Package 'Rpdb'

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`Rpdb-package` *Read, Write, Visualize and Manipulate PDB Files*

Description

Provides tools to read, write, visualize PDB files, and perform structural manipulations.

Details

This package enables users, e.g. computational chemists, to manipulate molecular structures stored in PDB files. It enables users ro read, write and visualize PDB files. Various basic structural manipulations are also supported. Conversion of Cartesian coordinates into fractional coordinates. Spliting a molecular structure into fragments. Computation of centers-of-geometry and centers-of-mass. Wrapping molecular structure using periodical boundary conditions. Translation, rotation and reflection of atomic coordinates. Calculate atomic bond lengths, angles and dihedrals.

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References

More information on the PDB format can be found here:
http://www.wwpdb.org/documentation/format33/v3.3.html

Examples

```
## Read a PDB file included in the package
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

## Visualize the PDB file
visualize(x, mode = NULL)

## From Cartesian to fractional coordinates and vice versa
x <- xyz2abc(x)
basis(x)
natom(x, x$atoms$resid)
range(x)
centres(x)
x <- abc2xyz(x)
basis(x)
natom(x, x$atoms$resid)
range(x)
centres(x)

## Split and unsplit
F <- x$atoms$resid
x <-   split(x, F)
x <- unsplit(x, F)

## Subset and merge
x.PCB.only <- subset(x, resname == "PCB")
x.DCB.only <- subset(x, resname == "DCB")
x <- merge(x.PCB.only, x.DCB.only)

## Duplicate and wrap
x <- replicate(x, a.ind = -1:1, b.ind = -1:1, c.ind = -1:1)
x <- wrap(x)
```

```
## Write the 'pdb' object 'x' to a temporary file.
write.pdb(x, file = tempfile())
```

---

addAxes *Add Axes or PBC Box to the 'rgl' Scene*

Description

Add lattice vectors, Cartesian axes or PBC box to the current 'rgl' scene.

Usage

```
addABC(x, lwd = 2, scale = NULL, labels = TRUE, cex = 2, adj.lab = 1.2)

addXYZ(lwd = 2, scale = NULL, labels = TRUE, cex = 2, dx = 5)

addPBCBox(x, scale = NULL, lwd = 2, col = "black", alpha = 0.25)

addBBox(x, lwd = 2, col = "black", alpha = 0.25)

bbox.pdb(x)
```

Arguments

x	an object of class 'crystal' containing the unit cell parameters.
lwd	a numeric value indicating the line width used to draw the axes or the PBC box.
scale	a scalar value, or a numeric vector of length 2 or 3 or 6, or a 3x3 matrix used to scale the PBC box or the axes; a length 3 vector is converted to a diagonal matrix, while vectors of length 2 or 4 or 6 are converted to a diagonal matrix for scaling and a relative shift;
labels	a logical value indicating whether to draw the labels of the axes.
cex	a numeric value indicating the magnification used to draw the labels of the axes.
adj.lab	numeric value performing relative adjustment of label position;
dx	a numeric value specifying the absolute length of the xyz axes-vectors;
col	colour used for the PBC box;
alpha	a numeric value specifying the transparency of the lines;

Details

addABC: Add the lattice vectors a, b and c to the current rgl device.
addXYZ: Add the Cartesian axes x, y and z to the current rgl device.
addPBCBox: Add a box representing the Periodic Boundary Conditions of a molecular system.
addBBox: Add a bounding box around the PDB molecule constructed using the lattice vectors.
bbox.pdb: Computes the bounding box around the PDB molecule.

Value

Returns invisibly a two-column data.frame containing the IDs and type indicators of the objects added to the scene.

bbox.pdb: Returns the coordinates of the bounding box.

See Also

visualize, rgl.open, par3d, addLabels

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, type = "l", xyz = FALSE, abc = FALSE, pbc.box = FALSE, mode = NULL)
addXYZ()
addABC(x$crystal)
addPBCBox(x$crystal)
```

---

addLabels *Add Labels to the 'rgl' Scene*

Description

Add Labels to the current 'rgl' scene.

Usage

```
addResLab(x, ...)

## S3 method for class 'atoms'
addResLab(x, at.centre = TRUE, col = "black", ...)

## S3 method for class 'pdb'
addResLab(x, at.centre = TRUE, col = "black", ...)

addEleLab(x, ...)

## S3 method for class 'atoms'
addEleLab(x, eleid = FALSE, col = "black", ...)

## S3 method for class 'pdb'
addEleLab(x, eleid = FALSE, col = "black", ...)

info3d(...)

## S3 method for class 'atoms'
```

```
info3d(x, id = rgl::rgl.ids(), col = "black", verbose = TRUE, adj = 0, ...)

## S3 method for class 'pdb'
info3d(x, id = rgl::rgl.ids(), col = "black", verbose = TRUE, adj = 0, ...)
```

Arguments

x	an R object containing atomic coordinates.
...	further arguments passed to or from other methods.
at.centre	a single element logical vector indicating if residue labels have to be added only at the position of the residue's centre-of-mass instead of at each atomic position.
col	the colors used to display the labels.
eleid	a single element logical vector indicating if the element ids have to be concatenated with the element names to prepare the labels.
id	vector of ID numbers of 'rgl' items, as returned by rgl.ids. The vertexes of these items are used to display the labels.
verbose	a logical value specifying if information have to be printed to the terminal.
adj	one value specifying the horizontal adjustment, or two, specifying horizontal and vertical adjustment respectively. See text3d

Details

addResLab add residue labels to the scene. If at.centre==TRUE only one label per residue is added at the centre of the residue. Otherwise, residue labels are added at each atomic positions. addEleLab add element labels to the scene at each atomic positions. info3d activate an interactive mode to add labels by selecting atoms by **right-clicking** on the current 'rgl' scene. To escape the interactive mode press the ESC key. The labels are as follow: "ResidResname:EleidElename"

Value

addResLab and addEleLab return (using invisible) a two-column data.frame containing the IDs and type indicators of the objects added to the scene.

See Also

pdb, visualize, measure

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, type = "l", mode = NULL)
addResLab(x)
x <- read.pdb(system.file("examples/Pentacene.pdb", package="Rpdb"))
visualize(x, type = "l", mode = NULL)
addEleLab(x)
```

atoms *Create 'atoms' Object*

Description

Creates an object of class 'atoms' containing the data related to ATOM and HETATM records of a PDB file.

Usage

```
atoms(...)

## S3 method for class 'pdb'
atoms(x, ...)

## S3 method for class 'atoms'
atoms(x, ...)

## Default S3 method:
atoms(
  recname,
  eleid,
  elename,
  alt,
  resname,
  chainid,
  resid,
  insert,
  x1,
  x2,
  x3,
  occ,
  temp,
  segid,
  basis = "xyz",
  symbol = NULL,
  isHetero = NULL,
  ...
)

is.atoms(x)
```

Arguments

...	arguments passed to methods.
x	an R object to be tested or from whom to extract the atoms component.

recname	a character vector containing the record name for each element.
eleid	a integer vector containing the element ID for each element.
elename	a character vector containing the element name for each element.
alt	a character vector containing the alternate location indicator for each element.
resname	a character vector containing the residue name for each element.
chainid	a character vector containing the chain ID for each element.
resid	a integer vector containing the residue ID for each element.
insert	a character vector containing the codes for insertion of residue of each element.
x1, x2, x3	a numeric vector containing the first, second and third coordinate for each element.
occ	a numeric vector containing the occupancie for each element.
temp	a numeric vector containing the temperature factor for each element.
segid	a character vector containing the segment ID for each element.
basis	a single element character vector indicating the type of basis vector used to express the atomic coordinates.
symbol	the chemical symbol of the atom.
isHetero	logical indicating if the record corresponds to the non-protein ligands.

Details

atoms is a generic function to create objects of class 'atoms'. The purpose of this class is to store ATOM and HETATM records from PDB files.

The default method creates an atoms object from its different components, i.e.: recname, eleid, elename, alt, resname, chainid, resid, insert, x1, x2, x3, occ, temp, segid and basis. All the arguments have to be specified, except basis, which by default is set to "xyz" (Cartesian coordinates).
is.atoms tests if an object is of class 'atoms', i.e. it only checks that the object inherits the "class" atoms.

Value

atoms returns a data.frame of class 'atoms' with the following components:

recname a character vector containing the record name for each element.

eleid a integer vector containing the element ID for each element.

elename a character vector containing the element name for each element.

alt a character vector containing the alternate location indicator for each element.

resname a character vector containing the residue name for each element.

chainid a character vector containing the chain ID for each element.

resid a integer vector containing the residue ID for each element.

insert a character vector containing the codes for insertion of residue for each element.

x1, x2, x3 a numeric vector containing the first, second and third coordinate for each element.

occ a numeric vector containing the occupencie for each element.

temp a numeric vector containing the temperature factor for each element.

segid a character vector containing the segment ID for each element.

basis a single element character vector indicating the type of basis vector used to express the atomic coordinates.

`is.atoms` returns TRUE if `x` is an object of class 'atoms' and FALSE otherwise.

See Also

`basis`, `coords`, `pdb`

Examples

```
x <- atoms(recname = c("ATOM","ATOM"), eleid = 1:2, elename = c("H","H"), alt = "",
  resname = c("H2","H2"), chainid = "", resid = c(1,1), insert = "",
  x1 = c(0,0), x2 = c(0,0), x3 = c(0,1), occ = c(0.0,0.0), temp = c(1.0,1.0),
  segid = c("H2","H2"))
print(x)
is.atoms(x)
```

---

basis *The Basis of an Object*

Description

Functions to get or set the basis of an object containing atomic coordinates.

Usage

```
basis(x)

## Default S3 method:
basis(x)

basis(x) <- value

## Default S3 replacement method:
basis(x) <- value

## S3 method for class 'pdb'
basis(x)

## S3 replacement method for class 'pdb'
basis(x) <- value
```

Arguments

x	an R object containing atomic coordinates.
value	a single element character vector use to set the basis of x.

Details

basis and basis<- are respectively generic accessor and replacement functions. The default methods get and set the basis attribute of an object containing atomic coordinates. This attribute indicate the type basis vector used to express atomic coordinates.
value must be equal to "xyz", for Cartesian, or "abc", for fractional coordinates.
The methods for objects of class 'pdb' get and set the basis attribute of its atoms component.

Value

For basis**:** NULL or a single element character vector. (NULL is given if the object has no basis attribute.)

For basis<-**:** the updated object. (Note that the value of basis(x) <- value is that of the assignment, value, not the return value from the left-hand side.)

See Also

coords, atoms, pdb

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
basis(x)
x <- xyz2abc(x)
basis(x)
```

---

bond-angle-dihedral *Atomic Bond Lengths, Angles and Dihedrals*

Description

Compute bond lengths, angles and dihedral from atomic coordinates.

Usage

```
bond(...)

## S3 method for class 'coords'
bond(x, sel1, sel2, ...)

## S3 method for class 'pdb'
bond(x, sel1, sel2, ...)
```

```
angle(...)

## S3 method for class 'coords'
angle(x, sel1, sel2, sel3, ...)

## S3 method for class 'pdb'
angle(x, sel1, sel2, sel3, ...)

dihedral(...)

