

# COST Training School - King's College

Danny Arends, Karl W. Broman, Ritsert C. Jansen

## Practical R and R/qtl



---

Groningen Bioinformatics Center

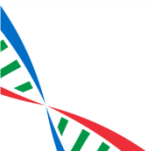
# Practical R and R/qtl

---

- Subset of:

<http://www.dannyarends.nl/pdf/Rintro.pdf>

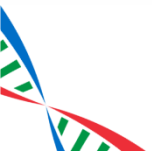
- R
  - Basic introduction
  - Lessons learned
  - Basic assignments
- R/qtl
  - Basic assignments



# R – Basic introduction

---

- `library("packagename")`
- `if(a < b)`
- `while(a < b)`
- `for(a in b)`
- `apply(matrix, 1, sum)`
- `lapply(vector, sum)`
- `which, any, match`

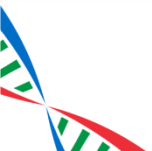


# R – Basic introduction

---

**Programming involves more than putting statements after each other**

- Structure
- Comments
- Principle of least surprise
- DRY
- Dead code
- Copyright

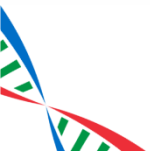


# An example

---

- A basic code example without any code

```
#  
# mycode.R  
#  
# Copyright (c) 2010-2014 - GBIC, Danny Arends and Ritsert C. Jansen  
# Last modified Feb, 2013  
# First written Jan, 2011  
#  
# R function to perform task XXX on matrix A and B  
#  
  
# Note: dim(A) == dim(B)  
fun <- function(A, B){  
  
}
```

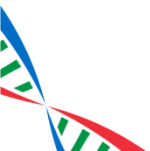


# Dead code

---

```
deadCode1 <- function(A, B){  
  C <- A + B  
  # C <- C*C  
  return(C)  
}
```

```
deadCode2 <- function(A, B){  
  C <- A + B  
  if(FALSE) C <- C*C  
  return(C)  
}
```



# R – Some tips and tricks

---

- Select probes within a region:

Code.R

```
> rows <- which(M[, "Mbp.start"] >= 5 & M[, "Mbp.end"] <= 10)
```

- ‘Force’ a numeric matrix

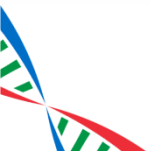
Code.R

```
> NM <- apply(M, 2, as.numeric)
```

- Perfectly tailored for linear modeling

Code.R

```
> result <- anova(lm(Y ~ X1 + X2 + X1:X2))
```



# R – Some tips and tricks

---

- Lapply and “[”

Code.R

```
> list
[[1]]
[1] 0, 4, 9
[[2]]
[1] 1, 5, 10

> lapply(list, "[", 1)
[1] 0, 1

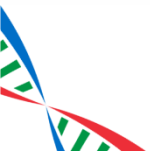
> lapply(list, "[", 2)
[1] 4, 5
```



# R – Lessons learned

---

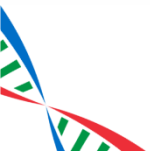
- **Distrust the type system**
  - Make sure the type of data is correct
    - **numeric != factor**
    - **matrix != data.frame**
    - **vector != list**
- **Use the package system**
  - Saves time in future (if you want to submit to CRAN)
  - Warns/Forces you to write manual files
  - Help files come with examples
    - R CMD BUILD packagename
    - Runs the examples as test suite



# R – Final remarks

---

- **LOTS** of packages
  - CRAN: 4701 packages (22<sup>th</sup> Juli 2013)
  - Bioconductor
    - Software (672)
    - AnnotationData (690)
    - ExperimentData (157)
- The type system sucks
- Code CLEAN
- Perfectly tailored to perform linear algebra
- Help is available



# R

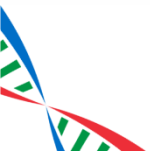
---

- Basic assignments:

<http://www.dannyarends.nl/docx/kingscollege.docx>

<http://www.dannyarends.nl/txt/kingscollegeanswers.txt>

- Install and Load the R/qtl package (Already Done)
- Format your own data
  - Load and Save
- Create a genetic map
- Effect mapping
- QTL mapping



# R/qtl

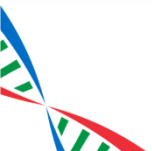
---

- Basic assignments :

<http://www.dannyarends.nl/docx/kingscollege.docx>

<http://www.dannyarends.nl/txt/kingscollegeanswers.txt>

- Format your data for use with R/qtl
- QTL scanning
  - scanone
- Plot routines
- Multiple QTL Mapping
  - Additive & Dominance models



# Additional assignments

---

- R
  - An LED
- R/qtl
  - Fix a genetic map
- Still hungry for more:  
<http://www.dannyarends.nl/pdf/Rintro.pdf>

