

Analyzing Hi-C data with the HiTC BioC package

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1 Introduction

The Hi-C technic was first introduced by [Lieberman-Aiden et al. \[2009\]](#) to simultaneously detect all chromosomal interactions in a single experiment. The Hi-C aims at measuring the population-averaged frequency at which two genomic loci physically interact in three-dimensional space. Briefly, after a first crosslink and digestion with a restriction enzyme, 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 an Illumina paired-end protocol.

After sequencing, raw reads have to be processed to generate the inter/intrachromosomal contact maps. The main steps of this processing are described in [Imakaev et al. \[2012\]](#). The raw paired-end reads are first independently aligned on a reference genome. The two mates from the same DNA fragment therefore define the two interacting loci on the genome. Imakaev et al. also proposed an iterative mapping procedure to rescue the reads spanning the ligation junction (and thus containing the two interactors in a single read). After the reads alignment, the Hi-C molecule generated from the DNA digestion and the ligation products are reconstructed using the position and direction of the sequenced mates. Self-circle ligations, single side reads and dangling ends are discarded, and the valid ligation products aligned to different restriction fragments and face toward the restriction site are used to reconstruct the contact maps. The interaction frequencies are therefore estimated by counting how many times two genomic bins (at a given resolution) were found as interactors. The data resolution usually depends on the sequencing depth. In their first paper, [Lieberman-Aiden et al. \[2009\]](#) generated data at a resolution of 1Mb (up to 100kb) and reveal the compartmentalization of the genome into regions of open and closed (active and inactive) chromatin as well as the three-dimensional structure of the genome (fractal globule). More recently, [Dixon et al. \[2012\]](#) generated 20 to 40kb contact maps in order to go deeper in the conformation structure and to study topological domains ([Nora et al. \[2012\]](#)).

The *HiTC* is designed to import processed data as contact maps. In order to generate these maps from raw sequencing reads a couple of pipeline are available on the web. We have recently developed the *HiC-Pro* software which is an optimized pipeline to process Hi-C data from raw reads to normalized contact maps. The outputs of *HiC-Pro* is fully compatible with the HiTC package.

This vignette is based on the analysis of the [Dixon et al. \[2012\]](#) contact maps, at a resolution of 40kb. These data are stored as a *HTClist* object, i.e. a list of inter/intrachromosomal contact maps, one for each pair of chromosomes. The goal of this vignette is to describe how the *HiTC* R package can be used to explore such data.

If you use *HiTC* for analyzing your data, please cite:

- Servant N., Lajoie B.R., Nora E.P., Giorgetti L., Chen C., Heard E., Dekker J., Barillot E. (2012) HiTC : Exploration of High-Throughput 'C' experiments. *Bioinformatics*.

2 Working with Hi-C data

The *HTCexp* (High-Throughput 'C' experiment) class aims at representing a single 'C' experiment, characterized by :

- A contact map (i.e a *Matrix*)
- Two *GRanges* objects that describe each features of the contact map, respectively, the x (i.e. columns) and y (i.e. rows) labels of the matrix. In the context of 5C, these two *GRanges* objects will describe the set of forward and reverse primers, and for the Hi-C the binned genomic intervals at a given resolution.

Whereas a 5C dataset is usually composed of a single intrachromosomal contact map (i.e. *HTCexp* object), a Hi-C dataset is represented by a list of inter/intrachromosomal contact maps, characterized by the physical interactions of each pair of chromosomes. The *HTClist* was designed as a list of *HTCexp* objects, with a couple of dedicated methods.

Working at a resolution of 40kb (or even at a lower resolution) can result in an intensive memory usage. Assuming that every restriction fragment could ligate to any other, there are on the order of 10^{11} possible HindIII restriction fragment pairs in the Human genome. In addition to the fact that the generation of a Hi-C library with enough complexity or sequence depth to cover all possible restriction fragment interactions is difficult, this will result in contact maps with a very high level of sparsity. The *HiTC* package provides an efficient memory storage of the data, based on the *sparseMatrix* class and the *Matrix* R package. In addition, binned intrachromosomal maps are expected to be symmetrical around the diagonal and can thus be stored as symmetrical matrix (*dsCMatrix* *Matrix* class). In the same way, the interchromosomal maps are also stored once as the chr1-chr2 map is expected to be the transposed of the chr2-chr1 map.

```
> require(HiTC)
> require(HiCDataHumanIMR90)
> data(Dixon2012_IMR90)
> show(hic_imr90_40)

HTClist object of length 325
25 intra / 300 inter-chromosomal maps

> class(intdata(hic_imr90_40$chr1chr1))

[1] "dsCMatrix"
attr(,"package")
[1] "Matrix"

> object.size(hic_imr90_40)

1161141408 bytes
```