## S3 method for class 'coords'
dihedral(x, sel1, sel2, sel3, sel4, ...)

## S3 method for class 'pdb'
dihedral(x, sel1, sel2, sel3, sel4, ...)

measure(...)

## Default S3 method:
measure(id = rgl::rgl.ids(), verbose = TRUE, ...)

## S3 method for class 'coords'
measure(x, id = rgl::rgl.ids(), verbose = TRUE, ...)

## S3 method for class 'pdb'
measure(x, id = rgl::rgl.ids(), verbose = TRUE, ...)
```

Arguments

`...`	further arguments passed to or from other methods.
`x`	an R object containing atomic coordinates.
`sel1`, `sel2`, `sel3`, `sel4`	an integer or logical vector used to select atoms defining bonds, angles or dihedrals. See details.
`id`	vector of ID numbers of 'rgl' items, as returned by `rgl.ids`. The vertexes of these items are used to compute the bond lengths, angles or dihedrals.
`verbose`	a logical value specifying if the information have to be printed to the terminal.

Details

The number of selected atoms with `sel1`, `sel2`, `sel3` and `sel4` must be the same. `sel1`, `sel2`, `sel3` and `sel4` respectively select the first, second, third and fouth atoms defining bonds, angles or dihedrals.

`measure` activate an interactive mode to compute bond lengths, angles and dihedrals by selecting atoms by **right-clicing** on the current 'rgl' scene. To escape the active mode press the ESC key.

Value

A numeric vector containing atomic bond lengths (in Angstrom), angles or dihedrals (in degrees)

See Also

coords, pdb, info3d, visualize

Examples

```
Pen <- read.pdb(system.file("examples/Pentacene.pdb", package="Rpdb"))
visualize(Pen, mode = NULL)
text3d(coords(Pen), texts = Pen$atoms$eleid)
bond(Pen, 3:4, 1:2)
angle(Pen, 3:4, 1:2, 5:6)
dihedral(Pen, 3:4, 1:2, 5:6, 6:5)
```

---

cellProperties *Properties of a Unit Cell*

Description

Compute the Cartesian coordinates of lattice vectors, the volume or the density of a unit cell.

Usage

```
cell.coords(...)

## Default S3 method:
cell.coords(abc, abg = c(90, 90, 90), digits = 3, ...)

## S3 method for class 'crystal'
cell.coords(x, digits = 3, ...)

## S3 method for class 'pdb'
cell.coords(x, digits = 3, ...)

cell.volume(...)

## S3 method for class 'crystal'
cell.volume(x, ...)

## S3 method for class 'pdb'
cell.volume(x, ...)

cell.density(...)
```

```
## Default S3 method:
cell.density(masses, volume, ...)

## S3 method for class 'pdb'
cell.density(x, ...)
```

Arguments

...	further arguments passed to or from other methods.
abc	a length 3 numeric vector containing the length of the a, b and c lattice vectors.
abg	a length 3 numeric vector containing the angles (degrees) between the a, b and c lattice vectors (alpha, beta, gamma).
digits	an integer used to round the lattice vectors coordinates.
x	an R object containing lattice parameters.
masses	a numeric vector containing atomic masses.
volume	a single element numeric vector containing the volume of the unit cell in Angstrom cube.

Details

`cell.coords` is a generic function which computes a 3x3 matrix whose columns contrain the Cartesian coordinates of lattice vectors. The 'a' and 'b' vectors are assumed to be respectively along the x-axis and in the xy-plane. The default method takes directly the lattice parameters as arguments. For objects of class `crystal` the lattice parameters are first extracted from the object and then the default method is called. For objects of class `pdb` the lattice parameters are extracted from their `crystal` component and the default method is called.

`cell.volume` is a generic function to compute the volume of a unit cell. For objects of class 'crystal', the unit cell parameters are directly used to compute the volume. For objects of class 'pdb', their `crystal` component is used.

`cell.density` is a generic function to compute the density of a unit cell. For objects of class 'pdb': First the volume of the unit cell is calculated by calling the `cell.volume` function on the `crystal` component of the 'pdb' object. Then the element names are converted into element symbols using the `toSymbols` function and their masses are taken from the `elements` data set. Finally the density is calculated using the sum of the atomic masses and the volume of the unit cell.

Value

`cell.coords` returns a 3x3 matrix containing the Cartesian coordinates of lattice vectors arranged by columns.
`cell.volume` returns a single element numeric vector containing the volume of the unit cell in Angstrom cube.
`cell.density` returns a single element numeric vector containing the density of the unit cell in g.cm-3.

See Also

crystal, pdb, xyz2abc

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
cell.volume(x)
cell.density(x)
cell.coords(x)
```

---

centres *Centres-of-Geometry and Centres-of-Mass*

Description

Computes centres-of-geometry and centres-of-mass of groups of atoms.

Usage

```
centres(x, ...)

## S3 method for class 'coords'
centres(x, factor = NULL, weights = NULL, unsplit = FALSE, na.rm = FALSE, ...)

## S3 method for class 'atoms'
centres(x, factor = NULL, weights = NULL, unsplit = FALSE, na.rm = FALSE, ...)

## S3 method for class 'pdb'
centres(x, factor = NULL, weights = NULL, unsplit = FALSE, na.rm = FALSE, ...)
```

Arguments

x	an R object containing atomic coordinates.
...	further arguments passed to or from other methods.
factor	a factor used to split the atomic coordinates by groups to compute multiple centres.
weights	a numerical vector containing atomic weights used to compute centres-of-mass.
unsplit	a logical value indicating whether the coordinates of the centres have to be unsplit to repeat their coordinates for each atom used for their calculation (used for wrapping by groups).
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.

Details

centres is a generic function to compute centres-of-geometry and centres-of-mass from an object containing atomic coordinates. For objects of class 'coords', 'atoms' and 'pdb', the coordinates of x are first splitted into groups defined by factor using the split function. For each group, the weighted mean of the x1, x2 and x3 components of x are calculated using weights. By default all atoms are assumed to have the same weight (calculation of centres-of-geometry). Finally, if unplit = TRUE the coordinates of the centres are unsplitted using the unsplit function to assign to each atom the coordinates of the centre to which they are attached (used for wrapping by groups).

For objects of class 'atoms' and 'pdb' by default factor is set to x$resid and x$coordinates$resid, respectively, to compute the centre-of-geometry of the different resdiues. Notice that coordinates can be neglected for the calculation of the centres using NA values in factor.

Value

Return an object of class 'coords' containing the coordinates of centres.

See Also

coords, atoms, pdb, elements

and split, unsplit, factor for details about splitting data sets.

Examples

```
# First lets read a pdb file
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

# Centres-of-geometry of the residues
centres(x)

# Centre-of-geometry of the whole structure
centres(x, factor = rep(1, natom(x)))
# or
centres(coords(x))

# Centres-of-geometry of the PCB and DCB residues
centres(x, factor = x$atoms$resname)

# Knowing the name of the elements forming
# the C60 of the PCBM molecules (PCB residues)
# we can compute the centres-of-geometry of
# the C60 by neglecting the other atoms of the
# PCB residues.
C60.elename <- paste0("C", sprintf("%0.3d", 1:60))

is.PCB <- x$atoms$resname == "PCB" # Produce a mask to select only the PCB residues
is.C60 <- is.PCB & x$atoms$elename %in% C60.elename # Produce a mask to keep only the C60

F <- x$atoms$resid # We use the residue IDs to split the coordinates
F[!is.C60] <- NA # We keep only the atoms of the C60
```

```
C60.centres <- centres(x, factor = F)

# Lets check the position of the C60 centres
visualize(x , mode = NULL)
spheres3d(C60.centres)
text3d(Ty(C60.centres, 2), text=paste0("PCB_", rownames(C60.centres)), cex=2)

# Centres-of-mass of the resdiues
symb <- toSymbols(x$atoms$elename) # Convert elename into elemental symbols
# Find the mass of the element in the periodic table
w <- elements[match(symb, elements[,"symb"]), "mass"]
centres(x, weights = w)
```

`centres.ppRoll` *Centres-of-Geometry: Rolling Window*

Description

Computes the geometric centres using a rolling window on a polypeptide chain

Usage

```
## S3 method for class 'ppRoll'
centres(x, window, ...)

## Default S3 method:
centres.ppRoll(x, window = 34, na.rm = TRUE, ...)

## S3 method for class 'atoms'
centres.ppRoll(x, window = 34, chain = NULL, na.rm = TRUE, ...)

## S3 method for class 'pdb'
centres.ppRoll(x, window = 34, chain = NULL, na.rm = TRUE, ...)
```

Arguments

`x`	an R object containing atomic coordinates (with additional class `ppRoll`).
`window`	size of the rolling window, specified as number of amino-acids;
`...`	further arguments passed to or from other methods.
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds.
`chain`	apply only to the respective chains, by default all chains;

Details

'centres.ppRoll' is a generic function to compute the geometric centres using a rolling window on an object containing atomic coordinates for a polypeptide chain. Due to limitations by CRAN check, the function is further referred as 'centres'.

The function may be useful to visualize the overall protein structure, but in a less cluttered way. Unlike the protein backbone, the centres may capture better the bulk of the protein.

Value

Return an object of class 'coords' containing the coordinates of the centres.

See Also

coords, atoms, pdb.

Examples

```
### Example 1: Toll-Like Receptor 2
# Download pdb file for TLR2: 2Z81;
# Read the pdb-file:
# x = read.pdb("pdb2z81.ent")

# Compute the centres:
# tmp = centres.ppRoll(x)

# Visualize the structure:
# visualize(x, type="p", pbc.box = FALSE)
# lines3d(tmp, lwd = 5, col = "red")

# Add Another "strand":
# tmp = centres.ppRoll(x, window = 8)
# lines3d(tmp, lwd = 5, col = "#FA3296")
```

`chains` *Extract Chain-Codes from a PDB Molecule Extract the codes of all chains from a PDB object.* `chains` *is a generic function to extract the ids of the chains from a PDB molecule.*

Description

Extract Chain-Codes from a PDB Molecule Extract the codes of all chains from a PDB object. `chains` is a generic function to extract the ids of the chains from a PDB molecule.

Usage

```
chains(x, ...)

## S3 method for class 'atoms'
chains(x, sorted = TRUE, ...)

## S3 method for class 'pdb'
chains(x, ...)
```

Arguments

x	Object of class pdb or class atoms;
...	arguments passed to other methods.
sorted	logical indicating if the returned chain-codes should be sorted;

Value

chains returns the codes of the individual chains in the molecule.

---

connect *Create 'connect' Object*

Description

Creates an object of class 'connect' containing the IDs of bonded atoms defining the connectivity of a molecular system.

