

Package ‘quaxnat’

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Title Estimation of Natural Regeneration Potential

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Description Functions for estimating the potential dispersal of tree species using regeneration densities and dispersal distances to nearest seed trees. A quantile regression is implemented to determine the dispersal potential. Spatial prediction can be used to identify natural regeneration potential for forest restoration as described in Axer et al (2021) <[doi:10.1016/j.foreco.2020.118802](https://doi.org/10.1016/j.foreco.2020.118802)>.

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URL <https://github.com/MaximilianAxer/quaxnat>

BugReports <https://github.com/MaximilianAxer/quaxnat/issues>

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extract_dist	<i>Extracting distances to nearest seed source for point data</i>
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Description

Extracts a distance for the inventory plots. The distance to the nearest seed source is used for the analysis of the regeneration potential.

Usage

```
extract_dist(raster, geom, species)
```

Arguments

raster	Raster dataset with tree species classification of specific tree species and tree species groups.
geom	Geodata representing the study area. This can be a polygon or point dataset. This describes the outer boundary of the study area. A buffer of 1000 m is placed around the Bounding box to possibly take into account seed trees outside the study area.
species	Represents the numerical value by which the tree species of interest was encoded in the raster dataset.

Value

Numeric vector with distances of every inventory plot to the nearest seed source of a specific tree species.

Examples

```
## Create raster data set
set.seed(2023)
rr <- terra::rast(
  matrix(sample(0:10, 20 * 20, replace = TRUE),
    nrow = 20, ncol = 20))
```

```
## Create vector data set
vec <- terra::vect(rbind(c(5,10), c(5,15)))

## Extract distance for the inventory plot
extract_dist(raster=rr, geom=vec, species="10")
```

k_exponential_power *Dispersal kernels from exponential power family*

Description

k_exponential_power computes the value, multiplied by N , of a dispersal kernel from the exponential power family that includes, as special cases, Gaussian kernels and kernels that follow an exponential function of the distance.

Usage

```
k_exponential_power(x, par, N = 1, d = NCOL(x))
```

Arguments

x	Numeric matrix of positions x relative to the seed source, or vector of distances $\ x\ $ to the seed source.
par	Numeric vector with two elements representing the log-transformed scale and shape parameters a and b .
N	The multiplier N .
d	The spatial dimension.

Details

The dispersal kernel, i.e. spatial probability density of the location of a seed relative to its source, is here given by

$$k(x) = \frac{b\Gamma(d/2)}{2\pi^{d/2}a^d\Gamma(d/b)}e^{-(\|x\|/a)^b},$$

which corresponds to a probability density of the distance given by

$$p(r) = \frac{b}{a^d\Gamma(d/b)}r^{d-1}e^{-(r/a)^b},$$

where d is the spatial dimension, $\| \cdot \|$ denotes the Euclidean norm and the normalizing constants involve the [gamma](#) function; see Bateman (1947), Clark et al. (1998), Austerlitz et al. (2004), Nathan et al. (2012) for the planar case. This means the b th power of the distance has a [gamma distribution](#) with shape parameter d/b and scale parameter a^b .

The kernel has its maximum at zero and represents a rather flexible family that includes, for $b = 2$ the classical Gaussian kernels and for $b = 1$, kernels decreasing exponentially with the distance. For $b < 1$ the distance distribution is fat-tailed in the sense of Kot et al. (1996). Such kernels have consequently been applied in a number of theoretical studies that address dispersal (Ribbens et al. 1994, Bullock et al. 2017).

Value

Numeric vector of function values $k(x)$ multiplied by N .

