R/QTL Part 2
QC, Non-F_2 Populations

Tom Kono
2017-03-14

First!
Plant Breeding Symposium

- http://plantsciencesymposium.umn.edu/

- 24 March, 2017, with a workshop on 23 March.

- Karl Broman, Briana Gross, Allison Miller, John Burke, John Doebley, among others...

Recall: QTL Mapping

- Identify genomic regions underlying variation in quantitative traits

- Usually involves structured populations with known genotype and phenotype

- R/QTL package by Karl Broman is one of the best, both in methodology and documentation

Get the Materials

```
$ git clone https://github.com/MorrellLAB/DoesNaughtCompute.git
$ cd DoesNaughtCompute/R_QTL_Part2/
```

In R:

```
> install.packages("qtl")
```

If you'd like to re-generate the sample dataset:

```
> install.packages("devtools")
> library(devtools)
> install_github("kbroman/simcross")
```

Sample Dataset

- F_2 and F_3 families, with no phenotypic data
- Genotyped with some markers on two chromosomes
- Some variation in marker density along chromosome
- Some markers have high missing data
- Some genotyping errors

F_2: Quick Review

- Use the `read.cross()` function to load the data

```
> pop <- read.cross(
    format="csv",
    file="Data/Simulated Genotypes F2.csv")
```

- Summarize the population

```
> summary(pop)
```

- Summarize the markers

```
> summary.map(pop)
```

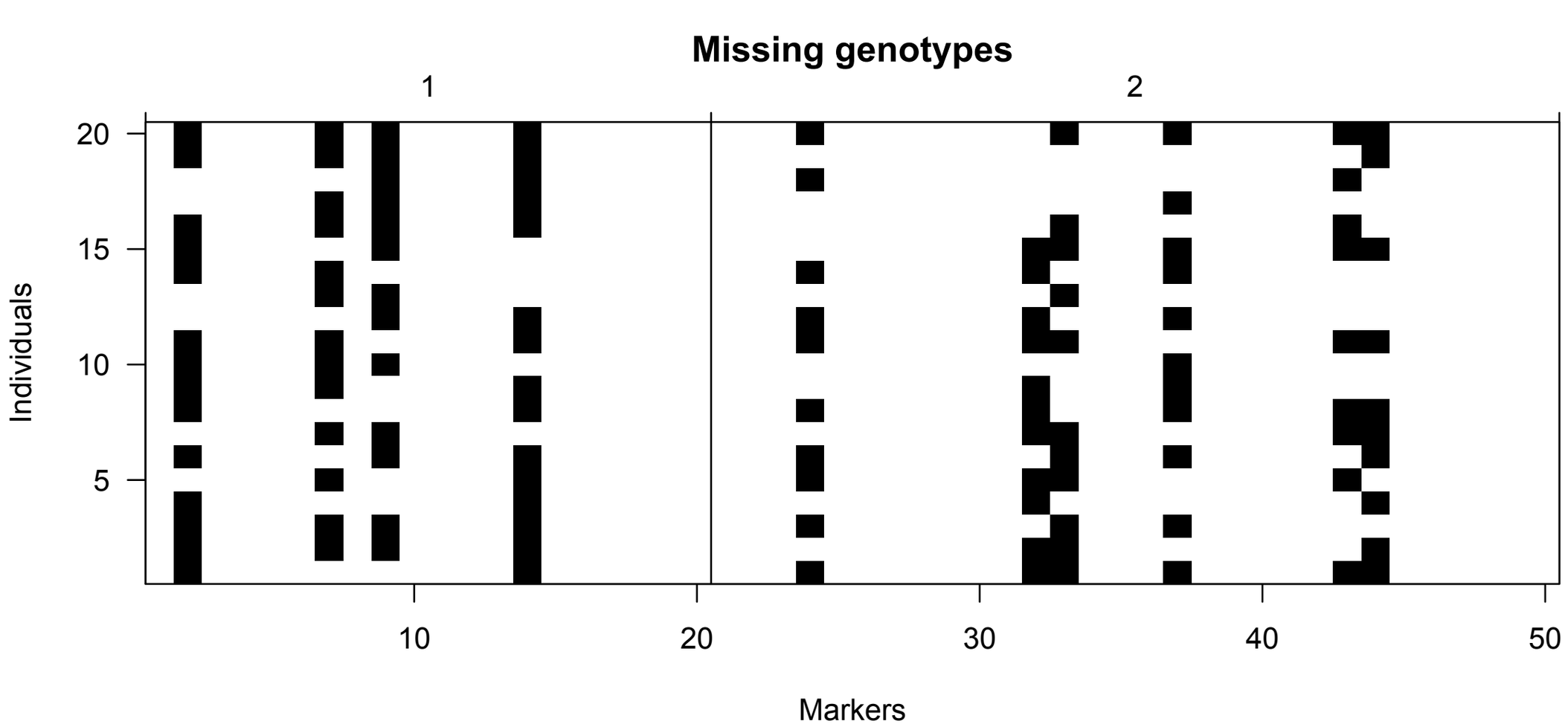
F_2: Quick Review

- How many individuals are in the F2 population?

