

# Package: growthmodels (via r-universe)

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**Title** Nonlinear Growth Models

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**Description** A compilation of nonlinear growth models.

**License** GPL-3

**URL** <https://github.com/drodriguezperez/growthmodels>

**BugReports** <https://github.com/drodriguezperez/growthmodels/issues>

**Suggests** testthat

**Roxygen** list(wrap = FALSE)

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

**RemoteUrl** <https://github.com/drodriguezperez/growthmodels>

**RemoteRef** HEAD

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growthmodels-package    *growthmodels: Nonlinear Growth Models*

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## Description

A compilation of nonlinear growth models.

## Details

Package: growthmodels  
Version: 1.2.0  
License: GPL-3

## Author(s)

Daniel Rodriguez <daniel.rodriguez.perez@gmail.com>

## References

- D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.
- M. M. Kaps, W. O. W. Herring, and W. R. W. Lamberson, "Genetic and environmental parameters for traits derived from the Brody growth curve and their relationships with weaning weight in Angus cattle.," *Journal of Animal Science*, vol. 78, no. 6, pp. 1436-1442, May 2000.
- A. Tsoularis and J. Wallace, "Analysis of logistic growth models.," *Math Biosci*, vol. 179, no. 1, pp. 21-55, Jul. 2002.
- A. Khamiz, Z. Ismail, and A. T. Muhammad, "Nonlinear growth models for modeling oil palm yield growth," *Journal of Mathematics and Statistics*, vol. 1, no. 3, p. 225, 2005.
- Michael J. Panik, "Growth Curve Modeling: Theory and Applications", John Wiley & Sons, December 2013.
- [http://en.wikipedia.org/wiki/Generalised\\_logistic\\_function](http://en.wikipedia.org/wiki/Generalised_logistic_function)

---

`blumberg`*Blumberg growth model*

---

**Description**

Computes the Blumberg growth model and its inverse

$$y(t) = \frac{\alpha * (t + t_0)^m}{w_0 + (t + t_0)^m}$$

**Usage**

```
blumberg(t, alpha, w0, m, t0 = 0)
```

```
blumberg.inverse(x, alpha, w0, m, t0 = 0)
```

**Arguments**

<code>t</code>	time
<code>alpha</code>	upper asymptote
<code>w0</code>	a reference value at $t = t_0$
<code>m</code>	slope of growth
<code>t0</code>	time shift (default 0)
<code>x</code>	size

**Author(s)**

Daniel Rodriguez

**References**

A. Tsoularis and J. Wallace, "Analysis of logistic growth models.," Math Biosci, vol. 179, no. 1, pp. 21-55, Jul. 2002.

**Examples**

```
growth <- blumberg(0:10, 10, 2, 0.5)

# Calculate inverse function
time <- blumberg.inverse(growth, 12, 2, 0.5)
```

---

brody

*Brody growth model*

---

### Description

Computes the Brody growth model and its inverse

$$y(t) = \alpha - (\alpha - w_0)\exp(-kt)$$

### Usage

```
brody(t, alpha, w0, k)
```

```
brody.inverse(x, alpha, w0, k)
```

### Arguments

t	time
alpha	upper asymptote
w0	the value at t = 0
k	growth rate
x	size

### Author(s)

Daniel Rodriguez

### References

M. M. Kaps, W. O. W. Herring, and W. R. W. Lamberson, "Genetic and environmental parameters for traits derived from the Brody growth curve and their relationships with weaning weight in Angus cattle.," *Journal of Animal Science*, vol. 78, no. 6, pp. 1436-1442, May 2000.

