Package ‘DCODE’

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Type Package

Title List Linear n-Peptide Constraints for Overlapping Protein Regions

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**Description**

Traversal graph algorithm for listing linear n-peptide constraints for overlapping protein regions.

**Author(s)**

S. Lebre

Maintainer: S. Lebre <sophie.lebre@umontpellier.fr>

**References**


**Examples**

```R
## Not run:
# 1) Build peptideList, used by function getConstraint.
mydata <- build_data()
aalist <- mydata$aaList
geneticCode <- mydata$geneticCode
peptidelist <- mydata$peptidelist

# 2) Ask for the constraint induced on a chosen peptide in a chosen overlapping frame

## amino acid contraints
getConstraint("C", frame = -2, code=geneticCode, pepList=peptidelist)
getConstraint("D", frame = 1, code=geneticCode, pepList=peptidelist)

## 3-peptide contraints
getConstraint("CWC", frame = -2, code=geneticCode, pepList=peptidelist)

## 5-peptide contraints
getConstraint("CWCCC", frame = -2, code=geneticCode, pepList=peptidelist)

## End(Not run)
```
build_data  

Function to build the elements aalist, geneticCode, peptideList, used by function getConstraint.

Description

To be run before the first use of function getConstraint. This function generates the variables aalist, geneticCode and peptideList, a list of all the peptides (up to length 5), used by function getConstraint.

Usage

build_data()

Value

- **aalist**: Vector of all amino acids.
- **geneticCode**: A list describing the standard genetic code.
- **peptideList**: A list of all the peptides (up to length 5).

Author(s)

Sophie Lebre <sophie.lebre@umontpellier.fr>

References


See Also

getConstraint

Examples

```r
## Not run:
# 1) Build peptideList, used by function getConstraint.
mydata <- build_data()
aaList <- mydata$aaList
geneticCode <- mydata$geneticCode
peptideList <- mydata$peptideList

# 2) Ask for the constraint induced on a chosen peptide in a chosen overlapping frame

## amino acid contraints
getConstraint("C", frame = -2, code=geneticCode, pepList=peptideList)
getConstraint("D", frame = 1, code=geneticCode, pepList=peptideList)
```
### Internal DCODE Functions

#### Description

Internal DCODE functions

#### Details

These are not to be called by the user (or in some cases are just waiting for proper documentation to be written).

#### getConstraint

Function giving the linear constraint associated with the chosen peptide and overlapping frame.

#### Description

This function prints the linear constraint to which the chosen peptide in the reference frame pep is subject when considering gene overlap with frameshift frame.

#### Usage

getConstraint(pep, frame, code, pepList)

#### Arguments

- **pep**: A chosen n-peptide in the reference frame (with length n<=5 if pepList is generated by function build_data).
- **frame**: The frameshift chosen in {-2, -1, 0, 1, 2}.
- **code**: The code used to translate codons into amino acids (which can be generated by function build_data).
- **pepList**: A list of all the peptide of length 1, 2, 3, ...required by the graph traversal algorithm (which can be generated by function build_data).

#### Author(s)

Sophie Lebre <sophie.lebre@umontpellier.fr>
getConstraint

References

See Also
build_data

Examples

# Not run:
# 1) Build peptideList, used by function getConstraint.
mydata <- build_data()
aaList <- mydata$aaList
geneticCode <- mydata$geneticCode
peptidelist <- mydata$peptidelist

# 2) Ask for the constraint induced on a chosen peptide in a chosen overlapping frame

# amino acid contraints
getConstraint("C", frame = -2, code = geneticCode, pepList = peptidelist)
getConstraint("D", frame = 1, code = geneticCode, pepList = peptidelist)

# 3-peptide contraints
getConstraint("CWC", frame = -2, code = geneticCode, pepList = peptidelist)

# 5-peptide contraints
getConstraint("CWCCC", frame = -2, code = geneticCode, pepList = peptidelist)

# End(Not run)
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