References

- Bateman, A. (1947). Contamination in seed crops: III. relation with isolation distance. *Heredity* **1**, 303–336. doi:10.1038/hdy.1947.20
- Kot, M., Lewis, M.A., van den Driessche, P. (1996). Dispersal Data and the Spread of Invading Organisms. *Ecology* **77**(7), 2027–2042. doi:10.2307/2265698
- Ribbens, E., Silander Jr, J.A., Pacala, S.W. (1994). Seedling recruitment in forests: calibrating models to predict patterns of tree seedling dispersion. *Ecology* **75**, 1794–1806. doi:10.2307/1939638
- Clark, J.S., Macklin, E., Wood, L. (1998). Stages and spatial scales of recruitment limitation in southern Appalachian forests. *Ecological Monographs* **68**(2), 213–235. doi:10.2307/2657201
- Clark, J.S. (1998). Why trees migrate so fast: confronting theory with dispersal biology and the paleorecord. *The American Naturalist* **152**(2), 204–224. doi:10.1086/286162
- Austerlitz, F., Dick, C.W., Dutech, C., Klein, E.K., Oddou-Muratorio, S., Smouse, P.E., Sork, V.L. (2004). Using genetic markers to estimate the pollen dispersal curve. *Molecular Ecology* **13**, 937–954. doi:10.1111/j.1365294X.2004.02100.x
- Bullock, J. M., Mallada González, L., Tamme, R., Götzenberger, L., White, S.M., Pärtel, M., Hooftman, D.A. (2017). A synthesis of empirical plant dispersal kernels. *Journal of Ecology* **105**, 6–19. doi:10.1111/13652745.12666
- Nathan, R., Klein, E., Robledo-Arnuncio, J.J., Revilla, E. (2012). Dispersal kernels: review, in Clobert, J., Baguette, M., Benton, T.G., Bullock, J.M. (eds.), *Dispersal ecology and evolution*, 186–210. doi:10.1093/acprof:oso/9780199608898.003.0015

Examples

```
k_exponential_power(2:5, par=c(0,0), d=2)
```

k_lognormal	<i>Dispersal kernels for log-normal distance distributions</i>
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Description

k_lognormal computes the value, multiplied by N , of a dispersal kernel based on seeds having a distance with a log-normal distribution from the their source.

Usage

```
k_lognormal(x, par, N = 1, d = NCOL(x))
```

Arguments

x	Numeric matrix of positions x relative to the seed source, or vector of distances $\ x\ $ to the seed source.
par	Numeric vector with two elements representing log-transformed scale and shape parameters, given by the median distance a and by the variance b of the underlying normal distribution.
N	The multiplier N .
d	The spatial dimension.

Details

The dispersal kernel, i.e. spatial probability density of the location of a seed relative to its source, is here given by

$$k(x) = \frac{\Gamma(d/2)}{2\pi^{d/2} \|x\|^d \sqrt{2\pi b}} e^{-\frac{1}{2b} (\log(\|x\|/a))^2} = \frac{\Gamma(d/2) e^{d^2 b/2}}{2\pi^{d/2} a^d \sqrt{2\pi b}} e^{-\frac{1}{2b} (\log \frac{\|x\|}{a} + db)^2},$$

which corresponds to a probability density of the distance given by

$$p(r) = \frac{1}{r \sqrt{2\pi b}} e^{-\frac{1}{2b} (\log(r/a))^2} = \frac{e^{b/2}}{a \sqrt{2\pi b}} e^{-\frac{1}{2b} (\log \frac{r}{a} + b)^2},$$

where d is the spatial dimension, $\| \cdot \|$ denotes the Euclidean norm and the normalizing constant of the kernel involves the [gamma](#) function; see Greene and Johnson (1989), Stoyan and Wagner (2001) for the planar case. Thus, the distance is assumed to have the [log-normal distribution](#) such that the log-distance has a normal distribution with mean $\log a$ and variance b . Here $\log k(x)$ is a quadratic function of $\log \|x\|$ with a maximum at $\log a - db$, while $\log p(r)$ is a quadratic function of $\log r$ with a maximum at $\log a - b$.

This kernel is particularly suitable if the maximum regeneration density is not directly at the seed source (e.g. Janzen–Connell effect), cf. Nathan et al. (2012).

Value

Numeric vector of function values $k(x)$ multiplied by N .

References

- Greene, D.F., Johnson, E.A. (1989). A model of wind dispersal of winged or plumed seeds. *Ecology* **70**(2), 339–347. doi:10.2307/1937538
- Stoyan, D., Wagner, S. (2001). Estimating the fruit dispersion of anemochorous forest trees. *Ecol. Modell.* **145**, 35–47. doi:10.1016/S03043800(01)003854
- Nathan, R., Klein, E., Robledo-Arnuncio, J.J., Revilla, E. (2012). Dispersal kernels: review, in Clobert, J., Baguette, M., Benton, T.G., Bullock, J.M. (eds.), *Dispersal ecology and evolution*, 186–210. doi:10.1093/acprof:oso/9780199608898.003.0015

Examples

```
k_lognormal(2:5, par=c(0,0), d=2)
```

k_power	Power-law dispersal kernels
---------	-----------------------------

Description

k_power computes the value, multiplied by N , of a dispersal kernel that follows a power law of a constant a plus the distance.