### Examples

```
growth <- brody(0:10, 10, 5, 0.3)

# Calculate inverse function
time <- brody.inverse(growth, 10, 5, 0.3)
```

---

chapmanRichards      *Chapman-Richards growth model*

---

**Description**

Computes the Chapman-Richards growth model and its inverse

$$y(t) = \alpha(1 - \beta \exp(-kt))^{1/(1-m)}$$

**Usage**

```
chapmanRichards(t, alpha, beta, k, m)
```

```
chapmanRichards.inverse(x, alpha, beta, k, m)
```

**Arguments**

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
m	slope of growth
x	size

**Author(s)**

Daniel Rodriguez

**References**

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

**Examples**

```
growth <- chapmanRichards(0:10, 10, 0.5, 0.3, 0.5)

# Calculate inverse function
time <- chapmanRichards.inverse(growth, 10, 0.5, 0.3, 0.5)
```

---

generalisedLogistic    *Generalised Logistic growth model*

---

### Description

Computes the Generalised Logistic growth model

$$y(t) = A + \frac{U - A}{1 + \beta \exp(-k(t - t_0))}$$

### Usage

```
generalisedLogistic(t, A, U, k, beta, t0)
```

```
generalisedLogistic.inverse(x, A, U, k, beta, t0 = 0)
```

### Arguments

t	time
A	the lower asymptote
U	the upper asymptote
k	growth range
beta	growth range
t0	time shift (default 0)
x	size

### Author(s)

Daniel Rodriguez

### References

[http://en.wikipedia.org/wiki/Generalised\\_logistic\\_function](http://en.wikipedia.org/wiki/Generalised_logistic_function)

### Examples

```
growth <- generalisedLogistic(0:10, 5, 10, 0.3, 0.5, 3)

# Calculate inverse function
time <- generalisedLogistic.inverse(growth, 5, 10, 0.3, 0.5, 3)
```

---

generalisedRichard     *Generalised Richard growth model*

---

### Description

Computes the Generalised Richard growth model and its inverse

$$y(t) = A + \frac{U - A}{(1 + \beta \exp(-k(t - t_0)))^{(1/m)}}$$

### Usage

```
generalisedRichard(t, A, U, k, m, beta, t0)
```

```
generalisedRichard.inverse(x, A, U, k, m, beta, t0 = 0)
```

### Arguments

t	time
A	the lower asymptote
U	the upper asymptote
k	growth range
m	slope of growth
beta	growth range
t0	time shift (default 0)
x	size

### Author(s)

Daniel Rodriguez

### References

[http://en.wikipedia.org/wiki/Generalised\\_logistic\\_function](http://en.wikipedia.org/wiki/Generalised_logistic_function)

### Examples

```
growth <- generalisedRichard(0:10, 5, 10, 0.3, 0.5, 1, 3)
```

```
time <- generalisedRichard.inverse(growth, 5, 10, 0.3, 0.5, 1, 3)
```

---

gompertz

*Gompertz growth model*

---

### Description

Computes the Gompertz growth model and its inverse

$$y(t) = \alpha \exp(-\beta \exp(-k^t))$$

### Usage

```
gompertz(t, alpha, beta, k)
```

```
gompertz.inverse(x, alpha, beta, k)
```

### Arguments

t	time
alpha	upper asymptote
beta	growth displacement
k	growth rate
x	size

### Author(s)

Daniel Rodriguez

### References

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

### Examples

```
growth <- gompertz(0:10, 10, 0.5, 0.3)

# Calculate inverse function
time <- gompertz.inverse(growth, 10, 0.5, 0.3)
```



---

janoschek

*Janoschek growth model*

---

### Description

Computes the Janoschek growth model and its inverse

$$y(t) = \alpha * (\alpha - \beta) \exp(-b * t^c)$$

### Usage

```
janoschek(t, alpha, beta, b, c)
```

```
janoschek.inverse(x, alpha, beta, b, c)
```

### Arguments

t	time
alpha	upper asymptote
beta	lower asymptote
b	growth parameter
c	shape parameter
x	size

### Author(s)

Daniel Rodriguez

### References

Michael J. Panik, "Growth Curve Modeling: Theory and Applications", John Wiley & Sons, December 2013.

