

## Annotation comparison Vetea Jacot

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# Chapter 1

## Namespace Index

### 1.1 Namespace List

Here is a list of all documented namespaces with brief descriptions:

<a href="#">CDScompR</a>	This script is used to compute the distance between two structural annotations of a same genome, one reference and one alternative annotation . . . . .	5
<a href="#">CDSmulticompR</a>	This script is used to compute the distance between multiple structural annotations of a same genome, one reference and one or more alternative annotations . . . . .	7



## Chapter 2

# Class Index

### 2.1 Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

<a href="#">cluster.Cluster</a>	This class represents clusters of overlapping loci computed by the function <code>construct_clusters</code> .	9
<a href="#">locus.Locus</a>	This class represents an annotation's locus identified from reading the associated GFF file with the <code>get_gff_borders</code> function . . . . .	13
<a href="#">intervals_utils.OrderedIntervals</a>	This class represents a list of intervals and implements multiple basic operations between intervals . . . . .	16



## Chapter 3

# Namespace Documentation

### 3.1 CDScompR Namespace Reference

This script is used to compute the distance between two structural annotations of a same genome, one reference and one alternative annotation.

#### Functions

- def `write_results` (all\_results, alt\_name, verbose=False)  
*This function writes to a new 'results.csv' file the results of the annotation comparison retrieved from the identities dictionary returned by the `annotation_match` function.*
- def `annotation_comparison` (ref\_path, alt\_path, verbose=False, create\_strings=False, exon\_mode=False)  
*Main function of this program.*
- def `usage` ()
- def `main` ()

#### 3.1.1 Detailed Description

This script is used to compute the distance between two structural annotations of a same genome, one reference and one alternative annotation.

It expects as input the paths to the annotation files (in GFF format), displays the computed distances between all annotation pairs, and creates a results CSV file detailing the loci comparisons between the annotations

#### 3.1.2 Function Documentation

##### 3.1.2.1 `annotation_comparison()`

```
def CDScompR.annotation_comparison (  
    ref_path,  
    alt_path,  
    verbose = False,  
    create_strings = False,  
    exon_mode = False )
```

Main function of this program.

Given a reference and alternative path, gets the corresponding GFF files and compares the two annotations to return their information about their loci's comparison

**Parameters**

<i>ref_path</i>	Path of the GFF file describing the reference annotation
<i>alt_path</i>	Path of the GFF file describing the alternative annotation
<i>verbose</i>	If True, triggers display of more information messages. Default is 'False'
<i>create_strings</i>	Boolean indicating whether to use the 'old' comparison function (old_compare_loci, 'True') or the new one (compare_loci, 'False')
<i>exon_mode</i>	Boolean indicating if the main comparison structures read from the file should be coding sequences (CDS, False) or exons (True). Default is 'False' (CDS comparison)

**See also**

compare\_loci()  
old\_compare\_loci()

**Returns**

Returns a list of lists of dictionaries describing the comparison of the structure identity between the loci of each annotation

**3.1.2.2 write\_results()**

```
def CDScompR.write_results (
    all_results,
    alt_name,
    verbose = False )
```

This function writes to a new 'results.csv' file the results of the annotation comparison retrieved from the identities dictionary returned by the annotation\_match function.

**See also**

annotation\_match()

**Parameters**

<i>results</i>	A dictionary of list of list of dictionaries containing results of the annotation comparison, as returned by annotation_match
<i>alt_name</i>	String indicating the name of the original alternative annotation file
<i>verbose</i>	If True, triggers display of more information messages. Default is 'False'

**See also**

annotation\_match()

**Remarks**

Results are written in CSV ('Comma-Separated Values') format

## 3.2 CDSmulticompR Namespace Reference

This script is used to compute the distance between multiple structural annotations of a same genome, one reference and one or more alternative annotations.

### Functions

- def **result\_to\_dict** (result)
- def **write\_multi\_results** (multi\_results, ref\_path, alt\_paths)
 

*Writes the results returned by the function multicomp into a results synthesis CSV file detailing the loci identity for each alternative.*
- def **multicomp** (ref\_path, alt\_paths, verbose, create\_strings, exon\_mode)
 

*Compares all alternative annotations given (alt\_paths) to the reference annotation (ref\_path) by calling annotation↔\_sort and appends the results dictionaries to a list.*
- def **usage** ()
- def **main** ()

### 3.2.1 Detailed Description

This script is used to compute the distance between multiple structural annotations of a same genome, one reference and one or more alternative annotations.

