

Genomic Data Analysis in R

Lecture 8

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Overview

I. R and Bioconductor Packages for Genomic Data

II. Tutorials

- **Analyzing Genomic Data**
- **Analyzing and Annotating Variants**
- **Analyzing Sequence Data**

Overview: Learning Objectives

I. R Bioconductor Packages for Genomic Data

- `GenomicRanges`, `VariantAnnotation`, `Rsamtools`

II. Tutorials

1. Genomic Data Analysis

- i. Load, inspect, query a BED/SEG file
- ii. Genomic regions overlap

2. Genomic Variants and Annotations

- i. Load, inspect, query a VCF file

3. Sequence Data Analysis

- i. Load, inspect, query a BAM alignment file
- ii. Extract sequences and qualities
- iii. Compute “pile-up” statistics at genomic loci

Tutorial #1: Genomic Data Analysis

1. Loading and querying BED/SEG text files
 - a. Use packages `GenomicRanges`, `data.table`
2. Concepts from Lecture 7: Slides 38-42.
3. Download the VCF and SEG files for this tutorial
 - <https://www.dropbox.com/sh/zoitjnobgp7I7c2/AABBIpTQcNA4IWYOFnV5dIMKa?dl=0>
 - BRCA.genome_wide_snp_6_broad_Level_3_scna.seg
 - GIAB_highconf_v.3.3.2.vcf.gz, GIAB_highconf_v.3.3.2.vcf.gz
 - GIAB_highconf_v.3.3.2.vcf.gz, GIAB_highconf_v.3.3.2.vcf.gz.tbi
4. R Markdown file for tutorial on GitHub: `Lecture8_GenomicData.Rmd`

Tutorial #2: Genomic Variant Annotations

1. Loading and querying UCSC and Ensemble transcript/gene databases in R
 - a. Use packages `VariantAnnotation`, `biomaRt` (Ensembl),
`TxDb.Hsapiens.UCSC.hg19.knownGene`
2. Download the VCF files for this tutorial
 - <https://www.dropbox.com/sh/zoitjnobgp7I7c2/AABBIpTQcNA4IWYOFnV5dIMKa?dl=0>
 - `GIAB_highconf_v.3.3.2.vcf.gz`, `GIAB_highconf_v.3.3.2.vcf.gz`
 - `GIAB_highconf_v.3.3.2.vcf.gz`, `GIAB_highconf_v.3.3.2.vcf.gz.tbi`
3. R Markdown file for tutorial on GitHub: `Lecture8_Annotations.Rmd`

Tutorial #3: Sequence Data Analysis

1. Loading and querying a BAM file using Rsamtools
 - a. Define the genomic coordinates and components to query (`ScanBamParam`)
 - b. Scanning the BAM file (`scanBam`)
2. We will use the example from Lecture 7: Slides 12-16.
3. Download the BAM file for this tutorial
 - <https://www.dropbox.com/sh/zoitjnobgp7I7c2/AABBIpTQcNA4IWYOFnV5dIMKa?dl=0>
 - BRCA_IDC_cfDNA.bam, BRCA_IDC_cfDNA.bam
 - BRCA_IDC_cfDNA.bam, BRCA_IDC_cfDNA.bam.bai
4. R Markdown file for tutorial on GitHub: `Lecture8_Rsamtools.Rmd`