3 Description of the Hi-C data

The *HiTC* package provides several methods to describe a *HTClist* object.

```
> ## 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 + the related 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$chr6chr6)

HTC object
Focus on genomic region [chr6:1-171115067]
CIS Interaction Map
Matrix of Interaction data: [4278-4278]
Binned data - window size = 40000
4278 genome intervals
Total Reads = 21565450
Number of Interactions = 3657661
Median Frequency = 1
Sparsity = 0.1

> ## 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

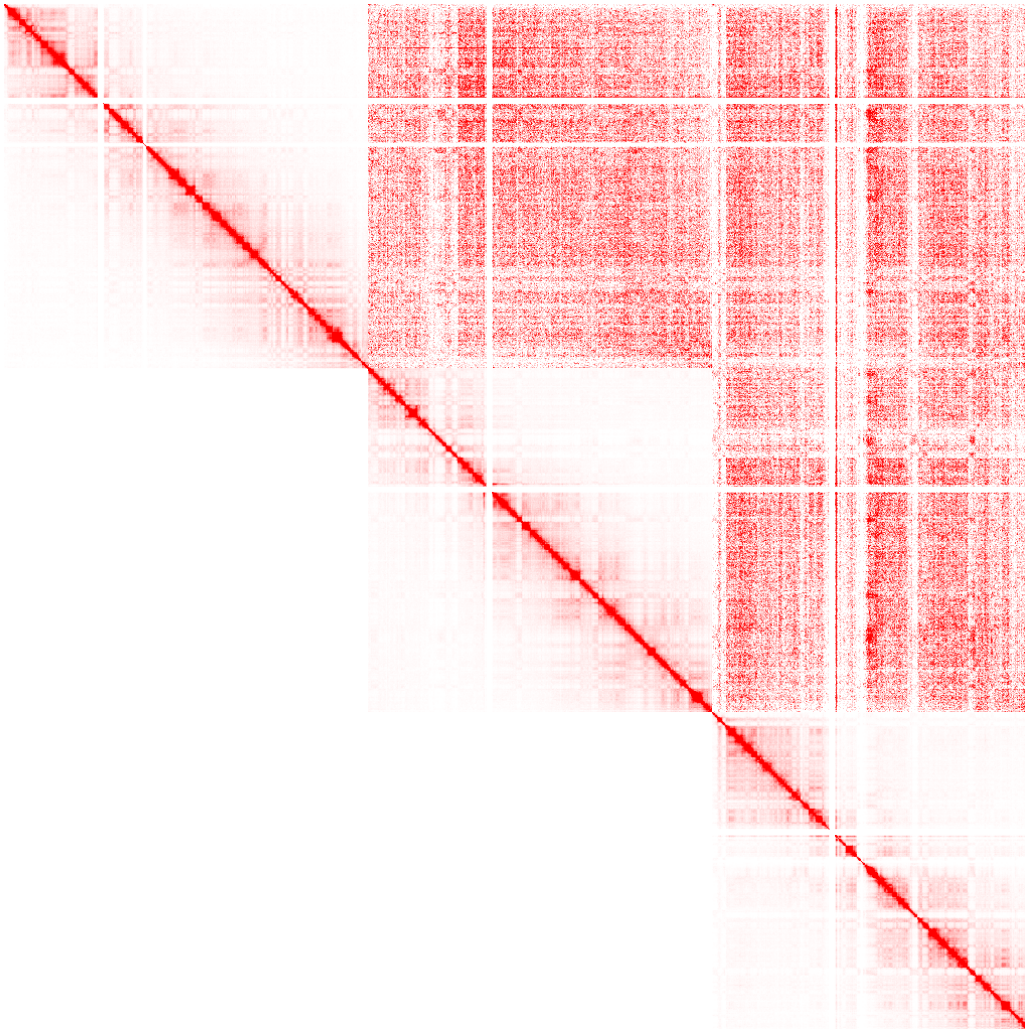
4 Hi-C Visualization

The Hi-C data can be visualized as contact maps, representing the contact frequencies between two chromosomes, or at the level of the genome. By default, objects from the *HTClist* class will be represented as an heatmap, whereas object from the *HTCexp* class (i.e. single map) as a triangle. Depending on what you want to visualize the resolution of the map can also be changed (from high to lower resolution).

