Some R package extensions to R/qtl2 for fine-mapping in multi-parent populations

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http://www.stat.wisc.edu/~yandell/talk/hort/2018_Rqtl2Extensions.pdf

overview of resources

- [R/qtl2](#)
- R/qtl2 extensions (on github)
  - [R/qtl2ggplot](#)   adds ggplot2 graphics
  - [R/qtl2pattern](#)   explores SNP patterns
  - [R/qtl2shiny](#)   offers interactive (shiny) app
  - [R/qtl2feather](#)   speeds up genotype probability access
- [Plant Systems Genetics Talk, Bangkok, Thailand, Jan 2017](#)
  - [intro slides 29-39](#)   overview of multi-parent population designs
  - various material on QTLs and on genomic selection from plant perspective

new style plot objects for R/qtl2

- R/qtl2 (and R/qtl) use base plot tools
  - easy to implement, but do not rescale well to devices
  - plot is basically a paper copy displayed on screen
- R/qtl2ggplot uses modern grammar of graphics tools (ggplot2)
  - plots are now objects that can be resized, saved, etc.
  - work well with modern "tidyverse" tools associated with RStudio
- extensions with R/qtl2ggplot
  - overlay multiple phenotypes
  - facets
  - extensible to R/qtl2pattern

new tools to look at small genomic region

- R/qtl2pattern unpacks SNP & SV patterns across founders
  - partition SNPs into groups based how founders differ
  - connect similar patterned SNPs to see simpler genetic pattern across region
  - impute new SNPs for each pattern
- drill into SNP information
  - identify top SNPs in genome database
  - relate SNPs to genes; refine to exon/intron
  - study 3-level SNP effects over region (additive & dominance)

interactive shiny tool for R/qtl2

- features
  - interactive, menu-driven
  - explore phenotypes in small region
  - extensible to multiple datasets
- dashboard menus
  - identify genome region and phenotype(s)
  - study LOD profile & SNP association for additive model
  - study additive and dominance relations