Usage

```
conect.default(eleid.1, eleid.2, ...)

connect(...)

## Default S3 method:
connect(eleid.1, eleid.2, ...)

## S3 method for class 'coords'
connect(x, radii = 0.75, safety = 1.2, by.block = FALSE, maxLimit = 3200, ...)

## S3 method for class 'atoms'
connect(x, safety = 1.2, by.block = FALSE, ...)

## S3 method for class 'pdb'
connect(x, safety = 1.2, by.block = FALSE, ...)

## S3 method for class 'character'
```

```
connect(pdbRec, atoms, ...)

is.connect(x)
```

Arguments

eleid.1	a integer vector containing the IDs of bonded atoms.
eleid.2	a integer vector containing the IDs of bonded atoms.
...	arguments passed to methods.
x, atoms	an R object containing atomic coordinates.
radii	a numeric vector containing atomic radii used to find neigbours.
safety	a numeric value used to extend the atomic radii.
by.block	a logical value indicating whether the connectivity has to be determine by block (see details).
maxLimit	integer value specifying the maximum number of atoms permitted to try connecting by distance.
pdbRec	the raw text lines from the pdb file.

Details

connect is a generic function to create objects of class 'connect'. The purpose of this class is to store CONNECT records from PDB files, indicating the connectivity of a molecular system.
The default method creates a connect object from its different components, i.e.: eleid.1 and eleid.2. Both arguments have to be specified.
The S3 method for an object of class 'coords' determines the connectivity from atomic coordinates. A distance matrix is computed, then, for each pair of atoms the distance is compared to a bounding distance computed from atomic radii. If this distance is lower than the bounding distance then the atoms are assumed to be connected.
The S3 method for object of class 'pdb' first uses the element names to search for atomic radii in the elements data set. Then atomic coordinates and radii are passed to connect.coords.
If by.block == TRUE, a grid is defined to determined the connectivity by block. The method is slow but allows to deal with very large systems.
The S3 method for object of class 'character' converts the raw string from a pdb file into a connect object.

is.connect tests if an object is of class 'connect', i.e. if it has a "class" attribute equal to connect.

Value

connect returns a two-column data.frame of class 'connect' whose rows contain the IDs of bonded atoms. The columns of this data.frame are described below:

eleid.1	an integer vector containing the elements IDs defining the connectivity of the system.
eleid.2	an integer vector containing the elements IDs defining the connectivity of the system.

is.connect returns TRUE if x is an object of class 'coords' and FALSE otherwise.

See Also

pdb

Examples

```
# If atom 1 is connected to atom 2, 3, 4 and 5
# then we can prepare the following 'connect' object:
x <- connect(rep(1,4), 2:5)
print(x)
is.connect(x)

# Compute connectivity from coordinates
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"), CONNECT = FALSE)
x$connect
x$connect <- connect(x)
x$connect
```

---

coords *The Atomic Coordinates of an Object*

Description

Get or set the atomic coordinates (either Cartesian or fractional coordinates) of an object.

Usage

```
coords(...)

coords(x) <- value

as.coords(...)

## Default S3 method:
coords(x1, x2, x3, basis = "xyz", ...)

## S3 method for class 'data.frame'
coords(x, basis = NULL, ...)

## S3 method for class 'matrix'
coords(x, basis = NULL, ...)

## S3 method for class 'coords'
coords(x, ...)
```

```
## S3 method for class 'atoms'
coords(x, ...)

## S3 replacement method for class 'atoms'
coords(x) <- value

## S3 method for class 'pdb'
coords(x, ...)

## S3 replacement method for class 'pdb'
coords(x) <- value

is.coords(x)
```

Arguments

...	further arguments passed to or from other methods.
x	an R object containing atomic coordinates.
value	an object of class 'coords' used for replacement
x1, x2, x3	numeric vectors containing the first, second and third coordinates.
basis	a single element character vector indicating the type of basis vector used to express the atomic coordinates.

Details

The purpose of the 'coords' class is to store the coordinates of a molecular system and facilitate their manipulation when passing from the Cartesian to fractional coordinates and vice versa.
coords and coords<- are generic accessor and replacement functions. as.coords is an alias to coords.
The default method of the coords function is actually a builder allowing to create a 'coords' object from its different components, i.e.: x1, x2, x3, and basis. All the arguments have to be specified except 'basis' which by default is set to "xyz" (Cartesian coordinates).

For an object of class 'atoms', the accessor function extracts its x1, x2 and x3 components as well as its basis attribute to create a 'coords' object.

The replacement function sets x1, x2 and x3 components, as well as the basis attribute.

For an object of class 'coords', the accessor function returns the 'coords' object as is.

For an object of class 'pdb', the accessor function extracts the x1, x2 and x3 components, as well as the basis attribute of its atoms component to create a 'coords' object. The replacement function sets the x1, x2 and x3 components as well as the basis attribute of its atoms component.

For 'matrix' and 'data.frame' objects, when basis == NULL this function searches x, y, z or a, b, c columns in x.
If x, y, z columns are found, they are used to set the first, second and third coordinates of the returned 'coords' object. In that case the basis set of x is set to "xyz".

If a, b, c columns are found they are used to a set the first, second and third coordinates of the returned 'coords' object. In that case the basis set of x is set to "abc".
If the function doesn't found neither the x, y, z nor the a, b, c columns an error is returned.
When basis!=NULL it has to be equal to "xyz" or "abc" and x must have exactly 3 columns.

is.coords tests if x is an object of class 'coords', i.e. if x has a "class" attribute equal to coords.

Value

The accessor function returns a data.frame of class 'coords' whose columns contain the three coordinates of the atoms of a molecular system. The coordinates can either be Cartesian (basis attribute equal to "xyz") or fractional coordinates (basis attribute equal to "abc").

The replacement function returns an object of the same class as x with updated coordinates.

is.coords returns TRUE if x is an object of class 'coords' and FALSE otherwise

See Also

basis

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
is.coords(x)
is.coords(x$atoms)

## Replace the coordinates of x by translated coordinates
coords(x) <- coords(Tz(x, 10))
coords(x)
```

---

crystal *Create 'crystal' Object*

Description

Create an object of class 'crystal' containing the unit cell parameters and the name of the space group to associate with an object of class 'pdb'. Note: the 'cryst1' class will be deprecated.

Usage

```
cryst1(...)

## Default S3 method:
crystal(abc, abg = c(90, 90, 90), sgroup = "P1", ...)

is.cryst1(x)

is.crystal(x)
```

Arguments

...	further arguments passed to or from other methods.
abc	a numeric vector of length 3 containing the norms of the lattice vectors a, b and c.
abg	a numeric vector of length 3 containing the angles between the lattice vectors α, β and γ.
sgroup	a character string giving the Hermann-Mauguin symbol of the space group.
x	an R object to be tested.

Details

`crystal` is a generic function to create objects of class 'crystal'. The purpose of this class is to store CRYST1 records from PDB files which contain the unit cell parameters and the name of the space group of a molecular system stored in a PDB file. The default method of the `crystal` function creates an object of class 'crystal' from its different components, i.e.: `abc`, `abg` and `sgroup`. At least `abc` has to be specified.

`is.crystal` tests if an object is of class 'crystal', i.e. if it has a "class" attribute equal to `crystal`.

Value

Function `crystal` returns a list of class 'crystal' with the following components:

abc	a numeric vector of length 3 containing the norms of the lattice vectors a, b and c.
abg	a numeric vector of length 3 containing the angles between the lattice vectors α, β and γ.
sgroup	a character string giving the Hermann-Mauguin symbol of the space group.

Function `is.crystal` returns TRUE if `x` is an object of class 'crystal' and FALSE otherwise.

See Also

`cell.coords`, `pdb`

Examples

```
x <- crystal(abc = c(10, 10, 10), abg = c(90,90,90), sgroup = "P1")
is.crystal(x)
```

distances *Inter-Atomic Distances*

Description

Computes inter-atomic distance vectors.

Usage

```
distances(...)

dist.point(...)

## Default S3 method:
distances(
  dx1 = numeric(0),
  dx2 = numeric(0),
  dx3 = numeric(0),
  basis = "xyz",
  ...
)

## S3 method for class 'coords'
distances(x, sel1, sel2, ...)

## S3 method for class 'atoms'
distances(x, sel1, sel2, ...)

## S3 method for class 'connect'
distances(x, data, ...)

## S3 method for class 'pdb'
distances(x, sel1, sel2, ...)

## Default S3 method:
dist.point(data, x, y = NULL, z = NULL, subset = NULL, ...)

is.distances(x)

norm(...)

## S3 method for class 'distances'
norm(x, type = "xyz", ...)

## S3 method for class 'connect'
norm(x, data, type = "xyz", ...)
```

Arguments

...	further arguments passed to or from other methods.
dx1, dx2, dx3	numeric arrays containing the first, second and third components of the distance vectors.
basis	a single element character vector indicating the type of basis vector used to express the coordinates.
x, y, z	an R object containing atomic coordinates, or a a connect object (for the corresponding method);
sel1, sel2	integer or logical vectors defining two atomic selections between which the distance vectors are computed.
data	an object of type pdb, atoms or coords, containing atomic coordinates.
subset	enables sub-setting the coords object;
type	a single element character vector indicating how to project the distances vectors before computing the norms. See details.

Details

The purpose of the 'distances' class is to store the inter-atomic distance vectors and facilitate their manipulation when passing from the Cartesian to fractional references and vice versa.
The default method of the distances function is actually a builder allowing to create a 'distances' object from its different components, i.e.: dx1, dx2, dx3, and basis. All the arguments have to be specified except 'basis' which by default is set to "xyz" (Cartesian reference).

For objects of class 'coords', 'atoms', 'pdb', two sets of atomic coordinates, defined by sel1 and sel2, are extracted and inter-atomic distance vectors are computed between these two sets. For objects of class 'connect', distances are computed for the atoms specified by the 'connect' object.

The method for the 'dist.point' function computes the inter-atomic distances between the atoms and a specified point.

The method of the norm function for objects of class 'distances' computes the norm of the distances vectors. type specify how to project the distance vectors before computing the norms. By default no projection is perform. The three dx, dy, and dz components of the distance vectors are used to compute the norm. type can take the following values:

- x: The distance vectors are projected over x.
- y: The distance vectors are projected over y.
- z: The distance vectors are projected over z.
- xy: The distance vectors are projected in the xy-plan.
- yz: The distance vectors are projected in the yz-plan.
- zx: The distance vectors are projected in the zx-plan.
- xyz: The distance vectors are not projected (The three components of the distance vectors are used to compute the norm).

is.distances tests if x is an object of class 'distances'; the test is limited to the class attribute.

Value

The distances and dist.point functions return an object of class 'distances' containing interatomic distance vectors. The norm function return an array, with the same dimensions as the dx1, dx2, dx3 components of the 'distances' object for which the norms have been computed, containing the norm of the distance vectors.

is.distances returns TRUE if x is an object of class 'distances' and FALSE otherwise.

See Also

coords, basis, xyz2abc, abc2xyz

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
is.DCB7 <- x$atoms$resname == "DCB" & x$atoms$resid == 7
is.DCB8 <- x$atoms$resname == "DCB" & x$atoms$resid == 8
d <- distances(x, is.DCB7, is.DCB8)
norm(d, type = "xyz")
norm(d, type = "xy")
norm(d, type = "x")
d <- dist.point(x, c(0,0,0), subset = is.DCB7)
norm(d, type = "xyz")
```

---

elements *Periodic Table of the Elements*

Description

This data set gives various information on chemical elements

Format

A data frame containing for each chemical element the following information.

num atomic number

symb elemental symbol

areneg Allred and Rochow electronegativity (0.0 if unknown)

rcov covalent radii (in Angstrom) (1.6 if unknown)

rbo "bond order" radii

rvdw van der Waals radii (in Angstrom) (2.0 if unknown)

maxbnd maximum bond valence (6 if unknown)

mass IUPAC recommended atomic masses (in amu)

elneg Pauling electronegativity (0.0 if unknown)

`ionization` ionization potential (in eV) (0.0 if unknown)

`elaffinity` electron affinity (in eV) (0.0 if unknown)

`red` red value for visualization

`green` green value for visualization

`blue` blue value for visualization

`name` element name

Source

Open Babel (2.3.1) file: element.txt

Created from the Blue Obelisk Cheminformatics Data Repository
Direct Source: http://www.blueobelisk.org/
http://www.blueobelisk.org/repos/blueobelisk/elements.xml includes furhter bibliographic citation information

- Allred and Rochow Electronegativity from http://www.hull.ac.uk/chemistry/electroneg.php?type=Allred-Rochow
- Covalent radii from http://dx.doi.org/10.1039/b801115j
- Van der Waals radii from http://dx.doi.org/10.1021/jp8111556

Examples

```
data(elements)
elements

# Get the mass of some elements
symb <- c("C","O","H")
elements[match(symb, elements[,"symb"]), "mass"]

# Get the van der Waals radii of some elements
symb <- c("C","O","H")
elements[match(symb, elements[,"symb"]), "rvdw"]
```

---

format.pdb.title *Format "Title" Field of PDB File*

Description

Formats the title field of a Protein Data Bank (PDB) file.