Usage

```
k_power(x, par, N = 1, d = NCOL(x))
```

Arguments

x	Numeric matrix of positions x relative to the seed source, or vector of distances $\ x\ $ to the seed source.
par	Numeric vector with two elements representing the log-transformed parameters a and b .
N	The multiplier N .
d	The spatial dimension.

Details

The dispersal kernel, i.e. spatial probability density of the location of a seed relative to its source, is here given by

$$k(x) = \frac{\Gamma(d/2)}{2\pi^{d/2}a^dB(d,b)}\left(1 + \frac{\|x\|}{a}\right)^{-(b+d)},$$

which corresponds to a probability density of the distance given by

$$p(r) = \frac{1}{a^dB(d,b)}r^{d-1}\left(1 + \frac{r}{a}\right)^{-(b+d)},$$

where d is the spatial dimension, $\| \cdot \|$ denotes the Euclidean norm and the normalizing constants involve the [beta](#) and [gamma](#) functions; see Nathan et al. (2012) for the planar case (with b replaced by $b - d$). This means the distance is $\frac{da}{b}$ times a random variable having an [F distribution](#) with $2d$ and $2b$ degrees of freedom. This is a fat-tailed distribution for all choices of the parameter b .

Value

Numeric vector of function values $k(x)$ multiplied by N .

References

- Nathan, R., Klein, E., Robledo-Arnuncio, J.J., Revilla, E. (2012). Dispersal kernels: review, in Clobert, J., Baguette, M., Benton, T.G., Bullock, J.M. (eds.), *Dispersal ecology and evolution*, 186–210. doi:10.1093/acprof:oso/9780199608898.003.0015
- Austerlitz, F., Dick, C.W., Dutech, C., Klein, E.K., Oddou-Muratorio, S., Smouse, P.E., Sork, V.L. (2004). Using genetic markers to estimate the pollen dispersal curve. *Molecular Ecology* **13**, 937–954. doi:10.1111/j.1365294X.2004.02100.x

Examples

```
k_power(2:5, par=c(0,0), d=2)
```

k_t

Dispersal kernels from spatial t distribution

Description

k_t computes the value, multiplied by N , of the dispersal kernel from Clark et al. (1999) that represents a multivariate t distribution.

Usage

```
k_t(x, par, N = 1, d = NCOL(x))
```

Arguments

x	Numeric matrix of positions x relative to the seed source, or vector of distances $\ x\ $ to the seed source.
par	Numeric vector with two elements representing the log-transformed parameters a and b .
N	The multiplier N .
d	The spatial dimension.

Details

The dispersal kernel, i.e. spatial probability density of the location of a seed relative to its source, is here given by

$$k(x) = \frac{\Gamma((b+d)/2)}{\pi^{d/2} a^d \Gamma(b/2)} \left(1 + \frac{\|x\|^2}{a^2}\right)^{-(b+d)/2},$$

which corresponds to a probability density of the distance given by

$$p(r) = \frac{2}{a^d B(d/2, b/2)} r^{d-1} \left(1 + \frac{r^2}{a^2}\right)^{-(b+d)/2},$$

where d is the spatial dimension, $\| \cdot \|$ denotes the Euclidean norm and the normalizing constants involve the [beta](#) and [gamma](#) functions; see Clark et al. (1999) and Austerlitz et al. (2004) for the planar case (with a, b replaced by $\sqrt{u}, 2p$ and $a, 2b - d$, respectively). This means the position is $\frac{a}{\sqrt{b}}$ times a random vector having a standard d -variate t distribution with b degrees of freedom (a standard Gaussian vector divided by $\sqrt{z/b}$, where z is independent and chi-squared distributed with b degrees of freedom), and the squared distance is $\frac{da^2}{b}$ times a random variable having an [F distribution](#) with d and b degrees of freedom.

