



# **Computational Biology LU 2014**

Bioinformatics Group
Institute for Knowledge Discovery
Graz University of Technology
http://genome.tugraz.at
Petersgasse 14, A-8010 Graz





#### **Outline**

- Computational Biology LU
- Facts on R
- Introduction
  - Data
  - Variables
  - Missing Data
  - Subsets





#### • Exercise dates:

02.06.2013 08:00 – 12:00 Introduction to R

02.06.2014 14:00 – 18:00 Microarrays

• 03.06.2013 08:00 – 12:00 miRNAs

• 04.06.2013 08:00 – 12:00 Networks

• 06.06.2013 08:00 – 12:00 Microbiome

■ 16.06.2013 09:00 — 13:00 Presentations

- 16.06.2013 15:00 — 18:00 Presentations

- You have to attend 4 out of 5 exercises and all presentations.
- Work in groups of at most two students.





## Computational Biology LU

- Deliver for each exercise a protocol until 14.07.2014.
- Email: <u>Gerhard.Thallinger@tugraz.at</u>
- For the protocol please make sure that:
  - It is a PDF file.
  - Important R code is discussed in the text appendix.
  - Images are included in the PDF file and discussed in the text. Axes of the images are labelled.
  - Include the R code or the Sweave file as an attachment
  - Make sure that the R code/Sweave file is executable without error (source() on a fresh R installation)





#### Facts on R

- Software environment for statistical computing and graphics
- Open source: <a href="http://cran.at.r-project.org/">http://cran.at.r-project.org/</a>
- Available for Windows, Linux and Mac OS
- Two major releases per year
- Provides data manipulation and display facilities.
- It can be extended with "packages" containing data, code and documentation.
- Currently 4556 (+671 Bioconductor) packages are available on the homepage.





## Simple usage

- Either R, or
- More comfortable: RStudio

- On the university PCs, R and RStudio have to be installed on USB Sticks and run from there.
- Install R first (http://www.r-project.org/)
- Afterwards RStudio (http://www.rstudio.com/)

## Executing the commands

- File with commands available on the course site: <u>http://genome.tugraz.at/ComputationalBiology/ComputerLab/</u>
- Open file in R (File->Open), position cursor at a certain line. "Ctrl+R" will send the line for execution to the console and go to the next line
- Comments are written after "#"
- R provides code completion (tab key)