

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 technics 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)
> ## 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" "chr10"
[11] "chr11" "chr12" "chr13" "chr14" "chr15" "chr16" "chr17" "chr18" "chr19" "chr20"
[21] "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.

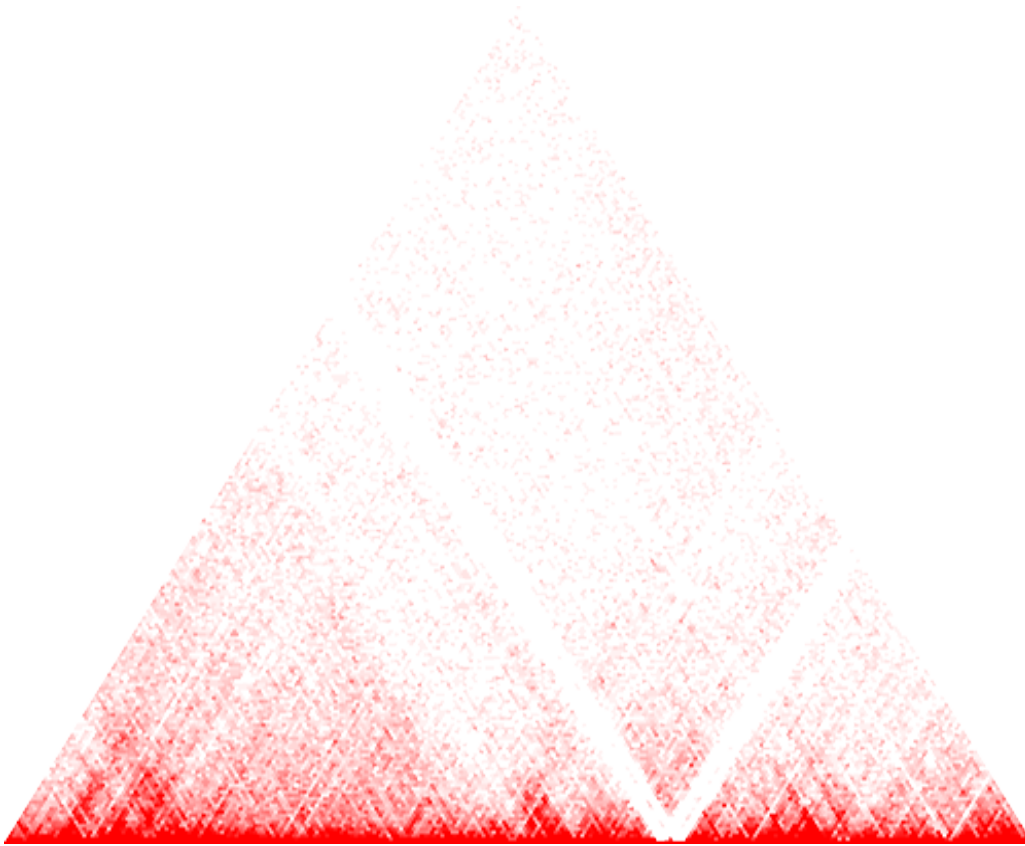
```
> show(tads_imr90)

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)
```



Package versions

This vignette was generated using the following package versions:

- R version 3.4.0 (2017-04-21), x86_64-pc-linux-gnu
- Running under: Ubuntu 16.04.2 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.5-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.5-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.22.0, GenomeInfoDb 1.12.0, GenomicRanges 1.28.0, HiCDataHumanIMR90 0.110.0, HiTC 1.20.0, IRanges 2.10.0, S4Vectors 0.14.0

- Loaded via a namespace (and not attached): Biobase 2.36.0, BiocParallel 1.10.0, BiocStyle 2.4.0, Biostrings 2.44.0, DelayedArray 0.2.0, GenomeInfoDbData 0.99.0, GenomicAlignments 1.12.0, Matrix 1.2-9, RColorBrewer 1.1-2, RCurl 1.95-4.8, Rcpp 0.12.10, Rsamtools 1.28.0, SummarizedExperiment 1.6.0, XML 3.98-1.6, XVector 0.16.0, backports 1.0.5, bitops 1.0-6, compiler 3.4.0, digest 0.6.12, evaluate 0.10, grid 3.4.0, htmltools 0.3.5, knitr 1.15.1, lattice 0.20-35, magrittr 1.5, matrixStats 0.52.2, rmarkdown 1.4, rprojroot 1.2, rtracklayer 1.36.0, stringi 1.1.5, stringr 1.2.0, tools 3.4.0, yaml 2.1.14, zlibbioc 1.22.0

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>.