This results from the kernel being defined as a mixture of Gaussian kernels with an inverse variance having a [gamma distribution](#) with shape parameter $\frac{b}{2}$ and inverse scale parameter $\frac{a^2}{2}$, which for $a = 1$ is a [chi-squared distribution](#) with b degrees of freedom.

The dispersal kernel always has its maximum at zero, and the distance has a fat-tailed distribution for all choices of b .

Value

Numeric vector of function values $k(x)$ multiplied by N .

References

- Clark, J.S., Silman, M., Kern, R., Macklin, E., HilleRisLambers, J. (1999). Seed dispersal near and far: patterns across temperate and tropical forests. *Ecology* **80**, 1475–1494. doi:10.1890/0012-9658(1999)080[1475:SDNAFP]2.0.CO;2
- Austerlitz, F., Dick, C.W., Dutech, C., Klein, E.K., Oddou-Muratorio, S., Smouse, P.E., Sork, V.L. (2004). Using genetic markers to estimate the pollen dispersal curve. *Molecular Ecology* **13**, 937–954. doi:10.1111/j.1365294X.2004.02100.x

Examples

```
k_t(2:5, par=c(0,0), d=2)
```

k_weibull

Dispersal kernels for Weibull distance distributions

Description

k_weibull computes the value, multiplied by N , of the dispersal kernel from Tufto et al. (1997) based on seeds having a distance with a Weibull distribution from their source.

Usage

```
k_weibull(x, par, N = 1, d = NCOL(x))
```

Arguments

- | | |
|-----|--|
| x | Numeric matrix of positions x relative to the seed source, or vector of distances $\ x\ $ to the seed source. |
| par | Numeric vector with two elements representing the log-transformed scale and shape parameters a and b of the distance distribution. |
| N | The multiplier N . |
| d | The spatial dimension. |

Details

The dispersal kernel, i.e. spatial probability density of the location of a seed relative to its source, is here given by

$$k(x) = \frac{b\Gamma(d/2)}{2\pi^{d/2}a^b} \|x\|^{b-d} e^{-(\|x\|/a)^b},$$

which corresponds to a probability density of the distance given by

$$p(r) = \frac{b}{a^b} r^{b-1} e^{-(r/a)^b},$$

where d is the spatial dimension, $\| \cdot \|$ denotes the Euclidean norm and the normalizing constants involve the [gamma](#) function; see Tufto et al. (1997) for the planar case. Thus, the distance is assumed to have the [Weibull distribution](#) with scale parameter a and shape parameter b . Equivalently, the b th power of the distance has an exponential distribution with scale parameter a^b .

Consequently, if and only if $b < 1$, the distance distribution has a heavier tail than an exponential distribution, although with tail probabilities still decreasing faster than any power law; it is a fat-tailed distribution in the sense of Kot et al. (1996). The kernel coincides with a Gaussian kernel in the special case $b = d = 2$.

Value

Numeric vector of function values $k(x)$ multiplied by N .

References

- Tufto, J., Engen, S., Hindar, K. (1997). Stochastic dispersal processes in plant populations, *Theoretical Population Biology* **52**(1), 16–26. doi:[10.1006/tpbi.1997.1306](#)
- Austerlitz, F., Dick, C.W., Dutech, C., Klein, E.K., Oddou-Muratorio, S., Smouse, P.E., Sork, V.L. (2004). Using genetic markers to estimate the pollen dispersal curve. *Molecular Ecology* **13**, 937–954. doi:[10.1111/j.1365294X.2004.02100.x](#)
- Kot, M., Lewis, M.A., van den Driessche, P. (1996). Dispersal Data and the Spread of Invading Organisms. *Ecology* **77**(7), 2027–2042. doi:[10.2307/2265698](#)
- Nathan, R., Klein, E., Robledo-Arnuncio, J.J., Revilla, E. (2012). Dispersal kernels: review, in Clobert, J., Baguette, M., Benton, T.G., Bullock, J.M. (eds.), *Dispersal ecology and evolution*, 186–210. doi:[10.1093/acprof:oso/9780199608898.003.0015](#)

Examples

```
k_weibull(2:5, par=c(0,0), d=2)
```

predict_quax

Prediction of potential regeneration densities

Description

Prediction of the potential regeneration density as a function of the distance to the nearest seed tree.

