

Annotation comparison Vetea Jacot

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1 Namespace Index	1
1.1 Namespace List	1
2 Namespace Documentation	3
2.1 CDScompare Namespace Reference	3
2.1.1 Detailed Description	3
Index	5

Chapter 1

Namespace Index

1.1 Namespace List

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

[CDScompare](#)

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3

Chapter 2

Namespace Documentation

2.1 CDScompare Namespace Reference

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Functions

- `main ()`

Variables

- `script_dir = os.path.join(os.path.dirname(os.path.abspath(__file__)), "python_util")`

2.1.1 Detailed Description

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This script is used to compute the similarities between two or more structural annotations of a same genome.

Author

: vetea, ranwez

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

Index

CDScompare, [3](#)