densify: An R package to prune sparse data frames of typological linguistic data

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Summary

The R package `densify` provides a procedure to prune input data frames containing empty cells (or cells with values {?} or {NA}) to denser sub-matrices with fewer empty cells. The pruning process trades off a series of variably weighted concerns, including data retention, coding density (proportion of non-empty cells) and taxonomic diversity of rows (representing for example phylogenetic relations). Users can adapt the relative weights given to these concerns through various parameters so that the densification process best fits their needs. As such, the software is useful for several purposes, including the densification of sparse input matrices and the subsampling of large input matrices according to a procedure that is sensitive to taxonomic structure.

Statement of Need

While the software will run on any data frame (with rows representing any entities with or without taxonomic structure and columns representing variables), it was primarily designed to prune data frames of linguistic typological data, where the rows are languages (taxa) and the columns typological features (sometimes also called characters, parameters or variables).

Linguistic typological data is increasingly available in large-scale databases, and many analyses that aim at exploring diversity or testing hypotheses rely on such databases. Some of these resources have information for nearly all features across nearly all languages in the database (i.e. they have complete or near-complete coding density), but the dataframe may be too large for certain computationally intensive analyses (e.g., PHOIBLE (Moran and McCloy 2019), Grambank (Skirgård et al. 2023)). Other databases (e.g., WALS (Dryer and Haspelmath 2013), AUTOTYP (Bickel et al. 2023), Lexibank (List et al. 2023)) exhibit features that are coded for different sets of languages, resulting in sparse language-feature matrices. Combining data from various databases via language identifiers like glottocodes (Hammarström et al. 2024) usually increases sparsity because the language samples do not match.

When datasets are too large or too sparse for computational applications, it can thus be necessary to generate and subsequently operate on a subset of the data represented in a smaller and denser matrix. Thereby, researchers might be particularly interested in maintaining taxonomic diversity in the languages represented, preferentially removing languages belonging to clades represented by many other languages in the sample and penalizing the removal of language isolates or languages which represent small language families.

While certain packages exist to generate sub-matrices from varying input matrices according to principled criteria (e.g., `admmDensestSubmatrix` (Ames and Bombina 2019), which identifies the densest sub-matrix of an input graph of a specified size; or `FSelector` (Romanski, Kotthoff, and Schratz 2023) and `varrank` (Kratzer and Furrer 2022), which perform attribute subset selection based on various tests and entropy measures to identify the most relevant attributes of a data input), `densify` adds sensitivity to taxonomic structure and generally more flexibility in parameter settings for the user. The pruning algorithm focuses both on the removal of rows and columns and does not require the size of the sub-matrix to be specified a priori.

Usage

The package `densify` provides the data from The World Atlas of Language Structures (WALS) (Dryer and Haspelmath 2013) and the language taxonomy provided by Glottolog v. 5.0 (Hammarström et al. 2024) as example data. The accompanying package vignette features a detailed demonstration of the utility and flexibility of `densify` to subsample an input matrix according to varying needs, using this data.

Preparing input

The data frame that requires subsetting must have rows representing taxa or observations (with taxon names provided in a dedicated column) and columns representing variables (and variable names as column names). Any cells with empty entries, not applicable or question marks must be coded as `NA`. If matrix densification should be sensitive to taxonomic structure, a taxonomy must be provided as (i) a `phylo` object (cf. Paradis and Schliep 2019), (ii) as an adjacency table (i.e. a data frame containing columns `id` and `parent_id`, with each row encoding one parent-child relationship), or (iii) the `glottolog_languoids` dataframe provided by the package. Every taxon in the input data frame must be included in the taxonomy (as a tip or node).

```r
install.packages("densify")
library(densify)

# prepare data: WALS and Glottolog
data(WALS)
data(glottolog_languoids)

# any question marks, empty entries, "NA"s must be coded as NA
WALS[WALS=="?"] <- NA
WALS[WALS=="NA"] <- NA
head(WALS)

# all taxa must be present in the taxonomy used for pruning
WALS <- WALS[which(WALS$Glottocode %in% glottolog_languoids$id), ]
```

Pruning

Iterative pruning of the input matrix is performed by the `densify()` function, which can be modulated by several parameters to, among others: specify to what extent taxonomic diversity of the sample should weigh in the pruning process; choose among various methods to calculate importance weights (e.g. via arithmetic or logit-transformed means of row-wise coding density); and choose the minimum variation required for a feature to be retained (e.g. constant variables might be of no interest). For a detailed discussion of the parameters, refer to the function documentation or to the vignette hosted in the software repository.

The output of the function is a `densify_result` object, documenting several summary statistics of all resulting sub-matrices. These include the number of available data points, the overall proportion of coded data in the matrix, the coding densities of the least well-coded taxon and variable, the coding densities of the most well-coded taxon and variable, the median coding densities of the all taxa and variables, and a taxonomic diversity index (Shannon diversity of the highest taxonomic level).

```r
set.seed(2024)
example_result <- densify(data = WALS,
                          taxonomy = glottolog_languoids,
                          taxon_id = "Glottocode",
                          density_mean = "log_odds",
                          min_variability = 3,
                          limits = list(min_coding_density = 1),
                          density_mean_weights = list(coding = 1, taxonomy = 1))
head(example_result)
```

Finding the optimal number of iterations and producing the sub-matrix

The functions `prune()` and `rank_results()` identify the optimal sub-matrix via a quality score, computed via a user-defined scoring function composed of any combination of available statistics from the `densify_result` object. The default scoring function maximizes the product of the number of available data points and the overall coding density.

The function `prune()` thereby retrieves the optimal sub-matrix, while `rank_results()` returns the relative ranks of all generated sub-matrices given the scoring function, the optimal sub-matrix receiving rank 1.

```r
# use prune() to obtain the optimum submatrix
# with the default scoring function
example_optimum_1 <- prune(example_result,
                           scoring_function = n_data_points*coding_density)

# with a scoring function that gives high weight to taxonomic diversity:
example_optimum_2 <- prune(example_result,
                           scoring_function = n_data_points*coding_density*taxonomic_index^3)

# use rank_results() to obtain a vector indicating the rank of each sub-matrix
example_ranks_1 <- rank_results(example_result,
                                scoring_function = n_data_points*coding_density)

example_ranks_2 <- rank_results(example_result,
                                scoring_function = n_data_points*coding_density*taxonomic_index^3)
```

The relative ranking of sub-matrices given the specified scoring function can also be visualized using `visualize()`, an alias of `plot()`.

```r
# use visualize() to illustrate quality scores and optimum
visualize(example_result, scoring_function = n_data_points*coding_density)
visualize(example_result, scoring_function = n_data_points*coding_density*taxonomic_index^3)
```

Conclusions

The R package `densify` provides users with a flexible and explicit method to generate sub-matrices from an input matrix in a mathematically principled way. This paper shows case examples using a standard sparse linguistic dataset (WALS) and the standard linguistic taxonomy provided by Glottolog. Additional examples and usage details are found in the vignette hosted in the software repository on GitHub.

Acknowledgements

The authors declare that there are no conflicts of interest.

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