It expects as input the paths to the annotation files (in GFF format), displays the computed distances between all annotation pairs, and creates results CSV files for each alternative and one global synthesis file

### 3.2.2 Function Documentation

#### 3.2.2.1 multicomp()

```
def CDSmulticompR.multicomp (
    ref_path,
    alt_paths,
    verbose,
    create_strings,
    exon_mode )
```

Compares all alternative annotations given (alt\_paths) to the reference annotation (ref\_path) by calling annotation↔\_sort and appends the results dictionaries to a list.

See also

annotation\_sort()

#### Parameters

<i>ref_path</i>	Path to the reference annotation file
<i>alt_path</i>	Path to the alternative annotation file
<i>verbose</i>	If True, triggers display of more information messages. Default is 'False'
<i>create_strings</i>	Boolean indicating wether to use the 'old' comparison function (old_compare_loci, 'True') or the new one (compare_loci, 'False')
<i>exon_mode</i>	Boolean indicating if the main comparison structures read from the file should be coding (CDS-Exon) or non-coding (CDS-Int). Default is 'False' (CDS-Int)

**See also**

`compare_loci()`  
`old_compare_loci()`

**Returns**

Returns the list of all results dictionaries of all alternatives

**3.2.2.2 write\_multi\_results()**

```
def CDSmulticompR.write_multi_results (
    multi_results,
    ref_path,
    alt_paths )
```

Writes the results returned by the function multicomp into a results synthesis CSV file detailing the loci identity for each alternative.

**See also**

[multicomp\(\)](#)

**Parameters**

<i>multi_results</i>	List of results dictionaries, as returned by multicomp
<i>ref_path</i>	Path to the reference annotation GFF file

## Chapter 4

# Class Documentation

### 4.1 cluster.Cluster Class Reference

This class represents clusters of overlapping loci computed by the function `construct_clusters`.

#### Public Member Functions

- `def __init__ (self, name, loci=None, end=-1)`  
*This method initialises the class.*
- `def get_loci (self)`  
*Retrieves the 'loci' attribute of the instance.*
- `def append_to_loci (self, annotation, value)`  
*Appends the given value to the list of the given annotation in the 'loci' attribute.*
- `def get_end (self)`  
*Retrieves the 'end' attribute of the instance.*
- `def set_end (self, value)`  
*Sets the given value as the 'end' attribute.*
- `def get_mRNAs (self, loc_id, ref)`  
*This method is used to retrieve the complete list of mRNAs of the locus of the cluster specified with its locus ID and a boolean indicating if the locus is to be searched for in the reference or alternative list.*
- `def get_details (self)`  
*Retrieves the class instance's 'loci' attribute as a human-readable dictionary of lists detailing each locus' mRNAs.*

#### Public Attributes

- `name`  
*name of the cluster*
- `loci`  
*list of Locus class instances present in the cluster*
- `end`  
*end coordinate of the cluster.*

### 4.1.1 Detailed Description

This class represents clusters of overlapping loci computed by the function `construct_clusters`.

It possesses only three attributes: 'loci', which is a dictionary of lists of instances of the class 'Locus' indicating the loci attributed to each cluster; 'name'; and 'end' which is the end coordinate of the last loci of the cluster

See also

`construct_clusters()`  
 Locus

### 4.1.2 Constructor & Destructor Documentation

#### 4.1.2.1 `__init__()`

```
def cluster.Cluster.__init__ (
    self,
    name,
    loci = None,
    end = -1 )
```

This method initialises the class.

Parameters

<i>name</i>	(optional) the name of the cluster
<i>loci</i>	(optional) the lists of loci for the cluster of the reference and alternative annotations, as a dictionary of lists
<i>end</i>	(optional) the end coordinate of the last locus of the cluster

### 4.1.3 Member Function Documentation

#### 4.1.3.1 `append_to_loci()`

```
def cluster.Cluster.append_to_loci (
    self,
    annotation,
    value )
```

Appends the given value to the list of the given annotation in the 'loci' attribute.

