

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 this 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 paper in the field for two main reasons: i) it was the first time than 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 |
| chr2chr1 | chr2 | chr1 | 504332 | 497291 | 1.0142 | 1 | 0.9869 |
| chr3chr1 | chr3 | chr1 | 440865 | 434917 | 1.0137 | 1 | 0.9859 |
| chr4chr1 | chr4 | chr1 | 456924 | 450005 | 1.0154 | 1 | 0.9849 |
| chr5chr1 | chr5 | chr1 | 399067 | 393926 | 1.0131 | 1 | 0.986 |
| chr6chr1 | chr6 | chr1 | 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:
```

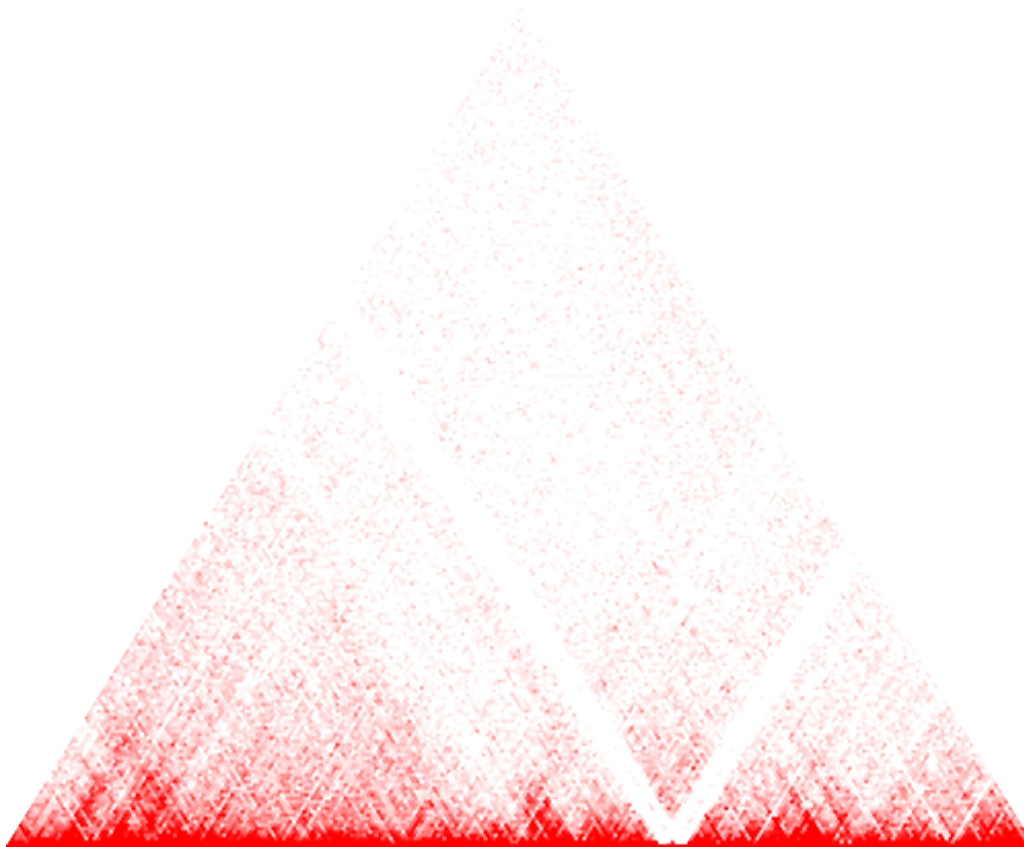
| | seqnames | ranges | strand |
|-------|----------|--------------------|--------|
| | <Rle> | <IRanges> | <Rle> |
| TAD-1 | chr1 | [770138, 1290137] | * |
| TAD-2 | chr1 | [1290138, 1850140] | * |
| TAD-3 | chr1 | [1850141, 2330140] | * |
| TAD-4 | chr1 | [2330141, 3610140] | * |
| TAD-5 | chr1 | [3770141, 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 3.1.2 (2014-10-31), i386-w64-mingw32
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.12.1, GenomInfoDb 1.2.3, GenomicRanges 1.18.3, HiCDataHumanIMR90 1.0.0, HiTC 1.10.0, IRanges 2.0.0, S4Vectors 0.4.0, XVector 0.6.0
- Loaded via a namespace (and not attached): BBmisc 1.8, BatchJobs 1.5, BiocParallel 1.0.0, BiocStyle 1.4.1, Biostrings 2.34.0, DBI 0.3.1, GenomicAlignments 1.2.1, Matrix 1.1-4, RColorBrewer 1.0-5, RCurl 1.95-4.4, RSQLite 1.0.0, Rsamtools 1.18.2, XML 3.98-1.1, base64enc 0.1-2, bitops 1.0-6, brew 1.0-6, checkmate 1.5.0, codetools 0.2-9, digest 0.6.4, fail 1.2, foreach 1.4.2, grid 3.1.2, iterators 1.0.7, lattice 0.20-29, rtracklayer 1.26.2, sendmailR 1.2-1, stringr 0.6.2, tools 3.1.2, zlibbioc 1.12.0

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>.