

# Package ‘primate’

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**Title** Tools and Methods for Primatological Data Science

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**Depends** R (>= 1.8.0), caroline

**Suggests** RJDBC

**Description** Data from All the World's Primates relational SQL database and other tabular datasets are made available via drivers and connection functions. Additionally we provide several functions and examples to facilitate the merging and aggregation of these tabular inputs.

**License** Apache License

**LazyLoad** yes

**NeedsCompilation** no

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`add.gnsp.clmn`                      *Add a genus species column*

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### Description

Adds a `genus_species` column to the specified dataframe

### Usage

```
add.gnsp.clmn(df, gn="Genus", sp="Species", rownames=FALSE, new.col=TRUE, gnsp.col = "gn_sp")
```

### Arguments

<code>df</code>	input data.frame
<code>gn</code>	column name for genus
<code>sp</code>	column name for species
<code>rownames</code>	use the new <code>gn_sp</code> column to assign data.frame rownames
<code>new.col</code>	TRUE if <code>gn_sp</code> column is to be retained, FALSE if it is to be removed
<code>gnsp.col</code>	the name of the new column to add, by default is "gn_sp"

### Value

modified data.frame (with genus species info concatenated and added)

### Examples

```
primates.tab <- AWP.read.pkg.tab(tab.nm='dbo_tblGrovesMonkeys', id.clmn='MonkeyNumberGroves')
primates.tab <- add.gnsp.clmn(primates.tab, gn="Genus", sp="Species", rownames=FALSE, new.col=TRUE)
```

---

`AWP.connect`                      *Create a connection to the SQL DB*

---

### Description

Connect to the All the World's Primate Database

### Usage

```
AWP.connect(drv=AWP.driver(), prefix='jdbc:jtds:sqlserver',
            server="s09.everleap.com", port=1433,
            db="DB_3918_atwpreview", user="DB_3918_atwpreview_user", pw="atwpreview_$_j")
```

**Arguments**

drv	driver (output from AWP.driver())
prefix	prefix to the URL (before "://")
server	domain name for the database server
port	port name used by the server's database
db	database name
user	database user name
pw	database user password

**Value**

a connection object for SQL

**Examples**

```
con <- AWP.connect(drv=AWP.driver())
```

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AWP.driver	<i>Load the driver to access the All the World's Primate remote SQL database</i>
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**Description**

Load the driver to utilize the database software

**Usage**

```
AWP.driver(drv.name="net.sourceforge.jtds.jdbc.Driver",
           drv.file=system.file("drivers","jtds-1.2.8.jar", package='primate'))
```

**Arguments**

drv.name	The name of the driver
drv.file	The file name for the database driver

**Value**

driver argument to AWP.connect

**Examples**

```
AWP.driver()
```

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AWP.get.lookup.table *Get a Lookup Table*

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### Description

Get the lookup table from the All the World's Primates SQL database

### Usage

```
AWP.get.lookup.table(con=AWP.connect(), tab.nm="TextType")
```

### Arguments

con	connection object
tab.nm	table name (for the parent table)

### Value

a data.frame corresponding to SQL table

### Examples

```
AWP.get.lookup.table(con=AWP.connect(), tab.nm="TextType")
```

---

AWP.get.SQL.table *Get a SQL Table*

---

### Description

Retrieve a table from the All the World's Primates SQL database

### Usage

```
AWP.get.SQL.table(con=AWP.connect(), tab.nm="tblGrovesMonkeys", c1mns=c('all'), xpnd=FALSE)
```

### Arguments

tab.nm	table name (defaults to the main primate species list)
con	connection object
c1mns	columns to return
xpnd	expand the lookup column codes into full text strings

**Value**

a data.frame corresponding to SQL table

**Examples**

```
online.version <- AWP.get.SQL.table(tab.nm='LMType') #a small example table
```

---

```
AWP.list.SQL.tables List the SQL tables
```

---

**Description**

List available tables from the All the World's Primates SQL database

**Usage**

```
AWP.list.SQL.tables(con=AWP.connect(), all=FALSE)
```

**Arguments**

con	connection object from AWP.connect
all	list all tables available

**Value**

a list (vector) of SQL table names

**Examples**

```
AWP.list.SQL.tables(con=AWP.connect(), all=FALSE)
```

---

AWP.read.pkg.tab	<i>Read a table from the All the World's primates example microarchive within this package</i>
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---

**Description**

Read an All the World's Primates table from the local package cache.

