

# Package ‘DASiR’

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**Type** Package

**Title** Distributed Annotation System in R

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**Description** R package for programmatic retrieval of information from DAS servers

**License** LGPL (>= 3)

**Depends** IRanges, GenomicRanges, XML, Biostrings

**LazyLoad** yes

**biocViews** Annotation

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DASiR-package

*Distributed Annotation System in R*

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## Description

R package for programmatic retrieval of information from DAS servers

## Details

Package: DASiR  
Type: Package  
License: LGPL(>= 3)

Distributed Annotation System (DAS) is a protocol for information exchange between a server and a client. Is widely used in bioinformatics and the most important repositories include a DAS server parallel to their main front-end.

DAS uses XML and HTTP protocols, so the requirements are much less than using MySQL or BioMart based alternatives.

This package provides a convenient R-DAS interface to programmatically access DAS servers available from your network. It supports only the basic features of DAS 1.6 protocol (DAS/2 is not supported) but these should be enough for most of the users.

Despite a large number (>1200 according official numbers on February 2013) are available, this package is designed with range-features (neither coverages nor sequences). DAS also supports querying genomic sequences and protein structures, but there are already better ways to access such static data in R.

In order to start with this package, you can give a look to basic metadata functions in [getDas-functions](#) man page and to the main functions [getDasFeature](#), [getDasSequence](#), [getDasStructure](#).

Basic support for graphical representation is also provided through [plotFeatures](#).

As a final consideration, you should have in mind that public available DAS servers are a valuable service and you should give them a reasonable use. Please, don't overload the servers with many or large queries.

## Author(s)

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## References

BioDas Wiki - <http://www.biodas.org/>

DAS 1.6 Specification - [http://www.ebi.ac.uk/~aj/1.6\\_draft7/documents/spec.html](http://www.ebi.ac.uk/~aj/1.6_draft7/documents/spec.html)

DAS servers catalog - <http://www.dasregistry.org/>

**Examples**

```
setDasServer(server="http://www.ensembl.org/das")
print(getDasServer())

#See the sources (supported organisms)
sources=getDasSource()
head(sources)

dsn_sources = getDasDsn()
head(dsn_sources)

#Notice that sources returns more information but we need the source ID given
#by getDasDsn, that corresponds to getDasSource$title in this server.

#The server we are quering is a genomic sequence server, so no gene information
#nor structure is available here

#Let's see what this sever supports for SCerevisiae
source = "Saccharomyces_cerevisiae.EF4.reference"
sources[grep(source, sources$title),] #das1:entry_points das1:sequence das1:features

#Ask for the entries
entries = getDasEntries(source)
head(entries)

#Retrive first 1000nts in the beginning of chromosomes I and II
range = GRanges(c("I", "II"), IRanges(start=1, end=1000))
seq = getDasSequence(source, range, class="DNAStringSet")

#Server supports features, but not types...
types = getDasTypes(source)
print(types) #Server returns null... So we will perform a query without types

#Let's see which features is returning the server
features = getDasFeature(source, range, NULL)
print(features)
#Features here are not genomic features (like genes), this is only sequence info

#In the webpage http://www.dasregistry.org/listSources.jsp
#We can see all the registred DAS servers and the information they provide

#Think that DASiR is only an interface to DAS servers! You should know what contains
#the server you are asking to and if it supports your desired features!

#Now let's retrieve genes in that region from another source
#This is UCSC Genome browser, which has access to all the features displayed in the webpage
setDasServer(server="http://genome.ucsc.edu/cgi-bin/das")
source = "sacCer3" #Notice that id now changes, we can retrieve it from getDasDsn()

#Retrieve the types
types = getDasTypes(source)
```

```

#We want the official genes from 'sdgGene' and the ENSEMBL predicted genes fro 'ensGene'
features = getDasFeature(source, range, c("sdgGene","ensGene"))
print(features)

#We obtain a total of 4 genes, 2 in chromosome I and 2 in chromosome II. Notice each gene
#appears 2 times, one as a sgdGene and another as ensGene.

#Now plot the features (but only from one reange at time!)
#Notice that with the default parameters each feature will appear with a different color
plotFeatures(features[features$segment.range == 1,])

#And that's all!

```

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getDas-functions      *DAS metadata information handling*

---

## Description

Functions to query metadata from the DAS server,

## Usage

```

setDasServer(server)
getDasServer()
getDasSource()
getDasDsn()
getDasEntries(source, as.GRanges=TRUE)
getDasTypes(source)

```

## Arguments

server	URL of the DAS server.
source	The data source id to get the metadata from. Be sure this information is coherent with those returned by <a href="#">getDasSource</a> . In some cases, depending on the server, you might need to use the source title, instead of the source id.
as.GRanges	For <a href="#">getDasEntries</a> , return a GRanges object instead of a data.frame (if possible)

## Details

The functions documented in this man page are used to set the session's DAS server and retrieve metadata from it.

