annmap: The base component for a framework of Genome analysis tools

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Important

The annmap package has similar methods to the deprecated exonmap package. We have tried to keep things as close as possible, but some functions, parameters and returned results are crucially different. Please make sure you have read the migration section on page 2 to see how to migrate your code from exonmap to annmap.

Contents

1 Introduction

annmap provides access to the genome annotation in the Annmap database (http://annmap.cruk.manchester.ac.uk). It is designed to be a base layer for interrogating genome and probeset annotation, and to be extensible, so that later packages for Microarray Expression analysis, deep sequencing, or proteomics data analysis can be added to extend the functionality of annmap.

The functions provided by annmap can be divided into five main groups:

1. Connect/disconnect to an instance of the database
2. Find genome features within a particular set of coordinates (e.g. geneInRange())
3. Find genome features by name (e.g. geneDetails())
4. Map between genome features (e.g. geneToExon())
5. Handle Affymetrix microarray annotation

For detailed examples showing how these tasks are performed, please see the cookbook document, supplied along with this package.

2 Migration from exonmap

2.1 Working with features previously in the 'other features' database

In exonmap if you wanted to find mappings to EST genes, you were required to pass a subset='est' parameter to the method of interest. EST genes are now integrated into the same database with the other features, so now there are seperate EST functions for you to call (probesetToEstGene, etc).

2.2 Range query parameter order

The parameter order for InRange queries has changed. The four parameters required are now in the order:

1. chr – Chromosome name as a character vector
2. start – Numeric start location
3. end – Numeric stop location
4. strand – Numeric strand direction (-1 or 1)

Alternatively, you can now pass a data.frame, a GRanges object or an IRanges object.

2.3 Gene plots

In exonmap there exist the functions gene.graph, gene.strip, and genePlot. These do not exist in the annmap package. Please see the cookbook pdf supplied with this package for alternatives.