRUE)</code> .

If `makeSigma = TRUE`, then the result has attribute `Sigma`, a list of covariance matrices corresponding to the levels of variable `cov`.

### See Also

The generic function [ranef](#).

---

simulate.egf

*Simulation and Parametric Bootstrapping*

---

### Description

Simulates incidence data conditional on a fitted nonlinear mixed effects model of epidemic growth. Optionally re-estimates the model given the simulated data, thus generating samples from the conditional distribution of the bottom level parameter vector.

### Usage

```
## S3 method for class 'egf'
simulate(object, nsim = 1, seed = NULL,
         bootstrap = FALSE,
         control = list(), parallel = egf_parallel(),
         trace = FALSE, ...)
```

### Arguments

object	an <a href="#">egf</a> object.
nsim	a positive integer indicating a number of replications.
seed	an integer used to set the <a href="#">RNG</a> state before simulation or, otherwise, <code>NULL</code> ; see <a href="#">simulate</a> .
bootstrap	a logical. If <code>TRUE</code> , then a bootstrapping step is performed.
control	passed to <a href="#">nlminb</a> .
parallel	an <a href="#">egf_parallel</a> object defining options for R level parallelization.
trace	a logical. If <code>TRUE</code> , then basic tracing messages indicating progress are printed. These may be mixed with optimizer output depending on <code>object[["control"]][["trace"]]</code> .
...	additional arguments passed from or to other methods.

**Details**

Bootstrap optimizations are typically expensive for nontrivial models. They are parallelized at the C++ level when there is OpenMP support and `object[["control"]][["omp_num_threads"]]` is set to an integer greater than 1. When there is no OpenMP support, they can still be parallelized at the R level with appropriate setting of argument `parallel`.

Arguments `control`, `parallel`, and `trace` are unused when `bootstrap = FALSE`.

**Value**

A list inheriting from class `simulate.egf`, with elements:

<code>simulation</code>	a data frame containing simulated incidence data. It has variables <code>ts</code> , <code>window</code> , <code>time</code> , and <code>X</code> , where <code>X</code> is a numeric matrix with <code>nsim</code> columns. It corresponds rowwise to <code>model.frame(object)</code> .
<code>bootstrap</code>	a numeric matrix with <code>nsim</code> columns, each a sample from the conditional distribution of the parameter vector represented by <code>coef(object)</code> . NULL if the method call did not set <code>bootstrap = TRUE</code> .

Attribute `RNGstate` preserves the RNG state prior to simulation, making the result reproducible.

**See Also**

The generic function `simulate`.

**Examples**

```
example("egf", package = "epigrowthfit")

zz <- simulate(m2, nsim = 6L, seed = 181952L, bootstrap = TRUE)
str(zz)

matplot(t(zz[["bootstrap"]][!m2[["random"]], ]),
        type = "o", las = 1, xlab = "simulation", ylab = "value")
```

---

`simulate.egf_model`      *Simulating Incidence Time Series*

---

**Description**

Simulates equally spaced incidence time series according to a specified nonlinear model. Top level nonlinear model parameters vary between time series according to a fixed intercept model  $\sim ts$  or random intercept model  $\sim(1 | ts)$ .

**Usage**

```
## S3 method for class 'egf_model'
simulate(object, nsim = 1, seed = NULL,
        mu, Sigma = NULL, tol = 1e-06, cstart = 0, tend = 100, ...)
```

**Arguments**

object	an <code>egf_model</code> object specifying a top level nonlinear model to be simulated.
nsim	a positive integer indicating a number of time series.
seed	an integer used to set the <code>RNG</code> state before simulation or, otherwise, <code>NULL</code> ; see <code>simulate</code> .
mu	a numeric vector listing means across time series of top level nonlinear model parameters (link scale). It is assumed that elements are ordered as <code>egf_top(object)</code> .
Sigma	a real, symmetric positive definite matrix to be used as the covariance matrix corresponding to <code>mu</code> . The default is equivalent to a zero matrix and is handled specially.
tol	a non-negative number indicating a tolerance for indefinite <code>Sigma</code> . Eigenvalues of <code>Sigma</code> must exceed <code>-tol</code> times its spectral radius. <code>diag(Sigma)</code> must be positive regardless of <code>tol</code> , as standard deviations are handled on a logarithmic scale.
cstart	a number indicating a threshold value of cumulative incidence. Left endpoints of suggested fitting windows are those times when cumulative incidence first exceeds this threshold.
tend	a positive number. Simulated time series run from time 0 to time <code>tend</code> with unit spacing. For nonlinear models of expected cumulative incidence with inflections, this argument is ignored and set to <code>tinfl+1</code> , where <code>tinfl</code> is the time of inflection.
...	unused optional arguments.