### Examples

```
growth <- janoschek(0:10, 10, 2, 0.5, 2)

# Calculate inverse function
time <- janoschek.inverse(growth, 12, 2, 0.5, 2)
```

---

logistic

*Logistic growth model*

---

### Description

Computes the Logistic growth model

$$y(t) = \frac{\alpha}{1 + \beta \exp(-kt)}$$

### Usage

```
logistic(t, alpha, beta, k)
```

```
logistic.inverse(x, alpha, beta, k)
```

### Arguments

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
x	size

### Author(s)

Daniel Rodriguez

### References

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

### Examples

```
growth <- logistic(0:10, 10, 0.5, 0.3)

# Calculate inverse function
time <- logistic.inverse(growth, 10, 0.5, 0.3)
```

---

loglogistic

*Log-logistic growth model*

---

### Description

Computes the Log-logistic growth model

$$y(t) = \frac{\alpha}{1 + \beta \exp(-k \log(t))}$$

### Usage

```
loglogistic(t, alpha, beta, k)
```

```
loglogistic.inverse(x, alpha, beta, k)
```

### Arguments

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
x	size

### Author(s)

Daniel Rodriguez

### References

A. Khamiz, Z. Ismail, and A. T. Muhammad, "Nonlinear growth models for modeling oil palm yield growth," *Journal of Mathematics and Statistics*, vol. 1, no. 3, p. 225, 2005.

### Examples

```
growth <- loglogistic(0:10, 10, 0.5, 0.3)

# Calculate inverse function
time <- loglogistic.inverse(growth, 10, 0.5, 0.3)
```

---

`mitcherlich`*Mitcherlich growth model*

---

**Description**

Computes the Mitcherlich growth model

$$y(t) = (\alpha - \beta k^t)$$

**Usage**

```
mitcherlich(t, alpha, beta, k)
```

```
mitcherlich.inverse(x, alpha, beta, k)
```

**Arguments**

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
x	size

**Author(s)**

Daniel Rodriguez

**References**

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

**Examples**

```
growth <- mitcherlich(0:10, 10, 0.5, 0.3)

# Calculate inverse function
time <- mitcherlich.inverse(growth, 10, 0.5, 0.3)
```

---

`mmf`*Morgan-Mercer-Flodin growth model*

---

**Description**

Computes the Morgan-Mercer-Flodin growth model

$$y(t) = \frac{(w_0\gamma + \alpha t^m)}{\gamma} + t^m$$

**Usage**

```
mmf(t, alpha, w0, gamma, m)
```

```
mmf.inverse(x, alpha, w0, gamma, m)
```

**Arguments**

t	time
alpha	upper asymptote
w0	the value at t = 0
gamma	parameter that controls the point of inflection
m	growth rate
x	size

**Author(s)**

Daniel Rodriguez

**References**

A. Khamiz, Z. Ismail, and A. T. Muhammad, "Nonlinear growth models for modeling oil palm yield growth," *Journal of Mathematics and Statistics*, vol. 1, no. 3, p. 225, 2005.

**Examples**

```
growth <- mmf(0:10, 10, 0.5, 4, 1)

# Calculate inverse function
time <- mmf.inverse(growth, 10, 0.5, 4, 1)
```

---

monomolecular

*Monomolecular growth model*

---

### Description

Computes the monomolecular growth model

$$y(t) = \alpha(1 - \beta \exp(-kt))$$

### Usage

```
monomolecular(t, alpha, beta, k)
```

```
monomolecular.inverse(x, alpha, beta, k)
```

### Arguments

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
x	size

### Author(s)

Daniel Rodriguez

### References

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

### Examples

```
growth <- monomolecular(0:10, 10, 0.5, 0.3)

# Calculate inverse function
time <- monomolecular.inverse(growth, 10, 0.5, 0.3)
```

---

negativeExponential    *Negative exponential growth model*

---

**Description**

Computes the negative exponential growth model

$$y(t) = \alpha(1 - \exp(-kt))$$

**Usage**

```
negativeExponential(t, alpha, k)
```

```
negativeExponential.inverse(x, alpha, k)
```

**Arguments**

t	time
alpha	upper asymptote
k	growth rate
x	size

**Author(s)**

Daniel Rodriguez

**References**

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

**Examples**

```
growth <- negativeExponential(0:10, 1, 0.3)

# Calculate inverse function
time <- negativeExponential.inverse(growth, 10, 0.3)
```

