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 simultaneoulsy 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 finaly 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 intrachromosomic 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 a 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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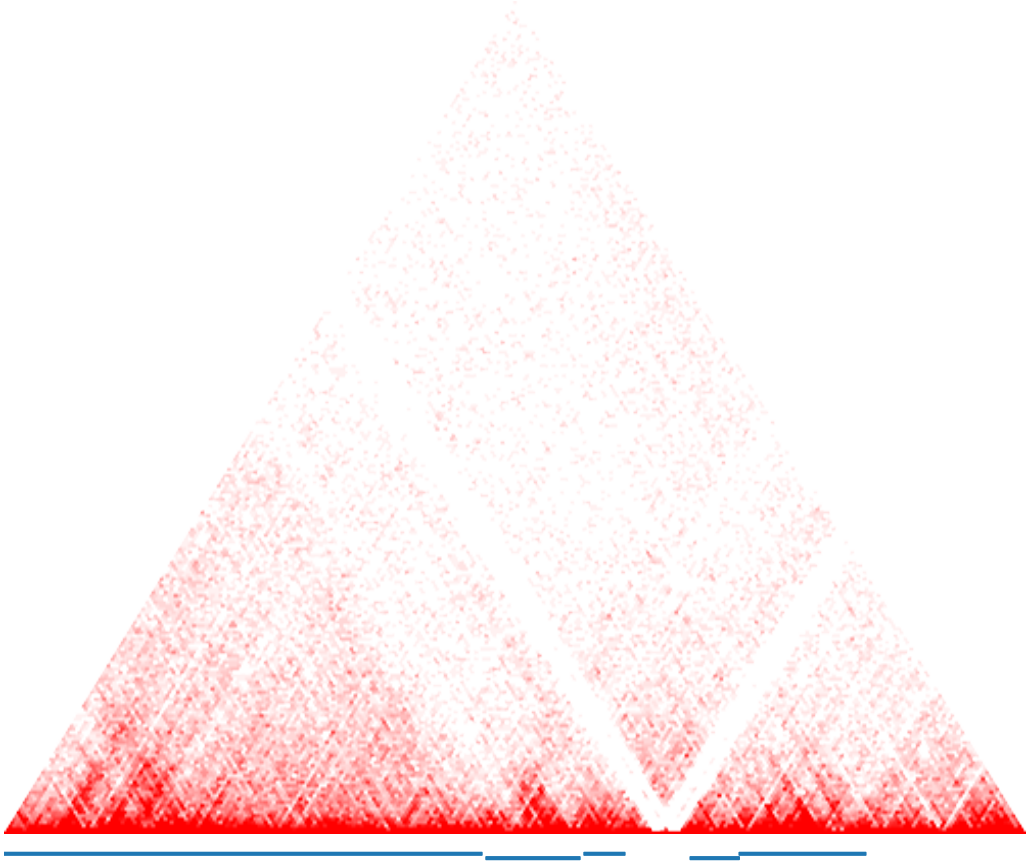

Package versions

This vignette was generated using the following package versions:

- R Under development (unstable) (2024-10-21 r87258), `x86_64-pc-linux-gnu`
- Running under: `Ubuntu 24.04.1 LTS`
- Matrix products: default
- BLAS: `/home/biocbuild/bbs-3.21-bioc/R/lib/libRblas.so`
- LAPACK: `/usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.12.0`
- Base packages: base, datasets, grDevices, graphics, methods, stats, stats4, utils
- Other packages: BiocGenerics 0.51.3, GenomeInfoDb 1.41.2, GenomicRanges 1.57.2, HiCDataHumanIMR90 1.25.0, HiTC 1.49.0, IRanges 2.39.2, S4Vectors 0.43.2
- Loaded via a namespace (and not attached): Biobase 2.65.1, BiocIO 1.15.2, BiocManager 1.30.25, BiocParallel 1.39.0, BiocStyle 2.33.1, Biostrings 2.73.2, DelayedArray 0.31.14, GenomeInfoDbData 1.2.13, GenomicAlignments 1.41.0, Matrix 1.7-1, MatrixGenerics 1.17.1, R6 2.5.1, RColorBrewer 1.1-3, RCurl 1.98-1.16, Rsamtools 2.21.2, S4Arrays 1.5.11, SparseArray 1.5.45, SummarizedExperiment 1.35.5, UCSC.utils 1.1.0, XML 3.99-0.17, XVector 0.45.0,

abind 1.4-8, bitops 1.0-9, cli 3.6.3, codetools 0.2-20, compiler 4.5.0, crayon 1.5.3, curl 5.2.3, digest 0.6.37, evaluate 1.0.1, fastmap 1.2.0, grid 4.5.0, htmltools 0.5.8.1, httr 1.4.7, jsonlite 1.8.9, knitr 1.48, lattice 0.22-6, matrixStats 1.4.1, parallel 4.5.0, restfulr 0.0.15, rjson 0.2.23, rlang 1.1.4, rmarkdown 2.28, rtracklayer 1.65.0, tools 4.5.0, xfun 0.48, yaml 2.3.10, zlibbioc 1.51.2

References

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