```

> ## Go back to a smaller dataset (chr21, 22, X) at lower resolution
> chrs.subset<-c("chr5chr5", "chr6chr6", "chr7chr7",
+               "chr5chr6", "chr6chr7", "chr5chr7")
> imr90_500 <- HTClist(mclapply(hic_imr90_40[chrs.subset], binningC,
+                             binsize=500000, bin.adjust=FALSE, method="sum", step=1))
> mapC(imr90_500)

```

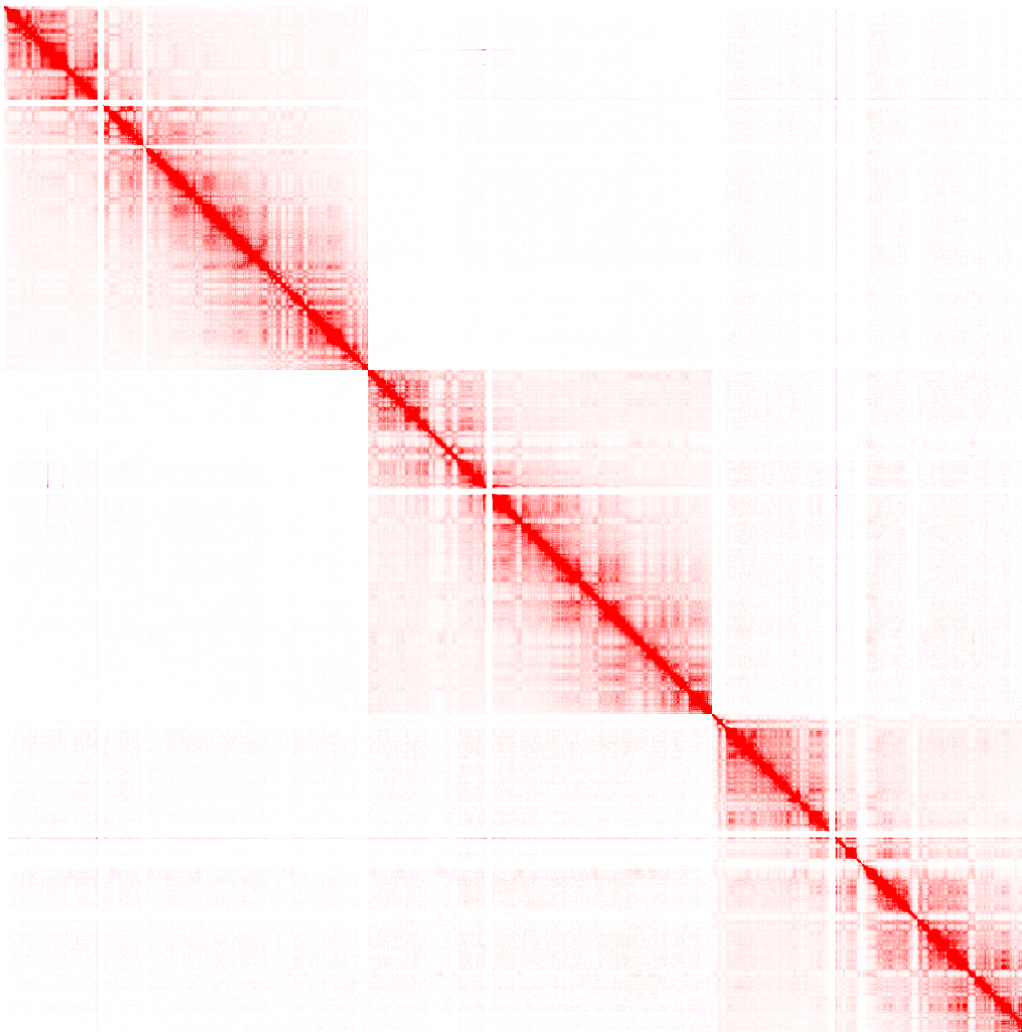


As we can see on this exemple, only half of the inter-chromosomal maps as stored and thus plotted. To display the full pairwise maps, methods such as `forcePairwise`, or `forceSymmetric` can be used to switch from a pairwise (and more memory consuming) form to a reduced form.

```

> mapC(forcePairwise(imr90_500), maxrange=500)

```



5 Hi-C Normalization

5.1 Back to restriction fragments

In addition to descriptive methods on the *HTClist* object, the *HiTC* package provides functions to extract biological information related to the data processing. These functions are useful for data normalization, in order to extract the expected bias at the level of the restriction fragment.