- [setDasServer](#) sets the URL of the DAS server to be used.
- [getDasServer](#) returns the URL of the DAS server used in this session
- [getDasSource](#) returns the id's, the titles and the capabilities of the data sources available in the server

- `getDasDsn` returns the id's of the dsn data sources available in the server
- `getDasEntries` returns the entry points of the given data source
- `getDasTypes` returns the types (a.k.a. tables) of the given data source

Please, be sure to pass the identifiers EXACTLY as the values returned by the functions available here (DAS is case-sensitive). It is also recommended that you check the capabilities for each of the data sources.

For performance reasons, the values in the main calls `getDasFeature`, `getDasSequence`, `getDasStructure` are not validated against the server. If you pass wrong values for `source`, `ranges` or `types` it will result in a NULL output of the function, but no error will rise.

### Value

For `getDasSever`, `getDasDsn` and `getDasTypes` a character vector

For `getDasSource` a `data.frame` with the information of the DBs

For `getDasEntries` a `GRanges` (as `GRanges=TRUE`) or `data.frame` otherwise

### Author(s)

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Anna Mantsoki <anna.mantsoki@bsc.es>

### See Also

[getDasFeature](#) [getDasSequence](#) [getDasStructure](#)

### Examples

```
#Set session server to EMBL-EBI Genomic DAS Server

setDasServer(server="http://www.ebi.ac.uk/das-srv/genomicdas/das")

print(getDasServer())

sources=getDasSource()
print(sources)

dsn_sources = getDasDsn()
print(dsn_sources)

entries = getDasEntries(sources$id[[1]])
print(entries)

types = getDasTypes(sources$id[[1]])
print(types)
```

---

`getDasFeature`*Query for features to session's DAS server*

---

### Description

This function retrieves information for the features for the given ranges and types using the corresponding data source id (or title) in the session's DAS server

### Usage

```
getDasFeature(source, ranges, types)
```

### Arguments

<code>source</code>	Data source id (or title). See <a href="#">getDasSource</a>
<code>ranges</code>	<a href="#">GRanges</a> object containing the seqname(s) and range(s) to query. Be sure this information is coherent with those returned by <a href="#">getDasEntries</a>
<code>types</code>	Names of the features to retrieve. They must match one or more of the values returned by <a href="#">getDasTypes</a>

### Details

This function queries the DAS server and returns the available information for the type(s) at the given range(s).

Please, be sure to pass the identifiers EXACTLY as the values returned by the functions available here (DAS is case-sensitive). It is also recommended that you check the capabilities for each of the data sources.

Please, notice that this function codes the parameters in a URL to query the server. This function could fail if you ask for many ranges or types. Also, notice that the speed of the query depends on the number of elements and the load in the server.

Please, use this function smartly and do not overload servers.

### Value

data.frame with the following columns: id, start, stop, version, label, type, method, score, orientation, phase, which match the contents of the specific annotation for the given ranges and types in the server (some of the fields are optional, so not all the servers provide information for all the above columns).

If there are not matching results, output is NULL.

### Author(s)

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**See Also**[getDas-functions](#)**Examples**

```
#Set session server to UniProt DAS Reference Server

setDasServer(server="http://www.ebi.ac.uk/das-srv/uniprot/das")
source = "uniprot-summary"
ranges=GRanges(seqnames=c("A0A000", "A0A001"), IRanges(start=c(1,1), end=c(394,591)))
types=c("description", "sequence-summary")

features = getDasFeature(source, ranges, types)
print(features)
```

---

getDasSequence	<i>Query nucleotide or amino acid sequence to session's DAS server</i>
----------------	--

---

**Description**

This function retrieves the nucleotide or amino acid sequence for the given ranges using the corresponding data source id (or title) in the session's DAS server

**Usage**

```
getDasSequence(source, ranges, class=c("character", "DNAStrngSet", "RNAStrngSet", "AAStrngSet"))
```

**Arguments**

source	Data source id (or title). See <a href="#">getDasSource</a>
ranges	<a href="#">GRanges</a> object containing the seqname(s) and range(s) to query. Be sure this information is coherent with those returned by <a href="#">getDasEntries</a>
class	Instance of the class to be used in the output. By default it returns a regular character vector, but we recomend using Biostring classes for retrieving large sequences. Most usual Biosting classes are <a href="#">DNAStrngSet</a> for genomic sequences, <a href="#">RNAStrngSet</a> for transcripts and <a href="#">AAStrngSet</a> for aminoacids.

