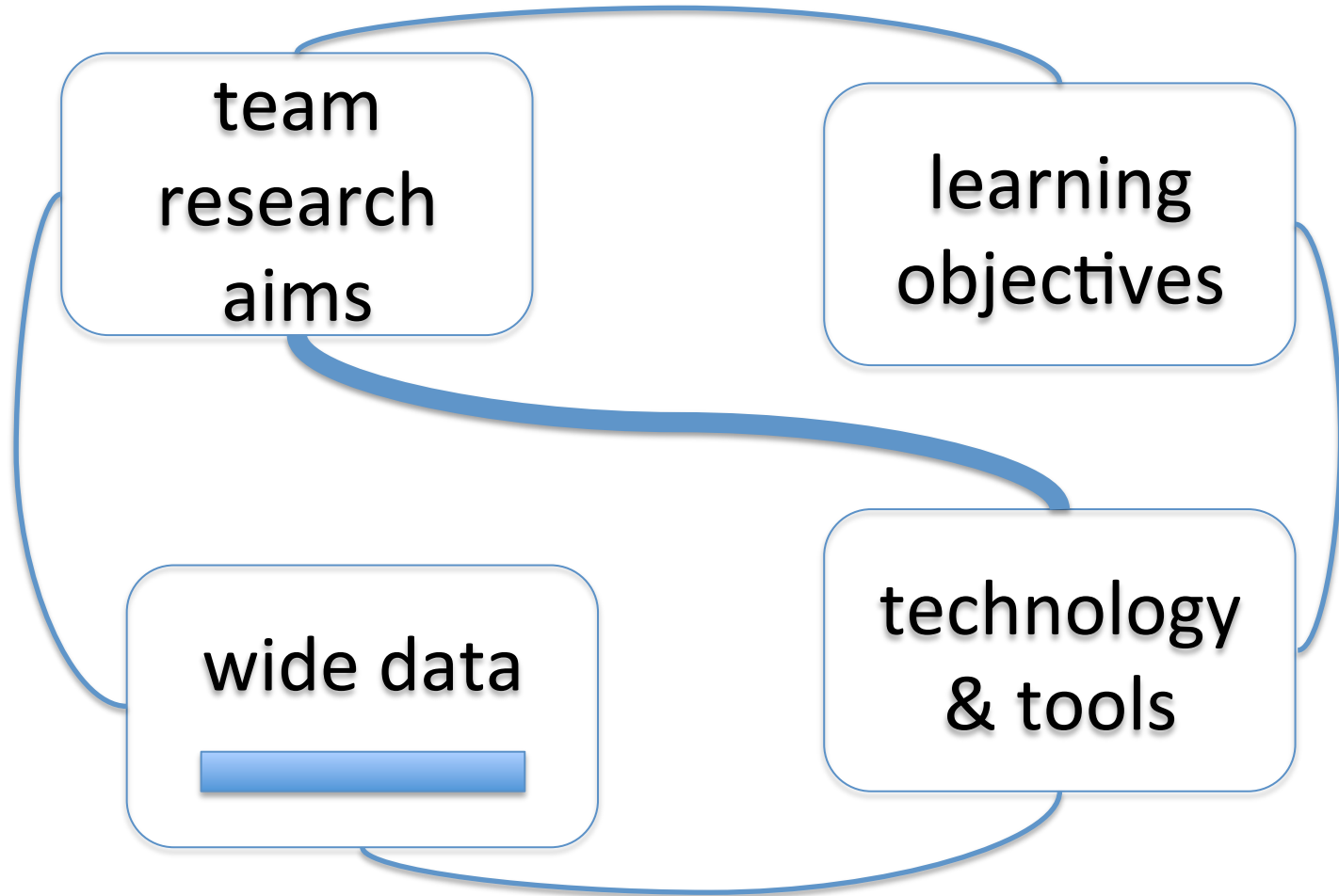
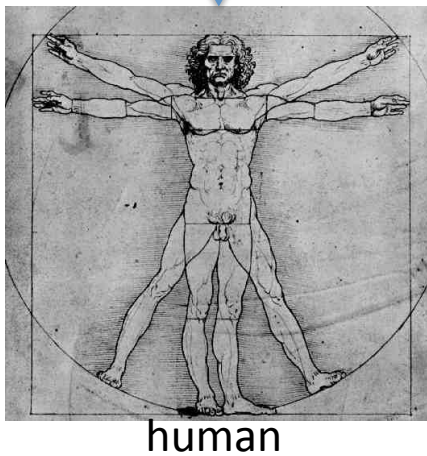
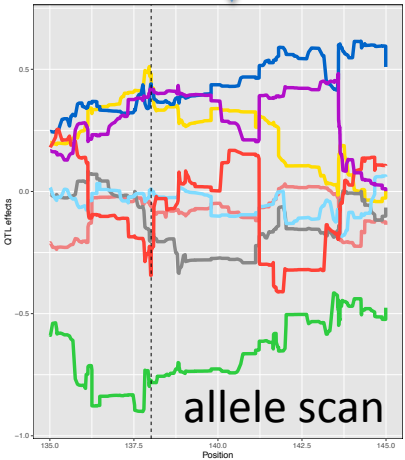
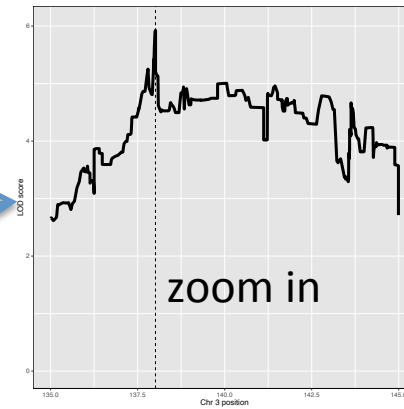
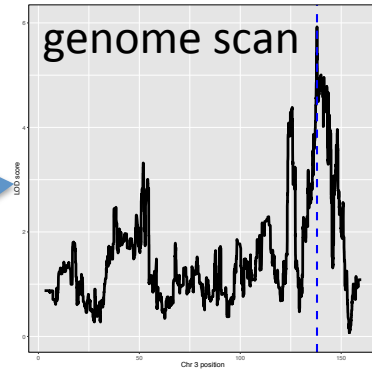
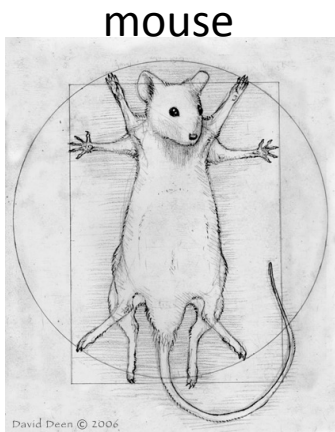