- How many markers are genotyped? How many on each chromosome?

F_2: Missing Data

- First QC step: visualize missing genotypes
  `> plotMissing(pop)`

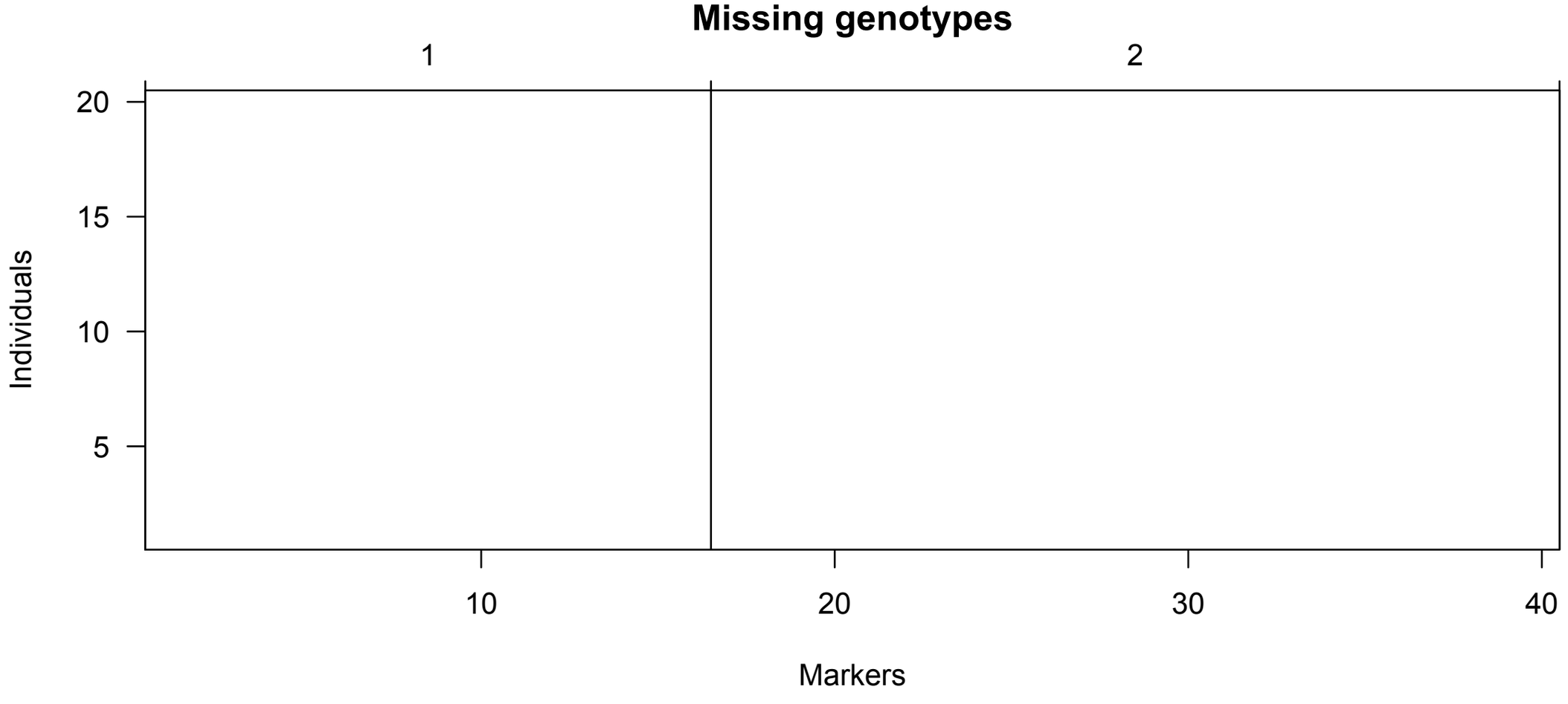


F_2: Missing Data

- Let's remove markers with lots of missing data:

```
> todrop <- markernames(pop)[nmissing(pop, what="mar") > 5]
> pop <- drop.markers(pop, todrop)
> plotMissing(pop)
```

