R/mpMap Workshop

Part 1: Overview

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Plan

Wednesday

- Part 1: Overview (20 min)
  - Introduction
  - Background
  - Installation
  - Documentation
  - Importing Data
- Exercises (5 min)
- Break/Questions (5 min)

Plan (Thursday)

8:30-9:30

- Part 2: Linkage Map Construction (45 min)
    - Estimating recombination fractions
    - Grouping
    - Ordering
    - Refinement
- Exercises (10 min)
- Break/Questions (5 min)

Plan

9:30-10:30

- Part 3: QTL Mapping (45 min)
    - Full Model
    - Association mapping
    - Meta-alleles
    - Mixed models
- Exercises (10 min)
- Break/Questions (5 min)

Plan

10:30-11:30

- Part 4: Advanced Topics (45 min)
    - Imputation
    - Selective phenotyping
    - Simulation
    - Haplotype Mosaics/Recombination
    - Visualization
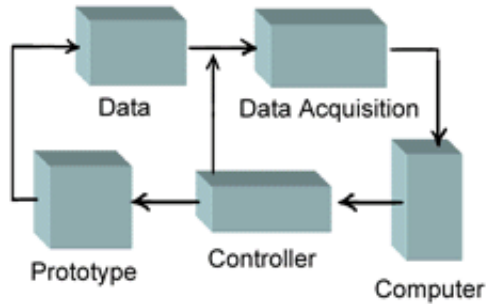- Exercises (10 min)
- Break/Questions (5 min)
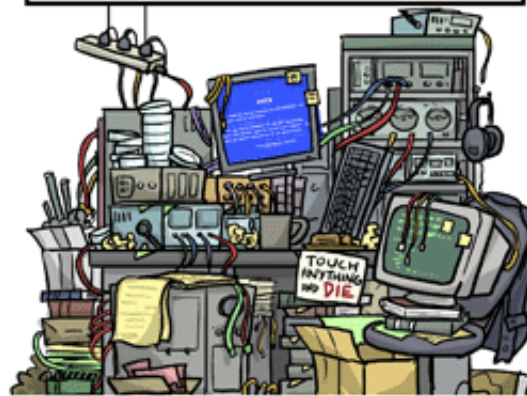
Part 1: Overview

Introduction

1998-2002
B.S. With Honors
Mathematics

2002-2007
Ph.D.
Biostatistics

2007-2015
Postdoc
Research Scientist
Senior Research Scientist
Statistical Genetics in Crops

At CSIRO

- 2009: Start of MAGIC linkage map construction

- 2011: Published R/mpMap

- 2013: Workshop @ NIAB on MAGIC-Type Populations

  - http://openwetware.org/wiki/MAGIC:Slides

- 2014: Genetics/G3 special collection

  - http://www.genetics.org/cgi/collection/multiparental_populations

- 2015: Workshop @ PAG Asia on Multiparental Populations

Collaborators

- Wheat MAGIC4/8, CSIRO

- Durum wheat MAGIC4, U. Bologna

- Barley MAGIC8, U. Bonn

- Tomato MAGIC8, INRA

- Arabidopsis MAGIC19, Cambridge, Oxford

- Chickpea MAGIC8, ICRISAT

- Rice MAGIC8/16, IRRI

- …

Going forward - less involvement with MAGIC

Associate Director in Population Analytics @ Janssen

- Focus on precision (personalized) medicine

Sep. 9-11 Wageningen, Netherlands

- EUCARPIA Biometrics in Plant Breeding

Nov. 16-18 China

- Nature Agrigenomics Conference

Background: why mpMap?