---

richard

*Richard growth model*

---

### Description

Computes the Richard growth model and its inverse

$$y(t) = \frac{\alpha}{(1 + \beta \exp(-kt))^{(1/m)}}$$

### Usage

```
richard(t, alpha, beta, k, m)
```

```
richard.inverse(x, alpha, beta, k, m)
```

### Arguments

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
m	slope of growth
x	size

### Author(s)

Daniel Rodriguez

### References

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

### Examples

```
growth <- richard(0:10, 10, 0.5, 0.3, 0.5)
```

```
time <- richard.inverse(growth, 10, 0.5, 0.3, 0.5)
```



---

schnute                      *Schnute growth model*

---

**Description**

Computes the Schnute growth model

$$y(t) = [r_0 + \beta \exp(kt)]^m$$

**Usage**

```
schnute(t, r0, beta, k, m)
```

```
schnute.inverse(x, r0, beta, k, m)
```

**Arguments**

t	time
r0	reference value
beta	growth displacement
k	growth rate
m	slope of growth
x	size

**Author(s)**

Daniel Rodriguez

**References**

A. Khamiz, Z. Ismail, and A. T. Muhammad, "Nonlinear growth models for modeling oil palm yield growth," *Journal of Mathematics and Statistics*, vol. 1, no. 3, p. 225, 2005.

**Examples**

```
growth <- schnute(0:10, 10, 5, .5, .5)

# Calculate inverse function
time <- schnute.inverse(growth, 10, 5, .5, .5)
```

---

`stannard`*Stannard growth model*

---

**Description**

Computes the Stannard growth model

$$y(t) = \alpha [1 + \exp(-(\beta + kt)/m)]^{-m}$$

**Usage**

```
stannard(t, alpha, beta, k, m)
```

```
stannard.inverse(x, alpha, beta, k, m)
```

**Arguments**

t	time
alpha	upper asymptote
beta	growth displacement
k	growth rate
m	slope of growth
x	size

**Author(s)**

Daniel Rodriguez

**References**

A. Khamiz, Z. Ismail, and A. T. Muhammad, "Nonlinear growth models for modeling oil palm yield growth," *Journal of Mathematics and Statistics*, vol. 1, no. 3, p. 225, 2005.

**Examples**

```
growth <- stannard(0:10, 1, .2, .1, .5)

# Calculate inverse function
time <- stannard.inverse(growth, 1, .2, .1, .5)
```

---

vonBertalanffy      *von Bertalanffy growth model*

---

**Description**

Computes the von Bertalanffy growth model

$$y(t) = (\alpha^{1-m} - \beta * \exp(-kt))^{1/(1-m)}$$

**Usage**

```
vonBertalanffy(t, alpha, beta, k, m)
```

```
vonBertalanffy.inverse(x, alpha, beta, k, m)
```

**Arguments**

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
m	slope of growth
x	size

**Author(s)**

Daniel Rodriguez

**References**

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

**Examples**

```
growth <- vonBertalanffy(0:10, 10, 0.5, 0.3, 0.5)

# Calculate inverse function
time <- vonBertalanffy.inverse(growth, 10, 0.5, 0.3, 0.5)
```

---

weibull                      *Weibull growth model*

---

**Description**

Computes the Weibull growth model

$$y(t) = \alpha - \beta \exp(-k * t^m)$$

**Usage**

```
weibull(t, alpha, beta, k, m)
```

```
weibull.inverse(x, alpha, beta, k, m)
```

**Arguments**

t	time
alpha	upper asymptote
beta	growth range
k	growth rate
m	slope of growth
x	size

**Author(s)**

Daniel Rodriguez

**References**

D. Fekedulegn, M. Mac Siurtain, and J. Colbert, "Parameter estimation of nonlinear growth models in forestry," *Silva Fennica*, vol. 33, no. 4, pp. 327-336, 1999.

**Examples**

```
growth <- weibull(0:10, 10, 0.5, 0.3, 0.5)

# Calculate inverse function
time <- weibull.inverse(growth, 10, 0.5, 0.3, 0.5)
```

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