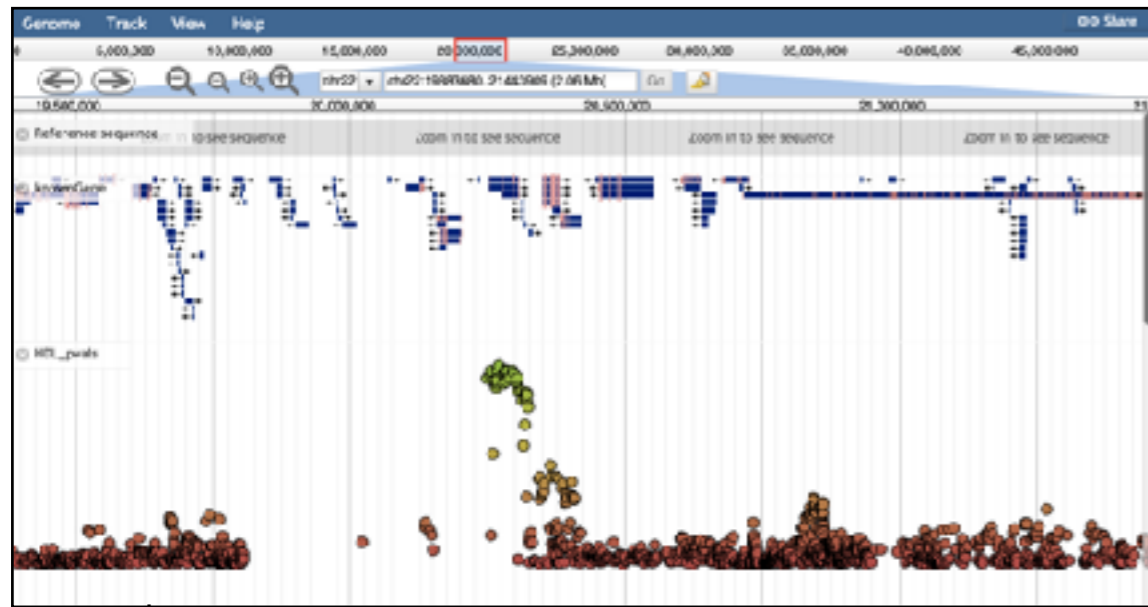


The JBrowse Cancer Genome Browser

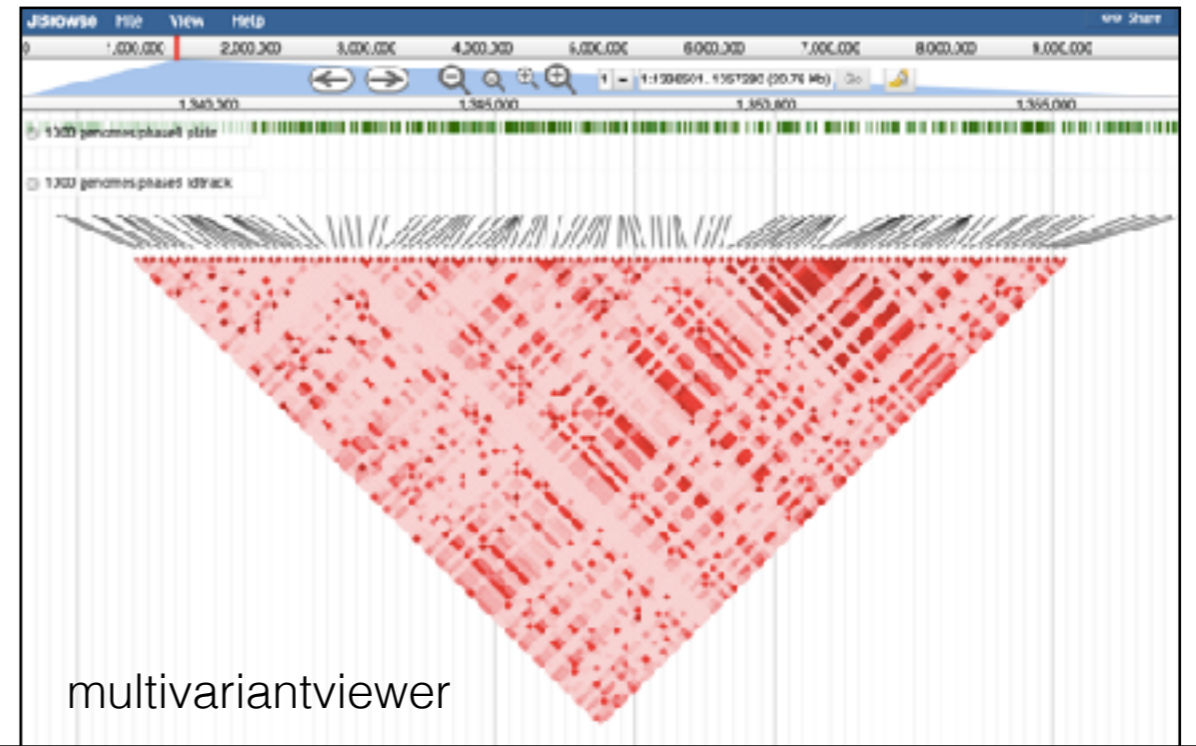
Ian Holmes
ITCR Meeting 2019

JBrowse

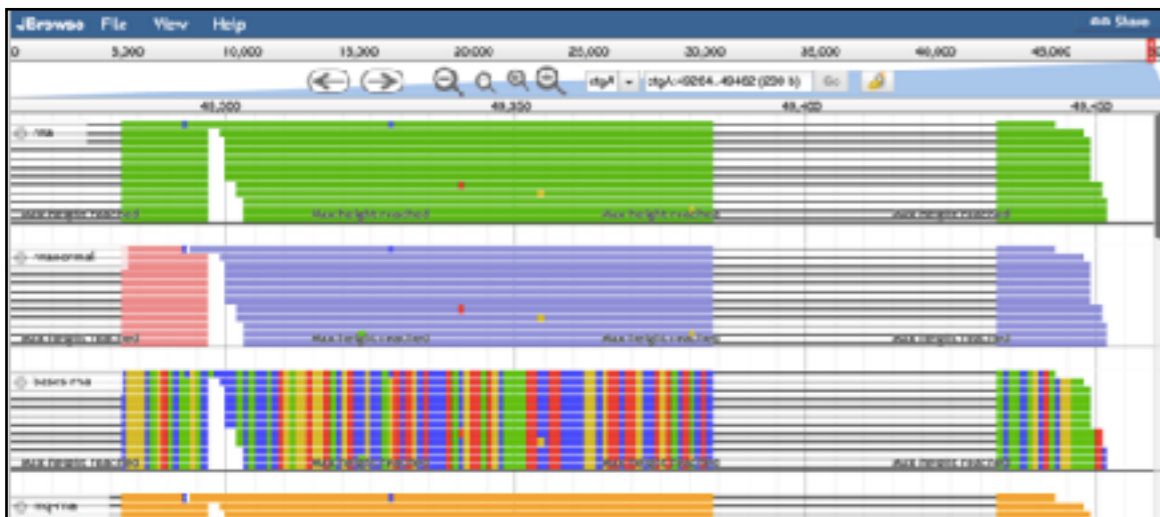
- All-JavaScript genome browser (can run as desktop app)
 - Grew out of the Generic Model Organism Database (GMOD) project, and its genome browser GBrowse
- Works as a static site: the most secure and performant way to web
 - Relies on fast pre-built indices (tabix, NCList)
- Emphasizes standards and code re-use
 - Parsers on GitHub for many standard formats (fasta, gff, bed, bigbed, sam, bam, wiggle, bigwig, cram, vcf...)
- >30k monthly active users, COSMIC one of biggest