- Alternatives:

  - HAPPY - applicable to general designs

  - R/qtl - more general

- Interfaces with both

- More specific: focus on MAGIC

- More general: broad range of tools

Installation

```
install.packages("devtools")
library(devtools)
install_github("behuang/mpMap")
library(mpMap)


## Loading required package: Rcpp
```

Documentation

- Should be the first stop for

    - inputs

    - outputs

    - related pages

    - examples

```
library(mpMap)
?mpMap

?read.mpcross
?mpcross
```

Importing Data

- Can be created using files or objects
- Necessary components
    - finals - progeny genotypes
    - founders - parental genotypes
    - pedigree - record of all crosses used in design
    - id - indices of rows in pedigree of genotyped finals
    - fid - indices of parental rows in pedigree
- Optional components
    - map
    - phenotypes

Common issues importing data

- Numeric genotypes
- Pedigree structure
- Indices

[((A x B) x (C x D)) x ((E x F) x (G x H))]-1-1-1-1-1-BP-BP-BP

A/B//C/D///E/F//G/H

ABCDEFGH

Simulated Data

```
map <- sim.map(len=100, n.mar=51, eq.spacing=T, include.x=F)
ped <- sim.mpped(4, 1, 2, 3, 1)
dat <- sim.mpcross(map, ped)

names(dat)


## [1] "founders" "finals"    "ibd"         "pheno"      "map"        "pedigree"
## [7] "id"        "fid"        "qtlgeno"


dat$founders[,1:5]


##     D1M1 D1M2 D1M3 D1M4 D1M5
## A     1    0    1    1    1
## B     1    1    0    1    1
## C     0    1    0    0    0
## D     1    0    0    1    1
```

Simulated Pedigree

ped

```
##    id Male Female Observed
## 1   1    0      0        0
## 2   2    0      0        0
## 3   3    0      0        0
## 4   4    0      0        0
## 5   5    1      2        0
## 6   6    3      4        0
## 7   7    5      6        0
## 8   8    5      6        0
## 9   9    7      7        0
## 10 10    9      9        0
## 11 11   10     10        1
## 12 12    8      8        0
## 13 13   12     12        0
## 14 14   13     13        1
```

Exercises

Installation and Documentation

- What version number is it?

- When was it last updated?

- Name three functions used for linkage map construction

- Name three visualization functions

- Name two other software packages to which mpMap can output files

Importing Data - Founders

- Which will work?

- What will cause problems?

```
##    D1M1 D1M2 D1M3 D1M4 D1M5
## A     0    0    1    0    0
## B     1    0    0    1    1
## C     0    0    0    1    0
## D     0    1    1    1    0
```

```
##    D1M1 D1M2 D1M3 D1M4 D1M5
## A   AA   AA   BB   AA   AA
## B   BB   AA   AA   BB   BB
## C   AA   AA   AA   BB   AA
## D   AA   BB   BB   BB   AA
```

Importing Data - Finals

- Which will work?

- What will cause problems?

```
##      D1M1  D1M2  D1M3  D1M4  D1M5
## L1      0     0     0     1     1
## L2      1     2     0     1     1
## L3      1     0     0     1     1
## L4      0     0     0     0     0
## L5      0     1     0     1     0
## L6      0     0     0     1     0
```

```
##      D1M1  D1M2  D1M3  D1M4  D1M5
## L1      0     0     0     1     1
## L2      1     0     0     1     1
## L3      1     0     0     1     1
## L4      0     0     0     0     0
## L5      0     1     1     1     0
```

Importing Data - Pedigree

- Which will work?

- What will cause problems?

```
##      id Male Female Observed
## L1  1    0      0         1
## L2  2    0      0         1
## L3  3    0      0         1
## L4  4    0      0         1
## L5  5    1      2         0
## L6  6    3      4         0
```

```
##      id Male Female Observed
## L1  1    0      0         0
## L2  2    0      0         0
## L3  3    0      0         0
## L4  4    0      0         0
## L5  5    1      2         0
```

Importing Data - Map

- Which will work?

- What will cause problems?

```
##     Marker Chr Pos
## 11    D1M1   1   0
## 12    D1M2   1   2
## 13    D1M3   1   4
## 14    D1M4   1   6
## 15    D1M5   1   8


##     Marker Chr Pos
## 12    D1M2   1   2
## 14    D1M4   1   6
## 15    D1M5   1   8
## 13    D1M3   1   4
## 11    D1M1   1   0
```

Questions