Parameters

<i>annotation</i>	string ('ref' or 'alt') indicating the origin of the value
<i>value</i>	Value to append to the 'loci' attribute

#### 4.1.3.2 get\_details()

```
def cluster.Cluster.get_details (
    self )
```

Retrieves the class instance's 'loci' attribute as a human-readable dictionary of lists detailing each locus' mRNAs.

##### Returns

Returns a dictionary of list detailing the content of the instance's 'loci' attribute

#### 4.1.3.3 get\_end()

```
def cluster.Cluster.get_end (
    self )
```

Retrieves the 'end' attribute of the instance.

##### Returns

Returns the 'end' attribute of the class instance

#### 4.1.3.4 get\_loci()

```
def cluster.Cluster.get_loci (
    self )
```

Retrieves the 'loci' attribute of the instance.

##### Returns

Returns the 'loci' attribute of the class instance

#### 4.1.3.5 get\_mRNAs()

```
def cluster.Cluster.get_mRNAs (
    self,
    loc_id,
    ref )
```

This method is used to retrieve the complete list of mRNAs of the locus of the cluster specified with its locus ID and a boolean indicating if the locus is to be searched for in the reference or alternative list.

**Parameters**

<i>loc</i> <sub>↔</sub> <i>_id</i>	Identifier of the locus from which to retrieve mRNAs
<i>ref</i>	Boolean indicating from which of the reference (True) or alternative (False) locus to retrieve the mRNAs

**Returns**

Returns the list of all mRNAs of the specified locus

**Remarks**

This method is intended to be used in unit tests to verify the clusters contains the intended loci

**4.1.3.6 set\_end()**

```
def cluster.Cluster.set_end (
    self,
    value )
```

Sets the given value as the 'end' attribute.

**Parameters**

<i>value</i>	Value to give to the 'end' attribute of the class instance
--------------	--

**4.1.4 Member Data Documentation****4.1.4.1 end**

```
cluster.Cluster.end
```

end coordinate of the cluster.

Equal to the end coordinate of the last cluster's locus

The documentation for this class was generated from the following file:

- /home/runner/work/CDScompR/CDScompR/script/cluster.py

## 4.2 locus.Locus Class Reference

This class represents an annotation's locus identified from reading the associated GFF file with the `get_gff_borders` function.

### Public Member Functions

- `def __init__ (self, name="", mRNAs=None, start=-1, end=-1, direction="")`  
*This method initialises the class with default values for each attribute.*
- `def mRNAs (self)`  
*This method is used to retrieve the 'mRNAs' attribute of an instance.*
- `def set_mRNAs (self, value)`  
*Sets the value of the 'mRNAs' attribute of the class instance.*
- `def contain_mrnas (self, **mrnas)`  
*This method is used to verify if all mRNAs of a dictionary are present in the class instance's 'mRNAs' attribute.*
- `def reverse (self, cluster_end)`  
*Reverses the coordinates of all mRNAs of the class instance.*
- `def show_init (self)`  
*This function was added for convenience as a way to easily retrieve the attribute values of the class instance as a formatted string.*

### Public Attributes

- `name`  
*name (identifier) of the locus*
- `mRNAs`  
*Dictionary of lists containing the CDS list of each mRNA of the locus.*
- `start`  
*start coordinate of the locus on the sequence*
- `end`  
*end coordinate of the locus on the sequence*
- `direction`  
*string indicating if the locus is on direct or reverse strand*

#### 4.2.1 Detailed Description

This class represents an annotation's locus identified from reading the associated GFF file with the `get_gff_borders` function.

It possesses multiple attributes describing the locus

See also

`get_gff_borders()`

#### 4.2.2 Constructor & Destructor Documentation

#### 4.2.2.1 `__init__()`

```
def locus.Locus.__init__ (
    self,
    name = "",
    mRNAs = None,
    start = -1,
    end = -1,
    direction = "" )
```

This method initialises the class with default values for each attribute.

