1 Introduction

Chromosome conformation capture (3C) is a cross-link based technique to detect spatial proximity of specific genomic distant loci [1], which has sparked a number of large-scale methods to study multiple interactions simultaneously [2]. Hi-C is a genome wide, unbiased version of 3C [3], in which all interactions are sampled by paired-end high-throughput sequencing.

2 Description

2.1 Data

The data were generated by Lieberman-Aiden et al. and published in 2009 [3]. In this study, the authors used lymphoblastoid human cells and two different restriction enzymes (HindIII and Ncol) in the HiC experiments. This package contains the reads mapped to hg18 (using Bowtie [4]) of the HindIII replicate SRR027956 for chromosome 20 (with options –seedmms 2, –seedlen 40, –solexa1.3-quals). The two ends of the paired reads were mapped separately. This data package is used in the GOTHiC package, that identifies significant interactions in HiC data.

> dirPath = system.file("extdata", package="HiCDataLymphoblast")
> fileName1 = list.files(dirPath, full.names=TRUE)[1]
> fileName2 = list.files(dirPath, full.names=TRUE)[2]
> library(ShortRead)
> alignedReads <- readAligned(fileName1, type="Bowtie")
> alignedReads <- readAligned(fileName2, type="Bowtie")

References

