

Human Fibroblast IMR90 Hi-C Data (Dixon et al.)

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1 Introduction

The Hi-C technic was first introduced by [Lieberman-Aiden et al. \[2009\]](#). In the continuity with 3C, 4C and 5C technics, the goal of the Hi-C is to simultaneously detect all chromosomal contacts in a single experiment. All these techniques aim at measuring the population-averaged frequency at which two genomic loci physically interact in three-dimensional space. In Hi-C, after a first crosslink and digestion, all genomic fragments are labeled with a biotinylated nucleotide before ligation. These junctions can then be purified efficiently by streptavidin-coated magnetic beads, and finally sequenced using a standard Illumina paired-end protocol.

The data available in this package were published by [Dixon et al. \[2012\]](#) and downloaded from the GEO website (GSE35156, sample GSM862724). This publication is one of the key papers in the field for two main reasons: i) it was the first time that Hi-C data were generated at such resolution (up to 20kb), ii) this resolution highlighted a new short range structure defined as topological domains (TADs), with high frequencies of intra-domain chromatin interactions but infrequent inter-domain chromatin interactions ([Nora et al. \[2012\]](#)).

If you use *HiCDataHumanIMR90*, please cite:

- Servant N (2014). *HiCDataHumanIMR90*: Human Fibroblast IMR90 HiC data from Dixon et al. 2012. R package version 1.1.0.
- Dixon JR, Selvaraj S, Yue F, Kim A et al. (2012) Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature* 485(7398):376-80.

2 Hi-C Data

The `hic_imr90_40` object is a *HTClist* object (see the *HiTC* package for more information ([Servant et al. \[2012\]](#))). It contains the complete genome-wide HiC data, with all inter and intrachromosomal contact maps at a resolution of 40kb.

```
> require(HiCDataHumanIMR90)
> require(HiTC)
> data(Dixon2012_IMR90)
```

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```
> ## Show data
> show(hic_imr90_40)

HTClist object of length 325
25 intra / 300 inter-chromosomal maps

> ## Is my data complete (i.e. composed of intra + inter chromosomal maps)
> isComplete(hic_imr90_40)

[1] TRUE

> ## Note that a complete object is not necessarily pairwise
> ## (is both chr1-chr2 and chr2-chr1 stored ?)
> isPairwise(hic_imr90_40)

[1] FALSE

> ## Which chromosomes ?
> seqlevels(hic_imr90_40)

[1] "chr1" "chr2" "chr3" "chr4" "chr5" "chr6" "chr7" "chr8" "chr9"
[10] "chr10" "chr11" "chr12" "chr13" "chr14" "chr15" "chr16" "chr17" "chr18"
[19] "chr19" "chr20" "chr21" "chr22" "chrX" "chrY" "chrM"

> ## Details about a given map
> detail(hic_imr90_40$chrXchrX)

HTC object
Focus on genomic region [chrX:1-155270560]
CIS Interaction Map
Matrix of Interaction data: [3882-3882]
Binned data - window size = 40000
3882 genome intervals
Total Reads = 15349610
Number of Interactions = 3362484
Median Frequency = 1
Sparsity = 0.112

> ## Descriptive statistics
> head(summary(hic_imr90_40))

      seq1 seq2  nbreads nbinteraction averagefreq medfreq sparsity
chr1chr1 chr1 chr1 25914788      4524734      5.7274      1  0.8835
chr1chr2 chr1 chr2  504332      497291      1.0142      1  0.9869
chr1chr3 chr1 chr3  440865      434917      1.0137      1  0.9859
chr1chr4 chr1 chr4  456924      450005      1.0154      1  0.9849
chr1chr5 chr1 chr5  399067      393926      1.0131      1  0.986
chr1chr6 chr1 chr6  382580      377654      1.013      1  0.9858
```

3 Topological Domains

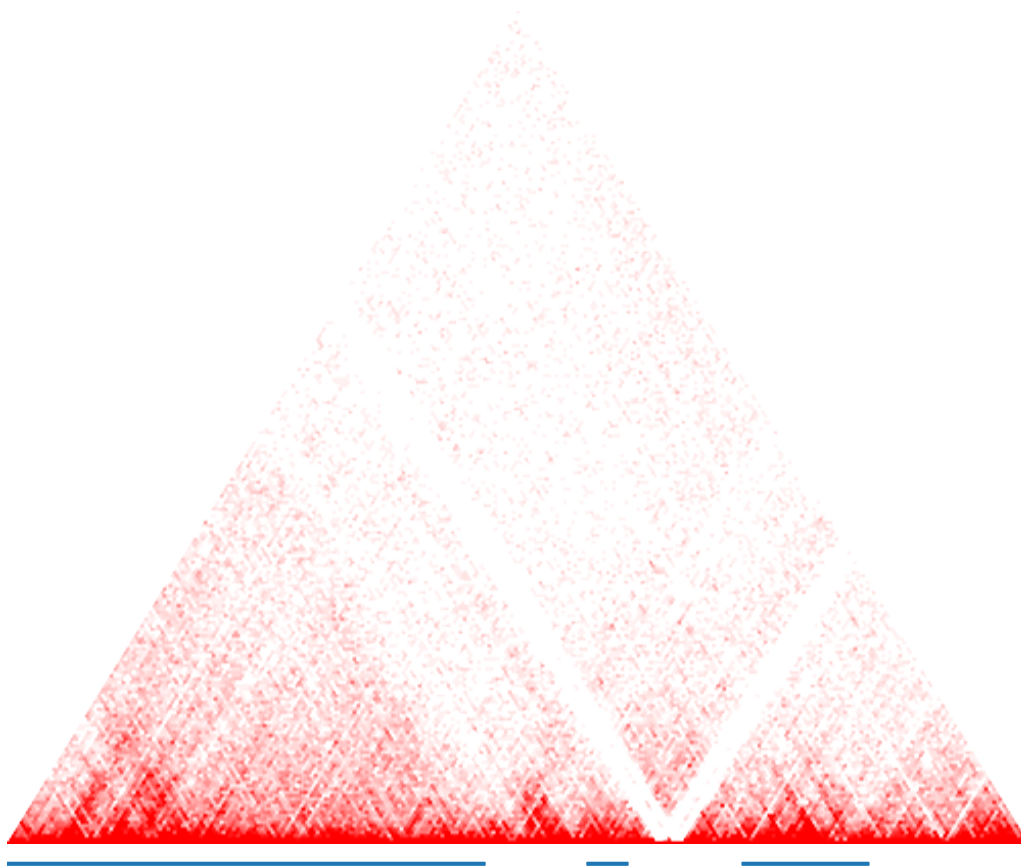
The `tads_imr90` object is a `GRanges` object with all TADs detected from this Hi-C data.

