

# Package ‘DCODE’

March 10, 2016

**Type** Package

**Title** List Linear n-Peptide Constraints for Overlapping Protein Regions

**Version** 1.0

**Date** 2016-03-10

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**Maintainer** Sophie Lebre <sophie.lebre@umontpellier.fr>

**Depends** R (>= 3.1.0), seqinr

**Description** Traversal graph algorithm for listing linear n-peptide constraints for overlapping protein regions. (Lebre and Gascuel, The combinatorics of overlapping genes, freely available from arXiv at : <http://arxiv.org/abs/1602.04971>).

**License** GPL (>= 2)

**LazyLoad** yes

**LazyData** no

**NeedsCompilation** no

**Repository** CRAN

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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**

Lebre and Gascuel, The combinatorics of overlapping genes (freely available from arXiv at: <http://arxiv.org/abs/1602.04971>).

**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 constraints
getConstraint("C", frame = -2, code=geneticCode, pepList=peptideList)
getConstraint("D", frame = 1, code=geneticCode, pepList=peptideList)

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

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

## End(Not run)
```

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build_data	<i>Function to build the elements aaList, geneticCode, peptideList, used by function <a href="#">getConstraint</a>.</i>
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### 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

Lebre and Gascuel, The combinatorics of overlapping genes (freely available from arXiv at: <http://arxiv.org/abs/1602.04971>).

### See Also

[getConstraint](#)

### 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 constraints
getConstraint("C", frame = -2, code=geneticCode, pepList=peptideList)
getConstraint("D", frame = 1, code=geneticCode, pepList=peptideList)
```

```

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

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

## End(Not run)

```

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DCODE-internal            *Internal DCODE Functions*

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### 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).

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

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### 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 $n \leq 5$ if pepList is generated by function <code>build_data</code> ).
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 <code>build_data</code> ).
pepList	A list of all the peptide of length 1, 2, 3, ...required by the graph traversal algorithm (which can be generated by function <code>build_data</code> ).

### Author(s)

Sophie Lebre <sophie.lebre@umontpellier.fr>

**References**

Lebre and Gascuel, The combinatorics of overlapping genes (freely available from arXiv at: <http://arxiv.org/abs/1602.04971>).

**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 constraints
getConstraint("C", frame = -2, code=geneticCode, pepList=peptideList)
getConstraint("D", frame = 1, code=geneticCode, pepList=peptideList)

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

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

## End(Not run)
```

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