Usage

```
predict_quax(distmap, quax)
```

Arguments

- | | |
|---------|--|
| distmap | A SpatRaster with distances to the nearest seed tree is used for the prediction of the potential regeneration densities. Usually a result of the <code>seed_tree_distmap()</code> function |
| quax | A quax object is used for the prediction. This is a parameterised dispersal function using quantile regression. |

Details

, defined by the study area. The potential regeneration density is calculated and given for each raster cell.

Value

A SpatRaster with the same resolution as the input raster containing the regeneration density on the same scale (e.g. numbers per hectare) as in the input data.

Examples

```
## Prepare artificial data:
set.seed(0)
r <- rgamma(200, shape=2, scale=150)
simulated.data <- data.frame(distance = r, density = rpois(length(r),
  k_lognormal(r, par=c(6,0), N=1000000, d=2)))

## Run quax function:
f1 <- quax(x = simulated.data$distance, y = simulated.data$density,
  tau = 0.9, fun = k_lognormal)

## Create raster data set
rr <- terra::rast(
  matrix(sample(0:10, 20 * 20, replace = TRUE),
    nrow = 20, ncol = 20))

## Compute distance for prediction area
distance <- seed_tree_distmap(raster = rr, species = "10")

## Prediction
p <- predict_quax(distmap = distance, quax = f1)
terra::plot(p)
```

quax

Estimating potential regeneration densities by quantile regression

Description

quax estimates parameters of a spatial dispersal kernel that describes the regeneration potential as the τ th quantile of the regeneration density. Here τ is between 0 and 1, with typical values close to 1 representing the situation that the full regeneration potential is realized only at a small fraction of all sites.

Usage

```
quax(...)

## Default S3 method:
quax(
```

```

    ...,
    y,
    tau,
    fun = k_lognormal,
    weights = 1,
    dim = 2,
    par = c(log.a = 8, log.b = 1)
)

## S3 method for class 'formula'
quax(
  formula,
  data,
  tau,
  fun = k_lognormal,
  subset,
  weights,
  na.action,
  offset,
  ...
)

```

Arguments

<code>...</code>	Vector of positions $x_1, \dots, x_n$ or distances to the seed source as required by the specific dispersal kernel. Optionally, further arguments passed to <code>optim</code> , to the default method or to the kernel.
<code>y</code>	Vector of observed values $y_1, \dots, y_n$ of the regeneration density of the inventory plot.
<code>tau</code>	Numeric value between 0 and 1. Specifies the quantile τ used in the regression.
<code>fun</code>	Function representing the dispersal kernel k_θ , multiplied by N , that is assumed for the regeneration potential. Values allowed are <code>k_lognormal</code> , <code>k_t</code> , <code>k_power</code> , <code>k_weibull</code> , <code>k_exponential_power</code> or a custom function with nonnegative values whose parameters include, in addition to the arguments in <code>...</code> not consumed by <code>optim</code> or the default method, the scaling factor N and the spatial dimension d (see Examples). The default, <code>k_lognormal</code> , is to fit a model with log-normal distance distributions.
<code>weights</code>	Numeric vector of optional non-negative weights w_i of the observations in the estimation procedure. Default is 1.
<code>dim</code>	The spatial dimension, by default equal to 2.
<code>par</code>	Numeric vector of initial values for the parameter vector θ .
<code>formula</code>	A formula of the form $y \sim x$.
<code>data, subset, na.action, offset</code>	For the formula interface: Further arguments passed to <code>model.frame</code> (along with <code>weights</code>).

Details

The function estimates the parameters N and θ of the regeneration potential Nk_θ by minimizing

