Package ‘ncbit’

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Type Package
Title retrieve and build NBCI taxonomic data
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Description making NCBI taxonomic data locally available and searchable as an R object
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
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R topics documented:

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ncbit retrieve and build NCBI taxonomic data

Description

making accessible the NCBI taxonomic data

Usage

ncbit(update = FALSE, ...)

1
Arguments

update whether to update database or to use the locally installed version
... additional arguments to be used if update=TRUE)

Details

This function will return a dataframe of the NCBI taxonomy, using either a freshly updated version (if update=TRUE) or a loaded version of the locally installed version. An internet connection must be functional and several utilities must be available and if updating the database: curl, gunzip, tar, perl, mv, and possibly rm. If any of the required utilities are unavailable, the function will issue an error. If updating the database, the database will be assembled in the data directory of the ncbi package and temporary files will be removed in the process. The removal of temporary files can be prevented with rm=FALSE in the call to ncbi.

Value

A dataframe of class 'taxdump' is returned with the following elements:

id a unique integer associated with the node
node a string descriptor of the node
unique a string describing the node
type the type of datum (e.g., scientific name, common name, synonym, etc.)
parent_id a unique integer associated with the parent node

References


Examples

ncbi=get(data(ncbi))
print(ncbi)
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