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6/29/11

How to convince Biologists to use R

Hans-Rudolf Hotz (hrh@fmi.ch)
Friedrich Miescher Institute for Biomedical Research
Basel, Switzerland

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How to convince Biologists to use R

....you force them to use R

Hans-Rudolf Hotz (hrh@fmi.ch)
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Basel, Switzerland

background

Friedrich Miescher Institute

- part of the Novartis Research Foundation
- affiliated institute of Basel University

314 employees

(incl. 96 PhD students, 95 Post Docs)

Epigenetics (8 research groups)

Growth Control (7 research groups)

Neurobiology (8 research groups)

Technology Platforms

Computational Biology – Cell Sorting – Imaging and Microscopy – Functional Genomics – Histology – Mass Spectrometry – Protein Structure

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Computational Biology Platform

five people supporting the wet lab scientists

dealing with all kind of data

~75 % of our work originates from NGS data

~75 % of our work is done with R (it used to be Perl)

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How to convince Biologists to use R
....you force them to use R

....you help them to use R

....they are forced to use R

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.....they are forced to use R

Biological research has changed from studying
a single gene/phenotype to genome wide analysis

→ a lot of (numeric) data

→ need for new software

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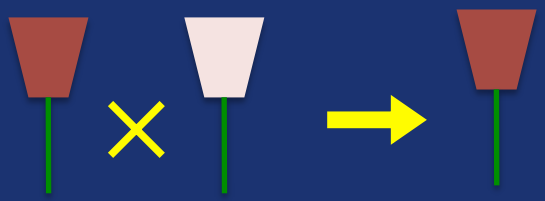
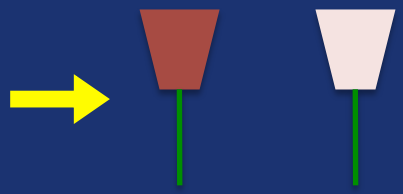
Biological reserach the classical experiment:



F1: 302:0 150:0



F2: 351:109 287:96

→ F2: 3:1

Biologists don't need R

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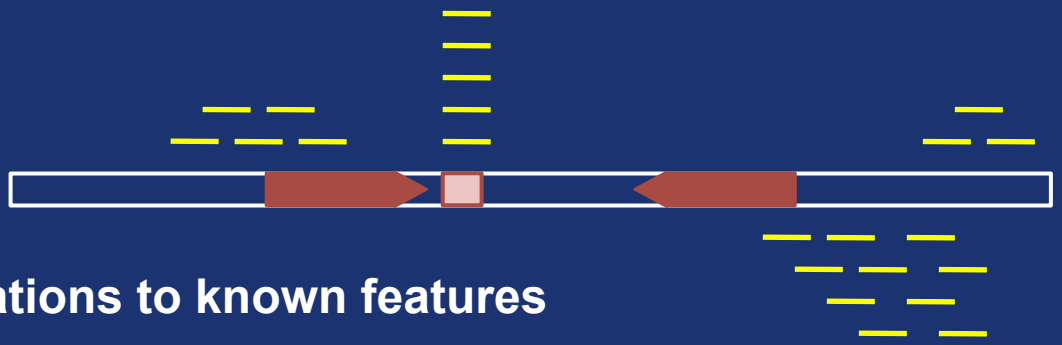
Biological reserach

the modern experiment:

100 million reads
from a DNA sequencer
(each 100 nucleotides long)

```
GATCGTGCCACC.....
GTGGCGAATGAT.....
CATCGTNCCACC.....
.....
```

align to the genome



compare the locations to known features
identify new features

Biologists need big computers
....and the right software!

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Software and Tools for Biologists

- commercial software	expensive, not up-to-date
- public website	limited data volume
- open source tools	not very flexible or address only single steps
- self written software	Biologists are not IT people
- “Bio* projects”	

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“Bio* projects

BioPerl, Biopython, BioJava.....Bioconductor

- open source
- ongoing development
- ‘easy’ to use
- can act as a ‘bridge’ to connect different open source tools / different data sets

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Bioconductor http://www.bioconductor.org/

"Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, more than 460 packages, and an active user community."

Depending on the nature of your research, Bioconductor might be the only available choice.

....they are forced to use R

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Biological reserach

use of Bioconductor

ShortRead, Biostrings

100 million reads
from a DNA sequencer
(each 100 nucleotides long)

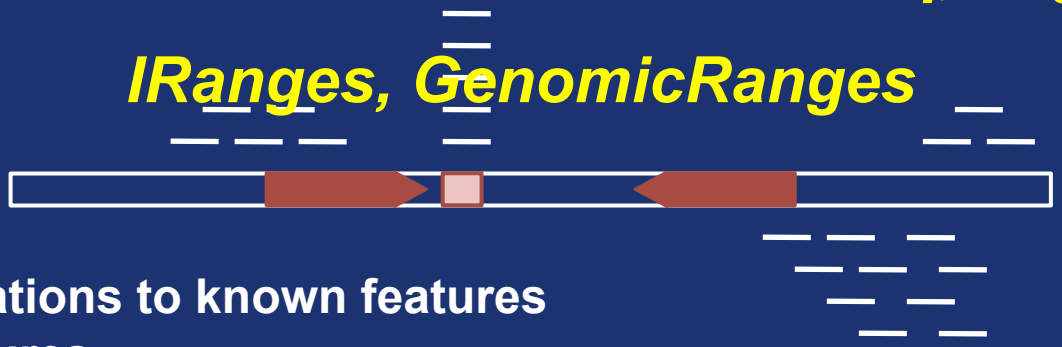
```
GATCGTGCCACC.....
GTGGCGAATGAT.....
CATCGTNCCACC.....
.....
```

