Iced Documentation

Release 0.2.3+git

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Recent technological advances allow the measurement, in a single Hi-C experiment, of the frequencies of physical contacts among pairs of genomic loci at a genome-wide scale.

Iced implements a fast and memory efficient of the ICE normalization strategy.

Contents:

CHAPTER 1

References

HiC-Pro: an optimized and flexible pipeline for Hi-C data processing *N. Servant, N. Varoquaux, B.R. Lajoie, E. Viara, C.J. Chen, J.-P. Vert, E. Heard, J. Dekker, E. Barillot, Genome Biology 2015

CHAPTER 2

Contacts

If you have any questions or suggestions, please email nelle dot varoquaux at ensmp dot fr, or open a ticket on Github

CHAPTER 3

Indices and tables

- genindex
- modindex
- search