Introduction to R and Bioconductor

Alex Sánchez

Unitat d'Estadística i Bioinformàtica (UEB)

June 7, 2014

Table of Contents

A bit of interaction

- What is your R knowledge, on a 0(beginner) to 2 (expert) scale?
- How deep is your knowledge with R packages related to NGS, on a 0(none) to 2 (good)scale?
- What analyses do you plan to do in R?

Objectives

- Quick review of *R* history and capabilities
- Overview of the Bioconductor project
- Bioconductor classes and methods for NGS

What is R?

1. an implementation of the S language (Bell Laboratories,Rick Becker, John Chambers and Allan Wilks)
2. R is an integrated suite of software for
   - data manipulation
   - calculation and
   - graphical display.

What is R?(c'ed)

1. R is a vehicle for newly developing methods of interactive data analysis
   - devolops rapidly
   - is being extenden by a large collection of packages
     - Comprehensive R Archive Network (CRAN)
     - Bioconductor
2. However, most programs written in R are essentially ephimeral, written for a single piece of data analysis

R specifics

- a suite of operators for calculations on arrays, in particular matrices.
- an "environment":
  - a fully planned and coherent system,
  - it can be *saved*, *loaded*, *exchanged*.

R and statistics

- R is an environment...
  - originally not designed for statistics,
  - many classical and modern statistical techiniques implemented,
- Difference with S, S-plus, SAS or SPSS...
  - minimal ouput
  - minimal number of object (in comparison with the).

R and the window system

- R comes with a graphical system on all plataform
  - console like: Unix
  - GUI and console: Mac, Windows
- Integrated Developer Interfaces (IDE) have been developed
  - StatET plugin (`http://www.walware.de/goto/statet`) for eclipse
  - **Rstudio** (`http://rstudio.org`)

Using R interactively

- Most of the time R is used interactively
- R console is vey similar to Unix/linux
  - `ls` command for listing,...
  - The syntax is only slightly different:
    - `ls()` instead of `ls`
- Documentation and help pages always avaliable:
  - through the "?" command (*perfect match*)
  - through the "?" command (*fuzzy matching*)
  - through `help.start()` if you have a windows system
  - searchable through `help.search()`

CRAN

- `http://cran.r-project.org`
- The comprehensive R Archive
  - 5578 packages! (26 May 2014)
  - easy to install
    - R CMD INSTALL (cmd line)
    - `install.packages()` (from within the environment

What is Bioconductor

- A software project for the analysis of genomic data
- **Open** source and **open** development.
- `http://bioconductor.org`
- A collection of R packages with *some* common structures
  - >1.100 packages (554 soft.,600 annot.)
  - >300 developers, >4.000 citations
- Gentleman et al. *Bioconductor: open software development for computational biology and bioinformatics*. Genome Biology (2004) vol. 5 (10) pp. R80