Rsamtools

align to the genome

DESeq, edgeR

IRanges, GenomicRanges



biomaRt,
rtracklayer

compare the locations to known features
identify new features

chipseq

....you help them to use R

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....you help them to use R

- running training courses
  - introductory
  - advanced
  - ‘RLunch’

- we don’t provide any help for Excel (you force them to use R)

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introductory training course

- 4 x ~2.5 hours plus ‘homework/exercises’
- based on “Introductory Statistics with R” by Peter Dalgaard
- offered every ~9 months
- 25 - 30 participants (split in two groups)

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session 1

Installing and running R

```
> hist(rnorm(1000))
```

Interacting with R

```
> 2 + 2
```

```
> x <- 2 + 2
```

Introducing the concept of vectors

```
> weight <- c(60, 72, 57, 72)
> mean(weight)
> weight + 1
```

participants are not familiar with working on the command line

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session 2

data types (numeric - logical - character - factor)

vector manipulation

higher data structures (matrix - data.frame - list)

```
> numbs <- c(1,2,3,4,5)
> chars <- as.character(numbs)
> as.numeric(chars) %% 2 == 0
[1] FALSE TRUE FALSE TRUE FALSE
```

participants are struggling
participants don't see the relevance to their work

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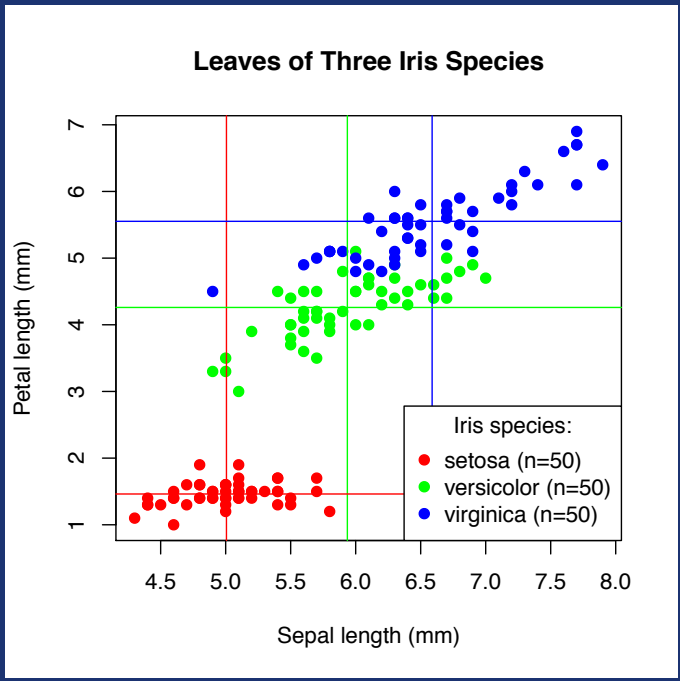
session 3

reading from text files
writing to text files

```
> read.delim("iris.txt")
```

visual data exploration

storing plots as image files



participants are starting to see the light.....
..... or we lose them completely

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session 4

statistical hypothesis testing

- fisher.test()
- cor()
- shapiro.test()
- t.test()
- wilcox.test()
- phyper()
- etc.

```
> D <- data.frame(DNAmet=c(T,F,T,T,T,T,F,T,F,F,T,F,F,F,F,F,F),
                  H3acet=c(T,T,F,T,T,T,F,T,F,F,F,F,F,F,F,F,F))
> ctD <- table(D)
> ctD
       H3acet
DNAmet FALSE TRUE
FALSE      9    1
TRUE       1    5

> fisher.test(ctD)

   Fisher's Exact Test for Count Data

data:  ctD
p-value = 0.0345
...
```

a simple Monte Carlo simulation

participants realize they lack basic statistics

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after the introductory training course

do we have 30 new R experts, now? no !

but:

- next time they knock at our door we don't have to start at point zero.
- they will go on statistic training
- they want to know more
  - advanced training course
  - bi-weekly 'RLunch'

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advanced training course

- 3 extra sessions
- working with Bioconductor packages

Using R for Short-Read Analysis (2 sessions)

Biostrings, IRanges, GenomicRanges, Rsamtools

Affymetrix microarray data analysis (1 session)

affy, limma

participants are overwhelmed

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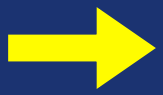
RLunch

- someone is presenting a ‘problem’ or ‘solution’

- introduction of (new) Bioconductor packages



mixture between a ‘journal club’
and a ‘progress report’

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Epigenetics

- Robert Ivanek

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