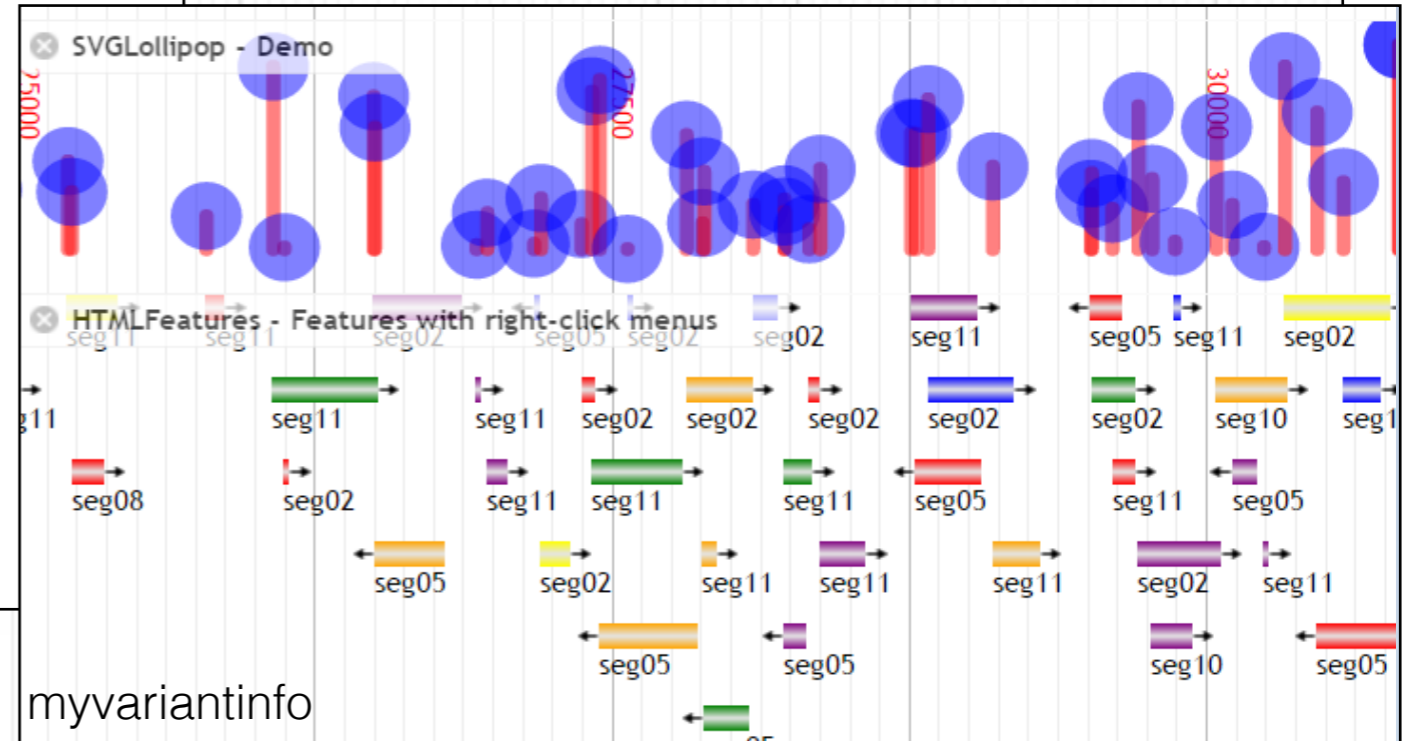
gwasviewer



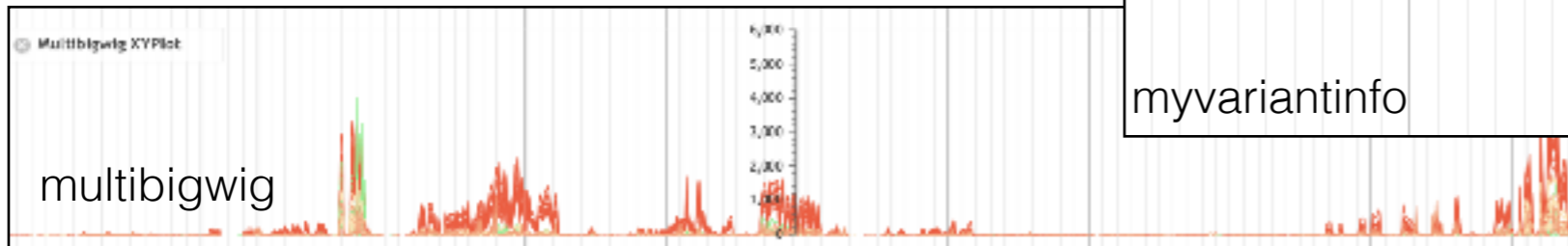
multivariantviewer



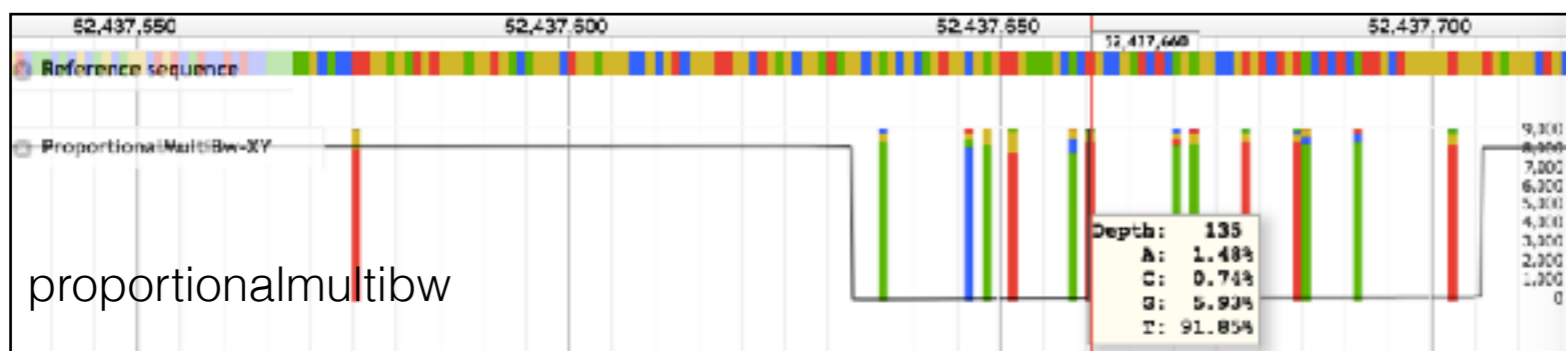
qualityglyphs



myvariantinfo



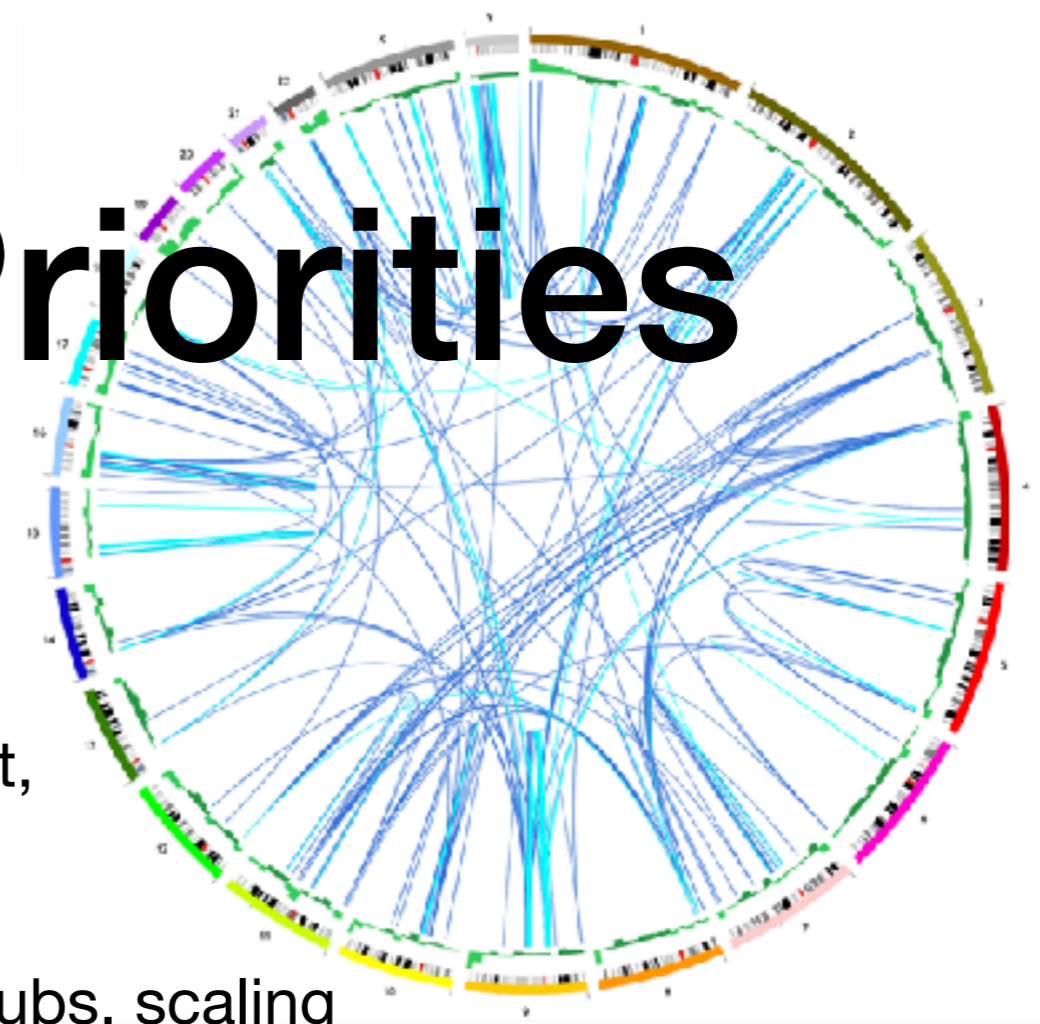
multibigwig



proportionalmultibw

JBrowse Plugin Registry
gmod.github.io/jbrowse-registry/

JBrowse 2: Priorities



- Modernization
 - **Web:** React components, state management, modularization, webpack/babel transpilation
 - **Genomics:** new formats (eg CRAM), track hubs, scaling
- Cancer applications
 - Genomic context of **structural variants**; breakpoints, circular view
 - Prebuilt human image at hg38.jbrowse.org (more to come)
 - Includes Dynamix (Monfort *et al*), an AI for track recommendation
- Rendering **genomic synteny** (c.f. GBrowse-Syn)

ITCR collaborations

- CIViC: protein variant browser (prototype)
- CNVnator: display output of CNVnator in JBrowse
- If you produce data that could benefit from visualization in genomic context, consider adapting a genome browser (they are extensible!) vs. developing your own

Thanks!

- Developers
 - **Rob Buels**
 - Colin Diesh
 - Garrett Stevens
 - Andrew Duncan
 - Eric Yao
- Outreach
 - Robin Haw
 - Scott Cain
- **Lincoln Stein**

