DFG PRIORITY PROGRAMME "ADAPTOMICS" 1529 R in Science | 10 - 11 February 2016





in Science: beginner's course

R is a high-level open source programming language and an environment for data analysis and graphics. This is a course about how to use R & RStudio and how to perform applications in statistics, phylogenetics, and data visualizations. The course includes several sessions and each contains a presentation and an exercise for practical training.

Day 1

Oral presentation about R

Essentials of the R language

- basic commands
- data import
- data export
- data re-arrangement

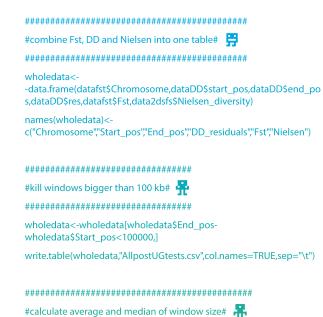
Day 2

Statistics and data visualization

- correlation
- GLMM (generalized linear mixed models)
- multiple comparison analysis in ANOVA (analysis of variance)
- PCA (principle component analysis)

Phylogenetics

- data import
- data modification
- data analysis
- data export



mean(wholedata\$End_pos-wholedata\$Start_pos)

genelist<-read.table("Alyrata_107_geneS.gff3")

c("Scaffold","?","gene_no","Start_pos","End_pos","?","?","ID")

Chromosome1<-genelist[genelist\$Scaffold=="scaffold_1",]
Chromosome2<-genelist[genelist\$Scaffold=="scaffold_2",]

Chromosome3<-genelist[genelist\$Scaffold=="scaffold_3",]
Chromosome4<-genelist[genelist\$Scaffold=="scaffold_4",]

#open list of A. lyrata genes#

#V4=start_pos

#V5=end_pos names(genelist)<-

median(wholedata\$End_pos-wholedata\$Start_pos)