##### Parameters

<i>name</i>	(optional) ID of the locus
<i>mRNAs</i>	(optional) Dictionary listing all mRNAs of the locus. Each key corresponds to the ID of the mRNA and each value to the list of all CDS coordinates as retrieved by the <code>get_gff_borders</code> function
<i>start</i>	(optional) Start coordinate of the locus
<i>end</i>	(optional) End coordinate of the locus
<i>direction</i>	(optional) String indicating if the locus is on the 'direct' or 'reverse' strand

##### See also

`get_gff_borders()`

### 4.2.3 Member Function Documentation

#### 4.2.3.1 `contain_mrnas()`

```
def locus.Locus.contain_mrnas (
    self,
    ** mRNAs )
```

This method is used to verify if all mRNAs of a dictionary are present in the class instance's 'mRNAs' attribute.

##### Parameters

<b><i>**mRNAs</i></b>	Dictionary with mRNA names as keys and CDS coordinates list as values
-----------------------	---

##### Returns

Returns a boolean indicating if all given mRNAs were found in the class instance's 'mRNAs' attribute

##### Remarks

This method is intended to be used in unit tests to verify the locus contains the intended mRNAs

#### 4.2.3.2 mRNAs()

```
def locus.Locus.mRNAs (
    self )
```

This method is used to retrieve the 'mRNAs' attribute of an instance.

##### Returns

Returns the 'mRNAs' attribute of the class instance

#### 4.2.3.3 reverse()

```
def locus.Locus.reverse (
    self,
    cluster_end )
```

Reverses the coordinates of all mRNAs of the class instance.

##### Parameters

<i>cluster_end</i>	End position coordinate of the cluster containing the locus
--------------------	---

##### Remarks

This method doesn't return anything and modifies directly the class instance. This method is used in case of loci on the reverse strand, and transforms the coordinates into coordinates from the end of the parent cluster

#### 4.2.3.4 set\_mRNAs()

```
def locus.Locus.set_mRNAs (
    self,
    value )
```

Sets the value of the 'mRNAs' attribute of the class instance.

##### Parameters

<i>value</i>	Value to be assigned to the 'mRNAs' attribute
--------------	---

#### 4.2.3.5 show\_init()

```
def locus.Locus.show_init (
```

*self* )

This function was added for convenience as a way to easily retrieve the attribute values of the class instance as a formatted string.

#### Returns

Returns a string describing the values of each attribute of the class instance

The documentation for this class was generated from the following file:

- /home/runner/work/CDScompR/CDScompR/script/locus.py

## 4.3 intervals\_utils.OrderedIntervals Class Reference

This class represents a list of intervals and implements multiple basic operations between intervals.

### Public Member Functions

- def `__init__` (self, `intervals`, include\_ub=False)  
*Initialises the class instance with the given intervals.*
- def `get_intervals_with_included_ub` (self)  
*Returns the class instance's intervals list including the upper bound of each interval.*
- def `total_length` (self)  
*Calculates the total length of all intervals.*
- def `union` (self, other)  
*Calculates the union an interval list with another interval list.*
- def `intersection` (self, other)  
*Calculates the intersection of this interval list with another interval list.*
- def `difference` (self, other)  
*Calculates the difference of this interval list with another interval list and returns the intervals of this list (asymmetric difference)*
- def `symmetric_difference` (self, other)  
*Calculates the difference of this interval list with another interval list and returns both intervals list (symmetric difference)*
- def `merge` (self, other, keep\_operator)  
*Merges this interval list with another interval list based on the specified operator.*

### Static Public Member Functions

- def `transform_intervals_to_exclude_ub` (`intervals`)  
*Excludes the upper bound of each interval of the given list.*
- def `new` (`intervals`, include\_ub=False)  
*Creates a new `OrderedIntervals` object.*

### Public Attributes

- `intervals`  
*List of sequence coordinates representing CDS intervals.*

### 4.3.1 Detailed Description

This class represents a list of intervals and implements multiple basic operations between intervals.

It is used to represent and compare lists of CDS bounds of compared loci in the mRNA comparison function `compute_matches_mismatches_EI_RF`

#### See also

`compute_matches_mismatches_EI_RF()`

#### Remarks

This class was adapted from <https://stackoverflow.com/a/20062829> by Vincent Ranwez, and translated into python using chatGPT

### 4.3.2 Constructor & Destructor Documentation

#### 4.3.2.1 `__init__()`

```
def intervals_utils.OrderedIntervals.__init__ (
    self,
    intervals,
    include_ub = False )
```

Initialises the class instance with the given intervals.