```
> ## Example on chromosome X
> ## GRanges of restriction fragments after HindIII digestion
> resFrag <- getRestrictionFragmentsPerChromosome(resSite="AAGCTT", overhangs5=1,
+                                                chromosomes="chr6",
+                                                genomePack="BSgenome.Hsapiens.UCSC.hg18")
> resFrag
```

```
[[1]]
GRanges object with 51298 ranges and 0 metadata columns:
      seqnames      ranges strand
   <Rle>         <IRanges> <Rle>
[1]   chr6      [  1, 10366]   +
[2]   chr6    [10367, 18359]   +
```



```

[51293] chr6 [170887666, 170887669] * | 269 584 0.555
[51294] chr6 [170888247, 170888250] * | 584 3119 0.555
[51295] chr6 [170891363, 170891366] * | 3119 2149 0.35
[51296] chr6 [170893509, 170893512] * | 2149 3232 0.405
[51297] chr6 [170896738, 170896741] * | 3232 3254 0.555

```

```

      GC_D      map_U      map_D
      <numeric> <numeric> <numeric>
[1]      0.37      <NA>      <NA>
[2]      0.35      <NA>      <NA>
[3]      0.26      <NA>      <NA>
[4]      0.34      <NA>      <NA>
[5]      0.335     <NA>      <NA>
...      ...      ...      ...
[51293] 0.465     <NA>      <NA>
[51294] 0.415     <NA>      <NA>
[51295] 0.29      <NA>      <NA>
[51296] 0.33      <NA>      <NA>
[51297] 0.475     <NA>      <NA>

```

seqinfo: 1 sequence from an unspecified genome; no seqlengths

```
> ## Annotation of Hi-C object
```

```
> imr90_500_chr6annot <- setGenomicFeatures(imr90_500$chr6chr6, cutSites)
```

```
> y_intervals(imr90_500_chr6annot)
```

GRanges object with 343 ranges and 3 metadata columns:

```

      seqnames      ranges strand |      len      GC
      <Rle>      <IRanges> <Rle> | <numeric> <numeric>
chr6:1-5e+05      chr6      [ 1, 500000] * | 127453 0.419
chr6:500001-1e+06 chr6      [ 500001, 1000000] * | 124817 0.419
chr6:1000001-1500000 chr6      [1000001, 1500000] * | 103076 0.433
chr6:1500001-2e+06 chr6      [1500001, 2000000] * | 127725 0.4
chr6:2000001-2500000 chr6      [2000001, 2500000] * | 122886 0.394
...      ...      ...      ...      ...
chr6:169000001-169500000 chr6 [169000001, 169500000] * | 110009 0.424
chr6:169500001-1.7e+08 chr6 [169500001, 170000000] * | 110434 0.411
chr6:170000001-170500000 chr6 [170000001, 170500000] * | 68293 0.473
chr6:170500001-1.71e+08 chr6 [170500001, 171000000] * | 114877 0.418
chr6:171000001-171115066 chr6 [171000001, 171115066] * | 0 NaN
      map
      <numeric>
chr6:1-5e+05      NaN
chr6:500001-1e+06 NaN
chr6:1000001-1500000 NaN
chr6:1500001-2e+06 NaN
chr6:2000001-2500000 NaN
...      ...
chr6:169000001-169500000 NaN
chr6:169500001-1.7e+08 NaN
chr6:170000001-170500000 NaN
chr6:170500001-1.71e+08 NaN

