pydamage

Release 0.1

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Contents:

Homepage: github.com/maxibor/pydamage

CHAPTER 1

Introduction

Pydamage, is a Python software to automate the process of contig damage identification and estimation. It uses a process akin to a likelihood ratio test to attempt to discriminate between truly ancient, and modern contigs originating from sample contamination.

1.1 Install

Pydamage is not yet on *pypi* nor *conda*, but you can already install it using pip, provided that you have access to this repository.

1.1.1 Install dependencies in conda environment

```
git clone git@github.com:maxibor/pydamage.git
cd pydamage
```

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```
conda env create -f environment.yml
conda activate pydamage
```

1.1.2 Install pydamage

- from source

```
python setup.py install
```

- from Github using pip

```
pip install git+ssh://git@github.com/maxibor/pydamage.git
```

1.2 CLI help

Command line interface help message

```
pydamage --help
```

See also *CLI*

CHAPTER 2

API

pydamage.main.**analyze**(*bam*, *wlen=30*, *show_al=False*, *mini=2000*, *cov=0.5*, *process=1*, *outdir=''*, *plot=False*, *verbose=False*, *force=False*)

Runs the pydamage analysis

Parameters

- **bam** (*str*) – Path to alignment (sam/bam/cram) file
- **wlen** (*int*) – window length
- **show_al** (*bool*) – print alignments representations
- **mini** (*int*) – Minimum numbers of reads aligned to consider contigs
- **cov** (*float*) – Minimum coverage to consider contig
- **process** (*int*) – Number of processes for parellel computing
- **outdir** (*str*) – Path to output directory
- **verbose** (*bool*) – verbose mode
- **force** (*bool*) – force overwriting of results directory

Returns pandas DataFrame containg pydamage results

Return type pd.DataFrame

CHAPTER 3

CLI

To access the help menu:

```
$ pydamage --help
```

The list of arguments of options is detailed below

3.1 pydamage

PyDamage: Damage parameter estimation for ancient DNA
Author: Maxime Borry
Contact: <borry[at]shh.mpg.de>
Homepage & Documentation: github.com/maxibor/pydamage

BAM: path to BAM/SAM/CRAM alignment file

```
pydamage [OPTIONS] BAM
```

Options

--version
Show the version and exit.

-w, --wlen <wlen>
Window length for damage modeling [default: 35]

-p, --process <process>
Number of processes [default: 2]

-m, --mini <mini>
Minimum reads aligned to consider reference [default: 1000]

-c, --cov <cov>
Minimum coverage to consider reference [default: 8]

-s, --show_al
Show alignments representations

-pl, --plot
Make the damage plots

--verbose
Verbose mode

-o, --outdir <outdir>
Output directory [default: pydamage_results]

--force
Force overwriting of results directory

Arguments

BAM
Required argument

CHAPTER 4

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