

# dRDataLoader

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dRDataLoader

*Function to load dnet built-in RData*

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## Description

dRDataLoader is supposed to load dnet built-in RData.

## Usage

```
dRDataLoader(RData = c(NA, "TCGA_mutations", "ig.DO", "ig.GOBP",
"ig.GOCC",
"ig.GOMF", "ig.HPCM", "ig.HPMA", "ig.HPMI", "ig.HPPA", "ig.MP",
"org.At.eg",
"org.At.egGOBP", "org.At.egGOCC", "org.At.egGOMF", "org.At.egPS",
"org.At.egSF", "org.At.string", "org.Ce.eg", "org.Ce.egGOBP",
"org.Ce.egGOCC",
"org.Ce.egGOMF", "org.Ce.egPS", "org.Ce.egSF", "org.Ce.string",
"org.Da.eg",
"org.Da.egGOBP", "org.Da.egGOCC", "org.Da.egGOMF", "org.Da.egPS",
"org.Da.egSF", "org.Da.string", "org.Dm.eg", "org.Dm.egGOBP",
"org.Dm.egGOCC",
"org.Dm.egGOMF", "org.Dm.egPS", "org.Dm.egSF", "org.Dm.string",
"org.Gg.eg", "org.Gg.egGOBP", "org.Gg.egGOCC", "org.Gg.egGOMF",
"org.Gg.egPS",
"org.Gg.egSF", "org.Gg.string", "org.Hs.eg", "org.Hs.egDGIdb",
"org.Hs.egDO",
"org.Hs.egGOBP", "org.Hs.egGOCC", "org.Hs.egGOMF", "org.Hs.egHPCM",
"org.Hs.egHPMA", "org.Hs.egHPMI", "org.Hs.egHPPA", "org.Hs.egMP",
"org.Hs.egMsigdbC1", "org.Hs.egMsigdbC2BIOCARTA",
"org.Hs.egMsigdbC2CGP",
"org.Hs.egMsigdbC2CP", "org.Hs.egMsigdbC2KEGG",
"org.Hs.egMsigdbC2REACTOME",
"org.Hs.egMsigdbC3MIR", "org.Hs.egMsigdbC3TFT", "org.Hs.egMsigdbC4CGN",
"org.Hs.egMsigdbC4CM", "org.Hs.egMsigdbC5BP", "org.Hs.egMsigdbC5CC",
"org.Hs.egMsigdbC5MF", "org.Hs.egMsigdbC6", "org.Hs.egMsigdbC7",
"org.Hs.egMsigdbH", "org.Hs.egPS", "org.Hs.egSF", "org.Hs.string",
"org.Mm.eg", "org.Mm.egDO", "org.Mm.egGOBP", "org.Mm.egGOCC",
"org.Mm.egGOMF",
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"org.Mm.egHPCM", "org.Mm.egHPMA", "org.Mm.egHPMI", "org.Mm.egHPPA",
"org.Mm.egMP", "org.Mm.egPS", "org.Mm.egSF", "org.Mm.string",
"org.Rn.eg",
"org.Rn.egGOBP", "org.Rn.egGOCC", "org.Rn.egGOMF", "org.Rn.egPS",
"org.Rn.egSF", "CLL", "org.Rn.string"), genome = c(NA, "Hs", "Mm",
"Rn",
"Gg", "Ce", "Dm", "Da", "At"), ontology = c(NA, "GOBP", "GOMF", "GOCC",
"PS", "PS2", "SF", "DO", "HPPA", "HPMI", "HPCM", "HPMA", "MP",
"MsigdbH",
"MsigdbC1", "MsigdbC2CGP", "MsigdbC2CP", "MsigdbC2KEGG",
"MsigdbC2REACTOME",
"MsigdbC2BIOCARTA", "MsigdbC3TFT", "MsigdbC3MIR", "MsigdbC4CGN",
"MsigdbC4CM",
"MsigdbC5BP", "MsigdbC5MF", "MsigdbC5CC", "MsigdbC6", "MsigdbC7",
"DGIdb"),
RData.location = "http://supfam.org/dnet/RData/1.0.7")