Bioconductor: history and overview

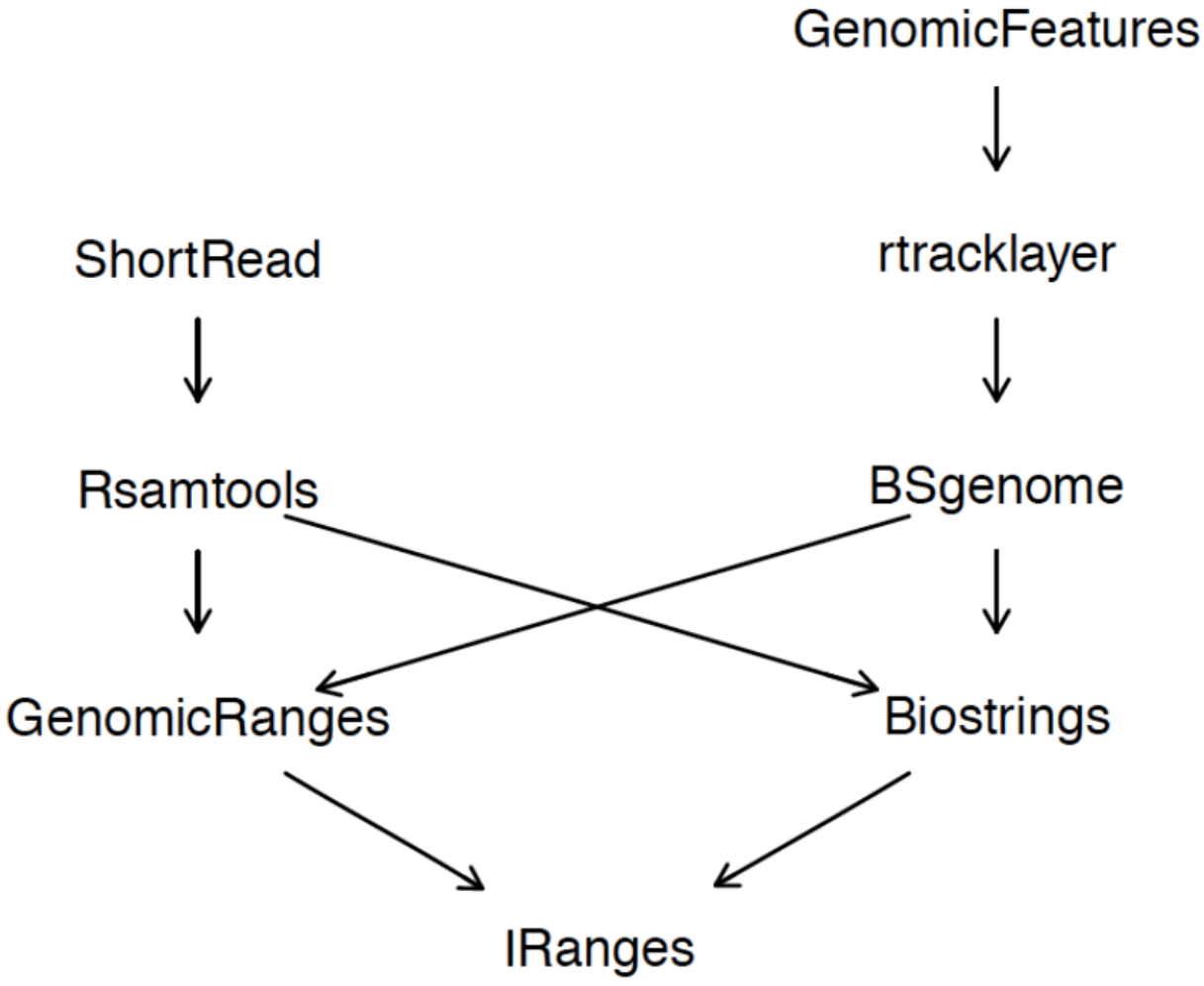
- Started in Harvard (2001) now hosted at Fred Hutchinson Cancer Research Center (FHCRC)
- Gentleman et al. *Bioconductor: open software development for computational biology and bioinformatics*. Genome Biology (2004) vol. 5 (10) pp. R80
- Focus on **Microarray** at first,
- and on **Next Generation Sequencing** as of 2008.

Bioconductor goals

- Provide access to powerful **statistical and graphical methods** for the analysis of biomedical and genomic data
- Facilitate the integration of **biological metadata** from WWW in the analysis of experimental data (e.g., GenBank, GO, LocusLink, PubMed)
- Allow the rapid development of **extensible, interoperable and scalable** software
- Promote **high-quality documentation** and **reproducible research**
- Provide **training** in computational and statistical methods

FHCRC,BIOC core packages

- Input and Output
  - rtacklayer, **Rsamtools, ShortRead**
- Sequence manipulation
  - **Biostrings**
- Range-based manipulations:
  - **IRanges, GenomicRanges**
- Annotations
  - **GenomicFeatures**, AnnotationDbi, BSgenome


GenomicFeatures
ShortRead
rtracklayer
Rsamtools
BSgenome
GenomicRanges
Biostrings
IRanges

53 Contributed packages (Sep. 2012)

- Chip-seq(14)
  - BayesPeak, CSAR, ChIPpeakAnno, ChiPseqR, ChIPsim, PICS, chipseq,...
- RNA-seq(18)
  - DEGseq, DESeq, Genominator, baySeq, edgeR, srnaSeqMao, goseq, gage, easyRNASeq,..

- **Infrastructure**: genomeIntervals, girafe, cqn
- **base calling**: Rolexa
- **Visualization**: HilbertVis, HilbertVisGUI
- **motif:** MotIV, rGADEM
- **domain-specific**: MEDIPS, OTUbase, R453Plus1Toolbox
- **database**: SRAdb, oneChannelGUI
- **smRNA**: segmentSeq

Installation

Two step installation

- First install R software: download from CRAN (`www.cran.r-project.org`)
- Install bioconductor
  - Download installer from Bioconductor website
    `> source("http://bioconductor.org/biocLite.R")`
  - Make default installation (installs some basic and some popular packages)
    `> biocLite()`
  - Add what you specifically need
    `> biocLite(goProfiles)`