#### Parameters

<i>intervals</i>	List of interval bounds to represent
<i>include_ub</i>	Boolean indicating wether to include the upper bounds of each interval of the list

#### Remarks

for CDS bounds of GFF annotations, `include_ub` needs to be 'True'

### 4.3.3 Member Function Documentation

#### 4.3.3.1 `difference()`

```
def intervals_utils.OrderedIntervals.difference (
    self,
    other )
```

Calculates the difference of this interval list with another interval list and returns the intervals of this list (asymmetric difference)

**Parameters**

<i>other</i>	Another <a href="#">OrderedIntervals</a> object.
--------------	--

**Returns**

A new [OrderedIntervals](#) object representing the difference between the two interval lists.

**Remarks**

This method returns the intervals of the first interval list not present in the second, but not those of the second not present in the first. To get both, use the `symmetric_difference` method

**See also**

[symmetric\\_difference\(\)](#)

**4.3.3.2 `get_intervals_with_included_ub()`**

```
def intervals_utils.OrderedIntervals.get_intervals_with_included_ub (
    self )
```

Returns the class instance's intervals list including the upper bound of each interval.

**Returns**

Returns the list of intervals of the class instance with their upper bounds

**4.3.3.3 `intersection()`**

```
def intervals_utils.OrderedIntervals.intersection (
    self,
    other )
```

Calculates the intersection of this interval list with another interval list.

**Parameters**

<i>other</i>	An <a href="#">OrderedIntervals</a> object.
--------------	---

**Returns**

A new [OrderedIntervals](#) object representing the intersection of the two interval lists.

#### 4.3.3.4 merge()

```
def intervals_utils.OrderedIntervals.merge (
    self,
    other,
    keep_operator )
```

Merges this interval list with another interval list based on the specified operator.

##### Parameters

<i>other</i>	Another <a href="#">OrderedIntervals</a> object.
<i>keep_operator</i>	A function that determines whether to keep an interval based on its presence in either list.

##### Returns

A new [OrderedIntervals](#) object representing the merged intervals.

#### 4.3.3.5 new()

```
def intervals_utils.OrderedIntervals.new (
    intervals,
    include_ub = False ) [static]
```

Creates a new [OrderedIntervals](#) object.

##### Parameters

<i>intervals</i>	List of integers representing the intervals.
<i>include_ub</i>	Boolean indicating if the upper bound should be included.

##### Returns

A new [OrderedIntervals](#) object.

#### 4.3.3.6 symmetric\_difference()

```
def intervals_utils.OrderedIntervals.symmetric_difference (
    self,
    other )
```

Calculates the difference of this interval list with another interval list and returns both intervals list (symmetric difference)

**Parameters**

<i>other</i>	Another <a href="#">OrderedIntervals</a> object.
--------------	--

**Returns**

A new [OrderedIntervals](#) object representing the difference between the two interval lists.

**Remarks**

This method returns the intervals of the first interval list not present in the second, and those of the second not present in the first. To get only the difference for this instance's list, use the difference method

**See also**

[difference\(\)](#)

**4.3.3.7 total\_length()**

```
def intervals_utils.OrderedIntervals.total_length (
    self )
```

Calculates the total length of all intervals.

**Returns**

The sum of the lengths of all intervals.

**4.3.3.8 transform\_intervals\_to\_exclude\_ub()**

```
def intervals_utils.OrderedIntervals.transform_intervals_to_exclude_ub (
    intervals ) [static]
```

Excludes the upper bound of each interval of the given list.

**Parameters**

<i>intervals</i>	Interval list to be transformed
------------------	---------------------------------

**Returns**

Returns the same list of intervals with each upper bound removed

#### 4.3.3.9 union()

```
def intervals_utils.OrderedIntervals.union (
    self,
    other )
```

Calculates the union an interval list with another interval list.

##### Parameters

<i>other</i>	An <a href="#">OrderedIntervals</a> object.
--------------	---

##### Returns

A new [OrderedIntervals](#) object representing the union of the two interval lists.

The documentation for this class was generated from the following file:

- /home/runner/work/CDScompR/CDScompR/script/intervals\_utils.py



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