

Package ‘GFFStrandLoc’

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Type Package

Title Strand-Wise Gene and Protein Extraction from GFF3 Files

Version 0.1.0

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Description Facilitates the extraction and organization of strand-specific genomic features from GFF3 files. In many species and variants, high quality genome annotations are not always available, necessitating de novo annotation using tools such as AUGUSTUS (Stanke et al., 2006; <doi:10.1093/nar/gkl200>). However, downstream processing of such annotations to obtain structured information, such as strand-wise gene locations, transcript regions, and associated protein identifiers—can be computationally intensive and complex. 'GFFStrandLoc' provides a streamlined framework to parse GFF3 files and generate structured outputs containing strand-wise and region-wise genomic coordinates for each transcript, along with their associated protein information. Additionally, it enables users to define custom promoter lengths and extract corresponding promoter region coordinates for genes in a strand-aware manner. By simplifying post-annotation processing, it enhances the usability of de novo annotated genomic datasets for downstream analysis and interpretation.

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Encoding UTF-8

RoxygenNote 7.3.3

NeedsCompilation no

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Description

Extracts strand-wise location of genomic features, UTRs, CDS, introns, exons, promoters, and associated protein sequences from a GFF3 file.

Usage

```
GFFStrandLoc(GFF3, PROMOTER_LEN, output_dir)
```

Arguments

GFF3	Path to GFF3 annotation file
PROMOTER_LEN	Integer specifying promoter length
output_dir	Directory where output CSV files will be saved

Value

Writes multiple CSV files to output directory

Examples

```
gff_file <- system.file("extdata", "example.gff3", package = "GFFStrandLoc")
outdir <- tempdir()
GFFStrandLoc(gff_file, 100, outdir)
```

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