

# DisperseR: Calculating Seed Dispersal In R

Samantha L. Davis

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## 1 Introduction

This is a small package intended to help users calculating seed dispersal in R. Although the R base machinery is capable of doing so, this package streamlines the process and enables you to focus more on the important aspects of data analysis instead of data generation or clean-up.

This code operates as follows. Ideally, you'll need a dataframe that contains the following data: (x,y) coordinates of each tree and seedling in a plot; and dbh measurements of any tree large enough. A tree is any individual that can be measured for diameter at breast height, and all trees are assumed to be reproductively active; a seedling is any individual that is new in the calendar year.

Spatial seed dispersal is characterized by a single equation,

$$R_i = STR * \sum_{k=1}^T \left( \frac{DBH_k}{30} \right)^2 e^{-Dm_{ik}^3} * \left( \frac{1}{n} \right) \quad (1)$$

where  $n$  is a normalizer function that standardizes the equation to values between 0 and 1,

$$n = \int_0^{\infty} e^{-Dm_{ik}^3} \quad (2)$$

and where  $STR$  is the standardized number of tree recruits,  $DBH$  is the diameter at breast height,  $D$  is a species-specific parameter estimated by this equation, and  $m$  is the distance between the measured point  $i$  and adult tree  $k$ , summed over each adult tree ( $k=1$  to  $T$  adult trees). These equations were originally established by Ribbens et al. (1994), in an experiment where seedling per  $m^2$  along a belt transect were correlated to the number and size of any adults within a  $20m$  radius.

The first piece of the equation, containing  $STR$ , establishes the number of recruits produced for a tree of a standard  $DBH$  (30cm), and the second piece of the equation establishes the mean density of recruits found in a  $1m^2$  quadrat centered at  $m$  distance away from the parent tree. Finally,  $\frac{1}{n}$  serves as a normalizer to standardize the equation across species.

The parameters *STR* and *D* are both needed by SORTIE-ND, an individual tree neighborhood dynamics forest gap model (say that five times fast!), to calculate seed dispersal for target species in its simulations. SORTIE-ND, unfortunately, does not come packaged with a magic bullet that offers species-specific parameters, and therefore, we must parameterize the model ourselves. This package is intended to help create estimates of both *STR* and *D* quickly, so that other parameters may be addressed.

What follows is a list of functions alongside example usage. To start, you must import or generate a plot map of all trees in a given area. This plot map must include a species identifier, an x coordinate, a y coordinate, and DBH (or NA) for each individual.

We can generate a sample plot easily with `generatePlotMap()`. As you can see below, this function generates a plot map with NA's for seedlings and actual values of DBH for adult trees. See `?generatePlotMap()` for information on how to customize your random plot map.

```
> library(disperseR)
> myplot <- generatePlotMap()
> head(myplot)
```

	species	x	y	dbh
1	1	54.6869423	54.22306	NA
2	1	0.6989224	48.65458	NA
3	1	36.4854372	70.25562	NA
4	1	11.3466584	19.18422	NA
5	1	65.2956505	14.86108	NA
6	1	74.8151938	27.04914	NA

```
> tail(myplot)
```

	species	x	y	dbh
55	3	21.576138	41.318587	17.422166
56	3	12.440960	38.173444	8.465424
57	3	11.524822	70.025328	91.295164
58	3	40.583205	17.483600	88.223219
59	3	7.775619	5.392415	2.301222
60	3	55.271426	98.093571	65.017483

## References

Ribbens, E., J. A. Silander, and S. W. Pacala, 1994. Seedling recruitment in forests : Calibrating models to predict patterns of tree seedling dispersion. *Ecology* **75**:1794–1806.