**Details**

This function allows to query the DAS server and returns the nucleotide or amino acid sequence available at the given ranges.

Please, be sure to pass the identifiers EXACTLY as the values returned by the functions available here (DAS is case-sensitive). It is also recommended that you check the capabilities for each of the data sources.

Please, notice that this function codes the parameters in a URL to query the server. This function could fail if you ask for many ranges. Also, notice that the speed of the query depends on the number of elements and the load in the server.

Please, use this function smartly and do not overload servers.

**Value**

Nucleotide or amino acid sequences that match the content of the annotation for the given ranges in the server.

If there are not matching results, output is NULL.

**Author(s)**

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**See Also**

[getDas-functions](#)

**Examples**

```
#Set session server to the UniProt DAS Reference Server
setDasServer(server="http://www.ebi.ac.uk/das-srv/uniprot/das")

print(getDasServer())

source = "uniprot" #Uniprot

ranges = GRanges(c("A0A000", "A0A001"), IRanges(start=c(1,1),end=c(394,591)))

sequences = getDasSequence(source, ranges)

print(sequences)
```

---

getDasStructure

*Query a protein 3D structure to session's DAS server*

---

**Description**

This function retrieves the 3D structure, including metadata and coordinates for the given query (ID of the reference structure) using the data source id (or title) in the session's DAS server.

**Usage**

```
getDasStructure(source, query)
```

**Arguments**

source	Data source id (or title). See <a href="#">getDasSource</a>
query	Query id



## Details

This function allows to query the DAS server and returns the the 3D structure,including metadata and coordinates for the given query (id of the reference structure).

Please, be sure to pass the identifiers EXACTLY as the values returned by the functions available here (DAS is case-sensitive). It is also recommended that you check the capabilities for each of the data sources.

Please, notice that this function codes the parameters in a URL to query the server. This function could fail if you ask for a reference structure that does not exist. Also, notice that the speed of the query depends on the number of elements and the load in the server.

Please, use this function smartly and do not overload servers.

## Value

data. frame with the following columns: x, y, z, atomName, atomID, occupancy, tempFactor, type, groupID, name, which match with the contents of the reference structure of the given query.

If there are not matching results, output is NULL.

## Author(s)

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## See Also

[getDasFeature](#) [getDas-functions](#) [getDasSequence](#)

## Examples

```
#Set DAS server
setDasServer(server="http://das.sanger.ac.uk/das")

#Get the sources with "structure" capability...
sources = getDasSource()
sources[grep("structure", sources$capabilities),]
source="structure" #...which name is also "structure"

query="1HCK" #PDB code

structure=getDasStructure(source,query)

head(structure)
```

---

 plotFeatures

*Basic plotting function for obtained features*


---

### Description

This functions creates a basic plot with the features retrieved by [getDasFeature](#) or adds them to an existing plot

### Usage

```
plotFeatures(df, col=NULL, col.start="start", col.end="end", col.id="label",
  col.type="type", box.height=4, box.sep=2, pos.label=c("middle", "top", "bottom", "no"),
  new=TRUE, legend=TRUE, ...)
```

### Arguments

df	<a href="#">data.frame</a> with the features. Columns <code>col.start</code> , <code>col.end</code> , <code>col.id</code> and <code>col.type</code> must be present.
col	Vector of colors for each box in df. If NULL, automatic rainbow coloring for different types will be used.
col.start, col.end, col.id, col.type	Names of the columns of the data.frame from which retrieve the values
box.height, box.sep	Height and separation between boxes (in percentual points respect y-axis)
pos.label	Position of the label respect the box. If <code>pos.label=="no"</code> , labels are disabled.
new	Open a new graphical device. If <code>new=FALSE</code> , boxes will be added to an existing plot (so, coordinate system must be coherent).
legend	Add legend to the plot
...	Other graphical parameters passed to <a href="#">plot.default</a>

### Details

This function provides a quick way to view (non-overlapped) boxes in a new or an existing plot with the features retrieved.

Notice that boxes will can be plotted overlapping the current open graphical device, so the x-coordinates must match.

### Value

(none)

### Author(s)

Oscar Flores <oflores@mmb.pcb.ub.es>

**See Also**

[getDasFeature](#)

**Examples**

```
#This is UCSC Genome browser
setDasServer(server="http://genome.ucsc.edu/cgi-bin/das")

source = "sacCer3" #Notice that id now changes, we can retrieve it from getDasDsn()
range = GRanges(c("I"), IRanges(start=1, end=2500))
type = c("sgdGene")

#We want the official genes from 'sgdGene' in the range I:1-2500
features = getDasFeature(source, range, type)
print(features)

plotFeatures(features)
```

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