Usage

```
## S3 method for class 'title'
format.pdb(x, ...)

## S3 method for class 'character'
format.pdb.title(x, ...)
```

Arguments

x	a vector of strings;
...	currently not used;

Details

This function is mostly used internally, e.g. by write.pdb, but may be useful in other instances as well.

Value

properly formatted text string.

See Also

write.pdb

Examples

```
format.pdb.title(c("Molecule 1", "is just an example"))
```

---

inertia *Moment of Inertia of a Molecular System*

Description

Computes the inertia tensor of a molecular system from atomic coordinates and masses.

Usage

```
inertia(...)

## S3 method for class 'coords'
inertia(x, m = NULL, ...)

## S3 method for class 'atoms'
inertia(x, m = NULL, ...)

## S3 method for class 'pdb'
inertia(x, m = NULL, ...)
```

Arguments

...	further arguments passed to or from other methods.
x	an R object containing atomic coordinates.
m	a numeric vector containing atomic masses.

Details

inertia is a generic function to compute the inertia tensor of a molecular system. For object of class 'coords' both atomic coordinates and masses have to be speifyed. For object of class 'atoms' the masses are determined from the elename component of the object (see toSymbols and masses). For object of class 'pdb' the atoms component is used.

Value

Return the inertia tensor in a 3x3 matrix.

See Also

toSymbols, masses, viewInertia

Examples

```
C70 <- read.pdb(system.file("examples/C70.pdb", package="Rpdb"))
inertia(C70)
visualize(C70, mode = NULL)
viewXY()
viewInertia(C70)
```

---

masses *Mass of Chemical Elements*

Description

Determine the mass of chemical elements

Usage

```
masses(...)

## Default S3 method:
masses(x, ...)

## S3 method for class 'pdb'
masses(x, ...)
```

Arguments

...	further arguments passed to or from other methods.
x	either a character or an integer vector containing element symbols or atomic numbers, or an object of class 'pdb' from which element symbols are determined (see details).

Details

masses is a generic function to determine the mass of chemical elements.

For objects of class 'pdb':

- First the element names are converted into element symbols using the toSymbols function.
- Then their masses are taken from the elements data set.

NA values are returned for unrecognized elements.

Value

Return a numeric vector containing the mass of chemical elements.

See Also

toSymbols

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb",package="Rpdb"))
masses(x)

masses(c("C","Cl",NA,"AA","N"))
```

---

merge.coords *Merging Molecular Systems*

Description

Merge two objects containing atomic coordinates

Usage

```
## S3 method for class 'coords'
merge(x, y, ...)

## S3 method for class 'atoms'
merge(x, y, reindex = TRUE, ...)

## S3 method for class 'pdb'
merge(x, y, reindex = TRUE, ...)
```

Arguments

x, y	objects of class coords to be merged.
...	further arguments passed to or from other methods.
reindex	a single element logical vector indicating if residue and element IDs have to be reindexed after merging.

Details

To merge x and y they must have the same basis attributes (see basis).

For objects of class 'coords' and 'atoms' the atomic coordinates are directly merged by row.

For objects of class 'pdb', the atoms and connect components of the two pdb objects are merged by row and the crystal component of x is used to build the returned object.

For objects of class 'atoms' and 'pdb' the residue and element IDs of y are shifted to avoid any confusion with those of x. If reindex == TRUE the reindex function is called to reinitialize the indexing of the returned object.

Value

Return an object of the same class as x and y merging x and y. If x and y have different basis attributes an error is returned.

See Also

coords, atoms, pdb, basis, merge, merge.data.frame

Examples

```
c1 <- coords( 1:3 ,  4:6 ,  7:9 , basis = "xyz")
c2 <- coords(10:12, 13:15, 16:18, basis = "xyz")
merge(c1,c2)


## Merging objects with different basis sets returns an error.
c2 <- coords(9:11, 12:14, 15:17, basis = "abc")
try(merge(c1,c2))


## Prepare a Pentacene/C70 dimer
C70 <- read.pdb(system.file("examples/C70.pdb", package="Rpdb"))
Pen <- read.pdb(system.file("examples/Pentacene.pdb", package="Rpdb"))
x <- merge(Tz(C70, 3.5, thickness=0.5), Pen)
```

mirror *Reflection of Atomic Coordinates*

Description

Perform a reflection (or mirror) operation on atomic coordinates with respect to a given reflection plane.

Usage

```
mirror(...)

## S3 method for class 'coords'
mirror(x, p1, p2 = NULL, p3 = NULL, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
mirror(x, p1, p2 = NULL, p3 = NULL, mask = TRUE, crystal = x$crystal, ...)
```

Arguments

...	further arguments passed to or from other methods.
x	an R object containing atomic coordinates.
p1	a numeric vector of length 3 containing the coordinates of the first point defining the reflexion plan. Can also be a 3x3 matrix or data.frame containing by row p1, p2 and p3.
p2	a numeric vector of length 3 containing the coordinates of the second point defining the reflexion plane.
p3	a numeric vector of length 3 containing the coordinates of the third point defining the reflexion plane.
mask	a logical vector indicating the set of coordinates to which to apply the reflexion.
crystal	an object of class 'crystal' used to convert fractional into Cartesian coordinates (when needed).

Details

mirror is a generic function. Method for objects of class 'coords' first convert the coordinates into Cartesian coordinates using crystal if needed. Once reflected, the coordinates are reconverted back to the original basis set using again crystal.

Method for objects of class 'pdb' first extract coordinates from the object using the function coords, perform the reflection, and update the coordinates of the 'pdb' object using the function coords<-.

Value

An object of the same class as x with reflected coordinates.

See Also

Helper functions for reflection with respect to a given Cartesian plane or a plane defined by two lattice vectors:
Mxy, Myz, Mzx, Mab, Mbc, Mca
Passing from Cartesian to fractional coordinates (or Vis Versa):
xyz2abc, abc2xyz

Examples

```
# First lets read a pdb file
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
cell <- cell.coords(x)
visualize(x, mode = NULL)

# Mirror operation with respect to the ab-plane
visualize(mirror(x, rep(0,3), p1=cell[, "a"], p2=cell[, "b"]), mode = NULL)
# Mirror operation with respect to the ab-plane for residue 1
visualize(mirror(x, rep(0,3), p1=cell[, "a"], p2=cell[, "b"],
   mask = x$atoms$resid == 1), mode = NULL)
```

`mirrorHelpers` *Helper Functions for reflection of Atomic Coordinates*

Description

Reflection of atomic coordinates with respect to a specific Cartesian plane or a plane defined by two lattice vectors.

Usage

```
Mxy(...)

## S3 method for class 'coords'
Mxy(x, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Mxy(x, mask = TRUE, crystal = x$crystal, ...)

Myz(...)

## S3 method for class 'coords'
Myz(x, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Myz(x, mask = TRUE, crystal = x$crystal, ...)

Mzx(...)
```

```
## S3 method for class 'coords'
Mzx(x, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Mzx(x, mask = TRUE, crystal = x$crystal, ...)

Mab(...)

## S3 method for class 'coords'
Mab(x, crystal, mask = TRUE, ...)

## S3 method for class 'pdb'
Mab(x, crystal = x$crystal, mask = TRUE, ...)

Mbc(...)

## S3 method for class 'coords'
Mbc(x, crystal, mask = TRUE, ...)

## S3 method for class 'pdb'
Mbc(x, crystal = x$crystal, mask = TRUE, ...)

Mca(...)

## S3 method for class 'coords'
Mca(x, crystal, mask = TRUE, ...)

## S3 method for class 'pdb'
Mca(x, crystal = x$crystal, mask = TRUE, ...)
```

Arguments

`...`	further arguments passed to or from other methods.
`x`	an R object containing atomic coordinates.
`mask`	a logical vector indicating the set of coordinates to which to apply the reflection.
`crystal`	an object of class 'crystal' used to convert fractional into Cartesian coordinates (when needed).

Details

These functions are helper functions to perform a reflection with respect to a specific Cartesian plan or a plan defined by two lattice vectors. All of them call the `mirror` function.

Value

An object of the same class as `x` with reflected coordinates.

See Also

mirror and xyz2abc, abc2xyz for passing from Cartesian to fractional coordinates (or Vice Versa).

Examples

```
# First lets read a pdb file
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, mode = NULL)

# Mirror operation with respect to the ab-plane
visualize(Mab(x), mode = NULL)
# Mirror operation with respect to the ab-plane for residue 1
visualize(Mab(x, mask = x$atoms$resid == 1), mode = NULL)
```

---

natom *Number of Atoms in an Object Containing Atomic Coordinates*

Description

Evaluates the number of atoms in an object containing atomic coordinates.

Usage

```
natom(x, ...)

## S3 method for class 'coords'
natom(x, factor = NULL, ...)

## S3 method for class 'atoms'
natom(x, factor = NULL, ATOM = TRUE, HETATM = TRUE, ...)

## S3 method for class 'pdb'
natom(x, factor = NULL, ATOM = TRUE, HETATM = TRUE, ...)
```

Arguments

x	an R object containing atomic coordinates.
...	further arguments passed to or from other methods.
factor	a factor used to split the object and evaluate the number of atoms in each group.
ATOM	a single element logical vector indicating if ATOM records have to be considered or not.
HETATM	a single element logical vector indicating if HETATM records have to be considered or not.

Details

natom is a generic function to evalute the number of atom in an object containing atomic coordinates. The atomic coordinates of the object are first filtered to keep ATOM and/or HETATM records as indicated by the 'ATOM' and 'HETATM' arguments. Then, if factor is specify, the object is splitted to evalute the number of atoms in each group defined by factor. If factor is not specify then the total number of atoms in the object is return.

Value

Return an integer or a vector of integer of lenght equal to nlevels(factor) (if factor is specify) indication the number of atoms in the object or in the groups defined by factor.

See Also

coords, atoms, pdb, factor, split

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

natom(x)
natom(x, x$atoms$resid)
natom(x, x$atoms$resname)
natom(x, HETATM = FALSE)
```

---

pdb *Create an Object of Class 'pdb'*

Description

Creates an object of class 'pdb'.