**Usage**

```
AWP.read.pkg.tab(tab.nm='dbo_tblGrovesMonkeys', id.c1mn=NA)
```

**Arguments**

tab.nm	table name
id.c1mn	id column of table

**Value**

data.frame corresponding to SQL table

**Examples**

```
primates.tab <- AWP.read.pkg.tab(tab.nm='dbo_tblGrovesMonkeys', id.c1mn='MonkeyNumberGroves')
```

---

AWP.run.SQL	<i>Run SQL queries</i>
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**Description**

Run arbitrary SQL queries on the All the World's Primate database

**Usage**

```
AWP.run.SQL(con=AWP.connect(), sql=NULL)
```

**Arguments**

con	connection object
sql	SQL string

**Value**

results of query

**Examples**

```
AWP.run.SQL(con=AWP.connect(), sql=NULL)
```

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regroup.equivalent	<i>Re-group data.frame by Genus_species in either old or new dataframe</i>
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**Description**

Regroup based on the old or the new data frame using a direction parameter.

**Usage**

```
regroup.equivalent(df, gnspl.old, gnspl.new, clmns, agg='mean', direction='old2new')
```

**Arguments**

df	a dataframe
gnspl.old	old nomenclature
gnspl.new	new nomenclature
clmns	the columns in the data.frame to re-group
agg	the aggregation type
direction	the aggregation priority

**Value**

a regrouped data frame

**Examples**

```
primates.tab <- AWP.read.pkg.tab(tab.nm='dbo_tblGrovesMonkeys', id.clmn='MonkeyNumberGroves')
primates.tab <- add.gnspl.clmn(primates.tab,gn="Genus",sp="Species",rownames=FALSE,gnspl.col='gn_sp')
primates.tab <- add.gnspl.clmn(primates.tab,gn="Genus",sp="Species",rownames=FALSE,gnspl.col='gnsplg')
pri.grpd <- regroup.gnspl(df=primates.tab,clmns=colnames(primates.tab), agg='max')
out <- regroup.equivalent(pri.grpd, gnspl.old=gn_sp, gnspl.new='gnsplg',
                          clmns='MonkeyNumberGroves', agg='paste', direction='old2new')
```

---

regroup.gnsp	<i>Re-group data.frame by Genus_species</i>
--------------	---

---

### Description

Regroup a given data.frame by a column designated as unique genus\_species combination. This function is essentially a wrapper for caroline::groupBy()

### Usage

```
regroup.gnsp(df, c1mns, agg='mean', by='gn_sp')
```

### Arguments

df	a dataframe
c1mns	columns
agg	type of aggregation to be used
by	the column name by which the data.frame should be re-grouped

### Value

returned value

### Examples

```
primates.tab <- AWP.read.pkg.tab(tab.nm='dbo_tblGrovesMonkeys', id.c1mn='MonkeyNumberGroves')
out <- regroup.gnsp(df=primates.tab, c1mns=colnames(primates.tab), agg='paste')
```

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updatevals	<i>Update the values of an AWP data.frame</i>
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### Description

Update the values in an old dataframe with the values in a new dataframe. Useful for comparing a pre-existing or self-assembled dataset with AWP.

### Usage

```
updatevals(x, y=NULL, v.old, v.new, verbose=TRUE, update=FALSE,
           na.only=TRUE, all=TRUE, missing.only=TRUE)
```



**Arguments**

x	first dataframe
y	second dataframe
v.old	variable old
v.new	variable new
verbose	get all the messages
update	update all the old with everything new
na.only	just update the missing values in the old dataframe
all	perform merge on all columns
missing.only	update only those that have missing values

**Value**

values of one data frame are updated to reflect new data in another

**Examples**

```
pri.tab <- AWP.read.pkg.tab(tab.nm='Locomotion')
#pri.AWP <- AWP.get.SQL.table(tab.nm='Locomotion')

dim(pri.tab) #should may be fewer cols or rows locally ...
#dim(pri.AWP) # than there are available online.

apply(pri.tab, 2, function(x) sum(is.na(x))) # also more missing values
#apply(pri.AWP, 2, function(x) sum(is.na(x))) # locally than online

# update the "Comment" column locally with the same online

vars <- c('LocomotionID', 'Comment')
#tmp <- merge(x=pri.tab[,c(vars)] ,y=pri.AWP[,c(vars)], by='LocomotionID')

#out <- updatevals(x=tmp,y=NULL,v.old='Comment.x',v.new='Comment.y')
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