

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
```

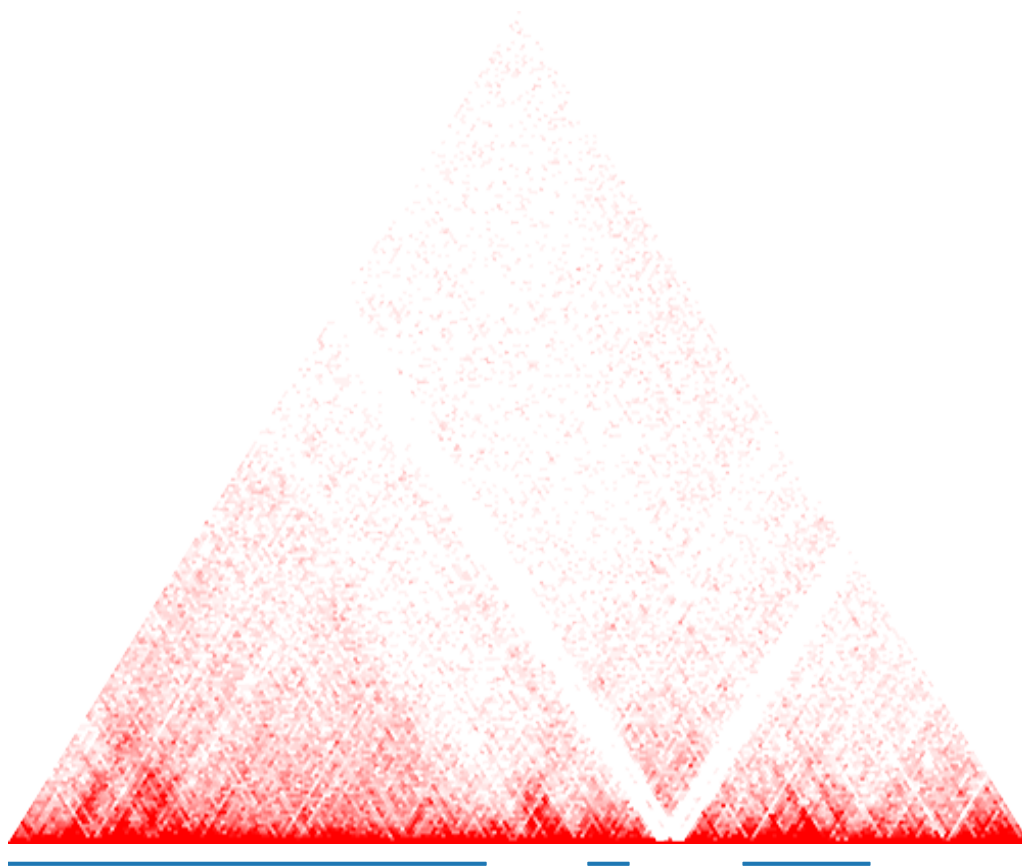
```
> regx <- extractRegion(hic_imr90_40$chrXchrX,
```

```
+ 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 4.6.1 (2026-06-24), x86_64-pc-linux-gnu
- Running under: Ubuntu 26.04.1 LTS
- Matrix products: default
- BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
- LAPACK:
/usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p0.3.32.so ;
LAPACK version 3.12.0
- Base packages: base, datasets, graphics, grDevices, methods, stats, stats4, utils
- Other packages: BiocGenerics 0.58.1, generics 0.1.4, GenomicRanges 1.64.0,
HiCDataHumanIMR90 1.32.0, HiTC 1.56.0, IRanges 2.46.0, S4Vectors 0.50.3,
Seqinfo 1.2.0
- Loaded via a namespace (and not attached): abind 1.4-8, Biobase 2.72.0,
BiocIO 1.22.0, BiocManager 1.30.27, BiocParallel 1.46.0, BiocStyle 2.40.0,
Biostrings 2.80.2, bitops 1.1-0, buildtools 1.0.0, cigarillo 1.2.1, cli 3.6.6,

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codetools 0.2-20, compiler 4.6.1, crayon 1.5.3, curl 8.0.0, DelayedArray 0.38.2, digest 0.6.39, evaluate 1.0.5, fastmap 1.2.0, GenomicAlignments 1.48.0, grid 4.6.1, htmltools 0.5.9, httr 1.4.9, knitr 1.52, lattice 0.23-1, maketools 1.3.2, Matrix 1.7-6, MatrixGenerics 1.24.0, matrixStats 1.5.0, parallel 4.6.1, R6 2.6.1, RColorBrewer 1.1-3, RCurl 1.98-1.20, restfulr 0.0.17, rjson 0.2.23, rlang 1.3.0, rmarkdown 2.32, Rsamtools 2.28.0, rtracklayer 1.72.0, S4Arrays 1.12.1, SparseArray 1.12.3, SummarizedExperiment 1.42.0, sys 3.4.3, tools 4.6.1, xfun 0.61, XML 3.99-0.25, XVector 0.52.0, yaml 2.3.12

References

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- E. P. Nora, B. R. Lajoie, E. G. Schulz, L. Giorgetti, I. Okamoto, N. Servant, T. Piolot, N. L. van Berkum, J. Meisig, J. Sedat, J. Gribnau, E. Barillot, N. Bluthgen, J. Dekker, and E. Heard. Spatial partitioning of the regulatory landscape of the x-inactivation centre. *Nature*, Apr 2012. doi: 10.1038/nature11049. URL <http://dx.doi.org/10.1038/nature11049>.
- 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>.