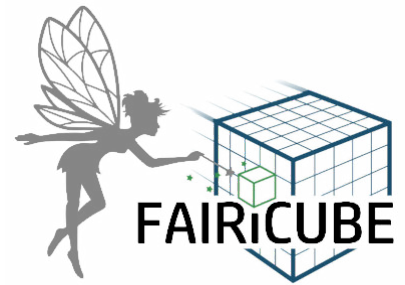


Summary of inserted values



Below is a summary of the entered values. Please check and eventually go back to correct before you submit values and generate metadata.

Username: *nilu*

Title: *Introducing gaps to genomics data (frequency and weights)*

Use case: *UC3*

Name of resource: *data processing*

ID: *C1DJCKP3NM*

Description: *Reading raw allele frequency and weights data and file that links chromosome arms (X,2L,2R,3L,3R,Y,4), chromatin state of the genome (Telomer, Euchromatin and Centromer) to positions in the raw data. subselecting chromose arm data and apply patterns of gaps according to real gap characteristics, writing data with and without synthetic gaps for each chromosome arm as csv*

Main category: *Pre-processing*

Publication date: *2024-05-30*

Objective: *data-transformation*

Platform: *Local Jupyter notebook*

Framework: *Pandas*

Architecture:

Approach:

Algorithm: *custom-method*

Processor: *cpu*

OS: *linux*

Keyword:

- pre-processing
- gap
- subselection
- slicing
- chromosome arm
- jupyter_notebook_available

Reference link:

-

Example:

Input data used:

1. data provided by Martin, not yet available online

Characteristics of input data:

1. <https://noULRavailable.com>

Biases and ethical aspects:

- 1.

Model configuration:

Output data obtained:

1. Europe_chromosomes_freq_chrom2L.csv Europe_chromosomes_freq_chrom4.csv
Europe_chromosomes_weight_chrom2R.csv Europe_chromosomes_weight_chromX.csv
Europe_chromosomes_freq_chrom2L_gap.csv
Europe_chromosomes_freq_chrom4_gap.csv
Europe_chromosomes_weight_chrom2R_gap.csv
Europe_chromosomes_weight_chromX_gap.csv
Europe_chromosomes_freq_chrom2R.csv Europe_chromosomes_freq_chromX.csv
Europe_chromosomes_weight_chrom3L.csv Europe_chromosomes_weight_chromY.csv
Europe_chromosomes_freq_chrom2R_gap.csv
Europe_chromosomes_freq_chromX_gap.csv
Europe_chromosomes_weight_chrom3L_gap.csv
Europe_chromosomes_weight_chromY_gap.csv
Europe_chromosomes_freq_chrom3L.csv Europe_chromosomes_freq_chromY.csv
Europe_chromosomes_weight_chrom3R.csv slicing_data.py.csv
Europe_chromosomes_freq_chrom3L_gap.csv
Europe_chromosomes_freq_chromY_gap.csv
Europe_chromosomes_weight_chrom3R_gap.csv
Europe_chromosomes_freq_chrom3R.csv Europe_chromosomes_weight_chrom2L.csv
Europe_chromosomes_weight_chrom4.csv
Europe_chromosomes_freq_chrom3R_gap.csv
Europe_chromosomes_weight_chrom2L_gap.csv
Europe_chromosomes_weight_chrom4_gap.csv

Characteristics of output data:

1. <https://noULRavailable.com>

Performance:

Conditions for access and use: MIT

Constraints:

Consumed resources filename: *slicing_data.py.csv*

Consumed resource:

Measure	Value
Data size in grid points	NaN
Largest allocated array in grid points	[483217, 226]
Data size (MB)	-53.66015625
Main memory available (GB)	30.974971771240234
Main memory consumed (GB)	2.4423894602805376
Sum of allocated variable sizes (GB)	1.7298487210646272
Description of CPU/GPU	Machine type: x86_64 Processor type: x86_64 Number of physical cores: 6 Number of logical cores: 12 Min CPU frequency: 800.0 GHz Max CPU frequency: 5100.0 GHz No GPU available
Wall time in seconds	3483.23264336586
Energy consumed (kw)	0.032916080377079
CO ₂ -equivalents [CO ₂ eq] (kg)	0.0009068380143885284
Network traffic (MB)	71.14130878448486
Programming language	Python
Essential libraries	sys numpy matplotlib.pyplot pandas os

Click on the button below to submit the data. The STAC-JSON metadata file will be created and uploaded to the FAIRiCUBE Knowledge Base and FAIRiCUBE Catalog.

The process of creating and uploading can require some time. At the end you will get a page informing you of the result of the workflow.

Please wait.

[Submit values and generate metadata](#)



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the European Union

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PROJECT

Project No: 101059238
Total cost: € 3,613,562.50
EU contribution: € 3,202,843.75
Duration of the project: 2022 – 2025 (36 months)

CONTACT US

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