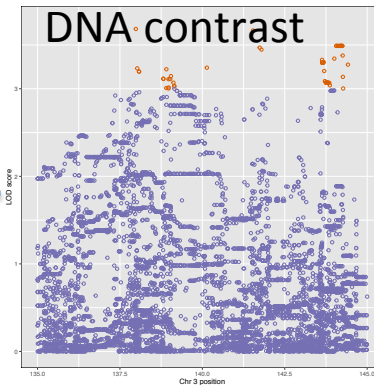
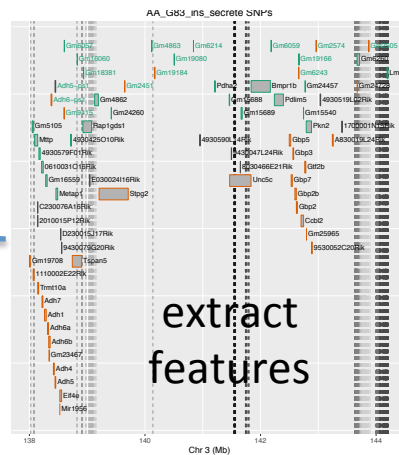
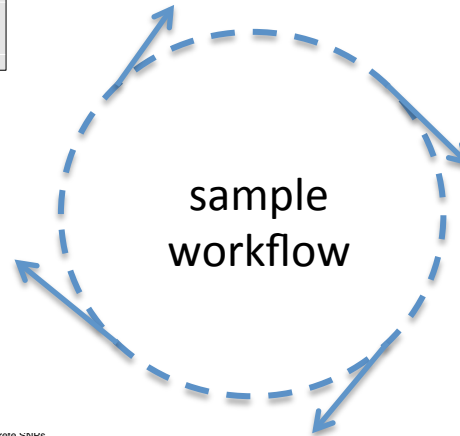
data @ uw  
brian.yandell@wisc.edu



