

NAME

bamdamage - Generates damage plots for a bam file.

SYNOPSIS

bamdamage [--mapquality *qual*] [--basequality *qual*] [--sample *name*] [*file.bam*]

bamdamage [-m *qual*] [-b *qual*] [-s *name*] [*file.bam*]

DESCRIPTION

bamdamage generates plots for the read length distribution, damage distribution, 5' damage pattern, 3' damage pattern in a pdf-file. The input is a single bam file either on the command line or given on standard input (stdin).

OPTIONS

--mapquality *qual*

-m *qual*

Skip reads with mapping quality smaller than *qual*. Default: 30.

--basequality *qual*

-b *qual*

Skip bases with base quality smaller than *qual*. Default: 20.

--samplename *name*

-s *name*

Use *name* for the legend in plots. Default is the file name.

EXAMPLE: Running bamdamage

Generate *AustralianAborigine_300000.pdf* with the sample labeled *Aborigine*.

bamdamage AustralianAborigine_300000.bam -s Aborigine

AUTHOR

When using **bamdamage** for a publication please cite:

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EXIT STATUS

bamdamage will exit with non-zero status if it discovers anything is wrong.

REPORTING BUGS

Report bugs to <bamdamage@tange.dk>.

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DEPENDENCIES

bamdamage uses Perl, R, and samtools.

SEE ALSO

bammds(1), **samtools(1)**, **R(1)**