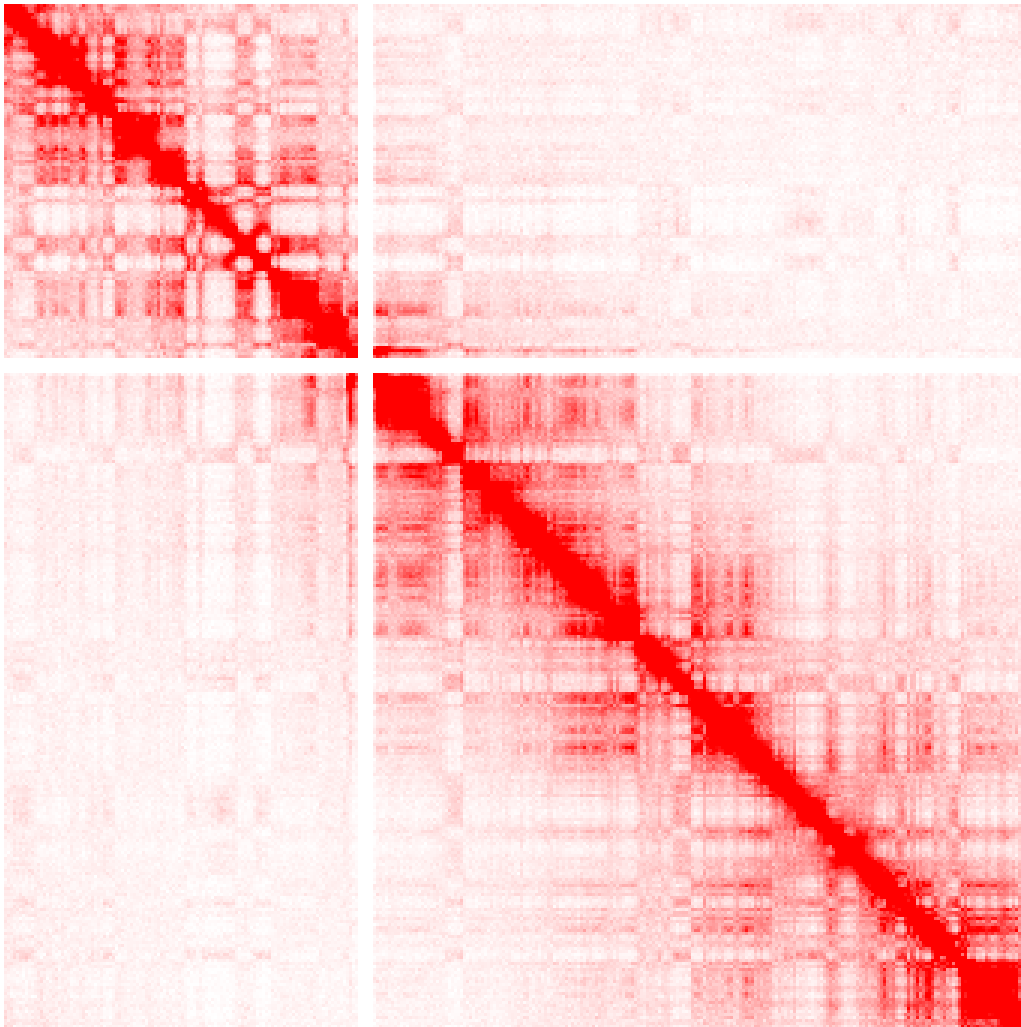
```

```
chr6:171000001-171115066      NaN
-----
seqinfo: 1 sequence from an unspecified genome; no seqlengths
> ## LGF normalization
> imr90_500_LGF <- normLGF(imr90_500_chr6annot)
```

5.3 Iterative correction and eigenvector decomposition (ICE) normalization

The ICE normalization is one of the most popular method to correct data from Hi-C bias. This method is based on the assumption of equal visibility of each genomic locus. The matrix of contact probabilities, M , for all given pairs of regions (i,j) is thus normalized such as $\sum_{i, i \neq j, j \pm 1} M_{ij} = 1$ for each region j . Note that running the ICE normalization method can be memory consuming because it uses the full genome matrix, and then store the bias vectors. If we advice to use apply the ICE normalization on a full Hi-C dataset (using inter and intrachromosomal maps), the *HiTC* package also allows to run it on a single intrachromosomal map.