```
> show(tads_imr90)

GRanges object with 2338 ranges and 0 metadata columns:
      seqnames      ranges strand
      <Rle>        <IRanges> <Rle>
TAD-1   chr1      770138-1290137   *
TAD-2   chr1     1290138-1850140   *
TAD-3   chr1     1850141-2330140   *
TAD-4   chr1     2330141-3610140   *
TAD-5   chr1     3770141-6077413   *
...     ...           ...         ...
TAD-2334 chrX 146992309-148552096   *
TAD-2335 chrX 148592096-149929342   *
TAD-2336 chrX 149929343-151969344   *
TAD-2337 chrX 152089345-152746806   *
TAD-2338 chrX 152786807-154946806   *
-----
seqinfo: 23 sequences from an unspecified genome; no seqlengths
```

```
> ## Extract region
> regx <- extractRegion(hic_imr90_40$chrXchrX,
+                       chr="chrX", from=95000000, to=105000000)
> ## Plot Hi-C data with TADs
> plot(regx, tracks=list(tads_imr90), maxrange=20)
```

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Package versions

This vignette was generated using the following package versions:

- R version 4.4.0 RC (2024-04-16 r86468), x86_64-pc-linux-gnu
- Running under: Ubuntu 22.04.4 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.20-bioc/R/lib/libRblas.so
- LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.10.0
- Base packages: base, datasets, grDevices, graphics, methods, stats, stats4, utils
- Other packages: BiocGenerics 0.51.0, GenomInfoDb 1.41.0, GenomicRanges 1.57.0, HiCDataHumanIMR90 1.25.0, HiTC 1.49.0, IRanges 2.39.0, S4Vectors 0.43.0
- Loaded via a namespace (and not attached): Biobase 2.65.0, BiocIO 1.15.0, BiocManager 1.30.22, BiocParallel 1.39.0, BiocStyle 2.33.0, Biostrings 2.73.0, DelayedArray 0.31.0, GenomInfoDbData 1.2.12, GenomicAlignments 1.41.0, Matrix 1.7-0, MatrixGenerics 1.17.0, R6 2.5.1, RColorBrewer 1.1-3, RCurl 1.98-1.14, Rsamtools 2.21.0, S4Arrays 1.5.0, SparseArray 1.5.0, SummarizedExperiment 1.35.0, UCSC.utils 1.1.0, XML 3.99-0.16.1, XVector 0.45.0, abind 1.4-5, bitops 1.0-7,

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cli 3.6.2, codetools 0.2-20, compiler 4.4.0, crayon 1.5.2, curl 5.2.1, digest 0.6.35, evaluate 0.23, fastmap 1.1.1, grid 4.4.0, htmltools 0.5.8.1, httr 1.4.7, jsonlite 1.8.8, knitr 1.46, lattice 0.22-6, matrixStats 1.3.0, parallel 4.4.0, restfulr 0.0.15, rjson 0.2.21, rlang 1.1.3, rmarkdown 2.26, rtracklayer 1.65.0, tools 4.4.0, xfun 0.43, yaml 2.3.8, zlibbioc 1.51.0

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References

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- N. Servant, B. R. Lajoie, E. P. Nora, L. Giorgetti, C. Chen, E. Heard, J. Dekker, and E. Barillot. Hitc : Exploration of high-throughput 'c' experiments. *Bioinformatics*, Aug 2012. doi: 10.1093/bioinformatics/bts521. URL <http://dx.doi.org/10.1093/bioinformatics/bts521>.