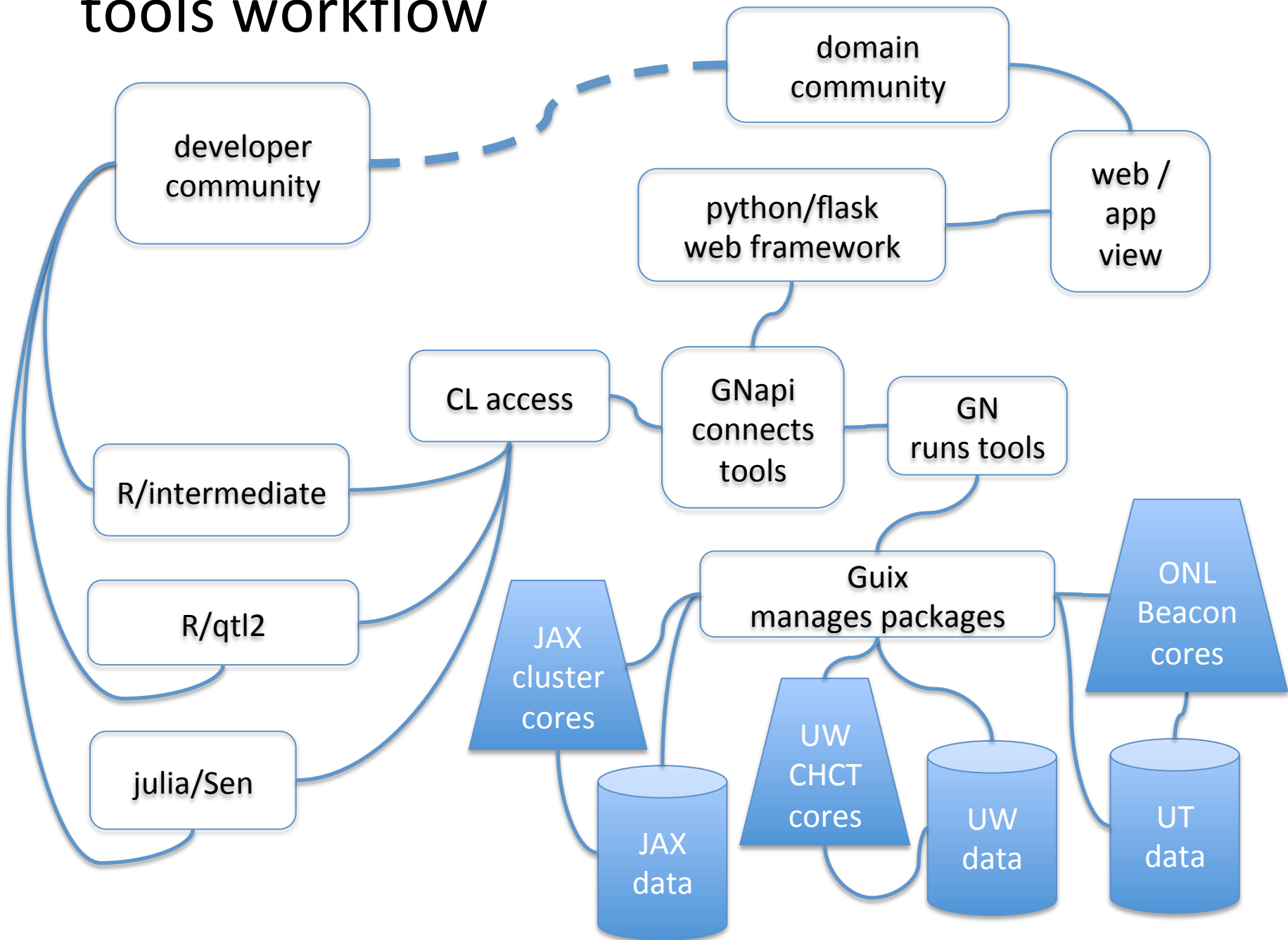
# team research aims



compare



# tools workflow



# qtl2 tasks

- develop [GNapi](#) (Prins, Broman, Sen)
  - data extraction tools created
  - data upload, workflow tools needed
- redesign qtl2 packages to use GNapi (Broman, Yandell)
  - data extraction, upload, etc.
  - CC and DO mouse SQL information
  - doqtl2 pipeline
- develop auxiliary qtl2 packages (Broman, Yandell)
  - qtl2ggplot, qtl2shiny, qtl2feature
  - qtl2d3plot
- rethink qtl2 data architecture (Broman, Yandell, Sen)
  - small master data object
  - data source indirection
  - rethink genotype probability object?

# learning objectives

- training next generation of young scientists
  - scalable integrative models
  - disease risk and treatment
- develop digital learning modules
  - blended / flipped learning environments
  - data & software carpentry
  - gateway to intermediate to advanced skills
  - reproducible research in teams