```
> imr90_500_ICE <- normICE(imr90_500, max_iter=10)
> mapC(HTClist(imr90_500_ICE$chr6chr6), maxrange=500)
```

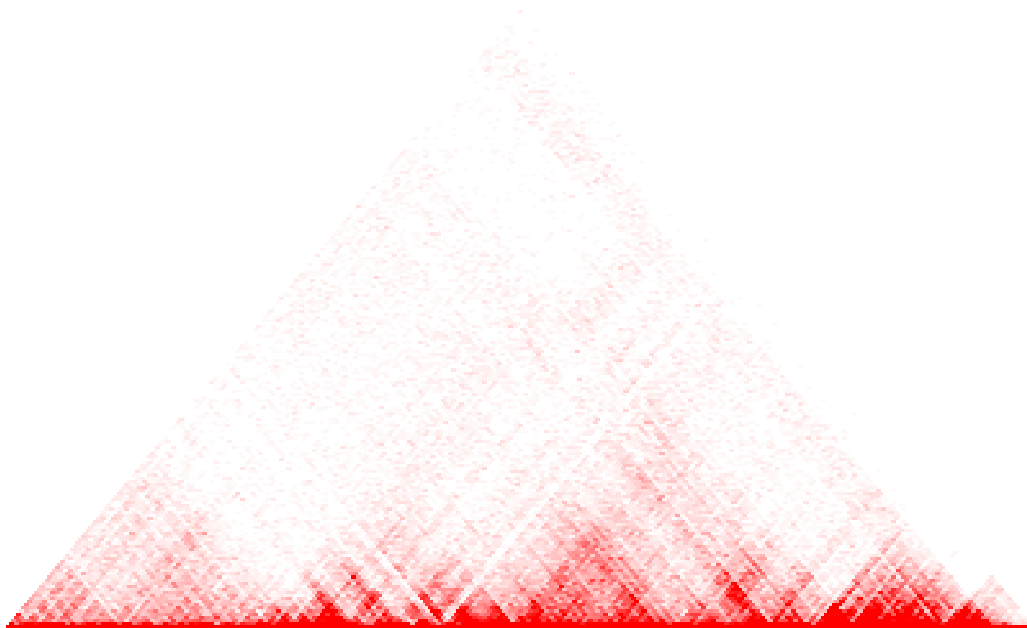


6 Detection of Topological Domains

Recent studies on a high resolution human and mouse Hi-C dataset have discovered that the genome organization can be further divided into megabase-long and evolutionarily conserved topological domains (TADs), with high frequencies of intra-domain chromatin interactions but infrequent inter-domain chromatin interactions ([Nora et al. \[2012\]](#), [Dixon et al. \[2012\]](#)). More recently, ? have demonstrated that the cell-type-specific chromatin organization seems to occur at the sub-megabase scale involving different ligation proteins and epigenomic mechanisms.

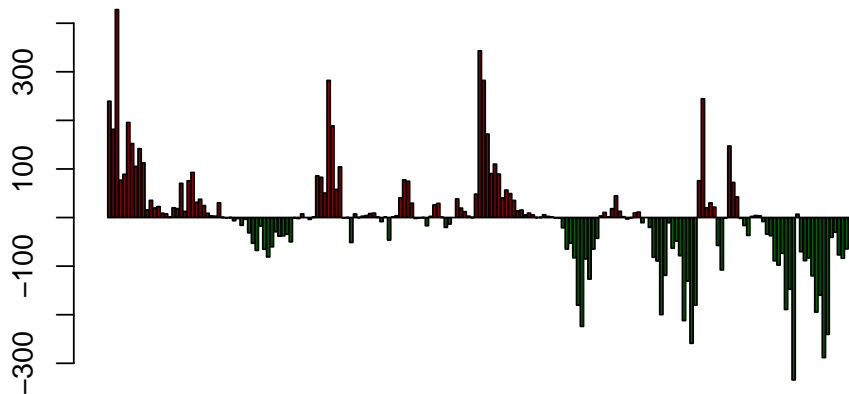
The following code shows how to focus on TADs, such as the ones describes in IMR90 around the Hox genes.

```
> hox <- extractRegion(hic_imr90_40$chr6chr6, chr="chr6", from=50e6, to=58e6)
> plot(hox, maxrange=50)
```



Different algorithms have been proposed to detect TADs. The directionality index was proposed by [Dixon et al. \[2012\]](#) as an input to their HMM model.

```
> di<-directionalityIndex(hox)
> barplot(di, col=ifelse(di>0,"darkred","darkgreen"))
```



Package versions

This vignette was generated using the following package versions:

- R version 3.2.0 RC (2015-04-08 r68161), x86_64-apple-darwin10.8.0
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.14.0, Biostrings 2.36.0, BSgenome 1.36.0, BSgenome.Hsapiens.UCSC.hg18 1.3.1000, GenomInfoDb 1.4.0, GenomicRanges 1.20.0, HiCDataHumanIMR90 0.101.1, HiTC 1.12.0, IRanges 2.2.0, rtracklayer 1.28.0, S4Vectors 0.6.0, XVector 0.8.0
- Loaded via a namespace (and not attached): BiocParallel 1.2.0, BiocStyle 1.6.0, bitops 1.0-6, futile.logger 1.4, futile.options 1.0.0, GenomicAlignments 1.4.0, grid 3.2.0, lambda.r 1.1.7, lattice 0.20-31, Matrix 1.2-0, RColorBrewer 1.1-2, RCurl 1.95-4.5, Rsamtools 1.20.0, tools 3.2.0, XML 3.98-1.1, zlibbioc 1.14.0

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References

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