assignment-7

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Package Title

vegan

Location

You can install 'vegan' from either:

CRAN directly

1. RStudio interface packages tab
2. r install.packages("vegan")
3. CRAN website (https://cran.r-project.org)

GitHub

1. git command: CMD build -> R CMD INSTALL
2. r remotes::install_github("vegandevs/began")

Vignettes

FAQ-vegan: FAQ and typical community ecology analyses help using metaMDS()

1. Dependencies

- depends on the **permute** package
- sometimes depends on the **MASS**, **mgcv**, **parallel**, **cluster**, **lattice** and **tcltk** packages

2. Similar packages `Environmetrics`, `Multivariate` and `Spatial`

3. Other documentaion

4. **vegan** homepage

Applications

- commonly used by community ecologists
- dealing with multivariate data, where data can consist of species (columns) by site/sample (rows)
- multivariate analyses for ecological communities + tools for diversity analyses
- often used to perform ordination fugures
- from microbiology to ecosystem biology, and beyond biology

Review

From my review of the **vegan** package, the primary purpose is to analyze community ecology data, or the data exploring multiple species or identities across an area (sample, site, region, etc.). This package is capable of 1. diversity analyses 2. community ordinations 3. dissimilarity analyses