Usage

```
pdb(...)

## Default S3 method:
pdb(
  atoms,
  crystal = NULL,
  connect = NULL,
  remark = NULL,
  title = NULL,
  resolution = NULL,
  ...,
  cryst1 = NULL
)
```

```
is.pdb(x)
```

Arguments

...	further arguments passed to or from other methods.
atoms	a data.frame of class atoms containing ATOM and HETATM records use to create the pdb object.
crystal	a list of class crystal containing the periodical boundary conditions and space group used to create the pdb object.
connect	a data.frame of class connect containing CONECT records use to create the pdb object.
remark	a character vector containing some REMARK records to be added to the pdb object.
title	a character vector containing some TITLE records to be added to the pdb object.
resolution	numeric value specifying the resolution; the unit should be specified as an attribute.
cryst1	will be deprecated and replaced by argument crystal.
x	an R object to be tested.

Details

This function is a generic function used to create objects of class 'pdb'. The purpose of this class is to store the data of molecular systems contained in PDB files. The default method of the pdb function creates an object of class 'pdb' from its different components, i.e.: title, remark, crystal, atoms and connect. At least an object of class 'atoms' has to be specified.

is.pdb tests if x is an object of class 'pdb', i.e. if x has a "class" attribute equal to pdb.

Value

pdb returns a list of class 'pdb' with the following components:

title	a character vector containing the TITLE records found in a PDB file.
remark	a character vector containing the REMARK records found in a PDB file.
crystal	a list of class 'crystal' containing the first CRYSTAL record found in a PDB file. All others are ignored.
atoms	a data.frame of class 'atoms' containing the ATOM and HETATM records found in a PDB file.
connect	a data.frame of class 'connect' containing the CONECT records found in a PDB file.

is.pdb returns TRUE if x is an object of class 'pdb' and FALSE otherwise.

See Also

atoms, coords, crystal, connect and read.pdb

Examples

```
title  <- "This is just an example"
remark <- NULL
crystal <- crystal(c(10,10,10))
atoms <- atoms(recname = c("ATOM","ATOM"), eleid = 1:2, elename = c("H","H"), alt = "",
               resname = c("H2","H2"), chainid = "", resid = c(1,1), insert = "",
              x1 = c(0,0), x2 = c(0,0), x3 = c(0,1), occ = c(0.0,0.0), temp = c(1.0,1.0),
               segid = c("H2","H2"))
connect <- connect(eleid.1 = c(1), eleid.2 = c(2))
x <- pdb(atoms = atoms, crystal = crystal, connect = connect, remark = remark, title = title)
is.pdb(x)
```

---

proj.line3d *Projections of Objects*

Description

Computes 3D Projections

Usage

```
proj.line3d(p, x, y, z, ...)

## S3 method for class 'line3d.numeric'
proj(p, x, y = NULL, z = NULL, ...)

## S3 method for class 'line3d.matrix'
proj(p, x, y = NULL, z = NULL, ...)
```

Arguments

p	numeric array or matrix with the x,y,z coordinates of the point or collection of points.
x, y, z	an R object containing the coordinates of the end-points of the line segment; can be specified either as individual values or as a matrix.
...	currently not used.

Details

The purpose of the 'proj' helper functions is to compute the spatial projections of various objects on other geometrical structures. Currently, only projection of points on a line segment are implemented.

The methods for the 'proj.line3d' function compute the projections of 1 point or a collection of points on a line segment defined by the 2 delimiting points.

The 'numeric' method projects a point, while the 'matrix' method projects a collection of points on another geometric object.

Value

The `proj.line3d` function returns an object of class 'proj' containing the 3-dimensional coordinates of the projected point, as well as a scalar value representing the fraction of the path on the line segment.

Examples

```
p = c(1,2,3)
line = matrix(c(0,5,2,3,1,4), nrow = 2)
proj.line3d(p, line)
```

`range.coords` *Range of Atomic Coordinates*

Description

Determines the range of atomic coordinates.

Usage

```
## S3 method for class 'coords'
range(x, na.rm = FALSE, finite = FALSE, ...)

## S3 method for class 'atoms'
range(x, na.rm = FALSE, finite = FALSE, ...)

## S3 method for class 'pdb'
range(x, na.rm = FALSE, finite = FALSE, ...)
```

Arguments

`x`	an R object containing atomic coordinates.
`na.rm`	logical, indicating if `NA`'s should be omitted.
`finite`	logical, indicating if all non-finite elements should be omitted.
`...`	further arguments passed to or from other methods.

Value

Return a data.frame whose columns contain the range of the first, second and third coordinates of x.

See Also

range, coords, atoms, pdb

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
range(x)
range(range(x))
```

---

read.pdb *PDB File Reader*

Description

Reads a Protein Data Bank (PDB) coordinates file.

Usage

```
read.pdb(
  file,
  ATOM = TRUE,
  HETATM = TRUE,
  CRYSTAL = TRUE,
  CONNECT = TRUE,
  TITLE = TRUE,
  REMARK = TRUE,
  MODEL = 1,
  CRYST1 = NULL,
  resolution = TRUE,
  verbose = TRUE
)
```

Arguments

file	a single element character vector containing the name of the PDB file to be read.
ATOM	a logical value indicating whether to read the ATOM records.
HETATM	a logical value indicating whether to read the HETATM records.
CRYSTAL	a logical value indicating whether to read the crystal cell parameters (from the CRYST1 pdb record).
CONNECT	a logical value indicating whether to read the CONNECT records.

TITLE	a logical value indicating whether to read the TITLE records.
REMARK	a logical value indicating whether to read the REMARK records.
MODEL	an integer vector containing the serial number of the MODEL sections to be read. Can also be equal to NULL to read all the MODEL sections or to NA to ignore MODEL records (see details).
CRYST1	will be replaced by the CRYSTAL argument; existing code should be migrated to use the CRYSTAL argument.
resolution	logical value indicating whether to extract the resolution (see details).
verbose	logical value indicating whether to print additional information, e.g. number of models.

Details

The read.pdb function reads the TITLE, REMARK, ATOM, HETATM, CRYSTAL and CONECT records from a PDB file. Three different reading modes can be used depending on the value of MODEL:

- When MODEL is a vector of integers, MODEL sections whose serial numbers match these integers are read.
- When MODEL == NULL, all MODEL sections are read.
- When MODEL == NA, MODEL records are ignored and all ATOM and/or HETATM records are merged together to return a single object.

When multiple models are specified, each of the models is actually stored as a separate pdb molecule in a list of pdb molecules. If the resolution parameter is set, the function attempts to extract the resolution from the REMARKS field. Note: The resolution is only meaningful for X-ray crystallography.

Value

When a single MODEL section is read, this function returns an object of class 'pdb' (a list with a class attribute equal to pdb) with the following components:

title	a character vector containing the TITLE records found in the PDB file.
remark	a character vector containing the REMARK records found in the PDB file.
crystal	a list of class 'crystal' containing the first CRYSTAL record found in the PDB file. All others are ignored.
atoms	a data.frame of class 'atoms' containing the ATOM and HETATM records found in the PDB file.
connect	a data.frame of class 'connect' containing the CONNECT records found in the PDB file.

When multiple MODEL sections are read, a list of object of class 'pdb' is returned.

References

PDB format has been taken from: http://www.wwpdb.org/documentation/format33/v3.3.html

See Also

write.pdb, pdb, crystal, atoms, connect

Examples

```
# Read a PDB file included with the package
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

# Visualize the PDB file
visualize(x, mode = NULL)

# Write the 'pdb' object 'x' in file "Rpdb.pdb" into the current directory
write.pdb(x, file = "Rpdb.pdb")

# Cleanup
unlink("Rpdb.pdb")
```

---

reindex *Reinitialize Object Indexing*

Description

Reinitialize the indexing of an object.

Usage

```
reindex(...)

## S3 method for class 'atoms'
reindex(x, eleid = TRUE, resid = TRUE, ...)

## S3 method for class 'pdb'
reindex(x, eleid = TRUE, resid = TRUE, ...)
```

Arguments

...	further arguments passed to or from other methods.
x	an R object.
eleid	a single element logical vector indicating if elements IDs have to reindexed.
resid	a single element logical vector indicating if residues IDs have to reindexed.

Details

reindex is a generic function to reinitialize the indexing of an object or its components. The methods for objects of class 'atoms' reinitialize the residue and element IDs starting from 1 and avoiding gaps in the indexes. For objects of class 'pdb' their atoms and connect components are reindexed consistently.

Value

Return an object of the same class as x with updated indexes.

See Also

pdb, atoms, subset.atoms, subset.pdb

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
x <- subset(x, x$atoms$eleid %in% sample(x$atoms$eleid, 10))
print(x)
x <- reindex(x)
print(x)
```

---

replicate *Replicate Atomic Coordinates*

Description

Replicate atomic coordinates using periodic boundary conditions.

Usage

```
replicate(x, ...)

## S3 method for class 'coords'
replicate(x, crystal = NULL, a.ind = 0, b.ind = 0, c.ind = 0, ...)

## S3 method for class 'atoms'
replicate(x, crystal = NULL, a.ind = 0, b.ind = 0, c.ind = 0, ...)

## S3 method for class 'pdb'
replicate(x, a.ind = 0, b.ind = 0, c.ind = 0, crystal = NULL, ...)
```

Arguments

x	an R object containing atomic coordinates to be replicated.
...	further arguments passed to or from other methods.
crystal	an object of class 'crystal' containing periodical boundary conditions used for replicating.
a.ind	a vector of integers indicating the positions of the replicated cells along the a-axis.
b.ind	a vector of integers indicating the positions of the replicated cells along the b-axis.
c.ind	a vector of integers indicating the positions of the replicated cells along the c-axis.

Details

The `replicate` function replicate a unit cell along the lattice vectors a, b and c as as many times as indicated by the `a.ind`, `b.ind` and `c.ind` arguments. Discontinuous integer vectors can be used for `a.ind`, `b.ind` and `c.ind` to create layered supercells (See examples).

Value

Return an object of class 'pdb' with replicated atomic coordinates.

See Also

`coords`, `atoms`, `pdb`, `crystal`

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

# Create a 3x3 supercell
y <- replicate(x, a.ind = 0:2, b.ind = 0:2, c.ind = 0:2)

# Create a 3x3 supercell which might need to be wrapped (if some molecules are outside the cell)
y <- replicate(x, a.ind = -1:1, b.ind = -1:1, c.ind = -1:1)

# Create a layered supercell with a vacuum layer in the bc-plan
y <- replicate(x, a.ind = c(0,2), b.ind = 0:2, c.ind = 0:2)
```

---

rotation *Rotation of Atomic Coordinates*

Description

Rotation of atomic coordinates around a given vector.

Usage

```
R(...)