```

## Arguments

RData	which built-in RData to load. It can be one of "TCGA_mutations", "ig.DO", "ig.GOBP", "ig.GOCC", "ig.GOMF", "ig.HPCM", "ig.HPMA", "ig.HPMI", "ig.HPPA", "ig.MP", "org.At.eg", "org.At.egGOBP", "org.At.egGOCC", "org.At.egGOMF", "org.At.egPS", "org.At.egSF", "org.At.string", "org.Ce.eg", "org.Ce.egGOBP", "org.Ce.egGOCC", "org.Ce.egGOMF", "org.Ce.egPS", "org.Ce.egSF", "org.Ce.string", "org.Da.eg", "org.Da.egGOBP", "org.Da.egGOCC", "org.Da.egGOMF", "org.Da.egPS", "org.Da.egSF", "org.Da.string", "org.Dm.eg", "org.Dm.egGOBP", "org.Dm.egGOCC", "org.Dm.egGOMF", "org.Dm.egPS", "org.Dm.egSF", "org.Dm.string", "org.Gg.eg", "org.Gg.egGOBP", "org.Gg.egGOCC", "org.Gg.egGOMF", "org.Gg.egPS", "org.Gg.egSF", "org.Gg.string", "org.Hs.eg", "org.Hs.egDGIdb", "org.Hs.egDO", "org.Hs.egGOBP", "org.Hs.egGOCC", "org.Hs.egGOMF", "org.Hs.egHPCM", "org.Hs.egHPMA", "org.Hs.egHPMI", "org.Hs.egHPPA", "org.Hs.egMP", "org.Hs.egMsigdbC1", "org.Hs.egMsigdbC2B", "org.Hs.egMsigdbC2CGP", "org.Hs.egMsigdbC2CP", "org.Hs.egMsigdbC2KEGG", "org.Hs.egMsigdbC2REACTOME", "org.Hs.egMsigdbC3MIR", "org.Hs.egMsigdbC3TFT", "org.Hs.egMsigdbC4CGN", "org.Hs.egMsigdbC4CM", "org.Hs.egMsigdbC5BP", "org.Hs.egMsigdbC5CC", "org.Hs.egMsigdbC5MF", "org.Hs.egMsigdbC6", "org.Hs.egMsigdbC7", "org.Hs.egMsigdbH", "org.Hs.egPS", "org.Hs.egSF", "org.Hs.string", "org.Mm.eg", "org.Mm.egDO", "org.Mm.egGOBP", "org.Mm.egGOCC", "org.Mm.egGOMF", "org.Mm.egHPCM", "org.Mm.egHPMA", "org.Mm.egHPMI", "org.Mm.egHPPA", "org.Mm.egMP", "org.Mm.egPS", "org.Mm.egSF", "org.Mm.string", "org.Rn.eg", "org.Rn.egGOBP", "org.Rn.egGOCC", "org.Rn.egGOMF", "org.Rn.egPS", "org.Rn.egSF", "CLL", "org.Rn.string". On the meanings, please refer to the Documentations at <a href="http://supfam.org/dnet/docs.html">http://supfam.org/dnet/docs.html</a>
genome	the genome identity. It can be one of "Hs" for human, "Mm" for mouse, "Rn" for rat, "Gg" for chicken, "Ce" for c.elegans, "Dm" for fruitfly, "Da" for zebrafish, and "At" for arabidopsis
ontology	the ontology supported currently. It can be "GOBP" for Gene Ontology Biological Process, "GOMF" for Gene Ontology Molecular Function, "GOCC" for Gene Ontology Cellular Component, "PS" for phylostratific age information, "PS2" for the collapsed PS version (inferred ancestors being collapsed into one with the known taxonomy information), "SF" for domain superfamily assignments, "DO" for Disease Ontology, "HPPA" for Human Phenotype Phenotypic Abnormality, "HPMI" for Human Phenotype Mode of Inheritance,

"HPCM" for Human Phenotype Clinical Modifier, "HPMA" for Human Phenotype Mortality Aging, "MP" for Mammalian Phenotype, and Drug-Gene Interaction database (DGIdb) and the molecular signatures database (Msigdb) only in human (including "MsigdbH", "MsigdbC1", "MsigdbC2CGP", "MsigdbC2CP", "MsigdbC2KEGG", "MsigdbC2REACTOME", "MsigdbC2BIOCARTA", "MsigdbC3TFT", "MsigdbC3MIR", "MsigdbC4CGN", "MsigdbC4CM", "MsigdbC5BP", "MsigdbC5MF", "MsigdbC5CC", "MsigdbC6", "MsigdbC7"). Note: These four ("GOBP", "GOMF", "GOCC" and "PS") are available for all genomes/species; for "Hs" and "Mm", these six ("DO", "HPPA", "HPMI", "HPCM", "HPMA" and "MP") are also supported; all "Msigdb" are only supported in "Hs". For details on the eligibility for pairs of input genome and ontology, please refer to the online Documentations at <http://supfam.org/dnet/docs.html>

**RData.location** the characters to tell the location of built-in RData files. By default, it remotely locates at <http://dnet.r-forge.r-project.org/RData>. Be aware of several versions and the latest one is matched to the current package version. 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 = "."*. Surely, the location can be anywhere as long as the user provides the correct path pointing to (otherwise, the script will have to remotely download each time). Here is the UNIX command for downloading all RData files (preserving the directory structure): *wget -r -l2 -A "\*.RData" -np -nH --cut-dirs=0 http://dnet.r-forge.r-project.org/RData*

### Value

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

### Note

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

### See Also

[dRDataLoader](#)

### Examples

```
org.Hs.egSF <- dRDataLoader(RData='org.Hs.egSF')
org.Hs.eg <- dRDataLoader(RData='org.Hs.eg')
org.Hs.egDGIdb <- dRDataLoader(RData='org.Hs.egDGIdb')
org.Hs.egMsigdbC2KEGG <- dRDataLoader(RData='org.Hs.egMsigdbC2KEGG')
org.Hs.egHPPA <- dRDataLoader(genome='Hs', ontology='HPPA')
ig.MP <- dRDataLoader(RData='ig.MP')
```