

NAME

insilicut.bash – manual page for insilicut.bash 1.2.0

SYNOPSIS

insilicut.bash [*OPTIONS*] ...

DESCRIPTION

'insilicut.bash' reports fragments when cutting genomic DNA with a restriction enzyme.

OPTIONS

-h, --help

display the help and exit

-V, --version output version information and exit

-v, --verbose verbosity level (0/default=1/2/3)

--gf path to the file containing the genomic DNA (fasta format)

--gn name of the genomic DNA (e.g. 'Athaliana')

--ef path to the file containing the restriction enzyme (fasta format)

--en name of the enzyme (e.g. 'ApeKI')

--ls lower bound on fragments size (default=100)

--us upper bound on fragments size (default=300)

--fullh

use full fasta header (e.g. keep "chr1 Atha" instead of "chr1")

--clean

remove temporary files

--p2i absolute path to the insilicut directory (default=) used for testing purposes only (e.g. in 'make check')

EXAMPLES

insilicut.bash --gf Athaliana_genome.fa --gn Athaliana --ef ApeKI.fa --en ApeKI

Remarks:

if R is installed, a histogram of fragments size is also produced

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REPORTING BUGS

Report bugs to <timothee.flutre@supagro.inra.fr>.

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