## S3 method for class 'coords'
R(obj, angle = 0, x = 0, y = 0, z = 1, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
R(obj, angle = 0, x = 0, y = 0, z = 1, mask = TRUE, crystal = obj$crystal, ...)
```

Arguments

...	further arguments passed to or from other methods.
obj	an R object containing atomic coordinates.
angle	the angle of the rotation in degrees.
x	the x-component of the rotation vector.
y	the y-component of the rotation vector.
z	the z-component of the rotation vector.
mask	a logical vector indicating the set of coordinates to which the rotation has to be applyed.
crystal	an object of class 'crystal' used to convert fractional into Cartesian coordinates (when needed).

Details

R is a generic function. Method for objects of class 'coords' first convert the coordinates into Cartesian coordinates using crystal if needed. Once rotated, the coordinates are reconverted back to the original basis set using again crystal. Method for objects of class 'pdb' first extracts coordinates from the object using the function coords, performs the rotation, and updates the coordinates of the 'pdb' object using the function coords<-.

Value

An object of the same class as x with rotated coordinates.

See Also

Helper functions for rotation around a given Cartesian vector:
Rx, Ry, Rz
Passing from Cartesian to fractional coordinates (or Vis Versa):
xyz2abc, abc2xyz

Examples

```
# First lets read a pdb file
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
cell <- cell.coords(x)
visualize(x, mode = NULL)

# Rotation of the structure around the c-axis
visualize(R(x, 90, x=cell["x","c"], y=cell["y","c"], z=cell["z","c"]),
          mode = NULL)
# Rotation of the residue 1 around the c-axis
visualize(R(x, 90, x=cell["x","c"], y=cell["y","c"], z=cell["z","c"], mask = x$atoms$resid == 1),
          mode = NULL)
```

`rotationHelpers` *Helper Functions for Rotation of Atomic Coordinates*

Description

Rotation of atomic coordinates along a specific Cartesian vector.

Usage

```
Rx(...)

## S3 method for class 'coords'
Rx(x, angle = 0, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Rx(x, angle = 0, mask = TRUE, crystal = x$crystal, ...)

Ry(...)

## S3 method for class 'coords'
Ry(x, angle = 0, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Ry(x, angle = 0, mask = TRUE, crystal = x$crystal, ...)

Rz(...)

## S3 method for class 'coords'
Rz(x, angle = 0, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Rz(x, angle = 0, mask = TRUE, crystal = x$crystal, ...)
```

Arguments

`...`	further arguments passed to or from other methods.
`x`	an R object containing atomic coordinates.
`angle`	the angle of the rotation in degrees.
`mask`	a logical vector indicating the set of coordinates to which the rotation has to be applied.
`crystal`	an object of class 'crystal' used to convert fractional into Cartesian coordinates when needed.

Details

These functions are helper functions to perform a rotation around a specific Cartesian vector. All of them call the `R` function.

Value

An object of the same class as x with rotated coordinates.

See Also

R and xyz2abc, abc2xyz for passing from Cartesian to fractional coordinates (or Vis Versa).

Examples

```
# First lets read a pdb file
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
cell <- cell.coords(x)
visualize(x, mode = NULL)

# Rotation of the structure around the z-axis
visualize(Rz(x, 90), mode = NULL)
# Rotation of the residue 1 around the c-axis
visualize(Rz(x, 90, mask = x$atoms$resid == 1), mode = NULL)
```

---

select *Select atoms*

Description

Select groups of atoms from a PDB object.

Usage

```
select(x, id, ...)

## S3 method for class 'pdb'
select(x, id, residue, chain, ...)

## S3 method for class 'atoms'
select(x, id, residue, chain, ...)
```

Arguments

x	an R object containing atoms;
id	an integer vector specifying the id of residues.
...	arguments passed to methods.
residue	a character vector specifying the residues to select.
chain	character vector specifying which chains to process;

Details

select is a generic function, which enables the selection of element IDs from molecules.

Value

`select` returns a vector with the element IDs.

`split.pdb` *Divide and Reassemble 'pdb' Objects*

Description

`split` divides a 'pdb' object by groups of atoms defined by `f`. `unsplit` reverses the effect of `split`.

Usage

```
## S3 method for class 'pdb'
split(x, f, drop = FALSE, ...)

## S3 method for class 'pdb'
unsplit(value, f, drop = FALSE, ...)
```

Arguments

`x`	an object of class 'pdb' to be divided into groups.
`f`	a 'factor' in the sense that `as.factor(f)` defines the grouping, or a list of such factors in which case their interaction is used for the grouping.
`drop`	logical indicating if levels that do not occur should be dropped (if `f` is a `factor` or a list).
`...`	further potential arguments passed to methods.
`value`	a list of 'pdb' objects compatible with a splitting of `x`. Recycling applies if the lengths do not match.

Details

`split` produce a list of 'pdb' objects with the same `crystal`, `title` and `remark` components as `x`. Only its `atoms` component is split while its `connect` component is cleaned to keep only the meaningful connectivity for each 'pdb' object of the list returned by the function. `unlist` produce a 'pdb' object with the same `crystal`, `title` and `remark` components as the first element of `value`. The `atoms` and `connect` components of all the elements of `value` are combined by row.

Value

The value returned from `split` is a list of 'pdb' objects containing the data for the groups of atoms. The components of the list are named by the levels of `f` (after converting to a factor, or if already a factor and `drop=TRUE`, dropping unused levels).
`unsplit` returns a 'pdb' object for which `split(x, f)` equals `value`.

See Also

`split`, `unsplit`, `pdb`

Examples

```
### Split a pdb file by residue IDs and write them into separate files
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

file.names <- paste0(x$atoms$resname, "_", x$atoms$resid, ".pdb")
file.names <- unique(file.names)
pdb.resid  <- split(x, x$atoms$resid)
length(pdb.resid)
useless <- mapply(write.pdb, pdb.resid, file.names)

# Cleanup
unlink(file.names)
```

`subset.atoms` *Subsetting 'atoms' and 'pdb' Objects*

Description

Return subsets of 'atoms' or 'pdb' objects which meet conditions.

Usage

```
## S3 method for class 'atoms'
subset(x, subset, drop = FALSE, reindex.all = TRUE, ...)

## S3 method for class 'pdb'
subset(x, subset, drop = FALSE, reindex.all = TRUE, ...)
```

Arguments

`x`	object to be subsetted.
`subset`	logical expression indicating elements or rows to keep: missing values are taken as false.
`drop`	passed on to [indexing operator.
`reindex.all`	a single element logical vector indicating if residues and elements IDs have to be reindexed after subsetting.
`...`	further arguments to be passed to or from other methods.

Details

For an 'atoms' object the method is similar to the data.frame method (see `subset`) but allow to directly reindex the elements and residues IDs. For a 'pdb' object subsetting is applied on the `atoms` and `connect` components of the object in a consistent way. First the `atoms` component is subsetted and then the `connect` component is filtered to keep only the connectivity for the subset.

Value

Return a subsetted object of the same class as x.

See Also

subset, pdb, atoms, reindex

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
y <- subset(x, x$atoms$eleid %in% sample(x$atoms$eleid, 10))
is(y)
y <- subset(x$atoms, x$atoms$eleid %in% sample(x$atoms$eleid, 10))
is(y)
x <- coords(x)
y <- subset(x, x < 0)
is(y)
```

---

toSymbols *Atomic Symbols Converter*

Description

Converts character strings or atomic numbers into atomic symbols.

Usage

```
toSymbols(x, ...)

## S3 method for class 'integer'
toSymbols(x, ...)

## S3 method for class 'numeric'
toSymbols(x, ...)

## S3 method for class 'character'
toSymbols(x, nletters = 3, na = NA, ...)
```

Arguments

x	a vector to be converted into atomic symbols.
...	further arguments passed to or from other methods.
nletters	an integer used to truncate the character strings before conversion.
na	the default value to use for invalid or missing element symbols.

Details

Each elements of x are converted into atomic symbols.
When x is an integer (or numeric) vector, atomic number are search into the elements data set to find associated atomic symbols.
When x is a character vector, toSymbols first removes all leading and trailing white spaces and numbers. Then translates the first character of the character strings to uppercase and all the others to lowercase. Finally, the character strings are tested for matching with element symbols provided by the elements data set. NA are produced for no matching.

Value

a character vector containing atomic symbols

See Also

elements

Examples

```
x <- c(1:10)
toSymbols(x)

x <- c("C  "," o","h1","1h","UU","SI0","cR")
toSymbols(x)

# 'nletters' can be used to truncate the character strings before
# conversion, if needed:
toSymbols("SIL", nletters=3) # return NA
toSymbols("SIL", nletters=2) # return "Si"
toSymbols("SIL", nletters=1) # return "S"
toSymbols("SIL", nletters=3, na="X") # return "X"
```

---

translate *Graphics Tools*

Description

Tools to modify or set rgl objects, scenes and the observer. translate performs a translation of the observer to a new position specified using relative shifts. trans is an abbreviated alias to function translate.

Usage

```
trans(x, y = 0, z = 0, auto = FALSE)

translate(x, y = 0, z = 0, auto = FALSE)
```

Arguments

x, y, z	amount to shift the observer in the x, y and z directions.
auto	If TRUE, the location will be set automatically by RGL to make the whole bounding box visible. Unfortunately, it may fail, as it seems there are some bugs in rgl.

Value

`translate` returns invisibly the old position of the observer.

`translation` *Translation of Atomic Coordinates*

Description

Translation of Cartesian or fractional coordinates.

Usage

```
Txyz(...)

## S3 method for class 'coords'
Txyz(
  obj,
  x = 0,
  y = 0,
  z = 0,
  mask = TRUE,
  thickness = NULL,
  crystal = NULL,
  ...
)

## S3 method for class 'pdb'
Txyz(
  obj,
  x = 0,
  y = 0,
  z = 0,
  mask = TRUE,
  thickness = NULL,
  crystal = obj$crystal,
  ...
)

Tabc(...)
```

```
## S3 method for class 'coords'
Tabc(
  obj,
  a = 0,
  b = 0,
  c = 0,
  mask = TRUE,
  thickness = NULL,
  crystal = NULL,
  ...
)

## S3 method for class 'pdb'
Tabc(
  obj,
  a = 0,
  b = 0,
  c = 0,
  mask = TRUE,
  thickness = NULL,
  crystal = obj$crystal,
  ...
)
```

Arguments

...	further arguments passed to or from other methods.
obj	an R object containing atomic coordinates.
x	the x-component of the translation vector.
y	the y-component of the translation vector.
z	the z-component of the translation vector.
mask	a logical vector indicating the set of coordinates to which to apply the translation.
thickness	a numeric value indicating the fraction of the thicknees of the selected atom to be added to the translation vector (Usually 0, 0.5 or 1. See details).
crystal	an object of class 'crystal' use to convert Cartesian into fraction coordinates (or Vis Versa) when need.
a	the a-component of the translation vector.
b	the b-component of the translation vector.
c	the c-component of the translation vector.

Details

Txyz and Tabc are generic functions. Method for objects of class 'coords' first convert the coordinates into Cartesian or fractional coordinates using crystal if needed to performed the translation.

