

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.

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```
> 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"
[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
```

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```
chr1chr5 chr1 chr5 399067 393926 1.0131 1 0.986
chr1chr6 chr1 chr6 382580 377654 1.013 1 0.9858
```

3 Topological Domains

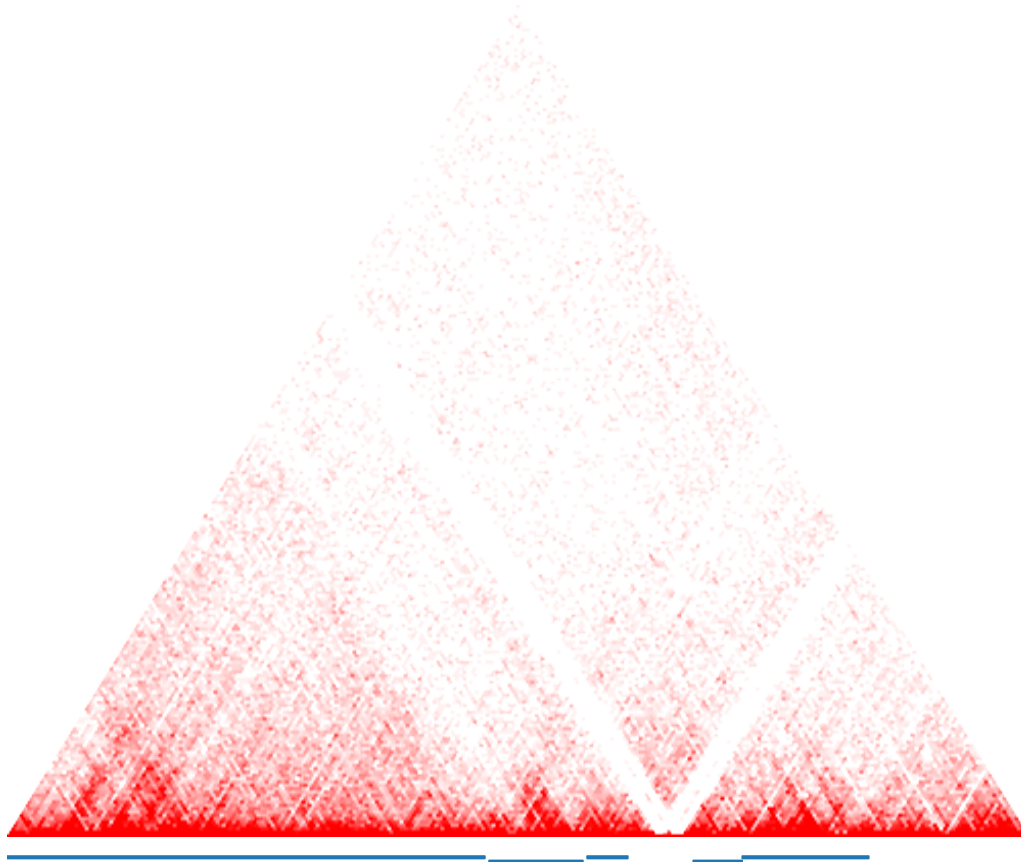
The `tads_imr90` object is a `GRanges` object with all TADs detected from this Hi-C data.

```
> 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 3.5.1 Patched (2018-07-12 r74967), x86_64-pc-linux-gnu
- Running under: Ubuntu 16.04.5 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.8-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.8-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.28.0, GenomInfoDb 1.18.0, GenomicRanges 1.34.0, HiCDataHumanIMR90 1.2.0, HiTC 1.26.0, IRanges 2.16.0, S4Vectors 0.20.0
- Loaded via a namespace (and not attached): Biobase 2.42.0, BiocManager 1.30.3, BiocParallel 1.16.0, BiocStyle 2.10.0, Biostrings 2.50.0, DelayedArray 0.8.0, GenomInfoDbData 1.2.0, GenomicAlignments 1.18.0, Matrix 1.2-14, RColorBrewer 1.1-2, RCurl 1.95-4.11, Rcpp 0.12.19, Rsamtools 1.34.0,

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SummarizedExperiment 1.12.0, XML 3.98-1.16, XVector 0.22.0, backports 1.1.2, bitops 1.0-6, compiler 3.5.1, digest 0.6.18, evaluate 0.12, grid 3.5.1, htmltools 0.3.6, knitr 1.20, lattice 0.20-35, matrixStats 0.54.0, rmarkdown 1.10, rprojroot 1.3-2, rtracklayer 1.42.0, tools 3.5.1, yaml 2.2.0, zlibbioc 1.28.0

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References

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