# dcRDataLoader

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dcRDataLoader         *Function to load dcGOR built-in RData*

## Description

dcRDataLoader is supposed to load RData that are used by package dcGOR.

## Usage

```
dcRDataLoader(RData = c(NA, "SCOP.sf", "SCOP.fa", "Pfam", "InterPro",
"Rfam",
"onto.GOBP", "onto.GOMF", "onto.GOCC", "onto.DO", "onto.HPPA",
"onto.HPMI",
"onto.HPON", "onto.MP", "onto.EC", "onto.KW", "onto.UP",
"SCOP.sf2GOBP",
"SCOP.sf2GOMF", "SCOP.sf2GOCC", "SCOP.sf2DO", "SCOP.sf2HPPA",
"SCOP.sf2HPMI",
"SCOP.sf2HPON", "SCOP.sf2MP", "SCOP.sf2EC", "SCOP.sf2KW", "SCOP.sf2UP",
"SCOP.fa2GOBP", "SCOP.fa2GOMF", "SCOP.fa2GOCC", "SCOP.fa2DO",
"SCOP.fa2HPPA",
"SCOP.fa2HPMI", "SCOP.fa2HPON", "SCOP.fa2MP", "SCOP.fa2EC",
"SCOP.fa2KW",
"SCOP.fa2UP", "Pfam2GOBP", "Pfam2GOMF", "Pfam2GOCC", "InterPro2GOBP",
"InterPro2GOMF", "InterPro2GOCC", "Rfam2GOBP", "Rfam2GOMF",
"Rfam2GOCC",
"Ancestral_domainome", "eTOL", "Feature2GOBP.sf", "Feature2GOMF.sf",
"Feature2GOCC.sf", "Feature2HPPA.sf", "Feature2GOBP.pfam",
"Feature2GOMF.pfam", "Feature2GOCC.pfam", "Feature2HPPA.pfam",
"Feature2GOBP.interpro", "Feature2GOMF.interpro",
"Feature2GOCC.interpro",
"Feature2HPPA.interpro"), domain = c(NA, "SCOP.sf", "SCOP.fa", "Pfam",
"InterPro", "Rfam"), ontology = c(NA, "GOBP", "GOMF", "GOCC", "DO",
"HPPA",
"HPMI", "HPON", "MP", "EC", "KW", "UP"), verbose = T,
RData.location = "http://dcgor.r-forge.r-project.org/data")
```

## Arguments

RData
: which built-in RData to load. If NOT NA, this RData will be always loaded. It can be: domains/RNAs (including 'SCOP.sf', 'SCOP.fa', 'Pfam', 'InterPro', 'Rfam'), ontologies (including 'onto.GOBP', 'onto.GOMF', 'onto.GOCC', 'onto.DO', 'onto.HPPA', 'onto.HPMI', 'onto.HPON', 'onto.MP', 'onto.EC', 'onto.KW', 'onto.UP'), annotations (including 'SCOP.sf2GOBP', 'SCOP.sf2GOMF', 'SCOP.sf2GOCC', 'SCOP.sf2DO', 'SCOP.sf2HPPA', 'SCOP.sf2HPMI', 'SCOP.sf2HPON', 'SCOP.sf2MP', 'SCOP.sf2EC', 'SCOP.sf2KW', 'SCOP.sf2UP', 'SCOP.fa2GOBP', 'SCOP.fa2GOMF', 'SCOP.fa2GOCC', 'SCOP.fa2DO', 'SCOP.fa2HPPA', 'SCOP.fa2HPMI', 'SCOP.fa2HPON', 'SCOP.fa2MP', 'SCOP.fa2EC', 'SCOP.fa2KW', 'SCOP.fa2UP', 'Pfam2GOBP', 'Pfam2GOMF', 'Pfam2GOCC', 'InterPro2GOBP', 'InterPro2GOMF', 'InterPro2GOCC', 'Rfam2GOBP', 'Rfam2GOMF', 'Rfam2GOCC'), domainome in eukaryotic genomes (including 'Ancestral_domainome', 'eTOL'), and databases used for predictiing ontology terms from input protein domain contents. On the meanings, please refer to the Documentations

domain
: domain part of annotation RData to load. When RData is NA and this plus next are NOT NA, then this plus next one are used to specify which annotation RData to load. In addition to NA, it can also be: 'SCOP.sf', 'SCOP.fa', 'Pfam' and 'InterPro'

ontology
: ontology part of annotation RData to load. This only works together with the previous 'domain' parameter. In addition to NA, it can also be: 'GOBP', 'GOMF', 'GOCC', 'DO', 'HPPA', 'HPMI', 'HPON', 'MP', 'EC', 'KW', 'UP'

verbose
: logical to indicate whether the messages will be displayed in the screen. By default, it sets to TRUE for display

RData.location
: the characters to tell the location of built-in RData files. By default, it remotely locates at "http://supfam.org/dcGOR/data" or "http://dcgor.r-forge.r-project.org/data". For the user equipped with fast internet connection, this option can be just left as default. But it is always advisable to download these files locally. Especially when the user needs to run this function many times, there is no need to ask the function to remotely download every time (also it will unnecessarily increase the runtime). For examples, these files (as a whole or part of them) can be first downloaded into your current working directory, and then set this option as: $RData.location = "."$. If RData to load is already part of package itself, this parameter can be ignored (since this function will try to load it via function data first)

## Value

any use-specified variable that is given on the right side of the assigement sign '<-', which contains the loaded RData.

## Note

If there are no use-specified variable that is given on the right side of the assigement sign '<-', then no RData will be loaded onto the working environment.

## See Also

[dcEnrichment](dcEnrichment)

## Examples

```
# Always, load from specified RData directly
SCOP.sf <- dcRDataLoader(RData=SCOP.sf)
Pfam <- dcRDataLoader(RData=Pfam)
InterPro <- dcRDataLoader(RData=InterPro)
Rfam <- dcRDataLoader(RData=Rfam)
onto.GOMF <- dcRDataLoader(RData=onto.GOMF)
# But for annotaion data, there are two ways to do so:
# 1) in a direct way
SCOP.sf2GOMF <- dcRDataLoader(RData=SCOP.sf2GOMF)
# 2) in an indirect way: specify both domain and ontology
SCOP.sf2GOMF <- dcRDataLoader(domain=SCOP.sf, ontology=GOMF)
```