

# Package ‘roverlaps’

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**Type** Package

**Title** Fast, Memory-Efficient Genomic Range Overlaps

**Version** 0.1.0

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**Description** Range overlaps between different sets of genomic intervals can be memory intensive and slow for huge (1M+) interval queries. Depending on the application, only part of a range overlap is needed (e.g. just the overlap mappings, not the actual ranges). This package implements fast, memory-efficient interval tree overlaps in C++ and provides flexibility for users to choose only what they need, thereby improving memory performance.

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**SystemRequirements** A C++11 compiler. Version 4.6.\* of g++ (as currently in Rtools) is insufficient; versions 4.8.\*, 4.9.\* or later will be fine.

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**Imports** Rcpp (>= 0.12.16), GenomicRanges, data.table, S4Vectors, methods, utils

**LinkingTo** Rcpp

**Suggests** testthat

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cpp_gr2dt	<i>Converts GRanges to data.table</i>
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**Description**

Converts GRanges to data.table and a field gr.lii which saves the (local) index that that gr was in its corresponding grl item

**Usage**

```
cpp_gr2dt(x)
```

**Arguments**

x	GRanges to convert
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**Value**

data.table of GRanges columns ('seqnames', 'start', 'end', 'strand', 'width') and metadata columns

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roverlaps	<i>roverlaps</i>
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**Description**

Description of your package

**Usage**

```
roverlaps(o1, o2, cores = 1, verbose = FALSE, index_only = FALSE)
```

**Arguments**

o1	Query ranges
o2	Subject ranges
cores	Maximum number of cores (processes in 1M chunks) [1]
verbose	Increase the output to stderr
index_only	Return only the indices (query.id and subject.id)

**Value**

data.table ('seqnames', 'start', 'end', 'strand', 'query.id', 'subject.id') of overlaps

**Author(s)**

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