NAME

gt-tirvish - Identify Terminal Inverted Repeat (TIR) elements,such as DNA transposons.

SYNOPSIS

gt tirvish [option …] -index INDEXNAME

DESCRIPTION

-index [*string*]

    specify the name of the enhanced suffix array index (mandatory) (default: undefined)

-seed [*value*]

    specify minimum seed length for exact repeats (default: 20)

-mintirlen [*value*]

    specify minimum length for each TIR (default: 100)

-maxtirlen [*value*]

    specify maximum length for each TIR (default: 1000)

-mintirdist [*value*]

    specify minimum distance of TIRs (default: 500)

-maxtirdist [*value*]

    specify maximum distance of TIRs (default: 10000)

-mat [*value*]

    specify matchscore for extension-alignment (default: 2)

-mis [*value*]

    specify mismatchscore for extension-alignment (default: -2)

-ins [*value*]

    specify insertionscore for extension-alignment (default: -3)

-del [*value*]

    specify deletionscore for extension-alignment (default: -3)

-xdrop [*value*]

    specify xdropbelowscore for extension-alignment (default: 5)

-similar [*value*]

    specify TIR similarity threshold in therange [1..100%] (default: 85.000000)

-overlaps […]

    specify no|best|longest|all (default: best)

-mintsd [*value*]

    specify minimum length for each TSD (default: 2)

-maxtsd [*value*]

    specify maximum length for each TSD (default: 11)

-vic [*value*]

    specify the number of nucleotides (to the left and to the right) that will be searched for TSDs around 5' and 3' boundary of predicted TIRs (default: 60)

-hmms

    profile HMM models for domain detection (separate by spaces, finish with --) in HMMER3 format
    Omit this option to disable pHMM search.

-pdomevalcutoff [*value*]

    global E-value cutoff for pHMM search
    default 1E-6

-pdomcutoff […]

    model-specific score cutoff
    choose from TC (trusted cutoff) | GA (gathering cutoff) | NONE (no cutoffs) (default: GA)

-maxgaplen [*value*]

    maximal allowed gap size between fragments (in amino acids) when chaining pHMM hits for a protein domain (default: 50)

-refseqs [*string*]

    specify the name of the gene sequences to scan for inside candidates (default: undefined)

-seqids [*yes|no*]

    use sequence descriptions instead of sequence numbers in GFF3 output (default: yes)

-md5 [*yes|no*]

    add MD5 hashes to seqids in GFF3 output (default: no)

-help

    display help for basic options and exit

-help+

    display help for all options and exit

-version

    display version information and exit

REPORTING BUGS

Report bugs to https://github.com/genometools/genometools/issues.