Once translated, the coordinates are reconverted back to the original basis set using again `crystal`. Method for objects of class 'pdb' first extract coordinates from the object using the function `coords`, perform the translation, and update the coordinates of the 'pdb' object using the function `coords<-`. The `thickness` argument can be use to translate selected atoms by a fraction of its thickness along the translation direction. This can be use when merging two fragments centered at the origin to build a dimer to avoid atomic overlap and set the inter-fragment distance (see examples).

Value

An object of the same class as `x` with translated coordinates.

See Also

Helper functions for translation along given Cartesian or lattice vector:
`Tx`, `Ty`, `Tz`, `Ta`, `Tb`, `Tc`
Passing from Cartesian to fractional coordinates (or Vis Versa):
`xyz2abc`, `abc2xyz`

Examples

```
# First lets read a pdb file
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, mode = NULL)
visualize(Txyz(x, y=10), mode = NULL)
visualize(Txyz(x, y=10,  mask = x$atoms$resid==1), mode = NULL)
visualize(Tabc(x, b= 1), mode = NULL)
visualize(Tabc(x, b= 1,  mask = x$atoms$resid==1), mode = NULL)

# Lets build a C70/Pentacene dimer with an inter-molecular distance equal to 3.5
C70 <- read.pdb(system.file("examples/C70.pdb", package="Rpdb"))
Pen <- read.pdb(system.file("examples/Pentacene.pdb", package="Rpdb"))
x <- merge(C70, Pen)
visualize(x, mode = NULL)
viewXY()
visualize(Txyz(x, x=0, y=0, z=3.5, mask = x$atoms$resname == "C70", thickness=0.5), mode = NULL)
viewXY()
```

`translationHelpers` *Helper Functions for Translation of Atomic Coordinates*

Description

Translation of atomic coordinates along a specific Cartesian or lattice vector.

Usage

```
Tx(...)

## S3 method for class 'coords'
Tx(obj, x = 0, mask = TRUE, thickness = NULL, crystal = NULL, ...)

## S3 method for class 'pdb'
Tx(obj, x = 0, mask = TRUE, thickness = NULL, crystal = obj$crystal, ...)

Ty(...)

## S3 method for class 'coords'
Ty(obj, y = 0, mask = TRUE, thickness = NULL, crystal = NULL, ...)

## S3 method for class 'pdb'
Ty(obj, y = 0, mask = TRUE, thickness = NULL, crystal = obj$crystal, ...)

Tz(...)

## S3 method for class 'coords'
Tz(obj, z = 0, mask = TRUE, thickness = NULL, crystal = NULL, ...)

## S3 method for class 'pdb'
Tz(obj, z = 0, mask = TRUE, thickness = NULL, crystal = obj$crystal, ...)

Ta(...)

## S3 method for class 'coords'
Ta(obj, a = 0, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Ta(obj, a = 0, mask = TRUE, crystal = obj$crystal, ...)

Tb(...)

## S3 method for class 'coords'
Tb(obj, b = 0, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Tb(obj, b = 0, mask = TRUE, crystal = obj$crystal, ...)

Tc(...)

## S3 method for class 'coords'
Tc(obj, c = 0, mask = TRUE, crystal = NULL, ...)

## S3 method for class 'pdb'
Tc(obj, c = 0, mask = TRUE, crystal = obj$crystal, ...)
```

Arguments

...	further arguments passed to or from other methods.
obj	an R object containing atomic coordinates.
x	the x-component of the translation vector.
mask	a logical vector indicating the set of coordinates to which to apply the translation.
thickness	a numeric value indicating the fraction of the thicknees of the selected atom to be added to the translation vector (Usually 0, 0.5 or 1. See details).
crystal	an object of class 'crystal' used to convert Cartesian into fractional coordinates (or Vice Versa) when need.
y	the y-component of the translation vector.
z	the z-component of the translation vector.
a	the a-component of the translation vector.
b	the b-component of the translation vector.
c	the c-component of the translation vector.

Details

These functions are helper functions to perform a translation along a specific Cartesian or lattice vector. All of them call either the Txyz or Tabc function.

Value

An object of the same class as x with translated coordinates.

See Also

Txyz, Tabc
Passing from Cartesian to fractional coordinates (or Vis Versa):
xyz2abc, abc2xyz

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, mode = NULL)
visualize(Ty(x, 10), mode = NULL)
visualize(Ty(x, 10, mask = x$atoms$resid==1), mode = NULL)
visualize(Tb(x, 1 ), mode = NULL)
visualize(Tb(x, 1 , mask = x$atoms$resid==1), mode = NULL)

# Lets build a C70/Pentacene dimer with an inter-molecular distance equal to 3.5
C70 <- read.pdb(system.file("examples/C70.pdb", package="Rpdb"))
Pen <- read.pdb(system.file("examples/Pentacene.pdb", package="Rpdb"))
x <- merge(C70, Pen)
visualize(x, mode = NULL)
viewXY()
visualize(Tz(x, z=3.5, mask = x$atoms$resname == "C70", thickness=0.5), mode = NULL)
```

```
viewXY()
```

`universalConstants` *Universal Constants*

Description

This data set provides various universal constants

Format

A data frame containing for each universal constant the following information.

`Quantity` a character vector containing a short description of the constants.

`Value` a numeric vector containing the value of the constants.

`Unit` a character vector indicating the unit of the constants.

Source

http://www.ebyte.it/library/educards/constants/ConstantsOfPhysicsAndMath.html

Examples

```
# Data for the speed of light
universalConstants["c",]

# Return the speed of light in m.s-1
universalConstants["c","Value"]

# Return the Planck constant in J.s
universalConstants["h","Value"]
```

`unsplit` *Reassemble Groups*

Description

`unsplit` reverses the effect of `split`.

Usage

```
unsplit(value, f, drop = FALSE, ...)

## Default S3 method:
unsplit(value, f, drop = FALSE, ...)
```

Arguments

value	a list of vectors or data frames compatible with a splitting of x. Recycling applies if the lengths do not match.
f	a 'factor' in the sense that as.factor(f) defines the grouping, or a list of such factors in which case their interaction is used for the grouping.
drop	logical indicating if levels that do not occur should be dropped (if f is a factor or a list).
...	further potential arguments passed to methods.

Details

unsplit is a generic functions with a default method (Method dispatch takes place based on the class of the first element of value) working with lists of vectors or data frames (assumed to have compatible structure, as if created by split). It puts elements or rows back in the positions given by f. In the data frame case, row names are obtained by unsplitting the row name vectors from the elements of value.
f is recycled as necessary and if the length of x is not a multiple of the length of f a warning is printed.
Any missing values in f are dropped together with the corresponding values of x.

Value

Returns a vector or data frame for which split(x, f) equals value

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

cut to categorize numeric values.
strsplit to split strings.

Examples

```
require(stats); require(graphics)
n <- 10; nn <- 100
g <- factor(round(n * runif(n * nn)))
x <- rnorm(n * nn) + sqrt(as.numeric(g))
xg <- split(x, g)
boxplot(xg, col = "lavender", notch = TRUE, varwidth = TRUE)
sapply(xg, length)
sapply(xg, mean)

### Calculate 'z-scores' by group (standardize to mean zero, variance one)
z <- unsplit(lapply(split(x, g), scale), g)

# or
```

```
zz <- x
split(zz, g) <- lapply(split(x, g), scale)

# and check that the within-group std dev is indeed one
tapply(z, g, sd)
tapply(zz, g, sd)


### Data frame variation

# Notice that assignment form is not used since a variable is being added

g <- airquality$Month
l <- split(airquality, g)
l <- lapply(l, transform, Oz.Z = scale(Ozone))
aq2 <- unsplit(l, g)
head(aq2)
with(aq2, tapply(Oz.Z,  Month, sd, na.rm=TRUE))


### Split a matrix into a list by columns
ma <- cbind(x = 1:10, y = (-4:5)^2)
split(ma, col(ma))

split(1:10, 1:2)
```

`vectorialOperations` *Basic Vectorial Operations*

Description

Basic vectorial operations such as scalar product and vectorial product

Usage

```
dotProd(U, V)

vectNorm(U)

rotVect(U, n = 1)

vectProd(U, V)
```

Arguments

`U`	a numeric vector of length 3.
`V`	a numeric vector of length 3.
`n`	an integer.

Value

- `dotProd` return a single element numeric vector.
- `vectNorm` return a single element numeric vector.
- `rotVect` return a numeric vector of length 3.
- `vectProd` return a numeric vector of length 3.

See Also

`matmult`

Examples

```
Vx <- c(3,0,0)
vectNorm(Vx)
Vx <- Vx / vectNorm(Vx)
Vy <- c(0,1,0)
Vz <- vectProd(Vx, Vy)
print(Vz)
```

---

viewAxis *Set the View of the 'rgl' Scene*

Description

Set the view of the current 'rgl' scene aligning one vector perpendicularly to the screen and placing another one in the horizontal plane.

Usage

```
viewAxis(V1, V2)

viewXY()

viewYZ()

viewZX()

viewAB(crystal)

viewBC(crystal)

viewCA(crystal)

viewInertia(x, m = NULL)
```

Arguments

V1	a length 3 numeric vector.
V2	a length 3 numeric vector.
crystal	an object of class 'crystal'.
x	an R object containing atomic coordinates.
m	a numeric vector containing atomic masses.

Details

viewAxis set the view of the current rgl scene (by setting UserMatrix; see par3d for more details) so that V1 is perpendicular to the screen and V2 is in the horizontal plane. The other functions documented here are helper functions calling viewAxis to set the view using particular Cartesian or lattice vectors. For functions viewAB, viewBC and viewCA a 'crystal' object has to be specified to define the lattice vectors used to set the view. The function viewInertia computes the inertia tensor from the atomic coordinates and masses (see inertia) and sets the view to its eigen vectors basis set.

Value

No return value, called for side effects.

See Also

visualize, cell.coords, par3d, rgl.open

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, mode = NULL)
viewAB(x$crystal)

C70 <- read.pdb(system.file("examples/C70.pdb", package="Rpdb"))
visualize(C70, mode = NULL)
viewXY()
viewInertia(C70)
```

---

visualize *Visualize a Molecular Structure*

Description

Use the rgl library to visualize in 3D a molecular structure.