**Value**

A list inheriting from class `simulate.egf_model`, with elements:

model	copy of argument object.
formula_ts	a formula, always <code>cbind(time, x) ~ ts</code> , expressing how simulated time series are stored in <code>data_ts</code> .
formula_windows	a formula, always <code>cbind(start, end) ~ ts</code> , expressing how fitting window endpoints are stored in <code>data_windows</code> .
formula_parameters	a formula specifying the generative model. If <code>Sigma = NULL</code> , then the formula is <code>~1</code> if <code>nsim = 1</code> and <code>~ts</code> if <code>nsim &gt; 1</code> . Otherwise, it is <code>~(1   ts)</code> .
data_ts	a data frame with variables <code>ts</code> , <code>time</code> , and <code>x</code> storing <code>nsim</code> simulated time series in long format.
data_windows	a data frame with <code>nsim</code> rows and variables <code>ts</code> , <code>start</code> , and <code>end</code> suggesting fitting window endpoints for each simulated time series. Start times are determined by <code>cstart</code> . End times are always the last time point in the corresponding time series.
init	a named list of the form <code>list(beta, theta)</code> giving the full bottom level parameter vector of the generative model.

**Y** a numeric matrix with `nsim` rows and `length(mu)` columns listing top level nonlinear model parameter values for each time series. If `Sigma = NULL`, then the row vectors of are all `mu`. Otherwise, `Y` is (conceptually) the result of `MASS::mvrnorm(nsim, mu, Sigma, tol)`.

**call** the call to `simulate`, allowing for updates to the `simulate.egf_model` object via `update`.

Attribute `RNGstate` preserves the RNG state prior to simulation, making the result reproducible.

### See Also

The generic function `simulate`.

### Examples

```
r <- 0.04
c0 <- 400
s <- 0.2

mu <- log(c(r, c0))
Sigma <- diag(rep.int(s^2, length(mu)))

zz <- simulate(object = egf_model(curve = "exponential", family = "pois"),
              nsim = 20L,
              seed = 202737L,
              mu = mu,
              Sigma = Sigma,
              cstart = 10)

str(zz)

mm <- egf(zz)
(pp <- cbind(actual = coef(zz), fitted = coef(mm)))
```

---

summary.egf

*Model Summaries*

---

### Description

Summarizes fitted values of top level nonlinear model parameters and gathers diagnostic information that can be used to quickly assess convergence of the optimizer.

### Usage

```
## S3 method for class 'egf'
summary(object, ...)
```

### Arguments

**object** an `egf` object.

**...** additional arguments passed from or to other methods.

**Value**

A list inheriting from class `summary.egf`, with elements:

<code>fitted</code>	a numeric matrix. Each column is the result of applying <code>summary.default</code> to a numeric vector listing the fitted values of a top level nonlinear model parameters. Fitted values are retrieved by <code>fitted.egf</code> .
<code>convergence</code>	an integer code returned by the optimizer, with 0 indicating successful convergence within the specified absolute or relative tolerance.
<code>value, gradient</code>	numeric vectors giving the value and gradient of the negative log marginal likelihood function at the parameter vector returned by the optimizer.
<code>hessian</code>	a logical flag indicating whether the Hessian matrix of the negative log marginal likelihood function is positive definite at the parameter vector returned by the optimizer. NA means that the matrix was not computed by <code>egf</code> , either because <code>se = TRUE</code> was not passed in the function call or because an error was thrown during computation.

**See Also**

The generic function `summary`.

**Examples**

```
example("egf", package = "epigrowthfit")

zz <- summary(m1)
str(zz)
```

---

terms.egf

*Model Terms*

---

**Description**

Extracts the `terms` object corresponding to a top level nonlinear model parameter.

**Usage**

```
## S3 method for class 'egf'
terms(x, top = egf_top(x), ...)
```

**Arguments**

<code>x</code>	an <code>egf</code> object.
<code>top</code>	a character string specifying a top level nonlinear model parameter.
<code>...</code>	unused optional arguments.



**Value**

A [terms](#) object.

**See Also**

The generic function [terms](#).

---

timescale	<i>Compute the Characteristic Time Scale</i>
-----------	--

---

**Description**

Computes characteristic time scales corresponding to exponential growth rates.

**Usage**

```
timescale(r, units)
```

**Arguments**

**r** a non-negative numeric vector listing exponential growth rates.  
**units** a character string indicating units for the result. If missing, then the result is “unitless”.

**Value**

1/r, as a [difftime](#) if units is not missing.

**See Also**

[R0](#), [finalsize](#).

**Examples**

```
r <- 10^(-2:0)
units <- "days"
stopifnot(all.equal(timescale(r), 1 / r),
          all.equal(timescale(r, units), .difftime(1 / r, units)))
```

---

`vcov.egf`*Model Covariance Matrices*

---

**Description**

Extracts (or, if necessary, computes) the covariance matrix of bottom level parameters beta and theta, corresponding to the output of `coef(object)`.

**Usage**

```
## S3 method for class 'egf'  
vcov(object, ...)
```

**Arguments**

<code>object</code>	an <code>egf</code> object.
<code>...</code>	unused optional arguments.

**Details**

If the resulting matrix is not finite or not positive definite, then the fit specified by `object` should be investigated, as the optimizer that produced the fit may have failed to converge.

**Value**

A real, symmetric matrix.

**See Also**

The generic function `vcov`.

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