$$\sum_{i=1}^n w_i \rho_\tau(y_i - Nk_\theta(x_i)),$$

where $\rho_\tau(u) = \int_0^u \tau - \mathbf{1}_{s < 0} \, ds = \begin{cases} u\tau & \text{if } u \geq 0 \\ u(\tau-1) & \text{if } u < 0 \end{cases}$ (Koenker and Bassett 1978, Chapter 6.6 in Koenker 2005). The preceding line, after subtracting the same expression for $N = 0$ and substituting $s = y_i - tk_\theta(x_i)$ in the integral, becomes $\int_0^N \sum_{i=1}^n w_i k_\theta(x_i) (\mathbf{1}_{y_i < tk_\theta(x_i)} - \tau) \, dt$, and any N such that the last integrand is ≤ 0 for $t < N$ and ≥ 0 for $t > N$, which can always be found as the integrand is increasing in t , minimizes this integral. The integrand being the difference of the sum of $w_i k_\theta(x_i)$ over the i with $y_i < tk_\theta(x_i)$ and τ times the sum over all i , with relevant terms for nonzero $k_\theta(x_i)$, this means that the estimate of N for a given vector θ can be computed as a τ th quantile. This is implemented as an inner, nested minimization, the result of which is minimized in θ using `optim`.

This is a rather naive approach to quantile regression that appears to work reasonably well for scaled dispersal kernels Nk_θ as considered here, see Appendix A in Axer et al. (2021). For general quantile regression problems the more sophisticated procedure `nlrq` in the package `quantreg`, based on Koenker and Park (1996), is expected to provide better results.

In particular, `quax` is subject to the usual numerical issues inherent in optimization: It can get stuck in a local minimum or altogether miss a minimum if the initial values (as specified by the argument `par`) are too far off or if the objective function exhibits bad behavior. Problems can further arise in the dispersal kernels if parameter values passed on a log scale become too large. It is therefore recommended to visually check the results (see Examples). Also, the `optim` arguments `method` and `control` can be added in `...` to select and tune the optimization algorithm, but note that the objective function is usually not differentiable.

See Koenker (2005) for a detailed exposition of quantile regression.

Value

An object of class `quax` containing the estimated function, including an attribute `o` containing the results of `optim`. Generic functions with methods defined for `quax` objects invoke these methods; see `summary.quax` for an example.

References

- Koenker, R., Bassett, G. (1978). Regression quantiles. *Econometrica* **46**(1), 33–50. doi:10.2307/1913643
- Axer, M., Schlicht, R., Wagner, S. (2021). Modelling potential density of natural regeneration of European oak species (*Quercus robur* L., *Quercus petraea* (Matt.) Liebl.) depending on the distance to the potential seed source: Methodological approach for modelling dispersal from inventory data at forest enterprise level. *Forest Ecology and Management* **482**, 118802. doi:10.1016/j.foreco.2020.118802
- Koenker, R., Park, B.J. (1996). An interior point algorithm for nonlinear quantile regression. *Journal of Econometrics* **71**(1–2), 265–283. doi:10.1016/03044076(96)845076
- Koenker, R. (2005). Quantile regression. Cambridge University Press. doi:10.1017/CBO9780511754098

See Also

Function `nlrq` in the package `quantreg`.

Examples

```
## Prepare artificial data:
set.seed(0)
r <- rgamma(200, shape=2, scale=150)
simulated.data <- data.frame(distance = r, density =
  rpois(length(r), k_lognormal(r, par=c(6,0), N=1000000, d=2)))
plot(density ~ distance, simulated.data)

## Run quax function:
f1 <- quax(x = simulated.data$distance, y = simulated.data$density,
  tau = 0.9, fun = k_lognormal)
summary(f1)
curve(f1(x), add=TRUE)

## Do the same using formula interface:
f1 <- quax(density ~ distance, simulated.data,
  tau = 0.9, fun = k_lognormal)
summary(f1)
#quantreg::nlrq(density ~ k_lognormal(distance,c(log.a,log.b),N=N,d=2),
# simulated.data, start = c(log.a=6,log.b=0,N=1e6), tau = 0.9) # similar

## Use another quantile:
f2 <- quax(density ~ distance, simulated.data,
  tau = 0.99, fun = k_lognormal)
summary(f2)
curve(f2(x), add=TRUE, lwd=0)

## Show effect of weights:
f3 <- quax(density ~ distance, simulated.data,
  tau = 0.9, fun = k_lognormal, weights = distance)
summary(f3)
curve(f3(x), add=TRUE, lty=3)

## Compare various dispersal models:
fun <- c("k_lognormal","k_t","k_weibull","k_power","k_exponential_power")
for (i in seq_along(fun))
  curve(quax(density ~ distance, simulated.data,
    tau = 0.9, fun = get(fun[i]), weights = distance)(x),
    add=TRUE, col=i, lty=3)
legend("topright", fun, col=seq_along(fun), lty=3)

## Use positions in computation:
simulated.data$position <- r *
  (\(a) cbind(cos(a),sin(a))) (rnorm(length(r)))
f3 <- quax(density ~ position, simulated.data,
  tau = 0.9, fun = k_lognormal, weights = distance)
summary(f3)
```

```
## Show problems with bad initial values and try another parameterization:
curve(quax(density ~ distance, simulated.data, par = c(log.a=0,log.b=0),
  tau = 0.99, fun = k_lognormal)(x), add=TRUE, lty=2)
curve(quax(density ~ distance, simulated.data, par = c(a=1,b=1),
  tau = 0.99, fun = function(x,par,N,d) if (any(par<=0)) rep(NA,NROW(x))
    else k_lognormal(x,log(par),N,d))(x), add=TRUE, lty=2)

## Use custom variant of lognormal model that includes a shift:
plot(simulated.data$position)
f4 <- quax(density ~ position, simulated.data,
  tau = 0.9, par = c(8, 1, 0, 0),
  fun = function(x, par, N, d)
    k_lognormal(x - rep(par[-(1:2)],each=NROW(x)), par[1:2], N, d)
)
summary(f4)
```