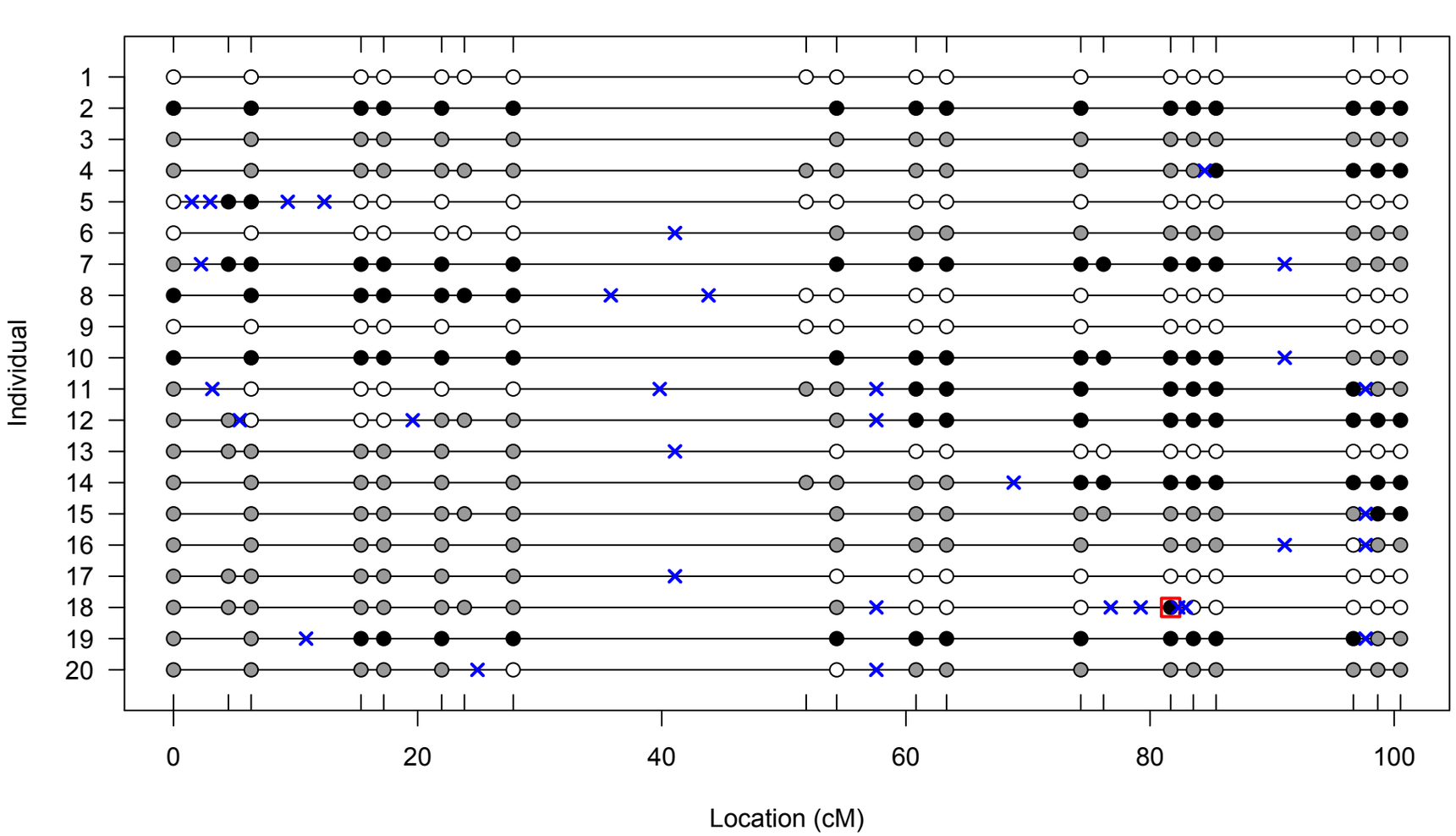
- How many markers remain?



F_2: Genotyping Errors

- Search for genotyping errors using the method of Lincoln and Lander (1992)

```
> pop <- calc.errorlod(pop, error.prob=0.01)
> plotGeno(pop, "1")
> plotGeno(pop, "2")
```



F_2: Genotyping Errors

- Unfortunately, R/QTL does not have a utility to fix genotyping errors

- Must go back to raw data

- If not, maybe set to missing and impute?

BC_sF_t: Read the Data

- R/QTL has limited support for more advanced populations: backcross and selfing

- The `read.cross()` function takes additional args:

```
> pop <- read.cross(
    format="csv",
    file="Data/Simulated_Genotypes.csv",
    BC.gen=0,
    F.gen=3)
```

- Plot the summaries, like in the F_2 case. Different?

BC_sF_t: Features

- Adjusts map distances and genotype probabilities for repeated backcrossing, selfing, or combinations of the two

- Similarly, these calculations trickle down to error detection and QTL scans

- Always read the docs! http://www.rqtl.org/tutorials/bcsft.pdf

More Complicated Designs?

- Nested Association Mapping populations: 'NAM' package
  https://cran.r-project.org/web/packages/NAM/NAM.pdf

- Multiparent Advanced Intercross populations: 'mpMap' package
  https://cran.r-project.org/web/packages/mpMap/mpMap.pdf

  Or, 'mpMap2'
  https://github.com/rohan-shah/mpMap2

A Note About the Data

- All the data used here was made up!
- Simulated with 'simcross' - also from Karl Broman http://kbroman.org/simcross/
- See 'simulate_genotypes.R' for script used to generate the data