Usage

```
windowRect0()

visualize(...)

## S3 method for class 'coords'
visualize(
  x,
  elename = NULL,
  crystal = NULL,
  connect = NULL,
  mode = NULL,
  type = "l",
  xyz = NULL,
  abc = NULL,
  pbc.box = NULL,
  lwd = 2,
  lwd.xyz = lwd,
  lwd.abc = lwd,
  lwd.pbc.box = lwd,
  cex.xyz = 2,
  cex.abc = 2,
  col = NULL,
  bg = "#FAFAD2",
  radii = "rvdw",
  scale.atoms = 1,
  add = FALSE,
  windowRect = c(0, 0, 800, 600),
  FOV = 0,
  userMatrix = diag(4),
  scale.box = 1,
  scale.axis = scale.box,
  alpha.box = 0.25,
  ...
)

## S3 method for class 'data.frame'
visualize(
  x,
  elename = NULL,
  crystal = NULL,
  connect = NULL,
  mode = NULL,
  type = "l",
  xyz = NULL,
  abc = NULL,
  pbc.box = NULL,
  lwd = 2,
```

```
  lwd.xyz = lwd,
  lwd.abc = lwd,
  lwd.pbc.box = lwd,
  cex.xyz = 2,
  cex.abc = 2,
  col = NULL,
  bg = "#FAFAD2",
  radii = "rvdw",
  add = FALSE,
  windowRect = c(0, 0, 800, 600),
  FOV = 0,
  userMatrix = diag(4),
  ...
)

## S3 method for class 'matrix'
visualize(
  x,
  elename = NULL,
  crystal = NULL,
  connect = NULL,
  mode = NULL,
  type = "l",
  xyz = NULL,
  abc = NULL,
  pbc.box = NULL,
  lwd = 2,
  lwd.xyz = lwd,
  lwd.abc = lwd,
  lwd.pbc.box = lwd,
  cex.xyz = 2,
  cex.abc = 2,
  col = NULL,
  bg = "#FAFAD2",
  radii = "rvdw",
  add = FALSE,
  windowRect = c(0, 0, 800, 600),
  FOV = 0,
  userMatrix = diag(4),
  ...
)

## S3 method for class 'atoms'
visualize(
  x,
  crystal = NULL,
  connect = NULL,
  mode = NULL,
```

```
  type = "l",
  xyz = NULL,
  abc = NULL,
  pbc.box = NULL,
  lwd = 2,
  lwd.xyz = lwd,
  lwd.abc = lwd,
  lwd.pbc.box = lwd,
  cex.xyz = 2,
  cex.abc = 2,
  col = NULL,
  bg = "#FAFAD2",
  radii = "rvdw",
  scale.atoms = 1,
  add = FALSE,
  windowRect = NULL,
  FOV = 0,
  userMatrix = diag(4),
  alpha.box = 0.25,
  ...
)

## S3 method for class 'pdb'
visualize(
  x,
  mode = NULL,
  type = "l",
  xyz = NULL,
  abc = NULL,
  pbc.box = NULL,
  lwd = 2,
  lwd.xyz = lwd,
  lwd.abc = lwd,
  lwd.pbc.box = lwd,
  cex.xyz = 2,
  cex.abc = 2,
  col = NULL,
  bg = "#FAFAD2",
  radii = "rvdw",
  scale.atoms = 1,
  add = FALSE,
  windowRect = NULL,
  FOV = 0,
  userMatrix = diag(4),
  ...
)

## S3 method for class 'character'
```

```
visualize(
  x,
  mode = NULL,
  type = "l",
  xyz = NULL,
  abc = NULL,
  pbc.box = NULL,
  lwd = 2,
  lwd.xyz = lwd,
  lwd.abc = lwd,
  lwd.pbc.box = lwd,
  cex.xyz = 2,
  cex.abc = 2,
  col = NULL,
  bg = "#FAFAD2",
  radii = "rvdw",
  add = FALSE,
  windowRect = NULL,
  FOV = 0,
  userMatrix = diag(4),
  ...
)
```

Arguments

...	further arguments passed to or from other methods.
x	an object or the name of a PDB file containing the molecular structure to visualize.
elename	a character vector containing the atomic names used to chose atom colors and radii.
crystal	an object of class 'crystal'. See crystal
connect	an object of class 'connect'. See connect
mode	a single element character vector indicating the visualization mode (See details).
type	a character string indicating the visualization style (See details).
xyz	a logical value indicating whether the x, y and z axes have to be added to the scene. See details.
abc	a logical value indicating whether the a, b and c axes have to be added to the scene. See details.
pbc.box	a logical value indicating whether the pbc box has to be added to the scene. See details.
lwd	a numeric value indication the line width used to plot the axes, the pbc box and atomic bonds when type = "l" (see details).
lwd.xyz	a numeric value indicating the line width used to plot the x, y and z axes.
lwd.abc	a numeric value indicating the line width used to plot the a, b and c axes.
lwd.pbc.box	a numeric value indicating the line width used to plot the pbc box.

cex.xyz	a numeric value indicating the magnification used to plot the labels of the x, y and z axes.
cex.abc	a numeric value indicating the magnification used to plot the labels of the a, b and c axes.
col	a vector indicating the colors to use to plot each atom.
bg	the color of the background
radii	either a character string indicating the type of radii or a numeric vector specifying the radii of each atom to use to plot atoms as spheres (see details).
scale.atoms	scalar value by which to scale the radii.
add	a logical value indicating whether the plot has be to added to a existing scene (see rgl.cur and open3d).
windowRect	a vector of four integers indicating the left, top, right and bottom of the displayed window in pixels (see par3d).
FOV	the field of view. This controls the degree of parallax in the perspective view (see par3d).
userMatrix	a 4 by 4 matrix describing user actions to display the scene (see par3d).
scale.box	scalar value or numeric vector used to scale the PBC box.
scale.axis	scalar value or numeric vector used to scale the axis-vectors.
alpha.box	a logical value specifying the transparency of the box-lines;

Details

Three different visualization styles are allowed.

- When type="p": Points are drawn at each atomic positions (very light visualization mode).
- When type="l": Lines are drawn between bonded atoms. The connectivity of the system has to be specifyed.
- When type="s": Spheres are drawn at each atomic positions (heavy visualization mode).
  The radii of the spheres are given by radii.
  - When radii="rcov": Covalent radii, taken from the elements data set, are used.
  - When radii="rvdw": Van der Waals radii, taken from the elements data set, are used.
  - When radii is a numeric vector: The numeric values are used to assign to each atom a radius. If length(radii) != natom(pdb) radii is recycled.

When xyz, abc or pbc.box are NULL, the axis or pbc box are are added depending if a 'crystal' object can be found.
Two different interactive visualization modes are avalable:

- When mode="measure": bond lengths, angles and dihedrals can be measured by **right-clicing** on the atoms.
- When mode="info": atomic labels can be added to the scene by **right-clicing** on the atoms. The labels are as follow: "ResidResname:EleidElename"

When mode=NULL the interactive mode is disabled. To escape the interactive mode press the ESC key.

Value

Return (using invisible) a two-column data.frame containing the IDs and type indicators of the objects added to the scene.

See Also

addXYZ, addABC, addPBCBox, par3d, select3d, measure, info3d

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
visualize(x, type = "l", mode = NULL)
visualize(x, type = "s", radii = "rcov", mode = NULL)
visualize(x, type = "s", radii = "rvdw", mode = NULL)
visualize(x, type = "p", mode = NULL)
visualize(subset(x, resid != 1), type = "l", mode = NULL)
visualize(subset(x, resid == 1), type = "s", add = TRUE, mode = NULL)

### Protein BackBone + Surface
# x = some protein (1 chain);
# visualize(x, type="l", lwd=4)
# visualize(x, type="s", alpha = 0.05, add = TRUE)
```

---

wrap *Wrap Atomic Coordinates*

Description

Wraps atomic coordinates using periodic boundary conditions.

Usage

```
wrap(x, ...)

## S3 method for class 'coords'
wrap(x, crystal = NULL, factor = NULL, ...)

## S3 method for class 'atoms'
wrap(x, crystal = NULL, factor = NULL, ...)

## S3 method for class 'pdb'
wrap(x, crystal = x$crystal, factor = NULL, ...)
```

Arguments

x	an R object containing atomic coordinates to be wrapped.
...	further arguments passed to or from other methods.

crystal	an object of class 'crystal' containing periodic boundary conditions used for wrapping.
factor	a factor used to wrap the atoms by groups.

Details

The wrap function translates all atoms out of the unit cell back into the unit cell using periodic boundary conditions. To do so, the wrap function first converts Cartesian into fractional coordinates. Then atoms with fractional coordinates greater than 1 or lower than 0 are respectively translated by -1 or +1. Finally, if the original atomic coordinates were Cartesian coordinates their are reconverted into Cartesian coordinates.

Value

Return an object of class 'pdb' with wrapped atomic coordinates.

See Also

coords, atoms, pdb, crystal, centres.pdb, xyz2abc

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

# Translation of the atoms along x-axis
x$atoms$x1 <- x$atoms$x1 + 10

# Wrapping the structure
y <- wrap(x)
```

---

write.pdb *PDB File Writer*

Description

Writes a Protein Data Bank (PDB) coordinate file from an object of class 'pdb'.

Usage

```
write.pdb(x, file = "Rpdb.pdb")
```

Arguments

x	an object, or a list of objects, of class 'pdb'.
file	a single element character vector containing the name of the PDB file to be created.

Details

All data stored in the 'pdb' object are written to a PDB file. A list of objects of class 'pdb' can be provided to write multiple MODEL data into a single file. In this case, each 'pdb' object of the list must have the same `crystal` and `connect` components.
To write only a subset of a 'pdb' object see function `subset.pdb`.

Value

No return value, called for side effects.

References

PDB format is described at: http://www.wwpdb.org/documentation/format33/v3.3.html

See Also

`read.pdb`, `pdb`, `crystal`, `atoms`, `connect`, `subset.pdb`

Examples

```
# Read a PDB file included with the package
pdb <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))

# Write the pdb object to file "Rpdb.pdb" in the current directory
write.pdb(pdb, file = "Rpdb.pdb")

# Cleanup
unlink("Rpdb.pdb")
```

---

xyz2abc *From Cartesian to Fractional Coordinates and Vice Versa*

Description

Converts Cartesian coordinates into fractional coordinates and vice versa.

Usage

```
xyz2abc(...)

## S3 method for class 'coords'
xyz2abc(x, crystal, ..., cryst1 = NULL)

## S3 method for class 'atoms'
xyz2abc(x, crystal, ...)

## S3 method for class 'pdb'
```

```
xyz2abc(x, crystal = x$crystal, ..., cryst1 = NULL)

## S3 method for class 'distances'
xyz2abc(x, crystal, ...)

abc2xyz(...)

## S3 method for class 'coords'
abc2xyz(x, crystal, ..., cryst1 = NULL)

## S3 method for class 'atoms'
abc2xyz(x, crystal, ...)

## S3 method for class 'pdb'
abc2xyz(x, crystal = x$crystal, ..., cryst1 = NULL)

## S3 method for class 'distances'
abc2xyz(x, crystal, ...)
```

Arguments

...	arguments passed to methods.
x	an R object containing atomic coordinates.
crystal	an object of class crystal.
cryst1	will be deprecated; use crystal instead.

Details

For atoms and pdb objects, the atomic coordinates are first extracted from x using the coords function. Then, using the periodic boundary conditions stored into crystal, the coordinates are converted from Cartesian to fractional (for the xyz2abc functions) or from fractional to Cartesian (for the abc2xyz functions) coordinates. Finally, for atoms and pdb objects, the new atomic coordinates are reassigned to the original x object using the coords<- function and x is returned.

Value

Return an object of the same class as x, with atomic coordinates expressed in a different basis set.

See Also

basis, coords, atoms, pdb, crystal

Examples

```
x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
basis(x)
x <- xyz2abc(x)
basis(x)
x <- abc2xyz(x)
```

```
basis(x)


  # This example returns an error because the coordinates stored
  # into the PDB file are already Cartesian coordinates.
  x <- read.pdb(system.file("examples/PCBM_ODCB.pdb", package="Rpdb"))
  try(x <- abc2xyz(x))
```

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