regeneration	<i>Regeneration densities at inventory plots and potential dispersal distances to nearest seed trees</i>
--------------	--

Description

A dataset containing the regeneration densities of beech, oak and Douglas fir of the inventory plots and the distance to the nearest conspecific nearest seed tree.

Usage

```
data(regeneration)
```

Format

A data frame with 484 rows and 7 variables

- `id`. An identifier for each inventory plot as an integer
- `distance_beech`. Distance in m from the plot to the nearest beech (0–3206.57)
- `distance_oak`. Distance in m from the plot to the nearest oak (0–1481.2)
- `distance_dgl`. Distance in m from the plot to the nearest Douglas fir (0–1807)
- `oak_regen`. Regeneration density of oak (N/ha) of the plot (0–30)
- `beech_regen`. Regeneration density of beech (N/ha) of the plot (0–30)
- `douglas_regen`. Regeneration density of Douglas fir (N/ha) of the plot (0–30)

seed_tree_distmap	<i>Distance map to nearest seed source</i>
-------------------	--

Description

Creation of a distance map for the study area. The distance to the nearest seed source is calculated for every raster cell.

Usage

```
seed_tree_distmap(raster, species)
```

Arguments

raster	Raster data set with tree species classification of specific tree species and tree species groups.
species	Represents the numerical value by which the tree species of interest is encoded in the raster data set.

Value

A SpatRaster object containing the distances to seed source. The object has the same resolution and extent as the input raster.

Examples

```
## Create raster data set
rr <- terra::rast(
  matrix(sample(0:10, 20 * 20, replace = TRUE),
    nrow = 20, ncol = 20))

## Compute distance for study area
distance <- seed_tree_distmap(raster = rr, species = "10")

## Plot the seed_tree_distmap
terra::plot(distance)
```

summary.quax	<i>Summarizing quantile regression fits of potential regeneration densities</i>
--------------	---

Description

This function is the summary method for class quax objects as returned by [quax](#).

Usage

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

Arguments

object	The function returned by <code>quax</code> .
...	not in use here

Details

The value component of the result can be used to compare the quality of the fit of different dispersal kernels for the same quantile to the same data.

Value

A list with the following components:

coefficients The parameters of the estimated dispersal kernel.

value The attained value of the objective function that is minimised in the quantile regression.

Examples

```
## Prepare artificial data:  
set.seed(0)  
r <- rgamma(200, shape=2, scale=150)  
simulated.data <- data.frame(distance = r, density =  
  rpois(length(r), k_lognormal(r, par=c(6,0), N=1000000, d=2)))  
plot(density ~ distance, simulated.data)  
  
## Fit a log-normal and a power-law dispersal kernel to the data:  
f1 <- quax(density ~ distance, simulated.data,  
  tau = 0.9, fun = k_lognormal)  
f2 <- quax(density ~ distance, simulated.data,  
  tau = 0.9, fun = k_power)  
  
## Compare both fits:  
summary(f1)  
summary(f2)
```


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